

Supplementary Table 1: Exonic candidate variants co-segregating with AD in the analyzed family members and likely being pathogenic.

Gene name	chromosome	begin	end	refGene.aachange	ExonicFunc.refGene	SIFT_pred	Polyphe2_HDIV_pred	Polyphe2_HVAR_pred	LRT_pred	MutationTaster_pred	PROVEAN_pred	fathmm-MKL_coding_pred	MetaSVM_pred	DELPREDSUM	DANN_score	CADD_raw	Condel	GERP++_RS	Sifhy_29w_ay_logOdds	DiseaseCausalProb_ExtVarTrainedModel	IsWithinCandidateGene	LODscore	AD-PP1 interactions	
ADAM17	chr2	9666348	9666349	ADAM17.NM_001145853:exon6:c.G644T;p.1215I	nonsynonymous SNV	D	D	F	D	D	D	D	D	T	7	0.978	4.685	0.506852763834606	3.65	11.201	0.14749289300958188	N	-1.2033	ADAM17<< >MMP14,ADAM17<< >MMP9,ADAM17<< >ACE,ADAM17<< >APP,ADAM17<< >NOTCH1,ADAM17<< >FURIN,ADAM17<< >NOTCH3,ADAM17<< >TIMP2,ADAM17<< >ADAM10,ADAM17<< >NOTCH2,ADAM17<< >SORT1,ADAM17<< >TIMPSF11,ADAM17<< >MMP2,ADAM17<< >TIMP1,ADAM17<< >MMP1,ADAM17<< >NGFR,ADAM17<< >TIMPSF1A,ADAM17<< >CXCL1,ADAM17<< >BONF,ADAM17<< >NOTCH4,ADAM17<< >KL,ADAM17<< >TIMPSF1B,ADAM17<< >CXCL12,ADAM17<< >MMP9,ADAM17<< >VEGFA,ADAM17<< >ADAM12,ADAM17<< >ERBB4,ADAM17<< >MMP3,ADAM17<<-BACE1
USP34	chr2	61566815	61566816	USP34.NM_014709:exon17:c.G2501T;p.G834V	nonsynonymous SNV	T	D	D	D	D	N	D	D	T	5	0.596	2.267	0.3425097549096623	6.59	19.588	0.2455167145666326	N	0.0000	
WFS1	chr4	6293694	6293695	WFS1.NM_001145853:exon6:c.G683A;p.R228H;WFS1.NM_006009:exon6:c.G683A;p.R228H	nonsynonymous SNV	D	D	D	D	D	N	D	D	T	7	1.000	8.866	0.8332741802088592	3.45	12.360	0.13150459923806931	N	0.0000	WFS1<<->GSK3A,WFS1<<->FTIC,WFS1<<->CDH23,WFS1<<->TCF7L2,WFS1<<->LHNA,WFS1<<->TPP1,WFS1<<->ELN
TBC1D14	chr4	6925579	6925580	TBC1D14.NM_001113361:exon2:c.C464T;p.S155F,T	nonsynonymous SNV	D	D	D	D	D	N	D	D	T	6	0.997	4.829	0.37223232523863044	6.73	16.872	0.21728023875477848	N	0.0000	
GRS125	chr4	22422614	22422615	GRS125.NM_145290:exon13:c.G1703A;p.R568H	nonsynonymous SNV	T	D	D	D	D	N	D	D	T	5	0.965	6.908	0.48120971734929573	5.1	18.051	0.21279519973079794	N	0.0000	
LIMCH1	chr4	41615578	41615579	LIMCH1.NM_001112719:exon2:c.C121T;p.R41C,LIMCH1.NM_001112720:exon2:c.C121T;p.R41C,LIMCH1.NM_001112717:exon7:c.C583T;p.R195C,LIMCH1.NM_001112718:exon7:c.C583T;p.R195C,LIMCH1.NM_014988:exon7:c.C583T;p.R195C	nonsynonymous SNV	D	D	D	N	D	D	D	D	T	6	0.899	7.293	0.48865070928314363	8.24	11.422	0.16255421454386143	N	0.0000	
TNIP1	chr5	150416472	15E408	TNIP1.NM_001252386:exon12:c.G1114C;p.E372Q,TNIP1.NM_001258456:exon12:c.G1273C;p.E425Q,TNIP1.NM_001258456:exon12:c.G1273C;p.E425Q,TNIP1.NM_001252385:exon13:c.G1273C;p.E425Q,TNIP1.NM_001252380:exon13:c.G1273C;p.E425Q,TNIP1.NM_001252391:exon13:c.G1273C;p.E425Q,TNIP1.NM_001252392:exon13:c.G1273C;p.E425Q,TNIP1.NM_001252393:exon13:c.G1273C;p.E425Q,TNIP1.NM_001258454:exon13:c.G1273C;p.E425Q,TNIP1.NM_000508:exon13:c.G1273C;p.E425Q	nonsynonymous SNV	T	D	D	D	D	N	D	D	T	5	0.998	6.136	0.4660015681088525	6.53	19.470	0.1921620000290765	N	0.0000	TNIP1<<->TNFAIP3,TNIP1<<->NFKB1
DAAM2	chr6	39869131	39869132	DAAM2.NM_001201427:exon24:c.G2866A;p.E956K	nonsynonymous SNV	D	D	F	D	D	D	D	T	7	0.999	5.809	0.49086129330090683	8.63	14.178	0.1828870149983611	N	0.0000	DAAM2<<->DVL1,DAAM2<<->CELSR2	
DDHD2	chr8	38107282	38107283	DDHD2.NM_001164232:exon11:c.A1306C;p.K436Q,DDHD2.NM_015214:exon11:c.A1306C;p.K436Q	nonsynonymous SNV	D	D	D	D	D	D	D	T	7	0.995	5.304	0.6272892683247199	8.8	15.094	0.306567171410914	N	-1.2033		
ADRA2A	chr10	112838908	113E08	ADRA2A.NM_000681:exon11:c.G1355C;p.K385N	nonsynonymous SNV	D	D	D	D	D	D	D	D	T	7	0.991	4.155	0.6219595917783705	-3.02	11.443	0.15734106894419156	N	0.0000	
TSC2D1	chr13	45147304	45147305	TSC2D1.NM_183422:exon1:c.A2906T;p.D969V	nonsynonymous SNV	D	D	D	D	D	D	D	T	7	0.992	4.006	0.43350670955132221	8.16	14.974	0.177355402267678	N	0.0000		

evidence for pathogenicity deleterious parameter

D deleterious D deleterious D deleterious D deleterious D deleterious D deleterious D deleterious sum of deleteri>DANN>0.9 CADD >1 Condel > 0.5 protein disruptive GERP>3 Sifhy > 10 P>0.3 Yes LODscore>1

number of rare (MAF<0.01) exonic and splicing variants seoregating with the disease
nonsynonymous 49
synonymous 23
frameshift indel 3
nonframeshift indel 5
splicing 7