

TECHNICAL STANDARDS FOR CLINICAL GENETICS LABORATORIES

2020 Revision, Revised March 2020

(For a General Overview of these Technical Standards, including Purpose and Disclaimer, see **Section A**)

E: CLINICAL CYTOGENETICS

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Note: This document contains hyperlinks between the table of content items on the first page and each section. It also contains hyperlinks to the original articles published in Genetics in Medicine journal, which are also included in appendices 1 to 9.

E1 Cell Culture, See D1.

E2 Records

E2.1 Retention of Case Materials

In addition to the general guideline (C3.6) for duration of **retention of case materials**, the following are specific to cytogenetics.

E2.1.1 Slides used for diagnostic tests have a limited lifespan. If stained with a "permanent" banding method (G-, C- or R-banded, NOR), slides should be kept at least 3 years or in compliance with state regulations. Retention time of those with fluorochrome stained chromosomes and cytogenomic array slides should be retained as defined by laboratory policy or procedure.

E2.1.2 Each laboratory should establish a policy to assure that any **residual original patient specimens** and/or cell cultures are retained until release of the final report.

E2.1.3 Processed patient specimens and/or cell pellets should be retained until two weeks after the final report has been signed. Long-term retention time of those with abnormal results is at the discretion of the laboratory director.

E2.1.4 Images for chromosome analysis and FISH images for non-neoplastic disorders, should be retained for at least 20 years, while FISH images for neoplastic disorders are to be retained for at least 10 years.

E2.1.5 For **cytogenomic microarray data**, see section E10 for the **retention of files and documentation**.

E3 Procedural Guidelines

E3.1 General Analytical Standards

E3.1.1 Terminology

Chromosome counts are defined as the number of centric chromosomes per metaphase cell. During the establishment of the modal number for a study, all aneuploid metaphase cells should be characterized for specific gain/loss.

Analyzed cells are defined as banded metaphase cells in which the individual chromosomes are evaluated in their entirety, either at the microscope or from intact digitized images or photographic

prints of intact cells.

Karyogrammed cells are defined as the cutout and paired chromosomes from photograph(s) or computer-generated image(s) from a single cell following the format in An International System for Human Cytogenomic Nomenclature 2016 (ISCN 2016) [McGowan-Jordan, Simons and Schmid, 2016].

Scored cells refer to cells evaluated for the presence or absence of a specific cytogenetic feature, usually indicated by either a particular clinical history or by the finding of one or two abnormal cells during the course of a study. Numbers of cells to be scored in most situations are left to the discretion of the laboratory director, unless otherwise specified in the guidelines.

Clone is defined as a cell population derived from a single progenitor cell. Clonal origin is inferred by the presence of at least two cells containing the same extra chromosome(s) or structural chromosome abnormality or by the presence of at least three cells that have lost the same chromosome [Second International Workshop on Chromosomes in Leukemia, 1980].

For the purpose of constitutional studies, the use of the terms **cell line** and **clone** are interchangeable.

Mosaicism is the presence of two or more cytogenetically distinguishable cell lines.

Pseudomosaicism refers to the presence of an abnormal cell(s) in cultured cells that arise from an in vitro culture artifact and do/does not represent the true karyotype.

Uniparental disomy is defined as a condition in which both homologous chromosomes are derived from a single parent.

E3.1.2 **Slide number** and **microscope stage coordinates** should be recorded for all metaphases analyzed or counted. If additional cells are evaluated in questions of mosaicism, slide number should be recorded for all cells that are scored and slide coordinates should be recorded for all abnormal metaphases or suspected abnormal metaphases.

E3.1.3 All laboratories must be able to perform studies using G- and/or R-banding, in addition to special stains and/or FISH, to characterize heteromorphisms or variants, when indicated and at the discretion of the laboratory director.

E3.1.4 Current ISCN must be used to describe all karyotypes.

E3.1.5 A number of different objective methods have been described for the calculation of band stage of resolution. One or more objective and reproducible method(s) must be used to assess **banding level of**

resolution and must be formally described in the laboratory standard operating procedures/protocol manual. [Kao et al., 1990]. Specific standards for resolution should be appropriate to the case and type of tissue studied. The 550-band stage should be the goal of all peripheral blood studies. A minimum of 400 bands should be reached for 90% of analyses from amniotic fluid and chorionic villi cells.

E3.1.6 Minimum standards established for **the numbers of cells to count and/or analyze and karyotype** during the "routine" component of a cytogenetic study are described in specific subsections appropriate to a specific tissue type, culture method and/or reason for referral. The numbers of cells to study in individual situations is dependent on the specific abnormality observed, the tissue being examined, whether the analysis involves prenatal diagnosis, etc. General recommendations are noted in the following subsections (see Table 1).

E3.1.6.1 Each laboratory should establish guidelines for procedures (e.g., numbers of cells to score) to follow for each general type of abnormality (hypodiploidy, hyperdiploidy and structural abnormality) with the recognition that uniformity among laboratories is not required.

E3.1.6.2 The laboratory's scoring guidelines should be based on current knowledge of the potential clinical significance of particular chromosome abnormalities and non-modal cells.

E3.1.6.3 Fewer cells than indicated under analytical standards may be studied in circumstances in which screening for a specific abnormality is the indication for the study (e.g., checking for a known familial abnormality) or when an abnormality is detected but no more cells are available (see [E3.2](#)).

E3.1.7 Analyses should be performed and/or evaluated by at least two qualified individuals.

E3.2 Abbreviated, Focused or Limited Chromosome Studies

E3.2.1 General Considerations

It is acknowledged that there are specific clinical circumstances for which an abbreviated or limited cytogenetic study may be appropriate. For example, in the tissue confirmation of an abnormal prenatal chromosome result or in peripheral blood chromosome studies on extended family members to exclude an identified chromosome rearrangement, limited analyses may be suitable.

E3.2.2 Analytical Standards

The laboratory should have established written criteria for which focused or abbreviated studies are permissible. Criteria should specifically address the rationale for such studies, the clinical reason for referral, the tissue type, and the minimum number of cells counted, analyzed and karyotyped under such circumstances.

E3.3 Maternal Cell Contamination (MCC): General Considerations

E3.3.1 Amniotic Fluid

E3.3.1.1 The overall frequency of MCC is approximately 0.5% of genetic amniocenteses [Hsu, 1992]. Factors that increase the chance of MCC include the gauge of needle used for the amniocentesis procedure [Ledbetter, 1993], the length of time in culture and the presence of blood in the sample.

It has also been documented that cultures initiated from the first 1-2 ml of amniotic fluid drawn at amniocentesis are at an increased risk for maternal cell contamination [Ledbetter, 1993]. It is recommended that the first few milliliters of fluid be labeled appropriately and kept separate from the remaining sample to minimize inclusion of maternal cells. The initial aliquot should be used for cytogenetic analysis only if absolutely necessary.

E3.3.1.2 Chorionic Villi Sampling (CVS)

The risk for MCC in CVS is significantly higher than for amniocentesis samples (1-2%) [Ledbetter et al., 1992]. A CVS specimen must be viewed under a dissecting microscope to allow for the gross identification and cleaning of villi from maternal decidua, blood vessels, membrane and other materials. It is recommended that sterile instruments (e.g., probes, scissors, forceps) be used to tease apart the sample to isolate the fetal chorionic villi from maternal decidua. It may be helpful to have two laboratory technologists clean or check the dissected tissue prior to initiating cultures.

E3.3.1.3 Products of Conception (POC)

Due to the manner in which abortus tissue and placenta samples are obtained and handled, there is a substantial risk of MCC, particularly in early fetal loss specimens. It is recommended that appropriate measures be taken to specifically identify fetal tissues and to dissect and culture only these tissues, as described above for prenatal CVS. Consultation with the referring physician may be warranted to determine the origin of the sample and/or the appropriateness of chromosome studies, particularly in cases for which the dissection of tissue appears to yield only maternal decidua.

E3.3.2 Analysis of Cultures with Known or Suspected MCC

Cultures with known or suspected MCC based on the condition of the specimen at receipt, or apparent maternal cells morphologically in culture, require variation in the normal analysis procedure. If XX cells are found in an otherwise XY study, the most likely explanation is MCC. Since the true fetal cells are probably represented by the XY complement, the full analysis and cell counts should be performed on these cells whenever possible. Counting and analyzing several cells with an XX constitution is recommended for documentation purposes. For prenatal testing, further studies may be warranted to exclude chimerism. Ultrasound examination to check the gender of the fetus, second amniocentesis or confirmatory amniocentesis after CVS and/or heteromorphism studies (molecular) between a maternal sample and the fetal sample may be required in the investigation.

If cell cultures initiated in the cytogenetics laboratory are to be used for molecular or biochemical testing,

any serious concerns about MCC in those cultures must be conveyed to the molecular or biochemical testing laboratory. In addition, if direct prenatal samples are sent out for testing, it is recommended that back-up cultures be grown and maintained until the molecular or biochemical testing is complete and reported.

E3.3.3 MCC Reporting and Quality Assurance

Reporting of MCC is case-dependent and is at the discretion of the laboratory director. Consultation with the referring physician is recommended, when appropriate. Any significant observation of MCC in a prenatal diagnosis sample should be interpreted in consultation with the physician who performed the procedure. For samples with a significant risk for MCC that produce a normal female karyotype, a disclaimer should be added to the report suggesting that analysis of maternal cells due to MCC cannot be excluded.

Any time that MCC is suspected or confirmed, the laboratory director must ensure that an attempt to determine the cause is documented as part of the laboratory's quality assurance program. Additionally, it is recommended that the ratio of XX:XY cases be monitored as a quality control check for CVS and POC cases. Monitoring the male cases for evidence of female cells is also important for quality control of MCC. FISH with probes for X/Y or molecular methods may be used on cell suspensions prior to culturing to screen for or to estimate the amount of MCC.

E4 Prenatal Diagnosis: General Considerations

Amniotic fluid contains single cells sloughed off of the amnion, fetal skin, lung, bladder, and digestive tract. A random sample of cells from the amniotic fluid is drawn and plated. These cells form true distinct colonies. In **chorionic villus sampling**, villi are usually retrieved from one or two sites and are likely to not be completely disaggregated.

Prenatal cytogenetic diagnosis can be performed on various tissues, each requiring different methods of culture and analysis.

A minimum of two cultures should be analyzed on each case whenever possible. FISH analysis for the chromosome of interest can be done on uncultured amniotic fluid cells in addition to chromosome analysis of cultured cells. The Benn and Hsu (2004) guidelines of workup should be followed for potential mosaicism.

If XX and XY cells are observed: Analyze 15 male colonies if available. If a mixture of XX and XY cells is present, it may be helpful to consult with the referring physician about evidence of a twin pregnancy.

Laboratories should have a protocol stating when to reflex to additional studies, such as increased counts,

and/or FISH, and/or a recommendation for high-resolution ultrasound, uniparental disomy, microarray, and study of a second tissue. While CVS may appear as colonies, they should be analyzed as any other disaggregated tissue.

Uniparental disomy testing should be considered if numeric mosaicism or structural abnormality of chromosomes 6, 7, 11, 14, or 15 is detected because these chromosomes are known to carry imprinted genes and uniparental disomy is associated with congenital abnormalities [Shaffer et al., 2001].

It is the laboratory director's responsibility to monitor quality and to ensure that analytical practices are consistent with the guidelines presented below. (Also see C4)

E4.1 Amniotic Fluid, Chorionic Villi and Percutaneous Umbilical Blood Sampling (PUBS)

E4.1.1 At least **two independent cell cultures** must be initiated and grown in separate incubators with independent electric circuits or emergency power systems, backup gas sources and emergency alarms.

E4.1.2 With the exception of PUBS, there must be a plan for maintaining **back-up cell culture(s)** pending the need for additional studies.

E4.1.3 If studies of parental chromosomes are necessary to help interpret a fetal chromosome abnormality or heteromorphism, the same laboratory should perform these studies, if possible and reasonable.

E4.1.4 The number of **test failures** (defined as failure to obtain final results from an adequate submitted specimen) should not exceed 1 per 100 consecutive samples (1%).

E4.1.5 Efforts must be made to determine the **cause of all test failures**. These records and records of corrective actions taken must be available for external review and kept for at least 2 years.

E4.1.6 With the exception of PUBS, at least 90% of final results must be completed and reported (verbal or written) within 14 calendar days from receipt of specimen, unless additional studies are necessary.

E4.1.7 Laboratories consistently failing to meet these standards should consider splitting or sending samples to another laboratory until the problems are resolved.

E4.1.8 Laboratories should have specific requirements for the acceptance and rejection of specimens that include the volume and quality of the specimen received.

E4.1.9 Where there is suspicion that MCC may be present (see E3.3), the laboratory director may want to consider analysis of additional cultures, increased colony counts, or molecular genetic analyses (PCR or QF-PCR) to rule out any confounding diagnosis.

E4.2 Amniotic Fluid

E4.2.1 Amniotic Fluid: Processing Standards

E4.2.1.1 If little or no cell pellet is apparent in the sample, the laboratory should consider the use of a method (e.g., assays for pH, protein, glucose, etc.) that will help to distinguish amniotic from other fluids.

E4.2.1.2 Notification of inadequate or poor cell culture growth should be made within 10 days of the amniocentesis procedure.

E4.2.1.3 A laboratory planning to establish amniotic fluid cytogenetic testing must arrange to split and successfully analyze at least 50 consecutive specimens with a laboratory performing such studies by established standards.

E4.2.1.4 The laboratory should investigate significantly increased chromosome instability in one or several concurrent patient samples.

E4.2.1.5 Sample quality and culture failures should be monitored.

E4.2.2 Amniotic Fluid: Analytical Standards (see also E3.1.6)

E4.2.2.1 **Analysis of in situ cultures** is the preferred method, since it is more reliable for evaluating mosaicism.

Count: a minimum of 15 cells from at least 15 colonies, distributed as equally as possible between at least 2 or more independently established cultures. Single metaphase colonies should only be used when multi-metaphase colonies are unavailable. Document any numerical/structural aberrations observed.

Analyze: 5 cells, each from a different colony, preferably from 2 independently established cultures. Band resolution should be appropriate to the reason for testing.

Karyotype: 2 cells. These cells can be from the 5 analyzed cells. If more than 1 abnormal cell line (as defined in Section E3.1.1) is found, karyotype at least 1 cell representative of each cell line.

If both abnormal and normal cells are observed in a colony, the colony is generally considered normal if the same abnormality was NOT seen in other colonies.

E4.2.2.2 Analysis from a combination of mixed in situ and subcultured cells

When it is impossible to complete the analysis by in situ only, subculturing may be necessary.

Count: Count as many colonies as possible and then increase the count to a total of 20 cells.

Analyze: 5 cells, distributed between 2 independently established cultures.

E4.2.2.3 Suspension Harvest Technique

Situations in which suspension harvest technique is appropriate include: suboptimal sample or when the primary concern is growing cells for other testing methodologies.

Count: a minimum of 20 cells, distributed as equally as possible among independently established cultures. Document any numerical/structural aberrations observed (see E4.2.2.1 for analysis and karyogram guidelines).

E4.3 Chorionic Villus Sample (CVS)

E4.3.1 Chorionic Villus Sample (CVS): Processing Standards

In cases of multiple gestations particularly in those of in vitro fertilization, one should be aware that a deceased co-twin with remaining viable placental material may be the source of a chromosome abnormality.

Confined placental mosaicism (CPM) is defined as at least two cell lines from a single fertilized egg seen in chorionic villi analysis that are only present in the placenta, not in the fetus itself. It is observed in about 1-2 % of CVS [Crane and Cheung, 1988]. Laboratories should have protocols to distinguish CPM from true mosaicism in the fetus. Additional studies may be recommended depending on the chromosome involved and the type of abnormality. These may include analysis of additional cultures and in some cases analysis of amniotic fluid cultures or fetal cord blood. In situ culture strategy is appropriate for CVS or any other tissues that grow in a monolayer, but the analysis protocols may differ from amniotic fluid.

The significance of mosaicism in CVS may differ based on the distribution of the abnormal cells in the direct and cultured preparations, as well as the chromosomes involved. When mosaicism is documented, in general, amniocentesis is recommended, since the amniotic fluid cells are more likely to represent the fetus.

E4.3.1.1 When direct (uncultured) preparations are used clinically, a cell culture technique (defined as longer than 48 hours) must also be used.

E4.3.1.2 Final written reports should include a summary of the analysis results of the cultured cells and direct preparation, if performed.

E4.3.1.3 A laboratory planning to establish CVS cytogenetics should already be testing amniotic fluid cells by established standards and methods. Prior to independent CVS analysis, the laboratory must split and confirm at least 25 samples (with an adequate volume) with a laboratory already performing CVS cytogenetics by established standards and methods. Note: During this period, samples that are too small to split should be sent to a qualified reference laboratory for culturing and analysis.

E4.3.2: Chorionic Villi: Analytical Standards (see also [E3.1.6](#))

E4.3.2.1 Direct (Uncultured) Preparations: should not be exclusively used in obtaining final results. (See Section E4.3.2.3 below.) Interphase FISH or molecular screening for sex chromosomes and common aneuploidies should be used to generate alternative preliminary results.

E4.3.2.2 Cultured Preparations

Count: a minimum of 20 cells distributed as equally as possible between at least 2 independently established cultures. Document any numerical/structural aberrations observed (see E 4.2.2 for analysis and karyogram guidelines).

E4.3.2.3 Combination of Direct Preparation and Culture Technique

Count: a minimum of 20 cells, at least 10 of which come from cultured preparations. Document any numerical/structural aberrations observed.

Analyze: 5 cells, preferably at least 4 cells from cultured preparations. Resolution should be appropriate to the reason for testing (see E 4.2.2 for karyogram guidelines).

E4.3.2.4 If mosaicism is documented in a CVS sample, cytogenetic studies of amniotic fluid are recommended.

E4.4 Fetal Blood: Percutaneous Blood Sampling (PUBS)

E4.4.1 Fetal Blood: Processing Standards

E4.4.1.1 Final results of PUBS should not be released until the sample has been confirmed to be fetal in origin.

E4.4.1.2 A minimum of 2 cultures should be established, if adequate specimen is submitted.

E4.4.1.3 Processing after 48 and 72 hours in culture is recommended.

E4.4.1.4 Final reports (verbal or written) should be available within 7 calendar days.

E4.4.2 Fetal Blood: Analytical Standards (see also [E3.1.6](#))

Count: a minimum of 20 cells (see E 4.2.2 for analysis and karyogram guidelines).

E4.5 Diagnostic cytogenetic testing following positive noninvasive prenatal screening (NIPS) results

[See [Genet Med 2017;19\(8\):845-850](#) OR [Appendix 1](#)]

E5 Peripheral Blood and Solid Tissue Constitutional Chromosome Study

E5.1 Peripheral Blood (Stimulated Lymphocytes): Routine Studies

E5.1.1 Peripheral Blood: Processing Standards

E5.1.1.1 At least 2 cultures should be established for each specimen.

E5.1.1.2 At least 90% of all routine peripheral blood analyses must have final written reports completed within 28 calendar days (21 calendar days is recommended) from receipt of the specimen. Clinical indications may dictate more rapid turn-around time. Specialized stains and studies may take longer.

E5.1.1.3 Test failures should not exceed 2% per year.

E5.1.1.4 The 550-band stage should be the goal of all constitutional studies to rule out a structural abnormality, particularly in cases of intellectual disability, birth defects, dysmorphology, or couples with recurrent pregnancy loss.

E5.1.2 Peripheral Blood: Analytical Standards (see also E3.1.6)

E5.1.2.1

Count: a minimum of 20 cells, documenting any numerical/structural abnormalities observed.

Analyze: 5 cells. Resolution should be appropriate to the reason for testing.

Karyotype: 2 cells. If more than 1 clone (as defined in Section E3.1.1) is found, karyotype 1 cell representative of each clone.

E5.1.2.2 Cases being studied for possible sex chromosome abnormalities, in which mosaicism is common, should include the standard 20-cell assessment. If mosaicism is confirmed, the analysis is complete. A minimum of 10 additional metaphase cells should be evaluated when one cell with a sex chromosome loss, gain or rearrangement is observed within the first 20 cells analyzed [Wiktor et al., 2009; Wolff et al., 2010].

E5.2 Peripheral Blood (Stimulated Lymphocytes): Focused High Resolution Analysis

Due to the improved detection rate for subtle chromosome deletions and duplications by genomic microarray analysis, complete high resolution chromosome analysis (resolution at the 850 band level) is no longer recommended as a standard test methodology.

E5.3 Peripheral Blood (Stimulated Lymphocytes): Complete High Resolution Analysis

E5.3.1 Complete High Resolution: Analytical Standards

E5.3.1.1 General processing and analytical standards for routine peripheral blood studies apply. In addition, complete high resolution chromosome analysis should include detailed evaluation of all regions on all chromosome pairs at a level of resolution above the 650-band stage (resolution at the 850 level is

recommended) [see also E5.1.2].

E5.4 Peripheral Blood (Stimulated Lymphocytes): Heritable Fragile Sites (Including Fragile X)

This section initially provided guidelines for the evaluation of patients for fragile X syndrome using the cytogenetic expression of the Xq27.3 (FRAXA) fragile site. Such chromosome testing has been replaced by molecular genetic DNA evaluation of the FMR1 locus, and specific College recommendations have been published to cover such testing (see Section FX, "Technical Standards and Guidelines for Fragile X") [Maddalena et al., 2001; Monaghan, Lyon and Spector, 2013]. For the most part, testing/culturing for fragile sites is no longer performed in the Cytogenetics Laboratory. However, individuals performing chromosome analyses should be aware of their occurrence (e.g. fra(10)(q25), fra(16)(q22), etc.) and are referred to Gardner, Sutherland and Shaffer, 4th edition of Chromosome Abnormalities and Genetic Counseling, for further guidance.

E5.5 Solid Tissues Constitutional Chromosome Study (Skin, Organs, Products of Conception, etc.)

E5.5.1 Solid Tissues Constitutional: Processing Standards

E5.5.1.1 Tissue biopsy specimens and small specimens should be transported in sterile cell culture medium with or without serum. Sterile saline solution may be used if medium is not available. Larger specimens should be transported according to written guidelines in each laboratory.

E5.5.1.2 At least two independent cultures should be established (three are recommended for resolving questions of mosaicism). These can be from explants of tissue grown in flasks or from enzyme-dissociated cells that can be processed in flasks or in situ.

E5.5.1.3 Except for products of conception (POC), test failure rates should not exceed 5% per year, in total. It is suggested that periodic monitoring of POCs be done to assure that the ratio of 46,XX: 46,XY results approximates 1:1.

E5.5.2 Solid Tissues Constitutional: Analytical Standards

See amniotic fluid guidelines (*E4.2.2*) for analytical standards.

E5.6 Bone marrow studies for constitutional disorders. In most laboratories, these studies have been replaced by analysis of short term (overnight) blood cultures and/or FISH analysis performed on interphase nuclei.

E5.7 Chromosome Instability Syndromes: Peripheral Blood Breakage Analyses

E5.7.1 General Standards

The rarity of chromosome instability syndromes requires that inexperienced laboratories should refer cases to reference laboratories with experience in diagnosing such disorders. Additionally, as research leads to the identification and cloning of the putative disease genes, molecular testing is recommended to supplement cytogenetic analysis.

G-banded or unbanded preparations may be applied, depending upon the particular goal of the study. Unbanded preparations are acceptable only if there is no need to identify abnormalities such as translocations or inversions that will not be visible in unbanded preparations. All abnormalities should be recorded using appropriate ISCN designations.

E5.7.2 Fanconi Anemia

Cytogenetic evaluation for Fanconi anemia (FA) should include analysis of crosslinking agent (e.g., mitomycin C [MMC], diepoxybutane [DEB]) induction of breakage in addition to baseline chromosome breakage.

E5.7.2.1 Fanconi Anemia: Culture Conditions

Each laboratory should have well-established negative control (non-Fanconi) and positive control (Fanconi) ranges for each culture (with and without mutagen) condition. Each new lot number of crosslinking agent should be appropriately quality controlled for its efficacy and potency for inducing chromosomal breakage. Given variability between drug lots, and the need to routinely prepare fresh stock and working solutions for most of the crosslinking agents, parallel testing of control specimens is recommended, as necessary. When a sufficient amount of blood specimen (and cell count) is available, two drug-treated cultures (e.g., either two different concentrations of either DEB or MMC, or one culture each of MMC and DEB) are recommended.

E5.7.2.2 Fanconi Anemia: Chromosome Breakage Analysis

Optimally, 50 metaphase cells (banded or unbanded) should be scored from each culture condition. The average rate of chromosomal aberrations per cell or the distribution of aberrations among cells should be compared to negative and positive control reference ranges. The percentage of cells demonstrating aberrations should be reported to enable identification of those patients who are mosaic for mutant and wild type cells.

E5.7.3 Bloom Syndrome

Traditionally, cytogenetic evaluation for Bloom syndrome included assessment of baseline sister chromatid exchange (SCE) rates. As the Bloom syndrome gene BLM has been cloned, molecular evaluation to identify the mutation should be performed. Nearly all affected individuals have mutations of the BLM gene.

E5.7.4 Ataxia Telangiectasia and Nijmegen Breakage Syndrome

Evaluation for ataxia telangiectasia (A-T) and Nijmegen Breakage Syndrome (NBS) should include evaluation of sensitivity to radiation. Although such sensitivity can be assessed by cytogenetic methods, it generally is evaluated by survival assays on lymphoblastoid or fibroblast cells.

As the A-T gene (ATM) and the NBS gene (NBN) have been cloned, molecular evaluation should be

performed for confirming the diagnosis in patients who have positive radiosensitivity assays. Again, nearly all affected individuals with AT or NBS have mutations of the ATM gene detectable by sequence analysis.

E5.7.5 Breakage Studies: Miscellaneous

Cytogenetic evaluation of chromosome breakage may also be undertaken for other reasons, e.g., prior exposure to clastogens. The specific culture methods utilized (e.g., timing of cultures) and the methods of analysis (G-banded vs. unbanded chromosomes) should be appropriate to the referral. The laboratory should have well established positive and negative control ranges for the specific analyses being conducted.

E6 Chromosome Studies for Acquired Abnormalities

E6.1–6.4 of the ACMG technical standards and guidelines: chromosome studies of neoplastic blood and bone marrow–acquired chromosomal abnormalities [See [Genet Med 2016;18\(6\):635-42](#) OR [Appendix 2](#)]

E6.5–6.8 of the ACMG technical standards and guidelines: chromosome studies of lymph node and solid tumor–acquired chromosomal abnormalities [See [Genet Med 2016;18\(6\):643-8](#) OR [Appendix 3](#)]

E7 Sex Chromatin

E7.1 The indirect nature of sex chromatin analysis has rendered the test obsolete. Any patient in whom the question of sex chromosome abnormality is being considered should have complete chromosome analysis.

E8 Reporting Standards

Final written reports of the results of diagnostic testing should include the following information:

E8.1 Case identification includes name (or other first identifier), date of birth of patient, date of collection and/or receipt of specimen, laboratory accession number(s), tissue type and name(s) of physician(s) or authorized person who ordered the test and to whom report is sent.

E8.2 Specific details of the study to be reported should include:

- Indication for study.
- Numbers of cells in which chromosomes were counted, analyzed and karyotyped.
- Cell culture times and conditions and banding methods employed, when they bear on the cytogenetic interpretation.
- Banding method, level of resolution and current ISCN karyotype designation(s) of cells analyzed.
- A statement of additional work done to resolve questions of mosaicism. Correlation with previous studies. When parallel controls are used for comparative purposes in a study, the results of those controls
- Interpretation of results to include: correlation with clinical information, indication of an abnormal result where applicable, recommendations for additional laboratory genetic studies for the patient and/or family, and a discussion of the significance of the findings, when appropriate. When appropriate, recommendations for genetic counseling should be made. The interpretation should be clear to a nongeneticist physician.
- When investigational procedures are employed, the investigational nature of the testing.
- Cautions as to possible inaccuracies and test limitations.
- Individuals qualified as under B3.1 must sign all final reports. Password protected electronic signatures can be used to fulfill this requirement.
- Specifics of any preliminary results given including what the preliminary result was, the date and the person to whom the report was given.
- Date of final report.

E8.3 Laboratory identification includes name, address, and phone number of the laboratory in which the study was performed.

E9 Fluorescence in Situ Hybridization (FISH)

ACMG technical standards and guidelines: Fluorescence in situ hybridization [See [Genet Med 2011;13\(7\):667-675](#) OR [Appendix 4](#)]

E10 Chromosomal Microarray Analysis for Constitutional Chromosome Abnormalities

ACMG standards and guidelines for constitutional cytogenomic microarray analysis, including postnatal and prenatal applications: revision 2013 [See [Genet Med 2013;15\(11\):901-909](#) OR [Appendix 5](#)]

This also includes:

- *Technical standards for the interpretation and reporting of constitutional copy-number variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics (ACMG) and the Clinical Genome Resource (ClinGen)* [See [Genet Med 2020;22\(2\):245-257](#) OR [Appendix 6](#)]
- *ACMG standards and guidelines for documenting suspected consanguinity as an incidental finding of genomic testing* [See [Genet Med 2013;15\(2\):150-2](#) OR [Appendix 7](#)]
- *ACMG recommendations for the design and performance expectations for clinical genomic copy number microarrays intended for use in the postnatal setting for detection of constitutional abnormalities* [See [Genet Med 2011;13\(7\):676-9](#)] [This document is retired]

E11 Chromosomal Microarray Analysis for Chromosome Abnormalities in Neoplastic Disorders

ACMG standards and guidelines: microarray analysis for chromosome abnormalities in neoplastic disorders [See [Genet Med 2013;15\(6\):484-494](#) OR [Appendix 8](#)]

This also includes:

- *Technical laboratory standards for interpretation and reporting of acquired copy-number abnormalities and copy-neutral loss of heterozygosity in neoplastic disorders: a joint consensus recommendation from the American College of Medical Genetics and Genomics (ACMG) and the Cancer Genomics Consortium (CGC)* [See [Genet Med 2019;21\(9\):1903-16](#) OR [Appendix 9](#)]

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Table 1: Chromosome Analysis Rubric

	Count (from at least 2 independent cultures)	Analyze	Karyotype
Chorionic Villi	20 metaphases (minimum 10 from cultured preparations)	5 metaphase cells	2 (1 per additional cell line)
Amniotic Fluid	15 in situ colonies 20 flask harvest 20 in situ and flask harvest	5 metaphase cells	2 (1 per additional cell line)
Blood	20 metaphases	5 metaphase cells	2 (1 per additional cell line)
Products of Conception/skin fibroblasts	20 metaphases	5 metaphase cells	2 (1 per additional cell line)
Bone Marrow/ Leukemic Blood/ Solid Tumor	20 metaphases	20 metaphases	2 (1 per additional side line / 2 per unrelated clone)

APPENDIX 1

**Diagnostic cytogenetic testing following positive noninvasive prenatal screening (NIPS) results
(See following page)**

Diagnostic cytogenetic testing following positive noninvasive prenatal screening results: a clinical laboratory practice resource of the American College of Medical Genetics and Genomics (ACMG)

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Noninvasive prenatal screening (NIPS) using cell-free DNA has been rapidly adopted into prenatal care. Since NIPS is a screening test, diagnostic testing is recommended to confirm all cases of screen-positive NIPS results. For cytogenetics laboratories performing confirmatory testing on prenatal diagnostic samples, a standardized testing algorithm is needed to ensure that the appropriate testing takes place. This algorithm includes diagnostic testing by either chorionic villi sampling or

amniocentesis samples and encompasses chromosome analysis, fluorescence in situ hybridization, and chromosomal microarray.

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Key Words: cell-free DNA; chromosome analysis; chromosomal microarray (CMA); noninvasive prenatal screening (NIPS); non-invasive prenatal testing (NIPT)

BACKGROUND

This document was generated to support clinical cytogenetics laboratories in the testing and management of positive noninvasive prenatal screening (NIPS) results and is designed to be a rubric that can guide laboratory practice. The American College of Medical Genetics and Genomics (ACMG) revised its position statement on the use of NIPS for fetal aneuploidy in July 2016.¹ This is meant to be a companion to that revised statement.

NIPS, also referred to as cell-free DNA (cfDNA) or noninvasive prenatal testing, has been available as a clinical

screening option for pregnant women since 2011.² Initially, NIPS was available primarily for the detection of trisomy 21,^{2,3} but it rapidly evolved to include the detection of trisomies 13 and 18, sex chromosome identification, and sex chromosome aneuploidies.^{4,5} NIPS has better performance as a screening test for trisomy 21 than for trisomies 13 or 18, or for sex chromosome aneuploidies.⁶ Recently, select microdeletion syndromes and smaller copy-number changes, as well as other autosomal aneuploidies, have been added by some laboratories as additional screening options.^{7,8} Various factors affect the accuracy of NIPS results, including confined

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placental mosaicism (CPM), maternal genomic contribution and technical or statistical issues.⁹ Follow-up diagnostic testing is uniformly recommended for all patients with positive NIPS results.^{1,10,11} This document establishes a standardized testing algorithm that is essential for the cytogenetics laboratory to ensure that the appropriate diagnostic testing has occurred and that the results are reliable, accurate, and reflective of the fetal karyotype.

DIAGNOSTIC TESTING

Follow-up prenatal diagnostic testing is recommended for all patients with positive NIPS results. This can be accomplished by either chorionic villus sampling (CVS) or amniocentesis. In general, diagnostic testing should be appropriate for the suspected anomaly (i.e., chromosomal microarray (CMA) for smaller copy-number changes). Some laboratories may opt to perform fluorescence in situ hybridization (FISH) for the aneuploidy or copy-number change in question and then reflex to either chromosome analysis or CMA, dependent on the FISH results. While FISH is possible for either type of copy-number change, it may not be as accurate, depending on the exact size of the anomaly or structural rearrangements.

Chromosome analysis on either CVS or amniocentesis demonstrating nonmosaic trisomy or sex chromosome aneuploidy consistent with the NIPS result is considered confirmation of a positive NIPS and therefore of an affected fetus. A full study (as defined by the ACMG laboratory guidelines¹²) on CVS or amniocentesis demonstrating a normal karyotype would not typically warrant additional metaphase cell counts or other analyses. However, a mosaic result on CVS should not be considered confirmatory. There are known physiological limitations of CVS that include the possibility of CPM and rare case reports of complete discordancy between the CVS karyotype and the fetal karyotype.^{13–16} While NIPS can be performed in the late first trimester of pregnancy, and CVS is a possibility for confirmatory studies (and often desired by the patient due to timing), CVS may simply reflect the same DNA/cells that were detected by NIPS, as both are derived from the placenta.¹⁷ Certain aneuploidies, including trisomy 13 and

monosomy X, are more likely to be found in the mosaic form on CVS, which may influence genetic counseling about the preferred diagnostic test for confirmatory studies.¹⁸ When CVS shows mosaicism for the suspected trisomy, it is impossible to determine if this is CPM or true fetal mosaicism (TFM). Therefore, a mosaic CVS result cannot be treated as confirmation of an affected fetus and a follow-up amniocentesis is warranted, as is recommended in all cases of mosaicism observed on CVS^{12,15,16} (Table 1).

Similarly, CMA testing on either CVS or amniotic fluid may be used as confirmatory diagnostic testing in cases with positive NIPS results, or as reflex testing in cases with initial normal results from chromosome analysis. Smaller copy-number changes are ideally confirmed by this method. Again, if the NIPS results and CMA results are concordant, no further testing is recommended. However, given that structural information is not available from CMA analysis, a reflex to chromosome analysis may be considered to evaluate the structural arrangement to inform recurrence risks, especially for those cases with trisomies 21 and 13.

On occasion, prenatal diagnostic testing may not be performed due to loss of the pregnancy before testing is possible. In such instances, testing of the products of conception and/or the fetus by either chromosome analysis or CMA should be considered on a case-by-case basis.

Other forms of abnormal result exist, such as “no calls” and the unanticipated findings rendered by special maternal medical circumstances (e.g., obesity, oocyte donations and prior transfusions). These are discussed at length in the revised ACMG position statement¹ but are beyond the scope of this laboratory algorithm.

POSITIVE PREDICTIVE VALUE

While most NIPS laboratories report a greater than 99% specificity and sensitivity for trisomy 21, the positive predictive value (PPV) is essential for patient care. The 2016 ACMG position statement¹ recommends that all laboratories reporting NIPS results also include the PPV, as well as the negative predictive value, detection rate, clinical specificity and fetal fraction. PPV answers an important question: “If NIPS is

Table 1 Prenatal diagnostic testing algorithm following positive NIPS results

NIPS positive for:	Recommended laboratory test	Sample type	Result/recommended further testing	
T13, T18, T21, SCA, other aneuploidy, triploidy	Chromosome analysis	CVS	Normal or abnormal c/w NIPS	No further testing/consider CMA
			Mosaic	Follow-up amniocentesis with mosaicism studies ^a
		AF	Normal or abnormal c/w NIPS or mosaic c/w NIPS	No further testing/consider CMA
Smaller copy-number changes	CMA	CVS or AF	Negative or abnormal c/w NIPS	No further testing
			Abnormal <i>not</i> c/w NIPS	Further testing may be warranted dependent on specific finding

AF, amniotic fluid; CMA, chromosomal microarray; CVS, chorionic villus sampling; c/w, consistent with; NIPS, noninvasive prenatal screening; SCA, sex chromosome aneuploidy; T13, trisomy 13; T18, trisomy 18; T21, trisomy 21.
^aSee the text for discussion of further testing options.

positive, what is the chance that the fetus is affected?" The PPV is affected by the analytic specificity and sensitivity of the test, as well as the prevalence of the disorder in the population.^{6,11,19} When the prevalence is age dependent, as it is for trisomies 13, 18 and 21, maternal age is a determining factor in the reliability of the test. Due to the higher incidence of aneuploidy associated with advanced maternal age, a 35-year-old woman with a positive result by NIPS has a higher PPV than a 25-year-old woman with a positive result. In addition, less common disorders, such as trisomy 13 and trisomy 18, would be expected to have lower PPVs than the more common trisomy 21. Very rare disorders (e.g., microdeletion syndromes and smaller copy-number changes), which are typically not associated with increased maternal age, would be expected to have even lower PPVs.⁷ The PPV can also be determined by comparing the NIPS results with the diagnostic testing results, with the caveat that these studies involve relatively low numbers of cases with wide confidence intervals.^{20–23}

SOURCES OF DISCORDANT RESULTS

The source of cfDNA in the maternal circulation is primarily of maternal origin, with a much lower proportion (typically around 10%) being derived from degraded trophoblastic cells of the placenta.²⁴ The primary reason for discordant NIPS and diagnostic cytogenetic testing is that the DNA tested is not solely representative of the fetus. This could be due to CPM or to a resorbed or unrecognized twin pregnancy. Furthermore, it has been reported that discordant results can be due to variations in the maternal DNA contribution, including low-level sex chromosome and autosomal chromosome mosaicism, maternal malignancies, and maternal copy-number variants.^{9,17,25–27} It is well known that some women may have low-level age-related losses and gains of the X chromosome.^{28,29} There are a few reports of concurrent maternal malignancies when multiple or rare aneuploidies (e.g., autosomal monosomies) are detected by NIPS.^{30,31} Other reasons for discordance might be technical or statistical.⁹ Since analytic algorithms differ between testing platforms and providers, there could be inconsistency in the reporting of aneuploidy results from the same pregnancy reported from different laboratories due to the utilization of different cutoffs, z-scores and/or comparison to different normalization controls. By necessity, reporting algorithms include screen-positive cases that are true negatives, to ensure that nearly all true positives would be identified by the screening test.

CPM AND TFM

When mosaicism is detected by CVS, cytogenetics laboratories attempt to distinguish between CPM and TFM. In general, regardless of the chromosome involved, this requires follow-up amniocentesis and often an extended chromosome analysis of this specimen with adherence to standard guidelines for distinguishing between pseudomosaicism and TFM.¹² This extended analysis could include screening

additional cells (or colonies) from independent cultures. Screening additional metaphase cells, however, has its limitations, and a very low level of fetal mosaicism can essentially never be ruled out. Theoretically, analyzing 15 amniotic fluid colonies from at least two independent coverslips will rule out a 19% level of mosaicism at the ninety-fifth confidence interval, while screening an additional 15 colonies will rule out a 10% level of mosaicism.³² Alternatively, interphase FISH for the mosaic aberration found at CVS might be useful, although it should be noted that laboratories need to validate and establish cutoff values for positivity for each probe utilized. Any value below these cutoff values or thresholds would be considered negative.³³ CMAs may also be ordered as part of the follow-up testing, although detection of low-level mosaicism may be more challenging than by chromosome analysis and/or interphase FISH analysis³⁴ (Table 1).

UNIPARENTAL DISOMY OF KNOWN IMPRINTED CHROMOSOMES

CPM can occur as a result of either postzygotic nondisjunction or aneusomy rescue. Given the latter, it is important to determine if the normal cell line represents uniparental disomy if an imprinted chromosome is involved.¹⁶ In these cases, discordance between the positive NIPS result and the diagnostic test result should be followed up with testing appropriate for detecting uniparental disomy of the particular chromosome of interest.

NIPS RESULTS WITH MULTIPLE ANEUPLOIDIES OR RARE ANEUPLOIDIES

Although reportedly rare, any NIPS result that is positive for more than one aneuploidy or one that shows rare aneuploidies, such as an autosomal monosomy, should include consideration of the possibility of a maternal malignancy. A wide variety of maternal malignancies have been described in the literature in association with unusual NIPS results^{30,31} and there are currently no guidelines for clinical evaluation following these rare results. Further evaluation and referral to an oncologist may be warranted.

SMALLER COPY-NUMBER CHANGES

Some NIPS laboratories offer screening for rare microdeletion syndromes and smaller copy-number changes. Again, diagnostic testing is necessary in these cases, particularly as most will be falsely positive due to lower PPVs, and some may represent variants of uncertain significance. In most cases that are positive by NIPS for smaller copy-number changes, the breakpoints and the base pair coordinate positions and sizes are not provided or reported by the testing laboratory.^{35,36} As a result, specific microdeletion FISH is not the appropriate diagnostic test, due to the possibility of incorrect or incomplete FISH probe coverage. In the vast majority of cases, a whole-genome CMA analysis should be used to determine the true fetal result. As well, it should be noted that maternal contribution may also

play a role in discordant results, either due to low-level maternal mosaicism or maternal copy-number changes²⁷ (Table 1).

NIPS cases positive for imprinted genetic disorders (e.g., Angelman or Prader–Willi syndrome) may come with the acknowledgment that the laboratory cannot distinguish between a deletion and uniparental disomy of the region in question. In such cases, methylation analysis, including

methylation-specific multiplex ligation-dependent probe amplification or similar methodology is the appropriate diagnostic test to confirm the fetal result. It should be noted that methylation may not be complete for all loci at the time of CVS, and amniocentesis or neonatal testing may be warranted. Laboratories performing methylation analyses should be consulted regarding the appropriate specimen type and requirements.

Table 2 Postnatal diagnostic testing algorithm following positive NIPS results

NIPS positive for	Clinical phenotype	Recommended laboratory test	Result/recommended further testing
T13, T18, T21, other aneuploidy, triploidy	Normal	No testing needed	N/A
	Abnormal c/w NIPS	Blood chromosome analysis	Abnormal or mosaic c/w NIPS: no further testing; Normal: additional cell counts or interphase FISH or CMA
	Abnormal <i>not</i> c/w NIPS	CMA	Further testing may be warranted depending on specific findings
SCA or discrepant sex chromosomes	Normal	Blood chromosome analysis	Abnormal or mosaic c/w NIPS: no further testing; Normal: no further testing
	Abnormal c/w NIPS or abnormal <i>not</i> c/w NIPS	Blood chromosome analysis	Abnormal or mosaic c/w NIPS: no further testing; Normal: further testing may be warranted depending on the phenotype
	Smaller copy-number changes	CMA	Abnormal c/w NIPS: parental studies, if indicated; Negative: no further testing; abnormal <i>not</i> c/w NIPS: Further testing may be warranted depending on specific findings

AF, amniotic fluid; CMA, chromosomal microarray; CVS, chorionic villus sampling; c/w, consistent with; N/A, not applicable; NIPS, noninvasive prenatal screening; SCA, sex chromosome aneuploidy; T13, trisomy 13; T18, trisomy 18; T21, trisomy 21.

Box 1 Points to consider following positive noninvasive screening results

- NIPS is a screening test. It is not a diagnostic test. Diagnostic testing is recommended as a follow-up for any positive NIPS result.
- The fetal contribution of the cfDNA studied by NIPS is of presumed placental origin and, therefore, NIPS results may not be representative of the fetus.
- Sources of discordant NIPS results include CPM, a resorbed or unrecognized twin, maternal chromosome abnormalities (either mosaic or nonmosaic), maternal malignancy, technical issues including low fetal fraction, or statistical errors.
- Mosaic CVS results should not be considered confirmation of a positive NIPS result. Follow-up amniocentesis is recommended.
- Chromosome analysis on follow-up amniotic fluid specimens with screening of additional cells, FISH, and/or CMA analyses may be considered to detect possible TFM in discordant cases. It should be understood that while the chance that TFM is present can be reduced to relatively low levels, it cannot be completely ruled out.
- CMA is recommended as follow-up testing for any smaller copy-number changes that are reported as positive by NIPS.
- Specific uniparental disomy analyses on CVS or amniotic fluid cells are recommended for any imprinted regions or chromosomes reportedly involved in positive NIPS cases with discordant results.
- For patients with screen-positive NIPS results, posttest access to genetic counseling by a genetics professional and accurate, balanced and up-to-date information are essential for guiding management.
- For unusual positive NIPS results (e.g., monosomy, or multiple or rare aneuploidies), an oncology consultation for possible maternal malignancy may be warranted.

NEWBORNS

In some cases, parents with a fetus suspected to have an anomaly by NIPS will decline diagnostic testing and choose the option of a neonatal assessment. If possible, at birth, a genetics consultation should be requested and a detailed physical examination performed. In NIPS cases positive for trisomies 13, 18 or 21, normal findings on a physical examination by a clinical geneticist may be sufficient to preclude further testing. Any suspicion of an abnormal phenotype related to the aneuploidy in question should prompt a cytogenetics evaluation. When warranted, an extended chromosome analysis to rule out low levels of mosaicism or FISH may be performed. If the neonate has an abnormal physical examination that is not suggestive of the trisomy in question, CMA is recommended. For sex chromosome aneuploidies, chromosome analysis or CMA is recommended, with the possibility of additional interphase FISH analysis if mosaicism is suspected. Any NIPS result indicating smaller copy-number changes should be confirmed by CMA. Extensive testing of placental tissue is not recommended, as this is not important in the clinical care of the infant. In most cases, peripheral blood chromosome analysis of the infant's mother to screen for mosaic sex chromosome gains or losses also may not be relevant and is typically not needed for patient care or for reproductive management.^{28,29} However, maternal chromosome analysis or CMA may be warranted depending on the maternal phenotype or medical history.

Finally, sex designation by NIPS may be discordant with physical examination. While sex designation by NIPS is relatively accurate, there are cases of XX or XY NIPS results with the opposite sexed infant.^{37,38} Blood chromosome analysis is recommended (Table 2). Clinical findings suggestive of a disorder of sexual differentiation may warrant follow-up by CMA or an appropriate gene panel.

IMPORTANCE OF GENETIC COUNSELING

Pretest counseling by the provider offering NIPS should include both the advantages and limitations of this screening test, as well as the alternatives.¹ For patients with positive NIPS results, posttest access to genetic counseling by a trained genetics professional is essential for guiding management. To ensure an informed decision regarding testing and diagnostic follow-up, patients undergoing this screening should be provided with up-to-date, balanced and accurate information about the limitations of NIPS, the implications of both negative and positive NIPS results, the potential for false positives and false negatives, and the role of diagnostic testing. Patients should understand that diagnostic testing is both available and voluntary. Furthermore, the education of providers is of paramount importance.

Several points to consider following a positive noninvasive screening result are listed in Box 1.

DISCLOSURE

A.M.C., Y.M.A., H.M.K., J.H.T. and J.M.M. are clinical laboratory directors at their respective institutions and perform the assays

described herein as a clinical service. The other authors declare no conflict of interest.

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APPENDIX 2

**ACMG technical standards and guidelines: chromosome studies of neoplastic blood and bone marrow–acquired chromosomal abnormalities
(See following page)**

Section E6.1–6.4 of the ACMG technical standards and guidelines: chromosome studies of neoplastic blood and bone marrow–acquired chromosomal abnormalities

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Disclaimer: These American College of Medical Genetics and Genomics standards and guidelines are developed primarily as an educational resource for clinical laboratory geneticists to help them provide quality clinical laboratory genetic services. Adherence to these standards and guidelines is voluntary and does not necessarily ensure a successful medical outcome. These standards and guidelines should not be considered inclusive of all proper procedures and tests or exclusive of other procedures and tests that are reasonably directed to obtaining the same results. In determining the propriety of any specific procedure or test, the clinical laboratory geneticist should apply his or her own professional judgment to the specific circumstances presented by the individual patient or specimen. Clinical laboratory geneticists are encouraged to document in the patient's record the rationale for the use of a particular procedure or test, whether or not it is in conformance with these standards and guidelines. They also are advised to take notice of the date any particular guideline was adopted, and to consider other relevant medical and scientific information that becomes available after that date. It also would be prudent to consider whether intellectual property interests may restrict the performance of certain tests and other procedures.

Cytogenetic analyses of hematological neoplasms are performed to detect and characterize clonal chromosomal abnormalities that have important diagnostic, prognostic, and therapeutic implications. At the time of diagnosis, cytogenetic abnormalities assist in the diagnosis of such disorders and can provide important prognostic information. At the time of relapse, cytogenetic analysis can be used to confirm recurrence of the original neoplasm, detect clonal disease evolution, or uncover a new unrelated neoplastic process. This section deals specifically with the standards and guidelines applicable to chromosome studies of neoplastic blood and bone marrow–acquired chromosomal abnormalities.

This updated Section E6.1–6.4 has been incorporated into and supersedes the previous Section E6 in Section E: Clinical Cytogenetics of the 2009 Edition (Revised 01/2010), American College of Medical Genetics and Genomics Standards and Guidelines for Clinical Genetics Laboratories.

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Key Words: bone marrow; cancer cytogenetics; clonal chromosomal abnormalities; cytogenetic analysis; hematological malignancies

6.1 GENERAL CONSIDERATIONS

6.1.1 Cytogenetic analyses of neoplastic blood and/or bone marrow–acquired clonal chromosomal abnormalities have been increasingly important in the clinical management of patients with hematological neoplasms. At time of diagnosis, cytogenetic abnormalities assist in the diagnosis of such disorders and can provide important prognostic information.¹ Furthermore, cytogenetic analysis can provide crucial information regarding specific genetically defined subtypes of these neoplasms that have targeted therapies. At time of relapse, cytogenetic analysis can be used to confirm recurrence of the original neoplasm, detect clonal disease evolution, or uncover a new unrelated neoplastic process.

6.1.2 These cytogenetic analyses include conventional G-banded chromosome analysis, fluorescence in situ hybridization (FISH),

and/or chromosomal microarray (CMA). Laboratories should work closely with oncologists and pathologists to determine the order of testing required to obtain relevant cytogenetic information in a cost-effective manner.

6.1.3 Laboratories offering cytogenetic analyses for hematological neoplasms should be familiar with the various chromosomal abnormalities associated with the different neoplasms and their clinical significance. The laboratory should be able to provide a robust analytical and interpretative service for the various hematological neoplasms. All results should be, to the extent possible, interpreted in the context of the clinical, pathologic, and molecular findings.^{1,2}

6.1.4 Tissue processing, analytical variables, and turnaround time (TAT) should be determined by the laboratory based on

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the indication for cytogenetic referral (e.g., initial diagnosis versus follow-up studies, pre- versus posttransplant studies, and lymphoid versus myeloid malignancies) and the clinical application of the cytogenetic results (e.g., selection of therapy).

6.1.5 Molecular genetics analyses are essential for diagnosis of some hematological neoplasms, and several molecular mutations, not detectable by cytogenetic analyses, provide important diagnostic and prognostic information. These are outside the scope of the current guidelines.

6.1.6 For quality assurance, the laboratory should monitor the numbers and types of hematological neoplasms received, percentage of cases with abnormal results, cell culture success rate, success rate of FISH and CMA studies, TAT, and correlation of FISH and CMA data with G-banded chromosome analysis results.

6.2 SPECIMEN COLLECTION AND PROCESSING

6.2.1 Specimen collection

6.2.1.1 Only those cells involved in the neoplastic process will harbor the abnormalities being sought. Therefore, the specimen type and culture techniques utilized should optimize the probability of detecting an abnormal clone.

6.2.1.2 In most cases, bone marrow is the tissue of choice for cytogenetic analyses of suspected hematological neoplasms. In some circumstances, alternative specimens may be used, including the following:

- a. Peripheral blood specimens may yield informative results when the circulating blast cell percentage is higher than 10%. In general, the abnormal clone can be identified in such specimens, albeit not as often as in bone marrow. Peripheral blood or bone marrow can be used in chronic lymphocytic leukemia (CLL).
- b. Bone marrow core biopsy specimens.
- c. Bone marrow smears and core biopsy touch imprints can be used for interphase FISH.
- d. Lymph node biopsy material or biopsy material from a suspected lymphoid mass are the preferred tissue in all lymphomas.
- e. Cerebrospinal fluid.
- f. Extramedullary leukemia (myeloid sarcoma, chloroma) tissue biopsy.

6.2.1.3 Specimens should be collected under sterile conditions in sodium heparin tubes for chromosome and/or FISH analyses. Bone marrow aspirate and biopsy specimens should preferably be collected in an appropriate transport medium tube with sodium heparin. The concentration of sodium heparin should be ~20 U/ml of specimen (per either bone marrow volume alone or per total volume of bone marrow and transport medium combined). EDTA tubes can be used for procedures that require genomic DNA extraction.

6.2.1.4 The volume of bone marrow available will differ for adults and children. An approximate specimen of 1 to 3 ml should be requested. During specimen procurement, several

draws are likely to be withdrawn. Because the first draw is more concentrated with neoplastic immature bone marrow cells, it is recommended that cytogenetics receive the first or second draw whenever possible.

6.2.1.5 Specimens should be received by the laboratory as soon as possible, ideally within 24 hours. Also, it is recommended that specimens be maintained at ambient temperature during transit. Extreme temperatures should be avoided.

6.2.1.6 If the specimen size precludes cell culture and conventional G-banded chromosome analysis, bone marrow smears or core biopsy touch imprints can be used for interphase FISH analysis.

6.2.2 Specimen processing

6.2.2.1 The laboratory should process the specimen as soon as possible after it is received. The methods that will be used to analyze the specimen should be determined prior to processing whenever possible. If chromosome analysis is requested, cell culture will be required. If FISH and/or CMA analyses are requested, a portion of the specimen can be used for direct harvest of interphase cells and/or genomic DNA extraction.

6.2.2.2 If a bone marrow core biopsy is obtained, it should be disaggregated to generate a cell suspension. This can be achieved by mechanical mincing and/or enzymatic digestion using collagenase. Culture conditions are the same as those for a bone marrow aspirate.

6.2.2.3 Cell culture conditions should be optimized for the specific hematological neoplasm suspected:

- a. Acute leukemias, including acute myeloid leukemia (AML), acute lymphoblastic leukemia (ALL), and acute biphenotypic leukemia: Unstimulated short-term cultures are recommended. If sufficient specimen is received, at least two cultures should be initiated, including direct, overnight, and/or 24-hour cultures. In pediatric ALL, an additional unstimulated 48-hour culture can be useful in characterizing the abnormal karyotype. The seeding density is usually 1 to 3 million cells per ml of medium.
- b. Myelodysplastic syndromes (MDS) and myeloproliferative neoplasms (MPN): Same as acute leukemias.
- c. Plasma cell dyscrasias, including multiple myeloma (MM) and plasma cell leukemia: Unstimulated 24- and 72-hour cultures as well as 120-hour IL-4-stimulated culture are recommended.³ For FISH and/or CMA analyses, if the bone marrow plasma cells percentage (as determined by flow cytometry) is below a certain cutoff value, plasma cell separation is recommended to enrich for the CD138⁺ plasma cell fraction.^{4,5} The laboratory needs to establish its cutoff value for plasma cell enrichment.
- d. Chronic lymphoproliferative disorders: Depending on the immunophenotype, additional cultures with B- or T-cell mitogens may be helpful. In CLL and other mature B-cell neoplasms, CpG-oligonucleotide cell stimulation

is recommended and has been shown to enhance the detection of clonal chromosomal abnormalities.^{6,7}

- e. Well-differentiated T-cell disorders (e.g., T-cell leukemias, T-cell lymphoma, Sézary syndrome, and mycosis fungoides): T-cell mitogens may be helpful.

6.3 ANALYSIS

6.3.1 Conventional G-banded chromosome analysis

6.3.1.1 Cell selection: metaphase cells should not be selected for analysis solely on the basis of good chromosome morphology. In general, the technologist should select an area of the slide to begin the analysis and then examine metaphase cells as they appear consecutively in the microscope field, only skipping cells for which extremely poor morphology precludes chromosome identification. This technique can also be performed using automated metaphase finders by examining metaphase cells consecutively captured by the system. Sufficient cells should be analyzed or examined to maximize the detection of an abnormal clone and establish the clonality of the abnormality found. For each abnormal clone identified, clonal cells with the best chromosome morphology should be analyzed, captured, and karyotyped to provide the most accurate breakpoint assignment.

When cells are skipped because of poor morphology, it is important to attempt to count the number of chromosomes. This is particularly true for possible hyperdiploid or hypodiploid pediatric ALL and hyperdiploid plasma cell dyscrasias. In addition, attempts should be made to identify possible structural chromosomal abnormalities, particularly if the disease under consideration is associated with a specific recurring abnormality (e.g., the t(9;22) in chronic myeloid leukemia (CML)).

6.3.1.2 Number of cells evaluated: The number of metaphase cells analyzed versus the number of cells counted or scored should be appropriate for the type of the study (e.g., initial diagnosis or follow-up studies) and the purpose of the study (e.g., detection of residual disease or response to therapy, monitoring for clonal evolution, or monitoring of allogeneic transplant engraftment).

6.3.1.3 Initial diagnostic studies:

- a. Analysis: Analyze a minimum of 20 cells from unstimulated cultures. For the mature B- and T-cell disorders, a combination of unstimulated and mitogen-stimulated cultures may be appropriate as described. Unstimulated CLL cultures infrequently yield CLL-related clonal chromosomal abnormalities; however, they can reveal MDS-related clonal abnormalities since some of these patients might have co-morbid MDS because of either prior therapy or age-related. Similarly, unstimulated 24-h MM cultures can reveal co-morbid MDS-related clonal abnormalities.
- b. Documentation:
 - For the abnormal cells:
 - If *only one* abnormal clone is present: two karyotypes.

- If *more than one* related abnormal clone is present: two karyotypes of the stemline and one of each sideline.
- If *unrelated clones* are present: two karyotypes for each stemline and one for each associated pertinent sideline.
- In instances when the sideline contains complex abnormalities, two karyotypes of each sideline may be required for better documentation.
- For the normal cells:
 - If *only normal* cells are present: two karyotypes.
 - If *normal and abnormal cells* are present: one karyotype of a normal cell.

6.3.1.4 Follow-up studies of patients who have had a previous cytogenetic study: For the following analytic guidelines, it is assumed that the laboratory has documentation of the patient's previous cytogenetic results. If the study has been performed elsewhere and there is minimal information available, it is recommended that, except for patients seen for the first time posttransplant, the analysis be considered the same as an initial diagnostic workup (see above).

- I. Patients who *have not* undergone allogeneic hematopoietic cell transplantation:
 - a. Analysis: analyze 20 cells. If all cells are normal, additional cells may be scored for a specific abnormality by G-banding or FISH if pathology is positive for the diagnosis in question. For some patients, follow-up cytogenetic study is ordered to rule out a therapy-associated malignancy (e.g., MDS) rather than disease recurrence.
 - b. Documentation:
 - For cases with both normal and abnormal cells or only abnormal cells:
 - One karyotype of a normal cell, if such a karyotype was not documented in a previous study by the laboratory; otherwise, one normal metaphase spread.
 - One or two karyotypes from each abnormal clone for a minimum total of two karyotypes.
 - For cases with all normal cells:
 - Two karyotypes.
- II. Patients who *have* undergone an allogeneic hematopoietic cell transplantation for whom donor versus recipient origin of the cells can be determined (by sex chromosome complement or cytogenetic heteromorphisms):

For studies aimed solely at determining engraftment status, molecular methods and/or interphase FISH (in the case of opposite sex transplant) are more sensitive than G-banded chromosome analysis and are the preferred methodologies. Therefore, in consultation with the referring physician, cancellation of test

requests for G-banded chromosome analysis for engraftment status should be considered.

During the course of the cytogenetic analysis, it will become evident whether there is chimerism for donor and recipient cells. It is expected that there will be different approaches used by different laboratories to address these studies.

- If *only donor* cells are present:
 - a. Analysis: analyze 20 cells.
 - b. Documentation: document two karyotypes for each cell line. In such cases, one is documenting either the constitutional karyotype (normal or abnormal of the donor) or the rare event of a malignant process arising in a donor cell.
- If *donor and recipient* cells are present:
 - a. Analysis: Analyze recipient cells completely for previously identified clonal chromosome abnormalities and any newly acquired abnormalities. In some cases there may be structural chromosomal abnormalities secondary to chromosome breakage or rearrangement induced by the pretransplant conditioning regimen. The laboratory should distinguish clonal from nonclonal changes and determine the significance of new abnormalities as much as possible.
Analyze all recipient cells present out of 20 cells analyzed. Evaluate each recipient cell for the presence of the abnormality present prior to transplantation (i.e., the diagnostic abnormality). Depending on the number of recipient cells present among the initial 20 metaphase cells scored, additional recipient cells may be analyzed completely and/or scored for the presence of the diagnostic abnormality.
Donor cells: analyze two donor cells if donor cells have not been analyzed in previous studies. Otherwise, simply score these cells as being of donor origin and count.
 - b. Documentation: for the recipient cells: Two karyotypes of the stemline and one of each sideline. For the donor cells: If donor cells have been documented previously, then provide a single metaphase spread. If donor cells have not been documented previously, then provide two karyotypes.
- If *only recipient* cells are present:
 - a. Analysis: analyze 20 cells following the guidelines set forth above with respect to the characterization of secondary abnormalities.
 - b. Documentation: same as noted above for abnormal recipient cells.

- III. Patients who *have* undergone an allogeneic hematopoietic cell transplantation for whom donor and recipient cells *cannot* be determined:
Analysis: analyze 20 cells. As in case scenarios outlined here, follow guidelines for recipient cells as set forth above.

6.3.2 FISH analysis

6.3.2.1 Interphase FISH analysis may be used as a primary testing methodology in conjunction with G-banded chromosome analysis for the evaluation of hematological neoplasms. FISH studies may be indicated to (i) provide a rapid result to aid in the differential diagnosis or planning of therapy; (ii) detect a cryptic chromosomal abnormality or gene rearrangement, especially when G-banded chromosome analysis yields normal results; (iii) detect clinically significant gene amplification, which may also require metaphase FISH analysis to document the tandem nature of this rearrangement on the same chromosome or the presence of double minutes; (iv) provide an alternative diagnostic method when no metaphase cells are obtained by blood or bone marrow cultures; and (v) detect abnormalities in samples that are not adequate or not suitable for G-banded chromosome analysis.

6.3.2.2 Characterization of the initial diagnostic interphase FISH abnormal signal pattern is important and will allow future monitoring of the patient's disease.

6.3.2.3 Metaphase FISH analysis and/or sequential G-banded chromosome analysis to metaphase FISH analysis may be useful and provides a useful methodology to characterize variant chromosomal abnormalities or gene rearrangements as demonstrated by a variant abnormal interphase FISH signal pattern.

6.3.2.4 Analysis and documentation of FISH studies should be in accordance with Section E9 of these standards and guidelines for clinical genetics laboratories.

6.3.3 CMA analysis

6.3.3.1 CMA analysis can add valuable information that will support and supplement both G-banded chromosome analysis and FISH. It can detect small cryptic clinically significant copy number changes (CNCs) in various hematological neoplasms. Additionally, CMA SNP platforms can also detect copy-neutral loss of heterozygosity (cnLOH). However, this technology cannot detect balanced chromosomal rearrangements.

6.3.3.2 The clinical utility of genome-wide CMAs in cancer diagnostics is growing rapidly. This technology is being used to better identify high-risk patients and predict clinical outcomes. In view of the rapid introduction of CMAs into clinical practice, it is important that laboratories stay up-to-date with this technology.

6.3.3.3 Analysis and documentation of CMA studies should be in accordance with Section E11 of these standards and guidelines for clinical genetics laboratories.

6.3.4 Recommended cytogenetic analysis scheme in hematological neoplasms

6.3.4.1 Acute leukemias

Bone marrow is the preferred specimen for acute leukemias, but peripheral blood can be used when >10% circulating blast cells are present.⁸ Interphase FISH analysis performed on bone marrow smears or core biopsy touch imprints is an alternative in cases with a dry tap and/or hemodiluted bone marrow aspirate and absent/low circulating blast cells. A strong collaboration with the oncologist and pathologist is important for

establishing the order of testing and additional tests that should be undertaken.⁹

1. AML

- G-banded chromosome analysis should preferably be performed first. However, interphase FISH analysis for *KMT2A (MLL)* gene rearrangement is highly recommended on all diagnostic AML samples because these abnormalities are often cryptic and have a pronounced prognostic impact.
- In case of a successful normal chromosome analysis with a clear diagnosis of AML by morphology and flow cytometry, additional interphase and metaphase FISH analyses are recommended to exclude cryptic rearrangements. Depending on the morphology and flow cytometry results, the following FISH probes can be added:
 - a. *RUNX1-RUNX1T1 (AML1-ETO)* fusion probes
 - b. *CBFB* rearrangement or *CBFB-MYH11* fusion probes: *inv(16)* and *t(16;16)* resulting in *CBFB-MYH11* fusion can be subtle in cases with sub-optimal G-banded chromosomes quality
 - c. *KMT2A (MLL)* rearrangement probes
 - d. *PML-RARA* fusion probes: *PML-RARA* fusion is diagnostic of acute promyelocytic leukemia (APL), which is usually strongly suspected at diagnosis based on the patient's presentation and blast cell morphology. A *RARA* break-apart probe can be used to detect variant translocations in which *RARA* fuses with a different partner
- In case of an incomplete/unsuccessful chromosome analysis or if the laboratory is unable to maintain a short TAT for chromosome analysis, then the following probes can be bundled in an AML FISH panel, which should be performed on the diagnostic specimen:
 - a. *RUNX1-RUNX1T1 (AML1-ETO)* fusion probes
 - b. *CBFB* rearrangement or *CBFB-MYH11* fusion probes
 - c. *KMT2A (MLL)* rearrangement probes
 - d. -5/5q- probes
 - e. -7/7q- probes
 - f. *PML-RARA* fusion probes: if there is suspicion of APL based on the patient's presentation and blast cell morphology
- *MECOM (EVII)* rearrangement probes should be considered when chromosome analysis is suggestive of an *inv(3)* or *t(3;3)*.
- Recent CMA studies revealed acquired CNCs and region of cnLOH that add independent prognostic impact in AML. CMA analysis can detect CNCs that are more specific to primary AML, whereas others are more specific to therapy-related AML.¹⁰ In addition, regions of cnLOH are more often detected in

patients with normal karyotypes than with abnormal karyotypes.^{11,12}

2. ALL

- B-lineage ALL is more frequent, accounting for 85% of pediatric ALL and 75% of adult ALL.¹
- In pediatric/young adult B-lineage ALL, G-banded chromosome analysis should be performed simultaneously with interphase FISH analysis using a panel that includes the following probes:
 - a. *BCR-ABL1* fusion probes
 - b. *KMT2A (MLL)* rearrangement probes
 - c. *ETV6-RUNX1* fusion probes: for *ETV6-RUNX1* fusion, *ETV6* deletion, and iAMP21 (intrachromosomal amplification of chromosome 21)
 - d. Centromeric probes for chromosomes 4 and 10: for trisomies of chromosomes 4 and 10
- In adult B-lineage ALL, G-banded chromosome analysis should be performed simultaneously with interphase FISH analysis using the following probes:
 - a. *BCR-ABL1* fusion probes
 - b. *KMT2A (MLL)* rearrangement probes
- In both pediatric and adult B-lineage ALL, and depending on the blast cell morphology, flow cytometry, chromosome analysis, and FISH results, additional interphase FISH testing should be considered, including:
 - a. *CRLF2* rearrangement probes: for *P2RY8-CRLF2* fusion and *IGH-CRLF2* fusion (Ph-like ALL)¹³
 - b. *PDGFRB* rearrangement probes (Ph-like ALL)¹³
 - c. *CDKN2A/B* (9p21.3) probe: 9p21.3 deletion is common in both B- and T-lineage ALLs, but its prognostic significance has been debated; however, it provides a clonal target for future monitoring of the patient's disease in the absence of other FISH targets
 - d. *PAX5* (9p13.2) probe
- *MYC* rearrangement and/or *IGH-MYC* fusion probes should be considered in both pediatric and adult ALL, where the morphology and flow cytometry results are suggestive of B-cell ALL (Burkitt leukemia variant)
- In T-lineage ALL, G-banded chromosome analysis should be performed first. Interphase FISH analysis is optional and could include the following probes:
 - a. *BCR-ABL1* fusion probes: for *BCR-ABL1* fusion and *ABL1* amplification
 - b. *KMT2A (MLL)* rearrangement probes
- In ALL, CMA analysis can be very helpful for detecting cryptic CNCs, with proven relevance to diagnosis, prognosis, and therapeutic response.¹⁴⁻¹⁶ Examples include deletions involving *PAX5* and *IKZF1* genes. It can also help clarify the structure of complex chromosomal rearrangements. Finally,

CMA SNP platforms can detect whole-chromosome cnLOH due to “doubling” of a near-haploid or low hypodiploid clone, which manifests in the form of a hyperdiploid or near-triploid karyotype. The prognosis of these two entities is very different.

6.3.4.2 Myelodysplastic syndromes

- Bone marrow is the preferred specimen for MDS.¹⁷ Interphase FISH analysis performed on bone marrow smears or core biopsy touch imprints is an alternative in cases with a dry tap and/or hemodiluted bone marrow aspirate. A strong collaboration with the oncologist and pathologist is important in MDS cases, where other non-neoplastic hematological disorders can have a similar presentation.
- G-banded chromosome analysis should preferably be performed first. In case of an incomplete/unsuccessful chromosome analysis or if the laboratory is unable to maintain a short TAT for chromosome analysis, the following probes can be bundled in an MDS FISH panel,¹⁸ which should be performed on the diagnostic specimen:
 - a. -5/5q- probes
 - b. -7/7q- probes
 - c. Centromeric probe for chromosome 8: for trisomy 8
 - d. 20q- probe
- Recent data suggest that MDS exhibits abundant clonal CNCs and cnLOH, often in the setting of a normal metaphase karyotype and with no previously identified clonal markers. CMA analysis is proving to be very useful in uncovering these genomic aberrations in MDS.^{19,20} Examples include cryptic 5q deletions distal to the *EGR1* gene (5q31). These can be missed by G-banded chromosome and FISH analyses.²¹

6.3.4.3 Myeloproliferative neoplasms and myelodysplastic syndromes/myeloproliferative neoplasms.

This is a heterogeneous group of clonal stem disorders that is broadly divided into three groups.^{9,22} The first is the classical MPN group, which includes CML (*BCR-ABL1* fusion positive), polycythemia vera, essential thrombocythemia, primary myelofibrosis, chronic neutrophilic leukemia, chronic eosinophilic leukemia not otherwise specified, mastocytosis, and MPN unclassified. The second group includes myeloid and lymphoid neoplasms associated with eosinophilia and abnormalities of *PDGFA*, *PDGFRB*, or *FGFR1*. The third is the MDS/MPN group, which includes chronic myelomonocytic leukemia, atypical CML (*BCR-ABL1* fusion negative), juvenile myelomonocytic leukemia, and MDS/MPN unclassified.

1. CML

- Bone marrow is the preferred specimen for CML; however, peripheral blood may be used if the level of blasts is >10%.
- The t(9;22)(q34;q11.2) is detectable in 90–95% of CML cases at diagnosis. The remaining 5–10% of

cases have either a variant t(9;22) or a cryptic *BCR-ABL1* fusion undetectable by chromosome analysis.

- Therefore, both G-banded chromosome analysis as well as interphase FISH analysis using *BCR-ABL1* fusion probes should be performed simultaneously at diagnosis.
- It is important to establish whether additional chromosome abnormalities are present at diagnosis, including an additional der(22), i(17q), and trisomy 8. These are warning signs that might be associated with inferior overall survival and increased risk of progression to accelerated phase.^{23,24}
- The CML National Comprehensive Cancer Network (NCCN) guidelines recommend that cytogenetic studies (both G-banded chromosome and *BCR-ABL1* fusion FISH analyses) and quantitative RT-PCR *BCR-ABL1* fusion testing be performed at diagnosis. If no *BCR-ABL1* fusion can be detected, molecular testing for mutations associated with other myeloproliferative conditions is indicated.

2. Other MPNs

- Bone marrow is the preferred specimen for other MPNs; however, peripheral blood may be used if there is peripheral involvement. With few exceptions, cytogenetic abnormalities are usually not specific in other MPNs. Typical abnormalities of myeloid neoplasms are usually observed and can be useful in demonstrating evidence of clonality.
- Interphase FISH analysis performed on bone marrow smears or core biopsy touch imprints is an alternative in cases with a dry tap and/or hemodiluted bone marrow aspirate. A strong collaboration with the oncologist and pathologist is important.
- The exclusion of *BCR-ABL1* fusion is necessary for the differential diagnosis of other MPNs from CML.
- Other specific FISH probes recommended in other MPNs based on the pathology input include *FIP1L1-PDGFA* fusion, *PDGFRB* rearrangement, and *FGFR1* rearrangement probes in myeloid/lymphoid neoplasms with eosinophilia. MPNs with these gene rearrangements can be treated with targeted therapies (i.e., tyrosine kinase inhibitors).

6.3.4.4 Plasma cell dyscrasias

- A bone marrow specimen is required for MM. For FISH and/or CMA analyses, plasma cell separation is recommended to enrich for the CD138⁺ plasma cell fraction in bone marrow samples with low plasma cell percentages (see Section 6.2.2.3).^{4,5}
- G-banded chromosome analysis should be performed (as described above) simultaneously with interphase FISH analysis using a panel that includes the following probes:^{25–27}
 - a. 1q21.3 probe (including *CKS1B*): for 1q21 copy gain, which has been linked to adverse prognosis

- b. 13q14.2q14.3 probes (including *RBI*): 13q14.2q14.3 deletion is common in MM but, when detected only by FISH, it is not predictive of survival in the absence of other adverse cytogenetic abnormalities. However, it provides a clonal target for future monitoring of the patient's disease in the absence of other FISH targets. 13q deletion detected by G-banded chromosome analysis still retains its prognostic value
- c. *IGH* rearrangement probes: if *IGH* is rearranged, including the classical gene disruption as well as deletion of either the 5' or 3' region of *IGH*, then reflex to *IGH-FGFR3*, *IGH-CCND1*, and *IGH-MAF* fusion probes.
- d. *TP53* (17p13.1) probe
- e. Probes for three of the odd-numbered chromosomes often trisomic in hyperdiploid MM (e.g., chromosomes 5, 9, 11, 15, and 19)
- The use of CMA analysis on the enriched plasma cell fraction has been shown to be very valuable in detecting clinically relevant CNCs.^{28–30}

6.3.4.5 Chronic lymphocytic leukemia

- CLL is a mature B-cell neoplasm diagnosed by B-cell count, morphology, and flow cytometry. Cytogenetically, either peripheral blood or bone marrow can be used in CLL. G-banded chromosome analysis should be performed simultaneously with interphase FISH analysis.³¹ CLL cell stimulation in culture using CpG-oligonucleotides greatly improves the detection rate of clonal cytogenetic abnormalities by G-banded chromosome analysis.^{6,7}
- To assign the patient into clinically relevant prognostic subgroups, the following panel of FISH probes is recommended:
 - a. *ATM* (11q22.3) probe
 - b. Centromeric probe for chromosome 12: for trisomy 12
 - c. 13q14.3 probe (including D13S319)
 - d. *TP53* (17p13.1) probe
- FISH can also be useful for the differential diagnosis with mantle cell lymphoma (MCL), for which FISH using the *IGH-CCND1* fusion probes is recommended.
- In CLL, CMA analysis has proven to be very effective in detecting CNCs and cnLOH at genomic regions with established prognostic significance, and it provides a much higher resolution compared to G-banded chromosome and FISH analyses.^{32,33} Examples include 13q14 deletions, which are quite heterogeneous.³⁴ Moreover, clinically relevant genomic alterations in CLL involve mostly deletions and duplications, whereas most balanced translocations are relatively rare and are of unclear significance.

6.3.4.6 B- and T-cell lymphomas

- For all lymphomas, the preferred tissue is lymph node or biopsy material from a suspected lymphoid mass. If fresh

material is available, G-banded chromosome analysis is recommended.

- Interphase FISH analysis using relevant probes performed on lymph node tissue sections, fine needle aspirate smears, and/or touch imprints should be included.
- For lymph node cytogenetic analysis in lymphomas, see Section E6.5-6.8.
- Bone marrow or peripheral blood analysis will not detect clonal chromosomal abnormalities if there is no evidence of infiltration. For FISH analysis, bone marrow smears or core biopsy touch imprints can be used.

6.4 TAT AND REPORTING

6.4.1 TAT

6.4.1.1 Specific chromosomal abnormalities are crucial for establishing a diagnosis and have direct relevance to specific treatment. Therefore, an effort should be made to expedite communicating the cytogenetic analyses results to the oncologist. It is recommended that the cytogenetics laboratory should have a written policy describing how cases are prioritized in the laboratory.

6.4.1.2 TAT guidance:

- a. Initial diagnostic workup: It is strongly recommended that the preliminary result should be reported within 7 calendar days, and the final results should be reported within 21 calendar days.
- b. Follow-up studies: It is strongly recommended that the final results should be reported within 21 calendar days.
- c. FISH studies: Reporting the FISH results within 3–5 working days from the time of receiving the specimen is recommended whenever possible.

6.4.2 Reporting

6.4.2.1 The most recent edition of the International System for Human Cytogenetic Nomenclature (ISCN) should be used to report the cytogenetics results.³⁵

6.4.2.2 The number of cells analyzed (both normal and abnormal) should be documented in the final report.

6.4.2.3 For CMA analysis, clones and subclones cannot be ascertained with certainty; however, the percentage of cells (levels of mosaicism) can be provided to give an estimate of possible clones/subclones and clonal diversity.

6.4.2.4 If a potential nonmosaic constitutional abnormality is observed, analysis of a PHA-stimulated peripheral blood sample during remission is strongly recommended to confirm that the abnormality is constitutional and not clonal.

6.4.2.5 At the time of initial diagnosis, finding a single abnormal metaphase cell, even one that is potentially significant, cannot be used as evidence of clonality unless there is strong supporting evidence of clonality for the same abnormality by either FISH or other molecular technique.

6.4.2.6 The final cytogenetic report of hematological acquired chromosomal abnormalities should contain the following information:

1. Patient identification using two different identifiers
2. Patient medical record number and/or laboratory identification number
3. Referring physician
4. Sample information (type, date of withdrawal and receipt, and date of report)
5. Reason for referral or suspected diagnosis
6. ISCN nomenclature of cytogenetic studies performed
7. Narrative description of the abnormalities observed, including modal chromosome number in each clone (to the extent possible), and numerical and structural abnormalities. The report should comment on the clinical significance of the abnormalities observed, including clinically relevant genes involved, possible disease association, and prognostic significance.
8. Literature references to support the clinical interpretation and to provide helpful information for the oncologist.

DISCLOSURE

All of the authors direct clinical cytogenetics laboratories that run the tests discussed in the current standards and guidelines on a fee-for-service basis.

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ERRATUM: Section E6.1–6.4 of the ACMG technical standards and guidelines: chromosome studies of neoplastic blood and bone marrow–acquired chromosomal abnormalities

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On page 5, in the left column, first paragraph under “AML,” a gene name is misspelled. The correct gene name is “*KMT2A (MLL)*.” The publisher regrets the error.

