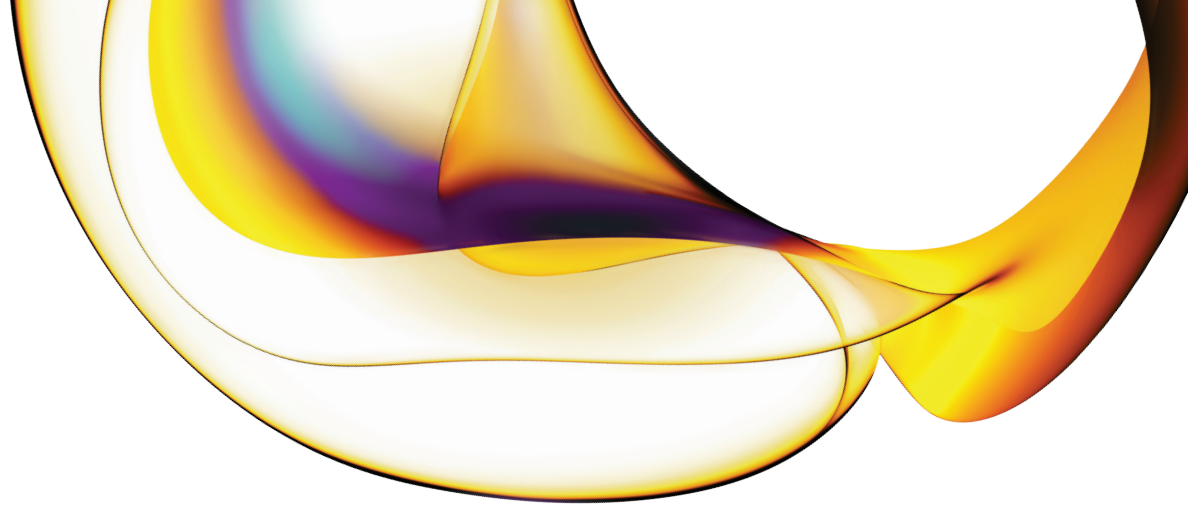

revvity

Short tandem repeat analysis by Whole Genome Sequencing

Historically, detection of repeat expansions has only been possible with polymerase chain reaction-based assays or Southern blots, which are costly and time-consuming methods. We are now able to rule out repeat expansion disorders by identifying and characterizing non-expanded (normal) alleles and to profile almost all genetic variations simultaneously using whole genome sequencing.

Gene	Condition
AFF2	Fragile X syndrome, FRAXE type
AR	Spinal bulbar muscular atrophy
ATN1	Dentatorubral-pallidoluysian atrophy
ATXN1	Spinocerebellar ataxia type 1
ATXN10	Spinocerebellar ataxia type 10
ATXN2	Spinocerebellar ataxia type 2, L-dopa responsive parkinsonism ALS type 13
ATXN3	Spinocerebellar ataxia type 3
ATXN7	Spinocerebellar ataxia type 7
ATXN8OS	Spinocerebellar ataxia type 8
C9orf72	Frontotemporal dementia, ALS type 1, hereditary ataxia
CACNA1A	Spinocerebellar ataxia type 6
CNBP	Myotonic dystrophy type 2
COMP	Pseudo-achondroplasia
CSTB	Unverricht-Lundborg disease
DIP2B	Intellectual developmental disorder, autosomal dominant, FRA12A type
DMPK	Myotonic dystrophy type 1

Gene	Condition
FMR1	Fragile X syndrome, fragile X-associated tremor/ ataxia syndrome
FOXL2	Blepharophimosis, ptosis, epicanthus inversus
FXN	Friedreich ataxia
HOXD13	Syndactyly, type V
NOP56	Spinocerebellar ataxia type 36
PABPN1	Oculopharyngeal muscular dystrophy
PHOX2B	Congenital central hypoventilation syndrome
PPP2R2B	Spinocerebellar ataxia type 12
RUNX2	Cleidocranial dysplasia
SOX3	Panhypopituitarism and intellectual disability with growth hormone deficiency
TBP	Spinocerebellar ataxia type 17
TBX1	Tetralogy of Fallot
TCF4	Fuchs endothelial corneal dystrophy
ZIC2	Holoprosencephaly type 5
ZIC3	VACTERL

The limit of detection of an expanded allele size on NGS based methods is currently not well established. Thus, if an allele is expanded, depending on the size, further confirmatory diagnostic testing may be required to fully characterize the repeat size to provide a definitive diagnosis.

Why choose Revvity Omics?

- State-of-the-art assay design curated by expertly trained, board-certified molecular geneticists based on gene/disease evidence and sequencing complexity
- Latest Technology and proprietary bioinformatics pipelines to integrate the detection of sequencing variants (SNVs), copy number variants (CNVs) and mitochondrial DNA (mtDNA) in a single assay.
- Variant interpretation and reporting performed by certified American Board of Medical Genetics and Genomics (ABMGG) Clinical Geneticists and Genetic Counselors
- Reporting structured to include interpretation and guidance for patients and clinicians according to guidelines of the American College of Medical Genetics and Genomics.
- Revvity Omics laboratories hold many accreditations depending upon lab location, including CLIA, CAP, ISO, JACHO, COLA, NABL, NSAI, and various U.S. state licenses and permits, including New York State.

How to order?

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