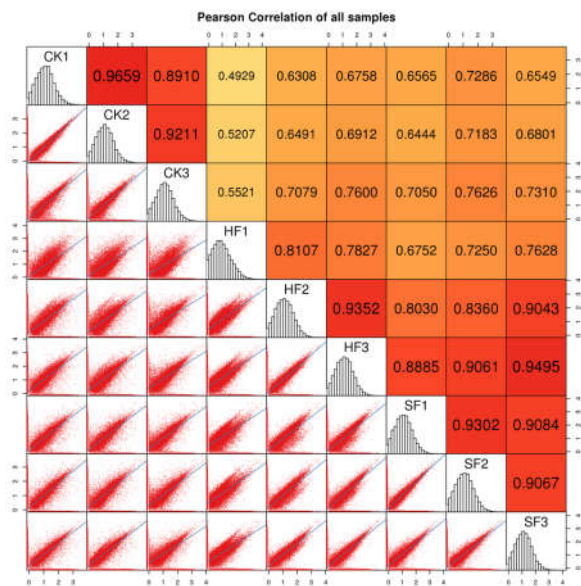


## Supplementary Table

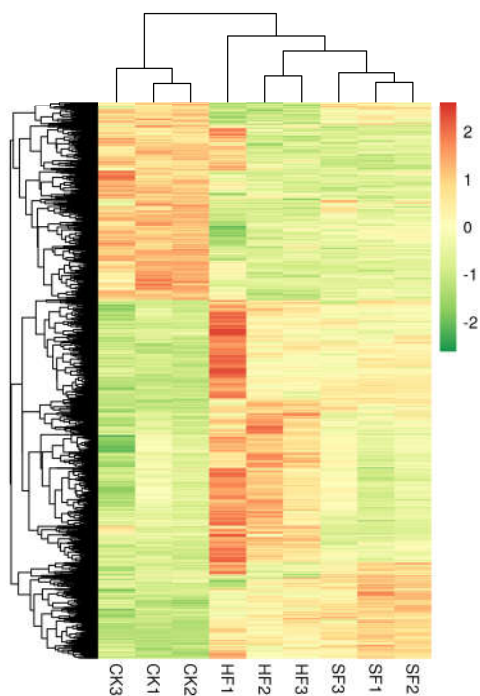
**Table S1.** The Sequences of primer for qRT-PCR validate analysis.

| Gene  | Primer sequences (5'-3')    |
|-------|-----------------------------|
| GAPDH | F: GTGCCAAGAAGGTTATCATCTCTG |
|       | R: CTCATGCTCATTAACACCAACAAC |
| UR1   | F: GCCATGGAAGTTTCAGGTGT     |
|       | R: ACCGGGCACTGCAGTATAAC     |
| UR2   | F: GGCTTTTTCTTCCTCCATCC     |
|       | R: GGAGTTCGCCAAGTGTGAAT     |
| UR3   | F: CTTCATGAATGGCCTCTGGT     |
|       | R: GCATACACTCTCGCTGATCG     |
| UR4   | F: TCCGTGCAGATGAAGAACTG     |
|       | R: CCGCGTTATCCCTCAGTTTA     |
| UR5   | F: CGATGAGCACTGCCAAGTAA     |
|       | R: GTCCCCCATTCACACAAAAC     |
| UR6   | F: ATCATCTCCCGCACATCTTC     |
|       | R: AAACGGTTACGTGGAGTTCG     |
| UR7   | F: GAAGCAAGCTCTGGTGGTTC     |
|       | R: CGATCCCTAATCTTCCACGA     |
| UR8   | F: AAAAGCTCCCTGTCTCCTC      |
|       | R: CCGCTAAAATCCATTCCAAC     |
| UR9   | F: CCATACCGTCGCGTTTTATT     |
|       | R: AGTCTTCTTCTGCCCCATT      |
| UR10  | F: AGCAACGAAAGCCAGAAAGA     |
|       | R: TTTAATGTCGGTGGGCTTC      |
| DR1   | F: ATCCCATCCCCTGGAATATC     |
|       | R: TTCTCCTCCAAGTCCCTCCT     |
| DR2   | F: TCCAATGACCACAAAAACGA     |
|       | R: TTCTTCTCCGCAGACCACTT     |
| DR3   | F: TGTACCCCCAAATCTCATCA     |
|       | R: TCTGGTGATGTGGTGCAGTT     |
| DR4   | F: CCAGCCTCCATCTCTCACTC     |
|       | R: GGCAGTATCGAAGGTTCCAA     |
| DR5   | F: CTCAAATGCAGAAGCCACAA     |
|       | R: TATGCACCAGAGGTGACAGC     |
| DR6   | F: AGATTGTGAGCATTGCGTTG     |
|       | R: TCCTATGGCATTAGCGGTTT     |