APPENDIX 3

**ACMG technical standards and guidelines: chromosome studies of lymph node and solid tumor–acquired chromosomal abnormalities
(See following page)**

Section E6.5–6.8 of the ACMG technical standards and guidelines: chromosome studies of lymph node and solid tumor–acquired chromosomal abnormalities

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Disclaimer: These ACMG standards and guidelines are developed primarily as an educational resource for clinical laboratory geneticists to help them provide quality clinical laboratory genetic services. Adherence to these standards and guidelines is voluntary and does not necessarily ensure a successful medical outcome. These standards and guidelines should not be considered inclusive of all proper procedures and tests or exclusive of other procedures and tests that are reasonably directed to obtaining the same results. In determining the propriety of any specific procedure or test, the clinical laboratory geneticist should apply his or her own professional judgment to the specific circumstances presented by the individual patient or specimen. Clinical laboratory geneticists are encouraged to document in the patient's record the rationale for the use of a particular procedure or test, whether or not it is in conformance with these standards and guidelines. They also are advised to take notice of the date any particular guideline was adopted, and to consider other relevant medical and scientific information that becomes available after that date. It also would be prudent to consider whether intellectual property interests may restrict the performance of certain tests and other procedures.

Cytogenetic analysis of tumor tissue is performed to detect and characterize chromosomal aberrations to aid histopathological and clinical diagnosis and patient management. At the time of diagnosis, known recurrent clonal aberrations may facilitate histopathological diagnosis and subtyping of the tumor. This information may contribute to clinical therapeutic decisions. However, even when tumors have a known recurrent clonal aberration, each tumor is genetically unique and probably heterogeneous. It is important to discover as much about the genetics of a tumor at diagnosis as is possible with the methods available for study of the tumor material. The information gathered at initial study will inform follow-up studies, whether for residual disease detection, determination of relapse and clonal evolution, or identifying a new disease clone.

This updated Section E6.5–6.8 has been incorporated into and supersedes the previous Sections E6.4 and E6.5 in Section E: Clinical Cyto-genetics of the 2009 Edition (Revised 01/2010), American College of Medical Genetics and Genomics Standards and Guidelines for Clinical Genetics Laboratories. This section deals specifically with the standards and guidelines applicable to lymph node and solid tumor chromosome analysis.

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Key Words: cancer cytogenetics; chromosome; guidelines; lymph node; solid tumor

6.5 GENERAL CONSIDERATIONS

6.5.1 Genetic analysis of solid tumors and lymphomas at diagnosis provides information critical for diagnosis and patient management.^{1,2} Analysis of tumor tissues may be accomplished by conventional chromosome analysis, fluorescence in situ hybridization (FISH) analysis, chromosomal microarray (CMA) analysis, molecular analysis, or a combination of methodologies. Because the genetic information aids in the differential diagnosis and provides direction for the most appropriate therapeutic management, including targeted therapies, tumor materials should be studied with available methods to gain as much

information as possible at the time of initial study. At a time of suspected disease recurrence or metastasis, the initial genetic data will be used to confirm recurrence or metastasis, assess clonal disease evolution, or reveal a new malignant process.

The method(s) chosen for evaluation of a tumor at the time of biopsy or resection will depend on the differential diagnosis, clinical indications, available tissue, available methodologies, and initial histopathology of the tumor tissue.

For disease staging, tumor samples may be accompanied or followed by other tissue samples for analysis, such as bone marrow and cerebrospinal fluid.

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6.5.2 The laboratory director and staff should be familiar with the chromosomal and molecular aberrations associated with tumor types/subtypes and their clinical significance. **Supplementary Tables S1–S5** online include common solid tumor and lymphoma chromosomal aberrations with known genes, potential FISH targets, clinical significance, and references.

6.5.3 Pediatric tumors should be cytogenetically analyzed whenever sufficient fresh tissue is available. Karyotyping, although low-resolution, provides a view of the entire genome. This genome view allows detection of cytogenetic aberrations that are commonly disease- or disease subtype-specific and have prognostic and therapeutic significance. Genetic analysis of adult tumors is indicated whenever such analysis may provide diagnostic, prognostic, or treatment-related information, especially if targeted therapies are available for the disorder undergoing study.

6.5.4 Methods for the processing of tumor material should be determined by the cytogenetic laboratory based on available clinical and pathologic findings. Laboratories should work with the oncologist and pathologist to determine the method(s) to gain the most genetic information cost-effectively. The laboratory should seek information about the suspected diagnosis and tissue type at the time of sample receipt to choose the most appropriate testing and tissue culture method(s) and to determine if DNA should be isolated from the fresh tumor. **Supplementary Table S6** online provides tumor nomenclature for tumor culture method selection.

6.5.5 Conventional cytogenetic, FISH, CMA, gene mutation panel, or sequencing analysis may be used as a primary or secondary method of evaluation of the tumor tissue. Multiple technologies may be needed for specific tumor types. The availability of fresh tissue, the differential diagnosis, a need for rapid diagnostic information, and the type of information needed should be used to prioritize testing such as conventional cytogenetic analysis, FISH, CMA, and/or mutation analysis.

6.5.6 Cytogenetic and molecular analysis results must be interpreted within the context of the pathologic and clinical findings.

6.5.7 For quality assurance, the laboratory may monitor the number and types of tumors received, the percentage of tumors with abnormal results, the cell culture success rate, and the success rate for FISH and CMA studies.

6.5.8 The presence or absence of specific aberrations should be available to the physician as soon as is feasible to contribute to the patient's plan of care.

6.6 SAMPLE COLLECTION AND PROCESSING

6.6.1 Sample collection

6.6.1.1 Tumor samples should be collected in a sterile manner. For conventional cytogenetic analysis, the tissue sample must be fresh. The sample selected for cytogenetic analysis should be "pure" tumor if possible, without necrosis. The sample must not be placed in fixative or frozen. Samples to be evaluated solely by FISH or CMA analysis may be fixed, frozen, or paraffin-embedded. If CMA analysis or sequencing is requested at the time of biopsy, DNA should be isolated from fresh tumor or formalin-fixed paraffin-embedded tumor rather than cultured

tumor cells because clonal aberrations may be lost during cell culture. Cultured tumor cells may be used for isolation of DNA if the karyotype is clonally abnormal. The use of formalin-fixed paraffin-embedded samples for FISH and DNA isolation allows a pathologist to identify and mark optimal areas of tumor to examine, specify the percentage of tumor in an area, and/or identify areas of necrosis or stromal tissue to avoid.

6.6.1.2 The laboratory should request a sample size of 0.5 to 1 cm³. If less tissue is available, the laboratory should accept as much as can be provided. If the sample size is very limited (e.g., fine needle aspirate or needle core biopsy), coverslip cultures are often successful. If the sample size precludes cell culture and conventional cytogenetic evaluation, touch preparations, cytopins, or paraffin-embedded tissue sections may be used for FISH analysis, or DNA may be isolated for CMA or sequencing analysis. See Section E6.5.2.

6.6.1.3 Fresh tumor should be transported in culture medium to the cytogenetics laboratory as soon as possible for immediate processing.

6.6.2 Sample processing

6.6.2.1 The cytogenetic laboratory should process the tumor sample as soon as possible after it is received. Prior to processing, it should be clear what methods will be used to analyze the sample (e.g., chromosome analysis, FISH, CMA, sequencing). If the sample is to be processed for CMA or sequencing, select a portion of the sample for DNA isolation. If the sample is for FISH analysis, touch preparations may be made or direct harvest performed. If the sample is for chromosome analysis, tissue culture will be required.

6.6.2.2 The fresh tumor sample should be inspected and details of the sample size, color, and attributes recorded. The time of sample collection and the time of sample receipt in the laboratory should be documented.

6.6.2.3 The cytogenetics laboratory should expect the sample submitted by a pathologist to be most representative of the tumor as determined by gross examination. However, if the fresh sample received by the laboratory is large and appears heterogeneous, portions of the sample may be cultured separately. If obvious normal, necrotic, or vascular tissues are present, the tumor should be separated from nontumor tissue for processing. Obvious necrotic tissue should be removed to reduce enzymatic damage induced by dying cells. If the tumor cannot be distinguished from normal or necrotic tissue, caution should be exercised and the entire sample processed.

6.6.2.4 For tissues from a body region with high concentrations of bacteria (e.g., tonsils, gut), treatment of the sample prior to disaggregation with antibiotic and/or antifungal solutions and addition of antibiotic and/or antifungals to the medium may be prudent.

6.6.2.5 Disaggregation methods should be optimized for different tissue types:

- a. Disaggregation of solid tumor samples for tissue culture is needed. Mechanical and/or enzymatic methods may

be used. If sufficient tumor material is submitted, both methods of disaggregation are recommended. For some tumor types, different growth characteristics can be seen with exposure to collagenase versus no exposure to collagenase. If sufficient material is available, cultures should be initiated with and without enzyme exposure.

- b. Disaggregation of lymphoid tissues into single cell suspension is necessary before culture initiation. The lymphoid cells in most tissues are readily disaggregated by mechanical means such as mincing with scalpels or curved scissors. The use of these methods is often advantageous if the tissue is easily dissociated because it will keep the loss of cells to a minimum and may help minimize stromal contamination because stromal cells are often locked in fibrous connective tissues. If cells are not readily liberated by mechanical means, enzymatic digestion may be necessary. When using enzymatic digestion, the tissue must first be minced and then incubated with the enzyme solution (e.g., collagenase) for 20 minutes to 16 hours depending on how quickly cell release occurs.

6.6.2.6 Culture methods, culture medium, and culture conditions should be chosen to best support the type of tumor received.

- a. The diagnosis and histopathology of a tumor can be helpful in determining culture and harvest methods. Different cell types can be expected to respond differently with growth medium, harvest method, and other factors (Table 6). If the diagnosis is unknown at culture initiation, it can be helpful to know whether the pathologist would classify the tumor as a “small round cell tumor” (SRCT), which includes lymphoproliferative disorders. SRCTs can be successfully grown in suspension, whereas non-SRCTs are best grown with monolayer (flask or coverslip) culture methods. Most, but not all, SRCTs (e.g., lymphoproliferative disorders) will also grow in monolayer culture. If adequate tissue is obtained, both culture types should be initiated for SRCTs. For very small tumor samples, coverslip cultures are recommended. Duplicate cultures should be established whenever possible.
- b. For lymphoid tissues, disaggregated cells are cultured in suspension using appropriate supportive growth medium. Tumor cells are spontaneously dividing; however, mitogens may be used for lymphoid disorders to encourage proliferation of the desired cell type.

6.6.2.7 Experience with solid tumor culture will provide the laboratory with information regarding optimal growth conditions and harvest methods for different tumor types.

- a. It can be helpful for the laboratory to maintain a database that documents how the different tumor types have grown and which culture and harvest conditions yield abnormal clones. This database can then be searched for

optimal processing and harvesting methods for any new tumor received in the laboratory.

- b. Short culture durations are preferred to optimize the mitotic index of early dividing tumor cells and to avoid growth of normal tissues. Depending on the amount of available tissue, a combination of direct, 24-hour, and/or 48-hour cultures are most often utilized for lymphoid disorders. Short-term cultures (e.g., direct or overnight cultures) may also be used in conjunction with longer-term cultures to capture actively dividing cells from solid tumors.
- c. Frequent (daily) observation of cells in culture is needed to determine cell growth rate and optimal time to harvest. Tumor cells should be harvested as soon as possible upon adequate growth to capture early dividing tumor cells and to prevent overgrowth by chromosomally normal cells.
- d. Conditions used for cell harvest will vary among tissue types (e.g., mitotic inhibitors) used (e.g., colcemid, velban, ethidium bromide), their concentration, and exposure duration, and they should be established by each laboratory.

6.7 ANALYTICAL METHODS

6.7.1 Conventional G-banded chromosome analysis

6.7.1.1 Cell selection. Analysis of metaphase chromosomes should include cells with both good and poor chromosome morphology when attempting to identify an abnormal clone. Once identified, clonal cells with the best chromosome morphology should be analyzed, karyotyped, and imaged to provide the most accurate breakpoint assignments.

Cells that cannot be completely analyzed because of poor morphology should be scanned for obvious structurally abnormal chromosomes and abnormal chromosome counts.

Clonal abnormalities should be documented in two independent cultures, if possible, to ensure that an *in vitro* culture artifact is not mistakenly identified as a clinically significant abnormality.

6.7.1.2 Analytic standards

6.7.1.2.1 Initial diagnostic studies

- a. Analysis
 - i. Analyze 20 metaphase cells and/or a sufficient number of cells to characterize all abnormal clones and subclones.
 - ii. If all cells show a complex karyotype where each cell is different, then analyze at least 10 cells with karyotyping.
- b. Documentation
 - i. For abnormal cells:
 1. If only one abnormal clone is present: two karyotypes.
 2. If more than one related abnormal clone is present: at least one karyotype of the stemline and at least one of each sideline.

3. If unrelated clones are present: at least one karyotype for each stemline and one for each associated pertinent sideline.
- ii. For normal cells:
 1. If only normal cells are present: two karyotypes.
 2. If normal and abnormal cells are present: one karyotype of a normal cell plus karyotypes for abnormal clone(s) as described.

6.7.1.2.2 Follow-up studies may be performed to assess stage of disease at the time of diagnosis or at the time of tumor recurrence.

- a. Analysis
 - i. Analysis should include a minimum of 20 metaphase cells.
 - ii. Additional cells may be scored for a specific abnormality identified in the diagnostic sample.
 - iii. In addition to looking for the known clonal aberration(s) from the diagnostic study, analysis of a sample after therapy should be performed with awareness of the possibility of new aberrations signifying clonal evolution and/or a new clonal process (i.e., therapy-related malignancy).
 - iv. FISH analysis may be considered in lieu of conventional chromosomal analysis for diagnoses characterized by an abnormality for which FISH testing is available.
- b. Documentation
 - i. If both normal and abnormal cells or if only abnormal cells are present:
 1. One or two karyotypes from each abnormal clone with a minimum of two karyotypes.
 2. One karyotype of a normal cell, if a normal karyotype was not documented in a previous study.
 3. If only normal cells are present: two karyotypes.

6.7.2 FISH analysis

6.7.2.1 FISH analysis may be used for primary, supplementary, or follow-up evaluation

- a. As a primary method for tumor evaluation, FISH is useful when (i) fresh tumor tissue is not available; (ii) rapid diagnostic information is needed to narrow the differential diagnosis; (iii) gene amplification or rearrangement for diagnostic or prognostic and/or therapeutic purposes is to be determined; (iv) no metaphase cells are obtained by culture of tumor material; or (v) conventional cytogenetic analysis yields a normal result.
- b. Supplemental FISH may be used as an adjunct to the initial conventional chromosomal analysis or CMA analysis to: (i) document a specific molecular event (e.g., gene rearrangement or fusion); (ii) provide a rapid result to aid in the differential diagnosis or planning of therapy; (iii) to assess gene copy number; (iv) clarify level of clonality; or (v) confirm a microarray variant.

- c. Follow-up FISH studies may be indicated to assess recurrent disease or disease progression and/or to differentiate recurrence of a tumor from a new disease process.
 - i. If initial studies failed to identify the clonal process unique to the tumor, then follow-up studies may provide another opportunity.

6.7.2.2 Characterization of interphase FISH aberrations and FISH signal patterns. Characterization of interphase FISH aberrations and the FISH signal patterns in diagnostic samples is useful for future monitoring of disease. Gene fusions may confirm a specific tumor diagnosis. If a particular patient's tumor has a unique FISH signal pattern, documentation of the pattern at diagnosis can prevent misinterpretation of FISH analysis at follow-up.

6.7.2.3 Sample types. Sample types that may be used for FISH include (i) paraffin-embedded tissue sections; (ii) touch preparations (TP); (iii) cytospin preparations; (iv) cultured or direct harvest tumor cells; (v) fixed cytogenetically prepared cells; or (vi) fresh-frozen tumor tissues.

- a. Paraffin-embedded tissue³
 - i. Before scoring a paraffin-embedded FISH slide, it is crucial for a pathologist to review a hematoxylin and eosin–stained slide and delineate the region of tumor cells that should be scored because it can be difficult to differentiate normal cells from malignant cells using only DAPI counterstain. The technologist should be clear, before scoring the slide, where the malignant cells of interest are located on the slide.
 - ii. Formalin-fixed, paraffin-embedded tissue is acceptable for FISH analysis. Tissues preserved in B5 fixative or decalcified are not suitable for FISH.
 - iii. Tumor sections cut 3 to 4 μ m thick and mounted on positively charged organosilane-coated (silanized) slides work well. The cytogenetics laboratory should request several unstained sections and one hematoxylin and eosin–stained sequentially cut section from the submitting laboratory.
- b. Touch preparations
 - i. A pathologist should make the TP or should be involved in selecting the tissue for TPs.
 - ii. TPs are helpful when tissue architecture is not crucial.
 - iii. TPs should be made by lightly touching the piece of tumor to a glass slide without smearing, followed by air drying.
- c. Cytospin preparations
 - i. Cytospin preparations are useful for a concentration of samples with very low cellularity (e.g., cerebrospinal fluid).
- d. Fixed cytogenetically prepared cells
 - i. Such preparations have multiple uses for both interphase and metaphase FISH evaluation including confirmation and clarification of suspected

chromosome aberrations or characterization of an apparently abnormal clone. Metaphase cell evaluation may help clarify specific chromosome rearrangements.

- e. Fresh-frozen tumor tissues
 - i. Such tissues may be useful in sequential analysis of recurring tumors or in evaluation of archived samples.

6.7.2.4 Documentation. Analysis and documentation of FISH results should be in accordance with Section E9 of these Standards and Guidelines for Clinical Genetics Laboratories.⁴

6.7.3 CMA analysis

6.7.3.1 CMA can provide valuable information to supplement that of chromosomal and FISH analyses. Isolated tumor DNA hybridized to whole-genome copy number and/or single-nucleotide polymorphism microarrays allows detection of loss, gain, and amplification of regions of DNA, which may not otherwise be detected. Single-nucleotide polymorphism probes allow detection of large regions of loss of heterozygosity, which may harbor tumor-suppressor genes.⁵

6.7.3.2 Sample types that may be used for CMA analysis include (i) fresh tumor tissue; (ii) paraffin-embedded tumor tissue; (iii) frozen tumor; and (iv) cultured cells, chromosomally characterized when possible.

- a. Fresh tumor tissue
 - i. If the tumor is homogeneous, fresh tumor is the optimal sample for CMA and can be procured at the time of sample processing for chromosomal analysis. A small piece of identified tumor should be transferred to the microarray laboratory as soon as possible for DNA isolation. For heterogeneous tumors with areas of necrosis, normal tissue, or prominent stroma, DNA isolation from histologically characterized formalin-fixed paraffin-embedded material may be needed to ensure that isolated DNA is from the tumor.
- b. Paraffin-embedded tumor
 - i. A pathologist should review the hematoxylin and eosin-stained section of the tumor to identify an area of concentrated tumor for DNA isolation.
- c. Fresh-frozen tumor
 - i. Frozen stored tumor should provide high-quality DNA for CMA. A pathologist's review of the original H&E-stained slides can assure the frozen sample contains adequate tumor.
- d. Cultured tumor cells
 - i. Tumor cells that have been placed into culture may be used for DNA isolation and CMA as long as they remain viable. An early decision to use cells for CMA is best to minimize growth of normal tissue components.
 - ii. DNA from cultured and harvested tumor cells that have been chromosomally characterized as abnormal may be used for CMA.

ACMG STANDARDS AND GUIDELINES

6.7.3.3 Documentation: analysis and documentation of CMA studies should be in accordance with Section E11 of these Standards and Guidelines for Clinical Genetics Laboratories.⁵

6.8 TURNAROUND TIME AND REPORTING

6.8.1 Turnaround time

6.8.1.1 TAT should be appropriate for clinical utility. The cytogenetics laboratory may want to have a written policy describing how tumor cases are prioritized (with respect to each other and with respect to other sample types) such that the genetic information provided can be used for patient management.

6.8.1.2 TAT guidance:

- a. Because of the multiplicity of tumor types and the different tumor growth characteristics in culture, TATs will vary. However, the final report for each tumor should be available as soon as possible given such factors. Final results should be available within 28 calendar days.
- b. Tumor FISH analysis results should be available within 1 to 4 days for most tumors and within 7 days for paraffin-embedded tumors.
- c. Preliminary verbal reports may be appropriate for some case studies. If preliminary results are communicated, then the date of preliminary report should be documented in the final report. The content of the preliminary report should be documented if it differs significantly from that of the final report.

6.8.2 Reporting

6.8.2.1 The most recent edition of the International System for Human Cytogenetic Nomenclature should be used to report the chromosomal, FISH, CMA, and sequencing results.⁶

6.8.2.2 Cells analyzed (both normal and abnormal) should be documented in the final report.

6.8.2.3 If an aberration is suspected to be constitutional, analysis of a phytohemagglutinin (PHA)-stimulated blood sample during remission is recommended to clarify the constitutional versus clonal nature of the aberration so genetic counseling may be recommended as appropriate.

6.8.2.4 The final report(s) for tumor samples should contain the following information:

1. Patient identification using two different identifiers
2. Patient medical record number and/or laboratory identification number
3. Name of referring physician
4. Sample information (type, dates of collection and receipt, date of report)
5. Reason for referral or suspected diagnosis
6. International System for Human Cytogenetic Nomenclature of all studies performed
7. Narrative description of the aberrations observed. The report should associate results if more than one study was performed on the same tissue. The interpretation should correlate the genetic testing results with the histopathology report and patient-specific clinical information.

Discussion can include the clinical significance of the results for the diagnosis, prognosis, and/or therapeutic management of the patient with reference to current literature.

8. Literature references should be included to support the interpretation and to provide helpful information for the health-care provider.

SUPPLEMENTARY MATERIAL

Supplementary material is linked to the online version of the paper at <http://www.nature.com/gim>

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DISCLOSURE

All of the authors direct clinical cytogenetics laboratories that run the tests discussed in the current standards and guidelines on a fee-for-service basis.

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Supplemental Table 1. Central Nervous system tumors with diagnostic or clinically significant chromosome aberrations

Tumor	Chromosome Aberrations	Genes Involved	Significance	References (PMID)
PEDIATRIC TUMORS				
• GLIAL				
- Pilocytic astrocytoma grade I	Most are normal; Loss 19p most common; Gain: 5, 6, 7, 8, 9, 11, 12, 15, 17, 19, 20, 22; Loss: 9q, 22q	<i>KIAA1549/BRAF</i> dup <i>BRAF</i> 7q34, amp <i>HIPK2</i> 7q34	<i>BRAF</i> dup prognosis variable; More common in cerebellum than supratentorial; Often with <i>NF1</i> , benign, non-aggressive	17086101 18716556 25664944 26378811 19016743
- Diffuse astrocytoma grade II	Rearrangement: 2p, 7q Gain: 7q, 8q Loss: 19p	<i>MYBL1</i>	Germline mutations of <i>TP53</i>	15269292 25461780 25664944 26061751 23633565
- Anaplastic astrocytoma grade III	Gain: 1q, 5q, 7q; Loss: 6q, 9p, 10q, 12q, 13q, 17p, 22q; Mutation: <i>TP53</i>	<i>FGFR1</i> <i>CDKN2A/B</i> <i>SMARCB1</i>	Gain of 1q may correlate with worse prognosis	11290570 25461780 25231549 25727226
- Glioblastoma	Gain: 1p, 1q, 2q, 3q, 7p, 16p, 17q, 21q Loss: 6q, 8q, 10q, 11q, 13q, 16q, 17q, 22q	<i>EGFR</i> <i>CDKN2A/B</i> <i>PTEN, IDH1, IDH2</i>	Amplification of genes worse outcome; <i>IDH1, IDH2</i> mutations longer survival; H3 mutations poor prognosis; Gain 3q, changes in 7, 10, 9p, 13q, 19 associated with glioblastoma progression	22064882 11290570 25461780 25727226 25752754 25231549 25754088 26328271
- Diffuse intrinsic pontine glioma	Gain: 1q, 7p, 7q Loss: 10q	amp <i>MYCN, MDM4, PDGFRA, EGFR, IRS2</i> <i>CDKN2A, PTEN</i>	Poor prognosis	22064882 23293772 24705252
• MENINGIOMA	Loss: 22q most common Loss: 1p, 14 as progresses, then loss of 4p, 6q, 7p, 10q, 11p, 18q, other whole arm loss	<i>NF2</i> mutations Loss <i>CDKN2A/B</i>	Loss 1p and other whole arm loss seen with progression / higher grade, additional losses as progresses further	20015288 23528542 21988727
• EPENDYMOMA	Rearrangement: 11q13.1 Gain: 1q, 7, 9	amp <i>ERBB2</i> Loss or	Gain 1q, homozygous loss	15269292 20516456

	Loss: 6q, 9p, 10, 11q, 13q, 17p, 19q	mutation <i>NF2</i> , <i>TP53</i> , <i>MEN1</i>	<i>CDKN2A</i> poor survival; Gain 9, 15q, 18, loss 6q favorable survival	24553141 24939246 20425037 21840481
- Spinal	Loss: 22q	homozygous loss <i>NF2</i> Loss <i>MEN1</i>	More common in adults	23528542
- Intracranial	Rearrangement: 2p Gain: 1q Loss: 6q23, 22q		Loss 6q have longer survival; Gain 1q poor survival, more common in pediatrics	24939246 20516456
• MEDULLOBLASTOMA	amp <i>MYCN</i> , <i>MYC</i> i(17)(q10) Loss: 10q	amp <i>MYCN</i> , <i>MYC</i> ; <i>BRCA2</i> , <i>ERBB2</i> , <i>SUFU</i> , <i>ERRB4</i> , <i>PTCH</i> , <i>APC</i> mutations	amp <i>MYCN</i> , <i>MYC</i> worse outcome	15269292 20425037 22358457 24264598 20823417
- WNT pathway	Loss: 6, 6q	<i>CTNNB1</i> , <i>AXIN1</i> , <i>APC</i>	Very good prognosis, more common in children	22134537 19255330 24493713 22358457
- SHH pathway	amp <i>GLI2</i> , <i>MYCN</i> Gain: 3q Loss: 9q, 10q	<i>GLI2</i> , <i>MYCN</i> <i>PTCH1</i> , <i>SMO</i> , <i>SUFU</i> ,	Good in infants, intermediate in children and adults	22134537 26195713 24651015 12068298 24077351
- Group 3	amp <i>MYC</i> Gain: 1q, 7, i(17)(q10), 18q Loss: 5q, 8, 10q, 11p, 16q	amp <i>MYC</i>	Poor prognosis, not seen in adults	22134537 19255330 22832581 25043047
- Group 4	amp <i>CDK6</i> , <i>MYCN</i> Gain: 7, 17q, i(17q), 18q, Loss: X, 8, 11p	amp <i>CDK4</i> , <i>MYCN</i>	Intermediate prognosis, mostly in children	22134537 19255330 22832581 25043047
• CHOROID PLEXUS				
- Carcinoma (CPC)	Gain: 1, 4, 7, 12p, 12q, 20p, 20q Loss: 3q22, 5p, 5q, 6p21, 18p, 18q, 22q	<i>PDGFR</i> <i>SMARCB1</i> , <i>TP53</i>	>36 mo of age more gains, <36 mo of age more losses, Loss 12q shorter survival; Mutation <i>TP53</i> more aggressive; Gain 9 and loss 10 associated with	24478045 23172371 11891207 9242217

				prolonged Survival
- Papilloma (CPP)	Gain: 5p, 5q, 6q, 7p, 7q, 8q, 9p, 12, 14, 20 Loss: 10q	<i>PDGFR, TWIST1, TP53, NOTCH2, NOTCH3</i>		23172371 11891207 12237235 24478045 9242217 25575132
- Supratentorial primitive neuroectodermal (sPNET)	amp <i>PDGFRA</i> , <i>MYB</i> , <i>KIT</i> Gain: 1q, 9q, 15, 18 Loss: 9, 13q, 19q Homozygous loss: <i>CDKN2A/B</i>	amp <i>PDGFRA, KIT, MYB</i> ; Mutation or loss <i>TP53, PTEN</i> <i>CDKN2A/B</i>	del 9p21.3 correlates with metastasis	20425037
- Atypical teratoid/rhabdoid (AT/RT)	Loss: 22q	<i>SMARCB1</i>	Distinguish from other tumors	23074045
ADULT TUMORS				
• GLIAL				
- Grade I	Gain: 7, 19, 20 Loss: 10, 22, X or Y			15269292 26061751
- Diffuse astrocytoma, Grade II	Loss: 17p (<i>TP53</i>), 17q (<i>NF1</i>), 6q, 13q, 22q	<i>TP53, ATRX IDH1, IDH2, RB1</i>	Survival of ~7 years	15269292 25664944 26061751
- Anaplastic, Grade III	Gain: 1q, 7p, 7q, 8p Loss: 1p, 6q, 9p, 10p, 10q, 13q, 14, 17p, 19q, 22	amp <i>EGFR, MDM2</i> ; <i>CDKN2A/B, PTEN</i> , <i>TP53, RB1</i> , <i>IDH1, IDH2</i> ,	Survival of ~4 years	15269292 11290570 26061751
- Glioblastoma, Grade IV	amp <i>PIK3C2B, MDM4</i> , <i>EGFR</i> , <i>MET, MYC, CDK4, GKI1</i> , <i>MDM2</i> Rearrangement: 1, 6, 7, 9, 11, 13, 16, 19 Gain: 4q, 7p, 7q, 19, 20q Loss: 1p, 6q, 9p 10p, 10q, 13q, 17p, 22q Homozygous loss <i>TP73</i> , <i>LRRC47, DFFB</i> , <i>CDKN2A/B, CACNA1B</i>	amp <i>MDM2, CDK4</i> amp <i>EGFR</i> , <i>PTEN, RB1, TP53</i> <i>CDKN2A/B, TP73</i> , <i>LRRC47, DFFB</i>	Short term survival, aggressive tumor, associated with <i>PTEN</i> loss, amp <i>EGFR</i>	11290570, 19609742 25461780
• OLIGODENDROGLIAL	der(1;19)(q10;p10)	<i>FUBP1</i>	Favorable outcome with	15269292

	Rearrangement: 4, 6, 7, 11, 13, 15, 18, 22 Loss: 1p, 4p, 4q, 9p, 13q, 18, 19q Mutation <i>IDH1</i>	<i>CDKN2A/B, CIC</i> <i>IDH1, IDH2</i>	der(1;19); Malignant progression with amp <i>CDK4</i> , or homozygous loss of <i>CDKN2A/B</i> or <i>RB1</i>	17047046 24918277 25664944 26061751
• OLIGOASTROCYTIC	der(1;19)(q10;p10)	<i>IDH1, IDH2</i>	Favorable outcome with der(1;19) and/or <i>IDH1</i> , <i>IDH2</i>	22039037 25143301
• MENINGIOMA	Gain: 1q25-32 Loss: 22; Higher grade loss 1p, 6q24-qter, 9p, 10, 14q, 18q	<i>NF2, CDKN2A/B</i>	<i>NF2</i> loss or mutation homozygous loss <i>CDKN2A/B</i> with progression; Loss 6q and 14q common in recurrent tumors	20015288 23528542 25347344
• EPENDYMONA				
- Spinal	Gain 5p, 7, 12. Loss 6p, 13, 14q, 10 Mostly deletions, del22q	<i>NF2</i>	More common in adults, better survival than intracranial	24939246 23528542
- Intracranial	3 groups: 1) gain 9, 15q, 18 or loss 6 2) balanced or one abnormality 3) gain 1q, loss <i>CDKN2A/B</i>	<i>CDKN2A/B</i>	1) good prognosis 2) intermediate risk 3) poor prognosis	24939246 21840481 20516456
• CHOROID PLEXUS				
- Papilloma (CPP)	Gain 5q, 6q, 15q, 18q Loss 22q	<i>ARL4A</i>	Indolent	12237235 11891207 23172371 24478045 25575132
- Atypical (aCPP - grade II)	Gain: 7, 20, 9, 12, 8, 18, 11, 15, 19 Loss: very few	<i>ARL4A</i>	Indolent	25575132
- Carcinoma (CPC - grade III)	Loss: 3, 6, 11, 16, 17p, 22q	<i>TP53, GTPBP2</i> <i>RSPH9, VEGFA,</i> <i>RBFOX1</i>	aggressive, poor outcome, with del/mutation <i>TP53</i> worse prognosis	25575132

Supplemental Table 2. Genitourinary tumors with diagnostic or clinically significant chromosome aberrations

Tumor	Chromosomal Aberrations	Genes Involved	Significance	References (PMID)
RENAL				23161685
• Renal cell carcinoma (RCC)				
- Clear cell RCC	der(3)t(3;5)(p11p21;q11q35) Gain: 5q, 7, 12, 20 Loss: 3(3p12p14, 3p21 and 3p25), 4p, 5q, 8p, 9p(p13p22), 13q, 14q, Y	<i>VHL, PBRMI, PTH1R, IGH</i>	Loss 3/3p with gain 5q favorable prognosis; Loss 3/3p and loss 5q correlated with metastasis	19124809 15122209 12407697
- Papillary RCC	Gain: 7, 12, 16, 17, 20 Loss: 9p(p21.3), Y	<i>CDKN2A, MET</i>	Adult papillary RCC	15122209 12407697
- t(X;V)(p11.23;V) RCC	t(X;1)(p11.23;q23.1) t(X;1)(p11.23;p34.3) t(X;17)(p11.23;q25.3) t(X;17)(p11.23;q23.1) inv(X)(p11.23q13.1)	<i>PRCC/TFE3</i> <i>SFPQ/TFE3</i> <i>ASPSCR1/TFE3</i> <i>CLTC/TFE3</i> <i>NONO/TFE3</i>	More common in pediatric RCC; Balanced t(X;17) in RCC vs unbalanced t(X;17) in ASPS	15122209 12407697
- t(6;11) RCC	t(6;11)(p21.1;q13.1)	<i>TFEB/ALPHA</i>	Pediatric/young adult RCC	15644781
• Chromophobe	Loss: 1, 2, 6, 10, 13, 17, 21 (monosomies)		Distinguish from oncocytoma	15122209
• Oncocytoma	t(5;11)(q35;q13.3) t(9;11)(p23;q13.3) Gain: 7 Loss: 1(1p), 14, Y	<i>CCND1</i>	Benign; Distinguish from chromophobe; Chromosome 1 abnormality more common in bilateral tumors	15122209 12407697
• Wilms tumor (Nephroblastoma)	der(16)t(1;16)(q10;p10) Gain: 1q,6, 7, 8, 12, 13, 18 Loss: 1p, 7p, 11p13, 16q, 17p, 22	<i>TP53, WT1, WTX, CTNNB1</i> mutations	Unfavorable histology; Augmented chemotherapy if loss 1p, 16q	21248786 12407697 11835232 21882282
• Clear cell sarcoma (CCSK)	t(10;17)(q22.3;p13.3)	<i>YWHAE/FAM22E</i>	t(10;17) in 12% of CCSK; t(10;17) also in endometrial stromal cell sarcoma	22294382
• Congenital mesoblasticnephrom	t(12;15)(p13.2;q25.3)	<i>ETV6/NTRK3</i>	Diagnostic	12407697 11801301

a (CMN)	Gain: 11, 17, 20			
• Rhabdoid tumor (RTK)	Loss: 11p15.5, 22 (22q11.23)	<i>SMARCB1</i>	Diagnostic; 11p loss may be secondary to 22q loss	8824720 12407697
• Mucinous tubular and spindle cell carcinoma (MTSCC)	Loss: 1, 4, 6, 8(8p), 9(9p), 13, 14, 15, 22		Favorable prognosis	12429795
• Bellini duct carcinoma (Collecting duct carcinoma)	Gain: 3 Loss: 1 (1q32), 6 (6p), 8p, 14, 15, 21q, 22	<i>FH</i>	Aggressive	12407697 15122209
• Papillary adenoma	Gain: 7, 17 Loss: Y		Distinguish from papillary RCC	12407697
PROSTATE				
- Adenocarcinoma	del(21)(q22.2q22.3) t(7;21)(p21.2;q22.3) t(17;21)(q21.31;q22.3) t(3;21)(q27.2;q22.3) t(8;21)(q24.22;q22.2) t(7;V)(p21.2;V) t(17;V)(q21.31;V) t(3;V)(q27.2;V) t(4;6)(q22;q15) Gain: 7 (7q31), 8q24 Loss: 8p21.3, 10q23.31, 13q, 17p13.1	<i>TMPRSS2/ERG</i> <i>TMPRSS2/ETV1</i> <i>TMPRSS2/ETV4</i> <i>TMPRSS2/ETV5</i> <i>NDRG1/ERG</i> <i>ETV1</i> <i>ETV4</i> <i>ETV5</i> <i>MYC, PTEN, TP53, LPL</i>	<i>ERG</i> amp <i>TMPRSS2/ERG</i> fusion+ poor OS <i>PTEN-, TP53-</i> poorest OS; Hormone independence and poor prognosis with gain 8q	23161685 18563191 18563191 17437846 12837920 19402094
BLADDER				23161685
- Urothelial cell carcinoma (Transitional cell carcinoma)	Gain: (Pseudodiploidy/pseudotetraploidy) Loss: 8p21.3, 9 (9p21.3), 11 (11p), 13q, 14q, 15q, 17p	<i>LZTS1, CDKN2A</i>	Loss of 9/9p early event; Homozygous deletion <i>CDKN2A</i> higher grade & stage; recurrence, progression; Loss 8p, 11/11p, 13q, 14q, 17p and tetraploidy late stage/invasive	16110317 11888856

- Bladder squamous cell carcinoma	Gain: 7 Loss: 3p, 8p, 9 (9p), 17p		Loss 9/9p also early event	11888856
REPRODUCTIVE				
- Endometrial stromal cell sarcomas	t(7;17)(p15.2-15.1;q11.2) t(6;7)(p21.32;p15.2-15.1) t(6;10)(p21.32;p11.22) t(6;10;10)(p21.32;q22;p11.22) t(10;17)(q22.3;p13.3)	<i>JAZF1/SUZ12JAZF1/PHF1</i> <i>EPC1/PHF1</i> <i>YWHAЕ/FAM22E</i>	Distinguish from non-EST uterine tumors; t(10;17) also common in renal clear cell sarcoma	21420714 24342291
- Endometrial carcinoma	i(1q) Gain: 1q, 2, 7, 10		More complex abnormalities seen in serous versus endometrioid carcinomas	7736425 9115961 8174089
- Uterine leiomyomata	t(6;V)(p21.31;V) or other rea(6p21.31) t(12;14)(q14.3;q23-24) del(7)(q22q23)	<i>HMGA1</i> <i>HMGA2</i>	Only 40% of uterine leiomyomata exhibit abnormal karyotypes; <i>MED12</i> mutations in ~80% of 46,XX myomas	16504804
GERM CELL (GCT)				
- Postpubertal GCTs	i(12p) Gain: 1q, 7, 8, 12p, 21, 22, X Loss: 1p, 4, 5, 11q, 13q, 18	<i>RET/NCOA4</i>	i(12p), amp(12p) distinguishes GCTs; Mediastinal GCT associated with Klinefelter syndrome	9461002 15738984
- Prepubertal GCTs	Gain: 1q, 2p, 3p, 13, 16p, 20q Loss: 1p, 4q, 6q		12p gain rare in prepubertal GCT distinguishes from adult GCT; Prepubertal GCT karyotypes generally less complex compared to adult GCTs	24577549

Supplemental Table 3. Gastrointestinal, dermal and neural crest tumors with diagnostic or clinically significant chromosome aberrations

Tumor	Chromosomal Aberrations	Genes Involved	Significance	References (PMID)
GASTROINTESTINAL				
• GIST	Loss: 1p, 14q, 15q, 13q, 22q Gain: 1q, 12q	<i>KIT, PDGFRA</i>	<i>KIT, PDGFRA</i> mutation diagnostic, response to TKIs	18623623, 18671247 16452129, 15095270 12072198, 20470368 15580284, 23942094
• LIVER				
- Hepatoblastoma	Gain: 1q, 2, 2q, 8, 20, der(4)t(1;4) Loss: 4q	Unknown genes	Distinguish from HCC, HMH	15981236, 20461752 25525853
- Hepatic mesenchymal hamartoma (HMH)	t(11;19)(q13;q13.4) t(19;V)(q13.4;V)	Unknown genes	Distinguish from hemangioma or malignant tumor	15325096
• SALIVARY GLAND				
- Pleomorphic adenoma	t(3;8)(p22.1;q12.1), t(12;V)(q14.3;V) Gain: 8	<i>CTNNB1/PLAG1, HMGA2</i>	Diagnostic; benign tumor	17693184, 15920557 18828159, 20055685 22987447
- Ca-ex-PA	<i>HMGA2, MDM2</i> amplification	<i>HMGA2, MDM2</i>	Amplification contributes to malignant transformation of PA	15920557, 22287457 22297681
- Mucoepidermoid cancer	t(11;19)(q21;p13.11) in 40-80%; Gain: 7, 8, X Loss: 6q	<i>CRTC1/MAML2</i>	Malignant; t(11;19) assoc with low / intermediate grade tumors	18486532, 16444749 23583282, 22847156
- Warthin's tumor	t(11;19)(q21;p13.11) in low percentage	<i>CRTC1/MAML2</i>	Benign; t(11;19) w/ metaplasia	18647217
DERMAL				
- DFSP and variants (GCF, Bednar, other)	t(17;22)(q22;q13.1), der(22)t(17;22) or r(22)t(17;22)	<i>COL1A1/PDGFB</i>	Diagnostic for DFSP; response to TKIs	20637435, 17124411 19890351, 12550751 21111450, 12661001 23327733
- Hidradenoma	t(11;19)(q21;p13.11), Gain: 7, 8, X Loss: 6q	<i>MAML2/CRTC1</i>	Clear cell variant	17334997, 15729701

- Cutaneous melanoma	Gain: 1q, 6p, 7, 8q, 11q, 17q, 20q Loss: 6q, 9, 9p, 10q	<i>CDKN2A, BRAF, PTEN</i>	<i>CDKN2A</i>	21732770, 21876842 25207365
- Uveal melanoma	Loss: 3 Gain: 8q	<i>GNA11, GNAQ</i>	Monosomy 3 correlates with metastatic disease	21083380, 1309305 22415057
BREAST				
- Invasive intraductal	dmin, hsr	<i>ERBB2</i> amp	Improved outcome with targeted therapy	19548375, 22417857 23539740
- Secretory Breast	t(12;15)(p13.2;q25.3)	<i>ETV6/NTRK3</i>	Favorable; distinguish from other breast lesions	22129193, 23944930
LUNG				
- NSCLC	<i>EGFR</i> high copy number or amplification, Loss: 3p Gain: 7 <i>MET</i> amplification inv(2)(p21p23.2) <i>ALK, ROS1, RET</i> rearrangements	<i>EGFR</i> <i>MET</i> <i>EML4/ALK</i>	Response to TKIs Response to TKIs	21670455, 21400669 20472851 25492085, 25055117 25806222 22311682, 22282074 25288236, 25077070 25806222
NEURAL CREST				
- Neuroblastoma	del(1p) with or without <i>MYCN</i> amplification 2p24.3 11q deletion Low <i>ALK</i> expression Gain 17q with or without <i>MYCN</i> amp del(3p) Triploidy without above aberrations	1p <i>MYCN</i> amp 11q23 band region <i>ALK</i> 17q In assoc with del(11q), lack <i>MYCN</i> amp	Unfavorable Unfavorable Unfavorable, inversely associated with <i>MYCN</i> Unfavorable Unfavorable Older age at diagnosis, unfavorable Favorable	22146831, 16306521, 19401703 15571958, 19401703 16306521, 19401703 21492432 22146831, 19171713 12538451, 15800319 19401703
amp-amplification; Ca-ex-PA-Carcinoma ex Pleomorphic Adenoma; DFSP-dermatofibrosarcoma protuberans; dmin-double minutes; GCF-giant cell fibroblastoma; GIST-gastrointestinal tumor; HCC-hepatocellular carcinoma; hsr-homogeneously stained regions; NSCLC-non-small cell lung carcinoma; TKI-tyrosine kinase inhibitor				

Supplemental Table 4. Bone and soft tissue tumors with diagnostic or clinically significant chromosome aberrations

Tumor	Chromosome Aberrations	Genes Involved	Significance	References (PMID)
BONE TUMORS				
- Aneurysmal bone cysts	t(1;17)(p34.3;p13.2) t(3;17)(q21.3;p13.2) t(9;17)(q22.31;p13.2) t(16;17)(q21;p13.2) t(17;17)(p13.2;q21.33)	<i>THRAP3/USP6</i> <i>CNBP/USP6</i> <i>OMD/USP6</i> <i>CDH11/USP6</i> <i>COL1A1/USP6</i>	Benign lesions but locally aggressive. Recurrences are common	11408073 11441369 15044915 15735689
- Chondrosarcoma	Structural abnormalities: 1, 6, 9, 12, 13, and 15 Gains and losses: 5, 7, 8, and 19		Presence of chromosome abnormalities correlates with increasing histological grade with complex aberrations mainly seen in high-grade disease 13q loss is an independent factor for metastasis, regardless of the tumor grade and size	8402563 10629543 11793445 11793371
- Enchondroma	Broad range of chromosomal abnormalities but chromosome 6 and 12 are more frequently affected		A common benign hyaline cartilaginous lesion	1458512 8402563 9452264 12606137 12742153
- Osteochondroma	Germ line losses; 8q24.11or 11p11.2	<i>EXT1</i> or <i>EXT2</i>	Most common benign bone tumor	7507706 9576285
- Osteosarcoma	Gains: 1q21, 3p26, 6p, 8q, 12p12p13, 14q24qter, 17p11p12, Xp12, and Xp11.2p21 Losses: 6q, 13q, and 17p	<i>RB1</i> and <i>TP53</i>	1q21 and 8q gains are associated with shorter survival 13q and 17p losses are poor prognostic signs	8344751 8636759 9140456 9685858 11950895
- Parosteal Osteosarcoma	12q13q15 amplification, ring chromosomes	<i>CDK4</i> , <i>MDM2</i>	Low grade malignant potential	22749040 20196171
SOFT TISSUE TUMORS				
• Adipocytic tumors				
- Lipoma	Translocations involving 12q14.3 t(3;12)(q28;q14.3) most common	<i>HMGA2</i> rearrangements <i>HMGA2/LPP</i> most common	65% of cases. Distinguish from liposarcoma	1988102 8453640 8812423 9403060

	Losses: 13q11q22, and 6p21p23 rearrangements		15-20% of lipomas without 12q14.3 rearrangements	9530339
- Chondroid lipoma	t(11;16)(q13.1;p13.12)	<i>C11orf95/MKL2</i>	Diagnostic	20607705
- Lipoblastoma	Rearrangements involving 8q12.1 Gains: 8 with or without 8q12.1 rearrangements	<i>PLAG1</i> rearrangements	Rare benign soft tissue tumor of embryonal fat	10987300 11549588
- Liposarcoma				
a) Well-differentiated liposarcoma	Ring and giant marker chromosomes usually involving 12q14q15	<i>MDM2, CDK4, and HMGA2</i> amplification	Low-grade malignancy that may recur locally but doesn't metastasize	1568170 8353809 8387391
b) Myxoid liposarcoma	t(12;16)(q13.3;p11.2)	<i>FUS/DDIT3</i>	Diagnostic	7503811 7805034 8510758
c) Pleomorphic liposarcoma	Complex karyotypic changes with no characteristic abnormalities		Highly malignant tumor	9591630
- Spindle cell lipoma/Pleomorphic lipoma	Losses: 2q21, 6q14q21, 10p, 13q, 16q22qter, and 17p		Distinguish from liposarcoma	7798294
• Fibroblastic/Myofibroblastic tumors				
- Angiofibroma	t(5;8)(p15.33;q13.3)	<i>AHRR/NCOA2</i>	Diagnostic. Benign tumor with local recurrence	22337624
- Adult fibrosarcoma	Complex karyotypes with no consistent abnormality detected			
- Infantile fibrosarcoma	t(12;15)(p13.2;q25.3) Gains: 8, 11, 17, and 20	<i>ETV6/NTRK3</i>	Diagnostic	1582636
- Inflammatory myofibroblastic tumor	t(1;2)(q21.3;p23.2) t(2;2)(p23.2;q12.3) t(2;17)(p23.2;q23.1) t(2;19)(p23.2;p13.12)	<i>TPM3/ALK</i> <i>RANBP2/ALK</i> <i>CLTC/ALK</i> <i>TPM4/ALK</i>	Rare soft tissue tumor at the edge between benign and malignant	10383129 10934142 12112524 12661011
- Low-grade fibromyxoid sarcoma	t(7;16)(q33;p11.2) in 70% of cases	<i>FUS/CREB3L2</i> associated with	Diagnostic	11106828 12960807

	Supernumerary ring chromosome in 25% of cases	both abnormalities		
- Solitary fibrous tumor	12q13 rearrangements	<i>NAB2/STAT6</i>	Diagnostic	23761323
• Smooth muscle tumor				
- Leiomyosarcoma	Complex karyotypes with no consistent abnormality detected	Involvement of <i>TP53, FANCA, RB1, PTEN, and ROR2</i>		8622088 12827608
• Skeletal muscle tumors				
- Alveolar rhabdomyosarcoma	t(2;13)(q36.1;q14.11) t(1;13)(p36.13;q14.11) Amplifications: 1p36, 2p24, 2q34qter, 12q13q15, 13q14, and 13q31	<i>PAX3/FOXO1</i> <i>PAX7/FOXO1</i>	Diagnostic translocations	8098985 8275086 11607823 12039929
- Embryonal rhabdomyosarcoma	Complex karyotypes with gains: 2, 8, and 13 Loss of heterozygosity at 11p15.5			8764111 12506174 18985676
- Spindle cell or sclerosing rhabdomyosarcoma	t(6;8)(q22.1;q13.3) t(8;11)(q13.3;p15.3)	<i>VGLL2/NCOA2</i> <i>TEAD1/NCOA2</i>	Congenital/infantile rhabdomyosarcoma	26501226 23463663
• Tumors of uncertain differentiation				
- Angiomatoid fibrous histiocytoma	t(12;16)(q13.12;p11.2) t(12;22)(q13.12;q12.2) t(2;22)(q33.3;q12.2)	<i>FUS/ATF1</i> <i>EWSR1/ATF1</i> <i>EWSR1/CREB1</i>	Diagnostic translocations	15884099 17188428 17724745 18094413
- Alveolar soft part sarcoma	der(17)t(X;17)(p11.23;q25.3)	<i>ASPSCR1/TFE3</i>	Diagnostic	1423174 11169942 11244503
- Clear cell sarcoma of the soft tissue	t(12;22)(q13.12;q12.2)	<i>EWSR1/ATF1</i>	Diagnostic	8401579 8552387
- Desmoplastic small round cell tumor	t(11;22)(p13;q12.2)	<i>EWSR1/WT1</i>	Diagnostic	1314522 8374894 8187063
- Ewing sarcoma	t(11;22)(q24.3;q12.2)	<i>EWSR1/FLI1</i>	90% of cases	3163261

	t(21;22)(q22.2;q12.2) t(7;22)(p21.2;q12.2)	<i>EWSR1/ERG</i> <i>EWSR1/ETV1</i>	Variant translocations in 5% of cases	1522903 8022439 7700648
- Undifferentiated small round cell sarcoma	t(4;19)(q35.2;q13.2) t(10;19)(q26.3;q13.2) t(X;19)(q13.1;q13.2) inv(X)(p11.4p11.22)	<i>CIC/DUX4</i> <i>CIC/DUX4L3</i> <i>CIC/FOXO4</i> <i>BCOR/CCNB3</i>	<i>EWSR1</i> negative, aggressive	25683183 25007147 24215322
- Extraskeletal myxoid chondrosarcoma	t(9;22)(q22.33;q12.2) t(9;17)(q22.33;q12) t(9;15)(q22.33;q21.3)	<i>EWSR1/NR4A3</i> <i>TAF15/NR4A3</i> <i>TCF12/NR4A3</i>	Diagnostic translocations	3967207 10602520
- Extrarenal rhabdoid tumor	Germ line deletions or translocations involving 22q11.23	<i>SMARCB1</i>	Poor prognosis	8092393 8545590 9892189 26216536
- Synovial sarcoma	t(X;18)(p11.23;q11.2) t(X;18)(p11.22;q11.2)	<i>SS18/SSX1</i> <i>SS18/SSX2</i>	Diagnostic translocations	3461881 3030536 3030537 7951320 9428816

Supplemental Table 5. Lymphomas with diagnostic or clinically significant chromosome aberrations

Tumor	Chromosomal Aberrations	Genes Involved	Significance	References (PMID)
• B-CELL				
- Burkitt lymphoma	t(8;14)(q24;q32)	<i>IGH/MYC</i>	Characteristic <i>MYC</i>	4113130
	t(2;8)(p12;q24)	<i>IGK/MYC</i>	disruption	946170
	t(8;22)(q24;q11.2)	<i>IGL/MYC</i>	Variant translocations	
	Gain: 1q21-q25, 7, 8, 12, 13q, 18 Loss: 6q, 13q, 17p		Secondary changes /Unfavorable: 13q	18923440 1869243 21207210 19895612
- Diffuse large B-cell lymphoma (DLBCL)	t(3;14)(q27;q32)	<i>IGH/BCL6</i>	Characteristic <i>BCL6</i>	8235596
	t(2;3)(p12;q27)	<i>IGK/BCL6</i>	disruption,	8506375
	t(3;22)(q27;q11.2)	<i>IGL/BCL6</i>	variant translocations	
	Gain: X, 3, 5, 7, 9, 12, 18, 1q23-q31, 1q31-q44, 3q, 6p, 7p, 7q31-q32, 8q2-2q24, 11q12-q13, 12q14-q24, 18q11q21, 22q12-qter		Unfavorable: 3, 1q Favorable: 5, 7q	11850073 15350300 10337996 12181265 21418177
	Loss: Y, 4, 6, 13, 15, 17, 1p36pter, 2p23pter, 4q32qter, 6q21q25, 8p12pter, 9p21pter, 11q23qter, 12p12p13, 14q23qter, 17p12p13, 18q21qter	<i>CDKN2A, TP53</i>	Unfavorable: 9p, 17p	18765795 20813005 17881637
	Rearrangement: 4p13, 6p22, 7p13, 8q24, 11q23, 13q14, 15q22, 17q11, 18q21	<i>MYC</i> <i>BCL2</i>	Unfavorable: <i>MYC</i> disruption <i>BCL2</i> disruption	21490439 24740248 22189900 15215171
- Follicular lymphoma	t(14;18)(q32;q21)	<i>IGH/BCL2</i>	Characteristic <i>BCL2</i>	7579360
	t(2;18)(p12;q21)	<i>IGK/BCL2</i>	disruption, Variant	2129304
	t(18;22)(q21;q11.2)	<i>IGL/BCL2</i>	translocations	
	Gain: X, 3, 5, 7, 8, 12, 18 (18q)		Unfavorable: X, 7, 12, 18, der(18)t(14;18)	10389925 8049424
	Loss: 1p36, 6q21, 6q23q26, 9p21, 10q22q24, 17p13	<i>CDKN2A, PTEN, TP53</i>	Unfavorable: 6q, 9p21, 10q22-q24, 17p13	9087572 9616165 17699855
	Rearrangement: 1p, 3q27, 6q23q26, 8q24, 11q, 12q13q15	<i>BCL6</i> <i>MYC</i>	<i>BCL6</i> disruption Unfavorable: <i>MYC</i> disruption	8167331 16075463 14736281
- Mantle cell lymphoma	t(11;14)(q13;q32)	<i>IGH/CCND1</i>	Characteristic <i>CCND1</i>	8499640

	Gain:3(3q), 12(12q)		disruption Unfavorable: 3q, 12	
	Loss: Y, 1p, 6q, 9(9p), 10q, 11q, 13q, 17p, 18	<i>CDKN2, TP53</i>	Unfavorable: 9p, 13q14, 17p	9559341 21945515
	Rearrangement: t(2;12)(p12;p13)	<i>IGK/CCND2</i>		
	t(12;14)(p13;q32)	<i>IGH/CCND2</i>		16861358
	t(6;14)(p21;q32)	<i>IGH/CCND3</i>		18391076
	8q24, 3q27	<i>MYC, BCL6</i>	Unfavorable: <i>MYC</i> disruption, complex karyotype	15138714
- B-cell chronic lymphocytic leukemia/small lymphocytic lymphoma (CLL/SLL)	Gain: 3, 12, 18, 2p24p25, 3q26q27, 8q24	<i>MYC</i>	Characteristic 12 gain Unfavorable: <i>MYC</i>	11486330
	Loss: 6q, 9p, 11q22, 13q, 14q24q32, 17p	<i>CDKN2A, ATM IGH, TP53</i>	Favorable: isolated 13q14.3 deletion	18477041 21749360
			Unfavorable: 6q, 17p, 9p	23001040
	Rearrangement: t(9;14)(p13;q32)	<i>IGH</i>		10784387
	t(11;14)(q13;q32)			23581835
	t(14;19)(q32;q13.3)			21502423
	8q24, 18q21	<i>MYC, BCL2</i>	Unfavorable: <i>MYC</i> disruption	19246886
- Splenic marginal zone lymphoma	Gain: 3q			11146574
	Loss: 6q, 7q31q32, 8p, 17p	<i>TP53</i>	Unfavorable: 7q, 8p/17p together	10329610 21115979 20479288 22816737
- Extranodal marginal zone lymphoma of mucosa-associated lymphoid tissue (MALT lymphoma)	t(11;18)(q21;q21)	<i>BIRC3/MALT1</i>		10979968
				10907943
	t(14;18)(q32;q21)	<i>IGH/MALT1</i>		12406890
	Gain:3 (3q), 9q, 18 (18q)		Unfavorable: partial or complete trisomy 18	17606442 16512826
	Loss: 6q, 9p, 17p	<i>CDKN2A,TP53</i>	Unfavorable: 9p, 17p	17525089
	Rearrangement: 1p22, 2q, 3p14.1	<i>BCL10, FOXP1</i>		20352431 9178679 10845924 15703784
- Nodal marginal zone lymphoma	Gain: 3, 7, 12, 18			16405665
	Loss: 6q, 11q	<i>ATM</i>		8547655 16156859
	Rearrangement: t(11;14)(q23;q32)	<i>IGH/DDX6</i>		22965301
	1q, 1p, complex karyotype			

- Lymphoplasmacytic lymphoma	Gain: 3, 12, 18 Loss: 6q, 7q, 13q, 17p		Unfavorable: 6q	23477936 12351413
- Primary mediastinal (thymic) large B-cell lymphoma	Gain: 2p15, 9p24, Xp11.4p21, Xq24q26	<i>REL, JAK2</i>		11241792 8608249 15572583 17728785
- ALK-positive DLBCL	Translocation: t(2;17)(p23;q23), variants	<i>ALK</i>		19521280 17509395
- B-cell, unclassifiable with features intermediate between DLBCL and Burkitt lymphoma	Rearrangement: 3q27, 8q24, 14q32, 18q21 Complex karyotypes	<i>BCL6, MYC, IGH, BCL2</i>	Unfavorable: <i>MYC</i> disruption combined with <i>BCL2</i> or <i>BCL6</i> (double hit)	23600716 25696840
- B lymphoblastic lymphoma	t(9;22)(q34;q11.2) t(4;11)(q21;q23), <i>KMT2A</i> variants t(12;21)(p13;q22) Gain: X, 4, 10, 14, 17, 21	<i>BCR/ABL1</i> <i>KMT2A/AFF1</i> <i>ETV6/RUNX1</i>	Unfavorable Unfavorable Favorable Favorable: 4, 10, 17	16304368 11071360 22580999 11392884
- B or T lineage lymphoblastic lymphoma	Rearrangement: 8p11	<i>FGFR1</i>	Unfavorable	23594707
• T-CELL				
- Anaplastic large cell, ALK-positive (ALCL) lymphoma	t(2;5)(p23;q35), variants Gain: X, 7, 9, 17p, 17q24-qter Loss: Y, 4q13-q21, 6q, 17, 11q14, 13q	<i>ALK</i>	Favorable	25533804 18385450 20660290 18275429
- Anaplastic large cell, ALK-negative (ALCL) lymphoma	Gain: 1q, 3p, 6p21, 7 Loss: 6q13p21, 13q, 15, 16pter, 16qter, 17p13			18275429 15111330
- Angioimmunoblastic T-cell lymphoma	Gain: X, 3 (3q), 5 (5q), 11q14, 19, 21, 22q Loss: 6q, 13q Rearrangement: 1p		Unfavorable: X Unfavorable: 1p31p32, Complex karyotypes	22586046 17044049 18341637 7919378 12780782 8636776
- Peripheral T-cell lymphoma, NOS	Gain: 1q, 3p, 5p, 7q22q31, 8q24qter,			18341637 7987800

	11q13, 17q, 12p13, 22q			8286748 10700871
	Loss: 4q, 5q, 6q, 9p, 10q,11p11, 12q, 13q, t(14;19)(q11;q13), TCRA/D variants t(5;9)(q33;q22)	<i>TCRA/TCRD</i>	Favorable: 5q, 10q, 12q Follicular variant	15111330 17696193 17582237 16341044
- T lymphoblastic lymphoma	t(10;11)(p13;q14)	<i>PICALM/MLLT10</i>		16826225
	t(7;14)(p14;q32)	<i>TRG,TCL1A</i>		24966976
	Loss: 9p Rearrangement: 7p14, 7q35, 14q11.2, 14q32, 11q23	<i>CDKN2A</i> <i>TCRG, TCRB, TCRA/D, IGH, KMT2A</i>		17369128
- Hepatosplenic T-cell lymphoma	Gain: 7, i(7q), 8			9264394 11807981
	Loss: X, Y			16941150
• HODGKIN				
- Classical Hodgkin lymphoma	Gain: 2p, 4p16,			10676635
	4q23q24, 9p23-p24, 12q			10190942
	Polyploid			
	Loss: 1p, 3p, 6q, 7q			21325169
	Rearrangement: 1p36, 6q15, 6q21, 7q22, 7q32, 8q24, 11q23, 12q24, 13p11, 14p11, 14q32, 15p11, 19p13			17510532
	complex karyotypes	<i>IGH</i>	Arising from follicular lymphoma	
- Nodular lymphocyte, predominant	Rearrangement: 3q27	<i>BCL6</i>		15339680,
	Similar rearrangements as in DLBCL- Complex karyotype			16049307
	Gain: Polyploid			16353293

Supplemental Table 6. Tumor nomenclature for solid tumor culture method selection

Tumors types may histologically be divided into small round cell tumors (SRCTs) and non-small round cell tumors (NSRCTs) based on cellular features. SRCTs may grow in suspension or attach to the culture dish and grow as a monolayer. NSRCTs will not grow in suspension. When the sample is received in the lab, if the histopathologic diagnosis is not yet known, it can be helpful if the pathologist can tell you if the tumor is a 'SRCT' for the purposes of initiating cultures. Some tumors may grow with either method. If sufficient sample is provided for a SRCT, initiate cultures using both methods. If a very small amount of tumor is received, a coverslip culture is best. Observation of growth will allow one to determine if cells attach or float. If cells float and form balls, a suspension microharvest can be done. Suspension direct or overnight harvest may provide material for FISH if culture growth fails.

Suspension only tumors

- Lymphoma or other lymphoproliferative disorders
- Histiocytosis
- Plasmacytoma

Suspension and monolayer - Small round cell tumors

- Ewing sarcoma or peripheral primitive neuroectodermal (pPNET)
- Medulloblastoma or central primitive neuroectodermal tumor (PNET)
- Neuroblastoma
- Osteosarcoma
- Retinoblastoma
- Rhabdomyosarcoma

Monolayer Culture - Non-small round cell tumors

Brain tumors

- Astrocytoma
- Choroid plexus tumors
- Ependymoma
- Glial tumors, glioblastoma, ganglioglioma
- Meningioma
- Oligodendroglioma

Mesenchymal tumors or sarcomas or “spindle cell” tumors

- Clear cell sarcoma
- Desmoplastic small round cell tumor
- Fibrosarcoma
- Hemangiosarcoma
- Hepatoblastoma, hepatocellular carcinoma
- Leiomyosarcoma, leiomyoma
- Liposarcoma, lipoma
- Malignant fibrous histiocytoma (MFH)
- Mesothelioma
- Synovial sarcoma
- Wilms tumor

Germ cell tumors

- Embryonal carcinoma, yolk sac tumors
- Seminoma
- Teratoma

Epithelial tumors (carcinomas)

- Breast
- Gastrointestinal
- Lung
- Prostate
- Renal cell

APPENDIX 4
ACMG technical standards and guidelines: Fluorescence in situ hybridization
(See following page)

Section E9 of the American College of Medical Genetics technical standards and guidelines: Fluorescence in situ hybridization

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Disclaimer: These standards and guidelines are designed primarily as an educational resource for clinical laboratory geneticists to help them provide quality laboratory genetic services. Adherence to these standards and guidelines does not necessarily ensure a successful medical outcome. These standards and guidelines should not be considered inclusive of all proper procedures and tests or exclusive of other procedures and tests that are reasonably directed to obtaining the same results. In determining the propriety of any specific procedure or test, the clinical laboratory geneticist should apply his or her own professional judgment to the specific clinical circumstance presented by the individual patient or specimen. It may be prudent, however, to document in the laboratory record the rationale for any significant deviation from these standards and guidelines.

Abstract: This updated Section E9 has been incorporated into and supersedes the previous Section E9 in Section E: Clinical Cytogenetics of the 2008 Edition (Revised 02/2007) American College of Medical Genetics Standards and Guidelines for Clinical Genetics Laboratories. This section deals specifically with the standards and guidelines applicable to fluorescence in situ hybridization analysis. *Genet Med* 2011; 13(7):667–675.

Key Words: fluorescence, hybridization, FISH, standards, guidelines

E9 FLUORESCENCE IN SITU HYBRIDIZATION

E9.1 General considerations

Fluorescence in situ hybridization (FISH) analyses can be performed on metaphase cells or on interphase nuclei. Metaphase studies are usually performed to gain information about chromosome structure that is not readily ascertainable by conventional banding techniques. Thus, metaphase studies are frequently considered an adjunct to conventional chromosome analysis. Common examples of metaphase analyses include detection of microdeletions, detection of cryptic rearrangements involving the ends (subtelomere regions) of chromosome arms, and characterization of structural abnormalities. Although meta-

phase FISH could be used to assess mosaicism, clinical situations for which this would be needed are rare.

Interphase FISH studies are performed to detect and, often, to quantify the presence of specific genomic targets in nondividing cells. Because mitotic cells are not required, interphase analysis makes it practical to examine large numbers of cells and cells from samples that have low (or no) mitotic index. Changes in the relative position of FISH signals in interphase nuclei can be used to detect rearrangements even though the chromosomes involved cannot be directly visualized. With careful design of the FISH probe sets and with the large number of nuclei that can be examined, FISH testing is often so sensitive as to make repeated chromosome analysis unnecessary for disease monitoring. Note, however, that FISH detects only its intended targets and may give no information about additional abnormalities that may signal disease progression or secondary disease. Examples of interphase FISH analyses include detection of aneuploidy in uncultured amniocytes and detection/quantification of abnormalities associated with neoplastic processes in hematological and solid tumor specimens.

It is recognized that technology and probe development may proceed at such a rapid pace that the standards and guidelines may not specifically address all situations. It is the laboratory director's responsibility to ensure quality assurance and proper pre- and postanalytical practices that are consistent with the general guidelines presented later.

These guidelines are not intended to address interphase FISH used in preimplantation genetics.

E9.2 Regulatory requirements

E9.2.1 Test ordering

As with other high-complexity tests, FISH tests may be ordered only by physicians and by other persons authorized by applicable state law.

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E9.2.2 Regulatory classification of FISH probes

With respect to the US Food and Drug Administration (FDA) regulation, FISH probes generally fall into one of four categories:

- Probes/kits whose analytical performance and clinical utility have been approved by the FDA (for in vitro diagnostics).
- Stand-alone probes manufactured according to good manufacturing practices and regulated for clinical use by the FDA as “analyte-specific reagents” (ASRs). FDA regulations prohibit manufacturers from making claims regarding the analytical performance or clinical utility of ASRs.
- Probes labeled for “research use only” (RUO) or for “investigational use only” (IUO) are subject to FDA approval but have not been approved by the FDA for clinical use. Laboratories may consider whether such probes could be used under the practice of medicine exemption or an investigational device exemption. When reporting results of tests that use RUOs or IUOs, the laboratory must disclose the FDA status of these reagents.
- Probes developed and used exclusively in-house, and not sold to other laboratories, are not actively regulated by the FDA at the present time. However, because they may be regulated in the future, the laboratory director should be aware of all applicable federal oversight requirements. A laboratory making its own probes should meet the standards set forth under Section G (Clinical Molecular Genetics).

Clinical laboratories should establish the performance characteristics for each test that uses such probes (42 CFR §493.1213). FDA regulations require the inclusion of a disclaimer on all reports for tests using probes that have not received FDA approval, 21 CFR §809.30(e).

Probes that have been approved by the FDA must be used exactly according to the manufacturer’s instructions. Because the performance characteristics of the probe/kit have been approved by the FDA, the laboratory need only ensure that the probe/kit is operating within the performance specifications stated in the product insert. Any changes to the procedure or substitution of reagents included in the FDA approved kit invalidate the approved status and make the laboratory responsible for establishing the performance characteristics of the test.

E9.2.3 Regulation of genetic testing laboratories

E9.2.3.1. Center for Medicare and Medicaid Services (formerly called Health Care Financing Administration), through CLIA ‘88, regulates all clinical laboratories and their practices. Thus, all laboratories providing FISH testing for clinical purposes are subject to Center for Medicare and Medicaid Services regulations and subject to inspection by Center for Medicare and Medicaid Services or other organization with “deemed” status.

E9.2.3.2. Many laboratories are also subject to regulation by state/local agencies and/or agencies representing the states from which their clinical samples may originate.

E9.2.3.3. Although the FDA has recently claimed responsibility for regulating laboratory developed tests, how this will impact FISH testing is, as yet, not clear.

E9.3 Development/validation of FISH tests

In the present context, a “test” is defined by the specific use of a probe or concurrent use of a set of probes, rather than by the generic “FISH” technology. Documentation of test validation is required under CLIA ‘88 for any test placed into clinical service after September 1994. In general, validation requirements for a FISH test will depend on its intended use.

Questions that should be considered in test development/validation include the following:

- Is the test intended to detect a condition that should be present in every cell (qualitative testing) or is it intended to detect a condition that may be present in only some cells (quantitative testing)?
- Is the test intended to detect the presence/absence of the DNA sequence complementary to the probe’s sequence or is it intended to detect a change in the relative position of targeted sequences (break-apart and fusion probe sets)?

Tests that fall into the latter category will also have the potential to yield information relating to the presence/absence of targeted sequences.

Because the effectiveness of a FISH test can vary with the type of tissue examined, the laboratory director should consider whether separate validations for each tissue type are warranted. Separate validations are always required if the test will be used for conventional cytogenetic preparations and preparations from paraffin-embedded tissues.

E9.3.1 Familiarization procedures

Factors such as reagent (including probe) concentrations and the temperature and timing of denaturation, hybridization, and slide washing contribute to the intensity of the probe signal and to the intensity of nonspecific fluorescence. Establishing the optimum conditions is an empirical process and is the first step in test development and validation.

For some FISH tests, there may be a limited number of alternative signal patterns, all of which can be anticipated before test development. For others and, in particular, for tests intended to detect abnormalities associated with neoplasia, there may be a large number of alternative signal patterns. In the latter situation, it may be helpful to identify alternative, unanticipated, signal patterns with a pilot study involving a small cohort of samples before beginning the validation process. If behavior of a new probe set is somewhat different from others of the same design (e.g., dual fusion and break apart), the pilot study might also help identify adjustments that need to be made to scoring criteria.

Other than for probes sold as FDA-approved reagents, there is no requirement for a manufacturer to demonstrate that the probe/probe set actually detects the abnormality of interest. For this reason, the laboratory should evaluate a known abnormal sample as part of its test development process. If this is not possible, the laboratory may wish (in some states, may be required) to include a disclaimer in the test report that acknowledges the fact that the test’s ability to detect the abnormality has not been confirmed.

E9.3.2 Probe localization

There are three methods that may be used to confirm that probes detect their intended targets. For any FISH probe, hybridization with concurrent 4’,6-diamidino-2-phenylindole banding or sequential G-/R- or Q-banding can be used to confirm that the probe’s signal is located over the intended chromosomal region. For break-apart and fusion probe sets, a sample known to contain the abnormality of interest could also be used. The latter approach has the advantage of also confirming the probe set’s ability to detect the abnormality and the advantage of confirming localization at the molecular level rather than the chromosomal region level.

Score a minimum of five metaphase cells to verify that each probe used in the test hybridizes to the appropriate chromosome target(s) and to no other chromosomes. Any source of meta-

phase cells may be used, but it is advisable to use cells prepared in a manner that, as closely as possible, mirrors the way cells will be prepared for clinical testing. To exclude cross-hybridization with loci on the Y chromosome, cells used for probe localization should be from male subjects whenever possible.

Use of a cell line containing the region of interest as a uniquely identifiable metaphase target (e.g., structural rearrangements and trisomy) is also an acceptable means for confirming correct localization of the probe as long as the cell line contains at least one copy of each chromosome (including the Y).

In addition to confirming that the probe targets the expected chromosome region, the localization process should also confirm that the probe mix is not contaminated with another probe and that the probe does not hybridize to other targets. Probes with significant cross-hybridization to other targets should not be used.

E9.3.3 Probe sensitivity and specificity

Probe sensitivity and specificity should be established by analysis of the hybridization of the probe to at least 40 chromosomes targeted by the probe. For autosomal targets, this will usually require scoring 20 metaphase cells. For targets located on sex chromosomes, this will usually require scoring 40 metaphase cells. If, as is often the case for many commercially available probes, the probe has perfect sensitivity and specificity (see later), no more than 40 targets need to be evaluated. If the sensitivity or the specificity is <100%, either the hybridization and evaluation should be repeated or the total number of targets evaluated should be increased to 100.

Cells from at least five chromosomally characterized males should be examined. To conserve probe, the patients may be pooled, but the laboratory should be aware that pooling may lead to overrepresentation of one individual's cells in this assessment.

E9.3.3.1. Probe sensitivity is the percentage of scorable metaphase chromosomes with the expected probe signal. A probe with perfect (100%) sensitivity will produce a detectable signal over the expected region of every target chromosome examined. A sensitivity of at least 95% is recommended for all probes used in clinical testing.

Assessment of the sensitivity for probes targeting repeated sequences is complicated by normal population variation in the size of the target. In rare individuals, the target may be difficult, or impossible, to detect. If such targets are used for clinical testing, recognition of this variation and the limitation it poses for interpretation of results should be documented during probe validation. The laboratory director should be aware of any probe limitations when interpreting results.

E9.3.3.2. Probe specificity is the percentage of all scored signals that occur at the expected location. A probe with perfect (100%) specificity will never produce signal over any chromosomal region other than the expected region on the target chromosome. Specificity is calculated by dividing the number of times the signal is seen at the correct chromosome location by the total number of signals seen over all chromosome locations. For clinical testing of metaphase cells, at least 98% of the signals should be located exclusively over the targeted region.

Targets that are comprised of repeated sequences may be especially prone to cross-hybridization. Adjustments to probe concentration and/or stringency of the hybridization may be required to achieve the desired specificity.

For testing of metaphase cells, the probe is sufficiently validated for use in the same sample type if its sensitivity and specificity are as high as recommended. The probe's sensitivity

and specificity are effectively equivalent to the test's analytical sensitivity and specificity (see later), and these values can be used to estimate the likelihood that a mixture of signal patterns is due to mosaicism.

For testing of interphase nuclei (e.g., detection of aneuploidy in uncultured amniocytes or detecting acquired changes in neoplasia), development of reporting criteria requires further evaluation, as follows.

E9.3.4 Analytical sensitivity and specificity

Although probe sensitivity and specificity are measures of how well a FISH probe detects a specific chromosomal target, analytical sensitivity and specificity are measures of how effectively a test based on one or more probes detects a particular condition. If the condition is the presence of a FISH signal at the targeted location in a metaphase chromosome, probe sensitivity/specificity is equivalent to analytical sensitivity/specificity. If the condition is aneuploidy, deletion/duplication or change in relative position of loci in interphase nuclei, factors other than the probe's sensitivity/specificity will also affect the test's ability to detect the condition of interest. For example, if a test based on a single probe is used to detect deletion of a locus, the test's effectiveness will be a function of the probe's sensitivity/specificity, but it will also be a function of signal size and nucleus size. Larger signals and smaller nuclei will increase the chance that two separate signals will appear to be a single signal. Analytical sensitivity/specificity may also be a function of the probe design and FISH strategy. Single-fusion translocation probe sets have relatively low specificity because coincidental juxtaposition of signals can mimic the abnormal gene fusion condition. An extra signal or a dual fusion strategy has greater specificity because there are few biological or technical conditions that can mimic the abnormal condition.

Analytical sensitivity is a measure of a test's ability to detect the analyte (condition) of interest. Analytical specificity is a measure of a test's ability to detect only the analyte of interest. Neither analytical sensitivity nor analytical specificity can be directly measured for most FISH applications because there is usually not a more accurate method for quantifying the presence/absence of the analyte. However, in FISH, the measurement of concern is usually the limit of detection, a term that is used interchangeably with analytical sensitivity by some authors.¹ The most practical method for establishing a FISH test's limit of detection is to calculate the upper limit of the abnormal signal pattern in normal cells. This upper limit constitutes the "normal cut-off value."

E9.3.5 Calculation of normal cut-off values

Three statistical methods have been used to calculate the upper limit of the confidence interval for abnormal FISH signal patterns. Unfortunately, none of the three is without drawbacks. Most widely used are the confidence interval around the mean and the inverse beta function. Less frequently, maximum likelihood has been used to calculate cut-off values. Although the latter may be most appropriate due to the fact that it makes no assumptions about the distribution of the data, the calculation itself is so complex as to make this approach unsuitable for most assays. Mean $\pm$ confidence interval and inverse beta functions are readily available in spreadsheet programs and, thus, are widely used despite the fact that the distribution of values in most FISH databases fits neither the normal distribution nor the binomial distribution. As currently used,² the inverse beta function may lead to conservative (high) cut-off values that yield some false-negative results and very few false-positive results. The confidence interval around the mean may lead to stringent

(low) cut-off values that yield few false-negative results at the expense of producing more false-positive results.

Because of these limitations, none of the three methods in current use is ideal for all applications. The laboratory should choose a method for calculating normal cut-off values that is compatible with its statistical analysis capabilities and with its FISH testing repertoire. When interpreting abnormal signal patterns, the laboratory should be aware of their method's inherent limitations. Regardless of the calculation used, borderline-positive and borderline-negative results should always be interpreted with great caution and in the context of other clinical and laboratory findings.

E9.3.6 Construction of the normal database

A confidence limit of at least 95% is desirable for FISH analyses. See the study by Dewald et al.³ for a discussion of the relationship between analytical sensitivity, frequency of the abnormal cell type, and the number of cells required to detect the abnormal cell type with a specified degree of confidence. In general, the evaluation of larger numbers of cells will lead to greater confidence in the ability to detect rare cell types.

For acquired abnormalities, an acceptable normal database should include at least 200 nuclei examined from at least 20 individuals who have no indication of having the condition/disease of interest. Databases that will be used for interphase analysis of presumed nonmosaic constitutional microduplications/microdeletions should be based on at least 50 nuclei from at least five individuals known not to have the abnormality of interest. Note that these databases only give information about the expectation for the abnormal signal pattern in normal cells and that an abnormal result for many nonmosaic microduplications should involve a much higher proportion of cells.

Databases that include more individuals may yield fewer false-positive results if the normal cut-off is calculated with the inverse beta method and fewer false-negative results if the confidence interval around the mean is used. The number of cells examined for database samples should reflect the number of cells that will be examined during the analysis itself. For FISH assays that have a low likelihood of yielding an abnormal signal pattern in normal cells, the assay's ability to detect low-frequency abnormal cells will improve if the number of nuclei examined during validation and analysis is larger.

Database samples should be analyzed using methods established during the familiarization step by staff members who would normally be involved in this testing. If an automated scanner is used for this testing, concurrent analysis by staff and the scanner should be performed. If the two data sets differ significantly, the automated scanner should be adjusted and the slides rescanned until the difference is insignificant.

A database and its resulting normal cut-off values are specific to the methodology and, to a lesser extent, to the personnel and equipment used in the laboratory that developed the database. Thus, a laboratory should not use a database developed by any other laboratory.

