

Whole Exome Sequencing

Gene package Multiple congenital anomaly, version 9, 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
A4GALT	607922	146	100	100	99
AAAS	605378	102	100	100	100
AAGAB	614888	59	100	100	97
AARS1	601065	89	100	100	96
AARS2	612035	122	100	100	100
AASS	605113	63	100	97	90
ABAT	137150	100	100	100	96
ABCA1	600046	92	100	100	97
ABCA12	607800	68	100	100	95
ABCA3	601615	107	100	100	98
ABCA4	601691	94	100	100	97
ABCB11	603201	67	100	100	96
ABCB4	171060	69	100	99	92
ABCB6	605452	110	100	100	100
ABCB7	300135	59	100	98	87
ABCC2	601107	76	100	99	95
ABCC6	603234	118	100	100	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ABCC8	600509	105	100	100	100
ABCC9	601439	65	100	100	95
ABCD1	300371	86	84	78	75
ABCD4	603214	108	100	100	100
ABCG5	605459	80	100	100	99
ABCG8	605460	149	100	98	95
ABHD12	613599	61	100	100	94
ABHD5	604780	74	100	100	98
ABL1	189980	141	100	100	100
ACAD8	604773	159	100	100	100
ACAD9	611103	95	100	100	100
ACADM	607008	66	100	100	96
ACADS	606885	121	100	100	100
ACADSB	600301	67	100	100	94
ACADVL	609575	114	100	100	98
ACAN	155760	150	93	93	92
ACAT1	607809	71	100	100	93
ACE	106180	108	100	100	100
ACO2	100850	146	100	98	94
ACOX1	609751	103	100	100	99
ACP5	171640	143	100	100	100
ACSF3	614245	149	100	100	100
ACSL4	300157	54	100	98	88
ACSL6	604443	83	100	100	98
ACTA1	102610	138	100	100	100
ACTA2	102620	167	100	100	100
ACTB	102630	192	100	100	100
ACTC1	102540	194	100	100	100
ACTG1	102560	188	100	100	100
ACTG2	102545	95	100	100	100
ACTN1	102575	118	100	100	100
ACTN4	604638	119	100	100	98
ACVR1	102576	73	100	100	99
ACVR1B	601300	81	100	100	94
ACVR2B	602730	105	100	100	98
ACVRL1	601284	102	100	100	95

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ACY1	104620	109	100	100	100
ADA	608958	85	100	100	96
ADA2	607575	96	100	100	99
ADAM10	602192	57	100	99	91
ADAM17	603639	67	100	99	94
ADAM9	602713	57	100	99	92
ADAMTS10	608990	112	100	100	100
ADAMTS13	604134	92	97	97	95
ADAMTS17	607511	100	97	95	92
ADAMTS18	607512	79	100	100	98
ADAMTS19	607513	67	100	93	86
ADAMTS2	604539	111	100	100	99
ADAMTSL2	612277	51	44	41	39
ADAMTSL4	610113	115	100	100	99
ADAR	146920	90	100	100	100
ADAT3	615302	152	100	100	100
ADCY5	600293	111	98	95	93
ADGRG1	604110	120	100	100	100
ADGRV1	602851	80	100	100	97
ADIPOQ	605441	87	100	100	100
ADK	102750	53	100	93	80
ADRB2	109690	117	100	100	100
ADSL	608222	89	100	100	96
AFF2	300806	57	100	99	92
AFG3L2	604581	77	99	95	90
AGA	613228	73	100	100	96
AGBL1	615496	74	98	98	97
AGK	610345	57	100	100	93
AGL	610860	72	100	100	95
AGPAT2	603100	142	100	100	96
AGPS	603051	61	100	99	90
AGRN	103320	140	100	98	95
AGT	106150	129	100	100	100
AGTR1	106165	55	100	100	100
AGXT	604285	133	100	100	100
AHCY	180960	151	96	96	96

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
AHDC1	615790	129	100	99	98
AHI1	608894	67	100	98	90
AHNAK2	608570	284	100	100	99
AICDA	605257	134	100	100	95
AIFM1	300169	55	100	96	82
AIMP1	603605	78	100	100	96
AIP	605555	134	100	100	100
AIPL1	604392	141	100	100	100
AIRE	607358	100	100	100	100
AK1	103000	124	100	100	100
AK2	103020	68	100	100	97
AKAP9	604001	76	100	100	96
AKR1C2	600450	71	91	91	85
AKR1D1	604741	64	100	100	97
AKT1	164730	147	100	100	100
AKT2	164731	112	100	100	100
AKT3	611223	70	100	99	90
ALAD	125270	104	100	100	100
ALAS2	301300	60	100	98	90
ALB	103600	63	100	100	95
ALDH18A1	138250	80	100	100	98
ALDH1A3	600463	88	100	100	97
ALDH2	100650	127	100	100	100
ALDH3A2	609523	64	100	99	93
ALDH4A1	606811	118	100	100	99
ALDH5A1	610045	66	100	97	91
ALDH6A1	603178	98	100	100	98
ALDH7A1	107323	69	100	100	91
ALDOA	103850	144	100	100	100
ALDOB	612724	102	100	100	100
ALG1	605907	61	91	79	73
ALG11	613666	73	100	100	99
ALG12	607144	158	100	100	100
ALG13	300776	50	100	97	83
ALG2	607905	81	100	100	99
ALG3	608750	95	100	100	100

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ALG6	604566	73	100	100	96
ALG8	608103	62	100	100	94
ALG9	606941	64	100	100	94
ALMS1	606844	100	100	100	99
ALOX12B	603741	113	100	100	99
ALOXE3	607206	111	100	100	98
ALPK1	607347	73	100	99	94
ALPL	171760	130	100	100	100
ALS2	606352	72	100	100	96
ALX1	601527	78	100	100	100
ALX3	606014	116	98	91	86
ALX4	605420	139	100	100	100
AMACR	604489	96	100	100	98
AMELX	300391	137	100	100	100
AMER1	300647	73	100	99	97
AMH	600957	104	100	100	100
AMHR2	600956	123	100	100	99
AMN	605799	89	100	93	83
AMPD1	102770	67	100	99	95
AMT	238310	130	100	100	100
ANG	105850	126	100	100	100
ANGPTL3	604774	59	100	100	95
ANK1	612641	113	100	100	98
ANK2	106410	74	100	100	98
ANKH	605145	91	100	100	99
ANKK1	608774	110	100	100	100
ANKRD11	611192	112	100	98	96
ANKRD26	610855	70	100	98	90
ANKS6	615370	89	95	93	90
ANO10	613726	57	100	99	88
ANO3	610110	61	93	92	87
ANO5	608662	77	100	100	96
ANO6	608663	70	100	100	97
ANOS1	300836	57	100	95	84
ANTXR1	606410	60	99	97	92
ANTXR2	608041	65	100	100	96

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
AP1S1	603531	84	100	100	96
AP1S2	300629	40	100	87	62
AP2S1	602242	100	100	100	100
AP3B1	603401	66	100	98	87
AP4B1	607245	81	100	100	100
AP4E1	607244	64	100	100	96
AP4M1	602296	130	100	100	99
AP4S1	607243	44	100	99	87
AP5Z1	613653	111	100	100	99
APCDD1	607479	125	100	100	100
APOA1	107680	130	100	100	100
APOA2	107670	90	100	100	100
APOA5	606368	179	100	100	100
APOB	107730	159	100	100	100
APOC2	608083	91	100	100	100
APOC3	107720	136	100	100	100
APRT	102600	81	100	100	100
APTX	606350	76	100	99	92
AQP2	107777	113	100	100	100
AQP5	600442	116	100	100	100
AR	313700	81	100	98	94
ARFGEF2	605371	83	100	100	96
ARG1	608313	75	100	100	98
ARHGAP26	605370	88	100	100	99
ARHGAP31	610911	103	100	100	99
ARHGEF10	608136	106	100	100	98
ARHGEF12	604763	67	100	99	94
ARHGEF6	300267	47	100	97	83
ARHGEF9	300429	50	100	99	85
ARID1A	603024	121	100	99	97
ARID1B	614556	102	100	100	98
ARL13B	608922	63	100	100	94
ARL2BP	615407	57	100	100	96
ARL6	608845	43	96	95	83
ARMC4	615408	67	98	96	92
ARNT	126110	53	100	99	91

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ARSA	607574	136	100	100	100
ARSB	611542	73	100	100	98
ARSL	300180	46	89	79	68
ARX	300382	46	89	79	68
ASAH1	613468	67	100	100	93
ASB10	615054	98	100	100	98
ASCC1	614215	52	100	93	81
ASCL1	100790	259	100	100	100
ASL	608310	117	100	100	99
ASNS	108370	73	100	100	92
ASPA	608034	55	100	99	91
ASPM	605481	71	100	100	97
ASPSCR1	606236	106	100	98	95
ASS1	603470	115	100	98	90
ASXL1	612990	107	100	98	98
ASXL3	615115	69	99	99	97
ATCAY	608179	116	100	100	96
ATIC	601731	62	100	100	96
ATL1	606439	72	100	100	93
ATL3	609369	56	100	99	93
ATM	607585	75	100	99	95
ATN1	607462	155	100	100	99
ATP13A2	610513	117	100	100	98
ATP1A2	182340	130	100	100	100
ATP1A3	182350	144	100	100	100
ATP2A1	108730	115	100	100	99
ATP2A2	108740	99	100	100	100
ATP2C1	604384	61	100	98	93
ATP5F1C	108729	52	100	93	74
ATP5F1E	606153	88	100	100	100
ATP6V0A2	611716	81	100	100	97
ATP6V0A4	605239	77	100	100	96
ATP6V1B1	192132	136	100	100	100
ATP7A	300011	49	100	98	84
ATP7B	606882	99	100	100	99
ATP8B1	602397	70	100	100	95

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ATPAF2	608918	73	100	100	100
ATR	601215	91	100	99	92
ATRX	300032	40	100	94	78
ATXN1	601556	116	100	100	100
ATXN10	611150	63	100	100	95
ATXN2	601517	75	97	93	86
ATXN3	607047	87	100	99	92
ATXN7	607640	90	100	97	93
ATXN8OS	603680	No coverage data			
AUH	600529	94	100	100	98
AURKC	603495	76	100	100	100
AVP	192340	64	100	97	86
AVPR2	300538	85	100	100	99
AXIN1	603816	127	100	99	97
AXIN2	604025	108	100	100	98
B2M	109700	94	100	100	100
B3GALNT2	610194	59	100	100	97
B3GALT6	615291	64	79	75	72
B3GAT3	606374	125	100	100	100
B3GLCT	610308	67	100	99	85
B4GALNT1	601873	111	100	100	100
B4GALT1	137060	95	100	100	100
B4GALT7	604327	126	100	100	98
B4GAT1	605517	154	100	100	100
B9D1	614144	90	100	100	100
B9D2	611951	82	100	100	100
BAAT	602938	73	100	100	87
BAG3	603883	196	100	100	100
BANF1	603811	115	100	100	100
BAP1	603089	121	100	100	100
BAX	600040	93	100	100	93
BBS1	209901	126	100	100	100
BBS10	610148	66	100	100	100
BBS12	610683	59	100	100	99
BBS2	606151	77	100	100	97
BBS4	600374	76	100	100	95

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
BBS5	603650	65	100	98	89
BBS7	607590	64	100	99	95
BBS9	607968	59	96	95	90
BCAP31	300398	83	100	100	97
BCHE	177400	71	100	100	99
BCKDHA	608348	160	100	100	100
BCKDHB	248611	64	100	99	94
BCKDK	614901	167	100	100	100
BCL10	603517	66	100	100	96
BCL2	151430	152	100	100	100
BCL7A	601406	110	100	100	100
BCO1	605748	74	100	100	97
BCOR	300485	78	100	99	94
BCR	151410	144	100	100	100
BCS1L	603647	170	100	100	100
BDNF	113505	104	100	100	100
BEAN1	612051	159	100	100	100
BEST1	607854	94	100	99	98
BFSP1	603307	98	100	100	96
BFSP2	603212	73	100	99	92
BGN	301870	87	100	100	98
BICD2	609797	133	100	100	99
BIN1	601248	105	100	100	94
BLK	191305	113	100	100	100
BLM	604610	82	100	100	96
BLNK	604515	60	100	98	88
BLOC1S3	609762	104	100	100	100
BLOC1S6	604310	46	100	100	84
BLVRA	109750	78	100	100	97
BMP1	112264	118	100	100	100
BMP15	300247	56	100	100	96
BMP2	112261	123	100	100	99
BMP4	112262	103	100	96	93
BMPER	608699	99	100	100	97
BMPR1A	601299	76	100	100	100
BMPR1B	603248	72	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
BMPR2	600799	65	100	100	98
BOLA3	613183	69	100	100	91
BPGM	613896	71	100	100	99
BPNT2	614010	146	100	100	97
BRAF	164757	68	100	100	94
BRAT1	614506	125	100	100	100
BRIP1	605882	55	100	99	91
BRWD3	300553	45	100	95	81
BSCL2	606158	101	100	100	100
BSND	606412	115	100	100	100
BTB	609019	89	100	100	100
BTK	300300	50	100	98	83
BUB1	602452	79	100	100	97
BUB1B	602860	70	100	99	94
C12orf57	615140	141	100	100	100
C12orf65	613541	78	100	100	100
C15orf41	615626	63	100	100	99
C19orf12	614297	186	100	100	100
C1GALT1C1	300611	47	100	100	95
C1QA	120550	155	100	100	100
C1QB	120570	121	100	100	100
C1QC	120575	150	100	100	100
C1QTNF5	608752	102	100	100	93
C1S	120580	96	100	100	98
C2	613927	106	100	100	100
C3	120700	127	100	100	99
C4A	120810	38	22	20	19
C4B	120820	36	24	22	21
C5	120900	72	100	98	94
C6	217050	65	100	99	94
C7	217070	79	100	99	96
C8A	120950	69	100	100	98
C8B	120960	100	100	100	98
C8orf37	614477	78	100	100	96
C9	120940	66	100	100	97
C9orf72	614260	56	100	100	96

