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Full name:	Hypertrophic cardiomyopathy (75 genes) - IPG
Type of panel:	Custom panel
Version number:	V4
Laboratory:	Centre de Génétique-Institut de Pathologie et de Génétique (IPG)
Created:	04 Jul 2019 - 09:55
Changed:	04 Dec 2023 - 11:06

Related Diseases

- Congenital fiber-type disproportion myopathy
- Fabry disease
- Familial dilated cardiomyopathy with conduction defect due to LMNA mutation
- Familial isolated dilated cardiomyopathy
- Familial isolated restrictive cardiomyopathy
- Fatal congenital hypertrophic cardiomyopathy due to glycogen storage disease
- Glycogen storage disease due to LAMP-2 deficiency
- Left ventricular noncompaction

Related Analytes

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
ACADVL	100.00	1	NM_000018.4
ACTA1	100.00	1	NM_001100.4
ACTC1	100.00	1	NM_005159.5
ACTN2	100.00	1	NM_001103.3
AGL	100.00	1	NM_000642.3

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
ALPK3	100.00	1	NM_020778.5
ANKRD1	100.00	1	NM_014391.2
ATAD3A	100.00	1	NM_001170535.3
ATP5F1E	100.00	1	NM_006886.4
BRAF	100.00	1	NM_001354609.2
CACNA1C	100.00	1	NM_000719.7
CALR3	100.00	1	NM_145046.5
CASQ2	100.00	1	NM_001232.3
CAV3	100.00	1	NM_033337.3
COA5	100.00	1	NM_001008215.3
CRYAB	100.00	1	NM_001289808.2
CSRP3	100.00	1	NM_003476.5
DES	100.00	1	NM_001927.4
FHL1	100.00	1	NM_001159699.2
FHOD3	100.00	1	NM_001281740.3
FLNC	100.00	1	NM_001458.4
FOXRED1	100.00	1	NM_017547.4
FXN	100.00	1	NM_000144.5
GAA	100.00	1	NM_000152.5
GLA	100.00	1	NM_000169.3

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
GLB1	100.00	1	NM_000404.4
GUSB	100.00	1	NM_000181.4
GYG1	100.00	1	NM_004130.4
HRAS	100.00	1	NM_005343.4
JPH2	100.00	1	NM_020433.5
KCNQ1	100.00	1	NM_000218.3
KLF10	100.00	1	NM_005655.4
LAMP2	100.00	1	NM_002294.3
LDB3	100.00	1	NM_001171610.2
LMNA	100.00	1	NM_170707.4
LZTR1	100.00	1	NM_006767.4
MAP2K1	100.00	1	NM_002755.4
MAP2K2	100.00	1	NM_030662.4
MIB1	100.00	1	NM_020774.3
MRPL3	100.00	1	NM_007208.4
MT-TI	100.00	1	
MT-TL1	100.00	1	
MYBPC3	100.00	1	NM_000256.3
MYH6	100.00	1	NM_002471.3
MYH7	100.00	1	NM_000257.4

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
MYL2	100.00	1	NM_000432.4
MYL3	100.00	1	NM_000258.3
MYLK2	100.00	1	NM_033118.4
MYO6	100.00	1	NM_004999.4
MYOM1	100.00	1	NM_003803.4
MYOZ2	100.00	1	NM_016599.5
MYPN	100.00	1	NM_032578.3
NEXN	100.00	1	NM_144573.3
NRAS	100.00	1	NM_002524.5
PDLIM3	100.00	1	NM_014476.6
PLN	100.00	1	NM_002667.5
PRKAG2	100.00	1	NM_016203.4
PTPN11	100.00	1	NM_002834.5
RAF1	100.00	1	NM_001354689.3
RYR2	100.00	1	NM_001035.3
SCO2	100.00	1	NM_005138.3
SLC25A3	100.00	1	NM_002635.4
SLC25A4	100.00	1	NM_001151.4
SOS1	100.00	1	NM_005633.3
TCAP	100.00	1	NM_003673.4

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
TMEM70	100.00	1	NM_017866.6
TNNC1	100.00	1	NM_003280.3
TNNI3	100.00	1	NM_000363.5
TNNT2	100.00	1	NM_001276345.2
TPM1	100.00	1	NM_001018005.2
TRIM63	100.00	1	NM_032588.3
TSFM	100.00	1	NM_005726.6
TTN	100.00	1	NM_001267550.2
TTR	100.00	1	NM_000371.4
VCL	100.00	1	NM_014000.3