

WES AMYOTROPHIC LATERAL SCLEROSIS, ALS DG 3.6

<i>Gene</i>	<i>Median coverage</i>	<i>% covered >10x</i>	<i>% covered >20x</i>	<i>OMIM disease ID</i>
ALS2	133.7	100.0	100.0	205100
ANG	120.7	100.0	100.0	611895
ANXA11	115.7	100.0	100.0	617839
CFAP410	141.1	100.0	100.0	No OMIM phenotype
CHCHD10	134.4	100.0	100.0	615911
CHMP2B	151.9	100.0	100.0	614696
ERBB4	146.1	100.0	99.9	615515
FIG4	155.8	100.0	100.0	612577
FUS	134.0	100.0	100.0	608030
GRN	136.9	100.0	100.0	607485
KIF5A	120.8	100.0	100.0	617921
MAPT	115.2	100.0	100.0	601104
MATR3	142.9	100.0	100.0	615515
NEK1	151.1	100.0	100.0	617892
OPTN	134.8	100.0	100.0	613435
PFN1	170.4	100.0	100.0	614808
SETX	144.1	100.0	100.0	602433
SIGMAR1	147.0	100.0	100.0	614373
SOD1	155.0	100.0	100.0	105400
SPG11	138.5	100.0	100.0	604360
SQSTM1	144.9	100.0	100.0	616437
TARDBP	135.9	100.0	100.0	612069
TBK1	149.6	100.0	100.0	616439
TUBA4A	208.1	100.0	100.0	616208
UBQLN2	103.8	100.0	100.0	300857

VAPB	143.8	100.0	100.0	608627
VCP	126.6	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](#)