

WES AMYOTROPHIC LATERAL SCLEROSIS, ALS DG 3.4

<i>Gene</i>	<i>Median coverage</i>	<i>% covered >10x</i>	<i>% covered >20x</i>	<i>OMIM disease ID</i>
ALS2	166.1	100.0	100.0	205100
ANG	207.3	100.0	100.0	611895
ANXA11	178.7	100.0	100.0	617839
CFAP410	269.9	100.0	100.0	No OMIM phenotype
CHCHD10	215.6	100.0	100.0	615911
CHMP2B	139.9	100.0	100.0	614696
ERBB4	187.6	100.0	100.0	615515
FIG4	160.5	100.0	100.0	612577
FUS	200.8	100.0	100.0	608030
GRN	229.2	100.0	100.0	607485
KIF5A	159.7	100.0	100.0	617921
MAPT	276.3	100.0	100.0	601104
MATR3	159.7	100.0	100.0	615515
NEK1	142.5	100.0	100.0	617892
OPTN	163.5	100.0	100.0	613435
PFN1	190.2	100.0	100.0	614808
SETX	171.6	100.0	100.0	602433
SIGMAR1	238.2	100.0	100.0	614373
SOD1	162.8	100.0	100.0	105400
SPG11	166.5	100.0	100.0	604360
SQSTM1	198.1	100.0	100.0	616437
TARDBP	180.1	100.0	100.0	612069
TBK1	130.0	100.0	100.0	616439
TUBA4A	275.0	100.0	100.0	616208
UBQLN2	224.5	100.0	100.0	300857

VAPB	154.5	100.0	100.0	608627
VCP	165.0	100.0	100.0	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.

TWIST is the default chemistry for all WES samples. Agilent V5 was the default chemistry until Q3 2021.

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 20x describes the percentage of a gene's coding sequence that is covered at least 20x.

Genes with no value for coverage are non protein coding genes.

Non protein coding genes are covered, but as coverage statistics are based on protein coding regions, statistics could not be generated.

OMIM release used for OMIM disease identifiers and descriptions: September 1st, 2021.

[EAS.GenProductCoverage.pdf.footer.ad01](#)