variantyx

Genomic Unity® Mitochondrial Analysis

Overview

Mitochondrial disorders are a clinically heterogeneous group of genetic disorders that affect the function of proteins or RNA molecules that reside in the mitochondria, the main energy factory for cells throughout the body.

Genomic Unity® Mitochondrial Analysis is an effective test for identifying the genetic cause underlying clinical symptoms consistent with mitochondrial disorders including: Mitochondrial complex deficiencies I, II, III, IV, and V; CPT deficiencies I and II; Diabetes mellitus and deafness (DAD); LHON; MELAS syndrome; Mitochondrial HMG-CoA synthase deficiency; MERRF and more.

Method

PCR free whole genome sequencing (WGS) is used as the underlying NGS technology. Its consistent read depth across >98% of the genome enables identification of multiple variant types from a single patient sample.

Proprietary algorithms optimized for each variant type are used to perform discrete in-silico analyses of the data which are brought together for collective interpretation, providing a complete genetic picture.

Rigorously trained variant scientists interpret all variant types in the context of the patient's phenotype and generate a unified clinical report.

Included analyses

- ✓ Sequencing analysis of nuclear mitochondrial genes
- ✓ Del/dup analysis of nuclear mitochondrial genes
- ✓ Mitochondrial genome analysis with heteroplasmy (≥5%), including large deletions

Test performance

Highly uniform sequencing depth

- 30X mean mappable coverage
- >98% of nucleotides covered at ≥8x
- >99% of HGMD and ClinVar annotated variants covered at ≥8x

Highly sensitive detection of SNVs and indels up to 50 bp

- 99.7% sensitivity
- 99.6% positive predictive value

Highly sensitive detection of structural variants

- 96% clinical sensitivity
- In most cases, the exact genomic coordinates (the breakpoints) of the structural variant can be determined

Accepted sample types

- Blood - optimally 5ml
- gDNA - 5µg minimum
- Saliva

Turnaround time

6-8 weeks after sample receipt

Reflex to Genomic Unity® Exome Plus Analysis

In the case that Genomic Unity® Mitochondrial Analysis does not identify causal variants, the option is given to reflex up to Genomic Unity® Exome Plus Analysis which looks more broadly for causal variants across all genes.

The reflex option is offered for a nominal patient pay price when not covered by the patient's insurance.

