WES IRON DISORDERS DG 3.6

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ABCB10	138.9	100.0	100.0	-
ABCB7	119.3	99.8	99.3	301310
ACVR1	128.3	100.0	99.9	102576
ALAS2	87.0	100.0	99.8	300751;300752
ATP4A	111.9	100.0	100.0	-
BMP6	128.0	100.0	100.0	-
C15orf41	141.9	100.0	99.9	615631
CALR	127.2	100.0	100.0	109091
CCL2	142.6	100.0	100.0	607948;182940;609423
CDAN1	139.2	100.0	100.0	224120
CP	143.5	100.0	100.0	604290
CYBRD1	119.4	100.0	100.0	-
EXOC6	149.7	100.0	100.0	-
FECH	140.8	100.0	100.0	177000
FTH1	128.3	100.0	100.0	615517
FTL	86.4	100.0	100.0	600886;606159;615604
FXN	140.2	100.0	100.0	229300
GATA1	94.0	100.0	100.0	314050;300835;300367;190685
GLRX5	129.5	100.0	100.0	205950
HAMP	115.9	100.0	100.0	613313
HEPH	96.2	99.8	99.3	-
HFE	152.9	100.0	100.0	614193;612635;235200;176200;140300;176100
HJV	126.9	100.0	100.0	602390
HMOX1	130.1	100.0	100.0	614034;606963
HSCB	141.5	100.0	100.0	-

HSPA9	134.5	100.0	100.0	182170
JAK2	148.4	100.0	100.0	147796
KIF23	141.0	100.0	100.0	-
KLF1	138.6	100.0	100.0	613673;613566;111150
LARS2	127.2	100.0	100.0	604544
LPIN2	134.5	100.0	100.0	605519
MPL	123.2	100.0	100.0	159530
NCOA4	127.8	100.0	100.0	-
NDUFB11	78.7	99.7	97.9	-
PANK2	143.8	100.0	100.0	234200;607236
PUS1	125.1	100.0	100.0	600462
SEC23B	134.0	100.0	100.0	224100
SF3B1	139.7	100.0	100.0	605590
SFXN4	129.1	100.0	100.0	615578
SLC11A2	125.3	100.0	100.0	206100
SLC19A2	146.0	100.0	100.0	249270
SLC25A37	141.5	100.0	100.0	-
SLC25A38	129.0	100.0	100.0	205950
SLC40A1	146.4	100.0	100.0	606069
SLC46A1	131.3	100.0	100.0	229050
STEAP3	122.5	100.0	100.0	615234
TF	127.1	100.0	100.0	209300
TFR2	117.3	100.0	100.0	604250
TFRC	134.3	100.0	100.0	-
TMEM14C	177.8	100.0	100.0	-
TMPRSS6	125.2	100.0	100.0	206200
TRNT1	152.6	100.0	100.0	612907
UROS	160.6	100.0	100.0	263700
YARS2	139.3	100.0	100.0	613561

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.

TWIST is the default chemistry for all WES samples. Agilent V5 was the default chemistry until Q3 2021.
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 no value for coverage are non protein coding genes.
Non protein coding genes are covered, but as coverage statistics are based on protein coding regions, statistics could not be generated.
OMIM release used for OMIM disease identifiers and descriptions: September 1st, 2021.