

Supplementary Material

Nutritional status affects the microRNA profile of the hypothalamus of female sheep

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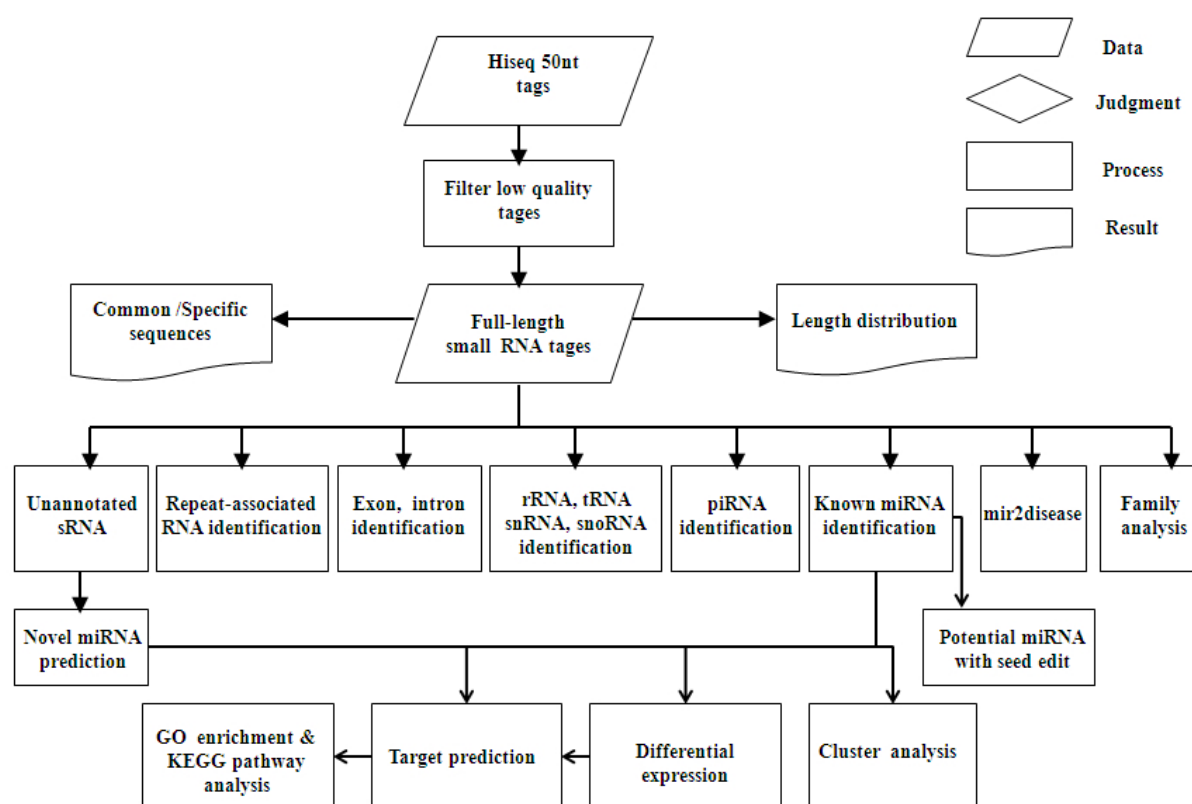
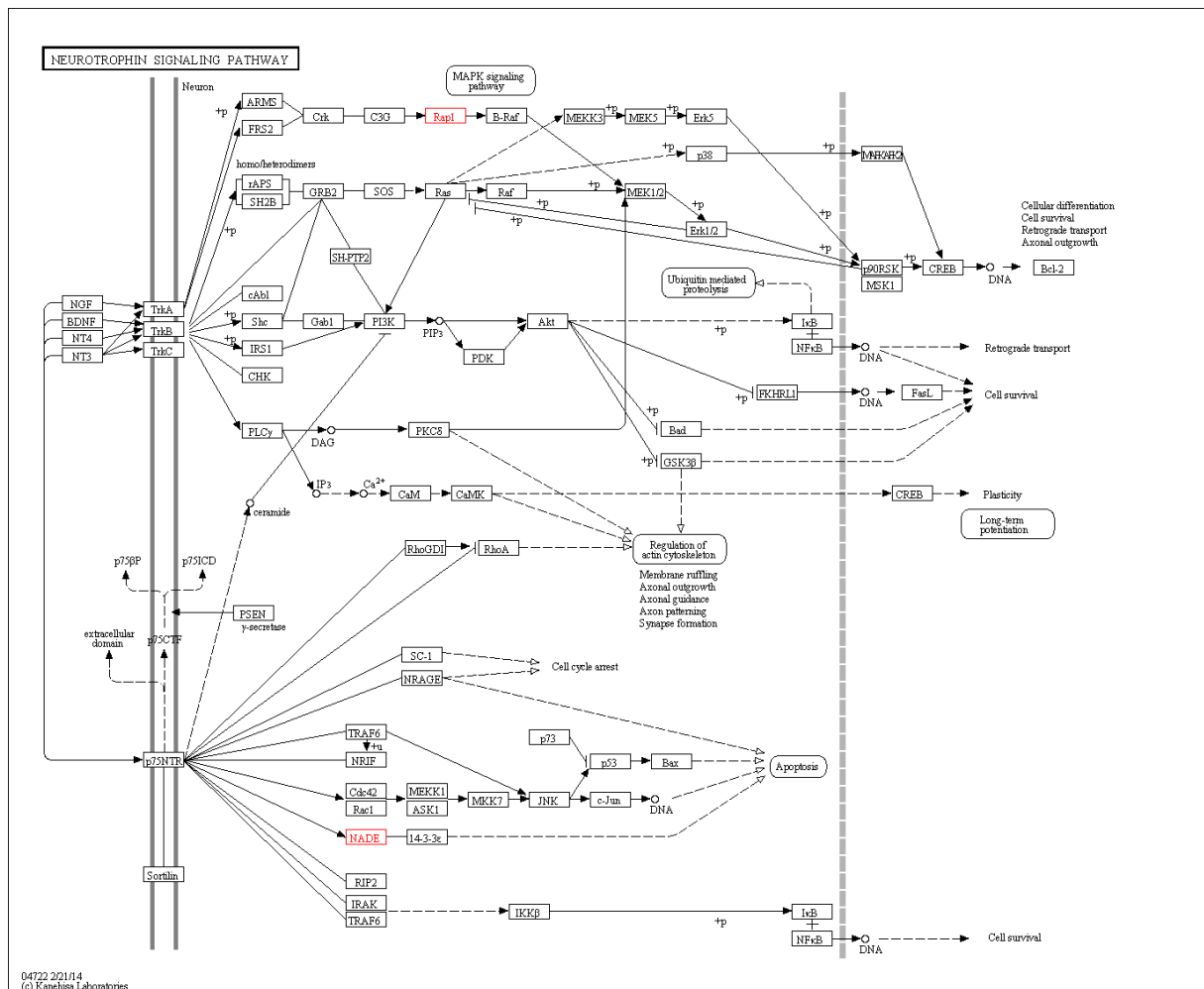
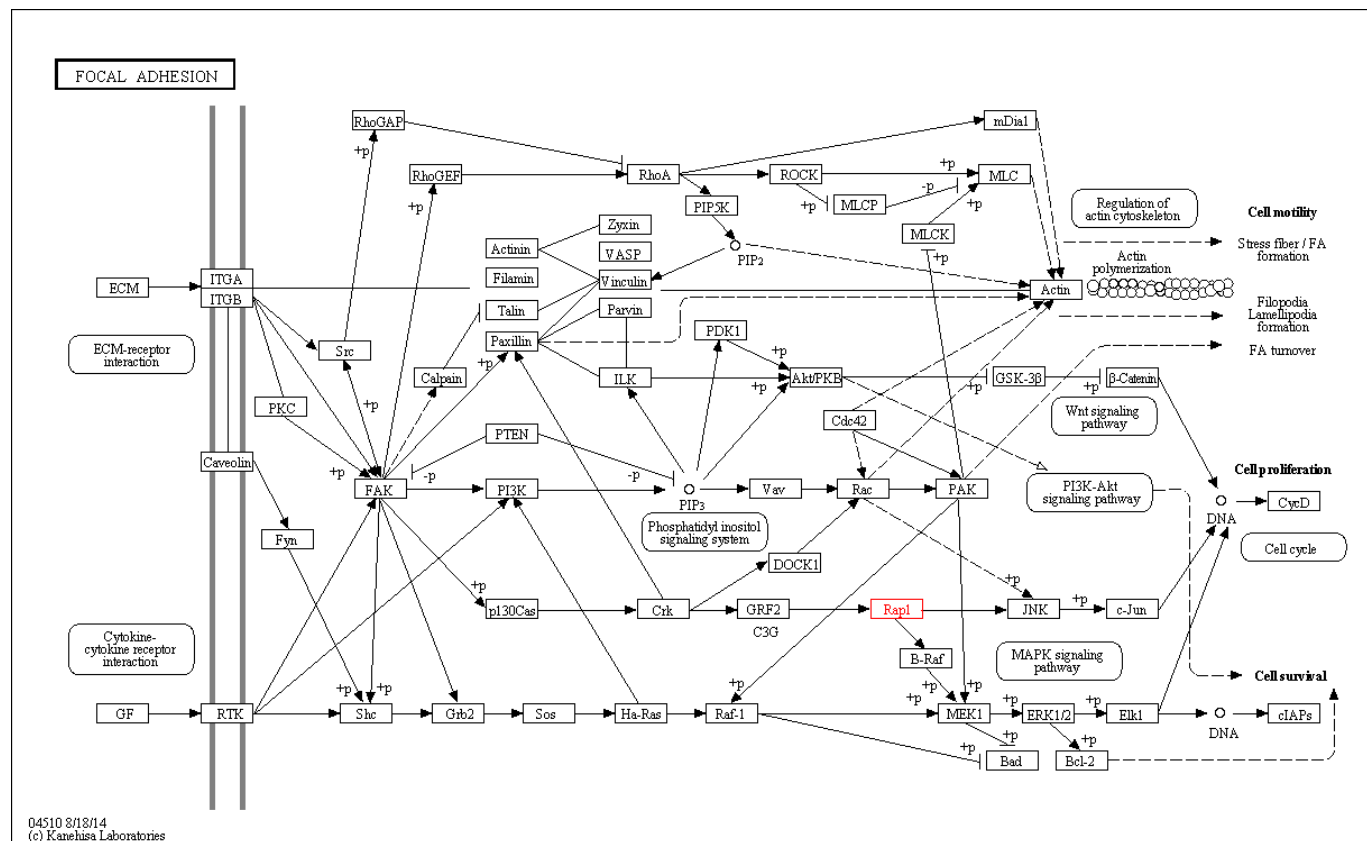


