SUPPLEMENTARY INFORMATION

Content

e-Methods

Whole-exome sequencing and whole-genome sequencing

Whole-exome sequencing was performed at the Institute for Molecular Medicine Finland (FIMM). For the index patient's sample target enrichment was done using Agilent SureSelect Human All Exon V5 kit (Agilent Technologies, Santa Clara, CA, USA). The sequencing was performed according to manufacturers' protocol on a Hiseq2500 platform (Illumina, San Diego, USA). Initial variant calling was done using the variant calling pipeline of FIMM and alignment was done to the human genome reference sequence hg19 (GRCh37). Initial data analysis of the index patient was performed with OmnomicsNGS software (Euformatics, Espoo, Finland) focusing on genes known to cause ALS and frontotemporal lobar degeneration. For the samples of patients 6-8 library preparation was done with Kapa HyperPrep kit, xGen® Dual Index UMI Adapters and target enrichment with NimbleGen MedExome kit.

Whole-genome sequencing was performed using the Illumina TruSeq DNA PCR Free library preparation kit and the HiSeq X10 sequencing system that produced 150 base pair paired-end reads according to the manufacturer's protocol. Raw sequence data was processed according to Broad Best Practices API (application program interface).

Adapters were trimmed with Trimmomatic[1], and sequences were aligned with BWA [2] using reference genome GRCh37. Further data processing and variant calling was done with GATK [3] version 3.7 using their best practice protocol[4]. After variant calling, the following hard filters were used for SNVs: Variant Confidence/Quality by Depth (QD) < 2.0, Phred-scaled p-value using Fisher's exact test to detect strand bias (FS) > 60.0, RMS Mapping Quality (MQ) < 35.0, Z-score From Wilcoxon rank sum test of Alt vs. Ref read mapping qualities (MQRankSum) < -12.5, Z-score from Wilcoxon rank sum test of Alt vs. Ref read position bias (ReadPosRankSum) < -8.0, Allele Balance for heterozygous calls (ABHet) <= 0.7. For indels, the hard filters were: QD < 2.0, FS > 200.0, ReadPosRankSum < -20.0.
Variants in genes indicated in ALS, other neurodegenerative diseases and the SOD1 pathway (eTable1) were extracted from the whole-exome and whole-genome sequencing data and remaining variants were annotated with ANNOVAR[5]. Genome aggregation database (gnomAD)[6], Combined Annotation Dependent Depletion and dbNSFP [7]database were used for annotation.
Possible causative variants were identified from the whole-exome and whole-genome derived data. First, bi-allelic, nonsynonymous, exonic or splice site SNVs and indels were selected. Then three different filtering strategies were used to identify putative disease contributing variants: 1) minor allele frequency (MAF) ≤0.001 2) MAF ≤ 0.01 and homozygous or possible compound heterozygote genotype 3) MetaLR prediction "Deleterious" and MAF≤0.01. Loci with read depth of less than 7, genotype quality score <30 and loci with only few reads supporting heterozygous genotype were excluded.

Table e-1 **Genes analyzed from the whole-exome and whole-genome sequencing data**

