Non-Syndromic Hearing Loss Panel

Test code: EA0201

Is a 138 gene panel that includes assessment of non-coding variants.

In addition, it also includes the maternally inherited mitochondrial genome. Is ideal for patients with a clinical suspicion of unilateral or bilateral non-syndromic hearing loss.

Is not ideal for individuals suspected to have syndromic hearing loss. Please refer to our Syndromic Hearing Loss Panel.

The inheritance of most types of non-syndromic hearing loss is autosomal recessive. However, also autosomal dominant as well as X-linked forms are present. Genes and mutations causative for sensorineural non-syndromic hearing loss are often population-specific and the clinical utility of this Panel varies consequently. In addition to non-syndromic hearing loss, this Panel have differential diagnostics power to some specific syndromes with hearing loss (for example Usher syndrome, Baraitser-Winter syndrome, branchio-oto-renal (BOR) syndrome), but in general, the Syndromic Hearing Loss Panel is recommended for genetic diagnostic of patients with hearing loss interlinked with symptoms affecting other parts of the body. In addition to protein coding regions, two disease causing intronic variants of HGF gene are targeted in this Panel. This Panel is included in the Comprehensive Hearing Loss and Deafness Panel.

About Non-Syndromic Hearing Loss

Sensorineural hearing loss is a genetically very heterogenous group of phenotypes varying in severity and causes. Non-syndromic sensorineural hearing loss is a partial or total loss of hearing that occurs without other associated clinical findings. Hearing loss can be unilateral or bilateral and it can be stable or progressive. In addition, specific types of non-syndromic hearing loss may show distinctive pattern of hearing loss for high, middle or low tones. Some 60-70% of congenital hereditary hearing impairment have non-syndromic origin, and the prevalence is estimated to be 3-4:10,000 neonates and increases with age. In many populations, mutations in GJB2 are the most prevalent explaining up to 50% of all non-syndromic hearing losses. Non-syndromic hearing loss is genetically heterogenous, as more than >60 autosomal dominant loci and >90 autosomal recessive loci have been identified ([http://www.hereditaryhearingloss.org](http://www.hereditaryhearingloss.org)).