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CA12	603263	73	100	100	99
CA2	611492	99	100	100	100
CA4	114760	100	100	100	100
CA5A	114761	175	100	100	100
CA8	114815	79	100	100	94
CABP2	607314	94	100	100	96
CABP4	608965	149	100	100	100
CACNA1A	601011	87	100	98	93
CACNA1C	114205	123	100	100	99
CACNA1D	114206	102	100	100	98
CACNA1F	300110	76	100	100	96
CACNA1G	604065	146	100	100	100
CACNA1S	114208	119	100	100	100
CACNA2D4	608171	86	100	100	98
CACNB2	600003	100	100	100	100
CACNB4	601949	57	100	100	94
CACNG2	602911	107	100	100	99
CALCOCO1	No ID	85	100	100	98
CALM1	114180	64	100	100	100
CALR	109091	136	100	100	100
CALR3	611414	67	100	100	97
CAMTA1	611501	161	100	99	97
CANT1	613165	128	100	100	100
CAPN3	114240	91	100	100	99
CAPN5	602537	143	100	100	99
CARD11	607210	108	100	100	99
CARD14	607211	112	100	99	99
CARD9	607212	122	100	100	99
CARS1	123859	83	100	98	92
CASK	300172	51	100	96	80
CASP10	601762	75	100	100	97
CASP8	601763	87	100	100	100
CASQ2	114251	65	100	100	97
CASR	601199	146	100	100	100
CAT	115500	70	100	100	93
CATSPER1	606389	109	100	100	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
CAV1	601047	95	100	100	100
CAV3	601253	150	100	100	100
CAVIN1	603198	172	100	100	100
CBL	165360	78	100	100	100
CBLIF	609342	No coverage data			
CBS	613381	127	100	100	100
CBX2	602770	176	100	100	100
CC2D1A	610055	132	100	100	100
CC2D2A	612013	66	100	100	95
CCBE1	612753	87	100	99	95
CCDC103	614677	83	100	100	100
CCDC114	615038	125	100	100	100
CCDC39	613798	80	100	99	94
CCDC40	613799	100	100	100	100
CCDC50	611051	73	100	100	98
CCDC65	611088	57	100	100	94
CCDC78	614666	123	100	100	100
CCDC8	614145	194	100	100	100
CCDC88C	611204	104	100	100	97
CCM2	607929	144	100	100	96
CCN6	603400	83	100	100	100
CCNQ	300708	62	81	81	81
CCT5	610150	85	100	100	91
CD151	602243	89	100	100	100
CD19	107265	107	100	100	99
CD247	186780	74	100	100	100
CD27	186711	95	100	100	100
CD2AP	604241	68	100	100	96
CD320	606475	95	100	100	100
CD36	173510	67	100	99	93
CD3D	186790	100	100	100	99
CD3E	186830	113	100	100	100
CD3G	186740	76	100	100	99
CD4	186940	103	100	100	100
CD40	109535	104	100	100	100
CD40LG	300386	67	100	100	97

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
CD59	107271	86	100	100	100
CD79A	112205	83	100	91	85
CD79B	147245	146	100	100	100
CD81	186845	146	97	90	90
CD8A	186910	100	100	100	97
CD96	606037	74	100	99	96
CDAN1	607465	95	100	100	98
CDC6	602627	65	100	100	98
CDC73	607393	75	100	100	97
CDH1	192090	92	100	100	99
CDH15	114019	125	100	100	100
CDH23	605516	135	100	100	100
CDH3	114021	124	100	100	100
CDHR1	609502	116	100	100	98
CDK5RAP2	608201	69	100	99	94
CDKL5	300203	58	100	97	87
CDKN1B	600778	163	100	100	100
CDKN1C	600856	74	90	83	76
CDKN2A	600160	139	100	100	100
CDON	608707	89	100	100	99
CDSN	602593	103	100	100	100
CDT1	605525	125	100	98	95
CEACAM16	614591	94	100	100	100
CEBPA	116897	130	100	93	75
CEBPE	600749	57	100	100	99
CEL	114840	151	94	90	87
CENPJ	609279	74	100	100	98
CEP135	611423	83	100	99	91
CEP152	613529	67	100	98	93
CEP164	614848	93	100	100	98
CEP19	615586	77	100	100	100
CEP290	610142	71	100	98	89
CEP41	610523	69	100	100	94
CEP57	607951	62	100	100	95
CERKL	608381	73	100	99	94
CERS3	615276	65	100	100	94

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
CES1	114835	126	77	77	76
CETP	118470	95	100	100	100
CFAP298	615494	75	100	100	96
CFAP53	614759	98	100	100	98
CFC1	605194	70	41	34	28
CFD	134350	99	100	98	90
CFH	134370	78	100	100	96
CFHR5	608593	75	100	100	97
CFI	217030	67	100	99	93
CFL2	601443	45	100	97	77
CFP	300383	68	100	95	86
CFTR	602421	93	100	100	97
CHAT	118490	130	99	92	88
CHD2	602119	72	100	100	96
CHD7	608892	87	100	100	97
CHKB	612395	111	100	100	100
CHM	300390	50	100	94	80
CHMP1A	164010	102	100	100	100
CHMP2B	609512	83	100	100	97
CHMP4B	610897	178	100	100	100
CHN1	118423	62	100	100	92
CHRD1	300350	48	100	100	92
CHRM3	118494	110	100	100	100
CHRNA1	100690	86	100	100	98
CHRNA2	118502	170	100	100	100
CHRNA4	118504	138	100	100	96
CHRNA1	100710	124	100	100	100
CHRNA2	118507	144	100	100	100
CHRNA3	100720	135	100	100	100
CHRNA4	100725	138	100	100	100
CHRNA5	100730	116	100	100	99
CHST14	608429	133	100	98	97
CHST3	603799	129	100	100	100
CHST6	605294	246	100	100	100
CHSY1	608183	79	98	95	92
CHUK	600664	66	100	99	92

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
CIB2	605564	195	100	100	100
CIITA	600005	117	100	100	99
CILK1	612325	59	100	99	91
CISD2	611507	137	100	100	100
CITED2	602937	93	100	100	100
CLCF1	607672	58	100	99	93
CLCN1	118425	101	100	100	100
CLCN2	600570	100	100	100	100
CLCN5	300008	59	100	100	96
CLCN7	602727	128	100	100	99
CLCNKA	602024	151	100	100	99
CLCNKB	602023	138	100	100	100
CLDN1	603718	115	100	100	100
CLDN14	605608	66	100	98	91
CLDN16	603959	73	100	100	97
CLDN19	610036	149	100	100	100
CLEC7A	606264	64	100	100	91
CLIC2	300138	40	100	90	69
CLMP	611693	73	100	100	100
CLN3	607042	111	100	100	100
CLN5	608102	70	100	100	100
CLN6	606725	120	100	100	99
CLN8	607837	129	100	100	100
CLPP	601119	125	100	100	100
CLRN1	606397	83	100	100	97
CNBP	116955	47	100	100	94
CNGA1	123825	62	96	91	86
CNGA3	600053	118	100	100	100
CNGB1	600724	112	100	100	99
CNGB3	605080	62	100	100	95
CNNM2	607803	161	100	100	99
CNNM4	607805	140	100	100	99
CNTN1	600016	70	100	100	97
CNTNAP2	604569	73	100	100	99
CNTNAP4	610518	86	100	99	95
COA5	613920	92	100	100	89

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
COASY	609855	139	100	100	100
COCH	603196	71	98	95	93
COG1	606973	96	100	100	98
COG4	606976	81	100	100	99
COG5	606821	66	100	99	91
COG6	606977	65	100	99	90
COG7	606978	83	100	100	98
COG8	606979	125	100	100	100
COL10A1	120110	90	100	100	99
COL11A1	120280	62	100	99	93
COL11A2	120290	110	100	100	100
COL17A1	113811	98	100	100	99
COL18A1	120328	143	100	100	97
COL1A1	120150	130	100	100	100
COL1A2	120160	70	100	100	97
COL2A1	120140	97	100	100	99
COL3A1	120180	122	100	100	100
COL4A1	120130	88	100	100	97
COL4A2	120090	102	100	100	99
COL4A3	120070	63	100	97	90
COL4A4	120131	70	100	100	96
COL4A5	303630	42	100	88	67
COL5A1	120215	136	100	100	98
COL5A2	120190	65	100	100	94
COL6A1	120220	147	100	100	100
COL6A2	120240	148	100	100	99
COL6A3	120250	104	100	100	99
COL7A1	120120	129	100	100	100
COL8A2	120252	95	100	100	98
COL9A1	120210	65	100	99	91
COL9A2	120260	100	100	99	96
COL9A3	120270	88	98	96	92
COLEC11	612502	168	100	100	100
COLQ	603033	83	100	100	98
COMP	600310	112	100	97	93
COQ2	609825	66	100	100	94

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
COQ6	614647	81	100	99	93
COQ8A	606980	129	100	100	100
COQ8B	615567	93	100	98	96
COQ9	612837	105	100	100	100
CORIN	605236	78	100	100	99
CORO1A	605000	122	92	92	91
COX10	602125	139	100	100	99
COX14	614478	138	100	100	100
COX15	603646	65	100	98	92
COX20	614698	53	100	97	83
COX4I2	607976	97	100	100	100
COX7B	300885	61	100	100	100
CP	117700	63	100	100	96
CPA6	609562	79	100	99	94
CPLANE1	614571	71	100	99	95
CPN1	603103	87	100	100	97
CPOX	612732	82	100	100	98
CPS1	608307	61	100	100	96
CPT1A	600528	109	100	100	98
CPT2	600650	106	100	100	99
CR2	120650	63	100	100	97
CRADD	603454	139	100	100	100
CRB1	604210	71	100	100	99
CRBN	609262	67	100	99	91
CREB1	123810	77	100	100	100
CREBBP	600140	85	100	99	94
CRELD1	607170	100	100	100	100
CRLF1	604237	105	96	91	89
CRPPA	614631	81	100	99	93
CRTAP	605497	86	100	100	99
CRTC1	607536	146	100	100	99
CRX	602225	196	100	100	100
CRYAA	123580	136	100	100	100
CRYAB	123590	79	100	100	100
CRYBA1	123610	74	100	100	100
CRYBA4	123631	106	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
CRYBB1	600929	97	100	100	100
CRYBB2	123620	181	100	100	100
CRYBB3	123630	105	100	100	100
CRYGB	123670	87	100	100	100
CRYGC	123680	86	100	100	100
CRYGD	123690	97	100	100	100
CRYGS	123730	104	100	100	100
CRYM	123740	76	100	100	99
CSF1R	164770	99	100	100	100
CSF2RA	306250	No coverage data			
CSF2RB	138981	132	100	100	100
CSF3R	138971	98	100	100	100
CSNK1D	600864	101	100	100	100
CSPP1	611654	83	100	100	97
CSRP3	600824	102	100	100	100
CST3	604312	97	100	100	92
CSTA	184600	60	100	100	96
CSTB	601145	84	100	100	100
CTC1	613129	100	100	100	100
CTCF	604167	98	100	100	100
CTDP1	604927	125	98	89	87
CTH	607657	76	100	100	98
CTHRC1	610635	80	100	97	91
CTNNA3	607667	61	100	100	96
CTNNB1	116806	62	100	100	97
CTNS	606272	118	100	100	100
CTSA	613111	124	100	100	100
CTSC	602365	75	100	100	97
CTSD	116840	137	100	100	100
CTSF	603539	94	100	94	91
CTSK	601105	65	100	100	98
CUBN	602997	82	100	100	96
CUL3	603136	73	100	97	88
CUL4B	300304	52	100	96	82
CUL7	609577	111	100	100	100
CXCR4	162643	82	83	83	82

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
CYB5A	613218	77	100	100	100
CYB5R3	613213	127	100	100	100
CYBA	608508	106	94	81	66
CYBB	300481	49	100	98	91
CYC1	123980	151	100	100	94
CYCS	123970	55	100	100	99
CYLD	605018	56	100	98	89
CYP11A1	118485	108	100	100	100
CYP11B1	610613	209	100	100	100
CYP11B2	124080	212	100	100	100
CYP17A1	609300	113	100	100	100
CYP19A1	107910	66	100	99	93
CYP1B1	601771	97	100	100	100
CYP21A2	613815	201	100	100	100
CYP24A1	126065	90	100	100	98
CYP26B1	605207	159	100	100	100
CYP26C1	608428	130	100	100	100
CYP27A1	606530	131	100	100	100
CYP27B1	609506	122	100	100	100
CYP2A6	122720	198	100	100	100
CYP2B6	123930	109	100	100	100
CYP2C19	124020	101	100	100	99
CYP2C8	601129	86	100	97	94
CYP2C9	601130	101	100	99	96
CYP2R1	608713	74	100	100	98
CYP2U1	610670	66	100	100	96
CYP46A1	604087	67	100	97	89
CYP4F22	611495	113	100	100	100
CYP4V2	608614	82	100	100	98
CYP7B1	603711	67	100	100	98
D2HGDH	609186	140	100	100	100
DAG1	128239	164	100	100	100
DARS1	603084	60	100	99	89
DARS2	610956	63	100	100	97
DBH	609312	136	100	100	100
DBT	248610	115	100	100	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
DCAF17	612515	75	100	100	94
DCC	120470	70	100	100	98
DCHS1	603057	128	100	100	100
DCLRE1C	605988	64	100	100	92
DCN	125255	69	100	100	100
DCTN1	601143	95	100	100	99
DCX	300121	57	100	98	92
DDB2	600811	113	100	100	99
DDC	107930	84	100	99	92
DDHD1	614603	107	100	98	92
DDHD2	615003	76	100	100	97
DDOST	602202	92	100	100	100
DDR2	191311	89	100	100	99
DDX11	601150	254	100	100	100
DDX3X	300160	76	100	100	98
DDX59	615464	62	100	98	92
DEPDC5	614191	83	100	100	97
DES	125660	106	100	100	100
DGKE	601440	106	100	100	98
DGUOK	601465	73	100	100	92
DHCR24	606418	119	100	100	100
DHCR7	602858	112	100	100	100
DHDDS	608172	69	100	100	99
DHFR	126060	76	100	100	98
DHH	605423	138	100	100	100
DHODH	126064	87	100	100	96
DHTKD1	614984	85	100	100	98
DIABLO	605219	105	100	100	99
DIAPH1	602121	84	100	99	93
DIAPH2	300108	44	100	92	75
DIAPH3	614567	61	100	99	93
DICER1	606241	77	100	99	95
DIP2B	611379	65	100	100	97
DIS3L2	614184	100	100	100	97
DKC1	300126	53	100	98	89
DLAT	608770	74	100	98	90

