WES FETAL AKINESIA DG 2.16

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ACTA1	95.3	99.8	97.9	161800;255310
ADCY6	162.8	100.0	100.0	616287
ADGRG6	135.7	99.8	98.7	616503
ALG3	106.5	100.0	99.9	601110
ASCC1	125.4	95.7	92.0	616867
BIN1	113.4	99.9	98.4	255200
CHAT	117.1	95.4	86.9	254210
CHRNA1	92.6	94.6	93.3	253290
CHRND	140.4	99.8	98.0	253290
CHRNE	167.8	100.0	100.0	608931
CHRNG	141.3	100.0	100.0	265000;253290
CHST14	160.6	99.9	98.9	601776
CNTNAP1	157.2	99.9	99.1	616286
COL6A1	158.8	100.0	99.8	158810
COL6A2	175.3	100.0	99.8	158810
COL6A3	154.0	100.0	99.8	158810
COX15	87.7	99.9	98.3	615119
DHCR24	155.8	100.0	99.9	602398
DHCR7	144.9	100.0	100.0	270400
DNM2	123.9	99.7	96.7	615368
DOK7	135.1	94.0	93.3	208150;254300
ECEL1	107.1	100.0	97.4	615065
EGR2	130.0	100.0	100.0	605253
ERBB3	113.3	99.9	99.2	607598
ERCC5	126.3	99.9	99.5	616570

ERCC6	158.2	100.0	99.9	214150
FBN2	142.2	100.0	99.8	121050
FKRP	153.3	100.0	100.0	613153
FLVCR2	124.8	100.0	100.0	225790
GBA	169.8	100.0	100.0	608013
GBE1	157.4	99.9	99.7	232500
GLDN	106.6	99.8	96.9	617194
GLE1	97.1	100.0	99.9	611890;253310
GMPPB	211.8	100.0	100.0	615351
IGHMBP2	108.3	99.6	97.4	604320
ISPD	110.2	99.6	97.5	614643
KIF5C	109.9	99.9	99.0	615282
KLHL40	130.6	100.0	100.0	615348
KLHL41	172.8	100.0	99.8	615731
LGI4	99.9	99.4	96.7	617468
LMNA	104.7	97.7	91.9	613205
LMOD3	128.6	100.0	99.8	616165
MEGF10	125.9	100.0	99.8	614399
MPZ	125.0	100.0	98.9	605253
MTM1	79.1	98.7	91.9	310400
MUSK	131.5	100.0	100.0	208150
MYBPC1	127.8	99.9	99.2	614915;614335
MYCN	173.8	100.0	100.0	164280
MYH3	94.1	99.9	98.3	178110;193700;601680
MYH8	115.4	100.0	99.4	158300
NEB	100.1	83.0	82.4	256030
NEK9	118.9	99.8	98.2	617022
PHGDH	106.6	100.0	99.3	256520
PIEZO2	104.2	99.9	99.2	108145;617146;114300
PIP5K1C	136.6	99.8	97.6	611369

PLOD1	131.9	99.8	97.3	225400
PSAT1	42.8	90.3	72.5	616038
RAPSN	149.0	99.8	97.7	208150;616326
RIPK4	167.5	100.0	100.0	263650
RYR1	117.1	98.7	95.7	255320
SCN4A	167.9	99.8	99.3	168300;170500;608390;613345
SELENON	131.0	84.9	83.9	255310
SLC5A7	100.2	100.0	99.9	617143
SLC6A9	148.8	100.0	100.0	617301
SMN1	97.6	99.8	96.9	253300
TBCD	136.2	98.2	94.3	617193
TNNI2	150.5	100.0	100.0	601680
TNNT3	146.3	100.0	99.8	601680
TPM2	105.2	100.0	99.7	609285;601680;108120
TPM3	74.3	89.5	88.0	255310
TRIP4	103.3	99.8	98.5	616866
TRPV4	138.4	100.0	99.8	156530;600175
TTN	163.0	98.6	98.1	608807;603689;600334
UBA1	130.5	99.6	98.1	301830
VIPAS39	114.7	100.0	99.9	613404
VPS33B	107.2	100.0	99.9	208085
WDR62	152.6	100.0	99.8	604317
ZC4H2	72.4	99.8	95.9	314580
ZMPSTE24	128.7	100.0	99.6	275210

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