

WES METABOLIC DISORDERS DG 3.00

<i>Gene</i>	<i>Median coverage</i>	<i>% covered >10x</i>	<i>% covered >20x</i>	<i>OMIM disease ID</i>
AASS	168.0	100.0	99.7	238700;268700
ABAT	105.5	100.0	99.4	613163
ABCC8	131.9	100.0	99.8	600509
ABCD1	78.1	75.8	71.6	300100
ABCD2	207.3	100.0	99.8	601081
ABCD3	125.8	99.8	97.7	170995
ABCD4	141.4	99.9	98.6	614857
ABCG5	173.9	100.0	100.0	210250
ABCG8	150.2	99.1	97.3	210250;611465
ABHD12	94.6	91.2	85.2	612674
ABHD5	224.8	100.0	100.0	275630
ACACA	133.5	98.4	98.1	613933
ACAD8	145.4	100.0	100.0	611283
ACAD9	141.7	100.0	99.9	611126
ACADM	154.1	99.8	99.0	201450
ACADS	129.3	99.9	98.2	201470
ACADSB	133.8	100.0	99.2	610006
ACADVL	138.0	99.4	97.3	201475
ACAT1	126.7	99.9	97.6	203750
ACAT2	142.8	100.0	100.0	614055
ACBD5	181.1	100.0	99.2	616618
ACO2	122.9	96.3	90.3	614559
ACOX1	143.2	100.0	99.9	264470
ACOX2	120.6	100.0	99.2	601641
ACSF3	148.4	100.0	99.9	614265

ACSL4	131.9	98.7	94.6	300387
ACY1	131.7	100.0	98.8	609924
ADA	105.4	100.0	99.7	102700
ADCK5	125.2	100.0	99.9	-
ADCY5	132.5	95.1	91.2	606703
ADK	96.9	84.1	81.0	614300
ADSL	150.2	99.2	98.7	103050
AGA	191.3	100.0	100.0	208400
AGK	123.5	90.6	88.6	259900
AGL	180.5	100.0	99.4	212350;614691
AGPAT2	146.1	99.6	96.1	232400
AGPS	82.8	99.3	95.4	608594
AGXT	150.4	100.0	100.0	600121
AHCY	117.4	100.0	99.2	613752
AK1	153.9	100.0	100.0	612631
AK2	115.9	98.9	94.9	267500
AKR1C1	141.4	95.9	89.7	-
AKR1D1	117.4	100.0	99.4	235555
ALAD	95.0	99.3	94.1	612740
ALAS2	88.1	98.9	94.9	300751;300752
ALDH18A1	142.2	100.0	99.9	219150
ALDH1A3	112.3	97.2	94.5	615113
ALDH2	131.7	100.0	100.0	610251
ALDH3A2	129.1	88.8	88.1	270200
ALDH4A1	125.0	100.0	99.4	239510
ALDH5A1	106.9	91.0	81.5	271980
ALDH6A1	126.0	100.0	99.9	614105
ALDH7A1	77.2	94.4	88.8	266100
ALDOA	172.4	98.9	96.9	611881
ALDOB	152.6	99.4	96.6	229600

ALG1	48.4	53.0	45.8	608540
ALG10	313.9	100.0	100.0	613688
ALG11	160.4	96.8	96.8	613661
ALG12	161.9	100.0	100.0	607143
ALG13	92.1	98.4	92.6	300884
ALG14	250.7	100.0	99.9	612866
ALG2	98.3	100.0	100.0	607906
ALG3	92.5	100.0	99.7	601110
ALG6	126.7	98.6	94.8	603147
ALG8	132.5	97.2	95.6	608104
ALG9	124.5	100.0	99.7	608776
ALOX12B	131.3	100.0	100.0	242100
ALPL	135.7	100.0	100.0	146300;241510;241500
AMACR	159.5	100.0	100.0	214950;614307
AMN	77.8	89.7	80.0	261100
AMPD1	142.3	99.9	98.6	615511
AMPD3	126.0	99.9	98.5	612874
AMT	153.3	100.0	100.0	605899
AP1S1	124.8	99.9	99.5	609313
AP3B2	127.7	93.3	89.5	617276
APOC2	110.2	100.0	100.0	207750
APRT	81.4	100.0	99.5	614723
ARG1	152.7	92.9	92.9	207800
ARSA	126.4	100.0	99.8	250100
ARSB	126.7	97.0	88.7	253200
ASAH1	158.2	99.7	98.6	159950;228000
ASL	113.6	100.0	99.6	207900
ASNS	98.7	99.4	95.2	108370
ASPA	151.4	99.9	98.3	271900
ASS1	110.2	95.4	87.9	215700