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
DLC1	604258	98	100	100	99
DLD	238331	77	100	100	98
DLG3	300189	61	100	97	88
DLL3	602768	100	100	96	89
DLX3	600525	137	100	100	84
DLX5	600028	109	100	100	100
DMD	300377	46	100	96	81
DMGDH	605849	75	100	100	99
DMP1	600980	80	100	100	97
DMPK	605377	117	100	100	99
DNA2	601810	93	100	100	96
DNAAF1	613190	131	100	100	99
DNAAF2	612517	124	100	100	100
DNAAF3	614566	98	100	100	99
DNAAF4	608706	54	100	99	89
DNAAF5	614864	104	96	86	79
DNAH11	603339	74	100	100	96
DNAH5	603335	74	100	100	96
DNAI1	604366	91	100	98	97
DNAI2	605483	131	100	100	99
DNAJB2	604139	103	100	100	100
DNAJB6	611332	66	100	99	93
DNAJC19	608977	75	100	100	96
DNAJC5	611203	217	100	100	100
DNAJC6	608375	84	100	100	98
DNAL1	610062	77	100	100	95
DNASE1L3	602244	67	100	100	98
DNHD1	617277	117	100	100	100
DNM1L	603850	70	100	99	94
DNM2	602378	111	100	100	99
DNMT1	126375	93	100	100	97
DNMT3B	602900	115	100	100	99
DOCK3	603123	84	100	100	98
DOCK6	614194	108	100	98	96
DOCK8	611432	74	100	99	94
DOK7	610285	119	96	93	92

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
DOLK	610746	136	100	100	100
DPAGT1	191350	76	100	100	100
DPM1	603503	79	94	89	85
DPM2	603564	76	100	100	100
DPM3	605951	227	100	100	100
DPP6	126141	82	100	97	90
DPY19L2	613893	90	98	95	88
DPYD	612779	66	100	99	95
DPYS	613326	75	100	100	98
DRC1	615288	81	100	100	98
DRD2	126450	113	100	100	100
DRD4	126452	107	100	90	82
DRD5	126453	239	100	100	100
DSC2	125645	184	100	100	100
DSC3	600271	73	100	99	89
DSG1	125670	80	100	99	95
DSG2	125671	158	100	100	99
DSG4	607892	77	100	100	98
DSP	125647	156	100	100	100
DSPP	125485	43	95	70	55
DST	113810	67	100	99	95
DSTYK	612666	77	100	98	93
DTNA	601239	84	100	100	100
DTNBP1	607145	94	100	100	96
DUOX2	606759	113	98	97	96
DUOXA2	612772	121	100	100	100
DUSP6	602748	144	100	100	100
DYM	607461	67	100	98	88
DYNC1H1	600112	96	100	100	99
DYNC2H1	603297	71	100	99	91
DYRK1A	600855	75	100	100	98
DYSF	603009	108	100	100	99
EARS2	612799	91	100	100	99
EBP	300205	93	100	100	100
ECE1	600423	114	97	97	97
ECEL1	605896	98	100	98	93

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ECM1	602201	125	100	100	100
EDA	300451	85	100	99	95
EDAR	604095	103	100	100	100
EDARADD	606603	65	100	100	98
EDN1	131240	92	100	100	93
EDN3	131242	90	100	100	98
EDNRA	131243	74	100	100	98
EDNRB	131244	96	100	100	100
EFEMP1	601548	99	100	100	99
EFEMP2	604633	103	100	100	100
EFNB1	300035	68	100	100	100
EFTUD2	603892	85	100	100	99
EGF	131530	74	100	100	97
EGFR	131550	87	100	100	98
EGLN1	606425	114	100	92	83
EGR2	129010	99	100	100	100
EHMT1	607001	126	99	99	99
EIF2AK3	604032	72	100	99	94
EIF2AK4	609280	73	100	99	95
EIF2B1	606686	79	100	100	100
EIF2B2	606454	77	100	98	91
EIF2B3	606273	58	100	100	94
EIF2B4	606687	89	100	100	100
EIF2B5	603945	72	100	100	98
EIF4A3	608546	68	100	100	97
EIF4G1	600495	100	100	100	100
ELAC2	605367	87	100	100	98
ELANE	130130	127	100	100	100
ELF4	300775	67	100	100	100
ELN	130160	85	100	100	98
ELOVL4	605512	71	100	100	98
ELP1	603722	No coverage data			
EMD	300384	105	100	100	100
EMG1	611531	78	100	100	100
EMX2	600035	164	100	100	100
ENAM	606585	60	100	100	98

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ENG	131195	98	100	100	99
ENO3	131370	148	100	100	100
ENPP1	173335	57	97	93	85
ENTPD1	601752	68	100	100	96
EOGT	614789	60	100	100	94
EP300	602700	109	100	100	97
EPAS1	603349	112	100	100	99
EPB41	130500	66	100	100	98
EPB42	177070	126	100	100	100
EPCAM	185535	58	100	100	93
EPG5	615068	69	100	100	97
EPHA2	176946	141	100	100	99
EPHB2	600997	147	98	98	98
EPHX1	132810	128	100	100	99
EPM2A	607566	86	89	87	85
EPX	131399	116	100	100	100
ERBB2	164870	134	100	98	98
ERBB3	190151	104	100	100	100
ERBB4	600543	65	100	99	93
ERCC1	126380	71	100	100	94
ERCC2	126340	97	100	99	98
ERCC3	133510	82	100	100	99
ERCC4	133520	83	100	100	97
ERCC5	133530	85	100	100	98
ERCC6	609413	88	100	100	97
ERCC6L2	615667	57	100	98	93
ERCC8	609412	81	100	99	91
ERF	611888	137	100	100	100
ERLIN2	611605	65	100	100	95
ESCO2	609353	58	100	100	95
ESPN	606351	101	97	88	81
ESR1	133430	115	100	100	99
ESRRB	602167	142	100	100	100
ETFA	608053	60	100	100	96
ETFB	130410	106	100	100	100
ETFDH	231675	85	100	100	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ETHE1	608451	113	100	100	98
ETV6	600618	131	100	100	99
EVC	604831	98	96	94	94
EVC2	607261	87	100	99	95
EWSR1	133450	72	100	100	95
EXOSC3	606489	114	100	100	96
EXPH5	612878	61	100	100	98
EXT1	608177	70	100	100	96
EXT2	608210	98	100	100	97
EXTL3	605744	150	100	100	100
EYA1	601653	86	100	100	98
EYA4	603550	62	100	100	94
EYS	612424	72	100	100	96
EZH2	601573	79	100	100	97
F10	613872	172	100	100	97
F11	264900	63	100	100	96
F12	610619	135	100	100	100
F13A1	134570	77	100	100	99
F13B	134580	83	100	100	98
F2	176930	102	100	100	99
F5	612309	113	100	100	97
F7	613878	138	100	100	100
F8	300841	48	100	99	88
F9	300746	58	100	100	96
FA2H	611026	83	100	99	91
FADD	602457	143	100	100	100
FAH	613871	99	100	100	100
FAM111A	615292	75	100	100	100
FAM111B	615584	65	100	100	99
FAM126A	610531	63	100	100	98
FAM161A	613596	64	100	100	96
FAM20A	611062	110	100	100	100
FAM20C	611061	125	100	100	100
FAM83H	611927	114	100	100	98
FAN1	613534	75	100	100	98
FANCA	607139	102	100	100	97

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
FANCB	300515	45	100	97	83
FANCC	613899	69	100	99	91
FANCD2	613984	71	100	100	96
FANCE	613976	123	100	99	90
FANCF	613897	170	100	100	100
FANCG	602956	126	100	100	100
FANCI	611360	72	100	100	98
FANCL	608111	57	100	99	88
FANCM	609644	75	100	99	95
FARS2	611592	111	100	100	100
FAS	134637	264	100	100	96
FASLG	134638	65	100	100	100
FAT1	600976	75	100	100	99
FAT4	612411	90	100	100	99
FBLN1	135820	117	100	99	99
FBLN5	604580	106	100	100	100
FBN1	134797	186	100	100	100
FBN2	612570	74	100	100	97
FBP1	611570	119	100	100	100
FBXL4	605654	67	100	100	98
FBXO38	608533	83	100	100	96
FBXO7	605648	86	100	100	97
FCGR3A	146740	244	100	100	98
FCGR3B	610665	210	100	100	100
FCN3	604973	103	100	100	97
FECH	612386	64	100	100	96
FERMT1	607900	70	100	99	92
FERMT3	607901	114	100	100	97
FGA	134820	110	100	100	98
FGB	134830	78	100	100	99
FGD1	300546	71	100	98	95
FGD4	611104	67	100	98	92
FGF10	602115	54	100	98	90
FGF14	601515	68	100	100	98
FGF16	300827	98	100	100	95
FGF17	603725	142	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
FGF23	605380	88	100	100	97
FGF3	164950	122	100	100	100
FGF8	600483	134	100	94	94
FGF9	600921	80	100	100	100
FGFR1	136350	102	100	100	98
FGFR2	176943	74	100	100	95
FGFR3	134934	122	100	100	98
FGG	134850	69	100	100	97
FH	136850	82	99	94	87
FHL1	300163	92	100	100	94
FIG4	609390	59	100	99	94
FIGLA	608697	86	100	100	96
FKBP10	607063	131	100	100	100
FKBP14	614505	96	100	100	99
FKRP	606596	143	100	100	100
FKTN	607440	85	100	100	100
FLCN	607273	127	100	100	100
FLG	135940	378	100	100	100
FLNA	300017	110	100	100	100
FLNB	603381	110	100	100	99
FLNC	102565	133	100	100	100
FLRT3	604808	70	100	100	100
FLT3	136351	68	100	100	94
FLT4	136352	132	100	100	100
FLVCR1	609144	98	100	100	96
FLVCR2	610865	140	100	100	99
FMO3	136132	69	100	100	95
FMR1	309550	41	100	96	76
FN1	135600	80	100	100	96
FOLR1	136430	111	100	100	100
FOXC1	601090	80	100	95	89
FOXC2	602402	137	100	100	100
FOXE1	602617	142	100	100	97
FOXE3	601094	74	87	79	74
FOXF1	601089	159	100	100	100
FOXG1	164874	127	97	90	84

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
FOXI1	601093	161	100	100	100
FOXL2	605597	114	100	94	88
FOXN1	600838	136	100	100	100
FOXO1	136533	93	100	98	96
FOXP1	605515	80	100	100	98
FOXP2	605317	72	100	100	98
FOXP3	300292	69	100	99	88
FOXRED1	613622	91	100	100	100
FRAS1	607830	79	100	100	97
FREM1	608944	83	100	100	98
FREM2	608945	104	100	100	100
FRMD7	300628	50	100	98	89
FSCN2	607643	139	100	100	100
FSHB	136530	81	100	100	100
FSHR	136435	71	100	100	98
FTCD	606806	96	99	96	93
FTL	134790	144	100	100	100
FTO	610966	90	100	100	99
FTSJ1	300499	91	100	100	93
FUCA1	612280	83	100	100	98
FUS	137070	77	100	100	97
FUT6	136836	228	100	100	100
FUZ	610622	109	100	100	100
FXN	606829	41	100	91	64
FXD2	601814	101	100	100	100
FYCO1	607182	115	100	100	99
FZD4	604579	90	100	100	99
FZD6	603409	62	100	100	98
G6PC	613742	113	100	100	100
G6PC3	611045	103	100	100	100
G6PD	305900	96	100	100	100
GAA	606800	156	100	100	100
GABRA1	137160	76	100	100	100
GABRB3	137192	95	100	100	98
GABRG2	137164	73	94	92	91
GAD1	605363	86	100	100	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
GALC	606890	54	100	99	89
GALE	606953	116	100	100	100
GALK1	604313	133	100	100	99
GALNS	612222	81	100	99	95
GALNT3	601756	69	100	100	97
GALT	606999	151	100	100	100
GAMT	601240	85	100	99	95
GAN	605379	86	100	100	99
GARS1	600287	72	100	100	97
GATA1	305371	75	100	100	96
GATA2	137295	100	100	100	100
GATA3	131320	203	100	100	100
GATA4	600576	81	100	87	80
GATA5	611496	78	100	99	95
GATA6	601656	128	100	95	91
GATAD1	614518	73	100	100	97
GATAD2B	614998	67	100	100	99
GATM	602360	65	100	100	98
GBA	606463	172	100	100	100
GBA2	609471	137	100	100	100
GBE1	607839	67	100	99	92
GCDH	608801	112	100	100	100
GCH1	600225	52	100	100	93
GCK	138079	127	100	100	100
GCLC	606857	88	100	100	97
GCM2	603716	84	100	100	100
GCNT2	600429	81	100	100	98
GCSH	238330	93	100	89	62
GDAP1	606598	77	100	100	100
GDF1	602880	69	100	93	81
GDF2	605120	122	100	100	100
GDF3	606522	120	100	100	100
GDF5	601146	143	100	100	100
GDF6	601147	124	100	100	100
GDI1	300104	97	100	100	100
GDNF	600837	81	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
GET3	601913	114	100	100	100
GFAP	137780	81	100	100	99
GFER	600924	86	100	100	100
GFI1	600871	136	100	100	100
GFI1B	604383	193	100	100	100
GFM1	606639	72	100	100	96
GFPT1	138292	59	100	100	92
GGCX	137167	82	100	100	100
GH1	139250	177	100	100	100
GHR	600946	77	100	100	98
GHRHR	139191	87	100	100	98
GHSR	601898	137	100	100	100
GIGYF2	612003	66	100	99	94
GIPC3	608792	115	100	95	93
GJA1	121014	101	100	100	100
GJA3	121015	138	100	100	100
GJA5	121013	211	100	100	100
GJA8	600897	145	100	100	100
GJB1	304040	91	100	100	99
GJB2	121011	150	100	100	100
GJB3	603324	182	100	100	100
GJB4	605425	208	100	100	100
GJB6	604418	75	100	100	99
GJC2	608803	85	96	86	76
GK	300474	46	99	88	66
GLA	300644	101	100	100	100
GLB1	611458	105	100	100	98
GLDC	238300	67	100	98	91
GLE1	603371	73	100	100	96
GLI2	165230	163	100	100	99
GLI3	165240	110	100	100	99
GLIS2	608539	117	100	100	100
GLIS3	610192	113	100	100	100
GLMN	601749	69	100	98	88
GLRA1	138491	85	100	100	96
GLRB	138492	63	100	100	98