Availability

Results in 3-4 weeks

Gene set description

<table>
<thead>
<tr>
<th>Gene</th>
<th>Associated phenotypes</th>
<th>Inheritance</th>
<th>ClinVar</th>
<th>HGMD</th>
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<tr>
<td>P2RX2</td>
<td>Deafness</td>
<td>AD</td>
<td>2</td>
<td>4</td>
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<tr>
<td>PCDH15</td>
<td>Deafness, Usher syndrome, type 1D</td>
<td>AR/Digenic</td>
<td>113</td>
<td>118</td>
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<td>PDE1C</td>
<td>Hearing loss</td>
<td>AD</td>
<td>2</td>
<td>2</td>
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<tr>
<td>PNPT1*,#</td>
<td>Deafness, Combined oxidative phosphorylation deficiency, 13</td>
<td>AR</td>
<td>11</td>
<td>13</td>
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<tr>
<td>POU3F4</td>
<td>Deafness</td>
<td>XL</td>
<td>25</td>
<td>80</td>
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<tr>
<td>POU4F3</td>
<td>Deafness</td>
<td>AD</td>
<td>9</td>
<td>33</td>
</tr>
<tr>
<td>Gene</td>
<td>Description</td>
<td>Inheritance</td>
<td>Gene 1</td>
<td>Gene 2</td>
</tr>
<tr>
<td>---------</td>
<td>------------------------------------------------------------------------------</td>
<td>-------------</td>
<td>--------</td>
<td>--------</td>
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<tr>
<td>PRPS1*</td>
<td>Phosphoribosylpyrophosphate synthetase I superactivity, Arts syndrome, Charcot-Marie-Tooth disease, X-linked recessive, 5, Deafness, X-linked 1</td>
<td>XL</td>
<td>27</td>
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<tr>
<td>RDX*</td>
<td>Deafness</td>
<td>AR</td>
<td>6</td>
<td>10</td>
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<tr>
<td>S1PR2</td>
<td>Deafness, autosomal recessive 68</td>
<td>AR</td>
<td>2</td>
<td>3</td>
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<tr>
<td>SERPINB6</td>
<td>Deafness</td>
<td>AR</td>
<td>2</td>
<td>3</td>
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<tr>
<td>SIX1</td>
<td>Deafness, Branchiootic syndrome, Branchiootorenal syndrome</td>
<td>AD</td>
<td>11</td>
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<td>SLC17A8</td>
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<td>AD</td>
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<tr>
<td>SLC22A4</td>
<td>Hearing loss</td>
<td>AR</td>
<td>2</td>
<td></td>
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<tr>
<td>SLC26A4</td>
<td>Deafness, Pendred syndrome, Enlarged vestibular aqueduct</td>
<td>AR</td>
<td>181</td>
<td>548</td>
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<td>SLC26A5</td>
<td>Deafness</td>
<td>AR</td>
<td>2</td>
<td>7</td>
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<tr>
<td>SLITRK6</td>
<td>Deafness and myopia</td>
<td>AR</td>
<td>3</td>
<td>5</td>
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<tr>
<td>SMPX</td>
<td>Deafness</td>
<td>XL</td>
<td>8</td>
<td>14</td>
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<td>STRC*,#</td>
<td>Deafness</td>
<td>AR</td>
<td>31</td>
<td>85</td>
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<tr>
<td>SYNE4</td>
<td>Deafness</td>
<td>AR</td>
<td>6</td>
<td>2</td>
</tr>
<tr>
<td>TBC1D24</td>
<td>Deafness, onychodystrophy, osteodystrophy, mental retardation, and seizures (DOORS) syndrome, Deafness, autosomal dominant, 65, Myoclonic epilepsy, infantile, familial, Epileptic encephalopathy, early infantile, 16, Deafness, autosomal recessive 86</td>
<td>AD/AR</td>
<td>43</td>
<td>55</td>
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<tr>
<td>TECTA</td>
<td>Deafness</td>
<td>AD/AR</td>
<td>36</td>
<td>120</td>
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<tr>
<td>TJP2</td>
<td>Cholestasis, progressive familial intrahepatic, Hypercholanemia, familial, Deafness, autosomal dominant 51</td>
<td>AD/AR</td>
<td>25</td>
<td>27</td>
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<tr>
<td>TMC1</td>
<td>Deafness, Deafness, autosomal dominant 36</td>
<td>AD/AR</td>
<td>33</td>
<td>91</td>
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<tr>
<td>TMEM132E</td>
<td>Hearing loss</td>
<td>AR</td>
<td>1</td>
<td></td>
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<tr>
<td>TMIE</td>
<td>Deafness</td>
<td>AR</td>
<td>9</td>
<td>10</td>
</tr>
<tr>
<td>TMPRSS3</td>
<td>Deafness</td>
<td>AR</td>
<td>25</td>
<td>82</td>
</tr>
<tr>
<td>TNC</td>
<td>Deafness</td>
<td>AD</td>
<td>3</td>
<td>6</td>
</tr>
<tr>
<td>TPRN</td>
<td>Deafness</td>
<td>AR</td>
<td>6</td>
<td>12</td>
</tr>
<tr>
<td>TRIOBP</td>
<td>Deafness</td>
<td>AR</td>
<td>22</td>
<td>40</td>
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<tr>
<td>TSPEAR*</td>
<td>Deafness</td>
<td>AR</td>
<td>2</td>
<td>7</td>
</tr>
<tr>
<td>USH1C</td>
<td>Deafness, Usher syndrome, type IC</td>
<td>AR</td>
<td>45</td>
<td>51</td>
</tr>
<tr>
<td>WBP2</td>
<td>Deafness, autosomal recessive 107</td>
<td>AR</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>WFS1</td>
<td>Wolfram syndrome, Deafness, Wolfram-like syndrome, autosomal dominant, Deafness, autosomal dominant 6/14/38, Cataract 41</td>
<td>AD/AR</td>
<td>69</td>
<td>362</td>
</tr>
</tbody>
</table>
*Some regions of the gene are duplicated in the genome. Read more.*

# The gene has suboptimal coverage (means <90% of the gene’s target nucleotides are covered at >20x with mapping quality score (MQ>20) reads), and/or the gene has exons listed under Test limitations section that are not included in the panel as they are not sufficiently covered with high quality sequence reads.

The sensitivity to detect variants may be limited in genes marked with an asterisk (*) or number sign (#)

Gene refers to the HGNC approved gene symbol; Inheritance refers to inheritance patterns such as autosomal dominant (AD), autosomal recessive (AR), mitochondrial (mi), X-linked (XL), X-linked dominant (XLD) and X-linked recessive (XLR); ClinVar refers to the number of variants in the gene classified as pathogenic or likely pathogenic in this database (ClinVar); HGMD refers to the number of variants with possible disease association in the gene listed in Human Gene Mutation Database (HGMD). The list of associated, gene specific phenotypes are generated from CGD or Mitomap databases.