ATIC	142.2	99.9	99.3	608688
ATP1A1	143.2	100.0	100.0	182310
ATP6AP1	104.8	98.2	92.1	300197
ATP6V0A2	133.7	100.0	99.5	219200;278250
ATP6V1A	156.0	99.9	98.7	607027
ATP6V1E1	82.2	93.1	88.3	108746
ATP7A	134.6	99.0	96.9	309400
ATP7B	146.0	99.9	99.2	277900
ATP8B1	141.0	96.5	94.0	243300
AUH	120.6	100.0	99.8	250950
B3GALNT1	158.6	100.0	99.8	615021
B3GALNT2	117.0	93.8	89.4	615181
B3GALT6	43.1	75.7	69.7	615291
B3GAT3	115.4	99.9	98.2	245600
B3GLCT	116.4	99.6	96.3	261540
B4GALT1	110.9	100.0	99.8	607091
B4GALT7	122.2	99.8	97.4	130070
B4GAT1	118.1	100.0	100.0	615287
BAAT	134.8	99.8	98.4	607748
BCAT1	177.0	100.0	100.0	113520
BCAT2	151.5	100.0	100.0	113530
BCKDHA	200.1	99.9	99.2	248600
BCKDHB	146.8	99.5	94.4	248600
BCKDK	215.7	100.0	100.0	614901
BCO1	144.1	100.0	100.0	115300
BLVRA	120.4	100.0	99.4	614156
BMP2	178.0	100.0	100.0	235200
BPGM	117.0	100.0	100.0	222800
BTD	127.0	83.1	83.0	253260
C1GALT1C1	167.0	100.0	99.5	300622

CA5A	106.3	87.4	85.2	114761
CAD	150.4	100.0	99.2	114010
CANT1	153.3	100.0	99.9	251450
CAT	160.2	100.0	100.0	614097
CBLIF	135.1	100.0	99.7	609342
CBS	124.5	99.8	98.3	236200
CCDC115	91.3	95.3	90.0	613734
CEL	159.3	89.7	88.0	609812
CERKL	124.1	99.5	96.9	608380
CERS3	114.6	99.9	98.9	615276
CFTR	140.6	99.6	97.9	167800;277180;219700;211400;614122
CHIT1	115.2	99.7	98.1	600031
CHKB	114.9	100.0	99.7	602541
CHST14	147.4	99.9	98.9	601776
CHST3	113.4	100.0	99.4	245600;143095
CHST6	197.7	100.0	100.0	217800
CHSY1	147.1	97.2	95.7	605282
CLCN7	142.0	99.7	98.4	618541
CLN3	133.0	92.5	91.8	204200
CLN5	125.9	69.3	66.3	256731
CLN6	141.3	99.9	97.1	601780
CLN8	173.9	83.5	83.5	600143
CLPB	135.7	94.9	94.9	616271
CMAS	108.5	99.9	97.8	603316
COG1	121.9	100.0	100.0	611209
COG2	146.1	99.9	98.5	606974
COG4	110.3	100.0	99.9	613489
COG5	154.6	99.7	97.6	613612
COG6	108.2	99.1	93.9	614576
COG7	125.0	100.0	100.0	608779

COG8	138.7	99.9	98.6	611182
COMT	152.3	100.0	99.9	167870;181500
COQ2	113.1	98.0	95.3	609825
COQ4	98.8	90.9	89.3	616276
COQ5	196.7	100.0	100.0	616359
COQ6	143.6	99.9	98.4	614647
COQ7	161.7	100.0	99.8	601683
COQ8A	164.9	100.0	99.5	606980
COQ8B	102.1	100.0	99.3	615567
COQ9	79.4	100.0	97.9	612837
CP	127.1	94.8	88.9	604290
CPOX	142.3	99.9	95.4	121300
CPS1	162.9	100.0	99.9	237300;265380
CPT1A	158.3	100.0	98.9	255120
CPT2	159.1	98.2	97.8	255110;608836;614212;600649
CRAT	126.1	100.0	99.8	600184
CRPPA	122.2	98.5	94.8	614643;616052
CTH	167.0	100.0	100.0	219500
CTNS	127.4	100.0	99.8	219800;219900;219750
CTSA	156.7	100.0	100.0	256540
CTSC	137.1	100.0	100.0	170650;245010;245000
CTSD	174.3	98.4	95.0	610127
CTSK	105.3	100.0	99.9	265800
CUBN	129.7	99.7	98.3	261100
CYB561	157.4	92.8	92.6	600019
CYB5R3	165.7	98.4	98.0	250800
CYP11A1	129.8	99.3	96.1	613743
CYP11B1	146.2	100.0	100.0	202010;103900
CYP11B2	138.4	100.0	100.0	610600;203400
CYP17A1	120.3	100.0	99.5	202110

