

Whole Exome Sequencing

Gene package Intellectual disability, version 10, 21-2-2020



Technical information

DNA was enriched using Agilent SureSelect DNA + SureSelect OneSeq 300kb CNV Backbone + Human All Exon V7 capture and paired-end sequenced on the Illumina platform (outsourced). The aim is to obtain 10 Giga base pairs per exome with a mapped fraction of 0.99. The average coverage of the exome is ~50x. Duplicate and non-unique reads are excluded. Data are demultiplexed with bcl2fastq Conversion Software from Illumina. Reads are mapped to the genome using the BWA-MEM algorithm (reference: <http://bio-bwa.sourceforge.net/>). Variant detection is performed by the Genome Analysis Toolkit HaplotypeCaller (reference: <http://www.broadinstitute.org/gatk/>). The detected variants are filtered and annotated with Cartagenia software and classified with Alamut Visual. It is not excluded that pathogenic mutations are being missed using this technology. At this moment, there is not enough information about the sensitivity of this technique with respect to the detection of deletions and duplications of more than 5 nucleotides and of somatic mosaic mutations (all types of sequence changes).



Dept. Clinical Genetics

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
A2ML1	610627	66	100	100	96
AARS1	601065	89	100	100	96
AASS	605113	100	97	90	90
ABAT	137150	100	100	96	96
ABCC9	601439	100	100	95	95
ABCD1	300371	84	78	75	75
ABCD4	603214	100	100	100	100
ABHD5	604780	100	100	98	98
ACAD8	604773	100	100	100	100
ACAD9	611103	100	100	100	100
ACO2	100850	100	98	94	94
ACOT9	300862	100	90	67	67
ACOX1	609751	100	100	99	99
ACSF3	614245	100	100	100	100
ACSL4	300157	100	98	88	88
ACTB	102630	100	100	100	100
ACTG1	102560	100	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ACVR1	102576	100	100	99	99
ACY1	104620	100	100	100	100
ADA2	607575	100	100	99	99
ADAM22	603709	100	99	94	94
ADAR	146920	100	100	100	100
ADAT3	615302	100	100	100	100
ADGRG1	604110	100	100	100	100
ADK	102750	100	93	80	80
ADNP	611386	100	100	100	100
ADSL	608222	100	100	96	96
AFF2	300806	100	99	92	92
AFF4	604417	100	99	93	93
AFG3L2	604581	99	95	90	90
AGA	613228	100	100	96	96
AGAP2	605476	100	99	96	96
AGO1	606228	100	100	99	99
AGO2	606229	99	96	90	90
AGPAT2	603100	100	100	96	96
AGTR2	300034	100	100	100	100
AHCY	180960	96	96	96	96
AHDC1	615790	100	99	98	98
AHI1	608894	100	98	90	90
AIFM1	300169	100	96	82	82
AIMP1	603605	100	100	96	96
AK1	103000	100	100	100	100
AKT1	164730	100	100	100	100
AKT3	611223	100	99	90	90
ALDH18A1	138250	100	100	98	98
ALDH3A2	609523	100	99	93	93
ALDH4A1	606811	100	100	99	99
ALDH5A1	610045	100	97	91	91
ALG1	605907	91	79	73	73
ALG11	613666	100	100	99	99
ALG12	607144	100	100	100	100
ALG13	300776	100	97	83	83

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ALG2	607905	100	100	99	99
ALG3	608750	100	100	100	100
ALG6	604566	100	100	96	96
ALG8	608103	100	100	94	94
ALG9	606941	100	100	94	94
ALMS1	606844	100	100	99	99
ALX1	601527	100	100	100	100
ALX4	605420	100	100	100	100
AMMECR1	300195	100	88	75	75
AMPD2	102771	100	100	100	100
AMT	238310	100	100	100	100
ANK3	600465	100	100	99	99
ANKEF1	No ID	100	100	97	97
ANKH	605145	100	100	99	99
ANKLE2	616062	100	99	95	95
ANKRD11	611192	100	98	96	96
ANO10	613726	100	99	88	88
ANTXR1	606410	99	97	92	92
AP1S1	603531	100	100	96	96
AP1S2	300629	100	87	62	62
AP3B1	603401	100	98	87	87
AP3B2	602166	100	100	98	98
AP4B1	607245	100	100	100	100
AP4E1	607244	100	100	96	96
AP4M1	602296	100	100	99	99
AP4S1	607243	100	99	87	87
APC2	612034	100	97	95	95
APTX	606350	100	99	92	92
ARFGEF2	605371	100	100	96	96
ARG1	608313	100	100	98	98
ARHGAP31	610911	100	100	99	99
ARHGAP4	300023	100	98	94	94
ARHGEF33	No ID	99	95	90	90
ARHGEF6	300267	100	97	83	83
ARHGEF9	300429	100	99	85	85

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ARID1A	603024	100	99	97	97
ARID1B	614556	100	100	98	98
ARID2	609539	100	100	96	96
ARL13B	608922	100	100	94	94
ARL6	608845	96	95	83	83
ARNT2	606036	100	100	97	97
ARSA	607574	100	100	100	100
ARSL	300180	100	99	92	92
ARX	300382	89	79	68	68
ASAH1	613468	100	100	93	93
ASCL1	100790	100	100	100	100
ASH1L	607999	100	100	97	97
ASL	608310	100	100	99	99
ASNS	108370	100	100	92	92
ASPA	608034	100	99	91	91
ASPM	605481	100	100	97	97
ASS1	603470	100	98	90	90
ASXL1	612990	100	98	98	98
ASXL2	612991	100	99	96	96
ASXL3	615115	99	99	97	97
ATAD3A	612316	98	95	92	92
ATAD3B	612317	98	95	90	90
ATCAY	608179	100	100	96	96
ATIC	601731	100	100	96	96
ATN1	607462	100	100	99	99
ATP1A2	182340	100	100	100	100
ATP1A3	182350	100	100	100	100
ATP2A2	108740	100	100	100	100
ATP6AP2	300556	100	91	64	64
ATP6VOA2	611716	100	100	97	97
ATP6V1B2	606939	100	100	99	99
ATP7A	300011	100	98	84	84
ATP8A2	605870	100	99	94	94
ATPAF2	608918	100	100	100	100
ATR	601215	100	99	92	92