AAAS AARS AARS2 AARSD1 AASDHPPT ABCA1 ABCA2 ABCB7 ABCC8 ABCD1 ABHD12 ABHD5 ACAT1 ACO1 ACO2 ACOT7 ACOX1 ACTB ACTN4 ADAR ADCK3 ADCY5 ADORA2B ADRB2 ADRM1 AFG3L2 AGRN AHNAK AHR AHSG AIFM1 AIMP1 AK2 AK9 AKR1C3 ALB ALDH18A1 ALDH3A2 ALDH7A1 ALDOA ALDOC ALG14 ALG2 ALKBH5 ALS2 AMFR AMPD2 ANAPC7 ANG ANGPT2 ANO10 ANO3 ANXA1 ANXA11 AP3D1 AP4B1 AP4E1 AP4M1 AP4S1 AP5Z1 APBA1 APEX1 API5 APLN APOA1 APOA1BP APOB APOE APOL2 APOPT1 APP APRT APTX AR ARHGEF10 ARHGEF28 ARL16 ARL6IP1 ARSA ARSI ASAH1 ASCC1 ASL ASPA ASS1 ATCAY ATF1 ATF4 ATL1 ATM ATP13A2 ATP1A1 ATP1A2 ATP1A3 ATP2B3 ATP5F1A ATP5F1B ATP6V1A ATP6V1B1 ATP6V1G2 ATP7A ATP7B ATP8A2 ATP8B3 ATXN1 ATXN10 ATXN2 ATXN3 ATXN7 ATXN8OS AUH AURKAIP1 AVIL B2M B4GALNT1 BACE1 BAD BAG3 BANF1 BASP1 BAX BCAP31 BCL2 BCL2L1 BCL2L13 BEAN1 BGLAP BICD2 BID BMP4 BOLA3 BSCL2 BTG2 BUB1 C10orf2 C11orf73 C12orf65 C19orf12 C1QA C21orf2 C4BPA C9orf72 CA2 CA8 CACNA1A CACNA1B CACNA1G CACNA1H CACNA1S CACNB4 CALCB CAMTA1 CAPN1 CARTPT CASP1 CASP12 CASP2 CASP3 CASP4 CASP7 CASP9 CAST CCAR2 CCDC88C CCL5 CCNC CCND1 CCNF CCNK CCNT1 CCS CCT2 CCT5 CCT7 CCT8 CD14 CD33 CD36 CD59 CDC42 CDH13 CDH2 CDK4 CDK5 CEBPA CENPV CEP55 CGA CGB3 CHAT CHCHD10 CHCHD2 CHGB CHMP2B CHRM1 CHRNA1 CHRNA4 CHRNB1 CHRND CHRNE CHRNG CIZ1 CKB CLCN2 CLCN5 CLDN17 CLEC4C CLN3 CLN5 CLN6 CLN8 CLU CNGA4 CNOT1 COASY COL19A1 COL1A1 COL4A1 COL4A2 COL6A3 COLQ COMMD1 COMT COPA COPG1 COX20 CP CPSF7 CREBBP CRYAB CRYM CRYZ CSF1R CSH1 CSH2 CTC1 CTDP1 CTNNB1 CTSA CTSD CTSF CUL4B CUTA CWF19L1 CXCR4 CYB561 CYCS CYP27A1 CYP2F1 CYP2U1 CYP7B1 CYP8B1 CYSLTR1 DAO DARS DARS2 DAXX DCAF17 DCC DCTN1 DCTN2 DCXR DDC DDHD1 DDHD2 DDX39B DENND2C DERL1 DES DHTKD1 DIABLO DNAH10 DNAH2 DNAH9 DNAJA1 DNAJB2 DNAJC12 DNAJC5 DNAJC6 DNM1L DNM2 DNMT1 DOK7 DPAGT1 DPP6 DPYSL3 DRAP1 DSG3 DSTN DSTYK DVL1 DYNC1H1 DYNC1I1 DYNC2LI1 DYNLT1 EARS2 EDN1 EEF1B2 EEF1D EEF1G EEF2 EGR1 EGR2 EHMT1 EIF1AX EIF2B1 EIF2B2 EIF2B3 EIF2B4 EIF2B5 EIF2S1 EIF3A EIF3D EIF3E EIF3H EIF3I EIF4A3 EIF4E1B EIF5A ELAVL1 ELOVL4 ELOVL5 ELP3 ENO3 ENTPD1 EPAS1 EPDR1 EPO EPRS ERBB3 ERBB4 ERCC6 ERCC8 ERLIN1 ERLIN2 ERVW-1 ETFB ETS2 EWSR1 EXOSC3 EXOSC6 EZR FA2H FAAP20 FAM126A FAM134B FANCD2 FAP FARSA FASLG FBLN5 FBXO32 FBXO7 FEN1 FGD4 FGF10