E9.3.7 Construction of an abnormal database

If the goal of testing is simply to detect the presence of abnormal cells, an abnormal database may have limited value. However, if the test will also be used to discriminate samples comprised entirely (or largely) of abnormal cells from samples with a mixture of cells, an abnormal database is also warranted. For instance, in prenatal detection of Down syndrome, one might want to discriminate nonmosaic trisomy 21 from mosaic trisomy 21 due to the fact that the phenotypic consequences of the latter are less predictable. An abnormal database based on patients shown by conventional

cytogenetics to have nonmosaic trisomy 21 would be one method for distinguishing between the two.

If an abnormal database is developed, the process used for development of the normal database should be followed except for the fact that the control samples would all be drawn from known affected individuals.

E9.3.8 Paraffin-embedded FISH analyses

For paraffin-embedded tissues, FISH may be performed either on 3–6 μm sections or on nuclei extracted from thick sections or cores from paraffin blocks. FISH performed on sections has the advantage of preserving specimen architecture, thus allowing the analysis to be focused on neoplastic tissue. However, sectioning causes nuclear truncation, resulting in possible loss of signals in some nuclei. The nuclear extraction technique yields whole nuclei, but nuclei from neoplastic cells cannot be distinguished from normal nuclei; therefore, nuclear extraction should not be used for specimens in which tissue architecture is integral to interpretation, such as *HER2 (ERBB2)* FISH in breast cancer.

Regardless of the preparation technique used, analyses performed on paraffin-embedded tissue should use their own databases. A database developed for detecting *MYC/IGH* gene rearrangements in conventionally prepared marrow should not be used for paraffin-embedded lymph nodes. Databases should be established based on tissue sections of consistent thickness, and this same thickness should be maintained for testing of all specimens. For example, a database determined using 6 μm sections should not be used for testing specimens that are cut at a thickness of 3 μm .

FISH testing of paraffin-embedded tissue using enumeration probes is generally not suitable for the detection of low-level mosaicism or minimal residual disease due to the fact that nuclear truncation and decreased hybridization efficiency will lead to relatively high normal cut-off values. However, this limitation may not apply to paraffin-embedded assays that rely on break-apart or fusion probe strategies. For paraffin-embedded FISH assays that are not used for detection of low-level mosaicism or minimal residual disease, databases may be based on fewer normal samples and on the analysis of a smaller number of cells. For example, the analysis of 50 nuclei from five normal samples each may be suitable for neoplasms or constitutional cases that are not expected to show genetic heterogeneity and in which a large percentage of the sample is expected to be composed of the cells of interest (e.g., a diagnostic sarcoma specimen) or when neoplastic cells can be distinguished from nonneoplastic cells. One hundred nuclei may be desirable for neoplasms known to exhibit genetic heterogeneity or in which neoplastic cells may be focally present against a background of nonneoplastic cells (e.g., certain lymphomas). However, scoring is best approached by scanning the entire area of hybridization for abnormal signal patterns and by correlating any abnormal FISH findings with histology.

A tissue source that mimics, as closely as possible, the tissues for which the assay is intended should be used for the database (e.g., tonsil for tests likely to involve lymph nodes).

Because metaphase cells are absent and specific chromosomes cannot be recognized in paraffin-embedded preparations, probe sensitivity and probe specificity cannot be directly assessed. Nevertheless, assessment with conventional cytogenetic preparations is recommended due to the fact that if a probe demonstrates suboptimal sensitivity and specificity on metaphase chromosome preparations, it is not likely to be acceptable for evaluation of paraffin-embedded tissue.

If the test will be used for detecting deletions, duplications, or genomic amplification, an internal control (second probe labeled in a different color) should be included in the probe mixture.

E9.3.9 Test precision

In FISH, test precision is a measure of the quantitative agreement between repeated assessments of the same sample. A test with perfect precision will find exactly the same percentage of abnormal cells in a given sample every time the test is performed.

Precision is usually not assessed for FISH tests due to the fact that inherent biological variation in samples confounds such assessment. The laboratory should be aware that FISH tests do not have perfect precision. Hence, when a test value falls just under or just over the cut-off value established for normal controls, the lack of perfect precision may contribute to a false-negative or a false-positive result. Care should be taken in reporting results near the cut-off values.

Appreciation of a test's precision can be achieved by comparing the analytical scores obtained from two different test readers. The laboratory director should have a method to measure agreement between readers and indirectly assess test precision and reproducibility. Discrepancies between two independent reads are often attributable to scoring technique, which should be controlled through training and on-going technologist competency assessment.

Note that varying culture conditions and, in particular, varying the length of the cell culture period may impact a test's precision and that these conditions should be controlled by following the laboratory's standard operating procedure.

E9.3.10 Probes included in FDA-approved kits

E9.3.10.1. Reagents sold in the form of FDA kits must be used exactly as described by the manufacturer or the approval status is invalidated. Demonstrating that a change in the recommended procedure yields no difference in probe signal intensity does not constitute revalidation of a kit. In effect, any change in the procedure results in a new test that must be validated, as appropriate, according to sections 9.3.1–9.3.9.

E9.3.10.2. If an FDA-approved kit is used for testing tissues other than those validated by the manufacturer, either the kit must be revalidated according to sections 9.3.1–9.3.9 or the test report must include a disclaimer that identifies the tissue for which the kit is approved and must note the fact that the kit has not been approved for other tissues.

E9.3.10.3. Although further validation is not needed when an FDA-approved kit is used according to the manufacturer's instructions, laboratories should confirm that the kit performs as expected by analyzing at least 10 samples whose status with respect to the test's targeted abnormality is known. At least one of these samples should have the abnormality of interest.

E9.3.11 Validation of probes used for characterization of copy number imbalances detected by microarray (array comparative genomic hybridization and single nucleotide polymorphism microarrays)

Whenever possible, characterization of array results and assessment of parent carrier status should be conducted with industry-standard FISH assays using probes already validated in the laboratory. It is recognized, however, that many such studies will require the use of novel FISH reagents prepared from the molecular constructs used in the array or from available con-

structs/clones overlapping the genomic region in question. Such reagents should be prepared as described for "home brew" probes (section E9.2.2.4) and should, at a minimum, be validated for localization and for probe sensitivity and specificity (sections E9.3.2–E9.3.3.2).

Before a FISH probe is used for copy number microarray follow-up, specific genomic coordinates of the construct should be documented and understood relative to the copy number change in question. Gross mapping of a FISH clone to a cytogenetic band is insufficient for precise molecular identification. When used following bacterial artificial chromosome-based copy number microarray, it is strongly recommended that the molecular identity of a "home brew" FISH clone be verified either by the commercial source of the clone or preferably by the laboratory reporting the results. For example, one could end sequence the clone or confirm an expected internal fragment by polymerase chain reaction.

Because oligonucleotide-based array findings are generally represented by numerous independently synthesized oligonucleotides, FISH characterization of an oligonucleotide array result generally provides independent confirmation of a probe's molecular identity.

It is generally not feasible to establish an extensive normal control database for probes used for characterization of copy number microarray findings. For nonmosaic abnormalities that can be confidently appreciated in metaphase preparations, the results of probe sensitivity/specificity assessment in normal controls are sufficient to document the normal condition (see section E9.3.3). If the abnormality in question is a duplication that can only be appreciated by interphase analysis, probe behavior in a minimum of 50 interphase cells from a representative normal control (or control pool) should be scored. This can be accomplished by adding interphase analysis to the sensitivity/specificity assessment as outlined in section E9.3.3. Very small tandem duplications (<500 kb) may not be resolvable by FISH and may require alternate methodologies (e.g., dual color FISH, fiber FISH, quantitative polymerase chain reaction, and multiplex ligation-dependent probe amplification) for assessment.

E9.4 Analytical standards

E9.4.1 General considerations

In many FISH tests, two or more targets/loci are routinely examined in a single assay. For tests that target only one locus, inclusion of a second probe is still recommended. The second probe provides an internal control for hybridization efficiency and can be used to tag the chromosome of interest or used to distinguish polysomy from polyploidy. If a probe is used for a target that might not be present in every sample (e.g., targets on the Y chromosome), another sample that is known to have the probe target should be run in parallel with the patient sample. When an internal control is not used, reverse banding on metaphase preparations should be used to confirm chromosomal location in all tests using the probe.

The laboratory should have a system for evaluating the technical quality of the slides used for FISH analyses. Factors such as disease state, tissue source, and age of the slides/fixed materials may result in nonspecific fluorescence or adversely impact the quality of the probe hybridization. Slides with poor technical quality should either not be examined or should be examined and interpreted with great caution. The laboratory should also have a written procedure for scoring that includes which cells should/should not be scored and methods for discriminating one signal from two.

The following analytical standards for testing presume that sensitivity and specificity are at least as recommended in section E9.3.3. If lower, a corresponding increase in the number of cells scored to attain comparable confidence levels is required.

Analytical criteria for FDA-approved probes supersede the general recommendations provided later.

E9.4.2 Metaphase FISH analyses

E9.4.2.1. Metaphase selection for analysis should be based on the observed hybridization of the control probe(s) and the target-specific probe to metaphase chromosome(s). Metaphases showing chromosome-bound background (signals located over nontarget sites) should not be scored.

E9.4.2.2. For nonmosaic microdeletion analyses, a minimum of 10 metaphase cells should be analyzed. If any metaphases are discordant, 10 additional metaphases should be examined. If suboptimal hybridization quality is a potential source of the discordance, the hybridization should be repeated. Assuming the probe's sensitivity and specificity meet the standards noted earlier, observation of three cells with loss of the same signal is, most likely, evidence of mosaicism.

E9.4.2.3. Because these abnormalities are often difficult to visualize in metaphase cell preparations, testing for microduplications should be based, at least in part, on the analysis of interphase nuclei (interpretation requires a reference database; see section E9.3.6). A minimum of 50 interphase nuclei should be examined.

E9.4.2.4. Concurrent testing of all chromosome subtelomere regions is usually performed in a format in which each probe mix is applied to a small region on the slide(s). Because few mitoses may be available in these regions, it is acceptable to examine five metaphase cells for each probe mix so long as abnormal findings are confirmed by the examination of at least 10 metaphase cells (may require a second, independent hybridization).

E9.4.2.5. For characterization of nonmosaic marker chromosomes or unidentified chromosome regions in derivative chromosomes, a minimum of five metaphase cells should be examined for each probe used in the characterization.

E9.4.2.6. Results of metaphase FISH analysis should be confirmed by at least two experienced individuals, one of whom may be the laboratory director.

E9.4.3 Interphase FISH analyses

E9.4.3.1. Selection of nuclei for analysis should be based on the observed hybridization of the probe(s). Nuclei that are broken, overlapped, or that have significant background "noise" should not be scored. If the assay uses more than one probe, different fluorochrome colors should be used to allow differentiation of the individual targets.

As noted in section E9.3.3.1, care should be exercised in the interpretation of results from studies based on repeated sequence probes. Although rare, individuals exist who have a low copy number of a repeat on one homolog. This could result in misleading results due to reduced hybridization and/or signal intensity. Whenever possible, concurrent examination of available metaphase cells should be performed in interphase analyses that use repeated sequence probes.

The presence of contamination by maternal cells (in prenatal cases), bacteria, or fungus can lead to false-positive or false-negative results. Routine processes to identify these contaminants are recommended, such as evaluating spun pellet for visible blood, which can indicate maternal cell contamination,

or evaluating slides for nonspecific background signals that could indicate fungal or bacterial contamination.

E9.4.3.2. For analysis of nonmosaic constitutional abnormalities (e.g., aneuploidies and microdeletions/microduplications), a minimum of 25 nuclei should be scored by each of two readers. If the scores from the two readers are discordant, the case should be read by a third qualified individual, or the test should be repeated.

If a result does not meet laboratory established reporting criteria, the study should be repeated. If no additional material is available, a third analysis (at least 50 nuclei) by a qualified individual can be performed in an attempt to account for questionable results (e.g., poor hybridization or background on a portion of the slide).

E9.4.3.3. Interphase FISH may be used as an adjunctive test to assess levels of mosaicism/chimerism in cell lines with abnormalities previously established by standard banded chromosome and/or metaphase FISH analysis. In this circumstance, at least 50 interphase nuclei should be examined.

E9.4.3.4. For analysis of acquired abnormalities, the total number of nuclei examined should reflect the number of nuclei examined in establishing the normal cut-off values (see E9.3.6). Half of the nuclei should be scored by each of two readers.

Exceptions to this requirement could be made if the abnormal cell type was extremely common in the test specimen. The laboratory director may establish conditions whereby the analysis of such specimens could be terminated before the standard number of nuclei is reached. See section E9.5.3.3.

E9.4.4 Paraffin-embedded FISH analyses

E9.4.4.1. For analysis of paraffin-embedded tissues, selection of nuclei should be based on location of cells of interest (e.g., if there are neoplastic cells and normal stroma on the same section, caution must be taken to score the appropriate cell type). Analysis of paraffin-embedded neoplastic specimens usually involves morphologic interpretation that requires participation by a pathologist. In some instances, depending on the type of specimen and amount of neoplastic tissue present, prehybridization identification (marking relevant neoplastic regions) by a pathologist may be sufficient to ensure analysis of appropriate cells. For some specimens, such as those containing a small amount of tumor admixed with abundant stroma or those in which *in situ* neoplasia needs to be distinguished from invasive cancer (e.g., breast cancer), this approach may not be sufficient and a pathologist may need to review the posthybridization slide at the microscope or captured images of the regions scored at a magnification that allows morphologic assessment. In specimens in which genetic heterogeneity could be present, such as in the setting of *HER2* amplification assessment in breast cancer, the entire area of hybridization should be evaluated.⁴ If areas containing an abnormal signal pattern are identified outside of regions previously marked by a pathologist, those areas should be reviewed by a pathologist to determine the clinical relevancy of the observation. With any paraffin-embedded FISH assay, interaction between the individuals scoring the FISH slide and a pathologist is strongly encouraged if there are any findings in question.

E9.4.4.2. Preparations from paraffin-embedded tissues tend to show more variability in hybridization quality and background fluorescence than conventional cytogenetic preparations. For this reason, care must be taken to score only areas with optimal probe hybridization. Areas with high tissue autofluorescence that could obscure signals should also be avoided. Signal scoring should involve focusing through the entire section to detect signals in different planes. Scoring of overlapping nuclei should be avoided.

Some types of probes are more problematic than others when used on paraffin-embedded tissues. For example, assessment of deletions in paraffin-embedded tissue is more difficult than assessment of gene rearrangements using break-apart or dual-fusion probe strategies. Evaluation for deletions should be performed with an appropriate control probe (e.g., use of a centromere or opposite arm probe). For tests not using an FDA-approved kit, distinguishing polyploidy from true amplification should also be evaluated in the context of an internal control probe on the same chromosome as the test probe.

E9.4.4.3. Appropriate internal control probes may not be readily available (e.g., amplification controls). In such cases, a negative (e.g., no amplification) and a positive (e.g., known amplification) control sample should be included in the analytical process.

E9.4.5 Analytical considerations for FISH following copy number microarray results

E9.4.5.1. In general, FISH used to confirm or visualize abnormal findings identified by copy number microarrays should follow the analysis guidelines established in sections E9.2.4.2 and E9.2.4.3. The following special considerations apply.

- **E9.4.5.1.1:** Whenever possible, parental FISH analyses should be performed by the same laboratory that performed the initial microarray and FISH evaluation of the proband. When this is not possible, the second laboratory should carefully review the array data to determine whether a suitable, previously validated probe is available. If a previously validated probe is not available, the laboratory should evaluate a specimen from the proband for validation and for positive control purposes. Without confirmation of the probe signal pattern in the proband, one cannot be certain that the probe used is capable of detecting the abnormality in question nor can subtle abnormalities such as small duplications be adequately interpreted in the parental samples.
- **E9.4.5.1.2:** For probes with which the laboratory has limited or no clinical experience, it is recommended that a normal control be run concurrently with patient material.
- **E9.4.5.1.3:** When a mosaic condition is suspected (e.g., copy number imbalances near the centromere or hybridization parameters suggestive of mosaicism), it is recommended that 30 metaphase cells be examined. Additionally, because the abnormality may represent a mosaic condition underrepresented in stimulated T cells, it is recommended that at least 50 interphase nuclei be examined in cases where metaphase FISH is nonconfirmatory. FISH examination of unstimulated preparations may be helpful.

E9.5 Interpretation and reporting

E9.5.1 General considerations

E9.5.1.1. For each FISH test performed, the report should, whenever possible, clearly and prominently state that the result is normal/negative or abnormal/positive. Other language such as “inconclusive,” “equivocal,” “borderline,” or “suspicious for” may be used for those situations where the result is not clearly normal or abnormal.

E9.5.1.2. In addition to information required on all clinical test reports, FISH test reports should identify the probe(s) used (either gene symbol or locus symbol), the manufacturer of each probe, and the number of cells evaluated. For FISH studies performed as a follow-up to copy number microarray testing,

the linear position of the probe construct, with corresponding genome build, should be referenced.

The report should also include a detailed description of the test results. Test results should also be described using the current International System for Human Cytogenetic Nomenclature. If multiple FISH assays are reported simultaneously, a separate nomenclature string should be used to describe the results of each.

E9.5.1.3. If a test yields normal results, images (photographic or digital) of two representative normal cells should be obtained. If the test yields abnormal results, images of at least two cells representing each of the abnormal signal patterns should be obtained. Images of normal cells are not required if there is a mixture of normal and abnormal cells.

For concurrent evaluation of all chromosome subtelomere regions, a normal result may be documented by a single image for each probe mix. If an abnormal result is obtained, a minimum of two images should be obtained to document each abnormal cell type.

E9.5.1.4. Pursuant to 21 CFR §809.30(e), the following specific disclaimer must be included in reports of all FISH testing using ASRs:

“This test was developed and its performance characteristics determined by [laboratory name] as required by CLIA ’88 regulations. It has not been cleared or approved for specific uses by the U.S. Food and Drug Administration.”

The wording of the above statement is mandatory and should not be changed. However, because the statement may cause some confusion regarding whether such tests are clinically necessary and reimbursable, laboratories may wish to add clarifying language, such as the following, after the disclaimer:

“The FDA has determined that such clearance or approval is not necessary. This test is used for clinical diagnostic purposes. It should not be regarded as investigational or for research.”

Laboratories also may wish to add language such as the following, if accurate:

“Pursuant to the requirements of CLIA ’88, this laboratory has established and verified the test’s accuracy and precision.”

E9.5.1.5. Limitations of the FISH assay should be stated in the report. For FDA-approved probes/kits, these limitations will be described in the manufacturer’s package insert. For tests based on ASRs, RUOs, IUOs, and modification of FDA-approved kits, the following limitations may merit reporting.

E9.5.1.6. If a database for interpreting mosaicism has not been developed for a particular probe (or probe set), caution should be exercised in any conclusion about the presence of mosaicism. Moreover, the test report should clearly state that the test’s sensitivity for detecting mosaicism is unknown.

E9.5.1.7. Care should be taken in the interpretation of negative results from studies based on repeated sequence probes because of rare individuals with small numbers of the repeated sequence target.

E9.5.2 Considerations for interpreting metaphase FISH tests

E9.5.2.1. Metaphase FISH analysis provides information only about the probe locus in question. It does not substitute for complete karyotypic analysis.

E9.5.2.2. Care should be taken in the interpretation of results when whole chromosome paints are used to characterize derivative chromosome regions of small size due to the fact that the painting library may not hybridize uniformly across the full length of a target chromosome.

E9.5.2.3. For most known microdeletions, there are also corresponding microduplications. Metaphase FISH analysis is suitable for detection of microdeletions, but microduplication testing should be based, at least in part, on the analysis of interphase nuclei (see E9.3.6 and E9.4.2.3 specifically). Contiguous duplications may result in FISH signals that are very close together, even in interphase.

If microdeletion testing is performed only on metaphase cells and does not include analysis of interphase nuclei, the test report should include a statement indicating that the test cannot exclude the presence of microduplications.

E9.5.2.4. When using metaphase FISH to document a microdeletion in which the missing signal is from a control probe, care should be taken in interpreting results unless the control's sensitivity and specificity were also assessed during the validation process.

E9.5.3 Considerations for interpreting interphase FISH tests

E9.5.3.1. As noted in E9.3.6, cut-off values for interphase FISH analyses are, at best, an estimate of the true upper limit for abnormal signal patterns in the normal population. **For this reason, borderline-positive and borderline-negative results should always be interpreted with great caution and in the context of other clinical and laboratory findings.** For example, bone marrow from a newly diagnosed chronic myeloid leukemia patient would not be expected to yield a borderline-positive result with *BCR/ABL1* FISH analysis. Similarly, one would not expect to have a low-level positive result for the common microduplication syndromes because the duplications are fairly large and because mosaicism is not expected.

E9.5.3.2. If interphase FISH testing is performed on rare sample types or on nonstandard cytogenetic preparations (such as destined, G-banded slides), the laboratory director should consider whether to include a disclaimer about the limitations of these materials in the report. For example, an overwhelmingly positive result with a rearrangement probe set probably needs no qualification in the report but a moderately positive result obtained with a probe used to detect deletions of the chromosome 5 long arm might.

E9.5.3.3. At the laboratory director's discretion, an abnormal interphase FISH result may be reported even though the number of nuclei is less than the standard number for the test. Testing of adequate samples may be terminated prematurely if each of the two readers finds as many, or more, abnormal nuclei as is required to exceed the normal cut-off value (if a full analysis had been performed). Similarly, samples with inadequate numbers of nuclei may be reported as abnormal if the number of abnormal nuclei among the available nuclei exceeds the number of abnormal nuclei that would have been required in a full study.

E9.5.3.4. Interphase FISH for acquired abnormalities may detect potentially abnormal signal patterns that were not anticipated during test development and validation. Such signal patterns should be interpreted with caution and considered in the context of the clinical indications for testing. Metaphase FISH may be helpful for clarifying these signal patterns.

E9.5.3.5. When using interphase FISH to detect a microdeletion or microduplication in which the probe does not target the critical gene responsible for the microdeletion/microduplication syndrome, normal results should be accompanied by a disclaimer stating the limitation of the test. Such a disclaimer may include information as given in the following example:

"The probe used, however, may give a normal result in cases that are due to very small deletions, point mutations or other genetic etiologies."

E9.5.3.6. For tests not using an FDA-approved kit, the presence/absence of gene amplification should be reported in the context of a control locus or in the context of positive and negative controls. A universal standard for what constitutes FISH evidence of gene amplification does not exist, at present, so the goal of this standard is to prevent polyploidy from being reported as gene amplification.

For some neoplasms, there are published conventions for when amplification should be reported. These are often based on clinical criteria, such as prognosis or response to therapy and, thus, may be disease specific (e.g., the cut-off ratio of >2.2 for *HER2* amplification in breast cancer is different from the cut-off ratio of >4 for amplification of *MYCN* in neuroblastoma). Whenever they are available, guidelines from consensus groups should be used for reporting gene amplification.

If dividing cells are available in the sample, a recommendation for conventional chromosome analysis (to detect homogeneously staining region, double minutes, etc) should be included in the report whenever amplification is detected.

E9.5.4 Considerations for interpreting FISH tests performed on paraffin-embedded tissues

E9.5.4.1. In situations where the fixation procedure is not known (e.g., an archived specimen or one received from an outside institution), and the hybridization fails, a note should be included in the report stating that variables such as type of fixative or age of paraffin block may negatively impact hybridization efficiency.

E9.5.4.2. If interphase FISH testing is performed on paraffin-embedded tissues prepared by another laboratory (i.e., not the same source as the samples used for the database), the possibility that the database may have limited applicability to this material should be acknowledged in the test report. This acknowledgment is not required for FDA-approved kits.

E9.5.5 Interpretive considerations for FISH used following copy number microarray

E9.5.5.1. Because it is impractical to establish normal cut-off values for all FISH tests used in copy number microarray follow-up studies, the laboratory should establish its own standard for interpreting microduplication test results. Two approaches have been used. In the first, the laboratory establishes an arbitrary cut-off (e.g., 50%) above which the results are considered abnormal and below which the result is considered uninformative. In the second, the laboratory establishes a flexible cut-off that is based on some multiple of the frequency of the abnormal pattern in a known normal sample (for instance three times the frequency). Again, the

test is interpreted as either abnormal or uninformative. Reporting the test result as uninformative acknowledges the fact that a normal finding will not always exclude very small duplications. Such duplications may be difficult to distinguish from normal and may require more extensive validation or alternative methodology for confirmation. This limitation should be acknowledged in all test reports in which the FISH analysis fails to confirm the microarray result.

E9.5.5.2. Occasionally, FISH and microarray results may be discordant. When this occurs, the following should be considered in the interpretation and resolution of the discordant findings.

The microarray or FISH data may be artifactual. The quality of the array and FISH data should be reviewed, and testing repeated, if warranted. Additionally, the molecular identity of the FISH probe should be verified, as well as the identity of the clone on the array (for bacterial artificial chromosome-based arrays). The commercial provider of the FISH construct and microarray should be notified of any suspicious manufacturing or labeling errors immediately.

The probe selected may not fully overlap the abnormality. Linear positions of the probe construct and the abnormality defined by the array should be carefully evaluated, using the same genomic build as a reference.

The abnormality in question may be a very small tandem duplication (<500 kb), yielding closely spaced signals that cannot be resolved by interphase FISH. In these cases, alternate confirmation methodologies may be required.

The abnormality identified by microarray may represent a mosaic condition underrepresented in stimulated T cells. See section E9.4.5.1.3.

E9.5.5.3. When parental samples are evaluated to assess the clinical significance of a finding in a proband, it is important to consider that finding the same abnormality by FISH in a parent and proband strongly suggests but does not prove an identical copy number state in both individuals. Laboratories may wish to add a disclaimer to their reports such as the following:

“Observation of the same abnormality by FISH in a parent and proband strongly suggests, but does not prove an identical copy number state in both individuals. The abnormality may have undergone further modification in the proband, or the parent may have undetected mosaicism for a normal cell line in a tissue not tested.”

Other factors that should be considered in assessing clinical significance are discussed more fully in the ACMG laboratory standards and guidelines for interpretation and reporting of postnatal constitutional copy number variants.⁵

E9.6 Quality assurance

E9.6.1

Probe localization, sensitivity, and specificity should be confirmed for each new lot of probe (as described in E9.3.2 and E9.3.3). Evaluation of new lots should include a written statement as to whether the lot passes or fails the quality assessment. Inclusion of a subjective assessment of signal quality is also desirable and may be useful for detecting trends.

E9.6.2

Biannual (twice per year) or continuous quality monitoring verification is required (42 CFR §493.1217) for all FISH assays.

This requirement can be met by continuous monitoring of test results. For example, important test characteristics to monitor

might include (1) correct number of signals (i.e., no contamination of probe and no degradation of probe) and (2) no excess background or other technical problems that would preclude interpretation. If continuous monitoring is used, the quality monitors should be assessed and documented at least twice per year.

Alternatively, quality monitoring may be accomplished by incorporating known normal or abnormal samples into the routine workflow of the laboratory and comparing the actual results for those samples to the expected results.

E9.6.3

Changes in equipment and changes in staff (or staff experience) may cause test results to “drift” away from values obtained during the establishment of normal/abnormal databases. The laboratory should have a method for ensuring that previously established normal range cut-offs are still appropriate or should have a plan for assessing the appropriateness of the database on at least an annual basis. One method for accomplishing the latter would be to periodically analyze known normal samples with the intent of adding to (or replacing) sample data in the test’s normal database.

E9.6.4 Proficiency testing

Laboratories must participate in proficiency testing (PT) for each FISH method they use at least twice per year. Metaphase FISH, interphase FISH performed on whole nuclei prepared with standard cytogenetic methods, interphase FISH performed on urine specimens, and interphase FISH performed on paraffin-embedded tissue each constitute a method and require their own PT process. If the laboratory does not participate in a commercially available PT program, the laboratory must have a documented alternate means for assessing proficiency.

Commercially available resources for FISH PT are somewhat limited. It is the laboratory director’s responsibility to ensure that such resources are sufficient for demonstrating proficiency with the methods used in his/her laboratory and, if they are not, developing alternate means for assessing this proficiency.

E9.6.5 Competency assessment

It is the laboratory director’s responsibility to ensure and document that technologists who perform FISH tests are appropriately trained and have demonstrated consistent ability to score cases likely to be assigned to them. At a minimum, each technologist’s competency should be assessed annually for each FISH method he/she participates in.

Although color blindness cannot be a condition for staff hiring, color blindness testing is recommended for all laboratory staff participating in the analysis, image capture, and image review for FISH testing.

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APPENDIX 5
ACMG standards and guidelines for constitutional cytogenomic microarray analysis,
including postnatal and prenatal applications: revision 2013
(See following page)

ACMG Standards and Guidelines for constitutional cytogenomic microarray analysis, including postnatal and prenatal applications: revision 2013

Sarah T. South, PhD^{1,2}, Charles Lee, PhD³, Allen N. Lamb, PhD^{1,2}, Anne W. Higgins, PhD⁴ and Hutton M. Kearney, PhD⁵; for the Working Group for the American College of Medical Genetics and Genomics (ACMG) Laboratory Quality Assurance Committee

Disclaimer: These American College of Medical Genetics and Genomics *Standards and Guidelines* are developed primarily as an educational resource for clinical laboratory geneticists to help them provide quality clinical laboratory genetic services. Adherence to these standards and guidelines is voluntary and does not necessarily assure a successful medical outcome. These *Standards and Guidelines* should not be considered inclusive of all proper procedures and tests or exclusive of other procedures and tests that are reasonably directed to obtaining the same results. In determining the propriety of any specific procedure or test, the clinical laboratory geneticist should apply his or her own professional judgment to the specific circumstances presented by the individual patient or specimen. Clinical laboratory geneticists are encouraged to document in the patient's record the rationale for the use of a particular procedure or test, whether or not it is in conformance with these *Standards and Guidelines*. They also are advised to take notice of the date any particular guideline was adopted, and to consider other relevant medical and scientific information that becomes available after that date. It also would be prudent to consider whether intellectual property interests may restrict the performance of certain tests and other procedures.

Microarray methodologies, including array comparative genomic hybridization and single-nucleotide polymorphism–detecting arrays, are accepted as an appropriate first-tier test for the evaluation of imbalances associated with intellectual disability, autism, and multiple congenital anomalies. This technology also has applicability in prenatal specimens. To assist clinical laboratories in validation of

microarray methodologies for constitutional applications, the American College of Medical Genetics and Genomics has produced the following revised professional standards and guidelines.

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Key Words: constitutional; guidelines; microarray; postnatal; prenatal; standards

GENERAL CONSIDERATIONS

Purpose of cytogenomic microarrays

Constitutional cytogenetic abnormalities include aneuploidy (extra or missing chromosomes) and structural aberrations (chromosomal gains and losses, translocations, inversions, insertions, and marker chromosomes). The cytogenomic microarray (CMA) platforms discussed in this guideline are those designed for the detection of DNA copy number gains and losses associated with unbalanced chromosomal aberrations. Regions with an absence of heterozygosity (AOH), also referred to as loss of heterozygosity, regions/runs of homozygosity, or long continuous stretches of homozygosity, may also be detected by platforms with single-nucleotide polymorphism (SNP)–detecting probes. Some regions with AOH may be indicative of uniparental isodisomy or regions of the genome identical by descent.

The utility of this technology for detection of gains and losses in patients with intellectual disabilities, autism, and/or congenital anomalies has been well documented, and CMA is now recommended as a first-tier test for these indications.^{1,2}

Advantages of CMAs

The benefits from the use of CMAs for detection of gains and losses of genomic DNA include:

1. Ability to analyze DNA from nearly any tissue, including archived tissue or tissue that cannot be cultured.
2. Detection of abnormalities that are cytogenetically cryptic by standard G-banded chromosome analysis.
3. Ability to customize the platform to concentrate probes in areas of interest.
4. Better definition and characterization of abnormalities detected by a standard chromosome study.
5. Interpretation of objective data, rather than a subjective visual assessment of band intensities.
6. Ability to detect copy neutral AOH with platforms incorporating SNP probes.
7. A ready interface of the data with genome browsers and databases.

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Limitations of CMAs

Limitations of the use of CMAs include:

1. For most platforms, the inability to detect genetic events that do not affect the relative copy number of DNA sequences, e.g., molecularly balanced chromosomal rearrangements. However, CMAs may reveal copy number changes in apparently “balanced” chromosomal rearrangements, i.e., gains or losses, at or near the chromosomal breakpoint sites.
2. Low-level mosaicism for unbalanced rearrangements and aneuploidy may not be detected by CMAs. The sensitivity of the microarray for detection of mosaicism will be influenced by the platform, sample type, copy number state, DNA quality, data quality, and size of imbalance.
3. The chromosomal mechanism of a genetic imbalance may not be elucidated.
4. Tetraploidy or other ploidy levels may not be detected or may be difficult to detect.
5. Copy number variations (CNVs) of genomic regions not represented on the platform will not be detected.
6. Current CMA technologies are not designed to detect duplications and deletions below the level of detection according to probe coverage and performance, point mutations, gene expression, and methylation anomalies that may contribute to the patient’s phenotype.
7. No microarray platform will detect all mutations associated with a given syndrome. Therefore, it must be understood that failure to detect a copy number alteration at any locus does not exclude the diagnosis of a disorder associated with that locus.

Microarray platform design and manufacture

Different types of CMA platforms are currently available for clinical testing. The probes for these platforms may use either bacterial artificial chromosome-based DNA or oligonucleotide-based DNA. The oligonucleotide-based DNA may be designed to detect only a copy number alteration of a sequence as compared with a control, or may also be able to determine a specific genotype (or allele) associated with the probe (a SNP-detecting probe). The copy number of a probe may be determined either through a directly competitive hybridization of differentially labeled patient and control DNA or a comparative hybridization of the labeled patient DNA to an *in silico* reference set. The copy number data are graphed as a $\log_2$ ratio of the probe intensities, with the expected normalized value equaling “0” (generally associated with two copies of genomic sequence), relative DNA gains having signals of greater intensity ($\log_2 > 0$), and relative DNA losses having less intensity ($\log_2 < 0$). For platforms with SNP-based probes, the copy number alteration should also correlate with the allelic information assuming sufficient coverage of the copy number alteration with SNP-detecting probes. For example, a region present in one copy should only have single SNP alleles identified in the region.

Microarray platform designs may have probes (i) targeted to specific regions of the genome for detection of imbalances known to be associated with congenital anomalies or neurocognitive impairments, (ii) distributed in a genome-wide manner with a specified distribution and spacing, or (iii) placed in both a targeted and genome-wide manner with varying distribution and spacing of probes for specific genomic regions as well as across the genome. The functional resolution of an array will be determined by both the intermarker probe spacing and the number of consecutive probes necessary to confidently identify a true CNV. The functional resolution may be different across different regions of the genome for a given platform due to probe density and may be different for a single copy number gain (two to three copies) versus a single copy number loss (two copies to one copy) of a DNA segment.

The American College of Medical Genetics and Genomics has published specific recommendations for the design and manufacture of CMA platforms.³ At a minimum, for whole-genome platforms, the design should allow for detection of both gains and losses of 400 kb or larger, genome-wide, with exceptions to this minimal size resolution as necessary due to features of genomic architecture such as segmental duplication-rich regions. It is also desirable to have enrichment of probes targeting dosage-sensitive regions or genes well associated with congenital anomalies or neurocognitive impairments.

All probe descriptions/content and annotations should be openly accessible to the performing laboratory (see also “Annotation/databases” section). Details regarding the microarray design, the synthesis verification, and all quality control (QC) steps taken to validate and assess the performance and reproducibility of the array should be documented and provided by the manufacturer.

FAMILIARIZATION WITH A NEW TECHNOLOGY FOR THE LABORATORY BEFORE VALIDATION

The laboratory with little or no experience with microarray technology should become familiar with all aspects of the new technology before beginning the validation process, regardless of the regulatory status of the array. Familiarization begins with understanding the processes, features, and capabilities of the technology selected. The laboratory should gain experience with the instrumentation, platform design, software, reagents, methodology, technological limitations, workflows, DNA quality parameters, etc., by experimental sample runs. Similarly, the laboratory should become familiar with the features of each sample type the laboratory will process, as different sample types may have unique considerations for microarray data quality and clinical applicability. The laboratory must also be familiar with the potential imbalances and rearrangements associated with the clinical indications.

The use of samples well characterized as “normal” and “abnormal” by another method is valuable during the familiarization process to gain experience in the recognition of CNVs that may represent true biological variation or a probe/platform performance issue. It is suggested that laboratories use a

combination of data from well-characterized cases processed and run on their platform(s), data from other laboratories, and/or data available from online databases to gain and broaden their experience. Data sharing should involve a spectrum of array results and data quality.

Laboratories need to be able to recognize nonperforming (or nonresponsive) probes, technically induced artifacts, and other issues affecting data quality. Laboratories should become familiar with CNVs that are benign and/or common and resources to aid in the recognition and interpretation of CNVs.³⁻⁸

VERIFICATION AND VALIDATION

Verification of a Food and Drug Administration–approved/cleared platform

At the time of the publication of these guidelines, there are no commercially available Food and Drug Administration (FDA)–approved or FDA-cleared microarrays for this application. However, laboratories are advised to keep abreast of new developments in this rapidly developing technology.

For any FDA-approved or FDA-cleared microarrays where the laboratory plans to claim the test as FDA-approved/cleared, the approved protocol and intended use (usually included in the package insert) must be followed. The laboratory must verify that it can obtain comparable performance specifications as those established by the manufacturer with regard to accuracy, precision, and reportable range of results.

At the onset of verification, pass/fail criteria for the verification protocol should be established. If the prespecified acceptance criteria are not met, and a repeat or evaluation of the reasons for the failure does not resolve the concern, the laboratory should consider whether or not the array is appropriate for clinical testing.

Accuracy testing will measure the ability of the platform and software to detect known abnormalities. The accuracy evaluation is accomplished by running a series of previously characterized abnormal cases (this may be accomplished through sharing samples with an established laboratory). A minimum of 15 cases is recommended. To the extent possible, the laboratory should use abnormal samples that represent abnormalities that the array is designed to detect. This evaluation should include both a comparison of the findings from the region(s) expected to be abnormal as well as a comparison of the rest of the genome analyzed by the platform. The laboratory must document the concordance of the expected results and any unexpected findings. Because this technology may detect true alterations not previously identified, any unexpected findings that fall within the determined reportable range (as defined in “Validation of a new platform for the laboratory” section) should be further investigated to determine whether the finding represents true biological variation. This will involve the use of an alternative technology or microarray platform for correlation of the unexpected finding.

Precision testing should measure the reproducibility of repeated tests for the same result. The precision of the platform is established by running a minimum of two abnormal

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samples, each run multiple times in separate experiments. The concordance of the repeated runs should be documented, and any alterations should be considered (variability of breakpoints, calls, and potential reasons for variation, i.e., segmental duplication-rich region) as they pertain to the reportable range, functional resolution, and potential variability around breakpoints. Some variability around breakpoints may be expected due to segmental duplications and individual probe performance. Precision testing can allow for an assessment of breakpoints and potential impact on the clinical interpretation. Breakpoint variability that does not alter the clinical interpretation would be less concerning than variability that does alter the interpretation. Samples with multiple abnormalities are preferable as they maximize the number of findings for the precision study.

Any modification to the FDA-approved use of the product (as specified in the package insert) will be considered as off-label use, and therefore the microarray must then be validated as a non-FDA-approved platform.

Validation of a non-FDA-approved platform

All platforms intended for clinical testing must be either FDA-approved/cleared and verified or must be validated by the performing laboratory. Validation is the process by which the laboratory measures the efficacy of the test in question by determining its performance characteristics when used as intended. This is necessary to demonstrate that it performs as expected and achieves the intended result. Validation is required when using laboratory-developed tests or modified FDA tests. The method and scope of the validation must be documented.

At the onset of validation, pass/fail criteria for the validation protocol should be established. If the prespecified acceptance criteria were not met, and a repeat or evaluation of the reasons for the failure does not resolve the concern, the laboratory should consider whether or not the array is appropriate for clinical testing.

The extent of work necessary for a validation can depend in part on whether the laboratory is validating a new microarray platform for the laboratory, validating a modified design of a previously validated platform, or adding additional sample types or intended uses to a previously validated platform. A new platform is defined as any new methodology or array introduced to the laboratory. A single microarray vendor may produce multiple similar platforms, but each must be validated independently. A modified design may include either minor modification to probe coverage, either through manufacturing of the array or by *in silico* probe filtering.

Validation of a new microarray platform for the laboratory

Through the validation process, the laboratory must establish the performance characteristics of the microarray platform and accompanying software. The performance characteristics that must be established include the accuracy and precision of results, the analytical sensitivity and specificity, and the reportable ranges. Validations should be documented for each array

platform used for clinical testing, regardless of whether the laboratory has prior experience with a different platform.

The reportable range of results includes criteria to identify a CNV and criteria to report a CNV. Laboratories, with consideration of the manufacturer's recommendations, should identify the parameters specific to their platform (number of consecutive probes, log₂ ratios, SNP allele ratios, QC metrics, etc.) that are necessary to conclude that a copy number call represents a true CNV. As the functional resolution is a combination of probe density and number of probes necessary to identify a true CNV, the reportable range should be at or above the functional resolution of the platform. The reportable range should be determined before the evaluation of the validation set, and data from the familiarization process should be utilized. The reportable range may exclude well-characterized benign CNVs. If the reportable range is altered for the laboratory, the validation data should be re-evaluated with the new reportable range. However, if the previously identified validation samples do not contain abnormalities that challenge the altered reportable range, additional samples should be evaluated.

The accuracy evaluation is accomplished by running a minimum of 30 previously characterized abnormal controls. To the extent possible, the laboratory should use abnormal controls that represent abnormalities that the array is designed to detect. This should include both autosomal and sex chromosome abnormalities as duplications and deletions on the sex chromosomes may behave differently in each sex. Furthermore, blinding the evaluators to the expected abnormalities has the additional benefit of validating the settings, evaluation of data, and reportable range. Samples used for validation should represent a variety of findings with various sizes of abnormalities, combinations of gains and losses, various regions of the genome, and some aberrations that challenge the technical limits of detection for reportable DNA gains and losses.

Sample exchanges with a laboratory that is proficient with a similar microarray platform can provide a good source of samples for validation. Exchange of validated data sets (e.g., array files) between laboratories is recommended for additional experience in data analysis.

This evaluation should initially include a full review of the data to identify aberrations that meet the reportable range while blinded to the expected abnormality (as would fit the clinical workflow), followed by an unblinded comparison of the findings from the region(s) expected to be abnormal, as well as an evaluation of the rest of the genome analyzed by the platform. An evaluation of the regions expected to be normal is also important in assessing the probe behavior across the genome. The laboratory must document the concordance of the expected results and any unexpected findings. Evaluation should also include breakpoint evaluation with regard to gene content and genomic architecture. The laboratory should also recognize nonresponsive probes in a region expected to show loss or gain (this may be due to either poor performance probes or underlying genomic architecture). As this technology may detect true alterations not previously identified, any unexpected

CNVs that fall within your laboratory-determined reportable range should be further investigated to determine whether the finding represents true biological variation. This may involve the use of an alternative technology or microarray platform for correlation of the unexpected finding. As both expected and unexpected findings are evaluated, careful selection of the 30 samples is important and the ability to evaluate unexpected findings in the 30 samples should be considered.

Sensitivity and specificity are determined by the number of true-positive, true-negative, false-positive, and false-negative results in a validation data set that meet reporting criteria. However, for a whole-genome assay, all true positives and true negatives are not known. Therefore, specificity and sensitivity for genome-wide array platforms cannot be calculated as traditionally defined.

Sensitivity is evaluated by comparison of expected versus observed abnormalities, and this is then extrapolated to the rest of the genome. Rather than a traditional calculation of specificity, an evaluation of the positive predictive value of the assay is desirable. Determination of the positive predictive value will involve the identification of copy number calls that fall within the laboratory's determined reportable range and a determination of the proportion of those calls that are true. To improve the specificity of the platform, if certain probes are recognized to repeatedly act as false positives, these probes should be removed from future analyses. The identification of false-positive probes may be due to technical or biological variables considering that not all regions of the genome are amenable to accurate locus-specific evaluation of copy number with this technology. If probe content is masked by the laboratory, these changes should be documented. If the changes are sufficient to alter the performance of the platform, an evaluation of the validation data with the altered probe content is required.

The precision testing should measure the closeness of repeated test results to one another. The precision of the platform is established by running a minimum of two abnormal samples, each run multiple times in separate experiments. The concordance of the repeated runs should be documented, and any alterations should be considered (variability of breakpoints, calls, and potential reasons for variation, i.e., segmental duplication-rich region) as they pertain to the reportable range, functional resolution, and potential variability around breakpoints. Some variability around breakpoints may be expected due to genomic architecture and individual probe performance. The precision testing can allow for an assessment of breakpoints and potential impact on the clinical interpretation. Breakpoint variability that does not alter the clinical interpretation would be less concerning than variability that does alter the interpretation. Samples with multiple abnormalities are preferable as they maximize the number of findings for the precision study.

Validation of a new version of a previously established platform

The definition of a new version should be limited to those situations in which a minimal number of probes are removed,

added, and/or replaced for the purpose of improved performance, and/or coverage is enhanced over a limited number of genomic regions. This would likely involve <10% of the total probe coverage, with no more than 5% probe removal. It should be recognized that these types of changes to an established platform are likely a rare event and most changes in platforms will require a full validation.

In the laboratory that is proficient with microarray technologies, a new version of a platform in use by the laboratory from the same manufacturer should be validated with a minimum of five abnormal samples.

Known abnormal samples from the previous version should be run using the new platform version for comparison to ensure that the performance meets the laboratory standards and to assess performance of probes added into higher-resolution platforms.

New content on an upgraded version should be assessed, if possible, using known abnormal sample(s) with variation in the region of the new content to determine performance.

The evaluation of this validation set of at least five samples should include data analyzed to determine whether the platform and software detected the expected abnormality. If other abnormalities are detected that meet the laboratory-reporting range, the validation should determine whether the findings represent true biological variation.

Validation of additional sample types on an established platform

It is expected that the initial validation will involve the most common sample type for the expected intended use. For example, if the intended use is postnatal evaluation, the sample type may be DNA extracted from peripheral blood. Because the quality of the DNA may vary from alternative tissue sources and this may add interference factors to the microarray analysis, use of DNA from alternative sample types requires an evaluation of the potential for interference.⁹

For a new sample type, an evaluation of the impact of the new sample type on data quality is necessary. The DNA extraction process should be part of the validation process. If there will be minimal changes to the processing or analysis, then a validation of the new sample type can involve equivalency of data quality with the new sample type. If alterations are made in the processing of the array or analysis (e.g., change of reference set), then a new validation is required. In addition, if the new sample type requires a different reportable range, then a new validation is required.

Validation of the allelic differentiation potential of SNP-detecting platforms

The detection of AOH is not in and of itself diagnostic but can identify a concern that would require additional testing such as sequence-based mutation analysis or uniparental disomy testing. However, as AOH may be reported by the laboratory, evaluation of the performance of the SNP-detecting probes to define regions of AOH should be included in the validation.

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Reports of these findings must clearly state that the finding is not diagnostic.

Given sufficient probe density, there should be a correlation between copy number state and SNP allele state.

A minimum of five samples need to contain expected copy neutral AOH in addition to CNVs. Interlaboratory comparisons of samples that contain known uniparental isodisomy or regions identical by descent are recommended. This comparison should address the data types that would be included in a report, such as approximate regions of AOH and approximate percentage of genome identical by descent. The detection and accurate size assessment of AOH by SNP-based arrays depend on the density of SNP probes. If the validation method does not address accuracy of breakpoints in AOH calls, reports should reflect this uncertainty. Inaccurate size estimation for regions of AOH could lead to unwarranted follow-up testing for uniparental isodisomy, somatic loss of heterozygosity, and/or autozygosity mapping.¹⁰

Mosaicism detection

Low-level mosaicism for unbalanced rearrangements and aneuploidy may not be detected by microarray analysis. In addition, the level of detectable mosaicism will vary by size, region of genome, copy number state, DNA quality and data quality. Therefore, it is not likely that a specific level of mosaicism can always be identified uniformly throughout the genome, and this limitation should be recognized.

Without extensive validation to determine specific levels of mosaic detection for a wide variety of CNV sizes and genomic regions, it is not recommended that this technology be used to rule out mosaicism. However, experience in mosaicism identification is desirable to maximize opportunity for detection. Methods for determining detectable levels of mosaicism include dilution studies and analysis of the sample by other quantitative methods. Fluorescence *in situ* hybridization analysis of fresh (uncultured) samples provides a reliable means to establish the level(s) of mosaicism detectable by microarray. Conventional cytogenetic analysis of metaphase cells provides information about mosaicism but may not accurately reflect levels of mosaicism. The laboratory director should determine the method used by the laboratory. More than one method is recommended.

For cells in suspension, dilution studies using samples with known CNVs may help to determine detectable levels of mosaicism. This method can provide an effective means to establish thresholds; however, it may have limitations as an artificial method. Dilution studies for SNP-detecting arrays may not be possible because they may introduce additional genotypes that complicate the analysis.

The detection of mosaicism may include information from both the log₂ ratio and the SNP allele pattern as applicable for each platform.

Be aware that microarray analysis gives a relative level of copy number across the cells within the sample but does not provide a cell-by-cell determination of copy number (e.g., trisomy in 60% vs. tetrasomy in 30% of cells).

Special considerations for validation of prenatal specimens

Experience with postnatal arrays and with common and rare CNVs is important for the processing and interpretation of array results for prenatal specimens. For validation, a distinction should be made between cultured amniocytes and chorionic villus sampling (CVS) cells and uncultured (direct) amniocytes and villi. The validation performed depends on whether the platform has been previously validated for postnatal use or is new to the laboratory and whether both cultured and uncultured cells will be used.

For cultured amniocytes and CVS cells, if prenatal array analysis is performed on an array platform new to the laboratory, the issues and process discussed in the “Validation of a new platform for the laboratory” section apply, and a minimum of 30 previously characterized cases should be processed. Due to the difficulty of obtaining abnormal prenatal specimens, this collection of 30 samples will likely include some previously characterized as normal cases. Therefore, additional experience with abnormal array findings through additional tissue types and data exchanges should occur, to ensure that a wide variety of abnormalities have been evaluated both in-house and *in silico*.

For a previously validated platform for postnatal use, the addition of prenatal specimens requires an understanding of the potential issues that these samples can present regarding data quality. The DNA extraction process should be part of the validation process. If the laboratory will perform analysis on cultured amniocytes and CVS, both sample types should be represented in the validation.

Prenatal samples (including products of conception). Healthy cultures established from amniocytes, villi, and fetal tissue yield an adequate quantity and quality of DNA and can be viewed as essentially equivalent for validation purposes. However, the laboratory should be aware of factors that can affect DNA yield and data quality including culture age, growth rate, confluency, and shipping conditions.

Because uncultured cells may yield different amounts and quality of DNA, additional validation is required to become familiar with potential differences as compared with cultured cells. Parameters to consider for uncultured amniocytes include method of DNA extraction, volume, and gestational age given that these parameters influence the amount and quality of DNA. For example, uncultured amniocytes yield less DNA than cultured cells; however, the quality of the DNA is generally higher from uncultured cells.

Because villi represent a more complicated tissue with different cell types/layers (syncytiotrophoblast, cytotrophoblast, and mesenchymal core), DNA may be extracted from all cell types, or the laboratory may eliminate or concentrate on different cell layers for DNA extraction.¹¹

Special quality assurance requirements for prenatal specimens. Back-up cultures of all prenatal samples undergoing array analysis should be established and maintained for the purposes of (i) possible array failures on direct extractions, (ii)

evaluation of possible mosaicism on an independent culture, and (iii) the need to perform metaphase chromosome or fluorescence in situ hybridization analysis to investigate CNVs.

Maternal cell contamination (MCC) analysis should be performed on all prenatal samples, unless contamination is otherwise excluded. MCC can result from direct samples of amniocytes with blood admixture, CVS samples not successfully cleaned of maternal decidua (a more frequent problem with products of conception), and cell cultures undergoing extensive subculturing resulting in expansion of maternal cells. When undetected, MCC can result in missed detection or misinterpretation of copy number changes, even in the context of a male result. Laboratories should understand that MCC can be detected by array software (i.e., SNP-based platforms) or, in the case of male fetuses, by a shift of the sex chromosome plots (mimicking mosaicism). Laboratories should also understand how the presence of MCC can affect detection of CNVs, including different types (gains and losses) and different sizes (small versus large gains and losses).

Mosaicism may be detected in prenatal samples and may represent culture artifact (pseudomosaicism), true fetal mosaicism, or, for CVS, confined placental mosaicism. Careful investigation may be required to determine the fetal genotype. For traditional chromosome analysis, algorithms have been developed to deal with confined placental mosaicism and pseudomosaicism. These algorithms will also need to be developed for microarray analysis and will depend on whether the analysis used direct or cultured cells, and if the mosaicism can be confirmed on an independent culture.

ESTABLISHING A REFERENCE DNA SET

Depending on the platform used, the reference DNA set may come from a single individual or multiple individuals and may be sex matched or mismatched, and may be used *in silico* or as a direct competitive hybridization. The laboratory should understand the benefits and limitations of each scenario. The laboratory should also consider how the data quality is affected by the source and components of the reference DNA set. For example, data quality is likely improved when the conditions used for data acquisition from the reference set closely match the experimental conditions used for the test.¹² Any changes to the reference DNA set require a verification of the quality and accuracy of results obtained with the new reference DNA set as compared with the previous reference DNA set, especially because changes to the control can result in variation of results, particularly within polymorphic regions. For arrays that use *in silico* controls, versioning should be documented.

SOFTWARE CONSIDERATIONS

The laboratory should recognize software limitations and the need for manual and visual inspection of the data for aberration and mosaicism detection because the software may not flag all relevant calls that may be identifiable by a visual inspection of the data. To verify that the method for result generation (including software calls and manual inspection) detects known

aberrations at certain mosaicism levels, the system should be challenged with different types of aberrations. During the familiarization phase, the settings should be explored and optimized for aberration detection and then established parameters should be used consistently throughout the validation process. Algorithmic parameter settings may be different for various sample types.

Changes to the software settings from those used during the validation may require a re-analysis of at least a subset of the validation data using the new settings to identify any changes to the performance characteristics of the microarray platform. Such changes may include, but are not limited to, new annotation libraries, changes to any *in silico* reference set, or any changes to the aberration-calling algorithm.

The laboratory should understand that most normalization algorithms assume a primarily diploid state, which may obscure the detection of polyploidy. In some situations, the allele pattern may assist with the detection of triploidy but may not identify tetraploidy. Both situations are likely rare in the postnatal constitutional population but may be present as mosaic findings as well as in prenatal settings.

The laboratory should document the software, parameters, and rules used in the analysis of the microarray, as well as all limitations of the analysis program.

QUALITY CONTROL

Identification

For each array, the slide identification number, sample sex, control sex, and sample-tracking control (if applicable) should be verified. Discrepancies in the documentation from the physical sample should be investigated and resolved before processing.

DNA requirements

The laboratory should establish the minimum DNA requirements to perform testing. Each laboratory should have established parameters for the determination of the sample quality and quantity and criteria for adequacy of each. If a sample does not meet these minimum requirements and is deemed suboptimal, the recommended action is to reject the specimen and request a repeat specimen.

Equipment calibration, maintenance, and QC

Equipment, instrumentation, and methodologies employed during the validation and use of microarray platforms should be calibrated, monitored for QC, and regularly maintained as appropriate. Quality metrics should be established whenever possible throughout the assay. Laboratories should ensure that documentation and safeguards are provided by the software manufacturer and that data are processed and summarized in a consistent fashion for every clinical analysis. Most analysis software provides a hierarchy of users with customizable permissions, which enable the laboratory director or supervisor to prevent modification of analysis settings so that all specimens are analyzed consistently. Any changes to data processing should be validated and documented.

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General QC metrics

Every microarray platform has defined quality metric values, e.g., adequate dye incorporation and/or amplification, fluorescence intensities, signal-to-background noise ratio, and standard deviation or standard error. Standard cutoff values and acceptable limits should be established for these metrics to ensure that the generated results are reliable and precise enough to be used for a clinical assessment. Quality metrics should be monitored for DNA labeling, hybridization efficiency, data generation and analysis, and other platform-specific parameters. The QC metrics should be incorporated into the laboratory quality assurance and quality improvement programs to monitor analytical variables.

Data quality

The quality of the data will affect the ability to detect genomic aberrations. Therefore, it is absolutely necessary for the laboratory to understand the within-array metrics provided by the analysis software and how each of these metrics reflects the quality of the data. There are a number of metrics that provide a measurement of signal to noise (i.e., artifactual random variance unrelated to genomic location) in the data, such as the difference between the log ratio values of consecutive probes and the spread of the derivative log ratio values after outlier rejection. Similar metrics of variance exist for each platform.

The laboratory should establish acceptable ranges for each QC metric chosen to represent data quality by the laboratory. These ranges are often provided by the manufacturer. However, the laboratory may want to modify these ranges on the basis of their experience with the arrays during the validation process. The laboratory should establish criteria for next steps, should the data fall outside of these established ranges.

Annotation/databases

An integral part of the data analysis is accessibility and use of private and public annotations/databases during the analysis process. Because these annotations are critical for interpretation, it is important that these tools are carefully constructed and applied by the laboratory or software manufacturer. All critical annotations should be thoroughly vetted, and the source(s) should be verified. For all reportable calls, the genomic content should be verified by an independent database source. The manufacturers should provide mechanism(s) for updates to these annotations. Documentation of resources and databases accessed for interpretation is recommended.

Verification of new lots of microarrays/reagents

Verification should ensure that new lots of microarray slides and/or reagents perform in the same manner as the previous lot. The manufacturer should supply documentation of the QC comparison between lots (e.g., oligonucleotide synthesis verification, accuracy of SNP calls or other defined control parameters). New lots of reagents (e.g., new labeling kits, consumables) should have documented equivalency between runs. This may be accomplished by documenting that the QC metrics meet certain set parameters for the new lot of reagents.

Confirmation of specific CNVs

With proper technical performance and analytical validation, it should not be necessary for the performing laboratory to further confirm a CNV called with the laboratory-validated parameters, after the validation stage. Each laboratory should establish a threshold (number of probes and/or genomic size, as well as other QC metrics) for declaring what constitutes a reportable abnormality with their assay. Features to keep in mind when assessing copy number changes are the appropriate log ratio difference between data, the presence of uniform contiguous probe behavior within and adjacent to call, sharp copy number state transitions at breakpoint boundaries, supportive SNP allele states (when applicable), and evaluation of least processed $\log_2$ ratio data (e.g., weighted versus not weighted). Any call-specific quality score provided by the software may be considered.

Given that it is desirable to maximize detection of aberrations of clinically important genes and of aberrations in mosaic form (which may not generate a robust copy number call), it is acceptable and appropriate at the discretion of the performing laboratory to evaluate calls that do not meet the laboratory-validated parameters. These calls may be flagged for review and correlated with the patient's clinical indication, but should be confirmed by an independent methodology if reported.

USE OF ALTERNATIVE TECHNOLOGIES FOR MECHANISM DETERMINATION

Determination of the mechanism leading to the detected CNV may be considered on a case-by-case basis because this may lead to better determination of recurrence risk. Some mechanisms can be identified through the combination of both the CNV and recognition of the genomic location of the altered material, or the genomic structure surrounding the alteration. Examples include both terminal and insertional translocations and ring or marker chromosomes. The appropriate alternative technology may depend on the size, type, and location of the identified CNV and the likely mechanism of formation. Therefore, use of these alternative technologies should be considered as separate testing and should use validated technologies performed and interpreted by appropriately trained personnel.

INTERPRETATION AND REPORTING

For further guidance on interpretation and reporting, refer to recently published guidelines from the American College of Medical Genetics and Genomics for interpretation and reporting of postnatal constitutional copy number variants¹³ and for reporting suspected consanguinity as an incidental finding of genomic testing.¹⁴

METHODOLOGY AND DISCLAIMERS

All reports should include a brief description of methodology, including platform specifics and reporting criteria. Disclaimers should be included as appropriate and required.

Example: testing limitations

Current microarray analysis technologies will detect only gains and losses of genomic segments. Therefore, a normal microarray result does not exclude mutations (nucleotide base-pair changes) in any gene represented on the microarray, gains and losses below the level of resolution of the platform, a balanced rearrangement, or epigenetic events. Additional testing may be appropriate for certain syndromes or conditions when the microarray analysis yields normal results.

Alternative example

This microarray platform will not detect truly balanced chromosomal rearrangements, point mutations, or imbalances of regions not represented on the microarray, and may not detect mosaicism. Failure to detect an alteration at any locus does not exclude all anomalies at that locus.

Example: disclaimer for a non-FDA-approved microarray platform

This test was developed and its performance characteristics determined by (your laboratory name here) as required by Clinical Laboratory Improvement Act (CLIA) 1988 regulations. It has not been cleared or approved for specific uses by the US Food and Drug Administration. Pursuant to the 1988 CLIA requirements, this laboratory has established and verified the test's accuracy and precision.

PROFICIENCY TESTING

The laboratory should participate in an external proficiency testing program through an appropriate deemed organization (e.g., the College of American Pathologists). The laboratory should also establish internal proficiency testing of normal and abnormal samples as part of the laboratory internal quality assurance program and ongoing quality improvement program. Correlation between microarray results run in parallel on different array platforms or correlation of microarray results with conventional cytogenetic and/or fluorescence *in situ* hybridization results may be sufficient to provide ongoing proficiency. Proficiency testing should be performed according to 1988 CLIA guidelines.

Documentation of participation and the performance results of all internal and external proficiency tests must be retained by the laboratory and made available to all accreditation agency inspectors.

LABORATORY ACCREDITATION AND PERSONNEL QUALIFICATIONS

Laboratory personnel must have documentation of education, degrees, and certifications as appropriate for level of testing, as well as training, competency assessments, and continuing education as required by appropriate regulatory bodies, e.g., College of American Pathologists, CLIA, Centers for Medicare & Medicaid Services. The testing laboratory must have CLIA certification and state certifications as required to provide clinical testing. College of American Pathologists accreditation is strongly encouraged.

RETENTION OF FILES AND DOCUMENTATION

Laboratories should make explicit in their policies which file types and what length of time each type will be retained and that data retention policy must be in accordance with local, state, and federal requirements. CLIA regulations (Sec. 493.1105) require storage of analytic systems records and test reports for at least 2 years. For more specific suggestions for microarray technologies, we recommend that the laboratory consider a minimum of 2-year storage of a file type that would allow regeneration of the primary results as well as re-analysis with improved analytic pipelines. In addition, laboratories should consider retention of the aberrations identified in the analysis, along with the final clinical test report interpreting the subset of clinically relevant variants, for as long as possible, given the likelihood of a future request for reinterpretation of variant significance.

CONCLUSIONS

Each new technological development in the field of genetics brings with it the desire to apply the technology to improve medical care. The transition of a new technology from the research bench into the clinical realm of diagnostic testing must be accompanied by extensive validation to ensure that the results reported to the health-care provider are accurate and reliable for use in patient-care decision making.

Microarray technologies provide a high-resolution view of the whole genome. Medical laboratory professionals must be prepared to identify, interpret, and report the results with clinical relevance, while keeping in mind the social, ethical, and legal responsibilities of reporting genetic information. The interpretation of the data from microarray analysis into clinically relevant information is a difficult and complex undertaking and is the practice of medicine. No algorithm for CNV interpretation can substitute for adequate training and knowledge in the field of genetics. We recommend that genomic microarray analysis be performed in laboratories overseen by individuals with appropriate professional training (American Board of Medical Genetics–certified clinical cytogeneticists or clinical molecular geneticists, or American Board of Medical Genetics/American Board of Pathology–certified molecular genetic pathologists) and that the interpretation and reporting of clinical genomic microarray findings be performed by these same certified individuals.

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DISCLOSURE

All members of this working group are directors of clinical laboratories that use genomic microarray technologies (please see affiliations for locations of clinical laboratories). S.T.S. has received honoraria from Affymetrix, a manufacturer of genomic microarray platforms, for speaking engagements. Also, S.T.S. is a consultant to Lineagen, a provider of genomic microarray testing services. The other authors declare no conflict of interest.

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APPENDIX 6

Technical laboratory standards for the interpretation and reporting of constitutional copy-number variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics (ACMG) and the Clinical Genome Resource (ClinGen)
(See following page)



Technical standards for the interpretation and reporting of constitutional copy-number variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics (ACMG) and the Clinical Genome Resource (ClinGen)

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Disclaimer: This technical standard is designed primarily as an educational resource for clinical laboratory geneticists to help them provide quality clinical laboratory genetic services. Adherence to this standard is voluntary and does not necessarily assure a successful medical outcome. This standard should not be considered inclusive of all proper procedures and tests or exclusive of other procedures and tests that are reasonably directed to obtaining the same results. In determining the propriety of any specific procedure or test, the clinical laboratory geneticist should apply his or her own professional judgment to the specific circumstances presented by the individual patient or specimen. Clinical laboratory geneticists are encouraged to document in the patient's record the rationale for the use of a particular procedure or test, whether or not it is in conformance with this standard. They also are advised to take notice of the date any particular standard was adopted, and to consider other relevant medical and scientific information that becomes available after that date. It also would be prudent to consider whether intellectual property interests may restrict the performance of certain tests and other procedures.

Purpose: Copy-number analysis to detect disease-causing losses and gains across the genome is recommended for the evaluation of individuals with neurodevelopmental disorders and/or multiple congenital anomalies, as well as for fetuses with ultrasound abnormalities. In the decade that this analysis has been in widespread clinical use, tremendous strides have been made in understanding the effects of copy-number variants (CNVs) in both affected individuals and the general population. However, continued broad implementation of array and next-generation sequencing-based technologies will expand the types of CNVs encountered in the clinical setting, as well as our understanding of their impact on human health.

Methods: To assist clinical laboratories in the classification and reporting of CNVs, irrespective of the technology used to identify them, the American College of Medical Genetics and Genomics has developed the following professional standards in collaboration with the National Institutes of Health (NIH)-funded Clinical Genome Resource (ClinGen) project.

Results: This update introduces a quantitative, evidence-based scoring framework; encourages the implementation of the five-tier classification system widely used in sequence variant classification; and recommends “uncoupling” the evidence-based classification of a variant from its potential implications for a particular individual.

Conclusion: These professional standards will guide the evaluation of constitutional CNVs and encourage consistency and transparency across clinical laboratories.

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Keywords: copy-number variant; interpretation; classification; CNV; scoring metric

INTRODUCTION

Genome-wide assessment of copy-number variants (CNVs), including losses (deletions) and gains (duplications) and

triplications), is recommended as a first-tier approach for the postnatal evaluation of individuals with intellectual disability, developmental delay, autism spectrum disorder, and/or multiple

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congenital anomalies, as well as for prenatal evaluation of fetuses with structural anomalies observed by ultrasound.^{1–3} For over a decade, CNV analysis by chromosomal microarray (CMA) has been broadly implemented in the clinical setting for detection of genomic imbalances at a much higher resolution than conventional cytogenetic methods (e.g., G-banded karyotype). In some cases, exon-focused array designs have also been used for detecting CNVs involving individual genes associated with monogenic disorders. More recently, next-generation sequencing (NGS)-based CNV analysis is increasingly used in clinical testing through genome, exome, or gene panel sequencing. Together, these methods have enabled genome-wide detection of CNVs, ranging in size from single exons to whole chromosomes in clinically affected individuals, as well as in the general population.

Though many recurrent CNVs (such as those flanked by segmental duplications) have been well characterized, most CNVs are unique, requiring further investigation to determine their potential clinical significance. This can be challenging for several reasons, including absent, limited, or conflicting associations with clinical phenotypes described in published literature and genomics databases. Accurate clinical interpretation of CNVs requires consistent methods of evaluating the genomic content of a CNV region and correlating clinical findings with those reported in the medical literature, with the ultimate goal of producing consistent, evidence-based clinical classification across laboratories.⁴ Inconsistency among laboratories can create confusion for clinicians and their patients, leaving them unable to confidently use genetic information to manage health-care decisions.⁵ Standards that are widely available, up-to-date, and flexible enough to incorporate lessons learned from the ever-evolving genomics knowledge base should help to reduce discordance in clinical classifications.

METHODS

To assist in the evaluation of CNVs and promote consistency and transparency in classification and reporting across clinical laboratories, the American College of Medical Genetics and Genomics (ACMG) and the National Institutes of Health (NIH)-funded Clinical Genome Resource (ClinGen) project⁶ formed a collaborative working group with the goal of updating the existing ACMG professional clinical laboratory practice standards for evaluating CNVs.⁷ The working group held an in-person meeting in the fall of 2015 to review the existing version of the interpretation standards⁷ and discuss how laboratories had incorporated them (and any modifications) into their clinical practice, as well as new resources, tools, and technologies that became available in the intervening years. Through group consensus, evidence categories most relevant to CNV classification were determined (including genomic content, dosage sensitivity predictions and curations, predicted functional effect, clinical overlap with patients in the medical literature, evidence from case and control databases, and inheritance patterns for individual CNVs), and a relative weight was assigned to each. In this manner, a

semiquantitative point-based scoring system was developed (described in detail in Supplemental Material 1).

Development of the new framework was an iterative process; working group members tested the analysis metrics using cases observed in their clinical laboratories and provided feedback for refinement that ensured objective and rigorous assessment of the available evidence. In 2017, after the framework had been developed and assessed by the working group, we identified a group of 11 additional board-certified clinical cytogeneticists to further evaluate both the performance of the analysis metrics and their usability in the clinical setting. Using both the outside reviewers and the committee members, we evaluated a total of 114 CNVs (58 deletions, 56 duplications); most CNVs ($n = 111$) were each evaluated by two independent reviewers. A full description of the validation process is provided in Supplemental Material 2. Feedback from this process led to the current version of the scoring metrics.

Proposed criteria for the evaluation of constitutional copy-number variants

These standards build upon the previous version⁷ by introducing a semiquantitative point-based scoring metric for CNV classification. Owing to the distinct properties and inherent differences between copy-number losses and copy-number gains, separate scoring metrics were developed for each (Tables 1 and 2, respectively); each scored evidence category is labeled (1A, 1B, etc.) for easy referencing. Full descriptions of each evidence category, including caveats to consider while scoring and illustrative examples, are provided in Supplemental Material 1. We strongly recommend the user to carefully review the explanatory material provided in the Supplement before utilizing these scoring metrics in clinical practice. Example cases scored using the metrics are provided in Supplemental Material 3.

As clinical laboratories incorporate more NGS-based techniques for CNV detection and integrate results from multiple technologies (some capable of identifying both copy-number and sequence variants), consistency across interpretation processes and reporting is critical. Thus, where possible, evidence categories and concepts presented in this CNV scoring system were developed to align with terminology and processes currently utilized for clinical sequence variant classification and interpretation.⁸

The point values assigned to each piece of evidence roughly correspond to the categorical strengths of evidence present in the sequence variant interpretation guidelines⁸ as well as recommendations put forth by the ClinGen Sequence Variant Interpretation (SVI) Working Group to model the ACMG/Association for Molecular Pathology (AMP) sequence variant interpretation guidelines into a more quantitative Bayesian framework;⁹ however, it is important to note that these numbers have not been statistically derived. In general, evidence receiving 0.90 points or higher is considered “very strong”; 0.45 points is considered “strong”; 0.30 points is considered “moderate”; and 0.15 points or lower is considered “supporting” evidence. Scores

Table 1 CNV interpretation scoring metric: copy-number loss

Section 1: Initial assessment of genomic content		Evidence	Suggested points/case	Max score
Evidence type				
Copy-number loss content	1A. Contains protein-coding or other known functionally important elements.		0 (Continue evaluation)	0
	1B. Does NOT contain protein-coding or any known functionally important elements.		−0.60	−0.60
Section 2: Overlap with established/predicted haploinsufficiency (HI) or established benign genes/genomic regions (Skip to section 3 if your copy-number loss DOES NOT overlap these types of genes/regions)				
Overlap with ESTABLISHED HI genes or genomic regions and consideration of reason for referral	2A. Complete overlap of an established HI gene/genomic region.		1.00	1.00
	2B. Partial overlap of an established HI genomic region		0 (Continue evaluation)	0
	• The observed CNV does NOT contain the known causative gene or critical region for this established HI genomic region OR • Unclear if known causative gene or critical region is affected OR • No specific causative gene or critical region has been established for this HI genomic region			
	2C. Partial overlap with the 5' end of an established HI gene (3' end of the gene not involved)...	See categories below		
	2C-1. ...and coding sequence is involved	0.90 (range: 0.45 to 1.00)		1.00
	2C-2. ...and only the 5' UTR is involved	0 (range: 0 to 0.45)		0.45
	2D. Partial overlap with the 3' end of an established HI gene (5' end of the gene not involved)...	See categories below		
	2D-1. ...and only the 3' untranslated region is involved.	0 (Continue evaluation)		0
	2D-2. ...and only the last exon is involved. Other established pathogenic variants have been reported in this exon.	0.90 (range: 0.45 to 0.90)		0.90
	2D-3. ...and only the last exon is involved. No other established pathogenic variants have been reported in this exon.	0.30 (range: 0 to 0.45)		0.45
	2D-4. ...and it includes other exons in addition to the last exon. Nonsense-mediated decay is expected to occur.	0.90 (range: 0.45 to 1.00)		1.00
	2E. Both breakpoints are within the same gene (intragenic CNV; gene-level sequence variant).	See ClinGen SVI working group PVS1 specifications	See categories at left	
			• PVS1 = 0.90 (Range: 0.45 to 0.90) • PVS1_Strong = 0.45 (Range: 0.30 to 0.90) • PVS1_Moderate or PM4 (in-frame indels) = 0.30 (Range: 0.15 to 0.45) • PVS1_Supporting = 0.15 (Range: 0 to 0.30)	

Table 1 continued

• N/A = No points, but continue evaluation -1 -1		
Overlap with ESTABLISHED benign genes or genomic regions	2F. Completely contained within an established benign CNV region.	-1
Haploinsufficiency predictors	2G. Overlaps an established benign CNV, but includes additional genomic material. 2H. Two or more HI predictors suggest that AT LEAST ONE gene in the interval is HI.	0 (Continue evaluation) 0.15
Section 3: Evaluation of gene number		
Number of protein-coding RefSeq genes wholly or partially included in the copy-number loss	3A. 0–24 genes	0
	3B. 25–34 genes	0.45
	3C. 35+ genes	0.90
Section 4: Detailed evaluation of genomic content using cases from published literature, public databases, and/or internal lab data (Skip to section 5 if either your CNV overlapped with an established HI gene/region in section 2, OR there have been no reports associating either the CNV or any genes within the CNV with human phenotypes caused by loss of function [LOF] or copy-number loss)		
Individual case evidence—de novo occurrences	Reported proband (from literature, public databases, or internal lab data) has either: • A complete deletion of or a LOF variant within gene encompassed by the observed copy-number loss OR • An overlapping copy-number loss similar in genomic content to the observed copy-number loss AND...	See categories below
	4A. ...the reported phenotype is highly specific and relatively unique to the gene or genomic region,	Confirmed de novo: 0.45 points each Assumed de novo: 0.30 points each (range: 0.15 to 0.45)
	4B. ...the reported phenotype is consistent with the gene/genomic region, is highly specific, but not necessarily unique to the gene/genomic region.	Confirmed de novo: 0.30 points each Assumed de novo: 0.15 point each (range: 0 to 0.45)
	4C. ...the reported phenotype is consistent with the gene/genomic region, but not highly specific and/or with high genetic heterogeneity.	Confirmed de novo: 0.15 point each Assumed de novo: 0.10 point each (range: 0 to 0.30)
Individual case evidence—inconsistent phenotype	4D. ...the reported phenotype is NOT consistent with what is expected for the gene/genomic region or not consistent in general.	0 points each (range: 0 to -0.30)
Individual case evidence—unknown inheritance	4E. Reported proband has a highly specific phenotype consistent with the gene/genomic region, but the inheritance of the variant is unknown.	0.10 points each (range: 0 to 0.15)
Individual case evidence—segregation among similarly affected family members	4F. 3–4 observed segregations	0.15
	4G. 5–6 observed segregations	0.30
	4H. 7 or more observed segregations	0.45
Individual case evidence—nonsegregations	4I. Variant is NOT found in another individual in the proband's family AFFECTED with a consistent, specific, well-defined phenotype (no known phenocopies).	-0.45 points per family (range: 0 to -0.45) (total)
	4J. Variant IS found in another individual in the proband's family UNAFFECTED with the specific, well-defined phenotype observed in the proband.	-0.30 points per family (range: 0 to -0.30) (total)

Table 1 continued

Case-control and population evidence	4K. Variant IS found in another individual in the proband's family UNAFFECTED with the nonspecific phenotype observed in the proband.	–0.15 points per family (range: 0 to –0.15)	–0.30 (total)
	4L. Statistically significant increase amongst observations in cases (with a consistent, specific, well-defined phenotype) compared with controls.	0.45 per study (range: 0 to 0.45 per study)	0.45 (total)
	4M. Statistically significant increase amongst observations in cases (without a consistent, nonspecific phenotype OR unknown phenotype) compared with controls.	0.30 per study (range: 0 to 0.30 per study)	0.45 (total)
	4N. No statistically significant difference between observations in cases and controls.	–0.90 (per study) (range: 0 to –0.90 per study)	–0.90 (total)
4O. Overlap with common population variation.			
–1 (range: 0 to –1)			
Section 5: Evaluation of inheritance pattern/family history for patient being studied			
Observed copy-number loss is de novo	5A. Use appropriate category from de novo scoring section in section 4.	Use de novo scoring categories from section 4 (4A–4D) to determine score	
Observed copy-number loss is inherited	5B. Patient with specific, well-defined phenotype and no family history. CNV is inherited from an apparently unaffected parent.	–0.30 (range: 0 to –0.45)	–0.45
	5C. Patient with nonspecific phenotype and no family history. CNV is inherited from an apparently unaffected parent.	–0.15 (range: 0 to –0.30)	–0.30
	5D. CNV segregates with a consistent phenotype observed in the patient's family.	Use segregation scoring categories from section 4 (4F–4H) to determine score	
Observed copy-number loss—nonsegregations	5E. Use appropriate category from nonsegregation section in section 4.	Use nonsegregation scoring categories from section 4 (4I–4K) to determine score	
Other	5F. Inheritance information is unavailable or uninformative.	0	0
	5G. Inheritance information is unavailable or uninformative. The patient phenotype is nonspecific, but is consistent with what has been described in similar cases.	0.10 (range: 0 to 0.15)	0.15
	5H. Inheritance information is unavailable or uninformative. The patient phenotype is highly specific and consistent with what has been described in similar cases.	0.30 (range: 0 to 0.30)	0.30

Only those CNVs otherwise meeting the reporting thresholds determined by your laboratory should be evaluated using this metric. See Supplemental Material 1 for a detailed description of each evidence category. Scoring: pathogenic 0.99 or more points, likely pathogenic 0.90 to 0.98 points, variant of uncertain significance 0.89 to –0.89 points, likely benign –0.90 to –0.98 points, benign –0.99 or fewer points. CNV copy-number variant, SVI sequence variant interpretation, UTR untranslated region.