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ATRIP	606605	100	100	97	97
ATRX	300032	100	94	78	78
AUH	600529	100	100	98	98
AUTS2	607270	100	100	98	98
AVPR2	300538	100	100	99	99
B3GALNT2	610194	100	100	97	97
B3GALT6	615291	79	75	72	72
B3GLCT	610308	100	99	85	85
B4GALNT1	601873	100	100	100	100
B4GALT1	137060	100	100	100	100
B4GALT7	604327	100	100	98	98
B4GAT1	605517	100	100	100	100
BBS1	209901	100	100	100	100
BBS10	610148	100	100	100	100
BBS12	610683	100	100	99	99
BBS2	606151	100	100	97	97
BBS4	600374	100	100	95	95
BBS5	603650	100	98	89	89
BBS7	607590	100	99	95	95
BBS9	607968	96	95	90	90
BCAP31	300398	100	100	97	97
BCKDHA	608348	100	100	100	100
BCKDHB	248611	100	99	94	94
BCL11A	606557	100	100	99	99
BCL11B	606558	100	97	92	92
BCOR	300485	100	99	94	94
BCORL1	300688	100	100	98	98
BCS1L	603647	100	100	100	100
BLM	604610	100	100	96	96
BRAF	164757	100	100	94	94
BRAT1	614506	100	100	100	100
BRF1	604902	100	100	100	100
BRPF1	602410	100	100	100	100
BRWD3	300553	100	95	81	81
BSCL2	606158	100	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
BTD	609019	100	100	100	100
BUB1B	602860	100	99	94	94
c12orf4	616082	100	100	95	95
C12orf57	615140	100	100	100	100
C12orf65	613541	100	100	100	100
C1orf167	No ID	100	97	94	94
C2CD3	615944	100	100	99	99
CA2	611492	100	100	100	100
CA5A	114761	100	100	100	100
CA8	114815	100	100	94	94
CACNA1A	601011	100	98	93	93
CACNA1C	114205	100	100	99	99
CACNA2D1	114204	100	99	91	91
CACNG2	602911	100	100	99	99
CAD	114010	100	100	100	100
CAMK2A	114078	100	99	95	95
CAMK2B	607707	100	100	95	95
CAMTA1	611501	100	99	97	97
CAPN10	605286	100	100	100	100
CASK	300172	100	96	80	80
CBL	165360	100	100	100	100
CBS	613381	100	100	100	100
CC2D1A	610055	100	100	100	100
CC2D2A	612013	100	100	95	95
CCBE1	612753	100	99	95	95
CCDC13	No ID	100	100	100	100
CCDC14	617147	100	100	96	96
CCDC174	616735	100	97	84	84
CCDC22	300859	100	94	92	92
CCDC78	614666	100	100	100	100
CCDC88C	611204	100	100	97	97
CCND2	123833	100	100	99	99
CDC5L	602868	100	99	90	90
CDH15	114019	100	100	100	100
CDK16	311550	100	100	97	97

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
CDK5	123831	100	100	100	100
CDK5RAP2	608201	100	99	94	94
CDK6	603368	100	100	96	96
CDKL5	300203	100	97	87	87
CDKN1C	600856	90	83	76	76
CDON	608707	100	100	99	99
CENPJ	609279	100	100	98	98
CEP104	616690	100	98	93	93
CEP135	611423	100	99	91	91
CEP152	613529	100	98	93	93
CEP290	610142	100	98	89	89
CEP41	610523	100	100	94	94
CEP63	614724	100	99	92	92
CEP89	615470	100	98	91	91
CERT1	604677	100	96	85	85
CHAMP1	616327	100	100	100	100
CHD2	602119	100	100	96	96
CHD3	602120	98	96	91	91
CHD4	603277	100	100	98	98
CHD7	608892	100	100	97	97
CHD8	610528	100	100	98	98
CHKB	612395	100	100	100	100
CHMP1A	164010	100	100	100	100
CHRNA4	118504	100	100	96	96
CIC	612082	100	100	99	99
CIT	605629	100	100	97	97
CKAP2L	616174	100	100	100	100
CLCN4	302910	100	100	98	98
CLCNKB	602023	100	100	100	100
CLIC2	300138	100	90	69	69
CLIP1	179838	100	99	93	93
CLN3	607042	100	100	100	100
CLN5	608102	100	100	100	100
CLN6	606725	100	100	99	99
CLN8	607837	100	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
CLP1	608757	100	100	100	100
CLPB	616254	100	100	100	100
CLTC	118955	100	98	94	94
CNKS2	300724	100	97	87	87
CNNM2	607803	100	100	99	99
CNOT3	604910	100	100	99	99
CNTNAP2	604569	100	100	99	99
COASY	609855	100	100	100	100
COG1	606973	100	100	98	98
COG4	606976	100	100	99	99
COG5	606821	100	99	91	91
COG6	606977	100	99	90	90
COG7	606978	100	100	98	98
COG8	606979	100	100	100	100
COL11A1	120280	100	99	93	93
COL12A1	120320	100	100	96	96
COL18A1	120328	100	100	97	97
COL4A1	120130	100	100	97	97
COL4A2	120090	100	100	99	99
COLEC11	612502	100	100	100	100
COQ2	609825	100	100	94	94
COQ4	612898	100	100	100	100
COQ8A	606980	100	100	100	100
COQ9	612837	100	100	100	100
COX10	602125	100	100	99	99
COX15	603646	100	98	92	92
COX6B1	124089	100	100	100	100
CPLANE1	614571	100	99	95	95
CPS1	608307	100	100	96	96
CRADD	603454	100	100	100	100
CRB2	609720	100	100	100	100
CRBN	609262	100	99	91	91
CREBBP	600140	100	99	94	94
CRLF1	604237	96	91	89	89
CRPPA	614631	100	99	93	93

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
CSNK2A1	115440	100	95	86	86
CSPP1	611654	100	100	97	97
CSTB	601145	100	100	100	100
CTBP1	602618	95	85	82	82
CTC1	613129	100	100	100	100
CTCF	604167	100	100	100	100
CTDP1	604927	98	89	87	87
CTNNB1	116806	100	100	97	97
CTNND1	601045	100	100	96	96
CTNND2	604275	97	94	90	90
CTSA	613111	100	100	100	100
CTSD	116840	100	100	100	100
CTTNBP2	609772	100	100	97	97
CUBN	602997	100	100	96	96
CUL3	603136	100	97	88	88
CUL4B	300304	100	96	82	82
CWF19L1	616120	100	100	92	92
CXorf56	301012	98	92	77	77
CYB5R3	613213	100	100	100	100
CYP27A1	606530	100	100	100	100
CYP2U1	610670	100	100	96	96
D2HGDH	609186	100	100	100	100
DAB1	603448	100	100	97	97
DAG1	128239	100	100	100	100
DARS2	610956	100	100	97	97
DBT	248610	100	100	99	99
DCAF17	612515	100	100	94	94
DCC	120470	100	100	98	98
DCHS1	603057	100	100	100	100
DCPS	610534	100	100	100	100
DCX	300121	100	98	92	92
DDC	107930	100	99	92	92
DDHD2	615003	100	100	97	97
DDX11	601150	100	100	100	100
DDX3X	300160	100	100	98	98

