

WES INTELLECTUAL DISABILITY DG 3.00

<i>Gene</i>	<i>Median coverage</i>	<i>% covered >10x</i>	<i>% covered >20x</i>	<i>OMIM disease ID</i>
AAAS	116.8	100.0	99.9	231550
AARS1	124.6	100.0	99.9	616339
AASS	168.0	100.0	99.7	238700;268700
ABAT	105.3	100.0	99.4	613163
ABCA2	129.9	99.7	98.9	618808
ABCC8	131.7	100.0	99.8	606176;240800;256450
ABCC9	173.0	100.0	99.9	239850
ABCD1	78.4	75.8	71.6	300100
ABCD4	141.1	99.9	98.6	614857
ABHD5	224.6	100.0	100.0	275630
ACAD9	141.5	100.0	99.9	611126
ACADS	129.1	99.9	98.2	201470
ACAT1	126.9	99.9	97.6	203750
ACO2	122.7	96.3	90.2	614559
ACOX1	143.0	100.0	99.9	264470
ACSF3	148.0	100.0	99.9	614265
ACSL4	133.0	98.8	94.7	300387
ACTB	74.1	99.7	96.0	243310;607371
ACTG1	121.3	100.0	100.0	614583
ACTL6A	150.7	99.8	98.6	-
ACTL6B	143.5	100.0	99.8	618470;618468
ACVR1	181.7	100.0	100.0	135100
ACY1	131.3	100.0	98.8	609924
ADAM22	154.4	99.9	99.6	617933
ADAR	122.0	100.0	99.8	615010

ADARB1	209.5	98.0	95.2	618862
ADAT3	89.9	100.0	99.7	615286
ADGRG1	163.4	100.0	100.0	606854;615752
ADK	97.1	84.1	81.0	614300
ADNP	229.0	90.5	90.5	615873
ADPRS	158.5	100.0	99.8	618170
ADSL	150.0	99.2	98.7	103050
AFF2	134.7	100.0	99.4	309548
AFF4	118.6	99.9	99.0	616368
AFG3L2	115.2	95.0	91.2	614487
AGA	191.5	100.0	100.0	208400
AGMO	133.3	99.2	96.0	-
AGO2	135.3	99.1	99.1	-
AGTPBP1	144.5	96.0	94.2	618276
AHCY	117.1	100.0	99.2	613752
AHDC1	121.2	100.0	99.2	615829
AHI1	154.7	99.7	97.9	608629
AHSG	186.0	99.9	99.5	203650
AIFM1	118.0	99.9	98.8	300816;310490
AIMP1	92.2	99.2	94.5	260600
AIMP2	155.7	89.0	86.0	618006
AKT3	103.6	98.8	94.5	615937
ALDH18A1	141.9	100.0	99.9	616586;601162;616603;219150
ALDH3A2	129.0	88.8	88.1	270200
ALDH4A1	124.7	100.0	99.4	239510
ALDH5A1	106.9	91.1	81.5	271980
ALDH7A1	77.2	94.5	88.9	266100
ALG1	48.3	53.0	45.7	608540
ALG11	160.5	96.8	96.8	613661
ALG12	161.4	100.0	100.0	607143

ALG13	92.8	98.4	92.7	300884
ALG14	250.7	100.0	99.9	619031
ALG2	98.2	100.0	100.0	616228;607906
ALG3	92.2	100.0	99.7	601110
ALG6	126.9	98.7	94.8	603147
ALG8	132.6	97.2	95.6	608104
ALG9	124.4	100.0	99.7	608776
ALKBH8	133.5	99.8	98.8	618504
ALMS1	203.4	99.8	99.5	203800
ALX3	124.5	77.9	73.3	136760
ALX4	137.4	100.0	99.3	613451
AMER1	108.5	99.9	98.4	300373
AMMECR1	95.1	100.0	99.1	300990
AMPD2	139.1	99.8	98.9	615809
AMT	152.9	100.0	100.0	605899
ANK3	171.9	99.3	99.0	615493
ANKH	132.0	100.0	100.0	-
ANKLE2	164.3	99.9	98.6	616681
ANKRD11	118.4	96.1	93.5	148050
ANKS1B	147.3	100.0	99.6	-
ANO10	131.7	99.8	98.0	613728
ANTXR1	127.7	99.7	97.9	230740
AP1S1	124.5	99.9	99.5	609313
AP1S2	67.0	77.9	69.9	304340
AP2M1	124.4	100.0	100.0	618587
AP3B1	140.6	99.2	95.9	608233
AP3B2	127.4	93.3	89.5	617276
AP3D1	125.0	99.8	98.6	617050
AP4B1	151.5	99.9	98.7	614066
AP4E1	120.8	99.8	98.6	613744

AP4M1	145.1	99.9	98.9	612936
AP4S1	89.3	78.9	71.3	614067
APC2	93.6	97.6	92.7	617169
APTX	122.5	94.9	92.4	208920
ARCN1	167.5	97.0	96.6	617164
ARF1	163.7	100.0	100.0	618185
ARFGEF2	146.2	99.9	99.1	608097
ARG1	152.6	92.9	92.9	207800
ARHGAP31	160.8	99.9	98.8	100300
ARHGEF6	151.3	99.5	96.2	-
ARHGEF9	59.7	76.5	74.1	300607
ARID1A	146.4	98.1	96.4	614607
ARID1B	153.3	96.2	95.2	135900
ARID2	182.8	99.8	98.5	617808
ARL13B	108.3	100.0	99.2	612291
ARL6	128.4	99.9	98.6	600151
ARMC9	152.0	100.0	99.8	617622
ARSA	126.1	100.0	99.8	250100
ARSL	103.2	99.0	93.1	302950
ARV1	128.5	100.0	99.9	617020
ARX	38.8	81.0	64.4	309510;308350;300215;300419;300004
ASAH1	158.3	99.7	98.6	159950;228000
ASH1L	174.4	98.7	98.6	617796
ASL	113.3	100.0	99.6	207900
ASNS	98.8	99.4	95.3	615574
ASPA	151.3	99.9	98.3	271900
ASPM	128.3	99.7	98.2	608716
ASS1	110.0	95.3	87.8	215700
ASXL1	145.5	99.8	99.3	605039
ASXL2	162.3	99.7	98.9	617190

ASXL3	161.7	99.9	99.7	615485
ATAD1	77.6	99.5	95.1	618011
ATAD3A	84.7	91.9	83.1	617183
ATIC	142.3	99.9	99.3	608688
ATL1	180.2	100.0	99.8	182600
ATN1	166.4	99.9	98.1	125370
ATP1A1	143.0	100.0	100.0	618314
ATP1A2	182.6	100.0	100.0	104290;602481
ATP1A3	173.1	100.0	99.9	614820
ATP2A2	162.9	100.0	100.0	124200
ATP6AP2	57.3	94.3	76.7	300423
ATP6V0A2	133.8	100.0	99.5	219200;278250
ATP6V1A	156.0	99.9	98.7	617403;618012
ATP6V1B2	143.7	100.0	99.3	616455
ATP7A	135.7	99.0	96.9	309400
ATP8A2	134.7	100.0	99.7	615268
ATR	178.5	99.9	99.4	210600
ATRX	103.1	99.4	96.4	309580;301040
AUH	120.8	100.0	99.8	250950
AUTS2	140.9	98.2	95.8	615834
AVPR2	112.1	100.0	99.4	304800
B3GALNT2	117.1	93.8	89.4	615181
B3GALT6	43.1	75.7	69.7	615349
B3GLCT	116.5	99.6	96.2	261540
B4GALNT1	156.5	99.3	94.9	609195
B4GALT7	122.0	99.8	97.4	130070
B4GAT1	117.9	100.0	100.0	615287
BAZ2B	157.1	99.9	99.0	-
BBS1	172.3	100.0	100.0	209900
BBS10	168.4	100.0	99.8	615987

BBS12	213.1	100.0	100.0	615989
BBS2	179.9	100.0	99.5	615981
BBS4	127.4	99.9	99.3	615982
BBS5	113.5	99.1	94.0	615983
BBS7	174.2	98.8	95.6	615984
BBS9	122.1	92.3	90.5	615986
BCAP31	80.5	92.7	83.2	300475
BCKDHA	199.7	99.9	99.2	248600
BCKDHB	147.1	99.5	94.4	248600
BCKDK	215.1	100.0	100.0	614923
BCL11A	144.3	97.7	96.0	617101
BCL11B	97.3	99.0	95.6	618092;617237
BCOR	117.7	99.6	97.4	300166;309800
BCORL1	167.8	99.6	97.9	301029
BCS1L	157.7	100.0	100.0	256000;262000;124000
BLM	133.6	99.8	98.3	210900
BOLA3	50.8	99.4	90.2	614299
BPTF	162.4	96.2	94.3	617755
BRAF	80.6	91.0	81.2	163950;613706;613707;115150
BRAT1	130.8	99.7	98.2	614498;618056
BRF1	108.7	99.9	98.4	616202
BRPF1	168.6	100.0	100.0	617333
BRSK2	117.8	99.5	97.4	-
BRWD3	131.3	99.3	97.2	300659
BSCL2	113.5	100.0	100.0	615924;269700
BTD	126.6	83.1	83.0	253260
BUB1B	141.2	99.6	98.9	257300
C12orf4	156.5	100.0	99.3	618221
C12orf57	144.5	100.0	98.9	218340
C12orf65	122.6	99.8	98.5	613559;615035