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
GLRX5	609588	68	100	91	81
GLUD1	138130	99	100	97	91
GLUL	138290	92	100	100	100
GLYCTK	610516	136	100	100	100
GM2A	613109	94	100	100	100
GMPPA	615495	114	100	100	100
GMPPB	615320	189	100	100	100
GMPS	600358	74	100	99	95
GNA11	139313	119	100	100	100
GNAI2	139360	125	100	100	100
GNAI3	139370	64	100	100	97
GNAL	139312	71	100	100	94
GNAO1	139311	98	100	100	99
GNAQ	600998	94	100	100	100
GNAS	139320	180	100	100	97
GNAT1	139330	166	100	100	100
GNAT2	139340	72	100	100	98
GNB4	610863	76	100	100	96
GNE	603824	93	100	100	99
GNMT	606628	105	100	100	100
GNPAT	602744	78	100	100	96
GNPTAB	607840	63	100	99	95
GNPTG	607838	153	100	99	94
GNRH1	152760	55	100	100	100
GNRHR	138850	98	100	100	99
GNS	607664	68	100	100	98
GOLGA5	606918	54	100	99	95
GORAB	607983	66	100	100	98
GOSR2	604027	66	100	95	90
GOT1	138180	88	100	100	100
GP1BA	606672	124	100	100	98
GP1BB	138720	65	100	99	84
GP6	605546	93	100	100	99
GP9	173515	187	100	100	100
GPC3	300037	53	100	99	91
GPC6	604404	76	100	100	97

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
GPD1	138420	80	100	100	100
GPD1L	611778	113	100	100	100
GPHN	603930	68	100	100	98
GPI	172400	130	100	100	100
GPR143	300808	43	100	89	76
GPR179	614515	135	100	100	100
GPSM2	609245	93	100	100	96
GRHL2	608576	81	100	100	99
GRHL3	608317	121	100	100	100
GRHPR	604296	96	100	100	100
GRIA3	305915	51	100	98	88
GRIK2	138244	94	100	100	98
GRIN1	138249	132	100	100	99
GRIN2A	138253	103	100	100	100
GRIN2B	138252	122	100	100	99
GRIP1	604597	84	100	100	99
GRK1	180381	114	100	100	99
GRM1	604473	136	100	100	99
GRM6	604096	127	100	95	90
GRN	138945	155	100	100	100
GRXCR1	613283	100	100	100	99
GSC	138890	131	100	100	100
GSDME	608798	94	100	100	100
GSN	137350	95	100	100	99
GSS	601002	89	100	100	99
GTF2H5	608780	53	100	100	100
GTPBP3	608536	148	100	100	100
GUCA1A	600364	108	100	100	100
GUCA1B	602275	156	100	100	100
GUCY1A1	139396	76	100	99	96
GUCY2C	601330	80	100	100	97
GUCY2D	600179	112	100	100	99
GUCY2F	300041	44	100	96	84
GUSB	611499	106	100	100	97
GYG1	603942	60	100	100	96
GYS1	138570	116	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
GYS2	138571	67	100	100	98
H19	103280	No coverage data			
H6PD	138090	170	100	100	100
HADH	601609	77	100	100	100
HADHA	600890	99	100	100	97
HADHB	143450	66	100	100	97
HAMP	606464	161	100	100	100
HAND2	602407	99	100	100	100
HARS1	142810	104	100	100	99
HARS2	600783	76	100	100	99
HAX1	605998	99	100	100	99
HBA1	141800	215	100	100	100
HBA2	141850	113	76	76	75
HBB	141900	125	100	100	100
HBD	142000	144	100	100	100
HBG1	142200	49	55	43	30
HBG2	142250	191	100	100	100
HCCS	300056	45	100	99	84
HCFC1	300019	79	100	97	92
HCN4	605206	103	100	100	99
HCRT	602358	139	100	100	100
HDAC4	605314	112	100	100	100
HDAC6	300272	85	100	100	97
HDAC8	300269	47	100	100	91
HEPACAM	611642	97	100	100	99
HERC2	605837	102	100	99	96
HES7	608059	61	95	86	76
HESX1	601802	71	100	100	95
HEXA	606869	86	100	100	98
HEXB	606873	119	100	100	97
HEY2	604674	160	100	99	96
HFE	613609	97	100	100	100
HFM1	615684	63	100	97	81
HGD	607474	63	100	100	96
HGSNAT	610453	70	94	94	92
HIBCH	610690	51	100	94	75

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
HINT1	601314	86	100	100	100
HJV	608374	117	100	100	100
HK1	142600	102	100	100	99
HLCS	609018	98	100	100	99
HMBS	609806	88	100	100	100
HMGCL	613898	94	100	100	100
HMGCS2	600234	78	100	100	99
HMOX1	141250	112	100	100	99
HMX1	142992	38	94	72	49
HNF1A	142410	157	100	100	100
HNF1B	189907	112	100	100	100
HNF4A	600281	116	100	100	98
HNRNPA1	164017	61	100	99	95
HOGA1	613597	122	100	100	100
HOXA1	142955	126	100	100	100
HOXA11	142958	72	100	100	100
HOXA13	142959	80	86	78	74
HOXB1	142968	115	100	100	100
HOXC13	142976	180	100	100	100
HOXD10	142984	139	100	100	100
HOXD13	142989	137	100	100	100
HPD	609695	107	100	100	99
HPGD	601688	73	100	100	98
HPRT1	308000	43	100	99	81
HPS1	604982	103	100	100	97
HPS3	606118	66	100	100	95
HPS4	606682	103	100	100	98
HPS5	607521	68	100	100	97
HPS6	607522	130	100	100	93
HPSE2	613469	73	100	98	92
HR	602302	111	100	99	97
HRAS	190020	179	100	100	100
HRG	142640	94	100	100	99
HSD11B1	600713	68	100	100	99
HSD11B2	614232	147	92	86	83
HSD17B10	300256	76	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
HSD17B3	605573	67	100	99	94
HSD17B4	601860	62	100	98	93
HSD3B2	613890	143	100	100	100
HSD3B7	607764	115	100	100	100
HSF4	602438	114	100	100	97
HSPB1	602195	116	100	100	98
HSPB3	604624	125	100	100	100
HSPB8	608014	220	100	100	98
HSPD1	118190	65	100	99	85
HSPG2	142461	105	99	99	99
HTR1A	109760	147	100	100	100
HTRA1	602194	93	96	87	83
HTRA2	606441	143	100	100	98
HUWE1	300697	53	100	96	83
HYAL1	607071	103	100	100	100
HYDIN	610812	46	82	69	57
HYLS1	610693	74	100	100	100
ICOS	604558	57	100	100	95
IDH2	147650	105	100	100	100
IDH3B	604526	117	100	100	100
IDS	300823	74	100	99	95
IDUA	252800	138	100	97	91
IER3IP1	609382	83	100	100	77
IFITM5	614757	131	100	100	100
IFNGR1	107470	68	100	100	95
IFT122	606045	111	100	100	99
IFT140	614620	113	100	100	98
IFT172	607386	75	100	100	96
IFT43	614068	75	100	100	100
IFT80	611177	62	100	98	87
IGBP1	300139	69	100	100	90
IGF1	147440	71	100	100	100
IGF1R	147370	120	100	100	100
IGF2R	147280	101	100	99	97
IGFALS	601489	103	100	100	100
IGFBP7	602867	60	100	95	87

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
IGHMBP2	600502	101	100	100	99
IGLL1	146770	132	100	100	100
IGSF1	300137	62	100	99	93
IHH	600726	133	100	100	100
IKBKB	603258	86	100	100	97
IKBKG	300248	24	38	33	31
IKZF1	603023	166	100	100	100
IKZF5	606238	85	100	100	99
IL10RA	146933	125	100	100	99
IL10RB	123889	69	100	100	97
IL11RA	600939	103	100	100	100
IL17F	606496	79	100	100	100
IL17RA	605461	125	100	100	100
IL17RD	606807	102	100	100	99
IL1RAPL1	300206	52	100	98	88
IL1RN	147679	76	100	100	90
IL21R	605383	113	100	100	100
IL2RA	147730	96	100	100	100
IL2RG	308380	54	100	99	91
IL31RA	609510	74	100	100	96
IL36RN	605507	82	100	100	100
IL7R	146661	60	100	100	99
ILDR1	609739	95	100	100	97
IMPDH1	146690	99	100	96	91
IMPG2	607056	68	100	100	97
INF2	610982	117	96	94	92
ING1	601566	156	100	100	100
INPP5E	613037	113	100	100	97
INPPL1	600829	111	100	100	99
INS	176730	106	100	100	100
INSL3	146738	69	93	78	78
INSR	147670	115	100	98	95
INVS	243305	81	100	100	97
IQCB1	609237	54	100	94	78
IQCE	617631	104	100	99	93
IQSEC2	300522	66	98	92	85

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
IRAK4	606883	72	100	99	91
IRF1	147575	107	100	100	98
IRF4	601900	147	100	100	100
IRF6	607199	121	100	100	100
IRF8	601565	136	100	100	99
IRGM	608212	54	78	78	78
IRX5	606195	99	100	100	100
ISCU	611911	75	100	100	100
ITCH	606409	61	96	95	90
ITGA2	192974	74	100	100	97
ITGA2B	607759	125	100	100	99
ITGA3	605025	137	100	100	100
ITGA6	147556	84	100	100	95
ITGA7	600536	117	100	97	96
ITGA8	604063	60	100	99	94
ITGB2	600065	140	100	100	100
ITGB3	173470	87	100	100	98
ITGB4	147557	135	99	98	97
ITK	186973	76	100	100	95
ITM2B	603904	79	100	100	97
ITPR1	147265	90	100	100	98
IVD	607036	107	100	100	98
IYD	612025	104	100	100	100
JAG1	601920	96	100	100	96
JAK2	147796	63	100	99	93
JAK3	600173	104	100	100	99
JAM3	606871	70	100	100	97
JPH2	605267	109	100	100	98
JPH3	605268	180	100	100	99
JUP	173325	106	100	100	98
KANK1	607704	105	100	100	99
KANSL1	612452	85	100	100	97
KARS1	601421	126	100	100	97
KAT6A	601408	95	100	100	99
KAT6B	605880	107	100	100	98
KBTBD13	613727	177	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
KCNA1	176260	126	100	100	100
KCNA5	176267	147	100	100	99
KCNC3	176264	91	94	78	64
KCND3	605411	167	100	100	99
KCNE1	176261	252	100	100	100
KCNE2	603796	81	100	100	100
KCNE3	604433	103	100	100	100
KCNH2	152427	121	100	100	99
KCNJ1	600359	60	100	100	100
KCNJ10	602208	171	100	100	100
KCNJ11	600937	128	100	100	100
KCNJ13	603208	73	100	100	99
KCNJ2	600681	96	100	100	100
KCNJ5	600734	148	100	100	100
KCNJ8	600935	103	100	100	99
KCNK3	603220	185	100	100	99
KCNK9	605874	129	100	100	100
KCNMA1	600150	88	100	100	96
KCNQ1	607542	160	97	94	93
KCNQ1OT1	604115	No coverage data			
KCNQ2	602235	131	100	100	100
KCNQ3	602232	108	100	100	96
KCNQ4	603537	147	98	95	91
KCNQ5	607357	85	100	98	95
KCNT1	608167	120	100	99	99
KCNV2	607604	130	100	100	100
KCTD1	613420	90	99	98	93
KCTD7	611725	159	100	100	100
KDM5C	314690	88	100	99	96
KDM6A	300128	52	100	95	80
KDM6B	611577	132	100	98	95
KDR	191306	68	100	99	96
KERA	603288	61	100	100	98
KHDC3L	611687	144	100	100	100
KIAA0586	610178	72	100	98	94
KIF11	148760	73	100	99	93

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
KIF1A	601255	101	100	100	98
KIF1B	605995	71	100	100	97
KIF1C	603060	141	100	100	100
KIF20A	605664	74	100	99	95
KIF21A	608283	68	100	99	93
KIF22	603213	158	100	100	100
KIF2A	602591	84	100	99	90
KIF5A	602821	90	100	100	96
KIF7	611254	107	98	96	93
KIFBP	609367	76	100	100	98
KIRREL3	607761	114	100	100	100
KISS1	603286	127	100	100	100
KISS1R	604161	165	100	100	100
KIT	164920	79	100	100	99
KITLG	184745	78	100	100	97
KL	604824	120	99	98	97
KLF1	600599	115	100	100	100
KLF11	603301	137	100	100	99
KLF6	602053	146	100	100	100
KLHDC8B	613169	90	100	100	100
KLHL10	608778	85	100	100	100
KLHL3	605775	86	100	100	97
KLHL40	615340	123	100	100	99
KLHL41	607701	77	100	100	100
KLHL7	611119	70	100	100	98
KLK4	603767	140	100	100	100
KLKB1	229000	74	100	100	96
KLLN	612105	98	100	100	100
KMT2A	159555	71	100	100	98
KMT2D	602113	114	100	100	99
KNL1	609173	60	100	99	95
KPTN	615620	150	100	100	100
KRAS	190070	83	100	100	87
KRIT1	604214	68	100	100	94
KRT1	139350	108	100	100	100
KRT10	148080	121	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
KRT12	601687	94	100	100	100
KRT13	148065	126	100	100	100
KRT14	148066	119	100	100	99
KRT16	148067	149	100	100	100
KRT17	148069	85	100	98	94
KRT18	148070	91	100	100	100
KRT2	600194	129	100	100	100
KRT3	148043	134	100	100	99
KRT4	123940	132	100	100	100
KRT5	148040	151	100	100	100
KRT6A	148041	213	100	100	100
KRT6B	148042	214	100	100	100
KRT6C	612315	164	100	100	100
KRT74	608248	151	100	100	100
KRT8	148060	91	100	100	97
KRT81	602153	113	76	72	70
KRT83	602765	131	100	100	100
KRT85	602767	124	100	100	99
KRT86	601928	126	79	75	73
KRT9	607606	119	100	100	100
L1CAM	308840	101	100	100	100
L2HGDH	609584	74	100	100	97
LAMA2	156225	71	100	99	96
LAMA3	600805	73	100	99	96
LAMA4	600133	71	100	100	97
LAMB1	150240	94	100	100	97
LAMB2	150325	153	100	100	100
LAMB3	150310	120	100	100	100
LAMC2	150292	106	100	100	99
LAMC3	604349	130	100	100	99
LAMP2	309060	44	100	95	77
LAMTOR2	610389	108	100	100	100
LARGE1	603590	97	100	100	99
LARP7	612026	67	100	99	92
LARS2	604544	79	100	100	99
LBR	600024	68	100	100	96