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
DEAF1	602635	100	97	90	90
DENND5A	617278	100	99	94	94
DEPDC5	614191	100	100	97	97
DHCR24	606418	100	100	100	100
DHCR7	602858	100	100	100	100
DHFR	126060	100	100	98	98
DHTKD1	614984	100	100	98	98
DIAPH1	602121	100	99	93	93
DIP2B	611379	100	100	97	97
DKC1	300126	100	98	89	89
DLG3	300189	100	97	88	88
DLG4	602887	100	100	100	100
DMD	300377	100	96	81	81
DMPK	605377	100	100	99	99
DNAJC12	606060	100	95	88	88
DNAJC19	608977	100	100	96	96
DNM1	602377	100	100	95	95
DNMT3A	602769	100	100	99	99
DNMT3B	602900	100	100	99	99
DOCK6	614194	100	98	96	96
DOCK7	615730	100	99	93	93
DOCK8	611432	100	99	94	94
DOLK	610746	100	100	100	100
DONSON	611428	100	91	75	75
DPAGT1	191350	100	100	100	100
DPF2	601671	100	99	94	94
DPH1	603527	100	100	100	100
DPM1	603503	94	89	85	85
DPP6	126141	100	97	90	90
DPYD	612779	100	99	95	95
DPYS	613326	100	100	98	98
DST	113810	100	99	95	95
DYM	607461	100	98	88	88
DYNC1H1	600112	100	100	99	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
DYRK1A	600855	100	100	98	98
EBP	300205	100	100	100	100
EDC3	609842	100	100	100	100
EDNRB	131244	100	100	100	100
EDRF1	No ID	100	99	95	95
EEF1A2	602959	100	100	100	100
EFCAB1	No ID	100	100	94	94
EFTUD2	603892	100	100	99	99
EHMT1	607001	99	99	99	99
EIF2AK3	604032	100	99	94	94
EIF4A3	608546	100	100	97	97
EIF4G1	600495	100	100	100	100
ELAC2	605367	100	100	98	98
ELOVL4	605512	100	100	98	98
ELP2	616054	100	100	99	99
EMC1	616846	100	100	99	99
EMG1	611531	100	100	100	100
EML1	602033	100	99	94	94
EMX2	600035	100	100	100	100
ENTPD1	601752	100	100	96	96
EOMES	604615	100	100	100	100
EP300	602700	100	100	97	97
EPB41L1	602879	100	100	99	99
EPG5	615068	100	100	97	97
ERCC1	126380	100	100	94	94
ERCC2	126340	100	99	98	98
ERCC3	133510	100	100	99	99
ERCC5	133530	100	100	98	98
ERCC6	609413	100	100	97	97
ERCC8	609412	100	99	91	91
ERLIN2	611605	100	100	95	95
ERMARD	615532	100	100	96	96
ESCO2	609353	100	100	95	95
ETFB	130410	100	100	100	100
ETHE1	608451	100	100	98	98

