

Whole Exome Sequencing

Gene package Intellectual disability, version 11, 30-9-2020



Technical information

DNA was enriched using Agilent SureSelect DNA + 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 Alissa Interpret 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	128	100	100	100
AARS1	601065	161	100	100	100
AASS	605113	87	100	98	93
ABAT	137150	142	100	100	100
ABCC9	601439	77	100	99	94
ABCD1	300371	178	100	100	100
ABCD4	603214	169	100	100	100
ABHD5	604780	116	100	96	92
ACAD8	604773	186	100	100	100
ACAD9	611103	186	100	100	100
ACO2	100850	270	100	100	100
ACOT9	300862	63	100	97	90
ACOX1	609751	126	100	100	98
ACSF3	614245	244	100	100	100
ACSL4	300157	47	97	86	72
ACTB	102630	253	100	100	100
ACTG1	102560	233	100	100	100
ACVR1	102576	104	100	100	99
ACY1	104620	215	100	100	100
ADA2	607575	157	100	100	100
ADAM22	603709	101	100	99	92
ADAR	146920	163	100	100	100
ADAT3	615302	319	100	100	100
ADGRG1	604110	233	100	100	100
ADK	102750	58	99	89	81

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ADNP	611386	160	100	100	98
ADSL	608222	178	100	100	100
AFF2	300806	70	100	97	90
AFF4	604417	119	100	98	94
AFG3L2	604581	107	96	96	93
AGA	613228	83	100	98	90
AGAP2	605476	215	100	100	100
AGO1	606228	134	100	100	100
AGO2	606229	184	99	97	93
AGPAT2	603100	227	100	100	100
AGTR2	300034	75	100	100	99
AHCY	180960	268	100	100	100
AHDC1	615790	285	100	100	100
AHI1	608894	65	96	86	77
AIFM1	300169	89	100	99	96
AIMP1	603605	70	99	88	81
AK1	103000	147	100	97	94
AKT1	164730	284	100	100	100
AKT3	611223	53	100	90	75
ALDH18A1	138250	169	100	100	99
ALDH3A2	609523	90	100	100	97
ALDH4A1	606811	315	100	100	100
ALDH5A1	610045	121	100	100	98
ALG1	605907	126	100	100	99
ALG11	613666	109	100	100	95
ALG12	607144	224	100	100	100
ALG13	300776	67	98	92	81
ALG2	607905	173	100	100	100
ALG3	608750	213	100	100	100
ALG6	604566	49	90	81	67
ALG8	608103	62	93	86	79
ALG9	606941	78	97	95	92
ALMS1	606844	116	100	99	96
ALX1	601527	188	100	100	94
ALX4	605420	206	100	99	97
AMMECR1	300195	93	100	100	100
AMPD2	102771	219	100	100	100
AMT	238310	225	100	100	100
ANK3	600465	118	100	99	98
ANKEF1	No ID	86	100	99	96
ANKH	605145	171	100	100	100
ANKLE2	616062	152	99	97	92
ANKRD11	611192	247	100	99	97

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ANO10	613726	82	98	93	85
ANTXR1	606410	116	99	98	95
AP1S1	603531	171	100	100	100
AP1S2	300629	33	95	74	53
AP3B1	603401	58	93	79	66
AP3B2	602166	182	100	100	100
AP4B1	607245	130	100	100	100
AP4E1	607244	66	97	87	75
AP4M1	602296	141	100	100	100
AP4S1	607243	50	100	96	78
APC2	612034	235	100	99	97
APTX	606350	166	100	98	90
ARFGEF2	605371	114	100	97	93
ARG1	608313	89	100	99	95
ARHGAP31	610911	186	100	100	100
ARHGAP4	300023	151	100	100	100
ARHGEF33	No ID	101	100	96	90
ARHGEF6	300267	51	99	91	78
ARHGEF9	300429	93	100	100	99
ARID1A	603024	182	100	98	97
ARID1B	614556	166	100	100	98
ARID2	609539	109	100	96	92
ARL13B	608922	56	100	90	72
ARL6	608845	44	98	88	79
ARNT2	606036	174	100	100	100
ARSA	607574	380	100	100	100
ARSL	300180	101	100	100	100
ARX	300382	100	92	89	84
ASAH1	613468	73	98	92	81
ASCL1	100790	249	100	100	100
ASH1L	607999	115	100	100	99
ASL	608310	294	100	100	100
ASNS	108370	82	100	98	91
ASPA	608034	103	100	98	94
ASPM	605481	64	94	87	75
ASS1	603470	215	100	98	96
ASXL1	612990	187	100	98	97
ASXL2	612991	150	97	97	97
ASXL3	615115	119	100	97	94
ATAD3A	612316	313	98	97	94
ATAD3B	612317	336	98	95	90
ATCAY	608179	200	100	100	100
ATIC	601731	84	100	99	94

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ATN1	607462	189	100	100	100
ATP1A2	182340	189	100	100	100
ATP1A3	182350	221	100	100	100
ATP2A2	108740	119	100	99	95
ATP6AP2	300556	54	100	93	81
ATP6V0A2	611716	120	100	97	91
ATP6V1B2	606939	94	100	99	98
ATP7A	300011	59	99	94	81
ATP8A2	605870	125	98	96	94
ATPAF2	608918	175	100	100	97
ATR	601215	76	98	92	83
ATRIP	606605	189	100	98	92
ATRX	300032	37	92	74	52
AUH	600529	81	100	98	91
AUTS2	607270	204	100	99	98
AVPR2	300538	182	100	100	100
B3GALNT2	610194	101	100	100	99
B3GALT6	615291	283	83	80	78
B3GLCT	610308	64	97	84	73
B4GALNT1	601873	269	100	100	100
B4GALT1	137060	136	100	100	100
B4GALT7	604327	254	100	100	100
B4GAT1	605517	291	100	100	100
BBS1	209901	225	100	100	100
BBS10	610148	100	100	100	99
BBS12	610683	118	100	100	98
BBS2	606151	117	100	99	94
BBS4	600374	100	100	100	93
BBS5	603650	52	91	66	47
BBS7	607590	68	95	82	75
BBS9	607968	73	99	94	88
BCAP31	300398	82	100	100	95
BCKDHA	608348	221	100	100	100
BCKDHB	248611	137	100	100	99
BCL11A	606557	271	100	100	100
BCL11B	606558	242	100	100	99
BCOR	300485	120	100	100	98
BCORL1	300688	135	100	100	99
BCS1L	603647	263	100	100	100
BLM	604610	64	99	90	76
BRAF	164757	84	100	99	94
BRAT1	614506	243	100	100	100
BRF1	604902	149	100	100	98