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
LCA5	611408	74	100	100	99
LCAT	606967	130	100	100	97
LCT	603202	114	100	100	100
LDB3	605906	123	100	100	100
LDHA	150000	62	100	99	88
LDHB	150100	58	100	100	98
LDLR	606945	209	100	100	100
LDLRAP1	605747	121	100	100	100
LEF1	153245	74	100	100	100
LEFTY2	601877	144	100	100	99
LEMD3	607844	84	100	100	96
LEP	164160	129	100	100	100
LEPR	601007	80	100	100	97
LFNG	602576	129	86	84	83
LGI1	604619	83	100	100	98
LHB	152780	99	100	100	100
LHCGR	152790	71	100	100	94
LHFPL5	609427	175	100	100	100
LHX3	600577	98	100	100	98
LHX4	602146	93	100	100	100
LIAS	607031	78	100	100	95
LIFR	151443	61	100	98	89
LIG1	126391	94	100	100	99
LIG4	601837	71	100	100	100
LIM2	154045	120	100	100	100
LINS1	610350	57	100	100	94
LIPA	613497	68	100	100	96
LIPC	151670	82	100	100	98
LIPH	607365	55	100	100	95
LIPN	613924	78	100	99	92
LITAF	603795	89	100	100	100
LMAN1	601567	72	100	97	86
LMBR1	605522	54	100	98	86
LMBRD1	612625	65	100	98	85
LMF1	611761	129	100	100	98
LMNA	150330	143	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
LMNB1	150340	66	100	100	97
LMOD3	616112	89	100	100	100
LMX1B	602575	118	100	100	99
LORICRIN	152445	83	100	100	100
LOX	153455	119	100	100	100
LOXHD1	613072	118	100	100	99
LPAR6	609239	87	100	100	100
LPIN1	605518	78	100	100	97
LPIN2	605519	77	100	100	98
LPL	609708	110	100	100	99
LPP	600700	97	100	100	100
LRAT	604863	159	100	100	100
LRBA	606453	65	100	99	94
LRIG2	608869	82	100	100	97
LRIT3	615004	78	100	100	100
LRMDA	614537	91	100	95	93
LRP2	600073	69	100	100	96
LRP4	604270	104	100	99	98
LRP5	603506	146	100	99	98
LRPAP1	104225	135	100	100	100
LRPPRC	607544	60	100	99	91
LRRC6	614930	79	100	99	93
LRRC8A	608360	174	100	100	100
LRRK2	609007	78	100	100	96
LRSAM1	610933	99	100	100	97
LRTOMT	612414	111	100	100	100
LTBP2	602091	106	100	100	99
LTBP3	602090	130	100	99	96
LTBP4	604710	139	100	100	99
LYST	606897	72	100	99	95
LYZ	153450	62	100	100	100
LZTFL1	606568	79	100	100	93
LZTS1	606551	132	100	100	100
MACF1	608271	68	100	99	94
MACROD2	611567	56	100	99	91
MAD1L1	602686	125	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
MAF	177075	80	84	80	76
MAFB	608968	136	100	100	100
MAGEL2	605283	88	100	98	93
MAGT1	300715	47	100	99	85
MAK	154235	82	100	100	97
MAML2	607537	90	100	100	99
MAMLD1	300120	96	100	99	95
MAN1B1	604346	122	100	100	100
MAN2B1	609458	115	100	100	100
MANBA	609489	85	100	100	95
MAOA	309850	49	100	99	92
MAP2K1	176872	79	100	100	96
MAP2K2	601263	117	100	100	95
MAP3K1	600982	69	100	98	94
MAP3K8	191195	68	100	100	100
MAPT	157140	120	100	100	100
MARS2	609728	157	100	100	100
MARVELD2	610572	92	100	100	97
MASP1	600521	112	100	100	99
MASP2	605102	85	100	100	97
MAST1	612256	143	100	100	100
MASTL	608221	65	99	99	96
MAT1A	610550	107	100	100	100
MAT2A	601468	83	100	100	96
MATN3	602109	73	98	90	84
MATR3	164015	63	100	100	95
MBD5	611472	81	100	100	99
MBTPS2	300294	46	100	99	90
MC2R	607397	102	100	100	100
MC4R	155541	71	100	100	100
MCC	159350	94	100	100	98
MCCC1	609010	74	100	100	94
MCCC2	609014	64	100	100	96
MCEE	608419	77	100	100	95
MCFD2	607788	87	100	100	100
MCM4	602638	88	100	100	97

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
MCM6	601806	70	100	100	97
MCOLN1	605248	129	100	100	100
MCPH1	607117	85	94	94	92
MECP2	300005	113	100	100	96
MED12	300188	68	100	100	97
MED13L	608771	73	100	100	97
MED17	603810	94	100	100	99
MED23	605042	63	100	100	96
MED25	610197	137	100	100	99
MEF2C	600662	93	100	99	96
MEFV	608107	105	100	100	100
MEGF10	612453	94	100	100	98
MEGF8	604267	134	100	99	98
MEN1	613733	182	100	100	100
MEOX1	600147	62	100	99	90
MERTK	604705	97	100	100	96
MESP2	605195	154	100	100	100
MET	164860	64	100	100	96
MFAP5	601103	50	100	100	92
MFN2	608507	114	100	100	98
MFRP	606227	100	100	100	100
MFSD8	611124	68	100	100	95
MGAT2	602616	104	100	100	100
MGME1	615076	58	94	94	92
MGP	154870	64	100	98	89
MIB1	608677	69	100	100	97
MICU1	605084	52	100	98	82
MID1	300552	89	100	100	93
MINPP1	605391	135	100	100	100
MIP	154050	123	100	100	100
MIR17HG	609415	No coverage data			
MIR184	613146	No coverage data			
MIR96	611606	No coverage data			
MITF	156845	87	100	100	99
MKKS	604896	80	100	100	100
MKRN3	603856	107	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
MKS1	609883	117	100	100	99
MLC1	605908	79	100	100	94
MLH1	120436	203	100	100	100
MLH3	604395	62	100	100	99
MLLT10	602409	79	100	100	97
MLLT11	604684	76	100	100	100
MLPH	606526	107	100	100	100
MLYCD	606761	65	100	96	92
MMAA	607481	78	100	100	98
MMAB	607568	82	100	100	98
MMACHC	609831	133	100	100	100
MMADHC	611935	63	100	100	90
MMP1	120353	63	100	100	98
MMP13	600108	78	100	100	95
MMP2	120360	125	100	100	100
MMP20	604629	68	100	100	95
MMP21	608416	81	100	96	88
MMP9	120361	118	100	100	97
MMUT	609058	75	100	100	95
MN1	156100	151	100	100	100
MNX1	142994	44	77	69	57
MOCS1	603707	105	100	100	99
MOCS2	603708	67	100	100	96
MOG	159465	91	100	100	100
MOGS	601336	130	100	100	100
MPC1	614738	74	100	100	92
MPDU1	604041	87	100	100	99
MPDZ	603785	69	100	99	95
MPI	154550	154	100	100	99
MPL	159530	109	100	100	100
MPLKIP	609188	56	100	100	100
MPO	606989	137	100	100	100
MPV17	137960	108	100	100	100
MPZ	159440	125	100	100	96
MRAP	609196	172	100	100	100
MRE11	600814	55	100	97	83

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
MRPL3	607118	64	100	100	90
MRPS16	609204	120	100	100	100
MRPS22	605810	75	100	100	96
MRTFA	606078	94	98	97	92
MS4A1	112210	80	100	100	98
MSH2	609309	191	100	100	100
MSH3	600887	81	100	100	97
MSH6	600678	213	100	100	100
MSR1	153622	94	100	99	92
MSRB3	613719	72	100	100	93
MSTN	601788	80	100	99	94
MSX1	142983	144	100	100	100
MSX2	123101	82	100	100	98
MTAP	156540	72	100	99	90
MTFMT	611766	78	100	100	90
MTHFR	607093	99	100	100	99
MTM1	300415	46	100	95	75
MTMR2	603557	72	100	100	95
MTO1	614667	116	97	94	93
MTPAP	613669	97	100	100	97
MTR	156570	80	100	100	97
MTRR	602568	87	100	100	98
MTTP	157147	67	100	100	97
MUC1	158340	78	98	92	87
MUSK	601296	85	100	100	99
MUTYH	604933	175	100	100	100
MVK	251170	100	100	100	100
MXI1	600020	66	97	93	88
MYBPC1	160794	62	100	100	94
MYBPC3	600958	169	100	100	98
MYCN	164840	169	100	100	100
MYD88	602170	157	100	100	100
MYF6	159991	132	100	100	100
MYH11	160745	136	100	100	99
MYH14	608568	114	100	99	97
MYH2	160740	85	100	100	98

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
MYH3	160720	95	100	100	98
MYH6	160710	145	100	99	98
MYH7	160760	176	100	100	100
MYH7B	609928	115	100	100	99
MYH8	160741	79	100	100	96
MYH9	160775	125	100	100	99
MYL2	160781	170	100	100	100
MYL3	160790	118	100	100	100
MYLK	600922	121	100	100	99
MYLK2	606566	111	100	100	100
MYO15A	602666	134	100	99	98
MYO1A	601478	97	100	100	100
MYO1E	601479	76	100	100	98
MYO3A	606808	73	100	99	95
MYO5A	160777	71	100	99	94
MYO5B	606540	103	100	100	98
MYO6	600970	82	100	99	94
MYO7A	276903	109	100	100	99
MYOC	601652	140	100	100	100
MYOT	604103	81	100	100	96
MYOZ2	605602	78	100	100	100
MYPN	608517	80	100	100	97
MYRF	608329	118	98	97	96
NAA10	300013	89	100	100	94
NAA15	608000	79	100	100	95
NAGA	104170	118	100	100	100
NAGLU	609701	112	100	97	93
NAGS	608300	110	100	100	100
NALCN	611549	69	100	100	97
NANOS1	608226	96	99	96	92
NBAS	608025	66	100	99	94
NBEAL2	614169	139	100	99	99
NBN	602667	68	100	99	88
NCF1	608512	108	68	65	61
NCF2	608515	94	100	100	98
NCF4	601488	121	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
NCOA4	601984	72	100	100	99
NCSTN	605254	91	100	100	98
NDE1	609449	109	100	100	100
NDN	602117	99	100	100	97
NDP	300658	77	100	100	100
NDRG1	605262	97	100	100	100
NDUFA1	300078	110	100	100	100
NDUFA10	603835	80	100	95	85
NDUFA11	612638	117	100	100	100
NDUFA12	614530	72	100	100	100
NDUFA2	602137	104	100	100	100
NDUFA9	603834	82	100	100	100
NDUFAF1	606934	63	100	100	95
NDUFAF2	609653	83	100	92	78
NDUFAF3	612911	130	100	100	100
NDUFAF4	611776	95	100	100	100
NDUFAF5	612360	70	100	100	96
NDUFAF6	612392	46	100	100	90
NDUFB3	603839	31	100	87	55
NDUFS1	157655	69	100	100	94
NDUFS2	602985	79	100	100	99
NDUFS3	603846	112	100	100	100
NDUFS4	602694	83	100	100	99
NDUFS6	603848	70	100	100	100
NDUFS7	601825	130	100	100	98
NDUFS8	602141	140	100	100	100
NDUFV1	161015	129	100	100	100
NDUFV2	600532	48	100	95	80
NEB	161650	69	88	87	84
NECTIN1	600644	112	100	100	100
NECTIN4	609607	121	100	100	100
NEFL	162280	157	100	100	100
NEK1	604588	56	100	98	89
NEU1	608272	155	100	100	100
NEUROD1	601724	115	100	100	100
NEUROG3	604882	161	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
NEXMIF	300524	48	100	100	95
NEXN	613121	85	100	100	99
NF1	613113	55	97	90	79
NF2	607379	141	100	100	100
NFIX	164005	154	100	100	100
NFKB2	164012	143	100	100	96
NFKBIA	164008	131	100	100	100
NFU1	608100	66	100	100	95
NGF	162030	131	100	100	100
NGLY1	610661	78	100	100	97
NHEJ1	611290	55	100	100	96
NHLRC1	608072	144	100	100	100
NHP2	606470	122	100	100	100
NHS	300457	57	100	96	90
NIN	608684	79	100	99	95
NIPA1	608145	107	100	100	97
NIPAL4	609383	97	100	100	99
NIPBL	608667	65	100	98	92
NKX2-1	600635	95	100	100	100
NKX2-5	600584	101	100	100	97
NKX2-6	611770	145	100	100	100
NKX3-2	602183	108	100	100	100
NLGN4X	300427	179	100	100	100
NLRP12	609648	135	100	100	100
NLRP3	606416	125	100	100	100
NLRP7	609661	167	100	100	100
NME8	607421	65	100	100	93
NMNAT1	608700	90	100	100	98
NNT	607878	67	100	100	96
NOBOX	610934	86	100	100	100
NOD2	605956	113	100	100	99
NODAL	601265	119	100	100	100
NOG	602991	198	100	100	100
NOL3	605235	132	100	100	100
NOP10	606471	147	100	100	100
NOP56	614154	93	100	100	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
NOTCH1	190198	117	100	99	98
NOTCH2	600275	98	100	99	98
NOTCH3	600276	111	99	95	91
NPC1	607623	87	100	100	99
NPC2	601015	95	100	100	100
NPHP1	607100	58	100	98	88
NPHP3	608002	66	100	99	94
NPHP4	607215	110	100	100	100
NPHS1	602716	102	100	100	100
NPHS2	604766	84	100	100	100
NPM1	164040	72	100	96	92
NPPA	108780	120	100	100	100
NPR2	108961	116	100	100	100
NR0B1	300473	120	100	100	99
NR0B2	604630	72	100	100	96
NR2E3	604485	123	100	100	99
NR2F1	132890	197	100	100	100
NR3C1	138040	80	100	100	98
NR3C2	600983	89	100	100	98
NR4A3	600542	114	100	100	100
NR5A1	184757	107	100	100	100
NRAS	164790	63	100	100	98
NRL	162080	108	100	100	100
NRXN1	600565	104	100	100	97
NSD1	606681	77	100	100	98
NSD3	607083	55	100	98	90
NSDHL	300275	68	100	100	93
NSMF	608137	96	100	95	95
NSUN2	610916	85	100	99	92
NT5C2	600417	54	100	98	89
NT5C3A	606224	61	100	99	89
NT5E	129190	90	100	100	98
NTF4	162662	176	100	100	100
NTRK1	191315	119	100	100	99
NTRK2	600456	92	100	100	96
NUBPL	613621	60	100	100	97