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
EXOSC2	602238	100	100	97	97
EXOSC3	606489	100	100	96	96
EZH2	601573	100	100	97	97
FA2H	611026	100	99	91	91
FAM126A	610531	100	100	98	98
FAR1	616107	100	100	96	96
FAT2	604269	100	100	99	99
FAT4	612411	100	100	99	99
FBN1	134797	100	100	100	100
FBN2	612570	100	100	97	97
FBXL4	605654	100	100	98	98
FBXO11	607871	100	96	85	85
FBXO31	609102	100	99	96	96
FGD1	300546	100	98	95	95
FGF12	601513	100	97	85	85
FGF14	601515	100	100	98	98
FGFR1	136350	100	100	98	98
FGFR2	176943	100	100	95	95
FGFR3	134934	100	100	98	98
FGL1	605776	100	99	90	90
FH	136850	99	94	87	87
FIBP	608296	100	100	100	100
FIG4	609390	100	99	94	94
FIGN	605295	100	100	100	100
FKRP	606596	100	100	100	100
FKTN	607440	100	100	100	100
FLNA	300017	100	100	100	100
FLVCR1	609144	100	100	96	96
FMN2	606373	100	94	89	89
FMR1	309550	100	96	76	76
FOXG1	164874	97	90	84	84
FOXP1	605515	100	100	98	98
FOXP2	605317	100	100	98	98
FRAS1	607830	100	100	97	97
FREM2	608945	100	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
FRMD4A	616305	100	97	90	90
FRMPD4	300838	100	99	95	95
FRRS1L	604574	85	79	70	70
FTCD	606806	99	96	93	93
FTO	610966	100	100	99	99
FTSJ1	300499	100	100	93	93
FUCA1	612280	100	100	98	98
GABRA1	137160	100	100	100	100
GABRB1	137190	100	100	97	97
GABRB3	137192	100	100	98	98
GAD1	605363	100	100	99	99
GALE	606953	100	100	100	100
GALT	606999	100	100	100	100
GAMT	601240	100	99	95	95
GAS6	600441	100	96	93	93
GATAD2B	614998	100	100	99	99
GATM	602360	100	100	98	98
GCDH	608801	100	100	100	100
GCH1	600225	100	100	93	93
GCSH	238330	100	89	62	62
GDI1	300104	100	100	100	100
GFAP	137780	100	100	99	99
GFM2	606544	100	99	92	92
GJA1	121014	100	100	100	100
GJB1	304040	100	100	99	99
GJC2	608803	96	86	76	76
GK	300474	99	88	66	66
GLB1	611458	100	100	98	98
GLDC	238300	100	98	91	91
GLI2	165230	100	100	99	99
GLI3	165240	100	100	99	99
GLYCK	610516	100	100	100	100
GM2A	613109	100	100	100	100
GMPPA	615495	100	100	100	100
GMPPB	615320	100	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
GNAO1	139311	100	100	99	99
GNAQ	600998	100	100	100	100
GNAS	139320	100	100	97	97
GNB1	139380	100	100	96	96
GNB5	604447	100	99	94	94
GNPAT	602744	100	100	96	96
GNPTAB	607840	100	99	95	95
GNS	607664	100	100	98	98
GPC3	300037	100	99	91	91
GPC4	300168	100	98	90	90
GPHN	603930	100	100	98	98
GPT2	138210	100	96	85	85
GRIA3	305915	100	98	88	88
GRID2	602368	100	100	99	99
GRIK2	138244	100	100	98	98
GRIK5	600283	100	100	99	99
GRIN1	138249	100	100	99	99
GRIN2A	138253	100	100	100	100
GRIN2B	138252	100	100	99	99
GRIN3B	606651	91	86	80	80
GRIP1	604597	100	100	99	99
GRM1	604473	100	100	99	99
GSE1	616886	100	100	100	100
GSS	601002	100	100	99	99
GTF2H5	608780	100	100	100	100
GTPBP3	608536	100	100	100	100
GUCY2F	300041	100	96	84	84
GUSB	611499	100	100	97	97
H19	103280	No coverage data			
HACE1	610876	100	100	94	94
HAX1	605998	100	100	99	99
HCCS	300056	100	99	84	84
HCFC1	300019	100	97	92	92
HCN1	602780	100	100	98	98
HDAC4	605314	100	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
HDAC6	300272	100	100	97	97
HDAC8	300269	100	100	91	91
HECTD1	No ID	100	97	88	88
HECW2	617245	100	97	90	90
HEPACAM	611642	100	100	99	99
HERC1	605109	100	99	94	94
HERC2	605837	100	99	96	96
HESX1	601802	100	100	95	95
HEXA	606869	100	100	98	98
HEXB	606873	100	100	97	97
HIVEP2	143054	100	100	98	98
HLCS	609018	100	100	99	99
HMGCL	613898	100	100	100	100
HNMT	605238	100	100	99	99
HNRNPH2	300610	100	100	100	100
HNRNPK	600712	96	84	66	66
HNRNPU	602869	100	100	95	95
HOXA1	142955	100	100	100	100
HPD	609695	100	100	99	99
HPRT1	308000	100	99	81	81
HRAS	190020	100	100	100	100
HSD17B10	300256	100	100	100	100
HSPA9	600548	100	99	93	93
HSPD1	118190	100	99	85	85
HUWE1	300697	100	96	83	83
IARS1	600709	100	98	88	88
IBA57	615316	100	100	97	97
IDS	300823	100	99	95	95
IDUA	252800	100	97	91	91
IER3IP1	609382	100	100	77	77
IFIH1	606951	100	100	96	96
IFT172	607386	100	100	96	96
IFT81	605489	99	94	82	82
IGBP1	300139	100	100	90	90
IGF1	147440	100	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
IKBKG	300248	38	33	31	31
IL1RAPL1	300206	100	98	88	88
IMPA1	602064	99	91	73	73
INPP5B	147264	100	100	98	98
INPP5E	613037	100	100	97	97
INPP5K	607875	100	100	98	98
INTS1	611345	100	99	96	96
INTS8	611351	100	98	84	84
IQSEC2	300522	98	92	85	85
ISG15	147571	100	100	100	100
ITGA7	600536	100	97	96	96
ITPR1	147265	100	100	98	98
ITPR2	600144	100	96	84	84
ITSN1	602442	100	97	91	91
IVD	607036	100	100	98	98
JAG1	601920	100	100	96	96
JAM3	606871	100	100	97	97
JMJD1C	604503	100	99	94	94
KALRN	604605	100	99	96	96
KANK1	607704	100	100	99	99
KANSL1	612452	100	100	97	97
KAT6A	601408	100	100	99	99
KAT6B	605880	100	100	98	98
KATNB1	602703	100	100	100	100
KCNA2	176262	100	100	100	100
KCNA4	176266	100	100	100	100
KCNB1	600397	100	100	100	100
KCNC3	176264	94	78	64	64
KCNH1	603305	100	100	98	98
KCNJ10	602208	100	100	100	100
KCNJ11	600937	100	100	100	100
KCNJ6	600877	100	100	100	100
KCNJ8	600935	100	100	99	99
KCNK9	605874	100	100	100	100
KCNMA1	600150	100	100	96	96

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
KCNQ1OT1	604115	No coverage data			
KCNQ2	602235	100	100	100	100
KCNQ3	602232	100	100	96	96
KCNQ5	607357	100	98	95	95
KCNT1	608167	100	99	99	99
KCTD7	611725	100	100	100	100
KDM1A	609132	100	100	93	93
KDM4B	609765	100	99	98	98
KDM5C	314690	100	99	96	96
KDM6A	300128	100	95	80	80
KDM6B	611577	100	98	95	95
KDSR	136440	100	100	96	96
KIAA0586	610178	100	98	94	94
KIAA1109	611565	100	100	97	97
KIAA1586	No ID	96	95	93	93
KIDINS220	615759	100	98	90	90
KIF11	148760	100	99	93	93
KIF1A	601255	100	100	98	98
KIF2A	602591	100	99	90	90
KIF4A	300521	100	96	79	79
KIF5C	604593	100	99	93	93
KIF7	611254	98	96	93	93
KIFBP	609367	100	100	98	98
KIRREL3	607761	100	100	100	100
KLHL15	300980	100	99	90	90
KMT2A	159555	100	100	98	98
KMT2B	606834	97	95	94	94
KMT2C	606833	100	99	96	96
KMT2D	602113	100	100	99	99
KMT2E	608444	100	100	97	97
KMT5B	610881	100	100	99	99
KNL1	609173	100	99	95	95
KPTN	615620	100	100	100	100
KRAS	190070	100	100	87	87
KRBOX4	300585	100	100	95	95

