

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

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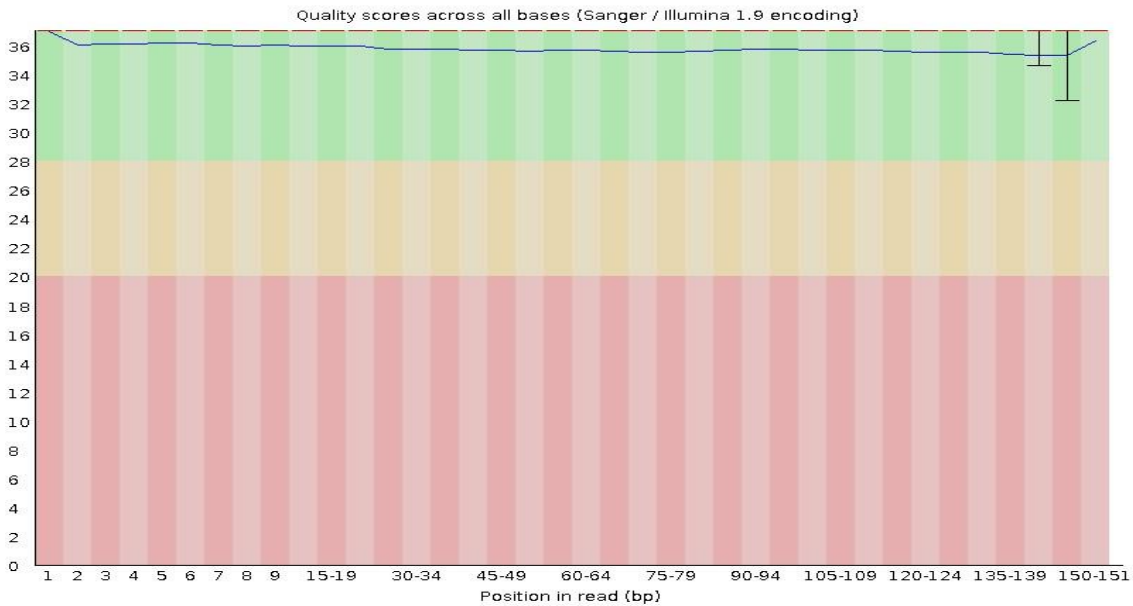
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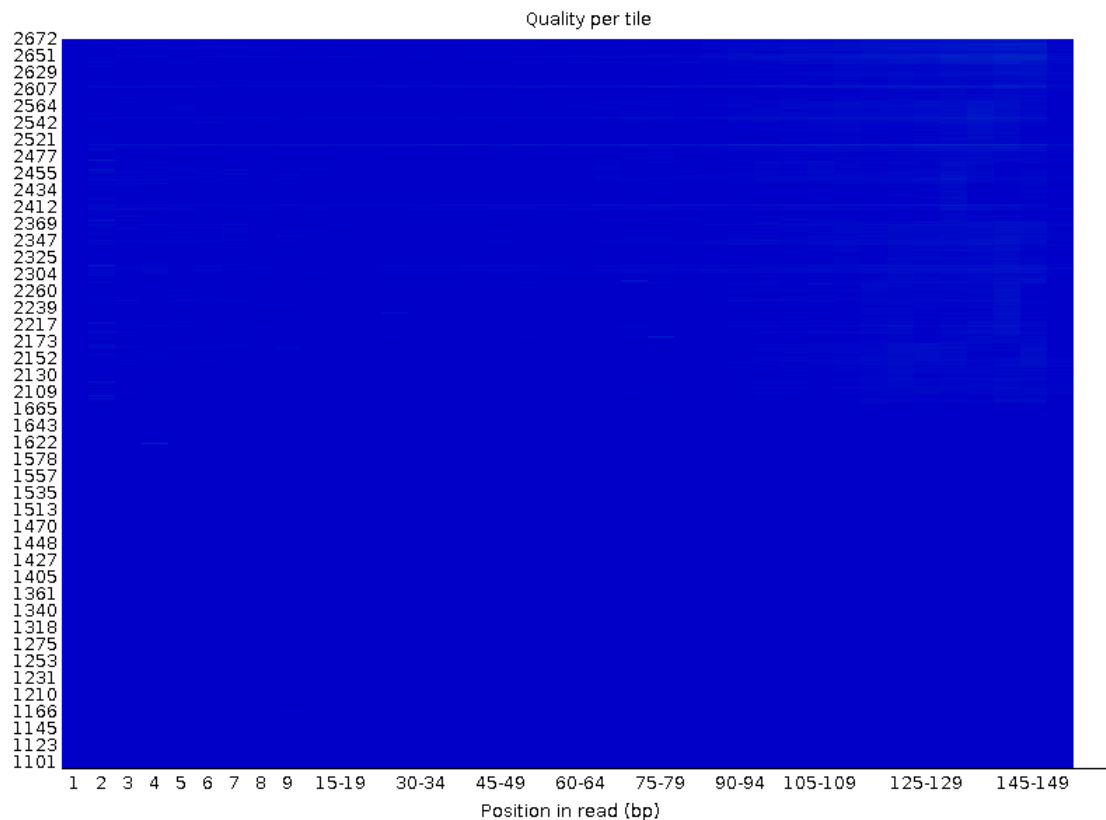
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**File S4.1.** Basic statistics of the of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 2).