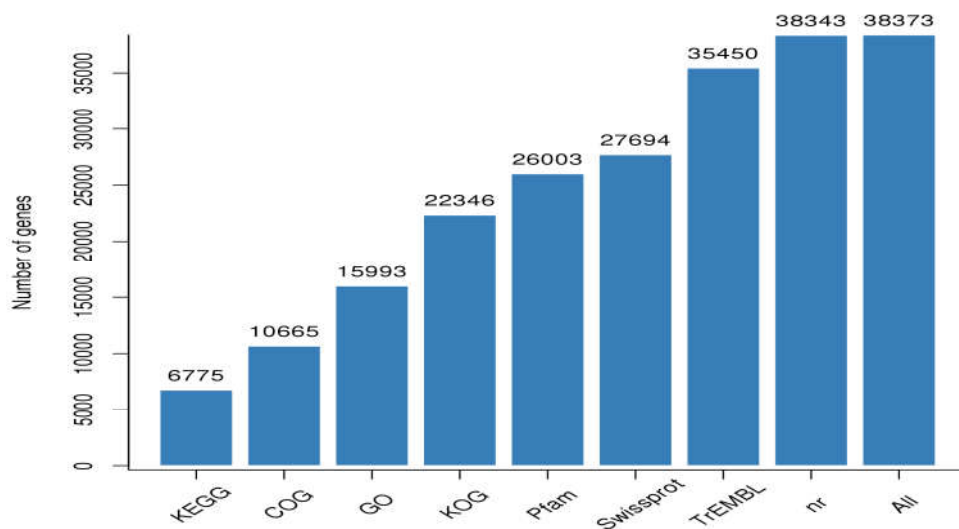
## Supplementary Figures



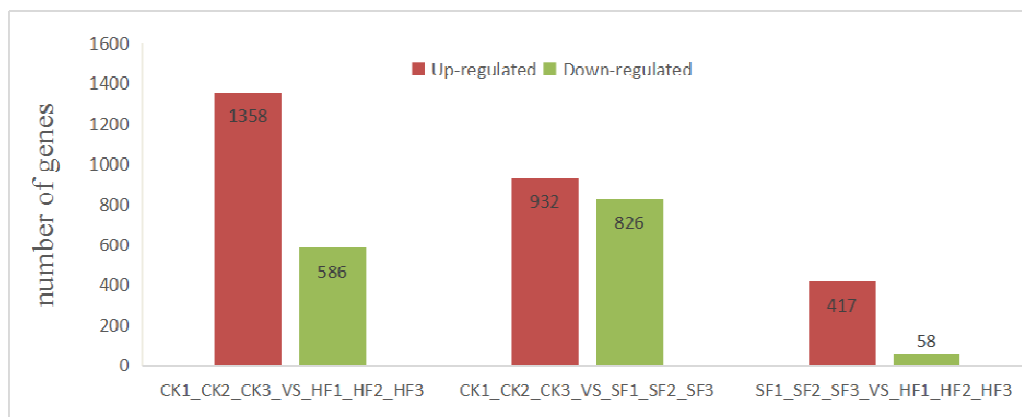
**Figure S1.** Pearson correlation of all samples.