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
BRPF1	602410	242	100	100	100
BRWD3	300553	47	98	89	77
BSCL2	606158	178	100	100	100
BTD	609019	195	100	100	100
BUB1B	602860	99	98	95	89
c12orf4	616082	57	94	84	74
C12orf57	615140	308	100	100	100
C12orf65	613541	100	100	94	58
C1orf167	No ID	218	100	100	100
C2CD3	615944	132	100	100	99
CA2	611492	116	100	100	100
CA5A	114761	147	100	100	100
CA8	114815	95	100	100	94
CACNA1A	601011	139	100	100	99
CACNA1C	114205	179	100	100	100
CACNA2D1	114204	61	91	79	70
CACNG2	602911	166	100	100	98
CAD	114010	218	100	100	100
CAMK2A	114078	199	100	100	100
CAMK2B	607707	187	100	100	100
CAMTA1	611501	210	100	98	95
CAPN10	605286	256	100	100	100
CASK	300172	60	96	86	70
CBL	165360	130	100	100	99
CBS	613381	430	100	100	100
CC2D1A	610055	228	100	100	100
CC2D2A	612013	88	98	93	86
CCBE1	612753	163	95	95	95
CCDC13	No ID	150	100	100	99
CCDC14	617147	98	94	90	82
CCDC174	616735	102	87	78	71
CCDC22	300859	158	100	100	100
CCDC78	614666	215	100	100	98
CCDC88C	611204	187	100	100	98
CCND2	123833	152	100	100	100
CDC5L	602868	68	99	91	81
CDH15	114019	235	100	100	100
CDK16	311550	117	100	100	100
CDK5	123831	223	100	100	100
CDK5RAP2	608201	113	99	94	90
CDK6	603368	137	98	94	93
CDKL5	300203	74	97	92	86
CDKN1C	600856	156	92	87	83

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CDON	608707	123	99	97	95
CENPJ	609279	97	97	93	89
CEP104	616690	94	100	99	95
CEP135	611423	42	92	74	57
CEP152	613529	79	93	86	81
CEP290	610142	35	74	58	45
CEP41	610523	83	100	94	91
CEP63	614724	50	97	81	65
CEP89	615470	103	95	89	87
CERT1	604677	95	96	92	89
CHAMP1	616327	157	100	100	100
CHD2	602119	82	98	92	84
CHD3	602120	152	98	96	95
CHD4	603277	129	100	99	97
CHD7	608892	167	100	99	97
CHD8	610528	185	100	100	99
CHKB	612395	373	100	100	100
CHMP1A	164010	202	100	100	100
CHRNA4	118504	386	100	100	99
CIC	612082	232	100	100	100
CIT	605629	131	100	100	99
CKAP2L	616174	100	88	88	84
CLCN4	302910	141	100	100	98
CLCNKB	602023	213	100	100	99
CLIC2	300138	52	100	95	82
CLIP1	179838	122	96	92	91
CLN3	607042	211	100	100	100
CLN5	608102	113	100	93	89
CLN6	606725	264	100	100	100
CLN8	607837	195	100	100	100
CLP1	608757	213	100	100	100
CLPB	616254	209	100	100	100
CLTC	118955	84	100	98	93
CNKS2	300724	49	96	82	65
CNNM2	607803	209	100	100	97
CNOT3	604910	203	100	100	99
CNTNAP2	604569	119	100	100	99
COASY	609855	239	100	100	100
COG1	606973	164	100	100	99
COG4	606976	150	100	100	100
COG5	606821	73	95	92	85
COG6	606977	66	94	83	74
COG7	606978	172	100	100	100

