Supplementary Table 5. *P* values and association parameters for the top 30 SNPs and their gene regions in genome wide association study of presence of thrombocytosis, 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)
BICF2P802523	1	68048836	LAMA2	Intron	G > A	0.453	0.313	0 (0–0.4)	0.0002	0.001	0.00008
BICF2S2352812	23	38926132	SLC9A9	Intron	T > C	0.344	0.438	3.6 (1.3–10)	0.0003	0.02	0.007
BICF2S23542873	1	68063413	LAMA2	Intron	G > A	0.438	0.313	0.1 (0–0.5)	0.0007	0.005	0.0004
BICF2P254642	6	26237831	SMG1	Intron	A > G	0.359	0.313	0.1 (0–0.7)	0.0007	0.02	0.001
BICF2P1067537	6	26265164	SMG1	CDS (L1442L)	A > G	0.359	0.313	0.1 (0–0.7)	0.0007	0.02	0.001
BICF2S22951013	30	36585555	NEO1	Intron	G > A	0.188	0.281	10.1 (1.2–87.9)	0.0008	0.01	0.003
BICF2P476932	18	25561545	ANO9	Intron	T > C	0.422	0.656	14.1 (1.7–116.5)	0.0009	0.004	0.0005
BICF2P306308	27	32508403	GRIN2B	Intron	T > C	0.438	0.313	0.1 (0–0.5)	0.001	0.008	0.0005
BICF2P892936	17	34151426	MTA3	Intron	A > G	0.172	0.188	17.7 (2.1–145.7)	0.001	0.003	0.0007
BICF2P315620	17	34250535	MTA3	CDS (D240D)	C > T	0.172	0.188	5.7 (1.2–26.4)	0.001	0.003	0.0007
BICF2P1043430	17	34285735	MTA3	Intron	C > T	0.172	0.188	9.1 (1.5–56.3)	0.001	0.003	0.0007
BICF2P1090053	11	24959634	SPOCK1	Intron	T > C	0.203	0.250	17.7 (2.1–145.7)	0.001	0.008	0.002
BICF2S23353659	11	40088521	MLLT3	Downstream	G > A	0.250	0.344	17.7 (2.1–145.7)	0.001	0.01	0.006
BICF2S2321031	2	56654634	ARHGEF28	Intron	G > A	0.313	0.188	8.2 (1.6–42)	0.001	0.004	0.0005
BICF2P1465211	2	56728504	ARHGEF28	Intron	G > A	0.297	0.219	17.5 (1.9–163.3)	0.001	0.009	0.002
BICF2G630247561	33	7961740	PCNP	Promotor	C > T	0.406	0.281	0.1 (0–0.6)	0.001	0.01	0.001
BICF2G630189318	5	47834654	KANK4	Intron	A > G	0.375	0.219	0 (0–0.4)	0.002	0.004	0.0004
BICF2G630189330	5	47838346	KANK4	3' UTR	A > G	0.375	0.219	0 (0–0.4)	0.002	0.004	0.0004
BICF2P704885	6	26206588	SMG1	Intron	T > C	0.328	0.281	0.1 (0–0.6)	0.002	0.02	0.001
BICF2P423478	6	26218520	SMG1	Intron	A > G	0.328	0.281	0.1 (0–0.6)	0.002	0.02	0.001
BICF2P912268	17	34165681	MTA3	Intron	G > A	0.203	0.188	25.9 (2.4–281.5)	0.002	0.002	0.0003
BICF2G630554507	7	27893234	MROH9	Intron	T > G	0.391	0.406	12.4 (1.6–97.7)	0.002	0.007	0.001
BICF2P118756	28	29891072	INPP5F	Intron	C > T	0.344	0.375	12.4 (1.6–95.6)	0.002	0.006	0.0008
BICF2P1167338	28	29915313	INPP5F	Intron	C > T	0.344	0.375	12.4 (1.6–95.6)	0.002	0.006	0.0008
BICF2P1455766	21	10748290	NOX4	Intron	A > G	0.406	0.438	0.1 (0–0.5)	0.002	0.009	0.0006
BICF2P1167348	6	26228768	SMG1	Promotor	G > T	0.391	0.344	0.1 (0–0.6)	0.002	0.01	0.002
BICF2P399880	24	37670948	NFATC2	Intron	A > G	0.438	0.500	14.2 (1.7–122.1)	0.002	0.006	0.0008
BICF2G630583531	6	32575445	GRIN2A	Intron	T > C	0.172	0.313	49 (3.8–637.8)	0.003	0.0007	0.0002
BICF2G630584076	6	31739230	CLEC16A	Intron	A > T	0.125	0.281	23.9 (2.1–276)	0.003	0.004	0.001
BICF2S23218636	2	30464167	NET1	Promotor	T > C	0.547	0.344	0.2 (0.1–0.8)	0.003	0.05	0.007

SNP, single nucleotide polymorphism; M > m, major allele to minor allele; MAF, minor allele frequency; CDS, the variant located in coding sequence region of a gene; Downstream, a variant located 3' of a gene within 5,000 bases; Promotor, a variant is located 5' of a gene within 5,000 bases; 3' UTR, the variant located in the 3' untranslated region (UTR) of a gene.