Table 2 CNV interpretation scoring metric: copy-number gain

Section 1: Initial assessment of genomic content		Evidence	Suggested points/case	Max score	
Evidence type					
Copy-number gain content	Section 2: Overlap with established triplosensitive (TS), haploinsufficient (HI), or benign genes or genomic regions (Skip to section 3 if the copy-number gain DOES NOT overlap these types of genes/regions)	1A. Contains protein-coding or other known functionally important elements.	0 (Continue evaluation)	0	
		1B. Does NOT contain protein-coding or any known functionally important elements	–0.60	–0.60	
Overlap with ESTABLISHED TS genes or genomic regions		2A. Complete overlap; the TS gene or minimal critical region is fully contained within the observed copy-number gain.	1	1	
		2B. Partial overlap of an established TS region • The observed CNV does NOT contain the known causative gene or critical region for this established TS genomic region OR • Unclear if the known causative gene or critical region is affected OR • No specific causative gene or critical region has been established for this TS genomic region.	0 (Continue evaluation)	0	
Overlap with ESTABLISHED benign copy-number gain genes or genomic regions		2C. Identical in gene content to the established benign copy-number gain.	–1	–1	
		2D. Smaller than established benign copy-number gain, breakpoint(s) does not interrupt protein-coding genes.	–1	–1	
		2E. Smaller than established benign copy-number gain, breakpoint(s) potentially interrupts protein-coding gene.	0 (Continue evaluation)	0	
		2F. Larger than known benign copy-number gain, does not include additional protein-coding genes.	–1 (range: 0 to –1.00)	–1	
Overlap with ESTABLISHED HI gene(s)	Breakpoint(s) within ESTABLISHED HI genes	2G. Overlaps a benign copy-number gain but includes additional genomic material.	0 (Continue evaluation)	0	
		2H. HI gene fully contained within observed copy-number gain.	0 (Continue evaluation)	0	
		2I. Both breakpoints are within the same gene (gene-level sequence variant, possibly resulting in loss of function [LOF]).	See ClinGen SVI working group PVS1 specifications • PVS1 = 0.90 (Range: 0.45 to 0.90) • PVS1_Strong = 0.45 (Range: 0.30 to 0.90) • N/A = 0 (Continue evaluation)	0	
		2J. One breakpoint is within an established HI gene, patient's phenotype is either inconsistent with what is expected for LOF of that gene OR unknown.	0.45	0.45	
		2K. One breakpoint is within an established HI gene, patient's phenotype is highly specific and consistent with what is expected for LOF of that gene.	0 (Continue evaluation)	0	
		2L. One or both breakpoints are within gene(s) of no established clinical significance.	0	0	
Breakpoints within other gene(s)	Section 3: Evaluation of gene number	3A. 0–34 genes	0	0	
		3B. 35–49 genes	0.45	0.45	
Number of protein-coding RefSeq genes wholly or partially included in the copy-number gain		0.90	0.90		
Section 4: Detailed evaluation of genomic content using cases from published literature, public databases, and/or internal lab data (Note: If there have been no reports associating either the copy-number gain or any of the genes therein with human phenotypes caused by triplosensitivity, skip to section 5)					
Individual case evidence—de novo occurrences		Reported proband (from literature, public databases, or internal lab data) has either: • complete duplication of one or more genes within the observed copy-number gain OR • an overlapping copy-number gain similar in genomic content to the observed copy-number gain AND ...	See categories below		
		4A. ...the reported phenotype is highly specific and relatively unique to the gene or genomic region.	Confirmed de novo: 0.45 points each Assumed de novo: 0.30 points each (range: 0.15 to 0.45)	0.90 (total)	
		4B. ...the reported phenotype is consistent with the gene/genomic region, is highly specific, but is not necessarily unique to the gene/genomic region.	Confirmed de novo: 0.30 points each Assumed de novo: 0.15 point each (range: 0 to 0.45)	0	
		4C. ...the reported phenotype is consistent with the gene/genomic region, but not highly specific and/or with high genetic heterogeneity.	Confirmed de novo: 0.15 point each Assumed de novo: 0.10 point each (range: 0 to 0.30)	0	
Individual case evidence—inconsistent phenotype consistent in general		4D. ...the reported phenotype is NOT consistent with the gene/genomic region or not consistent in general.	0 points each (range: 0 to –0.30)	–0.30 (total)	
		4E. Reported proband has a highly specific phenotype consistent with the gene/genomic region, but the inheritance of the variant is unknown.	0.10 points each (range: 0 to 0.15)	0.30 (total)	

Table 2 continued

Individual case evidence—segregation among similarly affected family members	4F. 3–4 observed segregations	0.15	0.45
	4G. 5–6 observed segregations	0.30	
	4H. 7 or more observed segregations	0.45	
Individual case evidence—nonsegregations	4I. Variant is NOT found in another individual in the proband's family AFFECTED with a consistent, specific, well-defined phenotype (no known phenocopies)	–0.45 points per family (range: 0 to –0.45)	–0.90 (total)
	4J. Variant IS found in another individual in the proband's family UNAFFECTED with the specific, well-defined phenotype observed in the proband.	–0.30 points per family (range: 0 to –0.30)	–0.90 (total)
	4K. Variant IS found in another individual in the proband's family UNAFFECTED with the nonspecific phenotype observed in the proband.	–0.15 points per family (range: 0 to –0.15)	–0.30 (total)
Case-control and population evidence	4L. Statistically significant increase among observations in cases (with a consistent, specific, well-defined phenotype) compared with controls.	0.45 per study (range: 0 to 0.45 per study)	0.45 (total)
	4M. Statistically significant increase among observations in cases (with a consistent, nonspecific phenotype or unknown phenotype) compared with controls.	0.30 per study (range: 0 to 0.30 per study)	0.45 (total)
	4N. No statistically significant difference between observations in cases and controls.	–0.90 per study (range: 0 to –0.90 per study)	–0.90 (total)
	4O. Overlap with common population variation.	–1 (range: 0 to –1)	–1
Section 5: Evaluation of inheritance patterns/family history for patient being studied			
Observed copy-number gain is de novo	5A. Use appropriate category from de novo scoring section in section 4.	Use de novo scoring categories from section 4 (4A–4D) to determine score	0.45
Observed copy-number gain is inherited	5B. Patient with a specific, well-defined phenotype and no family history. Copy-number gain is inherited from an apparently unaffected parent.	–0.30 (range: 0 to –0.45)	–0.45
	5C. Patient with nonspecific phenotype and no family history. Copy-number gain is inherited from an apparently unaffected parent.	–0.15 (range: 0 to –0.30)	–0.30
	5D. CNV segregates with consistent phenotype observed in the patient's family.	Use segregation scoring categories from in section 4 (4F–4H) to determine score	0.45
Observed copy-number gain—nonsegregations	5E. Use appropriate category from nonsegregation section in section 4.	Use nonsegregation scoring categories from section 4 (4I–4K) to determine score	–0.45
	5F. Inheritance information is unavailable or uninformative.	0	0
	5G. Inheritance information is unavailable or uninformative. The patient phenotype is nonspecific, but is consistent with what has been described in similar cases.	0.10 (range: 0 to 0.15)	0.15
	5H. Inheritance information is unavailable or uninformative. The patient phenotype is highly specific and consistent with what has been described in similar cases.	0.15 (range: 0 to 0.30)	0.30

Only those CNVs otherwise meeting the reporting thresholds determined by your laboratory should be evaluated using this metric. See Supplemental Material 1 for full description of each evidence category. Scoring: pathogenic 0.99 or more points, likely pathogenic 0.90 to 0.98 points, variant of uncertain significance 0.89 to –0.89 points, likely benign –0.90 to –0.98 points, benign –0.99 or fewer points. CNV copy-number variant, SVI sequence variant interpretation.

for each observed piece of evidence, both in support of (positive values) and refuting (negative values) pathogenicity, are summed to arrive at a CNV classification. CNVs with a final point value ≥ 0.99 are considered pathogenic, while point values between 0.90 and 0.98 are considered likely pathogenic; this approach aligns with the sequence variant interpretation guidelines⁸ (i.e., variants interpreted as pathogenic should have a 99% level of confidence and variants interpreted as likely pathogenic should have a 90% level of confidence). The variant of uncertain significance (VUS) category is the broadest, corresponding to points between -0.89 and 0.89 , while refuting evidence arriving at scores between -0.90 and -0.98 , or ≤ -0.99 are considered likely benign and benign, respectively.

To facilitate use of this semiquantitative system, a web-based CNV classification calculator based on these scoring metrics is publicly available (<http://cnvcalc.clinicalgenome.org/cnvcalc/>). This tool allows users to apply points for individual evidence categories for a given CNV and will automatically calculate the final point value and corresponding CNV classification. This tool will be continually supported and updated, allowing timely integration of new information as it emerges.

These standards were developed for evaluating evidence in the context of constitutional CNVs, including those detected during postnatal or prenatal testing. Laboratories may choose to use specific reporting practices based on factors such as CNV classification and clinical context, and these may vary across different test types and clinical settings (e.g., choosing to only report likely pathogenic or pathogenic variants associated with dominantly inherited conditions in a prenatal setting). These specific reporting practices should be documented in the laboratory's interpretation and reporting protocol.

These standards do not apply to acquired CNVs in neoplasia. In addition, this document does not address analytical validation of CNV detection methods, which have been addressed elsewhere, and assumes that any laboratory using the provided standards is confident that a reported CNV represents a true biological event.¹⁰ These standards serve as a reference for clinicians to enable them to understand the complexity of CNV interpretation and to appropriately communicate test results to patients and families. Although these standards attempt to comprehensively incorporate commonly available resources and processes used in CNV classification and interpretation, it is important to recognize that no singular algorithm will be applicable in all potential scenarios. The semiquantitative scoring framework is meant to serve as a guide. Professional judgment should always be used when evaluating the evidence surrounding a particular genomic variant and assigning a classification.

Recommended variant classification categories

Using the scoring metrics described in Supplemental Material 1, a laboratory geneticist should assign any CNV reported in a patient to one of five main classification categories. It is

strongly recommended that consistent terminology for these categories be used in clinical reporting to facilitate unambiguous communication of clinical significance throughout the medical community.

The classification categories represent a significant update from the previous version of these guidelines.⁷ To align closely with recommendations in the ACMG/AMP sequence variant interpretation guidelines⁸ and with the manner in which these terms are now commonly used, we have updated the existing three-tiered system of clinical significance (in which the term "variant of uncertain significance" had the optional qualifiers of "likely pathogenic" or "likely benign") to the five-tiered system described below.

Pathogenic

Pathogenic (P) CNVs are those that score 0.99 points or higher using the evidence scoring metric (Supplemental Material 1). Although the full clinical effect of a CNV on a patient's phenotype may not be known (due to zygosity or other reasons), the pathogenic nature of the CNV should not be in question.

Examples of P CNVs may include (1) CNVs reported in association with consistent clinical phenotypes across multiple peer-reviewed publications, with well-documented penetrance and expressivity, even if reduced and/or variable; (2) unique CNVs that overlap completely with an established dosage-sensitive region; and (3) multigenic CNVs in which at least one gene is known to be dosage sensitive,¹¹ even if the other genes are of uncertain significance.

Except for well-established cytogenetic heteromorphisms, this category will include most cytogenetically visible alterations (generally >5 Mb). In the absence of loci clearly associated with defined genetic syndromes within the interval, cytogenetically visible alterations should still be cautiously evaluated, taking the gene content into consideration.

Likely pathogenic

Likely pathogenic (LP) CNVs are those that score between 0.90 and 0.98 points using the evidence scoring metric. In general, these variants have strong evidence to suggest that they will ultimately be determined to be disease-causing, but not enough yet to definitively assert pathogenicity. Several evidence types outlined within the scoring metrics could be combined to reach the LP point threshold. However, some particularly strong pieces of evidence may result in the CNV being classified as P without the need for additional evidence (although additional information could be added to bring the classification to P). Examples of this type of evidence may include (1) deletions involving the 5' end (plus additional coding sequence) of established haploinsufficient (HI) genes (in scenarios where there are no known alternative start sites) (category 2C-1, deletion metric); (2) deletions involving multiple exons (through the 3' end of the gene) in an established HI gene (category 2D-4); and (3) deletions or duplications involving genes with multiple case reports reported in consistent, highly specific phenotypes.

Uncertain significance

Variants of uncertain significance (VUS) are those that score between -0.89 and 0.89 points using the evidence scoring metric. This represents a broad category and may include findings that are later demonstrated with additional evidence to be either pathogenic or benign. Some CNVs in this category may have more evidence than others to indicate involvement in disease and the likelihood of additional evidence surfacing through published literature may be higher. However, at the time of reporting, if insufficient evidence is available for confident determination of definitive clinical significance and the CNV meets the reporting criteria established by the laboratory, the CNV should be described as a variant of uncertain significance.

Examples of VUS may include (1) a CNV that exceeds a laboratory's size threshold for reporting but has no genes in the affected genomic interval (category 1B); (2) a CNV described in a small number of cases in the general population, but not at a high enough frequency to be considered a polymorphism ($>1\%$) (category 4O, with a downgraded score due to frequency); (3) a CNV that contains a small number of genes, but it is not known whether the genes in the interval are dosage sensitive (category 3A); (4) a CNV described in multiple contradictory publications and/or databases, without firm conclusions regarding clinical significance (multiple categories); (5) a CNV within an individual gene (category 2E, deletion metric, and 2I, duplication metric) with an unclear effect on the transcript reading frame.

Likely benign

Likely benign (LB) CNVs are those that score between -0.90 and -0.98 points using the evidence scoring metric. In general, these variants have strong evidence to suggest that they are likely not involved in Mendelian disease, but do not yet have enough evidence to state this definitively.

Examples of LB CNVs may include (1) variants with no statistically significant difference between observations in cases and controls (category 4N), and (2) variants observed frequently in the general population (although at a lower frequency than 1% , a conventionally accepted threshold for a common polymorphism [category 4O]).

Benign

Benign CNVs are those that score -0.99 or fewer points using the evidence scoring metric. These CNVs have typically been reported in multiple peer-reviewed publications or annotated in curated databases as benign variants, particularly if the nature of the copy-number variation has been well characterized (e.g., copy-number variation of the salivary amylase gene¹²) and/or the CNV represents a common polymorphism. To qualify as a benign polymorphism, the CNV should be documented in $>1\%$ of the population. It is important to carefully consider dosage of the CNV documented as a benign variant, given, for example, that duplications of some regions may be benign,

whereas deletions of the same interval may have clinical relevance.

Reporting guidelines for copy-number variants in the constitutional setting

In recent years, innovations in microarray and NGS technologies have expanded the diagnostic application of clinical CNV analysis and interpretation from chromosomal microarrays to single- and multigene sequencing panels, and exome or genome sequencing. Each of these tests may have distinct clinical reporting specifications. The following recommendations describe elements of a clinical laboratory report that are necessary to precisely describe the nature of a CNV and clearly communicate the evidence related to its classification and clinical significance. Other required elements of a clinical report (e.g., methodology and relevant disclaimers) are outlined in detail in the ACMG Technical Standards and Guidelines.

Reporting criteria

The laboratory report should include a description of the criteria used for both inclusion of a CNV in the report (e.g., classification type, CNV size) and classification of the CNV (e.g., the scoring metrics included in this document). Laboratories may or may not choose to disclose benign or likely benign CNVs, and this should be indicated in the report and their laboratory reporting protocol.

Description of each CNV detected

Each CNV should be described with the elements below. Appropriate nomenclature from the International System for Human Cytogenomic Nomenclature (ISCN) or the Human Genome Variation Society (HGVS) should be included in the report, but should not serve as a substitute for a clear description of the genomic imbalance for clinical professionals unfamiliar with these conventions.

- Cytogenetic location (chromosome number and cytogenetic band designation).
- CNV size and linear coordinates with the genome build specified. Genomic coordinates for the minimum predicted interval should be specified. When applicable, particularly when gene content of the CNV is unclear, the maximal genomic coordinates may also be provided.
- Copy-number state (e.g., single-copy gain or loss) with CNV mechanism specified when understood (e.g., tandem duplication). Assessment of mechanism may require additional testing methods.
- For intragenic CNVs: Appropriate naming conventions in this scenario may be dependent on the platform used to detect these variants. If the variant is identified using NGS-based technologies, HGVS nomenclature may be preferable, including gene name (using valid Human Genome Organisation Gene Nomenclature Committee [HGNC] nomenclature), transcript, and exons involved. If the variant is identified using CMA, ISCN nomenclature

is generally recommended. The naming convention selected should recognize a location, genomic content, and certainty or uncertainty of precise breakpoints.

Designation of genes in CNV interval

To the extent feasible, genes involved in a CNV should be specified in the laboratory report. For large imbalances, particularly those with well-established clinical significance, it is acceptable to provide only the name of the corresponding syndrome and/or the most clinically relevant genes in the interval. For CNVs of uncertain significance, it is suggested that all validated/curated (i.e., not predicted or hypothetical) genes in the interval be included, when possible, to facilitate periodic reviews of relevant medical literature. The incorporation of links to websites that list the genes in an interval is not recommended because the links may not faithfully direct the clinician to the appropriate gene content in the future. If all genes in the interval are not listed on the report, it is suggested that at least the total number of genes in the CNV interval be provided to highlight the extent of genomic imbalance; other potentially clinically relevant elements may also be noted.

Clear statement of variant classification and clinical significance

Regardless of the type of variant being assessed (CNV, sequence variant, etc.), determining a variant's classification should be performed independently from determining how it contributes to the diagnosis of the individual in whom it is discovered. Uncoupling variant classification (P, LP, etc.) from clinical significance in the context of an individual patient's diagnosis is key to objective and consistent interpretation of genomic variants. While the phenotype of the proband should be taken into account when assessing evidence supporting the pathogenicity of a CNV, classification should not be solely driven by the presentation of the patient under investigation (without consideration of other available evidence). For example, there is compelling evidence in the literature that deletion of a particular gene results in disease X; a laboratory evaluating a deletion of this gene is able to reach 0.99 points using the scoring metric, suggesting a classification of pathogenic. The laboratory should not then disregard all previously collected evidence and classify the variant as "uncertain significance" solely because their patient did not display features of disease X.

The classification of a particular variant should be based upon the evidence available to support or refute its pathogenicity at a given point in time; that body of evidence is ostensibly the same for every patient found to have that variant at that same point in time. As such, the variant should receive the same variant classification (P, LP, VUS, etc.), regardless of the clinical significance it has for each patient (which may differ). For example, there is substantial evidence demonstrating that a particular gene on the X chromosome causes disease via a loss-of-function mechanism. Given the body of evidence, deletions involving this gene should receive

the classification of pathogenic each time they are observed, regardless of whether they are observed in hemizygous males or heterozygous females. Within the report, the laboratory should explain the potential consequences of such a deletion for the patient under study—in a male this variant could represent a diagnostic finding; in a female this variant could represent carrier status. Therefore, each description of a CNV should include a clear statement of its classification and the evidence supporting it, as outlined in these recommendations, as well as the clinical significance of that variant for the patient being tested. See Supplemental Material 4 for examples of how these concepts may be conveyed during reporting.

Special considerations regarding reporting: clinically significant findings unrelated to the reason for referral

Occasionally, a CNV may be identified that, although unrelated to the patient's reason for referral, may indicate presymptomatic status for a late-onset disorder or may reveal an ongoing clinically unrecognized condition (i.e., an incidental finding¹³). Some examples of these include deletions involving known tumor suppressor genes,¹⁴ male infertility due to deletions involving the AZF region on the Y chromosome,¹⁵ a deletion disrupting a gene for hereditary spastic paraplegia in a child referred for autism,¹⁶ etc. It is often not possible to specifically avoid interrogation of the types of loci mentioned in the aforementioned cases, because such findings may occur as part of a large CNV involving multiple genes. It is impractical to provide a predefined list of all possible diagnoses to allow a patient to consent specifically to the interrogation of and reporting for each disorder. Therefore, referring clinicians must have a clear understanding of the potential for these discoveries, and patients/families should be duly informed before test ordering. An informed consent process is strongly recommended.

It is recommended that P or LP CNVs indicative of presymptomatic status be reported to facilitate appropriate and timely access to medical care. Individual laboratories may adopt nondisclosure policies for specific conditions and state them as such in their clinical reports.

The ACMG Secondary Findings Working Group has been established to identify genes "associated with highly penetrant genetic disorders and established interventions aimed at preventing or significantly reducing morbidity and mortality."¹³ When evaluating CNVs involving these genes, it is important to remember the mechanism of disease associated with each. If haploinsufficiency or triplosensitivity is not an established mutational mechanism for a specific gene, a deletion or duplication is not likely to be clinically relevant. If the mechanism of disease is consistent with haploinsufficiency or triplosensitivity, these CNVs should be reported. Dosage sensitivity evaluations of the genes currently on the ACMG secondary findings list are available at the following link: <https://www.ncbi.nlm.nih.gov/projects/dbvar/clingen/acmg.shtml>.

Clinically significant findings seemingly unrelated to the reason for referral represent another situation where it is important to separate the variant classification from clinical correlation. Historically, the reason for referral has influenced the CNV interpretation process; anecdotally, variants with clear evidence for pathogenicity have been classified as VUS because they did not “explain” the patient’s stated reason for referral. The reasons for referral provided to laboratories may not always represent a complete picture of the patient’s phenotypic features, and assumptions that a patient does or does not have a particular feature are not prudent without appropriate consultation with the referring clinician. Open channels of communication between the laboratory and the ordering physician are critical to guide clinical correlation.¹⁷

It is certainly appropriate to consider available phenotype information about a given patient as evidence in variant evaluation; if the patient undergoing testing has a phenotype that is consistent with the described phenotype for an observed CNV, this may be considered evidence supporting pathogenicity. It is not appropriate, however, to provide a different classification for the same CNV simply because it was identified in an individual with a different reason for referral. For example, there is substantial evidence demonstrating that loss-of-function variants in gene X result in hearing loss. If a laboratory observes a deletion of this gene in an individual referred for hearing loss, and the exact same deletion in another individual referred for speech delay, they should not interpret that variant as P in the former case and VUS in the latter. The variant should be classified as P in both instances. The variant is directly relevant to the reason for referral in the individual with hearing loss, but may represent an incidental finding or an explanation for an unobserved/unreported phenotype in the second. The pathogenicity of the variant, however, should not be in question given the depth of the supporting evidence. The reason for referral alone should not be used to justify varying classifications for the same CNV in different individuals.

Special considerations regarding reporting: carrier status

Detection of some CNVs, particularly deletions, will indicate carrier status for autosomal recessive or X-linked disorders mapping within the CNV interval. Although exhaustive reporting of carrier status may be considered difficult to standardize and beyond the intended scope of genome-wide microarrays (particularly for very large multigenic events), improvements in informatics could support reporting of such information in the future. Individual laboratories may choose to adopt specific disclosure policies for recessive conditions. If a laboratory chooses to include a list of carrier alleles, its reports should clearly separate the primary CNV results related to the reason for referral from a secondary list of carrier status alleles. If carrier status is not routinely assessed, reports should clearly state that carrier status may not be disclosed, and that any clinical concern for recessive disorders should be communicated to the reporting laboratory for

appropriate consideration. There are some situations when disclosure of carrier status is recommended:

1. Well-characterized disorders where loss of function is the established disease mechanism. In such cases, there may be justification for reporting carrier status to provide opportunity for reproductive counseling and additional testing in the proband or relevant family members, particularly when the carrier frequency is reasonably high, and/or screening is commonly available (e.g., cystic fibrosis). It should be recognized that these disclosures will represent serendipitous findings, and no claim should be made to the ordering clinician or patient that this test will routinely detect carrier status for any condition.
2. Disorders with clinical features consistent with the patient’s reason for referral. In such cases, a laboratory may have identified a CNV that represents one allele of an expected pair consistent with the referral diagnosis. The laboratory may then recommend ancillary molecular testing for this disorder in an effort to identify the other disease-causing allele. This should be restricted to well-described disorders with clear clinical consequence. The report should clearly state the recessive nature of the condition, and that the CNV is not diagnostic of affected status without confirmation of a second pathogenic variant.
3. CNVs involving dosage-sensitive genes on the X chromosome in females. Given the significant reproductive risk to female carriers of X-linked conditions, we recommend reporting these variants because it provides the opportunity for the patient and relevant family members to pursue additional testing/counseling as needed. Additionally, females may manifest symptoms in many X-linked disorders; these variants may ultimately have an impact on their medical management.

To make these nuances clearer to users of the laboratory report, we recommend dividing the report into sections describing primary variants considered relevant to the stated reason for referral separately from any variants that represent secondary or incidental findings or carrier status. Laboratories may decide at their discretion if additional subcategories are necessary.

Recommendation for appropriate clinical follow-up

The laboratory report should include recommendations for any necessary further cytogenetic characterization of the CNV, genetic counseling, and evaluation of relevant family members as appropriate. In addition, when a CNV is of uncertain significance, the report may include a recommendation for continued surveillance of the medical literature for new information that may alter the classification of the CNV and provide clarification on its clinical significance. The responsibility for monitoring the medical literature for a specific patient lies primarily with the physician with an ongoing patient relationship,¹⁸ but laboratories may choose to offer amended reports when reclassifications occur.

CONCLUDING REMARKS

Understanding the clinical relevance of CNVs is a complex, continually evolving process that constitutes the practice of medicine. As evident from the numerous considerations outlined in this document, no one formula or algorithm for CNV interpretation will substitute for adequate training in genetics and sound clinical judgment. We recommend that clinical reporting of constitutional CNVs be performed by individuals with appropriate professional training and certification (those individuals certified by the American Board of Medical Genetics and Genomics [ABMGG] in clinical cytogenetics, molecular genetics, and/or laboratory genetics and genomics). In addition, given the complexity of CNV interpretation, the different laboratory methodologies utilized for CNV characterization, and the evaluation of additional family members, an ideal laboratory setting for CNV analysis should include both cytogenetic and molecular genetic expertise.

This document for the first time lays out explicit guidance for interpreting CNVs that occur within individual genes. As detecting CNVs from sequencing-based platforms becomes more commonplace, it is important that CNV and single-nucleotide variant (SNV) analyses are appropriately aligned in their approaches to variant classification. Ideally, a CNV should receive the same classification whether it was detected on a CMA or an NGS platform, and whether or not it was interpreted by someone board-certified in cytogenetics or molecular genetics. The recommendations presented here (and in Supplemental Material 1) represent an initial effort to move toward more consistent CNV interpretation between laboratories and across technologies.

Systematic approaches to variant interpretation (such as this one) will evolve over time, particularly as knowledge regarding the relationships between genomic variation and human health improve. Groups are encouraged to use this framework as a guide, always using professional judgment when opting to incorporate emerging knowledge, methods, and resources, and documenting the process by which this evidence is used to arrive at a variant classification.

To summarize, major updates from the previous document⁷ include:

- CNV classification categories will change to the five-tier classification system recommended in the ACMG/AMP sequence variant interpretation guidelines.⁸
- Variants should be classified consistently between patients; while patient presentation and/or reason for referral may be used as evidence to support a particular classification, this information should not be used to justify disparate classifications of the same variant. Variant classifications should be based on evidence; at a given point in time, evidence supporting/refuting a given variant's pathogenicity should be the same. Therefore, the classification of that variant should be the same regardless of patient-specific factors such as reason for referral, sex, age, etc.
- Laboratories should consider utilizing headers or subsections in the clinical report to clearly communicate primary versus incidental or secondary findings, such as carrier status for autosomal recessive conditions, pathogenic variants unrelated to the stated reason for referral, etc. (examples may be found in Supplemental Material 4).
- Explicit new guidance for interpreting CNVs occurring within individual genes (intragenic deletions and duplications) (described in detail in Supplemental Material 1).
- Points-based scoring rubrics (Tables 1 and 2) to guide laboratories toward more consistent CNV interpretations. We anticipate that updates to these metrics will be required as laboratories gain experience using them, and as evidence and technologies change.

SUPPLEMENTARY INFORMATION

The online version of this article (<https://doi.org/10.1038/s41436-019-0686-8>) contains supplementary material, which is available to authorized users.

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DISCLOSURE

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The supplementary materials for the “Technical laboratory standards for the interpretation and reporting of constitutional CNVs” are listed below (with hyperlinks to the individual supplements):

1. Supplemental Figures
2. Supplemental Material 1: Using the copy number variation (CNV) scoring metrics
3. Supplemental Material 2: Validation of the CNV scoring metrics
4. Supplemental Material 3: Case examples
5. Supplemental Material 4: Example reports



Category 2A Complete overlap, similar in size

Category 2A Complete overlap, includes additional genomic material

Category 2A Known causative gene is fully contained

Category 2B Partial overlap, known causative gene is not included



Category 2A Complete overlap, similar in size

Category 2A Complete overlap, includes additional genomic material

Category 2A Known causative gene is fully contained

Category 2B Partial overlap, known causative gene is not included

Supplemental Figure 1.1: Illustrations of gain and loss scoring metric categories 2A-2B (overlap with established HI or TS region, causative gene/critical region known). **A)** A theoretical established haploinsufficient genomic region is shown in the context of several genes, one of which has been established as the main contributor to the phenotype associated with loss of this region. Example overlapping deletions are shown below, each representing a scenario described in the loss scoring metric (Table 1, Main Document). **B)** A theoretical established triplosensitive genomic region is shown in the context of several genes, one of which has been established as the main contributor to the phenotype associated with gain of this region. Example overlapping duplications are shown below, each representing a scenario described in the gain scoring metric (Table 2, Main Document). Red boxes represent deletions, blue boxes represent duplications. HI = haploinsufficient; TS = triplosensitive.

A) **Established HI Genomic Region** (Causative gene/critical region UNKNOWN)

Gene 1  Gene 2  Gene 3  Gene 4  Gene 5 

Category 2A Complete overlap, similar in size

Category 2A Complete overlap, includes additional genomic material

Category 2B Partial overlap, causative gene/critical region unknown

Category 2B Partial overlap, causative gene/critical region unknown

B) **Established TS Genomic Region** (Causative gene/critical region UNKNOWN)

Gene 1  Gene 2  Gene 3  Gene 4  Gene 5 

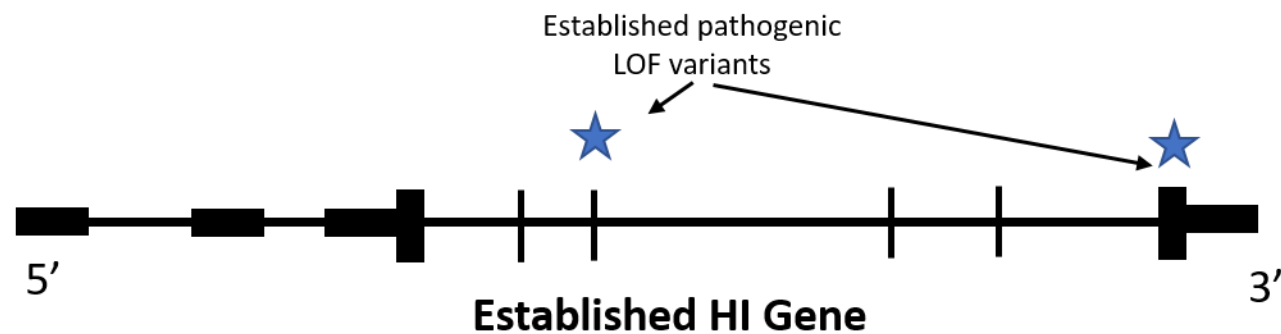
Category 2A Complete overlap, similar in size

Category 2A Complete overlap, includes additional genomic material

Category 2B Partial overlap, causative gene/critical region unknown

Category 2B Partial overlap, causative gene/critical region unknown

Supplemental Figure 1.2: Illustrations of scoring metric categories 2A-2B (overlap with established HI or TS region, causative gene/critical region unknown). **A)** A theoretical established haploinsufficient genomic region is shown in the context of several genes. In this example, no single gene or critical region has been established as the main contributor to the phenotype associated with loss of this region. Example overlapping deletions are shown below, each representing a scenario described in the loss scoring metric (Table 1, Main Document). **B)** A theoretical established triplosensitive genomic region is shown in the context of several genes. In this example, no single gene or critical region has been established as the main contributor to the phenotype associated with gain of this region. Example overlapping duplications are shown below, each representing a scenario described in the gain scoring metric (Table 2, Main Document). Red boxes represent deletions, blue boxes represent duplications. HI = haploinsufficient; TS = triplosensitive.



Category 2C-1

Overlap with 5' end, coding sequence involved

Category 2C-2

Only 5' UTR is involved

Category 2D-1

Only 3' UTR is involved

Category 2D-2

Only the last exon is involved; other established pathogenic variants have been reported in this exon

Category 2D-4

Overlap with 3' end; includes other exons in addition to the last exon; nonsense-mediated decay expected to occur

Category 2E

Both breakpoints are within the HI gene

Category 2H

HI gene fully contained within observed copy number gain

Category 2I

Both breakpoints are within the HI gene

One breakpoint within the HI gene

Category 2J or 2K

Supplemental Figure 1.3: Illustrations of scoring metric categories 2C-2E (loss metric) and 2H-2K (gain metric) - overlap with established haploinsufficient genes. A theoretical haploinsufficient gene is shown at the top. Example overlapping copy number variants are shown below, each representing a scenario described in the loss (Table 1, Main Document) or gain (Table 2, Main Document) scoring metric. Red boxes represent deletions, blue boxes represent duplications. HI = haploinsufficient; LOF = loss of function; UTR = untranslated region.

A) Established BENIGN Genomic Region

Gene 1  Gene 2  Gene 3  Gene 4 

Category 2F

Complete overlap, similar in size

Category 2F

Completely contained within an established benign genomic region

Category 2G

Overlaps, but includes additional genomic material

Category 2G

Partially overlaps, but includes additional genomic material

B) Established BENIGN Genomic Region

Gene 1  Gene 2  Gene 3  Gene 4 

Category 2C

Complete overlap, similar in size

Category 2D

Completely contained within an established benign genomic region; does not interrupt protein-coding genes

Category 2E

Completely contained within an established benign genomic region; potentially interrupts protein-coding genes

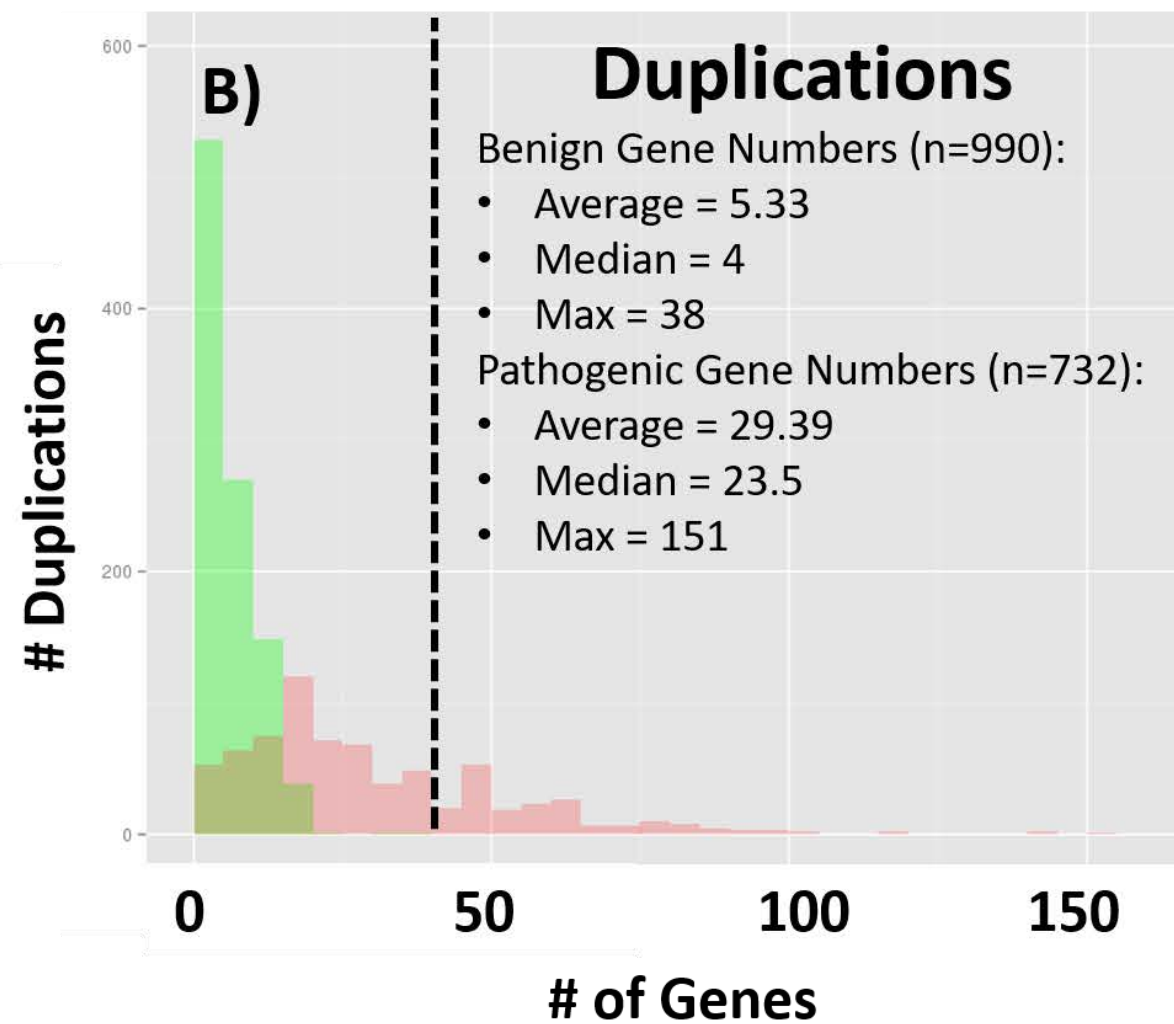
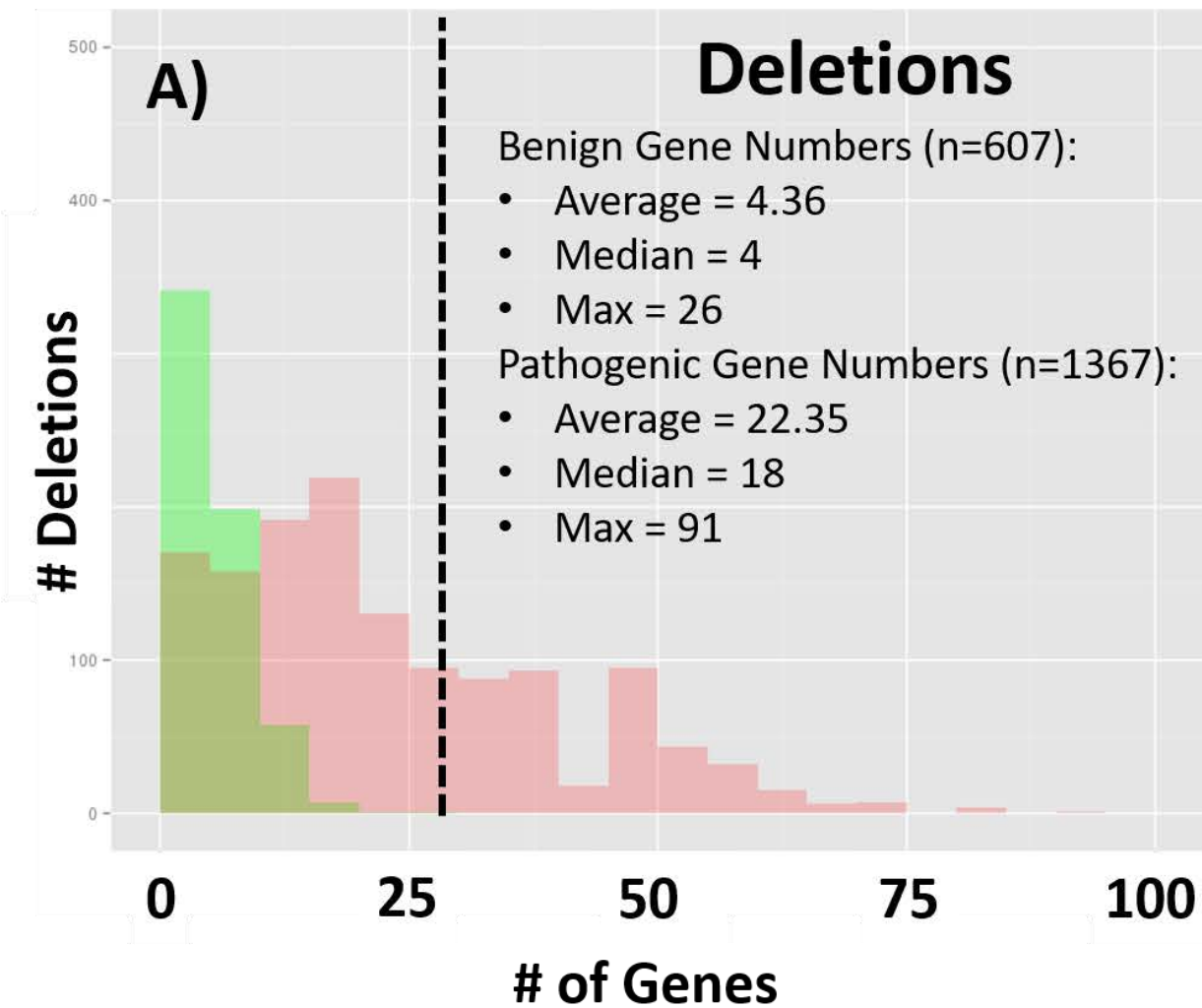
Category 2F

Overlaps, but does not include additional protein-coding genes

Category 2G

Overlaps, but includes additional genomic material

Supplemental Figure 1.4: Illustrations of scoring metric categories 2F-2G (loss metric) and 2C-2G (gain metric) - overlap with established benign genomic regions. **A)** A theoretical established benign genomic region is shown in the context of several genes. Example overlapping deletions are shown below, each representing a scenario described in the loss scoring metric (Table 1, Main Document). **B)** A theoretical established benign genomic region is shown in the context of several genes. Example overlapping duplications are shown below, each representing a scenario described in the gain scoring metric (Table 2, Main Document). Red boxes represent deletions, blue boxes represent duplications.



Classified as “Benign”
 Classified as “Pathogenic”

Supplemental Figure 1.5: Analysis of gene content across clinically-classified copy number variants (CNVs) in dbVar. CNVs involving autosomes with clinical classifications between 200 kb-5Mb within dbVar studies nstd37 and nstd101 were analyzed for gene content. Those CNVs involving known dosage sensitive genes or genomic regions (as documented in dbVar study nstd45) were excluded. Gene arrays and non-protein-coding genes were not included in gene counts. The average, median, and maximum number of genes noted within benign (green) and pathogenic (red) deletions (A) and duplications (B) are depicted.

Supplemental Material 1: Using the Copy Number Variation (CNV) Scoring Metrics

General Instructions

Appropriate Use of the Scoring Metrics

The use of these scoring metrics presumes that a CNV otherwise meets the laboratory's size and quality thresholds for reporting. It is recommended that any size restriction for inclusion of a CNV in a clinical report be based on the laboratory's consideration of the performance characteristics and limitations of the methodology used and generation of a reasonable amount of clinical follow-up, rather than assumptions regarding clinical significance based on size alone.

The scoring metrics (Table 1 and Table 2, Main Text) are intended primarily for the evaluation of CNVs associated with genes/genomic regions associated with dominant, Mendelian inheritance patterns. They were not developed with the intent of independently evaluating CNVs exhibiting non-Mendelian inheritance patterns; however, many of the concepts presented here may prove useful in the evaluation of such CNVs.

It should also be noted that many recurrent CNVs exhibiting incomplete penetrance and/or variable expressivity have already been evaluated by resources such as the ClinGen Dosage Sensitivity (DS) curation process, which provides ongoing review of these and other genes and genomic regions (<https://www.ncbi.nlm.nih.gov/projects/dbvar/clingen/>). Those CNVs with well-documented clinical features and significance replicated across multiple independent studies (e.g., 16p11.2 proximal region deletion, 22q11.2 proximal [DiGeorge/Velocardiofacial Syndrome] region duplication) have ClinGen DS scores of 3; such CNVs would be classified as Pathogenic utilizing Category 2A of the scoring metrics ("complete overlap with established dosage sensitive gene/genomic region"). Conversely, certain recurrent CNVs have been observed across multiple independent studies to lack any consistent phenotypic association, and to have evidence against dosage sensitivity when evaluated in case versus control

populations (e.g., 15q11.2 [BP1-BP2] region duplications, 15q13.3 [D-CHRNA7 to BP5, nested] region duplications). These regions have been given ClinGen Dosage Sensitivity scores of “dosage sensitivity unlikely.” As such, these would be classified as Benign utilizing category 2F in the deletion metric, or categories 2C, 2D, or 2F in the duplication metric (“overlap with established benign gene/genomic region”). Use of these metrics for recurrent regions other than those with definitive evidence classifications should be performed with caution.

The scoring metrics are intended primarily for the evaluation of the most commonly encountered CNVs (i.e. single copy gains and losses). However, they may also be adapted to evaluate CNVs other than typical losses (i.e., copy number of 1) or gains (i.e. copy number of 3), including the following:

Evaluation of other copy number states

The metrics may be adapted for use in the evaluation of other copy number states, such as homozygous deletions (copy number of 0), or gains beyond a single extra copy (copy number of 4 or more). When evaluating any case, regardless of copy number state, one must look for evidence identical or similar in scope to the CNV type under evaluation. For example, if one were evaluating a triplication (copy number of 4), one would go through the gain scoring metric (Table 2) focusing on evidence relating to tetrasomy, though overlapping gains with established triplosensitivity may also be appropriate to include. Another example would be evaluating homozygous deletions. In this scenario, one must evaluate using evidence relating to both haploinsufficiency and nullisomy. With both copies of the allele lost, the patient could be at risk for either a more severe presentation of an autosomal dominant disorder (i.e., if the loss of both copies were not lethal), or an autosomal recessive condition.

Complex Rearrangements

When dealing with complex rearrangements, such as unbalanced translocations, one should evaluate each CNV separately (for example, evaluate the deletion portion of the translocation using the deletion metric, and the duplication portion using the duplication metric). The overall classification for the event should default to the most deleterious classification (for example, if the deletion portion were classified as “pathogenic” and the duplication portion was classified as “uncertain significance,” the event as a whole should be classified as “pathogenic.” The mechanism and consequences of complex rearrangements, including recurrence risks, should be discussed in the report.

CNVs on the X Chromosome

The scoring metrics may be used to evaluate losses or gains on the X chromosome, which represent different copy number types in males (copy number of 0 or 2, respectively) and females (copy number of 1 or 3, respectively). In many circumstances, males are affected by X-linked disorders and females are asymptomatic carriers. However, there are also X-linked disorders in which females are the predominantly affected sex (due to male lethality), or in which carrier females are known to display symptoms of varying degrees of severity (due to skewed X-inactivation and/or other factors). When evaluating CNVs on the X-chromosome, utilize any appropriate evidence related to affected individuals, regardless of sex. Classification of losses involving X-linked recessive genes in females should be based on the predicted impact in a male (i.e. pathogenic), though overall clinical significance may be uncoupled. See Supplement 4, Example 6, for an example of how to report an X-linked deletion in a female.

Beginning the Evaluation

After selecting the appropriate scoring metric (Table 1 for deletions, Table 2 for duplications), work through each evidence category moving from top to bottom. If a section does not apply, skip to the next section. For example, if the observed CNV does not overlap any established

dosage sensitive or benign genes or genomic regions (Section 2 in both metrics), move on to Section 3.

When evaluating individual CNVs using case-based evidence from the literature or internal/external databases, the following may be considered relevant: CNVs (of the same copy number state/type) with identical or highly similar in genomic content to the one under evaluation; LOF variants involving individual genes within the deleted region; or whole gene duplications of individual genes within the duplicated region. For many CNVs, particularly those without an established HI or TS gene/genomic region, it is often difficult to identify other CNVs with identical or highly similar genomic content, and evaluating individual genes within the CNV itself may be the best approach to identifying evidence. It may be most appropriate to focus first on evaluating gene(s) within the interval that have established disease relationships. Resources with well-documented gene-disease annotations, such as OMIM (<https://omim.org>) and ClinGen (<https://search.clinicalgenome.org/kb/gene-validity/>) can a good starting point for evaluating phenotypic overlap, mechanism of pathogenicity, and inheritance patterns of individual genes.

The ClinGen Dosage Sensitivity map specifically annotates and scores genes and genomic regions in relation to dosage sensitivity, and should be used to interrogate most CNVs. When selecting the gene(s) to take through the scoring metric, give precedence to the genes in the region that are associated with dominantly inherited disorders caused by an appropriate mutational mechanism (see below). If a laboratory chooses to report on carrier status for autosomal recessive carrier status, they should consider only those conditions for which loss of function is an established disease mechanism. Resources useful for evaluating gene inheritance patterns include OMIM and the ClinGen Gene-Disease Validity curations.

When evaluating gene-level evidence, one must evaluate the given CNV in the context of the mutational mechanism observed in that gene. Dominant disorders may result from mechanisms other than dosage sensitivity (for example, gain of function or dominant negative mechanisms), and in some cases, differing dominant phenotypes may be associated with the same gene (e.g., gain of function/activating mutations in *FGFR1* result in skeletal dysplasias, whereas deletions/loss of function variants are associated with Kallmann syndrome¹). A full extra copy of a haploinsufficient gene should not be presumed to be disease-causing unless it is specifically known to also be associated with a triplosensitive disorder (e.g., *PMP22*, which is associated with Charcot-Marie-Tooth disease [MIM: 118220] when duplicated and Hereditary Neuropathy with liability to Pressure Palsies [MIM:162500] when deleted). Full-gene duplications are commonly present as benign variation in the human genome^{2, 3}.

Scoring Ranges

A range is provided for most scoring categories to allow the user flexibility when considering evidence of different relative strengths. For example, in Section 4, individual probands described in the literature, public databases, and/or internal laboratory data may be more or less convincing than others depending on factors such as the mode of ascertainment, depth of clinical data, phenotypic specificity, inheritance pattern, and/or the presence of additional or alternative genetic or non-genetic etiologies. Users should assign more points for particularly strong evidence (e.g., a well-phenotyped, *de novo* case involving the same genomic content as the CNV being evaluated) and fewer points to weaker evidence (e.g., a case with limited clinical data and no inheritance information). At times, the recommended range will include 0; just because a piece of evidence in a particular category is available does not mean it warrants points. For example, a case-control study involving the CNV under evaluation may be published, but, for whatever reason, the study is deemed to be of poor quality. The user is not obligated to assign points for a poorly-designed study; if a score of “0” is the most appropriate,

then that is what should be assigned. Whenever a laboratory opts to deviate from the default recommended points for a particular evidence category, the reasons should be documented in their internal tracking systems and/or in the clinical report in an effort to move toward greater transparency in variant classification.

Arriving at a Classification

Once a score of 0.99 or greater (or -0.99 or fewer) has been obtained, the CNV classification has been made (pathogenic or benign, respectively). However, one should consider working through the remaining sections of the metric (particularly section 4, focusing on literature evaluation) to determine if there is additional information of clinical relevance to report. Consider, for example, a deletion involving multiple genes. If one of those genes is an established HI gene, then 1.00 points may be assigned per category 2A (deletion metric), and the variant classification is “Pathogenic.” However, there may be mounting evidence that HI of a different gene in that interval could be involved in a different phenotype. This does not change the classification (the CNV is still pathogenic), but the laboratory may wish to also comment on the potential clinical significance of the loss of the other gene in the clinical report.

It is recommended that laboratories keep track of the CNVs they evaluate and the evidence that supports them to alleviate the need to start the evaluation from the beginning each time a particular CNV is observed. Once a CNV has reached a classification of “pathogenic” via this scoring metric, it is not always necessary to fully reevaluate the evidence each time it is observed, though laboratories should confirm that no new evidence contradicting pathogenicity has emerged since the variant was last evaluated.

The following text describes each section in the scoring metrics in detail, providing examples to illustrate various concepts. Note that the section numbers are the same in both the deletion and the duplication scoring metrics, but the individual categories therein may differ.

Section 1: Initial assessment of genomic content

In this first evidence category, genomic content within the CNV is evaluated in a general manner. If the CNV contains or overlaps protein-coding genes or other known functionally important elements⁴ (1A), further evaluation (using the subsequent evidence categories) of the CNV is required. Examples of functionally important elements include: the *SHOX* enhancer 160 kb downstream of the gene⁵, the zone of polarizing activity regulatory sequence (ZRS) affecting the *SHH* gene (reviewed

here: https://www.ncbi.nlm.nih.gov/projects/dbvar/clingen/clingen_region.cgi?id=ISCA-37467), etc.

CNVs that are completely void of gene content, including intronic sequence, repetitive elements or pseudogenes, fall into category 1B. The recommended point score for these types of events is -0.60. In these scenarios, there may not be any evidence to interrogate about the genomic region, as no genes are present. With no evidence supporting or refuting pathogenicity, the default classification should be one of uncertainty, which is reflected in the recommended default score. Additional information, however, could move a CNV like this toward either pathogenic (P) or benign (B) as appropriate. Inheritance information from the family being studied (considered in Section 5) could be used to classify this type of CNV as likely benign (LB) or B. However, the possible presence of functionally important elements, such as promoters, enhancers, or other regulatory regions near coding sequence, should be considered with clinical correlation for possible effects on gene expression. In addition, given that CNV breakpoints are not precisely mapped due to gaps in probe or bait coverage, it is important to consider all genes in the maximum CNV interval before presuming a CNV to be clinically benign (even though reporting is often done on the minimal interval only). Further evaluation may be necessary to clarify the genomic content of the CNV for appropriate clinical interpretation. Generally, it is acceptable to adopt a laboratory policy not to report these CNVs or report them in a

supplemental list, as there is no relevant literature to interrogate. An exception might be made if the CNV exceeds a size cutoff established by the laboratory.

Section 2: Overlap with Established (or Predicted) Pathogenic or Benign Dosage

Sensitive Genes/Genomic Regions

In this evidence category, the CNV is evaluated for overlap with established dosage sensitive genes or genomic regions, or any established benign genes or genomic regions (i.e., known to be copy number variable in the general population). To aid the genomics community in identifying those genes and genomic regions that are HI and/or TS, ClinGen has developed the Dosage Sensitivity Map⁶, a publicly available resource cataloging evidence supporting and/or refuting the role of dosage sensitivity for genes and genomic regions. For the purposes of this framework, “established dosage sensitive” (DS) genes or genomic regions are those that have been evaluated and shown to have sufficient evidence for HI and/or TS (i.e., a score of 3).

“Established benign” genes or genomic regions are those that have been evaluated and shown to be copy number variable in the general population (i.e. a score of “dosage sensitivity unlikely”). A list of genes and regions that have been evaluated using these criteria is updated daily and can be accessed at <https://www.ncbi.nlm.nih.gov/projects/dbvar/clingen/>.

Those CNVs completely containing established dosage sensitive genes or genomic regions may be considered “pathogenic” (category 2A; illustrated in Figures S1.1 and S1.2). If the CNV under evaluation partially overlaps an established dosage sensitive genomic region, further evaluation is required to determine whether the causative gene or critical region for the established region is known. If the critical gene/region has not yet been established (category 2B; illustrated in Figure S1.2), additional evidence will be necessary to determine the clinical relevance of the CNV under evaluation. For example, though the clinical significance of the 1p36 deletion (MIM: 607872) has been appreciated for some time, there is still no established causative gene or critical region^{7, 8}; deletions overlapping (but not completely encompassing this

region) would fall under category 2B, and would require further evidence to determine their classification and clinical significance. If the CNV partially overlaps a curated HI or TS gene, additional evaluation to determine the potential functional effect is required based on breakpoint location, involvement of coding sequence (for partial gene deletion/duplication) and evidence from the literature (categories 2C-2D in the deletion metric [Table 1], 2J-2K in the duplication metric [Table 2]; illustrated in Figure S1.3).

Similar logic applies when a CNV overlaps an established benign gene or genomic region. For the purposes of this framework, “established benign” genes or genomic regions are those evaluated and determined to be “dosage sensitivity unlikely” per the ClinGen Dosage Sensitivity Map. In general, these are CNVs that occur at high frequency in the general population (1% or higher), are not known to be more frequent in cases compared to controls and are not associated with any consistent phenotype. When a CNV under evaluation is contained completely within one of these genes/regions, it may be considered “benign” (category 2F in the deletion metric [Table 1], and categories 2C, 2D, and 2F in the duplication metric [Table 2]; illustrated in Figure S1.4). If the CNV under evaluation overlaps an established benign gene/region but is larger, it may contain clinically relevant genes or functionally important elements (such as regulatory regions for nearby HI genes) (category 2G; illustrated in Figure S1.4), and additional evaluation is recommended.

In general, if a CNV reaches a 1 or -1 score due to complete overlap with an established dosage sensitive gene or region, users of these metrics may not need to proceed further; however, for some CNVs, particularly those with incomplete penetrance and/or variability expressivity, additional evaluation may be necessary, and caution is recommended before interpreting a CNV based on this information alone. When reviewing ClinGen DS scores, it is important to note the date of last evaluation, as curations reflect a temporally static assessment.

New evidence may have emerged since the date of last evaluation, either supporting or refuting the original assessment.

Deletions partially overlapping established HI genes (categories 2C-2D in the deletion metric)

Special considerations may apply when a deletion partially overlaps an established HI gene. Note that these evidence categories are only applicable if the testing platform has sufficient resolution to identify such events. If the 5' end of the gene is involved, one must consider whether the deletion also involves additional coding sequence (category 2C-1), or if it is just restricted to the 5' untranslated region (UTR) (category 2C-2) (illustrated in Figure S1.3).

If additional coding sequence is involved, scoring should be based on the likelihood that a functional protein could still be produced. Deletions that include 5' UTR exons, first coding exons, or internal exons are typically deleterious in LOF genes. If the gene has alternative in-frame methionine downstream of the deletion, or if an alternatively spliced isoform is not encompassed by the deletion, consider downgrading from the suggested default number of points. If a significant portion of the gene is deleted, or if a known functional domain is deleted, consider upgrading the suggested default number of points. If the deletion only involves the 5' UTR, but the promoter is well-characterized and included in the deleted interval, consider upgrading the suggested default number of points.

When only the 5'UTR is involved, the recommended default score is 0. However, there are genes in which there is evidence supporting the role of 5'UTR variants in disease⁹. In these scenarios, it may be appropriate to upgrade within category 2C-2.

If a deletion partially overlaps the 3' end of the gene (category 2D; illustrated in Figure S1.1), one must consider whether or not the resulting protein product is expected to undergo nonsense-mediated decay (NMD). Deletions that involve the last exons of a LOF gene are not universally pathogenic if amino acids in the carboxyl terminus of the encoded protein are

dispensable. If only the 3' UTR is involved (category 2D-1), the recommended default score is 0. If the deletion involves only the last exon, the resulting protein product is expected to escape NMD. If, however, there is evidence to suggest that the last exon is critical to the protein's function (for example, if other established pathogenic variants have been documented in that exon), then such a deletion may be disease-causing (category 2D-2). Use the scoring range to reflect the level of confidence that the last exon is critical to gene function (e.g., increasing points with increasing number of documented pathogenic variants, functional studies showing that loss of the last exon results in disrupted function, the last exon is within an established variation hotspot, etc.). If there is no evidence to suggest that the last exon is critical to the gene function (for example, no other pathogenic variants have been reported in that exon) (category 2D-3), the recommended default score is 0.30. If a deletion overlaps the 3' end of the gene and includes exons other than the last exon (category 2D-4), NMD is expected to occur, and the recommended default score is 0.90. Consider upgrading from the default score if there is additional evidence to suggest a detrimental effect on the protein (for example, if a significant percentage of the protein is expected to be missing).

Deletions and duplications within individual genes (category 2E in the deletion metric; 2I in the duplication metric)

With the increasing resolution of array and NGS-based approaches, it is now possible to identify losses and gains of genomic material within individual genes. As opposed to multigenic CNVs (i.e., those CNVs involving more than one gene), these smaller, intragenic variants may be evaluated similarly to sequence-level variants. Guidelines for the interpretation of sequence variants already exist¹⁰, and additional efforts are underway to further clarify how best to utilize these¹¹⁻¹³. The ACMG/AMP sequence variant evidence category most directly applicable to intragenic deletions and duplications is PVS1, the rule that evaluates null variants in genes for which LOF is a known disease mechanism. The original publication, however, did not provide

specific guidance regarding when PVS1 should be applied, or scenarios in which PVS1 (a “very strong” piece of evidence) should be used at the original strength or downgraded. The ClinGen Sequence Variant Interpretation (SVI) working group recently put forth some additional considerations regarding use of the PVS1 rule¹⁴. To promote consistency and transparency across the field, we recommend that intragenic deletions and duplications within established HI genes⁶ be evaluated according to these criteria. A helpful flow-chart is provided in that manuscript that walks the user through how to determine the relative evidential strength of a given intragenic deletion or duplication. Each PVS1 category as described in that manuscript has been associated with a numerical point score in both the deletion (category 2E) and duplication (category 2I) metrics. Briefly, for intragenic deletions, one must consider: whether or not the deletion disrupts the reading frame; whether or not the deletion is predicted to undergo NMD; if the deleted exons are present in biologically-relevant transcript(s); if the truncated/alterd region is critical to protein function; the frequency of LOF variants in the involved exon(s) in the general population; and the amount of protein removed by the deletion. For intragenic duplications, one must consider: whether or not the duplication is in tandem; if the reading frame is disrupted; and if NMD is predicted to occur. Duplications affecting individual genes are typically expected to be in tandem rather than as insertions or translocations elsewhere in the genome¹⁵. Partial-gene duplications including terminal coding exons, i.e., either the first or last exons, of any type of gene are also often not deleterious because functional gene structure may be preserved. Surveys of benign variation have shown a preponderance of such duplications as well in the general population³. In contrast, duplications with breakpoints entirely within a gene and not involving terminal exons can be deleterious because they can disrupt the reading frame or splicing. In specific cases, it is essential to accurately determine the reading frame because it has known clinical implications (e.g., distinguishing between Duchenne and Becker muscular dystrophy).

When intragenic CNVs are being identified by chromosomal microarray (CMA), it is at times not possible to determine with certainty which elements may be involved, or whether or not the variant will disrupt the reading frame, due to array design and/or gaps in probe coverage. If information necessary to work through the PVS1 flow chart¹⁴ is not available, always default to the least impactful option. For example, if it is not clear whether a particular intragenic deletion disrupts the reading frame, select the arm of the flow chart that corresponds to deletions that preserve the reading frame. If available/feasible, one may also refer the patient for additional molecular testing to better characterize the event if the particular testing platform has technical limitations.

Evaluation of HI predictors (Section 2H, deletion metric only)

Computational (*in silico*) predictors of gene and variant function provide supportive evidence in the evaluation of sequence variants. Similarly, for the evaluation of CNVs, HI predictors may be used as supporting evidence for copy number losses. These types of *in silico* predictions do not need to be used for deletions that involve a gene which has been already established to cause disease due to HI or LOF (categories 2A-2E, deletion metric); use of this evidence is restricted to intervals encompassing genes of uncertain clinical significance.

Two HI predictors currently in common use are the gnomAD probability of loss of function intolerance (pLI) score¹⁶ and the DECIPHER HI index¹⁷. Note that these tools represent predictions; to our knowledge, the sensitivity and specificity of these tools to accurately predict haploinsufficiency have not been studied. Conservatively, both predictors must have strong HI scores to be included as supportive evidence. A deletion involving at least one gene with a gnomAD pLI score ≥ 0.9 (and upper bound of the observed/expected confidence interval <0.35) and a DECIPHER HI index of $\geq 10\%$ will qualify for scoring in this category. The points associated with this category should only be given once; do not count this piece of evidence multiple times, even if there is more than one gene in the region predicted to be HI.

Section 3: Evaluation of Gene Number

Though CNV size is generally used as a proxy for pathogenicity, exceptions often occur. Some CNVs that are very large, including cytogenetically visible imbalances, can be benign in nature¹⁸⁻²¹, while very small CNVs, such as focal gene and intragenic deletions and duplications, can be pathogenic due to dosage sensitivity.

In order to understand the impact of gene content on CNV pathogenicity, we evaluated the gene content of over 5000 clinically-classified copy number gains and losses from publicly available datasets (studies nstd37 and nstd101 in dbVar). Autosomal CNVs included in this study were classified using a 5-tier clinical classification system (benign, likely benign, uncertain, likely pathogenic, pathogenic). We controlled for CNV size (200 kb-5 Mb) and reduced the number of duplicate CNVs by only including a single representative CNV if all associated clinical classifications were the same. We excluded duplicate CNVs with multiple clinical classifications, non-protein coding genes, known dosage sensitive genes and known pathogenic or benign regions within dbVar study nstd45. **G**ene arrays were defined by greater than five genes in a family within a CNV and were reduced to count as one gene, by utilizing a custom script to identify genes with the same three starting characters.

We found that the median gene content of duplications classified as pathogenic (n=732) was 23.5 (average number of genes = 29.39, min=0, max=151), whereas for the median gene content of duplications classified as benign (n=990) was 4 (average number of genes = 5.33, min=0, max=38). Similarly, for deletions classified as pathogenic (n=1367), the median gene content was 18 (average number of genes = 22.35, min=0, max=91), and for deletions classified as benign (n=607), the median gene content was 4 (average number of genes = 4.36, min=0, max=26). We used over-lay of histograms (bin size = 10) of pathogenic and benign CNVs to determine optimal data segments (Figure S1.5).

Given these results, a stratified approach was developed that combined reported standard practice of participating laboratories with the results of gene content analysis. Deletions containing less than 24 genes and duplications containing less than 34 genes (category 3A) are not assigned any points; in general, pathogenicity in this gene range can be quite variable and very dependent upon the actual genes therein (i.e., whether or not one or more is dosage sensitive). Deletions containing between 25 and 34 genes, or duplications containing between 35-49 genes (category 3B) are assigned 0.45 points (a strong level of evidence). Deletions containing 35 or more genes, or duplications containing 50 or more genes (category 3C) are assigned 0.90 points (a very strong level of evidence). Note that, although these gene bins were determined using data from autosomes only, the relationship between gene count and pathogenicity should generally also apply to CNVs on the X-chromosome. Our results demonstrate that, in general, when a CNV contains a very large number of genes, it becomes more likely that loss or gain of this amount of genetic material will result in some demonstrable phenotypic consequence.

In practice, when using Section 3 in the gain and loss scoring metrics, err on the side of caution if a CNV involves clusters of genes or gene families, particularly those that are non-coding or lack any known clinical association. We recommend counting each cluster/family as a single gene. Exceptions include gene families in which individual genes are known to be associated with disease (such as the SCN gene cluster region at 2q24.3); in these cases, the disease genes may be counted individually.

Section 4: Detailed Evaluation of Genomic Content Using Cases from Published Literature, Public Databases, and/or Internal Laboratory Data

Many CNVs will not overlap established dosage sensitive genes or genomic regions; for these CNVs, gene content should be scrutinized for documented and relevant clinical association. When evaluating other data sources, such as published literature, public databases, and/or

internal laboratory data, one is looking for case-level or case-control data that support or refute the clinical significance of the genomic region under evaluation. The primary source for this type of information is peer-reviewed medical literature, however supportive information may also be obtained from public databases (ClinVar²², DECIPHER²³, etc.) or internal laboratory databases. We recommend that laboratories develop processes to document, track, and re-evaluate previously classified CNVs, including pathogenic CNVs, CNVs of uncertain significance, and CNVs that have been determined to represent benign variation, and share this information with the community through publicly available databases such as ClinVar.

Use judgment when opting to include data from a public or internal laboratory database as evidence. For data available in public databases, consider the amount of supporting evidence available to allow for independent evaluation of the clinical classification provided. For internal laboratory data, consider possible sources of bias, such as platform-specific artifacts and population sampling bias. Consider assigning higher or lower points based on the quantity and quality of the data available. Primary data should involve observations of related variants in humans, while *in vitro* or *in vivo* studies may be viewed as supportive. Use of evidence derived solely from model systems is generally discouraged, particularly for CNVs associated with non-specific conditions (e.g., intellectual disability) and/or limited evidence regarding gene function (e.g., the only information available for a gene is documented neuronal expression).

Individual Case Evidence

Case-level data includes other reported probands with CNVs similar in genomic content to the CNV under evaluation. For copy number losses, one may also consider probands with deletions or LOF variants of individual genes within the loss under evaluation; for copy number gains, one may also consider probands with full gene duplications of individual genes within the gain under evaluation. When evaluating case-level data reported in the literature, one must consider the clinical context in which the variant was observed. In general, probands with

similar, highly specific, well-defined phenotypes represent stronger evidence than probands with disparate or non-specific phenotypes. For the purposes of this framework, “highly specific, well-defined” phenotypes are those that are both distinct and have a known genetic etiology with limited genetic heterogeneity. Examples of “highly specific, well-defined” phenotypes include congenital anomalies (e.g., skeletal dysplasias, midline facial defects, holoprosencephaly, etc.) or a constellation of findings (e.g., coloboma, heart defects, choanal atresia, growth delays, genital anomalies, and ear abnormalities associated with CHARGE syndrome (MIM:214800)). “Non-specific” phenotypes are those that may be more common in the general population, have more considerable genetic heterogeneity, and/or can be caused by etiologies other than genetic variation. Examples of “non-specific” phenotypes include autism spectrum disorder and intellectual disability. Inheritance information, when available, can be used to modify the strength of case-level evidence. For example, a higher score should be assigned to cases with *de novo* occurrences or strong segregation amongst similarly affected family members compared to cases with unknown inheritance.

De novo Occurrences (categories 4A-D)

The fact that a variant occurred *de novo* in an affected individual with no family history of disease lends credence to that variant’s possible clinical significance; this information alone, however, is not enough to infer that a particular variant is disease-causing. The ClinGen SVI working group has developed parameters for evaluating the relative strength of *de novo* occurrence evidence based upon the phenotypic consistency, total number of *de novo* observations, and whether or not parental relationships have been confirmed

(https://www.clinicalgenome.org/site/assets/files/3461/svi_proposal_for_de_novo_criteria_v1_0.pdf).

Briefly, those cases with highly specific and relatively unique phenotypes (e.g., those with pathognomonic features for a specific condition) and confirmed parental relationships (i.e., both

maternity and paternity have been confirmed) constitute the strongest level of evidence (category 4A). Cases with highly specific (but not necessarily unique) phenotypes, consistent with what is expected for a given gene/genomic region, represent a moderate level of evidence (category 4B). Examples of this scenario may include phenotypes that are relatively rare in the general population but may also be associated with more than one known genetic cause, such as early infantile epileptic encephalopathy. Phenotypes that are consistent with what is expected for a given gene/genomic region but are not highly specific and are noted to have high genetic heterogeneity (e.g., intellectual disability, autism spectrum disorder, etc.) are considered supporting evidence (category 4C). In all categories, if parental relationships are assumed but not confirmed, relative strength is decreased, and points are subsequently reduced. A range is provided for all categories to allow for flexibility when assessing phenotypes of different relative specificity.

The ClinGen SVI *de novo* criteria recommendations were written for the evaluation of sequence-level variants within genes of known clinical significance and focus on the consistency of the observed phenotype with the phenotype that is known to be associated with variation in a particular gene. However, these concepts can be adapted for the process of CNV evaluation, which often requires the assessment of both genes of known and unknown clinical significance. When the gene(s) being assessed are of known clinical significance, points should be assigned for each reported *de novo* observation according to the appropriate category (4A-4D) up to a maximum total value of 0.90 points. For example, variation in gene X may be commonly associated with disease Y; however, gene X has not previously been evaluated by the ClinGen Dosage Sensitivity process, and it is unclear whether haploinsufficiency is the disease mechanism for disease Y. The CNV under evaluation is a deletion that includes gene X. There have been two reports of probands in the literature with *de novo* LOF variants in gene X and phenotypic features consistent with and highly specific for disease Y (Category 4A). One of

these probands has confirmed parental relationships (0.45 points), the other has assumed parental relationships (0.30 points). Based on this information 0.75 total points would be assigned in this section.

When the gene(s) being assessed are of unknown clinical significance, the expected phenotype associated with the gene is unknown. In this scenario, consistency of the observed phenotypes with each other, as well as their relative specificity is critical. Because there is no “expected” phenotype against which to compare, there must be at least two *de novo* cases with similar phenotypes before evidence can be counted. Each additional case observed with a consistent phenotype may be awarded additional points. For example, consider gene X as a gene of uncertain significance. There have been 3 reported *de novo* deletions in the literature, each with developmental delay. Developmental delay is a non-specific and highly heterogeneous phenotype; however, it is consistently observed across all three cases (Category 4C). All 3 cases have confirmed parental relationships. In this scenario, 0.15 points would be assigned to the first two cases, and an additional 0.15 would be assigned to the third, for a total of 0.30 points.

When there is only a single *de novo* case reported in the literature for in a gene of uncertain clinical significance, it may be unclear whether the observed phenotype is due to the observed *de novo* variant or some other cause entirely (genetic or otherwise). In this scenario, if the variant under evaluation by the laboratory is *de novo*, and the phenotype reported to the laboratory is consistent with the phenotype of the single reported *de novo* observation in the literature, these two cases could be used together to meet the consistency requirement. However, if this is the case, the proband under evaluation should not be assigned additional points in Section 5 of either scoring metric.

If the reported phenotype is either NOT consistent with what is expected for a given gene/genomic variant, or simply not consistent in general, clinical judgement should be used to

determine if this should result in 0 added points to the evaluation, or negative point values (i.e., evidence *against* a role in pathogenicity). Negative point values could be considered with increasing evidence of inconsistency. For example, consider a *de novo* deletion of a particular gene or genomic region reported twice in the literature - once in a seven-year-old with developmental delay, and once in a newborn with a congenital anomaly. Though the reported phenotypes are not the same, there is not enough information here to constitute evidence against a role in pathogenicity - the newborn may ultimately go on to be diagnosed with developmental delay, and it may be unclear whether the older child was assessed for the congenital anomaly. A scenario like this may warrant 0 points. Next consider a scenario in which *de novo* deletions have been observed in 5 cases in the literature - all in well-phenotyped, older individuals - 1 with developmental delay, 1 with a history of cardiac defect and normal development, 1 with a history of genitourinary anomalies and normal development, and 2 in individuals from the general population. In this scenario, with such disparate phenotypes and reasonable confidence that there are no overlapping phenotypes, negative points may be assigned.

Unknown Inheritance (category 4E)

Occasionally, particularly in older literature, there are probands with compelling phenotypes and CNVs similar in genomic content to the CNV under evaluation (or other variants appropriate for inclusion, such as LOF variants in genes included in copy number losses, or whole gene duplications of genes included within copy number gains, etc.) but without inheritance information. Caution should be used when deciding whether to include these cases as evidence, as knowing whether a particular variant is *de novo*, inherited from an affected parent, or inherited from an apparently unaffected parent constitute different levels of evidence in the clinical evaluation of that variant. It is recommended that these types of cases only be included as evidence if the phenotype in the proband is highly specific and consistent with that of other

probands for which inheritance is known, and only be assigned a minimal number of points. These types of cases should not be used in the setting of nonspecific phenotypes (e.g., developmental delay or autism spectrum disorder).

Segregation Among Similarly Affected Family Members (categories 4F-4H)

Segregation of a variant among similarly affected family members can lend support to the argument that the variant may be disease-causing. It is important to remember that segregation implicates a locus, not necessarily a particular gene or variant. While a given variant may be segregating within a family, it may be in linkage disequilibrium with the true causative variant. At least 3 documented segregations among affected individuals must be documented in order to assign points per this scoring metric; segregations may be added across families. In order to simplify the process of assessing segregation evidence, we recommend an approach consistent with the ClinGen gene-disease validity evaluation process²⁴; only those individuals with both the genotype and the phenotype, or individuals who are obligate carriers by virtue of their position in the pedigree, should be counted as evidence toward segregation. This is a conservative approach. Given the variability in literature reporting, it is often not possible to consistently gather accurate information on other family members' phenotypes and/or genotypes, and therefore we believe that such a conservative approach is appropriate. The number of segregations and suggested points included in categories 4F-4H serve as a guide; consider assigning fewer than the suggested number of points if the variant was observed via candidate gene sequencing only (as opposed to other genome-wide assessments, such as exome sequencing). Note that phenotypes segregating in a family may exhibit variable expressivity but may still be part of the same phenotypic spectrum. For example, autism spectrum disorder, intellectual disability, seizures, and schizophrenia observed in different individuals may all be caused by the same CNV as part of the developmental brain disorder spectrum²⁵.

Apparent Non-Segregation (categories 4I-4K)

Instances in which the variant appears NOT to segregate with affected status must be interpreted with caution. Apparent non-segregations include: 1) instances in which another *affected* individual in the family is found *not* to have the variant in question (category 4I), and 2) instances in which an *unaffected* individual *is* found to have the variant in question (categories 4J and 4K). In scenario 1 (category 4I), before considering this evidence against the pathogenicity of the variant and assigning negative points, one must consider whether there may be a biologically plausible explanation for this non-segregation, such as the presence of phenocopies. This scenario is more likely to occur in the setting of disorders that are more common in the general population (for example, breast cancer) and/or disorders that are known to have both genetic and non-genetic causes (for example, cardiomyopathy). Assign the default number of negative points (-0.45) when the individuals in the family are affected with similar, highly specific phenotypes (with no known phenocopies) and are not found to carry the same variant. Consider downgrading this evidence when phenocopies are a possibility.

In scenario 2 (categories 4J and 4K), one must consider whether the family member found to have the variant is truly unaffected. This can be difficult to determine, particularly in cases ascertained through the literature, public databases, or even internal laboratory databases, as it is often not possible to request additional clarifying information. Truly affected individuals may appear to be unaffected in the context of variable expressivity, reduced or age-dependent penetrance, disorders with subtle clinical manifestations, incomplete clinical evaluation, or novel disorders in which the phenotypic spectrum has not yet been well characterized. Specificity of the phenotype plays a role in how confident one can be in a family member's "unaffected" status, and the recommended point values vary accordingly (e.g., finding a variant in a person unaffected for a specific, unique phenotype [4J] is stronger evidence against pathogenicity than finding a variant in a person unaffected for a non-specific phenotype [4K]). For example: the phenotype under investigation is specific and well-defined, such as a rare eye phenotype only

appreciable with dilated eye examination. If the family member were evaluated by an ophthalmologist with dilated eye exam and found not to have said eye phenotype, assign the default number of negative points for a family member with the variant but unaffected with the specific, well-defined phenotype (-0.30 points, category 4J). If the family member were evaluated by a general practitioner, and it is unclear whether a dilated eye exam was performed, consider downgrading this evidence. In this scenario, 0 points may be appropriate if a dilated eye exam was not performed; there would be no way to know whether this individual was truly unaffected or not without this study.

Now consider a less specific phenotype, such as autism spectrum disorder. If the family member were thoroughly evaluated (for example, by a developmental pediatrician using validated measures of cognitive and social development) and said to be unaffected, consider awarding the default number of negative points for a family member with the variant but unaffected with a non-specific phenotype (-0.15 points, category 4K). Consider downgrading or not awarding any negative points at all if, for example, that family member is simply stated in a publication not to be affected, but no details of their evaluation are provided. Note that, when evaluating literature, public databases, and/or internal laboratory databases, points can be assigned per independent family observed up to the maximum number of points recommended for that particular category.

Case-Control or General Population Data (categories 4L-4O)

If the CNV has been studied as part of a well-powered case-control study with adequate numbers of cases and controls, points may be added or deducted based on enrichment (or lack thereof) in the clinical population. Interpretation of case-control data should include evaluation of significance (i.e. p-value), effect size (e.g. likelihood ratio), and clinical information (e.g. phenotypic specificity). Similar to categories defined for sequence variants¹⁰, CNVs in this category will be observed at a significantly higher frequency in cases versus controls ($p < 0.05$),

and with a strong effect size (odds ratio or likelihood ratio >5) and relatively narrow associated 95% confidence interval (lower bound >1). CNVs with the highest points values in this category will be observed in association with a consistent, specific, well-defined phenotype (0.45 points, category 4L); those lacking phenotypic specificity, but enriched nonetheless will also be counted (0.30 points, category 4M). Alternatively, CNVs that are not enriched are observed at similar (or higher) frequencies in controls compared to cases, may be deducted points, particularly when such CNVs are also relatively common (e.g. >0.1% frequency, -0.90 points, category 4N).

When evaluating case-control studies, be cognizant of the methods by which controls were ascertained, as well as the methods by which they were tested. Be aware of biases that might exist if alternate testing platforms were used for cases and controls. CNVs that have been observed in both affected and reportedly unaffected individuals, outside of the context of a disorder for which reduced penetrance and variable expressivity are well understood, should not be immediately dismissed as potentially causative variants without careful consideration.

Clinical judgment should be used to determine the appropriate classification for these types of CNVs. A points range (to 0, categories 4L-4N) is provided to account for case-control studies that are underpowered, biased, conflicting, and/or indicate weaker statistical associations.

Though a variant may not have been evaluated as part of a formal case control study, it is still possible to gather information about its presence or absence in the general population through resources which catalog copy number variation in reference populations, such as the Database of Genomic Variants (DGV)² or the gnomAD structural variant (SV) dataset

(<https://www.biorxiv.org/content/10.1101/531210v3>) (category 4O). The DGV compiles variation observed across multiple studies - these studies are often conducted on different platforms and at different levels of quality. To aid the user in identifying the most high-confidence, high quality CNVs observed in reference populations, DGV has developed a curated “Gold Standard” dataset. The Gold Standard dataset is a subset of the total DGV data that includes only those

CNVs from genome-wide, high resolution assays with the most accurate breakpoint resolution that have passed internal quality control metrics. Using these data, DGV can provide more accurate frequency estimates and population distribution information. This data is available as a standard track on the DGV website, <http://dgv.tcag.ca/dgv/app/home>. In 2019, the gnomAD database released a set of approximately 500,000 structural variant calls from approximately 15,000 genome sequencing samples with accompanying frequency information. Of note, population data for copy number variants has historically not been as robust as population data for sequence variants; as resources like DGV and gnomAD continue to add data and new populations, these datasets will become increasingly more valuable in the variant classification process. In general, for the purposes of clinical CNV evaluation, a CNV may be considered “common” in the general population if it is present at a frequency of 1% or greater in the DGV Gold Standard dataset (or other high confidence dataset); variation observed at this frequency in the general population may receive the default number of points for this category, -1 points. Consider assigning less weight if a variant is observed in the general population, but at a frequency lower than 1%. Note that expected carrier frequencies associated with autosomal recessive diseases may be higher than 1%; do not use this criterion to classify a CNV as “benign” if there is a well-known autosomal recessive disease gene (for which loss of function is the established disease mechanism) in the interval.

