

**Table S1. Primers for qRT-PCR**

gene	primers sequences	band length	NCBI №
Efα	GTTTATTTACCGCACAGGTTATCA ACACAGGGGCATATCCAGCA	70	NM_001087442.1
ODC	GCCAGTTCTAACAAAGAAACCCA TCTACGATACGATCCAGCCCA	93	NM_001086698.1
tbxt	CACCACCTACCTCAAGTCAGTA TTCCATTACTTATTCCTCCAGA	95	NM_001091696.1 NM_001090578.1
socs3.S	CACTCGAGAGCTGTTGATTAAATGT TCAGTTCTTCCGCACAGCAA	104	NM_001087305.2
mmp21.L	AAACAATCACCCCAAGGGCA TTGTGCTGACGACTTTCCA	105	NM_001085816.1
myf5	GATCTACAGACAAGTTTCT AATAGGGAGGGAGCATTGCT	108	NM_001101779.2 XM_018256033.2
fst.L	TGGATCTTGCAACTCCATTGT TCCAACAGTTTTGGGAGCTG	108	NM_001090590.1
frzb2.S	CTCTACCCGTAGAACAGTGCC CAAGTATTGGCTTGGAAGTGCT	80	XM_018261409.2 NM_001088556.1
tbx6.S	AGTCTATACTCCTGCAGCCCC TTCCGCTTGTCTTTGGCTG	117	XM_041578795.1
irx3	CTCGGTGTCTCTCACACAGCC ACTGTACTGGGTCGATCTGTT	104	NM_001090735.1 XM_018260411.2
cer1.S	ACCTTGCCCTTCACTCAGAATA TCGTCGATCTTGCTGATTTGGA	117	NM_001088331.2
adamts7.L	TGAAGGTTTTCTGTGTGGGA TCTGGACAGGGGCTTCTAGT	108	XM_041586924.1
shh.L	ACTGTTCTGGTCAAAGCAGAGAA GGTGCCACCAAATTCCACC	92	NM_001088313.1
gbx2.1.S	GGAGAAGATGGCAATAAGACCTACA CACGGACTGGACCCAGAGAA	88	NM_001090431.1
sfrp1	CCACGGTCACGAAAGACAGA TCAGAGCAAAGTCACTGGCG	97	NM_001087488.1
foxc2	GGGACAGACTGCTGCACCCT AAAGTCTGCTGCTGGGAGCC	90	NM_001096491.2 NM_001090451.1
lef1.S	GGGCCGGACCTACCTACATT CATATGGTGTGGATACCAGCC	87	NM_001096734.1
nalcn.S	GATTACCAGCTGGACGGTCA GTCTTGTCACCATTCTTCACA	105	XM_041584261.1
tbxt.2.S	CTGGTTACTCACAGTTGGGCA GATGGTATTGGCAGTGGCCC	103	NM_001085559.1
gsc	AGAGAGGAAAAAGTAGAGGTTT TCCACTTTTGGGCATTTTCTG	100	NM_001087809.1 XM_018230459.2
cd82	GCCGTGTACAAAGCGGGCT ACTCCCACGCAGACTCCCA	87	NM_001092348.1 NM_001091678.1
prss81.4.S	ACTTGGGCCTCCTTGGAATTT TGAAGGTGGGTTTGTGCTGG	109	XM_041577978.1
otx2	TGGGGGTATGGACTGTGGAT CTGGTTAAGGTGACTTGCTACT	117	NM_001090691.1 NM_001091486.1
LOC108716930 (tmem116)	ATTACTGCTGACCAACGGAA CACCCCATCAGGACCAGAA	119	XM_018263523.2
apobec2.L	CCGCTGCACTTACATTTGGA CGCTGTAATGTCAACAGCCC	113	NM_001092842.1
tnfrsf12a.L	CCGCAGGAAAAGCAAGTTCAC GTCCTATAGCTGTGACCTCTCG	102	NM_001090171.1
fbn3	AACTGCTTCCTGCAGTGTG GGATGGATACAGCATTGTGT	107	XM_041579837.1 XM_041579835.1
LOC108700343 (DDB_G0277449)	GCCCCGACTCAACTCATCA GACACATAACTCACCTGTCCAA	100	XM_018233450
foxc1.S	TCCTCCTCATCCAAAATGTCC TTCCGAGTTTAACTGTCCCA	93	NM_001088214.2

