SUPPLEMENTARY DATA

Patients and Controls

The 1168 SALS patients included in this study were recruited from different ALS Centres participating to the Italian SLAGEN Consortium. The SALS cohort was composed of 1119 cases and 49 individuals with concomitant ALS and FTD, while the FTD cohort comprised 203 patients (30 familial and 173 sporadic cases). All included patients fulfilled the El Escorial revised criteria for ALS and the Neary criteria for FTD diagnosis (Miller et al. 1999; Neary et al. 1998). The ALS cohort was characterized by a male to female sex ratio of 2:1 and a mean age of onset of 58.4±12.1; the FTD cohort presented a male to female sex ratio of 1:1 and a mean age of onset of 63.5 ± 9.5. SALS individuals included in the study were previously screened for *C9ORF72*, *SOD1*, *TARDBP* and *FUS* gene mutations as already reported (Ratti et al. 2012, Corrado et al. 2006; Corrado et al. 2009; Corrado et al. 2010; Del Bo et al. 2009); 78 SALS and 4 SALS-FTD patients carried a mutation in one of these genes. Mutations in *C9ORF72* or *GRN* genes were excluded in the FTD cohort considered in this analysis (Borroni et al. 2008).

The control group consisted of 1512 Italian healthy individuals (University and Hospital staff, blood donors) who did not have a personal or family history for neurodegenerative diseases.

Standard protocol approval and patient consent

We received approval for this study from the local ethical committees on human experimentation of each participating Institution. Written informed consent was designed according to the Declaration of Helsinki and obtained from all patients and healthy subjects participating to the study.

Mutational analysis

Genomic DNA was obtained from peripheral blood by standard methods. All the 3 coding exons of *PFN1* gene and at least 30bp of adjacent intronic sequences were amplified by PCR (Wu et al. 2012) and directly analyzed on ABI 3500 instrument (Applied Biosystems, Foster City, CA) using

the Big-Dye Terminator v3.1 kit (Applied Biosystems). Nucleotide numbering of *PFN1* gene mutations reflects cDNA numbering with +1 corresponding to the A of the ATG translation initiation codon of the GenBank reference sequence NM_005022.3. The initiation codon is Met 1.

Supplementary Table 1. SNP rs13204 genotype and allele frequencies in SALS, FTD and Control groups.

	ALS cases		FTD cases		Controls	
Genotype	**Genotype Frequency**	**Minor Allele Frequency**	**Genotype Frequency**	**Minor Allele Frequency**	**Genotype Frequency**	**Minor Allele Frequency**
CC	0.925	0.038	0.936	0.039	0.915	0.043
CT	0.074		0.049		0.082	
TT	0.001		0.015		0.003	

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