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
L1CAM	308840	100	100	100	100
L2HGDH	609584	100	100	97	97
LAMA1	150320	100	100	97	97
LAMA2	156225	100	99	96	96
LAMC1	150290	100	100	97	97
LAMC3	604349	100	100	99	99
LAMP2	309060	100	95	77	77
LARGE1	603590	100	100	99	99
LARP7	612026	100	99	92	92
LAS1L	300964	100	100	97	97
LIAS	607031	100	100	95	95
LIG4	601837	100	100	100	100
LINS1	610350	100	100	94	94
LMAN2L	609552	100	98	94	94
LONP1	605490	100	100	100	100
LRP2	600073	100	100	96	96
LRPPRC	607544	100	99	91	91
LZTFL1	606568	100	100	93	93
MAB21L2	604357	100	100	100	100
MACF1	608271	100	99	94	94
MACROD2	611567	100	99	91	91
MAF	177075	84	80	76	76
MAGEC3	300469	100	96	88	88
MAGEL2	605283	100	98	93	93
MAGT1	300715	100	99	85	85
MAN1B1	604346	100	100	100	100
MAN2B1	609458	100	100	100	100
MANBA	609489	100	100	95	95
MAOA	309850	100	99	92	92
MAP2K1	176872	100	100	96	96
MAP2K2	601263	100	100	95	95
MAPRE2	605789	100	98	90	90
MASP1	600521	100	100	99	99
MAST1	612256	100	100	100	100
MAT1A	610550	100	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
MBD5	611472	100	100	99	99
MBOAT7	606048	100	100	100	100
MBTPS2	300294	100	99	90	90
MCCC1	609010	100	100	94	94
MCCC2	609014	100	100	96	96
MCF2L	609499	100	99	97	97
MCM3AP	603294	100	99	96	96
MCOLN1	605248	100	100	100	100
MCOLN3	607400	100	94	83	83
MCPH1	607117	94	94	92	92
MDH2	154100	100	100	100	100
MECP2	300005	100	100	96	96
MECR	608205	100	100	99	99
MED12	300188	100	100	97	97
MED13L	608771	100	100	97	97
MED17	603810	100	100	99	99
MED23	605042	100	100	96	96
MED25	610197	100	100	99	99
MEF2C	600662	100	99	96	96
MEIS2	601740	100	100	99	99
METTL23	615262	100	100	98	98
MFSD2A	614397	100	100	98	98
MFSD8	611124	100	100	95	95
MGAT2	602616	100	100	100	100
MICU1	605084	100	98	82	82
MID1	300552	100	100	93	93
MID2	300204	100	96	82	82
MKKS	604896	100	100	100	100
MKS1	609883	100	100	99	99
MLC1	605908	100	100	94	94
MLYCD	606761	100	96	92	92
MMAA	607481	100	100	98	98
MMADHC	611935	100	100	90	90
MMUT	609058	100	100	95	95
MOCS1	603707	100	100	99	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
MOCS2	603708	100	100	96	96
MOGS	601336	100	100	100	100
MPDU1	604041	100	100	99	99
MPDZ	603785	100	99	95	95
MPLKIP	609188	100	100	100	100
MRPL3	607118	100	100	90	90
MRPS22	605810	100	100	96	96
MSL2	614802	100	100	99	99
MTFMT	611766	100	100	90	90
MTHFR	607093	100	100	99	99
MTHFS	604197	100	100	100	100
MTMR9	606260	100	100	97	97
MTOR	601231	100	100	97	97
MTR	156570	100	100	97	97
MTRR	602568	100	100	98	98
MVK	251170	100	100	100	100
MYCN	164840	100	100	100	100
MYH9	160775	100	100	99	99
MYO5A	160777	100	99	94	94
MYT1L	613084	100	100	97	97
NAA10	300013	100	100	94	94
NAA15	608000	100	100	95	95
NACC1	610672	100	100	100	100
NAGA	104170	100	100	100	100
NAGLU	609701	100	97	93	93
NALCN	611549	100	100	97	97
NANS	605202	100	99	94	94
NARS2	612803	99	97	92	92
NAT10	609221	100	99	96	96
NBEA	604889	99	97	91	91
NBN	602667	100	99	88	88
NCOR2	600848	99	94	86	86
NDE1	609449	100	100	100	100
NDP	300658	100	100	100	100
NDST1	600853	100	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
NDUFA1	300078	100	100	100	100
NDUFA11	612638	100	100	100	100
NDUFA12	614530	100	100	100	100
NDUFA2	602137	100	100	100	100
NDUFAF3	612911	100	100	100	100
NDUFAF5	612360	100	100	96	96
NDUFS1	157655	100	100	94	94
NDUFS2	602985	100	100	99	99
NDUFS3	603846	100	100	100	100
NDUFS4	602694	100	100	99	99
NDUFS6	603848	100	100	100	100
NDUFS7	601825	100	100	98	98
NDUFS8	602141	100	100	100	100
NDUFV1	161015	100	100	100	100
NDUFV2	600532	100	95	80	80
NECAP1	611623	100	100	100	100
NECTIN1	600644	100	100	100	100
NEDD4L	606384	100	99	94	94
NEU1	608272	100	100	100	100
NEXMIF	300524	100	100	95	95
NF1	613113	97	90	79	79
NFATC1	600489	100	100	100	100
NFE2L2	600492	100	99	94	94
NFIA	600727	100	100	98	98
NFIX	164005	100	100	100	100
NGLY1	610661	100	100	97	97
NHS	300457	100	96	90	90
NID1	131390	100	100	100	100
NIN	608684	100	99	95	95
NIPBL	608667	100	98	92	92
NKX2-1	600635	100	100	100	100
NLGN3	300336	100	100	98	98
NLGN4X	300427	100	100	100	100
NLRP3	606416	100	100	100	100
NONO	300084	98	91	76	76

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
NOVA2	601991	97	93	88	88
NPC1	607623	100	100	99	99
NPC2	601015	100	100	100	100
NPHP1	607100	100	98	88	88
NPRL3	600928	100	99	95	95
NR2F1	132890	100	100	100	100
NRAS	164790	100	100	98	98
NRXN1	600565	100	100	97	97
NSD1	606681	100	100	98	98
NSDHL	300275	100	100	93	93
NSUN2	610916	100	99	92	92
NTRK1	191315	100	100	99	99
NUP62	605815	100	100	100	100
OAT	613349	100	96	85	85
OCLN	602876	96	84	79	79
OCRL	300535	100	95	80	80
ODC1	165640	100	100	100	100
OFD1	300170	100	95	75	75
OPHN1	300127	100	96	84	84
ORC1	601902	100	100	97	97
OTC	300461	100	98	85	85
P2RX6	608077	100	95	91	91
PACS1	607492	100	100	97	97
PACS2	610423	100	99	96	96
PAFAH1B1	601545	100	96	90	90
PAH	612349	100	99	95	95
PAK3	300142	100	96	83	83
PANK2	606157	100	100	99	99
PANX1	608420	100	99	93	93
PAX1	167411	100	90	86	86
PAX6	607108	100	100	96	96
PAX8	167415	100	100	97	97
PBX1	176310	100	100	98	98
PC	608786	100	100	100	100
PCCA	232000	100	100	95	95