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
NUMA1	164009	129	100	100	98
NUP214	114350	111	100	100	98
NUP62	605815	107	100	100	100
NYX	300278	132	100	100	100
OAT	613349	64	100	96	85
OBSL1	610991	135	100	100	100
OCA2	611409	93	100	100	97
OCLN	602876	61	96	84	79
OCRL	300535	43	100	95	80
ODAPH	614829	88	100	100	96
OFD1	300170	43	100	95	75
OGG1	601982	101	100	100	100
OPA1	605290	59	100	98	89
OPA3	606580	130	100	100	100
OPHN1	300127	52	100	96	84
OPLAH	614243	132	100	100	99
OPN1LW	300822	121	89	89	88
OPN1MW	300821	47	54	45	42
OPN1SW	613522	78	100	100	100
OPTN	602432	81	100	100	96
ORAI1	610277	175	99	99	97
ORC1	601902	86	100	100	97
ORC4	603056	67	100	100	91
ORC6	607213	70	100	100	98
OSMR	601743	74	100	100	97
OSTM1	607649	79	100	100	97
OTC	300461	58	100	98	85
OTOA	607038	78	77	74	72
OTOF	603681	113	100	100	100
OTOG	604487	121	100	100	99
OTOGL	614925	76	100	100	95
OTX2	600037	100	100	100	100
OXCT1	601424	74	100	100	96
P2RX1	600845	103	100	100	100
P2RX2	600844	136	100	100	99
P2RY12	600515	67	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
P3H1	610339	123	100	100	100
P3H2	610341	65	100	100	95
PABPN1	602279	89	89	76	71
PACS1	607492	92	100	100	97
PAFAH1B1	601545	82	100	96	90
PAH	612349	68	100	99	95
PAK3	300142	48	100	96	83
PALB2	610355	69	100	100	97
PANK2	606157	81	100	100	99
PAPSS2	603005	94	100	100	95
PARK7	602533	68	100	99	87
PAX2	167409	144	100	100	98
PAX3	606597	104	100	100	100
PAX4	167413	74	100	100	99
PAX6	607108	73	100	100	96
PAX8	167415	111	100	100	97
PAX9	167416	215	100	98	98
PC	608786	141	100	100	100
PCARE	613425	105	100	100	98
PCBD1	126090	87	100	100	99
PCCA	232000	68	100	100	95
PCCB	232050	72	100	98	95
PCDH15	605514	72	100	100	95
PCDH19	300460	113	100	100	97
PCM1	600299	79	100	99	94
PCNT	605925	121	100	100	99
PCSK1	162150	68	100	100	97
PCSK9	607786	116	100	98	95
PCYT1A	123695	74	100	99	85
PDCD10	609118	48	100	99	82
PDE11A	604961	77	100	99	93
PDE4D	600129	70	100	97	94
PDE6A	180071	74	100	100	96
PDE6B	180072	125	100	100	100
PDE6C	600827	67	100	100	96
PDE6G	180073	147	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
PDE6H	601190	47	100	100	96
PDE8B	603390	72	100	99	96
PDGFB	190040	101	100	100	100
PDGFRA	173490	79	100	98	95
PDGFRB	173410	116	100	100	100
PDGFRL	604584	129	100	100	100
PDHA1	300502	49	100	94	84
PDHB	179060	65	100	100	95
PDP1	605993	87	100	100	100
PDS5B	605333	52	100	98	89
PDSS1	607429	60	100	93	85
PDSS2	610564	75	100	97	87
PDX1	600733	79	100	100	89
PDYN	131340	134	100	100	100
PDZD7	612971	84	100	100	99
PEPD	613230	100	100	100	98
PER2	603426	84	100	100	97
PET100	614770	85	92	66	66
PEX1	602136	62	100	99	94
PEX10	602859	100	100	100	97
PEX11B	603867	137	100	100	100
PEX12	601758	67	100	100	94
PEX13	601789	69	100	100	99
PEX14	601791	142	100	100	100
PEX16	603360	134	100	96	94
PEX19	600279	67	100	100	98
PEX2	170993	63	100	100	100
PEX26	608666	118	100	100	100
PEX3	603164	57	100	100	95
PEX5	600414	111	100	100	100
PEX6	601498	107	100	99	95
PEX7	601757	57	100	100	95
PFKM	610681	92	100	100	99
PFN1	176610	159	100	100	100
PGAM2	612931	156	100	100	100
PGAP2	615187	147	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
PGAP3	611801	115	100	100	100
PGK1	311800	47	100	100	89
PGM1	171900	72	100	100	99
PHEX	300550	48	100	98	89
PHF21A	608325	61	100	97	91
PHF6	300414	51	100	96	82
PHF8	300560	61	100	98	87
PHGDH	606879	138	100	100	100
PHKA1	311870	47	100	97	82
PHKA2	300798	56	100	99	90
PHKB	172490	76	100	100	98
PHKG2	172471	123	100	100	100
PHOX2A	602753	61	100	100	86
PHOX2B	603851	149	100	100	100
PHRF1	611780	143	100	100	98
PHYH	602026	121	100	100	94
PICALM	603025	60	100	98	85
PIEZO1	611184	136	100	100	99
PIEZO2	613629	70	100	99	94
PIGA	311770	67	100	100	97
PIGL	605947	98	100	100	100
PIGM	610273	85	100	100	100
PIGN	606097	63	100	99	89
PIGO	614730	126	100	100	100
PIGT	610272	138	100	100	100
PIGV	610274	96	100	100	100
PIK3CA	171834	85	100	99	96
PIK3CD	602839	137	100	99	98
PIK3R1	171833	80	100	100	97
PIK3R2	603157	89	95	93	90
PIK3R5	611317	107	100	100	100
PIKFYVE	609414	67	100	99	95
PINK1	608309	100	98	93	88
PIP5K1C	606102	130	100	95	95
PITPNM3	608921	99	100	99	97
PITX1	602149	109	100	100	97

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
PITX2	601542	149	100	100	100
PITX3	602669	96	100	100	100
PJKV	610219	93	100	100	99
PKD1	601313	93	97	95	90
PKD1L1	609721	69	100	98	91
PKD2	173910	62	100	97	89
PKHD1	606702	82	100	100	98
PKLR	609712	156	100	100	100
PKP1	601975	116	100	100	99
PKP2	602861	147	100	98	96
PLA2G4A	600522	68	100	100	96
PLA2G5	601192	89	100	100	100
PLA2G6	603604	118	100	100	99
PLA2G7	601690	99	100	100	97
PLAG1	603026	74	100	100	100
PLAU	191840	149	100	100	100
PLCB1	607120	60	100	99	94
PLCB4	600810	61	100	100	94
PLCD1	602142	115	100	100	100
PLCE1	608414	79	100	100	97
PLCG2	600220	107	100	100	99
PLEC	601282	146	100	100	100
PLEKHG5	611101	85	100	100	96
PLEKHM1	611466	174	100	100	99
PLG	173350	81	100	100	98
PLIN1	170290	96	100	100	99
PLN	172405	112	100	100	100
PLOD1	153454	100	100	100	99
PLOD2	601865	58	100	99	90
PLOD3	603066	100	100	100	99
PLP1	300401	93	100	99	97
PLS3	300131	48	100	96	83
PML	102578	136	100	100	100
PMM2	601785	72	100	100	97
PMP22	601097	105	100	100	100
PMPCA	613036	133	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
PMS2	600259	148	100	96	93
PNKP	605610	104	100	100	98
PNP	164050	70	100	100	97
PNPLA1	612121	102	100	100	99
PNPLA2	609059	114	100	100	100
PNPLA6	603197	123	100	100	99
PNPO	603287	69	100	100	94
PNPT1	610316	57	100	97	83
POC1A	614783	90	100	100	100
POF1B	300603	45	100	93	79
POFUT1	607491	114	100	100	100
POGLUT1	615618	54	100	98	91
POLD1	174761	114	100	99	96
POLE	174762	117	100	100	100
POLG	174763	114	100	100	99
POLG2	604983	140	100	100	95
POLH	603968	74	100	100	98
POLR1C	610060	92	100	100	98
POLR1D	613715	81	100	100	100
POLR3A	614258	84	100	100	98
POLR3B	614366	76	100	99	93
POMC	176830	132	100	100	100
POMGNT1	606822	93	100	100	99
POMGNT2	614828	154	100	100	100
POMP	613386	45	100	100	87
POMT1	607423	103	100	100	100
POMT2	607439	87	100	100	99
POR	124015	170	100	100	100
PORCN	300651	102	100	100	98
POU1F1	173110	83	100	100	100
POU3F4	300039	120	100	100	100
POU4F3	602460	247	100	100	100
PPA2	609988	70	100	94	76
PPARG	601487	71	100	100	100
PIIB	123841	96	100	100	100
PPM1D	605100	88	100	100	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
PPM1K	611065	77	100	100	98
PPOX	600923	106	100	100	100
PPP1CB	600590	54	100	100	95
PPP1R3A	600917	66	100	100	98
PPP2R1B	603113	77	100	100	96
PPP2R2B	604325	77	100	99	95
PPT1	600722	84	100	100	100
PQBP1	300463	100	100	100	100
PRCC	179755	114	100	100	96
PRCD	610598	83	100	100	100
PRDM16	605557	191	100	100	99
PRDM5	614161	76	100	100	96
PRDM6	616982	85	100	100	98
PRELID2	No ID	56	100	100	92
PRF1	170280	120	100	100	100
PRG4	604283	157	100	100	100
PRICKLE1	608500	76	100	100	98
PRICKLE2	608501	113	100	100	100
PRIMPOL	615421	49	95	89	78
PRKAG2	602743	123	100	100	97
PRKAR1A	188830	86	100	100	99
PRKCA	176960	126	100	100	100
PRKCE	176975	87	100	100	97
PRKCG	176980	122	100	100	99
PRKCSH	177060	142	100	100	98
PRKD1	605435	93	100	100	95
PRKG1	176894	69	100	100	98
PRKN	602544	96	100	100	99
PRKRA	603424	81	100	100	96
PRLR	176761	67	100	100	99
PRNP	176640	138	100	100	100
PROC	612283	149	100	100	100
PRODH	606810	98	100	95	86
PROK2	607002	61	100	100	99
PROKR2	607123	210	100	100	100
PROM1	604365	84	100	99	93

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
PROP1	601538	103	100	100	92
PROS1	176880	57	100	93	78
PRPF3	607301	77	100	98	94
PRPF31	606419	101	100	100	99
PRPF6	613979	108	100	100	99
PRPF8	607300	102	100	100	98
PRPH2	179605	162	100	100	100
PRPS1	311850	50	100	99	90
PRRT2	614386	123	100	100	100
PRRX1	167420	94	100	100	100
PRSS1	276000	239	100	100	100
PRSS12	606709	94	100	100	99
PRSS56	613858	95	100	100	100
PRX	605725	198	100	100	100
PSAP	176801	121	100	100	97
PSAT1	610936	64	100	100	97
PSENEN	607632	88	100	100	100
PSMB8	177046	124	100	100	100
PSMC3IP	608665	108	100	100	100
PSPH	172480	51	100	96	84
PSTPIP1	606347	109	100	100	99
PTCH1	601309	91	100	98	96
PTCH2	603673	108	100	100	100
PTDSS1	612792	66	100	100	98
PTEN	601728	115	85	78	76
PTF1A	607194	136	100	100	94
PTGIS	601699	101	100	100	95
PTH	168450	85	100	94	88
PTH1R	168468	123	100	100	100
PTHLH	168470	137	100	100	100
PTPN11	176876	77	100	99	90
PTPN12	600079	56	100	99	94
PTPN14	603155	110	100	100	98
PTPRC	151460	73	100	99	95
PTPRJ	600925	83	97	97	94
PTPRO	600579	72	100	100	98

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
PTPRQ	603317	80	100	99	95
PTS	612719	86	100	100	95
PUF60	604819	130	100	100	100
PUS1	608109	88	100	99	95
PYCR1	179035	93	100	100	100
PYGL	613741	84	100	100	96
PYGM	608455	112	100	100	100
QARS1	603727	108	100	100	100
QDPR	612676	94	100	100	97
RAB18	602207	85	100	100	97
RAB23	606144	104	100	100	100
RAB27A	603868	54	100	100	91
RAB28	612994	55	100	100	92
RAB33B	605950	74	100	100	100
RAB39B	300774	59	100	100	100
RAB3GAP1	602536	67	100	100	97
RAB3GAP2	609275	66	100	99	92
RAB40AL	300405	197	100	100	100
RAB7A	602298	91	100	100	100
RAC2	602049	99	100	100	100
RAD21	606462	69	100	99	92
RAD50	604040	98	100	100	98
RAD51	179617	52	88	88	85
RAD51C	602774	64	100	100	93
RAD54B	604289	89	100	99	95
RAD54L	603615	95	100	100	99
RAF1	164760	78	100	99	95
RAG1	179615	101	100	100	100
RAG2	179616	71	100	100	100
RAI1	607642	187	100	100	100
RALA	179550	51	90	80	72
RAP1GDS1	179502	75	100	100	98
RAPSN	601592	137	100	100	100
RARB	180220	85	100	100	99
RARS2	611524	66	100	99	93
RASA1	139150	61	100	98	90