FGF14 FGF19 FGF6 FGF8 FGFR1 FGGY FIG4 FKRP FKTN FLRT1 FLVCR1 FMR1 FOLR1 FOS FOSL2 FOXA1 FOXC1 FOXN3 FOXO3 FRRS1L FTH1 FTL FTMT FUBP1 FUCA1 FUS FXN FYN G6PD GAK GALC GAN GANAB GAPDH GAR1 GARS GBA GBA2 GBE1 GCDH GCH1 GCLC GCLM GDAP1 GDF1 GDI1 GDNF GFAP GFPT1 GH1 GH2 GJA1 GJB1 GJB3 GJC2 GLA GLB1 GLE1 GLO1 GLRX5 GLUL GMFB GMPPB GNAL GNAO1 GNAS GNB1 GNB4 GORASP1 GOSR2 GPX1 GPX3 GRID2 GRM1 GRN GRSF1 GSTA5 GSTK1 GSTM1 GSTM3 GSTM5 GSTP1 GTF2H4 GTF3C2 GUK1 H1F0 H1FX HAGH HARS HDAC10 HDAC6 HDDC3 HECW1 HENMT1 HEPACAM HES3 HEXA HEXB HINT1 HIST1H2AB HIST1H2AE HIVEP1 HIVEP3 HK1 HMGB1 HMGB3 HMOX1 HNF4A HNRNPA1 HNRNPA2B1 HNRNPAB HNRNPD HNRNPU HNRNPUL1 HOXD10 HPCA HPCAL1 HPRT1 HRAS HRNR HSBP1 HSD17B4 HSF1 HSP90AB1 HSP90B1 HSPA1A HSPA1B HSPA2 HSPA4 HSPA4L HSPA5 HSPA8 HSPA9 HSPB1 HSPB2 HSPB3 HSPB8 HSPD1 HSPE1 HSPH1 HTRA1 HTT HUWE1 IARS IBA57 ICAM1 IDH3A IDS IFI16 IFIH1 IFNG IFRD1 IGF1 IGHMBP2 IKBKAP IL10 IL1B IL1RN IL3 IL6 IL7 ILF2 IMPDH2 INF2 INHBA INS INVS IQGAP1 ISCA2 ITM2B ITPR1 ITPR2 JPT1 JRK JUN JUNB KARS KCNA1 KCNC3 KCNC4 KCND3 KCNJ10 KCNMA1 KCNT1 KCTD7 KIAA0196 KIAA0226 KIAA1755 KIDINS220 KIF1A KIF1B KIF1C KIF21A KIF5A KIF5B KIFAP3 KLC2 KMT2B KMT2C KPNB1 L1CAM L2HGDH LAMA2 LAMB2 LARGE LARS LBP LDHA LDHAL6A LDHB LEP LGMN LIMD1 LIMK1 LITAF LMNA LMNB1 LMNB2 LONP1 LPL LRRK2 LRSAM1 LUM LYRM7 MAG MAOB MAP4K1 MAPK14 MAPK3 MAPK8 MAPT MARCH5 MARCKSL1 MARS MARS2 MAT1A MAT2A MATR3 MAVS MCM2 MCM3 MCM4 MCM5 MCM6 MCOLN1 MDH2 MECP2 MECR MED25 MET METTL14 METTL22 MFF MFN2 MFSD8 MICAL1 MIF MLC1 MME MMP2 MMP9 MOB1B MPV17 MPZ MRE11A MRPL12 MRPS10 MT3 MT-CO1 MTFMT MTHFD1 MTMR2 MT-ND1 MT-ND4 MTOR MTPAP MTPN MTREX MTTP MUC1 MURC MUSK MYBBP1A MYBL1 MYH11 MYH3 MYH8 MYO3B MYOM1 NACA NAIP NAP1L4 NARS NCBP1 NCBP2 NDRG1 NDUFAF1 NDUFS1 NDUFV1 NDUFV3 NEFH NEFL NEFM NEK1 NEU1 NFE2L2 NFIL3 NFKBIA NFS1 NFU1 NGF NIPA1 NKX2-1 NKX6-2 NLRC5 NOP10 NOP56 NOS1 NOS2 NOTCH3 NPC1 NPC2 NPY NR4A2 NSUN2 NT5C2 NTM NTRK1 NUDT21 NUP62 NUP93 OBFC1 OCLN OPA1 OPA3 OPTN P2RX4 P2RX7 P2RY6 P3H1 P4HB PABPC4 PANK2 PARK2 PARK7 PAWR PAX6 PC PCMT1 PCP4 PDCD6 PDCD6IP PDE10A PDE6B PDGFB PDGFRB PDIA3 PDIA4 PDIA6 PDK3 PDYN PEX1 PEX10 PEX11B PEX12 PEX13 PEX14 PEX16 PEX19 PEX2 PEX26 PEX3 PEX5 PEX6 PEX7 PFDN2 PFN1 PGAP1 PGK1 PHB PHF21A PHGDH PHKA1 PHOX2A PHYH PINK1 PIP5K1C PITPNA PITPNB PITX2 