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
PCCB	232050	100	98	95	95
PCDH19	300460	100	100	97	97
PCGF2	600346	100	99	96	96
PCLO	604918	100	99	98	98
PCNT	605925	100	100	99	99
PDE4D	600129	100	97	94	94
PDHA1	300502	100	94	84	84
PDP1	605993	100	100	100	100
PDSS1	607429	100	93	85	85
PDSS2	610564	100	97	87	87
PEPD	613230	100	100	98	98
PET100	614770	92	66	66	66
PEX1	602136	100	99	94	94
PEX10	602859	100	100	97	97
PEX11B	603867	100	100	100	100
PEX12	601758	100	100	94	94
PEX13	601789	100	100	99	99
PEX16	603360	100	96	94	94
PEX19	600279	100	100	98	98
PEX2	170993	100	100	100	100
PEX26	608666	100	100	100	100
PEX3	603164	100	100	95	95
PEX5	600414	100	100	100	100
PEX6	601498	100	99	95	95
PEX7	601757	100	100	95	95
PGAP1	611655	100	99	90	90
PGAP2	615187	100	100	100	100
PGAP3	611801	100	100	100	100
PGK1	311800	100	100	89	89
PHC1	602978	100	97	94	94
PHF21A	608325	100	97	91	91
PHF23	612910	100	100	100	100
PHF6	300414	100	96	82	82
PHF8	300560	100	98	87	87
PHGDH	606879	100	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
PHIP	612870	100	98	90	90
PI4KA	600286	100	99	96	96
PIGA	311770	100	100	97	97
PIGC	601730	100	100	100	100
PIGG	616918	100	100	98	98
PIGL	605947	100	100	100	100
PIGN	606097	100	99	89	89
PIGO	614730	100	100	100	100
PIGT	610272	100	100	100	100
PIGV	610274	100	100	100	100
PIGW	610275	100	100	100	100
PIGY	610662	100	100	94	94
PIK3CA	171834	100	99	96	96
PIK3R2	603157	95	93	90	90
PLA2G6	603604	100	100	99	99
PLCB1	607120	100	99	94	94
PLK4	605031	100	99	91	91
PLP1	300401	100	99	97	97
PLXNA3	300022	98	97	95	95
PLXND1	604282	100	99	96	96
PMM2	601785	100	100	97	97
PMPCA	613036	100	100	100	100
PNKP	605610	100	100	98	98
PNP	164050	100	100	97	97
POC1A	614783	100	100	100	100
POGZ	614787	100	100	97	97
POLG	174763	100	100	99	99
POLR3A	614258	100	100	98	98
POLR3B	614366	100	99	93	93
POMGNT1	606822	100	100	99	99
POMGNT2	614828	100	100	100	100
POMK	615247	100	100	100	100
POMT1	607423	100	100	100	100
POMT2	607439	100	100	99	99
PORCN	300651	100	100	98	98

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
POU1F1	173110	100	100	100	100
POU3F3	602480	77	68	62	62
PPFIA4	603145	100	99	95	95
PPM1D	605100	100	100	99	99
PPOX	600923	100	100	100	100
PPP1CB	600590	100	100	95	95
PPP1R15B	613257	100	100	98	98
PPP2CA	176915	100	100	93	93
PPP2R1A	605983	100	100	100	100
PPP2R5B	601644	100	100	100	100
PPP2R5C	601645	97	89	78	78
PPP2R5D	601646	100	100	98	98
PPP3CA	114105	100	99	90	90
PPT1	600722	100	100	100	100
PQBP1	300463	100	100	100	100
PRIM1	176635	100	95	79	79
PRKAR1A	188830	100	100	99	99
PRKCE	176975	100	100	97	97
PRMT7	610087	100	100	98	98
PRODH	606810	100	95	86	86
PRPS1	311850	100	99	90	90
PRR12	616633	100	96	90	90
PRSS12	606709	100	100	99	99
PSAP	176801	100	100	97	97
PSMD12	604450	98	86	70	70
PTCH1	601309	100	98	96	96
PTCHD1	300828	100	100	98	98
PTDSS1	612792	100	100	98	98
PTEN	601728	85	78	76	76
PTF1A	607194	100	100	94	94
PTGR1	601274	99	94	83	83
PTPN11	176876	100	99	90	90
PTRH2	608625	100	100	100	100
PTRHD1	617342	100	100	100	100
PTS	612719	100	100	95	95

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
PUF60	604819	100	100	100	100
PUM1	607204	100	100	98	98
PURA	600473	100	100	100	100
PUS1	608109	100	99	95	95
PUS3	616283	100	99	96	96
PUS7	616261	100	98	90	90
PYCR1	179035	100	100	100	100
PYCR2	616406	100	100	100	100
QARS1	603727	100	100	100	100
QDPR	612676	100	100	97	97
RAB18	602207	100	100	97	97
RAB27A	603868	100	100	91	91
RAB39B	300774	100	100	100	100
RAB3GAP1	602536	100	100	97	97
RAB3GAP2	609275	100	99	92	92
RAB40AL	300405	100	100	100	100
RAC1	602048	100	100	97	97
RAD21	606462	100	99	92	92
RAD50	604040	100	100	98	98
RAF1	164760	100	99	95	95
RAI1	607642	100	100	100	100
RALA	179550	90	80	72	72
RARB	180220	100	100	99	99
RARS2	611524	100	99	93	93
RBBP8	604124	100	99	92	92
RBFOX1	605104	100	100	99	99
RBM10	300080	100	96	88	88
RBM28	612074	100	100	96	96
RBPJ	147183	100	99	89	89
RCBTB1	607867	100	100	99	99
RELN	600514	100	100	97	97
RERE	605226	97	92	86	86
REV3L	602776	100	99	95	95
RFT1	611908	100	99	93	93
RHEB	601293	86	60	36	36

