

Supplementary Table 2. *P* values and association parameters for the top 30 SNPs and their gene regions in genome wide association study of ACVIM class, sorted in ascending order of line regression *p* values

Marker	Chromosome	Position	Gene name	Variant	Allele (M > m)	MAF (cases)	MAF (controls)	<i>p</i> value (correlation/trend)	R-value (correlation/trend)	<i>p</i> value (line regression)	Slope (line regression)
BICF2G630597771	32	13650453	CCSER1	Intron	G > A	0.391	0.094	0.0001	0.562	0.00003	0.858
BICF2G630719698	1	34717853	AIG1	Intron	A > C	0.281	0.063	0.0002	0.549	0.00005	1.055
BICF2S22955672	1	31263680	ABRACL	Intron	G > A	0.188	0.031	0.0002	0.541	0.00007	1.134
BICF2G630113839	16	31910129	NRG1	Intron	C > T	0.313	0.063	0.0003	0.531	0.0001	0.891
BICF2S23654432	13	8847168	EIF3E	Intron	C > A	0.094	0.000	0.0003	0.530	0.0001	1.643
BICF2S2348307	5	21285791	ALG9	Intron	G > C	0.234	0.031	0.0003	0.527	0.0001	1.053
BICF2P344497	16	53450034	WDR17	Promotor	C > A	0.500	0.250	0.0003	0.527	0.0001	0.787
BICF2P826959	17	20219378	RAB10	Intron	A > G	0.203	0.031	0.0003	0.527	0.0001	1.189
BICF2P792699	17	20242118	RAB10	Intron	G > A	0.203	0.031	0.0003	0.527	0.0001	1.189
BICF2P635675	17	20254811	RAB10	Intron	G > A	0.203	0.031	0.0003	0.527	0.0001	1.189
BICF2P844340	17	20269538	RAB10	Downstream	T > A	0.203	0.031	0.0003	0.527	0.0001	1.189
BICF2G630597735	32	13669627	CCSER1	Intron	T > A	0.297	0.094	0.0003	0.527	0.0001	1.003
BICF2S23531583	26	29367235	ARVCF	Promotor	T > C	0.172	0.438	0.0004	-0.519	0.0002	-0.922
BICF2P1290654	6	7954357	CUX1	Intron	T > C	0.375	0.156	0.0004	0.514	0.0002	0.927
BICF2G630155016	27	44221153	CACNA1C	Intron	G > A	0.484	0.250	0.0004	0.513	0.0002	0.698
BICF2G630155028	27	44246648	CACNA1C	Intron	A > G	0.484	0.250	0.0004	0.513	0.0002	0.698
BICF2G630155029	27	44248683	CACNA1C	Intron	T > C	0.484	0.250	0.0004	0.513	0.0002	0.698
BICF2G630155030	27	44254253	CACNA1C	Intron	G > A	0.484	0.250	0.0004	0.513	0.0002	0.698
BICF2G630155042	27	44277814	CACNA1C	Intron	T > C	0.484	0.250	0.0004	0.513	0.0002	0.698
BICF2G630155011	27	44213022	CACNA1C	Intron	T > C	0.500	0.250	0.0004	0.513	0.0002	0.706
BICF2G630155032	27	44257504	CACNA1C	Intron	A > G	0.500	0.250	0.0004	0.513	0.0002	0.706
BICF2G630155044	27	44278322	CACNA1C	Intron	C > T	0.500	0.250	0.0004	0.513	0.0002	0.706
BICF2S22952579	16	31914602	NRG1	Intron	C > T	0.266	0.031	0.0005	0.509	0.0002	0.825
BICF2S23913673	32	13735479	CCSER1	Intron	A > G	0.313	0.125	0.0005	0.508	0.0002	0.964
BICF2P115550	1	36878165	EPM2A	Intron	C > T	0.359	0.719	0.0005	-0.505	0.0003	-0.733
BICF2S2335909	32	13567826	CCSER1	Intron	T > C	0.391	0.125	0.0005	0.504	0.0003	0.739
BICF2G630847123	16	14810816	ATP6V0E2	Intron	C > G	0.188	0.031	0.0006	0.504	0.0003	1.163
BICF2G630847146	16	14825580	ATP6V0E2	Promotor	C > A	0.188	0.031	0.0006	0.504	0.0003	1.163
BICF2G630716870	1	30536547	KIAA1244	Intron	G > A	0.313	0.625	0.0006	-0.501	0.0003	-0.782
BICF2G630765420	36	4140801	CCDC148	Intron	C > A	0.391	0.688	0.0006	-0.500	0.0003	-0.711

SNP, single nucleotide polymorphism; M > m, major allele to minor allele; MAF, minor allele frequency; Promotor, a variant is located 5' of a gene within 5,000 bases; Downstream, a variant located 3' of a gene within 5,000 bases.