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COG8	606979	164	100	100	100
COL11A1	120280	86	99	95	89
COL12A1	120320	105	97	95	92
COL18A1	120328	247	100	100	100
COL4A1	120130	121	100	99	96
COL4A2	120090	196	100	100	99
COLEC11	612502	234	100	100	100
COQ2	609825	79	98	92	82
COQ4	612898	176	100	100	97
COQ8A	606980	250	100	100	100
COQ9	612837	123	100	100	100
COX10	602125	177	100	99	94
COX15	603646	137	100	100	100
COX6B1	124089	158	100	100	100
CPLANE1	614571	75	97	93	86
CPS1	608307	101	100	100	99
CRADD	603454	228	100	100	96
CRB2	609720	229	100	100	100
CRBN	609262	78	95	93	86
CREBBP	600140	275	99	99	98
CRLF1	604237	269	93	91	91
CRPPA	614631	76	97	84	77
CSNK2A1	115440	110	100	94	94
CSPP1	611654	68	99	91	80
CSTB	601145	132	100	100	100
CTBP1	602618	244	100	94	92
CTC1	613129	174	100	100	100
CTCF	604167	114	100	96	92
CTDP1	604927	173	100	100	100
CTNNB1	116806	133	100	100	99
CTNND1	601045	149	100	99	95
CTNND2	604275	154	98	96	95
CTSA	613111	181	100	100	100
CTSD	116840	278	100	100	100
CTTNBP2	609772	124	100	99	95
CUBN	602997	107	100	99	96
CUL3	603136	51	95	83	70
CUL4B	300304	43	90	77	62
CWF19L1	616120	91	100	94	88
CXorf56	301012	66	100	100	96
CYB5R3	613213	188	100	100	100
CYP27A1	606530	295	100	100	100
CYP2U1	610670	143	100	100	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
D2HGDH	609186	269	100	100	100
DAB1	603448	135	100	98	93
DAG1	128239	269	100	100	100
DARS2	610956	79	100	96	94
DBT	248610	70	100	93	83
DCAF17	612515	71	100	99	93
DCC	120470	114	100	100	98
DCHS1	603057	292	100	100	100
DCPS	610534	179	100	100	100
DCX	300121	102	100	96	89
DDC	107930	112	100	95	92
DDHD2	615003	71	100	94	87
DDX11	601150	196	100	100	100
DDX3X	300160	56	100	98	91
DEAF1	602635	191	100	100	100
DENND5A	617278	136	100	100	98
DEPDC5	614191	157	100	100	98
DHCR24	606418	207	100	100	100
DHCR7	602858	243	100	100	100
DHFR	126060	57	93	71	43
DHPS	600944	286	100	100	100
DHTKD1	614984	128	100	100	99
DIAPH1	602121	101	100	99	96
DIP2B	611379	119	100	100	99
DKC1	300126	73	100	93	88
DLD	238331	65	99	90	76
DLG3	300189	120	100	100	98
DLG4	602887	214	100	100	100
DMD	300377	68	98	93	87
DMPK	605377	233	100	100	100
DNAJC12	606060	97	100	98	92
DNAJC19	608977	70	100	98	85
DNM1	602377	172	100	100	99
DNMT3A	602769	198	100	100	100
DNMT3B	602900	192	100	98	94
DOCK6	614194	255	100	100	100
DOCK7	615730	72	99	94	87
DOCK8	611432	118	100	99	96
DOLK	610746	430	100	100	100
DONSON	611428	78	95	93	89
DPAGT1	191350	151	100	100	100
DPF2	601671	164	100	100	100
DPH1	603527	216	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
DPM1	603503	79	98	89	73
DPP6	126141	139	100	95	91
DPYD	612779	73	94	92	86
DPYS	613326	160	100	100	98
DST	113810	91	99	96	91
DYM	607461	82	100	99	93
DYNC1H1	600112	161	100	100	99
DYRK1A	600855	111	100	97	92
EBP	300205	110	100	100	100
EDC3	609842	226	100	100	100
EDNRB	131244	135	100	99	94
EDRF1	No ID	66	99	93	82
EEF1A2	602959	218	100	100	100
EFCAB1	No ID	57	89	85	78
EFTUD2	603892	124	100	100	100
EHMT1	607001	176	99	99	98
EIF2AK3	604032	95	97	93	90
EIF2S3	300161	54	99	90	78
EIF4A3	608546	94	100	98	94
EIF4G1	600495	178	100	100	99
ELAC2	605367	162	100	100	100
ELOVL4	605512	98	98	89	81
ELP2	616054	86	98	91	83
EMC1	616846	147	100	100	99
EMG1	611531	153	100	100	100
EML1	602033	103	100	100	98
EMX2	600035	176	100	99	95
ENTPD1	601752	102	100	100	99
EOMES	604615	171	100	100	100
EP300	602700	158	99	98	94
EPB41L1	602879	174	100	100	100
EPG5	615068	106	100	99	98
ERCC1	126380	143	100	100	100
ERCC2	126340	262	100	100	100
ERCC3	133510	178	100	100	100
ERCC5	133530	87	99	96	89
ERCC6	609413	128	100	100	98
ERCC8	609412	81	100	94	84
ERLIN2	611605	110	100	100	100
ERMARD	615532	102	96	82	73
ESCO2	609353	88	97	89	81
ETFB	130410	179	100	100	100
ETHE1	608451	197	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
EXOSC2	602238	107	100	100	100
EXOSC3	606489	208	100	100	100
EZH2	601573	77	98	94	91
FA2H	611026	182	100	100	100
FAM126A	610531	96	100	100	94
FAR1	616107	69	100	92	82
FAT2	604269	229	100	100	100
FAT4	612411	170	100	99	98
FBN1	134797	141	100	100	99
FBN2	612570	139	100	100	99
FBXL4	605654	94	100	99	95
FBXO11	607871	63	100	96	87
FBXO31	609102	210	100	100	100
FGD1	300546	126	100	100	100
FGF12	601513	145	100	100	100
FGF14	601515	93	100	97	89
FGFR1	136350	185	100	100	100
FGFR2	176943	145	100	100	99
FGFR3	134934	241	100	100	100
FGL1	605776	64	90	89	83
FH	136850	83	100	100	98
FIBP	608296	172	100	100	100
FIG4	609390	88	100	96	91
FIGN	605295	185	100	100	100
FKRP	606596	339	100	100	100
FKTN	607440	104	90	81	68
FLNA	300017	206	100	100	100
FLVCR1	609144	132	100	95	85
FMN2	606373	113	99	94	86
FMR1	309550	39	96	84	63
FOXG1	164874	424	100	97	94
FOXP1	605515	121	100	100	100
FOXP2	605317	83	100	98	94
FRAS1	607830	141	100	99	99
FREM2	608945	189	100	100	99
FRMD4A	616305	174	100	100	100
FRMPD4	300838	105	100	100	96
FRRS1L	604574	75	100	92	80
FTCD	606806	270	100	99	98
FTO	610966	149	100	100	100
FTSJ1	300499	155	100	100	100
FUCA1	612280	172	100	100	100
GABRA1	137160	96	100	99	97