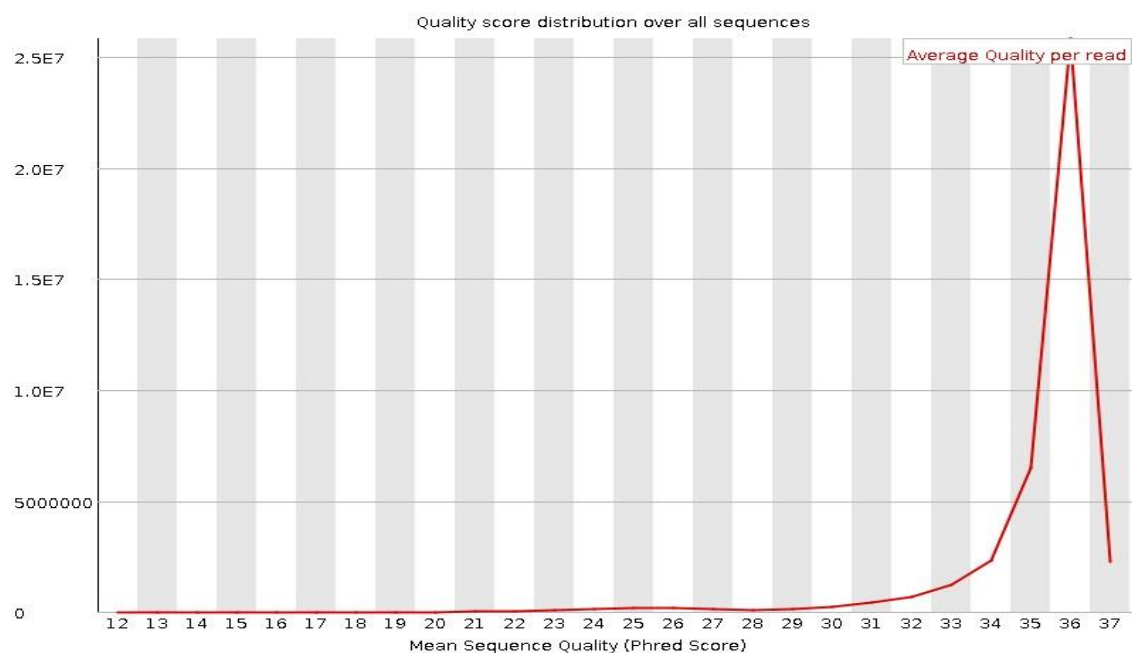
Measure	Value
Filename	trim.2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	41083929
Sequences flagged as poor quality	0
Sequence length	20-151
%GC	44



