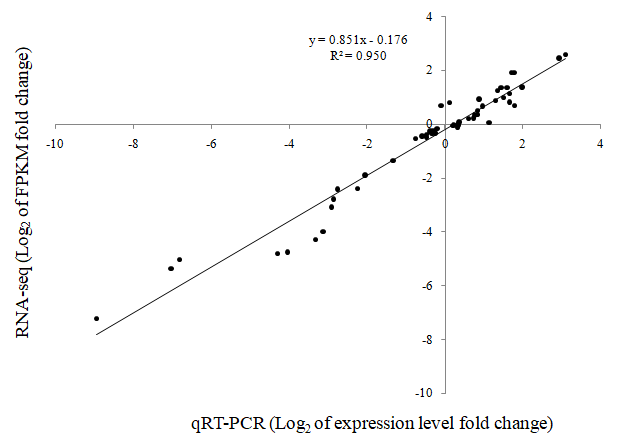
Comparative analysis of latex transcriptomes reveals the potential mechanisms underlying the rubber molecular weight variations among *Hevea brasiliensis* clones RRIM600 and Reyan7-33-97

Shichao Xin, Yuwei Hua, Ji Li, Xuemei Dai, Xianfeng Yang, Jinu Udayabhanu, Huasun Huang\* and Tiandai Huang\*



**Fig. S2.** Correlation analyses of the RNA-Seq (FPKM) and qRT-PCR results. The values of log2 of expression levels fold change in qRT-PCR (x-axis) were plotted against the values of log2 of FPKM fold changes in transcriptome data (y-axis) for the 17 selected genes in four latex samples.