six3	GCCGCTAAGAACAGGCTTCA CGTCGAAGGAGACTCGGC	105	XM_018265033.2 NM_001085702.1
otx1.S	AACTGACCTCACTGACCCCG TAACGGGTCTTGGCGAACAG	95	XM_041564173.1
aplnr.S	GCTTCTTATCCTTATGTACTGTGCC TGTTAAGGCTCCCCCTCTCT	117	NM_001086378.1
frmpd1.L	CACAAACATCTCCAGGTTCAAA TTTTGAGTTTCTCTGGTGCCT	102	XM_041562636
cebpa	TGTTCTGGAAAAATAAAGAAATGCC AAAACAAGGATATGCGGTTGT	87	NM_001086806 NM_001091687
col9a1.L	GCCAAGGACCTGCTGGTAG GATTCAGGCCGACGTAGACT	112	NM_001093327.1
LOC121394313	GGATGCGGCTTTCCTGAGAA GGTGTAATGGAGGGGAGTGG	120	XR_005961647.1
angptl4.L	GAAGGAGAAAAGTCCAGCGGT AACAGTCCACCCTGCATCTGA	99	XM_018255009
xmc	GGATACCCTTTCCCCAACTGA TGGACAATTCTGCCTCCAGC	120	NM_001088686.1
chst3.L	CCTAAGGCAGCAGTGTGTGG CACACGGTCTGTGTTTATCTTGT	98	XM_018225493
neurog2.L	GACTCGACCCAACTCACCTG TGTCGCAAGTGACAATGCTG	94	NM_001088333
serpinh1.S	CAGCCATGATCTCCAGAAACA TGGCCAGGTAGAGGTCCTTC	110	NM_001086790
bmpr1b.L	CGATGCATATCGGGAGGTATACTA TGTGGGCCGTAATCTCCTG	120	XM_041590765
stx1a.L	CACCTACAGAAGAACAGGGTGA TGACTGCCTTCTTGGTGTCA	105	XM_018246184
nek5.L	GCTCCGAGACTTGTAGAAGGG AACTTTACTCCACCCTCAGC	110	XM_018247613
cdx4	AAGACTCTCTGAAAGACAGGTAAA CTCTGCACAGAACACATGCC	111	NM_001087251 XM_018232950
ankfn11.L	ATCATCTCATTGACTACTTCCCA CGGAGCAGGAATGAGATCTGT	85	XM_041577568
ccn11.L	CTGCTGCCTGTCATTGGGAT GCAGGAGGCTTCCATCAGTT	108	NM_001091541
gypc.L	TGCTTGTGGATCTGCCTGAC CATTCTCTGCAGGTGGCGTT	116	XM_041576187.1
itga2.L	AGCCTGGAGAGAAATCGGAA GAAGAAGCCGAGCTTCCACA	110	XM_018266172.2
cdx1.L	CAGACATCCAGCGCCTTG ACCAGATTTTTACCTGCCGT	120	XM_018251931.2
kctd12.L	AGCACTGGAATGGACAACCT GCTCCCAGAATCCCCAACA	97	NM_001094975
hes3.L	AGAGAAAGCTGGAGAAAGCAGAT TGTACAGTTGAGTTCCGTGAATA	90	XM_018226118.2
gpx3.S	AGATGGGGCTCAAACCTAGGG AGTTGTAGCAATCCACCGATTTT	105	NM_001092673
snai2.L	CGCACTGAAAATGCCACGA ATGGGGAGATGATCACTGTATGG	104	NM_001086282
helq.S	GTCAAACCTGTAAAACTAGTGCAGA GAATTTTGACAGACACATGCCA	113	XM_041579752
chad.L	CCACCCTACAGAGCCTAGCA CTGCCATCTATCCACCTCCG	85	XM_018235299.2
ppp1r9b.L	CGCTACAAGAGAAGGTTGCAG ACAAGCAGTAAGCACCACCA	120	XM_018234825.2
neurog1.L	CACACGAGCTCATTGCACAG TCCATGTTGGAAGCCATTATCA	113	XM_018252019.2
c2orf50.L	CCGAGTGCCAAGGAGAAGG TCCCCAATTCTCATGCCAGC	120	XM_018264012.2
LOC108701132	AGCAGCAAGAGACCGAGATG CTGGATTGCACTTGATGCCG	99	XM_018235361.2

LOC108696684 (interleukin-11)	AATCATACCACAACCTTTAAAGCCA ACAGCATTTCATTGAGACTACAGG	85	XM_018226270.2
tshb.S	CCCTGCCCCAAAAGAGAACCA AAACACACACGAAAGCAGGC	91	XM_018249167.2
LOC108699267 (neuropeptide Y receptor type 2)	CGGAAGGCAACATCCCATAAG GCTTCAGACATCCTTTGCACC	112	XM_018231250.2
tbx6r.L	GTGTGACGGGCTACAGGTTT GAAGTTGGGCCCCAGAGAG	101	NM_001097074
LOC121398071 (histone H2A type 1-like)	TCACTATCGCTCAGGGTGGA AGCTCACTTGCTCTTAGCCG	95	XM_041576621.1
LOC108702520 (Hox-B8)	ATGAGACCACAAGCCGCC TTTCGGGTCAGGTAGGGGTT	107	XM_018238034.2
ddit3.L	CCAGTTGTTTTAGAGCAGGAGA TGTCCACGAGCAAAGGAGAC	91	NM_001089166
acsbg2.S	CTCTCAAAGAGCAGGTTCCA TGTCTGCATTACATTGCACTTA	105	XM_041579918
jam3.S	AGGACAAATGATGAGGGCGA GTTAAGAGAGGAGTGGCGGG	100	XM_018227682.2
fstl1.L	GAGCTGAGACCCAAGTCCAA ATCCCCCTCCTTCCCTTAC	92	NM_001095580
hgf.S	GAAGTACAAGTGCAAGGATCTGA TTATCTGTGAGCAGTGCCAATACG	116	XM_018255753.2
rgs20.L	GGATGGCGTGTGAAGACCTC GGAGTCCAAGCTGACCTCTTT	119	NM_001093411
slc25a12.L	AGACCACCTACACTGGGGTT GCGAAACACTCGAGCTCCT	98	NM_001091799
gcnt1.L	TTTGGCTGTCATTGTGGTCC TGACGAATGGCACGAAGTGA	115	NM_001087338