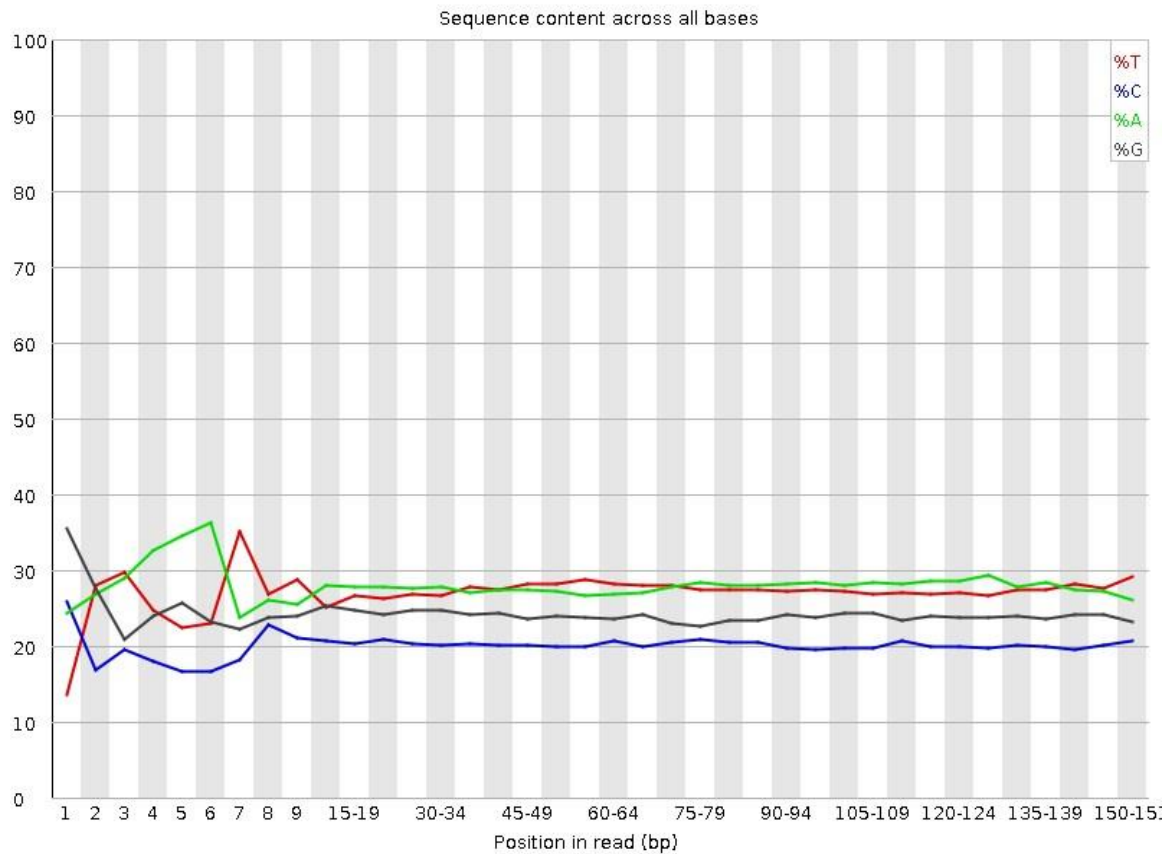
**File S4.2.** Summary of per base sequence quality of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 2).



