

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

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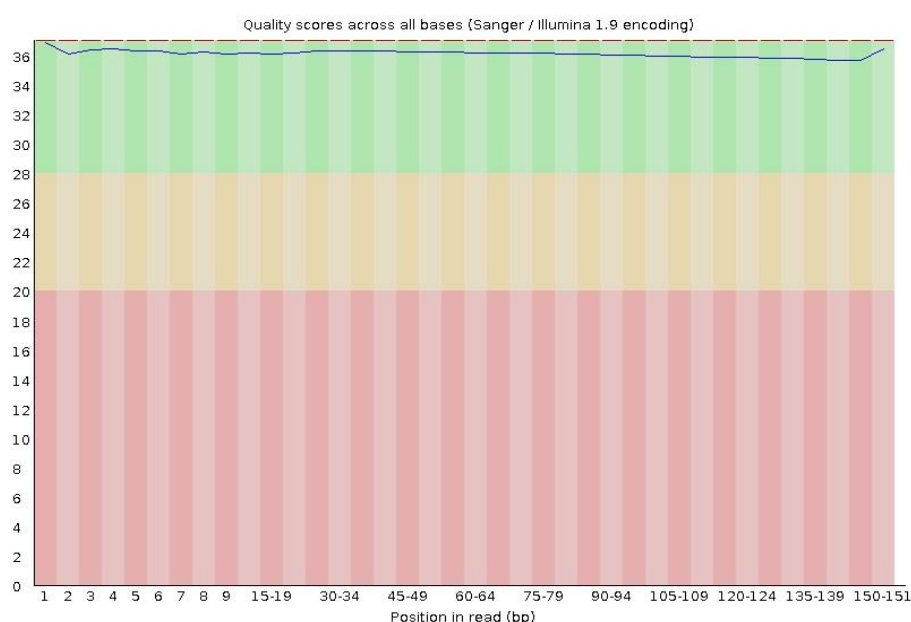
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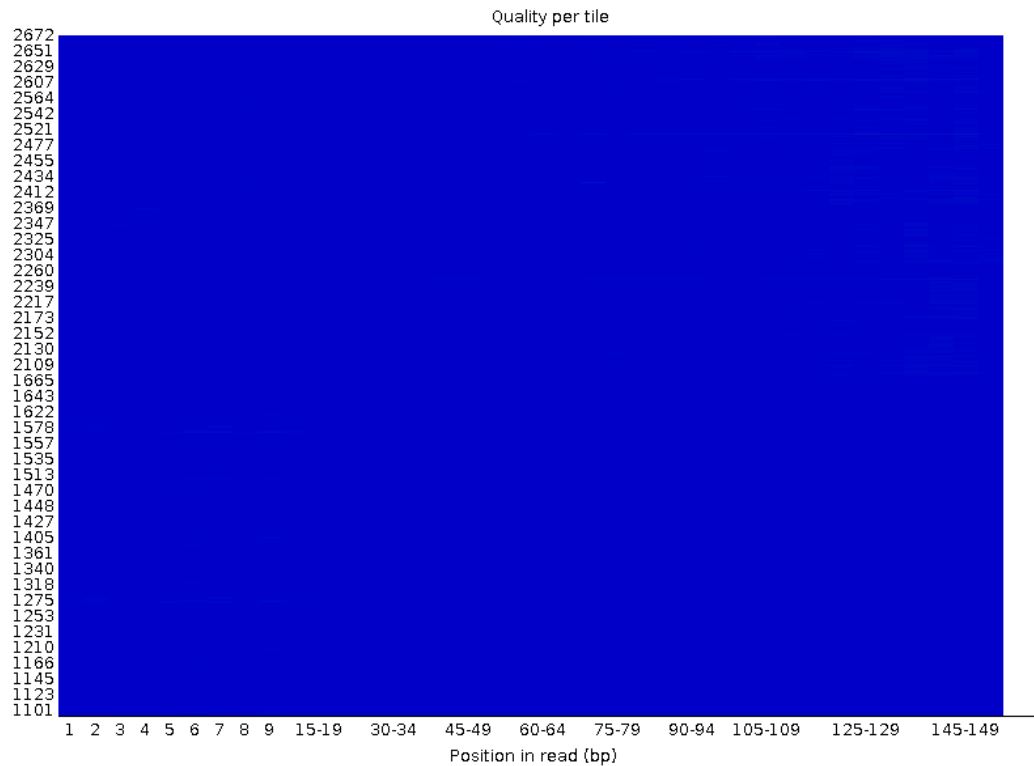
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**File S3.1.** Basic statistics of the of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).

