

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

Hassan S. Al-Zahrani^a, Tarek A. A. Moussa^{a,b*}, Hameed Alsamadany^a, Rehab M. Hafez^b and Michael P. Fuller^c

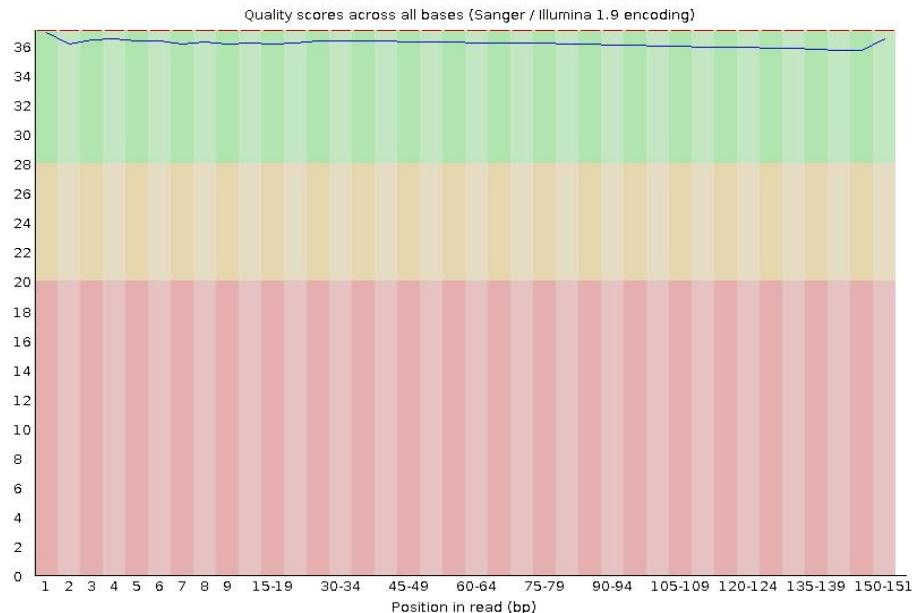
^a Biological Sciences Department, Faculty of Science, King Abdulaziz University, Jeddah, Saudi Arabia

^b Botany and Microbiology Department, Faculty of Science, Cairo University, Giza 12613, Egypt

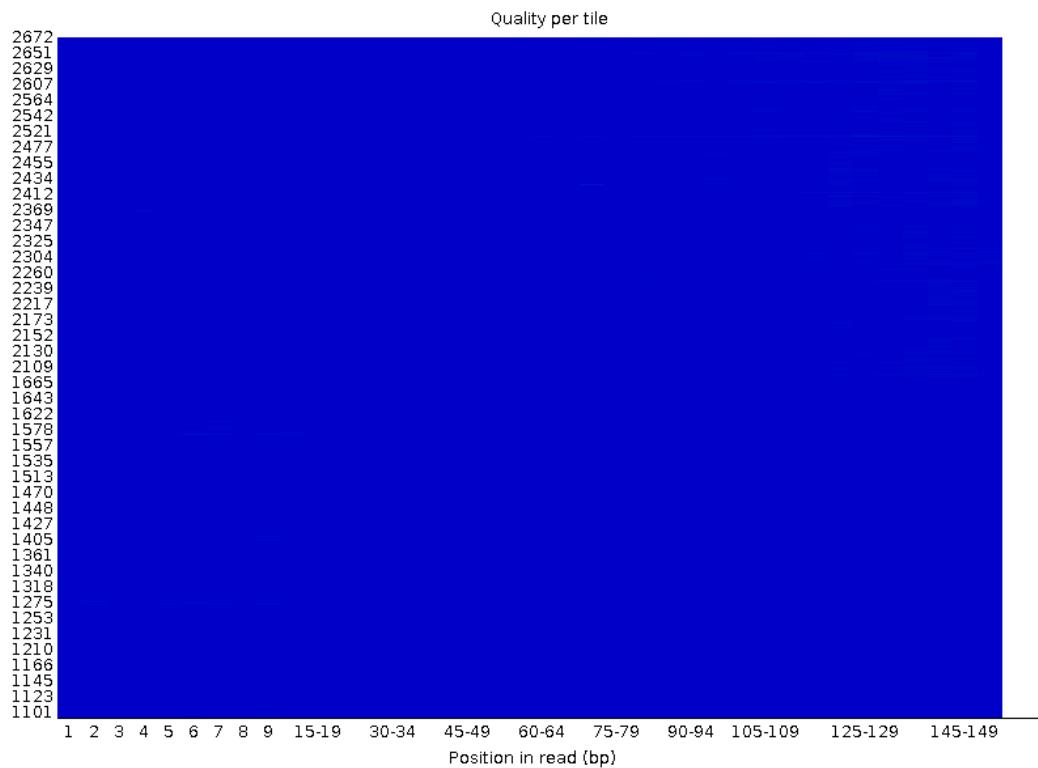
^c School of Biological and Marine Science, Faculty of Science and Engineering, University of Plymouth, Plymouth, UK

