WES IRON DISORDERS DG 3.00

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ABCB10	68.9	77.4	71.2	1
ABCB7	148.3	99.5	98.2	301310
ACVR1	181.9	100.0	100.0	102576
ALAS2	88.1	98.9	94.9	300751;300752
ATP4A	136.5	99.9	98.9	2
BMP6	133.8	95.7	93.6	3
C15orf41	121.0	85.9	85.6	615631
CALR	124.4	94.8	89.1	109091
CCL2	181.5	100.0	100.0	607948;182940;609423
CDAN1	120.4	100.0	99.6	224120
CP	127.1	94.8	88.9	604290
CYBRD1	154.1	100.0	99.9	4
EXOC6	122.7	99.2	96.3	5
FECH	120.3	100.0	100.0	177000
FTH1	78.3	94.0	76.6	615517
FTL	144.1	98.5	89.4	600886;606159;615604
FXN	72.3	95.5	80.1	229300
GATA1	108.4	99.8	98.4	314050;300835;300367;190685
GLRX5	129.2	97.3	89.1	205950
HAMP	192.7	100.0	100.0	613313
HEPH	78.4	98.8	91.9	6
HFE	127.9	100.0	99.7	614193;612635;235200;176200;140300;176100
HJV	156.1	100.0	100.0	602390
HMOX1	137.4	98.4	89.9	614034;606963
HSCB	108.0	100.0	98.7	7

HSPA9	97.6	88.5	84.5	182170;8
JAK2	127.4	98.1	95.8	147796
KIF23	167.9	99.5	96.3	9
KLF1	87.9	100.0	97.8	613673;613566;111150
LARS2	143.2	100.0	100.0	604544
LPIN2	119.0	100.0	100.0	605519
MPL	140.2	100.0	99.5	159530
NCOA4	119.9	96.4	93.0	14
NDUFB11	108.7	99.5	96.5	15
PANK2	185.6	100.0	99.3	234200;607236
PUS1	118.0	100.0	99.5	600462
SEC23B	156.2	99.9	99.3	224100
SF3B1	158.2	99.7	98.6	605590
SFXN4	128.8	99.9	98.9	615578;10
SLC11A2	112.0	98.2	98.0	206100
SLC19A2	110.3	100.0	99.7	249270
SLC25A37	238.3	100.0	100.0	11
SLC25A38	112.2	97.9	95.3	205950
SLC40A1	134.9	100.0	99.5	606069
SLC46A1	116.3	99.9	98.5	229050
STEAP3	162.7	100.0	99.7	615234
TF	128.4	100.0	100.0	209300
TFR2	120.0	99.1	97.8	604250
TFRC	166.7	100.0	99.8	12
TMEM14C	122.8	100.0	99.8	13
TMPRSS6	113.0	99.9	99.1	206200
TRNT1	108.4	99.5	96.5	612907
UROS	122.0	100.0	99.9	263700
YARS2	194.6	100.0	99.8	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.
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 10x 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