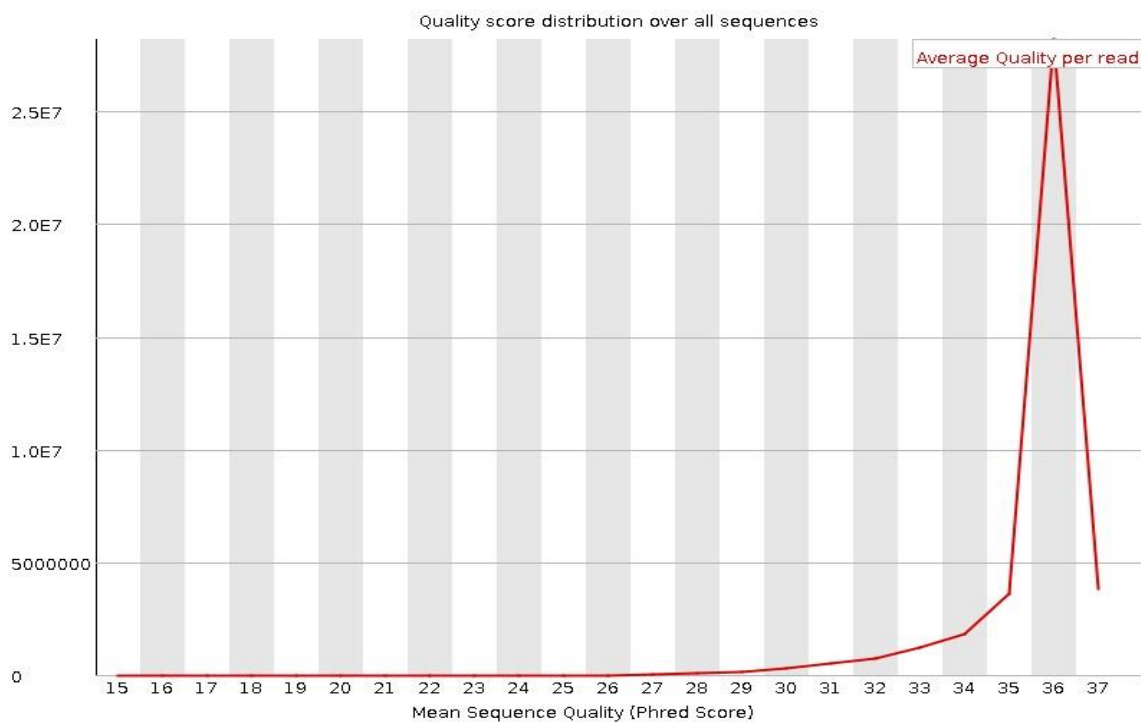
Measure	Value
Filename	trim.1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	41083929
Sequences flagged as poor quality	0
Sequence length	20-151
%GC	44