C2CD3	140.3	95.8	95.6	615948
CA2	172.2	100.0	100.0	259730
CA5A	106.2	87.4	85.2	615751
CA8	126.5	99.6	97.4	613227
CACNA1A	94.8	93.1	90.0	141500;617106
CACNA1B	143.4	97.6	95.7	618497
CACNA1C	163.1	99.9	99.2	601005
CACNA1D	155.6	98.0	97.9	615474
CACNA1E	142.6	100.0	99.9	618285
CACNA1G	151.5	100.0	99.6	616795;618087
CACNA2D2	136.6	94.0	93.2	618501
CAD	150.0	100.0	99.2	616457
CAMK2A	129.9	99.9	99.0	617798;618095
CAMK2B	110.7	100.0	99.8	617799
CAMK2G	126.8	99.9	98.1	618522
CAMTA1	189.4	100.0	99.5	614756
CANT1	152.9	100.0	99.9	251450
CARS2	131.3	100.0	100.0	616672
CASK	104.6	97.3	94.3	300749;300422
CBL	152.3	97.3	97.1	613563
CBS	124.3	99.8	98.3	236200
CC2D1A	151.3	100.0	99.3	608443
CC2D2A	131.6	98.5	96.5	216360;612285
CCBE1	81.0	99.8	98.9	235510
CCDC115	91.2	95.2	89.9	616828
CCDC174	140.3	99.5	97.2	616816
CCDC22	110.0	99.6	96.6	300963
CCDC32	118.3	100.0	99.5	-
CCDC47	189.1	99.4	97.5	618268
CCDC88A	106.8	96.5	93.1	617507

CCDC88C	110.9	100.0	99.3	236600
CCND2	141.6	100.0	100.0	615938
CCNK	106.7	92.6	89.8	618147
CDC42	121.8	98.0	91.0	616737
CDC42BPB	155.4	100.0	99.3	-
CDC6	172.5	100.0	100.0	613805
CDH11	153.1	100.0	100.0	211380
CDH15	146.7	99.9	98.7	612580
CDK10	124.6	100.0	99.9	617694
CDK13	146.0	98.0	92.6	617360
CDK19	160.6	100.0	99.9	618916
CDK5RAP2	130.2	99.8	98.9	604804
CDK8	185.4	99.7	98.0	-
CDKL5	121.8	91.7	90.3	300672
CDKN1C	67.0	88.0	77.8	614732
CDON	132.4	100.0	99.5	614226
CENPF	145.1	99.8	98.5	243605
CENPJ	156.2	100.0	99.6	613676;608393
CEP104	131.2	100.0	99.2	616781
CEP120	170.7	100.0	99.5	617761
CEP135	104.9	99.1	93.7	614673
CEP152	184.3	99.7	98.2	613823
CEP290	97.4	96.2	90.2	610188;615991
CEP41	92.7	99.8	97.4	614464
CEP55	138.6	100.0	99.8	236500
CEP57	100.0	99.2	93.1	614114
CEP83	133.5	99.8	97.3	615862
CEP89	159.0	96.0	94.5	-
CERT1	136.3	90.2	87.4	616351
CHAMP1	200.3	100.0	100.0	616579

CHD1	137.8	99.3	95.0	617682
CHD2	151.3	99.4	99.2	615369
CHD3	111.3	94.8	92.6	618205
CHD4	133.6	100.0	99.9	617159
CHD7	158.3	100.0	99.5	214800
CHD8	151.4	100.0	99.9	615032
CHKB	114.6	100.0	99.7	602541
CHMP1A	131.8	100.0	99.8	614961
CHRNA4	108.7	98.3	96.2	600513
CIC	71.5	63.3	63.3	617600
CIT	127.6	100.0	99.3	617090
CKAP2L	194.5	99.7	98.6	272440
CLCN4	117.9	99.9	98.9	300114
CLIC2	74.9	99.9	96.6	300886
CLIP1	141.5	100.0	99.0	-
CLN3	132.7	92.5	91.8	204200
CLN5	126.0	69.3	66.3	256731
CLN6	141.0	99.9	97.2	204300;601780
CLN8	173.3	83.5	83.5	600143;610003
CLP1	139.9	100.0	100.0	615803
CLPB	135.3	94.9	94.9	616271
CLTC	183.9	100.0	99.9	617854
CNKSR2	96.3	95.5	90.9	301008
CNNM2	197.5	100.0	100.0	616418
CNOT1	158.8	100.0	99.9	-
CNOT2	155.1	99.9	99.5	-
CNOT3	146.5	100.0	100.0	-
CNPY3	82.9	100.0	99.3	617929
CNTNAP2	153.8	100.0	99.8	610042
COA8	92.7	81.9	80.7	220110

COASY	180.6	100.0	100.0	615643
COG1	121.6	100.0	100.0	611209
COG4	110.1	100.0	99.9	618150;613489
COG5	155.0	99.7	97.6	613612
COG6	108.4	99.1	93.9	614576;615328
COG7	124.8	100.0	100.0	608779
COG8	138.4	99.9	98.6	611182
COL4A1	115.4	98.8	97.4	175780;607595
COL4A2	120.7	100.0	99.6	614483
COLEC11	177.8	100.0	100.0	265050
COQ2	113.4	98.0	95.3	607426
COQ4	98.7	90.9	89.3	616276
COQ8A	164.7	100.0	99.5	612016
COQ9	79.2	100.0	97.9	614654
COX10	211.4	100.0	100.0	256000;220110
COX15	106.0	99.9	98.7	256000
COX6B1	189.3	100.0	100.0	220110
CPLANE1	149.1	99.7	98.4	614615;277170
CPLX1	90.3	100.0	100.0	617976;194190
CPS1	163.0	100.0	99.9	237300
CRADD	122.7	99.5	96.2	614499
CRBN	152.7	88.2	87.7	607417
CREBBP	123.9	99.7	98.5	180849
CRLF1	127.4	91.0	89.7	272430
CRPPA	122.3	98.5	95.0	614643
CSDE1	184.9	99.9	99.5	-
CSF1R	125.3	99.9	99.2	221820;618476
CSNK2A1	108.2	81.6	77.8	617062
CSNK2B	139.9	100.0	100.0	-
CSPP1	132.7	99.8	98.7	615636

CSTB	84.9	99.5	89.9	254800
CTBP1	96.5	93.2	86.9	617915;194190
CTC1	127.7	100.0	99.6	612199
CTCF	149.7	100.0	99.3	615502
CTDP1	129.0	88.4	84.3	604168
CTNNA2	118.7	100.0	99.8	618174
CTNNB1	146.7	100.0	99.9	615075
CTNND2	112.7	93.5	91.1	-
CTSA	156.4	100.0	100.0	256540
CTSD	174.1	98.4	95.0	610127
CTTNBP2	128.5	99.5	97.3	-
CTU2	134.4	99.7	97.7	618142
CUL4B	93.3	98.0	91.1	300354
CUX1	129.9	96.4	94.8	618330
CUX2	132.6	99.9	99.1	618141
CWC27	106.0	99.3	96.5	250410
CWF19L1	127.0	100.0	99.8	616127
CXorf56	92.7	99.8	96.9	301013
CYB5R3	165.3	98.4	98.0	250800
CYFIP2	137.4	100.0	99.4	618008
CYP27A1	180.3	98.9	96.7	213700
CYP2U1	159.9	94.8	91.5	615030
D2HGDH	135.1	99.2	97.2	600721
DAG1	202.8	100.0	100.0	616538;613818
DARS1	158.0	100.0	99.3	615281
DARS2	143.7	94.9	94.3	611105
DBT	135.0	99.8	98.1	248600
DCAF17	107.6	98.9	93.3	241080
DCC	147.1	100.0	100.0	617542;157600
DCHS1	147.7	99.8	99.1	601390

DCPS	146.9	91.3	91.2	616459
DCX	115.5	100.0	99.9	300067
DDC	121.3	99.7	96.4	608643
DDHD2	145.0	100.0	99.5	615033
DDX11	108.5	85.1	80.7	613398
DDX3X	77.1	81.2	78.9	300958
DDX59	172.3	100.0	100.0	174300
DDX6	73.6	97.7	88.8	618653
DEAF1	114.4	97.4	88.8	615828;617171
DEGS1	165.3	100.0	100.0	618404
DENND5A	118.4	100.0	99.4	617281
DEPDC5	145.0	100.0	99.8	604364
DHCR24	165.6	97.7	97.7	602398
DHCR7	151.8	100.0	100.0	270400
DHDDS	92.9	99.0	95.0	617836
DHFR	52.0	92.3	79.0	613839
DHPS	131.3	100.0	99.7	618480
DHTKD1	145.4	99.9	98.9	204750
DHX30	163.1	100.0	99.9	617804
DIAPH1	119.5	99.8	99.0	616632
DIP2B	155.2	100.0	99.3	136630
DIS3L2	164.1	100.0	99.7	267000
DKC1	109.2	99.8	98.7	305000
DLD	135.9	100.0	99.7	246900
DLG3	86.8	99.0	93.2	300850
DLG4	165.1	99.1	99.0	-
DMD	134.0	99.6	98.6	310200
DMPK	158.4	99.8	98.4	160900
DMXL2	184.1	99.9	99.1	616113
DNAJC12	188.9	87.4	87.4	617384

