

De novo transcriptome analysis of *Solanum lycopersicum* cv. super strain B under drought stress

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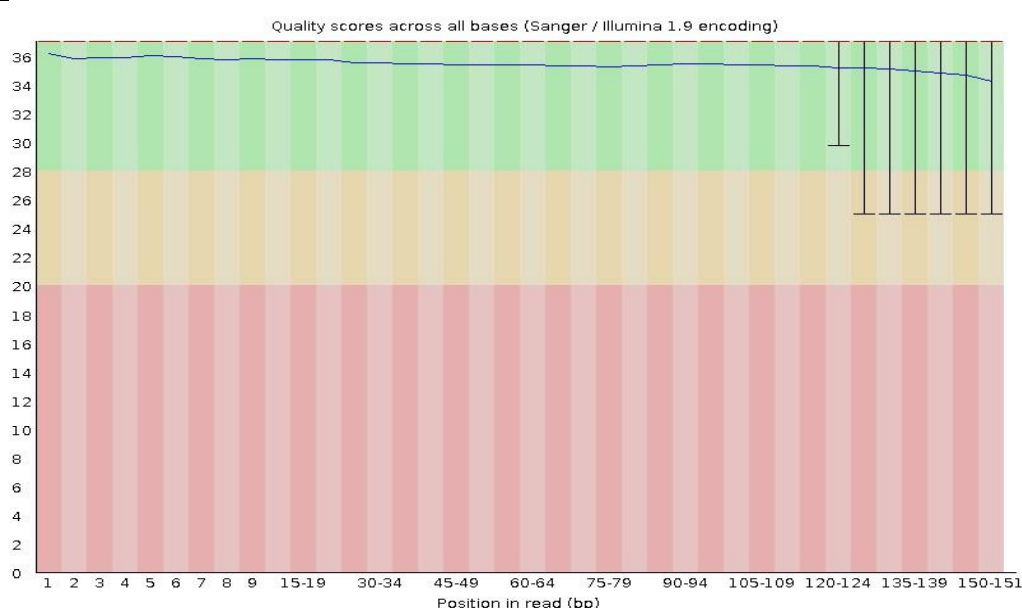
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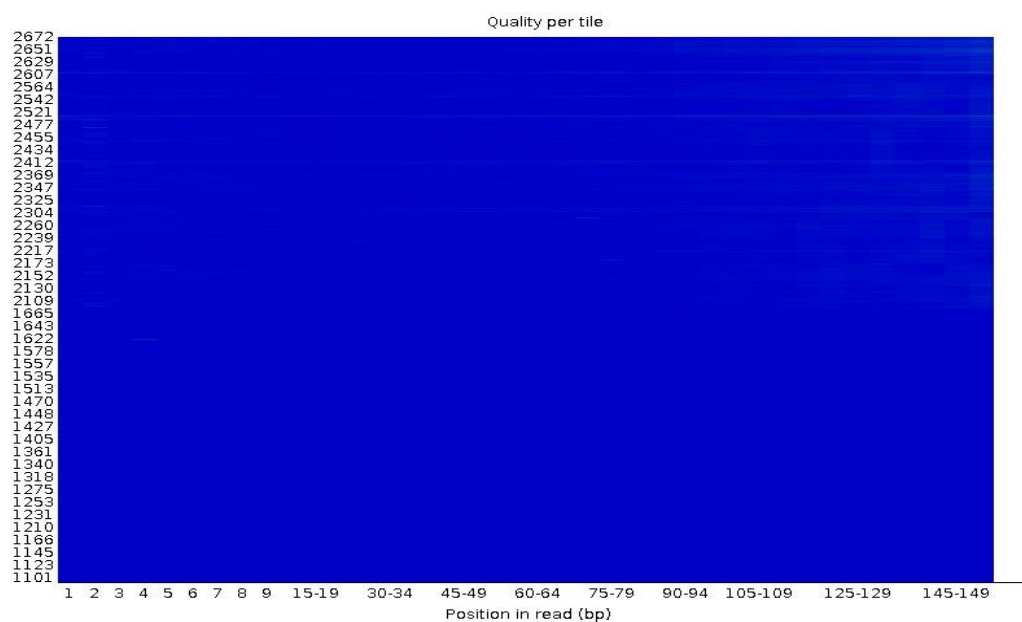
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File S2.1. Basic statistics of the of the raw data in the cv. super strain B transcriptome under drought stress (fastq 2).

