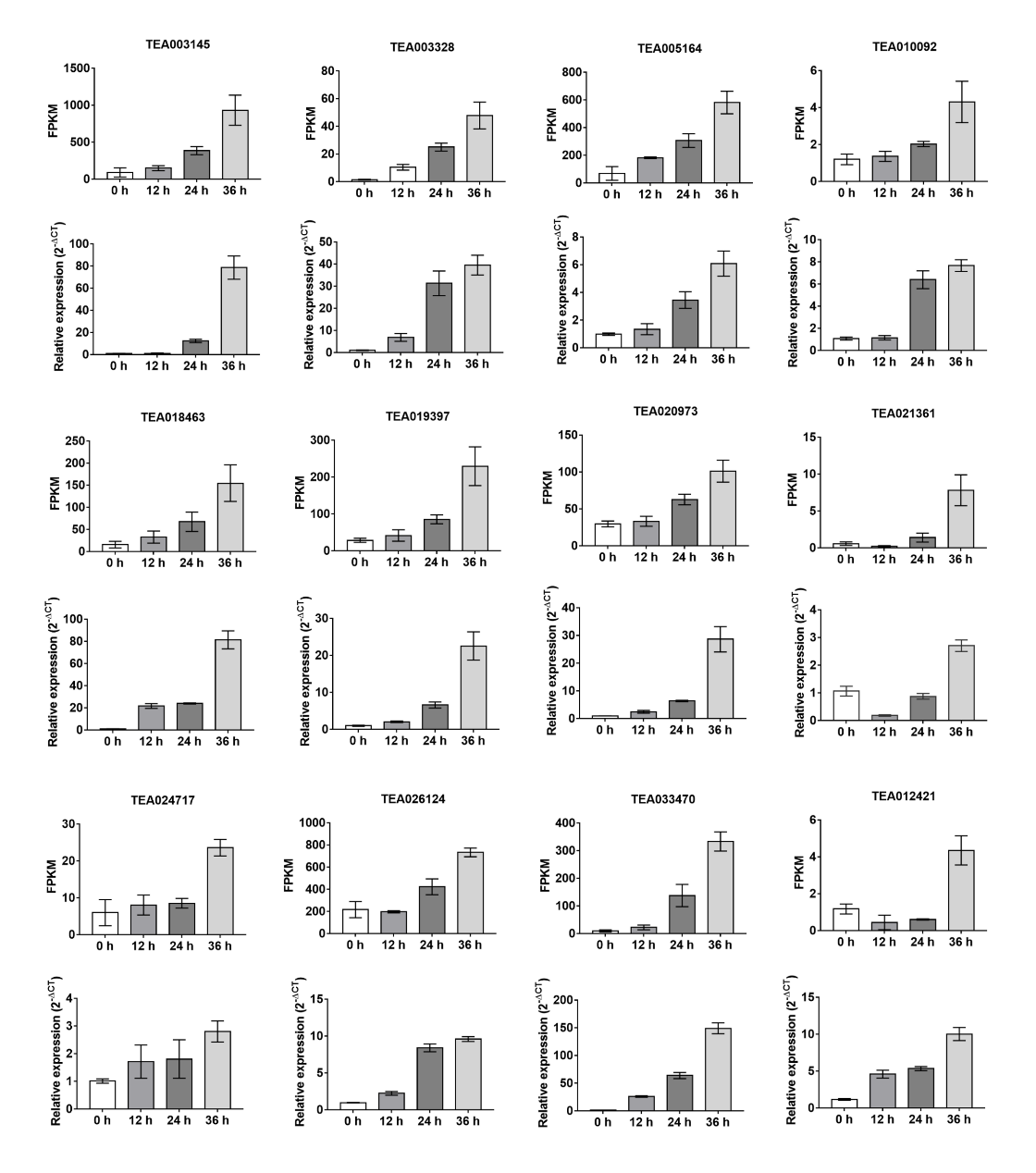
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**Fig. S6.** The expression patterns of the 12 key hub genes identified from the co-expression networks based on RNA-seq and RT-PCR analysis. The data represent the mean + SD (n = 3).