WES IRON DISORDERS DG 3.2

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ABCB10	55.7	77.6	68.9	-
ABCB7	122.8	99.5	97.1	301310
ACVR1	145.3	100.0	99.9	102576
ALAS2	78.1	98.7	93.2	300751;300752
ATP4A	132.1	100.0	98.6	-
BMP6	124.7	96.3	94.0	-
C15orf41	109.1	85.9	85.7	615631
CALR	104.3	94.5	87.5	109091
CCL2	159.9	100.0	100.0	607948;182940;609423
CDAN1	111.5	100.0	99.9	224120
CP	108.0	92.6	85.2	604290
CYBRD1	124.5	100.0	99.7	-
EXOC6	108.4	98.5	95.7	-
FECH	101.9	99.9	99.8	177000
FTH1	71.0	91.9	73.8	615517
FTL	134.8	98.6	88.5	600886;606159;615604
FXN	66.0	98.3	84.7	229300
GATA1	106.2	99.9	98.5	314050;300835;300367;190685
GLRX5	118.9	97.2	89.6	205950
HAMP	184.2	100.0	100.0	613313
HEPH	69.8	98.0	89.0	-
HFE	101.9	99.9	97.8	614193;612635;235200;176200;140300;176100
HJV	147.9	100.0	100.0	602390
HMOX1	142.5	97.7	90.1	614034;606963
HSCB	96.5	99.8	97.6	-

HSPA9	76.1	87.1	82.8	182170
JAK2	106.8	97.6	95.2	147796
KIF23	142.4	98.2	94.0	-
KLF1	97.5	100.0	99.6	613673;613566;111150
LARS2	123.2	100.0	100.0	604544
LPIN2	105.3	99.9	99.7	605519
MPL	132.8	100.0	99.8	159530
NCOA4	103.3	93.9	90.4	-
NDUFB11	100.6	99.1	94.8	-
PANK2	159.3	100.0	99.7	234200;607236
PUS1	117.5	99.9	98.0	600462
SEC23B	134.5	99.9	99.1	224100
SF3B1	135.0	99.5	98.2	605590
SFXN4	102.7	99.6	97.4	615578
SLC11A2	96.4	98.1	97.4	206100
SLC19A2	95.1	100.0	98.5	249270
SLC25A37	231.1	100.0	100.0	-
SLC25A38	98.1	97.4	93.3	205950
SLC40A1	118.9	99.9	98.6	606069
SLC46A1	103.5	100.0	98.5	229050
STEAP3	175.6	100.0	99.7	615234
TF	104.6	100.0	99.9	209300
TFR2	123.6	99.3	96.9	604250
TFRC	132.5	99.9	99.6	-
TMEM14C	97.1	100.0	99.7	-
TMPRSS6	116.2	100.0	99.3	206200
TRNT1	84.7	99.7	97.4	612907
UROS	100.1	100.0	99.9	263700
YARS2	171.1	99.9	99.4	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.

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