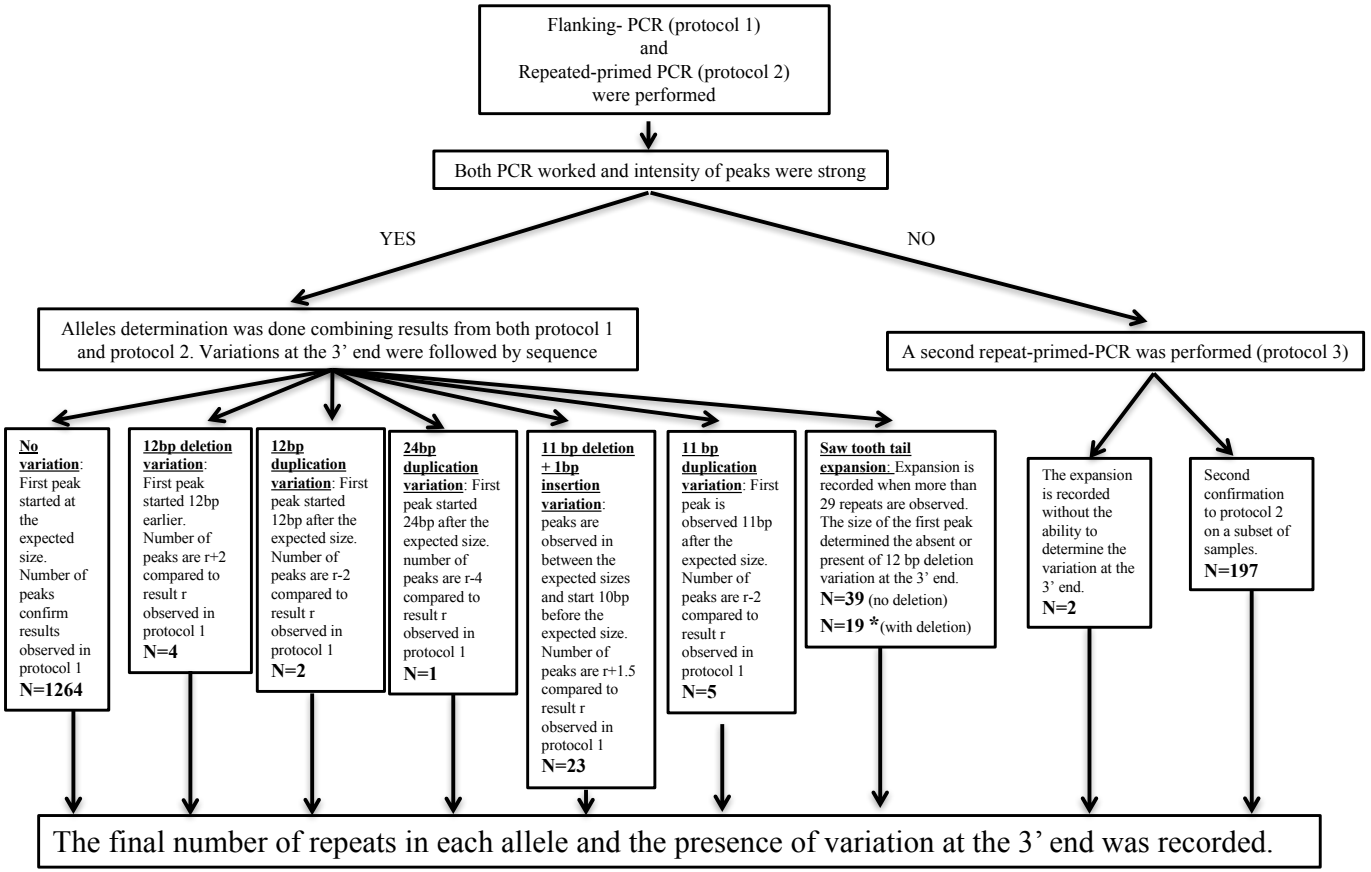
Supplement Table 1. Primers used for *C9orf72* intron 1 characterization in ALS patients and controls. **A**. Primers used for hexanucleotide repeat number determination. **B**. Primers used for genotyping sequence variations adjacent to the repeat. **C**. Primers used to genotype six SNPs that define the risk haplotype.