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
RAX2	610362	78	100	100	100
RB1	614041	163	100	100	98
RB1CC1	606837	63	100	99	92
RBBP8	604124	57	100	99	92
RBM10	300080	81	100	96	88
RBM20	613171	136	100	100	100
RBM28	612074	70	100	100	96
RBM8A	605313	99	100	100	100
RBP4	180250	128	100	100	100
RBPJ	147183	77	100	99	89
RD3	180040	153	100	100	100
RDH12	608830	104	100	100	100
RDH5	601617	149	100	100	100
RDX	179410	54	100	93	76
RECQL4	603780	148	100	100	99
REEP1	609139	72	100	100	99
RELN	600514	74	100	100	97
REN	179820	93	100	100	100
RET	164761	173	100	100	100
RETREG1	613114	73	100	98	86
RFT1	611908	67	100	99	93
RFTN2	618215	73	100	98	92
RFX5	601863	100	100	100	98
RFX6	612659	91	100	99	95
RFXANK	603200	118	100	100	100
RFXAP	601861	148	100	100	100
RGR	600342	101	100	98	91
RGS9	604067	108	100	100	98
RGS9BP	607814	153	100	100	100
RHAG	180297	62	100	100	94
RHBDF2	614404	100	100	99	96
RHCE	111700	207	100	100	99
RHO	180380	131	100	100	100
RIMS1	606629	94	100	100	98
RIN2	610222	102	100	100	99
RIPK4	605706	171	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
RIT1	609591	72	100	100	100
RLBP1	180090	111	100	100	100
RMND1	614917	67	100	100	93
RMRP	157660	No coverage data			
RNASEH2A	606034	109	100	100	100
RNASEH2B	610326	62	100	98	88
RNASEH2C	610330	323	100	100	100
RNASEL	180435	85	100	100	99
RNASET2	612944	106	100	100	99
RNF123	614472	114	100	100	100
RNF135	611358	83	100	100	99
RNF139	603046	91	100	100	100
RNF145	No ID	50	99	90	68
RNF168	612688	93	100	100	99
RNF170	614649	69	100	97	85
RNF212	612041	87	100	100	97
RNF216	609948	66	100	97	86
RNF6	604242	73	100	100	99
ROBO2	602431	76	100	100	98
ROBO3	608630	106	100	100	100
ROBO4	607528	91	100	100	98
ROGDI	614574	90	100	98	93
ROM1	180721	110	100	100	100
ROR2	602337	134	100	100	99
RP1	603937	73	100	100	97
RP1L1	608581	165	100	100	100
RP2	300757	67	100	100	98
RPE65	180069	72	100	100	98
RPGR	312610	39	81	72	60
RPGRIP1	605446	88	100	100	96
RPGRIP1L	610937	60	98	96	89
RPIA	180430	77	100	100	98
RPL11	604175	62	100	100	100
RPL35A	180468	86	100	100	100
RPL5	603634	54	99	93	85
RPS10	603632	61	100	100	97

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
RPS14	130620	134	100	100	100
RPS17	180472	2	5	5	5
RPS19	603474	97	100	100	92
RPS24	602412	105	100	100	100
RPS26	603701	81	100	100	100
RPS6KA3	300075	46	100	92	70
RPS7	603658	54	100	100	89
RPSA	150370	84	100	100	100
RRAS2	600098	68	100	99	86
RRM2B	604712	90	100	100	100
RS1	300839	44	100	99	74
RSPH1	609314	80	100	100	95
RSPH4A	612647	100	100	100	100
RSPH9	612648	125	100	100	100
RSPO1	609595	93	100	100	100
RSPO4	610573	116	100	100	100
RTEL1	608833	131	100	100	99
RTN2	603183	135	100	100	100
RTTN	610436	71	100	99	94
RUNX1	151385	76	100	100	98
RUNX2	600211	107	100	100	100
RXFP2	606655	54	100	99	90
RYR1	180901	152	99	99	99
RYR2	180902	128	100	100	97
SACS	604490	70	100	100	99
SAG	181031	97	100	100	98
SALL1	602218	120	100	100	99
SALL4	607343	155	100	100	97
SAMD9	610456	68	100	100	100
SAMHD1	606754	64	100	99	88
SAR1B	607690	79	100	100	97
SARS2	612804	86	100	100	99
SART3	611684	94	100	100	97
SAT1	313020	66	100	100	97
SATB2	608148	95	100	100	97
SBDS	607444	79	100	100	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
SBF2	607697	72	100	100	95
SC5D	602286	88	100	100	100
SCARB2	602257	89	100	100	98
SCARF2	613619	101	100	99	97
SCN10A	604427	110	100	100	99
SCN11A	604385	88	100	100	97
SCN1A	182389	92	100	100	99
SCN1B	600235	169	100	97	93
SCN2A	182390	95	100	100	97
SCN2B	601327	117	100	100	100
SCN3A	182391	84	100	100	97
SCN3B	608214	92	100	100	100
SCN4A	603967	143	100	100	100
SCN4B	608256	111	100	100	100
SCN5A	600163	192	100	100	100
SCN8A	600702	110	100	100	98
SCN9A	603415	84	100	100	98
SCNN1A	600228	108	100	100	98
SCNN1B	600760	109	100	100	99
SCNN1G	600761	122	100	100	98
SCO1	603644	99	100	100	99
SCO2	604272	125	100	100	100
SCP2	184755	54	100	100	92
SDCCAG8	613524	92	100	100	96
SDHA	600857	134	100	97	91
SDHAF1	612848	82	100	100	100
SDHAF2	613019	140	100	100	100
SDHB	185470	149	100	100	100
SDHC	602413	170	100	100	100
SDHD	602690	164	100	100	100
SEC23A	610511	61	100	97	90
SEC23B	610512	74	100	100	97
SEC63	608648	54	100	99	87
SECISBP2	607693	82	100	100	95
SELENON	606210	132	90	90	90
SEMA3E	608166	64	100	100	94

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
SEMA4A	607292	108	100	100	100
SEPSECS	613009	78	100	100	96
SEPTIN12	611562	85	100	100	99
SEPTIN9	604061	125	100	100	100
SERAC1	614725	65	100	99	86
SERPINA1	107400	90	100	100	100
SERPINA3	107280	106	100	100	100
SERPINA6	122500	106	100	100	100
SERPINA7	314200	50	100	98	85
SERPINB6	173321	85	100	100	98
SERPINB7	603357	70	100	100	97
SERPINC1	107300	96	100	100	99
SERPIND1	142360	77	100	100	99
SERPINE1	173360	132	100	100	100
SERPINF1	172860	111	100	99	95
SERPINF2	613168	150	100	100	98
SERPING1	606860	112	100	100	99
SERPINH1	600943	159	100	100	100
SERPINI1	602445	73	100	100	98
SETBP1	611060	102	99	98	97
SETD1A	611052	135	100	99	98
SETD5	615743	85	100	100	98
SETX	608465	70	100	100	97
SF3B1	605590	69	100	100	94
SF3B4	605593	84	100	100	99
SFTPA2	178642	191	100	100	100
SFTPB	178640	86	100	100	99
SFTPC	178620	100	100	100	100
SFXN4	615564	74	100	100	99
SGCA	600119	149	100	98	96
SGCB	600900	54	100	95	89
SGCD	601411	60	100	100	97
SGCE	604149	84	100	100	94
SGCG	608896	78	100	100	98
SGSH	605270	103	100	94	90
SH2B3	605093	115	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
SH2D1A	300490	56	100	98	83
SH3BP2	602104	127	91	91	91
SH3PXD2B	613293	122	100	100	99
SH3TC2	608206	89	100	100	99
SHANK3	606230	117	99	93	86
SHH	600725	119	100	100	99
SHOC2	602775	61	100	99	95
SHOX	312865	No coverage data			
SHROOM4	300579	70	100	100	97
SI	609845	60	100	99	92
SIGMAR1	601978	135	100	100	100
SIL1	608005	100	100	100	100
SIM1	603128	99	100	100	99
SIX1	601205	119	100	100	100
SIX3	603714	158	100	100	96
SIX5	600963	75	100	95	85
SIX6	606326	233	100	100	100
SKI	164780	123	100	100	99
SKIV2L	600478	124	100	100	100
SLC10A2	601295	78	100	100	96
SLC11A2	600523	57	100	99	90
SLC12A1	600839	72	100	100	98
SLC12A3	600968	113	100	100	100
SLC12A6	604878	67	100	99	94
SLC16A1	600682	83	100	100	99
SLC16A12	611910	89	100	100	100
SLC16A2	300095	75	100	100	95
SLC17A5	604322	86	100	100	97
SLC17A8	607557	66	100	100	99
SLC19A2	603941	68	100	100	99
SLC19A3	606152	73	100	100	98
SLC1A3	600111	99	100	100	100
SLC20A2	158378	99	100	100	95
SLC22A12	607096	117	100	100	97
SLC22A18	602631	107	100	100	98
SLC22A5	603377	118	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
SLC24A1	603617	105	100	100	99
SLC24A5	609802	77	100	100	100
SLC25A1	190315	102	100	100	100
SLC25A12	603667	88	100	100	97
SLC25A13	603859	98	100	99	93
SLC25A15	603861	132	100	100	98
SLC25A19	606521	105	100	100	100
SLC25A20	613698	66	100	100	97
SLC25A22	609302	122	100	100	100
SLC25A3	600370	105	100	100	100
SLC25A38	610819	109	100	100	100
SLC25A4	103220	112	100	100	100
SLC26A2	606718	68	100	100	100
SLC26A3	126650	72	100	100	95
SLC26A4	605646	68	100	100	94
SLC26A5	604943	61	100	100	96
SLC26A8	608480	64	100	99	93
SLC27A4	604194	133	100	100	100
SLC29A3	612373	152	100	99	99
SLC2A1	138140	127	100	100	100
SLC2A10	606145	125	100	100	100
SLC2A2	138160	63	100	100	96
SLC2A9	606142	107	100	100	97
SLC30A10	611146	148	100	100	100
SLC30A2	609617	104	100	100	100
SLC33A1	603690	68	100	98	86
SLC34A1	182309	136	100	100	100
SLC34A2	604217	120	100	100	99
SLC34A3	609826	121	100	98	93
SLC35A1	605634	66	100	100	97
SLC35A2	314375	75	100	100	99
SLC35C1	605881	146	100	100	100
SLC35D1	610804	57	100	99	85
SLC36A2	608331	102	100	100	100
SLC37A4	602671	96	100	100	95
SLC38A8	615585	83	100	99	94

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
SLC39A13	608735	129	100	100	100
SLC39A4	607059	125	100	100	100
SLC3A1	104614	93	100	100	97
SLC40A1	604653	63	100	100	97
SLC45A2	606202	93	100	100	97
SLC46A1	611672	121	100	100	98
SLC4A1	109270	122	100	100	100
SLC4A11	610206	125	100	100	99
SLC4A4	603345	61	100	100	97
SLC52A3	613350	109	100	100	100
SLC5A1	182380	104	100	100	96
SLC5A2	182381	113	100	100	99
SLC5A5	601843	94	100	99	95
SLC5A7	608761	82	100	100	99
SLC6A19	608893	115	100	100	100
SLC6A20	605616	139	100	100	100
SLC6A3	126455	102	100	100	100
SLC6A5	604159	85	100	100	96
SLC6A8	300036	103	100	98	95
SLC7A14	615720	112	100	100	100
SLC7A7	603593	79	100	100	97
SLC7A9	604144	100	100	100	99
SLC9A3R1	604990	116	100	100	100
SLC9A6	300231	64	100	96	84
SLCO1B1	604843	61	100	99	90
SLCO1B3	605495	66	100	99	92
SLCO2A1	601460	97	100	100	99
SLITRK1	609678	89	100	100	100
SLITRK6	609681	75	100	100	99
SLURP1	606119	98	100	100	100
SLX4	613278	118	100	100	99
SMAD2	601366	69	100	100	97
SMAD3	603109	188	100	100	100
SMAD4	600993	79	100	100	98
SMAD6	602931	165	100	97	87
SMAD9	603295	85	100	100	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
SMARCA2	600014	94	98	98	96
SMARCA4	603254	127	100	100	100
SMARCAD1	612761	61	100	98	89
SMARCAL1	606622	88	100	100	98
SMARCB1	601607	130	100	100	99
SMARCC2	601734	74	100	100	94
SMC1A	300040	71	100	100	97
SMC3	606062	69	100	97	88
SMCHD1	614982	63	100	98	89
SMN1	600354	4	7	7	7
SMO	601500	124	100	100	100
SMOC1	608488	106	100	100	97
SMOC2	607223	88	100	99	94
SMPD1	607608	131	100	100	99
SMPX	300226	51	100	100	83
SMS	300105	42	95	89	68
SNAI2	602150	66	100	100	100
SNAP29	604202	148	100	100	100
SNCA	163890	52	100	100	98
SNCB	602569	130	100	100	100
SNIP1	608241	100	100	100	100
SNRNP200	601664	102	100	100	98
SNRPE	128260	37	100	97	69
SNRPN	182279	96	100	100	100
SNTA1	601017	111	100	94	82
SNX10	614780	77	100	100	98
SOBP	613667	165	100	98	95
SOD1	147450	74	100	100	100
SOS1	182530	71	100	100	95
SOST	605740	163	100	100	100
SOX10	602229	72	100	97	89
SOX17	610928	157	100	100	100
SOX18	601618	73	95	90	81
SOX2	184429	183	100	100	100
SOX3	313430	64	100	95	89
SOX9	608160	157	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
SP110	604457	61	100	100	96
SP7	606633	129	100	100	100
SPAG1	603395	64	100	99	91
SPART	607111	71	100	100	98
SPAST	604277	64	100	100	94
SPATA16	609856	64	100	100	98
SPATA7	609868	62	100	99	94
SPECC1L	614140	64	100	99	92
SPG11	610844	84	100	100	97
SPG21	608181	66	100	95	88
SPG7	602783	125	100	100	97
SPINK1	167790	79	100	100	97
SPINK5	605010	66	100	99	95
SPINT2	605124	94	100	100	100
SPR	182125	102	100	100	100
SPRED1	609291	57	100	98	92
SPRY4	607984	104	100	100	96
SPTA1	182860	68	100	100	96
SPTAN1	182810	95	100	100	98
SPTB	182870	124	100	100	100
SPTBN2	604985	121	100	100	100
SPTLC1	605712	62	100	99	94
SPTLC2	605713	81	100	100	96
SQSTM1	601530	129	100	100	96
SRC	190090	119	100	100	100
SRCAP	611421	139	100	100	100
SRD5A2	607306	56	100	99	86
SRD5A3	611715	111	100	100	96
SRP72	602122	56	100	99	89
SRPX2	300642	59	100	99	95
SRY	480000	159	100	100	100
SSTR5	182455	168	100	100	100
ST14	606797	111	100	100	99
ST3GAL3	606494	79	100	100	96
ST3GAL5	604402	55	99	92	84
STAC3	615521	82	100	100	98

