**Table S1** Analysis of transcriptional sequence assembly and alignment of blueberry under drought stress

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Raw reads | Raw bases | Clean reads | Clean bases | Q30(%) | GC content(%) | Mapped reads | Mapped ratio |
| CK\_L1 | 50168622 | 7575461922 | 49608216 | 7375914970 | 91.33 | 46.29 | 45952855 | 92.63% |
| CK\_L2 | 53044662 | 8009743962 | 52620364 | 7853068229 | 92.13 | 46.18 | 48953435 | 93.03% |
| CK\_L3 | 46948118 | 7089165818 | 46385738 | 6908394495 | 90.59 | 46.74 | 43082322 | 92.88% |
| MD\_L1 | 63374360 | 9569528360 | 62816610 | 9339224348 | 92.06 | 46.41 | 58164107 | 92.59% |
| MD\_L2 | 54039612 | 8159981412 | 53611098 | 7985011226 | 91.87 | 46.07 | 49455453 | 92.25% |
| MD\_L3 | 56562812 | 8540984612 | 56036110 | 8326204281 | 91.52 | 46.12 | 51577733 | 92.04% |
| SD\_L1 | 51084954 | 7713828054 | 50695132 | 7535114245 | 95.93 | 46.73 | 47389270 | 93.48% |
| SD\_L2 | 67027100 | 10121092100 | 66527718 | 9873712333 | 95.92 | 46.45 | 62046895 | 93.26% |
| SD\_L3 | 61876142 | 9343297442 | 61354442 | 9106147231 | 95.58 | 46.56 | 57307386 | 93.40% |
| CK\_R1 | 57134796 | 8627354196 | 56599088 | 8434553494 | 92.17 | 46.49 | 46912888 | 82.89% |
| CK\_R2 | 48648626 | 7345942526 | 48228068 | 7182169909 | 92.14 | 45.85 | 34916212 | 72.40% |
| CK\_R3 | 50573454 | 7636591554 | 50188132 | 7480643420 | 92.86 | 46.38 | 43051629 | 85.78% |
| MD\_R1 | 43590858 | 6582219558 | 43181666 | 6436894542 | 91.10 | 46.15 | 36664230 | 84.91% |
| MD\_R2 | 45705760 | 6901569760 | 45291266 | 6758524390 | 91.78 | 46.16 | 32260969 | 71.23% |
| MD\_R3 | 43109142 | 6509480442 | 42739344 | 6369476251 | 92.11 | 45.56 | 33768356 | 79.01% |
| SD\_R1 | 38802292 | 5859146092 | 30486924 | 5742864153 | 92.03 | 45.95 | 23468953 | 76.98% |
| SD\_R2 | 46168078 | 6971379778 | 45711232 | 6818247954 | 91.74 | 46.08 | 37037413 | 81.02% |
| SD\_R3 | 47317614 | 7144959714 | 46945344 | 7006355724 | 92.45 | 45.43 | 32900084 | 70.08% |