### Non-coding disease causing variants covered by the panel

<table>
<thead>
<tr>
<th>Gene</th>
<th>Genomic location HG19</th>
<th>HGVS</th>
<th>RefSeq</th>
<th>RS-number</th>
</tr>
</thead>
<tbody>
<tr>
<td>DFNA5</td>
<td>Chr7:24746007</td>
<td>c.991-15_991-13delTTC</td>
<td>NM_004403.2</td>
<td>rs727505273</td>
</tr>
<tr>
<td>DIAPH3</td>
<td>Chr13:60738072</td>
<td>c.-172G&gt;A</td>
<td>NM_001042517.1</td>
<td></td>
</tr>
<tr>
<td>DIAPH3</td>
<td>Chr13:60738073</td>
<td>c.-173C&gt;T</td>
<td>NM_001042517.1</td>
<td></td>
</tr>
<tr>
<td>EYA4</td>
<td>Chr6:133833847</td>
<td>c.1282-12T&gt;A</td>
<td>NM_004100.4</td>
<td></td>
</tr>
<tr>
<td>EYA4</td>
<td>Chr6:133833997</td>
<td>c.1341-19T&gt;A</td>
<td>NM_004100.4</td>
<td></td>
</tr>
<tr>
<td>GJB2</td>
<td>Chr13:20763744</td>
<td>c.-22-2A&gt;C</td>
<td>NM_004004.5</td>
<td>rs201895089</td>
</tr>
<tr>
<td>GJB2</td>
<td>Chr13:20766920</td>
<td>c.-23+2T&gt;A</td>
<td>NM_004004.5</td>
<td></td>
</tr>
<tr>
<td>GJB2</td>
<td>Chr13:20766921</td>
<td>c.-23+1G&gt;A</td>
<td>NM_004004.5</td>
<td>rs80338940</td>
</tr>
<tr>
<td>GJB2</td>
<td>Chr13:20766922</td>
<td>c.-23G&gt;T</td>
<td>NM_004004.5</td>
<td>rs786204734</td>
</tr>
<tr>
<td>GJB2</td>
<td>Chr13:20767158</td>
<td>c.-259C&gt;T</td>
<td>NM_004004.5</td>
<td></td>
</tr>
<tr>
<td>GJB2</td>
<td>Chr13:20767159</td>
<td>c.-260C&gt;T</td>
<td>NM_004004.5</td>
<td></td>
</tr>
<tr>
<td>GRHL2</td>
<td>Chr8:102505149</td>
<td>c.20+133delA</td>
<td>NM_024915.3</td>
<td></td>
</tr>
<tr>
<td>GRHL2</td>
<td>Chr8:102505272</td>
<td>c.20+257delT</td>
<td>NM_024915.3</td>
<td></td>
</tr>
<tr>
<td>GRHL2</td>
<td>Chr8:102505561</td>
<td>c.20+544G&gt;T</td>
<td>NM_024915.3</td>
<td></td>
</tr>
<tr>
<td>GRXCR1</td>
<td>Chr4:42965170</td>
<td>c.627+19A&gt;T</td>
<td>NM_001080476.2</td>
<td>rs201824235</td>
</tr>
<tr>
<td>HGF</td>
<td>Chr7:81384504</td>
<td>c.482+1991_482+2000delGATGATGAAAA</td>
<td>NM_000601.4</td>
<td>rs900334407</td>
</tr>
<tr>
<td>HGF</td>
<td>Chr7:81384516</td>
<td>c.482+1986_482+1988delTGA</td>
<td>NM_000601.4</td>
<td></td>
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<tr>
<td>MYO3A</td>
<td>Chr10:26409593</td>
<td>c.1777-12G&gt;A</td>
<td>NM_017433.4</td>
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</tr>
<tr>
<td>MYO6</td>
<td>Chr6:76593963</td>
<td>c.2417-1758T&gt;G</td>
<td>NM_004999.3</td>
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</tr>
<tr>
<td>MYO7A</td>
<td>Chr11:76839534</td>
<td>c.-48A&gt;G</td>
<td>NM_000260.3</td>
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</tr>
<tr>
<td>MYO7A</td>
<td>Chr11:76893448</td>
<td>c.3109-21G&gt;A</td>
<td>NM_000260.3</td>
<td></td>
</tr>
</tbody>
</table>
### Test Strengths