Genes analyzed

AARS2, ABCB6, ABCB7, ACAD8, ACAD9, ACADM, ACADS, ACADSB, ACADVL, ACAT1, ACO2, ACSF3, AFG3L2, AGK, AGL, AIFM1, AK2, ALAS2, ALDH18A1, ALDH2, ALDH3A2, ALDH4A1, ALDH5A1, ALDH6A1, ALDH7A1, AMACR, AMT, APTX, ATP5A1, ATP5E, ATP7B, ATP8B1, ATPAF2, ATXN2, AUH, BAX, BCKDHA, BCKDHB, BCKDK, BCL2, BCS1L, BOLA3, C12ORF65, C19ORF12, CA5A, CARS2, CAVIN1, CHCHD10, CISD2, CLPB, CLPP, COA5, COA6, COA8, COQ2, COQ4, COQ6, COQ8A, COQ8B, COQ9, COX10, COX14, COX15, COX20, COX4I2, COX6A1, COX6B1, COX7B, CPT1A, CPT1C, CPT2, CYC1, CYCS, CYP11A1, CYP27A1, D2HGDH, DARS2, DBT, DDHD1, DECR1, DGMDH, DGUOK, DHODH, DHTKD1, DIABLO, DLAT, DLD, DNA2, DNAJC19, DNM1L, EARS2, ECHS1, ELAC2, ETFA, ETFB, ETFDH, ETHE1, FAH, FARS2, FASTKD2, FBXL4, FDX10, FH, FOXRED1, FXN, G6PC, GAA, GAMT, GATM, GBE1, GCDH, GCSH, GDAP1, GFER, GFM1, GFM2, GLDC, GLRX5, GLUD1, GPI, GPT2, GPX1, GRHPR, GSR, GSS, GTPBP3, GYS1, GYS2, HADHA, HADHB, HARS2, HAX1, HCCS, HK1, HMGCL, HMGCS2, HOGA1, HSD17B10, HSD3B2, HSPA9, HSPD1, HTRA2, IARS2, IBA57, IDH2, IDH3B, ISCA2, ISCU, IVD, KIF1B, L2HGDH, LARS2, LGHA, LIAS, LIPT1, LONP1, LRPPRC, LYRM4, LYRM7, MARS2, MCCC1, MCCC2, MCEE, MECR, MFF, MFN2, MGME1, MICU1, MLYCD, MMAA, MMAB, MMACHC, MMADHC, MMUT, MOCS1, MPC1, MPV17, MRPL12, MRPL3, MRPL44, MRPS16, MRPS22, MRPS7, MSRB3, MTFMT, MTO1, MTPAP, NADK2, NAGS, NARS2, NDUFA1, NDUFA10, NDUFA11, NDUFA12, NDUFA2, NDUFA4, NDUFA9, NDUFAF1, NDUFAF2, NDUFAF3, NDUFAF4, NDUFAF5, NDUFAF6, NDUFAF7, NDUFB11, NDUFB3, NDUFB9, NDUFS1, NDUFS2, NDUFS3, NDUFS4, NDUFS6, NDUFS7, NDUFS8, NDUFV1, NDUFV2, NFA1, NFU1, NNT, NUBPL, OAT, OGDH, OGG1, OPA1, OPA3, OXCT1, PAM16, PANK2, PARS2, PC, PCCA, PCCB, PCK2, PDHA1, PDHB, PDHX, PDK3, PDSS1, PDSS2, PET100, PFKM, PGAM2, PHKA1, PHKA2, PHKB, PHKG2, PHYH, PINK1, PKLR, PNPLA8, PNPT1, POLG, POLG2, PPM1K, PRKAG2, PRODH, PRPS1, PTRH2, PUS1, PYCR1, PYCR2, PYGM, QARS1, RANBP2, RARS2, REEP1, RMND1, RNASEH1, RNASEL, RRM2B, SARDH, SARS2, SCO1, SCO2, SDHA, SDHAF1, SDHAF2, SDHB, SDHC, SDHD, SERAC1, SFXN4, SLC19A2, SLC19A3, SLC22A5, SLC25A1, SLC25A12, SLC25A13, SLC25A15, SLC25A19, SLC25A20, SLC25A22, SLC25A3, SLC25A38, SLC25A4, SLC25A46, SLC37A4, SLC6A8, SOD2, SPG7, STAR, SUCLA2, SUCLG1, SURF1, TACO1, TARS2, TAZ, TIMM44, TIMM8A, TK2, TMEM126A, TMEM70, TMLHE, TPI1, TPK1, TRIT1, TRMU, TRNT1, TSFN, TTC19, TUFM, TWNK, TXNRD2, TYMP, UNG, UQCC2, UQCC3, UQCRB, UQCRC2, UQCRQ, VARS2, WDR81, WFS1, XPNPEP3, YARS2

The *PRODH* gene is not fully covered by this test, therefore pathogenic variants may not be detected in this gene.

Mitochondrial genes analyzed

MT-ATP8, MT-ATP6, MT-CO1, MT-CO2, MT-CO3, MT-CYB, MT-ND1, MT-ND2, MT-ND3, MT-ND4L, MT-ND4, MT-ND5, MT-ND6, MT-RNR2, MT-TA, MT-TR, MT-TN, MT-TD, MT-TC, MT-TE, MT-TQ, MT-TG, MT-TH, MT-TI, MT-TL1, MT-TL2, MT-TK, MT-TM, MT-TF, MT-TP, MT-TS1, MT-TS2, MT-TT, MT-TW, MT-TY, MT-TV, MT-RNR1, MT-RNR2