DNAJC19	139.9	98.9	96.4	610198
DNM1	144.6	92.6	89.1	616346
DNMT3A	134.5	99.8	98.6	615879
DNMT3B	133.3	100.0	100.0	242860
DOCK3	134.7	100.0	99.0	618292
DOCK6	122.0	99.3	98.9	614219
DOCK7	150.6	99.8	98.2	615859
DOLK	186.8	100.0	100.0	610768
DONSON	113.5	91.7	85.4	617604
DPAGT1	90.4	100.0	100.0	608093;614750
DPF2	121.1	99.9	98.4	618027
DPH1	165.9	100.0	99.9	616901
DPM1	155.8	98.3	91.4	608799
DPP6	139.3	99.7	97.8	616311
DPYD	173.1	99.7	97.7	274270
DPYS	137.0	100.0	99.9	222748
DYM	122.4	97.4	96.5	223800
DYNC1H1	157.2	99.9	99.4	158600;614228;614563
DYNC1I2	61.8	84.4	68.8	618492
DYRK1A	158.6	100.0	100.0	614104
EBF3	151.7	100.0	100.0	617330
EBP	73.6	99.7	95.7	302960;300960
ECHS1	108.4	99.9	99.0	616277
EDC3	134.0	100.0	99.9	616460
EED	84.4	96.5	91.4	617561
EEF1A2	188.9	100.0	100.0	616409;616393
EFNB2	174.8	100.0	99.8	-
EFTUD2	123.6	100.0	99.8	610536
EHMT1	138.4	94.5	93.7	610253
EIF2AK1	151.3	98.8	95.4	618878

EIF2AK2	160.3	100.0	99.7	618877
EIF2AK3	174.9	97.2	94.5	226980
EIF2B4	138.4	100.0	99.9	603896
EIF2B5	119.7	100.0	99.1	603896
EIF2S3	92.7	95.4	89.1	300148
EIF3F	75.7	96.7	83.9	618295
EIF4A3	106.1	100.0	99.5	268305
ELAC2	124.5	100.0	99.7	615440
ELOVL4	122.8	100.0	99.5	614457
ELP2	137.0	99.9	98.8	617270
EMC1	133.3	100.0	99.2	616875
EML1	152.5	99.7	98.4	600348
EMX2	159.0	100.0	100.0	269160
ENTPD1	160.7	100.0	100.0	615683
EP300	191.7	99.8	99.0	613684;180849
EPG5	137.8	99.5	98.5	242840
ERCC1	88.0	100.0	99.3	610758
ERCC2	135.0	100.0	99.7	601675;610756;278730
ERCC3	107.7	96.9	96.3	616390;610651
ERCC5	143.3	100.0	99.7	616570
ERCC6	197.1	100.0	100.0	278800;133540;214150
ERCC8	103.4	99.5	95.9	216400
ERLIN2	140.7	100.0	99.9	611225
ESCO2	139.8	98.8	95.3	269000;268300
ETFB	122.1	100.0	99.8	231680
ETHE1	96.1	99.9	97.4	602473
EXOSC2	117.4	100.0	100.0	617763
EXOSC3	125.9	99.5	94.9	614678
EXOSC9	173.7	99.7	97.2	618065
EXTL3	198.7	100.0	100.0	617425

EZH2	171.4	100.0	99.4	277590
FA2H	96.1	92.1	83.2	612319
FAM126A	146.5	100.0	99.4	610532
FAM149B1	118.0	99.5	95.4	618763
FAM20C	132.0	100.0	100.0	259775
FAR1	85.0	97.6	92.8	616154
FARS2	206.4	100.0	100.0	614946;617046
FARSB	94.4	98.8	94.6	613658
FAT4	227.0	100.0	100.0	616006;615546
FBXL3	237.0	100.0	100.0	606220
FBXL4	200.8	100.0	100.0	615471
FBXO11	101.9	96.9	92.7	618089
FBXO31	112.2	96.0	93.1	615979
FDFT1	147.6	97.7	96.0	618156
FGD1	91.7	97.3	92.8	305400
FGF12	124.6	99.9	98.1	617166
FGF14	225.8	100.0	100.0	609307
FGFR1	137.4	100.0	99.9	101600;147950;166250;613001;615465
FGFR2	133.9	97.7	97.1	123790;101400;101600;609579;101200;207410;123500
FGFR3	122.3	99.8	97.6	616482;602849;187600;100800;146000;610474
FH	147.2	92.1	88.3	606812
FIBP	143.3	100.0	100.0	617107
FIGN	150.0	100.0	100.0	-
FKRP	124.1	100.0	100.0	236670;606612;613153
FKTN	128.8	99.7	96.9	613152;236670;611588;253800
FLNA	139.3	100.0	99.8	300049;304120;311300;300321;309350;305620
FLVCR1	153.3	100.0	99.0	609033
FLVCR2	140.4	100.0	100.0	225790
FMN2	106.7	85.5	82.5	616193
FMR1	96.8	96.1	92.3	300624;300623

FOLR1	130.3	100.0	100.0	613068
FOXG1	144.5	88.7	82.1	613454
FOXJ1	74.5	99.9	98.4	618699
FOXP1	143.9	100.0	99.8	613670
FOXP2	153.9	99.5	99.2	602081
FOXRED1	135.7	100.0	99.9	618241
FRAS1	140.1	100.0	99.4	219000
FRMD4A	129.2	90.8	87.3	616819
FRMPD4	120.1	97.5	96.5	300983
FRRS1L	134.5	79.7	69.1	616981
FTCD	101.1	95.8	91.0	229100
FTO	114.9	83.8	83.7	612938
FTSJ1	132.7	98.0	93.9	309549
FUCA1	132.3	100.0	99.9	230000
FUT8	150.2	100.0	99.2	618005
GABBR2	127.2	96.1	92.0	617904;617903
GABRA1	196.8	100.0	100.0	615744
GABRA2	180.7	99.7	98.6	618557
GABRA3	95.0	98.7	94.4	-
GABRA5	168.7	100.0	99.9	618559
GABRB1	204.1	100.0	100.0	617153
GABRB2	156.7	100.0	99.9	617829
GABRB3	147.5	99.6	98.2	617113
GABRG2	167.0	90.8	90.2	618396
GAD1	141.7	100.0	99.9	603513
GALC	117.3	99.8	98.4	245200
GALE	149.4	100.0	100.0	230350
GALNT2	132.6	99.7	97.1	618885
GALT	167.0	100.0	99.7	230400
GAMT	112.7	93.1	82.7	612736

GATAD2B	120.1	100.0	100.0	615074
GATM	156.4	100.0	100.0	612718
GCH1	81.0	99.9	95.7	233910
GCSH	33.5	75.8	69.3	605899
GDI1	158.4	99.8	98.7	300849
GFAP	103.8	91.8	89.6	203450
GFER	91.2	99.6	93.8	613076
GFM1	131.5	99.9	99.4	609060
GFM2	137.8	99.0	95.3	618397
GJA1	187.0	100.0	100.0	257850;164200
GJB1	169.9	100.0	100.0	302800
GJC2	37.1	78.2	58.8	613206;608804
GK	57.1	89.2	70.8	307030
GLB1	89.6	99.9	97.4	230650;230600;230500
GLDC	70.8	90.0	81.9	605899
GLI2	155.3	99.1	97.4	610829;615849
GLI3	140.6	98.5	98.0	175700;146510
GLIS3	135.9	98.6	98.2	610199
GLUD1	72.9	94.1	82.9	606762
GLYCTK	155.0	98.8	97.3	220120
GM2A	131.0	100.0	100.0	272750
GMPPA	168.8	100.0	100.0	615510
GMPPB	245.2	100.0	100.0	615352;615351;615350
GNAI1	92.9	99.0	94.0	-
GNAO1	172.5	93.8	93.8	615473;617493
GNAS	168.9	86.9	85.1	612463;219080;612462;103580
GNB1	183.2	100.0	100.0	616973
GNB5	132.6	100.0	98.8	617182;617173
GNPAT	153.9	99.7	97.4	222765
GNPTAB	167.3	100.0	99.9	252500;252600

GNPTG	155.7	99.1	94.3	252605
GNS	111.5	98.3	94.7	252940
GOT2	95.5	97.5	90.9	618721
GPAA1	111.2	98.8	95.9	617810
GPC3	91.0	99.1	94.8	312870
GPC4	120.3	100.0	99.6	301026
GPHN	175.6	100.0	99.5	615501
GPSM2	147.0	99.9	99.2	604213
GPT2	135.7	99.1	93.6	616281
GRIA3	101.9	99.7	96.1	300699
GRIA4	153.3	99.8	99.0	617864
GRID2	179.0	100.0	99.8	616204
GRIK2	155.9	96.2	95.4	611092
GRIN1	164.0	100.0	100.0	617820;614254
GRIN2A	160.9	100.0	100.0	245570
GRIN2B	173.9	99.8	99.1	616139;613970
GRIN2D	76.1	79.9	65.5	617162
GRIP1	136.8	100.0	99.7	617667
GRM1	170.0	100.0	99.7	614831;617691
GRN	165.8	100.0	100.0	614706;607485
GSE1	129.7	99.8	97.7	-
GSS	102.2	96.5	96.4	266130
GTF2H5	76.2	72.5	72.2	616395
GTPBP2	140.1	100.0	99.3	617988
GTPBP3	162.8	100.0	99.8	616198
GUSB	111.2	92.9	91.8	253220
H1-4	102.0	100.0	100.0	617537
H4C3	109.7	100.0	100.0	-
HACE1	172.2	100.0	99.3	616756
HADH	127.1	99.0	97.5	609975