Fig. S1. Data analysis process.

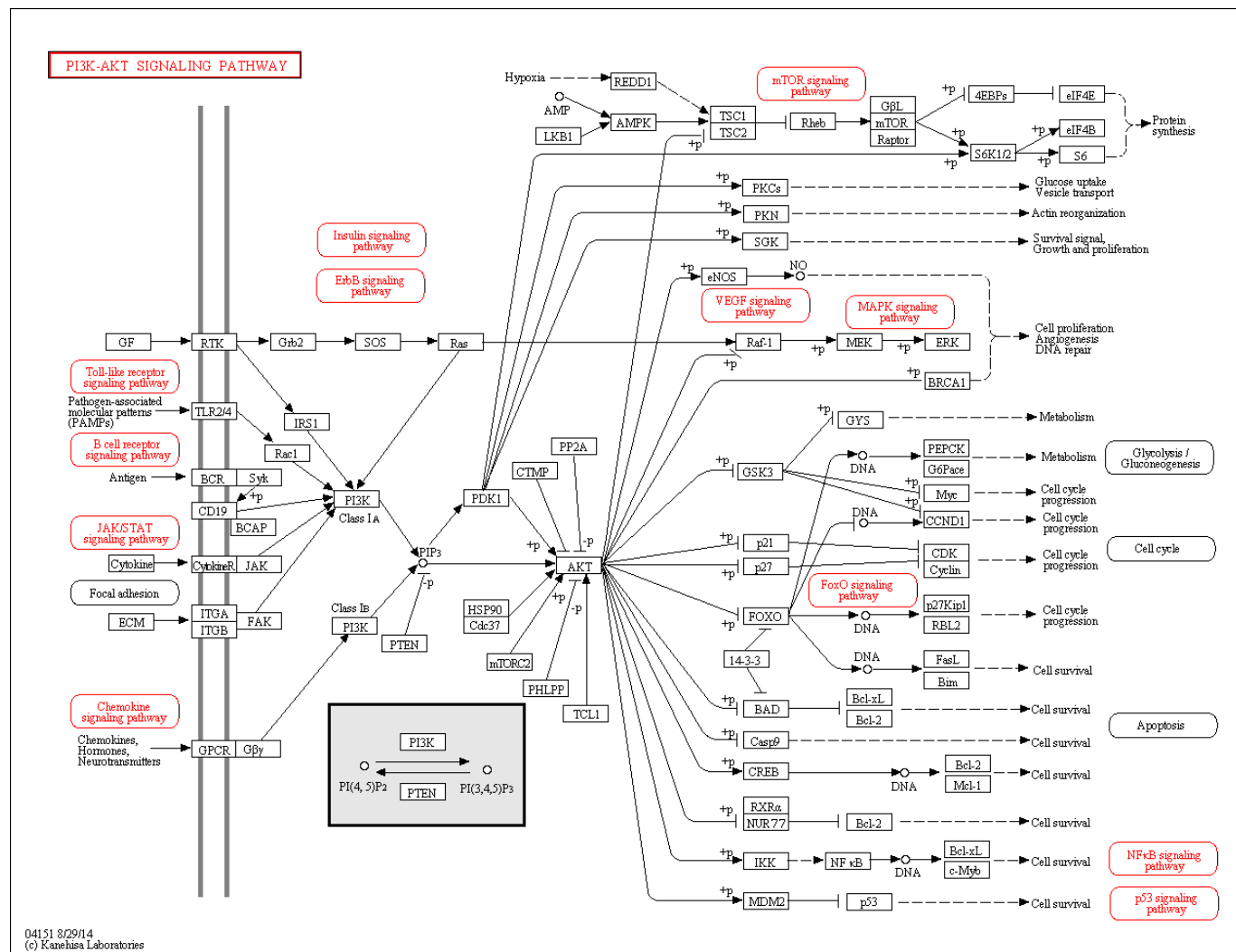
Fig. S2. The most enriched KEGG pathways of target genes for differentially expressed miRNAs in estrous sheep. The pathway map was downloaded in KEGG database (<http://www.genome.jp/kegg/>).



