

WES METABOLIC DISORDERS DG 2.16

<i>Gene</i>	<i>Median coverage</i>	<i>% covered >10x</i>	<i>% covered >20x</i>	<i>OMIM disease ID</i>
AASS	131.5	99.9	99.4	268700;238700
ABAT	83.2	99.9	98.3	613163
ABCC8	125.8	100.0	99.9	600509
ABCD1	87.4	77.2	75.0	300100
ABCD2	164.3	100.0	99.7	601081
ABCD3	108.1	99.5	97.3	170995
ABCD4	129.0	99.8	98.4	614857
ABCG5	139.5	100.0	99.9	210250
ABCG8	133.9	99.7	98.2	611465;210250
ABHD12	93.1	100.0	98.9	612674
ABHD5	180.9	100.0	100.0	275630
ACACA	109.9	98.3	97.5	613933
ACAD8	122.1	100.0	99.9	611283
ACAD9	124.3	99.9	99.1	611126
ACADM	129.5	99.8	99.2	201450
ACADS	148.2	100.0	100.0	201470
ACADSB	113.1	99.9	97.3	610006
ACADVL	115.8	99.8	98.0	201475
ACAT1	110.2	99.7	98.3	203750
ACAT2	132.1	100.0	100.0	614055
ACBD5	145.1	99.6	98.0	616618
ACO2	115.3	95.8	89.5	614559
ACOX1	123.7	100.0	100.0	264470
ACOX2	111.0	100.0	99.3	601641
ACSF3	145.8	99.9	99.1	614265

ACSL4	102.8	98.6	93.5	300387
ACY1	118.5	100.0	98.6	609924
ADA	104.6	100.0	99.6	102700
ADCK5	128.6	100.0	99.7	-
ADCY5	131.8	97.8	94.7	606703
ADK	102.4	99.8	98.0	614300
ADSL	138.6	99.2	98.6	103050
AGA	142.7	100.0	100.0	208400
AGK	108.5	99.5	95.7	259900
AGL	146.9	100.0	99.4	614691;212350
AGPAT2	162.6	99.1	94.8	232400
AGPS	75.4	99.5	97.8	608594
AGXT	160.8	100.0	100.0	600121
AHCY	111.6	99.9	97.7	613752
AK1	136.9	100.0	99.9	612631
AK2	96.1	98.7	94.4	267500
AKR1D1	91.5	99.6	95.7	235555
ALAD	94.9	99.5	94.7	612740
ALAS2	74.7	98.9	94.7	300751;300752
ALDH18A1	113.7	100.0	99.8	219150
ALDH1A3	102.4	99.7	97.0	615113
ALDH2	126.5	100.0	100.0	610251
ALDH3A2	113.5	95.3	94.3	270200
ALDH4A1	123.9	100.0	99.8	239510
ALDH5A1	91.0	99.3	93.2	271980
ALDH6A1	104.9	100.0	99.6	614105
ALDH7A1	66.7	93.5	86.1	266100
ALDOA	120.4	76.5	74.5	611881
ALDOB	135.3	100.0	99.3	229600
ALG1	46.5	53.2	50.2	608540

ALG10	274.1	100.0	100.0	613688
ALG11	129.3	96.8	96.3	613661
ALG12	155.7	100.0	99.9	607143
ALG13	77.3	98.5	92.1	300884
ALG14	199.4	100.0	100.0	612866
ALG2	103.2	100.0	100.0	607906
ALG3	106.5	100.0	99.9	601110
ALG6	101.6	99.1	95.6	603147
ALG8	118.5	96.6	96.2	608104
ALG9	113.0	100.0	99.6	608776
ALOX12B	125.6	100.0	99.8	242100
ALPL	154.8	100.0	99.7	241500;146300;241510
AMACR	157.7	100.0	100.0	614307;214950
AMN	101.5	98.1	90.6	261100
AMPD1	115.8	99.9	98.6	615511
AMPD3	117.2	99.9	98.9	612874
AMT	142.7	100.0	100.0	605899
AP1S1	101.0	100.0	99.8	609313
APOC2	103.7	100.0	100.0	207750
APRT	93.2	100.0	100.0	614723
ARG1	159.1	100.0	100.0	207800
ARSA	138.5	100.0	100.0	250100
ARSB	109.4	99.9	98.9	253200
ASAH1	125.7	99.3	97.2	228000;159950
ASL	123.6	100.0	98.5	207900
ASPA	116.1	99.7	96.9	271900
ASS1	97.4	95.0	87.1	215700
ATIC	113.9	100.0	99.7	608688
ATP1A1	111.1	100.0	99.6	182310
ATP6AP1	105.6	99.8	96.9	300197