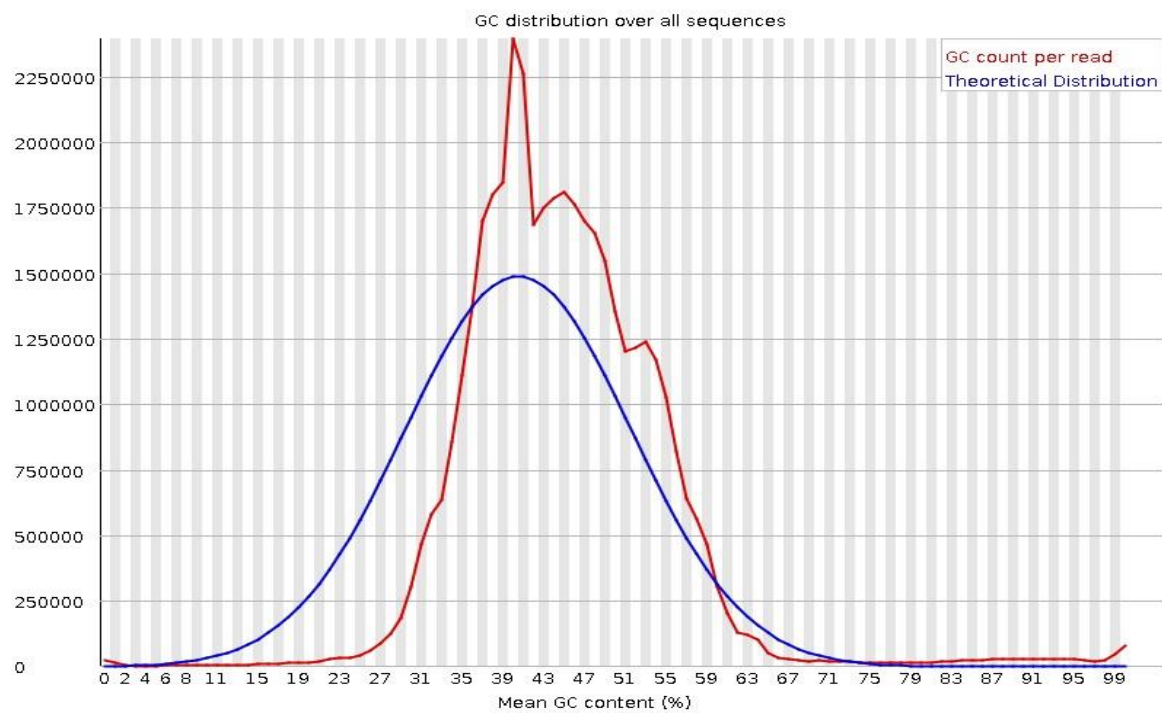
**File S4.3.** Summary of per tile sequence quality of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 2).



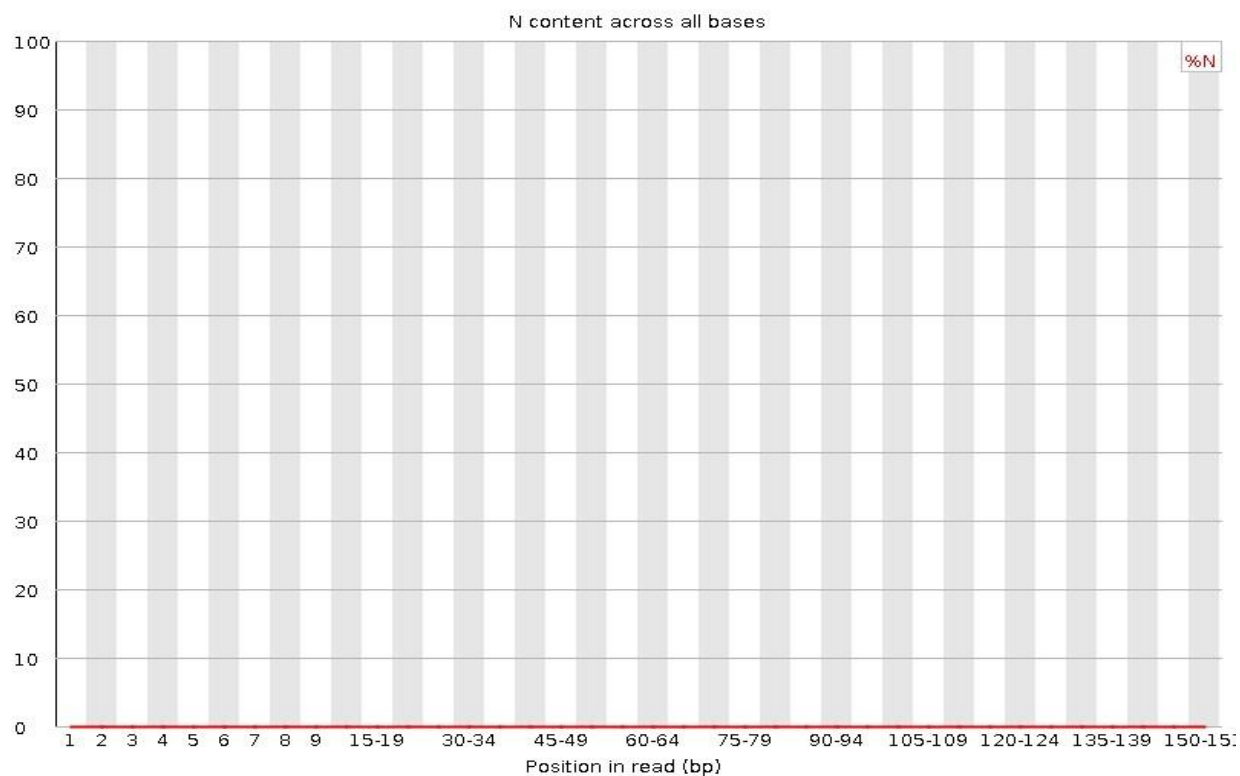
**File S4.4.** Summary of per sequence quality scores of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 2).



