WES IRON DISORDERS DG 2.16

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ABCB10	60.9	85.4	71.8	1
ABCB7	126.2	99.9	98.6	301310
ALAS2	74.7	98.9	94.7	300751;300752
ATP4A	136.3	100.0	99.6	2
BMP6	137.8	99.0	96.6	3
C15orf41	122.0	100.0	99.6	615631
CALR	111.8	98.1	91.7	109091
CCL2	133.0	100.0	100.0	182940;609423;607948
CDAN1	112.4	100.0	99.6	224120
CP	100.6	93.1	87.4	604290
CYBRD1	122.5	100.0	99.6	4
EXOC6	104.0	99.0	96.5	5
FECH	104.0	100.0	99.7	177000
FTH1	66.2	98.7	87.9	615517
FTL	145.2	99.7	96.7	600886;615604;606159
FXN	64.9	99.7	96.8	229300
GATA1	92.9	99.9	98.2	300367;300835;314050;190685
GLRX5	137.6	99.6	96.1	205950
HAMP	169.0	100.0	100.0	613313
HEPH	68.3	97.8	89.2	6
HFE	108.0	100.0	98.9	614193;140300;235200;176100;612635;176200
HFE2	150.1	100.0	100.0	602390
HMOX1	137.4	96.5	90.7	614034;606963
HSCB	104.8	99.5	97.2	7
HSPA9	82.6	89.5	84.2	8

JAK2	103.5	97.6	95.0	147796
KIF23	144.7	99.4	96.8	9
KLF1	115.3	100.0	99.9	613673;111150;613566
LARS2	122.8	100.0	100.0	604544
LPIN2	97.8	100.0	99.6	605519
MPL	125.8	100.0	99.8	159530
NCOA4	101.7	96.7	92.2	14
NDUFB11	103.3	98.6	95.0	15
PANK2	154.1	100.0	100.0	234200;607236
PUS1	113.3	99.8	97.5	600462
SEC23B	131.0	99.8	99.0	224100
SF3B1	130.9	99.6	98.3	605590
SFXN4	124.0	100.0	99.7	615578;10
SLC11A2	96.2	99.9	98.7	206100
SLC19A2	101.3	100.0	99.6	249270
SLC25A37	212.0	100.0	100.0	11
SLC25A38	94.5	99.1	95.2	205950
SLC40A1	120.8	100.0	99.8	606069
SLC46A1	111.1	99.9	98.4	229050
STEAP3	166.9	100.0	99.4	615234
TF	101.6	100.0	99.7	209300
TFR2	124.0	99.6	98.3	604250
TFRC	132.0	99.9	99.0	12
TMEM14C	95.6	100.0	97.8	13
TMPRSS6	107.0	100.0	99.4	206200
TRNT1	101.5	99.2	96.5	612907
UROS	103.8	100.0	99.7	263700
YARS2	175.2	99.9	99.6	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