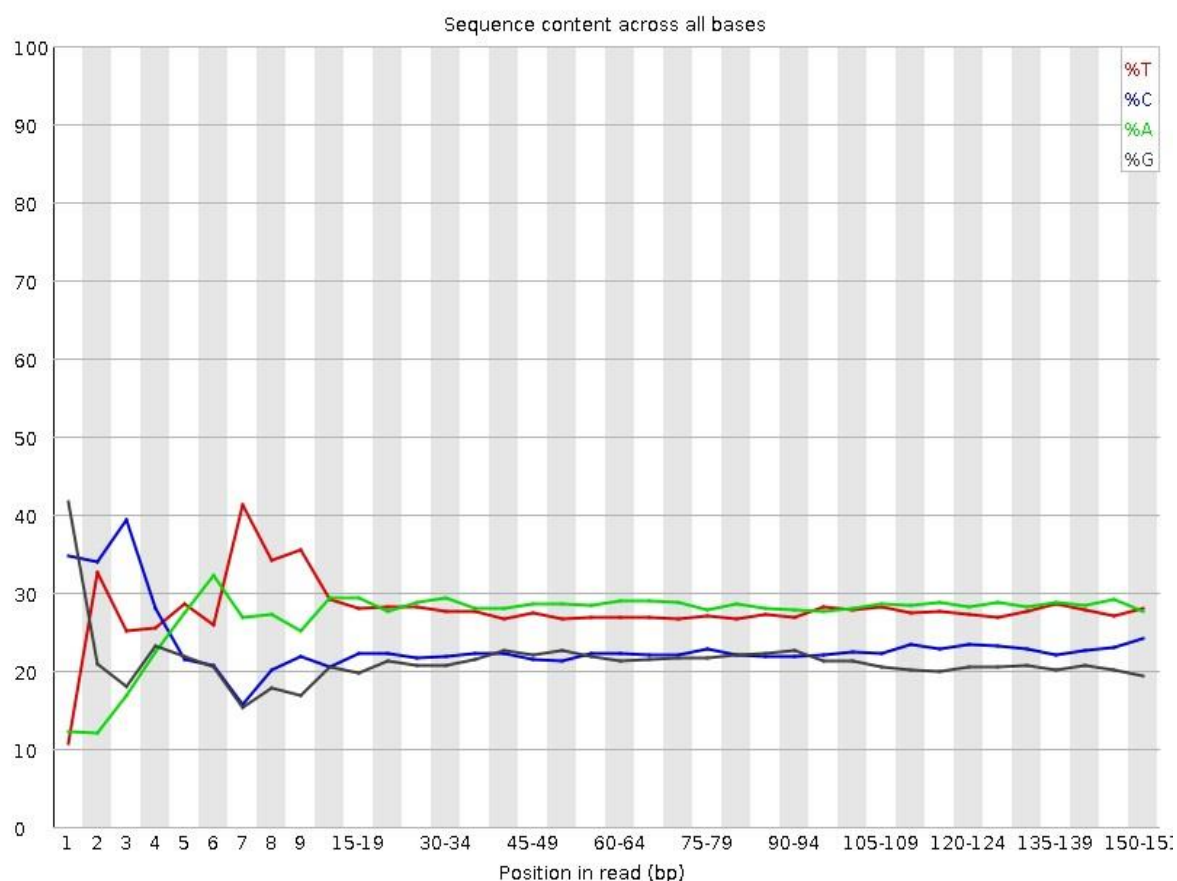
**File S3.2.** Summary of per base sequence quality of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).



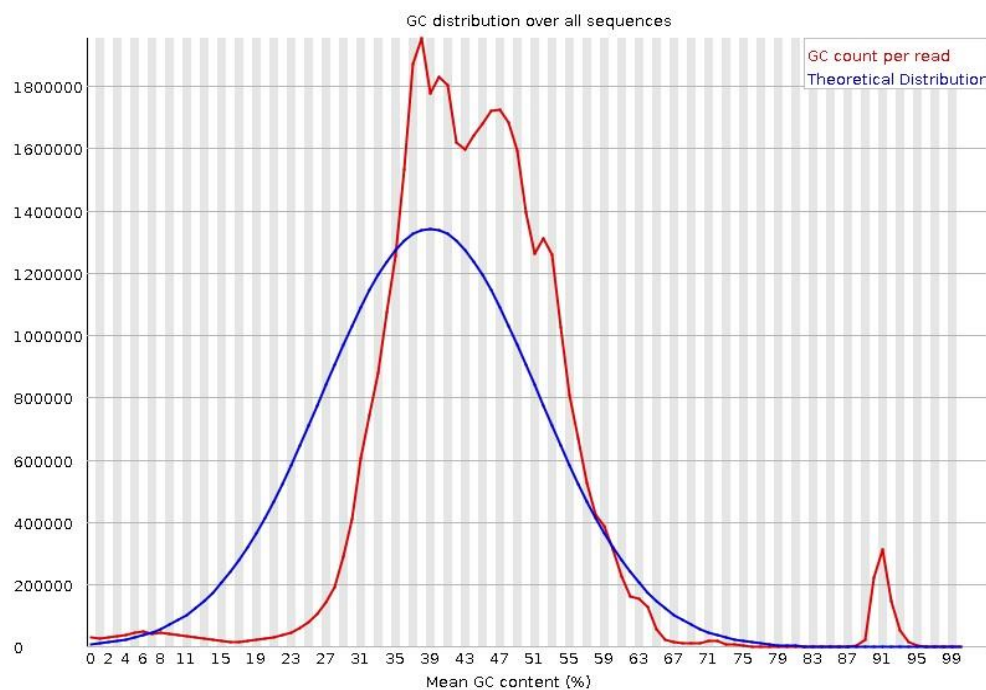
**File S3.3.** Summary of per tile sequence quality of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).