PLA2G4C PLA2G4E PLA2G6 PLAA PLEKHG2 PLEKHG5 PLN PLP1 PMM2 PMP22 PMPCA PNKD PNKP PNPLA6 POLG POLG2 POLR1C POLR2E POLR3A POLR3B POMGNT1 POMT1 POMT2 PON1 PON2 PON3 POU2F1 PPA1 PPARG PPARGC1A PPARGC1B PPIA PPIAL4G PPM1A PPM1B PPP1R12A PPP2R1A PPP2R2B PPP3CA PPP3CB PPT1 PRCC PRDX2 PRDX4 PRDX5 PRDX6 PRICKLE1 PRKCG PRKCSH PRKRA PRL PRNP PRPH PRPS1 PRR12 PRRT2 PRRX1 PRSS1 PRX PSAP PSAT1 PSEN1 PSEN2 PSMA2 PSMA6 PSMB5 PSMB6 PSMB7 PSMB8 PSMC1 PSMC2 PSMC5 PSMC6 PSMD11 PSMD14 PSMD2 PSMD4 PSME2 PTBP1 PTGR1 PTGS2 PTMS PTPN21 PTRF PYCR2 QARS RAB21 RAB25 RAB39B RAB3GAP2 RAB7A RAB9A RAC1 RACK1 RAP1A RAPSN RARS RAVER1 RB1 RBBP6 RBM12 RBM12B RBM15 RBM15B RBM3 RBM45 RBM4B RBM8A RBMS2 RCAN1 RDX REEP1 REEP2 RET RHOA RINL RNASEH2A RNASEH2B RNASEH2C RNASET2 RNF170 RNF19A RNF216 RNH1 RPA3 RPGRIP1 RPL30 RPLP1 RRAS2 RRM2B RTN2 RTRAF RUNX2 RUVBL1 RUVBL2 S100A11 SACS SAE1 SAMD9L SAMHD1 SARS SBF1 SBF2 SCG5 SCN10A SCN1A SCN4A SCN8A SCN9A SCP2 SCYL1 SDHA SDHAF1 SEPT9 SERPINA10 SERPINH1 SETX SFN SGCE SH3BGRL3 SH3TC2 SIGMAR1 SIL1 SIRT1 SIRT5 SKP1 SLC11A2 SLC12A6 SLC16A2 SLC17A5 SLC19A3 SLC1A2 SLC1A3 SLC1A4 SLC20A2 SLC25A12 SLC25A15 SLC25A20 SLC25A4 SLC25A5 SLC27A4 SLC2A1 SLC30A10 SLC33A1 SLC39A14 SLC40A1 SLC52A1 SLC52A2 SLC52A3 SLC5A7 SLC6A3 SMAD2 SMN1 SMPD1 SNCA SNCG SND1 SNORD118 SNX14 SOD1 SOD2 SOST SOX10 SP1 SP7 SPAST SPG11 SPG20 SPG21 SPG7 SPIN1 SPP1 SPR SPTAN1 SPTB SPTBN2 SPTLC1 SPTLC2 SQSTM1 SRCAP SRP19 SRPK2 SRRT SS18L1 SSB SSR4 STAT1 STAT4 STIM1 STIP1 STK36 STMN1 STUB1 STXBP2 STXBP5L SUCLA2 SUMF1 SUMO2 SURF1 SV2A SYNE1 SYNE2 SYNJ1 SYP SYT14 TAB1 TAF1 TAF15 TAF1L TAGLN2 TARDBP TBCA TBK1 TBP TDP1 TECPR2 TF TFG TFRC TGFB1 TGFBR2 TGM6 TH THAP1 THSD7B TIA1 TIMM13 TK2 TKT TLN1 TMEM240 TMSB4X TNF TNFAIP3 TNFRSF10B TNFSF11 TNNI2 TNNT3 TOR1A TP53 TPD52 TPI1 TPM2 TPP1 TPR TRAP1 TREM2 TREX1 TRIM2 TRIM28 TRNAU1AP TRPM7 TRPM8 TRPV4 TRRAP TSFM TTBK2 TTC19 TTPA TTR TUBA1A TUBA1B TUBA4A TUBA8 TUBB2B
TUBB3 TUBB4A TUFM TYMP TYROBP UBA1 UBC UBE2M UBE2N UBE3A UBQLN1 UBQLN2 UCHL1 ULK1 UNC13A USH2A USP8 USP9X UTS2 VAC14 VAMP1 VAPA VAPB VARS VAT1 VCAM1 VCL VCP VEGFA VGF VIP VLDLR VPS11 VPS13A VPS13C VPS35 VPS37A VRK1 WDR45 WDR48 WDR6 WDR81 WFS1 WNK1 WTAP WWOX WWP2 XBP1 XIAP XK XPR1 XRCC5 XRCC6 YARS YES1 YWHAB YWHAG YWHAQ YWHAZ ZC3H18 ZFR ZFYVE26 ZFYVE27 ZNF34