CYP19A1	161.8	98.8	96.8	613546;139300
CYP1B1	97.2	100.0	100.0	231300;604229
CYP21A2	101.0	97.8	88.4	201910
CYP27A1	180.7	98.9	96.7	213700
CYP27B1	133.7	99.9	99.3	264700
CYP2R1	147.8	99.4	95.6	600081
CYP2U1	160.0	94.8	91.5	615030
CYP7B1	131.5	98.0	92.8	270800;613812
D2HGDH	135.3	99.2	97.2	600721
DAO	120.0	100.0	100.0	181500
DBH	167.2	100.0	100.0	223360
DBT	134.8	99.8	98.0	248600
DCXR	175.3	98.6	93.6	260800
DDC	121.6	99.7	96.4	608643
DDHD1	164.0	97.9	95.8	609340
DDOST	127.8	100.0	99.9	614507
DEGS1	165.2	100.0	100.0	615843
DGAT1	146.5	91.9	87.6	2
DGKE	130.4	99.8	98.1	615008
DGUOK	124.5	100.0	99.4	251880
DHCR24	165.8	97.7	97.7	602398
DHCR7	152.1	100.0	100.0	270400
DHDDS	93.1	99.0	95.0	608172
DHFR	51.8	92.1	78.9	613839
DHODH	112.7	100.0	100.0	263750
DLD	135.6	100.0	99.7	246900
DMGDH	171.4	100.0	99.7	605850
DNAJC12	188.9	87.4	87.4	606060
DNAJC19	139.7	98.9	96.2	610198
DNM1L	139.3	99.9	98.5	614388

DNM2	138.9	98.1	94.5	606482;160150
DNMT1	131.2	99.2	99.0	614116
DNMT3B	133.6	100.0	100.0	242860
DOLK	187.5	100.0	100.0	610768
DPAGT1	90.7	100.0	100.0	608093;614750
DPM1	155.7	98.2	91.3	608799
DPM2	98.8	100.0	98.7	615042
DPM3	225.1	100.0	100.0	612937
DPYD	173.0	99.7	97.7	274270
DPYS	137.1	100.0	99.9	222748
DTYMK	130.6	100.0	99.8	188345
EBP	73.3	99.7	95.8	302960
ECHS1	108.6	99.9	99.0	616277
ELOVL1	94.0	99.8	97.6	611813
ELOVL4	122.7	100.0	99.5	600110;614457
ENO3	186.4	100.0	99.9	612932
EOGT	125.8	79.4	78.4	614789
EPHX1	137.1	99.9	98.8	189800;607748
EPHX2	120.2	99.5	96.2	143890
ETFA	160.1	100.0	100.0	231680
ETFB	122.5	100.0	99.8	231680
ETFDH	141.8	100.0	99.8	231680
ETHE1	96.2	99.9	97.4	602473
EXT1	114.3	99.9	98.4	133700;215300
EXT2	145.0	100.0	99.3	133701
FA2H	96.4	92.0	83.1	612319
FAH	135.8	100.0	100.0	276700
FAR1	84.8	97.6	92.8	616107
FBP1	101.3	93.7	93.3	229700
FCSK	98.1	97.7	95.4	608675

FDFT1	147.8	97.7	96.0	184420
FECH	120.3	100.0	100.0	177000
FH	147.0	92.1	88.3	606812
FKRP	124.4	100.0	100.0	613153;606612;606596;607155
FKTN	128.6	99.7	97.0	613152;611615;611588;253800
FLAD1	190.8	100.0	99.8	610595
FMO3	168.0	99.9	99.7	602079
FOLR1	130.7	100.0	100.0	613068
FTCD	101.3	95.7	91.0	229100
FUCA1	132.6	100.0	99.9	230000
FUT2	180.4	100.0	100.0	612542
FUT6	147.5	100.0	100.0	613852
FUT8	150.1	100.0	99.2	602589
G6PC	185.9	100.0	100.0	232200
G6PC3	113.2	100.0	99.9	612541
G6PD	114.5	99.3	98.0	134700;611162
GAA	156.2	100.0	99.9	232300
GAD1	141.6	100.0	99.9	603513
GALC	117.3	99.8	98.3	245200
GALE	149.9	100.0	100.0	230350
GALK1	142.1	100.0	99.1	230200
GALM	106.1	100.0	99.9	137030
GALNS	115.7	100.0	99.8	253000
GALNT2	133.0	99.6	97.0	618885
GALNT3	149.7	99.8	99.0	601756
GALT	167.6	100.0	99.7	230400
GAMT	113.1	93.1	82.7	612736
GANAB	129.4	99.9	99.0	104160
GATM	156.2	100.0	100.0	612718
GBA	202.3	100.0	100.0	230900;127750;231005;231000;168600;608013;230800