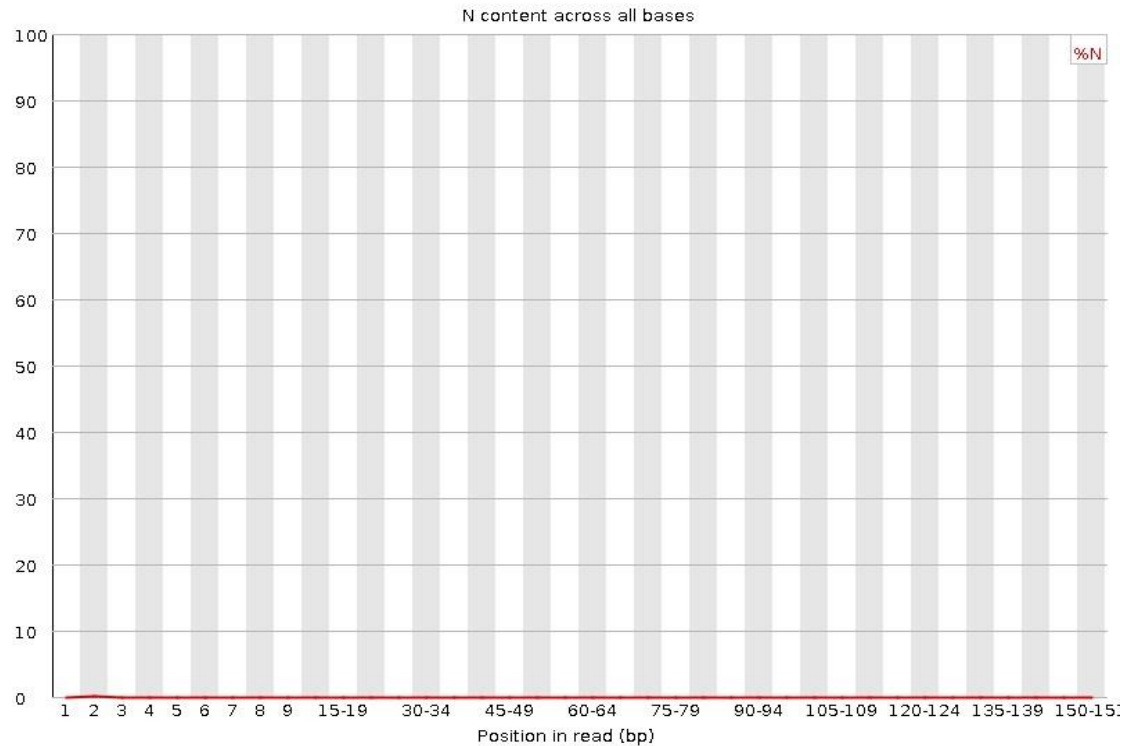
**File S3.4.** Summary of per sequence quality scores of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).