The strengths of this test include:

- CAP accredited laboratory
- CLIA-certified personnel performing clinical testing in a CLIA-certified laboratory
- Powerful sequencing technologies, advanced target enrichment methods and precision bioinformatics pipelines ensure superior analytical performance
- Careful construction of clinically effective and scientifically justified gene panels
- Some of the panels include the whole mitochondrial genome (please see the Panel Content section)
- Our Nucleus online portal providing transparent and easy access to quality and performance data at the patient level
- Our publicly available analytic validation demonstrating complete details of test performance
- ~2,000 non-coding disease causing variants in our clinical grade NGS assay for panels (please see 'Non-coding disease causing variants covered by this panel' in the Panel Content section)
- Our rigorous variant classification scheme
- Our systematic clinical interpretation workflow using proprietary software enabling accurate and traceable processing of NGS data
- Our comprehensive clinical statements

### Test Limitations

The following exons are not included in the panel as they are not sufficiently covered with high quality sequence reads: OTOA (NM_144672:22-27), STRC (NM_153700:1-18). Genes with suboptimal coverage in our assay are marked with number sign (#) and genes with partial, or whole gene, segmental duplications in the human genome are marked with an asterisk (*) if they...
overlap with the UCSC pseudogene regions. Gene is considered to have suboptimal coverage when >90% of the gene’s target nucleotides are not covered at >20x with mapping quality score (MQ>20) reads. The technology may have limited sensitivity to detect variants in genes marked with these symbols (please see the Panel content table above).

**This test does not detect the following:**

- Complex inversions
- Gene conversions
- Balanced translocations
- Some of the panels include the whole mitochondrial genome but not all (please see the Panel Content section)
- Repeat expansion disorders unless specifically mentioned
- Non-coding variants deeper than ±20 base pairs from exon-intron boundary unless otherwise indicated (please see above Panel Content / non-coding variants covered by the panel).

**This test may not reliably detect the following:**

- Low level mosaicism in nuclear genes (variant with a minor allele fraction of 14.6% is detected with 90% probability)
- Stretches of mononucleotide repeats
- Low level heteroplasmia in mtDNA (>90% are detected at 5% level)
- Indels larger than 50bp
- Single exon deletions or duplications
- Variants within pseudogene regions/duplicated segments
- Some disease causing variants present in mtDNA are not detectable from blood, thus post-mitotic tissue such as skeletal muscle may be required for establishing molecular diagnosis.

The sensitivity of this test may be reduced if DNA is extracted by a laboratory other than Blueprint Genetics.

For additional information, please refer to the Test performance section and see our Analytic Validation.

**Test performance**

The Blueprint Genetics non-Syndromic hearing loss panel covers classical genes associated with sensorineural hearing loss, unilateral and bilateral, non-syndromic genetic deafness, Usher syndrome, Baraitser-Winter syndrome and Branchio-oto-renal (BOR) syndrome. The genes on the panel have been carefully selected based on scientific literature, mutation databases and our experience.

Our panels are sliced from our high-quality whole exome sequencing data. Please see our sequencing and detection performance table for different types of alterations at the whole exome level (Table).

Assays have been validated for different starting materials including EDTA-blood, isolated DNA (no FFPE), saliva and dry blood spots (filter card) and all provide high-quality results. The diagnostic yield varies substantially depending on the assay used, referring healthcare professional, hospital and country. Blueprint Genetics’ Plus Analysis (Seq+Del/Dup) maximizes the chance to find a molecular genetic diagnosis for your patient although Sequence Analysis or Del/Dup Analysis may be a cost-effective first line test if your patient’s phenotype is suggestive of a specific mutation type.

The genes on the panel have been carefully selected based on scientific literature, mutation databases and our experience.

Our panels are sectioned from our high-quality, clinical grade NGS assay. Please see our sequencing and detection performance table for details regarding our ability to detect different types of alterations (Table).