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
GABRB1	137190	110	100	100	96
GABRB3	137192	160	100	100	100
GAD1	605363	139	100	100	99
GALE	606953	200	100	100	100
GALT	606999	231	100	100	100
GAMT	601240	284	100	100	100
GAS6	600441	202	99	97	96
GATAD2B	614998	153	100	100	100
GATM	602360	105	100	100	99
GCDH	608801	239	100	100	100
GCH1	600225	207	94	94	94
GCSH	238330	43	100	85	69
GDI1	300104	130	100	100	99
GFAP	137780	176	100	100	100
GFM2	606544	73	100	94	88
GJA1	121014	143	100	100	100
GJB1	304040	137	100	100	99
GJC2	608803	283	100	100	98
GK	300474	27	83	59	35
GLB1	611458	149	100	100	100
GLDC	238300	118	100	100	98
GLI2	165230	260	100	100	100
GLI3	165240	243	100	100	100
GLYCTK	610516	298	100	100	100
GM2A	613109	183	100	100	100
GMPPA	615495	180	100	100	100
GMPPB	615320	281	100	100	100
GNAO1	139311	173	100	100	99
GNAQ	600998	137	100	100	100
GNAS	139320	269	100	100	100
GNB1	139380	172	100	100	100
GNB5	604447	134	100	100	100
GNPAT	602744	80	97	94	86
GNPTAB	607840	87	100	99	95
GNS	607664	105	100	100	99
GPC3	300037	86	100	98	92
GPC4	300168	93	100	99	97
GPHN	603930	87	100	96	94
GPT2	138210	169	100	100	96
GRIA3	305915	62	98	91	79
GRID2	602368	117	100	100	98
GRIK2	138244	66	99	93	86
GRIK5	600283	239	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
GRIN1	138249	259	100	100	100
GRIN2A	138253	408	100	100	99
GRIN2B	138252	237	100	100	99
GRIN3B	606651	217	97	95	93
GRIP1	604597	117	100	100	98
GRM1	604473	210	100	100	99
GSE1	616886	210	100	100	100
GSS	601002	188	100	100	100
GTF2H5	608780	81	100	100	100
GTPBP3	608536	237	100	100	100
GUCY2F	300041	69	100	99	93
GUSB	611499	222	100	100	100
H19	103280	No coverage data			
HACE1	610876	59	97	89	77
HAX1	605998	120	100	100	100
HCCS	300056	64	100	98	90
HCFC1	300019	207	100	100	100
HCN1	602780	193	100	99	97
HDAC4	605314	227	100	99	97
HDAC6	300272	145	100	100	100
HDAC8	300269	73	100	100	95
HECTD1	No ID	83	96	93	88
HECW2	617245	142	100	100	99
HEPACAM	611642	195	100	100	100
HERC1	605109	116	100	99	97
HERC2	605837	144	99	94	90
HESX1	601802	47	79	62	57
HEXA	606869	162	100	100	100
HEXB	606873	73	97	91	84
HIVEP2	143054	196	100	100	99
HLCS	609018	163	100	100	99
HMGCL	613898	168	100	100	100
HNMT	605238	84	100	100	91
HNRNPH2	300610	110	100	100	100
HNRNPK	600712	69	97	89	77
HNRNPU	602869	88	95	94	92
HOXA1	142955	294	100	100	100
HPD	609695	196	100	100	100
HPRT1	308000	40	95	80	55
HRAS	190020	426	100	100	100
HSD17B10	300256	123	100	100	100
HSPA9	600548	114	100	99	97
HSPD1	118190	67	99	90	77

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
HUWE1	300697	90	100	98	93
IARS1	600709	94	100	97	94
IBA57	615316	227	100	100	100
IDS	300823	91	100	98	94
IDUA	252800	224	100	100	98
IER3IP1	609382	147	100	95	85
IFIH1	606951	70	99	91	80
IFT172	607386	143	100	100	98
IFT81	605489	37	96	78	54
IGBP1	300139	86	100	98	89
IGF1	147440	117	100	100	100
IKBKG	300248	35	36	26	26
IL1RAPL1	300206	56	100	92	78
IMPA1	602064	63	94	85	79
INPP5B	147264	132	100	100	99
INPP5E	613037	259	100	100	100
INPP5K	607875	174	100	100	100
INTS1	611345	223	100	99	99
INTS8	611351	53	92	77	67
IQSEC2	300522	128	100	99	98
ISG15	147571	418	100	100	100
ITGA7	600536	219	100	100	100
ITPR1	147265	120	100	99	97
ITPR2	600144	83	95	93	88
ITSN1	602442	109	98	95	91
IVD	607036	170	100	100	100
JAG1	601920	213	100	100	100
JAM3	606871	129	100	100	100
JMJD1C	604503	93	95	90	84
KALRN	604605	153	100	99	99
KANK1	607704	177	100	100	100
KANSL1	612452	188	100	100	100
KAT6A	601408	140	100	100	99
KAT6B	605880	131	99	95	92
KATNB1	602703	334	100	100	100
KCNA2	176262	209	100	100	100
KCNA4	176266	165	100	100	100
KCNB1	600397	279	100	100	100
KCNC3	176264	321	94	88	87
KCNH1	603305	163	100	100	99
KCNJ10	602208	271	100	100	100
KCNJ11	600937	382	100	100	100
KCNJ6	600877	177	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
KCNJ8	600935	559	100	100	100
KCNK9	605874	267	100	100	100
KCNMA1	600150	122	100	98	96
KCNQ10T1	604115	No coverage data			
KCNQ2	602235	274	100	100	100
KCNQ3	602232	186	100	100	98
KCNQ5	607357	107	100	99	93
KCNT1	608167	236	100	100	100
KCTD7	611725	259	100	100	100
KDM1A	609132	90	98	95	90
KDM4B	609765	285	100	100	100
KDM5B	605393	106	100	99	96
KDM5C	314690	130	100	100	99
KDM6A	300128	57	95	86	73
KDM6B	611577	250	100	100	99
KDSR	136440	104	100	100	99
KIAA0586	610178	62	96	86	75
KIAA1109	611565	71	99	95	88
KIAA1586	No ID	35	95	80	57
KIDINS220	615759	106	100	98	93
KIF11	148760	46	95	80	64
KIF1A	601255	260	100	100	100
KIF2A	602591	58	95	79	65
KIF4A	300521	54	100	91	73
KIF5C	604593	99	99	93	87
KIF7	611254	224	100	100	98
KIFBP	609367	117	100	100	100
KIRREL3	607761	297	100	100	100
KLHL15	300980	92	100	100	100
KMT2A	159555	118	100	100	98
KMT2B	606834	247	99	98	97
KMT2C	606833	126	98	96	92
KMT2D	602113	341	100	100	100
KMT2E	608444	101	98	91	86
KMT5B	610881	86	99	95	89
KNL1	609173	80	99	96	92
KPTN	615620	242	100	100	100
KRAS	190070	59	90	78	77
KRBOX4	300585	149	100	100	97
L1CAM	308840	164	100	100	100
L2HGDH	609584	73	97	96	93
LAMA1	150320	140	100	99	98
LAMA2	156225	96	100	98	93