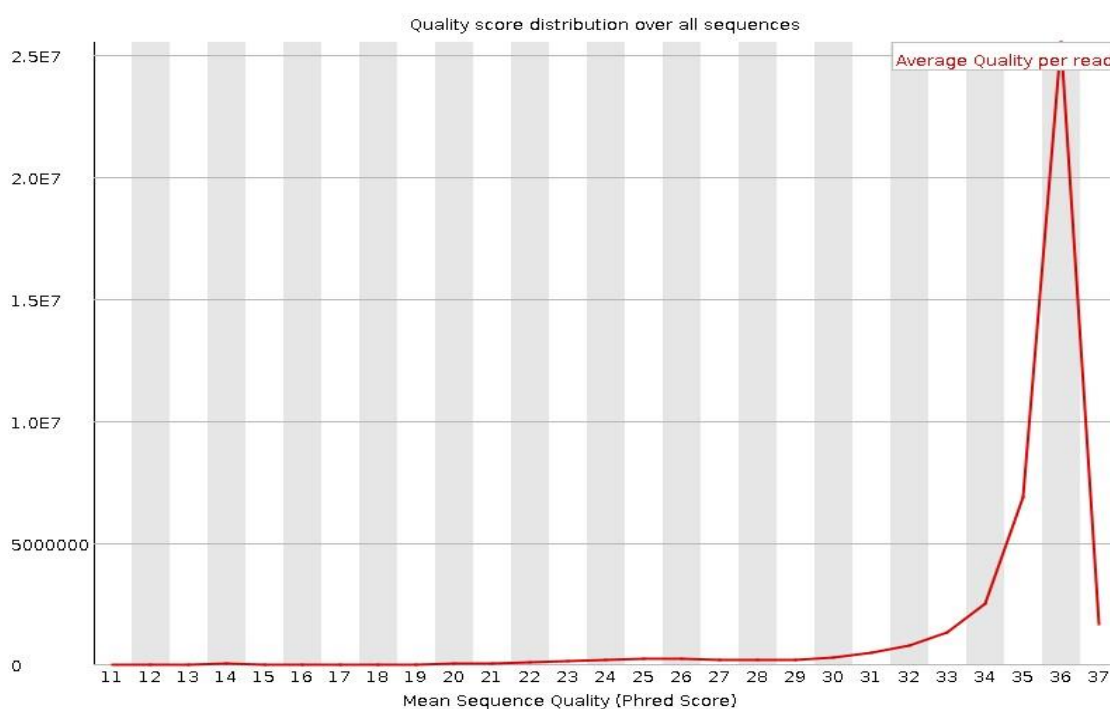
Measure	Value
Filename	2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	41779729
Sequences flagged as poor quality	0
Sequence length	151
%GC	44



File S2.2. Summary of per base sequence quality of the raw data in the cv. super strain B transcriptome under drought stress (fastq 2).