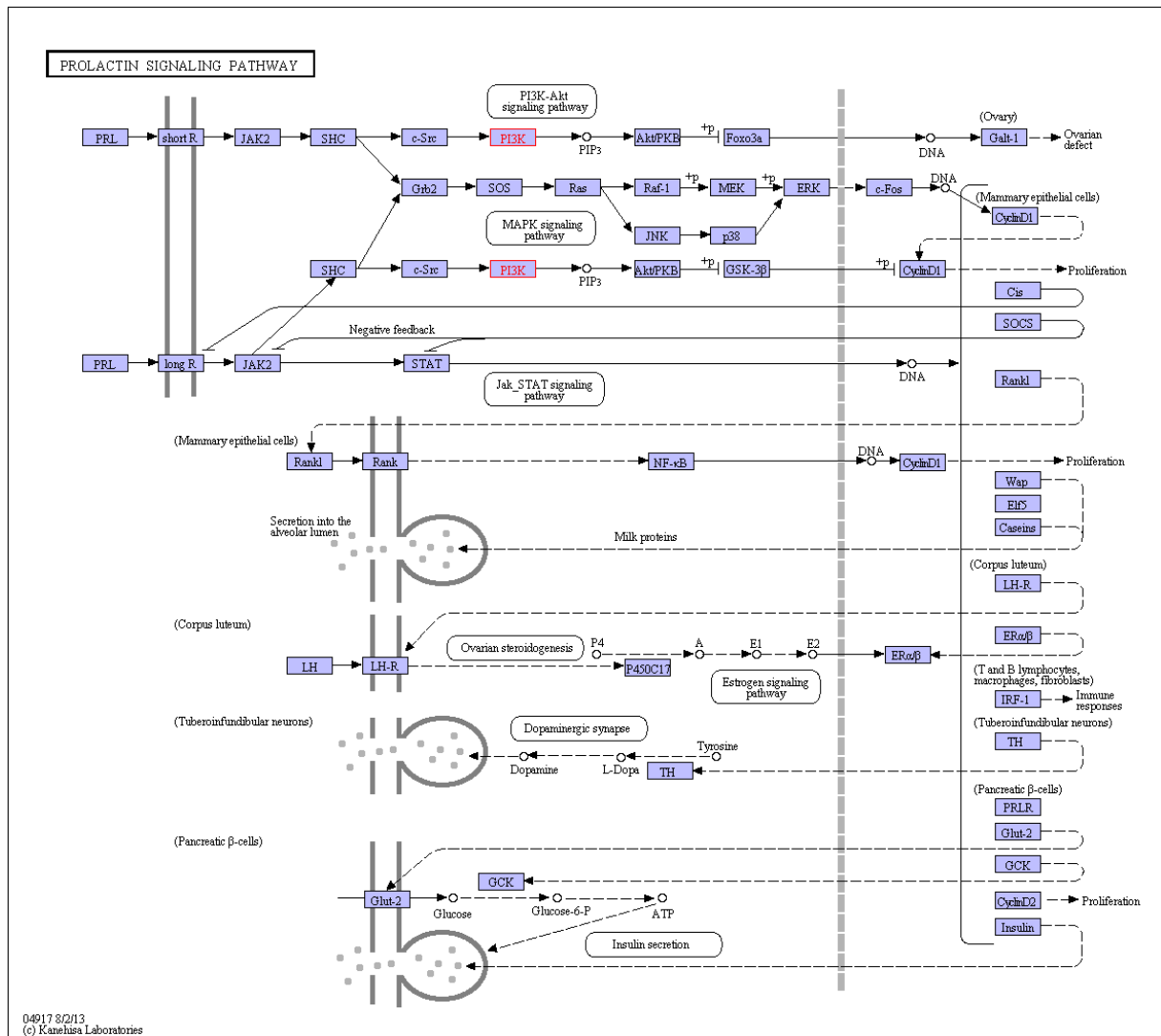
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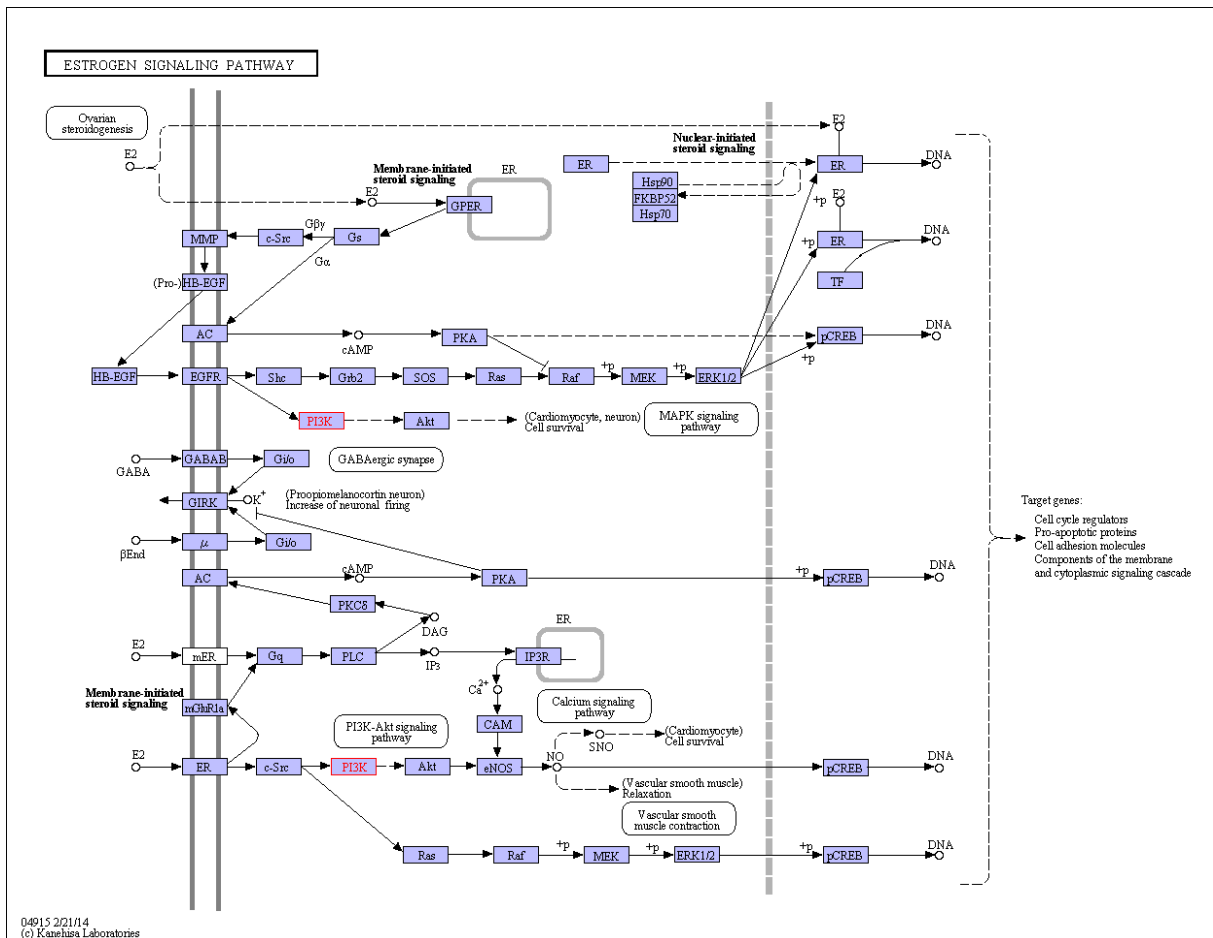