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
LAMC1	150290	152	100	98	95
LAMC3	604349	249	100	100	100
LAMP2	309060	54	100	89	76
LARGE1	603590	204	100	100	100
LARP7	612026	37	95	79	62
LAS1L	300964	128	100	100	99
LIAS	607031	78	95	93	87
LIG4	601837	86	100	97	93
LINS1	610350	80	100	96	89
LMAN2L	609552	141	100	100	100
LONP1	605490	264	100	100	100
LRP2	600073	118	100	99	97
LRPPRC	607544	61	98	90	79
LZTFL1	606568	43	84	76	70
MAB21L2	604357	511	100	100	100
MACF1	608271	104	100	99	97
MACROD2	611567	58	96	90	83
MAF	177075	206	89	85	82
MAGEC3	300469	106	100	100	99
MAGEL2	605283	355	100	100	100
MAGT1	300715	69	93	87	78
MAN1B1	604346	251	100	100	100
MAN2B1	609458	213	100	100	100
MANBA	609489	93	100	99	94
MAOA	309850	74	100	99	92
MAP2K1	176872	148	100	100	99
MAP2K2	601263	276	100	100	100
MAPRE2	605789	98	100	100	98
MASP1	600521	195	100	100	100
MAST1	612256	274	100	100	100
MAT1A	610550	273	100	100	100
MBD5	611472	141	100	99	97
MBOAT7	606048	228	100	100	100
MBTPS2	300294	52	99	94	81
MCCC1	609010	111	100	96	95
MCCC2	609014	99	100	98	95
MCF2L	609499	230	100	100	100
MCM3AP	603294	161	100	99	98
MCOLN1	605248	216	100	100	100
MCOLN3	607400	65	100	97	89
MCPH1	607117	114	87	84	81
MDH2	154100	167	100	100	100
MECP2	300005	200	100	100	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
MECR	608205	137	100	100	99
MED12	300188	99	100	100	98
MED13L	608771	124	100	100	100
MED17	603810	82	97	87	68
MED23	605042	79	100	97	92
MED25	610197	200	100	100	100
MEF2C	600662	157	100	100	99
MEIS2	601740	161	100	100	100
METTL23	615262	109	100	100	100
MFSD2A	614397	161	100	100	100
MFSD8	611124	82	99	93	83
MGAT2	602616	328	100	100	100
MICU1	605084	88	98	92	84
MID1	300552	112	100	100	97
MID2	300204	81	99	94	87
MKKS	604896	251	100	100	100
MKS1	609883	157	100	100	100
MLC1	605908	181	100	100	95
MLYCD	606761	134	100	100	99
MMAA	607481	82	100	99	95
MMADHC	611935	56	85	85	80
MMUT	609058	101	100	95	92
MOCS1	603707	198	100	100	100
MOCS2	603708	81	100	100	97
MOGS	601336	229	100	100	100
MPDU1	604041	164	100	100	100
MPDZ	603785	104	100	99	95
MPLKIP	609188	126	100	100	100
MRPL3	607118	104	100	96	87
MRPS22	605810	72	100	98	85
MSL2	614802	128	100	100	100
MTFMT	611766	93	100	100	97
MTHFR	607093	191	100	100	100
MTHFS	604197	138	100	100	100
MTMR9	606260	94	100	99	94
MTOR	601231	147	100	100	100
MTR	156570	119	100	100	98
MTRR	602568	95	100	100	96
MVK	251170	207	100	100	100
MYCN	164840	275	100	100	100
MYH9	160775	156	100	100	99
MYO5A	160777	106	96	93	90
MYT1L	613084	174	100	97	91

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
NAA10	300013	98	100	100	100
NAA15	608000	59	99	91	78
NACC1	610672	272	100	100	100
NAGA	104170	226	100	100	100
NAGLU	609701	182	100	100	100
NALCN	611549	87	100	97	90
NANS	605202	140	100	100	99
NARS2	612803	79	97	93	84
NAT10	609221	146	99	96	96
NBEA	604889	68	98	93	82
NBN	602667	57	98	83	71
NCOR2	600848	183	100	100	99
NDE1	609449	133	100	100	100
NDP	300658	155	100	100	100
NDST1	600853	243	100	100	100
NDUFA1	300078	106	100	100	100
NDUFA11	612638	243	100	100	100
NDUFA12	614530	119	100	100	100
NDUFA2	602137	189	100	100	100
NDUFAF3	612911	230	100	100	100
NDUFAF5	612360	73	96	94	87
NDUFS1	157655	90	100	99	96
NDUFS2	602985	143	100	100	100
NDUFS3	603846	180	100	100	100
NDUFS4	602694	88	100	100	98
NDUFS6	603848	99	100	100	95
NDUFS7	601825	250	100	100	100
NDUFS8	602141	334	100	100	100
NDUFV1	161015	257	100	100	100
NDUFV2	600532	68	98	90	77
NECAP1	611623	150	100	100	100
NECTIN1	600644	175	100	100	100
NEDD4L	606384	98	98	96	93
NEU1	608272	238	100	100	100
NEXMIF	300524	94	100	100	100
NF1	613113	88	97	91	85
NFATC1	600489	265	100	100	100
NFE2L2	600492	137	100	100	99
NFIA	600727	112	100	100	100
NFIX	164005	273	100	100	100
NGLY1	610661	70	100	97	89
NHS	300457	96	100	99	97
NID1	131390	181	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
NIN	608684	97	98	94	91
NIPBL	608667	93	98	90	82
NKX2-1	600635	216	100	100	100
NLGN3	300336	154	100	100	99
NLGN4X	300427	201	100	100	100
NLRP3	606416	404	100	100	100
NONO	300084	75	100	90	83
NOVA2	601991	210	99	96	94
NPC1	607623	138	100	100	99
NPC2	601015	119	100	100	99
NPHP1	607100	89	97	96	89
NPRL3	600928	184	100	100	100
NR2F1	132890	208	100	99	96
NRAS	164790	107	100	100	99
NRXN1	600565	190	100	99	98
NSD1	606681	208	100	99	98
NSDHL	300275	88	100	100	95
NSUN2	610916	113	100	99	94
NTRK1	191315	272	100	100	100
NUP62	605815	345	100	100	100
OAT	613349	75	89	83	73
OCLN	602876	100	85	81	69
OCRL	300535	75	100	98	91
ODC1	165640	94	100	100	98
OFD1	300170	51	97	80	64
OPHN1	300127	71	100	99	91
ORC1	601902	148	100	100	100
OTC	300461	49	99	86	71
P2RX6	608077	254	100	100	100
PACS1	607492	151	100	99	97
PACS2	610423	210	100	100	99
PAFAH1B1	601545	72	86	86	85
PAH	612349	121	100	100	99
PAK3	300142	41	94	88	73
PANK2	606157	117	100	99	97
PANX1	608420	112	100	100	97
PAX1	167411	289	100	100	100
PAX6	607108	267	100	100	100
PAX8	167415	221	100	100	100
PBX1	176310	97	100	100	96
PC	608786	344	100	100	100
PCCA	232000	71	98	93	87
PCCB	232050	159	100	98	95