Table e-2 Presumed shared haplotype of the patients (P1-8) with the *SOD1* mutation p.Ala90Val on chromosome 21 determined by rare single nucleotide polymorphism (SNP) marker alleles. The rare SNP alleles are concordant for one or both rare alleles in all patients, which is consistent with a shared haplotype although the phases of the genotypes are not determined.
The physical locations of the SNP markers are relative to the human genome build GRCh37/hg19. Chr21:33039600 is the physical location of the *SOD1* mutation p.Ala90Val. The SNP markers were first screened from the WGS data of patients P2-P5 and then Sanger sequenced for P1 and P6-P8. The alternative allele frequency is from the Finnish gnomAD database population.

Marker rs number	Physical location on chr21 (GRCh37/hg19)	Alleles ref/alt	Alternative allele frequency	P1	P2	P3	P4	P5	P6	P7	P8
rs182973529	32723906	[G/A]	0.02119	G_A	G_A	G_A	G_A	G_A	G_A	G_A	G_A
rs117515869	32811845	[C/T]	0.005152	C_T	C_T	C_T	C_T	C_T	C_T	C_T	C_T
rs112208200	32827409	[C/T]	0.01005	C_T	C_T	C_T	C_T	C_T	C_T	C_T	C_T
rs2833409	32829700	[C/T]	0.03177	C_T	C_T	C_T	C_T	C_T	C_T	C_T	C_T
rs17652514	32846040	[C/T]	0.008309	C_T	C_T	C_T	C_T	C_T	C_T	C_T	C_T
rs9983512	32901528	[A/G]	0.01379	A_G	A_G	A_G	A_G	A_G	A_G	A_G	A_G
rs78530452	33017124	[C/T]	0.02291	C_T	C_T	C_T	C_T	C_T	C_T	T_T	C_T
	33039600	[C/T]	0.00004485	C_T	C_T	C_T	C_T	C_T	C_T	C_T	C_T
rs527967648	33103636	[G/A]	0.02232	G_A	G_A	G_A	G_A	G_A	G_A	A_A	G_A

Figure e-1 Pedigrees of patients P1-8. Unaffected individuals known to carry the *SOD1* p.Ala90Val mutation are colored gray, age at the time of the study or age of death of deceased individuals is shown for the family members, when known. P8 was the only individual in the family with both pAla90Val and p.Asp91Ala mutations. The family members with white symbols are unaffected and not genetically tested except for two individuals in family P6: individual marked with * is a carrier of *ANG* p.Lys78Glu and individual marked with - has been tested and is not a carrier of *SOD1* p.Ala90Val or *ANG* p.Lys78Glu. The number of siblings of P2 and P3 is unknown. The pedigrees have been anonymized with the consequence of some loss of information, but the evidence for the reduced penetrance of *SOD1* p. Ala90Val should still be clear.

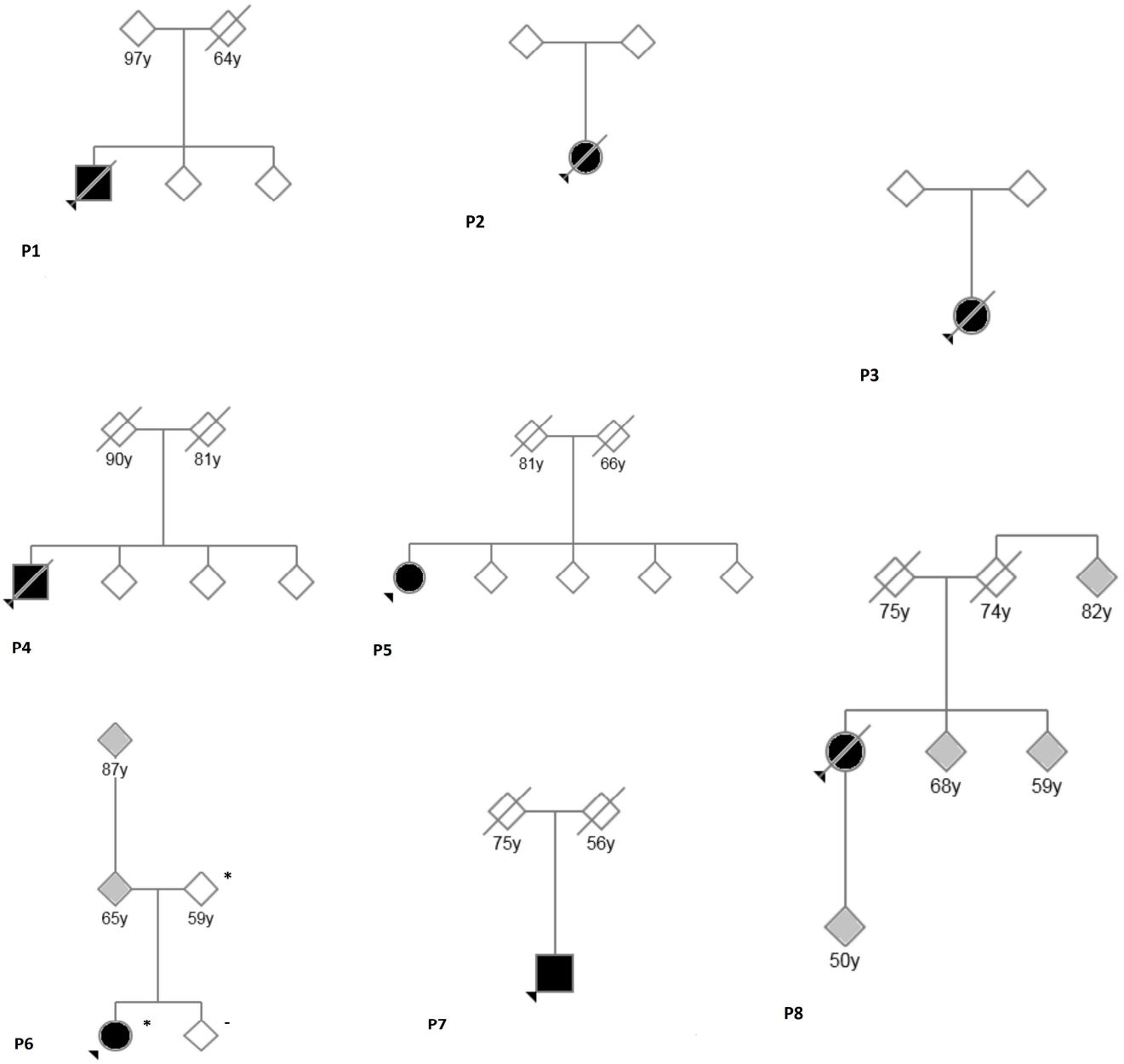

Table e-3 Additional variants identified in WES/WGS of P1-8.