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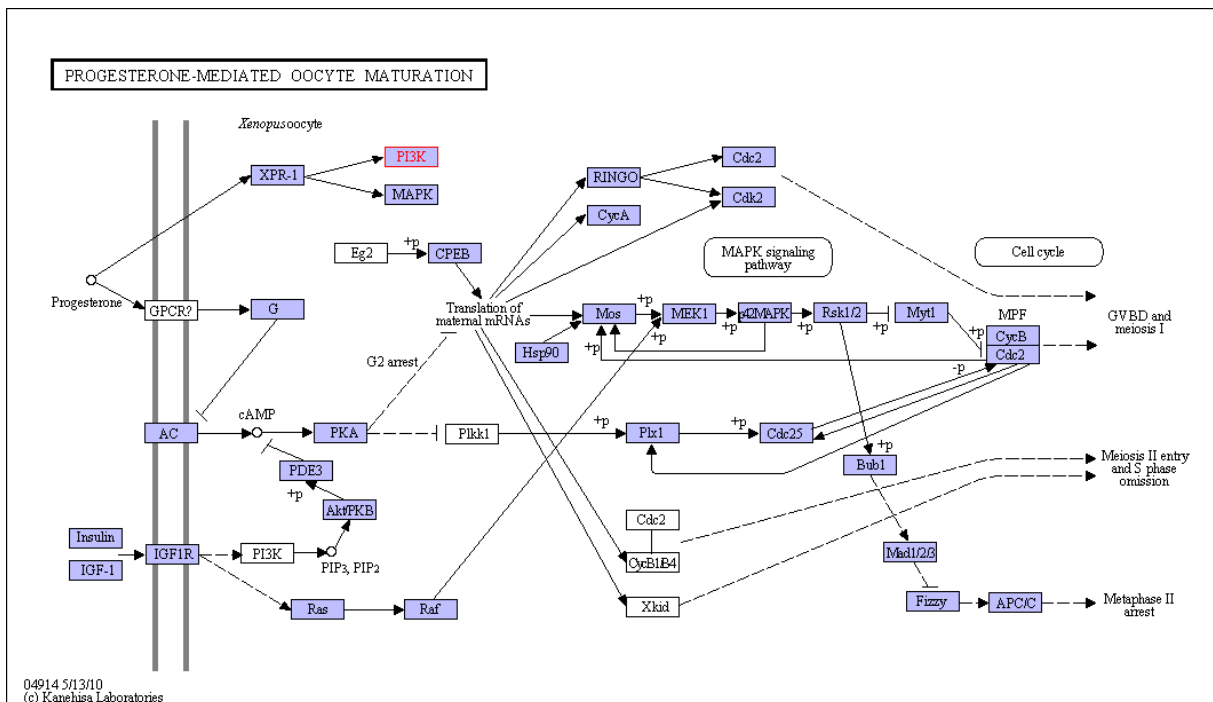