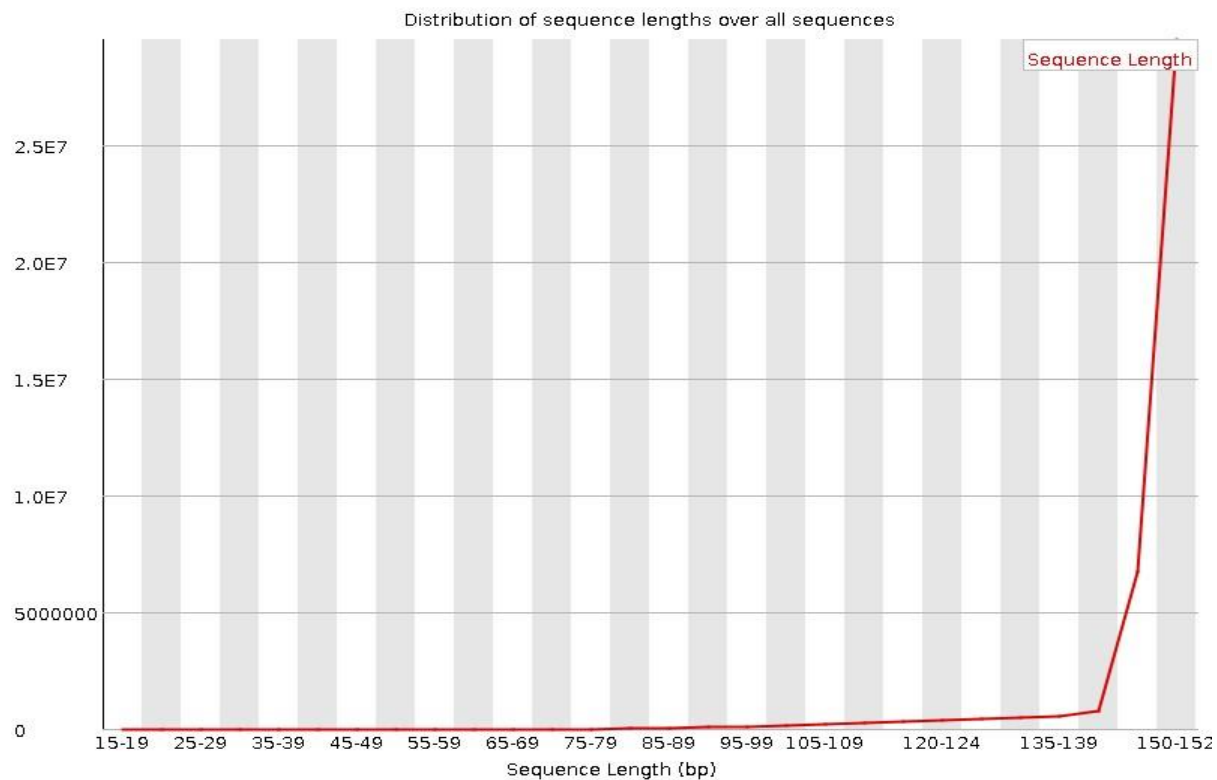
**File S4.5.** Summary of per base sequence content of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 2).



