TABLE S4. Sequences identified with the *Genomatix* software as RBP- or TCF-binding consensus in the different promoters. The underlined sequence corresponds to the core of the motif

Gene	RBP consensus	Position from-to
EphB3	ACAATGGGAGAGTTG CTAACTTCTCACTCT	-2074 / -2088 -1721 / -1735
NOX1	ACAATGGGAAACTGG	+204 / +218
SOX9	AGAGTTTCCCAATGC	-1684 / -1698
KLF5	TGTGTGGGAAAACGT GGAGTGGGAAAAACC	-705 / -719 -670 / -684
Hes1	ACTGTGGGAAAGAAA GGAAGTTTCACACGA	-74 / -88 -54 / -68
Gene	**TCF consensus**	**Position from-to**
Jagged1	CACCCTTCAAAGGAAGT AGTTTTTCAAAGTTCCC	-1100 / -1126 -558 / -574