Consider downgrading if there are reasons to question the reported population frequency of a variant. When evaluating variation in the general population, consider the number of samples the variant was observed in compared to the number of the samples where that particular locus was examined; when the frequency is extremely high (i.e., >99%), it may be because the locus was only examined in a very small proportion of the overall cases, and/or the variant may represent a reference artifact. Additionally, consider the genomic architecture in the area under investigation; common population variants may occur near known disease-causing regions. For

example, there are segmental duplications around the promoter and first exon of *KANSL1*, the gene that has been established as causative of Koolen-Devries syndrome^{26, 27}. As a result, variation around the 5' end of this gene appears frequently in the general population.

Additional considerations when evaluating case-control or general population data include:

- ï Dosage of copy number imbalance reported in the general population studies. The CNV observed in the general population might exclusively represent a copy number gain. If the CNV in question overlaps the same region, but is a copy number loss, a pathogenic outcome cannot be excluded. The opposite situation also applies. Similarly, a CNV observed commonly as a heterozygous deletion in the general population may have a pathogenic outcome when present in a homozygous state.
- ï Size of the reported benign CNV relative to the CNV in question. One should ensure that the CNV reported in the general population includes the same gene content as the CNV being interrogated. Different array platforms represented in public databases can lead to differences in reported sizes of identical CNVs.
- ï Sex of individual in database relative to patient sex. This consideration is particularly important for X-linked CNVs in males, as many of the variants are seen in females who may be non-manifesting carriers of the condition. In addition, consider that contributors to these databases may have excluded the sex chromosomes from analysis; therefore, CNVs mapping to the X and Y chromosomes may be under-represented.
- ï Validity of the CNV reported in general population databases. The majority of CNVs reported from large population studies have not been experimentally validated; therefore, CNVs reported in a single study or through use of a single platform should be interpreted with caution.
- ï Clinical characterization of “normal” individuals. One should consider the extent of clinical characterization of individuals represented in the database. Each population

series is selected based on defined criteria, usually outlined in the primary reference. Consider how these individuals were selected for inclusion and how likely it is that the clinical phenotype presented in the patient of interest might be present in the “normal” population. Factors such as incomplete penetrance, variable expressivity, age of onset, and parent of origin imprinting effects need to be considered before classification of a CNV as benign in all instances. CNVs occurring with relatively high frequency in the general population and in multiple publications may be interpreted with more confidence as benign in nature. Of note, many publications use the same reference set (e.g., HapMap); therefore, a CNV represented in multiple publications may represent the same individual studied multiple times.

Section 5: Evaluation of Inheritance Pattern/Family History for the Patient Being Studied

When available, inheritance and family history information for the patient being studied may provide evidence supporting or refuting the pathogenicity of the observed variant. Although this is a very relevant line of evidence by which to gauge clinical significance, it is important to stress that it is difficult and often imprudent to attribute clinical significance based on the inheritance pattern of a CNV in a single family. It is only through ascertainment of significantly large families with multiple affected and unaffected family members segregating a given CNV or ascertainment of multiple individuals with the same CNV that a true measure of clinical significance can be confidently assessed. For this reason, the ACMG strongly supports efforts to collect and curate de-identified patient data from clinical studies to facilitate rapid and unambiguous assessment of the clinical significance of CNVs^{23, 28, 29}.

Points should be assigned for inheritance information in the patient being studied (i.e., *de novo*, inherited from an unaffected family member, inherited from an affected family member) using the same considerations and with the same caveats as discussed in the section above about

scoring inheritance information for subjects obtained from the literature, public databases, or internal laboratory databases. If inheritance information is unknown or uninformative (for example, only one parent is available for follow-up, and the CNV is not found in the parent available for study), and no information is known about the patient phenotype, no points can be awarded (category 5F). As discussed above, when a CNV is found in a parent or other relative, the carrier parent and other relevant family members should have a thorough medical evaluation for the presence or absence of the clinical features present in the proband. When this information is not provided to the laboratory, this should be included in the report with a recommendation for correlation with parental clinical features. Do not add or deduct points for inheritance from a parent if the affected status of that parent is unknown.

When inheritance information is unavailable or uninformative, but the patient phenotype is consistent with what has been described in similar cases (categories 5G and 5H), points may be assigned dependent upon the relative specificity of the phenotype. In general, cases under evaluation by the clinical laboratory should be scored in a similar manner to relevant cases observed in the scientific literature (e.g., *de novo* cases scored similarly to literature *de novo* cases, inherited cases scored similarly to other cases with the same inheritance pattern, etc.). In categories 5G and 5H, the ranges allow the laboratory to upgrade or downgrade evidence from their observed case based upon their presumed ability to obtain more detailed clinical information, including pertinent negatives (e.g., phenotypes reported in the literature that the patient under evaluation has been determined NOT to have), from the referring clinician, something that is typically not possible in literature cases. If this is not possible, or if any questions remain about how well a patient's phenotype matches with what has been previously described, score as you would an additional case observed in the literature.

When evaluating inheritance in the context of "affected" vs. "unaffected" family members, consider the specificity of the phenotype, as discussed above. Special considerations that

preclude confident inference and may only be well defined after ascertainment of multiple families include the following:

- ï Incomplete penetrance: The CNV may be pathogenic but non-penetrant in the carrier parent^{30, 31}.
- ï Variable expressivity: The carrier parent may have subclinical features that will later be shown to be in the spectrum of the disorder caused by the CNV³².
- ï Parent of origin imprinting effects: The CNV region may be imprinted, such that the disorder only manifests when inherited from a particular sex (and the carrier parent is not manifesting the disorder because of chance inheritance)^{33, 34}.
- ï Sex-limited traits: Expression of the phenotype may be limited to one sex or the other. For example, the phenotype may only be confined to the prostate, ovaries, oocytes, sperm, etc.
- ï Second variant not detectable by original testing methodology: The proband may be manifesting a recessive disorder (e.g., a deletion may be inherited from an unaffected carrier parent and an undetectable variant inherited in a gene within the interval from the other parent). Alternatively, the proband may have one or more “modifier” genes/DNA elements not present in the unaffected parent.
- ï Mosaic CNV in parent: The CNV may not be present in all tissues of the parent, and therefore, the parent may not manifest all clinical features associated with the CNV^{35, 36}.

In general, however, points should not be deducted in the context of “non-segregation” if a parent with a CNV in the mosaic state does not exhibit the same features as a proband with the same CNV observed constitutionally. The same logic applies for hemizygous CNVs inherited from unaffected heterozygous mothers; in general, these should not be considered non-segregations.

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Supplemental Material 2: Validation of the CNV Scoring Metrics

Development of the copy number variant (CNV) scoring metrics (Tables 1 and 2 in the main document) was an iterative process using expert opinion regarding evidence sources and relative strengths, refined across multiple rounds of internal and external testing (Tables 1 and 2). Committee members discussed their internal laboratory evaluation processes, including the evidence types and resources they used most frequently and felt were most integral. These types of evidence were aggregated into the categories represented in Tables 1 and 2. Through discussion and case examples, the committee assigned relative weights to each evidence type. The scoring metric for deletions (Table 1) was developed and tested by committee members first, followed by development of the duplication scoring metric (Table 2) in order to retain consistency across similar evidence categories. The two metrics differ only where necessary due to the different potential impacts of deletions and duplications on overall gene-level pathogenicity. The duplication metric was also tested by the committee members upon completion.

The metrics were tested using CNV cases observed and reported from committee members' clinical laboratories (36 deletions and 34 duplications for a total of 70 CNVs). Committee members were not assigned to test the cases submitted by their own clinical laboratories; each CNV was "new" to the assigned reviewers. For a subset of 25 of these CNVs (15 deletions and 10 duplications), committee members were first asked to evaluate them as they typically would in their clinical laboratories, without using the proposed scoring metrics (henceforth referred to as "baseline" evaluations). These 25 CNVs were then evaluated using the scoring metrics by different committee members. An additional 45 CNVs were evaluated using only the scoring metrics, for a total of 70 CNVs. Overall, 33 of the deletions (91.7%) and all of the duplications (100%) were independently evaluated by 2 individuals using the metrics; 3 of the deletions

(8.3%) were evaluated by a single individual. In total, committee members made 137 individual classifications using the metrics.

In order to evaluate additional CNVs and to gain perspective from community members not directly involved in the scoring metric development process, 11 additional clinical cytogeneticists (8 based in the United States, 2 based in the United Kingdom, and 1 based in Australia) were invited to test the scoring metrics. External reviewers were only given the information in Tables 1 and 2; they did not have access to the full manuscript or Supplemental Material 1, as these documents were not completed at the time of external reviewer testing. The external reviewers evaluated 44 additional CNVs previously observed and reported from internal committee members' clinical laboratories (22 deletions and 22 duplications). Following the model used during internal committee testing, a subset of 22 of these CNVs (11 deletions and 11 duplications) were first evaluated using typical laboratory practices ("baseline"), then evaluated (by different external reviewers) using the scoring metrics. All CNVs assessed by external reviewers were independently evaluated by 2 individuals, for a total of 88 individual classifications using the scoring metrics. A summary of CNVs evaluated and individual classifications obtained during the testing period are described in Table S2.1; a complete listing of all CNVs evaluated is available in a separate file, Table S2.2.

Table S2.1: Number of CNVs evaluated by category

	Internal Committee Members			External Reviewers			Total
	# Deletions	# Duplications	# Total CNVs	# Deletions	# Duplications	# Total CNVs	
Baseline	15 (30*)	10 (20*)	25 (50*)	11 (22*)	11 (22*)	22 (44*)	47 (94*)
With Metric	36 (69*)	34 (68*)	70 (137*)	22 (44*)	22 (44*)	44 (88*)	114 (225*)

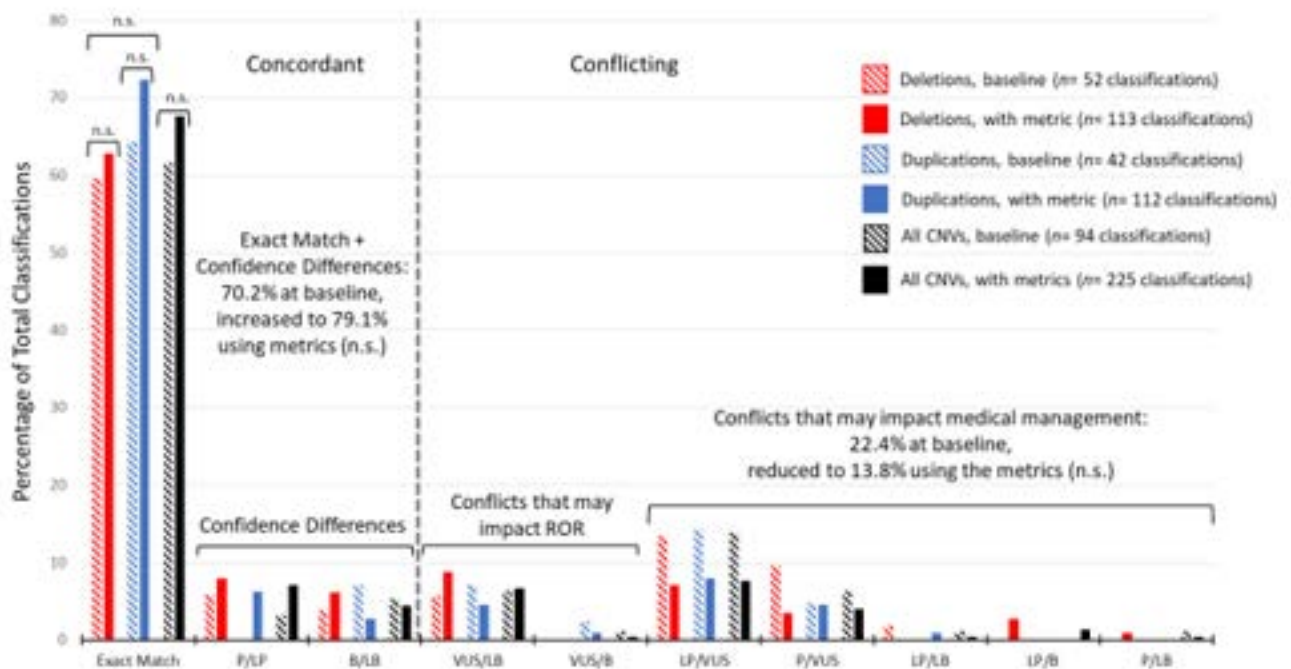
*Indicates total number of independent classifications

The testing process aimed to answer three questions: 1) how often could individual reviewers match the original clinical laboratory classification; 2) how often could reviewers evaluating the same CNV reach the same classification (i.e., concordance); and 3) were classifications reached using the scoring metrics the appropriate classifications in the opinion of the expert reviewers.

Comparison to Original Laboratory Classifications

To address the first question, the original laboratory classifications, which were previously reported as part of clinical testing, were considered the “reference classifications” to which the individual reviewers’ classifications were compared. Comparisons to the original laboratory classifications were made for both the “baseline” set of CNVs ($n=47$ CNVs, 94 individual classifications) as well as the full set of CNVs evaluated ($n=114$ CNVs, 225 classifications in total) using the scoring metrics. Results are depicted in Figure S2.1.

Figure S2.1: Original Laboratory Comparisons: The percentage of classifications matching the original clinical laboratory classification are displayed at baseline (diagonal striped boxes) and using the CNV scoring metrics (solid boxes). Results are shown for deletions (red), duplications (blue), and all CNVs combined (black). n.s. = Not statistically significant; ROR = return of result; P = pathogenic; LP = likely pathogenic; VUS = uncertain significance; LB = likely benign; B = benign.



Percentages were compared using a two-sample t-test between proportions. While the percentage of exact matches (meaning that the individual classification was exactly the same as the classification from the original clinical laboratory) was greater when reviewers used the CNV scoring metrics compared to baseline; these differences were not statistically significant (deletions: $t(163) = 0.393$, $p = 0.6948$; duplications: $t(223) = 1.522$, $p = 0.1295$; all CNVs: $t(317) = 1.013$, $p = 0.3118$). Additionally, there was no significant difference between the proportion of exact match classifications obtained with the deletion scoring metric compared to the duplication scoring metric ($t(223) = 1.522$, $p = 0.1295$).

In addition to those classifications designated as “exact matches,” there were other reviewer classifications that represented confidence differences from the original laboratory classifications (i.e., pathogenic (P) and likely pathogenic (LP), or benign (B) and likely benign (LB)). In ClinVar, a National Centers of Biotechnology Information (NCBI) database cataloging human variation and its relationship to disease, these types of classifications are considered

concordant, and not in conflict with one another

(<https://www.ncbi.nlm.nih.gov/clinvar/docs/clinsig/#conflicts>). Anecdotally, confidence differences appear to be managed clinically in a similar manner (LP variants treated as P, LB variants treated as B). Considering both “exact match” and “confidence difference” categories as concordant, the overall percentage of classifications concordant with the original laboratory classification was 70.2% at baseline ($n=94$ classifications) and 79.1% using the scoring metrics ($n=225$ classifications). Additionally, the overall percentage of classification discrepancies possibly impacting medical management (e.g., uncertain significance (VUS) versus P, etc.) decreased to 13.8% using the scoring metrics compared to 22.4% at baseline. While these results indicate a trend toward improvement using the scoring metrics, they are also not statistically significant (comparison of classifications concordant with the original laboratory classification: $t(317) = 1.013$, $p = 0.3118$; comparison of classifications possibly impacting medical management: $t(317) = 1.874$, $p = 0.0619$).

Concordance Comparisons

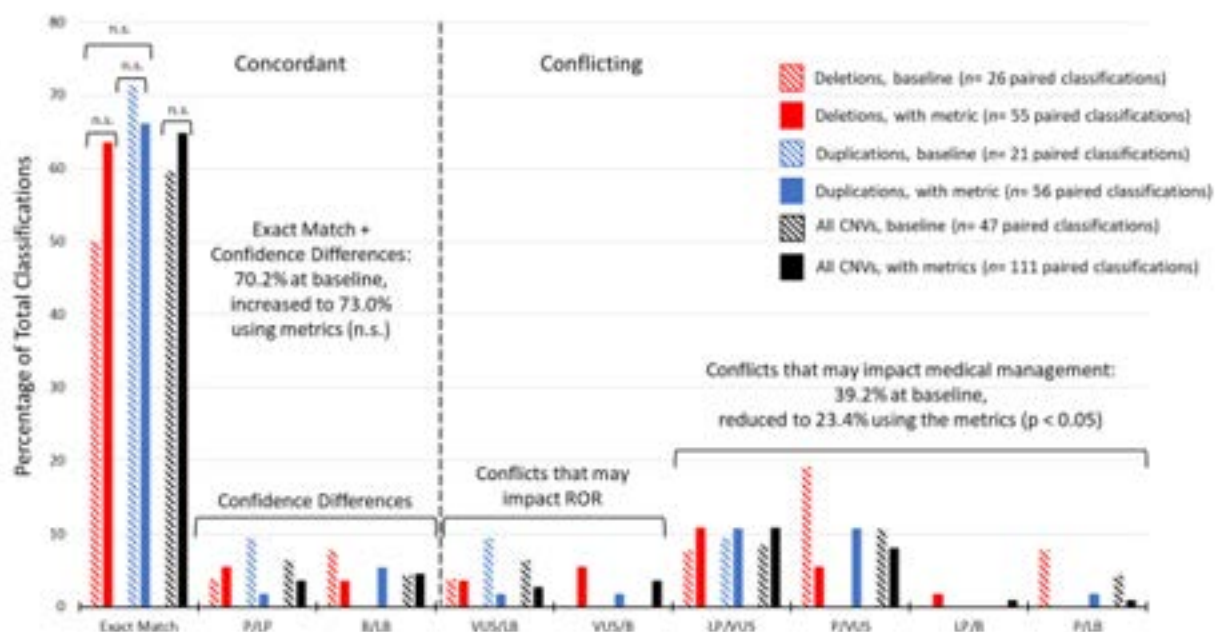
To address the second question (how often reviewers evaluating the same CNV came to the same classification), only the 111 CNVs (55 deletions, 56 duplications) evaluated by 2 independent reviewers were considered. In this scenario, the classifications of the 2 reviewers were compared to each other. As in the original laboratory classification assessment, a subset of the total CNVs were initially reviewed using internal laboratory procedures as a baseline ($n=26$ deletions, 21 duplications), then reviewed again by different individuals as part of the full set of CNVs evaluated using the scoring metrics. Results are depicted in Figure S2.2.

Figure S2.2: Concordance Comparisons: For those cases evaluated by 2 independent reviewers ($n = 111$), the percentage in which both reviewers' classifications matched are displayed at baseline (diagonal striped boxes) and using the CNV scoring metrics (solid boxes).

Results are shown for deletions (red), duplications (blue), and all CNVs combined (black). n.s.

= Not statistically significant; ROR = return of result; P = pathogenic; LP = likely pathogenic;

VUS = uncertain significance; LB = likely benign; B = benign.



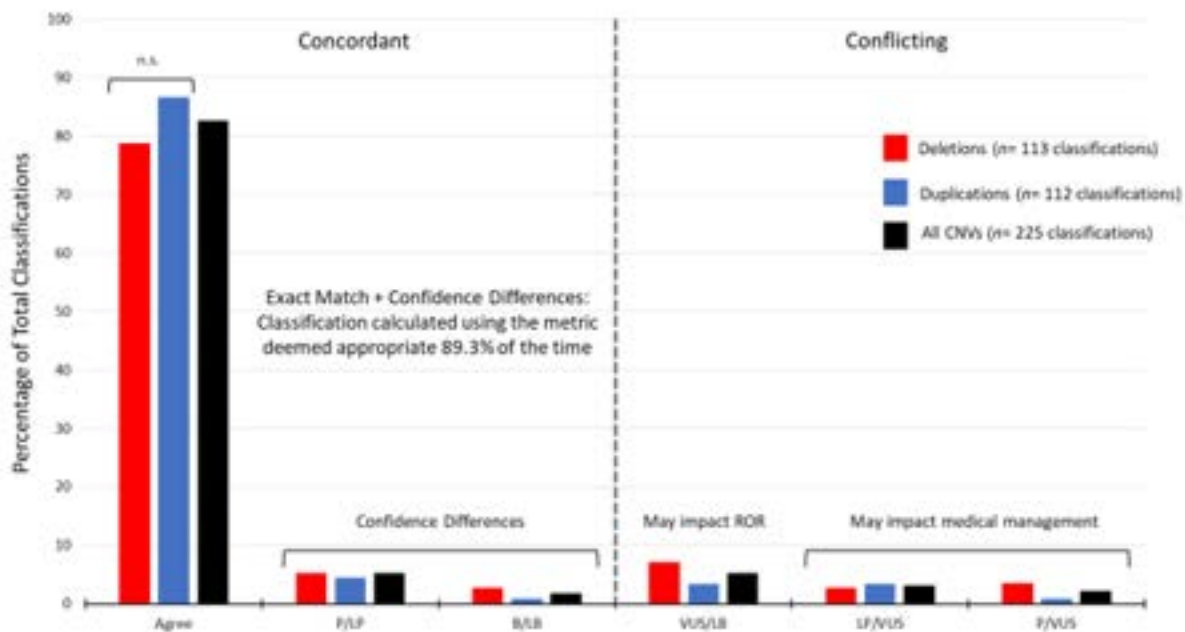
Expanding the definition of concordance to include classifications representing confidence differences, reviewers were concordant with one another 73.0% of the time using the CNV scoring metrics ($n = 111$ paired classifications); this level of concordance is similar to the level observed at baseline (70.2%, $n = 47$ paired classifications). However, the percentage of cases involving conflicts that could affect medical management was significantly lower when using the scoring metrics (23.4%, $n = 111$ paired classifications) than at baseline (39.2%, $n = 47$ paired classifications) ($t(156) = 2.02$, $p = 0.0451$).

Appropriateness of classifications calculated using the metrics

For each case evaluated using the CNV scoring metrics, individual reviewers were asked if they believed the classification calculated using the metric was appropriate; if they indicated “no,” they were asked to provide the classification they thought was warranted in each case. There

was a total of 225 individual answers to this question (113 responses for deletions, 112 responses for duplications). Responses are depicted in Figure S2.3

Figure S2.3: Appropriateness of classifications calculated using the metrics: For each case evaluated using the scoring metrics, individual reviewers were asked if they believed the classification they obtained using the metrics was appropriate, and, if not, what they thought was the appropriate classification. Results are shown for deletions (red), duplications (blue), and all CNVs combined (black). n.s. = Not statistically significant; ROR = return of result; P = pathogenic; LP = likely pathogenic; VUS = uncertain significance; LB = likely benign; B = benign.



In general, reviewers were satisfied with the classifications generated by the scoring metrics; in 82.7% of cases ($n = 225$), the individual reviewer completely agreed with the calculated classification. The reviewer had a difference in confidence level from the calculated classification (P vs. LP, B vs. LB) in an additional 6.7% of cases; combined with those cases demonstrating complete agreement, reviewers' opinions were concordant with the calculated

classifications in 89.3% of cases. In 5.3% of cases, the reviewer's opinion differed from the calculated classification in a manner that could affect medical management (LP vs. VUS, P vs. VUS).

Discussion

It has been well established that clinical laboratories at times interpret the same variants differently. This has been documented for both CNVs and sequence variants, and can occur for a number of different reasons, including different access to evidence, different interpretations of the significance of given pieces of evidence, and the emergence of new evidence over time. Technical standards for the evaluation and classification of variants, such as the previous CNV standard¹ and the current sequence variant standards², were created in an effort to guide users toward more consistent, transparent evidence evaluation practices and, ultimately, more consistent variant classifications. The points-based scoring metrics presented in this manuscript are intended to further refine this process for CNVs.

Like previous and current variant classification standards, education and practice will be required for users to familiarize themselves with the nuances of this new system. Our data show that, with relatively little practice (each reviewer was assigned an average of 9 CNVs to evaluate with the scoring metrics), reviewers could match levels of concordance with the original laboratory classification and with each other similar to baseline, with trends toward improvement. At a minimum, these metrics mirror the methods that are currently being used in clinical practice, but provide more structure and guidance to the assessment process. This initial positive performance trend is similar to data obtained following the release of the current ACMG/AMP sequence variant guidelines². Amendola et al.³ described the experience of 9 clinical diagnostic laboratories using the ACMG/AMP sequence variant guidelines to evaluate a total of 99 variants within a year of the guidelines' publication. Similar to our experience with

initial tests of the metrics, these authors demonstrated that shortly after initial publication, use of the ACMG/AMP guidelines to classify variants did not result in a statistically significant increase in inter-laboratory concordance over variant classification using internal laboratory methods. These particular laboratories were able to reach exactly the same classifications using the ACMG/AMP guidelines 34% of the time. This is comparable to our concordance comparison; using our scoring metrics, our reviewers were able to reach exactly the same classifications 64.9% of the time.

Over time, however, as laboratories gained experience with the sequence variant guidelines, variant classification consistency has improved. Harrison et al.⁴ reported variant classification concordance for over 6000 sequence variants submitted to ClinVar by four different clinical laboratories approximately 2 years after the sequence guidelines were published. In this study, the laboratories were able to reach exactly the same classifications using these methods 62.3% of the time, a marked improvement over the observations made in the previous study. We anticipate similar results for the CNV scoring metrics; with increased education, familiarity, and experience, we expect to see steady improvements in inter-laboratory concordance. We will continue to study trends in inter-laboratory concordance using these metrics, as well as usability and user experience, and plan to use this information to guide future iterations of the scoring metrics.

REFERENCES

1. Kearney HM, Thorland EC, Brown KK, Quintero-Rivera F, South ST, Working Group of the American College of Medical Genetics Laboratory Quality Assurance Committee. American College of Medical Genetics standards and guidelines for interpretation and reporting of postnatal constitutional copy number variants. *Genet Med*. 2011;13(7):680-685. doi: 10.1097/GIM.0b013e3182217a3a [doi].
2. Richards S, Aziz N, Bale S, et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med*. 2015;17(5):405-424. doi: 10.1038/gim.2015.30 [doi].
3. Amendola LM, Jarvik GP, Leo MC, et al. Performance of ACMG-AMP Variant-Interpretation Guidelines among Nine Laboratories in the Clinical Sequencing Exploratory Research Consortium. *Am J Hum Genet*. 2016;98(6):1067-1076. doi: S0002-9297(16)30059-3 [pii].
4. Harrison SM, Dolinsky JS, Knight Johnson AE, et al. Clinical laboratories collaborate to resolve differences in variant interpretations submitted to ClinVar. *Genet Med*. 2017;19(10):1096-1104. doi: 10.1038/gim.2017.14 [doi].

Supplemental Material 3: Case Examples

The following case examples are meant to illustrate how one would use the CNV scoring metrics to assess a given CNV. This supplement includes the following examples:

- Example Case 1: A multi-gene deletion illustrating use of case-level evidence. This example also illustrates how classification may be affected by additional information regarding patient phenotype.
- Example Case 2: A multi-gene duplication with final classification of Uncertain. This example provides insight on how to prioritize genes within the CNV for evaluation.
- Example Case 3: An inherited deletion with final classification of Benign. This example illustrates use of population data.
- Example Case 4: A recurrent duplication with final classification of Pathogenic. This example illustrates use of the ClinGen Dosage Sensitivity Map.

These classifications were made based on evidence available as of August 2019. Classifications may change over time as additional evidence emerges. Additional case examples will be provided at www.clinicalgenome.org.

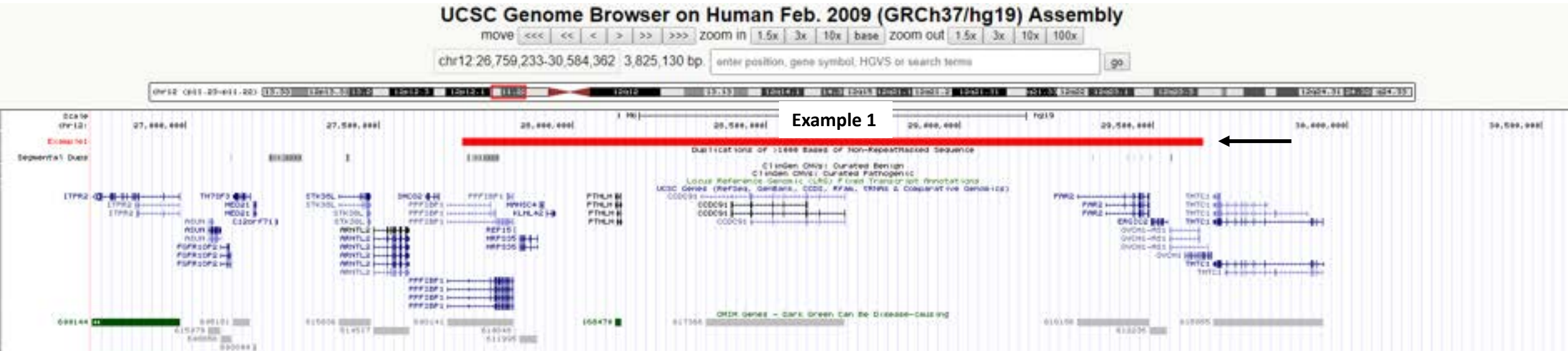
Example Case 1:

```
arr(GRCh37) 12p11.23p11.22  
  (2771551_29628080)x1
```

Case 1: Deletion with case-level evidence

- `arr(GRCh37)12p11.23p11.22(27715516_29628080)x1 dn`
- No additional clinical information provided
- Use the LOSS scoring metric

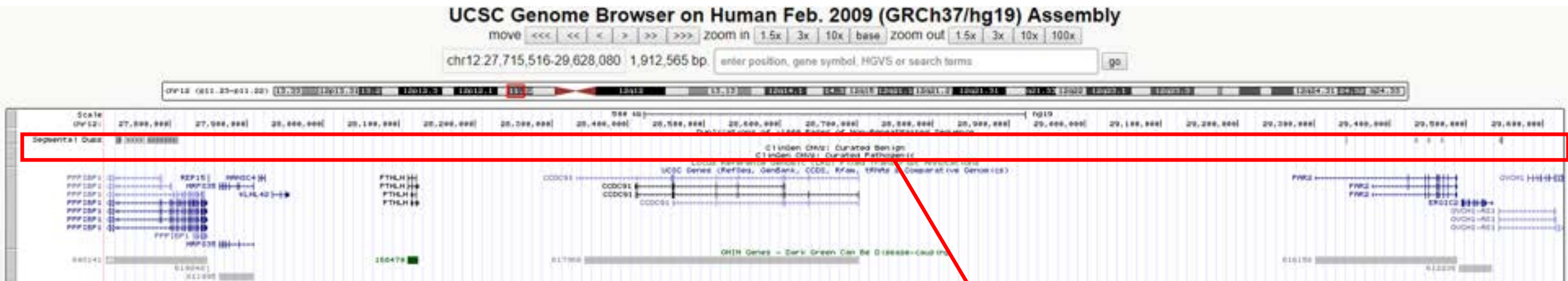
Section 1: Initial Assessment of Genomic Content



- Would apply category 1A (contains protein-coding or other known functionally important elements), as this deletion includes several protein-coding genes
- 0 points awarded, continue evaluation

Total: 0 points

Section 2: Overlap with Established/Predicted HI or Established Benign Genes/Genomic Regions



ClinGen CNVs: Curated Benign
ClinGen CNVs: Curated Pathogenic

There are no established HI or benign genes/genomic regions within the observed interval.

Section 2: Overlap with Established/Predicted HI or Established Benign Genes/Genomic Regions



ClinGen Dosage Sensitivity Curation Page

Location Search Results

<https://www.ncbi.nlm.nih.gov/projects/dbvar/clingen/>

Submitted location: chr12:27,715,516-29,628,080

"N/A" indicates that this gene has not yet been evaluated

Location search results

Gene Symbol	Haploinsufficiency score	Triplosensitivity score	Curation Status	Region Location (GRCh37)	ExAC pLI	OMIM	Relationship to Submitted Location	ISCA ID
PTHLH	2	1	Complete	chr12:28,111,017-28,124,916	0.921	168470	Contained	ISCA-17209
PPFIBP1	N/A	N/A	Awaiting Review	chr12:27,677,045-27,848,497	0.0	602141	Overlap	ISCA-10221
LOC100506578	N/A	N/A	Reopened	chr12:27,745,391-27,746,972			Contained	ISCA-16181
REP15	N/A	N/A	Awaiting Review	chr12:27,849,428-27,850,566	0.001	610848	Contained	ISCA-30108
HMGB1P49	N/A	N/A	Awaiting Review	chr12:27,855,271-27,855,839			Contained	ISCA-32863
MRPS35	N/A	N/A	Awaiting Review	chr12:27,863,706-27,909,237	0.041	611995	Contained	ISCA-7936
MANSC4	N/A	N/A	Awaiting Review	chr12:27,915,599-27,924,209			Contained	ISCA-8474
KLHL42	N/A	N/A	Awaiting Review	chr12:27,933,187-27,955,973	0.439		Contained	ISCA-2790
RN7SKP15	N/A	N/A	Awaiting Review	chr12:27,959,015-27,959,323			Contained	ISCA-38098

One gene has been evaluated by the ClinGen Dosage Sensitivity group, but HI score is 2.

Section 2: Overlap with Established/Predicted HI or Established Benign Genes/Genomic Regions

- Sections 2A-2G: N/A
 - Does not overlap an established HI gene or genomic region
 - Does not overlap an established benign gene or genomic region

Total: 0 points

Section 2H: Haploinsufficiency Predictors

- Use DECIPHER to quickly assess pLI score (currently pulled from ExAC) and HI Index

Search results for 'position:12:27715516-29628080' ([Refine Search](#))

[Open-access patients](#) **56**
[CNV Syndromes](#) **0**
[DDD Research Variants](#) **2**
[Genes](#) **14**
[Results](#)
[Browser](#)

Genes: 1 to 10 of 10 (out of 14 total)

Show: ☐ OMIM ☐ Morbid ☐ DDG2P ☒ Protein coding

Name	Location	Description	OMIM	Morbid	DDG2P	%HI	pLI	Links
PTHLH	12 28111017 28125638	parathyroid hormone like hormone	✓	✓	Y	5.77	0.92	View
FAR2	12 29302036 29493913	fatty acyl-CoA reductase 2	✓	-	-	65.22	0.92	View
KLHL42	12 27932953 27955973	kelch like family member 42	-	-	-	53.28	0.44	View
ERGIC2	12 29490285 29534122	ERGIC and golgi 2	✓	-	-	12.72	0.32	View
MRPS35	12 27663706 27909228	mitochondrial ribosomal protein S35	✓	-	-	39.99	0.04	View
PPFIBP1	12 27676364 27648497	PPFIA binding protein 1	✓	-	-	48.49	0.00	View
REP15	12 27849428 27850566	RAB15 effector protein	✓	-	-	78.52	0.00	View
CCDC91	12 28286182 28732883	coiled-coil domain containing 91	✓	-	-	29.75	0.00	View
OVCH1	12 29565407 29650619	ovochoymase 1	-	-	-	90.08	0.00	View
MANSC4	12 27915671 27924209	MANSC domain containing 4	-	-	-	83.29	-	View

Search results for 'position:12:27715516-29628080' ([Refine Search](#))

[Open-access patients](#) **56**
[CNV Syndromes](#) **0**
[DDD Research Variants](#) **2**
[Genes](#) **14**
[Results](#)
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Genes: 1 to 10 of 10 (out of 14 total)

Show: ☐ OMIM ☐ Morbid ☐ DDG2P ☒ Protein coding

Name	Location	Description	OMIM	Morbid	DDG2P	%HI	pLI	Links
PTHLH	12 28111017 28125638	parathyroid hormone like hormone	✓	✓	Y	5.77	0.92	View
FAR2	12 29302036 29493913	fatty acyl-CoA reductase 2	✓	-	-	65.22	0.92	View
KLHL42	12 27932953 27955973	kelch like family member 42	-	-	-	53.28	0.44	View
ERGIC2	12 29490285 29534122	ERGIC and golgi 2	✓	-	-	12.72	0.32	View
MRPS35	12 27663706 27909228	mitochondrial ribosomal protein S35	✓	-	-	39.99	0.04	View
PPFIBP1	12 27676364 27648497	PPFIA binding protein 1	✓	-	-	48.49	0.00	View
REP15	12 27849428 27850566	RAB15 effector protein	✓	-	-	76.52	0.00	View
CCDC91	12 28286182 28732883	coiled-coil domain containing 91	✓	-	-	29.75	0.00	View
OVCH1	12 29565407 29650619	ovochoymase 1	-	-	-	90.08	0.00	View
MANSC4	12 27915671 27924209	MANSC domain containing 4	-	-	-	83.29	-	View

This gene has pLI of >0.90 AND HI <10% and looks promising! However, since we know the pLI is being pulled from ExAC, let's double check in gnomAD...

However...

gnomAD browser

Search by gene, region, or variant

About Downloads Terms Contact

This is a new version of the gnomAD browser. The old version is available at <http://gnomad-old.broadinstitute.org>

PTHLH

parathyroid hormone-like hormone

Ensembl gene ID

ENSG00000087494

Ensembl transcript ID

ENST00000395872 (canonical)

UCSC Browser

12:28111018-28125639

GeneCards

PTHLH

OMIM

168470

Dataset

gnomAD v2.1.1

gnomAD SVs

Gene Constraint

Category	Exp. SNVs	Obs. SNVs	Constraint metrics
Synonymous	44.9	33	Z = 1.39 o/e = 0.74 (0.56 - 0.98) 0 1
Missense	107.7	74	Z = 1.15 o/e = 0.69 (0.57 - 0.83) 0 1
LoF	9.9	1	pLI = 0.81 o/e = 0.1 (0.04 - 0.48) 0 1

genome

Save plot

The pLI is no longer >0.90, AND the upper bound of the observed/expected confidence interval is >0.35. Do not assign points in category 2H.

LoF

9.9

1

pLI = 0.81

o/e = 0.1 (0.04 - 0.48)

0 1

Total: 0 points

Section 3: Evaluation of Gene Number

 About Browse ▾ DDD(UK) [Join](#) [Login](#)

Search results for 'position:12:27715516-29628080' ([Refine Search](#))

Open-access patients **56** CNV Syndromes **0** DDD Research Variants **2** **Genes 14**

Results **Browser**

Genes: 1 to 10 of 10 (out of 14 total) Show: ☐ OMIM ☐ Morbid ☐ DDG2P ☒ Protein coding

Name	Location	Description	OMIM	Morbid	DDG2P	%HI	pLI	Links
PTHLH	12 28111017 28125638	parathyroid hormone like hormone	✓	✓	Y	5.77	0.92	View
FAR2	12 29302036 29493913	fatty acyl-CoA reductase 2	✓	-	-	65.22	0.92	View
KLHL42	12 27932953 27955973	kelch like family member 42	-	-	-	53.28	0.44	View
ERGIC2	12 29490285 29534122	ERGIC and golgi 2	✓	-	-	12.72	0.32	View
MRPS35	12 27863706 27909228	mitochondrial ribosomal protein S35	✓	-	-	39.99	0.04	View
PPFIBP1	12 27676364 27848497	PPFIA binding protein 1	✓	-	-	48.49	0.00	View
REP15	12 27849428 27850566	RAB15 effector protein	✓	-	-	78.52	0.00	View
CCDC91	12 28286182 28732883	coiled-coil domain containing 91	✓	-	-	29.75	0.00	View
OVCH1	12 29565407 29650619	ovochymase 1	-	-	-	90.08	0.00	View
MANSC4	12 27915671 27924209	MANSC domain containing 4	-	-	-	83.29	-	View

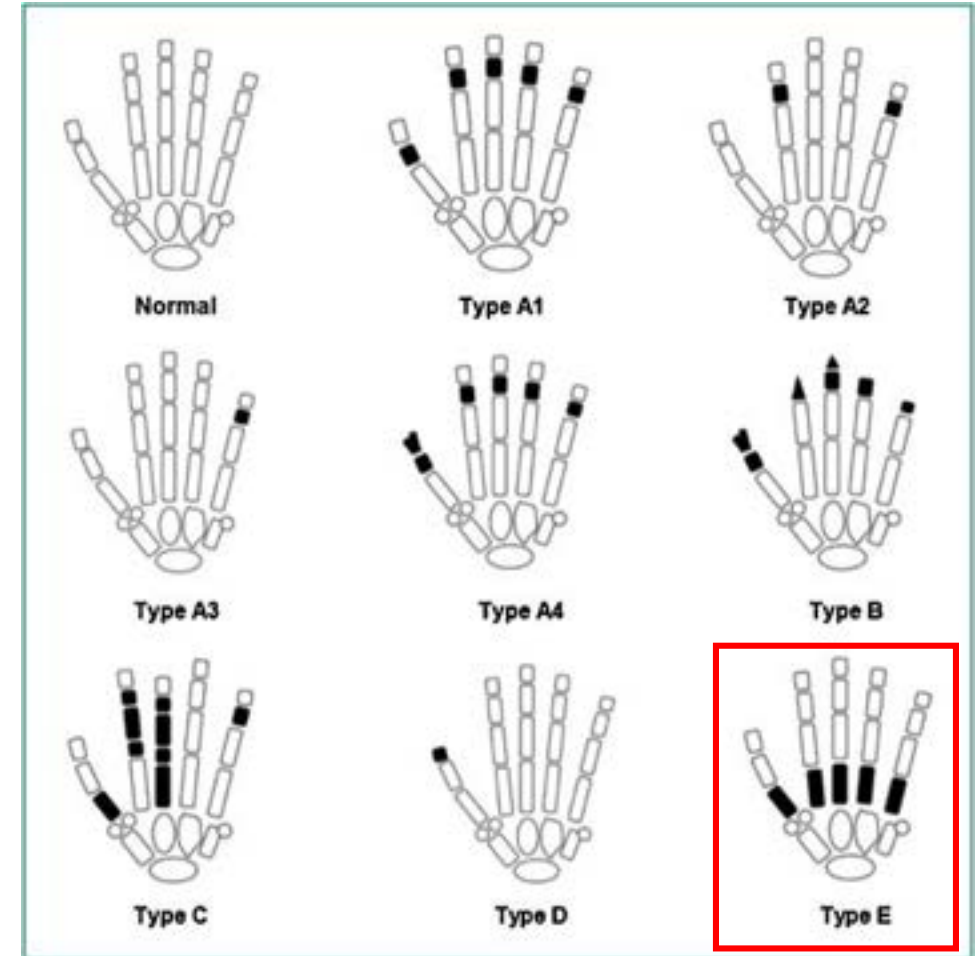
Total: 0 points

Section 4: Detailed Evaluation of Genomic Content

- Where to start the evaluation?
 - 10 protein-coding genes in the interval
 - Are any OMIM-Morbid?
 - Yes – *PTHLH*
 - Per OMIM: Associated with autosomal dominant Brachydactyly, type E2 (BDE)
 - Of note, this gene is the only gene in the interval with complementary DECIPHER HI and ExAC pLI scores
 - Though the pLI score is not within range when calculated using the gnomAD dataset, this still flags the gene as one of potential interest to follow-up on
 - If NO OMIM-Morbid genes:
 - Look at any genes documented in OMIM
 - Look at genes with complementary HI predictor scores
- At any time: search the literature for the entire CNV interval
 - Keep in mind that results may be too broad for use (e.g., “12p11 deletions”)

PTHLH and Autosomal Dominant Brachydactyly Type E (BDE)

- Shortening of the digits, mainly in the metacarpals (III-V) and metatarsals
 - Wide variability in the number of digits affected, including within the same family
- May also be associated with short stature, delayed tooth eruption and/or oligodontia
- Intelligence generally unaffected



PTHLH and Autosomal Dominant Brachydactyly Type E (BDE)

- Brachydactyly *in general* may occur as an isolated malformation or as part of a syndrome
 - Searching OMIM clinical synopses for “brachydactyly” yields over 250 results
- Brachydactyly type E specifically is more rare
 - Similar OMIM search using “brachydactyly type E” yields 4 results
- Isolated BDE has also been associated with variants in *HOXD13*
 - Similar radiologic features are also seen in:
 - pseudopseudohypoparathyroidism (variants in *PPHP*) - this syndrome is also marked by cognitive defects and cataracts
 - Hypertension and brachydactyly syndrome (variants in *PDE3A*) – this syndrome is also marked by severe hypertension
 - 2q37 deletions (including *HDAC4*) – also marked by intellectual disability
- Given the relatively limited heterogeneity of BDE, this may be considered a “highly specific, but not necessarily unique” phenotype
 - Brachydactyly, type unspecified, would be considered “not highly specific and/or with high genetic heterogeneity”

De Novo variants

Category 4B → Default: confirmed parental relationships = 0.30; assumed = 0.15; Range: 0-0.45

- Thomas-Teinturier et al. 2016 (PMID: 26640227):
 - The authors describe a female proband with BDE and no reported family history.
 - Single gene sequencing of PTHLH was performed, and a heterozygous de novo deletion was detected (c.101+3delAAGT).
 - Per the authors, "this alteration deletes four nucleotides from position 3–6 of intron V...[it] is predicted to cause a moderate decrease in the consensus sequence value of the natural donor splice site (WT 84.38; Mut 60.23; Var.% 28.62). As a result, novel additional potential donor sites with a higher consensus value could be created. Use of these sites is predicted to lead to aberrant transcripts with a premature stop codon, as in the first family."
 - Parental relationships were not confirmed.
 - Default for assumed parental relationships: 0.15
 - Opting to downgrade to 0.10: Other genetic causes of BDE were not effectively ruled out.

Total: 0.10 points

De Novo variants

Category 4B → Default: confirmed parental relationships = 0.30; assumed = 0.15; Range: 0-0.45

- Pereda et al. 2017 (PMID: 28211986):
 - Female proband with BDE and no reported family history.
 - Single gene sequencing of PTHLH revealed a heterozygous c.166C>T (p.R56*) variant; this variant has been described in an unrelated individual with BDE by Jamsheer et al. 2016.
 - The variant was also detected in a mosaic state in the girl's unaffected father (10-20% of blood cells, not detected via buccal swab or hair sample).
 - Per ClinGen [gene curation scoring guidelines](#), if a variant is detected in a mosaic state in the proband's parent, it can be "counted" as a *de novo* variant.
 - Maternal relationship was not confirmed.
 - Default for assumed parental relationships: 0.15
 - Opting to downgrade to 0.10: Other genetic causes of BDE were not effectively ruled out.

Total: 0.20 points

De Novo variants

Category 4B → Default: confirmed parental relationships = 0.30;
assumed = 0.15; Range: 0-0.45

- Jamsheer et al. 2016 (PMID: 26763883):
 - Female proband with BDE and no reported family history.
 - Single gene sequencing of *PTHLH* revealed a heterozygous c.166C>T (p.R56*) variant
 - This variant has been described in an unrelated individual with BDE by Pereda et al. 2017.
 - Variant was said to be *de novo*, but no information regarding confirmation of parental relationships was presented.
 - Default for assumed parental relationships: 0.15
 - Opting to downgrade to 0.10: Other genetic causes of BDE were not effectively ruled out.

Total: 0.30 points

Variants of unknown inheritance

Category 4E → Default: 0.10; Range: 0-0.15

- Klopocki et al. 2010 (PMID: 20170896):
 - One individual with a heterozygous nonsense variant (p.K120X) (Individual II-1 in Family 5)
 - The authors note that this variant is located more than 50bp away from the 3' boundary of the second-to-last exon, thus expected to undergo NMD.
 - The individual presented with brachydactyly type E (shortened metacarpals III-V), short stature, and oligodontia.
 - The individual was said to have an affected sister and nephew, though it is unclear whether these individuals were tested for the variant.
 - Parental testing was not performed.
 - Default points awarded (0.10).
 - Note: this category is being used because BDE is a relatively specific phenotype. If the phenotype under evaluation was non-specific, this category would not be used.

Total: 0.40 points

Segregation Among Similarly Affected Family Members

- Note: Segregations may be added across families.
- Reyes et al. 2018 (PMID: 30458061):
 - The authors describe a female proband with brachydactyly type E (BDE) and no evidence for abnormal calcium or phosphate regulation.
 - Whole exome sequencing (WES) revealed "a novel heterozygous A>G change at nucleotide -3 up-stream of PTHLH exon 3 that encodes the last two amino acids of the pro-sequence and the mature PTHrP...[resulting in] a heterozygous insertion of genomic nucleotides -2 and -1 causing a frame-shift after residue 34 of the preprosequence and thus 29 novel residues without homology to PTHrP or any other protein."
 - This variant was also found in her affected mother, maternal aunt, and monozygous twin sons, but not in her unaffected daughter or sister.
 - Number of segregations counted = 3

Total # of Segregations: 3

Segregation Among Similarly Affected Family Members

- Bae et al. 2018 (PMID:29947179):
 - Male proband with BDE and normal calcium and phosphate levels.
 - WES of the proband, his affected mother, and his unaffected father revealed a shared c.169C>T (p.Arg57*) variant for the proband and his affected mother.
 - The family history indicates that there are at least 7 other affected relatives across 4 generations of the family, though no other individuals were tested.
 - Number of segregations counted = 1
 - Only counting genotype +/-phenotype + individuals

Total # of Segregations: 4

Segregation Among Similarly Affected Family Members

- Thomas-Teinturier et al. 2016 (PMID: 26640227):
 - The authors describe a female proband and her mother with BDE.
 - Single gene sequencing of *PTHLH* was performed. A heterozygous deletion, c.47_101+73del128 "compris[ing] bases 47–101 of exon V and 73 bases of intron V (total deletion: 128 bp)" was found in the proband and her mother (NM_198965.1).
 - Per the authors: "The c.47_101p73del128 defect removes the canonical donor site of exon V. Consequently, new potential splice sites localized before or after the deletion breakpoint are predicted to be used. These aberrant splicings are expected to produce transcripts with premature stop codon 5' to the last 50 nucleotides of the penultimate exon [Holbrook et al., 2004], which are predicted to be degraded by nonsense-mediated mRNA decay."
 - Number of segregations counted = 1

Total # of Segregations: 5

Segregation Among Similarly Affected Family Members

- Jamsheer et al. 2016 (PMID: 26763883):
 - The authors describe a female proband with BDE; her full sister and father were also reported to be affected.
 - Single-gene sequencing revealed a NM_198965.1 c.258delC (p.N87Tfs*18) in exon 4 of PTHLH in the proband and her affected family members, but not in her unaffected mother, sister, or paternal aunt.
 - Number of segregations counted = 2
- Total number of segregations across all families = 7
- Category 4H: 7 or more segregations = 0.45 points

Total # of Segregations: 7

Total: 0.85 points

Case-control and population evidence

- No known case-control evidence available for the observed CNV (Categories 4L-4N = 0 points)
- Population Data:

gnomAD SVs



DGV Gold Standard Set



Multiple small events are observed throughout the region. Though some in DGV are at high frequencies, they are much smaller than the observed CNV, and the information is not enough to constitute “anti” evidence for this CNV (0 points).

Total: 0.85 points

Section 5: Evaluation of Inheritance Pattern/Family History for Patient Being Studied

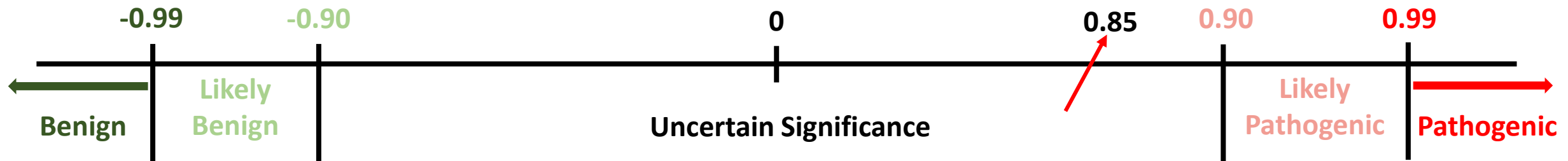
- Though we know this variant is *de novo*, we have not been provided any information about the patient's phenotype or family history.
 - Without any further information, the most appropriate category would be 5F, "Inheritance information is unavailable or uninformative" (0 points).
- Option: Call the ordering provider and request additional information.
 - If the proband is noted to have brachydactyly: Could award an additional 0.15-0.30 points (depending on whether parental relationships are confirmed) for another *de novo* observation of a highly specific (but not necessarily unique) phenotype (Category 5A).
 - This additional information would bring the total points to **1.0** (or greater) for a classification of **PATHOGENIC**.

What if my patient does not have BDE?

- The full body of documented supporting evidence should not be completely discounted because your patient does not have BDE.
 - Total points do not suddenly change from 0.85 to -0.90 or less; there is no cause to classify this CNV as “likely benign” or “benign” simply because your patient does not exhibit the expected phenotype.
- Carefully evaluate what this may mean in the context of the other evidence.
- Just as consistent phenotype information from your patient can be scored as a case, inconsistent phenotype information can also be scored as a case (Category 4D; Default = 0 points, Range = 0 to -0.30 points).
 - Decide whether this represents a lack of information or truly negative information.
 - For example: Who determined that the proband did not have brachydactyly?
 - Did the doctor’s office call the parent, ask if the child had short fingers, and the parent told them he didn’t? (Consider 0 points)
 - Did the child have an X-ray of the hand where BDE was specifically ruled out by a radiologist? (Consider negative points)
- Classifications should be driven by all available evidence, not swayed by a single case; this is the intent of the “uncoupling” recommendation.

What if no additional phenotypic information is available?

- Current point total without proband phenotype: 0.85 points



- Very close to likely pathogenic (LP) – is variant of uncertain significance really appropriate?
- Use your clinical judgement
 - Evaluate the full body of evidence – does it warrant an upgrade? Is there any contradictory information?
 - Document your rationale

In this case...

- There are additional pieces of information available about *PTHLH* that could support an argument to bump this CNV up to LP:
 - Deletions overlapping our example CNV (including *PTHLH*) have been observed segregating within families with BDE (Klopocki *et al.* 2010 [PMID: 20170896]; Huang *et al.* 2019 [PMID:31283647]).
 - Why don't we just count these in our evaluation? Both of these publications represent additional segregation information; we have already obtained the maximum segregation score of 0.45 points.
 - Missense variants in *PTHLH* with functional information suggesting a loss of function mechanism have also been observed in individuals with BDE (Klopocki *et al.* 2010 [PMID: 20170896]).

Conclusion

- Final points based on publicly available evidence: 0.85
- Classification may change as additional evidence becomes available:
 - If phenotype information confirms proband has BDE:
 - This is an additional case - add 0.15-0.30 points (depending on confirmation of parental relationships) (Category 5A [4B])
 - Classification: Pathogenic
 - If contradictory evidence is available (e.g., your patient is radiologically confirmed not to have BDE):
 - This additional (contradictory) case information could subtract up to 0.30 points from your total. (Category 5A [4D]). Final points could range anywhere from 0.85 to 0.55 points.
 - In any scenario, the total number of points remain in the “Uncertain” range.
 - If phenotype information is unavailable or uninformative (no contradictory evidence):
 - Additional, unscored evidence supports the upgrade from 0.85 points to 0.90 points (evidence documented on previous slide)
 - Classification: Likely Pathogenic

Example Case 2:

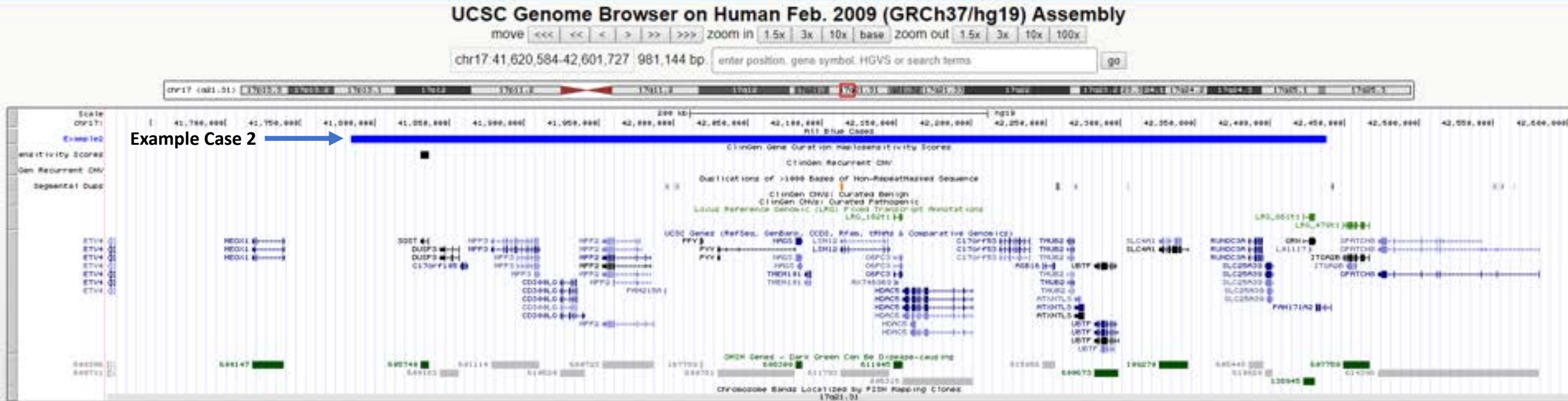
`arr(GRCh37)`

`17q21.31(4178410_42438203)x3`

arr(GRCh37)17q21.31(41784108_42438203)x3

- No clinical information provided
- No parental testing available
- Use the GAIN scoring metric

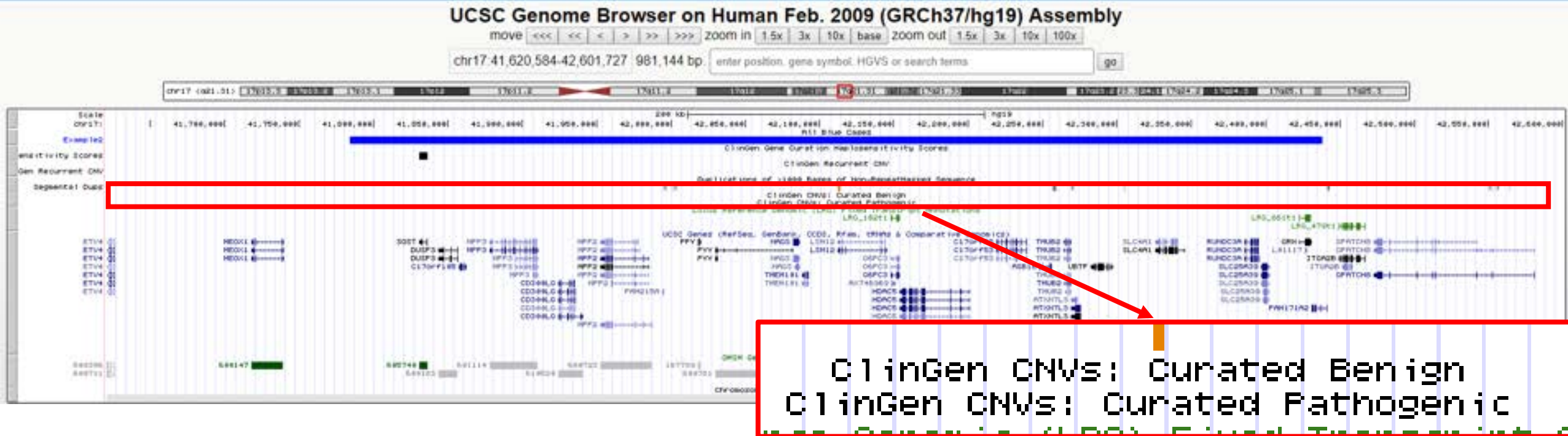
Section 1: Initial Assessment of Genomic Content



- Would apply category 1A (“contains protein-coding or other known functionally important elements”), as this duplication includes several protein-coding genes
- 0 points awarded, continue evaluation

Total: 0 points

Section 2: Overlap with Established Triplosensitive (TS), Haploinsufficient (HI) or Benign Genes/Genomic Regions



- There are no established TS, HI, or Benign genes/genomic regions within the observed interval (0 points).

Total: 0 points

Section 3: Evaluation of Gene Number

DECIPHER GRCh37 About Browse + DDD(UK) Search DECIPHER

Search results for 'position:17:41784108-42438203' (Refine Search)

Open-access patients 18 CNV Syndromes 8 DDD Research Variants 1 **Genes 29**

Results **Browser**

Genes: 1 to 10 of 23 (out of 29 total)

Show: ☐ OMIM ☐ Morbid ☐ DDG2P ☒ Protein coding Filter...

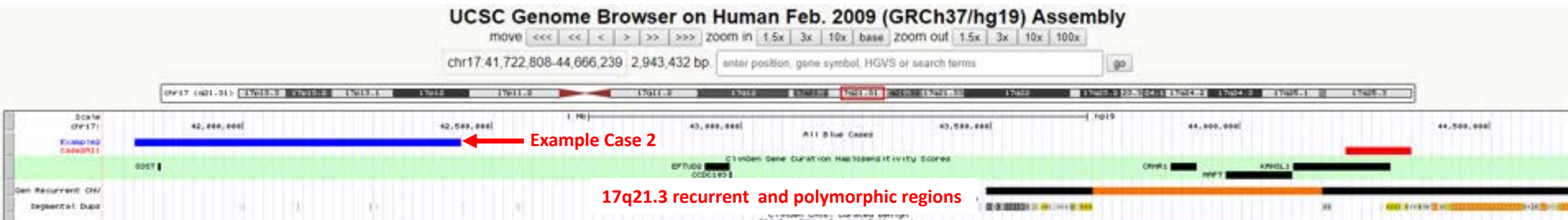
Name	Location	Description	OMIM	Morbid	DDG2P	%HI	pLI	Links
ASB16	17 42347815 42356451	ankyrin repeat and SOCS box containing 16	✓	-	-	52.95	0.00	View
ATXN7L3	17 42269173 42277401	ataxin 7 like 3	-	-	-	34.92	0.95	View
C17orf105	17 41857803 41864900	CFAP97 domain containing 1	-	-	-	54.42	-	View
C17orf53	17 42219274 42239044	chromosome 17 open reading frame 53	-	-	-	71.65	0.00	View
CD300LG	17 41924516 41940997	CD300 molecule like family member g	✓	-	-	94.75	0.03	View
DUSP3	17 41843489 41856356	dual specificity phosphatase 3	✓	-	-	46.04	0.74	View
FAM171A2	17 42430583 42441243	family with sequence similarity 171 member A2	-	-	-	59.23	-	View
G6PC3	17 42148103 42153709	glucose-6-phosphatase catalytic subunit 3	✓	✓	-	43.93	0.00	View
GRN	17 42422814 42430470	granulin precursor	✓	✓+	-	64.61	0.06	View
HDAC5	17 42154114 42201070	histone deacetylase 5	✓	-	-	4.31	1.00	View

Section 3: Evaluation of Gene Number

- 23 protein-coding genes
 - Category 3A (“0-34 genes”) → 0 points
- DECIPHER is a useful resource for identifying which genes in the interval may be most appropriate to pursue within Section 4 (OMIM Morbid, OMIM, etc.)
 - List is sortable

Total: 0 points

Section 4: Detailed Evaluation of Genomic Content Using Published Literature, Public Databases, and/or Internal Lab Data



- Starting literature search with “17q21.31” may produce irrelevant results due to other well-studied recurrent regions in this area.
- Consider searching for evidence related to genes within the interval.

Which genes should I start with?

- Has ClinGen evaluated any genes in this region?

Submitted location: chr17:41,784,108-42,438,203
"N/A" indicates that this gene has not yet been evaluated

 ClinGen
Clinical Genome Resource

ClinGen Dosage Sensitivity Curation Page

Gene Issues (35) Region Issues (0)

Location search results

Items 1 - 20 of 35 Page 1 of 2

Gene Symbol	Haploinsufficiency score	Triplosensitivity score	Curation Status	Region Location (GRCh37)	ExAC pLI	OMIM	Relationship to Submitted Location	ISCA ID
SOST	30: Gene associated with autosomal recessive phenotype	0	Complete	chr17:41,831,999-41,836,156	0.38	605749	Contained	ISCA: 29515
WHSC1L2P	N/A	N/A	Awaiting Review	chr17:41,795,882-41,797,884			Contained	ISCA: 15903
DUSP3	N/A	N/A	Awaiting Review	chr17:41,843,489-41,856,360	0.737	606183	Contained	ISCA: 34867
C17orf105	N/A	N/A	Awaiting Review	chr17:41,857,803-41,862,854			Contained	ISCA: 26388
MPP3	N/A	N/A	Awaiting Review	chr17:41,873,197-41,910,562	0.0	601118	Contained	ISCA: 14814
CD300LG	N/A	N/A	Awaiting Review	chr17:41,924,516-41,940,897	0.03	618520	Contained	ISCA: 32860
MPP2	N/A	N/A	Awaiting Review	chr17:41,952,727-41,987,079	0.903	606723	Contained	ISCA: 12689
FAM215A	N/A	N/A	Awaiting Review	chr17:41,994,576-41,995,355			Contained	ISCA: 18668
LRRC37A1BP	N/A	N/A	Awaiting Review	chr17:42,000,144-42,003,768			Contained	ISCA: 37819
LINC01976	N/A	N/A	Awaiting Review	chr17:42,015,629-42,016,330			Contained	ISCA: 45329
PPY	N/A	N/A	Awaiting Review	chr17:42,019,170-42,019,835	0.983	167280	Contained	ISCA: 12948
PYY	N/A	N/A	Awaiting Review	chr17:42,030,101-42,061,837	0.954	601660	Contained	ISCA: 11368
NAG3	N/A	N/A	Awaiting Review	chr17:42,062,832-42,068,436	0.0	608300	Contained	ISCA: 15495
TMEM101	N/A	N/A	Awaiting Review	chr17:42,068,556-42,100,519	0.162		Contained	ISCA: 14909
LSM12	N/A	N/A	Awaiting Review	chr17:42,112,003-42,144,967	0.832	611793	Contained	ISCA: 1740
OSPC3	N/A	N/A	Awaiting Review	chr17:42,148,998-42,153,712	0.0	612541	Contained	ISCA: 8152

- Can sort by TS score
- One gene has been evaluated with a score of 0; others are awaiting review.

Which genes should I start with?

- Are there any OMIM Morbid genes in the region?

DECIPHER GRCh37 About Browse DDD(UK) Search DECIPHER Join Login

Search results for 'position: 17:41784108-42438203' (Refine Search)

Open-access patients 18 CNV Syndromes 1 DDD Research Variants 1 Genes 29

Results Browser

Genes: 1 to 10 of 23 (out of 29 total)

List is sortable

Morbid DDG2P Protein coding Filter...

Name	Location	Description	OMIM	Morbid	DDG2P	%HI	pLI	Links
SLC4A1	17 42325753 42345509	solute carrier family 4 member 1 (Diego blood group)	✓	✓+	Y	46.73	0.91	View
SOST	17 41831099 41836156	sclerostin	✓	✓+	-	25.56	0.38	View
GRN	17 42422614 42430479	granulin precursor	✓	✓+	-	54.61	0.06	View
NAGS	17 42081914 42086431	N-acetylglutamate synthase	✓	✓	Y	57.83	0.00	View
G6PC3	17 42148183 42153709	glucose-6-phosphatase catalytic subunit 3	✓	✓	-	43.93	0.00	View
UBTF	17 42282481 42298964	upstream binding transcription factor	✓	✓	P	3.63	1.00	View
DUSP3	17 41843488 41856356	dual specificity phosphatase 3	✓	-	-	46.04	0.74	View
C17orf105	17 41857003 41864960	CFAP97 domain containing 1	-	-	-	54.42	-	View
MRP3	17 41878167 41890536	membrane palmitoylated protein 3	✓	-	-	50.67	0.00	View
CD300LG	17 41824516 41840997	CD300 molecule like family member g	✓	-	-	94.75	0.03	View

- Yes! Next step: check the mechanism.

OMIM Morbid Genes in the Region

- All genes completely encompassed within duplicated interval
 - Review of OMIM record and quick literature search indicates that triplosensitivity is not an established mechanism for any of these disorders
 - Would not take any of these genes further through the scoring metric
- *SLC4A1*
 - Cryohydrocytosis (AD)
 - Ovalocytosis, SA type (AD)
 - Renal tubular acidosis, distal (AD)
 - Renal tubular acidosis, distal (AR)
 - Spherocytosis, type 4 (AD)
 - *SOST* (ClinGen TS Score 0)
 - Craniodiaphyseal dysplasia (AD)
 - Sclerosteosis 1 (AR)
 - Van Buchem disease (AR)
 - *GRN*
 - Aphasia, primary progressive (AD)
 - Ceroid lipofuscinosis, neuronal, 11 (AR)
 - Frontotemporal lobar degeneration with ubiquitin-positive inclusions (AD)
 - *NAGS*
 - N-acetylglutamate synthase deficiency (AR)
 - *G6PC3*
 - Dursun syndrome (AR)
 - Neutropenia, severe congenital 4 (AR)
 - *UBTF*
 - Neurodegeneration, childhood-onset, with brain atrophy (AD)

Total: 0 points

What next?

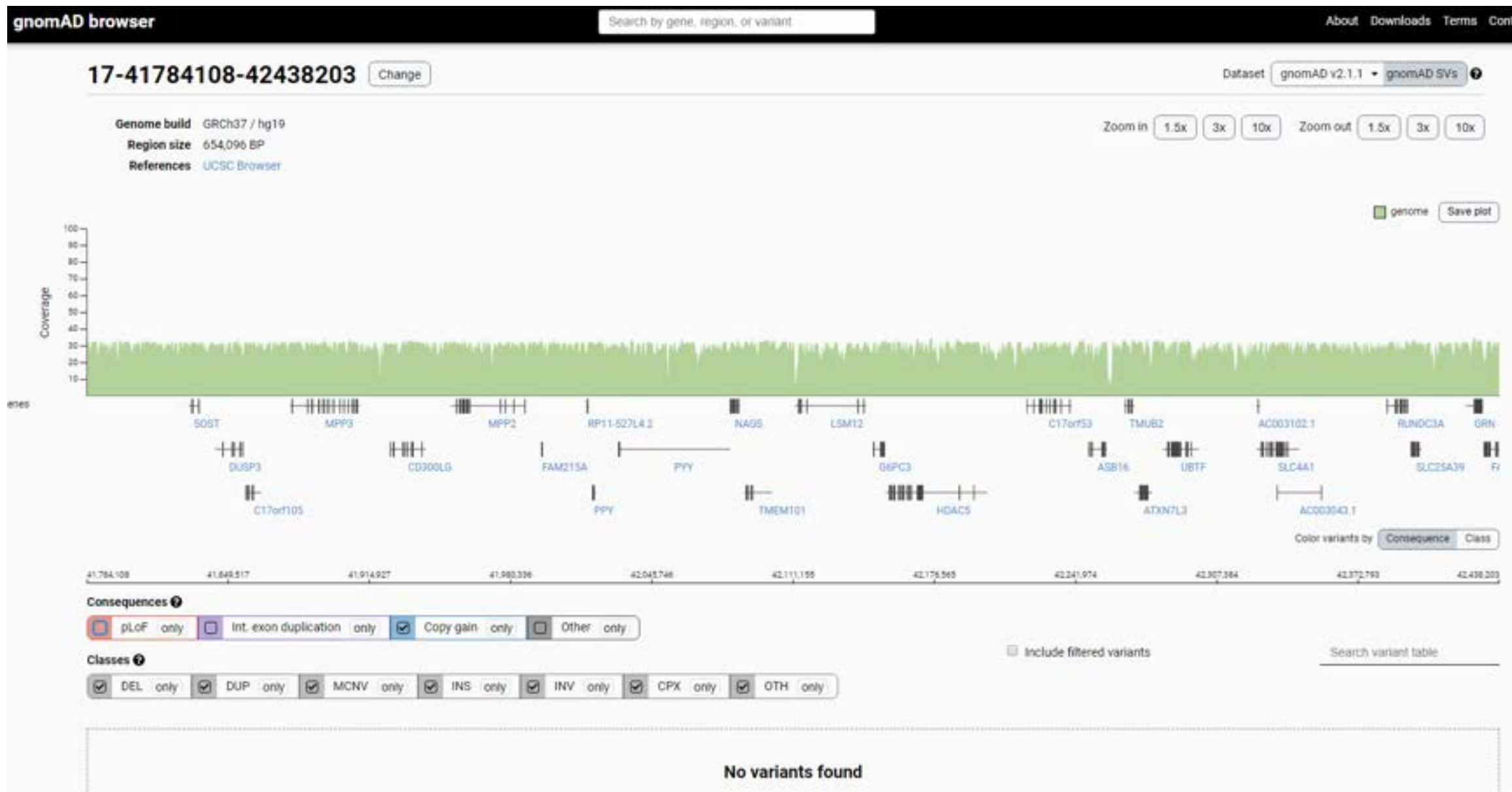
- Quick review of remaining OMIM genes – no evidence to suggest any of these genes causes disease by triplosensitivity (0 points)

Name	Location	Description	OMIM	Morbid	DDG2P	%HI	pLI	Links
DUSP3	17 41843489 41856356	dual specificity phosphatase 3	✓	-	-	46.04	0.74	View
MPP3	17 41878167 41910538	membrane palmitoylated protein 3	✓	-	-	50.67	0.00	View
CD300LG	17 41924516 41940997	CD300 molecule like family member g	✓	-	-	94.75	0.03	View
MPP2	17 41952725 41967068	membrane palmitoylated protein 2	✓	-	-	53.42	0.00	View
PPY	17 42018172 42019836	pancreatic polypeptide	✓	-	-	56.98	0.56	View
PYY	17 42030106 42081837	peptide YY	✓	-	-	58.10	0.05	View
LSM12	17 42112003 42144987	LSM12 homolog	✓	-	-	8.10	0.93	View
HDAC5	17 42154114 42201070	histone deacetylase 5	✓	-	-	4.31	1.00	View
ASB16	17 42247815 42256451	ankyrin repeat and SOCS box containing 16	✓	-	-	52.95	0.00	View
RUNDC3A	17 42385781 42396039	RUN domain containing 3A	✓	-	-	46.63	0.96	View
SLC25A39	17 42396993 42402238	solute carrier family 25 member 39	✓	-	-	58.14	0.00	View

Section 4: Detailed Evaluation of Genomic Content

- Sections 4A-4K are non-applicable for this particular duplication
 - None of the included genes has evidence to suggest triplosensitivity as a disease mechanism
- Next: Evaluate for case-control and population data
 - This CNV is not recurrent; unlikely to be part of case-control studies
 - Check population data in gnomAD, DGV gold standard datasets

gnomAD – No relevant copy gains found



A curated catalogue of human genomic structural variation

chr17:41,784,108..42,438,203

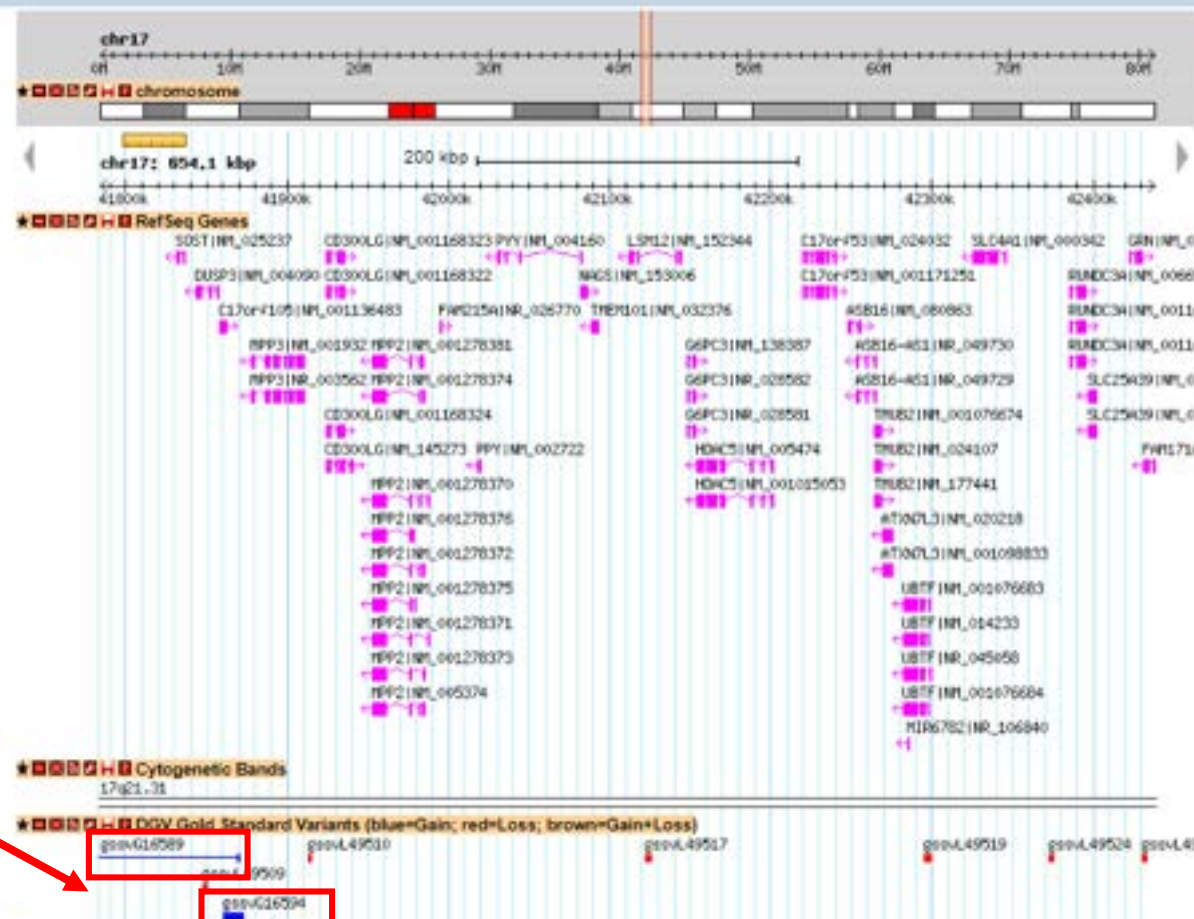
ScrollZoom:

Show 654.1 kbp

⊕ ⊗ ⊙ Flip

 Flip

Two small duplications are present; the top duplication was observed in 4 samples in 2 studies and has a stated frequency of 0.03%. The bottom duplication was observed in 2 samples from 2 studies with a stated frequency of 0.08%. Both of these events are much smaller than our CNV and are not relevant to our case (0 points).



Section 5: Evaluation of Inheritance Patterns/Family History of Patient Being Studied

- No information was provided on the patient's presentation or their family history. Parental testing was not performed.
 - Category 5F: Inheritance information is unavailable or uninformative (0 points).
- **Total points: 0** **Proposed Classification: Uncertain**
- Should this be Likely Benign (LB)?
 - In this scenario, there is no concrete evidence supporting pathogenicity, but also no concrete evidence supporting a classification of "benign."
 - While we cannot say definitively that this CNV has no effect on current or future phenotype, we can convey the sentiment that this is unlikely to cause a phenotype in the report (see Example Report 7).
- Should we test parents?
 - In this scenario, where our baseline score is 0, testing parents would not garner enough points to take this CNV out of the VUS range.