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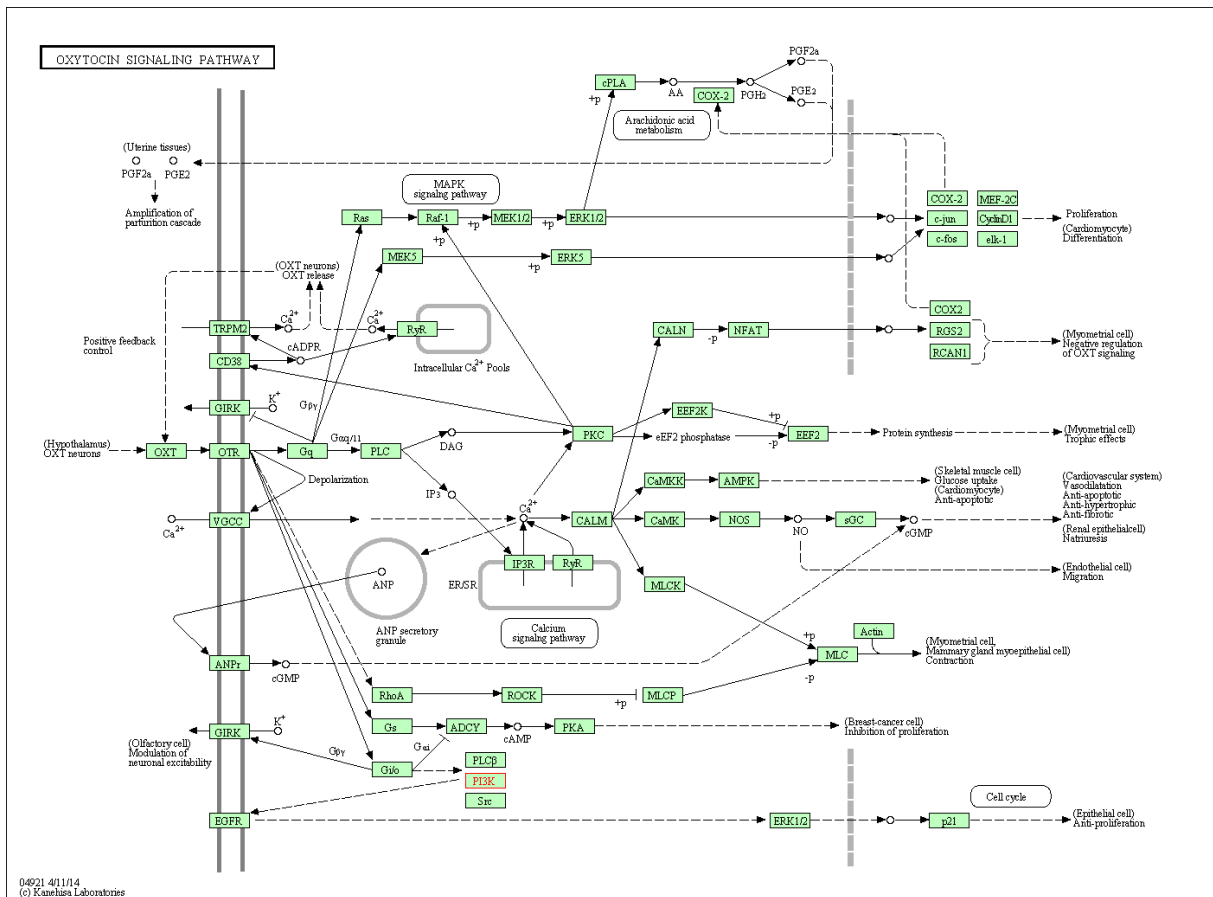
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