ATP6V0A2	117.4	99.9	99.0	219200;278250
ATP6V1A	133.4	99.6	97.3	607027
ATP6V1E1	66.5	92.3	85.9	108746
ATP7A	111.2	99.5	96.7	309400
ATP7B	128.7	99.9	99.1	277900
ATP8B1	114.0	97.5	94.6	243300
AUH	127.0	100.0	99.7	250950
B3GALNT1	124.4	100.0	99.6	615021
B3GALNT2	93.9	92.9	91.0	615181
B3GALT6	81.7	82.6	77.6	615291
B3GAT3	121.0	99.6	96.5	245600
B3GLCT	96.6	99.7	99.1	261540
B4GALT1	112.2	99.8	97.7	607091
B4GALT7	123.9	99.8	98.1	130070
B4GAT1	136.9	100.0	100.0	615287
BAAT	103.0	99.8	97.3	607748
BCKDHA	176.9	100.0	99.8	248600
BCKDHB	123.3	98.6	92.8	248600
BCO1	129.2	100.0	100.0	115300
BLVRA	111.9	100.0	99.9	614156
BMP2	163.4	100.0	100.0	235200
BPGM	101.3	100.0	100.0	222800
BTD	126.6	99.9	99.7	253260
C1GALT1C1	139.9	100.0	99.0	300622
CA5A	93.2	99.6	95.7	114761
CAD	136.7	99.9	99.2	114010
CANT1	144.9	100.0	100.0	251450
CAT	136.9	100.0	100.0	614097
CBS	123.3	99.9	99.0	236200
CCDC115	77.9	88.9	87.1	613734

CEL	146.5	94.0	90.4	609812
CERKL	114.1	99.4	97.2	608380
CERS3	95.2	99.8	98.2	615276
CFTR	113.5	99.4	97.4	219700;277180;167800;614122;211400
CHIT1	110.6	99.7	98.0	600031
CHKB	115.4	100.0	100.0	602541
CHST14	160.6	99.9	98.9	601776
CHST3	133.8	100.0	100.0	245600;143095
CHST6	279.8	100.0	100.0	217800
CHSY1	125.9	99.3	97.9	605282
CLN3	114.7	92.6	91.9	204200
CLN5	138.7	99.9	98.8	256731
CLN6	132.3	100.0	99.9	601780
CLN8	144.5	83.5	83.5	600143
CLPB	125.6	99.8	97.9	616271
COG1	108.4	100.0	99.9	611209
COG2	124.6	99.7	98.1	606974
COG4	94.5	100.0	99.6	613489
COG5	126.3	99.9	98.4	613612
COG6	90.4	99.1	96.0	614576
COG7	106.1	100.0	99.7	608779
COG8	145.0	100.0	98.5	611182
COMT	161.8	100.0	99.9	181500;167870
COQ2	103.5	97.6	97.1	609825
COQ4	105.0	91.3	90.2	616276
COQ5	168.1	100.0	100.0	616359
COQ6	127.5	99.9	98.6	614647
COQ7	138.3	99.9	99.6	601683
COQ8A	161.8	100.0	99.9	606980
COQ8B	99.5	100.0	99.8	615567

COQ9	73.8	100.0	98.1	612837
CP	100.6	93.1	87.4	604290
CPOX	134.1	99.5	97.2	121300
CPS1	133.8	100.0	99.9	237300;265380
CPT1A	131.5	99.9	98.4	255120
CPT2	139.2	98.3	98.2	600649;255110;608836;614212
CTH	141.0	100.0	99.8	219500
CTNS	112.6	100.0	99.5	219900;219800;219750
CTSA	132.9	100.0	99.9	256540
CTSC	116.2	100.0	100.0	245000;245010;170650
CTSD	171.0	99.8	97.8	610127
CTSK	86.3	100.0	99.8	265800
CUBN	103.2	99.6	97.6	261100
CYB561	145.0	92.8	92.7	600019
CYB5R3	152.1	99.2	98.3	250800
CYP11A1	121.2	99.2	95.0	613743
CYP11B1	155.9	100.0	100.0	202010;103900
CYP11B2	156.0	100.0	100.0	203400;610600
CYP17A1	108.5	100.0	99.6	202110
CYP19A1	125.7	99.4	97.3	139300;613546
CYP1B1	134.4	100.0	100.0	231300;604229
CYP21A2	91.6	99.2	93.4	201910
CYP27A1	173.0	100.0	99.7	213700
CYP27B1	147.1	100.0	99.7	264700
CYP2R1	130.7	99.7	96.8	600081
CYP2U1	134.3	98.4	95.5	615030
CYP7B1	103.8	99.6	96.6	613812;270800
D2HGDH	142.0	100.0	99.4	600721
DAO	105.1	100.0	99.7	181500
DBH	145.6	100.0	99.9	223360

