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| **TableS1 Statistics of filtering and removing joints of each sample data for small RNAs** |
| Sample | PS (%\*) | TS (%\*) | SS (%\*) |
| Total reads | 15687101 | 15980089 | 12262330 |
| (100.00%) | (100.00%) | (100.00%) |
| High quality | 15374878 | 15653777 | 11989204 |
| (98.02%) | (97.96%) | (97.78%) |
| 3'Adapter null | 31176 | 51919 | 20778 |
| (0.20%) | (0.34%) | (0.17%) |
| Insert null | 97840 | 96620 | 90338 |
| (0.62%) | (0.63%) | (0.78%) |
| 5'Adapter contaminants | 21209 | 24125 | 18839 |
| (0.14%) | (0.15%) | (0.16%) |
| Smaller than 18nt | 518331 | 964549 | 903122 |
| (3.34%) | (6.10%) | (7.62%) |
| Poly A | 342 | 244 | 143 |
| (0.00%) | (0.00%) | (0.00%) |
| Clean tags | 14705980 | 14516320 | 10955984 |
| (95.70%) | (92.77%) | (91.27%) |
| \*The ratio is equal to the separate reads divided by the total raw reads |
| PS, TS and SS represent the three stages of stem development of *Populus trichocarpa*, primary growth stage, the transition stage from primary to secondary growth, and the secondary growth stage. |