**Supplementary table 1. RNA-seq data quality summary**

| **Sample1** | **Raw reads2** | **Raw data3** | **Effective4** | **Error5** | **Q20(%)6** | **Q30(%)** | **GC(%)7** |
| --- | --- | --- | --- | --- | --- | --- | --- |
| A1 | 63684194 | 9.6 | 98.34 | 0.02 | 97.90 | 94.33 | 53.88 |
| A4 | 72810934 | 10.9 | 97.83 | 0.03 | 97.57 | 93.99 | 54.55 |
| A5 | 66817782 | 10.0 | 98.42 | 0.02 | 97.94 | 94.41 | 53.73 |
| A3 | 48215378 | 7.2 | 98.65 | 0.03 | 97.87 | 94.31 | 54.56 |
| A2 | 59626720 | 8.9 | 98.83 | 0.02 | 97.94 | 94.32 | 54.12 |
| A6 | 59526612 | 8.9 | 98.34 | 0.02 | 97.98 | 94.48 | 54.21 |

1Sample: sample name (A1-A3 for RIL resistant bulks and A4-A6 for susceptible RIL bulks).  
2Raw reads: total amount of reads of raw data.

3Raw data: (raw reads) \* (sequence length =150 bp), calculated in Gbp.

4Percentage of effective reads: (clean reads/raw reads)\*100  
5Error: base error rate in percentage   
6Q20, Q30: base count of Phred value > 20 or 30\*100 / Total base count  
7GC: G & C base count \*100/ total base count