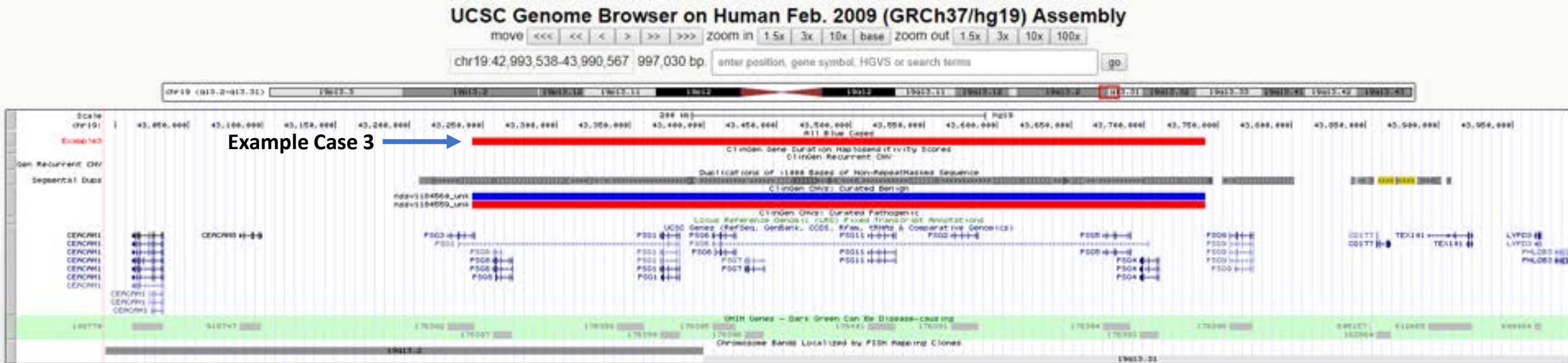
Example Case 3:

arr(GRCh37) 19q13.3
(43242796_43741310) x 1

arr(GRCh37) 19q13.3(43242796_43741310) x 1 mat

- Reason for referral: 3-year-old male referred for aniridia and genitourinary anomalies
- Inherited from apparently normal mother
- Use the LOSS scoring metric

Section 1: Initial Assessment of Genomic Content



- Would apply category 1A (“contains protein-coding or other known functionally important elements”), as this duplication includes several protein-coding genes
- 0 points awarded, continue evaluation

Total: 0 points

Section 3: Evaluation of Gene Number

DECIPHER GRCh37 About Browse DDD(UK) Search DECIPHER Join Login

Search results for 'position:19:43242796-43741310' (Refine Search)

Open-access patients 7 CNV Syndromes 8 DDD Research Variants 0 **Genes 16**

Results **Browser**

Genes: 1 to 10 of 10 (out of 16 total)

Show: ☐ OMIM ☐ Morbid ☐ DDG2P ☒ Protein coding Filter...

Name	Location	Description	OMIM	Morbid	DDG2P	%HI	pLI	Links
PSG1	19 43370016 43383974	pregnancy specific beta-1-glycoprotein 1	✓	-	-	95.19	0.00	View
PSG11	19 43511808 43530664	pregnancy specific beta-1-glycoprotein 11	✓	-	-	96.60	0.00	View
PSG2	19 43568363 43587197	pregnancy specific beta-1-glycoprotein 2	✓	-	-	97.00	0.00	View
PSG3	19 43225790 43244721	pregnancy specific beta-1-glycoprotein 3	✓	-	-	96.93	0.00	View
PSG4	19 43886854 43711451	pregnancy specific beta-1-glycoprotein 4	✓	-	-	97.98	0.00	View
PSG5	19 43870408 43890668	pregnancy specific beta-1-glycoprotein 5	✓	-	-	85.23	0.00	View
PSG6	19 43486231 43423715	pregnancy specific beta-1-glycoprotein 6	✓	-	-	98.36	0.00	View
PSG7	19 43428266 43441330	pregnancy specific beta-1-glycoprotein 7 (gene/pseudogene)	✓	-	-	-	-	View
PSG8	19 43256838 43358843	pregnancy specific beta-1-glycoprotein 8	✓	-	-	97.33	0.00	View
PSG9	19 43715843 43773882	pregnancy specific beta-1-glycoprotein 9	✓	-	-	96.25	0.00	View

Section 3: Evaluation of Gene Number

- 10 protein-coding genes
 - Category 3A (“0-24 genes”) → 0 points
 - Note: multiple members of the same gene family are within the CNV. If the genes within the gene family are not known to be associated with disease, consider counting them as 1 (as opposed to 10 distinct genes) to avoid artificially inflating the gene count. In this scenario, there are less than 24 genes any way, so this doesn’t affect the score.

Total: 0 points

Section 4: Detailed Evaluation of Genomic Content Using Published Literature, Public Databases, and/or Internal Lab Data

- Sections 4A-4K are non-applicable for this particular deletion
 - None of the included genes has evidence to suggest a relationship with human disease
- Next: Evaluate population data (Category 4O)
 - gnomAD, DGV gold standard datasets

Total: 0 points

19-43242796-43741310

Change

Dataset gnomAD v2.1.1 gnomAD SVs ?

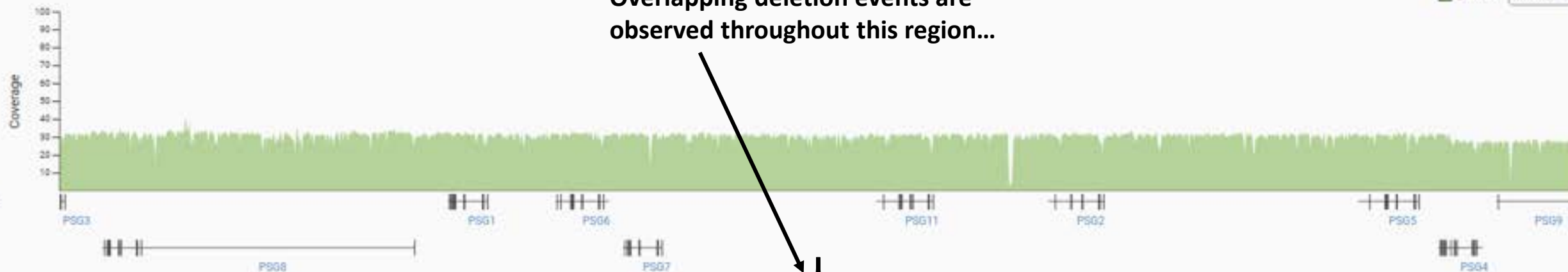
Genome build GRCh37 / hg19

Region size 498,515 BP

References [UCSC Browser](#)

Zoom in 1.5x 3x 10x Zoom out 1.5x 3x 10x

genome Save plot



Overlapping deletion events are
observed throughout this region...



...at very high frequencies (some as high as almost 3.5%!) 

43,242,79643,292,84743,342,49843,392,39043,442,20143,492,05543,541,90443,591,75543,641,60743,691,45843,741,310									
Consequences ?									
☒ pLoF only ☐ Int. exon duplication only ☐ Copy gain only ☐ Other only									
Classes ?									
☒ DEL only ☒ DUP only ☒ MCNV only ☒ INS only ☒ INV only ☒ CPX only ☒ OTH only									
							☐ Include filtered variants		Search variant table
Variant ID	Source	Consequence	Class	Position	Size	Allele Count	Allele Number	Allele Frequency	Number of Homozygotes
DEL_19_203513	G	● loss of function	deletion	43240000 - 43265000	25.0 kb	14	21156	6.62e-4	1
DEL_19_203516	G	● loss of function	deletion	43252700 - 43277025	24.3 kb	67	20884	3.21e-3	1
DEL_19_203517	G	● loss of function	deletion	43259179 - 43261136	1.96 kb	2	21476	9.3e-5	0
DEL_19_203519	G	● loss of function	deletion	43260063 - 43264479	4.42 kb	1	21476	4.7e-5	0
DEL_19_203520	G	● loss of function	deletion	43265181 - 43271102	5.92 kb	68	21280	3.19e-3	1
DEL_19_203524	G	● loss of function	deletion	43292603 - 43603303	311 kb	538	21476	2.51e-2	6
DEL_19_203526	G	● loss of function	deletion	43316928 - 43645531	329 kb	538	21476	2.51e-2	6
DEL_19_203527	G	● loss of function	deletion	43316984 - 43485863	169 kb	538	21476	2.51e-2	6
DEL_19_203528	G	● loss of function	deletion	43317433 - 43745515	428 kb	208	21436	9.7e-3	7
DEL_19_203533	G	● loss of function	deletion	43352131 - 43393674	41.5 kb	510	21476	2.37e-2	6
DEL_19_203535	G	● loss of function	deletion	43382581 - 43529434	147 kb	539	21476	2.51e-2	6
DEL_19_203539	G	● loss of function	deletion	43420778 - 43440033	19.3 kb	569	21462	2.65e-2	10
DEL_19_203542	G	● loss of function	deletion	43455418 - 43546255	90.8 kb	492	21360	2.3e-2	5
DEL_19_203543	G	● loss of function	deletion	43455566 - 43789432	334 kb	676	21468	3.15e-2	9
DEL_19_203544	G	● loss of function	deletion	43469163 - 43624537	155 kb	454	21122	2.15e-2	10
DEL_19_203550	G	● loss of function	deletion	43507886 - 43753337	245 kb	676	21468	3.15e-2	9
DEL_19_203553	G	● loss of function	deletion	43519150 - 43555000	35.9 kb	747	21472	3.48e-2	12
DEL_19_203555	G	● loss of function	deletion	43547647 - 43603780	56.1 kb	519	21448	2.42e-2	8
DEL_19_203560	G	● loss of function	deletion	43603132 - 43790133	187 kb	679	21474	3.16e-2	9
DEL_19_203563	G	● loss of function	deletion	43645614 - 43745072	99.5 kb	491	21216	2.31e-2	8

Similar information in DGV...



Multiple high-frequency deletions across the region; highest frequency (purple box) is 2.88%; event encompassing most of our CNV (green box) is at 1.39%.

Total: -1 points

Section 5: Evaluation of Inheritance Patterns/Family History of Patient Being Studied

- Inherited from apparently normal mother
 - Should we continue to deduct points, using category 5B?
 - You could, but in this case, this is not necessary, as we have already reached a classification of Benign.
 - CAUTION
 - What if the mother had the same phenotype as the patient? Would we add points using Category 5D, taking this variant out of “Benign”?
 - No!
 - Strong population data supports a Benign classification for this variant.
 - Just because the mother and patient share a phenotype does not make this the causative variant.
 - More likely: the mother and patient have a different, yet-to-be-identified variant causing the phenotype.
 - Always use clinical judgement.

• Total points: -1

Proposed Classification: Benign

Example Case 4:

arr[GRCh37]

22q11.21(18912231_21465672)x3

arr[GRCh37] 22q11.21(18912231_21465672)x3

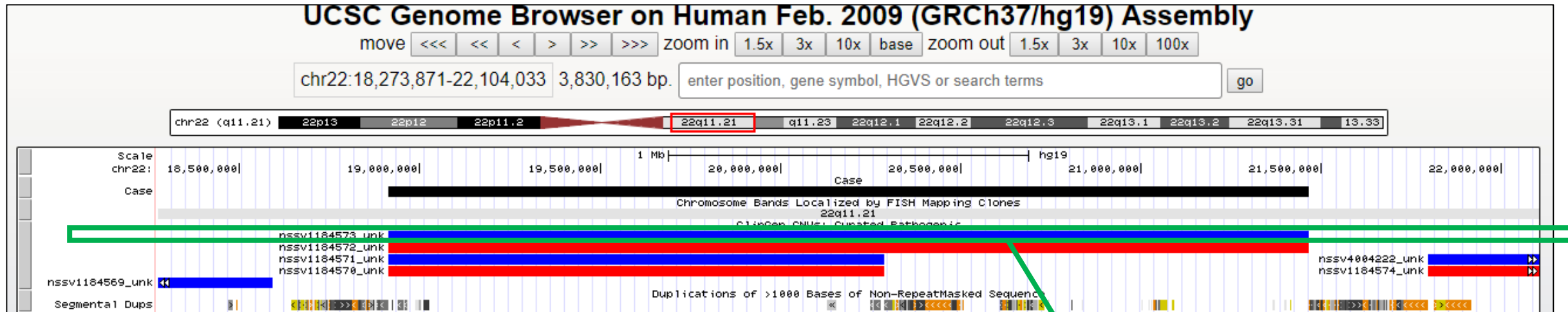
- Reason for referral: 8 y/o female referred for failure to thrive, short stature, fine motor delay, gross motor delay, speech delay, learning disability, autism
- Inherited from apparently unaffected father
- Use the GAIN scoring metric

Example Case 4



- Total: 0 points**

Section 2: Overlap with Established Triplosensitive (TS), Haploinsufficient (HI) or Benign Genes/Genomic Regions



ClinGen CNVs: Curated Pathogenic

- This duplication completely encompasses a ClinGen “Dosage Sensitivity 3 Score” genomic region (category 2A), a recurrent CNV mediated by rearrangements involving flanking segmental duplication regions
- This warrants 1.0 points and a classification of PATHOGENIC. Users may need not proceed further through the metric, however, for the sake of this example, we will walk through the subsequent examples.

Total: 1 point

Section 3: Evaluation of Gene Number

DECIPHER GRCh37 About Browse + DDD(UK) Search DECIPHER Join Login

Search results for 'position:22:18912231-21465672' (Refine Search)

Open-access patients 70% CNV Syndromes 2 DDD Research Variants 8 Genes 81

Results Browser

Genes: 1 to 10 of 44 (out of 81 total)

Show: ☐ OMIM ☐ Morbid ☐ DDG2P ☒ Protein coding Filter...

Name	Location	Description	OMIM	Morbid	DDG2P	%HI	pLI	Links
AIFM3	22 21319396 21335649	apoptosis inducing factor mitochondria associated 3	✓	-	-	38.59	0.00	View
ARVCF	22 19957419 20004331	ARVCF delta catenin family member	✓	-	-	54.56	0.00	View
C22orf29	22 19833661 19842419	retrotransposon Gag like 10	-	-	-	89.11	0.00	View
C22orf39	22 19338891 19435755	chromosome 22 open reading frame 39	-	-	-	70.44	0.00	View
CDC45	22 19466982 19500135	cell division cycle 45	✓	✓	Y	8.40	0.07	View
CLDN5	22 19510547 19515068	claudin 5	✓	-	-	50.93	0.74	View
CLTCL1	22 19168906 19279239	clathrin heavy chain like 1	✓	-	-	72.86	0.00	View

Section 3: Evaluation of Gene Number

- 44 protein-coding genes
 - Category 3B (“35-49 genes”) → 0.45 points
- Note: multiple non-coding genes are also present in this CNV, many of which localize within segmental duplications in this region. These genes should not be counted in the evaluation of gene number.

Section 4: Detailed Evaluation of Genomic Content Using Published Literature, Public Databases, and/or Internal Lab Data

- Since this duplication completely encompasses a known triplosensitive region, and a recurrent CNV with well-characterized phenotypic variability and incomplete penetrance, sections 4A-40 would not need to be performed. We refer users to resources such as the ClinGen Dosage Sensitivity Map as a starting point to review of the literature
- NOTE: use of these metrics for recurrent regions other than those with definitive evidence classifications should be performed with caution.

Section 4, continued

- We refer users to resources such as the ClinGen Dosage Sensitivity Map as a starting point to review of the literature for established dosage sensitive genes and regions



ClinGen Dosage Sensitivity Curation Page

22q11.2 recurrent (DGS/VCFS) region (proximal, A-D) (includes TBX1)

Note the date of last evaluation, particularly for reviews resulting in scores < 3. Check literature to make sure no contradictory evidence has emerged since this date.

Curation Status: Complete

Id: ISCA-37446

Date last evaluated: 2018-08-31

Issue Type: ClinGen Region Curation

ClinGen Haploinsufficiency Score: 3

ClinGen Triplosensitivity Score: 3



Location Information

22q11.21

GRCh37/hg19 chr22: 18,912,231-21,465,672

View: [NCBI](#) | [Ensembl](#) | [UCSC](#)

GRCh38/hg38 chr22: 18,924,718-21,111,383

View: [NCBI](#) | [Ensembl](#) | [UCSC](#)

https://www.ncbi.nlm.nih.gov/projects/dbvar/clingen/clingen_region.cgi?id=ISCA-37446

Section 4, continued

Genome View

Evidence for Haploinsufficiency Phenotypes

Evidence for Triplosensitive Phenotypes

Triplosensitivity score: 3

Strength of Evidence (disclaimer): Sufficient evidence for dosage pathogenicity

Triplosensitivity phenotype: [CHROMOSOME 22q11.2 DUPLICATION SYNDROME](#)

Evidence for gain of function phenotype

PubMed ID	Description
20301749	Firth. GeneReviews: 22q11.2 Duplication. Review of the phenotype associated with duplication of proximal 22q11.2. Similar to the reciprocal deletion, this review combines data from reports of patients with both A-D (3 Mb) and A-B (1.5 Mb) region duplications. The phenotype is described as, "generally mild and highly variable; findings range from apparently normal to intellectual disability/learning disability, delayed psychomotor development, growth retardation, and/or hypotonia. The high frequency with which the 22q11.2 duplication is found in an apparently normal parent of a proband suggests that many individuals can harbor a duplication of 22q11.2 with no discernible phenotypic effect."
19254783	Portnoi (2009) reviewed the literature and summarized findings from approximately 50 unrelated cases of duplications involving proximal 22q11.2. The author noted, "The phenotype of patients is extremely variable, ranging from multiple defects to mild learning difficulties, sharing features with DGS/VCFS, including heart defects, urogenital abnormalities, velopharyngeal insufficiency with or without cleft palate, and with some individuals being essentially normal."
18414210	Ou et al. (2008) reviewed clinical findings of 22q11.2 CNV carriers from a cohort of 7000 clinical aCGH cases. Three probands (Pts 1-3) and two relatives of patient 1 (sibling and mother) with A-D (3 Mb) region duplications were reported. Clinical findings in common in at least two carriers included developmental delay, speech delay, variable dysmorphic features, hypernasal speech, hearing impairment, and behavioral abnormalities. Parental samples were unavailable for patients 2 and 3.

Triplosensitivity phenotype comment:

Duplication of the 22q11.2 proximal (A-D) region* is associated with a highly variable clinical phenotype, ranging from apparently normal to expression a broad range of clinical features, including nonspecific phenotypes (intellectual disability, learning disability, developmental delays, autism, psychiatric disorder growth delays, hypotonia) as well as phenotypes that overlap clinical findings of DGS/VCFS. 22q11.2 duplications are frequently inherited; incomplete penetrance has been demonstrated. This duplication is enriched in the clinical population.

*The 22q11.2 region contains a cluster of low copy repeats (LCRs) that mediate recurrent copy number changes through non-allelic homologous recombination. Proximal 22q11.2 rearrangements involve the centromeric LCR22A and either LCR22B (A-B, approximate size 1.5 Mb) or LCR22D (A-D, approximate size 3.0 Mb) (note in some literature these LCRs are referred to as LCR22-2, 3a and -4, respectively). This review refers to patients with the more common A-D rearrangement. The phenotypes in individuals with A-B and A-D duplications are largely indistinguishable. Note that genes used as landmarks are not necessarily causative of the phenotype(s) associated with the region.

Additional relevant literature is summarized below:

Section 5: Evaluation of Inheritance Patterns/Family History of Patient Being Studied

- Inherited from apparently unaffected father
 - Reported phenotype (failure to thrive, short stature, fine motor delay, gross motor delay, speech delay, learning disability, autism) is relatively non-specific
 - Category 5C, 0 points (see NOTE)
- NOTE: for any CNV that has well-documented phenotypic variability and/or incomplete penetrance, including many recurrent CNVs, this section of the metrics will not apply and should not be used to add or deduct points from an already classified CNV (for example, even if this 22q11.2 duplication was inherited from an unaffected parent, we should not deduct points as incomplete penetrance is established). The points ranges allow one to assign 0 points for such cases.
- Total points: 1 (from Section 2A); Proposed Classification: Pathogenic

Supplemental Material 4: Example Reports

The following example reports are meant to illustrate how certain concepts might be conveyed on a clinical report, such as:

- A single CNV that represents a cause for the reason for referral, an incidental finding, and is indicative of carrier status (Example Report 1)
- Incidental findings (Example Report 2)
- Carrier status (Example Report 3)
- Variants associated with low penetrance/variable expressivity...
 - ...that are seemingly related to the reason for referral (Example Report 4.1)
 - ...that are seemingly unrelated to the reason for referral (Example Report 4.2)
- Multiple CNVs observed in a single proband (Example Report 5)
- X-linked findings in a female (Example Report 6)
- A variant classified as “uncertain” that is unlikely to be of clinical relevance (Example Report 7)

Note that several of the examples are populated with generic information (“Gene X,” “Disease Y,” etc.). In general, this is to keep the focus on the reporting concepts, rather than the underlying data. In other examples, actual well-known genes and genomic regions are used in the hopes that familiarity with the underlying data would help solidify the reporting concept.

These examples are not meant to represent complete reports. For brevity, many important aspects are omitted, such as dates, sample information, test limitations, detailed follow-up recommendations, etc. The wording choices presented here represent suggestions; the clinical laboratory is ultimately responsible for deciding how information is presented on their clinical reports.

Example Report 1: Single CNV involving multiple genes, related to reason for referral, incidental finding, and carrier status

Patient Name: Jane Doe DOB: 01/01/2010 Laboratory ID: 1234567 Test ordered: Chromosomal Microarray	<i>Include any other important header information, such as: relevant dates, additional patient demographics, ordering provider information, sample information, etc.</i>
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Reason For Referral (RFR): Jane Doe is 9 year old female referred for autism spectrum disorder.

Report Summary: A PATHOGENIC 1.4 Mb deletion of 3q11.2 involving 10 protein-coding genes, including Gene X, was identified. Heterozygous loss of function (LOF) variants in Gene X have been identified in individuals with neurodevelopmental disorders, such as developmental delay, intellectual disability, and autism (see discussion of Gene X below for more detailed information). THIS FINDING IS BELIEVED TO BE CAUSATIVE OF THIS INDIVIDUAL'S CLINICAL FINDINGS. Genetic counseling is recommended.

This deletion also includes Gene Y. Heterozygous loss of function variants in Gene Y have been identified in individuals with autosomal dominant progressive sensorineural hearing loss (see discussion of Gene Y below for more detailed information). Jane Doe was not reported to have hearing loss; this may represent an incidental finding, or provide a cause for a phenotype that was either not reported or may be observed in the future. Clinical correlation is recommended.

This deletion also includes Gene Z. Biallelic loss of function variants in Gene Z have been identified in individuals with Disease 1, an autosomal recessive condition. This finding indicates that Jane Doe is at least a carrier for Disease 1. Note that this variant alone is insufficient to cause Disease 1 (see discussion of Gene Z below for more detailed information). Clinical correlation is recommended to determine if additional testing to identify a second pathogenic variant in Gene Z is warranted.

Copy Number Variation (CNV): 1.4 Mb 3q11.2 Deletion

ISCN	Type	Size	Inheritance	Zygosity	Classification
arr [GRCh37] 3q11.2 (XXXXXXX-XXXXXXX) x 1	Deletion	1.4 Mb	De Novo	Heterozygous	Pathogenic

Relevant Genomic Content:

This deletion includes 10 protein-coding genes, including the following, which are relevant to this report:

Gene	Disease	Mode of Inheritance	Relevance Category	Notes
Gene X	Neurodevelopmental Disorder (NDD)	AD	Related to RFR	This finding is thought to be causative for the reported RFR. Genetic counseling is recommended.
Gene Y	Progressive sensorineural hearing loss (SNHL)	AD	Incidental Finding	Though Jane Doe was not reported to have hearing loss, she is thought to be at risk to develop hearing loss given this finding. Clinical correlation is recommended.
Gene Z	Disease 1	AR	Carrier Status	This variant alone is insufficient to cause Disease 1. A second pathogenic variant on the opposite allele (<i>in trans</i>) is necessary to cause disease. Clinical correlation is required to determine if additional testing is warranted.

Gene X

Include a more detailed description of Gene X and its relationship to Neurodevelopmental Disorder 1, including any appropriate references. Describe the evidence supporting Gene X that led the CNV to be classified as Pathogenic.

Gene Y

Include a more detailed description of Gene Y and its relationship to progressive sensorineural hearing loss, including any appropriate references.

Gene Z

Include a more detailed description of Gene Z and its relationship to Disease 1, including any appropriate references.

Other genes included in this deletion are: Gene A, Gene B, Gene C, Gene D, Gene E, Gene F, and Gene G. [Optional. If the gene list is extensive, the laboratory may not wish to note them all. May include any other relevant information, links, etc. regarding the other genes in the interval.]

Include any other relevant report information, such as methods, quality metrics, disclaimers, resources, etc.

Example Report 2: CNV involving multiple genes, unrelated to reason for referral (incidental finding)

Patient Name: Jane Doe
DOB: 01/01/2010
Laboratory ID: 1234567
Test ordered: Chromosomal Microarray

Include any other important header information, such as: relevant dates, additional patient demographics, ordering provider information, sample information, etc.

Reason For Referral (RFR): Jane Doe is 9 year old female referred for developmental delay and autism spectrum disorder.

Report Summary: This test did not identify any variants that can explain the patient’s reported clinical features at this time. However, a PATHOGENIC 1.4 Mb deletion of 3q11.2 involving 10 protein-coding genes, including Gene Y, was identified. Heterozygous loss of function (LOF) variants in Gene Y have been identified in individuals with autosomal dominant progressive sensorineural hearing loss (see discussion of Gene Y below). Jane Doe was not reported to have hearing loss; this may represent an incidental finding, or a cause for a phenotype that was not reported or that may be observed in the future. Clinical correlation and genetic counseling are recommended.

Copy Number Variant (CNV): 1.4 Mb 3q11.2 Deletion

ISCN	Type	Size	Inheritance	Zygosity	Classification
arr [GRCh37] 3q11.2 (XXXXXXXX-XXXXXXXX) x 1	Deletion	1.4 Mb	De Novo	Heterozygous	Pathogenic

Relevant Genomic Content:

This deletion includes 10 protein-coding genes, including the following, which are relevant to this report:

Gene	Disease	Mode of Inheritance	Relevance Category	Notes
Gene Y	Progressive sensorineural hearing loss (SNHL)	AD	Incidental Finding	Though Jane Doe was not reported to have hearing loss, she is thought to be at risk to develop hearing loss given this finding. Clinical correlation and genetic counseling are recommended.

Gene Y

Include a more detailed description of Gene Y, its relationship to progressive sensorineural hearing loss, and the evidence leading to the classification, including any appropriate references.

Other genes included in this deletion are: Gene A, Gene B, Gene C, Gene D, Gene E, Gene F, Gene G, Gene H, and Gene X. [Optional. If the gene list is extensive, the laboratory may not wish to note them all. May include any other relevant information, links, etc. regarding the other genes in the interval.]

Include any other relevant report information, such as methods, quality metrics, disclaimers, resources, etc.

Example Report 3: CNV involving genes conferring carrier status ONLY

Patient Name: Jane Doe
DOB: 01/01/2010
Laboratory ID: 1234567
Test ordered: Chromosomal Microarray

*Include any other important header information, such as:
relevant dates, additional patient demographics,
ordering provider information, sample information, etc.*

Reason For Referral (RFR): Jane Doe is 9 year old female referred for developmental delay and autism spectrum disorder.

Report Summary: This test did not identify any variants that can explain the patient’s reported clinical features at this time. However, a PATHOGENIC 1.4 Mb deletion of 3q11.2 was identified involving GeneZ, a gene associated with an autosomal recessive condition, Disease 1. This finding indicates that Jane Doe is at least a CARRIER for Disease 1. Note that this variant alone is insufficient to cause autosomal recessive Disease 1. Clinical correlation is recommended; if warranted, consider additional testing to determine a genetic etiology for the stated reason for referral and/or to identify a second variant in Gene Z. Genetic counseling is also recommended.

Copy Number Variant (CNV): 1.4 Mb 3q11.2 Deletion

ISCN	Type	Size	Inheritance	Zygosity	Classification
arr [GRCh37] 3q11.2 (XXXXXXXX-XXXXXXXX) x 1	Deletion	1.4 Mb	De Novo	Heterozygous	Pathogenic

Relevant Genomic Content:

This deletion includes 10 protein-coding genes, including the following, which are relevant to this report:

Gene	Disease	Mode of Inheritance	Relevance Category	Notes
Gene Z	Disease 1	AR	Carrier status	This variant alone is <i>insufficient</i> to cause disease; a second pathogenic variant on the opposite allele (<i>in trans</i>) is required. This finding alone DOES NOT explain the patient’s reported phenotype. Clinical correlation is required to determine if additional testing is warranted.

Gene Z

Include a more detailed description of Gene Z, its relationship to Disease 1, and the evidence leading to the classification, including any appropriate references.

Other genes included in this deletion are: Gene A, Gene B, Gene C, Gene D, Gene E, Gene F, Gene G, Gene H, and Gene X. *[Optional. If the gene list is extensive, the laboratory may not wish to note them all. May include any other relevant information, links, etc. regarding the other genes in the interval.]*

Include any other relevant report information, such as methods, quality metrics, disclaimers, resources, etc.

Example Report 4.1: CNV associated with low penetrance, matching phenotype

Patient Name: Jane Doe DOB: 01/01/2010 Laboratory ID: 1234567 Test ordered: Chromosomal Microarray	<i>Include any other important header information, such as: relevant dates, additional patient demographics, ordering provider information, sample information, etc.</i>
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Reason For Referral (RFR): Jane Doe is 9 year old female referred for developmental delay and autism spectrum disorder.

Report Summary: A PATHOGENIC duplication of 22q11.21 was identified. This duplication is approximately 2.5 Mb in size and corresponds to the recurrent 22q11.2 proximal region involving breakpoints A-D. Duplications of this region are associated with LOW PENETRANCE AND VARIABLE EXPRESSIVITY; these duplications have been observed in individuals with neurodevelopmental disorders (references) as well as in apparently normal individuals, even within the same family (see below for additional information). This duplication is likely contributing to Jane Doe’s reported phenotype. Clinical correlation is recommended to determine if additional testing is warranted.

Copy Number Variant (CNV): 2.5 Mb 22q11.21 Duplication

ISCN	Type	Size	Inheritance	Zygosity	Classification
arr [GRCh37] 22q11.21 (18912231_21465672) x3	Duplication	2.5 Mb	De Novo	Heterozygous	Pathogenic

Relevant Genomic Content:

This deletion includes a known recurrent genomic region relevant to this report:

Genomic Region	Disease	Mode of Inheritance	Relevance Category	Notes
Recurrent 22q11.2 proximal region, breakpoints A-D	Neurodevelopmental disorders	AD	Related to RFR; Low penetrance and variable expressivity	Variant known to be associated with neurodevelopmental disorders, but with LOW PENETRANCE and VARIABLE EXPRESSIVITY. Clinical correlation is recommended to determine if additional testing is warranted.

Duplication 22q11.21, proximal regions, breakpoints A-D

Include a more detailed description of duplications of the 22q11.21 proximal region (breakpoints A-D), the evidence supporting this classification, and the spectrum of associated clinical observations, including any appropriate references.

Include any other relevant report information, such as methods, quality metrics, disclaimers, resources, etc.

Example Report 4.2: CNV associated with low penetrance, non-matching phenotype

Patient Name: Jane Doe

DOB: 01/01/2010

Laboratory ID: 1234567

Test ordered: Chromosomal Microarray

Include any other important header information, such as: relevant dates, additional patient demographics, ordering provider information, sample information, etc.

Reason For Referral (RFR): Jane Doe is 9 year old female referred for hearing loss.

Report Summary: This test did not identify any variants that can explain the patient’s reported clinical features at this time. However, a PATHOGENIC duplication of 22q11.21 was identified. This duplication is approximately 2.5 Mb in size and corresponds to the recurrent 22q11.2 proximal region involving breakpoints A-D. Duplications of this region are associated with LOW PENETRANCE AND VARIABLE EXPRESSIVITY; these duplications have been observed in individuals with neurodevelopmental disorders (references) as well as in apparently normal individuals, even within the same family (see below for additional information).

Jane Doe was not reported to have features of a neurodevelopmental disorder; this may represent an incidental finding, or a cause for a phenotype that was not reported. This finding alone DOES NOT diagnose Jane Doe with a specific neurodevelopmental disorder, such as autism; such diagnoses are made based on clinical presentation. Genetic counseling and clinical correlation are recommended to determine the significance of this finding for Jane Doe and her family. Clinical correlation is also recommended to determine if additional testing is warranted to further investigate genetic etiologies for her hearing loss.

Copy Number Variant (CNV): 2.5 Mb 22q11.21 Duplication

ISCN	Type	Size	Inheritance	Zygosity	Classification
arr [GRCh37] 22q11.21 (18912231_21465672) x3	Duplication	2.5 Mb	De Novo	Heterozygous	Pathogenic

Relevant Genomic Content:
This deletion includes a known recurrent genomic region relevant to this report:

Genomic Region	Disease	Mode of Inheritance	Relevance Category	Notes
Recurrent 22q11.2 proximal region, breakpoints A-D	Neurodevelopmental disorders	AD	Related to RFR; Low penetrance and variable expressivity	Variant known to be associated with neurodevelopmental disorders, but with LOW PENETRANCE and VARIABLE EXPRESSIVITY. Clinical correlation is recommended to determine if additional testing is warranted.

Duplication 22q11.21, proximal regions, breakpoints A-D

Include a more detailed description of duplications of the 22q11.21 proximal region (breakpoints A-D), the evidence supporting this classification, and the spectrum of associated clinical observations, including any appropriate references.

Include any other relevant report information, such as methods, quality metrics, disclaimers, resources, etc.

Example Report 5: Multiple CNVs

Patient Name: Jane Doe

DOB: 01/01/2010

Laboratory ID: 1234567

Test ordered: Chromosomal Microarray

*Include any other important header information, such as:
relevant dates, additional patient demographics,
ordering provider information, sample information, etc.*

Reason For Referral (RFR): Jane Doe is 9 year old female referred for developmental delay and autism spectrum disorder.

Report Summary: A PATHOGENIC 1.4 Mb deletion at 3q11.2 involving 10 protein-coding genes, including Gene X, was identified. Heterozygous loss of function (LOF) variants in Gene X have been identified in individuals with neurodevelopmental disorders, such as developmental delay, intellectual disability, and autism (see discussion of Gene X below for more detailed information). This finding is believed to be causative of this individual’s clinical findings. Genetic counseling is recommended.

The 3q11.2 deletion also includes Gene Y. Heterozygous loss of function variants in Gene Y have been identified in individuals with autosomal dominant progressive sensorineural hearing loss (see discussion of Gene Y below). Jane Doe was not reported to have hearing loss; this may represent an incidental finding, a cause for a phenotype not reported, or a phenotype not yet observed. Clinical correlation is recommended.

A second copy number variant (CNV), a 350 kb duplication at 5q13.1 was also identified. This CNV is a VARIANT OF UNCERTAIN SIGNIFICANCE; it is unclear at this time what effect (if any) this variant may have on Jane Doe’s current or future health. See below for additional information. Genetic counseling is recommended.

Copy Number Variant (CNV) #1: 1.4 Mb 3q11.2 Deletion

ISCN	Type	Size	Inheritance	Zygosity	Classification
arr [GRCh37] 3q11.2 (XXXXXXX-XXXXXXX) x 1	Deletion	1.4 Mb	De Novo	Heterozygous	Pathogenic

This deletion includes 10 protein-coding genes, including the following, which are relevant to this report:

Gene	Disease	Mode of Inheritance	Relevance Category	Notes
Gene X	Neurodevelopmental Disorder (NDD)	AD	Related to RFR	This finding is thought to be causative for the reported RFR. Genetic counseling is recommended.
Gene Y	Progressive sensorineural hearing loss (SNHL)	AD	Incidental Finding	Though Jane Doe was not reported to have hearing loss, she is thought to be at risk to develop hearing loss given this finding. Clinical correlation is recommended.

Gene X
Include a more detailed description of Gene X, its relationship to Neurodevelopmental Disorder 1, and the evidence leading to the classification, including any appropriate references.

Gene Y
Include a more detailed description of Gene Y and its relationship to progressive sensorineural hearing loss, including any appropriate references.

Other genes included in this deletion are: Gene A, Gene B, Gene C, Gene D, Gene E, Gene F, Gene G, and Gene H.
[Optional. If the gene list is extensive, the laboratory may not wish to note them all. May include any other relevant information, links, etc. regarding the other genes in the interval.]

Copy Number Variant (CNV) #2: 350 kb 5q13.1 Duplication

ISCN	Type	Size	Inheritance	Zygoty	Classification
arr [GRCh37] 5q13.1 (XXXXXXX-XXXXXXX) x 3	Duplication	350 kb	De Novo	Heterozygous	Uncertain Significance

This duplication includes 2 protein-coding genes:

Gene I
Describe any available information about Gene I, the evidence (or lack thereof) leading to the classification, including any appropriate references.

Gene K
Describe any available information about Gene K, the evidence (or lack thereof) leading to the classification, including any appropriate references.

Include any other relevant report information, such as methods, quality metrics, disclaimers, resources, etc.

Example Report 6: X-linked finding in a female

Patient Name: Jane Doe
DOB: 01/01/2010
Laboratory ID: 1234567
Test ordered: Chromosomal Microarray

Include any other important header information, such as: relevant dates, additional patient demographics, ordering provider information, sample information, etc.

Reason For Referral (RFR): Jane Doe is 9 year old female referred for hearing loss.

Report Summary: This test did not identify any variants that can explain the patient’s reported clinical features at this time. However, a maternally inherited, PATHOGENIC 124 kb deletion of Xq21.1 (involving the *ATP7A* gene) was identified. Hemizygous loss of function variants in this gene have been associated with Menkes disease in MALES; as Jane Doe is a FEMALE, this finding likely represents CARRIER STATUS for Menkes disease. Female carriers of pathogenic *ATP7A* variants are typically asymptomatic, though unfavorably skewed X-inactivation could result in clinical findings related to this disorder. Genetic counseling and clinical correlation are recommended to discuss the potential reproductive implications of this finding and to determine if additional testing is warranted to identify a genetic etiology for Jane Doe’s hearing loss.

Copy Number Variant (CNV): 124 kb Xq21.1 Deletion

ISCN	Type	Size	Inheritance	Zygosity	Classification
arr [GRCh37] Xq21.1 (77226076-77350000) x 1	Deletion	124 kb	Maternal	Heterozygous	Pathogenic

Relevant Genomic Content:
This deletion includes a single gene relevant to this report:

Gene	Disease	Mode of Inheritance	Relevance Category	Notes
ATP7A	Menkes disease	X-linked	Carrier Status	Female heterozygous carriers of pathogenic variants in <i>ATP7A</i> TYPICALLY DO NOT display overt clinical features of Menkes syndrome, an X-linked condition affecting predominantly males. This finding DOES NOT explain the patient’s reported clinical features. Clinical correlation is recommended to determine if additional testing is warranted.

ATP7A
Include a more detailed description of ATP7A, Menkes disease, and the evidence supporting this classification, including any appropriate references.

Include any other relevant report information, such as methods, quality metrics, disclaimers, resources, etc.

Example Report 7: 17q21.31 dup

Patient Name: Jane Doe
DOB: 01/01/2010
Laboratory ID: 1234567
Test ordered: Chromosomal Microarray

Include any other important header information, such as: relevant dates, additional patient demographics, ordering provider information, sample information, etc.

Reason For Referral (RFR): Jane Doe is 9 year old female. No reason for referral was reported.

Report Summary: This test did not identify any variants of predicted clinical relevance at this time. However, an UNCERTAIN 654 kb duplication at 17q21.31 was identified. This duplication includes 23 protein-coding genes, but, at this time, none of them are known to cause human disease as the result of the presence of an extra copy (triplosensitivity). Please note that the classification of this variant could change over time as additional evidence emerges. Further, because no clinical indication for testing was provided, full clinical correlation could not be performed by the laboratory. Clinical correlation is recommended to determine if additional testing is necessary to identify a genetic etiology for Jane Doe's clinical features.

Copy Number Variant (CNV): 654 kb 17q21.31 Duplication

ISCN	Type	Size	Inheritance	Zygosity	Classification
arr [GRCh37] 17q21.31 (41784108-42438203) x 3	Duplication	654 kb	Unknown; parental testing not performed	Heterozygous	Uncertain

This deletion includes 23 protein-coding genes. At this time, none of the genes in the region have been reported to cause disease when present as an extra copy.

The classification of this CNV is UNCERTAIN at this time per the 2019 ClinGen/ACMG constitutional copy number variant interpretation standards (reference). While this duplication does include protein-coding elements (Category 1A, 0 points), it does not overlap any known dosage sensitive genes/genomic regions (Section 2, all categories, 0 points). Twenty-three protein-coding genes are duplicated (Category 3A, 0 points), but, per literature evaluation, triplosensitivity is not a known mechanism for disease for any of these genes (Categories 4A-K, 0 points). There is no significant case-control or population variant overlap with this duplication (Category 4L-O, 0 points). Finally, no information was provided about the patient's phenotype, her family history, or the inheritance of the observed CNV (Category 5 F, 0 points). The final tallied score is 0 points, which corresponds to a variant classification of UNCERTAIN (0 total points).

Include any other relevant report information, such as methods, quality metrics, disclaimers, resources, etc.

APPENDIX 7
ACMG standards and guidelines for documenting suspected consanguinity
as an incidental finding of genomic testing
(See following page)

American College of Medical Genetics and Genomics: standards and guidelines for documenting suspected consanguinity as an incidental finding of genomic testing

Catherine W. Rehder, PhD¹, Karen L. David, MD, MS^{2,3}, Betsy Hirsch, PhD⁴, Helga V. Toriello, PhD⁵, Carolyn M. Wilson, MS⁶ and Hutton M. Kearney, PhD⁶

Genomic testing, including single-nucleotide polymorphism-based microarrays and whole-genome sequencing, can detect long stretches of the genome that display homozygosity. The presence of these segments, when distributed across multiple chromosomes, can indicate a familial relationship between the proband's parents. This article describes the detection of possible consanguinity by genomic testing and the factors confounding the inference of a specific parental

relationship. It is designed to guide the documentation of suspected consanguinity by clinical laboratory professionals and to alert laboratories to the need to establish a reporting policy in conjunction with their ethics review committee and legal counsel.

Genet Med 2013;15(2):150–152

Key Words: consanguinity; homozygosity; laboratory guideline

Many genomic microarray platforms use a combination of probes designed to assess copy number and probes to genotype single-nucleotide polymorphisms. In addition to copy-number changes (i.e., deletions, duplications), these array platforms can identify genomic regions that display an absence of heterozygosity, often in the form of one or more long contiguous stretch of homozygosity. Large regions of homozygosity, when observed on a single chromosome, can be indicative of uniparental disomy;¹ however, when these regions are distributed throughout the genome, they usually represent segments of autozygosity or regions that are identical by descent (IBD). These autozygous segments originate from a common ancestor and can indicate a consanguineous relationship between the proband's parents. The health impact of consanguinity has been recently reviewed.² Whole-genome and potentially whole-exome sequencing strategies can also detect long contiguous stretches of homozygosity. Because the results obtained using any of these technologies can point to a familial relationship or consanguinity between parents, these technologies could reveal situations suspicious for potential abuse, especially, but not limited to, situations when the mother is disabled or a minor.³

The guidelines presented here are designed to assist clinical laboratories in the management of microarray and exome/genome sequencing findings that suggest parental consanguinity, with a primary focus on detection and reporting results back to the ordering clinician.

DETECTION OF CONSANGUINITY

Genomic regions that are IBD originate from a common ancestor, with the proportion of the genome that is autozygous

increasing as the parental relationship becomes closer. The average proportion of the autosomal genome that is IBD in the offspring of related parents is given by the coefficient of inbreeding (F).⁴ For example, on average, 6.25% or 1/16th of the genome of offspring of first cousins ($F = 1/16$) is IBD. Although the coefficient of inbreeding provides a theoretical value, significant deviations from the expected values do occur.

Because smaller stretches of homozygosity (<3 Mb) spread throughout the genome are common even in outbred populations, laboratories typically set a size threshold, below which segments are not considered significant. In theory, in the offspring of a second-cousin mating, an average of four 12.5 Mb stretches of homozygosity per genome will be present, although both the number and the size of homozygous segments are known to be highly variable.⁵ When long contiguous stretches of homozygosity involving multiple chromosomes are present, the percentage of the genome that is IBD can be estimated by the sum of the sizes of the homozygous segments divided by the total autosomal genomic length (~2,881 Mb for GRCh37/hg19). The sex chromosomes are typically excluded from the calculation because males have only a single X and Y chromosome and therefore cannot have homozygosity at any locus outside of the pseudoautosomal regions. This calculation is likely an underestimation of the actual percentage of the genome that is IBD because only those segments of homozygosity meeting the threshold set by the laboratory will be flagged for inclusion in the calculation.⁶ This percentage can then be compared with the theoretical value derived from the coefficient of inbreeding for any given parental relationship. These theoretical values are found in many genetics texts and resources.⁵

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Because recombination during meiosis is a somewhat random process, the variation from the theoretical value increases with each meiosis⁷ such that third cousins may share more DNA sequences than second cousins. Even among the progeny of first cousins, in whom the average percentage of the genome that is IBD is 6.25%, the SD is 2.43%.⁵ The expected percentages are based on a single common ancestor; however, multiple loops of consanguinity or multiple generations of breeding within a relatively closed community could complicate the estimation of the degree of relationship. These variations from the expected or theoretical values are more pronounced for more distantly related individuals⁵ and may be caused by stochastic events, multiple loops of consanguinity, small gene pools, and unknown family structures (e.g., adoptions, nonpaternity). Because of these variables, the specific familial relationship or degree of relatedness between the parents cannot always be extrapolated from the percentage of the genome that is IBD. Single-nucleotide polymorphism array analysis is not designed to be a paternity test, nor should it be used to definitively assign a specific relationship between the parents of the proband.

Concerns for abuse arise when IBD proportions suggest that the parents of the proband are first- or second-degree relatives, particularly when the mother is a minor or intellectually disabled. Among the progeny of first- ($F = 1/4$) and second-degree ($F = 1/8$) relative matings, the number of meioses separating the parents is sufficiently low such that the SD is relatively low. Therefore, when high percentages of the genome ($\geq 10\%$) are IBD and several large segments of absence of heterozygosity are present, it is reasonable to suspect a close parental relationship.

RECOMMENDATIONS FOR PRETEST COUNSELING

It is recommended that each patient/family undergoing microarray and exome/genome testing receive pretest counseling.

RECOMMENDATIONS FOR REPORTING FINDINGS OF CONSANGUINITY TO THE ORDERING CLINICIAN

It is important to recognize that the detection of one or more long contiguous stretch of homozygosity, in and of itself, is not abnormal. However, the detection of segments that are homozygous does increase the likelihood that the proband has inherited two copies of a deleterious allele for an autosomal recessive disorder. Clinicians may find utility in this knowledge if the patient's phenotype matches that of an autosomal recessive disorder for which one or more candidate genes are located within one of these segments. Because there is clinical utility in the detection of excessive homozygosity, even when the percentage of the genome that is IBD is quite low ($<3\%$), many laboratories may choose to report this finding back to the ordering clinician to encourage consideration of recessive mechanisms and facilitate autozygosity mapping. Laboratories may choose to include a percentage or proportion of the genome that is homozygous in their reports. In general, caution should be exercised when using an automated calculation of the percentage of the genome

that is IBD. Some analysis programs generate this calculation using all segments displaying absence of heterozygosity, regardless of size or mechanism, which can include deletions. This automated calculation is also typically inflated by small regions of homozygosity that are more likely representative of regions of suppressed recombination or linkage disequilibrium (identity by state). Limiting this calculation to segments $>2\text{--}5\text{ Mb}$ is more likely to result in the inclusion of segments that are truly IBD. Each laboratory should establish parameters for calculating the percentage of the genome that is IBD and determine a threshold for reporting back the results.

In general, laboratories have very limited information regarding the structure of the proband's family (e.g., maternal age, adoptions, multiple loops of consanguinity, other familial relationships). Therefore, speculation of a specific relationship in written reports is strongly discouraged. An example of suggested language is as follows:

"Several large regions of homozygosity ($\geq 2\text{ Mb}$ or larger) were detected, encompassing $> 10\%$ of the genome. Although this result is not diagnostic of a specific condition, it raises the possibility of a recessive disorder with a causative gene located within one of these regions. A genetics consultation is recommended."

SPECIAL CONSIDERATIONS

The observation of a possible first- or second-degree parental relationship, particularly when the mother of the proband is known to be a minor or has an intellectual disability, raises a suspicion for abuse involving the mother of the proband. Laboratories do not typically have information regarding the mother's age, intellectual status, or family structure; therefore, they do not have adequate information to communicate a suspicion for abuse to any authoritative agency. Therefore, when the percentage of homozygosity reaches a level that could be consistent with a first- or second-degree parental relationship ($>10\%$ with multiple regions of homozygosity $2\text{--}5\text{ Mb}$ or larger), laboratory reports should indicate that the results could be associated with possible consanguinity to ensure that the ordering clinician (geneticist or nongeneticist) understands the implications of the results. An example of suggested language is as follows:

"Several large regions of homozygosity ($\geq 2\text{ Mb}$ or larger) were detected, encompassing $> 10\%$ of the genome. Although this result is not diagnostic of a specific condition, it raises the possibility of a recessive disorder with a causative gene located within one of these regions. Additionally, these results could indicate a familial relationship (first or second degree) between this individual's parents. A genetics consultation is recommended."

Laboratories are encouraged to engage the ordering clinician when a first- or second-degree mating is suspected based on the results of the analysis. The clinician is the most appropriate

person to correlate laboratory results with family history and cultural traditions and to investigate any concern for abuse. Clinicians should be aware that many states have mandatory reporting statutes requiring that anyone with cause to suspect that a child, juvenile, or disabled adult has been the victim of abuse, including rape or sexual assault, report his/her concern to the appropriate governmental authorities.^{8,9} These same statutes provide protection for the reporting individual as long as the concern is raised in good faith. It is advised that each laboratory or hospital consult with its ethics review committee and legal counsel for policy development concerning the requirements for and manner of reporting.

CONCLUDING REMARKS

The ability to detect regions of homozygosity is an important clinical tool with clear utility in the context of the detection of autosomal recessive conditions and uniparental disomy. A secondary consequence of the observation of regions of homozygosity is the possible discovery of a consanguineous relationship between the proband's parents. Although a specific relationship cannot be determined using the currently available technologies, this information may be useful to the clinician caring for the patient and family. It is the responsibility of the clinician, not the laboratorian, to perform clinical correlation and investigate any concern for abuse. The laboratorian's duty is to effectively communicate the possibility of a familial relationship between the parents to the ordering clinician when a first- or second-degree relationship is suspected based on the results of the analysis. Laboratories are encouraged to develop

a reporting policy in conjunction with their ethics review committee and legal counsel.

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DISCLOSURE

The authors declare no conflict of interest.

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APPENDIX 8
ACMG standards and guidelines: microarray analysis for chromosome abnormalities
in neoplastic disorders
(See following page)

American College of Medical Genetics and Genomics technical standards and guidelines: microarray analysis for chromosome abnormalities in neoplastic disorders

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Disclaimer: These American College of Medical Genetics and Genomics Standards and Guidelines are developed primarily as an educational resource for clinical laboratory geneticists to help them provide quality clinical laboratory genetic services. Adherence to these Standards and Guidelines is voluntary and does not necessarily ensure a successful medical outcome. These Standards and Guidelines should not be considered inclusive of all proper procedures and tests or exclusive of other procedures and tests that are reasonably directed to obtaining the same results. In determining the propriety of any specific procedure or test, the clinical laboratory geneticist should apply his or her own professional judgment to the specific circumstances presented by the individual patient or specimen. Clinical laboratory geneticists are encouraged to document in the patient's record the rationale for the use of a particular procedure or test, whether or not it is in conformance with these Standards and Guidelines. They also are advised to take notice of the date any particular standard or guideline was adopted and to consider other relevant medical and scientific information that becomes available after that date. It also would be prudent to consider whether intellectual property interests may restrict the performance of certain tests and other procedures.

Microarray methodologies, to include array comparative genomic hybridization and single-nucleotide polymorphism-based arrays, are innovative methods that provide genomic data. These data should be correlated with the results from the standard methods, chromosome and/or fluorescence *in situ* hybridization, to ascertain and characterize the genomic aberrations of neoplastic disorders, both liquid and solid tumors. Over the past several decades, standard methods have led to an accumulation of genetic information specific to many neoplasms. This specificity is now used for the diagnosis and classification of neoplasms. Cooperative studies have revealed numerous correlations between particular genetic aberrations and therapeutic outcomes. Molecular investigation of chromosomal abnormalities identified by standard methods has led to discovery of genes, and

gene function and dysfunction. This knowledge has led to improved therapeutics and, in some disorders, targeted therapies. Data gained from the higher-resolution microarray methodologies will enhance our knowledge of the genomics of specific disorders, leading to more effective therapeutic strategies. To assist clinical laboratories in validation of the methods, their consistent use, and interpretation and reporting of results from these microarray methodologies, the American College of Medical Genetics and Genomics has developed the following professional standard and guidelines.

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Key Words: cancer; guidelines; microarray; neoplastic; tumor

Neoplastic processes are a complex group of disorders that develop as a result of the accumulation of genetic alterations including gene mutations, chromosomal rearrangements, gain and loss of genetic material, epigenetic changes, loss of heterozygosity (LOH), and various other genetic changes. Defining and understanding the genetic alterations of specific neoplastic disorders influences the diagnoses, prognoses, and therapeutic choices for patients with both malignant and benign neoplasms.^{1–7}

Published clinically applicable data now show the utility of DNA microarray analysis in the assessment of multiple neoplastic disorders.^{8–13} Data indicate that microarray technologies provide information about gain and loss of genetic material in neoplastic disorders, including hematologic malignancies and solid

tumors.^{14–17} These gains and losses, represented as an increase or decrease in the proportion of genetic material as compared with a reference genome, are collectively referred to as copy-number variants (CNVs). Microarray methodologies are appropriate complementary methods to standard methods of chromosome and fluorescence *in situ* hybridization (FISH) analyses for detection of genetic anomalies in neoplastic disorders.

DNA microarray technologies should confirm genetic imbalances identified by conventional and molecular cytogenetic or FISH analyses and provide further detail of the aberrations.^{15–17} However, additional important information about the genetics of specific disorders may be revealed, e.g., leukemia with normal cytogenetic and FISH analyses.^{18–23}

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DNA MICROARRAY PLATFORMS

Different types of DNA microarray platforms currently available for clinical testing include bacterial artificial chromosome–based array comparative genomic hybridization, oligonucleotide-based array comparative genomic hybridization, oligonucleotide plus single-nucleotide polymorphism (SNP)-based arrays that contain both copy-number (intensity-only) and SNP (allele-differentiating) probes, as well as SNP-only-based arrays.^{9,24–26}

For comparative genomic hybridization–based microarrays, patient DNA and reference DNA are labeled with different fluorochromes and hybridized to probes on the microarray. SNP-based arrays use a single color dye compared with an *in silico* reference. A scanner measures differences in the intensities of the fluorochromes, and the data are expressed as having more or less signal as compared with the reference. For genomic regions with two copies of the DNA sequence, copy-number data are graphed as a $\log_2$ ratio with the expected normal copy number equaling “0.” Duplications will have signals of greater intensity ($\log_2 > 0$) and deletions less intensity ($\log_2 < 0$). Microarrays that incorporate SNP probes allow simultaneous detection of DNA copy-number changes and absence of heterozygosity (AOH) by providing information about the intensity of the signals at the loci. AOH may be due to LOH, hemizygosity, or homozygosity.

Advantages of DNA microarray analysis

Advantages of DNA microarray analyses include:

- The ability to use any sample that yields DNA of sufficient quality,
- Assessment of the genome at very high resolution,
- Interpretation of raw data using objective biostatistical algorithms,
- The ability to detect copy-number-neutral runs or regions of homozygosity (ROHs or AOH) with SNP-array technology, and
- A ready interface of the digital data with genome browsers and Web-based genome-annotated databases.

Limitations of DNA microarray analysis

Limitations of DNA microarray analyses include:

- Inability to detect molecularly balanced chromosomal rearrangements,²⁷
- Inability to detect tumor-specific changes (acquired clonality) with a low ratio of tumor cells to normal cells,
- Inability to determine the chromosomal mechanisms of the genetic imbalance, e.g., insertion, tandem duplication; chromosome and/or FISH studies may be needed,
- Inability or difficulty in detection of tetraploidy or other ploidy levels; platforms that include SNP probes may facilitate detection, and

- Inability to characterize clonal and subclonal populations; the $\log_2$ ratio may provide an indication of clonal heterogeneity.

Because of these limitations, results using microarray technologies at diagnosis should be correlated with other established methodologies (chromosome analysis, FISH). Microarray analysis is neither established nor recommended as a method for posttherapy follow-up or for minimal residual disease detection.

It should be understood that the current copy-number genomic microarray technologies are not designed to detect point mutations, gene expression levels, methylation anomalies, and microRNA anomalies, all of which may contribute to tumorigenesis. Detection of a “small” insertion or deletion, e.g., intragenic, will be affected by platform resolution, probe spacing, gene coverage, laboratory software parameters, and sample DNA quality.

Microarray platform design and verification

The laboratory should choose a microarray design with probe coverage suitable for detection of known copy-number aberrations associated with the neoplasm of interest. Microarray platform design may be (i) targeted to specific regions of the genome for detection of known cancer-associated unbalanced genomic alterations, (ii) genome-wide with a specified distribution and spacing of probes, or (iii) both targeted and genome-wide, with varying distribution and spacing of probes in specific regions and across the entire genome.

Manufacturers of microarrays should verify the identity of each clone or probe on the platform used for clinical testing. Probes selected from the public domain should be listed with their physical and cytogenetic positions on the human genome. All probe descriptions and annotations should be openly accessible. Details regarding the microarray design, the synthesis verification, and all quality control (QC) steps taken to validate and assess the performance and reproducibility of the microarray should be documented and provided by the manufacturer. Additional information may be found in the American College of Medical Genetics and Genomics recommendations for the design and performance expectations for clinical genomic copy-number microarray devices.²⁸

Microarrays should be designed with consideration of the statistical algorithms to be used for determining abnormal thresholds. The number and density of probes within a given region of interest, i.e., within a region known to be associated with a cancer gene or feature, should provide the sensitivity needed for detection of a copy-number variation.

VERIFICATION AND VALIDATION OF HARDWARE, SOFTWARE, REAGENTS, AND PROCESSES

Definitions

Verification. Verification is a confirmation, through provision of objective evidence, that specified requirements have been fulfilled. This is a one-time process completed to determine or

confirm test performance characteristics before the test system is used for patient testing. Verification is a quality assurance process to determine that instruments, software, and associated data are accurate per the manufacturer's description and specifications, i.e., does the system (hardware, software, probes) function as described by the vendor/manufacturer?

Validation. Validation is a confirmation through the provision of objective evidence that requirements for a specific intended use or application have been fulfilled. Validation is a QC process to determine that the data from test samples are accurate for the intended use when compared with a validated method, i.e., does the system (processes) provide the correct (accurate, reproducible) result(s) when test samples or test data are analyzed?

Platform

Initiation of microarray technologies requires the laboratory verify that the instrumentation, software, and probes perform as specified by the vendor. All platforms intended for clinical testing must be verified and validated. The method and scope of the verification and validation must be documented. A new platform is defined as any new methodology or microarray type introduced into the laboratory. A single microarray vendor may produce multiple similar platforms, but each must be assessed independently. A new version is defined as a minor modification to probe coverage, either through manufacturing of the microarray or by *in silico* probe filtering.

Laboratory with little or no experience with microarray technologies

The laboratory with little or no experience with microarray technology should become familiar with all aspects of the new technology through the verification process, consultation with vendor support, and if possible, other laboratories with demonstrated proficiency using the same platform before beginning the validation process. Familiarization includes understanding the processes, features, and capabilities of the technology selected. The laboratory should gain experience with the instrumentation, platform design, software, reagents, methodologies, technological limitations, workflows, and DNA quality parameters by experimental sample runs. Similarly, the laboratory should become familiar with the features of each sample type the laboratory will process.

It is strongly suggested that laboratories use a combination of data from well-characterized controls and/or data from public databases to gain and broaden their experience. Sample exchanges with a laboratory proficient with a similar microarray platform can provide a good source of samples for validation. Exchange of validated data sets between laboratories provides additional experience in data analysis. Samples chosen for validation studies should have aberrations that challenge the technical limits of detection for reportable deletions and duplications.

Laboratories must be able to recognize nonperforming probes, technically induced artifact and quality issues.

Laboratories should become familiar with benign and/or common CNVs and resources to aid in recognition and interpretation of CNVs, whether in a constitutional or neoplastic setting.

The laboratory should demonstrate expertise in technical aspects of the processing of sample types to be used for clinical testing, technical performance of the microarray, reproducibility of results, and data analysis and interpretation. Expertise should be documented for each microarray platform used for clinical testing, regardless of whether the laboratory has prior experience with a different platform.

New platform

A minimum of 30 samples should be processed and interpreted by the laboratory to verify and validate any new platform. This includes changing to a platform of the same type from a different manufacturer or a different platform type, e.g., array comparative genomic hybridization to SNP. Samples with known abnormalities should be used to gain expertise with the new methodology and assess performance.

New/different version of an established platform

Analysis of a minimum of five known abnormal samples should be run on a new platform version. Data from a new version should be compared with data from the established version to determine if the platform and software perform as expected to detect known CNVs. New probe additions for enhanced coverage or improved performance should be investigated with samples known to have variation in the region of new content (when possible).

New versions of established platforms will vary with the manufacturer and platform type. A manufacturer may define minor upgrades as new versions. There are no definitive criteria for a new version; however, a different version should be limited to minimal probe changes, e.g., removal and/or replacement of probes to improve performance and/or coverage over a limited number of genomic regions. These types of changes to an established platform are likely to be rare, with most changes of platforms requiring a full validation.

Validation of a new clinical test or assay

Any assay intended for clinical diagnosis must be verified and validated before offering as a clinical test. Proficiency in test performance, analysis, and interpretation must be demonstrated.

It is understood that the microarray platform employed by the laboratory may be used to analyze multiple sample types and multiple neoplastic disorders. Inherent differences in obtainable results from different biological materials require that the laboratory determine the performance characteristics of the microarray for each sample type, e.g., bone marrow/blood, fresh or frozen tissue/tumor, formalin-fixed paraffin-embedded (FFPE) tumor, to be used for clinical testing. A surgical pathologist should be involved in the collection of optimal solid tumor samples to ensure a minimum of 25% tumor in the sample.

Laboratories that plan to offer clinical testing for different neoplastic disorders using different sample types should

prepare by processing and analyzing a sufficient number of each type to establish proficiency. Disease-specific samples for which clinical testing will be offered should be included in the validation sample collection. The laboratory should run technical replicates of multiple samples during the validation process to ensure that the assay results are accurate and reproducible. Discrepancies between replicates should be investigated and documented.

Each laboratory should use judgment and experience to determine the number of samples of a particular type of neoplastic disorder to include in their preclinical testing validation. Laboratories will also need to use judgment and experience to determine differences and issues of processing various sample types and adjust sample numbers of each type accordingly, with the goal of optimizing quality and analytic interpretation of results.

Sample assays for a specific diagnosis may be validated by comparison of results with those obtained by other methods, e.g., conventional cytogenetics, FISH, or another validated microarray assay. During the validation process, all genomic imbalances identified by standard method(s) should be detected by the microarray within the limits of clonality detection levels established by the laboratory for the diagnosis or sample type. Reportable abnormalities, e.g., CNVs or LOH detected by microarray but not by cytogenetic analysis, should be confirmed by another method, e.g., multiplex ligation-dependent probe amplification (MLPA), quantitative PCR (qPCR), FISH, or a different microarray platform, during the validation process to gain sufficient expertise and confidence in data interpretation.

Exchanging samples with another laboratory conducting similar assays in a blind, split-sample comparison using both normal and abnormal samples and comparing results at the appropriate detection levels declared by the laboratories can provide valuable feedback during the validation process. After the validation period, sample sharing can be used for external proficiency testing (PT). All validation data for each disease and sample type, including discordant results and limitations, should be documented.

Clonality detection and limits

Samples from neoplastic disorders can be expected to have varying amounts of nonneoplastic cells admixed with neoplastic cells. The proportion of clonal and nonclonal cells may or may not be clinically relevant but will affect assay sensitivity. Detectable clonality can be influenced by several factors including microarray platform used, sample source, DNA quality, size and copy-number state of the abnormality, and probe coverage. Noise from poor-quality DNA may mask clonality. Each laboratory will need to challenge their microarray with mosaic, aneuploid, and clonally diverse samples to gain experience in their detection. The various factors should be considered with data analysis.

Visual inspection and manual review of the data should be employed to detect clonality and gain experience with data interpretation. The software may not flag low-level clonality. A

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call made by visual/manual inspection, when the call was not made by the software, should be verified by another method, e.g., interphase FISH, qPCR.

Determination of levels of detectable clonality

Methods to evaluate levels of detectable clonality will differ with sample type, e.g., fresh, fixed, or FFPE. Dilution studies are one method that may be used to create different levels of clonality for test purposes.²⁹ Flow cytometric analysis and interphase FISH analysis of fresh (uncultured) samples provide reliable methods for confirmation of clonality level(s). Conventional cytogenetic analysis of metaphase cells provides information about clonal populations but does not reliably reflect levels of clonality.

Dilution studies for SNP arrays require nonneoplastic and tumor DNA from the same patient. Buccal cells or blood may provide a source of nonneoplastic patient DNA.

Assessment of levels of neoplastic to nonneoplastic cells or sizes of different clonal populations in fresh or fixed (FFPE) tissue samples is more difficult. Dissection of fresh tumor with an inverted microscope can reduce the amount of nonneoplastic tissues. Microdissection of FFPE tumors can enrich the DNA sample for tumor. Estimation of clonality in tumor tissue samples can be useful when analyzing data from these tumor types.^{11,29}

Determination of ploidy

Polyploidy may be detected by microarray analysis but may be difficult to appreciate. The allelic states of SNP probes can assist in determining ploidy levels. The validation process should include samples with varying levels of ploidy to gain experience in analysis and recognition of different ploidies. The manufacturer should provide the method used for normalization. The laboratory must understand the effect that normalization may have on polyploidy detection and subsequent interpretation of gains and losses in the context of polyploidy.

Clonal diversity

Clonal diversity, common to neoplastic disorders, should be visible by microarray when the cell populations of different clones reach the threshold for detection. However, determination of the composition of clones or the sequence of progression of clonal evolution will not be possible. Correlation with conventional cytogenetic analysis may facilitate interpretation of the microarray results.

Software experience and evaluation

Software may not be specifically designed for analysis of cancer specimens. Laboratories may choose to design their own software programs or modify parameters of the platform's standard software program. The laboratory should recognize software limitations and the need for manual and visual inspection of the data for aberration and clonality detection.

A comprehensive evaluation of any software to be used to analyze microarray data should be performed. The laboratory

must determine and document the ability of the software to define accurately the limits of copy-number variations, i.e., deletions, duplications, and/or amplifications, according to software rules and parameters. When applicable, the laboratory should also determine the ability of the assay to define the end points of copy-neutral ROHs according to the software settings. Limits should be reestablished whenever the microarray platform, probes, software, or analysis rules change. The laboratory should challenge the software with a variety of aberrations, especially copy-number variations that help define the limits of detection. The limits, rules, and parameters for detection of clonality should be determined. The laboratory should document the software parameters and rules used in the analysis of the microarray, as well as all limitations of the analysis program.

REFERENCE DNA

Comparative genomic hybridization–based microarray analysis requires comparison of sample DNA to reference DNA. Selection of an appropriate reference DNA is essential. Constitutional DNA from blood or normal tissue from the same individual may be used. Constitutional patient DNA will mask constitutional CNVs and reduce the complexity of postanalytic interpretation. However, novel underlying germline abnormalities that could contribute to disease will not be detected.

Laboratories may establish their own reference DNAs. Reference DNA may be from a set of normal individuals with common CNVs identified for a specific type of microarray. The laboratory should characterize any reference DNA to identify CNVs that may have an effect on the interpretation of patient data.

Male and female controls should be established. Laboratory policies should detail how reference DNAs will be used, i.e., for mismatched opposite-sex or same-sex comparisons, as single male or single female references, or as pools from multiple male or multiple female DNA samples. The laboratory should document the rationale for the use of reference DNA types and have provisions for use in different situations. The advantages and limitations of different approaches should be understood and considered during interpretation of data.

Each new reference DNA or new lot of purchased reference DNA for array comparative genomic hybridization should be compared by microarray analysis to the previous lot of reference DNA.

SNP-based microarray analysis requires comparison of the sample result with established references or an *in silico* reference library. If sufficient data are available for a control population, a laboratory may establish its own *in silico* reference that mimics the typical study population. New reference data should be established for new SNP-based array designs.

QUALITY CONTROL

Identification

For each microarray, the slide ID, sample sex, control sex (when appropriate), and sample-tracking control (for multiplex microarrays) should be verified. Discrepancies in the documentation

from the physical sample should be investigated and resolved before processing.

Sample requirements

The laboratory should establish parameters for the minimum DNA quality and quantity requirements for each sample type used for clinical testing. The laboratory should demonstrate proficiency in sample preparation, DNA extraction, and DNA purification for each sample type. Fresh or frozen tumor tissue is preferable to fixed tumor tissue for quality. FFPE tumor samples should be evaluated by a surgical pathologist to assess the quality and quantity of tumor in the sample used for microarray analysis. A minimum of 25% tumor is recommended to prevent masking of clonal changes by normal tissue DNA.

DNA extraction, purification, measurement, and amplification with different sample types

DNA extraction methods should ensure the highest-quality DNA possible from the sample type(s) tested by the laboratory. Samples from neoplastic disorders present unique challenges for generating high-quality, tumor-specific DNA. Written protocols should be available in the laboratory procedure manual and/or quality management program for optimizing DNA extraction and labeling, DNA quantification (e.g., fluorometer, spectrophotometer), DNA quality and concentration (e.g., examination by gel electrophoresis), DNA fragmentation (e.g., via sonication or digestion), fluorescent labeling (e.g., examination by gel electrophoresis, visual inspection, ultraviolet/visible spectroscopy), and amplification (e.g., significant increase in product). For any labeling method, acceptable ranges should be determined for proper dye incorporation. Protocols for optimization, e.g., reextraction, repurification, tumor cell enrichment for hematological samples (cell sorting or concentration), and/or microdissection for paraffin-embedded tumor, should be available as appropriate. Laboratories should be aware that fixatives other than formalin may influence DNA quality and that decalcification of bony tumors may adversely affect DNA quality.

Suboptimal samples

The laboratory should establish sample adequacy requirements. Samples that do not meet the laboratory requirements should be rejected with a repeat sample requested from the referring physician.

When a repeat sample is not available, whole-genome amplification may be a reasonable alternative if the laboratory has expertise with the method and if potential biases inherent in the technique are detailed in the report. Laboratory policies and protocols should describe when and how whole-genome amplification is performed.

Equipment calibration, maintenance, and QC

Equipment, instrumentation, and methodologies employed during the validation and use of microarray platforms should be calibrated, receive regular maintenance, and be monitored for QC. Quality metrics should be established for each step of the assay.

QC metrics

Every microarray platform has defined quality metric values, e.g., adequate dye incorporation and/or amplification, fluorescence intensities variance, signal-to-background-noise ratio, and SD or error. Standard cutoff values and acceptable limits should be established for these metrics to ensure that the generated results are reliable and sufficiently precise to be used for a clinical assessment. Quality metrics should be monitored for DNA labeling, hybridization efficiency, data generation and analysis, and other platform-specific parameters. QC metrics should be incorporated into the laboratory quality assurance and quality improvement programs to monitor analytical variables.

Microarray content

It is not feasible for a laboratory to validate the identity and copy-number responsiveness of every probe on a microarray. The laboratory should obtain documentation from the microarray manufacturer that the probes on each microarray are the intended sequence, located appropriately by the software, empirically selected for appropriate copy-number responsiveness and/or SNP allele specificity, and stable for these assessments from lot to lot.

Data quality

Detection of genomic aberrations is dependent on the size of the DNA targets, the probe density, the probe performance, and the distance between the sequences naturally located on the chromosome. The quality of the data will affect the ability to detect genomic aberrations; thus, the laboratory needs to understand the within-array metrics provided by the analysis software and how each metric reflects the quality of the data. One metric that provides a measurement of noise or random variance unrelated to genomic location in the data is the derivative log ratio. The derivative log ratio is the difference between the log ratio values of consecutive probes (derivative log ratio spread), i.e., the spread of the derivative log ratio values after outlier rejection. For SNP arrays, quality may be assessed using data from such parameters as call rates and variability (spread) of allele frequency.

Other features to be kept in mind when assessing copy-number changes are the appropriate log ratio difference between patient and control samples, presence of nonrandom contiguous probe behavior, sharp copy-number state transitions, and supportive SNP allele states (when applicable). The software manufacturer should provide confidence metrics for a copy-number call or SNP allele state/genotype based on the algorithms used by the software for aberration calls.

The laboratory should establish acceptable ranges for each QC metric chosen to assess data quality. The manufacturer often provides these ranges; however, the laboratory may want to modify these ranges based on their experience with the microarrays during the validation process. The laboratory should establish criteria for next steps should the data fall outside of these established ranges.

Custom and public annotations/databases are integral to data analysis. Because these annotations are critical for interpretation, it is important that these tools are carefully constructed and applied by the software manufacturer. Manufacturers should provide updates to these annotations as they become available. The laboratory should check any inconsistencies with an additional data source, e.g., compare results from the University of California, Santa Cruz (UCSC) genome browser with those from the Ensembl browser. Custom annotations from the laboratory should be verified.

Laboratories should ensure that the software manufacturer provides documentation and safeguards such that data are processed and summarized in a consistent manner for every clinical analysis. Most analysis software provides a hierarchy of users with customizable permissions, which enables the laboratory to prevent modification of analysis settings so that all specimens are analyzed consistently. Any changes to data processing should be validated and documented.

Verification of new lots of microarrays and/or reagents

Verification should ensure that new lots of microarray slides and/or reagents perform in the same manner as the previous lot. The manufacturer should supply documentation of the QC comparison between lots of microarray slides, e.g., oligo synthesis verification, accuracy of SNP calls, or other defined control parameters. A new lot of microarray slides should be tested to ensure equivalency by testing, either before or concurrently with new patient specimens, preferably using a patient specimen with an abnormal result that has been tested on a previous lot. Manufacturers may include a normal control and request that it be run. New lots of reagents, e.g., new labeling kits and consumables, should have documented equivalency between runs. This may be accomplished by documenting that the QC metrics meet certain set parameters for the new lot of reagents.

QUALITY ASSURANCE**Laboratory accreditation and personnel qualifications**

Laboratory personnel must have documentation of education, degrees, and certifications as appropriate for the level of testing, as well as training, competency assessments, and continuing education as required by appropriate regulatory bodies, e.g., College of American Pathologists (CAP), Clinical Laboratory Improvement Amendments (CLIA), Center for Medicare and Medicaid Services (CMS). The testing laboratory must have CLIA certification and state certifications as required to provide clinical testing. CAP accreditation is strongly encouraged.

Indications and ordering for microarray analysis of neoplastic disorders

Microarray analysis of tumors should be limited to specimens that contain ample tumor, e.g., diagnostic or relapse. The sample should be accompanied by an appropriate indication for the test. Clinical testing should be limited to neoplastic disorders for which unbalanced genomic anomalies are well documented to have diagnostic, prognostic, and/or therapeutic implication(s).

Microarray analysis is not indicated for tumor surveillance or detection of minimal or residual disease because of insensitivity of the test for low levels of disease. Alternative methods should be recommended to monitor patient response to treatment and for residual disease detection, e.g., FISH, qPCR. A clonal abnormality identified and confirmed at diagnosis may be used for follow-up. The same method used for confirmation, e.g., qPCR or FISH, is recommended for use in follow-up studies. Alternatively, DNA or cells may be saved and used as a control when follow-up samples are assessed for residual disease.

Laboratories may facilitate appropriate ordering by providing a directive or disease-specific testing menu. The test requisition should provide sufficient clinical and/or pathological information for the laboratory to assess the appropriateness of the test order.

Proficiency testing (PT)

The laboratory should participate in PT for sample types and tumor types that are included in the laboratory test menu by participating in an external PT program when available through an appropriate-deemed organization, e.g., CAP. In addition, the laboratory may establish external PT of normal and abnormal specimens by the exchange of DNAs, in a blinded manner, with another laboratory performing microarray testing for neoplastic disorders.

The laboratory should also establish internal PT of normal and abnormal samples as part of the laboratory internal quality assurance program and ongoing quality improvement program. Correlation between microarray results run in parallel on different microarray platforms or correlation of microarray results with conventional cytogenetic and/or FISH results may be sufficient to provide ongoing proficiency. PT should be performed according to the CLIA '88 guidelines.

Documentation of participation and the performance results of internal and external PT must be retained by the laboratory and made available to all accreditation agency inspectors.

Failure to achieve agreement on external or internal proficiency tests should be documented and followed by investigation of the discrepancy with resolution. If indicated, appropriate remediation should be undertaken.

Turnaround time

Laboratory policies should define acceptable standards for microarray analysis test prioritization and turnaround times. Turnaround time should be clinically appropriate so the results are available for patient care management decisions.

It is suggested that 90% of cases should have a final written report by 21 calendar days. A longer turnaround time is acceptable when custom probes, oligos, or primer sequences must be designed, ordered, validated, and used. Normal or preliminary abnormal results should be available within 14 calendar days.

Documentation of problems

A logbook, database, or sample processing form should be created and used to track problems that may occur throughout the processing of samples for neoplasia, from sample intake to final report, e.g., sample adequacy and/or errors. Data from the QC metrics program can provide information for oversight of all processes. Ongoing collection of sample or process variances allows patterns or trends to be recognized and promptly addressed.

ANALYSIS OF DATA INCLUDING ANALYTICAL SOFTWARE ALGORITHMS

Analytical software algorithms differ between platforms. Microarray software is designed to determine gain, loss, or long ROHs in a chromosomal region. Most software manufacturers provide standard algorithms to set cutoff values for calls. However, each laboratory should thoroughly test the rules or filters during the validation process and determine the parameters for cutoff values, e.g., the number of consecutive probes deleted or amplified and the log₂ ratio to call a CNV, depending on probe density. It may be necessary to set different parameters for different chromosome regions or specific genes of interest while keeping in mind the potential for a false-positive call.

Ratio values for mosaic cases will be less than expected for nonmosaic cases and may fall below the standard cutoff value. Clonality may be apparent by visualization or by examination of the moving averages across the chromosomes. The sensitivity of the microarray for detection of clonality should be determined during the platform validation process.

The laboratory must be familiar with the principles of the software program for any platform used. However, the laboratory should never depend solely on the software for analysis. A visual inspection of the moving average across each chromosome and a review of the allele frequency for SNP arrays should be done to identify appropriate and inappropriate results for the disorder being tested. Analysis should be continued until all inconsistencies are resolved.

RESULTS EVALUATION AND INTERPRETATION

The laboratory should be consistent in the analysis, interpretation, and reporting of microarray results. The laboratory should have a record of and be familiar with the microarray coverage, including known cancer-associated genes and regions, benign and/or common population CNVs, and common genetic disorders caused by genomic CNVs and/or LOH.

Systematic evaluation and interpretation of DNA microarrays

The laboratory should establish the methods for microarray result analysis and interpretation using the following recommendations.

Disease-associated genetic aberrations

Analysis and interpretation of microarray data from a neoplastic disorder should take into account the working diagnosis, the clinical information provided, and other disorders in the

differential diagnosis. The indication or working diagnosis may prove to be incorrect after the diagnostic workup is complete; thus, the laboratory should be aware of other disorders that may be in the differential.

The laboratory should be familiar with recurrent, clonal aberrations associated with particular diagnoses. In addition, the laboratory should be familiar with specific genes known to be pathogenic or to contribute to the pathogenesis of a particular disorder. The medical literature should be used to stay abreast of current disease-specific genetic aberrations, as well as the diagnostic, prognostic, and therapeutic significance of aberrations.

CNV interval size and cancer-associated genes

The size of a CNV is relevant, as larger CNVs encompassing multiple genes are more likely to have a clinical impact; however, very small CNVs that interrupt or delete an established cancer-associated gene may be clinically significant. A single laboratory-established CNV size cutoff or threshold for determination of inclusion of a CNV in a clinical report should not be used as the sole determinant of a call. The laboratory should establish methods for detection of clinically significant CNVs that fall below laboratory-established thresholds, particularly in regions of known cancer-associated genes.

Genomic content in CNV interval

The genomic content of the CNV should be carefully examined for genes relevant to disorders in the differential diagnosis, gene-rich sequences, or genes known to have a clinical association. CNVs encompassing known oncogenes or tumor suppressor genes may have significance, although the implications of the CNV for the particular disorder or patient being studied may not be clear based on current literature.