**Figure S2.** Heat map of gene expressions in the three libraries with three replicates.

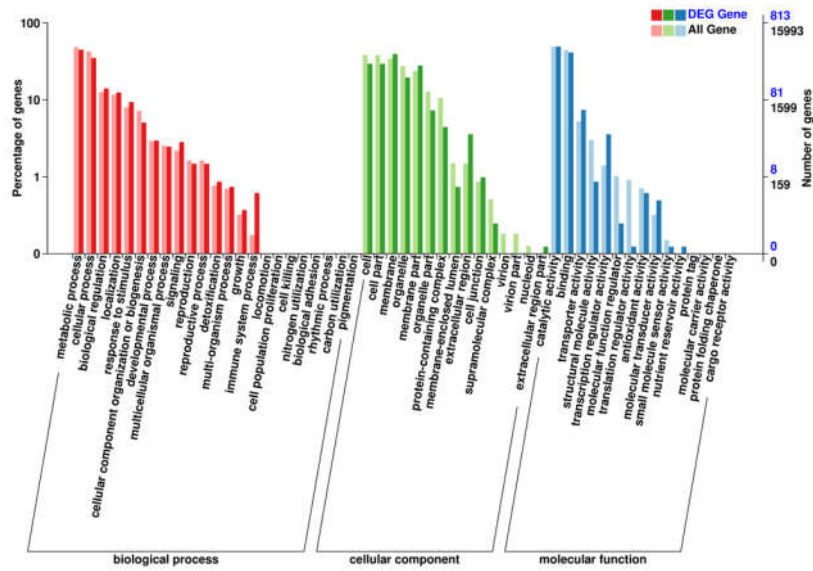


**Figure S3.** The number of the unigenes annotated in the databases.

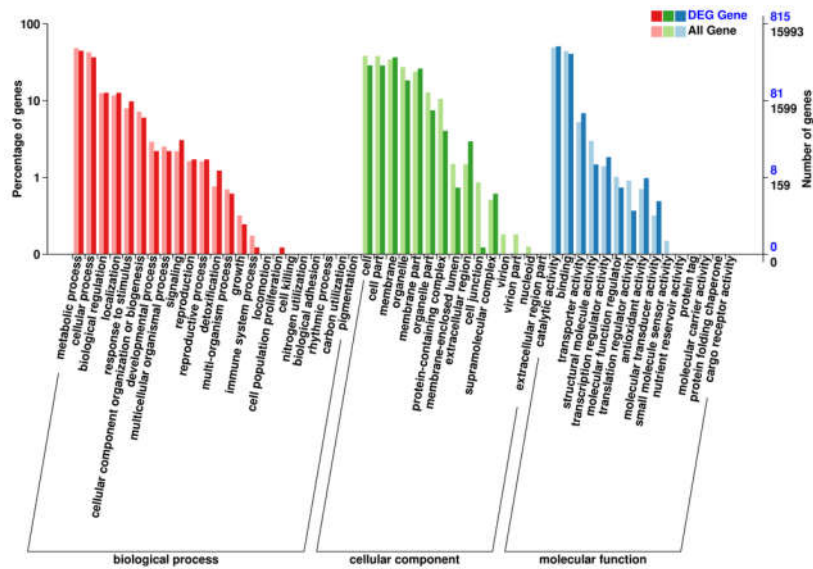


**Figure S4.** The number of the identified DEGs in the three libraries.

A



B



**Figure S5.** The GO terms classification of all gene and DEGS. (A) GO classification annotation in CK1\_CK2\_CK3\_vs\_SF1\_SF2\_SF3. (B) GO classification annotation in CK1\_CK2\_CK3\_vs\_HF1\_HF2\_HF3.