Table S1 The statistic of sequencing, filtering and assembling in transcriptome analysis

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| Sample | Sequencing and Filtering | Unigene Assembling |
| Total Raw Reads(M) | Total Clean Reads(M) | Total Clean Bases(Gb) | Clean Reads Q20(%) | Total Number | Total Length | Mean Length | N50 |
| white1 | 55.54 | 55.52 | 8.33 | 96.75 | 104278 | 94491519 | 906 | 1339 |
| white2 | 65.44 | 65.43 | 9.81 | 96.53 | 109198 | 98634405 | 903 | 1327 |
| white3 | 66.35 | 66.33 | 9.95 | 96.72 | 107669 | 98650570 | 916 | 1361 |
| purple1 | 40.04 | 40.03 | 6 | 96.52 | 85919 | 75605924 | 879 | 1318 |
| purple2 | 55.74 | 55.73 | 8.36 | 96.82 | 100405 | 87834032 | 874 | 1297 |
| purple3 | 50.61 | 50.6 | 7.59 | 96.83 | 96399 | 84890351 | 880 | 1319 |
| Total | 333.72 | 333.64 | 50.04 | 580.17 | 197769 | 2.26E+08 | 1140 | 1762 |