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
RHOBTB2	607352	100	100	99	99
RIT1	609591	100	100	100	100
RLIM	300379	100	100	90	90
RMND1	614917	100	100	93	93
RMRP	157660	No coverage data			
RNASEH2A	606034	100	100	100	100
RNASEH2B	610326	100	98	88	88
RNASEH2C	610330	100	100	100	100
RNASET2	612944	100	100	99	99
RNF113A	300951	100	100	100	100
RNF125	610432	100	100	100	100
RNF135	611358	100	100	99	99
ROGDI	614574	100	98	93	93
RORA	600825	100	100	97	97
RPGRIP1L	610937	98	96	89	89
RPL10	312173	100	100	100	100
RPS6KA3	300075	100	92	70	70
RSPRY1	616585	100	98	90	90
RTEL1	608833	100	100	99	99
RTTN	610436	100	99	94	94
RUBCN	613516	100	98	96	96
RUSC2	611053	100	100	100	100
RXYLT1	605862	100	100	94	94
SALL1	602218	100	100	99	99
SAMHD1	606754	100	99	88	88
SATB2	608148	100	100	97	97
SBDS	607444	100	100	99	99
SC5D	602286	100	100	100	100
SCAF4	616023	100	98	90	90
SCN1A	182389	100	100	99	99
SCN1B	600235	100	97	93	93
SCN2A	182390	100	100	97	97
SCN3A	182391	100	100	97	97
SCN8A	600702	100	100	98	98
SCO1	603644	100	100	99	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
SCO2	604272	100	100	100	100
SDHA	600857	100	97	91	91
SEMA3E	608166	100	100	94	94
SEPSECS	613009	100	100	96	96
SERAC1	614725	100	99	86	86
SETBP1	611060	99	98	97	97
SETD1A	611052	100	99	98	98
SETD2	612778	100	100	98	98
SETD5	615743	100	100	98	98
SF1	601516	90	84	79	79
SGSH	605270	100	94	90	90
SH3KBP1	300374	99	89	69	69
SHANK2	603290	100	99	96	96
SHANK3	606230	99	93	86	86
SHH	600725	100	100	99	99
SHOC2	602775	100	99	95	95
SIK1	605705	100	100	99	99
SIL1	608005	100	100	100	100
SIN3A	607776	100	100	97	97
SIX3	603714	100	100	96	96
SKI	164780	100	100	99	99
SLC12A6	604878	100	99	94	94
SLC13A5	608305	100	100	98	98
SLC16A2	300095	100	100	95	95
SLC17A5	604322	100	100	97	97
SLC19A3	606152	100	100	98	98
SLC1A1	133550	100	100	98	98
SLC1A2	600300	100	100	98	98
SLC1A4	600229	100	100	100	100
SLC25A12	603667	100	100	97	97
SLC25A15	603861	100	100	98	98
SLC25A19	606521	100	100	100	100
SLC25A22	609302	100	100	100	100
SLC2A1	138140	100	100	100	100
SLC33A1	603690	100	98	86	86

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
SLC35A1	605634	100	100	97	97
SLC35A2	314375	100	100	99	99
SLC35A3	605632	100	99	92	92
SLC35C1	605881	100	100	100	100
SLC39A12	608734	100	97	87	87
SLC39A8	608732	100	99	95	95
SLC4A4	603345	100	100	97	97
SLC6A1	137165	100	100	100	100
SLC6A17	610299	100	100	100	100
SLC6A3	126455	100	100	100	100
SLC6A8	300036	100	98	95	95
SLC7A7	603593	100	100	97	97
SLC9A6	300231	100	96	84	84
SMAD4	600993	100	100	98	98
SMARCA2	600014	98	98	96	96
SMARCA4	603254	100	100	100	100
SMARCB1	601607	100	100	99	99
SMARCC2	601734	100	100	94	94
SMARCE1	603111	100	100	93	93
SMC1A	300040	100	100	97	97
SMC3	606062	100	97	88	88
SMOC1	608488	100	100	97	97
SMPD1	607608	100	100	99	99
SMPD4	610457	100	100	98	98
SMS	300105	95	89	68	68
SNAP25	600322	100	100	98	98
SNAP29	604202	100	100	100	100
SNIP1	608241	100	100	100	100
SNRNP70	180740	100	100	98	98
SNRPN	182279	100	100	100	100
SNX14	616105	100	99	91	91
SOBP	613667	100	98	95	95
SON	182465	99	96	90	90
SOS1	182530	100	100	95	95
SOS2	601247	100	99	95	95

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
SOX10	602229	100	97	89	89
SOX11	600898	100	100	100	100
SOX2	184429	100	100	100	100
SOX3	313430	100	95	89	89
SOX5	604975	100	100	96	96
SPAST	604277	100	100	94	94
SPATA5	613940	100	100	97	97
SPG11	610844	100	100	97	97
SPOCK1	602264	100	100	97	97
SPRED1	609291	100	98	92	92
SPTAN1	182810	100	100	98	98
SPTBN2	604985	100	100	100	100
SRCAP	611421	100	100	100	100
SRD5A3	611715	100	100	96	96
SRPX2	300642	100	99	95	95
SSR4	300090	100	100	99	99
ST3GAL3	606494	100	100	96	96
ST3GAL5	604402	99	92	84	84
STAG1	604358	100	98	83	83
STAMBP	606247	100	100	97	97
STIL	181590	100	100	97	97
STRA6	610745	100	100	100	100
STRADA	608626	100	100	98	98
STT3A	601134	100	100	98	98
STT3B	608605	100	100	97	97
STX1B	601485	100	100	99	99
STXBP1	602926	100	100	99	99
SUCLA2	603921	100	97	86	86
SUCLG1	611224	100	100	100	100
SUCO	No ID	100	99	94	94
SUMF1	607939	100	100	99	99
SUOX	606887	100	100	100	100
SURF1	185620	94	89	87	87
SUZ12	606245	100	98	92	92
SYN1	313440	100	99	85	85

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
SYNCRIP	616686	97	89	76	76
SYNE1	608441	100	100	97	97
SYNGAP1	603384	98	98	98	98
SYP	313475	100	100	98	98
SYT1	185605	100	100	99	99
SYT14	610949	100	95	86	86
SZT2	615463	100	100	100	100
TAF1	313650	100	97	87	87
TAF2	604912	100	99	92	92
TALPID3	610178	100	98	94	94
TAT	613018	100	100	98	98
TBC1D20	611663	100	93	93	93
TBC1D24	613577	100	100	100	100
TBC1D7	612655	100	98	85	85
TBCD	604649	100	99	96	96
TBCE	604934	100	97	88	88
TBCK	616899	100	99	91	91
TBL1XR1	608628	100	98	90	90
TBP	600075	100	100	96	96
TBR1	604616	100	100	99	99
TBX1	602054	94	85	80	80
TCF12	600480	100	100	98	98
TCF20	603107	100	100	100	100
TCF4	602272	100	100	96	96
TCN2	613441	100	100	100	100
TCTN3	613847	100	100	97	97
TDP2	605764	100	100	99	99
TECPR2	615000	100	100	99	99
TECR	610057	100	100	100	100
TELO2	611140	100	97	93	93
TFAP2A	107580	100	100	100	100
TGFBR1	190181	94	93	93	93
TGFBR2	190182	100	100	100	100
TGIF1	602630	100	100	100	100
TH	191290	100	99	94	94

