

### PATIENT

Name: **Patient, Sample**  
 Accession #: 00-00000  
 DOB: 01/01/2016  
 Sex at Birth: Female  
 MRN: 00000  
 Indication: Diagnostic

### TEST INFORMATION

Portal Order #: 000000  
 Family #: 000000  
 Specimen #: N/A  
 Specimen type: Blood EDTA (Purple top)  
 Collection date: N/A  
 Received date: N/A  
 Final Report: 00/00/2021

### MEDICAL PROFESSIONAL

Physician, Sample, MD  
 Sample Facility

### ADDITIONAL RECIPIENTS

Sample Client

## UNCERTAIN: CNV of Uncertain Significance Detected

### Results

Change	Chromosome Region	Classification	Genomic Coordinates	Min Size	Max Size
LOSS	1p36.33	Uncertain Significance	849467 - 1264880	415 kb	1.268 Mb

SNP Array Result: arr[GRCh37] 1p36.33(849467\_1264880)x1

### Interpretation

#### COPY NUMBER VARIATIONS

The results of this test indicate a terminal copy number **LOSS** at **1p36.33**. This copy number loss is a minimum of 415 kb in size and involves 31 genes (see RefSeq genes below). Overlapping copy losses of a larger size and gene content have been reported in the literature in individuals presenting with **1p36 deletion syndrome**. Individuals with 1p36 deletion syndrome most commonly present with intellectual disability, dysmorphic features, hypotonia, short stature, seizures, heart defects, hearing loss, ophthalmologic abnormalities, and behavioral concerns (Rocha, 2016; Shimada, 2015). However, copy losses of a similar size and gene content as the current patient have not been reported in the literature at this time. Additionally, the current patient's copy loss does not involve any of the candidate genes that have been proposed to lead to the features noted in monosomy 1p36 (Jordan, 2015; Zaveri, 2014). Due to the lack of information currently available regarding copy losses of a similar size and gene content, the clinical significance of this alteration is uncertain. Clinical correlation is recommended.

Genetic testing for variants of unknown significance (VUS) in family members may be pursued (at cost) to determine the inheritance. However, it is not expected to clarify the VUS significance or identify at-risk individuals at this time.

#### REGIONS OF HOMOZYGOSITY

No regions of homozygosity were detected.

Genetic counseling is a recommended option for all patients undergoing genetic testing.

Electronically Signed By **Sample Director**, on 00/00/2021 at 0:00:00 PM

All content hereafter is supplemental information to the preceding report.

## References

- Jordan VK, *et al.* (2015) *Appl Clin Genet* **8**:189-200. [PMID:26345236](#)
- Rocha CF, *et al.* (2016) *Genet. Mol. Res.* **15**(1):34-41. [PMID:26910004](#)
- Shimada S, *et al.* (2015) *Brain Dev.* **37**(5):515-26. [PMID:25172301](#)
- Zaveri HP, *et al.* (2014) *PLoS ONE* **9**(1):e85600. [PMID:24454898](#)

## RefSeq Genes

The **1p36.33** region contains 31 gene(s): *LOC100130417*, *SAMD11*, *NOC2L*, *KLHL17*, *PLEKHN1*, *PERM1*, *HES4*, *ISG15*, *AGRN*, *LOC100288175*, *RNF223*, *C1orf159*, *LINC01342*, *MIR200B*, *MIR200A*, *MIR429*, *TLL10*, *TNFRSF18*, *TNFRSF4*, *SDF4*, *B3GALT6*, *FAM132A*, *UBE2J2*, *SCNN1D*, *ACAP3*, *MIR6726*, *SNORD167*, *PUSL1*, *CPSF3L*, *MIR6727*, *CPTP*.

## SNP Array Assay Information

**General Information:** Genomic imbalances are an underlying cause of congenital anomalies, developmental delay, intellectual disability, autism, dysmorphism and numerous genetic syndromes. Routine karyotype analysis can detect some common chromosomal imbalances such as aneuploidies but cannot detect smaller DNA rearrangements. Chromosomal Microarray Analysis (CMA) is a technique that allows for high resolution genome-wide detection of unbalanced structural and numerical chromosomal abnormalities. In addition, SNP probes are used to detect copy-neutral chromosomal changes, such as regions of homozygosity (ROH), including patterns consistent with uniparental disomy (UPD), consanguinity, and/or identity by descent. Importantly, not all copy-neutral chromosomal changes will be detectable by the methodology due to the underlying genetic mechanism. The level of resolution of SNP Array depends primarily on the number and spacing of the oligonucleotide probes on the array.

**Methodology:** Genomic deoxyribonucleic acid (gDNA) is isolated from the patient's specimen using a standardized kit, quantified, labeled and hybridized to an oligonucleotide array with more than 1.9 million copy number probes and nearly 750,000 SNP probes used for genotyping and copy number analysis. This array allows for detection of loss of copy number (deletion), gain of copy number (duplication), and regions of homozygosity.

