WES AMYOTROPHIC LATERAL SCLEROSIS, ALS DG 3.00

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ALS2	176.4	100.0	99.9	205100
ANG	210.9	100.0	100.0	611895
ANXA11	101.5	100.0	98.5	617839
CHCHD10	25.2	59.1	43.9	615911
CHMP2B	94.7	99.7	96.7	614696
ERBB4	157.2	100.0	99.5	615515
FIG4	190.3	100.0	99.8	612577
FUS	135.1	99.2	96.4	608030
KIF5A	141.4	100.0	99.9	617921
MATR3	100.4	97.0	93.4	615515
OPTN	119.9	100.0	99.9	613435
PFN1	176.9	100.0	100.0	614808
SETX	182.3	100.0	99.8	602433
SIGMAR1	134.5	100.0	100.0	614373
SOD1	144.8	100.0	99.9	105400
SPG11	135.0	100.0	99.3	604360
SQSTM1	125.7	98.8	95.5	616437
TARDBP	150.0	100.0	100.0	612069
TBK1	121.6	99.7	97.2	616439
TUBA4A	170.9	100.0	100.0	616208
UBQLN2	123.7	100.0	99.4	300857
VAPB	114.2	100.0	99.9	608627
VCP	122.7	100.0	99.2	613954

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