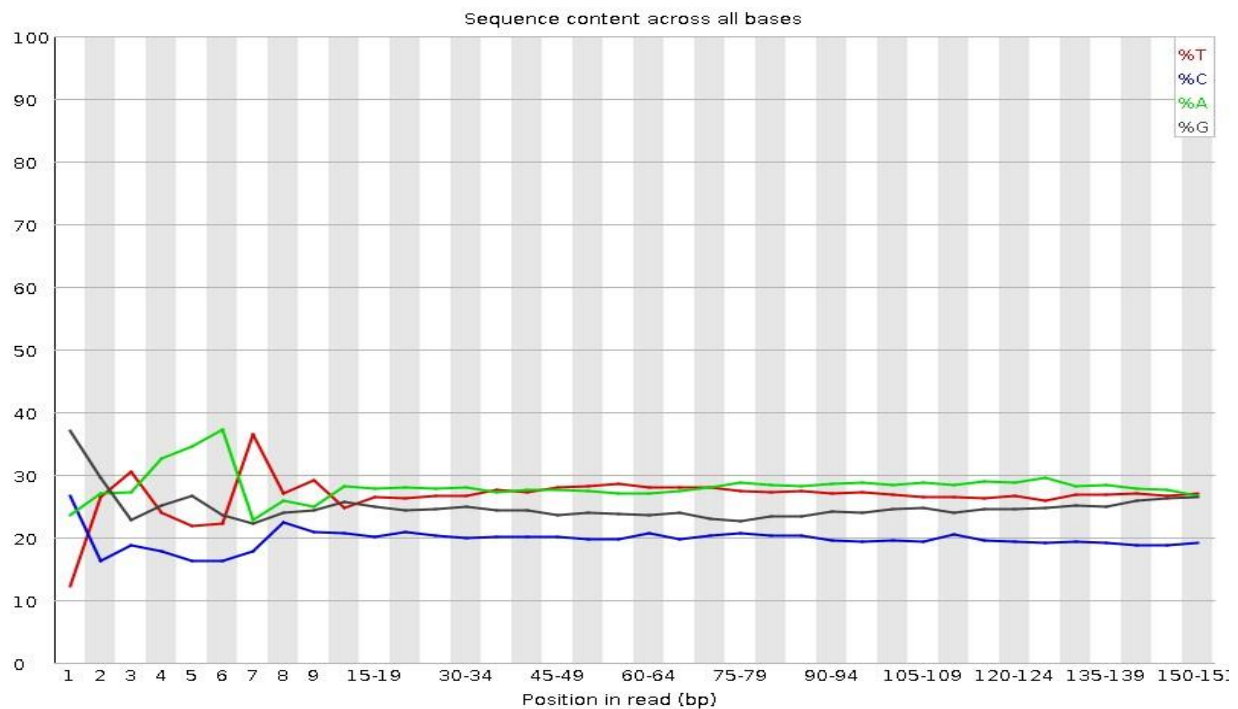


File S2.3. Summary of per tile sequence quality of the raw data in the cv. super strain B transcriptome under drought stress (fastq 2).

