**Table S1.** **Telomeric repeat motif candidates identification in TRIP.**

|  |  |  |
| --- | --- | --- |
| **Parameters for TRM candidates\*** | **Criteria** | **Purpose** |
| (1) avg\_genome\_cov  (2) rpt\_reads\_num | ≥ 10x  ≥ 12,000 | Ensure sufficient amount of input data  Make sure the simple repeats were not pre-filtered in the raw data |
| (3) repeats\_len\_per\_million\_reads | ≥ 4 Kb | Meet a minimum total repeat length requirement (telomeres consist of hundreds to thousands base pairs). |
| (4) percent\_repeats\_len\_per\_read | ≥ 50% | Exclude intersperse short-tandem repeats (telomeres are tandem repeats with a large number of copies). |
| (5) unit\_len | ≥ 5 bp | Meet a minimum of TRM unit length requirement (all known telomere motifs are 5 bp or longer). |

\* See Table S1 for definitions.