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

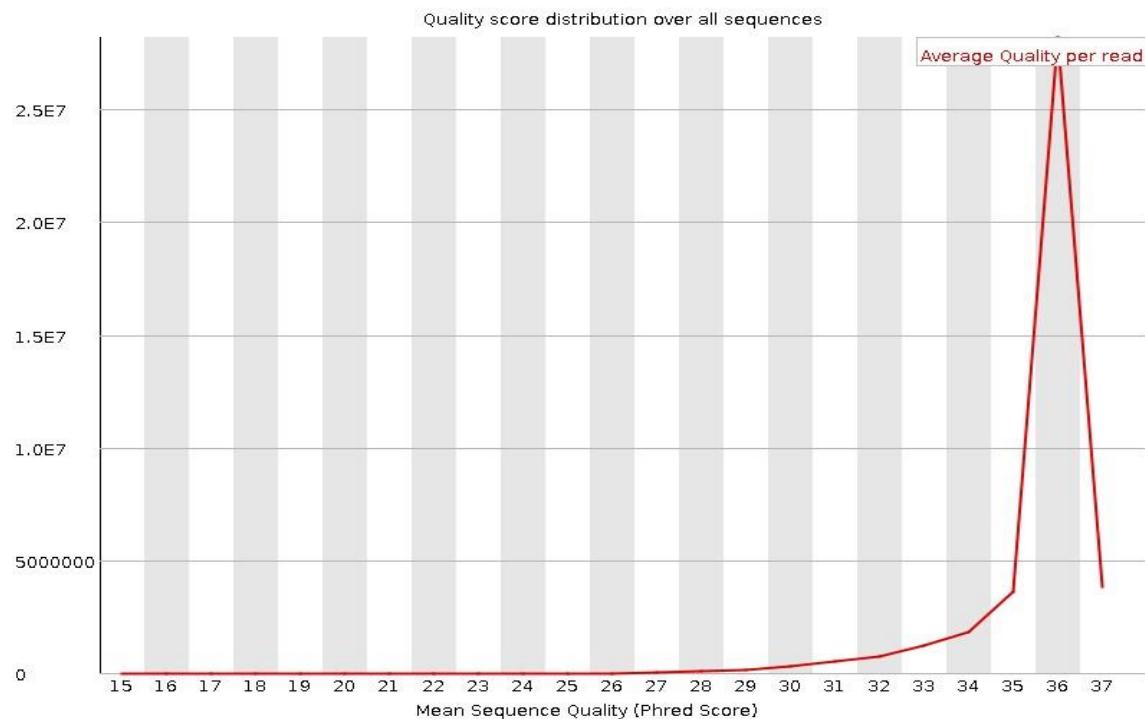
Measure	Value
Filename	trim.1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	41083929
Sequences flagged as poor quality	0
Sequence length	20-151
%GC	44