GBA2	165.1	100.0	99.7	614409
GBE1	200.1	100.0	99.6	263570;232500
GCDH	158.1	100.0	99.2	231670
GCH1	80.7	99.9	95.5	233910;128230
GCK	124.0	95.4	95.4	125853;606176;125851;602485
GCLC	169.3	99.8	98.0	608446;230450
GCLM	111.3	99.6	95.8	608446
GCSH	33.4	75.7	68.9	605899
GFPT1	190.8	100.0	99.4	610542;608931
GK	56.7	88.9	70.4	307030
GLA	81.9	91.1	88.2	301500
GLB1	89.8	99.9	97.4	230650;253010;230600;230500
GLDC	70.9	89.9	82.0	605899
GLRA1	116.2	100.0	99.8	149400
GLRX5	129.2	97.3	89.1	205950
GLS	95.2	96.3	87.2	138280
GLUD1	72.8	94.2	82.9	606762
GLUL	76.6	74.4	73.2	610015
GLYCTK	155.6	98.8	97.3	220120
GM2A	131.5	100.0	100.0	272750
GMPPA	169.3	100.0	100.0	615495
GMPPB	245.6	100.0	100.0	615352;615351;615350
GMPS	143.9	99.1	96.1	601626
GNE	132.7	100.0	99.7	269921;600737;605820
GNMT	134.7	100.0	100.0	606664
GNPAT	154.0	99.7	97.3	222765
GNPTAB	167.2	100.0	99.9	252500;252600
GNPTG	156.0	99.1	94.3	252605
GNS	111.6	98.4	94.8	252940
GOT1	126.4	100.0	99.3	614419

GOT2	95.7	97.5	90.9	138150
GPD1	107.5	100.0	100.0	614480
GPD1L	143.0	100.0	99.8	611777
GPHN	175.6	100.0	99.5	252150
GPI	163.9	100.0	100.0	613470
GPT2	136.1	99.2	93.6	138210;616281
GPX1	50.2	95.9	86.4	614164
GRHPR	108.1	84.2	81.3	260000
GSS	102.4	96.5	96.4	231900;266130
GUSB	111.3	92.9	91.7	253220
GYG1	151.7	99.9	99.2	613507
GYS1	131.5	100.0	98.6	611556
GYS2	155.0	99.8	99.0	240600
H6PD	190.9	99.0	99.0	604931
HADH	127.1	99.0	97.5	231530;609975
HADHA	87.5	97.2	91.6	609015;609016
HADHB	90.7	98.8	89.7	609015
HAGH	147.9	100.0	99.7	614033
HEXA	108.9	93.8	93.3	272800
HEXB	187.8	99.6	96.9	268800
HFE	127.9	100.0	99.7	235200
HGD	119.5	100.0	100.0	203500
HGSNAT	125.5	86.4	86.3	252930
HIBADH	130.6	94.4	91.2	608475
HIBCH	83.8	98.2	88.5	250620
HK1	140.2	100.0	100.0	235700
HLCS	179.3	100.0	100.0	253270
HMBS	103.3	99.9	99.4	176000
HMGCL	129.1	100.0	99.8	246450
HMGCS2	122.6	100.0	99.6	605911

HMOX1	137.4	98.4	89.9	614034;606963
HNF1A	171.3	100.0	99.8	142410
HNF4A	143.0	99.9	99.0	600281
HOGA1	156.5	100.0	96.4	613616
HPD	174.6	100.0	100.0	140350;276710
HPDL	200.6	100.0	100.0	619026;619027
HPRT1	74.2	99.3	91.8	300323;300322
HS6ST1	54.3	92.9	84.5	614880
HSD11B1	126.6	100.0	99.6	614662
HSD11B2	167.3	86.0	82.7	218030
HSD17B10	109.8	100.0	99.1	300438;300705;300220
HSD17B3	142.1	97.8	97.8	264300
HSD17B4	130.0	95.4	93.1	261515;233400
HSD3B2	151.4	100.0	99.7	201810
HSD3B7	142.9	99.1	95.5	607765
HTRA2	138.0	100.0	99.9	606441
HYAL1	115.0	100.0	100.0	601492
IDH2	111.5	99.7	97.4	613657
IDH3B	150.2	95.4	95.4	612572
IDI1	70.2	99.8	97.6	604055
IDS	110.5	99.9	98.0	309900
IDUA	128.6	93.7	86.8	607015;607014;607016
IMPAD1	157.7	100.0	100.0	614078
IMPDH1	57.5	87.9	80.2	180105;613837
INPP5E	107.5	97.1	92.7	610156
INPPL1	131.0	98.4	94.5	258480
INSR	138.2	97.8	94.7	147670
IREB2	154.2	100.0	99.8	147582
ITCH	133.7	91.6	91.3	606409
ITPA	149.2	100.0	100.0	147520