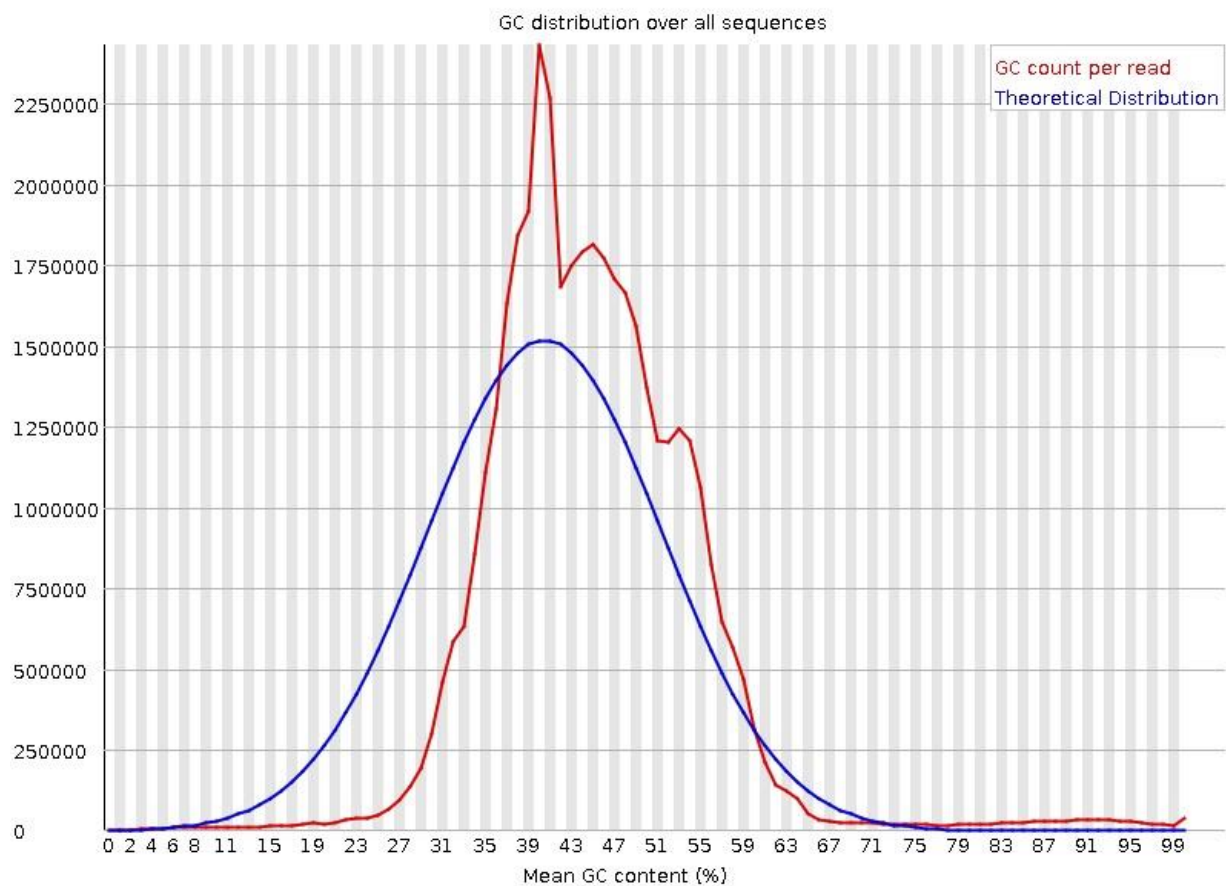


File S2.4. Summary of per sequence quality scores of the raw data in the cv. super strain B transcriptome under drought stress (fastq 2).

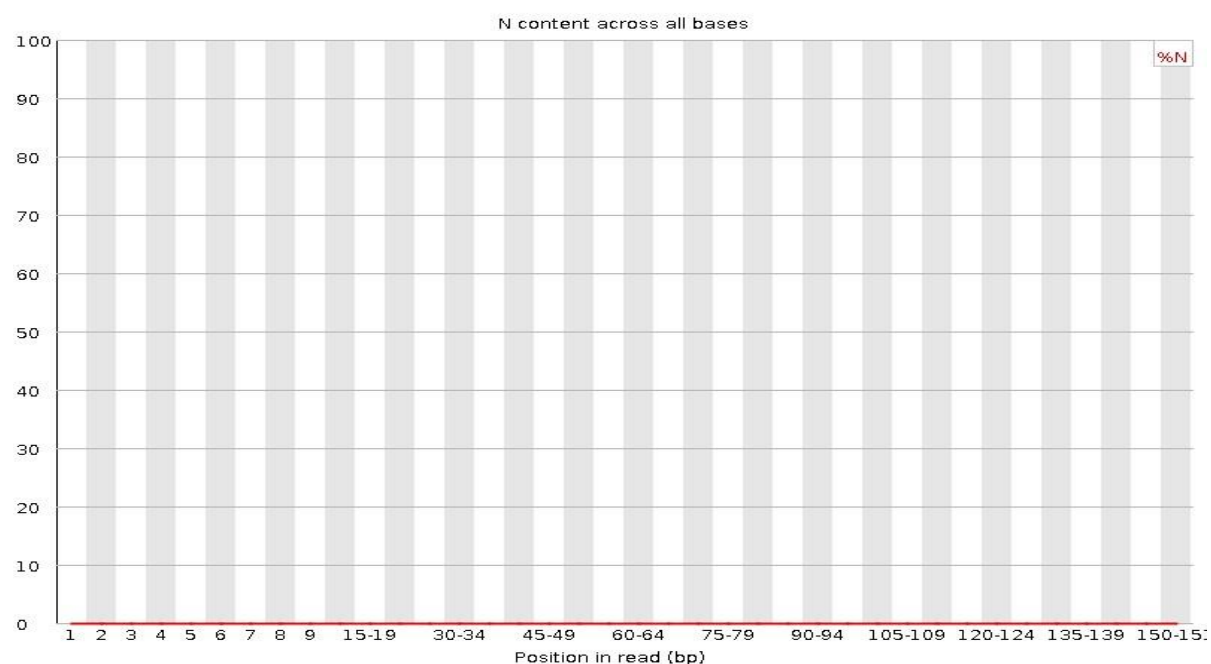
File S1.5. Summary of per base sequence content of the raw data in the cv. super strain B transcriptome under drought stress (fastq 1).