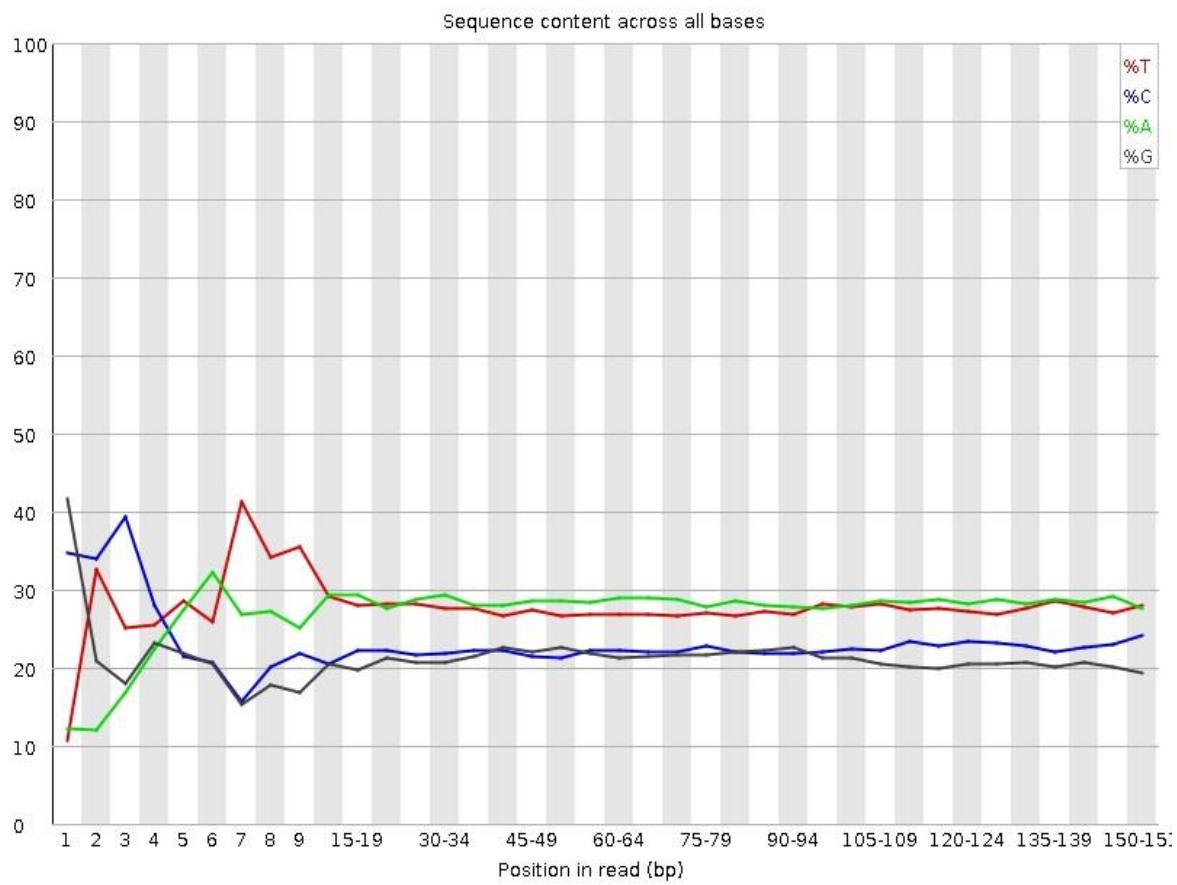
File S3.2. Summary of per base sequence quality of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).



