WES CONGENITAL HEARTDISEASE [1] DG 2.16

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ACTC1	111.1	100.0	98.9	102540
ACVR2B	115.6	99.7	97.0	602730
ALDH1A2	105.1	99.9	98.6	603687
ANKRD1	98.1	99.9	98.6	609599
BRAF	72.5	92.4	80.2	164757
CFAP53	131.8	99.1	97.0	614759
CFC1	125.8	91.0	80.1	605194
CHD7	137.0	99.9	99.4	608892
CITED2	149.7	99.2	99.0	602937
CRELD1	98.9	99.8	95.9	607170
EHMT1	127.7	94.6	94.2	607001
ELN	103.1	100.0	98.9	130160
FBN1	137.1	100.0	99.8	134797
FLT4	160.3	99.2	99.1	136352
FOXC2	122.3	100.0	100.0	602402
FOXH1	84.5	100.0	99.5	603621
FOXL1	144.0	100.0	99.4	603252
GATA4	87.6	95.9	86.7	600476
GATA5	74.0	100.0	99.2	611496
GATA6	110.2	98.3	92.5	601656
GDF1	50.7	97.8	84.7	602880
GJA5	207.8	100.0	100.0	121013
HAND1	162.9	100.0	100.0	602406
HAND2	85.1	100.0	99.2	602407
HEY2	162.7	99.4	96.6	604674

JAG1	133.7	99.2	97.1	601920
KMT2D	136.2	100.0	99.7	602113
KRAS	67.2	99.4	97.3	190070
LEFTY2	69.3	99.5	91.7	601877
MCTP2	120.6	99.5	97.4	616297
MED13L	108.5	99.9	99.6	608771
MMP21	94.9	100.0	98.0	608416
MYH11	122.1	100.0	99.5	160745
MYH6	95.5	99.0	95.3	160710
MYH7	92.2	99.5	96.4	160760
NKX2-5	120.8	100.0	99.9	600584
NKX2-6	139.9	100.0	100.0	611770
NODAL	144.8	100.0	100.0	601265
NOTCH1	141.8	99.8	98.9	190198
NOTCH2	123.7	100.0	99.6	610205
NR2F2	236.6	100.0	100.0	107773
PKD1L1	108.7	100.0	99.3	609721
PLD1	116.4	99.9	99.3	602382
PTPN11	78.3	98.6	90.7	176876
RAF1	108.3	100.0	99.9	164760
SHROOM3	151.4	99.9	99.1	604570
SMAD6	180.5	98.8	89.1	602931
SOS1	102.0	99.6	97.4	182530
TAB2	170.6	99.9	99.5	605101
TBX1	101.2	93.0	86.9	602054
TBX20	108.2	100.0	99.9	606061
TBX5	135.3	100.0	100.0	601620
TDGF1	120.9	99.7	94.8	187395
TFAP2B	168.3	99.2	96.8	601601
TLL1	129.8	100.0	99.9	606742

TNNI3K	105.8	99.9	99.3	613932
ZFPM2	155.6	100.0	99.8	603693
ZIC3	140.9	100.0	99.8	300265

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