*Previously reported mutation[8-10]. Genes previously associated with ALS are bolded. het=heterozygous, hemi=hemizygous (X-chromosomal in male). Mutations previously found in ALS cases or variants predicted to be deleterious in genes previously associated with ALS are here classified as "probably pathogenic", other variants are classified as "possibly pathogenic". This classification is used here to assess the variants effect on the phenotype of the patients. Prediction programs SIFT and Polyphen predictions on the deleteriousness of the variants: D= damaging, B=benign, T=tolerated, P=possibly damaging. CADD phred scores of 20 or more can be considered probably deleterious. GnomAD database v2.1 was accessed in February 2019.

Selection criteria of the variants included in the probably pathogenic category:

P1: Heterozygous *ARHGEF28* mutations have been previously reported in ALS, also in combination with *SOD1* mutations [11]

P3: *UNC13A* is a known ALS risk gene (common SNPs). Rare *UNC13A* missense mutations of unclear significance have been reported in ALS patients[12, 13], however, the missense variant found here is predicted to be deleterious by all three *in silico* prediction tools.

P4: Heterozygous p.T109I mutation in *ARHGEF10* has been reported in hereditary motor and sensory neuropathy and p.R338T variant in Charcot-Marie-Tooth disease with decreased nerve conduction velocities[14, 15]

P5: Heterozygous pathogenic p.R1465W mutation in *ADGRB2* (rs778361520) has been reported in a patient with spastic paraparesis[16].

P6: The same mutation in *ANG* has been previously reported in ALS[10].

P7: Heterozygous deletions leading to a frameshift and a premature stop codon in the *SPG11* gene have been previously reported in ALS [17] and the same mutation has been previously reported in a hereditary spastic paraplegia patient as a recessive mutation[8]. Compound heterozygous loss-of-function mutations in *CACNA1H* have been previously found in an ALS patient [18, 19].

P8: *SOD1* p.D91A is a known recessive ALS mutation[9], it is considered probably pathogenic here as a compound heterozygote with *SOD1* p.A90V. *SOD1* p.D91A has been previously reported as a compound heterozygote with another *SOD1* mutation[20]

Gene	Category	Variant	rs number	ref seq	Geno-type	European (non-Finnish) gnomAD v2.1 MAF	European (non-Finnish) gnomAD v2.1 MAF non-neuro	gnomAD v2.1 MAF Finnish	gnomAD v2.1 MAF Finnish non-neuro	Patient	Possibly pathogenic	Probably pathogenic	CADD phred	Poly-phen	Sift
ARHGEF28	ALS	c.C743G,p.T248R	rs375000790	NM_001080479	het	7,79E-06	0	6,79E-04	6,74E-04	P1		X	24,7	D	D
AVPR2	neurodegen	c.G236C,p.G79A	rs782026554	NM_001146151	hemi	0	0	1,85E-04	2,81E-04	P1	X		0,943	B	T
EPHB3	neurodegen	c.G2234T,p.G745V	rs774373853	NM_004443	het	0	0	4,62E-05	5,98E-05	P1	X		26,2	D	D
FAM170A	neurodegen	c.A782G,H261R	rs199949750	NM_182761	het	4,35E-04	4,18E-04	1,20E-04	1,12E-04	P1	X		20,4	B	T
POU2F1	neurodegen	c.A826G,p.T276A	rs142378150	NM_002697	het	4,83E-03	4,58E-03	6,25E-03	6,09E-03	P1	X		21,8	D	D
RDX	neurodegen	c.G37T,p.D13Y	-	NM_002906	het	0	0	0	0	P1	X		34	D	D
ALOX15	SOD1 path	c.G82A,p.G28S	rs147708465	NM_001140	het	3,71E-04	2,48E-04	3,20E-04	2,80E-04	P2	X		35	D	D
AR	neurodegen	c.C341A,p.A114D	rs1800053	NM_001011645	het	2,32E-03	2,33E-03	4,04E-04	3,27E-04	P2	X		14,25	B	D