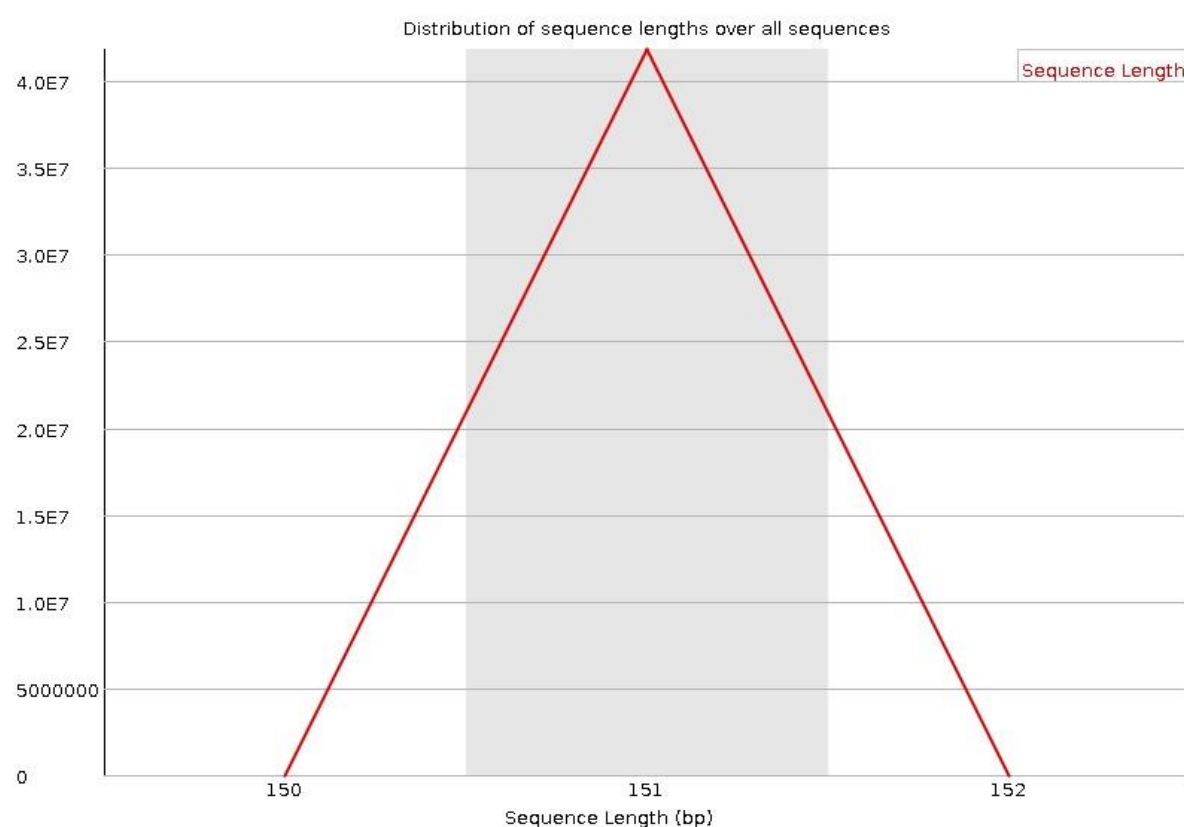
File S2.5. Summary of per base sequence content of the raw data in the cv. super strain B transcriptome under drought stress (fastq 2).