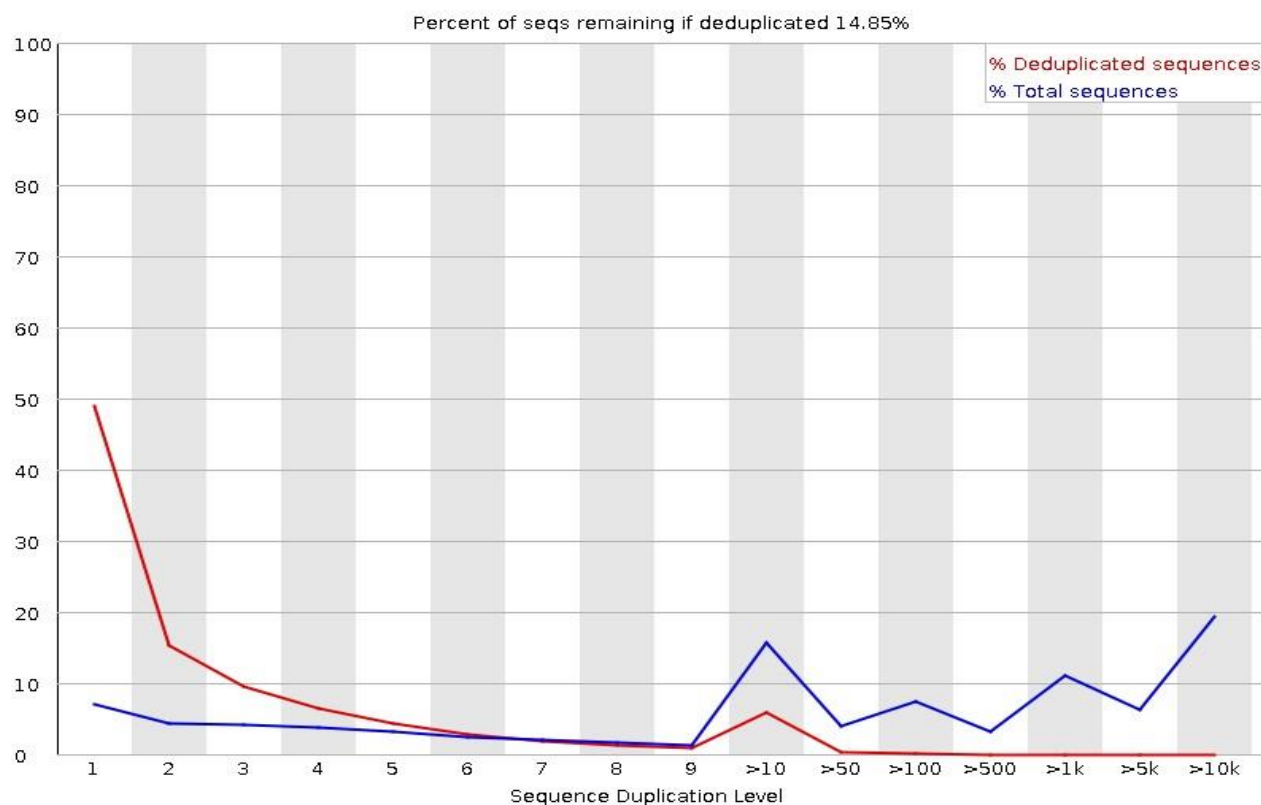
**File S4.6.** Summary of per sequence GC content of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 2).