HADHA	87.4	97.2	91.6	609015
HAX1	166.3	100.0	100.0	610738
HCCS	111.4	99.7	97.6	309801
HCFC1	97.6	98.3	93.6	309541
HCN1	151.3	98.5	98.2	615871
HDAC4	127.0	100.0	99.8	-
HDAC6	121.1	99.5	97.4	300863
HDAC8	106.6	86.5	85.1	300882
HECW2	130.8	100.0	99.1	617268
HEPACAM	125.9	85.8	78.9	604004;613925;613926
HERC1	172.0	100.0	100.0	617011
HERC2	115.0	79.9	77.2	176270;615516
HESX1	80.5	99.7	97.4	182230
HEXA	109.0	93.8	93.3	272800
HEXB	188.2	99.6	97.0	268800
HGSNAT	125.5	86.4	86.3	252930
HIBCH	83.9	98.3	88.7	250620
HIVEP2	189.4	100.0	100.0	616977
HK1	139.8	100.0	100.0	618547
HLCS	179.1	100.0	100.0	253270
HMGCL	128.9	100.0	99.8	246450
HNMT	177.0	100.0	99.8	616739
HNRNPH1	126.6	99.4	96.1	-
HNRNPH2	146.3	100.0	100.0	300986
HNRNPK	77.0	91.6	82.9	616580
HNRNPU	170.6	99.9	98.9	617391
HOXA1	167.4	100.0	100.0	601536
HPD	174.4	100.0	100.0	276710
HPRT1	74.9	99.3	92.4	300322
HRAS	177.5	100.0	100.0	218040;163200

HSD17B10	110.5	100.0	99.1	300438
HSD17B4	130.2	95.5	93.1	261515;233400
HSPA9	97.6	88.6	84.5	616854
HSPD1	92.0	98.8	93.7	612233
HTRA2	137.9	100.0	99.9	617248
HUWE1	95.0	99.3	95.9	309590
HYLS1	183.3	100.0	100.0	236680
IARS1	150.2	100.0	99.6	617093
IARS2	170.7	100.0	99.9	616007
IBA57	116.9	93.6	90.0	615330
IDS	111.2	99.9	98.0	309900
IDUA	128.4	93.8	86.8	607014
IER3IP1	102.8	92.2	82.6	614231
IFIH1	137.5	99.7	98.3	615846
IFT172	107.6	99.9	99.1	615630;616394
IFT81	108.5	93.5	90.2	617895
IGBP1	111.9	99.5	96.2	300472
IGF1	102.5	100.0	99.9	608747
IGF1R	128.4	100.0	99.9	270450
IKBKG	63.2	84.1	77.2	308300
IL1RAPL1	127.0	99.8	98.7	300143
IMPA1	84.1	97.1	87.2	617323
INPP5E	107.3	97.0	92.7	610156;213300
INPP5K	108.9	100.0	100.0	617404
INTS1	119.0	99.8	98.4	618571
IQSEC1	93.2	89.1	86.3	618687
IQSEC2	72.9	96.8	88.8	309530
IRF2BPL	160.0	99.5	94.9	618088
ISCA2	125.9	100.0	98.8	616370
ITGA7	141.9	99.6	98.0	613204

ITPA	149.1	100.0	100.0	616647
ITPR1	152.2	100.0	99.9	206700;117360
IVD	100.8	100.0	100.0	243500
JAG1	147.0	97.7	96.9	118450
JAM3	149.6	100.0	99.9	613730
JMJD1C	161.4	99.9	99.2	-
KANK1	140.2	100.0	100.0	612900
KANSL1	180.3	99.9	99.2	610443
KAT6A	175.6	100.0	99.8	616268
KAT6B	171.0	99.6	98.3	606170;603736
KAT8	118.2	99.9	98.8	618974
KATNB1	136.1	100.0	99.9	616212
KCNA2	160.5	100.0	99.6	616366
KCNA4	148.3	100.0	100.0	618284
KCNB1	156.6	100.0	99.6	616056
KCNC1	156.5	100.0	100.0	616187
KCNC3	113.2	78.6	65.8	605259
KCNH1	173.1	98.7	98.7	611816;135500
KCNJ10	156.9	89.3	89.0	612780;274600
KCNJ11	176.4	100.0	100.0	606176
KCNJ6	190.9	100.0	100.0	614098
KCNK4	182.4	99.1	97.4	618381
KCNK9	152.8	97.3	97.3	612292
KCNMA1	122.2	94.4	93.6	617643;618729
KCNQ2	113.4	91.3	89.8	121200;613720
KCNQ3	123.8	100.0	99.4	121201
KCNQ5	164.3	97.8	95.5	617601
KCNT1	129.5	96.0	95.2	615005;614959
KCNT2	125.1	99.4	97.2	617771
KCTD3	144.2	100.0	99.7	-

KCTD7	163.3	95.0	95.0	611726
KDM1A	149.2	98.2	95.3	616728
KDM3B	139.2	97.5	96.3	-
KDM5B	132.3	94.6	92.3	618109
KDM5C	109.8	99.8	98.0	300534
KDM6A	115.7	96.2	88.9	147920;300867
KDM6B	161.0	98.8	97.9	618505
KIAA0586	144.0	97.3	93.2	616490
KIAA1109	170.8	99.8	99.2	617822
KIDINS220	167.3	100.0	100.0	617296
KIF11	105.5	97.6	94.8	152950
KIF14	143.5	99.6	97.8	617914
KIF1A	114.4	97.4	95.1	614213;614255
KIF2A	121.5	99.6	95.8	615411
KIF3B	114.3	100.0	99.7	-
KIF4A	94.8	99.4	95.7	300923
KIF5A	141.0	100.0	99.9	617235
KIF5C	123.5	99.9	98.8	615282
KIF7	99.8	93.6	90.5	200990;607131
KIFBP	176.4	96.1	96.1	609460
KIRREL3	127.9	99.8	98.8	612581
KLF7	137.7	100.0	99.7	-
KLHL15	174.9	100.0	99.7	300982
KMT2A	154.5	100.0	99.9	605130
KMT2B	146.5	95.8	94.0	617284
KMT2C	167.4	92.2	91.0	617768
KMT2D	141.7	100.0	99.4	147920
KMT2E	189.2	99.8	98.5	618512
KMT5B	201.9	99.9	99.1	617788
KNL1	121.3	99.2	98.1	604321

KPTN	142.8	100.0	100.0	615637
KRAS	84.7	99.5	96.9	615278;609942;163200
L1CAM	135.6	99.9	99.1	307000;304100;303350
L2HGDH	145.2	99.1	97.2	236792
LAMA1	141.8	100.0	99.7	615960
LAMA2	155.7	100.0	99.6	618138;607855
LAMB1	171.6	100.0	99.9	615191
LAMC3	151.1	98.6	97.1	614115
LAMP2	109.8	99.3	95.7	300257
LARGE1	129.2	100.0	99.6	236670;608840;613154
LARP7	78.1	88.5	78.5	615071
LAS1L	93.4	99.7	97.2	309585
LIAS	151.7	100.0	99.0	614462
LIG4	223.2	100.0	99.9	606593
LINGO1	167.2	100.0	100.0	618103
LINS1	139.9	100.0	99.1	614340
LMAN2L	138.9	100.0	99.7	616887
LONP1	141.5	100.0	99.8	600373
LRP2	170.9	100.0	99.9	222448
LRPPRC	151.8	99.9	99.1	220111
LYST	169.5	99.6	98.3	214500
LZTFL1	132.2	99.9	99.2	615994
LZTR1	136.6	100.0	99.9	616564;605275
MAB21L1	191.4	100.0	100.0	-
MAB21L2	180.8	100.0	100.0	615877
MACF1	145.4	99.7	99.3	618325
MAF	79.1	83.5	78.0	601088
MAG	160.5	100.0	100.0	616680
MAGEL2	115.6	93.0	87.2	176270;615547
MAN1B1	129.1	100.0	99.7	614202