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
THOC2	300395	100	94	72	72
THOC6	615403	100	100	100	100
THRB	190160	100	100	99	99
TIMM8A	300356	100	100	100	100
TINF2	604319	100	100	100	100
TLK2	608439	97	82	66	66
TM4SF20	615404	100	100	96	96
TMCO1	614123	100	100	96	96
TMEM165	614726	100	100	100	100
TMEM231	614949	100	95	90	90
TMEM237	614423	100	98	87	87
TMEM240	616101	100	100	100	100
TMEM67	609884	100	100	94	94
TMEM70	612418	100	100	95	95
TMLHE	300777	89	81	67	67
TMPRSS7	No ID	100	99	92	92
TMTC3	617218	100	99	93	93
TMX2	616715	100	94	88	88
TNIK	610005	100	98	92	92
TOE1	613931	100	100	98	98
TPI1	190450	100	98	96	96
TPO	606765	100	100	100	100
TPP1	607998	100	100	100	100
TRAIP	605958	100	100	100	100
TRAPPC11	614138	100	97	90	90
TRAPPC6B	610397	100	95	78	78
TRAPPC9	611966	100	100	98	98
TREX1	606609	100	100	100	100
TRIM32	602290	100	100	100	100
TRIO	601893	99	99	97	97
TRIP12	604506	100	99	95	95
TRMT1	611669	100	99	94	94
TRMT10A	616013	100	100	94	94
TRPM3	608961	100	100	98	98
TSC1	605284	100	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
TSC2	191092	100	100	100	100
TSEN15	608756	100	100	100	100
TSEN54	608755	100	96	96	96
TSHB	188540	100	100	100	100
TSPAN7	300096	100	98	83	83
TTC19	613814	100	92	77	77
TTC37	614589	100	99	93	93
TTC8	608132	100	100	93	93
TTI2	614426	100	100	98	98
TUBA1A	602529	100	100	100	100
TUBA8	605742	100	100	100	100
TUBB	191130	100	99	97	97
TUBB2A	615101	99	82	74	74
TUBB2B	612850	100	87	78	78
TUBB3	602661	100	99	95	95
TUBB4A	602662	100	100	99	99
TUBG1	191135	100	100	100	100
TUBGCP2	617817	100	97	91	91
TUBGCP4	609610	100	98	94	94
TUBGCP6	610053	100	100	99	99
TUSC3	601385	100	100	95	95
TWIST1	601622	100	100	95	95
TWNK	606075	100	100	100	100
UBA5	610552	100	91	67	67
UBE2A	312180	100	99	81	81
UBE3A	601623	100	100	96	96
UBE3B	608047	100	100	99	99
UBR1	605981	100	99	93	93
UNC80	612636	100	100	97	97
UPB1	606673	100	100	100	100
UPF3B	300298	100	98	87	87
UQCC2	614461	100	100	100	100
UQCRQ	612080	100	100	100	100
UROC1	613012	100	100	99	99
USP18	607057	95	95	93	93

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
USP27X	300975	100	100	100	100
USP7	602519	97	89	71	71
USP9X	300072	100	98	94	94
UTRN	128240	100	100	97	97
VLDLR	192977	100	100	97	97
VPS11	608549	100	100	98	98
VPS13B	607817	100	99	96	96
VPS13C	608879	100	97	85	85
VPS37A	609927	100	99	86	86
VPS53	615850	100	100	96	96
VRK1	602168	100	99	92	92
VWA3B	614884	100	98	92	92
WAC	615049	100	98	91	91
WASHC4	615748	100	97	90	90
WASHC5	610657	100	100	94	94
WBP11	618083	96	74	54	54
WDR13	300512	100	100	98	98
WDR19	608151	100	100	97	97
WDR26	617424	100	94	81	81
WDR4	605924	100	100	100	100
WDR45	300526	100	100	100	100
WDR62	613583	100	100	100	100
WDR73	616144	100	100	97	97
WDR81	614218	100	100	100	100
WFS1	606201	100	100	100	100
WWOX	605131	100	100	100	100
XIAP	300079	100	95	80	80
XPA	611153	100	100	93	93
XPC	613208	100	100	98	98
XPNPEP3	613553	100	100	96	96
XYLT1	608124	100	97	93	93
YAP1	606608	100	99	94	94
YME1L1	607472	100	95	83	83
YWHAE	605066	100	100	91	91
YY1	600013	100	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ZBTB16	176797	100	100	100	100
ZBTB18	608433	100	100	99	99
ZBTB20	606025	100	100	100	100
ZBTB24	614064	100	100	100	100
ZC3H14	613279	100	99	93	93
ZC4H2	300897	100	99	93	93
ZDHC15	300576	100	99	89	89
ZDHC9	300646	100	97	83	83
ZEB2	605802	100	100	100	100
ZFYVE26	612012	100	100	98	98
ZIC1	600470	100	100	100	100
ZIC2	603073	96	95	93	93
ZIC4	608948	100	100	99	99
ZMYND11	608668	100	100	98	98
ZNF101	603983	100	100	93	93
ZNF292	616213	100	98	95	95
ZNF407	615894	100	100	100	100
ZNF41	314995	100	99	93	93
ZNF592	613624	100	100	100	100
ZNF674	300573	100	99	93	93
ZNF711	314990	100	96	85	85
ZNF81	314998	100	100	90	90
ZSWIM6	615951	96	93	88	88

- OMIM release used: 8-9-2019

- The statistics above are based on a set of 100 samples

- Median depth is the median of the mean sequence depth over the protein coding exons (± 10 bp flanking introns) of the longest transcript

- % Covered 10x , 20x and 30 x describes the percentage of a gene's coding sequence (± 10 bp flanking introns) that is covered at least 10x, 20x or 30x