COL4A1	neurodegen	c.C401T,p.P134L	rs140517831	NM_001845	het	3,33E-04	3,01E-04	2,87E-03	2,74E-03	P2	X		20,9	D	T
FBXW8	SOD1 path	c.C712T,p.R238C	rs202064358	NM_153348	het	6,97E-05	2,91E-05	1,19E-04	1,68E-04	P2	X		34	D	D
NOB1	SOD1 path	c.T862A,p.C288S	rs144374127	NM_014062	het	2,56E-04	2,62E-04	3,58E-04	4,47E-04	P2	X		24,8	D	D
PMM2	neurodegen	c.G422A,p.R141H	rs28936415	NM_000303	het	5,43E-03	5,31E-03	8,35E-03	7,99E-03	P2	X		34	P	D
TPP1	neurodegen	c.C14A,p.A5D	rs138976576	NM_000391	het	2,18E-03	2,17E-03	2,79E-03	2,79E-03	P2	X		15,34	B	D
ADA2	SOD1 path	c.G14C,p.G5A	rs200930463	NM_001282228	het	3,87E-05	4,47E-05	0	0	P3	X		24,3	D	T
APTX	neurodegen	c.C431A,p.S144Y	rs34778324	NM_001195249	het	9,76E-03	9,75E-03	2,99E-03	3,19E-03	P3	X		0,004	B	D
BICD2	ALS	c.T1179A,p.N393K	rs144427583	NM_015250	het	8,00E-04	7,88E-04	2,39E-04	2,80E-04	P3	X		9,538	B	T
C17orf107	neurodegen	c.472_473insGGGGTCTGCA,p.R158fs	rs746824055	NM_001145536	het	5,41E-05	6,48E-05	0	0	P3	X		-	-	-
CACNA1H	ALS	c.C2759T,p.T920M	rs59052554	NM_021098	het	3,36E-03	3,43E-03	4,19E-04	3,88E-04	P3	X		13,5	B	T
CDH23	SOD1 path	c.A3301G,p.I1101V	rs199510686	NM_022124	het	2,99E-04	3,16E-04	8,40E-04	8,43E-04	P3	X		23	B	-
LAMB2	neurodegen	c.C1886T,p.P629L	rs148491867	NM_002292	het	4,11E-04	4,27E-04	4,38E-04	5,03E-04	P3	X		24,1	P	D
MYH11	SOD1 path	c.G5890C,p.E1964Q	rs768140376	NM_001040114	het	9,67E-05	1,01E-04	4,62E-05	0	P3	X		21,6	P	D
NME8	SOD1 path	c.A169G,p.N57D	rs759876007	NM_016616	het	1,76E-05	1,12E-05	0	0	P3	X		18,54	D	T
PRRT2	neurodegen	c.G640C,p.A214P	rs745594874	NM_145239	het	3,79E-03	4,05E-03	8,71E-04	7,51E-05	P3	X		23,3	D	D
QARS	neurodegen	c.A2261G,p.D754G	rs142480574	NM_005051	het	4,10E-04	4,27E-04	4,38E-04	5,03E-04	P3	X		31	D	D
SLC26A10	neurodegen	c.T1247G,p.L416R	rs111924104	NM_133489	het	7,27E-03	7,25E-03	2,55E-03	2,68E-03	P3	X		27,5	D	D
SLC26A10	neurodegen	c.G1206A,p.W402X	rs113207856	NM_133489	het	6,13E-03	6,08E-03	2,55E-03	2,68E-03	P3	X		39	-	-
UNC13A	ALS	c.C892T,p.R298W	rs201739401	NM_001080421	het	6,37E-04	6,28E-04	5,95E-04	6,91E-04	P3		X	24,4	D	D
ARHGEF10	neurodegen	c.C700A,p.P234T	-	NM_001308153	het	0	0	0	0	P4		X	25,2	D	D
FAM126A	neurodegen	c.G1480A,p.V494I	rs151228394	NM_032581	het	7,70E-04	7,56E-04	3,58E-04	3,35E-04	P4	X		5,833	B	T