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
PCDH19	300460	221	100	100	98
PCGF2	600346	190	100	100	100
PCLO	604918	135	100	99	97
PCNT	605925	234	100	96	94
PDE4D	600129	88	100	96	90
PDHA1	300502	78	100	94	87
PDP1	605993	194	100	100	100
PDSS1	607429	69	100	96	82
PDSS2	610564	152	99	93	88
PEPD	613230	216	100	100	100
PET100	614770	178	100	100	100
PEX1	602136	80	95	94	90
PEX10	602859	266	100	100	100
PEX11B	603867	105	100	99	95
PEX12	601758	131	100	100	100
PEX13	601789	113	100	100	100
PEX16	603360	212	100	100	100
PEX19	600279	205	100	100	100
PEX2	170993	93	100	100	100
PEX26	608666	151	100	100	100
PEX3	603164	60	100	97	88
PEX5	600414	172	100	100	100
PEX6	601498	253	100	100	99
PEX7	601757	94	100	100	94
PGAP1	611655	42	92	74	56
PGAP2	615187	219	100	100	100
PGAP3	611801	208	100	100	100
PGK1	311800	89	100	100	95
PHC1	602978	141	100	100	98
PHF21A	608325	110	100	97	95
PHF23	612910	172	100	100	100
PHF6	300414	22	86	52	22
PHF8	300560	98	100	100	98
PHGDH	606879	199	100	100	100
PHIP	612870	68	94	90	84
PI4KA	600286	153	100	100	99
PIGA	311770	62	100	99	86
PIGC	601730	139	100	100	100
PIGG	616918	146	100	99	96
PIGL	605947	159	100	100	100
PIGN	606097	50	92	79	65
PIGO	614730	253	100	100	100
PIGT	610272	194	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
PIGV	610274	186	100	100	100
PIGW	610275	131	100	100	100
PIGY	610662	69	100	100	100
PIK3CA	171834	69	100	95	89
PIK3R2	603157	272	96	94	93
PLA2G6	603604	287	100	100	100
PLCB1	607120	80	98	94	87
PLK4	605031	77	98	90	83
PLP1	300401	86	100	98	92
PLXNA3	300022	179	100	100	100
PLXND1	604282	243	100	99	99
PMM2	601785	115	100	100	99
PMPCA	613036	189	100	100	100
PNKP	605610	246	100	100	100
PNP	164050	329	100	100	98
POC1A	614783	216	100	100	100
POGZ	614787	154	100	100	99
POLG	174763	188	100	100	100
POLR3A	614258	143	100	100	99
POLR3B	614366	93	100	97	92
POMGNT1	606822	228	100	100	100
POMGNT2	614828	358	100	100	100
POMK	615247	206	100	100	100
POMT1	607423	155	100	100	100
POMT2	607439	154	100	100	97
PORCN	300651	129	100	100	99
POU1F1	173110	65	92	91	85
POU3F3	602480	134	81	72	68
PPFIA4	603145	219	100	100	100
PPM1D	605100	133	100	100	98
PPOX	600923	195	100	100	100
PPP1CB	600590	90	100	100	97
PPP1R15B	613257	183	100	100	100
PPP2CA	176915	86	99	94	81
PPP2R1A	605983	241	100	100	100
PPP2R5B	601644	155	100	100	100
PPP2R5C	601645	84	95	89	79
PPP2R5D	601646	172	100	100	100
PPP3CA	114105	97	100	99	93
PPT1	600722	145	100	100	100
PQBP1	300463	124	100	100	100
PRIM1	176635	68	91	87	79
PRKAR1A	188830	98	100	100	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
PRKCE	176975	205	100	100	100
PRMT7	610087	208	100	100	99
PRODH	606810	222	100	99	98
PRPS1	311850	70	100	98	92
PRR12	616633	202	100	100	100
PRSS12	606709	157	100	100	100
PSAP	176801	134	100	100	99
PSMD12	604450	69	100	98	92
PTCH1	601309	201	100	100	98
PTCHD1	300828	101	100	100	99
PTDSS1	612792	101	100	100	100
PTEN	601728	100	99	94	87
PTF1A	607194	138	100	97	93
PTGR1	601274	87	100	98	96
PTPN11	176876	80	98	94	89
PTRH2	608625	192	100	100	100
PTRHD1	617342	264	100	100	100
PTS	612719	119	100	100	100
PUF60	604819	237	100	100	100
PUM1	607204	145	100	100	100
PURA	600473	481	100	100	100
PUS1	608109	233	100	100	100
PUS3	616283	128	100	100	99
PUS7	616261	88	100	96	93
PYCR1	179035	285	100	100	100
PYCR2	616406	201	100	100	100
QARS1	603727	206	100	100	100
QDPR	612676	134	100	100	100
RAB18	602207	68	91	90	85
RAB27A	603868	88	100	100	97
RAB39B	300774	156	100	100	99
RAB3GAP1	602536	86	100	99	95
RAB3GAP2	609275	96	97	91	81
RAB40AL	300405	174	100	100	100
RAC1	602048	113	100	95	86
RAD21	606462	63	100	98	93
RAD50	604040	51	94	76	57
RAF1	164760	124	100	98	97
RAI1	607642	405	100	100	100
RALA	179550	45	80	75	65
RARB	180220	98	100	98	92
RARS2	611524	70	100	93	77
RBBP8	604124	53	99	89	79

