

Table S5. Analysis of the transcription factor-binding sites of the SNP rs80934526A>G in the promoter sequence of the porcine *HHEX* gene.

TF	SEQUENCE	SCORE	Q-VALUE	MATCHED SEQUENCE
TFAP2D	rs80934526A	7.86179	0.0043	TGCCTGGAGCCCC <u>T</u>
MLXIPL	rs80934526A	11.2936	0.0017	CCTGGAGCCCC <u>T</u> AGCGTGC
THAP11	rs80934526A	7.78947	0.00668	CCTGGAGCCCC <u>T</u> AGCGTGCGGG
ZBTB7A	rs80934526A	10.7576	0.00349	GAGCCCC <u>T</u> AGCGTG
ZBTB7A	rs80934526A	11.5303	0.00398	TGGAGCCCC <u>T</u> AGCG
ZNF423	rs80934526A	-1.57143	0.00205	GAGCCCC <u>T</u> AGCGTGC
FOXA2	rs80934526A	9.19737	0.000551	CGGGCCGGGGTGCCTGGAGCCCC <u>G</u> A
SP4	rs80934526A	6.28283	0.00147	CGGGCCGGGGTGCCTGGAGCCCC <u>G</u>
POU5F1	rs80934526A	14.2105	0.000435	GGCCGGGGTGCCTGGAGCCCC <u>G</u>
BRD4	rs80934526A	9.31169	0.00139	GGCCGGGGTGCCTGGAGCCCC <u>G</u>
EP300	rs80934526A	7.44156	0.000966	GGCCGGGGTGCCTGGAGCCCC <u>G</u> AGC
MYB	rs80934526A	9.96053	0.000485	GCCGGGGTGCCTGGAGCCCC <u>G</u> AGCG
FOXA2	rs80934526G	9.98684	0.000551	GCCGGGGTGCCTGGAGCCCC <u>G</u> AGCG
MYC	rs80934526G	8.44737	0.00205	GCCGGGGTGCCTGGAGCCCC <u>G</u> A
ZBTB17	rs80934526G	9.72368	0.0066	GCCGGGGTGCCTGGAGCCCC <u>G</u> AG
BRD4	rs80934526G	9.28571	0.00139	CGGGGTGCCTGGAGCCCC <u>G</u> AGC
POU5F1	rs80934526G	9.09211	0.000783	GGGGTGCCTGGAGCCCC <u>G</u> AGCG
HDAC2	rs80934526G	8.7	0.000889	GGGTGCCTGGAGCCCC<u>G</u>AGCGTGCG
TFAP2C	rs80934526G	10.9242	0.00715	GGTGCCTGGAGCCCC <u>G</u>
HDAC2	rs80934526G	13	0.000233	GTGCCTGGAGCCCC<u>G</u>AGCGTGCGGG
HCFC1	rs80934526G	7.03947	0.00742	GTGCCTGGAGCCCC <u>G</u> AGCGTGC
GTF2I	rs80934526G	7.31579	0.00757	GTGCCTGGAGCCCC <u>G</u> AGCGTGC
UBTF	rs80934526G	10.4737	0.00372	CCTGGAGCCCC <u>G</u> AGCG
REST	rs80934526G	9.07792	0.00109	CCTGGAGCCCC <u>G</u> AGCGTGCGGGCAG
POU5F1	rs80934526G	11.5395	0.000532	CTGGAGCCCC <u>G</u> AGCGTGCGGGC
TFAP2D	rs80934526G	6.0102	0.00418	TGGAGCCCC <u>G</u> AGCG
BRD4	rs80934526G	7.97403	0.00183	GGAGCCCC <u>G</u> AGCGTGCGGGCAG
RELA	rs80934526G	8.64474	0.00276	AGCCCC <u>G</u> AGCGTGCGGGCAGC
BRD3	rs80934526G	10.6842	0.00327	GCCCC <u>G</u> AGCGTGCGGG
NCOR1	rs80934526G	6.98485	0.00329	GCCCC <u>G</u> AGCGTGCGGGCA
SPI1	rs80934526G	15.0658	0.000404	CCCC <u>G</u> AGCGTGCGGGC
RUNX1	rs80934526G	10.2368	0.00258	CCCC <u>G</u> AGCGTGCGGGC
BRCA1	rs80934526G	11.3026	0.0031	CCCC <u>G</u> AGCGTGCGGG
SPI1	rs80934526G	10.8684	0.00234	CCCC <u>G</u> AGCGTGCGGG
SUMO2/SUMO3	rs80934526G	10.6974	0.000992	CCCC <u>G</u> AGCGTGCGGGC
THAP1	rs80934526G	9.52632	0.0062	CCCC <u>G</u> AGCGTGCGG
MED1	rs80934526G	9.32857	0.00618	CCCC <u>G</u> AGCGTGCGGG
RELA	rs80934526G	8.78947	0.0091	CCCC <u>G</u> AGCGTGCGG
SRF	rs80934526G	7.65789	0.00255	CCCC <u>G</u> AGCGTGCGGGCAGCTGG