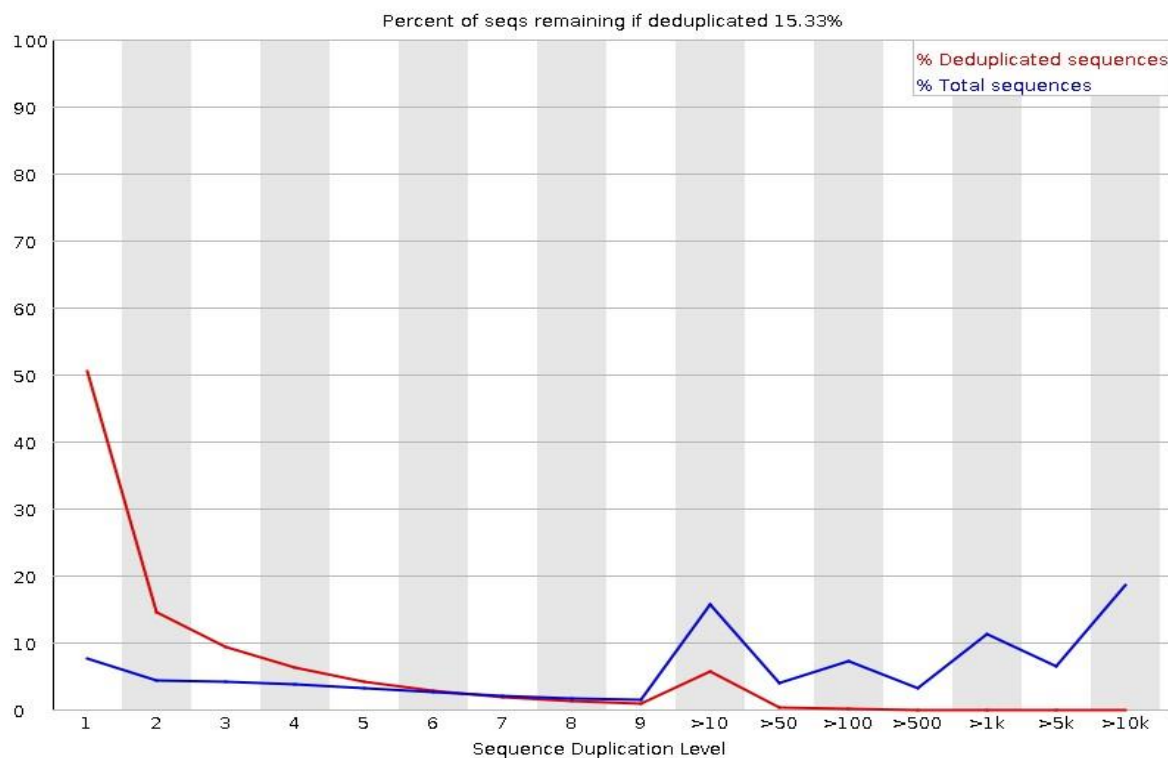
File S2.6. Summary of per sequence GC content of the raw data in the cv. super strain B transcriptome under drought stress (fastq 2).



