Table S2: Genomic comparison statistics of sequenced reads.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sample | Uniquely Mapped Reads | Multiple Mapped Reads | Sample | Uniquely Mapped Reads | Multiple Mapped Reads |
| Q\_H1 | 88.01% | 8.17% | S\_H1 | 93.81% | 3.18% |
| Q\_H2 | 90.76% | 5.84% | S\_H2 | 93.15% | 3.50% |
| Q\_H3 | 87.49% | 8.51% | S\_H3 | 92.73% | 3.89% |
| Q\_H4 | 87.53% | 8.59% | S\_H4 | 93.23% | 3.31% |
| Q\_H5 | 91.38% | 4.54% | S\_H5 | 93.79% | 3.13% |
| Q\_L1 | 81.07% | 14.30% | S\_L1 | 93.33% | 3.51% |
| Q\_L2 | 89.60% | 6.70% | S\_L2 | 92.88% | 3.42% |
| Q\_L3 | 87.00% | 8.81% | S\_L3 | 92.52% | 4.01% |
| Q\_L4 | 85.19% | 5.88% | S\_L4 | 91.66% | 4.39% |
| Q\_L5 | 87.00% | 8.81% | S\_L5 | 92.50% | 3.88% |