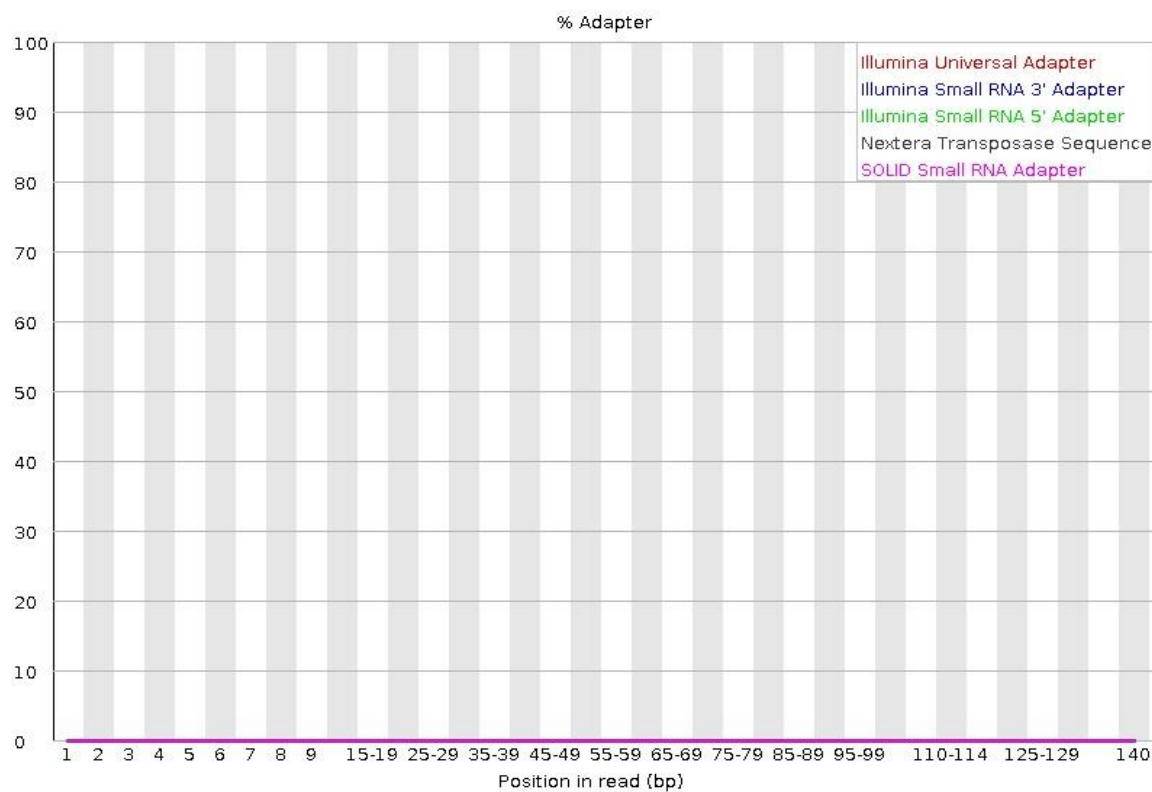
**File S4.7.** Per base N content plot of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 2).



**File S4.8.** Sequence length distribution plot of quality scores of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 2).



**File S4.9.** Sequences duplicated levels vs total sequences percentage of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 2).



**File S4.10.** Adapter content percentages of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 2).

**File S4.11.** Summary of overrepresented sequences of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 2).

[illegible]

GGGAGGTATCCCAATAGGAGGTTTCCTCCTATGGTTTTCAAACAATCAC	50031	0.12177754469393616	No Hit
TGGACATTAATTAGGGCTGAAAGCCCTAACTTAATGGACGGGAGGTATCC	47149	0.1147626362610061	No Hit
GCGTCGGCATCCAGACCGTCGGCTGATCGTGGTTTTACTAGGCTAGACTA	46984	0.11436101936599101	No Hit
TGGGAGTATTTGCACTTGTGGTAACGGTATTTGCATTATTGATGGTTTTT	44791	0.10902316572497242	No Hit
CTCGTAACCAAACATGCACAGCGGTCAAACAGTATGTCCCAAGGGGACTT	44429	0.1081420425977272	No Hit
CAAAGAATATCCCAATTATCCATAAACTGTAAC TAAGTGAGGCTCTCTC	44174	0.10752136194179482	No Hit
GCCCAAGCTGCTCACAGTATACGGGCGTCGGCATCCAGACCGTCGGCTGA	41532	0.10109062353797758	No Hit