

Table S1. Summary of high-throughput sequencing statistics obtained for each sample evaluated in the present study.

| Sample ID | Raw reads | Clean reads | Effective reads | AvgLen (bp) | GC (%) | Effective (%) |
|------------------|------------------|--------------------|------------------------|--------------------|---------------|----------------------|
| Ma1 | 107096 | 107086 | 104526 | 477 | 54.20 | 97.60 |
| Ma2 | 107705 | 107687 | 105482 | 477 | 53.78 | 97.94 |
| Ma3 | 102341 | 102330 | 101997 | 477 | 53.45 | 99.66 |
| Gg1 | 103479 | 103462 | 101319 | 477 | 53.90 | 97.91 |
| Gg2 | 109241 | 109227 | 107829 | 477 | 54.60 | 98.71 |
| Gg3 | 104496 | 104485 | 102215 | 477 | 53.87 | 97.82 |
| Sb1 | 107840 | 107806 | 104571 | 477 | 52.46 | 96.97 |
| Sb2 | 103788 | 103769 | 101632 | 477 | 53.25 | 97.92 |
| Sb3 | 106675 | 106652 | 104240 | 477 | 53.07 | 97.72 |
| Cc1 | 106511 | 106505 | 100088 | 477 | 54.68 | 93.97 |
| Cc2 | 102145 | 102131 | 99879 | 477 | 55.07 | 97.78 |
| Cc3 | 104643 | 104637 | 103106 | 477 | 54.98 | 98.53 |

Average length (bp) is the average sequence length of all samples. GC (%) is the percentage of G and C type bases in the total base. Effective (%) is the percentage of effective reads in raw reads.