

SUPPLEMENTARY TABLES

Supplementary Table 1. The upstream and downstream sequence of primers in Real time PCR.

Primer	Primer sequences	
	Forward	Reverse
CPEB3	5-CCAACTGAGTCCA GCGTAT-3	5-AGGAGCGGTGATTCCATCT-3
MYC	5-GCCCCTCAA CGTTA GCTTCA-3	5-AGTTCTCCTCCTCGTCGCA G-3
TGFB1	5-GATGTCA CCGGA GTTGTGC-3	5-GAACCCGTTGATGTCCACTT-3
JAK1	5-ACTGAGGTGAACCTGGA GGC-3	5-ACTGCCCA GCCGGA GG-3
SMAD2	5-GGAATTTGCTGCTCTTCTGG-3	5-CTGCCTTCGGTATTCTGCTC-3
STAT3	5-GAGCTGGCTGACTGGAA GA G-3	5-TGTTGACGGGTCTGAA GTTG-3
ATG3	5-TGCTATAAGCGGTGCAACA-3	5-CGGCTTCCGTTATTCTGTGA-3
STAT6	5-CACTGGAA GCA GGAA GAACTCA-3	5-AGACACTTGGCCA GCCTCA-3
PIK3C3	5-TCATGGCAA GCTGTACGG-3	5-TCAGCCA CAGGAACTGACTG-3
RB1	5-CACATTCCTCGAA GCCCTTA-3	5-GTTGGTGTGGCA GACCTTC-3
E2F3	5-TGCACTGTCTGA GGATGG-3	5-GGTGCA GCTTTGGATCA GTT-3
GAPDH	5-GAAGGTGAA GGTCCGA GT-3	5-GAAGATGGTGTGGGATTTTC-3

Supplementary Table 2. Read count for sample (CPEB3) and control (IgG) in total, and in ribosomal RNAs (rRNAs).

Sample ID	Raw reads	Clean reads	Clean ratio*	rRNA trimmed	rRNA ratio**
CPEB3	23063600	22537635	97.72%	8656239	61.59%
IgG	21692675	18560899	85.56%	12404800	33.17%

*: Clean ratio=(clean reads/Raw reads)%; **:rRNA ratio=[(Clean reads -rRNA trimmed)/Clean reads]

Supplementary Table 3. Percentage of mapped reads in CPEB3 and control IgG group.

Sample ID	All reads	Mapped reads	Mapped ratio*
CPEB3	8656239	4759549	54.89%
IgG	12404800	2300735	18.55%

*: Mapped ratio=(Mapped reads/All reads)%