NRF1	rs80934526G	11.6711	0.00236	CCC <u>G</u> AGCGTGCGGG
SRC	rs80934526G	10.1579	0.00103	CCC <u>G</u> AGCGTGCGGGCAGCTGGG
ZNF143	rs80934526G	10.1184	0.00266	CCC <u>G</u> AGCGTGCGGGCA
POU5F1	rs80934526G	9.73684	0.000697	CCC <u>G</u> AGCGTGCGGGCAGCTGGG
SMARCA4	rs80934526G	9.77922	0.00119	CCC <u>G</u> AGCGTGCGGGCAGCTGGGCAC
E2F1	rs80934526G	12.9079	0.00154	CC <u>G</u> AGCGTGCGG
NRF1	rs80934526G	11.8571	0.00214	CC <u>G</u> AGCGTGCGG
SPI1	rs80934526G	11.2105	0.00319	CC <u>G</u> AGCGTGCGG
FOXA2	rs80934526G	9.61842	0.000551	CC <u>G</u> AGCGTGCGGGCAGCTGGGCACG
RELA	rs80934526G	8.4	0.00431	CC <u>G</u> AGCGTGCGGGCAG
RELA	rs80934526G	8.82895	0.00818	CC <u>G</u> AGCGTGCGG
BRD4	rs80934526G	7.18421	0.000896	CC <u>G</u> AGCGTGCGGGCAGCTGGGCACG
HIF1A	rs80934526G	11.1327	0.00871	CC <u>G</u> AGCGTGCGG
ZBTB7B	rs80934526G	5.40816	0.00356	CC <u>G</u> AGCGTGCGGGCAGCTGGGC
NOTCH1	rs80934526G	7.27632	0.00769	CC <u>G</u> AGCGTGCGGGCAGCTGGG
SRC	rs80934526G	8	0.00158	CC <u>G</u> AGCGTGCGGGCAGCTGGGC
ETS1	rs80934526G	13.6053	0.000759	C <u>G</u> AGCGTGCGGGCAGCTGGGCA
SPI1	rs80934526G	11.7895	0.00349	C <u>G</u> AGCGTGCGGG
HIF1A	rs80934526G	12.3119	0.00389	C <u>G</u> AGCGTGCGGG
NRF1	rs80934526G	8.46053	0.0061	C <u>G</u> AGCGTGCGGG
NRF1	rs80934526G	9.17143	0.00315	C <u>G</u> AGCGTGCGG
RELA	rs80934526G	8.7	0.00749	C <u>G</u> AGCGTGCGGG
MZF1	rs80934526G	10.4079	0.0039	<u>G</u> AGCGTGCGGGCAG
EP300	rs80934526G	10.6842	0.00302	<u>G</u> AGCGTGCGGGCAGCTGGGCACGGG
POU5F1	rs80934526G	10.0526	0.000677	<u>G</u> AGCGTGCGGGCAGCTGGGCAC
HDAC2	rs80934526G	7.77143	0.00105	<u>G</u> AGCGTGCGGGCAGCTGGGCACGGG

The mutation sites are highlighted in bold and underlined.