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
STAMPB	606247	72	100	100	97
STAR	600617	118	100	100	100
STAT1	600555	64	100	99	94
STAT3	102582	90	100	100	99
STAT5B	604260	107	100	100	97
STIL	181590	65	100	100	97
STIM1	605921	95	100	100	99
STK11	602216	161	100	100	100
STK4	604965	82	100	100	99
STOX1	609397	62	89	89	89
STRA6	610745	98	100	100	100
STRADA	608626	96	100	100	98
STRC	606440	66	53	48	46
STS	300747	90	97	97	95
STXBP1	602926	76	100	100	99
STXBP2	601717	121	100	100	100
SUCLA2	603921	56	100	97	86
SUCLG1	611224	88	100	100	100
SUFU	607035	104	100	100	100
SUGCT	609187	73	100	100	93
SUMF1	607939	88	100	100	99
SUMO1	601912	72	100	97	85
SUOX	606887	136	100	100	100
SURF1	185620	88	94	89	87
SYCP3	604759	45	100	100	89
SYN1	313440	60	100	99	85
SYNE1	608441	77	100	100	97
SYNE2	608442	77	100	100	96
SYNE4	615535	107	100	100	100
SYNGAP1	603384	158	98	98	98
SYNJ1	604297	62	100	99	92
SYP	313475	69	100	100	98
SYT14	610949	61	100	95	86
SZT2	615463	117	100	100	100
TAB2	605101	76	100	100	99
TAC3	162330	93	100	100	95

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
TACR3	162332	136	100	100	100
TACSTD2	137290	228	100	100	100
TAF1	313650	54	100	97	87
TAF2	604912	64	100	99	92
TAL1	187040	64	97	89	82
TAL2	186855	87	100	100	100
TALDO1	602063	136	100	100	100
TAP1	170260	125	100	100	100
TAP2	170261	106	100	100	100
TAPBP	601962	106	100	100	100
TARDBP	605078	124	100	100	95
TAT	613018	65	100	100	98
TAZ	300394	97	100	98	90
TBC1D20	611663	74	100	93	93
TBC1D24	613577	158	100	100	100
TBCE	604934	59	100	97	88
TBP	600075	80	100	100	96
TBX1	602054	94	94	85	80
TBX15	604127	77	100	100	99
TBX19	604614	126	100	100	99
TBX20	606061	80	100	100	97
TBX21	604895	139	100	100	99
TBX22	300307	60	100	99	90
TBX3	601621	100	100	100	99
TBX4	601719	145	100	100	100
TBX5	601620	77	100	100	99
TBXAS1	274180	74	100	99	93
TCAP	604488	102	100	100	100
TCF12	600480	72	100	100	98
TCF4	602272	73	100	100	96
TCIRG1	604592	117	100	100	97
TCN2	613441	118	100	100	100
TCOF1	606847	115	100	100	99
TCTN1	609863	94	100	100	98
TCTN2	613846	84	100	100	97
TCTN3	613847	66	100	100	97

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
TDGF1	187395	127	100	100	100
TDP1	607198	53	100	100	92
TDRD7	611258	70	100	100	98
TEAD1	189967	82	100	100	98
TECPR2	615000	102	100	100	99
TECR	610057	140	100	100	100
TECTA	602574	123	100	100	98
TEK	600221	80	100	100	99
TENM3	610083	86	100	100	99
TERC	602322	No coverage data			
TET2	612839	71	100	100	99
TEX28	300092	No coverage data			
TF	190000	79	100	100	99
TFAP2A	107580	95	100	100	100
TFAP2B	601601	142	100	100	100
TFE3	314310	71	100	99	90
TFG	602498	87	100	100	94
TFR2	604720	101	100	100	97
TG	188450	97	100	100	99
TGFB1	190180	111	100	99	95
TGFB2	190220	88	100	100	98
TGFB3	190230	104	100	100	100
TGFB1	601692	82	100	100	98
TGFBR1	190181	171	94	93	93
TGFBR2	190182	210	100	100	100
TGIF1	602630	152	100	100	100
TGM1	190195	125	100	100	100
TGM5	603805	113	100	100	100
TGM6	613900	117	100	100	99
TH	191290	93	100	99	94
THAP1	609520	87	100	100	98
THBD	188040	195	100	100	100
THOC6	615403	210	100	100	100
THPO	600044	118	100	100	100
THRA	190120	121	100	100	100
THRB	190160	88	100	100	99

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
TIA1	603518	73	100	100	96
TIMM8A	300356	138	100	100	100
TIMP3	188826	104	100	100	100
TINF2	604319	155	100	100	100
TJP2	607709	83	100	100	99
TK2	188250	66	100	100	95
TLL1	606742	67	100	100	96
TLR4	603030	61	100	100	99
TMC1	606706	61	100	100	94
TMC6	605828	86	100	100	97
TMC8	605829	118	100	100	100
TMCO1	614123	108	100	100	96
TMEM126A	612988	68	100	100	93
TMEM138	614459	54	100	100	100
TMEM165	614726	108	100	100	100
TMEM181	613209	83	100	100	97
TMEM216	613277	87	100	100	95
TMEM231	614949	96	100	95	90
TMEM237	614423	57	100	98	87
TMEM38B	611236	68	100	100	98
TMEM67	609884	77	100	100	94
TMEM70	612418	93	100	100	95
TMIE	607237	85	100	100	99
TMLHE	300777	32	89	81	67
TMPRSS15	606635	68	100	98	91
TMPRSS3	605511	74	100	100	99
TMPRSS6	609862	118	100	100	100
TNC	187380	110	100	100	98
TNFRSF10B	603612	95	100	100	99
TNFRSF11A	603499	97	95	95	95
TNFRSF11B	602643	91	100	100	99
TNFRSF13B	604907	106	100	100	100
TNFRSF13C	606269	78	100	91	73
TNFRSF1A	191190	97	100	98	94
TNFSF11	602642	56	100	100	94
TNNC1	191040	127	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
TNNI2	191043	151	100	100	100
TNNI3	191044	165	100	100	97
TNNT1	191041	88	100	99	94
TNNT2	191045	149	100	100	100
TNNT3	600692	114	100	100	100
TNXB	600985	151	94	92	91
TOP1	126420	76	100	100	93
TOP2A	126430	71	100	100	97
TOPORS	609507	73	100	100	100
TP53	191170	167	100	100	100
TP63	603273	115	100	100	98
TPI1	190450	123	100	98	96
TPK1	606370	59	100	100	89
TPM1	191010	145	100	100	100
TPM2	190990	98	100	100	100
TPM3	191030	69	100	100	99
TPMT	187680	75	100	100	89
TPO	606765	116	100	100	100
TPP1	607998	97	100	100	100
TPRN	613354	94	92	86	79
TRAPPC11	614138	60	100	97	90
TRAPPC2	300202	52	100	91	70
TRAPPC9	611966	100	100	100	98
TRDN	603283	53	100	94	79
TREM2	605086	107	100	100	100
TREX1	606609	234	100	100	100
TRHR	188545	94	100	100	100
TRIM24	603406	72	100	100	97
TRIM32	602290	107	100	100	100
TRIM33	605769	66	100	99	92
TRIM37	605073	61	100	100	94
TRIOBP	609761	182	100	99	97
TRIP11	604505	66	100	98	90
TRMU	610230	97	100	100	98
TRPA1	604775	61	100	98	88
TRPC6	603652	86	100	100	96

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
TRPM1	603576	85	100	100	99
TRPM4	606936	124	100	100	99
TRPM6	607009	75	100	100	96
TRPS1	604386	85	100	100	100
TRPV3	607066	106	100	100	99
TRPV4	605427	109	100	100	100
TSC1	605284	167	100	100	100
TSC2	191092	184	100	100	100
TSEN2	608753	63	87	86	78
TSEN34	608754	87	100	100	100
TSEN54	608755	105	100	96	96
TSFM	604723	77	100	100	100
TSG101	601387	78	100	100	93
TSHB	188540	95	100	100	100
TSHR	603372	100	100	100	99
TSHZ1	614427	142	98	98	98
TSPAN12	613138	67	100	100	92
TSPAN7	300096	55	100	98	83
TSPEAR	612920	105	100	100	100
TSPYL1	604714	133	100	100	100
TTBK2	611695	74	100	100	99
TTC19	613814	53	100	92	77
TTC21B	612014	75	100	99	94
TTC37	614589	58	100	99	93
TTC7A	609332	110	100	100	99
TTC8	608132	66	100	100	93
TTI2	614426	66	100	100	98
TTN	188840	68	100	99	97
TPPA	600415	61	100	98	91
TTR	176300	93	100	100	100
TUBA1A	602529	110	100	100	100
TUBA8	605742	118	100	100	100
TUBB1	612901	153	100	100	99
TUBB2A	615101	99	99	82	74
TUBB2B	612850	119	100	87	78
TUBB3	602661	269	100	99	95

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
TUBB4A	602662	242	100	100	99
TUBG1	191135	190	100	100	100
TUBGCP6	610053	159	100	100	99
TUFM	602389	158	100	100	100
TULP1	602280	108	100	100	100
TUSC3	601385	72	100	100	95
TWIST1	601622	132	100	100	95
TWIST2	607556	150	100	100	100
TWINK	606075	145	100	100	100
TYK2	176941	128	100	100	99
TYMP	131222	102	100	100	100
TYR	606933	83	100	100	98
TYROBP	604142	108	100	100	100
TYRP1	115501	73	100	100	98
UBA1	314370	94	100	100	100
UBE2A	312180	57	100	99	81
UBE3A	601623	61	100	100	96
UBE3B	608047	116	100	100	99
UBIAD1	611632	173	100	100	100
UBQLN2	300264	79	100	100	100
UBR1	605981	61	100	99	93
UGT1A1	191740	130	100	100	100
UMOD	191845	95	100	100	97
UMPS	613891	74	100	100	98
UNG	191525	104	100	100	100
UPB1	606673	96	100	100	100
UPF3B	300298	74	100	98	87
UQCRB	191330	75	100	100	100
UQCRC2	191329	95	100	100	96
UQCRQ	612080	123	100	100	100
UROC1	613012	112	100	100	99
UROD	613521	87	100	100	97
UROS	606938	60	100	100	97
USB1	613276	93	100	100	99
USH1C	605242	80	100	98	92
USH1G	607696	180	100	100	100

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
USH2A	608400	82	100	100	98
USP21	604729	150	100	100	99
USP9Y	400005	76	100	98	93
UTP4	607456	85	100	100	97
UVSSA	614632	123	100	100	99
VANGL1	610132	99	100	100	100
VANGL2	600533	131	100	100	100
VAPB	605704	71	100	100	98
VAX1	604294	104	97	91	87
VCAN	118661	67	100	100	99
VCL	193065	89	100	99	93
VCP	601023	90	100	100	98
VDR	601769	87	100	100	100
VHL	608537	183	100	100	100
VIM	193060	106	100	100	96
VIPAS39	613401	64	100	100	98
VKORC1	608547	113	100	100	99
VLDLR	192977	70	100	100	97
VPS13A	605978	72	100	99	91
VPS13B	607817	75	100	99	96
VPS33B	608552	80	100	100	98
VPS35	601501	68	100	99	94
VPS37A	609927	46	100	99	86
VPS45	610035	74	100	100	98
VRK1	602168	53	100	99	92
VSX1	605020	87	100	100	99
VSX2	142993	96	100	100	100
VWF	613160	90	98	98	96
WAS	300392	66	97	84	76
WASHC5	610657	62	100	100	94
WBP11	618083	49	96	74	54
WDPCP	613580	72	100	99	93
WDR11	606417	83	100	100	96
WDR19	608151	71	100	100	97
WDR34	613363	116	100	100	100
WDR35	613602	62	100	100	94

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
WDR36	609669	74	100	100	95
WDR45	300526	92	100	100	100
WDR60	615462	80	100	99	94
WDR62	613583	139	100	100	100
WDR72	613214	70	100	100	96
WDR81	614218	155	100	100	100
WFS1	606201	196	100	100	100
WHRN	607928	119	100	100	100
WIPF1	602357	73	100	100	96
WNK1	605232	90	100	100	99
WNK4	601844	130	100	100	100
WNT1	164820	199	100	100	100
WNT10A	606268	126	100	100	100
WNT10B	601906	129	100	100	100
WNT3	165330	151	100	100	99
WNT4	603490	231	100	92	92
WNT5A	164975	127	100	100	99
WNT7A	601570	150	100	100	100
WRAP53	612661	148	100	100	100
WRN	604611	63	100	100	95
WT1	607102	117	100	100	98
WWOX	605131	92	100	100	100
XDH	607633	81	100	100	96
XIAP	300079	47	100	95	80
XK	314850	62	100	100	96
XPA	611153	71	100	100	93
XPC	613208	108	100	100	98
XPNPEP3	613553	63	100	100	96
YAP1	606608	73	100	99	94
YARS1	603623	96	100	100	99
YARS2	610957	127	100	100	99
ZAP70	176947	151	100	100	100
ZBTB16	176797	128	100	100	100
ZBTB24	614064	73	100	100	100
ZC4H2	300897	78	100	99	93
ZDHHC9	300646	44	100	97	83

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	median depth	% covered >10x	% covered >20x	% covered >30x
ZEB1	189909	84	100	100	98
ZEB2	605802	85	100	100	100
ZFP57	612192	101	100	100	100
ZFPM2	603693	82	100	100	100
ZFYVE26	612012	90	100	100	98
ZFYVE27	610243	99	100	100	100
ZIC1	600470	255	100	100	100
ZIC2	603073	161	96	95	93
ZIC3	300265	101	100	100	97
ZMPSTE24	606480	59	100	100	96
ZMYND10	607070	130	100	100	100
ZNF335	610827	110	100	100	100
ZNF423	604557	166	100	100	100
ZNF469	612078	169	100	100	100
ZNF513	613598	121	100	100	100
ZNF592	613624	141	100	100	100
ZNF644	614159	63	100	100	99
ZNF711	314990	54	100	96	85
ZNF750	610226	146	100	100	100
ZNF81	314998	49	100	100	90
ZSWIM6	615951	71	96	93	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