

Article

Transcriptome analysis of ovaries in mice with premature ovarian failure after treatment with Zishen Yutai pills

Supplementary materials

Table S1. The sequences of primers.

Primers	Primers sequences(5'-3')
s100a8	F: ACAAGGAAATCACCATGCCCT R: TTTGTGAGATGCCACACCCA
cxcl13	F: CTCCAGGCCACGGTATTCTG R: CCAGGGGGCGTAACTTGAAT
cxcl5	F: CGGTTCCATCTCGCCATTCA R: GCTATGACTGAGGAAGGGGC
caspase-3	F: GTCATCTCGCTCTGGTACGG R: CACACACACAAAGCTGCTCC

Table S2. Statistics of RNA-Seq data.

Sample Name	Clean Reads	Clean Bases	≥Q30 (%)	GC content (%)
H053A	24,032,632	7,209,789,600	95.25	49.15
H054A	22,445,557	6,733,667,100	94.10	48.03
H055A	24,138,141	7,241,442,300	94.40	47.69
H068A	24,103,230	7,230,969,000	94.35	48.31
H069A	24,132,287	7,239,686,100	94.12	47.97
H070A	24,128,637	7,238,591,100	94.27	48.10
H098A	24,143,150	7,242,945,000	95.08	47.82
H099A	24,085,506	7,225,651,800	94.48	47.85
H0100A	24,063,439	7,219,031,700	94.47	47.78

Note: Clean Reads: Total sequencing reads; Clean Bases: The product of the number of clean reads and their length, represents the total number of bases sequenced; GC content (%): the percentage of G and C bases in the total bases in reads; ≥Q30 (%): Bases with mass values ≥30 accounted for a percentage of the total bases in reads. H053-55A: Model group, H068-70A: Normal group, H098-100A: ZSYTP group.