**Table S1 Summary of RNA sequencing and assembly**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Samples**  | **Clean Reads** | **Map Rate** | **GC Content** | **≥Q30%** |
| C1 | 21,328,777 | 94.20% | 45.49% | 92.09% |
| C2 | 20,756,335 | 93.77% | 45.63% | 92.38% |
| C3 | 24,382,509 | 94.24% | 45.52% | 92.72% |
| Cp1 | 20,234,220 | 94.00% | 45.60% | 92.61% |
| Cp2 | 24,501,034 | 93.04% | 45.64% | 92.36% |
| Cp3 | 23,168,691 | 93.96% | 45.59% | 92.66% |
| P1 | 22,605,631 | 94.10% | 45.48% | 92.41% |
| P2 | 20,647,526 | 93.61% | 45.36% | 92.23% |
| P3 | 21,922,069 | 93.93% | 44.89% | 92.61% |
| Sp1 | 20,373,363 | 89.08% | 45.89% | 92.25% |
| Sp2 | 20,237,184 | 89.25% | 46.07% | 92.26% |
| Sp3 | 19,736,617 | 85.52% | 45.62% | 91.61% |
| St1 | 22,041,182 | 93.62% | 46.05% | 93.07% |
| St2 | 22,082,739 | 92.60% | 45.46% | 92.28% |
| St3 | 20,944,987 | 92.82% | 45.89% | 92.25% |