DBT	109.9	99.6	96.9	248600
DCXR	169.1	100.0	99.9	260800
DDC	97.9	99.5	95.0	608643
DDHD1	161.6	99.9	98.4	609340
DDOST	114.0	100.0	99.8	614507
DGAT1	150.3	96.7	92.0	2
DGKE	127.8	99.8	98.3	615008
DGUOK	119.4	99.9	97.9	251880
DHCR24	155.8	100.0	99.9	602398
DHCR7	144.9	100.0	100.0	270400
DHDDS	81.0	97.1	93.8	608172
DHFR	50.0	94.1	83.1	613839
DHODH	98.8	100.0	100.0	263750
DLD	119.2	99.9	99.7	246900
DMGDH	134.7	100.0	99.8	605850
DNAJC12	140.7	87.4	87.4	606060
DNAJC19	93.8	98.4	92.3	610198
DNM1L	119.5	99.9	98.7	614388
DNM2	123.9	99.7	96.7	606482;160150
DNMT1	114.3	99.2	98.7	614116
DNMT3B	116.4	100.0	99.9	242860
DOLK	157.2	100.0	100.0	610768
DPAGT1	87.5	100.0	99.9	608093;614750
DPM1	134.7	95.2	88.2	608799
DPM2	88.5	99.8	97.6	615042
DPM3	200.5	100.0	100.0	612937
DPYD	141.6	99.5	96.4	274270
DPYS	117.5	100.0	99.8	222748
DTYMK	108.5	100.0	100.0	188345
EBP	63.2	99.5	95.2	302960

ECHS1	103.8	100.0	99.7	616277
ELOVL1	85.9	99.8	97.5	611813
ELOVL4	104.4	99.9	99.1	600110;614457
ENO3	173.2	100.0	100.0	612932
EOGT	102.7	79.3	78.1	614789
EPHX1	116.0	99.2	96.0	189800;607748
EPHX2	97.7	99.6	97.4	143890
ETFA	132.7	100.0	99.8	231680
ETFB	116.8	100.0	100.0	231680
ETFDH	114.4	100.0	99.3	231680
ETHE1	97.3	99.9	97.8	602473
EXT1	88.6	99.6	98.0	215300;133700
EXT2	118.0	99.9	99.1	133701
FA2H	92.7	98.8	92.5	612319
FAH	128.4	100.0	99.8	276700
FAR1	73.7	97.2	91.8	616107
FBP1	105.5	100.0	99.3	229700
FDFT1	136.3	100.0	99.6	184420
FECH	104.0	100.0	99.7	177000
FH	128.0	95.0	88.5	606812
FKRP	153.3	100.0	100.0	606596;613153;607155;606612
FKTN	107.5	99.7	96.1	611588;613152;611615;253800
FLAD1	170.7	100.0	99.6	610595
FMO3	131.9	100.0	99.3	602079
FOLR1	107.4	100.0	99.9	613068
FTCD	116.8	98.7	95.2	229100
FUCA1	125.9	100.0	99.9	230000
FUK	104.4	99.4	97.8	608675
FUT2	154.5	100.0	100.0	612542
FUT6	142.5	100.0	100.0	613852

