

Supplementary Data

Linkage to the 8p21.1 Region Including the *CLU* Gene in Age at Onset Stratified Alzheimer's Disease Families

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Table S1
Microsatellite markers analyzed in 8p21.3-p11.21 with the 16 fine-mapping markers in bold

Marker	Location (deCODE Kosambi cM)	Start position (bp, NCBI Build v.36.3)
D8S1116	37.35	21,474,679
D8S1733	39.46	22,576,582
D8S1734	40.75	22,851,217
364H17-001N12-002H5	n.p.	24,356,916 (Build_34) ^a
398M23-45O20	n.p.	25,347,905 (Build_34) ^a
D8S1048	46.42	26,867,735
D8S1820	47.61	28,053,522
D8S1809	47.81	28,247,393
263c6-1	n.p.	28,905,395 (Build_34) ^a
29H12-1	n.p.	31,326,763 (Build_34) ^a
244L21-8557	n.p.	32,222,736 (Build_34) ^a
D8S278	53.64	32,667,932
D8S1709	54.23	33,744,523
D8S283	n.p.	33,747,507
D8S535	n.p.	33,810,144
D8S505	54.23	34,570,479
D8S1121	55.41	35,920,931
D8S1803	55.41	36,514,271
DG8S21	n.p.	37,982,718 (Build_34) ^a
D8S1791	n.p.	38,273,218
D8S515	n.p.	39,709,842
D8S532	59.76	40,907,577

n.p. marker is not present in deCODE genetic map. ^aMarker is not included in the NCBI public database Build v.36.3.

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Table S2

Primer and PCR conditions used for sequencing the coding regions including approximately 100 bp into the introns in the *CLU* gene

Amplified gene region	Primers	PCR conditions
Exon 1	F 5' AGATGGGCACGCGAGTTCA R 5' TGGCTTCCTGGGCTCCGT	95°C 10', (95°C 30'', 60°C 30'', 72°C 30'') × 16 -0.3°C/cycle, (95°C 30'', 55°C 30'', 72°C 30'') × 25, 72°C 10'
Exon 2	F 5' AGTGCAGCAGTGCCTGCTGT R 5' TGCACGCAGAGCCTGAACCA	95°C 10', (95°C 30'', 64°C 30'', 72°C 30'') × 16 -0.3°C/cycle, (95°C 30'', 59°C 30'', 72°C 30'') × 25, 72°C 10'
Exon 3	F 5' CATGCTGCTGCCTGCTGGCA R 5' TGCAGCCTCAGCATCAGCTGA	95°C 10', (95°C 30'', 64°C 30'', 72°C 30'') × 16 -0.3°C/cycle, (95°C 30'', 59°C 30'', 72°C 30'') × 25, 72°C 10'
Exon 4	F 5' AACTGGAGCAAGGGTAGGCA R 5' TACCAATGGAGCATGGCAACT	95°C 10', (95°C 30'', 60°C 30'', 72°C 30'') × 16 -0.3°C/cycle, (95°C 30'', 55°C 30'', 72°C 30'') × 25, 72°C 10'
Exon 5	F 5' TGACTGTTACAGCCATGGGCA R 5' TCGAGATGACACCCGCTGAG	95°C 10', (95°C 30'', 64°C 30'', 72°C 30'') × 16 -0.3°C/cycle, (95°C 30'', 59°C 30'', 72°C 30'') × 25, 72°C 10'
Exon 6	F 5' GCACACCTGTAGTCTCAGCT R 5' AAGCTGCATGAGGCTCAGGA	95°C 10', (95°C 30'', 62°C 30'', 72°C 30'') × 16 -0.3°C/cycle, (95°C 30'', 57°C 30'', 72°C 30'') × 25, 72°C 10'
Exon 7	F 5' CAGTTTGTGGCCATCCCTTA R 5' TGCCGTGTGATAAATGCTCAGT	95°C 10', (95°C 30'', 64°C 30'', 72°C 30'') × 16 -0.3°C/cycle, (95°C 30'', 59°C 30'', 72°C 30'') × 25, 72°C 10'
Exon 8 + 9	F 5' AGGACTTCCTTATCAGAAGCCT R 5' AGTGTTAGAGTGCAGGATCCA	95°C 10', (95°C 30'', 64°C 30'', 72°C 30'') × 16 -0.3°C/cycle, (95°C 30'', 59°C 30'', 72°C 30'') × 25, 72°C 10'
rs11136000	F 5' AGTGCTGGGATTACAGGTGT R 5' TGCCTACCCTTGCTCCAGTT	95°C 10', (95°C 30'', 67°C 30'', 72°C 30'') × 16 -0.3°C/cycle, (95°C 30'', 57°C 30'', 72°C 30'') × 25, 72°C 10'
3'UTR		
Part 1	F 5' TGGATCCTGCACTCTAACACT R 5' ATTTGGACTTCTGGGCACCA	95°C 10', (95°C 30'', 58°C 30'', 72°C 30'') × 15 -0.3°C/cycle, (95°C 30'', 53°C 30'', 72°C 30'') × 25, 72°C 10'
Part 2	F 5' TGGTGGCCAGAAGTCCAAAT R 5' AAGTAACTTTTGAACAGTGTGA	95°C 10', (95°C 30'', 58°C 30'', 72°C 30'') × 15 -0.3°C/cycle, (95°C 30'', 53°C 30'', 72°C 30'') × 25, 72°C 10'

Table S3

Identified SNPs by sequencing *CLU* in 58 AD chromosomes from 28 families

SNP	Position ^b , change	Location	Minor allele ^c	Observed MAF (%)
rs2070926	g.27523738C>G	intron 2	G	41
rs11136000 ^d	g.27520436A>G	intron 3	A	38
rs7982 ^a	g.27518398C>T	exon 5 H315H	T	30
rs28541694	g.27517925G>C	intron 5	C	25
rs3216167	g.27517690delT	intron 6	delT	29
rs3087554	g.27511359A>G	3'UTR	G	24
rs9331942	g.27511031T>C	3'UTR	C	3
rs9331945	g.27510874T>C	3'UTR	C	5
rs9331947	g.27510794T>C	3'UTR	C	2
rs9331949	g.27510603A>G	3'UTR	G	3
rs9331950	g.27510599C>T	3'UTR	T	19
rs10503814	g.27510492G>A	3'UTR	A	3

^aSNPs with strongest association to LOAD in GWASs reported by [6, 7]. ^bSNP position in bp according to NCBI.Buuld 36.3 ref.assembly. ^cAlleles were coded on the forward strand of the gene, i.e., the reverse strand of the genome.