IVD	101.1	100.0	100.0	243500
KCNA2	160.9	100.0	99.6	616366
KCNJ11	177.3	100.0	100.0	600937
KMT2A	154.8	100.0	99.9	605130
KMT2D	142.1	100.0	99.4	147920
L2HGDH	145.2	99.0	97.2	236792
LAMP2	108.9	99.2	95.6	300257
LARGE1	129.6	100.0	99.6	1
LCAT	117.2	99.0	93.8	136120;245900
LCT	134.2	99.8	98.5	223000
LDHA	79.1	95.0	91.7	612933
LDHB	110.4	94.7	84.3	614128
LFNG	107.3	87.9	86.4	609813
LIAS	151.6	100.0	99.1	607031
LIPA	131.2	99.2	95.2	278000
LIPC	115.4	100.0	99.4	614025;125853;612797
LIPT1	227.5	100.0	99.9	610284
LIPT2	70.0	94.9	75.2	617659
LMBRD1	114.6	94.7	90.2	277380
LPIN1	147.0	99.6	97.3	268200
LPIN2	119.0	100.0	100.0	609628
LPL	154.1	100.0	100.0	144250;238600
LRAT	283.9	100.0	100.0	268000;613341
LTC4S	63.7	74.2	68.5	614037
LYST	169.3	99.6	98.3	214500
MAN1B1	129.3	100.0	99.7	614202
MAN2B1	142.3	99.8	97.9	248500
MAN2B2	151.8	99.9	99.1	-
MANBA	128.8	87.8	86.5	248510
MAOA	119.7	100.0	99.7	300615

MAT1A	158.1	99.7	97.7	250850
MBOAT7	108.6	100.0	99.5	617188
MCCC1	175.5	100.0	99.8	210200
MCCC2	140.4	99.9	98.4	210210
MCEE	155.7	100.0	100.0	251120
MCOLN1	159.0	99.8	98.4	252650
MDH1	112.8	100.0	99.0	154200
MFSD2A	140.6	99.7	98.5	614397
MFSD8	143.3	100.0	99.7	610951
MGAT2	156.4	100.0	100.0	212066
MINPP1	174.7	100.0	99.5	188470
MLYCD	92.6	96.0	90.4	248360
MMAA	210.3	100.0	100.0	251100
MMAB	110.4	100.0	99.6	251110
MMACHC	227.1	100.0	100.0	277400
MMADHC	101.0	94.4	83.5	277410
MMUT	166.1	99.8	98.3	251000
MOCOS	178.8	99.8	97.7	613274
MOCS1	93.1	99.2	95.1	252150
MOCS2	166.1	99.6	99.5	252150
MOGS	146.7	100.0	99.9	606056
MPDU1	112.0	100.0	100.0	609180
MPI	123.7	100.0	99.9	602579
MRPL44	140.0	99.9	98.7	615395
MRPS36	69.7	95.2	77.6	611996
MSMO1	57.0	96.3	88.9	607545
MTHFD1	144.1	100.0	99.5	601634
MTHFR	117.2	97.3	96.0	181500;236250;188050;601634
MTM1	95.6	99.0	93.3	310400
MTMR2	120.1	100.0	99.0	601382

MTR	163.3	100.0	100.0	250940;601634
MTRR	156.8	100.0	99.6	236270
MVK	120.8	90.9	90.5	175900;260920;610377
NADK2	199.4	99.9	97.2	615787
NAGA	152.2	100.0	100.0	609242;609241
NAGLU	118.0	92.9	89.9	252920
NAGS	85.0	99.7	95.0	237310
NANS	114.3	100.0	99.9	605202
NAXD	142.8	100.0	100.0	618321
NAXE	85.1	100.0	99.8	608862
NBAS	169.2	100.0	99.6	608025
NEU1	146.4	99.7	97.7	256550
NGLY1	166.1	100.0	99.8	610661
NMNAT1	131.6	100.0	99.2	608553
NNT	143.9	96.4	95.9	614736
NPC1	136.4	99.6	98.7	257220
NPC2	160.5	100.0	99.6	607625
NPL	134.8	100.0	99.9	611412
NSD1	175.5	100.0	99.9	130650;601626;117550
NSDHL	148.1	100.0	98.7	308050;300831
NT5C3A	80.9	97.8	88.2	266120
NT5E	165.5	100.0	99.9	211800
NUS1	62.4	60.0	44.5	610463
OAT	87.0	85.2	76.3	258870
OCRL	127.1	99.9	98.6	300555;309000
OPA3	124.4	100.0	99.0	258501
OPLAH	136.3	100.0	99.8	260005
OTC	134.9	100.0	100.0	311250
OXCT1	154.2	99.8	98.1	245050
PAH	157.4	100.0	100.0	261600