Copy-number-neutral ROHs detected by SNP analysis

Thresholds or minimal criteria to identify clinically important ROHs consistent with LOH (LOH or AOH) should be established. ROHs associated with parental consanguinity or uniparental disomy should be distinguished from acquired LOH. Distinction of acquired versus constitutional AOH may be facilitated by detection of the clonal aberration in affected tissue (acquired LOH) and/or detection (or not) of the aberration in unaffected tissue (constitutional LOH). Homozygosity in a region that contains a tumor suppressor gene may be associated with an inherited cancer predisposition syndrome. Constitutional analysis should be recommended as appropriate.

Comparison of CNV to internal and external databases

Public databases and the medical literature should be used in determining the significance of CNVs. Available databases include (all last accessed 26 January 2013) the following:

- Database of Genomic Variants (<http://projects.tcag.ca/variation/>),

- Online Mendelian Inheritance in Man (<http://www.ncbi.nlm.nih.gov/omim/>),
- DECIPHER (<http://www.sanger.ac.uk/research/areas/>),
- dbVar—database of Structural Variation (<http://www.ncbi.nlm.nih.gov/dbvar>),
- dbGaP—database of Genotypes and Phenotypes (<http://www.ncbi.nlm.nih.gov/gap>),
- Memorial Sloan-Kettering Cancer Center (<http://cbio.mskcc.org/CancerGenes>),
- The Cancer Genome Anatomy Project (<http://www.ncbi.nlm.nih.gov/ncicgap/>),
- UCSC Genome Bioinformatics (<http://genome.ucsc.edu/cgi-bin/hgGateway>),
- The Cancer Genome Atlas (<http://cancergenome.nih.gov/>),
- Ensembl (http://uswest.ensembl.org/Homo_sapiens/Gene/Summary),
- The International Standards for Cytogenomics Arrays Consortium (<https://www.iscaconsortium.org/>), and
- Wellcome Trust Sanger Institute (<http://www.sanger.ac.uk/genetics/CGP/cosmic/>).

Laboratories should document pathogenic CNVs, CNVs of uncertain significance, benign CNVs, and CNVs thought or determined to be constitutional. The intralaboratory data should be used along with external data as a reference for interpretation of data from new studies.

Categories of clinical significance

Using the guidelines outlined above for systematic investigation of a CNV for clinical significance, it is recommended that the interpreting laboratory geneticist use the following categories for reporting. Consistent terminology will facilitate unambiguous communication of clinical significance. Taking into account that tumors may be genetically complex, it may not be feasible to provide a detailed interpretation of every CNV and/or AOH region detected. In such cases, a narrative to describe variants and their clinical significance and interpretation should be provided to communicate the desired information. When feasible, the laboratory should provide details of specific CNV and AOH anomalies.

Pathogenic

Acquired. The CNV is a documented clinically significant and/or disease-associated clonal genetic aberration.

Constitutional. Microarray analysis will inevitably reveal common benign and rare constitutional CNVs. Rare constitutional CNVs should be noted and investigated for clinical significance, e.g., cancer-predisposing gene aberration and/or deletion or duplication associated with a known constitutional syndrome. Evaluation and reporting of constitutional CNVs should follow the guidelines set forth in the American College of Medical Genetics and Genomics Standards and Guidelines for interpretation and reporting of constitutional CNVs.³⁰

Uncertain clinical significance

This category may include CNVs that are not known to be associated with disease but meet the reporting criteria established by the laboratory. A CNV in this category is not clearly pathogenic, and there is insufficient evidence for an unequivocal determination of clinical significance. The laboratory should interpret novel CNVs in light of the available clinical and/or pathological information and current literature. Reporting CNVs of uncertain significance is at the discretion of the laboratory. If reported, they may be categorized as follows:

Uncertain clinical significance, acquired, likely pathogenic. Many neoplastic disorders have well-recognized and/or well-characterized aberrations. However, microarray resolution may reveal uncharacterized CNVs. If reported, the discussion should avoid speculation as to the pathogenicity or clinical significance of the CNV without supporting evidence.

Examples: (i) A CNV described in a single case report of a similar neoplasm. (ii) A CNV with a gene in the interval that has potential or relevant function as an oncogene or tumor suppressor gene or that belongs to another known gene family that has an association with neoplastic processes but not the neoplastic process being studied. (iii) A CNV that appears related to the clonal neoplastic process being studied by having a similar $\log_2$ ratio as the clonal process being studied but is not a recognized aberration. Evolution and heterogeneity of a clonal neoplastic process is common. Microarray is likely to reveal new, but uncharacterized, aberrations that may be reported in this category.

Collection of the data of CNVs of uncertain significance is encouraged to build a database for intralaboratory reference, for correlation with clinical parameters, and for sharing in publications. The eventual understanding of the clinical significance will depend on accumulation of sufficient information and correlation with clinical features.

Uncertain clinical significance, likely constitutional. Refer to the American College of Medical Genetics and Genomics Standards and Guidelines for interpretation and reporting of constitutional CNVs.³⁰

Uncertain clinical significance, not otherwise specified. A CNV that meets the laboratory parameters for reporting but has no features to categorize it further.

Benign. Reporting of benign CNVs is at the discretion of the laboratory. The laboratory should be familiar with common benign CNVs, stay current with the literature, and interpret results with this knowledge. This category will include: (i) CNVs reported in multiple peer-reviewed publications or curated databases as a benign variant and (ii) CNVs without relevant genetic content that meet criteria for reporting. It should be recognized, however, that cancer-associated anomalies that occur in known variant regions might not be benign.

REPORTING GUIDELINES FOR MICROARRAY ANALYSIS OF NEOPLASTIC DISORDERS

The following guidelines describe the elements of the clinical report that are necessary to communicate clearly and completely the clinical significance of microarray analysis results.

Reporting criteria

Microarray reports should be written so the result is understandable to a nongeneticist health-care provider and so that the clinical significance of the result for patient management is clear.

Care and special consideration should be given to reporting of certain results in children, e.g., disease-predisposing genes and adult-onset disease-associated genes.

To the extent possible, the current International System for Human Cytogenetic Nomenclature should be used to describe known recurrent, disease-associated, or clinically significant aberrations. FISH and chromosome studies used for confirmation analysis should be described using this nomenclature, which provides a format to report microarray results with the nucleotide boundaries for copy-number gains or losses. Breakpoints should be given to the extent possible given the employed technology.

The laboratory may choose to list relevant genes within the altered region. The specific genome-build nucleotide numbering should be specified, e.g., February 2009 assembly, NCBI37/hg19.

Verbal discussion of microarray results with the health-care provider is encouraged to facilitate communication and understanding of microarray results and clinical significance.

Written report

The written report should include the following:

1. Case identification with at least two unique patient identifiers: patient name, date of birth, or other unique identifier, e.g., medical record number.
2. Laboratory accession number(s), date of collection and/or receipt of specimen, specimen type, and name(s) of physician(s) or authorized persons to whom the report is to be provided.
3. Indication for the study, e.g., clinical information or diagnosis and/or pathological diagnosis.
4. List of specific CNVs with the following information when relevant:
 - Chromosome location (chromosome number and band designation),
 - LOH and CNVs with linear coordinates and genome build,
 - Genes of potential significance within interval(s), when indicated,
 - Dosage (copy-number loss, gain, amplification with confirmed ploidy/normalization), and
 - Clonality or ploidy, if applicable.
5. Confirmation testing method(s) and results, when applicable, and a statement of additional analyses performed to resolve questions of clonality, as appropriate.

6. Narrative interpretation to correlate the microarray result with patient-specific clinical or laboratory information, e.g., histopathology, immunophenotype, and/or flow cytometric data. The discussion should include the clinical significance of the results for the diagnosis, prognosis, and/or therapeutic management of the patient with reference to current literature. A note/disclaimer should be included to encourage clinicians to consider the results/data along with other laboratory tests, clinical findings, and recent literature.
7. Clinically significant constitutional CNVs should be discussed with recommendations for further testing as appropriate.
8. If a CNV of uncertain clinical significance is reported, a discussion of the possible relationship or significance to the diagnosis with supporting literature should be provided.
9. References as appropriate for the interpretation and that provide helpful information for the health-care provider.
10. Documentation of date of verbal communication of preliminary or final results to health-care provider(s) with notes regarding discussion of acquired and/or constitutional CNVs or abnormalities and the clinical significance, as appropriate.
11. Recommendation(s) for additional testing as appropriate.
12. Recommendation(s) for genetic counseling as appropriate.
13. Technical information for the testing platform and software, e.g., commercial source, coverage, version, and National Center for Biotechnology Information (NCBI) build used for data analysis. Limitations of the testing platform, e.g., detection of LOH, balanced rearrangements, ploidy, and/or low-level clonality. Biases and limitations of whole-genome amplification when appropriate. Methods summary including criteria for calls, e.g., minimum number of consecutive probes and/or length of area of LOH.
14. Qualified individuals must sign all final reports. Password-protected electronic signatures can be used fulfill this requirement.
15. Date of final report.
16. Disclaimers as appropriate, e.g., when and what investigational procedures are employed. Disclaimers as required.

CONCLUSIONS

Each new technological development in the field of genetics brings with it the desire to apply the technology to improve medical care. The transition of a new technology from the research bench into the clinical realm of diagnostic testing must be accompanied by extensive clinical validation to ensure the results reported to the health-care provider are accurate and reliable for use in patient-care decision making. The validation involves extensive comparison to the existing trusted methodologies to demonstrate that the new method has reliable and consistent results and interpretation. Sufficient comparative data must be accumulated and evaluated before the new method becomes a first-tier method. When the new

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technology provides additional information that is unattainable by the existing method, data accumulation and correlation with clinical parameters can expand the benefit provided by the new technology.

Microarray technologies provide a high-resolution view of the whole genome, which may yield massive amounts of new information. Medical laboratory professionals must be prepared to identify, interpret, and report results with clinical relevance while being mindful of the social, ethical, and legal responsibilities of reporting genetic information. Interpretation of the data from microarrays into clinically relevant information is a difficult and complex undertaking and is the practice of medicine. No algorithm for CNV interpretation can substitute for adequate training and knowledge in the fields of oncology, pathology, and medical genetics. Individuals with appropriate professional training and board certification, i.e., American Board of Medical Genetics clinical cytogenetics, clinical molecular genetics, or molecular genetic pathology should provide the interpretation of genomic microarrays for the clinical investigation of neoplastic disorders.

DISCLOSURE

All authors direct clinical testing laboratories that use the technologies and/or perform tests related to those described in this guideline.

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APPENDIX 9

Technical laboratory standards for interpretation and reporting of acquired copy-number abnormalities and copy-neutral loss of heterozygosity in neoplastic disorders: a joint consensus recommendation from the American College of Medical Genetics and Genomics (ACMG) and the Cancer Genomics Consortium (CGC)
(See following page)



Technical laboratory standards for interpretation and reporting of acquired copy-number abnormalities and copy-neutral loss of heterozygosity in neoplastic disorders: a joint consensus recommendation from the American College of Medical Genetics and Genomics (ACMG) and the Cancer Genomics Consortium (CGC)

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Disclaimer: This laboratory standard is designed primarily as an educational resource for clinical laboratory geneticists to help them provide quality clinical laboratory genetic services. Adherence to this standard is voluntary and does not necessarily assure a successful medical outcome. This standard should not be considered inclusive of all proper procedures and tests or exclusive of other procedures and tests that are reasonably directed to obtaining the same results. In determining the propriety of any specific procedure or test, the clinical laboratory geneticist should apply his or her own professional judgment to the specific circumstances presented by the individual patient or specimen.

Clinical laboratory geneticists are encouraged to document in the patient's record the rationale for the use of a particular procedure or test, whether or not it is in conformance with this standard. They also are advised to take notice of the date any particular standard was adopted, and to consider other relevant medical and scientific information that becomes available after that date. It also would be prudent to consider whether intellectual property interests may restrict the performance of certain tests and other procedures.

The detection of acquired copy-number abnormalities (CNAs) and copy-neutral loss of heterozygosity (CN-LOH) in neoplastic disorders by chromosomal microarray analysis (CMA) has significantly increased over the past few years with respect to both the number of laboratories utilizing this technology and the broader number of tumor types being assayed. This highlights the importance of standardizing the interpretation and reporting of acquired variants among laboratories. To address this need, a clinical laboratory-focused workgroup was established to draft recommendations for the interpretation and reporting of acquired CNAs and CN-LOH in neoplastic disorders. This project is a collaboration between the American College of Medical Genetics and Genomics (ACMG) and the Cancer Genomics Consortium (CGC). The recommendations put forth by the workgroup are based on literature review, empirical data, and expert consensus of the workgroup members. A four-tier evidence-based categorization system for acquired CNAs and CN-

LOH was developed, which is based on the level of available evidence regarding their diagnostic, prognostic, and therapeutic relevance: tier 1, variants with strong clinical significance; tier 2, variants with some clinical significance; tier 3, clonal variants with no documented neoplastic disease association; and tier 4, benign or likely benign variants. These recommendations also provide a list of standardized definitions of terms used in the reporting of CMA findings, as well as a framework for the clinical reporting of acquired CNAs and CN-LOH, and recommendations for how to deal with suspected clinically significant germline variants.

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Keywords: copy-number abnormalities; acquired variants; cancer; chromosomal microarray; interpretation

INTRODUCTION

Genomic testing of hematologic malignancies and solid tumors at the time of disease presentation provides information that is crucial for diagnosis and management. This evaluation may include G-banded chromosome analysis, fluorescence in situ hybridization (FISH) analysis, chromosomal microarray analysis (CMA), gene expression and fusion studies, targeted gene sequencing, as well as gene sequencing panels.

The somatic genomic variants detected in the tumor tissue play a critical role in the patient's clinical management by aiding in the diagnosis, providing prognostic information, and helping in the choice of appropriate therapy. The types of somatic variants observed include numerical and structural chromosomal abnormalities, single-nucleotide variants (SNVs), nucleotide-level deletions, duplications and insertions (i.e., indels), and gene-level deletions and duplications. One type of somatic structural chromosomal rearrangements

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common in neoplastic disorders are copy-number abnormalities (CNAs), which are changes that represent acquired gains and losses of chromosomal material. High-resolution genome-wide CMA is being widely used in clinical laboratories to detect acquired CNAs and copy-neutral loss of heterozygosity (CN-LOH) in neoplastic disorders, and is providing important insights into the unique genomic copy-number profile of different tumor tissues. In recent years, the clinical utility of CMA has been well established in the diagnosis of several neoplastic disorders.^{1–7}

The American College of Medical Genetics and Genomics (ACMG) technical standards and guidelines for CMA in neoplastic disorders includes a section on CMA results evaluation and interpretation.⁸ This document provided the initial framework for interpreting CMA results in neoplastic disorders; however, it describes broad principles. The use of CMA in neoplastic disorders has significantly increased over the past few years with respect to both the number of laboratories utilizing this technology and the broader number of tumor types being assayed. In practice, the interpretation of CMA results remains relatively subjective and lacks standardization, resulting in inconsistent practices between clinical laboratories. The CNAs and CN-LOH detected by CMA in neoplastic disorders are in many cases critical for optimal patient care. This necessitates standardized interpretation and reporting of acquired variants using an evidence-based system to accurately establish their clinical significance.

To address this need, a clinical laboratory-focused workgroup was established to draft recommendations for the interpretations and reporting of acquired CNAs and CN-LOH in neoplastic disorders. This project is a collaboration between the ACMG Laboratory Quality Assurance (QA) Committee and the Cancer Genomics Consortium (CGC). The workgroup developed recommendations for categorizing CNAs and CN-LOH detected by CMA in neoplastic disorders into specific standard categories (i.e., tiers) of clinical significance based on objective criteria using an evidence-based weighting system. The term “acquired variants” is used in this document to refer to both acquired CNAs and CN-LOH.

These newly developed recommendations, which are described in detail below, include:

1. Standardized definitions of terms used to describe single variants or patterns of variants detected by CMA
2. A four-tier evidence-based categorization system for acquired CNAs and CN-LOH, which is based on the level of available evidence regarding their diagnostic, prognostic, and therapeutic relevance
3. CNA and CN-LOH examples in tiers 1 and 2 in various hematologic malignancies and solid tumors
4. Considerations regarding the interpretation and reporting of unanticipated clinically significant germline variants
5. A framework to standardize the clinical reporting of acquired CNAs and CN-LOH

Even though these proposed technical laboratory standards are intended for interpretation and reporting of acquired

variants detected by CMA in neoplastic disorders, the newly developed recommendations should be applicable to acquired structural variants (including CNAs) detected by sequencing-based approaches, as the clinical testing practices move increasingly toward these technologies.

METHODS

These technical laboratory standards were informed by a review of the literature and current guidelines. Resources consulted included PubMed; current World Health Organization (WHO) and National Comprehensive Cancer Network (NCCN) guidelines; and relevant ACMG, Association for Molecular Pathology (AMP), and College of American Pathologists (CAP) guidelines. The workgroup members also used their expert opinion and empirical data to inform their recommendations. The proposed four-tier evidence-based categorization system for CNAs and CN-LOH was refined and extensively tested among the workgroup members using clinical cases from the members' diagnostic laboratories. In addition, input from the greater cancer genomics community was solicited during the annual CGC meeting when this tier system was first presented. Any conflicts of interests for workgroup members are listed at the end of the paper. The ACMG Laboratory QA Committee reviewed the document providing further input on the content, and a final draft was presented to the ACMG Board of Directors for review and approval to post on the ACMG website for member comment. Upon posting to the ACMG website, an email and link were sent to all ACMG members inviting participation in the 30-day open comment process. All members' comments and additional evidence received were assessed by the authors, and these recommendations were incorporated into the document as deemed appropriate. Member comments and author responses were reviewed by representatives of the ACMG Laboratory QA Committee and the ACMG Board of Directors. The final document was approved for publication by the ACMG and the CGC Board of Directors.

DEFINITIONS OF SPECIFIC TERMS USED TO DESCRIBE SINGLE VARIANTS OR PATTERNS OF VARIANTS DETECTED BY CMA

In an attempt to standardize the terminology used to communicate results of clinical CMA, the workgroup reached consensus on the definitions of specific terms shown in Box 1, which describe genomic variants commonly detected by CMA in neoplastic disorders.^{9–11}

PROPOSED FOUR-TIER EVIDENCE-BASED CATEGORIZATION SYSTEM FOR ACQUIRED CNAS AND CN-LOH

The interpretation of clinical significance of acquired genomic variants is based on their impact on clinical care, including diagnostic, prognostic, and therapeutic significance. The weight of clinical impact of a genomic variant is gauged by the level of available evidence regarding its association with a specific diagnosis, disease outcome, and/or response to a

Box 1: Specific terms used to describe single variants or patterns of variants detected by CMA

- **Size/location of variant:**

Focal: Relatively small change (typically less than 5 Mb) that usually contains a known or suspected driver cancer gene

Whole arm: Change that involves the entire chromosome short (p) or long (q) arm

Whole chromosome: Change that involves the entire chromosome

Interstitial: Change mediated by at least two breaks within a chromosome p or q arm

Terminal: Change that includes the end of the p or q arm of the chromosome

Intragenic: Change that occurs within a single gene

Proximal/distal: Describes a position relative to the centromere and moving outward on the chromosome p or q arm

- **Type of variant:**

Gain/loss: Type of copy-number change observed. It is recommended that the term “gain” be used rather than “duplication.” Attempts should be made to determine the relative gain/loss in polyploid samples.

Copy-number abnormalities (CNAs): Neoplastic disease-associated changes that represent acquired gains or losses of chromosome material.

Copy-neutral loss of heterozygosity (CN-LOH): Allelic imbalance without an associated copy-number change. This is a somatic process occurring in tumors, and terms such as absence of heterozygosity (AOH), identity by descent (IBD), and uniparental disomy (UPD) should be used when the change is germline.

Amplification: High copy-number gain of sequences, typically containing oncogene(s) that are important for the cancer being studied. Note that the term should not be used to describe a single copy gain of chromosomal material or to describe gain due to polysomy. Standard thresholds used to represent amplification typically range from 3–5 fold increases over baseline ploidy (e.g., intrachromosomal amplification of chromosome 21 [iAMP21] in B-ALL) to >100 copies per genome (e.g., *MYCN* amplified neuroblastoma) and will vary depending on the type of tumor. The laboratory should establish specific copy-number threshold cutoffs that will be used to identify clonally amplified regions by correlating CMA results to established methodologies for different tumor types.

Chromothripsis: A copy-number profile that has alternating copy states in a single region—typically a single chromosome or chromosome arm—that contains at least ten distinct alternating copy-number segments.^{9–11}

Intrachromosomal complexity: Summary of chromosomal regions that include more than two copy-number states, are largely confined to a single chromosome or chromosome arm, and contain at least five distinct copy-number segments. If clinically significant abnormalities (tiers 1 or 2) fall within a complex region, they may be reported individually.

Genomic complexity: Pattern of chromosome instability predominantly due to structural alterations resulting in widespread gains and losses of chromosomes or chromosomal regions in the majority of chromosomes.

particular treatment. The evidence used for variant categorization is weighted differently based on its likely impact on clinical decision-making. Additionally, the type and size of study providing this evidence is considered in the interpretation of the variants, with professional practice guidelines, large collaborative studies, and replicated studies carrying more weight than individual case reports. Based on literature review and workgroup consensus, the workgroup proposes categorizing genomic variants detected by CMA in neoplastic disorders into four tiers according to the level of evidence for their clinical significance as described below (Fig. 1). The workgroup adapted the levels of evidence published by the Oxford Centre for Evidence-Based Medicine (CEBM).¹² An attempt was made to keep these newly developed recommendations aligned, to the extent possible, with the recently published standards and guidelines for the interpretation and reporting of sequence variants in cancer.¹³ The sequence variant guidelines introduce the concept that the

interpretation of somatic variants should focus on their impact on clinical care. In addition to their oncogenic role, they may be associated with a favorable or adverse prognosis, with sensitivity, resistance, or toxicity to a specific therapy, with eligibility for clinical trials, and/or with better diagnostic accuracy. The principles put forward for interpretation of somatic sequence variants are applicable for interpretation of somatic CNAs and CN-LOH, which can also serve as biomarkers of prognosis, sensitivity, or resistance to targeted therapies, and/or can support a diagnosis of a particular tumor type. In addition, there is an increasing trend in genomic oncology testing to use consolidated sequencing-based assays to detect somatic SNVs, indels, CNAs, and abnormal gene fusions in selected cancer-related genes. Reporting results of such integrated assays would not be practical if disparate sets of rules had to be applied for interpretation of SNVs and indels versus CNAs and CN-LOH. With the prediction that unbiased genome-wide evaluation

Tier 1: Variants with strong clinical significance <i>(Diagnostic, prognostic, and/or therapeutic)</i>	Tier 1A - Acquired variants that define a specific entity in the WHO classification, are included in professional guidelines (e.g., NCCN, COG, IPSS), and/or can be treated with an FDA-approved drug - Germline pathogenic variants associated with cancer predisposition
	Tier 1B Acquired variants associated with a specific neoplasm, prognosis, or treatment response, as shown by <u>high or good quality evidence</u> (Levels 1, 2, and 3 CEBM evidence) with expert consensus and/or confirmed and reproduced by independent groups
Tier 2: Variants with some clinical significance <i>(Diagnostic, prognostic, and/or therapeutic)</i>	- Recurrent acquired variants observed in different neoplasms but <u>not</u> specific to a particular tumor type -----OR----- - Acquired variants associated with a specific neoplasm, prognosis, or treatment response, as shown by <u>average quality evidence</u> (Levels 4 and 5 CEBM evidence)
Tier 3: Clonal variants with no documented neoplastic disorder association	- Acquired variants with no documented neoplastic disorder association - All variants that <u>do not</u> meet the criteria for Tiers 1 and 2, and cannot be classified as constitutional benign or likely benign
Tier 4: Benign or likely benign Variants	- Constitutional benign or likely benign variants that are listed in the ClinGen curated benign variants and/or in the Database of Genomic Variants (DGV) with $\geq 1\%$ population frequency - They usually do not encompass COSMIC cancer genes

Fig. 1 Four-tier evidence-based categorization system for acquired copy-number abnormalities (CNAs) and copy-neutral loss of heterozygosity (CN-LOH) detected by chromosomal microarray analysis (CMA). CEBM Oxford Centre for Evidence-Based Medicine, COG Children's Oncology Group, COSMIC Catalogue of Somatic Mutations in Cancer, IPSS International Prognostic Scoring System for myelodysplastic syndromes, NCCN National Comprehensive Cancer Network, WHO World Health Organization.

for different types of genetic and genomic variants (including both sequence variants and numerical and structural chromosome rearrangements) may become feasible for cancer samples in the near future, a unified approach for the clinical interpretation, classification, and reporting of all somatic variants will become a necessity.

Tables 1 and 2 provide examples of CNAs and CN-LOH in tiers 1 and 2 in various hematologic malignancies and solid tumors.

I. Tier 1 (variants with strong clinical significance): Variants with strong diagnostic, prognostic, and/or therapeutic clinical significance. They have been demonstrated to play a critical role in the oncogenic process under investigation. Based on the level of evidence available, tier 1 variants are further subdivided into:

- a. **Tier 1A:** Acquired variants or a specific pattern of acquired variants that fulfill one or more of the following criteria:
 - Define a specific entity in the WHO classification.
 - Are included in professional clinical practice guidelines as clinically significant variants (e.g., NCCN, Children's Oncology Group (COG), Myelodysplastic Syndromes (MDS) International

Prognostic Scoring System, International Myeloma Working Group Criteria).

- Can be treated by a targeted FDA approved drug. Tier 1A also includes germline pathogenic variants associated with cancer predisposition.

b. **Tier 1B:** Acquired variants or a specific pattern of acquired variants with either:

- High quality evidence (levels 1 and 2 CEBM evidence) in the literature that shows association with a specific neoplasm, prognosis, or treatment response. This includes well-powered studies in the form of randomized controlled clinical trials, systematic review and meta-analysis of these studies, and cohort studies with consensus from experts in the field.
- Good quality evidence (level 3 CEBM evidence) in the literature that shows association with a specific neoplasm, prognosis, or treatment response. This includes multiple (at least two) smaller clinical studies in the form of cohort or case-control studies that have been confirmed and reproduced by different independent groups.

II. Tier 2 (variants with some clinical significance): Acquired variants or a specific pattern of acquired

Table 1 Tier examples in hematologic malignancies

Disease	Tier 1A	Reference (PMID)	Tier 1B	Reference (PMID)	Tier 2	Reference (PMID)
Myeloid						
Acute myeloid leukemia (AML)	–5/5q del ^P –7 ^P	NCCN 27895058	KMT2A (MLL) partial tandem duplication ^P 13q CN-LOH ^P	12149299 22417203 26033747 11585760 25270908	9q del ^R	8207990
Myelodysplastic syndromes (MDS)	–5/5q del ^{D,P,T} –7/7q del ^{D,P} Trisomy 8 ^P 11q del ^{D,P} 12p del ^{D,P} –13/13q del ^{D,P} 17p del ^{D,P} 4q12 del resulting in FIP1L1-PDGFR fusion ^{D,P,T}	WHO 2016 NCCN MDS IPSS-R	7q CN-LOH ^P 11q CN-LOH ^P	17954704 21285439	1p CN-LOH ^R 1q gain ^R Trisomy 21 ^R	21285439 24123380
Myeloid/lymphoid neoplasms with eosinophilia		WHO 2016				
Lymphoid						
B-lymphoblastic leukemia/lymphoma	Xp22.33/Yp11.32 del resulting in P2RY8-CRLF2 fusion ^{D (Ph-like),P,T} 5q32q33 del resulting in EBF1-PDGFRB fusion ^{D (Ph-like),P,T} 9q34.1 dup resulting in NUP214-ABL1 fusion ^{D (Ph-like),P,T} iAMP21 CNAs pattern ^{D,P} Hyperdiploid B-ALL with typical pattern of gains ^{D,P} Hypodiploid B-ALL with typical pattern of losses and doubled near-haploid/hypodiploid B-ALL ^{D,P}	WHO 2016 25207766	IKZF1 del (7p12.2) ^P ERG del (21q22.2) ^{D,P}	27815723 26202931 24064621 27776115	CDKN2A/2B del (9p21.3) ^R ETV6 del (12p13.2) ^R PAX5 del (9p13.2) ^R RB1 del (13q14.2) ^R	17344859 23508010
T-lymphoblastic leukemia/lymphoma						
			TCR rearrangements with CNAs at the breakpoints or in the unbalanced form ^D 9q34.1 amp resulting in NUP214-ABL1 fusion ^{D,P,T} 1p33 del resulting in STIL-TAL1 fusion ^D	28671688 18835836 17609427 15361874 18923437 19562638 25304610	6q del ^R CDKN2A/2B biallelic del (9p21.3) ^R	9552025 2207332 18838613
Chronic lymphocytic leukemia (CLL)	11q22.3 del (ATM and/or BIRC3) ^{P,T} Trisomy 12 ^P 13q14.2 del (MIR15A/16-1) ^P 17p13.1 del (TP53) ^{P,T}	WHO 2016 NCCN	2p12p25.3 gain (MYCN) ^P 9p21.3 del (CDKN2A) in CLL transformed to RS ^P	19406473 21749360 23044996 24004666 9531609	Trisomy 19 ^R 6q del ^R 14q24.1q32.3 del ^R	17593029 21788947 14712287 21281237 10482982 24729385 20649559
Plasma cell neoplasms	Hyperdiploidy with trisomies of odd-numbered chromosomes ^P 1q21 gain ^P –17/17p13.1 del (TP53) ^P	IMWG 21292777 21292778 25212883 27249749	1p del ^P	19448682 20929319 23892719 24460694	14q del ^{R,P} 16q del ^{R,P}	20616218 27157252 22565645 27157252 23716545
Burkitt-like lymphoma with 11q aberration	11q CNAs pattern ^{D,P}	WHO 2016 26980727				

This table lists examples of tiers 1 and 2 genomic variants and is not intended to provide a comprehensive list of variants in each disease. It reflects the evidence available at the time the current technical standards were written.

amp amplification, CMA copy-number abnormality, CN-LOH copy-neutral loss of heterozygosity, D diagnostic, del deletion, iAMP21 intrachromosomal amplification of chromosome 21, IMWG International Myeloma Working Group, IPSS-R Revised International Prognostic Scoring System for myelodysplastic syndromes, NCCN National Comprehensive Cancer Network, P prognostic, R recurrent, RS Richter syndrome, T therapeutic, WHO World Health Organization.

Table 2 Tier examples in solid tumors

Disease	Tier 1A	Reference (PMID)	Tier 1B	Reference (PMID)	Tier 2	Reference (PMID)
Central nervous system (CNS)						
Pilocytic astrocytoma	7q34 dup/del resulting in <i>KIAA1549-BRAF</i> fusion ^D 17q11.2 del (<i>NF1</i>) ^{GL}	WHO 2016				
Supratentorial ependymoma	11q13.1 del resulting in <i>C11orf95-RELA</i> fusion ^D	WHO 2016	Chromothripsis 11q ^D	24553141 25965575		
Ependymoma	–22/22q12.2 del (<i>NF2</i>) ^D	WHO 2016	1q gain ^P 9p21.3 del (<i>CDKN2A</i>) ^P	28371821 22338015 20516456		
ETMR, C19MC-altered	19q13.42 gain/amp ^D + 2 with 19q13.42 gain/amp ^D	WHO 2016				
MB WNT pathway	Monosomy 6 ^D	WHO 2016				
MB SHH pathway	9q22.32 del/LOH (<i>PTCH1</i>) ^D 10q23.31 del/LOH (<i>PTEN</i>) ^D <i>GLI2</i> amp ^D <i>MYCN</i> amp ^D 10q24.32 del (<i>SUFU</i>) ^{GL} 17p13.1 del/LOH (<i>TP53</i>) ^{D,P,GL}	WHO 2016 25403219	Chromothripsis 17p ^{D,P}	22265402 24651015 29753700		
MB non-WNT/non-SHH	17p del and/or 17q gain idic(17p11.2) ^D <i>MYC</i> amp ^{D,P} <i>MYCN</i> amp ^D	WHO 2016				
Glioblastoma IDH wild type—adult	+7, –10 (<i>PTEN</i>) ^{D,P} 9p21.3 del/LOH (<i>CDKN2A</i>) ^{D,P} –13/13q14.2 del (<i>RB1</i>) ^{D,P} <i>PDGFRA</i> amp ^D <i>EGFR</i> amp ^D	WHO 2016				
Glioblastoma—pediatric	+7, 17p13.1 del/LOH (<i>TP53</i>) ^{D,P} <i>PDGFRA</i> amp ^{D,P}	WHO 2016 27582545	<i>MET</i> amp ^{D,T}	28966033 27748748		
Oligodendroglioma	1p and 19q co-del ^{D,T}	WHO 2016				
Meningioma, acoustic neuroma	22q12.2 del (<i>NF2</i>) ^{GL} –22/22q del ^D	WHO 2016	9p del (<i>CDKN2A</i>) ^P	11485924 11958372		
Atypical teratoid/rhabdoid tumor	–22/22q del ^D 22q11.23 del/LOH (<i>SMARCB1</i>) ^{D,GL} 19p13.2 del/LOH (<i>SMARCA4</i>) ^{D,GL}	WHO 2016				
Choroid plexus carcinoma	17p13.1 del (<i>TP53</i>) ^{GL}	WHO 2016				
Chordoma	22q11.23 del (<i>SMARCB1</i>) ^D	29119645	10q23.31 del (<i>PTEN</i>) ^D 9p21.3 del (<i>CDKN2A</i>) ^D	24983247 21602918		
Hemangioblastoma	3p25.3 del (<i>VHL</i>) ^{GL}	20301636 (Gene Reviews)				
Pineoblastoma	14q32.13 del (<i>DICER1</i>) ^{D,GL} 13q14.2 del (<i>RB1</i>) ^{GL}	WHO 2016				
Pediatric embryonal tumors						
Neuroblastoma	<i>MYCN</i> amp ^{D,P} 1p del ^P 11q del and 17q gain ^{D,P} <i>ALK</i> amp ^P Near-triploid ^P	26389190 (NCI guidelines)			3p del ^P 14q del ^R	15800319 12538451 11729208
Wilms tumor	11p del/LOH ^{D,P,GL} 17p13.1 del (<i>TP53</i>) ^P 1q gain, 16q del ^{D,P}	26389282 (NCI guidelines) 20301471 (Gene Reviews)				
Alveolar rhabdomyosarcoma	<i>PAX-FOXO1</i> gene fusion amp ^P	22447499				
Renal cell carcinoma (RCC)						
Clear cell RCC	3p25.3 del/LOH (<i>VHL</i>) ^D <i>VHL</i> , <i>FLCN</i> del ^{GL}	WHO 2016 26448938 24550497 23797736	14q loss ^P 9p loss ^P	26448938 21725288 26790128 25315157		
Papillary RCC-type I	Gain 7 and 17 ^D	WHO 2016 26448938 25790038 28780132			Gain 12, 16, 20, -Y ^R	26448938
Chromophobe RCC	Hypodiploidy with loss 1, 2, 6, 10, 13, 17, 21 ^{D,R} 17p11.2 del (<i>FLCN</i>) ^{GL}	WHO 2016 19562744 26448938				
Breast	<i>ERBB2</i> amp ^P	29523670 (NCCN guidelines)	6q25.1 tandem dup resulting in <i>ESR1-CCDC170</i> fusion ^P	25099679	<i>CCND1</i> amp ^T	26059247
Lung	<i>EGFR</i> amp ^T	23552377	6q22.1 del resulting in <i>GOPC-ROS1</i> fusion ^T <i>FGFR1</i> amp ^T <i>MET</i> amp ^{T,P}	25870798 25535693 21160078 27664533		
Soft tissue						
Liposarcoma, atypical lipomatous tumors	<i>MDM2</i> , <i>CDK4</i> amp ^D	WHO 2013				
Desmoid-type fibromatosis	5q22.2 del (<i>APC</i>) ^{GL}	24554300				
Infantile fibrosarcoma			+8, +11, +17, +20 ^{D,R}	11801301		
Lipoblastoma					Gain 8 ^R	11549588
Bone						
Osteochondroma	8q24.11 del (<i>EXT1</i>) ^{GL} 11p11.2 del (<i>EXT2</i>) ^{GL}	20301413 (Gene Reviews)				
Osteosarcoma	17p13.1 del (<i>TP53</i>) ^D	WHO 2013	<i>MDM2</i> , <i>CDK4</i> amp ^D	20196171 21336260		

Table 2 continued

Disease	Tier 1A	Reference (PMID)	Tier 1B	Reference (PMID)	Tier 2	Reference (PMID)
Ewing sarcoma					1q gain, 16q loss ^D Gain 8 ^R	11672775
Gastrointestinal stromal tumor (GIST)			–1p, –14, –22 ^D	10919666 16982739 23942094		
Mesothelioma	3p21.1 del (<i>BAP1</i>) ^{GL}	28713672			3p del (<i>BAP1</i>) ^R 9p del (<i>CDKN2A</i>) ^R –22 (<i>NF2</i>) ^R	21642991 26928227 28713672

This table lists examples of tiers 1 and 2 genomic variants and is not intended to provide a comprehensive list of variants in each disease. It reflects the evidence available at the time the current technical standards were written.

amp amplification, *D* diagnostic, *del* deletion, *dup* duplication, *ETMR* embryonal tumor with multilayered rosettes, *GL* germline, *LOH* loss of heterozygosity, *MB* medulloblastoma, *NCCN* National Comprehensive Cancer Network, *NCI* National Cancer Institute, *P* prognostic, *R* recurrent, *T* therapeutic, *WHO* World Health Organization.

variants with some diagnostic, prognostic, and/or therapeutic clinical significance. They include:

- Recurrent variants observed in different neoplasms but *not* specific to a particular tumor type, and usually encompassing Catalogue of Somatic Mutations in Cancer (COSMIC) census cancer genes(s).
- Acquired variants or a specific pattern of acquired variants with average quality evidence (levels 4 and 5 CEBM evidence) in the literature that shows association with a specific neoplasm, prognosis, or treatment response. This includes a small case series or multiple (at least two) case reports that describe the association.

III. **Tier 3 (clonal variants with no documented neoplastic disorder association):** Acquired clonal variants with no documented neoplastic disorder association. All variants that *do not* meet the criteria for tiers 1 and 2 and cannot be classified as constitutional benign or likely benign, can be classified as tier 3 variants. Tier 3 variants are defined as “acquired clonal variants with no documented neoplastic disorder association” rather than “acquired clonal variants with uncertain clinical significance.” This is because an “acquired clonal variant” is by default significant for this particular patient because it can be used as a marker for the neoplastic clone to monitor residual disease and/or relapse.

IV. **Tier 4 (benign or likely benign variants):** Constitutional benign or likely benign variants that are listed in the ClinGen curated benign variants and/or in the Database of Genomic Variants (DGV) with $\geq 1\%$ population frequency, and usually do not encompass COSMIC cancer gene(s). It is not recommended to report tier 4 variants.

GENERAL AND SPECIAL CONSIDERATIONS

1. The interpretation of clinical significance of CNAs and CN-LOH using this tier system should be performed in the context of the clinical/pathologic diagnosis, as well as other laboratory tests including G-banded karyotype, FISH, and other relevant tests. This is crucial because
2. some acquired variants will have different clinical significance in different neoplastic disorders. For example, 1q gain is associated with adverse prognosis in multiple myeloma (MM) (tier 1A),^{14,15} while it does not have major prognostic significance in MDS (tier 2).¹⁶ CNAs may also have different clinical significance depending on other cytogenetic or molecular diagnostic abnormalities present in the tumor. For example, loss of chromosome 7 or 7q deletion are typically associated with an inferior outcome in myeloid malignancies (tier 1A), but in acute myeloid leukemia (AML) with a *CBFB* gene rearrangement, they do not appear to significantly change the prognosis (tier 2).¹⁷
3. This tier system can be used to classify a specific pattern of CNAs and/or CN-LOH that is diagnostic of a specific neoplastic disease entity. This includes a characteristic pattern of whole chromosome gains/losses (e.g., hyperdiploid and hypodiploid B-ALL) and whole chromosome CN-LOH (e.g., doubled hypodiploid/near-haploid B-ALL).¹⁸ It also includes a characteristic signature of gains and losses along one chromosome (e.g., intrachromosomal amplification of chromosome 21 [*IAMP21*] in B-ALL).¹⁹ The pattern of acquired gains/losses can be classified collectively using the tier system.
4. Diagnostic balanced chromosomal abnormalities (e.g., translocations, inversions, and insertions) detected by G-banded karyotype and/or FISH testing but not by CMA should be discussed in the CMA report but should not be included in the classification using the tier system or listed in the results table/nomenclature string. When present in the unbalanced form and detected by CMA with breakpoints mapping within genes known to be associated with a specific gene fusion, these abnormalities can be classified using the tier system and listed in the results table/nomenclature string (e.g., the presence of an extra copy of the Philadelphia chromosome *der*(22)t(9;22)(q34;q11.2) in CML or ALL,¹⁸ or an extra copy of the *der*(21)t(12;21)(p13;q22) in B-ALL, and the unbalanced *der*(19)t(1;19)(q23;p13) in B-ALL).²⁰
5. An interstitial loss or gain involving one chromosome arm with recurring breakpoints in genes known to be involved in a specific gene fusion can be classified using

this tier system (e.g., 4q12 deletion that results in *FIP1L1-PDGfra* fusion, PAR1 deletion at Xp22.33/Yp11.32 that results in *P2RY8-CRLF2* fusion, and 9q34.1 gain that results in *NUP214-ABL1* fusion).^{18,21}

5. Interstitial or terminal losses or gains involving two chromosome arms with breakpoints within genes known to be associated with a specific gene fusion as a result of an interchromosomal rearrangement (e.g., translocation or insertion) or intrachromosomal rearrangement (e.g., inversion) should be interpreted according to the level of supporting evidence. They can be classified using this tier system with later confirmation of the gene fusion by other molecular techniques if there is enough supporting evidence, including the clinical/pathologic diagnosis, visible recurrent rearrangement by G-banded karyotype, and/or other acquired variant known to be associated with the gene fusion in question. In the absence of such supporting evidence, the report should describe the possibility of a gene fusion but without classifying the variants using the tier system until the fusion is confirmed by other molecular techniques.
6. Correlation of the CMA results with the G-banded karyotype and FISH results is strongly recommended because some professional clinical practice guidelines used to classify tier 1A variants are technique specific. For example, some chromosomal abnormalities can only be considered diagnostic/prognostic if detected by G-banded karyotype (e.g., MDS and MM prognostic criteria).
7. CMA has the potential to identify acquired variants associated with comorbid neoplastic disorders. For example, comorbid MDS-related variants may be identified in patients treated for chronic lymphocytic leukemia (CLL) or MM either because of prior therapy or age-related disease. These variants should be interpreted in the context of the clinical/pathologic diagnosis and correlated with G-banded karyotypes from both stimulated and unstimulated CLL or MM cultures. CMA performed in MM on CD138+ enriched cells is helpful in identifying MM-specific acquired variants.⁷
8. The term “CN-LOH” is used in this document to refer to a region with acquired allelic imbalance (i.e., homozygosity) without an associated copy-number change (i.e., copy-neutral), which is a common finding in cancer. The term “copy-neutral” is used to allow distinction from loss of heterozygous single-nucleotide polymorphism (SNP) calls due to a one copy-number loss (i.e., heterozygous deletion). However, in some cases LOH can also be observed with a copy-number gain. Examples include high-level amplification involving only one allele, and the copresence of a clone with trisomy of a particular chromosome and a subclone that lost one copy of that chromosome resulting in whole chromosome LOH.
9. Regions of CN-LOH may have a higher level of clinical significance if they span a gain-of-function variant in an oncogene and/or loss-of-function variant in a tumor suppressor gene documented in this patient. This is

especially relevant in laboratories that do integrated reporting of CNAs, regions of CN-LOH, and sequence variants results.

DATABASES AND RESOURCES FOR INTERPRETATION OF CNAS AND CN-LOH IN NEOPLASTIC DISORDERS

A wealth of genomic information has been generated for different tumor types through chromosome analysis and large-scale genome sequencing projects, and the data have been consolidated into many public databases. However, the majority of such databases house information at a gene and variant level, and resources focused on incidence and significance of acquired CNAs and CN-LOH in neoplastic disorders are limited. In the absence of CNA-specific information, gene and variant-centered databases can be used to support interpretation of CNAs involving specific genes.

To allow utilization of gene and variant-focused data for informing interpretation of CNAs and CN-LOH in oncology samples, it is important to annotate the mechanism of action for genes and variants related to cancer. Such mechanisms typically include loss of function of tumor suppressors, gain of function of oncogenes, abnormal gene fusions, and translocations involving regulatory regions. If variants affecting a gene are proven to be loss-of-function variants, it can be extrapolated that a deletion of the same gene or a larger region containing that gene would also confer a loss of function.

A brief overview of resources that are useful in interpretation of CMA results in oncology is provided in Table 3. Such resources include:

1. Databases and data portals focusing directly on acquired CNAs and CN-LOH
2. Databases and data portals focusing on acquired sequence variants, which allow the evaluation of whether specific genes within the region affected by a CNA have been associated with the tumor type of interest
3. Knowledge bases that contain curated information on the significance of individual genes and acquired sequence variants in different tumor types
4. Chromosome-level databases and knowledge bases that compile data from conventional cytogenetic analysis and curations regarding the significance of chromosome aberrations detected by karyotyping
5. Databases of benign and pathogenic germline variants that allow exclusion of benign germline variants and interpretation of germline secondary findings

To facilitate review and interpretation of acquired CNAs data, laboratories are advised to curate and maintain lists of genes and regions of clinical relevance in a variety of tumor types. These lists support comprehensive and efficient recognition of disease-relevant loci, and allow consistency in interpretation. A laboratory can also opt to develop lists of predefined pertinent positives and negatives per tumor

Table 3 Selected databases relevant for interpretation of acquired CNAs

Resource type and utility	Resource name and description	Location (web address)
General/summary	Video tutorial: 'Introduction to Publicly Available Knowledge Bases to Aid Interpretations of Genomic Findings in Oncology' Provides overview of types and utility of online resources	Cancer Genomics Consortium YouTube channel: (https://www.youtube.com/watch?v=4dBh1Qkp8os) http://portals.broadinstitute.org/tcga/gistic/browseGisticAnalyses
Databases and knowledge bases of acquired CNAs in neoplastic disorders (Can be used to search for recurrent CNAs in the tumor of interest)	The Cancer Genome Atlas (TCGA) Copy Number Portal: Allows one to search and review high-resolution copy-number data from cancer samples in The Cancer Genome Atlas project The Compendium of Cancer Genome Aberrations (CCGA): A knowledge base developed by the Cancer Genomics Consortium that compiles information about clinical significance of CNAs, CN-LOH, and balanced structural abnormalities in different tumors	http://www.ccgai.io
Pan-cancer gene list	Catalog of Somatic Mutations in Cancer (COSMIC) database Cancer Gene Census	https://cancer.sanger.ac.uk/census
Cancer gene and variant databases and data portals (Can be used to evaluate the role of a particular gene (or genes) within a CNA or CN-LOH region in pathogenesis of the tumor type being tested; these resources may have overlapping data sets (from the same large-scale studies) but offer different solutions for data visualization and searches)	Catalog of Somatic Mutations in Cancer (COSMIC): A large source of manually curated somatic variant information hosted by the Sanger Institute; contains data from >35,000 cancer genomes from large-scale genome screening studies including TCGA and the International Cancer Genomics Consortium (ICGC) ICGC Data Portal: An international consortium established to launch and coordinate worldwide large-scale genome sequencing projects for various tumor types; data from specific projects is available through the ICGC portal cBioPortal: A source for visualization, analysis, and download of large-scale cancer genomics data sets, initially developed at Memorial Sloan Kettering Cancer Center and now maintained by a multi-institution team National Cancer Institute (NCI) Genomic Data Commons (GDC): An information system that contains genomic and clinical data from NCI-funded projects as the Cancer Genome Atlas (TCGA) and the Therapeutically Applicable Research to Generate Effective Treatments (TARGET) program, as well as other cancer studies PeCan Data Portal (Pediatric Cancer focused): A data portal developed and hosted by St. Jude Children's Research Hospital, which provides interactive visualizations of pediatric cancer variant data from large-scale childhood cancer genomic studies	http://cancer.sanger.ac.uk/cosmic https://dcc.icgc.org/ http://www.cbioportal.org/ https://portal.gdc.cancer.gov/ https://pecan.stjude.org/home
Chromosome-level data sources (Contain data and knowledge about conventional cytogenetic studies in cancer)	Mitelman Database: A database that contains karyotype information for >69,000 tumor cases and allows searches based on abnormality, tumor type, and other criteria Atlas of Genetics and Cytogenetics in Oncology and Haematology: An expert curated knowledge base devoted to cytogenetics findings in cancer	https://cgap.nci.nih.gov/Chromosomes/Mitelman http://atlasgeneticsoncology.org/
Knowledge bases with cancer gene and variant curation (Contain expert curated information and summaries about the clinical significance of genes and variants in cancer)	Information about commonly used knowledge-bases compiled by the Variant Interpretation for Cancer Consortium (VICC): A driver project of the Global Alliance for Genomics and Health (GA4GH) Clinical Interpretation of Variants in Cancer (CIViC): An open access, open source, community-driven knowledge base developed by researchers at the Genome Institute at Washington University School of Medicine My Cancer Genome: A knowledge base developed and hosted by the Vanderbilt University Cancer Center OncoKB: A knowledge base developed and hosted by the Memorial Sloan Kettering Cancer Center Precision Medicine Knowledgebase (PMKB): A knowledge base developed and hosted by the Institute of Precision Medicine at Weill Cornell Medicine	http://cancervariants.org/resources/ http://www.civicdb.org https://www.mycancergenome.org/ http://oncokb.org/#/ https://pmkb.weill.cornell.edu/
Population database of benign CNVs (Allows to exclude CNVs that are common in the general population)	Database of Genomic Variants (DGV): A comprehensive catalog of normal structural variation in the human genome; the database contains copy-number variants and other structural variations identified in healthy control samples	http://dgv.tcag.ca/dgv/app/home
Databases and data portals of genes, variants, and CNVs associated with constitutional genetic disorders (May assist in interpretation of findings that are suspected to be germline)	dbVar Human Structural Variant Data Hub: Catalogs CNVs identified through the course of routine clinical cytogenomic testing in postnatal populations, with clinical assertions as classified by the original submitter DECIPHER (Database of genomic variation and Phenotype in Humans using Ensembl Resources): A database of sequence variants or copy-number variants and main clinical findings from patients with genetic disorders Online Mendelian Inheritance in Man: A catalog of genes implicated in single-gene (Mendelian) disorders ClinVar: A National Center for Biotechnology Information (NCBI) maintained catalog of variants found in patient samples, with assertions made regarding their clinical significance, information about the submitter, and other supporting data; focused mostly on constitutional variants, may have utility in the interpretation of suspected germline findings ClinGen: A National Institutes of Health (NIH)-funded central resource that defines the clinical relevance of genes and variants for use in precision medicine and research	https://www.ncbi.nlm.nih.gov/dbvar/content/human_hub/ https://decipher.sanger.ac.uk/ http://www.ncbi.nlm.nih.gov/omim/ http://www.ncbi.nlm.nih.gov/clinvar/ https://www.clinicalgenome.org/
Sequence repositories (collect, store, and disseminate the nucleotide and amino acid sequence data) and genome browsers (provide context and visualization for genome features, such as genes or disease loci)	NCBI Genome: A NIH-sponsored sequence repository Ensembl: A genome browser developed and maintained by the European Molecular Biology Laboratory (EMBL) UCSC Genome Browser: A genome browser developed and maintained by the University of California–Santa Cruz	https://www.ncbi.nlm.nih.gov/genome https://www.ensembl.org/index.html?redirect=no https://genome.ucsc.edu/

CNA copy-number abnormalities, CN-LOH copy-neutral loss of heterozygosity, CNV copy-number variant.

type, and perform systematic careful evaluation for their presence.

The curated clinical-grade disease-specific gene lists can be maintained in both a spreadsheet and .bed file format. It is useful for such lists to be converted into a format compatible with the CMA software, so they can be uploaded and used as custom annotation tracks during case review. This allows quickly recognizing acquired CNAs that contain genes implicated in the tumor of interest. A comprehensive list of genes shown to contain variants causally implicated in cancer (so-called Cancer Gene Census) is maintained in the COSMIC database, and can be downloaded from its website (<https://cancer.sanger.ac.uk/census>).

Because the databases and data portals for search and visualization of acquired CNAs in neoplastic disorders are rare, clinical interpretation typically requires a review of primary literature. Such interpretation remains a complex and time-consuming task that requires appropriate professional training and certification in clinical cytogenetics and/or molecular diagnostics. It also necessitates familiarity with the CMA assay and an understanding of the specific tumor biology.

CONSIDERATIONS REGARDING INTERPRETATION AND REPORTING OF UNANTICIPATED CLINICALLY SIGNIFICANT GERMLINE VARIANTS

In addition to acquired clonal abnormalities, genome-wide analysis of tumor samples also detects constitutional germline copy-number variants (CNVs) and regions of absence of heterozygosity (AOH). These may include benign population variants, germline CNVs directly related to the neoplasm under investigation (e.g., germline deletions of tumor suppressor genes), and pathogenic CNVs that are diagnostic or predictive of a presymptomatic or unrecognized genetic condition unrelated to the patient's tumor. With the exception of CNVs that are associated with an increased risk of neoplasia, other germline variants are unanticipated and unrelated to the reason for CMA. Referring clinicians must have a clear understanding of the potential for these discoveries; the best practice would also include informing the patients and their families about the possibility of secondary findings before the test is ordered, and implementing a formal informed consent process. Before offering clinical CMA testing for oncology samples, laboratories should develop a process for appropriate follow-up if an unanticipated, likely germline abnormality is observed.

Indications that a detected CNV or AOH may be germline

Distinguishing between acquired CNAs/CN-LOH and constitutional CNVs/AOH in CMA may be challenging. The possibility that a variant may be germline should be considered in the following scenarios:

1. Involvement of 100% of the cells in a sample. Often, acquired variants involve only a subset of cells corresponding to the tumor clone. Review of the log₂ ratio and SNP data allows determining if a variant is present in all or only a subset of cells in a sample. However, it is important to be aware of the following caveats:
 - a. Some specimens may consist of pure tumor tissue and have acquired variants that involve close to 100% of the cells (e.g., a bone marrow specimen packed with leukemic blasts or a dissected tumor section).
 - b. Copy-number losses encompassing cancer predisposition genes are particularly difficult to interpret by CMA alone. For small abnormalities with insufficient SNP data, CMA may not reliably differentiate a heterozygous loss in 100% of the cells from a homozygous loss in 50% of the cells. If CMA shows copy-number losses encompassing cancer predisposition genes, it might not be possible to distinguish between a germline heterozygous deletion of the gene in question in 100% of the cells versus acquired biallelic loss of the gene in 50% of the cells. Frequently encountered examples include the Fanconi anemia/DNA repair pathway genes (including *BRCA1* and *BRCA2*), *NF1*, *RB1*, and *PAX5*. Follow-up interphase FISH analysis using gene-specific probes can be helpful in distinguishing between these two possibilities.
2. Higher proportion of cells involved by a variant than expected by pathologic findings. For hematologic malignancies, a finding may be germline if it appears to involve a significantly greater proportion of cells than that expected based on the blast cell count or degree of involvement determined by morphology or flow cytometry. Correlation with hematopathology and flow cytometry/immunophenotyping data is valuable, and efforts to obtain this information are recommended. For solid tumors, a finding may be germline if the estimate of involvement by CMA is significantly greater than the estimation of tumor cell fraction provided by the submitting pathologist. However, estimating tumor fraction in solid tumors is often challenging and involves subjective judgment; this estimate may not always be perfectly correlated with CMA results.
3. Supporting clinical information may suggest that a CMA variant is germline:
 - a. Some tumor types are frequently associated with the presence of predisposing germline variants. Examples include Wilms tumor, tuberous sclerosis complex (TSC1/TSC2) tumors, neurofibromas, adrenocortical carcinoma, and rhabdoid tumor (Supplementary Table 1). Laboratories should have an increased level of suspicion for germline variants when performing CMA for these tumor types.
 - b. CNVs/AOH including known cancer predisposition genes (Supplementary Table 1) may be suspected as germline in patients with features of hereditary cancer syndromes, including diagnosis at unusually

young age, development of bilateral or multifocal tumors, or family/personal history of cancer.

- c. CNVs involving genes and regions associated with known pathogenic microdeletion/microduplication syndromes may be suspected as germline in patients who have reported features consistent with the disorder in question. If the provided clinical information is limited, the laboratory may request additional details to allow accurate interpretation of the findings.

Interpretation and reporting of suspected germline variants

When reporting variants that are suspected to be germline, CNVs predisposing to cancer should be distinguished from variants unrelated to the patient's cancer diagnosis.

Germline CNVs directly related to the neoplasm under investigation (e.g., germline deletion of a tumor suppressor gene) should be reported as being of strong clinical significance (tier 1A) and discussed in the interpretation section of the report. This includes germline CNVs involving cancer predisposition genes listed in the 2016 ACMG secondary findings document.²²

For likely germline CNVs not related to the neoplasm under investigation:

- a. Laboratories should have an established policy for reporting CNVs that are likely germline and have been curated as pathogenic by ClinGen (including pathogenic CNVs associated with disorders that show incomplete penetrance) and/or span known haploinsufficient or triplosensitive genes.²³ These findings can influence clinical care for the patient and the family; as such, they should be included in the report and discussed as potentially constitutional clinically significant variants (see below).
- b. Possibly constitutional CNVs unrelated to the patient's cancer diagnosis should not be classified into the tier system. For unambiguous reporting, the laboratory may have a separate section of the report for describing these variants.

Follow-up recommendations for suspected germline variants

If CMA of a tumor sample detects suspected germline CNVs/AOH, the report should contain recommendations for appropriate follow-up, including the following:

- a. Referral to a genetic specialist for evaluation and counseling.
- b. Confirmation of germline status by testing noninvolved tissue. For patients with solid tumors, a peripheral blood sample may be tested. For patients with hematologic malignancies, the optimal samples for germline testing are cultured skin fibroblasts, although a buccal swab or a

peripheral blood sample at the time of complete remission may be acceptable.

Suggested language for reporting suspected constitutional findings:

Suspected germline variant

Based on (percent of cells involved, supporting clinical information, etc.), this finding may represent a germline variant. Genetic testing of a tissue that is not involved in the neoplastic process is recommended when the patient is in clinical remission to determine whether this is a germline or an acquired variant and to aid in determination of its clinical significance. If the variant is germline, genetic counseling is recommended for additional information about this variant and its clinical significance.

REPORTING RECOMMENDATIONS FOR ACQUIRED CNAS AND CN-LOH

The laboratory must ensure that the clinical report accurately describes the findings and clearly communicates their clinical significance. The report should include the preanalytic, analytic, and postanalytic factors that are relevant to the clinical interpretation of the findings, as well as elements that represent regulatory requirements (which are outlined in the ACMG Laboratory Standards and Guidelines; Section E8). Despite the large amount of information that must be included, the report should be as simple and concise as possible, formatted in a way that allows the results to be easily seen and understood, and the clinically critical information should appear at the beginning. Displaying the results in tables may be helpful to increase the overall clarity of the report, provided that the tables can be integrated into the medical record.

In contrast to reporting results of CMA testing for constitutional variants, reports for oncology specimens should not be limited to positive findings. In some cases, what the test does not detect may be of the same or even greater significance than the positive findings. It is strongly recommended that pertinent negatives relevant for clinical management are included in a disease-specific manner. This will typically include tier 1A variants that are used for clinical decision-making (as key prognostic markers or predictors of response or resistance to targeted treatments).

Detected CNAs and CN-LOH should be classified into the four-tier system described above. In complex cases, laboratories may opt not to specify tier classification for every variant individually, but should accurately point out and discuss in the interpretation section all the variants with strong or some clinical significance (tiers 1 and 2). It is not recommended that tier 4 variants (benign/likely benign) be included in the report.

If there is doubt about a variant being "acquired/clonal" versus "germline/constitutional," this should be discussed in the report, and such variants should not be tiered using the

classification system for acquired variants until this uncertainty is clarified.

For clear communication of the relevant and required information, it is recommended that the CMA clinical report be organized into the following sections: results, interpretation, recommendations (if applicable), references, and method description and disclaimers.

Results section

CMA results should be reported according to the current version of the International System for Human Cytogenomic Nomenclature (ISCN).²⁴ According to ISCN 2016, results can be reported using a table, as a nomenclature string, or both at the discretion of the laboratory director. If the results are displayed in a table, the following information should be included:

- Required
 - Chromosomes and corresponding bands involved in the variant
 - Type of variant (loss, gain, amplification, CN-LOH)
 - Genomic coordinates with designated genome build
- Recommended
 - Copy-number state and percentage of cells involved, estimated based on the log2 ratio and SNP data
 - Tier classification
- Optional
 - Variant size in kb or Mb
 - COSMIC cancer census genes within the affected region

Variants that constitute a diagnostic pattern may be classified collectively in the table using the tier system. The results table can be included either at the beginning or at the end of the report. In complex cases, it may be helpful to clinicians to emphasize clinically significant findings at the beginning of the report, and to place the complete results table at the end. In such cases, laboratories should consider including an additional abridged summary table with clinically significant variants at the beginning of the report.

While the clone structure cannot be ascertained with certainty by CMA, it is recommended to report the approximate percentage of cells (levels of mosaicism) for acquired variants to give an estimate of possible clones and subclones.

Full interpretation of clinically significant variants and a text summary integrating results

The full interpretation should include comments on the following variants:

- Clinically significant CNAs and/or CN-LOH (tier 1 and 2 variants).

- Clinically significant pattern of CNAs and/or CN-LOH (tier 1 and 2 variants).
- CNAs and/or CN-LOH of potential clinical significance (cannot be tiered at the time of reporting). This category addresses point 5 in “General and special considerations” when there is uncertainty about an acquired variant being indicative of a specific gene fusion in the absence of supporting evidence at the time of reporting.
- Optional: other clonal variants (tier 3 variants).

The comments may contain information about the prevalence and functional, prognostic, or predictive significance of the detected CNAs or CN-LOH in a particular tumor type. The laboratory may want to specifically point out the presence of abnormalities that are associated with response to a targeted treatment, in particular if they predict sensitivity to an FDA approved drug. However, specific treatment recommendations are not encouraged. A text summary should integrate CMA results and correlate them with the results of G-banded karyotype and FISH studies. This summary can be included at the beginning or at the end of the interpretation section. Key abnormalities detected by karyotyping and FISH should not be classified into tiers, but should be discussed in the summary with correlation to the CMA findings.

Recommendations

A recommendation section may be included when necessary based on the findings. For example, appropriate follow-up should be recommended in cases in which CMA findings may be germline (see “Follow-up recommendations for suspected germline variants”). Recommendations should also include molecular confirmation of clinically significant abnormalities that are predicted but cannot be established based solely on CMA results (this includes breakpoints suggestive of a particular abnormal gene fusion, CN-LOH suggestive of a variant in a particular oncogene or a tumor suppressor gene, etc.). Treatment recommendations (for the use of specific targeted therapies or enrollment into specific clinical trials) typically should not be included, considering that a treatment choice depends on many factors (other than the diagnosis provided on a test requisition and the CMA findings) that are unknown to the laboratory.

References

Key publications that were used as evidence to classify detected variants into tiers should be listed in the final report.

Methodology and disclaimers

Methodologic details should be presented at the bottom of the report and should include a brief description of the array platform and assay performance characteristics; this may include size resolution and limitations of the assay (e.g., lack of sensitivity for detecting abnormalities present in a low proportion of cells in the sample, inaccuracy in ploidy determination, inability to detect balanced rearrangements,

etc.). Criteria for inclusion of findings in the report and criteria for tier classification should be briefly stated.

The order of different report sections is at the discretion of the laboratory director. Laboratories should have the freedom to choose their own reporting format as long as the report includes the required information outlined above and clearly communicates clinically relevant findings. Laboratory report formats may be limited by a specific reporting system used by the associated hospital, medical center, or commercial entity. Several report examples for different tumor types, including cases with both simple and complex findings, are provided in the supplementary materials of this document.

SUMMARY

The technical standards for interpretation and reporting of acquired CNAs and CN-LOH in neoplastic disorders described were developed in response to an urgent need to standardize the interpretation and reporting of these acquired variants using an evidence-based system with objective criteria. These recommendations represent an expert consensus of the workgroup members based on literature review, empirical data, and their professional judgment. These recommendations describe a four-tier evidence-based categorization system for acquired CNAs and CN-LOH. They outline the variant classification criteria for each tier based on the level of evidence available, and provide examples in tiers 1 and 2 in various hematologic malignancies and solid tumors. This document also provides a list of standardized definitions of terms used in the reporting of these variants, and recommendations for handling suspected clinically significant germline variants. Finally, this document outlines a framework for the clinical reporting of acquired CNAs and CN-LOH. The workgroup believes that the technical standards presented here will help clinical laboratories in achieving better standardized interpretation of CMA results. The workgroup will be constantly reviewing and revising these recommendations based on feedback from the cancer genomic community through a follow-up evaluation mechanism established in collaboration with the ACMG and CGC.

SUPPLEMENTARY MATERIALS

- Supplementary Table 1 illustrating selected tumor suppressor genes associated with germline predisposition to cancer.
- CMA report examples in hematologic malignancies and solid tumors.
- Supplementary figures illustrating examples of amplification, chromothripsis, intrachromosomal complexity, and genomic complexity. The same pattern of acquired CNAs suggestive of a specific disease entity is demonstrated using different CMA platforms. To illustrate the clinical utility of this tier classification system in the interpretation of acquired CNAs derived from whole genome sequencing

(WGS), examples of such abnormalities derived from WGS data are also included.

SUPPLEMENTARY INFORMATION

The online version of this article (<https://doi.org/10.1038/s41436-019-0545-7>) contains supplementary material, which is available to authorized users.

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DISCLOSURE

All members of this workgroup are directors of clinical laboratories that use chromosomal microarray technologies.

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The supplementary materials for the “Technical laboratory standards for interpretation and reporting of acquired CNAs and CN-LOH in neoplastic disorders” are listed below (with hyperlinks to the individual supplements):

1. **Supplementary table 1**
2. **CMA report templates**
3. **CMA report examples**
4. **Supplementary figures**

Supplementary Table 1

Selected tumor suppressor genes associated with germline predisposition to cancer (Deletions of these genes may prompt germline testing)

Gene Symbol	Gene Name (HGNC)	Tumor Types	Cancer Syndrome (OMIM #)
<i>APC</i>	APC regulator of WNT signaling pathway	Colorectal; pancreatic; desmoid; hepatoblastoma; glioma; other CNS	Adenomatous polyposis coli; Turcot syndrome (OMIM 175100)
<i>ATM</i>	ATM serine/threonine kinase	Leukemia; lymphoma; medulloblastoma; glioma	Ataxia-telangiectasia (OMIM 208900)
<i>BRCA1</i>	BRCA1 DNA repair associated	Breast; ovarian	Hereditary breast/ovarian cancer (OMIM 604370)
<i>BRCA2</i>	BRCA2 DNA repair associated	Breast; ovarian; pancreatic; leukemia (FANCD1)	Hereditary breast/ovarian cancer (OMIM 612555)
<i>CDH1</i>	cadherin 1	Gastric	Familial gastric carcinoma (OMIM 137215)
<i>CDKN1B</i>	cyclin dependent kinase inhibitor 1B	Pituitary; parathyroid	Multiple endocrine neoplasia type IV (OMIM 610755)
<i>CDKN2A</i>	cyclin dependent kinase inhibitor 2A	Melanoma; pancreatic	Familial malignant melanoma (OMIM 155755)
<i>CHEK2</i>	checkpoint kinase 2	Breast	Familial breast cancer (OMIM 114480)
<i>DICER1</i>	dicer 1, ribonuclease III	Pleuropulmonary blastoma	Familial pleuropulmonary blastoma or DICER1 syndrome (OMIM 601200)
<i>FANCA</i>	FA complementation group A	AML; leukemia	Fanconi anemia A (OMIM 227650)
<i>FANCC</i>	FA complementation group C	AML; leukemia	Fanconi anemia C (OMIM 227645)
<i>FANCD2</i>	FA complementation group D2	AML; leukemia	Fanconi anemia D2 (OMIM 227646)
<i>FANCE</i>	FA complementation group E	AML; leukemia	Fanconi anemia E (OMIM 600901)
<i>FANCF</i>	FA complementation group F	AML; leukemia	Fanconi anemia F (OMIM 603467)
<i>FANCG</i>	FA complementation group G	AML; leukemia	Fanconi anemia G (OMIM 614082)
<i>FH</i>	fumarate hydratase	Leiomyomatosis; renal	Hereditary leiomyomatosis and renal cell cancer (OMIM 150800)
<i>LZTR1</i>	leucine zipper like transcription regulator 1	Glioblastoma; schwannoma	Schwannomatosis-2 (OMIM 615670)
<i>MAX</i>	MYC associated factor X	Pheochromocytoma	Susceptibility to pheochromocytoma (OMIM154950)

<i>MEN1</i>	menin 1	Parathyroid adenoma; pituitary adenoma; pancreatic islet cell; carcinoid	Multiple endocrine neoplasia type 1 (OMIM 131100)
<i>MLH1</i>	mutL homolog 1	Colorectal; endometrial; ovarian; CNS	Hereditary non-polyposis colorectal cancer; Turcot syndrome (OMIM 609310)
<i>MSH2</i>	mutS homolog 2	Colorectal; endometrial; ovarian	Hereditary non-polyposis colorectal cancer (OMIM 120435)
<i>MSH6</i>	mutS homolog 6	Colorectal; endometrial; ovarian	Hereditary non-polyposis colorectal cancer (OMIM 614350)
<i>MUTYH</i>	mutY DNA glycosylase	Colorectal	Adenomatous polyposis coli (OMIM 608456)
<i>NF1</i>	neurofibromin 1	Neurofibroma; glioma	Neurofibromatosis type 1 (OMIM 162200)
<i>NF2</i>	neurofibromin 2	Meningioma; acoustic neuroma	Neurofibromatosis type 2 (OMIM 101000)
<i>PALB2</i>	partner and localizer of BRCA2	Wilms tumor; medulloblastoma; AML; breast (FANCN)	Fanconi anemia N; breast cancer susceptibility (OMIM 610355)
<i>PHOX2B</i>	paired like homeobox 2B	Neuroblastoma	Familial neuroblastoma (OMIM 613013)
<i>PMS2</i>	PMS1 homolog 2, mismatch repair system component	Colorectal; endometrial; ovarian; medulloblastoma; glioma	Hereditary non-polyposis colorectal cancer; Turcot syndrome (OMIM 614337)
<i>POLD1</i>	DNA polymerase delta 1, catalytic subunit	Colorectal	Colorectal cancer susceptibility (OMIM 612591)
<i>PTCH1</i>	patched 1	Skin basal cell; medulloblastoma	Nevoid basal cell carcinoma syndrome (OMIM 109400)
<i>PTEN</i>	phosphatase and tensin homolog	Hamartoma; glioma; prostate; endometrial	Cowden syndrome; Bannayan-Riley-Ruvalcaba syndrome (OMIM 601728)
<i>RB1</i>	RB transcriptional corepressor 1	Retinoblastoma; sarcoma; breast; small cell lung carcinoma	Familial retinoblastoma (OMIM 180200)
<i>RECQL4</i>	RecQ like helicase 4	Osteosarcoma; skin basal cell; skin squamous cell	Rothmund-Thompson syndrome (OMIM 268400)
<i>SBDS</i>	SBDS ribosome maturation factor	AML; MDS	Schwachman-Diamond syndrome (OMIM 260400)
<i>SDHA</i>	succinate dehydrogenase complex flavoprotein subunit A	Paraganglioma	Paragangliomas-5 (PGL5) (OMIM 614165)
<i>SDHAF2</i>	succinate dehydrogenase complex assembly factor 2	Paraganglioma	Familial paraganglioma (OMIM 601650)
<i>SDHB</i>	succinate dehydrogenase complex iron sulfur subunit B	Paraganglioma; pheochromocytoma	Gastrointestinal stromal tumor (OMIM 606764); Paraganglioma and gastric stromal sarcoma (OMIM 606864); Paragangliomas 4 (OMIM 115310), Pheochromocytoma (OMIM 171300)

<i>SDHC</i>	succinate dehydrogenase complex subunit C	Paranglioma; pheochromocytoma	Gastrointestinal stromal tumor (OMIM 606764); Paranglioma and gastric stromal sarcoma (OMIM 606864); Parangliomas 3 (OMIM 605373)
<i>SDHD</i>	succinate dehydrogenase complex subunit D	Paranglioma; pheochromocytoma	Paranglioma and gastric stromal sarcoma (OMIM 606864); Parangliomas 1, with or without deafness (OMIM 168000); Pheochromocytoma (OMIM 171300)
<i>SMAD4</i>	SMAD family member 4	Gastrointestinal polyp	Juvenile polyposis (OMIM 175050)
<i>SMARCB1</i>	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	Malignant rhabdoid	Rhabdoid predisposition syndrome (OMIM 609322)
<i>SMARCA4</i>	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	Rhabdoid tumor; small cell carcinoma of the ovary hypercalcemic type	Rhabdoid tumor predisposition syndrome type 2 (OMIM 613325)
<i>SMARCE1</i>	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	Meningioma	Meningioma susceptibility (OMIM 607174)
<i>STK11</i>	serine/threonine kinase 11	Jejunal hamartoma; ovarian; testicular; pancreatic	Peutz-Jeghers syndrome (OMIM 175200)
<i>SUFU</i>	SUFU negative regulator of hedgehog signaling	Medulloblastoma	Medulloblastoma predisposition (OMIM 155255)
<i>TERT</i>	telomerase reverse transcriptase	Melanoma	Dyskeratosis congenita (OMIM 613989)
<i>TGFBR2</i>	transforming growth factor beta receptor 2	colorectal	Hereditary Nonpolyposis Colorectal Cancer type 6 (OMIM 614331)
<i>TMEM127</i>	transmembrane protein 127	Pheochromocytoma; renal cell carcinoma	Susceptibility to pheochromocytoma (OMIM 613403)
<i>TP53</i>	tumor protein p53	Breast; sarcoma; adrenocortical carcinoma; glioma; multiple other tumor types	Li-Fraumeni syndrome (OMIM 191170)
<i>TSC1</i>	TSC complex subunit 1	Hamartoma; renal cell carcinoma; tuberous sclerosis tuber	Tuberous sclerosis 1 (OMIM 191100)
<i>TSC2</i>	TSC complex subunit 2	Hamartoma; renal cell carcinoma; tuberous sclerosis tuber	Tuberous sclerosis 2 (OMIM 613254)
<i>VHL</i>	von Hippel-Lindau tumor suppressor	Renal; hemangioma; pheochromocytoma	Von Hippel-Lindau syndrome (OMIM 193300)
<i>WRN</i>	Werner syndrome RecQ like helicase	Osteosarcoma; meningioma; other tumor types	Werner syndrome (OMIM 277700)
<i>WT1</i>	WT1 transcription factor	Wilms tumor	Denys-Drash syndrome; Frasier syndrome; familial Wilms tumor (OMIM 607102)

CMA Report Template 1

Patient name:

Medical record #:

Date of birth:

Lab #:

Indication for the study:

Type of specimen:

Date sample collected:

Date sample received:

Report date:

Array platform:

CMA results according to GRCh** (ISCN):

Interpretation:

Chromosomal microarray (CMA) analysis revealed multiple clonal copy number abnormalities (CNAs) and/or regions of copy-neutral loss of heterozygosity (CN-LOH) in the DNA from the _____ tissue from this patient including gain of chromosomes _____, loss of chromosomes _____, copy number gains in the _____ chromosome regions, copy number losses in the _____ chromosome regions, and _____ CN-LOH in the _____ chromosome regions.

- **Clinically significant CNAs and/or CN-LOH (Tier 1 and 2 variants)**

Tier classification	Chr.	Variant type (% of cells involved)	Cytogenetic locus	Genomic coordinates (GRCh**)	Size (Mb)	COSMIC census cancer gene(s) within the region

Narrative interpretation

- **Clinically significant pattern of CNAs and/or CN-LOH (Tier 1 and 2 variants)**

Tier classification	Chr.	Variant type (% of cells involved)	Cytogenetic locus	Genomic coordinates (GRCh**)	Size (Mb)	COSMIC census cancer gene(s) within the region

Narrative interpretation

- **CNAs and/or CN-LOH of potential clinical significance (cannot be tiered at the time of reporting)**

Chr.	Variant type (% of cells involved)	Cytogenetic locus	Genomic coordinates (GRCh**)	Size (Mb)	COSMIC census cancer gene(s) within the region

Narrative interpretation and recommended confirmatory testing

- **Other clonal variants** (Tier 3 variants)

Tier classification	Chr.	Variant type (% of cells involved)	Cytogenetic locus	Genomic coordinates (GRCh**)	Size (Mb)	COSMIC census cancer gene(s) within the region

Result and interpretation summary:

References:

Recommendations:

Methodology and disclaimer:

CMA Report Template 2

Patient name:

Medical record #:

Date of birth:

Lab #:

Indication for the study:

Type of specimen:

Date sample collected:

Date sample received:

Report date:

Array platform:

*** Result and interpretation summary:**

** In this template, the summary of the results and the interpretation are provided at the beginning of the report, so that clinically relevant information is emphasized and easy to find. For simple cases, this is followed by detailed results provided in a table format. For complex cases, the nomenclature strings 'arr(1-22,X,Y)cx or arr(1-22,X)cx' can be used; it is still recommended to provide a table with result details, but the table can be moved to the end of the report (see example for Case 4). The provided report templates are examples only; the report format and the order of report sections are at the discretion of the laboratory director, but the clinically significant information should be prioritized.*

CMA results according to GRCh:**

Chr.	Start band	End band	Genomic position – start	Genomic position – end	Variant type (% of cells involved)	COSMIC census cancer gene(s) within the region	Tier classification

Interpretation:

Chromosomal microarray analysis (CMA) revealed multiple clonal abnormalities, including:

- Gain of chromosomes
- Loss of chromosomes
- Copy number gains in cytogenetic regions
- Copy number losses in cytogenetic regions

Tier 1: strong diagnostic, prognostic, and/or therapeutic clinical significance

Narrative interpretation

Tier 2: acquired variants with some clinical significance

Narrative interpretation

Tier 3: acquired clonal variants with no documented neoplastic disorder association

Narrative interpretation

References:

Recommendations:

Methodology and disclaimer:

Example, Case 1, Template 1:

B-cell Acute Lymphoblastic Leukemia/Lymphoma (B-ALL)

Patient name:

Medical record #:

Date of birth:

Lab #:

Indication for the study: B-ALL, new diagnosis

Type of specimen: BM aspirate

Date sample collected:

Date sample received:

Report date:

Array Platform: Agilent 4x180k aCGH+SNP

CMA results according to GRCh38 (ISCN):

arr[GRCh38] Xp22.33 or Yp11.32(1285856_1528518)x1,
5q33.3(157844969_159909736)x1,
12q24.11q24.12(110343572_111746376)x1,
15q26.1(91791442_93027044)x1,
19p13.3(1272199_4418045)x1,
21q21.1(19199045_20602261)x4,
21q21.1q21.2(20629500_23114127)x6,
21q21.2q22.3(23130506_44049398)x5,
21q22.3(44052418_46664244)x1

Interpretation:

Chromosomal microarray (CMA) analysis revealed multiple clonal copy number abnormalities (CNAs) in the DNA from the bone marrow sample from this patient, including copy number gains in the 21q21.1, 21q21.1q21.2 and 21q21.2q22.3 regions and copy number losses in the Xp22.33 or Yp11.32, 5q33.3, 12q24.11q24.12, 15q26.1 and 21q22.3 chromosome regions.

- **Clinically significant pattern of CNAs and/or CN-LOH** (Tier 1 and 2 variants)

Tier classification	Chr.	Variant type	Cytogenetic locus	Genomic coordinates (GRCh38)	Size (Mb)	COSMIC census cancer gene(s) within the region
Tier 1A (Strong significance)	21	CNAs pattern	21q21.1-21q22.3	19,199,045-46,664,244	~27.5	<i>RUNX1</i>

Four complex contiguous CNAs were detected involving the long (q) arm of chromosome 21, consisting of a two copy gain at band 21q21.1 (~1.4 Mb in size), a four copy gain at bands 21q21.1q21.2 (~2.48 Mb in size), a three copy gain at bands 21q21.2q22.3 (~20.96 Mb in size) that spans the *RUNX1* gene, and a terminal one copy loss at band 21q22.3 (~2.61 Mb in size). This pattern

of chromosome 21q CNAs is consistent with the intrachromosomal amplification of chromosome 21 (iAMP21) signature (WHO 2016, Harrison CJ et al. Leukemia 2014, and Li Y et al. Nature 2014).