MAN2B1	142.1	99.8	97.9	248500
MANBA	128.9	87.8	86.5	248510
MAOA	120.5	100.0	99.7	300615
MAP1B	145.5	99.3	97.7	-
MAP2K1	110.9	99.8	97.0	163950;615279
MAP2K2	122.7	98.5	95.1	615280
MAPK8IP3	162.4	99.4	99.0	-
MAPRE2	184.8	100.0	99.3	616734
MASP1	146.2	100.0	99.9	257920
MAST1	155.1	100.0	99.5	618273
MAT1A	157.8	99.7	97.7	250850
MBD5	169.7	99.9	99.9	156200
MBOAT7	108.4	100.0	99.5	617188
MBTPS2	134.1	100.0	99.0	308205
MCCC1	175.6	100.0	99.8	210200
MCCC2	140.6	99.9	98.4	210210
MCOLN1	158.8	99.8	98.4	252650
MCPH1	149.6	100.0	99.3	251200
MDH2	116.7	98.0	97.9	617339
MECP2	150.2	100.0	98.8	300260;312750;300673;300055
MECR	115.0	100.0	98.8	617282
MED12	101.7	99.8	96.7	300895;305450;309520
MED13	179.9	100.0	99.9	-
MED13L	136.2	100.0	99.8	616789
MED17	148.2	96.3	93.6	613668
MED23	162.2	100.0	99.7	614249
MED25	151.6	100.0	99.8	616449
MEF2C	163.3	99.9	95.9	613443
MEGF8	137.9	99.9	99.0	614976
MEIS2	149.2	100.0	100.0	600987

METTL23	139.0	100.0	100.0	615942
METTL5	145.1	99.3	98.5	-
MFF	100.8	94.3	90.0	617086
MFSD2A	140.3	99.7	98.5	616486
MFSD8	143.5	100.0	99.7	610951
MGAT2	156.2	100.0	99.9	212066
MGP	159.6	98.8	95.2	245150
MICU1	126.3	98.9	95.3	615673
MID1	160.2	99.8	98.8	300000
MID2	122.0	99.8	98.7	300928
MKKS	232.7	100.0	100.0	605231
MKS1	104.6	99.8	97.8	615990;617121
MLC1	102.9	100.0	99.0	604004
MLYCD	92.5	96.0	90.3	248360
MMAA	210.2	100.0	100.0	251100
MMAB	110.2	100.0	99.5	251110
MMACHC	226.3	100.0	100.0	277400
MMADHC	101.2	94.4	83.5	277410
MMUT	166.3	99.8	98.3	251000
MN1	108.2	100.0	99.3	618774
MOCS1	92.8	99.2	95.1	252150
MOCS2	166.2	99.6	99.5	252160
MOGS	146.3	100.0	99.9	606056
MPDU1	111.6	100.0	100.0	609180
MPDZ	159.6	99.8	98.8	615219
MPLKIP	106.5	100.0	99.4	234050
MRAS	110.5	100.0	99.6	618499
MRPS22	153.4	99.8	99.1	611719
MSL3	80.1	84.6	77.7	-
MSMO1	57.3	96.2	88.9	616834

MTFMT	165.7	100.0	99.8	614947;618248
MTHFR	116.9	97.3	96.0	236250
MTO1	165.2	91.3	90.4	614702
MTOR	131.6	100.0	99.5	607341;616638
MTR	163.4	100.0	100.0	250940
MTRR	156.7	100.0	99.6	236270
MVK	120.6	91.0	90.5	610377
MYCN	140.0	100.0	99.9	164280
MYH9	134.5	100.0	99.3	603622
MYO5A	136.2	99.8	98.9	214450
MYO9A	168.9	99.9	99.1	-
MYT1L	137.3	87.0	86.2	616521
NAA10	117.4	99.7	98.5	300855;309800
NAA15	105.7	95.8	91.0	617787
NACC1	152.8	100.0	99.8	617393
NAGA	151.5	100.0	100.0	609242;609241
NAGLU	117.8	92.9	89.9	252920
NALCN	138.9	100.0	99.5	616266;615419
NANS	114.1	100.0	99.9	610442
NARS2	146.1	98.3	97.4	616239
NAXE	85.0	100.0	99.7	617186
NBEA	146.9	92.0	90.6	-
NBN	109.9	99.9	98.7	251260
NCAPG2	149.3	99.9	99.2	618460
NDE1	107.2	100.0	100.0	605013;614019
NDP	89.5	100.0	99.8	310600
NDST1	190.0	100.0	100.0	616116
NDUFA1	197.8	99.8	99.3	301020
NDUFA11	117.7	100.0	100.0	618236
NDUFA12	198.9	100.0	100.0	618244

NDUFA2	127.0	100.0	100.0	618235
NDUFAF3	129.2	100.0	99.9	618240
NDUFAF5	139.2	100.0	99.5	618238
NDUFAF8	37.9	62.6	61.1	618776
NDUFS1	178.8	100.0	99.6	618226
NDUFS2	118.4	100.0	100.0	618228
NDUFS3	140.9	90.7	90.6	618230
NDUFS4	190.9	100.0	99.4	252010
NDUFS6	137.6	100.0	99.8	618232
NDUFS7	125.2	100.0	99.1	618224
NDUFS8	133.9	100.0	99.4	618222
NDUFV1	157.9	98.0	96.1	618225
NDUFV2	85.1	87.0	76.9	618229
NEDD4L	116.6	72.0	71.6	617201
NEU1	146.1	99.7	97.7	256550
NEXMIF	153.9	100.0	99.5	300912
NF1	131.8	92.6	90.2	162200;601321
NFIA	188.3	99.2	98.8	613735
NFIB	131.9	97.5	96.6	618286
NFIX	176.9	100.0	99.5	602535;614753
NFU1	72.3	98.8	91.1	605711
NGLY1	166.3	100.0	99.8	615273
NHS	128.9	95.4	93.9	302350
NIPBL	143.1	98.9	97.0	122470
NKAP	105.1	99.3	95.4	301039
NKX2-1	57.3	98.6	85.6	118700;610978
NLGN2	140.2	92.9	88.5	-
NLGN3	152.5	99.9	98.9	300425
NLGN4X	160.0	99.9	98.9	300495
NONO	98.0	100.0	98.4	300967

NOVA2	118.4	99.0	94.6	-
NPC1	136.2	99.6	98.7	257220
NPC2	159.9	100.0	99.6	607625
NPHP1	152.3	100.0	99.1	609583
NR2F1	182.8	100.0	100.0	615722
NR4A2	138.5	100.0	100.0	-
NRAS	185.8	100.0	100.0	249400;613224;163200
NRROS	265.0	100.0	100.0	618875
NRXN1	161.2	97.4	96.9	614325
NSD1	175.3	100.0	99.9	117550
NSD2	148.4	99.9	99.2	-
NSDHL	149.0	100.0	98.6	308050;300831
NSUN2	118.1	96.0	95.1	611091
NT5C2	148.2	98.0	96.7	613162
NTNG2	154.1	98.5	96.7	618718
NTRK1	138.7	99.8	98.2	256800
NTRK2	166.5	100.0	99.9	613886;617830
NUBPL	112.1	99.7	98.4	618242
NUP62	116.3	100.0	100.0	271930
NUS1	62.6	59.9	44.6	617831;617082
OAT	87.2	85.3	76.3	258870
OCLN	204.3	100.0	100.0	251290
OCRL	128.1	99.9	98.6	300555;309000
ODC1	155.0	100.0	99.8	-
OFD1	61.6	88.2	74.0	300804;311200;300209
OGT	135.3	99.9	99.0	300997
OPA3	124.2	100.0	99.0	258501
OPHN1	104.9	99.5	97.7	300486
ORC1	110.5	100.0	99.4	224690
OSGEP	107.2	100.0	99.4	617729

OTC	135.9	100.0	100.0	311250
OTUD6B	122.8	99.9	98.8	617452
OTX2	151.9	100.0	99.7	610125
OXR1	123.8	99.4	97.0	213000
P4HTM	154.8	99.0	97.4	-
PACS1	115.8	98.7	96.9	615009
PACS2	155.2	99.3	96.3	618067
PAFAH1B1	102.0	94.1	87.1	607432
PAH	157.4	100.0	100.0	261600
PAK1	133.3	100.0	99.6	618158
PAK3	96.1	99.3	96.0	300558
PANK2	185.6	100.0	99.3	234200;607236
PANX1	148.5	100.0	100.0	-
PARN	134.5	81.2	81.1	616353
PAX1	165.6	92.4	87.9	615560
PAX6	141.5	100.0	100.0	194072
PAX7	134.9	100.0	100.0	618578
PAX8	101.4	100.0	99.8	218700
PBX1	146.8	100.0	99.4	617641
PC	161.4	99.7	97.3	266150
PCCA	116.0	99.5	96.7	606054
PCCB	133.1	97.8	96.0	606054
PCDH12	207.7	100.0	100.0	251280
PCDH19	176.8	100.0	98.9	300088
PCGF2	114.2	100.0	99.5	618371
PCLO	162.6	99.7	98.7	608027
PCNT	113.8	99.6	97.1	210720
PCYT2	149.6	99.8	97.1	618770
PDE4D	124.9	95.7	93.5	614613
PDGFRB	147.3	99.2	97.4	616592