**Analytical Range:** The Amry CMA: SNP Microarray (Affymetrix® CytoScan™ HD Array, Santa Clara, CA) backbone probe spacing is set at an average of 1.1 kb throughout the entire human genome and an average of 880 basepairs in intragenic regions throughout the genome. A copy loss of size greater than 200kb and copy gain of size greater than 400kb is reported, unless the copy number variant (CNV) is classified as benign or likely benign based on a multifactorial classification scheme or does not include any coding sequence. Smaller copy number change may be reported when it includes a gene(s) with potential clinical relevance. The array detects currently known microdeletion/duplication syndromes, UPD due to isodisomy and most disorders detected by chromosomal analysis and FISH tests, excluding balanced rearrangements and polyploidy. Genomic regions with lower complexity or significant sequence homology may have decreased probe density and/or analytic sensitivity. Copy number alterations restricted to the pseudoautosomal regions of the sex chromosomes are not routinely reported. Copy number neutral ROHs greater than 10 Mb in size are reported. ROH totaling 2.5% or greater of the covered genome will be reported.

**Expected (Normal) Value:** Diagnostic: No significant copy number changes or regions of homozygosity were detected. Family History or Carrier Screen: No significant copy number changes or regions of homozygosity were detected.

**Result Reports:** The CNV location is reported by region and location on the chromosome, and includes the min/max size (Mb) of the span of loss or gain. Minimum size (Min size Mb/kb) represents the distance between the first deviated proximal and last deviated distal probes of the CNV. Maximum size (Max size Mb/kb) represents the distance between the first non-deviated proximal and distal probes flanking the CNV, and genomic coordinates are reported based on the combination of the deviated copy number and SNP probes at the CNV boundaries. Array nomenclature is based on the ISCN (International System for Human Cytogenetic Nomenclature) 2016 guidelines. Analysis is based on genome assembly GRCh 37/hg19. CNVs in the following classifications are always reported and are based on the following definitions:

- **Pathogenic:** CNV with sufficient evidence to classify as pathogenic.
- **Likely Pathogenic:** CNV with strong evidence in favor of pathogenicity.
- **Uncertain Clinical Significance:** CNV with limited and/or conflicting evidence regarding pathogenicity.

**Reclassification Reports:** The SNP array analysis and CNV(s) classification and interpretation are performed based on the information and literature available as of the date the proband SNP array report was issued. Over time, as new information evolves and becomes available, the CNV(s) classification and interpretation may change. Clients should recontact the laboratory with any pertinent changes in clinical phenotype and periodically to determine if a reported alteration has been reclassified. An unsolicited reclassification report may also be issued if the laboratory identifies new information that impacts the overall classification and interpretation of the reported SNP array results.

### Resources:

The following references are used in copy number variation classification when applicable for observed alterations.

1. HGMD® [Internet]: Stenson PD et al. *Genome Med.* 2009;1(1):13 World Wide Web URL: [www.hgmd.cf.ac.uk](http://www.hgmd.cf.ac.uk).
2. Online Mendelian Inheritance in Man, OMIM®. McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University (Baltimore, MD), Copyright© 1966-2017. World Wide Web URL: <http://omim.org>
3. DECIPHER database [Internet]: Bragin E, et al. *Nucleic Acids Res* 2014;42(Database issue):D993-D1000 World Wide Web URL: <http://decipher.sanger.ac.uk>
4. Database of Genomic Variants: MacDonald JR, et al. *Nucleic Acids Res* 2014 Jan;42(Database issue):D986-92. World Wide Web URL: <http://dgv.tcag.ca/dgv/app/home>
5. UCSC Genome Browser: Kent WJ, et al. *Genome Res* 2002 Jun;12(6):996-1006. World Wide Web URL: <https://genome.ucsc.edu/>
6. ClinGen. Rehm H.L, et al. *N Engl J Med* 2015 372(23):2235-42. World Wide Web URL: <https://www.clinicalgenome.org/>

**Disclaimer:** This test was developed, and its performance characteristics were determined by Amry Genetics Corporation. It has not been cleared or approved by the US Food and Drug Administration. The FDA does not require this test to go through premarket FDA review. It should not be regarded as investigational or for research. This test should be interpreted in context with other clinical findings. The Amry Test: SNP Array will only detect net gain or loss of genomic material and regions of homozygosity (ROH) meeting reporting criteria and therefore is not intended to analyze the following types of chromosomal aberrations: balanced translocations, Robertsonian translocations, balanced insertions, inversions, point mutations, low level mosaicism, epigenetic abnormalities, heterodisomic or mosaic UPD or any microdeletions and duplications that are under the resolution of the array or not represented on the array. A negative result from the analysis cannot rule out the possibility that a tested individual carries an aberration in the undetectable group. Although molecular tests are highly accurate, rare diagnostic errors may occur. Possible diagnostic errors include sample mix-up, technical errors, and clerical errors. This report does not represent medical advice. Any questions, suggestions, or concerns regarding interpretation of results should be forwarded to a genetic counselor, medical geneticist, or physician skilled in interpretation of the relevant medical literature. This laboratory is certified under the Clinical Laboratory Improvement Amendments (CLIA) as qualified to perform high complexity clinical laboratory testing.