G6PC	146.8	100.0	99.9	232200
G6PC3	114.6	100.0	100.0	612541
G6PD	114.4	99.5	97.4	134700;611162
GAA	160.8	100.0	99.9	232300
GAD1	112.7	99.9	99.7	603513
GALC	102.9	99.8	98.8	245200
GALE	140.0	100.0	100.0	230350
GALK1	165.2	100.0	99.9	230200
GALM	91.9	100.0	99.9	137030
GALNS	108.3	100.0	99.3	253000
GALNT3	125.8	99.9	98.7	601756
GALT	152.6	100.0	100.0	230400
GAMT	112.5	98.3	91.5	612736
GANAB	107.1	99.9	98.3	104160
GATM	137.3	100.0	100.0	612718
GBA	169.8	100.0	100.0	608013;231005;168600;231000;127750;230900;230800
GBA2	141.5	100.0	99.6	614409
GBE1	157.4	99.9	99.7	232500;263570
GCDH	145.9	100.0	99.1	231670
GCH1	84.8	100.0	99.5	128230;233910
GCK	138.6	100.0	100.0	125853;125851;606176;602485
GCLC	143.7	99.3	95.8	230450;608446
GCLM	101.7	99.7	97.2	608446
GCSH	32.1	88.4	69.8	605899
GFPT1	146.0	99.9	99.1	610542;608931
GIF	110.1	100.0	99.2	609342
GK	44.1	84.9	63.9	307030
GLA	73.6	99.5	95.8	301500
GLB1	82.6	99.7	95.4	230600;230500;230650;253010
GLDC	59.2	90.6	79.2	605899

GLRA1	96.8	100.0	99.7	149400
GLRX5	137.6	99.6	96.1	205950
GLUD1	65.5	98.1	87.5	606762
GLUL	77.0	99.7	96.5	610015
GLYCTK	161.3	100.0	99.5	220120
GM2A	122.0	100.0	100.0	272750
GMPPA	147.2	100.0	99.8	615495
GMPPB	211.8	100.0	100.0	615351;615350;615352
GMPS	120.6	98.2	94.2	601626
GNE	113.8	100.0	99.3	269921;600737;605820
GNMT	126.9	99.9	98.7	606664
GNPAT	127.2	99.5	96.8	222765
GNPTAB	148.0	100.0	99.3	252500;252600
GNPTG	177.6	100.0	98.5	252605
GNS	94.5	99.6	95.2	252940
GOT1	107.7	100.0	99.4	614419
GOT2	80.3	95.8	89.5	138150
GPD1	87.7	100.0	99.4	614480
GPD1L	128.0	100.0	99.9	611777
GPHN	144.7	99.9	98.8	252150
GPI	141.4	100.0	99.8	613470
GPT2	121.7	100.0	99.4	616281
GPX1	50.6	99.6	95.9	614164
GRHPR	99.6	84.2	81.7	260000
GSS	93.3	100.0	99.2	231900;266130
GUSB	99.5	92.5	90.5	253220
GYG1	125.6	100.0	99.4	613507
GYS1	109.6	100.0	98.6	611556
GYS2	120.1	99.7	98.0	240600
H6PD	193.5	99.0	99.0	604931

HADH	111.1	99.3	98.8	231530;609975
HADHA	72.9	96.3	89.3	609015;609016
HADHB	77.6	96.7	83.8	609015
HAGH	139.7	100.0	99.8	614033
HEXA	106.3	93.7	92.4	272800
HEXB	163.0	99.7	98.5	268800
HFE	108.0	100.0	98.9	235200
HGD	98.2	100.0	99.8	203500
HGSNAT	98.3	87.2	86.2	252930
HIBADH	106.3	97.3	92.8	608475
HIBCH	69.9	96.3	79.8	250620
HK1	116.5	100.0	99.7	235700
HLCS	142.3	100.0	100.0	253270
HMBS	97.3	100.0	98.4	176000
HMGCL	119.4	99.9	98.7	246450
HMGCS2	102.4	100.0	99.4	605911
HMOX1	137.4	96.5	90.7	614034;606963
HOGA1	149.6	100.0	99.1	613616
HPD	148.1	100.0	99.7	140350;276710
HPRT1	59.8	98.3	88.2	300322;300323
HS6ST1	72.8	97.7	92.0	614880
HSD11B1	113.8	100.0	99.0	614662
HSD11B2	165.6	94.3	87.3	218030
HSD17B10	92.4	100.0	98.4	300438;300705;300220
HSD17B3	116.4	100.0	99.9	264300
HSD17B4	109.4	96.3	93.6	233400;261515
HSD3B2	131.8	100.0	99.9	201810
HSD3B7	143.7	99.5	96.2	607765
HTRA2	132.6	100.0	99.6	606441
HYAL1	110.7	100.0	100.0	601492

