

Supplementary Table S4. Statistically over-represented TFBS motifs identified within the promoter regions of the genes within cluster 65.

Motif^a	Family	Raw score^b	P value^c	Promoters containing TFBS motif
Broad-complex 1	Zinc finger, C2H2	15.4	0.003	<i>Ascl2, Ccl20, Cftr, Es31, Fgf15, Fgfr4, Gm4738, Kcnj15, Mycl1, Ubd</i>
NFYA	CAAT-box	10.2	0.001	<i>Ascl2, Calcb, Cftr, Es31, Gp2, Gm4738, Rps6kl1</i>
REL	NF-κB	7.74	0.001	<i>Ccl20, Cftr, Clca2, Fgfr4, Gpr133, Kcna1, Psg18, Rps6kl1, Ubd</i>
DI 2	REL	7.43	0.002	<i>Ccl20, Cftr, Clca2, Fgfr4, Kcna1, Kcnj15, Psg18, Ubd</i>
NF-κB	NF-κB	6.87	0.001	<i>Ccl20, Clca2, Fgfr4, Gpr133, Kcna1, Psg18, Ubd</i>
NHLH1	bHLH	6.3	0.001	<i>Gpr133, Gm4738, Gulo, Ubd</i>
RELA	NF-κB	5.99	0.001	<i>Ccl20, Clca2, Fgfr4, Kcna1, Psg18, Ubd</i>
HNF1α	Homeobox	3.87	0.002	<i>Es31, Gm4738, Kcnj15</i>
TBP	TATA-box	3.63	0.008	<i>Anxa10, Calcb, Ccl20, Fgf15, Gp2, Gpr133, Gm4738, Mycl1</i>
Sox17	HMG	3.28	0.002	<i>Ascl2, Kcnj15, Mycl1, Psg18</i>
Sox9	HMG	1.66	0.01	<i>Ascl2, Ccl20, Kcnj15, Mycl1, Psg18</i>

^a, Data are presented in order of clover score, with the highest score (most thermodynamically stable pairing) first.

^b, Quantifies the degree of over-representation of motifs when compared to the background set of all mouse promoters.

^c, Probability of obtaining the raw score by chance. Values calculated by randomly sampling the background set of all mouse promoters.