PDHA1	102.5	99.4	97.1	312170
PDHX	159.5	99.9	99.4	245349
PDP1	150.7	100.0	100.0	608782
PDSS1	129.7	94.7	87.5	614651
PDSS2	126.1	99.7	97.2	614652
PEPD	109.3	100.0	98.7	170100
PET100	106.7	100.0	99.6	220110
PEX1	155.7	99.9	99.4	601539;214100
PEX10	101.6	96.8	89.7	614871;614870
PEX11B	108.5	100.0	99.6	614920
PEX12	150.3	100.0	100.0	266510
PEX13	208.8	100.0	100.0	614883
PEX16	157.9	97.8	94.2	614876;614877
PEX19	103.6	99.9	98.5	614886
PEX2	158.8	100.0	100.0	614866;614867
PEX26	93.8	100.0	100.0	614873
PEX3	126.1	100.0	99.3	614882;617370
PEX5	123.9	99.9	99.0	616716;202370;214110
PEX6	112.8	94.5	86.7	614863
PEX7	136.2	87.7	80.7	215100;614879
PGAP1	129.5	99.1	94.7	615802
PGAP2	157.4	100.0	99.9	614207
PGAP3	70.5	63.5	59.6	615716
PGK1	51.0	92.9	79.4	300653
PGM3	177.2	100.0	99.8	615816
PHACTR1	118.6	100.0	99.7	618298
PHF21A	120.7	100.0	99.9	-
PHF6	69.1	97.9	88.6	301900
PHF8	91.4	99.7	96.8	300263
PHGDH	115.8	99.9	98.8	601815

PHIP	154.9	98.7	96.2	617991
PI4KA	107.9	92.6	88.8	616531
PIBF1	82.5	99.5	96.2	617767
PIGA	86.1	93.8	86.9	300868
PIGB	115.2	99.9	97.9	618580
PIGC	103.4	99.1	90.7	617816
PIGG	175.1	100.0	99.7	616917
PIGH	83.8	81.9	68.2	618010
PIGK	87.5	99.2	95.1	618879
PIGL	141.4	100.0	100.0	280000
PIGN	117.5	93.8	91.5	614080
PIGO	155.9	100.0	99.9	614749
PIGP	97.1	95.7	87.3	617599
PIGS	101.9	100.0	100.0	618143
PIGT	174.3	98.1	98.1	615398
PIGU	104.5	100.0	99.1	618590
PIGV	144.5	100.0	100.0	239300
PIGW	178.0	100.0	99.8	616025
PIGY	95.4	100.0	99.9	616809
PIK3CA	151.7	98.0	97.8	615108;602501
PIK3R2	105.0	90.7	89.6	603387
PITRM1	122.7	98.4	96.1	-
PLA2G6	112.7	92.2	90.6	610217;256600
PLAA	188.2	99.9	99.2	617527
PLCB1	161.1	100.0	99.8	613722
PLK4	178.7	99.9	98.1	616171
PLP1	142.5	100.0	99.2	312920;312080
PLPBP	111.8	98.2	90.1	617290
PLXND1	114.6	98.9	96.1	-
PMM2	145.5	100.0	99.9	212065

PMPCA	123.1	97.6	94.1	213200
PMPCB	146.2	100.0	99.7	617954
PNKP	111.8	100.0	100.0	613402;616267
PNP	124.4	99.8	98.9	613179
PNPLA6	139.4	100.0	99.7	215470;275400;245800
POGZ	141.8	99.4	99.0	616364
POLA1	124.0	99.3	95.5	301030
POLG	111.3	100.0	99.3	607459;203700;613662
POLR1C	102.6	90.5	87.0	616494
POLR2A	182.4	100.0	100.0	618603
POLR3A	136.7	100.0	99.7	264090;607694
POLR3B	157.2	99.9	98.6	607694;614381
POMGNT1	131.1	100.0	99.9	613151;253280;613157
POMGNT2	185.3	100.0	100.0	618135;614830
POMK	180.0	100.0	100.0	615249;616094
POMT1	150.2	99.3	97.5	609308;236670;613155
POMT2	110.6	99.4	96.4	613156;236670;613158;613150
PORCN	121.5	100.0	99.0	305600
POU1F1	137.5	100.0	99.2	613038
POU3F3	32.1	73.2	59.5	-
PPM1D	177.8	100.0	99.9	617450
PPP1CB	128.2	99.9	99.3	617506
PPP1R12A	140.8	97.6	95.3	618820
PPP1R15B	135.4	100.0	99.6	616817
PPP1R21	146.3	99.6	96.0	-
PPP2CA	186.7	100.0	100.0	618354
PPP2R1A	136.1	91.6	91.5	616362
PPP2R5B	128.0	100.0	100.0	-
PPP2R5C	118.7	97.7	93.1	-
PPP2R5D	176.9	100.0	100.0	616355

PPP3CA	143.4	99.8	98.5	617711
PPT1	164.4	90.3	90.3	256730
PQBP1	138.3	100.0	100.0	309500
PRKAR1A	94.4	99.3	93.5	101800;610489
PRMT7	129.1	100.0	99.9	617157
PRODH	89.1	85.0	80.6	239500
PRPS1	119.3	86.4	86.4	301835;311070;300661
PRR12	126.0	98.7	97.2	-
PRSS12	159.9	100.0	99.9	249500
PRUNE1	139.6	93.6	93.5	617481
PSAP	112.1	100.0	100.0	249900
PSAT1	52.6	95.2	81.5	610992
PSMD12	94.9	98.6	92.9	617516
PSPH	147.1	100.0	100.0	614023
PTCH1	126.9	99.2	97.6	109400;610828
PTCHD1	167.1	100.0	99.9	300830
PTDSS1	140.4	100.0	100.0	151050
PTEN	167.3	99.5	97.2	605309;158350
PTF1A	87.0	95.8	85.5	609069
PTPN11	100.2	99.1	93.8	163950;151100
PTPN23	150.5	100.0	100.0	618890
PTRH2	258.3	100.0	100.0	616263
PTRHD1	170.7	100.0	100.0	-
PTS	119.2	99.9	99.1	261640
PUF60	183.9	100.0	99.3	615583
PUM1	148.0	100.0	99.9	617931
PURA	147.4	99.0	95.1	616158
PUS1	117.8	100.0	99.5	600462
PUS3	191.9	100.0	100.0	617051
PUS7	177.1	100.0	99.8	618342

PYCR1	94.0	99.9	97.7	612940;614438
PYCR2	118.0	100.0	99.1	616420
QARS1	150.8	100.0	100.0	615760
QDPR	112.8	100.0	99.7	261630
QRICH1	151.3	100.0	99.9	617982
RAB11B	201.3	100.0	100.0	617807
RAB18	95.2	99.5	97.4	614222
RAB23	131.4	100.0	99.5	201000
RAB27A	163.3	100.0	100.0	607624
RAB39B	110.6	100.0	100.0	311510;300271
RAB3GAP1	137.0	99.4	98.9	600118
RAB3GAP2	108.1	99.6	97.1	614225;212720
RAC1	140.2	99.9	96.1	617751
RAC3	113.0	97.4	94.4	618577
RAD21	103.3	99.2	96.6	614701
RAF1	125.7	100.0	100.0	611553
RAI1	187.0	100.0	100.0	182290
RALA	140.7	94.7	88.0	-
RALGAPA1	58.2	74.6	63.9	618797
RARB	109.5	100.0	100.0	615524
RARS1	115.0	94.2	91.6	616140
RARS2	123.0	100.0	99.8	611523
RBBP8	147.6	100.0	99.7	606744;251255
RBFOX1	180.0	89.2	88.9	-
RBM10	122.3	99.5	97.1	311900
RBM28	154.8	100.0	100.0	612079
RBPJ	89.9	98.4	92.9	614814
RCBTB1	119.8	99.9	99.5	617175
RECQL4	149.4	99.8	98.1	268400;218600
RELN	158.1	100.0	99.8	257320

RERE	85.6	96.2	91.4	616975
REV3L	164.3	97.6	97.2	-
RFT1	126.4	99.8	99.6	612015
RFX3	174.4	100.0	100.0	-
RHEB	43.9	88.9	75.6	-
RHOBTB2	213.4	100.0	100.0	618004
RIC1	162.1	100.0	99.9	618761
RIMS2	148.9	96.7	95.3	618970
RIT1	178.2	100.0	100.0	615355
RLIM	124.1	100.0	99.0	300978
RMND1	165.5	100.0	98.5	614922
RMRP				607095
RNASEH2A	150.3	100.0	100.0	610333
RNASEH2B	116.7	80.6	78.1	610181
RNASEH2C	279.8	100.0	99.5	610329
RNASET2	115.2	97.4	93.1	612951
RNF113A	143.2	100.0	100.0	300953
RNF125	210.7	99.9	99.2	616260
RNF13	95.4	95.4	81.9	618379
ROGDI	103.5	98.4	95.2	226750
ROR2	168.0	100.0	99.9	268310
RORA	117.7	96.7	90.2	618060
RPGRIP1L	155.7	96.7	95.6	216360;611560
RPIA	109.4	98.6	94.9	608611
RPL10	79.6	97.4	89.2	300998
RPS19	92.6	100.0	99.6	105650
RPS6KA3	105.3	98.5	94.7	300844;303600
RRM2B	164.2	100.0	99.7	612075
RSPRY1	173.0	100.0	100.0	616723
RSRC1	80.1	99.8	97.0	618402