IDH2	98.5	100.0	99.6	613657
IDH3B	128.2	95.5	95.4	612572
IDS	100.9	99.9	97.1	309900
IDUA	148.1	98.9	94.6	607015;607014;607016
IMPAD1	170.4	100.0	99.9	614078
IMPDH1	53.6	95.3	84.1	180105;613837
INPP5E	116.8	100.0	98.6	610156
INPPL1	127.9	99.8	98.0	258480
IREB2	130.2	100.0	99.5	147582
ISPD	110.2	99.6	97.5	616052;614643
ITPA	130.2	100.0	100.0	147520
IVD	100.0	100.0	99.9	243500
KMT2A	133.0	100.0	99.9	605130
KMT2D	136.2	100.0	99.7	147920
L2HGDH	124.0	99.0	96.7	236792
LAMP2	92.3	97.9	92.8	300257
LARGE1	115.2	100.0	99.7	1
LCAT	140.7	99.4	95.1	136120;245900
LCT	118.8	99.8	97.9	223000
LDHA	55.6	96.6	88.0	612933
LDHB	86.0	94.8	82.9	614128
LFNG	117.6	92.8	87.7	609813
LIAS	125.3	99.9	98.7	607031
LIPA	105.0	96.5	94.4	278000
LIPC	98.5	100.0	99.1	612797;125853;614025
LIPT1	203.2	100.0	99.9	610284
LIPT2	91.2	99.9	99.3	617659
LMBRD1	100.1	98.9	94.1	277380
LPIN1	123.4	99.1	96.4	268200
LPIN2	97.8	100.0	99.6	609628

LPL	128.2	100.0	99.9	238600;144250
LRAT	240.7	100.0	100.0	613341;268000
LTC4S	83.3	94.2	79.5	614037
LYST	136.3	99.4	97.8	214500
MAN1B1	125.5	100.0	99.8	614202
MAN2B1	128.6	99.9	98.6	248500
MANBA	118.3	99.5	97.5	248510
MAOA	98.9	100.0	99.0	300615
MAT1A	144.1	99.8	98.4	250850
MCCC1	137.6	100.0	99.4	210200
MCCC2	119.0	100.0	99.7	210210
MCEE	121.1	100.0	99.9	251120
MCOLN1	157.1	99.9	99.0	252650
MFSD2A	114.3	100.0	99.3	614397
MFSD8	121.3	100.0	99.6	610951
MGAT2	145.4	100.0	100.0	212066
MINPP1	163.8	100.0	99.5	188470
MLYCD	95.7	99.4	96.5	248360
MMAA	168.5	100.0	100.0	251100
MMAB	94.6	100.0	99.7	251110
MMACHC	196.0	100.0	100.0	277400
MMADHC	81.2	92.7	79.5	277410
MOCS1	91.2	98.8	95.7	252150
MOCS2	137.7	99.6	99.5	252150
MOGS	141.0	100.0	100.0	606056
MPDU1	102.4	100.0	99.6	609180
MPI	110.1	100.0	99.9	602579
MSMO1	51.6	95.8	88.5	607545
MTHFD1	115.4	99.8	97.4	601634
MTHFR	114.9	98.2	96.4	601634;181500;236250;188050

MTM1	79.1	98.7	91.9	310400
MTMR2	99.1	99.9	98.5	601382
MTR	131.4	99.9	99.4	601634;250940
MTRR	131.1	100.0	99.0	236270
MUT	131.3	99.9	98.9	251000
MVK	121.4	91.0	90.5	610377;175900;260920
NADK2	163.3	99.9	99.0	615787
NAGA	121.7	100.0	100.0	609241;609242
NAGLU	117.7	97.1	94.1	252920
NAGS	104.3	100.0	99.9	237310
NANS	97.2	99.9	98.4	605202
NBAS	138.5	99.9	99.1	608025
NEU1	141.3	99.3	96.4	256550
NMNAT1	113.5	100.0	98.5	608553
NNT	124.6	100.0	98.5	614736
NPC1	117.8	100.0	99.2	257220
NPC2	124.7	100.0	99.9	607625
NPL	111.5	100.0	99.9	611412
NSD1	147.0	100.0	99.8	117550;130650;601626
NSDHL	125.8	99.7	97.1	300831;308050
NT5C3A	64.1	97.2	85.7	266120
NT5E	151.4	100.0	99.9	211800
NUS1	53.3	71.5	44.1	610463
OAT	68.2	81.7	70.1	258870
OCRL	106.2	99.8	98.3	300555;309000
OPA3	156.6	100.0	99.2	258501
OPLAH	141.5	100.0	99.9	260005
OTC	111.4	100.0	99.7	311250
OXCT1	125.5	99.7	98.2	245050
PAH	126.4	100.0	100.0	261600