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
RBFOX1	605104	143	95	95	91
RBM10	300080	130	100	100	100
RBM28	612074	110	100	99	97
RBPJ	147183	79	99	91	81
RCBTB1	607867	129	100	100	96
RELN	600514	114	100	99	97
RERE	605226	243	100	100	99
REV3L	602776	86	98	96	91
RFT1	611908	134	100	95	89
RHEB	601293	28	90	59	39
RHOBTB2	607352	232	100	100	100
RIT1	609591	123	100	100	100
RLIM	300379	59	100	100	94
RMND1	614917	87	95	83	77
RMRP	157660	No coverage data			
RNASEH2A	606034	265	100	100	100
RNASEH2B	610326	60	100	99	89
RNASEH2C	610330	261	100	100	100
RNASET2	612944	99	93	92	84
RNF113A	300951	95	100	100	100
RNF125	610432	101	100	97	84
RNF135	611358	145	100	100	98
ROGDI	614574	222	100	99	97
RORA	600825	125	100	98	93
RPGRIP1L	610937	80	95	91	83
RPL10	312173	136	100	100	100
RPS6KA3	300075	37	96	80	55
RSPRY1	616585	93	100	96	94
RTKL1	608833	260	100	100	100
RTTN	610436	74	98	94	87
RUBCN	613516	163	100	100	100
RUSC2	611053	241	100	100	100
RXYLT1	605862	75	99	91	82
SALL1	602218	214	100	100	100
SAMHD1	606754	97	100	99	93
SATB1	602075	106	100	100	97
SATB2	608148	139	100	100	99
SBDS	607444	131	100	100	99
SC5D	602286	79	100	98	90
SCAF4	616023	104	98	95	90
SCN1A	182389	97	100	97	91
SCN1B	600235	224	100	100	100
SCN2A	182390	93	98	94	86

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
SCN3A	182391	92	100	96	90
SCN8A	600702	137	100	100	98
SCO1	603644	245	100	100	100
SCO2	604272	377	100	100	100
SDHA	600857	155	100	100	100
SEMA3E	608166	91	93	91	87
SEPSECS	613009	88	99	96	90
SERAC1	614725	98	98	95	89
SETBP1	611060	171	100	100	99
SETD1A	611052	215	100	99	99
SETD2	612778	113	100	99	98
SETD5	615743	121	100	99	96
SF1	601516	130	92	86	82
SGSH	605270	272	99	94	94
SH3KBP1	300374	85	100	97	92
SHANK2	603290	323	98	98	98
SHANK3	606230	246	99	98	97
SHH	600725	259	100	100	100
SHOC2	602775	74	100	100	96
SIK1	605705	309	100	100	100
SIL1	608005	202	100	100	98
SIN3A	607776	114	100	100	99
SIX3	603714	279	100	100	100
SKI	164780	208	100	100	98
SLC12A6	604878	98	100	97	95
SLC13A5	608305	194	100	100	100
SLC16A2	300095	101	100	100	100
SLC17A5	604322	82	100	94	85
SLC19A3	606152	108	100	100	100
SLC1A1	133550	114	100	100	99
SLC1A2	600300	139	100	100	100
SLC1A4	600229	125	100	100	100
SLC25A12	603667	94	100	100	97
SLC25A15	603861	152	100	100	100
SLC25A19	606521	168	100	100	100
SLC25A22	609302	317	100	100	100
SLC2A1	138140	354	100	100	100
SLC33A1	603690	147	98	93	85
SLC35A1	605634	69	100	99	95
SLC35A2	314375	196	100	100	99
SLC35A3	605632	49	93	85	76
SLC35C1	605881	329	100	100	100
SLC39A12	608734	85	100	97	88

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
SLC39A8	608732	91	100	93	85
SLC4A4	603345	110	100	99	96
SLC6A1	137165	177	100	100	98
SLC6A17	610299	180	100	100	100
SLC6A3	126455	226	100	100	100
SLC6A8	300036	134	100	100	97
SLC7A7	603593	146	100	100	100
SLC9A6	300231	89	98	88	81
SLC9A7	300368	70	100	96	91
SMAD4	600993	78	100	97	95
SMARCA2	600014	95	100	98	96
SMARCA4	603254	225	100	100	100
SMARCB1	601607	216	100	100	100
SMARCC2	601734	143	100	100	100
SMARCE1	603111	102	100	94	83
SMC1A	300040	96	100	96	95
SMC3	606062	46	93	80	60
SMOC1	608488	133	100	99	97
SMPD1	607608	377	100	100	100
SMPD4	610457	243	100	99	97
SMS	300105	61	100	93	86
SNAP25	600322	96	100	100	96
SNAP29	604202	107	100	100	95
SNIP1	608241	141	100	100	98
SNRNP70	180740	159	100	100	100
SNRPN	182279	141	100	100	100
SNX14	616105	43	83	65	53
SOBP	613667	172	100	98	97
SON	182465	170	100	98	94
SOS1	182530	74	94	89	79
SOS2	601247	64	95	80	67
SOX10	602229	381	100	100	100
SOX11	600898	201	100	100	100
SOX2	184429	257	100	100	100
SOX3	313430	155	100	100	100
SOX5	604975	117	100	100	98
SPAST	604277	82	99	84	69
SPATA5	613940	95	100	99	94
SPG11	610844	105	99	94	88
SPOCK1	602264	143	100	100	98
SPRED1	609291	108	100	100	98
SPTAN1	182810	147	100	99	98
SPTBN2	604985	211	100	99	98

