WES IRON DISORDERS DG 3.4

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ABCB10	155.9	100.0	100.0	-
ABCB7	157.8	99.7	99.5	301310
ACVR1	171.2	100.0	100.0	102576
ALAS2	182.2	100.0	100.0	300751;300752
ATP4A	195.6	100.0	100.0	-
BMP6	191.2	100.0	100.0	-
C15orf41	157.0	100.0	100.0	615631
CALR	202.9	100.0	100.0	109091
CCL2	163.6	100.0	100.0	607948;182940;609423
CDAN1	177.8	100.0	100.0	224120
CP	161.2	100.0	100.0	604290
CYBRD1	180.9	100.0	100.0	-
EXOC6	143.2	100.0	100.0	-
FECH	159.7	100.0	100.0	177000
FTH1	197.4	100.0	100.0	615517
FTL	141.9	100.0	100.0	600886;606159;615604
FXN	163.7	100.0	100.0	229300
GATA1	226.4	100.0	100.0	314050;300835;300367;190685
GLRX5	178.2	100.0	100.0	205950
HAMP	172.6	100.0	100.0	613313
HEPH	164.5	100.0	100.0	-
HFE	187.7	100.0	100.0	614193;612635;235200;176200;140300;176100
HJV	228.4	100.0	100.0	602390
HMOX1	195.4	100.0	100.0	614034;606963
HSCB	181.3	100.0	100.0	-

HSPA9	142.4	100.0	100.0	182170
JAK2	156.9	100.0	100.0	147796
KIF23	151.8	100.0	100.0	-
KLF1	237.6	100.0	100.0	613673;613566;111150
LARS2	171.4	100.0	100.0	604544
LPIN2	158.2	100.0	100.0	605519
MPL	219.1	100.0	100.0	159530
NCOA4	192.1	100.0	100.0	-
NDUFB11	155.8	100.0	99.9	-
PANK2	192.2	100.0	100.0	234200;607236
PUS1	178.0	100.0	99.2	600462
SEC23B	158.5	100.0	100.0	224100
SF3B1	177.0	100.0	100.0	605590
SFXN4	143.9	100.0	100.0	615578
SLC11A2	155.4	100.0	100.0	206100
SLC19A2	184.4	100.0	100.0	249270
SLC25A37	206.3	100.0	100.0	-
SLC25A38	161.7	100.0	100.0	205950
SLC40A1	178.5	100.0	100.0	606069
SLC46A1	221.9	100.0	100.0	229050
STEAP3	215.2	100.0	100.0	615234
TF	169.3	100.0	100.0	209300
TFR2	196.7	100.0	100.0	604250
TFRC	154.5	100.0	100.0	-
TMEM14C	184.8	100.0	100.0	-
TMPRSS6	205.3	100.0	100.0	206200
TRNT1	142.5	100.0	100.0	612907
UROS	177.5	100.0	100.0	263700
YARS2	196.1	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.

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