Primer pair #	**Primer 1**	**Primer 2**	**Anchor primer**	**Expected size (3 repeats, including anchor)- bp**
A. Primers used for determining the number of repeats.				
1.- protocol 1	6-FAM-TACTCGCTGAGGGTGAACAA	GCCTCCTCACTCACCCACT	-	241
2.- protocol 2	6- FAM- AGTCGCTAGAGGCGAAAGCCCGAC	**TACGCATCCCAGTTTGAGACG**GGGGCCGGGGCCGGGGCCGGGG	**TACGCATCCCAGTTTGAGACG**	299
3. - protocol 3	6- FAM- CAAGGAGGGAAACAACCGCAGCC	**TACGCATCCCAGTTTGAGACG**CCCCGGCCCCGGCCCCGGCCCC	**TACGCATCCCAGTTTGAGACG**	101
B. Primers used for genotyping sequence variations adjacent to the repeat.			**Expected size without del/ins (3 repeats, in bp)**	
1.	AGTCGCTAGAGGCGAAAGCCCGAC	TACTCGCTGAGGGTGAACAA	389	
2.	CCACCAGTCGCTAGAGGCGAAAG	TACTCGCTGAGGGTGAACAA	394	
3.	GCCTCCTCACTCACCCACT	TACTCGCTGAGGGTGAACAA	241	
C. Primers used to genotype six SNPs that define the risk haplotype			**rs number**	**Expected size (bp)**
1.	ccaagaaagacaagaagatgaaatgtg	acaccAtagaggctacacgcacca	rs10967965	246
2.	gcatagtcttttgcctgcctgtct	cgcaagggttgttcagagtctttt	rs1537712	376
3.	ccctgcagatcataggagaaatatca	tgaacactttcatctgcaaagctagg	rs700791	303
4.	tggtggttaatactagcatccccagt	tgcatacagagccattttcaccat	rs1982915	273
5.	gctcccatttatccagattacagca	ccatttatatcacactggcaaccaga	rs2783010	599
6.	ttgcagcctcagaaaacacagaag	cagcctacagtccagggtctcaaa	rs10967993	487

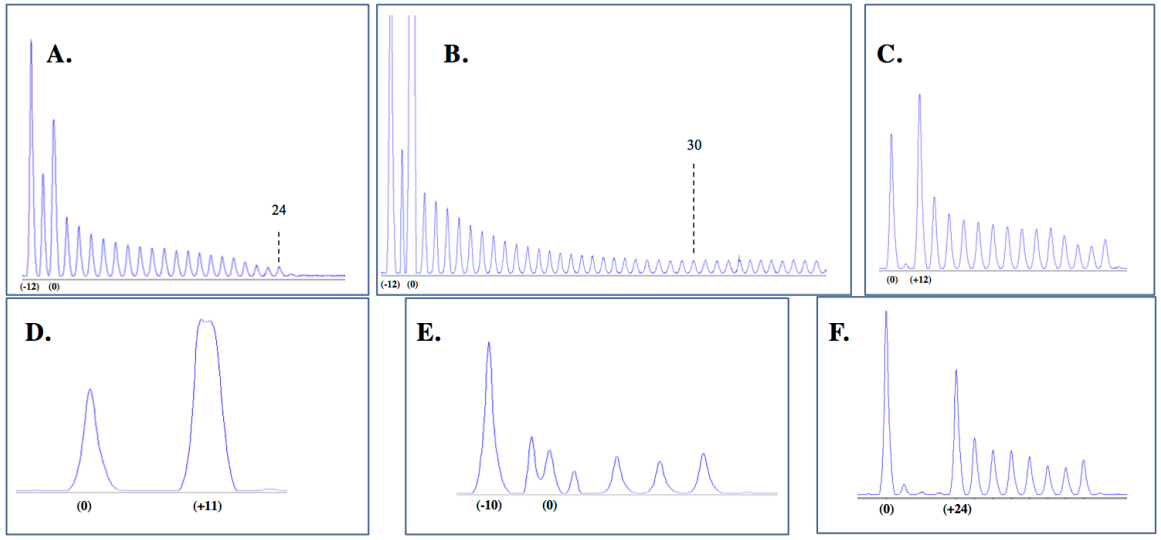
Supplement Table 2. *C9orf72* G_4C_2 hexanucleotide repeat allele distribution in the Jewish population.

