

Table S1 Total primers used and small RNA sequence

Name	Sequence (5'-3')
DRD2-P1-F	CG <u>ACGCGT</u> CGGGGGTTGTGGAGGGATCGCT
DRD2-P2-F	CG <u>ACGCGT</u> CGGGGCACCAGCTAGTAAGACG
DRD2-P3-F	CG <u>ACGCGT</u> CGCTGGGAATGGGGGTGATGAT
DRD2-P-R	CCC <u>AAGCTT</u> GGGGCCAGGACCCAGCAAATCGG
PCR-DRD2-rs1110730503 -F	CGAGCGGGCAGAGTTTCCAA
PCR-DRD2-rs1110730503 -R	CCTCCCTCCTCGACTGAATC
PCR-DRD2-rs1107428594-F	GGAAGCTATCTGAGTGAGTC
PCR-DRD2-rs1107428594-R	CAGGATGAATCAGGAATAAG
DRD2-A/T-WT-F	<u>CGACGCGT</u> CGCAACTGCCCCATAGGGAGAA
DRD2-A/T-WT-R	CCC <u>AAGCTT</u> GGGGGAGAGTAGAGCGAGAACCA
DRD2-A/T-MUT-F	CTCCACATTTAaGTGACTTGAGACTTTTCAGCTTCTAAG
DRD2-A/T-MUT-R	GTCACiTAAATGTGGAGATGCGAAAACAACCC
IRF1-WT-F	CG <u>ACGCGT</u> CGCCATCTTAGGTCAATTCCAA
IRF1-WT-R	CCC <u>AAGCTT</u> GGGACCCCAAAGTAACACCCTAT
IRF1-MUT-F	TCgggaaCTGACCTCTTGGATGCAAAGTGC
IRF1-MUT-R	AAGAGGTCAGttcccGAGGAGCCTGGTCCAAGGAC
IRF2-WT-F	CG <u>ACGCGT</u> CGGGGCACCAGCTAGTAAGACG
IRF2-WT-R	CCC <u>AAGCTT</u> GGGGCCAGGACCCAGCAAATCGG
IRF2-MUT-F	CTCCACATTTcctgtACTTGAGACTTTTCAGCTTCTAAGGA
IRF2-MUT-R	GTacaggAAATGTGGAGATGCGAAAACAA
ChIP-IRF1-F	AGCACAGAACTAACCAAAGG
ChIP-IRF1-R	TTTGAGGAGTCAGAGTGTAG
ChIP-IRF2-F	CGAGCGGGCAGAGTTTCCAA
ChIP-IRF2-R	CGGCACATTAGGGTGTAGGA

ChIP-Non-specific-F	GGATTCAGTCTGGAAGGAGC
ChIP-Non-specific-R	GCAGGTCAGAAAATACGAGC
siIRF1-1 sense	GGGCUGAUCUGGAUUAUATT
siIRF1-1 antisense	UAUUAUCCAGAUCAAGCCCTT
siIRF1-2 sense	CUCCCUGCCAGAUUAUUGAATT
siIRF1-2 antisense	UUCAAUAUCUGGCAGGGAGTT
siIRF2-1 sense	GGGCUUAGUAAUGGAGUAATT
siIRF2-1 antisense	UUACUCCAUAUACUAAGCCCTT
siIRF2-2 sense	GCACCACUCUUUAGAAACUTT
siIRF2-2 antisense	AGUUUCUAAAGAGUGGUGCTT

Table S2 Primer sequences for transcripts used in real-time quantitative PCR

Gene	Primer sequence (5'→3')	Tm	Product length (bp)	amplification efficiency
BAX	Forward: CCGAAATGTTTGCTGACG	87	154	102%
	Reverse: AGCCGATCTCGAAGGAAGT			
BCL-2	Forward: TTCTTTGAGTTCGGTGGGG	87	195	101%
	Reverse: CCAGGAGAAATCAAATAGAGGC			
DRD2	Forward: TGGCAAACCCGGACCTCCC	87	227	105%
	Reverse: TGGGGTTCACGGCGCTGTTG			
IRF1	Forward: GTGAAGGACCAGAGCAGGAA	87	276	107%
	Reverse: TGACAGTGCTGGAGTAAGGG			
IRF2	Forward: TGGACAGCACCATTGAGGAT	88	304	108%
	Reverse: TTGGAAGTGACGAAGGTTGC			
GAPDH	Forward: GATGGTGAAGGTCGGAGTG	88	446	107%
	Reverse: CGAAGTTGTCATGGATGACC			

Table S3 The promoter prediction of porcine dopamine receptor D2 (*DRD2*) gene by Promoter 2.0

	position	score	likelihood
<i>DRD2</i>	400 (-1900)	0.545	Marginal prediction
	1800(-500)	0.577	Marginal prediction

Table S4 The promoter prediction of porcine *DRD2* gene by Neural Network Promoter Prediction

	Start	End	Score	Promoter Sequence
<i>DRD2</i>	432(-1818)	482-1768)	0.91	GGGGCGGGGCCTGTCTCAGGGGCGGGGCCCGAGGCGCCCCATGGCCCCGC
	448(-182)	498(-1752)	0.88	CAGGGGCGGGGCCCGAGGCGCCCCATGGCCCCGCCCCCTCCCTCCCGCGC
	573(-1677)	623(-1627)	0.84	CTCCGCGCCGGGTCCCTGCGCCTCACGCCCCGCCCCGCGCCGGCCCCGCCC
	584(-1666)	634(-1616)	0.81	GTCCCTGCGCCTCACGCCCCGCCCCGCGCCGGCCCCGCCCCACCCCGCCCC
	607(-1643)	657(-1593)	0.87	CGCGCCGGCCCCGCCCCACCCCGCCCCGCCGCGGCGGTCCACTGCTCCC
	636(-1614)	686(-1564)	0.82	CGCGGCCGGTCCACTGCTCCCAGCGGGTCCGAGCCGGCCGAGCGGCTGCC
	683-1567)	733(-1517)	0.89	GCCCGCCGGGGCTCTGAACGGCGCGGGCGGGGAGCCAGGGACCCGC

Table S5 The CpG islands prediction of porcine *DRD2* gene by Meth Primer

	Size(bp)	Start	End
Island 1	507	356 (-1894)	862 (-1388)
Island 2	421	874 (-1376)	1294 (-956)
Island 3	106	1391 (-859)	1496 (-754)
Island 4	115	1597 (-653)	1711 (-539)