WES IRON DISORDERS DG 2.14

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ABCB10	75.2	75.6	67.1	1
ABCB7	131.5	99.9	98.4	301310
ALAS2	89.7	99.6	97.1	300751;300752
ATP4A	148.5	100.0	99.0	2
BMP6	107.9	92.9	90.0	3
C15orf41	124.9	99.9	97.9	615631
CCL2	138.4	100.0	100.0	182940;609423;607948
CDAN1	97.6	97.6	95.2	224120
CP	120.0	93.9	89.6	604290
CYBRD1	131.6	100.0	100.0	4
EXOC6	87.6	96.9	90.4	5
FECH	121.9	99.9	99.4	177000
FTH1	96.4	95.4	84.2	615517
FTL	147.7	99.0	93.2	600886;615604;606159
FXN	75.2	85.7	75.9	229300
GATA1	83.5	99.6	95.7	300367;300835;314050;190685
GLRX5	108.2	92.6	83.8	205950
HAMP	175.6	100.0	100.0	613313
HEPH	86.4	98.9	93.7	6
HFE	142.0	100.0	99.7	614193;140300;235200;176100;612635;176200
HFE2	116.8	100.0	100.0	602390
HMOX1	128.7	95.8	89.5	614034;606963
HSCB	90.1	99.1	95.1	7
HSPA9	91.6	91.1	85.9	8
KIF23	170.1	96.2	94.5	9

KLF1	52.1	90.8	81.7	613673;111150;613566
NCOA4	130.6	94.8	91.3	14
NDUFB11	109.6	94.4	88.0	15
PANK2	146.6	99.3	93.1	234200;607236
PUS1	127.2	98.6	93.9	600462
SEC23B	161.1	97.5	96.4	224100
SFXN4	131.7	100.0	99.1	615578;10
SLC11A2	135.2	100.0	99.3	206100
SLC19A2	119.5	99.8	97.8	249270
SLC25A37	194.0	100.0	100.0	11
SLC25A38	111.4	99.8	98.1	205950
SLC40A1	155.7	99.9	99.4	606069
SLC46A1	106.0	99.4	96.4	229050
STEAP3	199.0	100.0	99.8	615234
TF	125.9	100.0	100.0	209300
TFR2	104.4	98.2	93.5	604250
TFRC	157.2	99.9	99.1	12
TMEM14C	114.2	100.0	99.7	13
TMPRSS6	101.7	100.0	99.1	206200
UROS	108.3	100.0	99.9	263700
YARS2	173.2	99.8	98.9	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