

Supplementary data

Synthesis of gene primers

Table S1. Primer sequence information.

Primer name	species	Forward Primer(5'-3')	Reverse Primer(5'-3')
<i>ACER2</i>	canis	TCCCTAATATGCAGTGAAAATGCAA	AGGTGCATTTGAAGGTCCCA
<i>ANXA9</i>	canis	CAGACCACACAGAAGCTGGT	TCCTTTGGGTACATGGGTGC
<i>APBB1IP</i>	canis	GGTGAGTCCAACGACGACAT	CAGCTCTGGGTGGTTTGGAT
<i>CLDN1</i>	canis	CGCGGTACCCCGTC	CAGGAAGGCCAGCAGGAAG
<i>CYP1B1</i>	canis	TCACCATTCTCATGCCACC	AGAACCGGGCTGGATCAAAG
<i>CYTH1</i>	canis	GACGACAGCTACGTTCCCAG	CTGCCCATGGCTACCTGTTT
<i>DDR2</i>	canis	GGGTAGGGTTCCTGCAAACA	CAAGCCCACAAAAGTGAAGC
<i>DNAJB6</i>	canis	GATCAGTCAGCGTAGGGACG	AGAGTTGAAAAGGAGCCGGG
<i>DPP4</i>	canis	GCACCTCAAAACAGCATGTCA	TTGCGAACACAGAAGTCCCT
<i>DSG3</i>	canis	TCAAGGAGCTTCCGCTTTGT	GGTTGCACGAGAGAACCAGA
<i>FOCAD</i>	canis	AGTGGCACCGTGCAATTTTC	AGTTGCAAGTCCAGCTCTCC
<i>HAS2</i>	canis	GTGGAGTGCGAATGTGGAGA	GGCATGCTGTGTGTTTCGTT
<i>ITGA6</i>	canis	GTGCATAACCGACCAGGGAA	CTGGGGAAGGGCAAAGAGAG
<i>ITGB8</i>	canis	AAGCGTTTGCACAAGAGCAG	AAGTGGACAACCAGCAACCA
<i>ITPKB</i>	canis	TTGCTATGGCAAGGTCTGGG	CCCCAATCTGCTGGGGATTT
<i>MOG</i>	canis	TGCCATGTCGCATCTATCCC	TTACCTTCCCCTCGCCATA
<i>NID2</i>	canis	ACAGCGGCCAGTTTACTGAT	ATTTACTTTCTTCTGCTGGGC
<i>NPNT</i>	canis	CCAGGATAAGGTGCCAGCTC	TGTGGCTTGATGATCCAGGG
<i>NTN1</i>	canis	CCTGCAAGTGCCCCAAAATC	ATCACCAGGCTGCTCTTGTC
<i>ONECUT1</i>	canis	AGCACAGGTCAGCAATGGAA	CCGGAATTGAGTTTGCTCCA
<i>PLPP3</i>	canis	TCTTGAACGTCTGCAACCCCT	GGACACAAAAGAAAACCAACAA
<i>PSEN1</i>	canis	TGGCGGCAAGTGAAGAGTAG	GGGGTGCAGGTAAGTCTGTC
<i>TJP2</i>	canis	AGCTGTCCGAACACTCGAAG	GTTCAAGTCCCACATCTCCG
<i>VAPA</i>	canis	GCCCACCGACCTCAAATTCA	TAGGCCTCACACAGTACCGA
<i>VAV1</i>	canis	GGCCAGGGCCATAGCAATAA	GTTCTTAGCACCTGGCATGA
<i>WDPCP</i>	canis	AATGACAGCCCAGAATGGCA	ACCACAGGTGCAGTTCACTC
<i>ARFIP1</i>	canis	CGTGATGCAAACACTCTGCC	CAGCAATGGCGTTGTGGA
<i>BCAS3</i>	canis	TTGTGGGATCCGGAACAGGG	CCATCCCGAACACCTGCTTT
<i>FLRT2</i>	canis	CTGGAAACGCACGTGAACAA	CCTACCGGGGAGGGAACATA
<i>SNAI2</i>	canis	GGACTCTTTAGGTCGCTCGG	CGGTAATGGGGCTGTATGCT
<i>ERBB3</i>	canis	GGGGGTAGAGAATGTGTCCC	GAGCACGATCTCGAGGTCC
<i>STAB2</i>	canis	GCGGACATAGGAAAAGCCCT	ATGATTCCAACGACGCCAGA
<i>EPHA1</i>	canis	ACATTCTGCACTTCCGCTCA	GGGCTCAGTCCTTGAATCCC
<i>SMAGP</i>	canis	GTTTCTGTGGCTGCCCAATG	CACTAGTTGACCAGGCAGGG
<i>AKAP12</i>	canis	GATGCCCTGGTGGAGTAACC	CTCCTCCTGCCCATCCTTTG
<i>EFNA5</i>	canis	CTGTGAAACAACCCCCAGGA	GAGCCCTGTCTTGGGGAAAA
<i>LIMS2</i>	canis	AAGGAGGTGGAGTGGTGACT	GAAGAGCCCCCTCAGGGAATG
<i>DENND6A</i>	canis	AGTCATCTTAGCTGTGGGCA	CGAAATGGAATGCGGGGACT