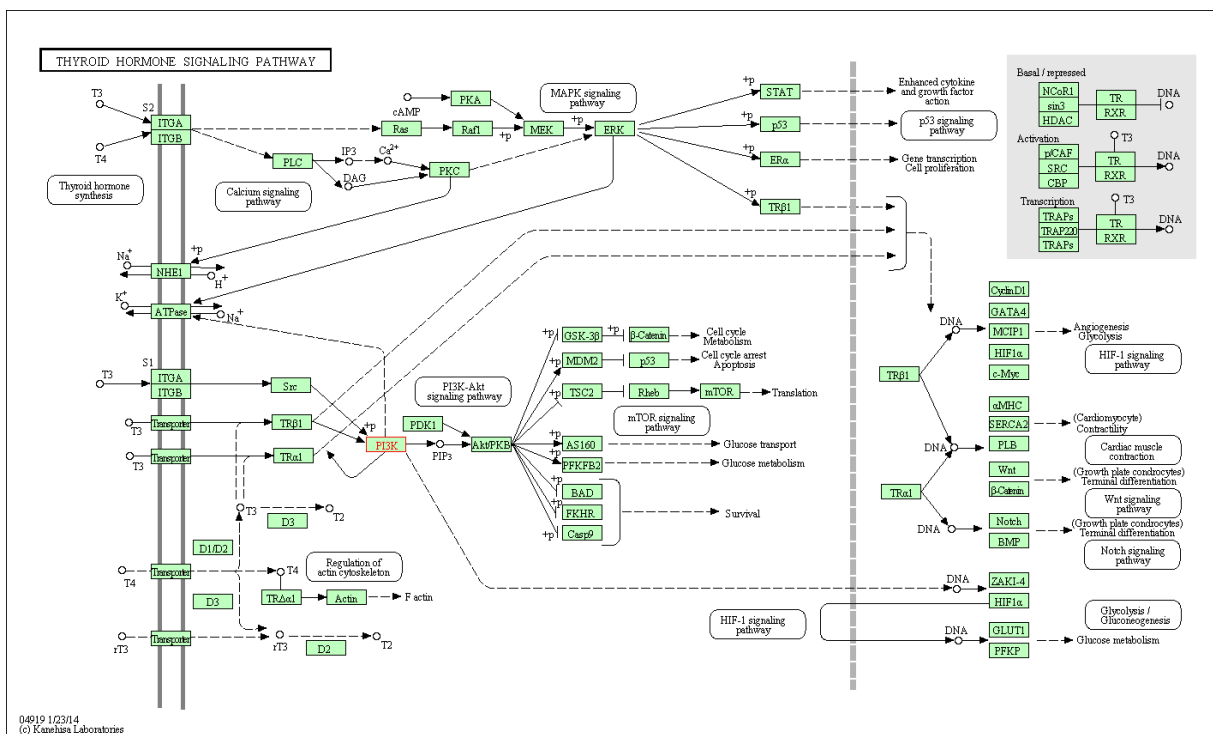
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map04510_org_2015012701230430589