<table>
<thead>
<tr>
<th>Type of Alteration</th>
<th>Sensitivity % (TP/(TP+FN))</th>
<th>Specificity %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Single nucleotide variants</td>
<td>99.89% (99,153/99,266)</td>
<td>&gt;99.9999%</td>
</tr>
<tr>
<td>Insertions, deletions and indels by sequence analysis</td>
<td>96.9% (7,563/7,806)</td>
<td>&gt;99.9999%</td>
</tr>
</tbody>
</table>

https://blueprintgenetics.com/
### Performance of Blueprint Genetics Mitochondrial Sequencing Assay.

<table>
<thead>
<tr>
<th></th>
<th>Sensitivity %</th>
<th>Specificity %</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>ANALYTIC VALIDATION</strong> (NA samples; n=4)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Single nucleotide variants</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Heteroplasmic (45-100%)</td>
<td>100.0% (50/50)</td>
<td>100.0%</td>
</tr>
<tr>
<td>Heteroplasmic (35-45%)</td>
<td>100.0% (87/87)</td>
<td>100.0%</td>
</tr>
<tr>
<td>Heteroplasmic (25-35%)</td>
<td>100.0% (73/73)</td>
<td>100.0%</td>
</tr>
<tr>
<td>Heteroplasmic (15-25%)</td>
<td>100.0% (77/77)</td>
<td>100.0%</td>
</tr>
<tr>
<td>Heteroplasmic (10-15%)</td>
<td>100.0% (74/74)</td>
<td>100.0%</td>
</tr>
<tr>
<td>Heteroplasmic (5-10%)</td>
<td>100.0% (3/3)</td>
<td>100.0%</td>
</tr>
<tr>
<td>Heteroplasmic (&lt;5%)</td>
<td>50.0% (2/4)</td>
<td>100.0%</td>
</tr>
<tr>
<td><strong>CLINICAL VALIDATION</strong> (n=76 samples)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>All types</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Single nucleotide variants n=2026 SNVs</td>
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</table>
### Insertions and deletions by sequence analysis n=40 indels

<table>
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<tr>
<th>Heteroplasmic (%)</th>
<th>1-10bp</th>
<th>1-10bp</th>
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<tbody>
<tr>
<td>(45-100%)</td>
<td>100.0% (32/32)</td>
<td>100.0%</td>
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<tr>
<td>(5-45%)</td>
<td>100.0% (3/3)</td>
<td>100.0%</td>
</tr>
<tr>
<td>(&lt;5%)</td>
<td>100.0% (5/5)</td>
<td>99.997%</td>
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</table>

### SIMULATION DATA / (mitomap mutations)

<table>
<thead>
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<th>Insertions, and deletions 1-24 bps by sequence analysis; n=17</th>
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</thead>
<tbody>
<tr>
<td>Homoplasmic (100%) 1-24bp</td>
</tr>
<tr>
<td>(100%) 1-24bp</td>
</tr>
<tr>
<td>(50%) 1-24bp</td>
</tr>
<tr>
<td>(25%) 1-24bp</td>
</tr>
<tr>
<td>(20%) 1-24bp</td>
</tr>
<tr>
<td>(15%) 1-24bp</td>
</tr>
<tr>
<td>(10%) 1-24bp</td>
</tr>
<tr>
<td>(5%) 1-24bp</td>
</tr>
<tr>
<td>Homoplasmic (100%) 500 bp, 1kb, 5 kb</td>
</tr>
<tr>
<td>100.0%</td>
</tr>
<tr>
<td>(50%) 500 bp, 1kb, 5 kb</td>
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<tr>
<td>100.0%</td>
</tr>
<tr>
<td>(30%) 500 bp, 1kb, 5 kb</td>
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<tr>
<td>100.0%</td>
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<tr>
<td>(20%) 500 bp, 1kb, 5 kb</td>
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<tr>
<td>99.7%</td>
</tr>
<tr>
<td>(10%) 500 bp, 1kb, 5 kb</td>
</tr>
<tr>
<td>99.0%</td>
</tr>
</tbody>
</table>

### Copy number variants (separate artificial mutations; n=1500)

<table>
<thead>
<tr>
<th>Homoplasmic (100%) 500 bp, 1kb, 5 kb</th>
</tr>
</thead>
<tbody>
<tr>
<td>100.0%</td>
</tr>
<tr>
<td>Heteroplasmic (50%) 500 bp, 1kb, 5 kb</td>
</tr>
<tr>
<td>100.0%</td>
</tr>
<tr>
<td>Heteroplasmic (30%) 500 bp, 1kb, 5 kb</td>
</tr>
<tr>
<td>100.0%</td>
</tr>
<tr>
<td>Heteroplasmic (20%) 500 bp, 1kb, 5 kb</td>
</tr>
<tr>
<td>99.7%</td>
</tr>
<tr>
<td>Heteroplasmic (10%) 500 bp, 1kb, 5 kb</td>
</tr>
<tr>
<td>99.0%</td>
</tr>
</tbody>
</table>