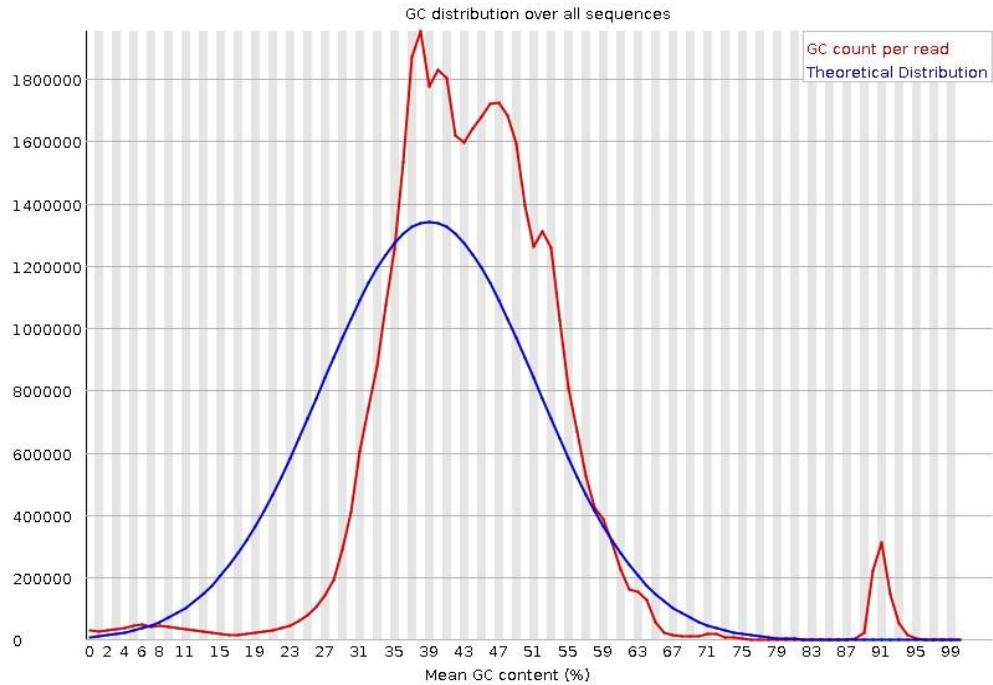
File S3.3. Summary of per tile sequence quality of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).



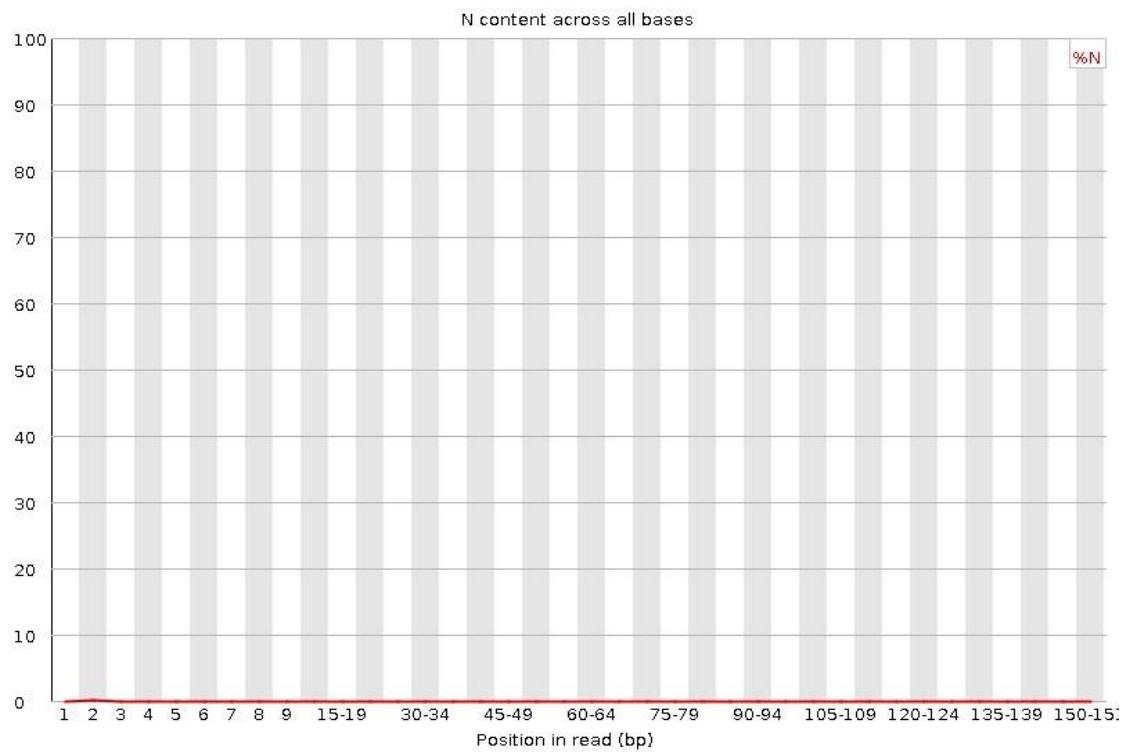
File S3.4. Summary of per sequence quality scores of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).