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
SRCAP	611421	186	100	100	100
SRD5A3	611715	138	100	100	100
SRPX2	300642	102	100	100	100
SSR4	300090	139	100	100	100
ST3GAL3	606494	156	100	100	100
ST3GAL5	604402	100	100	93	92
STAG1	604358	73	95	89	83
STAMBP	606247	126	100	92	92
STIL	181590	192	100	99	95
STRA6	610745	229	100	100	100
STRADA	608626	154	100	100	96
STT3A	601134	119	100	100	100
STT3B	608605	67	99	92	83
STX1B	601485	139	100	100	100
STXBP1	602926	126	100	100	100
SUCLA2	603921	74	100	98	88
SUCLG1	611224	90	100	100	96
SUCO	No ID	73	93	90	82
SUMF1	607939	174	100	100	100
SUOX	606887	254	100	100	100
SURF1	185620	158	100	98	95
SUZ12	606245	49	79	75	65
SYN1	313440	151	100	100	100
SYNCRIP	616686	88	100	98	90
SYNE1	608441	113	100	98	95
SYNGAP1	603384	201	100	98	98
SYP	313475	110	100	100	99
SYT1	185605	69	97	88	79
SYT14	610949	71	100	94	82
SZT2	615463	206	100	100	100
TAF1	313650	71	100	99	95
TAF2	604912	66	98	89	80
TALPID3	610178	62	96	86	75
TAT	613018	141	100	100	100
TBC1D20	611663	149	100	100	96
TBC1D24	613577	390	100	100	100
TBC1D7	612655	94	95	85	85
TBCD	604649	210	99	97	95
TBCE	604934	69	100	96	87
TBCK	616899	56	95	88	76
TBL1XR1	608628	68	100	90	81
TBP	600075	140	100	99	90
TBR1	604616	270	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
TBX1	602054	131	94	90	87
TCF12	600480	94	100	99	96
TCF20	603107	182	100	100	100
TCF4	602272	145	100	99	97
TCN2	613441	190	100	100	100
TCTN3	613847	126	100	100	98
TDP2	605764	121	89	88	84
TECPR2	615000	195	100	99	97
TECR	610057	156	100	100	100
TELO2	611140	246	100	100	100
TFAP2A	107580	236	100	100	100
TGFBR1	190181	110	97	94	92
TGFBR2	190182	214	100	100	99
TGIF1	602630	133	100	100	100
TH	191290	266	100	100	100
THOC2	300395	34	82	62	47
THOC6	615403	231	100	100	100
THRB	190160	137	100	100	100
TIMM8A	300356	98	100	100	100
TINF2	604319	229	100	100	100
TLK2	608439	83	98	90	80
TM4SF20	615404	75	100	100	99
TMCO1	614123	96	91	89	82
TMEM165	614726	92	100	99	93
TMEM231	614949	271	100	100	98
TMEM237	614423	77	98	98	95
TMEM240	616101	287	100	100	100
TMEM67	609884	61	90	74	62
TMEM70	612418	103	100	98	94
TMLHE	300777	63	89	86	82
TMPRSS7	No ID	106	100	100	97
TMTC3	617218	47	96	79	62
TMX2	616715	147	100	100	100
TNIK	610005	107	100	98	92
TOE1	613931	204	100	100	100
TPI1	190450	190	100	100	100
TPO	606765	222	100	100	99
TPP1	607998	223	100	100	100
TRAIP	605958	175	100	100	100
TRAPPC11	614138	77	97	94	90
TRAPPC6B	610397	41	91	56	49
TRAPPC9	611966	213	100	100	100
TREX1	606609	313	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
TRIM32	602290	222	100	100	100
TRIO	601893	159	99	99	97
TRIP12	604506	87	100	99	97
TRMT1	611669	217	100	100	100
TRMT10A	616013	63	100	94	84
TRPM3	608961	179	100	100	99
TSC1	605284	153	100	100	100
TSC2	191092	314	100	100	100
TSEN15	608756	92	99	93	93
TSEN54	608755	201	100	100	98
TSHB	188540	84	100	100	97
TSPAN7	300096	97	100	100	99
TTC19	613814	101	100	98	93
TTC37	614589	65	99	96	91
TTC8	608132	104	96	91	86
TTI2	614426	133	100	100	100
TUBA1A	602529	219	100	100	100
TUBA8	605742	185	100	100	100
TUBB	191130	186	100	100	100
TUBB2A	615101	109	100	90	81
TUBB2B	612850	113	100	90	80
TUBB3	602661	330	100	100	97
TUBB4A	602662	233	100	100	100
TUBG1	191135	334	100	100	100
TUBGCP2	617817	193	100	100	100
TUBGCP4	609610	122	100	100	98
TUBGCP6	610053	356	100	100	100
TUSC3	601385	101	100	100	96
TWIST1	601622	187	100	100	98
TWINK	606075	231	100	100	100
UBA5	610552	52	93	78	66
UBE2A	312180	96	100	98	80
UBE3A	601623	79	98	89	83
UBE3B	608047	134	100	100	99
UBR1	605981	71	96	92	85
UNC80	612636	125	100	100	98
UPB1	606673	213	100	100	100
UPF3B	300298	40	83	64	48
UQCC2	614461	124	100	100	100
UQCRQ	612080	169	100	100	91
UROC1	613012	245	100	100	100
USP18	607057	132	95	95	95
USP27X	300975	106	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
USP7	602519	80	99	95	90
USP9X	300072	45	96	86	71
UTRN	128240	72	99	94	85
VLDLR	192977	120	100	100	98
VPS11	608549	184	100	100	100
VPS13B	607817	98	99	95	89
VPS13C	608879	63	96	87	77
VPS37A	609927	61	100	92	80
VPS53	615850	133	100	100	100
VRK1	602168	56	100	89	72
VWA3B	614884	101	100	99	94
WAC	615049	78	96	88	82
WASHC4	615748	45	93	80	65
WASHC5	610657	82	100	94	87
WBP11	618083	96	98	90	83
WDR13	300512	199	100	100	100
WDR19	608151	75	100	96	92
WDR26	617424	80	100	96	92
WDR4	605924	188	100	100	100
WDR45	300526	161	100	100	100
WDR62	613583	214	100	100	100
WDR73	616144	194	100	100	100
WDR81	614218	293	100	100	100
WFS1	606201	268	100	100	100
WWOX	605131	128	100	94	94
XIAP	300079	63	94	89	81
XPA	611153	49	99	92	75
XPC	613208	138	100	100	99
XPNPEP3	613553	157	100	100	99
XYLT1	608124	191	100	98	95
YAP1	606608	104	100	100	97
YIF1B	No ID	196	100	100	100
YME1L1	607472	68	93	88	80
YWHAE	605066	85	87	85	82
YY1	600013	156	100	100	99
ZBTB16	176797	309	100	100	100
ZBTB18	608433	289	100	100	100
ZBTB20	606025	302	100	100	100
ZBTB24	614064	155	100	100	100
ZC3H14	613279	76	98	96	88
ZC4H2	300897	88	100	100	100
ZDHHC15	300576	50	96	68	56
ZDHHC9	300646	77	100	100	98

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ZEB2	605802	289	100	100	100
ZFYVE26	612012	176	100	100	99
ZIC1	600470	322	100	100	100
ZIC2	603073	171	95	93	91
ZIC4	608948	291	100	100	100
ZMYND11	608668	86	100	99	93
ZNF101	603983	106	100	100	100
ZNF292	616213	98	100	99	98
ZNF407	615894	224	100	100	100
ZNF41	314995	87	100	99	96
ZNF592	613624	263	100	100	100
ZNF674	300573	77	100	95	77
ZNF711	314990	58	99	92	81
ZNF81	314998	59	100	99	93
ZSWIM6	615951	118	97	94	91

- 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