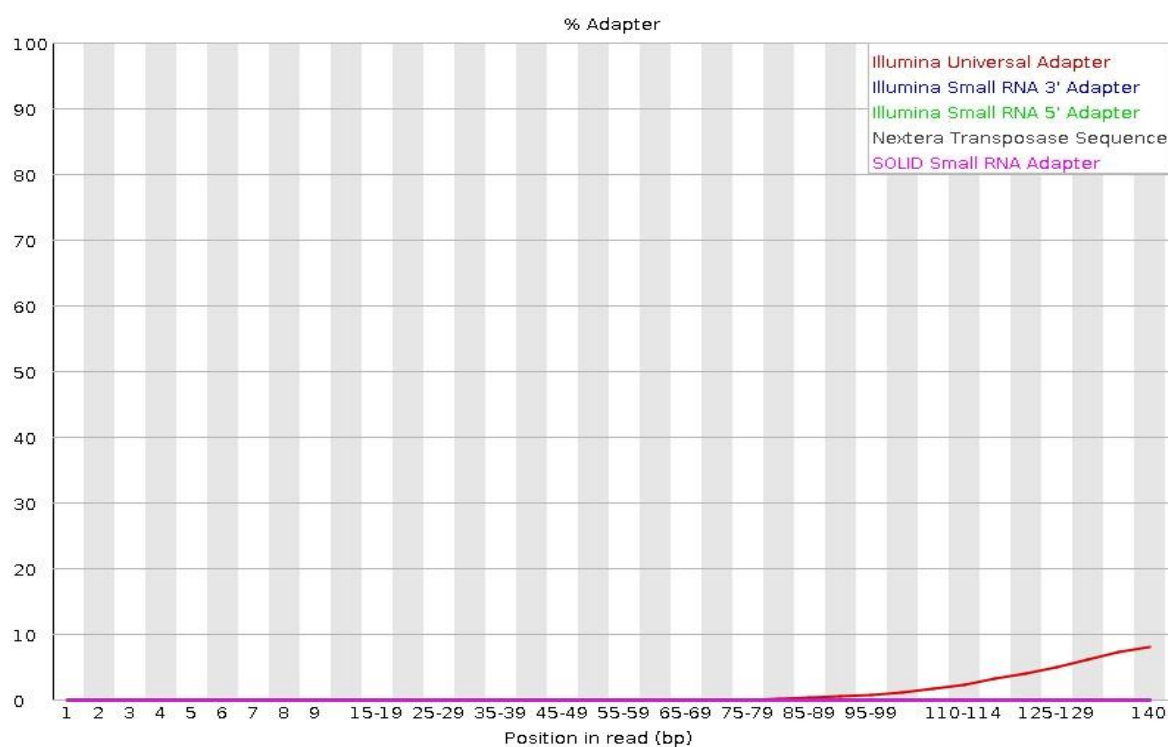
File S2.7. Per base N content plot of the raw data in the cv. super strain B transcriptome under drought stress (fastq 2).



File S2.8. Sequence length distribution plot of quality scores of the raw data in the cv. super strain B transcriptome under drought stress (fastq 2).



File S2.9. Sequences duplicated levels vs total sequences percentage of the raw data in the cv. super strain B transcriptome under drought stress (fastq 2).



File S2.10. Adapter content percentages of the raw data in the cv. super strain B transcriptome under drought stress (fastq 2).

File S2.11. Summary of overrepresented sequences of the raw data in the cv. super strain B transcriptome under drought stress (fastq 2).

[illegible]

TGGACATTAATTAGGGCTGAAAGCCCTAACTTAATGGACGGGAGGTATCC	48088	0.11509887965046399	No Hit
AGAGGTAGGAATGGGAGTATTTGCACTTGTGGTAACGGTATTTGCATTAT	46416	0.11109693890068076	No Hit
CTCGTAACCAAACATGCACAGCGGTCAAACAGTATGTCCCAAGGGGACTT	45974	0.11003900958763999	No Hit
TGGGAGTATTTGCACTTGTGGTAACGGTATTTGCATTATTGATGGTTTTT	45827	0.10968716431837076	No Hit
CAAAGAATATCCCAATTATCCATAAACTGTAAGTAAGTGAGGCTCTCTC	44740	0.10708542412996504	No Hit
GCCCAAGCTGCTCACAGTATACGGGCGTCGGCATCCAGACCGTCGGCTGA	43703	0.1046033592032155	No Hit