RTEL1	127.3	99.5	96.7	615190
RTN4IP1	97.0	99.9	98.6	616732
RTTN	138.8	98.9	98.0	614833
RUBCN	114.2	99.3	97.5	615705
RUSC2	180.4	100.0	100.0	617773
RXYLT1	168.9	99.5	96.8	615041
SALL1	133.3	99.9	99.0	107480
SAMD9	186.2	100.0	99.9	617053
SAMHD1	162.4	98.7	98.4	612952
SARS1	131.4	100.0	99.3	617709
SATB2	126.3	99.7	97.4	612313
SBDS	198.0	100.0	100.0	260400
SC5D	192.8	100.0	99.5	607330
SCAMP5	127.8	100.0	100.0	-
SCAPER	177.9	99.7	98.2	618195
SCN1A	144.0	99.9	99.5	607208
SCN1B	177.9	98.0	96.4	617350
SCN2A	165.0	99.6	97.6	613721
SCN3A	173.4	99.8	99.3	617935;617938
SCN8A	189.4	100.0	99.8	614306;614558
SCO1	115.4	97.0	93.8	220110
SCO2	106.8	100.0	100.0	604377
SCYL1	155.0	100.0	100.0	616719
SDCCAG8	138.1	100.0	99.9	615993
SDHA	99.6	85.8	80.4	256000;252011
SEC31A	134.2	99.3	97.1	618651
SEMA3E	158.0	99.2	98.9	214800
SEPSECS	192.3	100.0	100.0	613811
SERAC1	134.7	99.9	99.5	614739
SET	65.8	98.3	90.5	618106

SETBP1	140.9	99.8	98.7	269150;616078
SETD1A	157.5	100.0	99.8	-
SETD1B	170.2	98.2	97.5	-
SETD2	159.1	100.0	99.9	616831
SETD5	170.1	100.0	99.8	615761
SGPL1	159.7	100.0	100.0	617575
SGSH	148.7	94.5	94.1	252900
SHANK2	157.5	97.7	97.6	613436
SHANK3	110.2	91.5	81.6	606232
SHH	128.4	100.0	99.5	147250
SHOC2	164.4	99.9	99.5	607721
SHROOM4	104.0	100.0	99.0	300434
SIAH1	164.3	100.0	100.0	-
SIK1	115.4	98.7	94.4	616341
SIL1	157.5	99.2	96.7	248800
SIN3A	137.1	100.0	99.0	613406
SIX3	154.1	99.9	98.6	157170
SKI	101.8	99.3	94.9	182212
SLC12A5	116.0	83.9	83.8	616645
SLC12A6	146.8	100.0	100.0	218000
SLC13A5	156.7	100.0	99.9	615905
SLC16A2	72.2	99.2	93.9	300523
SLC17A5	153.6	99.6	97.0	604369;269920
SLC19A3	156.2	97.8	97.6	607483
SLC1A1	163.7	99.9	99.6	222730
SLC1A2	112.0	96.1	95.4	617105
SLC1A4	148.9	98.9	95.8	616657
SLC25A1	97.6	95.9	88.5	615182
SLC25A12	187.7	99.9	99.5	612949
SLC25A15	176.3	99.8	98.2	238970

SLC25A22	114.8	98.6	95.8	609304
SLC25A24	146.5	99.4	99.2	612289
SLC2A1	164.6	92.8	92.8	606777;608885;612126;601042
SLC33A1	156.5	99.9	98.9	614482
SLC35A1	151.0	100.0	99.7	603585
SLC35A2	116.3	99.9	98.4	300896
SLC35A3	85.6	80.6	78.6	615553
SLC35C1	161.6	99.9	98.7	266265
SLC39A14	108.8	100.0	99.3	617013
SLC39A8	145.2	100.0	99.8	616721
SLC46A1	115.9	99.9	98.5	229050
SLC4A4	139.4	99.8	99.2	604278
SLC5A6	175.6	100.0	100.0	618973
SLC6A1	137.3	96.7	96.7	616421
SLC6A17	182.5	100.0	100.0	616269
SLC6A19	134.4	100.0	100.0	234500;242600
SLC6A3	147.4	100.0	100.0	613135
SLC6A8	56.6	93.6	81.7	300352
SLC6A9	155.2	100.0	100.0	617301
SLC7A7	126.5	100.0	99.9	222700
SLC9A6	119.6	95.2	91.8	300243
SLC9A7	91.4	97.6	90.4	301024
SMAD4	127.1	100.0	99.9	139210
SMARCA1	118.4	99.6	97.6	-
SMARCA2	125.9	96.7	96.2	601358
SMARCA4	157.1	99.9	99.0	614609
SMARCB1	209.8	100.0	100.0	614608
SMARCC2	114.2	99.0	96.5	618362
SMARCD1	141.8	94.2	89.3	-
SMARCE1	86.1	95.6	88.8	616938

SMC1A	102.5	100.0	98.7	300590
SMC3	91.8	95.2	91.0	610759
SMG9	111.9	100.0	100.0	616920
SMOC1	132.2	99.9	98.3	206920
SMPD1	171.0	100.0	100.0	257200
SMPD4	96.0	99.4	94.2	618622
SMS	81.2	91.5	78.9	309583
SNAP25	138.5	100.0	99.9	616330
SNAP29	140.1	100.0	100.0	609528
SNIP1	173.7	98.9	97.0	614501
SNORD118				614561
SNRPB	93.0	100.0	99.3	117650
SNRPN	106.9	100.0	97.0	209850;176270
SNX14	95.5	99.6	95.9	616354
SNX27	134.0	100.0	99.5	-
SOBP	193.5	97.5	92.9	613671
SON	126.0	98.8	94.9	617140
SOS1	123.9	99.8	98.4	610733
SOS2	123.7	100.0	99.2	616559
SOX10	70.1	99.9	97.9	609136;611584
SOX11	180.8	100.0	100.0	615866
SOX2	207.0	100.0	100.0	206900
SOX3	60.6	91.7	75.6	300123
SOX4	83.7	97.3	90.9	-
SOX5	112.8	99.9	98.9	616803
SOX6	122.8	99.9	99.4	618971
SPART	153.2	99.7	96.8	275900
SPAST	111.7	99.8	98.6	182601
SPATA5	167.7	100.0	99.7	616577
SPECC1L	135.6	96.0	95.6	145410

SPG11	135.1	100.0	99.3	616668;604360
SPOCK1	123.5	100.0	99.5	-
SPOP	167.7	100.0	100.0	618828
SPR	170.0	99.8	96.3	612716
SPRED1	171.5	100.0	99.0	611431
SPTAN1	126.3	99.1	98.6	613477
SPTBN2	120.2	100.0	99.3	615386;600224
SPTBN4	91.3	97.3	91.0	617519
SRCAP	167.6	99.4	98.9	136140
SRD5A3	140.5	99.9	99.1	612713;612379
SRPX2	77.3	99.8	96.5	300643
SSR4	112.1	100.0	99.7	300934
ST3GAL3	104.1	68.8	68.6	611090;615006
ST3GAL5	117.5	85.0	84.2	609056
STAG1	137.2	99.6	97.4	617635
STAG2	86.8	97.7	89.9	301022
STAMPB	118.0	100.0	99.4	614261
STIL	192.8	100.0	99.8	612703
STRA6	130.4	100.0	99.8	601186
STRADA	132.6	100.0	98.9	611087
STT3A	160.5	100.0	100.0	615596
STT3B	150.9	100.0	99.6	615597
STX1B	162.9	100.0	100.0	616172
STXBP1	120.0	96.8	96.5	612164
SUCLA2	62.9	89.5	82.2	612073
SUCLG1	122.2	99.9	99.8	245400
SUMF1	104.0	97.5	90.9	272200
SUOX	189.2	100.0	100.0	272300
SUPT16H	90.4	98.6	93.6	-
SURF1	94.6	89.4	88.2	256000

SUZ12	132.6	91.5	86.2	-
SVBP	142.8	100.0	100.0	-
SYN1	69.6	82.0	73.3	300491
SYNCRIP	76.0	97.7	87.3	-
SYNGAP1	167.1	99.4	98.1	612621
SYNJ1	157.9	99.9	99.4	617389;615530
SYP	73.0	99.9	96.7	300802
SYT1	176.1	99.8	98.5	618218
SZT2	152.9	99.6	99.5	615476
TAF1	109.6	99.8	97.8	300966
TAF13	106.1	100.0	100.0	617432
TAF2	137.9	99.9	98.6	615599
TAF6	140.8	99.8	98.9	617126
TANC2	165.1	100.0	99.5	-
TANGO2	132.7	100.0	99.3	616878
TAOK1	152.3	99.5	97.9	-
TASP1	147.7	99.7	98.9	-
TAT	136.0	100.0	100.0	276600
TBC1D20	127.4	94.2	94.2	615663
TBC1D23	113.7	99.7	97.2	617695
TBC1D24	171.9	100.0	100.0	220500;615338
TBC1D2B	120.6	99.3	97.6	-
TBC1D7	127.3	100.0	99.3	248000
TBCD	146.7	96.2	94.4	617193
TBCE	146.8	99.8	97.4	617207;241410
TBCK	126.0	99.2	96.8	616900
TBL1XR1	75.6	96.5	84.9	602342;616944
TBP	114.5	100.0	99.9	168600
TBR1	138.1	99.9	97.9	606053
TBX1	89.6	87.0	77.5	188400;192430

