Table S8 Potential transcription factors binding sites identified using LASAGNA2, assuming a threshold of $E < 0.001$ (see Methods).

SNP ID	Chr	SNP position CanFam3.1	Location relative to closest gene	Gene symbol	Gene position (CanFam3.1)	Allele	Transcription Factors (TF)
BICF2P1103910	3	60,627,895	-18,237 5'-upstream	*ADRA2C*	60,646,132-60,647,722	C	Not binding TF
						T	HNF-3
BICF2G630460099 rs23187455	34	24,997,821	intron	*ATP13A4*	24,903,358-25,015,885	T	Not binding TF
						G	CCAAT box YY1
BICF2P1348247 rs8579426	18	14,783,296	intron	*ATXN7L1*	14,764,456-14,816,374	A	C/EBP
						C	AP-4
BICF2S23653049	21	37,676,665	-756 5'-upstream	*CRSP3*	37,676,841-37,680,643	C	AP-1 COMP-1
						T	CAAT
BICF2S23056947	11	59,372,782	126,320 3'-downstream	*CYLC2*	59,233,061-59,246,462	A	NF-1 YY1
						G	ISRE Pax-2
TIGRP2P326458 rs9245895	25	19,685,756	122,854 3'-downstream	*DNMT3A*	19,492,193-19,562,902	A	Not binding TF
						G	AP2-rep
BICF2G630133149 rs23978953	37	27,776,287	intron	*EPHA4*	27,677,566-27,809,643	A	Not binding TF
						G	YY1
BICF2S2364842 rs24136831	4	39,487,456	intron	*ERGIC1*	39,436,405-39,540,037	C	c-Myb PPARalpha RORalpha2
						T	AP-1 NF-2E XFD-3
BICF2G630662694	13	32,140,606	257,806 3'-downstream	*GAPDHS* homolog	31,881,600-31,882,800	A	GATA-X
						G	HNF-4
BICF2S22912847	10	9,289,666	23,049 3'-downstream	*HNRNPA1* homolog uncharacterised in dog	9,265,652-9,266,617	C	FOXJ2
						T	AP-4 MyoD NF-1 Tal-1

BICF2S2298493	19	29,638,300	-129,385 5’-upstream	*INHBB*	29,767,685- 29,768,479	A	AP-4 Gfi-1
						T	C/EBP Gfi-1 XFD-1
BICF2S23651627	10	8,629,969	-353 5’-upstream	*LLPH*	8,630,322- 8,638,520	G	CdxA
						T	COMP-1 HNF-4 NRSF PPARG
BICF2P1396496	1	24,322,562	-65,718 5’-upstream	*MC2R*	24,388,280- 24,389,164	T/C	Nucleotide substitution does not change binding of TF
BICF2G630509420 rs23187455	24	11,907,423	intron	*MKKS*	11,900,097- 11,913,740	C T	NF-1 Not binding TF
TIGRP2P367127 rs8543245	29	33,726,769	-191,715 5’-upstream	*MMP16*	33,918,484- 34,207,979	A	GATA1 Lmo2 complex
						G	Not binding TF
BICF2G630560144 rs24457899	7	55,945,622	intron	*NOL4*	55,618,488- 56,009,178	A	AP-1 HNF-1
						G	GCNF
TIGRP2P197019 rs8772369	15	17,371,288	gene	*OR1B1* (human) homolog	-	C/T	Nucleotide substitution does not change binding of TF
BICF2S23454833	16	210,603	10,650 3’-downstream	*PKD1L1*	123,726-199,953	A	GC box
						C	Ik-3
BICF2G630842234	16	196,716	intron	*PKD1L1*	123,726-199,953	A/G	Nucleotide substitution does not change binding of TF
BICF2S2298493	19	5,405,052	-437,119 5’-upstream	*PCDH18*	4,967,933- 4,983,273	A	FOXD3 HFH-1 HNF-3 TCF11:MafG XFD-3
						G	FOXD3 HNF-3 TCF11:MafG XFD-3
BICF2P433473	19	5,365,804	-397,871 5’-upstream	*PCDH18*	4,967,933- 4,983,273	A	ARP-1 Brachyury

							CRE_BP1 ER RORalpha1
						C	NRSF
BICF2P886804 rs8850580	24	21,610,316	intron	*POFUT1*	21,608,905-21,636,579	A/G	Nucleotide substitution does not change binding of TF
TIGRP2P97765 rs8917688	7	46,745,071	365,573 3-downstream	*SETBP1*	45,951,185-46,379,498	A/G	Nucleotide substitution does not change binding of TF
BICF2P40264	31	no mapping	gene	*SH3BGR* homolog	-	A/G	Nucleotide substitution does not change binding of TF
BICF2P1363919	31	39,884,152	652 3’-downstream	*V1R* homolog	39,882,640-39,883,500	A	AP-2 C/EBP
						G	HNF-4