### The performance presented above reached by following coverage metrics at assay level (n=66)

<table>
<thead>
<tr>
<th>Mean of medians</th>
<th>Median of medians</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean sequencing depth MQ0 (clinical)</td>
<td>18224X</td>
</tr>
<tr>
<td>Nucleotides with &gt;1000x MQ0 sequencing coverage (%) (clinical)</td>
<td>100%</td>
</tr>
</tbody>
</table>
Bioinformatics

The target region for each gene includes coding exons and ±20 base pairs from the exon-intron boundary. In addition, the panel includes non-coding variants if listed above (Non-coding variants covered by the panel). Some regions of the gene(s) may be removed from the panel if specifically mentioned in the “Test limitations” section above. The sequencing data generated in our laboratory is analyzed with our proprietary data analysis and annotation pipeline, integrating state-of-the-art algorithms and industry-standard software solutions. Incorporation of rigorous quality control steps throughout the workflow of the pipeline ensures the consistency, validity and accuracy of results. Our pipeline is streamlined to maximize sensitivity without sacrificing specificity. We have incorporated a number of reference population databases and mutation databases such as, but not limited, to 1000 Genomes Project, gnomAD, ClinVar and HGMD into our clinical interpretation software to make the process effective and efficient. For missense variants, in silico variant prediction tools such as SIFT, PolyPhen, MutationTaster are used to assist with variant classification. Through our online ordering and statement reporting system, Nucleus, the customer has an access to details of the analysis, including patient specific sequencing metrics, a gene level coverage plot and a list of regions with inadequate coverage if present. This reflects our mission to build fully transparent diagnostics where customers have easy access to crucial details of the analysis process.

Clinical interpretation

We provide customers with the most comprehensive clinical report available on the market. Clinical interpretation requires a fundamental understanding of clinical genetics and genetic principles. At Blueprint Genetics, our PhD molecular geneticists, medical geneticists and clinical consultants prepare the clinical statement together by evaluating the identified variants in the context of the phenotypic information provided in the requisition form. Our goal is to provide clinically meaningful statements that are understandable for all medical professionals regardless of whether they have formal training in genetics.

Variant classification is the cornerstone of clinical interpretation and resulting patient management decisions. Our classifications follow the Blueprint Genetics Variant Classification Schemes based on the ACMG guideline 2015. Minor modifications were made to increase reproducibility of the variant classification and improve the clinical validity of the report. Our experience with tens of thousands of clinical cases analyzed at our laboratory allowed us to further develop the industry standard.

The final step in the analysis of sequence variants is confirmation of variants classified as pathogenic or likely pathogenic using bi-directional Sanger sequencing. Variant(s) fulfilling the following criteria are not Sanger confirmed: the variant quality score is above the internal threshold for a true positive call, and visual check-up of the variant at IGV is in-line with the variant call. Reported variants of uncertain significance are confirmed with bi-directional Sanger sequencing only if the quality score is below our internally defined quality score for true positive call. Reported copy number variations with a size <10 exons are confirmed by orthogonal methods such as qPCR if the specific CNV has been seen less than three times at Blueprint Genetics.

Our clinical statement includes tables for sequencing and copy number variants that include basic variant information (genomic coordinates, HGVS nomenclature, zygosity, allele frequencies, in silico predictions, OMIM phenotypes and classification of the variant). In addition, the statement includes detailed descriptions of the variant, gene and phenotype(s) including the role of the specific gene in human disease, the mutation profile, information about the gene’s variation in population cohorts and detailed information about related phenotypes. We also provide links to the references used, congress abstracts and mutation variant databases used to help our customers further evaluate the reported findings if desired. The conclusion summarizes all of the existing information and provides our rationale for the classification of the variant.

Identification of pathogenic or likely pathogenic variants in dominant disorders or their combinations in different alleles in recessive disorders are considered molecular confirmation of the clinical diagnosis. In these cases, family member testing can be used for risk stratification within the family. In the case of variants of uncertain significance (VUS), we do not recommend family member risk stratification based on the VUS result. Furthermore, in the case of VUS, we do not recommend the use of genetic information in patient management or genetic counseling.

