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

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**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.