Supplementary Table 4. *P* values and association parameters for the top 30 SNPs and their gene regions in genome wide association study of presence of leukocytosis, sorted in ascending order of allelic *p* values

Marker	Chromosome	Position	Gene name	Variant	Allele (M > m)	MAF (cases)	MAF (control)	OR (95% CI)	*p* value (alleles)	*p* value (genotype)	*p* value (linear regression)
BICF2S23731803	29	28008653	ZNF704	Intron	G > A	0.375	0.219	15.2 (1.9–124.5)	0.0002	0.001	0.0003
BICF2P360314	14	59117383	CPED1	Intron	G > T	0.203	0.313	12.3 (1.7–87.1)	0.0002	0.005	0.0009
BICF2P409762	23	46354770	AADAC	Intron	C > T	0.156	0.156	85.7 (4.6–1608.3)	0.0002	0.0003	0.00005
BICF2P158364	14	59109058	CPED1	Intron	C > A	0.172	0.313	10.9 (1.3–93.4)	0.0002	0.005	0.002
TIGRP2P178665	13	44472531	FRYL	Intron	G > T	0.484	0.344	0.1 (0–0.6)	0.0005	0.009	0.0006
BICF2P427858	18	16480966	RELN	Intron	G > A	0.359	0.531	12.7 (1.6–98.8)	0.0009	0.002	0.0009
BICF2P693293	35	17037652	DEK	Intron	T > C	0.359	0.469	6.9 (1.5–31.4)	0.0009	0.008	0.003
BICF2P192591	17	54399594	CD101	Promotor	C > T	0.438	0.406	0.1 (0–0.7)	0.001	0.02	0.002
BICF2S23642683	10	62058722	COMMD1	3' UTR	A > G	0.422	0.469	0.1 (0–0.7)	0.001	0.005	0.0009
BICF2P205119	23	51723523	RSRC1	Intron	G > T	0.469	0.375	8.2 (1.5–46)	0.001	0.002	0.002
TIGRP2P178653	13	44442703	FRYL	Intron	G > A	0.531	0.406	13 (1.8–95)	0.001	0.01	0.002
BICF2P1349041	5	22674087	ZC3H12C	Intron	T > C	0.234	0.313	17.3 (1.8–166.7)	0.002	0.003	0.0009
BICF2P686334	35	2120293	GMDS	Intron	A > C	0.250	0.094	3.3 (1.1–9.3)	0.002	0.003	0.0009
BICF2G630202095	17	49247030	DUSP11	Intron	A > G	0.313	0.313	17.3 (1.8–166.7)	0.002	0.03	0.02
BICF2P634344	4	73231391	PRLR	Intron	T > C	0.453	0.344	5.7 (1.4–24)	0.002	0.02	0.005
BICF2G630136177	37	30897806	CLN8	Intron	T > A	0.281	0.094	6.5 (1.4–29.5)	0.002	0.008	0.001
TIGRP2P118688	8	63235556	PPP4R4	Intron	C > T	0.203	0.156	10 (1.5–65.4)	0.003	0.008	0.003
BICF2P1194681	12	10053247	NCR2	Intron	C > T	0.344	0.438	10 (1.5–65.4)	0.003	0.008	0.003
BICF2P186881	18	43730865	CHST1	Intron	A > G	0.438	0.406	0.1 (0–0.9)	0.003	0.03	0.004
BICF2S23637714	31	25290094	KRTAP15-1	Intron	C > T	0.422	0.375	0 (0–0.5)	0.003	0.01	0.0008
BICF2P446760	13	38583430	LIMCH1	Intron	A > G	0.469	0.313	0.1 (0–1)	0.003	0.04	0.007
BICF2P1029983	18	16472126	RELN	Intron	G > A	0.313	0.438	14 (1.6–125.9)	0.004	0.007	0.002
BICF2G630368171	23	45718686	MED12L	Intron	C > T	0.297	0.250	14 (1.6–125.9)	0.004	0.007	0.002
TIGRP2P255581	18	46923214	NAP1L4	Downstream	G > A	0.328	0.250	6.7 (1.4–33)	0.004	0.02	0.006
BICF2S2309194	1	68658546	SAMD3	Downstream	C > T	0.453	0.344	0.1 (0–0.7)	0.004	0.02	0.005
TIGRP2P178488	13	43751269	NFXL1	Intron	G > A	0.516	0.406	0.1 (0–0.6)	0.004	0.009	0.001
BICF2P1186789	13	43753527	NFXL1	Intron	A > T	0.516	0.406	4.5 (1.2–16.5)	0.004	0.009	0.001
BICF2P878006	13	43783081	NFXL1	CDS (A604A)	T > C	0.516	0.406	16.4 (1.7–160.9)	0.004	0.009	0.001
TIGRP2P178533	13	43842335	CNGA1	Intron	G > A	0.453	0.531	5.7 (1.3–25.1)	0.004	0.009	0.001
BICF2P475301	3	50082580	AGBL1	NMD_trans	A > G	0.375	0.281	0.1 (0–0.6)	0.004	0.01	0.003

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; 3' UTR, the variant located in the 3' untranslated region (UTR) of a gene; Downstream, a variant located 3' of a gene within 5,000 bases; CDS, the variant located in coding sequence region of a gene; NMD_trans, a variant in a transcript that is already the target of nonsense-mediated decay (NMD).