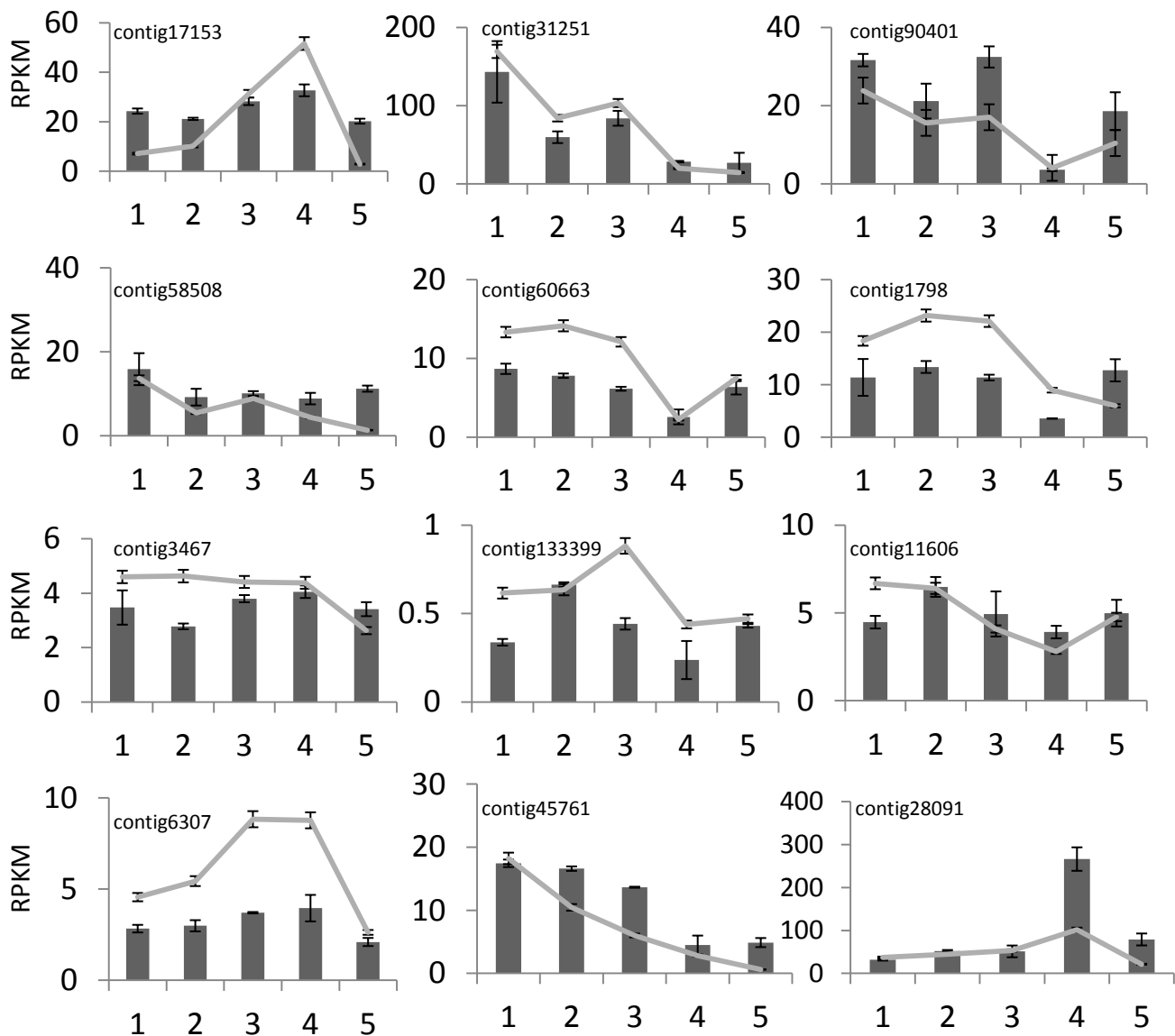R2X[1]=0.375; R2X[2]=0.258

**Supplemental Figure 1.** Principle Component Analysis for metabolites from  different leaves and stem

**Supplemental Table S1**: Number of reads get from five tissues of tea plants and quality of transcriptome sequencing

| Sample | Number of reads | GC% | Q20% | Q30% |
|--------|-----------------|-----|------|------|
| Bud-1 | 33833529 | 42 | 0.999782 | 0.97464 |
| Bud-2 | 38754301 | 43 | 0.999762 | 0.974404 |
| FL-1 | 25833070 | 42 | 0.999802 | 0.966952 |
| FL-2 | 26044289 | 42 | 0.999812 | 0.968461 |
| ML-1 | 31705267 | 47 | 0.999766 | 0.965772 |
| ML-2 | 25758852 | 44 | 0.999814 | 0.968212 |
| SL-1 | 29076645 | 42 | 0.999827 | 0.968581 |
| SL-2 | 27800431 | 42 | 0.999794 | 0.96766 |
| Stem-1 | 30996807 | 43 | 0.999819 | 0.968278 |
| Stem-2 | 26347796 | 43 | 0.999807 | 0.96791 |
| Total | 148075493.5 | | | |

**Supplemental Table S2**: Primers used for q-PCR in this study

| Gene | Forward Primer | Reverse Primer |
|---|---|---|
| contig17153 | CAGGAAACCCACTCTTCCAA | CTTCTTCCCCAAAAACGACA |
| contig31251 | TCCGAGTTCGTGAGTGTCAG | GAAGTCCTTTGCCCCATACC |
| contig90401 | AATCGAGCAGATTTGCAAGG | TTCCCAGAGATGCCGATTAC |
| contig58508 | CCTTCCACTCTTCGTCCTGA | GGTCTCAAGCTCCGCAATTA |
| contig60663 | TGGCCTTTCGAGGTCTATTG | TTCTGTCCATACCGAGCTGTC |
| contig1798 | TTCTAACCTGCCCACTCCAC | GAATCCATGGAAGCCTTTGA |
| contig3467 | TTCCTGACCACCCTCGTTAG | AGCACTTCACCTCCTGATGC |
| contig133399 | TCTTACTCTACACGACGCTCTTCC | TTGGGTTGTTCTTCACAGAGC |
| contig11606 | GACAGGATTGGAGCCGTAAA | AAAGAGCCGAGAGGAGGAAG |
| contig6307 | ATTGTCCGTCTTCCATGCTC | GTGGAGCACCTCAAACATCC |
| contig45761 | GGGATGAGGGAGACCAAAAT | CAAACTCCCTTCCACCTCAA |
| contig28019 | CAACAGAGGAGTCTGCACCA | CTTTAGGGCTTCCCGACATT |

**Supplemental Figure 2.** Q-PCR results showing that the expression patterns of the 12 genes were in accordance with those of RNA-Seq. 1, 2, 3, 4, 5 means Bud, FL, SL, ML and Stem respectively.