map04722_org_2015012701212023696

Table S1. Real-time quantitative PCR primers

Primer sequences for QRT-PCR of six randomly selected significantly different miRNAs

MiR_name	Primer
oar-miR-200a	GGGGTAACACTGTCTGGTAACGATGTT
oar-miR-200b	GGGGTAATACTGCCTGGTAATGATG
oar-miR-200c	GGTAATACTGCCGGGTAATGATGGA
novel_mir_278	GCGTGGAAGACTAGTGATTTTGTTGT
novel_mir_294	GCGCCCATAAAGTAGAAAGCACTA
novel_mir_146	GGGTAGCAGCACAGAAATGTTGGT

Gene	Primer	
GNAQ	R:GCTCGAGTTTCCCAACCCAT	F:CGGCCGCCCCAGCCCA
ITPR1	R:CCCAGATTCTTAGATTACCTC	F:CTCCTTGTTGCTGTCCC
PRKCB	R:GCGGGTCACTGCTCTAT	F:CCTTCCTCCTGGCTCA
CREB	R:GCCACNTTAGCCCAGGTNTC	F:GAATCGGTTACACTNTCCA
GNA1	R:CGCTGAGTGACTACGAC	F:GAGGGCTCTTCTTGATT
MAP3K1	R: AGGAGACAGCCCAGACA	F:CGAGACGGAGCTTTGA
GPR54	R:CGGACTTAATGTTCTGCTGT	F:ACCGAGACCTGCTGGATGTA
KISS1	R:GCCTGATCCCGGCTCCGA	F:CGTAGCGCAGGCCGAAGGAG
GnRH	R:TCCTGCTGACTTTCTGTG	F:CTTAGGTTCTACTGGCTGAT
β -actin	R:TCGTTGTAGAAGGTGTGGT	F:AGAGCAAGAGAGGCATCC

Table S2. (a–d) Distribution of total small RNAs reads by Solexa sequencing.

Table S3. All miRNA expression level comparison HEN vs HAN libraries.

Table S4. The significantly different expressed known miRNA.

Table S5. The significantly different expressed novel miRNA.