Our interpretation team analyzes millions of variants from thousands of individuals with rare diseases. Thus, our database, and our understanding of variants and related phenotypes, is growing by leaps and bounds. Our laboratory is therefore well positioned to re-classify previously reported variants as new information becomes available. If a variant previously reported by

https://blueprintgenetics.com/
Blueprint Genetics

Blueprint Genetics is re-classified, our laboratory will issue a follow-up statement to the original ordering health care provider at no additional cost.

#}

**ICD codes**

Commonly used ICD-10 codes when ordering the Non-Syndromic Hearing Loss Panel

<table>
<thead>
<tr>
<th>ICD-10</th>
<th>Disease</th>
</tr>
</thead>
<tbody>
<tr>
<td>F84.2</td>
<td>Rett syndrome</td>
</tr>
<tr>
<td>H90.5</td>
<td>Sensorineural hearing loss, unilateral and bilateral</td>
</tr>
<tr>
<td>H35.50</td>
<td>Usher syndrome, type IV</td>
</tr>
<tr>
<td>H49.40</td>
<td>Progressive external ophthalmoplegia</td>
</tr>
<tr>
<td>Q87.89</td>
<td>Branchio-oto-renal (BOR) syndrome</td>
</tr>
<tr>
<td>G11.9</td>
<td>Hereditary ataxia</td>
</tr>
<tr>
<td>C94.2</td>
<td>Acute Megakaryoblastic Leukemia</td>
</tr>
<tr>
<td>K59.8</td>
<td>Chronic Intestinal Pseudoobstruction</td>
</tr>
<tr>
<td>T36.5</td>
<td>Adverse effect of aminoglycosides</td>
</tr>
<tr>
<td>G93.41</td>
<td>Metabolic Encephalopathy</td>
</tr>
<tr>
<td>H49.81</td>
<td>Kearns Sayre Syndrome</td>
</tr>
<tr>
<td>E88.42</td>
<td>MERFF Syndrome</td>
</tr>
<tr>
<td>H47.013</td>
<td>Nonarteritic Anterior Ischemic Optic Neuropathy</td>
</tr>
<tr>
<td>G60.2</td>
<td>Neuropathy in association with hereditary ataxia</td>
</tr>
<tr>
<td>G30</td>
<td>Alzheimer's Disease</td>
</tr>
<tr>
<td>G25.5</td>
<td>Chorea</td>
</tr>
<tr>
<td>G40</td>
<td>Epilepsy and recurrent seizures</td>
</tr>
<tr>
<td>I42</td>
<td>Cardiomyopathy</td>
</tr>
<tr>
<td>N26.9</td>
<td>Focal Segmental Glomerulosclerosis</td>
</tr>
<tr>
<td>G31.82</td>
<td>Leigh's Disease</td>
</tr>
<tr>
<td>H47.2</td>
<td>Leber's hereditary optic neuropathy</td>
</tr>
<tr>
<td>G71.3</td>
<td>Mitochondrial Myopathy</td>
</tr>
<tr>
<td>I42.1</td>
<td>Hypertrophic Cardiomyopathy</td>
</tr>
<tr>
<td>E11.9</td>
<td>Non-Insulin Dependent Diabetes Mellitus</td>
</tr>
</tbody>
</table>
Z86.74  Personal history of sudden cardiac arrest
H90.3  Sensorineural Hearing Loss

Accepted sample types

- EDTA blood, min. 1 ml
- Purified DNA, min. 3μg*
- Saliva (Oragene DNA OG-500 kit)

Label the sample tube with your patient’s name, date of birth and the date of sample collection.

Note that we do not accept DNA samples isolated from formalin-fixed paraffin-embedded (FFPE) tissue.

Resources

- Action on Hearing Loss
- American Society for Deaf Children
- British Deaf Association
- Cortical Foundation
- GeneReviews - BOR Syndrome
- GeneReviews - Baraitser-Winter syndrome
- GeneReviews - Deafness and Hereditary Hearing Loss
- GeneReviews - Usher Syndrome, type I
- GeneReviews - Usher Syndrome, type II
- Hearing Link
- Hearing Loss Association of America
- Hereditary Hearing loss
- NORD - BOR Syndrome
- NORD - Usher Syndrome
- National Association of the Deaf US
- The Cain Foundation for BOR syndrome
- Usher Syndrome Coalition