WES CONGENITAL HEARTDISEASE * DG 2.14

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ACTC1	164.1	100.0	99.6	102540
ACVR1	165.1	100.0	100.0	102576
ACVR2B	140.5	97.1	94.7	602730
ALDH1A2	114.8	100.0	99.6	603687
ANKRD1	101.7	99.5	96.8	609599
CFAP53	146.6	97.6	94.2	614779
CFC1	74.5	82.7	71.3	605194
CHD7	150.7	99.9	98.9	608892
CITED2	111.6	99.2	99.0	602937
CRELD1	114.4	99.9	97.8	607170
CRKL	166.4	100.0	99.8	602007
ELN	91.1	99.4	97.4	130160
FBN1	159.8	99.9	99.5	134797
FLT4	155.9	98.6	97.9	136352
FOXH1	47.2	98.5	85.0	603621
GATA4	87.4	68.6	60.7	600576
GATA5	44.2	98.3	84.4	611496
GATA6	61.7	83.7	72.1	601656
GDF1	19.5	65.0	48.4	602880
GJA5	268.4	100.0	100.0	121013
HAND1	84.8	100.0	98.9	602406
HAND2	32.2	87.8	67.9	602407
HEY2	146.1	99.2	92.8	604674
IRX4	90.0	95.8	92.3	606199
JAG1	148.4	98.1	97.5	601920

LEFTY2	42.3	91.3	77.1	601877
MED13L	134.6	100.0	99.6	608771
MMP21	93.3	90.2	84.6	608416
MYH11	132.6	100.0	99.3	160745
MYH6	113.3	99.0	96.1	160710
MYH7	111.4	99.4	96.8	160760
NKX2-5	83.2	100.0	99.5	600584
NKX2-6	104.4	100.0	99.7	611770
NODAL	160.7	100.0	99.9	601265
NOTCH1	137.5	99.1	98.0	190198
NOTCH2	172.4	100.0	99.9	610205
NR2F2	246.1	98.7	94.3	107773
PITX2	147.8	99.7	97.5	601542
PKD1L1	123.8	100.0	99.6	617205
PTPN11	103.1	97.9	92.5	176876
SHROOM3	137.3	99.9	98.9	604570
SMAD6	100.5	80.0	72.0	602931
TAB2	210.5	99.7	97.6	605101
TBX1	75.3	77.1	67.4	602054
TBX20	142.8	99.9	99.3	606061
TBX5	141.3	100.0	100.0	601620
TDGF1	151.4	99.8	96.4	187395
TFAP2B	153.5	98.8	96.3	601601
TLL1	140.1	100.0	99.9	606742
TNNI3K	118.8	98.8	96.0	613932
ZFPM2	196.3	100.0	99.6	603693
ZIC3	113.7	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