TCF20	152.3	100.0	100.0	618430
TCF4	132.3	100.0	99.8	610954
TCF7L2	178.4	99.9	98.8	-
TCN2	177.9	100.0	100.0	275350
TCTN2	149.1	100.0	99.5	616654
TCTN3	136.3	100.0	100.0	614815
TDP2	198.9	100.0	99.4	616949
TECPR2	151.3	100.0	100.0	615031
TECR	123.8	100.0	99.0	614020
TELO2	112.2	99.7	96.2	616954
TENM3	175.2	100.0	99.6	615145
TET3	170.6	94.4	94.4	618798
TFAP2A	119.1	99.4	94.3	113620
TGDS	109.0	99.4	96.8	616145
TGFBR1	182.1	93.7	93.6	609192
TGIF1	160.2	100.0	100.0	142946
TH	88.4	99.3	96.0	605407
THOC2	99.7	98.9	93.9	300957
THOC6	258.7	100.0	100.0	613680
THRB	182.5	100.0	99.7	188570
TIMM50	129.4	98.3	94.4	617698
TIMM8A	63.1	98.0	90.4	304700
TINF2	187.0	100.0	100.0	127550;268130;613990
TKFC	137.1	100.0	99.5	618805
TKT	122.4	98.7	97.8	617044
TLK2	108.4	99.1	95.0	618050
TMCO1	86.4	88.0	87.4	213980
TMEM106B	149.3	99.9	98.8	617964
TMEM165	134.0	100.0	100.0	614727
TMEM216	114.2	99.9	98.1	608091

TMEM231	106.4	100.0	99.6	614970
TMEM237	141.9	100.0	99.9	614424
TMEM240	125.1	100.0	100.0	607454
TMEM63A	103.3	100.0	99.9	618688
TMEM67	97.1	99.4	95.0	613550;610688;216360
TMEM70	130.8	98.0	94.0	614052
TMLHE	100.6	99.5	97.1	300872
TMTC3	111.1	99.6	96.5	617255
TMX2	150.6	100.0	99.8	618730
TNIK	136.4	100.0	99.3	617028
TNRC6B	140.3	100.0	99.8	-
TOE1	170.1	100.0	100.0	614969
TP53RK	50.8	92.5	79.5	617730
TPI1	112.6	99.8	97.5	615512
TPO	147.1	99.9	98.1	274500
TPP1	145.9	100.0	100.0	204500
TPRKB	81.2	81.2	76.0	617731
TRAF7	161.6	100.0	99.8	618164
TRAIP	132.3	100.0	100.0	616777
TRAPPC11	151.3	100.0	99.3	615356
TRAPPC4	137.8	100.0	100.0	618741
TRAPPC6B	97.5	99.9	98.0	617862
TRAPPC9	143.9	100.0	99.6	613192
TREX1	248.1	100.0	100.0	225750;192315
TRIM32	130.8	100.0	100.0	615988
TRIM8	125.4	99.3	97.2	-
TRIO	136.0	99.2	97.5	617061
TRIP12	167.0	99.9	99.2	617752
TRIT1	133.0	100.0	100.0	617873
TRMT1	131.2	99.4	96.2	618302

TRMT10A	158.0	100.0	99.7	616033
TRNT1	108.6	99.6	96.6	616084
TRPM3	134.1	100.0	99.5	-
TRRAP	158.7	99.9	99.5	-
TSC1	137.7	99.8	98.7	607341;191100
TSC2	143.4	100.0	99.6	607341;613254
TSEN15	74.5	79.0	77.2	617026
TSEN2	118.8	100.0	99.6	612389
TSEN54	113.6	96.3	94.2	277470;225753
TSFM	139.8	100.0	99.5	610505
TSHB	286.1	100.0	100.0	275100
TSPAN7	134.9	100.0	100.0	300210
TTC19	89.7	81.5	73.8	615157
TTC37	166.1	100.0	99.3	222470
TTC5	97.4	100.0	99.9	-
TTC8	135.2	99.6	98.1	615985
TTI2	116.8	100.0	100.0	615541
TUBA1A	76.5	99.9	97.0	611603
TUBA8	154.6	99.9	99.5	613180
TUBB	125.0	97.3	93.8	615771;156610
TUBB2A	65.7	97.0	95.7	615763
TUBB2B	65.4	100.0	99.5	610031
TUBB3	113.5	98.2	96.9	600638;614039
TUBB4A	76.8	95.9	94.0	612438
TUBG1	178.3	100.0	100.0	615412
TUBGCP2	101.6	99.7	96.1	618737
TUBGCP4	123.3	99.1	96.4	616335
TUBGCP6	157.4	100.0	99.3	251270
TUSC3	190.6	100.0	99.5	611093
TWIST1	96.5	100.0	98.9	101400;617746

TWNK	202.1	100.0	100.0	607459;271245;609286
U2AF2	125.0	99.9	98.2	-
UBA5	94.1	97.9	87.0	617132
UBE2A	128.4	99.7	96.2	300860
UBE3A	96.1	99.1	94.9	105830
UBE3B	133.2	100.0	99.9	244450
UBR1	144.0	99.9	99.1	243800
UBTF	128.7	100.0	99.4	617672
UFC1	137.3	100.0	100.0	618076
UFM1	144.2	74.1	69.5	617899
UGDH	164.7	99.9	99.0	618792
UGP2	154.8	99.0	98.6	618744
UNC13A	130.0	99.4	97.7	-
UNC80	128.5	97.9	97.4	616801
UPB1	160.5	100.0	100.0	613161
UPF3B	61.6	92.4	84.2	300676
UROC1	149.5	100.0	100.0	276880
USP27X	188.4	100.0	100.0	300984
USP7	100.3	91.3	87.9	-
USP9X	110.4	98.3	93.1	300919;300968
VAMP1	153.0	100.0	100.0	108600
VAMP2	131.4	99.5	97.7	-
VAR51	131.0	100.0	99.9	617802
VLDLR	157.4	100.0	99.8	224050
VPS11	131.1	94.9	93.6	616683
VPS13B	164.1	99.5	98.2	216550
VPS37A	70.7	91.6	78.6	614898
VPS53	133.5	91.5	90.7	615851
VRK1	157.2	99.7	98.5	607596
VWA3B	148.6	100.0	99.7	616948

WAC	174.2	100.0	99.7	616708
WARS2	140.7	100.0	99.5	617710
WASF1	104.2	99.9	96.5	-
WASHC4	131.0	99.1	95.5	615817
WDFY3	151.5	100.0	99.6	617520
WDPCP	122.2	98.2	94.4	-
WDR13	113.9	99.9	98.6	-
WDR26	96.9	88.8	84.0	617616
WDR37	148.7	86.5	86.2	618652
WDR4	161.0	100.0	100.0	618347
WDR45	82.9	98.1	92.5	300894
WDR45B	80.8	98.0	89.2	617977
WDR62	157.2	100.0	99.5	604317
WDR73	180.6	100.0	100.0	251300
WDR81	174.7	100.0	100.0	610185
WFS1	192.5	100.0	99.9	222300
WVOX	137.9	100.0	100.0	616211;614322
XPA	83.9	99.6	95.6	278700
XRCC4	166.5	99.9	99.3	616541
XYLT1	147.6	97.4	89.6	615777
YME1L1	133.6	99.0	95.2	617302
YWHAE	161.7	100.0	100.0	-
YWHAG	213.0	100.0	100.0	617665
YY1	105.8	100.0	99.8	617557
ZBTB11	200.2	99.9	99.6	618383
ZBTB16	152.9	100.0	99.9	612447
ZBTB18	209.6	100.0	99.9	612337
ZBTB20	185.9	100.0	100.0	259050
ZBTB24	167.8	100.0	100.0	614069
ZC3H14	181.6	99.9	98.9	617125

ZC4H2	88.4	100.0	99.0	314580
ZDHHC9	60.5	99.9	93.8	300799
ZEB2	158.7	99.9	99.1	235730
ZFYVE26	116.5	100.0	99.1	270700
ZIC1	219.4	100.0	100.0	616602
ZIC2	110.1	100.0	98.7	609637
ZMIZ1	153.6	99.4	98.3	-
ZMYND11	147.6	100.0	99.6	616083
ZNF142	135.8	100.0	99.9	618425
ZNF148	187.8	99.9	99.6	617260
ZNF292	150.8	99.6	98.3	-
ZNF335	136.8	100.0	99.9	615095
ZNF407	166.4	99.9	99.3	-
ZNF41	114.0	100.0	99.6	-
ZNF462	195.5	100.0	99.9	-
ZNF711	128.7	99.8	98.3	300803
ZSWIM6	142.3	95.5	91.9	603671;617865

Gene symbols used follow HGNC guidelines: Gray KA, Yates B, Seal RL, Wright MW, Bruford EA. Nucleic Acids Res. 2015 Jan;43(Database issue):D1079-85.

Median Coverage describes the average number of reads seen across 50 exomes.

% Covered 10x describes the percentage of a gene's coding sequence that is covered at least 10x.

% Covered 20x describes the percentage of a gene's coding sequence that is covered at least 20x.

Genes with Median Coverage and % Covered 10x/20x denoting NC are non-coding genes for which coverage statistics could not be generated.

OMIM release used for OMIM disease identifiers and descriptions : October 1st, 2016.

Ad 1. "No OMIM phenotype" signifies a gene without a current OMIM association Ad 2. OMIM phenotype descriptions between {} signify risk factors