PANK2	154.1	100.0	100.0	234200;607236
PC	155.4	99.9	98.7	266150
PCBD1	103.9	100.0	99.7	264070
PCCA	99.2	99.3	95.5	606054
PCCB	111.8	99.3	96.9	606054
PCK1	119.4	100.0	99.9	614168
PCK2	164.9	100.0	100.0	614095
PCYT1A	95.6	97.9	94.4	608940;123695
PDSS1	104.8	96.7	87.7	607429
PDSS2	112.9	99.6	96.1	610564
PEPD	117.4	100.0	99.6	170100
PEX1	127.9	99.9	99.3	214100;601539
PEX10	113.3	99.9	97.4	614870;614871
PEX11B	87.9	100.0	99.4	614920
PEX12	120.6	100.0	100.0	614859
PEX13	179.6	100.0	100.0	614883;614885
PEX14	130.5	99.8	97.8	614887
PEX16	140.8	98.6	94.8	614876;614877
PEX19	84.9	100.0	98.9	614886
PEX2	134.9	100.0	100.0	614867;614866
PEX26	94.3	100.0	99.6	614872;614873
PEX3	113.9	99.9	99.2	614882
PEX5	107.9	100.0	99.2	214110;202370
PEX6	106.5	98.5	92.0	614862;614863
PEX7	111.0	91.2	89.3	614879;215100
PFKM	113.7	100.0	99.2	232800
PGAM2	163.6	100.0	100.0	261670
PGAP1	110.9	99.1	95.8	611655
PGAP2	134.7	100.0	99.5	614207
PGAP3	70.3	63.5	59.9	611801

PGK1	44.7	90.9	75.9	300653
PGM1	128.8	100.0	99.8	612934;614921
PGM3	149.3	99.9	99.6	172100
PHGDH	106.6	100.0	99.3	601815
PHKA1	90.2	97.4	91.6	300559
PHKA2	93.7	99.9	98.7	306000
PHKB	125.3	99.9	99.1	172490
PHKG1	112.6	99.9	97.5	172470
PHYH	74.0	99.9	96.9	266500
PIGA	70.9	92.9	84.0	300868;300818
PIGC	85.9	99.3	92.2	601730
PIGL	122.1	99.7	99.6	280000
PIGM	148.9	100.0	100.0	610293
PIGN	106.3	93.6	91.1	614080
PIGO	144.5	100.0	99.9	614749
PIGP	89.3	94.8	86.0	605938
PIGQ	134.6	94.0	92.2	605754
PIGT	159.3	98.1	98.1	610272
PIGV	124.4	100.0	100.0	239300
PIGW	145.0	100.0	99.8	610275
PIGY	90.3	100.0	99.9	610662
PIK3CA	127.7	100.0	99.8	162900;211980;612918;114500;167000;615108;182000;114480;613659;114550;603387;602501
PIK3R1	124.3	99.9	98.9	615214
PIK3R2	104.3	93.9	90.2	603387
PIK3R5	120.7	100.0	99.9	615217
PIKFYVE	136.4	99.9	99.7	121850
PIP5K1C	136.6	99.8	97.6	611369
PKLR	169.2	100.0	99.7	266200;102900
PLA2G5	104.8	100.0	100.0	228980
PLA2G6	111.9	99.8	98.2	256600;610217;612953