Group/ # of repeats	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20**	**21**	**22**	**23**	**24**	**25**	**exp**	**# alleles**	**# individuals**
AJ-ALS	427	0	10	64	10	6	74	7	15	12	10	7	4	1	2	1	0	1	0	0	0	0	1	0	46	698	349
AJ- Controls	797	7	4	122	23	8	134	18	18	29	12	11	3	2	3	2	1	2	0	0	1	1	0	0	2	1200	600
MJ-ALS	72	1	0	26	7	0	25	1	4	3	3	0	3	0	0	0	0	0	1	0	0	0	0	0	6	152	76
NAJ-ALS (non Moroccan)	41	0	2	9	1	1	5	2	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	4	68	34
MJ-Controls	294	4	6	82	30	2	107	5	25	20	4	0	10	1	0	3	0	1	0	0	0	1	0	2	3	600	300
Total	**1631**	**12**	**22**	**303**	**71**	**17**	**345**	**33**	**63**	**64**	**29**	**19**	**21**	**4**	**5**	**6**	**1**	**4**	**1**	**0**	**1**	**2**	**1**	**2**	**61**	**2718**	**1359**

Supplementary Figure 1. C9orf72 G4C2 hexanucleotide repeat allele determination scheme. Two PCR were performed on all samples. Flanking PCR (protocol 1) uses primers flanking the repeat and has a detection level of up to 32 repeats. Repeated-primed PCR (protocols 2 and 3) can detect the number of repeats in the longest allele. Protocol 2 can also detect variations at the 3' end adjacent to the repeat. Five different variations were observed in alleles with repeats less than 30. One variation was observed in expanded alleles (12 bp deletions). N= number of individuals. * =One sample out of the 19 did not yield any PCR product in protocol 1, and had at least one expanded allele that had a 12 bp deletion observed in protocol 2. This individual most likely has two expanded alleles.



Supplementary Figure 2. C9orf72 repeat- primed PCR results reveal variation at the 3' end. Zero represents the position of the first peak from an allele with no variation at the 3' end (defined as "the expected size"). A. Twenty-four repeats are observed with the first peak starting 12 bp before the expected size. B. More than 30 repeats are observed with the first peak starting 12 bp before the expected size. C. Sixteen repeats are observed with the first peak starting 12 bp after the expected size. D. One allele is represented with one peak starting 11 bp after the expected size. E. Eight repeats are observed with the first peak starting 10 bp before the expected size. F. Ten repeats are observed with the first peak starting 24 bp after the expected size. G. The same DNA sample failed to produce a saw tooth pattern with protocol 2 (G1), but worked with protocol 3 (G2). H. Deletions, insertions and indel allele sequences and frequencies. No deletions, insertions or indels were observed in 2661 alleles carrying any number of repeats (from 2 to expansion). Five different variations were observed downstream the repeat. 12 bp deletion was observed in 23 individuals, mostly with alleles of 20 repeats or more (22/23 cases). 12 bp duplication was extremely rare (was observed twice). 11 bp duplication was observed only in chromosomes bearing 3 repeats. Indels were observed in 24 cases, rarely adjacent to 4, or 5 repeats, and more often with 8 repeats (20/24). 24 bp insertion was observed only once. In bold letters and underlined are the variations. In box are the number of repeats (r) and in parentheses the number of cases if variation was observed more than once, and the section in the figure representing that case. For two expanded alleles, in which protocol 2 failed, characterization of the variation at the 3' end is lacking.



Variation	# of repeats	Sequence at 3' end	# of alleles
Reference	GGGGCC GGGGCC (2r or higher)	GGGGCGTGGTC GGGGCGGGCCCG GGGGCGGGCCCGGGGCGGGGCT	2661
12 bp deletion	2r, 20r, 23r, 24r (A), Exp (x19,B)	GGGGCGTGGTC - - - - - - - - - - GGGGCGGGCCCGGGGCGGGGCT	23
12 bp duplication	15r, 16r (C)	GGGGCGTGGTC GGGGCGGGCCCG **GGGGCGGGCCCG** GGGGCGGGCCCGGGGCGGGGCT	2
11 bp duplication	3r (x5,D)	GGGGCGTGGTC **GGGGCGTGGTC** GGGGCGGGCCCG GGGGCGGGCCCGGGGCGGGGCT	5
Indel	4r (x2), 5r (x2), 8r (x20,E)	GGGG**G**CGTGGTC G - - - - - - - - - - GGGGCGGGCCCGGGGCGGGGCT	24
24 bp insertion	10r (F)		1
		Total	2716