GRWD1	SOD1 path	c.C1172T,p.A391V	rs377325041	NM_031485	het	2,13E-04	1,78E-04	4,10E-05	5,83E-05	P4	X		22,7	B	T
HEXB	neurodegen	c.C214T,p.L72F	rs147155126	NM_000521	het	1,00E-02	1,02E-02	8,01E-03	7,60E-03	P4	X		17,95	P	D
ITPR1	neurodegen	c.A3416G,p.D1139G	rs61751570	NM_001168272	het	1,93E-03	1,83E-03	7,67E-03	8,15E-03	P4	X		15,18	P	T
MARS	neurodegen	c.C617T,p.P206L	rs138776588	NM_004990	het	1,36E-03	1,30E-03	1,59E-04	1,12E-04	P4	X		22,9	B	T
POLG2	neurodegen	c.714_716del,p.238_239del	rs782339619	NM_007215	het	0	0	0	0	P4	X		-	-	-
ADGRB2/ BAI2	SOD1 path neurodegen	c.C188T,p.S63L	rs367550636	NM_001294336	het	3,21E-05	4,03E-05	0	0	P5		X	24,5	P	D
CACNA1H	ALS	c.C4817T,p.T1606M	rs59286323	NM_021098	het	7,92E-03	7,71E-03	4,15E-03	4,31E-03	P5	X		24,5	P	T
CHRNB1	neurodegen	c.42_44del,p.14_15del	rs767124946	NM_000747	het	6,74E-05	8,28E-05	7,83E-04	7,32E-04	P5	X		-	-	-
CHRNB1	neurodegen	c.44_45insAA,p.A15fs	rs752322425	NM_000747	het	0	0	0	0	P5	X		-	-	-
GALC	neurodegen	c.C437T,p.A146V	rs763635404	NM_001201402	het	0	0	2,40E-04	3,37E-04	P5	X		22,8	D	T
HTT	SOD1 path , neurodegen	c.G8215A,p.A2739T	rs772607321	NM_002111	het	1,49E-04	1,37E-04	1,20E-04	1,69E-04	P5	X		5,327	B	T
ITPR1	neurodegen	c.G5320A,p.G1774R	rs373359869	NM_001168272	het	1,80E-04	1,85E-04	1,08E-03	1,18E-03	P5	X		25,9	P	D
XK	neurodegen	c.T1108G,p.Y370D	rs145996031	NM_021083	het	3,43E-03	3,19E-03	4,14E-03	4,23E-03	P5	X		26,3	D	D
ADCY5	neurodegen	c.C130A,p.H44N	rs189868197	NM_183357	het	0	0	5,95E-04	1,19E-03	P6	X		2,557	B	T
AHNAK	neurodegen	c.A13381G,p.M4461V	rs114666146	NM_001620	het	6,43E-04	6,50E-04	3,98E-05	5,59E-05	P6	X		9,553	P	T
AHNAK	neurodegen	c.C16348T,p.P5450S	rs139375615	NM_001620	het	2,04E-03	1,85E-03	8,76E-04	8,94E-04	P6	X		22,7	D	D
ANG	ALS	c.A232G,p.K78E*	rs141055235	NM_001145	het	3,10E-04	2,42E-04	1,59E-04	1,68E-04	P6		X	24,8	B	D
ATP7A	neurodegen	c.A2448C,p.Q816H	rs782104223	NM_000052	het	0	0	6,25E-05	8,21E-05	P6	X		25,1	D	D
KIAA1755	ALS	c.C676T,p.Q226X	rs766143998	NM_001348708	het	0	0	4,62E-05	5,98E-05	P6	X		29,5	-	-

KMT2C	ALS	c.C10432G,p.Q3478E	rs142835638	NM_170606	het	5,49E-03	5,15E-03	3,74E-03	4,02E-03	P6	X		22,4	D	D
MYOM1	muscle	c.A4357T,p.M1453L	rs181642354	NM_003803	het	2,11E-04	2,03E-04	1,76E-04	0	P6	X		7,428	B	T
POU2F1	neurodegen	c.C829T,p.R277C	rs145849668	NM_002697	het	1,94E-04	1,84E-04	7,96E-05	1,12E-04	P6	X		29,7	D	D
CACNA1H	ALS	c.C3691T,p.R1231C	rs781510850	NM_021098	het	9,35E-06	1,20E-05	0	0	P7		X	28,2	D	D
PGAM4	neurodegen	c.G79A,p.D27N	rs191844393	NM_001029891	hemi	6,70E-04	5,94E-04	9,12E-04	8,43E-04	P7	X		17,51	P	D
SPG11	ALS	c.C5623T,p.Q1875X*	rs141848292	NM_025137	het	6,16E-05	6,70E-05	0	0	P7		X	37	-	-
CAPN1	neurodegen	c.C1037T,p.T346I	rs192790363	NM_005186	het	1,09E-04	1,07E-04	3,36E-03	3,20E-03	P8	X		29	P	D
CHAT	neurodegen	c.C74G,p.T25R	-	NM_020549	het	0	0	0	0	P8	X		4,612	B	D
GALC	neurodegen	c.A256G,p.T86A	rs147313927	NM_001201402	het	4,02E-03	4,22E-03	2,60E-03	2,08E-03	P8	X		23	D	T
KIF1B	neurodegen	c.G4388A,p.R1463H	rs201477179	NM_015074	het	7,77E-06	0	1,23E-03	1,17E-03	P8	X		35	D	D
SOD1	ALS	c.A272C, p.D91A*	rs80265967	NM_000454.4	het	7,43E-04	6,11E-04	1,19E-02	1,15E-02	P8		X	0,265	B	T

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