<i>VPS33B</i>	canis	ATCGGATCGCCAATGTCTCC	CGCATGTTCTTGATGCGAGG
<i>BCAS3</i>	canis	TTGTGGGATCCGGAACAGGG	CCATCCCGAACACCTGCTTT
<i>STX16</i>	canis	CCAGTTAGTGCTGGTGGAGC	ATCAGGACCCAAATCCCTGC
<i>APBB1IP</i>	canis	GGTGAGTCCAACGACGACAT	CAGCTCTGGGTGGTTTGGAT
<i>AKAP12</i>	canis	GATGCCCTGGTGGAGTAACC	CTCCTCCTGCCCATCCTTTG
<i>TNS2</i>	canis	GGAATGTTCCAGGCAGCAGG	AGTCCCTCACCTGGTAGTT
<i>CNN3</i>	canis	GAACAGGAACGAACGGGTCT	TCGCCGTATTGGTAATCCCG
<i>SPINT2</i>	canis	GTGCCGGGGCAATAAAAACA	GGACCACCACTTTAGTGCCA
<i>LYPD3</i>	canis	TGACTGCAGCGAATGTGACT	CAGGACAAGGGGTGGGATTC
<i>GCNT2</i>	canis	AAACAGCTCTTGGGGCAACT	GATTCTTTTGCTGAAGCGGC
<i>GRB7</i>	canis	AAAGTCGGGACACCCTCCTA	GGGTCCGAAGTCTGGTTCTG
<i>TEK</i>	canis	GGCCCAAGCCTTCCAAAATG	TCCTTCTTGATGCGTGCCTT
miR-175	canis	TGGCAGCCGAGCCCCGAC	AGTGCAGGGTCCGAGGTATT
miR-123	canis	TGCCCCGCCGGGTCGGCCG	AGTGCAGGGTCCGAGGTATT
miR-371	canis	ACTCAAAAAATGGCGGCACTTT	AGTGCAGGGTCCGAGGTATT
miR-172	canis	GCGCCCGGGGAAGCTAGCCT	AGTGCAGGGTCCGAGGTATT
<i>U6</i>	canis	CTCGCTTCGGCAGCACA	AGTGCAGGGTCCGAGGTATT
<i>GAPDH</i>	canis	GAACATCATCCCTGCTTCCA	CAGGTCAGATCCACAACCTGATAC

Table S2. All the valid URLs of the bioinformatics analysis software.

Software	URL
SOAPnuke(1.5.0)	https://github.com/BGI-flexlab/SOAPnuke
cmsearch (1.1.2)	https://omictools.com/cmsearch-tool
miRDeep2 (0.1.3)	https://github.com/rajewsky-lab/mirdeep2
Piano	http://ento.njau.edu.cn/Piano.html
DEGSeq(v1.36.0)	http://bioinfo.au.tsinghua.edu.cn/software/degseq/
RNAhybrid(0.1)	https://bibiserv.cebitec.uni-bielefeld.de/rnahybrid
miRanda (V22)	http://www.microrna.org/microrna/home.do
TargetScan (7.1)	http://www.targetscan.org/vert_72/
Mfuzz(2.60.0)	http://www.bioconductor.org/packages/release/bioc/html/Mfuzz.html
HISAT2(v2.2.1)	http://www.ccb.jhu.edu/software/hisat
Bowtie2 (v2.4.5)	http://bowtie-bio.sourceforge.net/Bowtie2/index.shtml
RSEM (v1.3.1)	http://deweylab.biostat.wisc.edu/rsem/rsem-calculate-expression.html
GO	http://geneontology.org
KEGG	http://www.kegg.jp/kegg/rest/keggapi.html
WGCNA (v1.71)	https://labs.genetics.ucla.edu/horvath/CoexpressionNetwork/Rpackages/WGCNA