- **Clinically significant CNAs and/or CN-LOH (Tier 1 and 2 variants)**

Tier classification	Chr.	Variant type	Cytogenetic locus	Genomic coordinates (GRCh38)	Size (Mb)	COSMIC census cancer gene(s) within the region
Tier 1A (Strong significance)	X or Y	1 copy loss	Xp22.33 or Yp11.32	1,285,856-1,528,518	0.24	<i>P2RY8</i> , <i>CRLF2</i>
Tier 2	5	1 copy loss	5q33.3	157,844,969-159,909,736	2	<i>EBF1</i>
Tier 2	12	1 copy loss	12q24.11q24.12	110,343,572-111,746,376	1.4	<i>SH2B3</i>

- One copy loss was detected in the very distal region of the short (p) arm of chromosome X or Y in the pseudoautosomal region 1 (PAR1) at bands Xp22.33 or Yp11.32, respectively. This interstitial PAR1 deletion is approximately 242 kb in size, encompasses the 3' region of the *P2RY8* gene as well as five other RefSeq genes and is expected to result in *P2RY8-CRLF2* gene fusion (Ph-like ALL) (WHO 2016, Mullighan CG et al. Nat Genet 2009, and Roberts KG et al. N Engl J Med 2014).
- One copy loss was observed in the distal region of the q arm of chromosome 5 at band 5q33.3. This interstitial deletion is approximately 2.06 Mb in size and encompasses nine annotated RefSeq genes including one census cancer gene as shown in the COSMIC (Catalogue of somatic mutations in cancer) database, namely *EBF1*. *EBF1* gene deletions have been reported in 4-6% of pediatric B-lineage ALL patients with a reported higher frequency during relapse (Mullighan CG et al. Nature 2007 and Yang JJ et al. Blood 2008).
- One copy loss was detected in the distal region of the q arm of chromosome 12 at bands 12q24.11q24.12. This interstitial deletion is approximately 1.4 Mb in size and encompasses 20 annotated RefSeq genes including one census cancer gene, namely *SH2B3*. *SH2B3*, which encodes the JAK2 negative regulator LNK, has been reported to be deleted in some B-ALL cases with *CRLF2* gene rearrangements (Roberts KG et al. N Engl J Med 2014).

- **Other clonal variants (Tier 3 variants)**

Tier classification	Chr.	Variant type	Cytogenetic locus	Genomic coordinates (GRCh38)	Size (Mb)	COSMIC census cancer gene(s) within the region
Tier 3	15	1 copy loss	15q26.1	91,791,442-93,027,044	1.23	
Tier 3	19	1 copy loss	19p13.3	12,721,99-44,18,045	3.14	<i>TCF3</i> , <i>GNA11</i> , <i>MAP2K2</i> , and <i>SH3GL1</i>

- One copy loss was observed in the distal region of the q arm of chromosome 15 at band 15q26.1. This interstitial deletion is approximately 1.23 Mb in size and encompasses seven annotated RefSeq genes.
- One copy loss was detected in the distal region of the p arm of chromosome 19 at band 19p13.3. This interstitial deletion is approximately 3.14 Mb in size and encompasses approximately 100 annotated RefSeq genes including four census cancer genes, namely *TCF3*, *GNA11*, *MAP2K2*, and *SH3GL1*.

Interpretation summary:

Copy number abnormalities (CNAs) of high clinical significance (Tier 1) detected in this BM sample include the pseudoautosomal region 1 (PAR1) deletion that results in *P2RY8-CRLF2* gene fusion (Ph-like ALL), and a pattern of chromosome 21 CNAs that is consistent with the intrachromosomal amplification of chromosome 21 (iAMP21).

References:

- Harrison CJ, Moorman AV, Schwab C, Carroll AJ, Raetz EA, Devidas M, Strehl S, Nebral K, Harbott J, Teigler-Schlegel A, Zimmerman M. An international study of intrachromosomal amplification of chromosome 21 (iAMP21): cytogenetic characterization and outcome. *Leukemia* 2014;28(5):1015.
- Li Y, Schwab C, Ryan SL, Papaemmanuil E, Robinson HM, Jacobs P, Moorman AV, Dyer S, Borrow J, Griffiths M, Heerema NA. Constitutional and somatic rearrangement of chromosome 21 in acute lymphoblastic leukaemia. *Nature* 2014;508(7494):98.
- Mullighan CG, Collins-Underwood JR, Phillips LA, Loudin MG, Liu W, Zhang J, Ma J, Coustan-Smith E, Harvey RC, Willman CL, Mikhail FM. Rearrangement of CRLF2 in B-progenitor-and Down syndrome-associated acute lymphoblastic leukemia. *Nat Genet* 2009;41(11):1243.
- Mullighan CG, Goorha S, Radtke I, Miller CB, Coustan-Smith E, Dalton JD, Girtman K, Mathew S, Ma J, Pounds SB, Su X. Genome-wide analysis of genetic alterations in acute lymphoblastic leukaemia. *Nature* 2007;446(7137):758.
- Roberts KG, Li Y, Payne-Turner D, Harvey RC, Yang YL, Pei D, McCastlain K, Ding L, Lu C, Song G, Ma J. Targetable kinase-activating lesions in Ph-like acute lymphoblastic leukemia. *N Engl J Med* 2014;371(11):1005-15.
- Yang JJ, Bhojwani D, Yang W, Cai X, Stocco G, Crews K, Wang J, Morrison D, Devidas M, Hunger SP, Willman CL. Genome-wide copy number profiling reveals molecular evolution from diagnosis to relapse in childhood acute lymphoblastic leukemia. *Blood* 2008;112(10):4178-83.

Methodology and disclaimer:

This array CGH analysis was performed using the Agilent 4x180k aCGH+SNP oligonucleotide (oligo) array, which contains ~110,000 oligo probes for the detection of copy number changes (deletions, duplications, amplifications, and unbalanced translocations/insertions) and ~60,000 SNP probes for the detection of copy-neutral loss of heterozygosity (CN-LOH). It contains genome-wide coverage with an average probe spacing of ~25 kb. It is designed to detect copy number changes with a minimum size of ~50 kb across the genome. This test will not detect truly balanced chromosomal rearrangements, imbalances of regions not represented on the array, low-level mosaicism, and point mutations. The failure to detect an alteration at any locus does not exclude all abnormalities at that locus. This test was developed and its performance characteristics determined by the 'Laboratory Name' as required by CLIA '88 regulations. It has not been cleared or approved for specific uses by the U.S. Food and Drug Administration.

Positive evaluation criteria:

- Genomic DNA copy gain/loss >50 kb involving clinically significant census cancer genes (520 in the COSMIC Database).
- Genomic DNA copy loss >1 Mb or gain >2 Mb outside known clinical oncology significant regions spanning at least one annotated RefSeq gene.
- Long stretch of allele homozygosity >15 Mb on a single chromosome, which is consistent with copy-neutral loss of heterozygosity (CN-LOH). These regions suggest clonal evolution associated with the acquisition of homozygosity for a gene mutation within the homozygotic stretch. Candidate gene(s) within these CN-LOH regions will be reported.

Example, Case 1, Template 2:

B-cell Acute Lymphoblastic Leukemia/Lymphoma (B-ALL)

Patient name:

Medical record #:

Date of birth:

Lab #:

Indication for the study: B-ALL, new diagnosis

Type of specimen: BM aspirate

Date sample collected:

Date sample received:

Report date:

Array Platform: Agilent 4x180k aCGH+SNP

Result and interpretation summary:

Copy number abnormalities (CNAs) of high clinical significance (Tier 1) detected in this BM sample include the pseudoautosomal region 1 (PAR1) deletion that results in a *P2RY8-CRLF2* gene fusion (Ph-like ALL), and a pattern of chromosome 21 CNAs that is consistent with the intrachromosomal amplification of chromosome 21 (iAMP21).

CMA results according to GRCh38:

Chr.	Start -End band	Genomic position: start-end	Variant type	Size (Mb)	COSMIC census cancer gene(s) within the region	Tier classification
X or Y	Xp22.33 or Yp11.32	1,285,856-1,528,518	1 copy loss	0.24	<i>P2RY8, CRLF2</i>	Tier 1A
5	q33.3	157,844,969-159,909,736	1 copy loss	2	<i>EBF1</i>	Tier 2
12	q24.11q24.12	110,343,572-111,746,376	1 copy loss	1.4	<i>SH2B3</i>	Tier 2
15	q26.1	91,791,442-93,027,044	1 copy loss	1.23		Tier 3
19	p13.3	12,721,99-44,18,045	1 copy loss	3.14	<i>TCF3, GNA11, MAP2K2, and SH3GL1</i>	Tier 3
21	q21.1	19,199,045-20,602,261	2 copy gain	1.4		Tier 1A (pattern)
21	q21.1q21.2	20,629,500-23,114,127	4 copy gain	2.48		
21	q21.2q22.3	23,130,506-44,049,398	3 copy gain	20.9	<i>RUNX1</i>	

21	q22.3	44,052,418-46,664,244	1 copy loss	2.6		
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Interpretation:

Chromosomal microarray analysis (CMA) revealed multiple clonal abnormalities, including:

- Copy number gains in the 21q21.1, 21q21.1q21.2 and 21q21.2q22.3 regions
- Copy number losses in the Xp22.33 or Yp11.32, 5q33.3, 12q24.11q24.12, 15q26.1 and 21q22.3 regions

Tier 1: strong diagnostic, prognostic, and/or therapeutic clinical significance

- Four complex contiguous copy number abnormalities (CNAs) were detected involving the long (q) arm of chromosome 21 and consisting of a two copy gain at band 21q21.1 (~1.4 Mb in size), a four copy gain at bands 21q21.1q21.2 (~2.48 Mb in size), a three copy gain at bands 21q21.2q22.3 that spans the *RUNX1* gene (~20.96 Mb in size), and a terminal one copy loss at band 21q22.3 (~2.61 Mb in size). This pattern of chromosome 21 CNAs is consistent with the intrachromosomal amplification of chromosome 21 (iAMP21) signature (WHO 2016, Harrison CJ et al. Leukemia 2014, and Li Y et al. Nature 2014).
- One copy loss was detected in the very distal region of the short (p) arm of chromosome X or Y in the pseudoautosomal region 1 (PAR1) at bands Xp22.33 or Yp11.32, respectively. This interstitial PAR1 deletion is approximately 242 kb in size, encompasses the 3' region of the *P2RY8* gene as well as five other RefSeq genes and is expected to result in *P2RY8-CRLF2* gene fusion (Ph-like ALL) (WHO 2016, Mullighan CG et al. Nat Genet 2009, and Roberts KG et al. N Engl J Med 2014).

Tier 2: acquired variants with some clinical significance

- One copy loss was observed in the distal region of the q arm of chromosome 5 at band 5q33.3. This interstitial deletion is approximately 2.06 Mb in size and encompasses nine annotated RefSeq genes including one census cancer gene as shown in the COSMIC (Catalogue of somatic mutations in cancer) database, namely *EBF1*. *EBF1* gene deletions have been reported in 4-6% of pediatric B-lineage ALL patients with a reported higher frequency during relapse (Mullighan CG et al. Nature 2007 and Yang JJ et al. Blood 2008).
- One copy loss was detected in the distal region of the q arm of chromosome 12 at bands 12q24.11q24.12. This interstitial deletion is approximately 1.4 Mb in size and encompasses 20 annotated RefSeq genes including one census cancer gene, namely *SH2B3*. *SH2B3*, which encodes the JAK2 negative regulator LNK, has been reported to be deleted in some patients with *CRLF2* gene rearrangements (Roberts KG et al. N Engl J Med 2014).

Tier 3: acquired clonal variants with no documented neoplastic disorder association

- One copy loss was observed in the distal region of the q arm of chromosome 15 at band 15q26.1. This interstitial deletion is approximately 1.23 Mb in size and encompasses seven annotated RefSeq genes.
- One copy loss was detected in the distal region of the p arm of chromosome 19 at band 19p13.3. This interstitial deletion is approximately 3.14 Mb in size and encompasses approximately 100 annotated RefSeq genes including four census cancer genes, namely *TCF3*, *GNA11*, *MAP2K2*, and *SH3GL1*.

References:

- Harrison CJ, Moorman AV, Schwab C, Carroll AJ, Raetz EA, Devidas M, Strehl S, Nebral K, Harbott J, Teigler-Schlegel A, Zimmerman M. An international study of intrachromosomal

amplification of chromosome 21 (iAMP21): cytogenetic characterization and outcome. *Leukemia* 2014;28(5):1015.

- Li Y, Schwab C, Ryan SL, Papaemmanuil E, Robinson HM, Jacobs P, Moorman AV, Dyer S, Borrow J, Griffiths M, Heerema NA. Constitutional and somatic rearrangement of chromosome 21 in acute lymphoblastic leukaemia. *Nature* 2014;508(7494):98.
- Mullighan CG, Collins-Underwood JR, Phillips LA, Loudin MG, Liu W, Zhang J, Ma J, Coustan-Smith E, Harvey RC, Willman CL, Mikhail FM. Rearrangement of CRLF2 in B-progenitor- and Down syndrome-associated acute lymphoblastic leukemia. *Nat Genet* 2009;41(11):1243.
- Mullighan CG, Goorha S, Radtke I, Miller CB, Coustan-Smith E, Dalton JD, Girtman K, Mathew S, Ma J, Pounds SB, Su X. Genome-wide analysis of genetic alterations in acute lymphoblastic leukaemia. *Nature* 2007;446(7137):758.
- Roberts KG, Li Y, Payne-Turner D, Harvey RC, Yang YL, Pei D, McCastlain K, Ding L, Lu C, Song G, Ma J. Targetable kinase-activating lesions in Ph-like acute lymphoblastic leukemia. *N Engl J Med* 2014;371(11):1005-15.
- Yang JJ, Bhojwani D, Yang W, Cai X, Stocco G, Crews K, Wang J, Morrison D, Devidas M, Hunger SP, Willman CL. Genome-wide copy number profiling reveals molecular evolution from diagnosis to relapse in childhood acute lymphoblastic leukemia. *Blood* 2008;112(10):4178-83.

Methodology and disclaimer:

This array CGH analysis was performed using the Agilent 4x180k aCGH+SNP oligonucleotide (oligo) array, which contains ~110,000 oligo probes for the detection of copy number changes (deletions, duplications, amplifications, and unbalanced translocations/insertions) and ~60,000 SNP probes for the detection of copy-neutral loss of heterozygosity (CN-LOH). It contains genome-wide coverage with an average probe spacing of ~25 kb. It is designed to detect copy number changes with a minimum size of ~50 kb across the genome. This test will not detect truly balanced chromosomal rearrangements, imbalances of regions not represented on the array, low-level mosaicism, and point mutations. The failure to detect an alteration at any locus does not exclude all abnormalities at that locus. This test was developed and its performance characteristics determined by the '*Laboratory Name*' as required by CLIA'88 regulations. It has not been cleared or approved for specific uses by the U.S. Food and Drug Administration.

Positive evaluation criteria:

- Genomic DNA copy gain/loss >50 kb involving clinically significant census cancer genes (520 in the COSMIC Database).
- Genomic DNA copy loss >1 Mb or gain >2 Mb outside known clinical oncology significant regions spanning at least one annotated RefSeq gene.
- Long stretch of allele homozygosity >15 Mb on a single chromosome, which is consistent with copy-neutral loss of heterozygosity (CN-LOH). These regions suggest clonal evolution associated with the acquisition of homozygosity for a gene mutation within the homozygotic stretch. Candidate gene(s) within these CN-LOH regions will be reported.

Example, Case 2, Template 1:

Neuroblastoma

Patient name:

Medical record #:

Date of birth:

Lab #:

Indication for the study: Poorly differentiated neuroblastoma

Type of specimen: Right retroperitoneal mass

Date sample collected:

Date sample received:

Report date:

Array Platform: CytoScan HD, Thermofisher

CMA results according to GRCh37 (ISCN):

arr[GRCh37] 1p36.33p34.3(849466_38448665)x1-2,
1p34.3q44(38484877_249224684)x2-3,
2p24.3(16039832_16445487)x28-38,
2p24.2(17064164_17235911)x14,
2p22.3(32592069_32825190)x1-2,
2q22.3q23.3(145128059_153658276)x3,
2q23.3q37.3(153800773_242783384)x3,
17q21.31q25.3(43710150_81041938)x3

Interpretation:

Chromosomal microarray (CMA) analysis revealed multiple clonal copy number abnormalities (CNAs) in the DNA from the tumor tissue (neuroblastoma) from this patient, including a loss of 37.6 Mb in 1p36.33p34.3, a gain of 210.7 Mb in 1p34.3q44, a complex rearrangement with 4 gains and 1 loss in chromosome 2 (including a 406 kb amplification in 2p24.3 involving the *MYCN* gene), and a gain of 37.3 Mb in 17q21.31q25.3.

- **Clinically significant CNVs and/or CN-LOH (Tier 1 and 2 variants)**

Tier classification	Chr.	Variant type	Cytogenetic locus	Genomic coordinates (GRCh37)	Size (Mb)	COSMIC census cancer gene(s) within the region
Tier 1B	1	1 copy loss	p36.33p34.3	849,466 - 38,448,665	37.59	
Tier 1A	2	Amplification (38 copies)	p24.3	16,039,832 - 16,445,487	0.4	<i>MYCN</i>
Tier 1B	17	1 copy gain	q21.31q25.3	43,710,150 - 81,041,938	37.32	

MYCN amplification is associated with unfavorable prognosis in neuroblastoma [1]. Loss of 1p and gain of 17q are often observed with *MYCN* amplification and have also been described as unfavorable prognostic markers [1,2].

- **Other clonal variants** (Tier 3 variants)

Tier classification	Chr.	Variant type	Cytogenetic locus	Genomic coordinates (GRCh37)	Size (Mb)	COSMIC census cancer gene(s) within the region
Tier 3	1	1 copy gain	p34.3q44	38,484,877 - 249,224,684	210.7	
Tier 3	2	Amplification (14 copies)	p24.2	17,064,164 - 17,235,911	0.17	
Tier 3	2	1 copy loss	p22.3	32,592,069 - 32,825,190	0.23	<i>BIRC6</i>
Tier 3	2	1 copy gain	q22.3q23.3	145,128,059 - 153,658,276	8.53	
Tier 3	2	1 copy gain	q23.3q37.3	153,800,773 - 242,783,384	88.98	

Interpretation summary:

Copy number abnormalities (CNAs) of high clinical significance (Tier 1) detected in this sample include amplification of the *MYCN* locus, which is associated with an unfavorable outcome in neuroblastoma, and loss of 1p and gain of 17q, which are also known markers of poor prognosis and frequently co-occur with *MYCN* amplification.

References:

1. Cohn SL, Pearson AD, London WB, Monclair T, Ambros PF, Brodeur GM, Faldut A, Hero B, Iehara T, Machin D, Mosseri V. The International Neuroblastoma Risk Group (INRG) classification system: an INRG task force report. *J Clin Oncol* 2009;27(2):289-97.
2. Monclair T, Brodeur GM, Ambros PF, Brisse HJ, Cecchetto G, Holmes K, Kaneko M, London WB, Matthay KK, Nuchtern JG, von Schweinitz D. The International Neuroblastoma Risk Group (INRG) staging system: an INRG task force report. *J Clin Oncol* 2009;27(2):298-303.

Methodology and disclaimer:

SNP microarray analysis was performed using the CytoScan TM HD platform for the sole purpose of identifying DNA copy number gains and losses and regions of loss of heterozygosity. The array contains more than 2.6 million copy number markers, including 750,000 SNPs, with a median spacing of 0.88 kb within genes. Patient DNA is extracted, amplified, enzymatically fragmented, and hybridized to oligonucleotide probes. The array is washed, scanned, and the results are analyzed and interpreted. Gains or losses greater than 35 markers within or including a known clinically significant cancer related gene, or greater than 1 Mb outside known clinical oncology significant regions, and loss of heterozygosity greater than 10 Mb, are reported. The analysis is based on the GRCh37/hg19 assembly.

This assay will not detect balanced chromosomal aberrations, imbalance of regions not represented on the microarray, or point mutations. Failure to detect an alteration at any locus does not exclude any particular diagnosis. The results of this test should be considered in the context of the clinical phenotype. The detection threshold for mosaicism is variable, depending on the size of the segment. Common population copy number variants (CNVs) cited in the Database of Genomic Variants are not reported.

This test was developed by Affymetrix, Inc (Santa Clara, CA, USA) and its performance determined by '*Laboratory Name*' as required by CLIA '88 regulations. This assay has not been cleared or approved by the U.S. Food and Drug Administration. The FDA has determined that such clearance or approval is not necessary. Pursuant to the requirement of CLIA '88, this laboratory has established and verified the test's accuracy and precision.

Example, Case 2, Template 2:

Neuroblastoma

Patient name:

Medical record #:

Date of birth:

Lab #:

Indication for the study: Poorly differentiated neuroblastoma

Type of specimen: Right retroperitoneal mass

Date sample collected:

Date sample received:

Report date:

Array Platform: CytoScan HD, Thermofisher

Result and interpretation summary:

Copy number abnormalities (CNAs) of high clinical significance (Tier 1) detected in this sample include amplification of the *MYCN* locus, which is associated with an unfavorable outcome in neuroblastoma, and loss of 1p and gain of 17q, which are also known markers of poor prognosis and frequently co-occur with *MYCN* amplification.

CMA results according to GRCh37:

Chr.	Start -End Band	Genomic position: start-end	Variant type	Size (Mb)	COSMIC census cancer gene(s) within the region	Tier classification
1	p36.33p34.3	849,466 - 38,448,665	1 copy loss	37.59		Tier 1B
2	p24.3	16,039,832 - 16,445,487	Amplification (38 copies)	0.4	<i>MYCN</i>	Tier 1A
2	p24.2	17,064,164 - 17,235,911	Amplification (14 copies)	0.17		Tier 3
2	p22.3	32,592,069 - 32,825,190	1 copy loss	0.23	<i>BIRC6</i>	Tier 3
2	q22.3q23.3	145,128,059 - 153,658,276	1 copy gain	8.53		Tier 3
2	q23.3q37.3	153,800,773 - 242,783,384	1 copy gain	88.98		Tier 3
17	q21.31q25.3	43,710,150 - 81,041,938	1 copy gain	37.32		Tier 1B

Interpretation:

Chromosomal microarray (CMA) analysis revealed the following copy number abnormalities (CNAs):

- A loss of 37.6 Mb in 1p36.33p34.3,
- A gain of 210.7 Mb in 1p34.3q44,
- A complex rearrangement with 4 gains and 1 loss in chromosome 2, including a 406 kb amplification in 2p24.3 (*MYCN* gene amplified, 38 copies) and a 172 kb amplification in 2p24.2 (14 copies) with no known genes
- A gain of 8.53 Mb in 2q22.3q23.3
- A gain of 88.98 Mb in q23.3q37.3
- A gain of 37.3 Mb in 17q21.31q25.3

Tier 1: strong diagnostic, prognostic, and/or therapeutic clinical significance

Amplification of the *MYCN* locus is associated with an unfavorable outcome in neuroblastoma. Additionally, loss of 1p and gain of 17q are also known markers of poor prognosis and frequently co-occur with *MYCN* amplification.

Tier 3: acquired clonal variants with no documented neoplastic disorder association

Copy number gains in 1p34.3q44 (210.7 Mb), 2q22.3q23.3 (8.5 Mb), and 2q23.3q37.3 (88.9 Mb), and a copy number loss in 2p22.3 (0.23 Mb) were observed as acquired clonal variants.

References:

1. Cohn SL, Pearson AD, London WB, Monclair T, Ambros PF, Brodeur GM, Faldut A, Hero B, Iehara T, Machin D, Mosseri V. The International Neuroblastoma Risk Group (INRG) classification system: an INRG task force report. *J Clin Oncol* 2009;27(2):289-97.
2. Monclair T, Brodeur GM, Ambros PF, Brisse HJ, Cecchetto G, Holmes K, Kaneko M, London WB, Matthay KK, Nuchtern JG, von Schweinitz D. The International Neuroblastoma Risk Group (INRG) staging system: an INRG task force report. *J Clin Oncol* 2009;27(2):298-303.

Methodology and disclaimer:

SNP microarray analysis was performed using the CytoScan TM HD platform for the sole purpose of identifying DNA copy number gains and losses and regions of loss of heterozygosity. The array contains more than 2.6 million copy number markers, including 750,000 SNPs, with a median spacing of 0.88 kb within genes. Patient DNA is extracted, amplified, enzymatically fragmented, and hybridized to oligonucleotide probes. The array is washed, scanned, and the results are analyzed and interpreted. Gains or losses greater than 35 markers within or including a known clinically significant cancer related gene, or greater than 1 Mb outside known clinical oncology significant regions, and loss of heterozygosity greater than 10 Mb, are reported. The analysis is based on the GRCh37/hg19 assembly.

This assay will not detect balanced chromosomal aberrations, imbalance of regions not represented on the microarray, or point mutations. Failure to detect an alteration at any locus does not exclude any particular diagnosis. The results of this test should be considered in the context of the clinical phenotype. The detection threshold for mosaicism is variable, depending on the size of the segment. Common population copy number variants (CNVs) cited in the Database of Genomic Variants are not reported.

This test was developed by Affymetrix, Inc (Santa Clara, CA, USA) and its performance determined by '*Laboratory Name*' as required by CLIA '88 regulations. This assay has not been cleared or approved by the U.S. Food and Drug Administration. The FDA has determined that such clearance or approval is not necessary. Pursuant to the requirement of CLIA '88, this laboratory has established and verified the test's accuracy and precision.

Example, Case 3, Template 1:

Medulloblastoma/Germline Tier 1 Variant

Patient name:

Medical record #:

Date of birth: 10-1-1995

Lab #:

Indication for the study: Intracranial mass,
left cerebellar tumor, suspected medulloblastoma.
Patient has clinical diagnosis of Neurofibromatosis

Type of specimen: FFPE tissue

Date sample collected:

Date sample received:

Report date:

Array platform: Infinium® OExPls CytoConsortium Array BeadChip

Specimen Description: Block ID: A1 (90% tumor)

A pathologist reviewed this case and determined the tumor content on an H&E slide from this formalin-fixed paraffin-embedded (FFPE) patient specimen.

CMA results according to GRCh37 (ISCN):

arr[GRCh37] 9q21.11q34.3(70984372_141213431)x2 hmz[0.95]
13q11q34(18964272_115031453)x3[0.13]
17q11.2(29097182_30286085)x1?c[1.0]

Pertinent negative results:

MYCN: no amplification

MYC: no amplification

TP53: no copy number aberrations or CN-LOH

Interpretation:

Chromosomal microarray (CMA) analysis of an FFPE specimen from a cerebellar tumor revealed copy-neutral loss of heterozygosity (CN-LOH) in the long (q) arm of chromosome 9 present in approximately 95% of the cells and gain of chromosome 13 present in approximately 13% of the cells. A likely constitutional deletion in 17q11.2 including the *NFI* gene was also detected.

- **Clinically significant CNAs and/or CN-LOH (Tier 1 and 2 variants)**

Tier classification	Chr.	Variant type (% of cells involved)	Cytogenetic locus	Genomic coordinates (GRCh37)	Size (Mb)	COSMIC census cancer gene(s) within the region
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Tier 1A	9	CN-LOH (95%)	9q21.11q34.3	70984372_141213431	70.2	<i>PTCH1</i>
Tier 1A	17	1 copy loss (100%)	q11.2	29097182_30286085	1.18	<i>NF1</i>
Tier 2	13	1 copy gain (13%)	13q11q34	18964272_115031453	96	Whole chromosome

- A relatively stable genetic profile with allelic loss in 9q, together with nuclear negativity for beta-catenin and positivity for GAB (per concurrent IHC staining), are most consistent with the SHH subtype of medulloblastoma [1-3]. Abnormalities of 9q, including the *PTCH1* gene, have been strongly associated with a diagnosis of the SHH subtype of medulloblastoma (WHO 2016) [3]. Adult SHH medulloblastomas often demonstrate *SMO* mutations and show responsiveness to inhibitors of the receptor *SMO*, especially if tumors are negative for *MYCN* and *GLI2* amplification (like in this tumor) [4].
- The 1.18 Mb deletion encompassing *NF1* likely represents a constitutional abnormality, based on this individual's known history of Neurofibromatosis 1 and the presence of the deletion in all the cells in the sample. Germline loss-of-function mutations and deletions of *NF1* predispose patients to the development of CNS tumors including medulloblastomas [5,6].
- Gain of chromosome 13 has been observed as a recurrent finding in medulloblastoma but has not been associated with a particular genetic subtype [2].

Interpretation summary:

CN-LOH in 9q detected by CMA is consistent with the SHH subtype of medulloblastoma (WHO 2016). Deletion in 17q11.2 involving *NF1* likely represents a germline abnormality and is consistent with the patient's clinical diagnosis of Neurofibromatosis 1.

References:

1. Ellison DW, Dalton J, Kocak M, et al. Medulloblastoma: clinicopathological correlates of SHH, WNT, and non-SHH/WNT molecular subgroups. *Acta Neuropathologica* 2011;121(3):381-96.
2. Kool M, Korshunov A, Remke M, et al. Molecular subgroups of medulloblastoma: an international meta-analysis of transcriptome, genetic aberrations, and clinical data of WNT, SHH, Group 3, and Group 4 medulloblastomas. *Acta Neuropathologica* 2012;123(4):473-84.
3. Louis DN, Ohgaki H, Wiestler OD, Cavenee WK (2016) World Health Organization Histological Classification of Tumours of the Central Nervous System. International Agency for Research on Cancer, France.
4. Lassaletta A, Ramaswamy V. Medulloblastoma in adults: they're not just big kids. *Neuro Oncol.* 2016;18(7):895-7.
5. Rosenfeld A, Listernick R, Charrow J, Goldman S. Neurofibromatosis type 1 and high-grade tumors of the central nervous system. *Child's Nervous System* 2010;26(5):663-7.
6. Pascual-Castroviejo I, Pascual-Pascual SI, Viaño J, et al. Posterior fossa tumors in children with neurofibromatosis type 1 (NF1). *Child's Nervous System* 2010;26(11):1599-603.

Recommendations:

Testing of a tissue that is not involved in the neoplastic process (peripheral blood) for the detected *NF1* deletion is recommended to determine whether this is a germline or an acquired variant, and to aid in accurate determination of its clinical significance. If the variant is germline, genetic counseling and evaluation of other family members at risk are recommended.

The CN-LOH in 9q may suggest the presence of a *PTCH1* mutation in tumor cells; if clinically indicated, sequencing based testing for *PTCH1* mutations may be considered.

Methodology and disclaimer:

Microarray-based chromosome analysis was performed using the I Scan® System with the Infinium® OExPls CytoConsortium Array BeadChip. This microarray consists of >800,000 genetic markers. The markers provide information on the copy number status of the entire genome and provide single nucleotide polymorphism (SNP) genotyping that allows for detection of mosaicism, uniparental disomy (UPD), loss of heterozygosity (LOH) and identity by descent. Patient hybridization data was compared to a compilation of information obtained from multiple controls including the HapMap set of 270 control individuals. Criteria for designating a reportable aberration include deletions larger than 200 kb with a minimum of 20 consecutive markers disrupted and duplications larger than 500 kb, unless the area is associated with benign copy number variation. Smaller aberrations are reported only if the regions have a likely clinical significance. Stretches of homozygosity are reported when the region is greater than 3 Mb. Genomic linear positions are given relative to NCBI build 37. Results were compared with a public database of known, common copy number variations seen in healthy controls (DGV), DECIPHER (Database of Chromosomal Imbalance and Phenotype in Humans Using Ensembl Resources), and ICCG (The International Collaboration for Clinical Genomics), and common population variants were excluded from the secondary analysis. The lower limit of detection for mosaic or clonal abnormalities is 5-10% depending on the aberration and the probe coverage. Classification and reporting of the detected variants was performed following the ‘*Reference*’ standards and recommendations.

This test was developed and its appropriate performance characteristics determined by the ‘*Laboratory Name*’ of the ‘*Institution*’. It has not been cleared or approved by the U.S. Food and Drug Administration.

Example, Case 4, Template 2:

Osteosarcoma/Complex

Patient name:

Medical record #:

Date of birth:

Lab #:

Indication for the study: H/O osteosarcoma (recurrence)

Type of specimen: FFPE

Date sample collected:

Date sample received:

Report date:

Array Platform: OncoScan FFPE Assay (Affymetrix)

Result and interpretation summary:

Numerous and widespread CNAs, including deletions of the *TP53* and *RB1* loci, are consistent with the diagnosis of osteosarcoma.

CMA results according to GRCh37 (ISCN):

arr(1-22,X,Y)cx

Please see 'Result table' for detailed information about detected abnormalities.

Interpretation:

Chromosomal microarray (CMA) analysis revealed numerous copy number abnormalities (CNAs) affecting almost all the chromosomes.

Tier 1: strong diagnostic, prognostic, and/or therapeutic clinical significance

- A complex profile of CNAs, with gains, losses and regions of loss of heterozygosity involving almost every chromosome, is a characteristic finding in osteosarcoma [1,2].
- The 15 Mb deletion at 17p12p13.3 that spans the *TP53* gene. Loss-of-function mutations and deletions involving *TP53* occur in osteosarcoma in up to 75% of the cases [3,4].
- The 48 Mb deletion at 13q12.12q21.33 that spans the *RB1* gene. *RB1* abnormalities are observed in up to 70% of osteosarcomas [5,6].
- The 17p and 13q deletions detected by CMA may be unmasking mutations in the remaining alleles of the *TP53* and *RB1* tumor suppressor genes.

References:

1. Morrow JJ, Khanna C. Osteosarcoma genetics and epigenetics: Emerging biology and candidate therapies. *Critical Reviews™ in Oncogenesis* 2015;20(3-4).
2. Selvarajah S, Yoshimoto M, Maire G, et al. Identification of cryptic microaberrations in osteosarcoma by high-definition oligonucleotide array comparative genomic hybridization. *Cancer Genet Cytogenet* 2007;179(1):52–61.
3. Fletcher CD, Hogendoorn P, Mertens F, Bridge J. WHO Classification of Tumours of Soft Tissue and Bone. 4th ed. Lyon, France: IARC Press; 2013.
4. Martin JW, Squire JA, Zielenska M. The genetics of osteosarcoma. *Sarcoma* 2012;2012:627254.
5. Belchis DA, Meece CA, Benko FA, et al. Loss of heterozygosity and microsatellite instability at the retinoblastoma locus in osteosarcomas. *Diagn Mol Pathol* 1996;5(3):214–9.

CMA results according to GRCh37:

Tier classification	Chr.	Variant type	Cytogenetic locus	Genomic coordinates (GRCh37)	Size (Mb)	COSMIC census cancer gene(s) within the region
Tier 3	1	Gain	p36.33p21.2	754191_1001261191	100.1	<i>TNFRSF14, PDE4B, SFPQ, EPS15, MPL, MDS2, RPL5, FHL3, JAK1, FUBP1, PLEKHG5, MTOR, TAL1, MUTYH, STIL, ABCA4, CDKN2C, SDHB, PAX7, PRDM16, MYCL1, SPEN, THRAP3, MFN2, PINK1, BCL10, GNB1, RPL22, LCK, JUN, RPL11, ARID1A, CAMTA1</i>
Tier 3	2	Gain	p25.3p24.3	21493_16,137237	16.1	<i>MYCN, RPS7</i>
Tier 3	2	Loss	q12.3q37.3	109388845_243052331	133.6	<i>NUP35, ERCC3, HOXD13, SLC4A10, PMS1, PAX3, SCN9A, LRP1B, ATIC, IKZF2, CASP8, SF3B1, BARD1, TTN, IL1B, ZEB2, DIS3L2, ACSL3, ERBB4, TTL, PAX8, CASP10, COL3A1, CREB1, ACKR3, CHN1, FAP, HOXD11, IDH1, FEV, ACVR1, GLI2, NFE2L2, AGAP1, RANBP2</i>
Tier 3	3	Loss	p22.1p11.1	41267751_90473621	49.2	<i>FHIT, NCKIPSD, MITF, PTPRG, BAP1, PBRM1, SETD2, FOXPI, RASSF1, PRKCD, CDC25A, CTNNB1</i>

Tier 3	3	Loss	q12.3 q22.3	101901464_137685956	35.7	<i>RPN1, BTLA, CNBP, GATA2, CBLB</i>
Tier 3	3	Loss	q22.3q25.31	137708154_155755327	18.0	<i>FOXL2, CHST2, WWTR1, GPR171, GMPS, ATR</i>
Tier 3	3	Loss	q25.31q26.1	155773202_161221705	5.4	<i>MLF1</i>
Tier 3	3	Loss	q26.1q26.32	163898427_176923441	13.0	<i>MECOM, TERC, SI, MYNN, TBLIXR1</i>
Tier 3	3	Loss	q29	194255121_195517124	1.2	<i>MUC4</i>
Tier 3	4	Loss	p16.3q32.1	69403_160690431	160.6	<i>TLR2, IL2, BMPR1B, CHIC2, SMIM20, SLC34A2, AFF1, GABRG1, LPHN3, WHSC1, GARI, RHOH, PHOX2B, FGF2, LEF1, KDR, FAM175A, PDGFRA, KIT, FGFR3, FIP1L1, TET2, FBXW7, RAP1GDS1</i>
Tier 3	4	Loss	q32.1q35.2	160800702_190915650	30.1	<i>PALLD, VEGFC, FAT1, FRG1</i>
Tier 3	6	Loss	p25.3p24.3	204908_7445997	7.2	<i>IRF4, RIPK1</i>
Tier 3	6	Loss	q13q22.31	71661009_121220244	49.5	<i>ROS1, FHL5, CASP8AP2, GOPC, PRDMI, ATG5, FOXO3, EPHA7</i>
Tier 3	6	Gain	q22.31q23.2	121283136_133962467	12.6	<i>STL</i>
Tier 3	6	Loss	q23.2q27	133969150_170131934	36.1	<i>IGF2R, TNFAIP3, MYB, STX11, PLEKHG1, FGFR1OP, EZR, MLLT4, ECT2L, QKI</i>
Tier 3	6	Gain	q27	170149792_170913051	0.76	
Tier 3	7	Loss	p22.3q36.3	41420_159118443	159.0	Whole Chromosome
Tier 3	8	Loss	p23.3p21.2	172416_25045912	24.8	<i>CSMD1, PCM11</i>
Tier 3	8	Loss	p21.2p11.22	25051874_39186857	14.1	<i>WRN, WHSC1L1, FGFR1</i>
Tier 3	8	Loss	q11.1q12.3	46896971_63335905	16.4	<i>TOX, PLAG1, TCEA1, CHCHD7, CHD7, RAB2A</i>
Tier 3	8	Gain	q12.3q12.3	63346633_63963847	0.61	
Tier 3	8	Loss	q12.3q21.11	63977367_75426804	11.4	<i>MYBL1, NCOA2</i>
Tier 3	8	Gain	q21.11q21.13	75448056_81741000	6.2	<i>HEY1</i>
Tier 3	8	Gain	q21.3q22.1	91887024_95282065	3.39	<i>RUNX1T1</i>
Tier 3	8	Gain	q22.1q23.2	96725931_110626130	13.9	<i>COX6C, RIMS2</i>
Tier 3	8	Gain	q23.3q24.12	115705861_120233910	4.5	<i>EXT1, RAD21</i>
Tier 3	8	Gain	q24.13q24.21	125872783_127885910	2.0	
Tier 3	8	Loss	q24.22q24.23	136038122_139835605	3.79	

Tier 3	9	Loss	p24.3 p24.1	204737_8233804	8.0	<i>JAK2, PDCD1LG2, AK3, CD274, KDM4C</i>
Tier 2	9	Loss	p24.1p13.1	8297667_38589146	30.29	<i>PSIP2, NFIB, MLLT3, CDKN2B, PAX5, CDKN2A, ZCCHC7, PTPRD, FANCG</i>
Tier 3	9	Gain	q13q34.11	68170420_130446493	62.27	<i>NTRK2, OMD, NR4A3, XPA, TGFBRI, PTCH1, TAL2, GNAQ, SLC44A1, CNTRL, SYK, FANCC</i>
Tier 3	9	Loss	q34.11q34.3	130802334_139145503	8.3	<i>TSC1, SET, NUP214, FBNP1, RALGDS, BRD3, ABL1</i>
Tier 3	10	Loss	p15.3q26.3	126069_135434303	135.3	Whole Chromosome
Tier 3	11	Loss	q11q25	54795356_134938847	80.1	<i>COLCA2, MEN1, VEGFB, NXF1, KMT2A, PCSK7, BIRC3, MRE11A, PAFAH1B2, MAML2, ZBTB16, ARHGEF12, POLD3, EED, FLI1, RAB30, POU2AF1, NUMA1, MALAT1, SDHD, NPAT, RELA, CLP1, SDHAF2, PICALM, DDX6, ATM, CBL, CCND1, DDX10</i>
Tier 3	12	Loss	p13.33q13.11	189399_48239835	48.0	<i>PTPRO, PIK3C2G, ATF7IP, ARID2, ERC1, CLEC12A, ZNF384, CCND2, KDM5A, KRAS, CLEC12B, ETV6, CDKN1B</i>
Tier 3	12	Loss	q13.11q24.33	48333749_133818115	85.4	<i>HOXC11, SH2B3, PTPN11 -Isoform 1, BTG1, ALDH2, LRIG3, HMGA2, MDM2, BCL7A, PMEL, POLE, ERBB3, CDK4, WIF1, HNF1A, HOXC13, TBK1, NACA, KMT2D, DIP2B, ATF1, DDIT3</i>
Tier 1B	13	Loss	q12.12q21.33	23586808_72425891	48.8	<i>RB1, TNFSF11, DLEU1, LCP1, BRCA2, PDS5B, DLEU2, LHFP, FLT1, MIR16-1, MIR15A, CDX2, ELF1, FLT3, PAN3, SERP2, FOXO1A</i>
Tier 3	13	Gain	q21.33q22.1	72444460_74212656	1.7	<i>DIS3</i>
Tier 3	13	Loss	q22.1q31.2	74221200_89092933	14.8	
Tier 3	13	Gain	q31.2q31.2	89098615_89391172	0.29	
Tier 3	13	Loss	q31.2q33.1	89415869_103296243	13.8	

Tier 3	13	Gain	q33.1q33.2	103504516_106089052	2.5	<i>ERCC5</i>
Tier 3	13	Loss	q33.2q34	106101354_110405663	4.3	
Tier 3	13	Gain	q34	110465026_112308757	1.8	
Tier 3	13	Loss	q34	112316276_113907391	1.59	
Tier 3	14	CN-LOH	q22.3q31.3	55721591_87560170	31.8	<i>GPHN, MAX, TSHR, OTX2, KTN1, RAD51B</i>
Tier 3	15	Loss	q13.1q23	28391421_72265173	43.8	<i>NUTM1, RAB27A, TCF12, SCG5, SPRED1, FLJ27352, BMF, NOP10, BUB1B, HMGN2P46, TGM7, MAP2K1, GREM1, CASC5</i>
Tier 3	16	Loss	p13.3q24.3	83886_90158005	90.0	Whole Chromosome
Tier 1A	17	Loss	p13.3p12	400958_15717546	15.3	<i>MAP2K4, PER1, GAS7, USP6, RABEP1, GPS2, WRAP53, YWHAE, TP53</i>
Tier 3	21	Loss	q11.2q22.3	14621423_48097610	33.47	Whole Chromosome
Tier 3	22	Loss	q11.1q13.2	16054712_42485292	26.4	<i>EWSR1, SMARCB1, VPREB1, IGLL1, NF2, MAPK1, CHEK2, MYH9, MN1, BCR, CRKL, PATZ1, PDGFB, MKL1, SEPT5, EP300, HIC2, HIRA, PNUTL1, IGL, CLTCL1</i>
Tier 3	22	Loss	q13.2q13.33	42636686_51213826	8.5	<i>HDAC10, BRD1</i>
Tier 3	X	Loss	q21.1q21.2	81785485_85266946	3.4	
Tier 3	X	Loss	q21.31q22.1	86637361_99079378	12.4	
Tier 3	Y	Gain	q11.221q11.23	16198904_28799935	12.6	

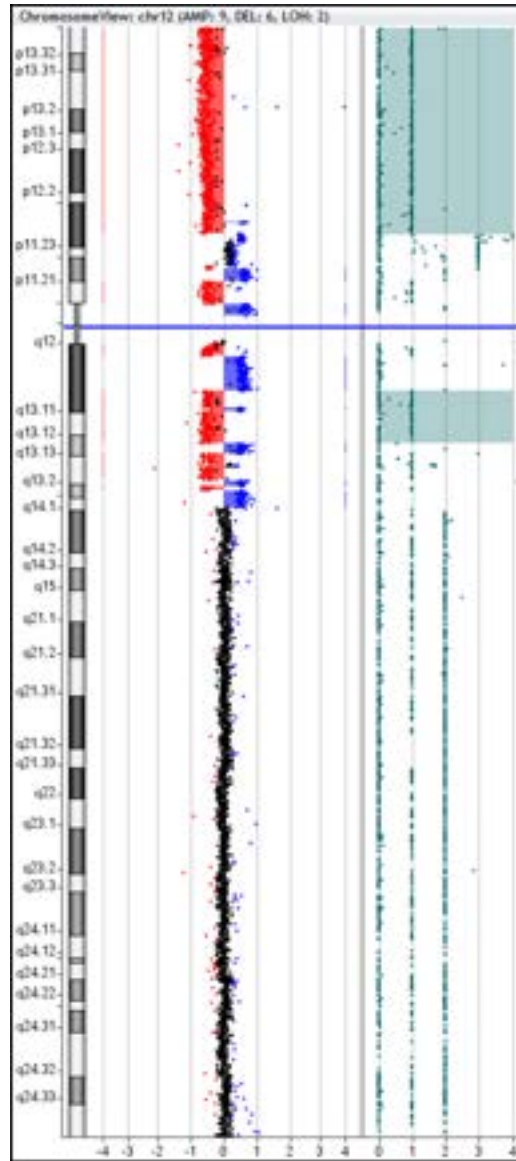
Methodology and disclaimer:

Genomic DNA was extracted from frozen tissue (S17-4489-C), using a commercially available kit (Qiagen Gentra Puregene Tissue Kit). Chromosomal microarray (CMA) analysis of tumor samples was performed using the Affymetrix OncoScan FFPE Assay, which utilizes Molecular Inversion Probe (MIP) technology to obtain accurate genome-wide copy number and loss-of-heterozygosity (LOH) profiles. The assay contains 220,000 probes across the genome and targeted cancer regions, allowing for detection of copy number abnormalities at 50–100kb resolution in ~900 cancer genes and at 300 kb resolution in other chromosomal regions. Patient hybridization results are compared to data derived from over 300 FFPE samples from unaffected tissues. Depending on the quality of the data, copy number abnormalities involving fewer than 25 consecutive probes may not be reliably detected, and may not be reviewed in routine analysis. Detected copy number abnormalities (CNAs) are reported when found to have clear or suspected clinical relevance; copy number changes which correspond to benign variants frequently observed in the general population will not be reported. Long stretches of homozygosity will only be reported if they most likely represent somatic events in tumor cells, or when their size exceeds 5,000kb. Genomic linear positions are given relative to NCBI build GRCh37/hg 19 (February 2009).

The OncoScan FFPE Assay and associated software (Chromosome Analysis Suite) are manufactured by Affymetrix and used to identify copy number gains and losses throughout the genome. This array platform can also reveal extended regions of copy-neutral LOH, which in tumor specimens are frequently associated with the presence of molecular mutations in oncogenes and tumor-suppressor genes mapping within the affected regions. CMA analysis does not detect balanced rearrangements (such as inversions and reciprocal translocations), small deletions and duplications, point mutations, some forms of polyploidy and some mosaic conditions. Based on the results of internal validation studies, abnormalities present in a mosaic state are reliably detected if the mosaicism level (percentage of tumor cells in a specimen) is 23% or higher. While this assay has been extensively validated by the '*Laboratory name*' and other clinical laboratories per ACMGG guidelines, it is not feasible to validate every potential genomic imbalance in the human genome. Furthermore, this technique only identifies the regions of imbalance; it does not provide information regarding the arrangement or mechanisms responsible. For these reasons, it may be recommended that some CMA analysis results be further characterized by fluorescence in situ hybridization (FISH) or standard chromosome analysis.

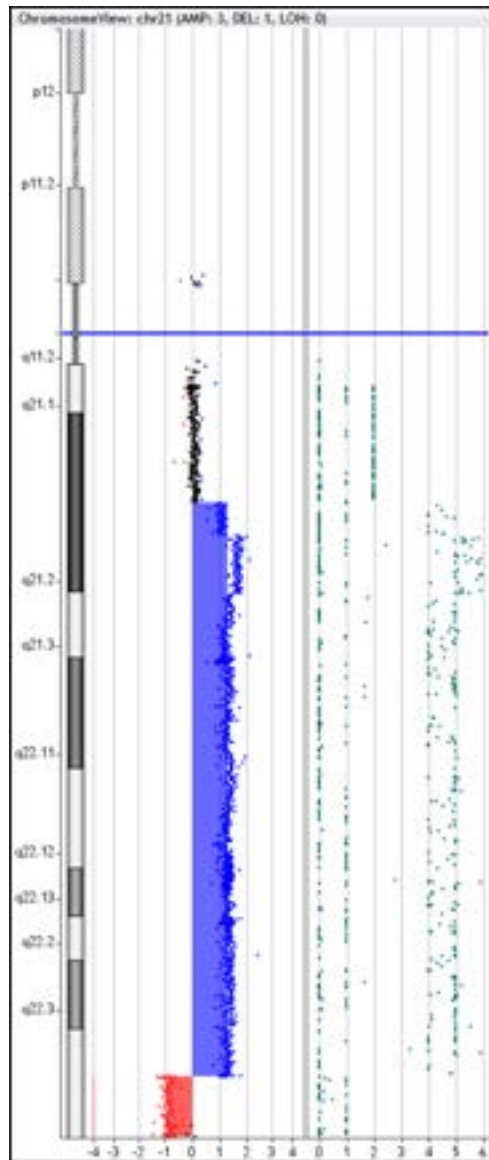
This test was developed and its performance characteristics determined by '*Laboratory Name*' in compliance with CLIA'88. It has not been cleared or approved by the Food and Drug Administration (FDA). The FDA has determined that such clearance or approval is not necessary. The assay is used for clinical purposes and should not be regarded as investigational and/or research. The testing was performed at the '*Laboratory name and address*' which is certified under the Clinical Laboratory Improvement Amendments of 1988 (CLIA '88) for performing high complexity clinical laboratory testing.

Supplementary Figures



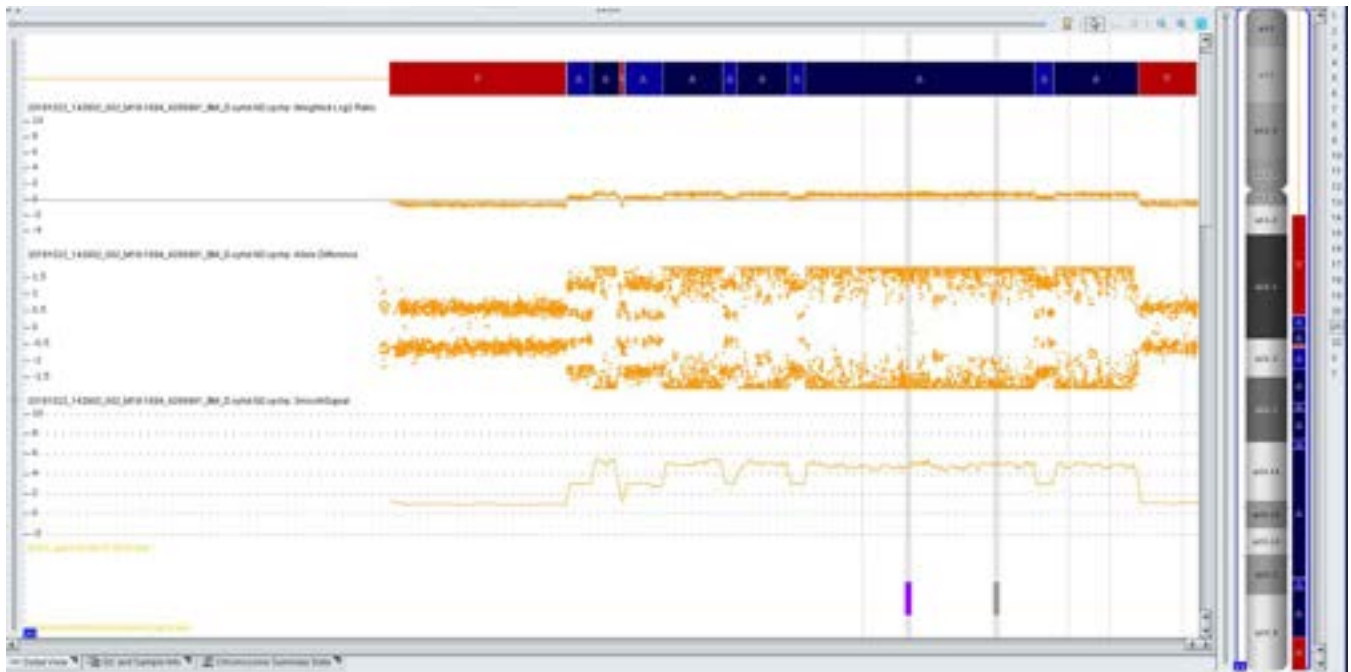
Chromosome 12

Supplementary Figure 1: Adult B-precursor ALL bone marrow sample. CMA plot of chromosome 12 demonstrating 14 alternating CNAs involving the proximal region of the short (p) and long (q) arms of chromosome 12. This pattern of alternating CNAs is suggestive of 'Chromothripsis'. In addition, there is a deletion of the remaining distal portion of 12p. Bone marrow sample was tested using the Agilent 180k aCGH+SNP oligo array, and data analysis was performed using the Agilent CytoGenomics software v4.0

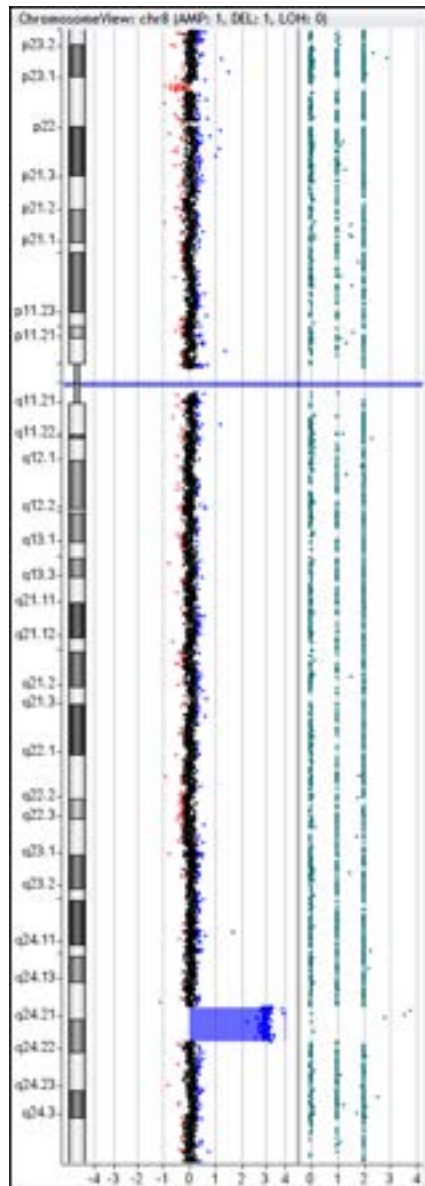


Chromosome 21

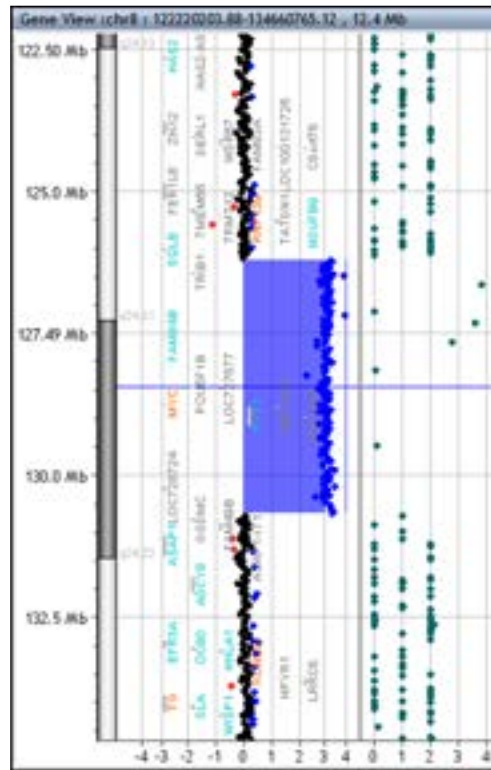
Supplementary Figure 2: Pediatric B-precursor ALL bone marrow sample. CMA plot of chromosome 21 demonstrating 4 complex contiguous CNAs involving the long (q) arm of chromosome 21, consisting of a 2 copy gain at band 21q21.1 (~1.4 Mb), a 4 copy gain at bands 21q21.1q21.2 (~2.48 Mb), a 3 copy gain at bands 21q21.2q22.3 that spans the *RUNX1* gene (~20.96 Mb), and a terminal one copy loss at band 21q22.3 (~2.61 Mb). This pattern of chromosome 21q CNAs represents the 'intrachromosomal amplification of chromosome 21 (iAMP21)' signature (Tier 1A). Bone marrow sample was tested using the Agilent 180k aCGH+SNP oligo array, and data analysis was performed using the Agilent CytoGenomics software v4.0



Supplementary Figure 3: Pediatric B-precursor ALL bone marrow sample. CMA plot of chromosome 21 demonstrating numerous CNAs including a terminal one copy loss and a gain of extra copies of the region encompassing the *RUNX1* gene. This pattern of chromosome 21q CNAs represents the 'intrachromosomal amplification of chromosome 21 (iAMP21)' signature (Tier 1A). The bone marrow sample was tested using the Cytoscan HD Assay from Affymetrix/ThermoFisher, and data analysis was performed using the Chromosome Analysis Suite (ChAS) software

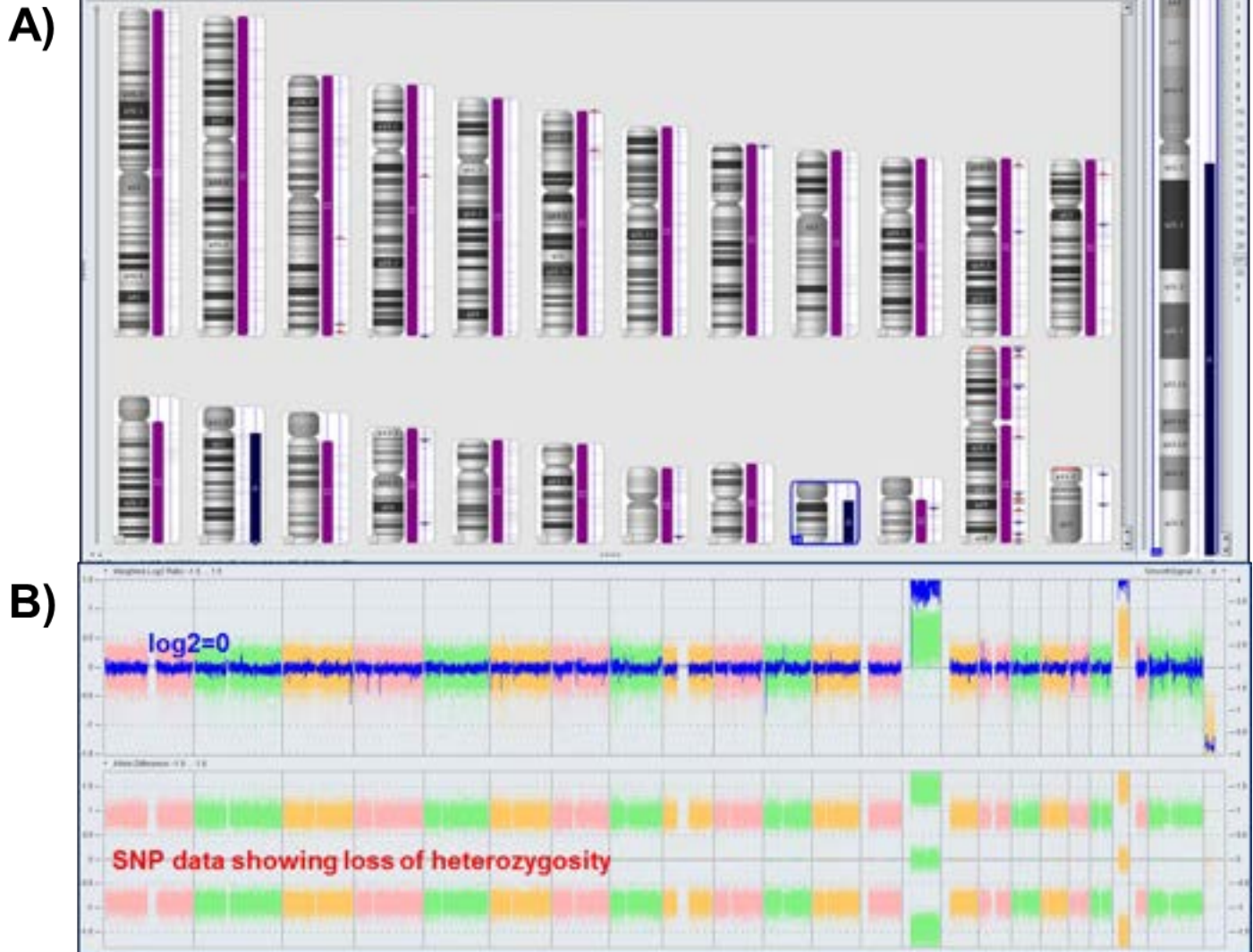


Chromosome 8

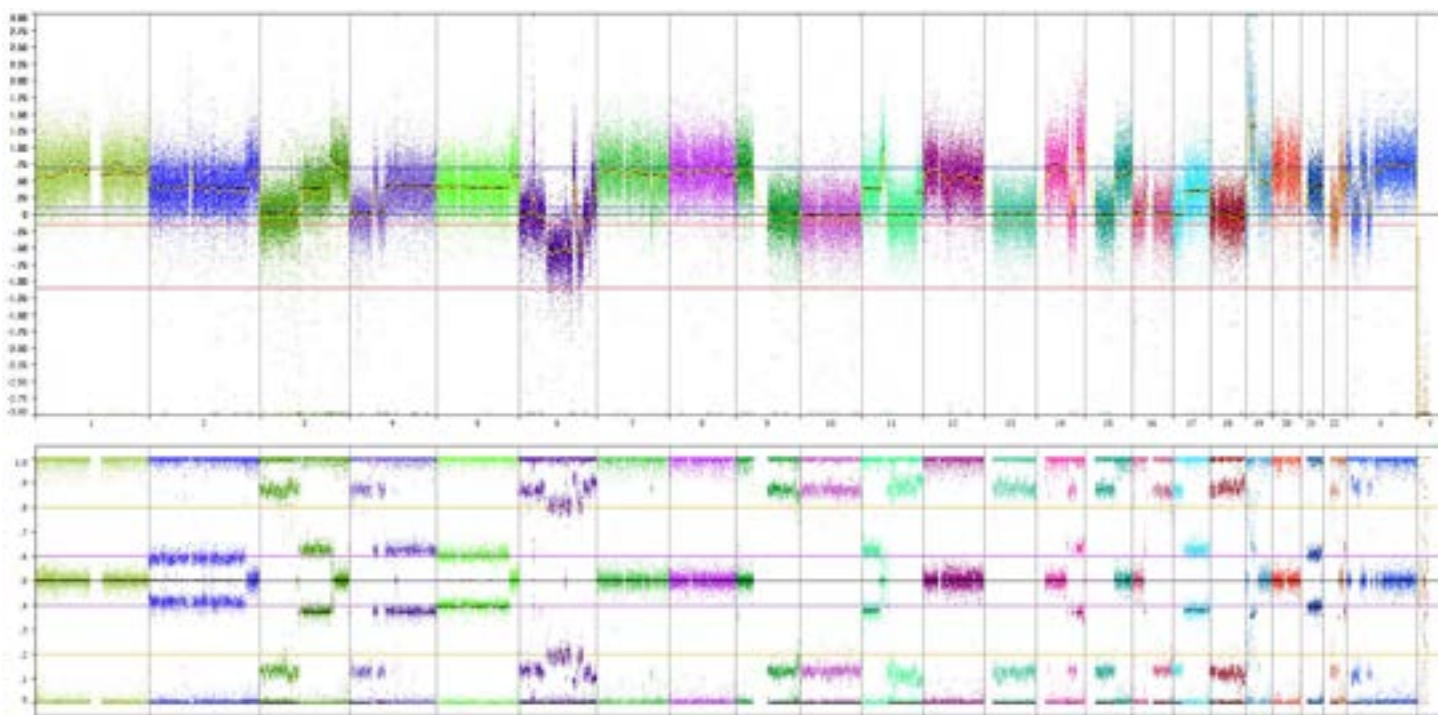


Zoomed in view of the amplified region that spans *MYC*

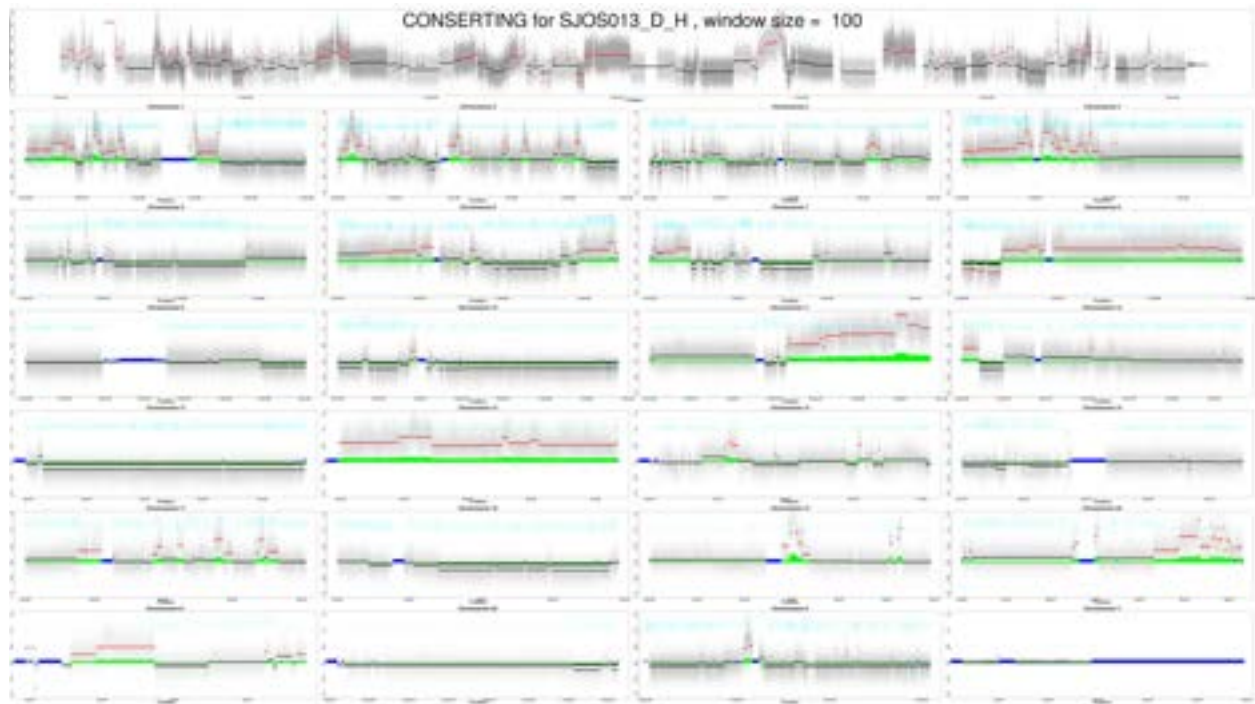
Supplementary Figure 4: Adult AML bone marrow sample. CMA plot of chromosome 8 demonstrating an 8~10 copy number gain (~4.46 Mb) involving the distal region of the long (q) arm of chromosome 8 at bands 8q24.13q24.21 that spans the *MYC* gene (i.e., *MYC* gene amplification) (Tier 1B). This *MYC* amplification is due to the presence of numerous 'double-minutes' in the leukemic cells as shown by G-banded chromosome and FISH analyses. Bone marrow sample was tested using the Agilent 180k aCGH+SNP oligo array, and data analysis was performed using the Agilent CytoGenomics software v4.0



Supplementary Figure 5: Pediatric B-precursor ALL bone marrow sample. CMA plot shows CN-LOH for chromosomes 1-13, 15-20, 22 and X (panel A, purple bars) and gain of two extra copies of chromosomes 14 and 21 (panel A blue bars). This pattern is consistent with near-haploidy (Tier 1A) with doubling of all the chromosomes in the abnormal clone. The figure shows screenshots from the “Chromosome Analysis Suite (ChAS)” software, with the ‘Karyoview’ in panel A and ‘whole genome view’ in panel B. The bone marrow sample was tested using the Cytoscan HD Assay from Affymetrix/ThermoFisher, and data analysis was performed using the Chromosome Analysis Suite (ChAS) software

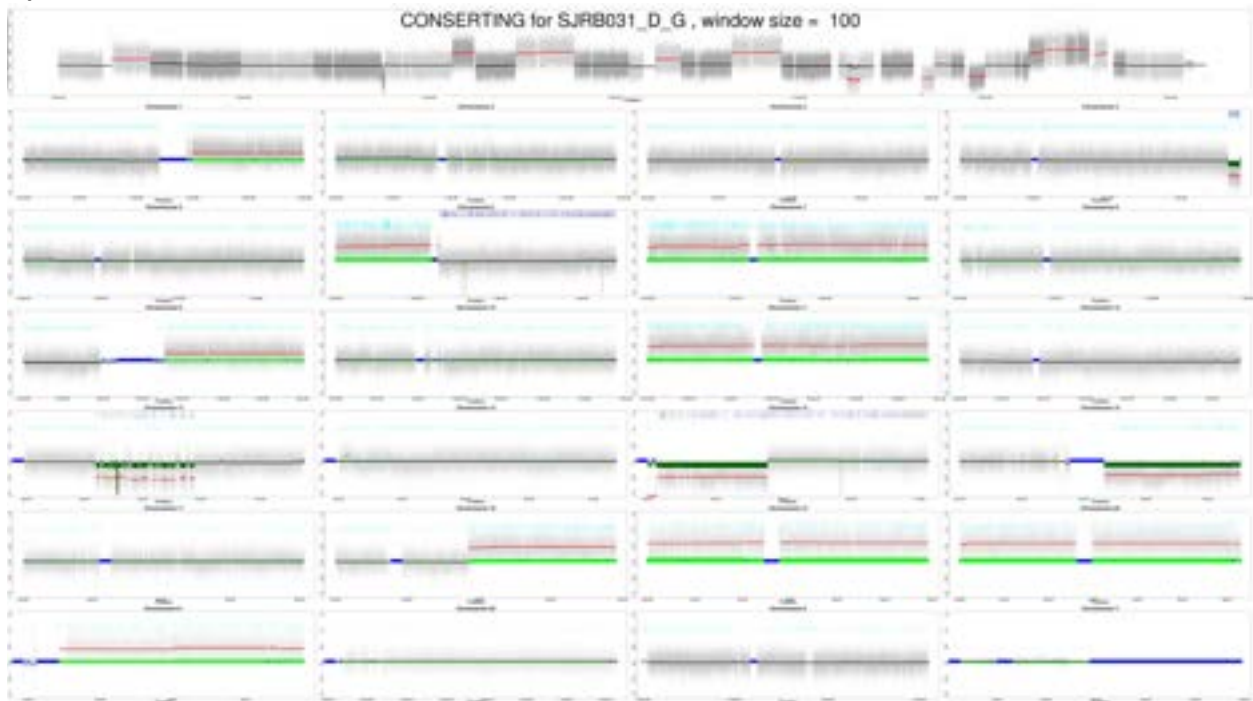


Supplementary Figure 6: Whole genome view showing numerous and widespread CNAs involving almost all the chromosomes. Complex patterns of genome-wide CNAs is characteristic for Osteosarcoma (Tier 1B). Osteosarcoma sample was tested using the OncoScan FFPE Assay from Affymetrix/ThermoFisher, and data analysis was performed using the Nexus 10.0 software from Biodiscovery

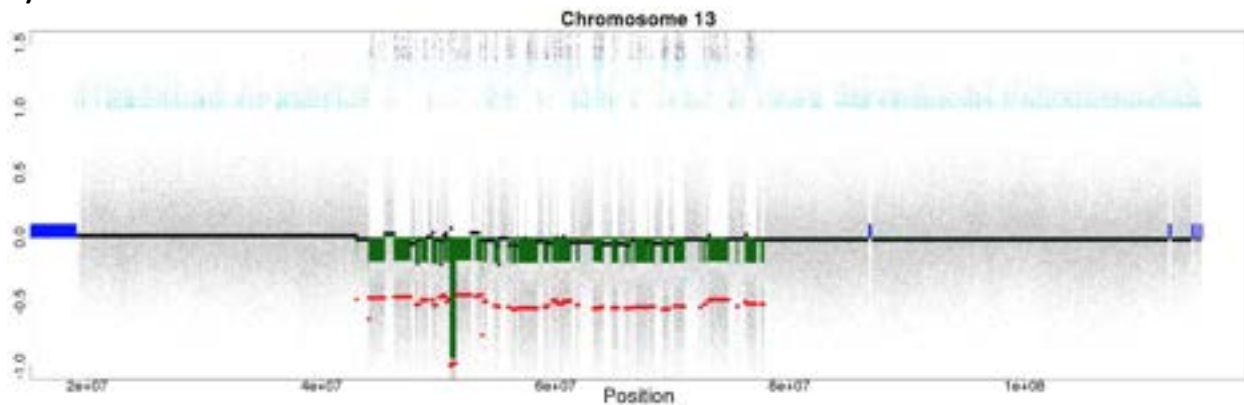


Supplementary Figure 7: Genomic complexity in an Osteosarcoma sample (Rusch et al., Nature Commun 2018). Copy number profile was generated from whole genome sequencing using read counts from 100 bp bins. Normalization and segmentation was performed using the CONSERTING algorithm (Chen et al., Nat Methods 2015). Grey scatterplots show log₂ ratio of normalized read count bins, horizontal lines show copy number segments; those with an absolute log₂ ratio shift of >0.25 are highlighted in red. A complex copy number profile can be appreciated genome wide, is consistent with Osteosarcoma and is given a Tier 1B classification (Smida et al., Int J Cancer 2017)

A)

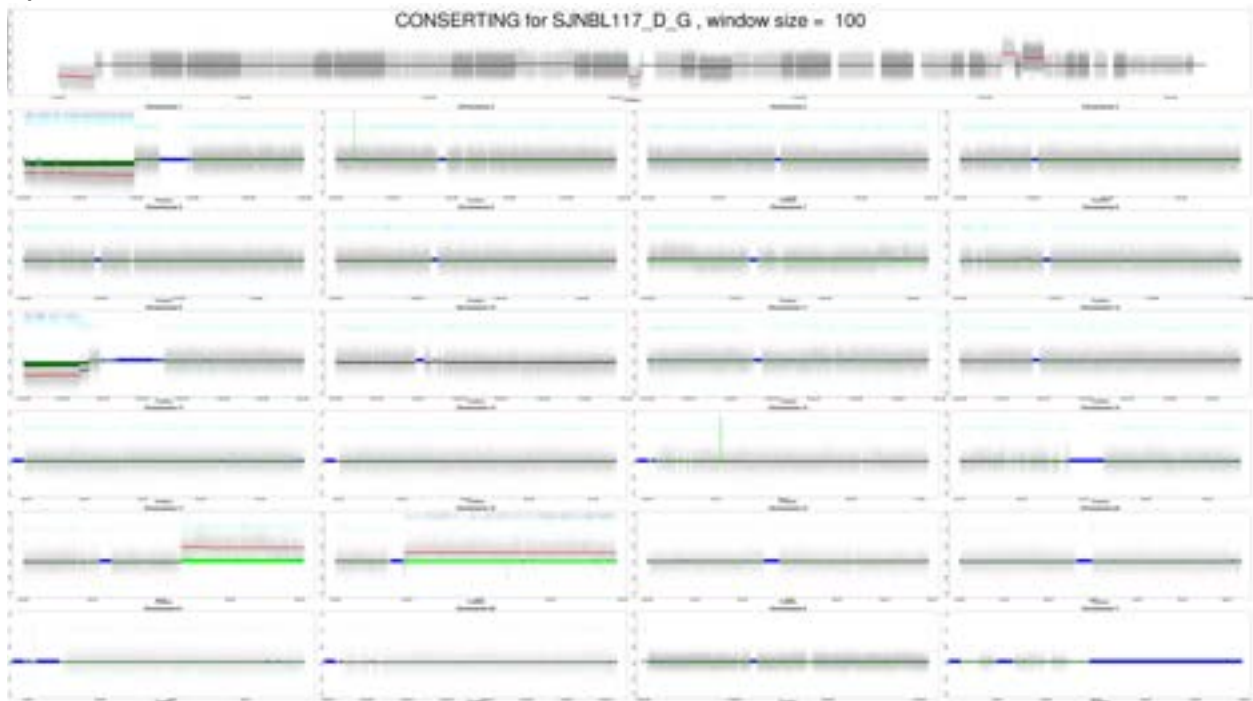


B)

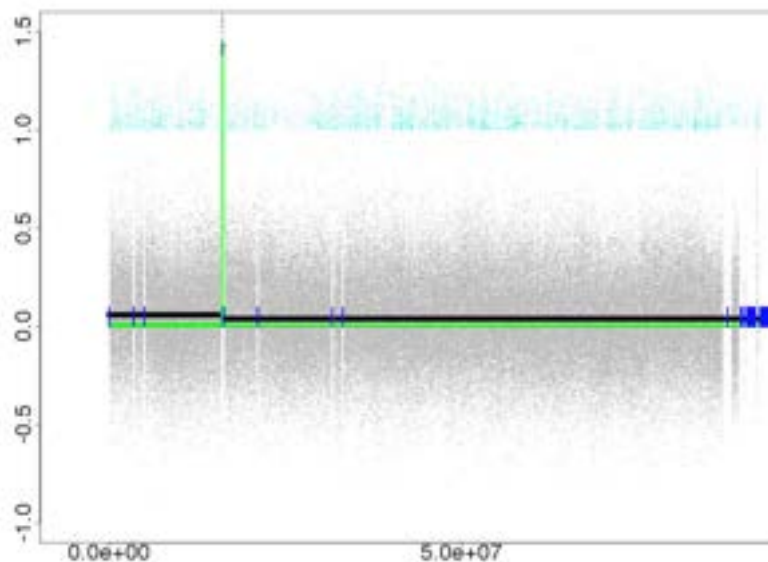


Supplementary Figure 8: A) Genome wide copy number profile of a Retinoblastoma sample. Copy number profile was generated from whole genome sequencing using the CONSERTING algorithm as above. Dark blue scatterplots towards the top of the chromosome plots show regions of loss of heterozygosity; CN-LOH can be observed on regions of 6q and 15q (both Tier 3). Additionally, a gain of 6p is found that may be consistent with an isochromosome of 6p, a recurrent abnormality found in retinoblastoma (Tier 1B). The remaining abnormalities can be placed in tiers 2 and 3 (Kooi et al., PLoS ONE 2016) **B)** Chromothripsis of 13q between approximately 45 and 75 Mb shows a copy number state alternating between two and one copies of each genomic region (log2 ratio of zero and - 0.5). A focal homozygous deletion of *RB1* (48-49 Mb; log2 ratio = -1) is observed within the chromothripsis region (Tier 1A)

A)



B)



Supplementary Figure 9: A) Genome wide copy number profile of a Neuroblastoma sample. Copy number profile was generated from whole genome sequencing using the CONSERTING algorithm as above. Copy number profile shows loss of 1p (Maris et al., JCO 2000) and gain of 17q (Bown et al., N Engl J Med 1999) (both Tier 1B). Other gross chromosomal abnormalities including a region of LOH at elevated copy number on 18q are classified as Tier 3. **B)** A focal amplification on 2p including *MYCN* (Bagatell et al., JCO 2009) is observed (Tier 1A). Loss of 1p and gain of 17q are often observed with the *MYCN* amplification, and have also been described as unfavorable prognostic markers