PLA2G7	120.9	99.8	98.6	147050;600807;614278
PLCB1	134.9	100.0	99.7	613722
PLCB4	102.5	99.8	98.0	614669
PLCD1	116.1	100.0	99.3	151600
PLCE1	125.0	99.8	99.0	610725
PLCG2	105.8	100.0	99.3	614878;614468
PLIN1	93.1	100.0	99.3	613877
PLOD1	131.9	99.8	97.3	225400
PLOD2	121.3	99.6	97.3	609220
PLOD3	109.7	100.0	99.9	612394
PLPBP	95.3	99.6	95.3	604436
PMM2	127.7	100.0	99.7	212065
PNLIP	133.9	100.0	97.7	614338
PNMT	106.0	100.0	99.8	145500
PNP	108.6	100.0	99.5	613179
PNPLA2	142.7	100.0	99.8	610717
PNPLA6	137.9	99.9	99.5	612020
PNPO	74.4	100.0	99.3	610090
POFUT1	134.6	99.9	99.4	607491
POGLUT1	101.2	100.0	98.7	615618
POLR3A	116.8	100.0	99.9	607694
POLR3B	129.8	99.7	98.2	614381;607694
POMGNT1	115.5	100.0	99.6	613151;613157;253280
POMGNT2	201.7	100.0	100.0	614830
POMK	138.7	100.0	100.0	616094;615249
POMT1	130.6	99.7	97.8	236670;609308;613155
POMT2	103.3	100.0	98.4	236670;613150;613156;613158
PPCS	148.5	100.0	99.3	609853
PPM1K	132.5	100.0	100.0	615135
PPOX	95.2	99.8	97.5	176200

PPT1	136.6	90.2	89.2	256730
PRKAG2	129.9	99.7	97.4	602743
PRKCSH	152.6	99.5	94.8	177060
PRODH	81.8	89.0	81.7	239500;600850
PRPS1	111.6	100.0	99.9	301835;311070;304500;300661
PSAP	98.1	100.0	99.3	610539;249900;611722;611721
PSAT1	42.8	90.3	72.5	610992
PSPH	126.6	100.0	99.8	614023
PTEN	129.7	99.6	97.0	188470;275355;276950;176807;607174;605309;155600;608089;158350;153480;613028
PTGIS	113.7	99.5	96.4	145500
PTPN11	78.3	98.6	90.7	607785;163950;156250;151100
PTS	101.5	99.8	98.4	261640
PYCR1	96.0	99.7	97.4	614438;612940
PYGL	141.0	100.0	100.0	232700
PYGM	121.1	100.0	99.9	232600
QDPR	97.9	100.0	99.2	261630
RBCK1	107.9	100.0	99.2	610924
RDH12	80.7	99.8	97.2	612712
RDH5	167.7	100.0	100.0	136880
RFT1	105.7	100.0	99.2	612015
RPE65	131.9	100.0	99.8	204100;613794
RPIA	113.0	100.0	98.8	608611
SARDH	129.1	92.9	91.4	268900
SAT1	122.5	100.0	98.9	308800
SC5D	153.6	99.8	99.3	607330
SCARB2	105.8	99.8	99.1	254900
SCP2	107.8	99.7	96.4	613724
SCYL1	146.2	100.0	100.0	607982
SEC23B	131.0	99.8	99.0	610512
SELENBP1	121.6	100.0	99.8	604188

SEPSECS	159.6	100.0	99.6	613811
SERAC1	111.0	99.7	99.0	614739
SGSH	140.2	97.6	94.7	252900
SI	118.7	99.4	95.9	222900
SLC10A7	111.0	99.9	99.2	611459
SLC12A1	144.2	100.0	99.8	600839
SLC13A3	89.5	100.0	99.5	606411
SLC16A1	138.1	100.0	99.2	245340
SLC17A5	137.7	99.8	96.1	269920;604369
SLC22A12	117.7	100.0	99.8	607096
SLC22A5	129.7	100.0	100.0	212140
SLC25A1	103.2	99.3	95.1	615182
SLC25A13	120.1	99.8	98.9	603471
SLC25A15	146.8	97.9	93.6	238970
SLC25A19	77.4	99.9	97.8	607196
SLC25A20	90.7	100.0	100.0	212138
SLC25A21	122.3	99.9	99.4	607571
SLC25A32	128.2	100.0	99.9	610815
SLC25A38	94.5	99.1	95.2	205950
SLC25A42	130.0	99.9	98.5	610823
SLC28A1	130.4	100.0	99.7	606207
SLC2A1	148.9	92.8	92.8	606777
SLC2A2	158.1	100.0	99.9	227810
SLC2A9	104.8	100.0	98.7	606142
SLC30A10	176.1	100.0	100.0	613280
SLC33A1	132.0	99.7	97.7	614482;612539
SLC35A1	127.1	100.0	99.4	603585
SLC35A2	104.8	99.8	98.1	314375
SLC35A3	66.6	80.6	78.3	605632
SLC35C1	187.8	100.0	99.8	266265