PANK2	185.6	100.0	99.3	234200;607236
PC	161.8	99.8	97.3	266150
PCBD1	112.5	100.0	99.6	264070
PCCA	115.9	99.5	96.7	606054
PCCB	133.2	97.9	96.0	606054
PCK1	136.1	100.0	100.0	614168
PCK2	169.7	100.0	100.0	614095
PCYT1A	113.2	98.9	95.5	123695;608940
PCYT2	149.9	99.8	97.1	602679
PDSS1	129.8	94.7	87.6	607429
PDSS2	125.9	99.8	97.1	610564
PEPD	109.7	100.0	98.8	170100
PEX1	155.5	99.9	99.4	601539;214100
PEX10	101.8	96.8	89.7	614871;614870
PEX11B	109.0	100.0	99.6	614920
PEX12	150.7	100.0	100.0	614859
PEX13	208.9	100.0	100.0	614885;614883
PEX14	132.7	96.7	90.8	614887
PEX16	158.6	97.9	94.2	614876;614877
PEX19	103.7	99.9	98.5	614886
PEX2	158.8	100.0	100.0	614866;614867
PEX26	94.0	100.0	100.0	614872;614873
PEX3	125.7	100.0	99.3	614882
PEX5	124.0	99.9	99.0	202370;214110
PEX6	113.0	94.5	86.7	614862;614863
PEX7	135.9	87.8	80.7	215100;614879
PFKM	135.4	100.0	99.5	232800
PGAM2	168.8	100.0	100.0	261670
PGAP1	129.1	99.0	94.4	611655
PGAP2	157.8	100.0	99.9	614207

PGAP3	70.6	63.5	59.6	611801
PGK1	50.7	92.8	79.3	300653
PGM1	147.7	94.2	94.2	614921;612934
PGM3	177.0	100.0	99.8	172100
PHGDH	116.1	99.9	98.8	601815
PHKA1	113.5	99.2	95.3	300559
PHKA2	112.3	100.0	99.7	306000
PHKB	151.1	99.9	99.2	172490
PHKG1	114.4	99.9	97.8	172470
PHKG2	169.5	100.0	99.9	172471
PHYH	89.1	100.0	99.6	266500
PI4K2A	106.9	91.9	86.4	-
PIGA	85.7	93.8	86.7	300818;300868
PIGB	115.0	99.9	97.8	604122
PIGC	103.7	99.2	90.9	601730
PIGL	141.3	100.0	100.0	280000
PIGM	158.5	100.0	100.0	610293
PIGN	117.3	93.8	91.5	614080
PIGO	156.3	100.0	99.9	614749
PIGP	96.9	95.8	87.3	605938
PIGQ	132.0	92.8	90.8	605754
PIGT	174.8	98.1	98.1	610272
PIGV	145.1	100.0	100.0	239300
PIGW	177.8	100.0	99.8	610275
PIGY	95.5	100.0	99.9	610662
PIK3CA	151.3	98.0	97.8	114480;182000;603387;114550;167000;602501;612918;211980;114500;615108;613659;162900
PIK3R1	148.2	99.8	99.0	615214
PIK3R2	105.2	90.7	89.6	603387
PIK3R5	126.8	100.0	99.9	615217
PIKFYVE	164.2	99.9	99.4	121850

PIP5K1C	138.1	98.0	95.8	611369
PKLR	183.1	100.0	99.2	102900;266200
PLA2G5	144.8	100.0	100.0	228980
PLA2G6	112.9	92.2	90.7	610217;256600;612953
PLA2G7	151.3	99.9	99.0	614278;600807;147050
PLCB1	160.9	100.0	99.8	613722
PLCB4	117.7	99.9	98.8	614669
PLCD1	124.5	99.9	97.8	151600
PLCE1	149.9	99.9	99.3	610725
PLCG2	125.6	100.0	99.8	614878;614468
PLIN1	85.0	99.6	94.9	613877
PLOD1	147.6	100.0	98.4	225400
PLOD2	148.2	99.3	97.3	609220
PLOD3	113.0	99.8	98.0	612394
PLPBP	111.9	98.2	90.1	604436
PMM2	145.4	100.0	100.0	212065
PNLIP	172.3	100.0	99.8	614338
PNMT	88.3	99.6	96.7	145500
PNP	124.6	99.8	98.9	613179
PNPLA2	128.9	99.7	96.1	610717
PNPLA6	139.7	100.0	99.7	612020
PNPO	78.4	99.9	97.7	610090
POFUT1	150.4	100.0	99.0	607491
POGLUT1	123.6	99.4	94.6	615618
POLR3A	136.9	100.0	99.7	607694
POLR3B	157.1	99.9	98.6	607694;614381
POMGNT1	131.5	100.0	99.9	613151;253280;613157
POMGNT2	186.0	100.0	100.0	614830
POMK	180.7	100.0	100.0	615249;616094
POMT1	150.5	99.3	97.5	609308;236670;613155

