Supplementary Table 3. *P* values and association parameters for the top 30 SNPs and their gene regions in genome wide association study of presence of MVP, sorted in ascending order of allelic *p* values

Marker	Chromosome	Position	Gene name	Variant	Allele (M > m)	MAF (cases)	MAF (controls)	OR (95% CI)	*p* value (alleles)	*p* value (genotype)	*p* value (linear regression)
BICF2S22953701	24	35459972	PREX1	Intron	A > G	0.516	0.219	4.9 (1.8–13.3)	0.00004	0.00001	0.000002
BICF2G630719698	1	34717853	AIG1	Intron	A > C	0.281	0.063	22.1 (2.9–168.2)	0.0004	0.0001	0.00003
BICF2G630847123	16	14810816	ATP6V0E2	Intron	C > G	0.188	0.031	3.5 (1.6–7.9)	0.001	0.0005	0.0001
BICF2G630847146	16	14825580	ATP6V0E2	Promotor	C > A	0.188	0.031	5.6 (1.9–16.9)	0.001	0.0005	0.0001
BICF2P677273	17	1889414	TSSC1	Intron	C > T	0.391	0.063	6.2 (2–19.8)	0.000008	0.0002	0.0002
BICF2S23028719	34	19270341	FETUB	Intron	G > A	0.156	0.031	6.2 (2–19.8)	0.0005	0.0006	0.0002
BICF2G630847762	16	15628450	PRKAG2	Intron	C > T	0.141	0.031	15.2 (3.5–65.8)	0.001	0.0006	0.0003
BICF2P389796	23	48297678	ARHGEF26	Intron	G > A	0.109	0.281	21.1 (2.4–187.5)	0.002	0.002	0.0003
BICF2G630777293	35	20097889	SOX4	Promotor	G > A	0.422	0.500	9.6 (2.2–41.8)	0.001	0.001	0.0003
BICF2P932119	4	17368888	CTNNA3	Downstream	T > C	0.391	0.125	5.7 (1.5–21.5)	0.0004	0.001	0.0003
BICF2P739518	4	17382382	CTNNA3	Intron	C > T	0.391	0.125	3.7 (1.5–9.2)	0.0004	0.001	0.0003
BICF2G630813604	16	45227982	UFSP2	Downstream	T > A	0.344	0.125	3.7 (1.5–9.2)	0.0001	0.001	0.0003
BICF2P618015	17	6196342	MBOAT2	Intron	C > T	0.234	0.063	5.9 (1.9–18.6)	0.0005	0.002	0.0004
BICF2G630460824	34	24262493	IQCJ	Intron	T > C	0.453	0.125	6.3 (1.9–20.6)	0.0008	0.0005	0.0004
BICF2P134702	4	18127172	CTNNA3	Intron	A > C	0.375	0.125	4.2 (1.6–11.3)	0.0009	0.0009	0.0005
BICF2G630765420	36	4140801	CCDC148	Intron	C > A	0.391	0.688	4.2 (1.6–11.3)	0.002	0.002	0.0008
BICF2G630576688	6	49783656	DBT	Intron	C > T	0.359	0.063	4.2 (1.6–11.3)	0.001	0.003	0.0008
BICF2G630780037	35	23781532	SLC17A1	Intron	T > C	0.156	0.031	4.2 (1.6–11.3)	0.001	0.002	0.0008
BICF2S23539509	17	2058552	TRAPPC12	Intron	G > A	0.468	0.188	4.2 (1.6–11.3)	0.00005	0.002	0.0009
BICF2G630369796	23	44154775	TM4SF1	Intron	A > G	0.531	0.375	0.2 (0–0.5)	0.001	0.007	0.001
BICF2P241728	1	24795748	LDLRAD4	Intron	C > T	0.094	0.344	23.4 (2.6–209.3)	0.002	0.01	0.001
BICF2G630155016	27	44221153	CACNA1C	Intron	G > A	0.484	0.250	16.9 (1.9–149.9)	0.001	0.008	0.001
BICF2G630155028	27	44246648	CACNA1C	Intron	A > G	0.484	0.250	17.2 (3.1–94.5)	0.001	0.008	0.001
BICF2G630155029	27	44248683	CACNA1C	Intron	T > C	0.484	0.250	17.2 (3.1–94.5)	0.001	0.008	0.001
BICF2G630155030	27	44254253	CACNA1C	Intron	G > A	0.484	0.250	3.9 (1.5–9.9)	0.001	0.008	0.001
BICF2G630155042	27	44277814	CACNA1C	Intron	T > C	0.484	0.250	5.7 (1.8–18.4)	0.001	0.008	0.001
BICF2G63069877	38	17960385	LMX1A	Intron	C > T	0.531	0.438	4.3 (1.6–11.5)	0.001	0.009	0.001
BICF2P281121	1	24617129	LDLRAD4	NMD_trans	C > T	0.563	0.250	0.2 (0–0.7)	0.0007	0.005	0.002
BICF2G630791371	1	83354309	TRPM6	Intron	C > T	0.578	0.219	0.2 (0.1–0.6)	0.0007	0.01	0.002
BICF2P1030134	17	7287630	HPCAL1	Intron	T > C	0.250	0.031	0.1 (0–0.5)	0.0005	0.006	0.002

SNP, single nucleotide polymorphism; MVP, mitral valve prolapse; 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; NMD_trans, a variant in a transcript that is already the target of nonsense-mediated decay (NMD), i.e. stop codon is not in last exon nor within 50 bases of the end of the second-to-last exon.