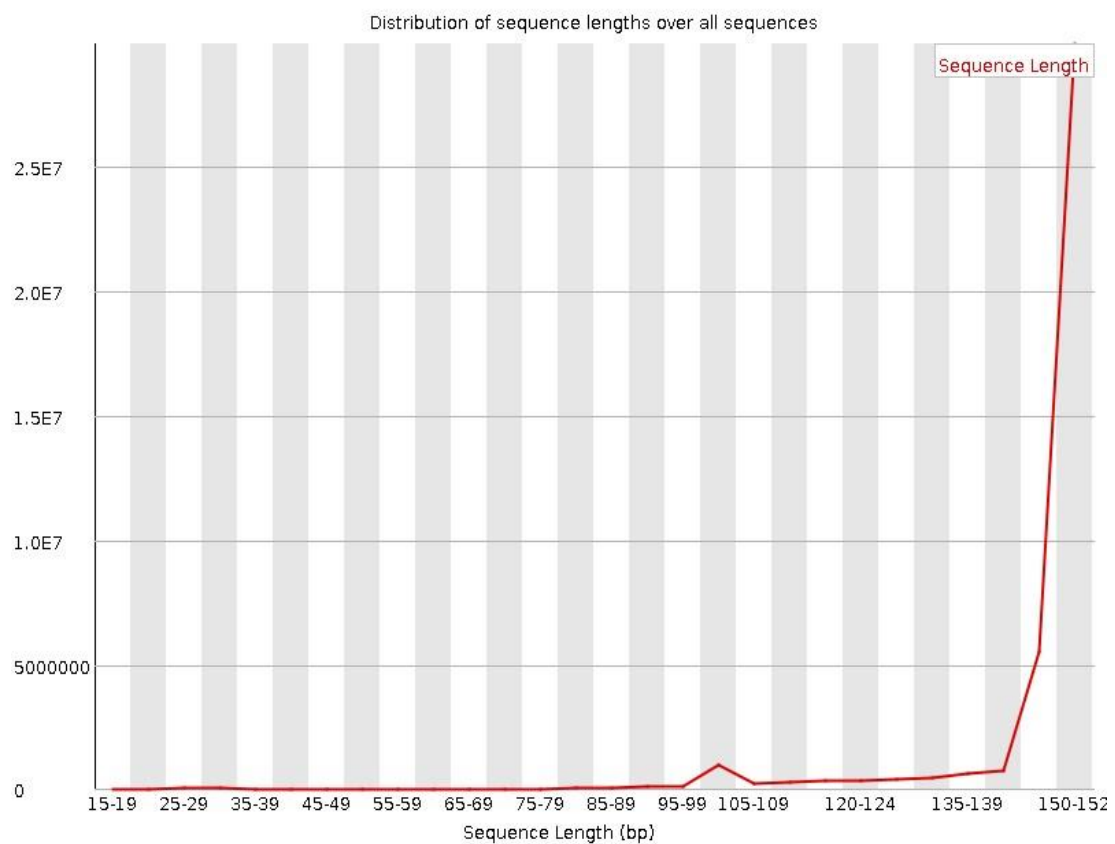
**File S3.5.** Summary of per base sequence content of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).



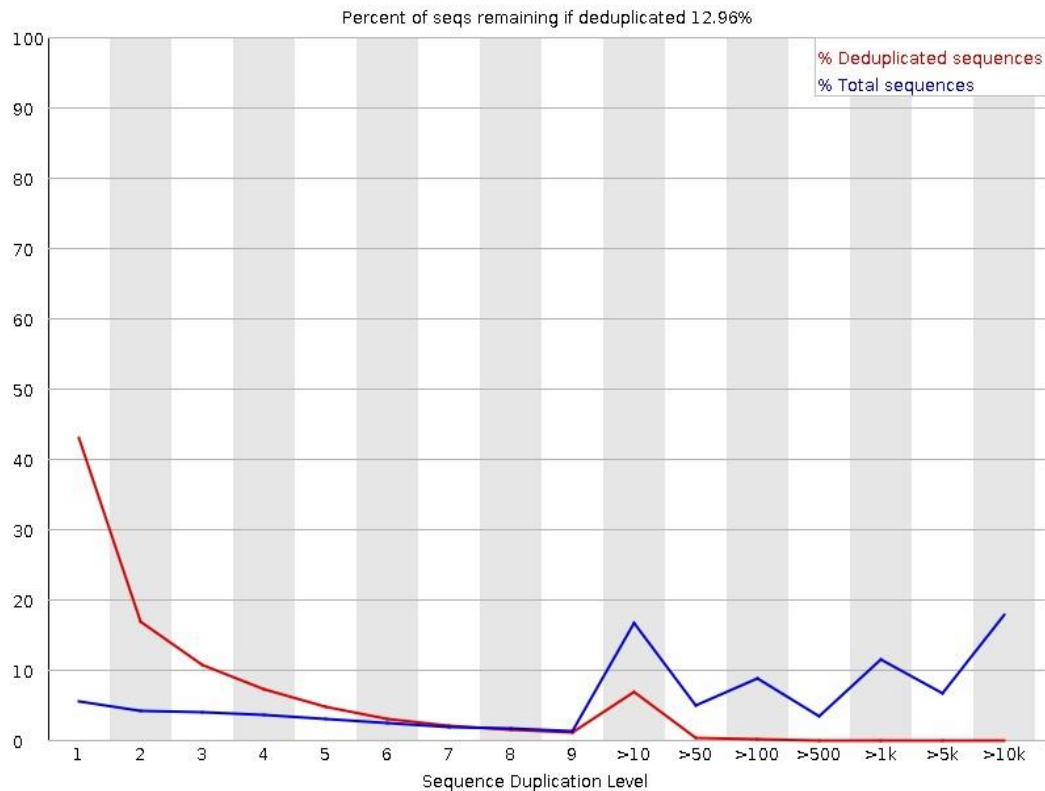
**File S3.6.** Summary of per sequence GC content of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).