POMT2	110.7	99.4	96.4	613156;236670;613158;613150
PPCS	139.9	99.8	99.5	609853
PPM1K	159.6	100.0	100.0	615135
PPOX	109.9	99.7	96.8	176200
PPT1	164.4	90.3	90.3	256730
PRKAG2	152.4	99.1	96.7	602743
PRKCSH	160.1	99.8	95.4	177060
PRODH	89.3	85.0	80.6	600850;239500
PRPS1	118.4	86.4	86.4	304500;301835;311070;300661
PSAP	112.4	100.0	100.0	611722;610539;249900;611721
PSAT1	52.6	95.3	81.6	610992
PSPH	147.3	100.0	100.0	614023
PTEN	166.6	99.5	97.0	176807;155600;607174;188470;158350;608089;153480;613028;275355;605309;276950
PTGIS	125.5	98.2	95.1	145500
PTPN11	100.3	99.1	93.7	163950;156250;607785;151100
PTS	118.8	99.9	99.1	261640
PUS3	192.1	100.0	100.0	616283
PYCR1	94.2	99.9	97.7	612940;614438
PYCR2	118.2	100.0	99.1	616420
PYGL	146.6	100.0	100.0	232700
PYGM	138.7	100.0	99.9	232600
QDPR	112.9	100.0	99.7	261630
RBCK1	105.6	99.9	98.2	610924;615895
RDH12	102.1	100.0	98.6	612712
RDH5	162.8	100.0	99.9	136880
RFT1	126.6	99.8	99.6	612015
RINT1	195.2	99.9	98.6	610089
RPE65	153.2	99.8	97.8	204100;613794
RPIA	109.4	98.6	94.9	608611
RXYLT1	168.9	99.5	96.8	615041

SARDH	121.7	93.7	91.7	268900
SAT1	138.7	99.9	98.5	308800
SC5D	192.4	100.0	99.5	607330
SCARB2	121.3	100.0	99.8	254900
SCP2	130.8	100.0	99.2	613724
SCYL1	155.2	100.0	100.0	607982
SEC23B	156.2	99.9	99.3	610512
SELENBP1	136.9	100.0	100.0	604188
SEPSECS	192.2	100.0	100.0	613811
SERAC1	134.6	99.9	99.5	614739
SGSH	149.1	94.4	94.1	252900
SI	146.2	99.2	96.1	222900
SLC10A7	130.8	99.7	98.0	611459
SLC12A1	167.4	96.2	96.1	600839
SLC13A3	100.7	99.4	97.5	606411
SLC16A1	162.9	100.0	99.3	245340
SLC17A5	153.4	99.6	97.0	604369;269920
SLC18A2	124.9	100.0	99.7	193001
SLC22A12	113.2	100.0	99.8	607096
SLC22A5	145.5	100.0	100.0	212140
SLC25A1	97.8	95.8	88.6	615182
SLC25A13	146.4	100.0	99.7	603471
SLC25A15	176.5	99.8	98.1	238970
SLC25A19	94.0	100.0	98.5	607196
SLC25A20	106.4	100.0	100.0	212138
SLC25A21	142.7	100.0	99.7	607571
SLC25A32	145.3	100.0	100.0	610815
SLC25A38	112.2	97.9	95.3	205950
SLC25A42	131.7	96.5	93.2	610823
SLC28A1	145.8	100.0	98.8	606207

