

Table S4. Analysis of the transcription factor-binding sites of the SNP rs80901185T>C in the promoter sequence of the porcine *HHEX* gene.

TF	SEQUENCE	SCORE	Q-VALUE	MATCHED SEQUENCE
ZBTB17	rs80901185T	10.1667	0.00684	TCGCTTGAATCCGCCTTCC
POLR2A	rs80901185C	10.7632	0.00216	GTGTTCCCACCGGGGCTACAG <u>CC</u>
CDK9	rs80901185C	8.38158	0.00452	TGTTCCCACCGGGGCTACAG <u>CC</u>
POLR2A	rs80901185C	8.40789	0.00588	TGTTCCCACCGGGGCTACAG <u>CC</u>
TAF1	rs80901185C	11.8158	0.000828	GTTCCCACCGGGGCTACAG <u>CC</u>
TAF1	rs80901185C	12.0263	0.00123	TTCCCACCGGGGCTACAG <u>CC</u> CGC
TBP	rs80901185C	9.09639	0.00558	TCCCACCGGGGCTACAG <u>CC</u> CGCT
EP300	rs80901185C	-1.44286	0.00414	CCCACCGGGGCTACAG <u>CC</u> CGC
YY1	rs80901185C	6.93421	0.00275	CCACCGGGGCTACAG<u>CC</u>CGCTTG
TBP	rs80901185C	11.0921	0.00272	CACCGGGGCTACAG <u>CC</u> CGCTTGA
YY1	rs80901185C	8.68421	0.00637	CACCGGGGCTACAG<u>CC</u>
TAF1	rs80901185C	12.5263	0.000834	CCGGGGCTACAG <u>CC</u> CGC
YY1	rs80901185C	9.68421	0.0025	CCGGGGCTACAG<u>CC</u>CGC
SUZ12	rs80901185C	10.2237	0.00345	CCGGGGCTACAG <u>CC</u> CGC
POLR2A	rs80901185C	9.23684	0.00618	CCGGGGCTACAG <u>CC</u> CGC
POLR2A	rs80901185C	9.57895	0.00538	CGGGGCTACAG <u>CC</u> CGCT
ZNF589	rs80901185C	11.0198	0.00305	GGGCTACAG <u>CC</u> CGCTTG
POLR2A	rs80901185C	10.2632	0.00456	GCTACAG <u>CC</u> CGCT
STAT3	rs80901185C	15.1714	0.000282	CTACAG <u>CC</u> CGCTTGAATCCGCCT
SPI1	rs80901185C	8.84286	0.0061	AG <u>CC</u> CGCTTGAATCCGCCTTCCAGGC

The mutation sites are highlighted in bold and underlined.