

TOP hits for transcription factor with predicted binding sites in the dog genomic sequence in S9 Fig.

adjusted P (minimum)	ID	name	family
0.00211691856384277	MA0131.2	HINFP	Factors with multiple dispersed zinc fingers
0.00358247756958008	MA0471.1	E2F6	E2F-related factors
0.00879335403442383	MA0470.1	E2F4	E2F-related factors
0.0169353485107422	MA0814.1	TFAP2C(var.2)	AP-2
0.0192151069641113	MA0812.1	TFAP2B(var.2)	AP-2
0.0276827812194824	MA0003.3	TFAP2A	AP-2

For each matrix ID the minimum of the Bonferroni corrected (N=1316) p values is presented. For the detailed descriptions of predicted binding sites for each matrix ID, see S8 Table.