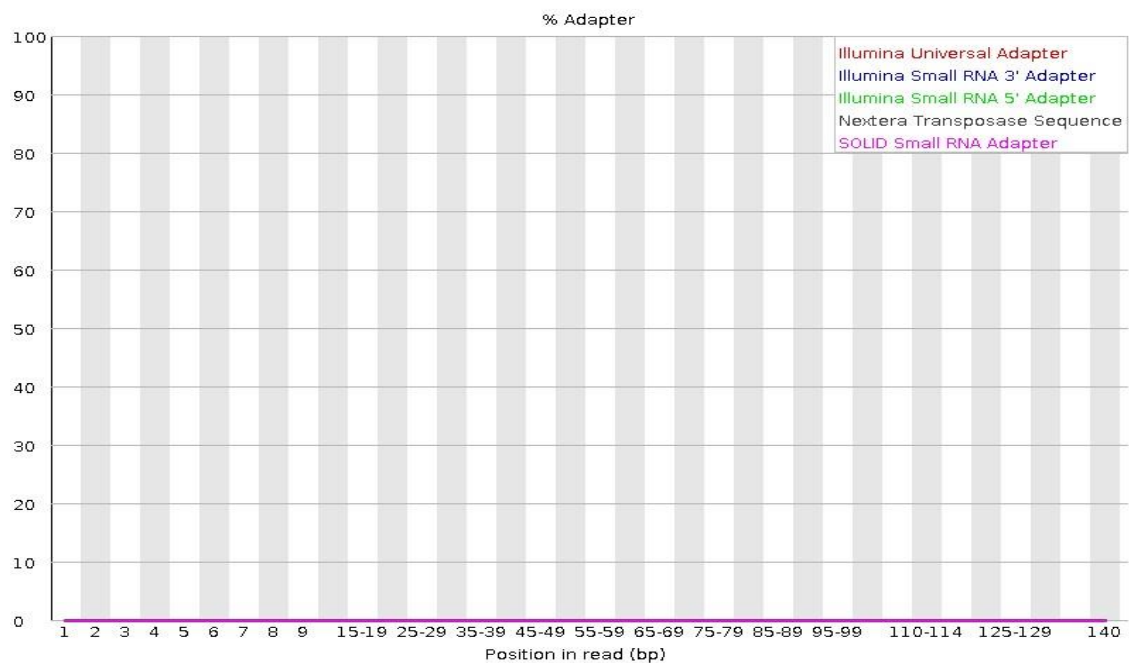
**File S3.7.** Per base N content plot of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).



**File S3.8.** Sequence length distribution plot of quality scores of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).



**File S3.9.** Sequences duplicated levels vs total sequences percentage of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).



**File S3.10.** Adapter content percentages of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).

**File S3.11.** Summary of overrepresented sequences of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).

[illegible]