SLC2A1	164.9	92.8	92.8	606777
SLC2A2	183.6	100.0	100.0	227810
SLC2A9	122.5	99.8	96.1	606142
SLC30A10	168.1	100.0	100.0	613280
SLC33A1	156.2	99.9	98.9	612539;614482
SLC35A1	150.9	100.0	99.7	603585
SLC35A2	115.7	99.9	98.4	314375
SLC35A3	85.2	80.7	78.6	605632
SLC35C1	162.1	99.9	98.7	266265
SLC35D1	135.3	100.0	97.7	610804
SLC37A4	124.2	100.0	99.2	232220
SLC39A14	109.2	100.0	99.4	608736
SLC39A4	100.1	99.5	95.5	201100
SLC39A8	145.0	100.0	99.7	608732
SLC3A1	161.7	100.0	99.8	220100
SLC44A1	178.3	98.2	98.2	606105
SLC46A1	116.3	99.9	98.5	229050
SLC52A1	205.9	100.0	100.0	615026
SLC52A2	170.8	100.0	100.0	614707
SLC52A3	125.5	100.0	100.0	211530
SLC5A1	143.0	100.0	100.0	606824
SLC5A2	131.5	100.0	100.0	233100
SLC6A19	134.7	100.0	100.0	608893
SLC6A5	135.3	100.0	100.0	614618
SLC6A8	56.3	93.5	81.6	300352
SLC6A9	155.4	100.0	100.0	617301
SLC7A7	126.7	100.0	99.9	222700
SLC7A9	145.8	100.0	99.9	220100
SLCO1B1	63.6	99.2	93.7	237450
SLCO1B3	57.8	98.8	90.8	237450

SMPD1	171.4	100.0	100.0	257200;607616
SMS	80.6	91.5	78.5	309583
SNX14	95.2	99.6	95.9	616354
SOD1	144.8	100.0	99.9	618598;105400
SOD2	228.2	100.0	100.0	147460
SPR	170.3	99.8	96.3	612716
SPTLC1	132.2	99.2	95.4	162400
SPTLC2	158.5	100.0	100.0	613640
SQOR	108.8	100.0	97.8	617658
SRD5A2	81.7	99.9	99.0	264600
SRD5A3	140.7	99.9	99.1	612713;612379
SSR4	111.5	100.0	99.7	300934
ST3GAL3	104.3	68.8	68.6	611090;615006
ST3GAL5	117.5	85.0	84.2	609056
STAR	148.9	100.0	100.0	201710
STS	98.3	97.1	95.5	308100
STT3A	160.4	100.0	100.0	601134
STT3B	150.6	100.0	99.6	608605
SUCLA2	62.7	89.5	82.2	612073
SUCLG1	122.6	99.9	99.8	245400
SUCLG2	72.5	96.7	86.3	603922
SUGCT	162.0	99.9	98.5	231690;277410
SUMF1	104.0	97.5	90.8	272200
SUOX	189.7	100.0	100.0	272300
TALDO1	151.8	100.0	97.9	606003
TANGO2	133.1	100.0	99.3	616830
TAT	136.4	100.0	100.0	276600
TAZ	101.2	99.1	95.5	302060
TBXAS1	151.1	100.0	100.0	614158;231095
TCIRG1	116.3	97.6	90.1	259700

TCN2	178.3	100.0	100.0	275350
TECR	124.1	100.0	99.0	614020
TH	88.5	99.3	96.1	605407
TIMM50	129.7	98.3	94.4	607381
TK2	119.9	99.2	96.3	609560
TKFC	137.3	100.0	99.5	615844
TKT	122.7	98.7	97.8	606781
TMEM106B	148.7	99.9	98.8	617964
TMEM165	133.8	100.0	100.0	614727
TMEM199	118.1	100.0	99.9	616815
TMEM70	130.2	98.0	93.9	612418
TMLHE	99.9	99.5	97.1	300872
TPI1	112.9	99.8	97.5	615512
TPK1	121.5	99.8	99.0	606370
TPMT	45.1	99.1	90.1	610460
TPP1	146.4	100.0	100.0	204500
TRAK1	158.4	93.3	92.9	608112
TRAPPC11	151.1	100.0	99.2	614138
TRAPPC2L	213.9	100.0	100.0	610970
TREH	147.9	96.9	92.1	612119
TUSC3	190.4	100.0	99.5	611093
TYMP	97.1	100.0	97.0	603041
TYMS	147.8	99.9	99.6	188350
TYR	164.5	100.0	100.0	203100;103470;601800;606952
TYRP1	183.7	100.0	99.8	612271;203290
UGT1A1	227.3	100.0	100.0	237900;143500;601816;218800;606785
UMPS	174.8	100.0	99.4	258900
UPB1	160.9	100.0	100.0	613161
UROC1	149.7	100.0	100.0	276880
UROD	158.6	98.9	96.1	176100

UROS	122.0	100.0	99.9	263700
VMA21	89.1	99.0	94.6	300913
VPS13B	163.9	99.5	98.2	607817
VPS33A	113.2	91.3	89.8	617303
XDH	110.6	100.0	99.9	278300
XYLT1	148.0	97.4	89.6	608124
XYLT2	149.8	100.0	98.3	608125
ZBTB11	199.9	99.9	99.6	-

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