

The Invitae Boosted Exome provides a clear evidence-based analysis of an individual's exome through systematic evaluation of genetic variants informed by the patient's clinical presentation and history. Invitae's medical team has extensive experience performing clinical exome and genome sequencing.

THE INVITAE BOOSTED EXOME INCLUDES:

- **Advanced NGS capture technology** with customized and improved coverage of medically relevant genes
- **Customized capture baits** to enhance the coverage of hard-to-sequence areas of the exome and allow detection of intragenic copy number variants (learn more in the metrics table on the next page)
- **Phenotype selection tool**, an Invitae-developed online interface that supports a personalized analysis so you can collaborate in selecting the genes to analyze
- **Gene coverage data**, provided to ordering clinicians, ensuring full transparency prior to placing an order
- **Rigorous custom-developed bioinformatics** to ensure that clinically important variants are reliably identified

INVITAE'S MEDICAL GENETICS EXPERTS WILL ANALYZE:

- Genes identified by applying a phenotype-to-gene matching tool based on the Human Phenotype Ontology system plus OMIM and other relevant databases
- Genes that were not identified with the phenotype-to-gene matching tool but have protein-truncating or splice site-altering variants
- Genes with variants that, based on trio analysis, appear to be de novo, compound heterozygous in trans, or homozygous with biparental inheritance
- Genes selected by ordering clinicians

All genes that contain rare variants and satisfy the above criteria are rigorously curated for gene-disease relationships to ensure an up-to-date analysis. Invitae does not routinely report variants in candidate genes that lack evidence of association with Mendelian disease.

For more information, please visit www.invitae.com/exome.

INVITAE BOOSTED EXOME METRICS

What do we cover?	What do we evaluate?	What do we report?
Proband <ul style="list-style-type: none"> Overall, > 97% of the exome is covered Average 150x coverage (per base) across all included exons with >99.4% of reportable exons covered at $\geq 20x$ Invitae's high-quality variant calling detects: <ul style="list-style-type: none"> single nucleotide variants insertions/deletions (indels) intragenic copy number variants* 	Proband <ul style="list-style-type: none"> Novel and known heterozygous missense variants rare or absent in population databases (e.g., gnomAD) Hemizygous, presumed compound heterozygous and homozygous variants Variants predicted to cause loss of function All variants above are evaluated post gene-curation 	Proband <ul style="list-style-type: none"> A clinical summary describing relevant findings Detailed information including: <ul style="list-style-type: none"> list of analyzed genes pathogenic and likely pathogenic variants related to the indication for testing, and some variants of uncertain significance that follow an appropriate inheritance mode, and closely match the patient's phenotype description of evidence for variant classification with relevant citations in-depth description of technical coverage medically important incidental findings Optional secondary findings report (based on the latest ACMG recommendations) for all sequenced individuals Additional variants in genes not evaluated by Invitae due to absent or poor relationship to reported phenotype (please contact us for details and access to this information)
Trio <ul style="list-style-type: none"> Exome sequencing of all three samples with joint calling 	Trio <ul style="list-style-type: none"> Everything interpreted in the proband, plus Variants segregating in certain patterns as autosomal recessive (e.g., in trans) or X-linked alleles, plus De novo variants 	Trio <ul style="list-style-type: none"> Inheritance patterns associated with all reported variants

* In contrast to Invitae's gene panel sequencing where single-exon del/dups are detected, the greater variability in depth of coverage across an exome permits reliable detection of del/dups spanning 4 exons or more with high confidence; smaller events are also often detected and will be reported when sufficient resolution exists.

TURNAROUND TIME: 6–8 weeks on average

SPECIMEN TYPES: Blood or saliva

PRICE: Proband \$1,250; Duo/Trio \$2,500, with insurance billing, institutional billing, and patient pre-pay options available. Full billing options available at www.invitae.com/billing.

Questions? Our team is ready to assist you! Please contact us at 800-436-3037 or clientservices@invitae.com.