SLC35D1	125.0	99.5	97.2	610804
SLC37A4	114.3	100.0	99.6	232220
SLC39A14	95.4	99.9	97.9	608736
SLC39A4	114.2	100.0	99.0	201100
SLC39A8	140.9	100.0	99.8	608732
SLC3A1	144.5	100.0	99.4	220100
SLC46A1	111.1	99.9	98.4	229050
SLC52A1	198.3	100.0	100.0	615026
SLC52A2	185.4	100.0	100.0	614707
SLC52A3	118.8	100.0	99.8	211530
SLC5A1	110.7	100.0	99.3	606824
SLC5A2	135.0	100.0	100.0	233100
SLC6A19	129.3	100.0	100.0	608893
SLC6A8	53.5	96.1	83.8	300352
SLC7A7	105.5	100.0	99.6	222700
SLC7A9	119.8	100.0	98.8	220100
SLCO1B1	53.5	97.4	89.9	237450
SLCO1B3	50.9	97.5	87.9	237450
SMPD1	146.4	100.0	99.2	257200;607616
SMS	63.0	88.9	73.1	309583
SOD1	123.6	100.0	100.0	105400
SPR	145.7	100.0	99.8	612716
SPTLC1	108.6	98.5	93.4	162400
SPTLC2	142.8	100.0	99.9	613640
SRD5A2	85.6	100.0	98.1	264600
SRD5A3	139.9	99.8	98.3	612379;612713
SSR4	109.5	100.0	99.7	300934
ST3GAL3	134.7	100.0	99.5	615006;611090
ST3GAL5	101.8	89.0	84.9	609056
STAR	135.0	100.0	100.0	201710

STS	78.7	99.3	95.2	308100
STT3A	123.1	100.0	99.9	601134
STT3B	127.4	99.9	99.6	608605
SUCLA2	58.8	91.7	82.6	612073
SUCLG1	102.9	99.9	99.6	245400
SUCLG2	58.1	91.8	79.3	603922
SUGCT	127.1	99.4	95.8	277410;231690
SUMF1	89.7	99.7	96.8	272200
SUOX	167.2	100.0	100.0	272300
TALDO1	148.2	100.0	99.6	606003
TANGO2	127.3	100.0	100.0	616830
TAT	115.0	100.0	100.0	276600
TAZ	114.5	99.3	95.8	302060
TBXAS1	128.8	100.0	100.0	614158;231095
TCIRG1	131.4	99.2	96.6	259700
TCN2	148.5	100.0	100.0	275350
TECR	124.9	100.0	99.6	614020
TH	96.3	100.0	98.2	605407
TIMM50	122.9	99.9	98.7	607381
TK2	103.8	100.0	99.2	609560
TKT	115.6	98.7	98.1	606781
TMEM165	148.2	100.0	99.8	614727
TMEM199	118.4	100.0	99.8	616815
TMEM5	159.1	99.7	97.8	615041
TMEM70	117.9	99.8	97.6	612418
TMLHE	87.4	99.1	94.8	300872
TPI1	112.1	99.9	96.4	615512
TPK1	94.0	100.0	98.7	606370
TPMT	42.2	96.7	83.3	610460
TPP1	123.7	100.0	99.9	204500

TRAK1	149.3	100.0	99.6	608112
TRAPPC11	125.6	99.9	99.0	614138
TRAPPC2L	198.9	100.0	100.0	610970
TREH	141.3	98.2	93.2	612119
TUSC3	155.1	99.9	99.5	611093
TYMP	120.9	100.0	100.0	603041
TYR	147.9	100.0	99.9	601800;103470;203100;606952
TYRP1	152.3	100.0	100.0	203290;612271
UGT1A1	184.1	100.0	100.0	218800;601816;143500;237900;606785
UMPS	149.3	100.0	98.8	258900
UPB1	143.0	100.0	100.0	613161
UROC1	132.8	100.0	99.9	276880
UROD	130.8	98.9	95.6	176100
UROS	103.8	100.0	99.7	263700
VPS13B	134.5	99.3	98.0	607817
XDH	93.8	100.0	99.7	278300
XYLT1	128.1	99.9	98.2	608124
XYLT2	147.5	99.7	98.1	608125

Gene symbols used follow HGCN 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