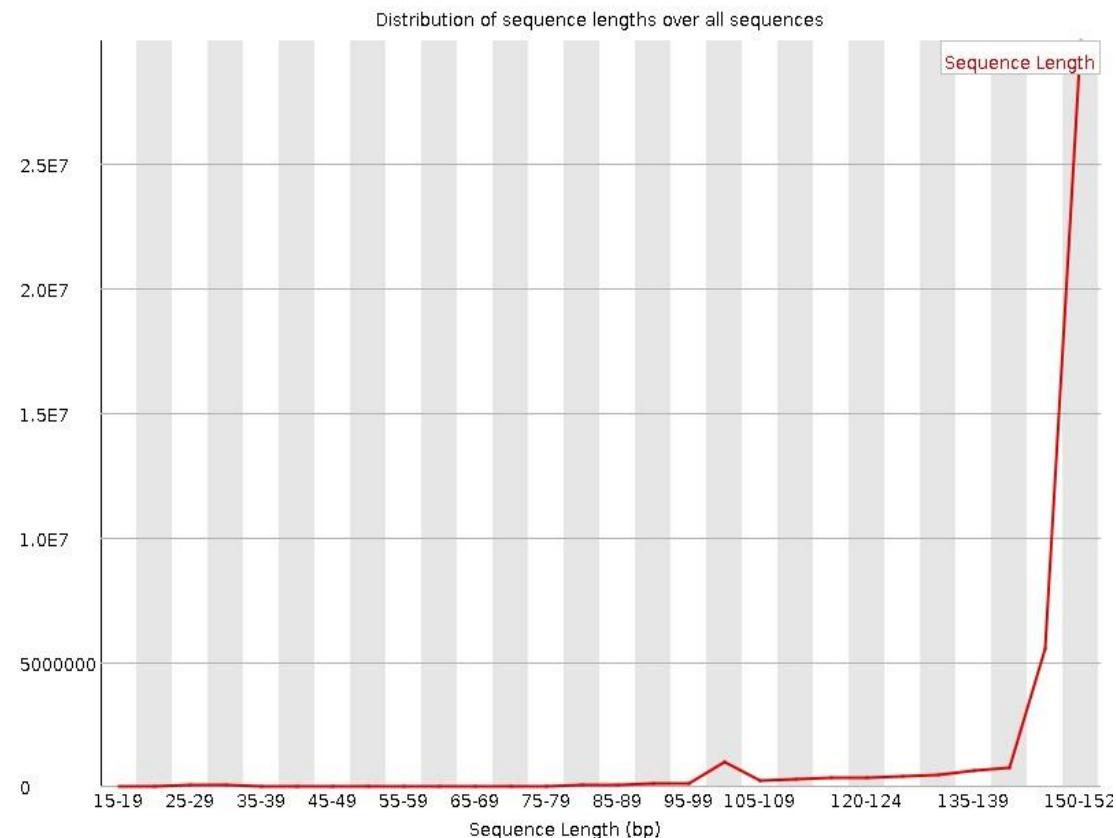
File S3.5. Summary of per base sequence content of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).



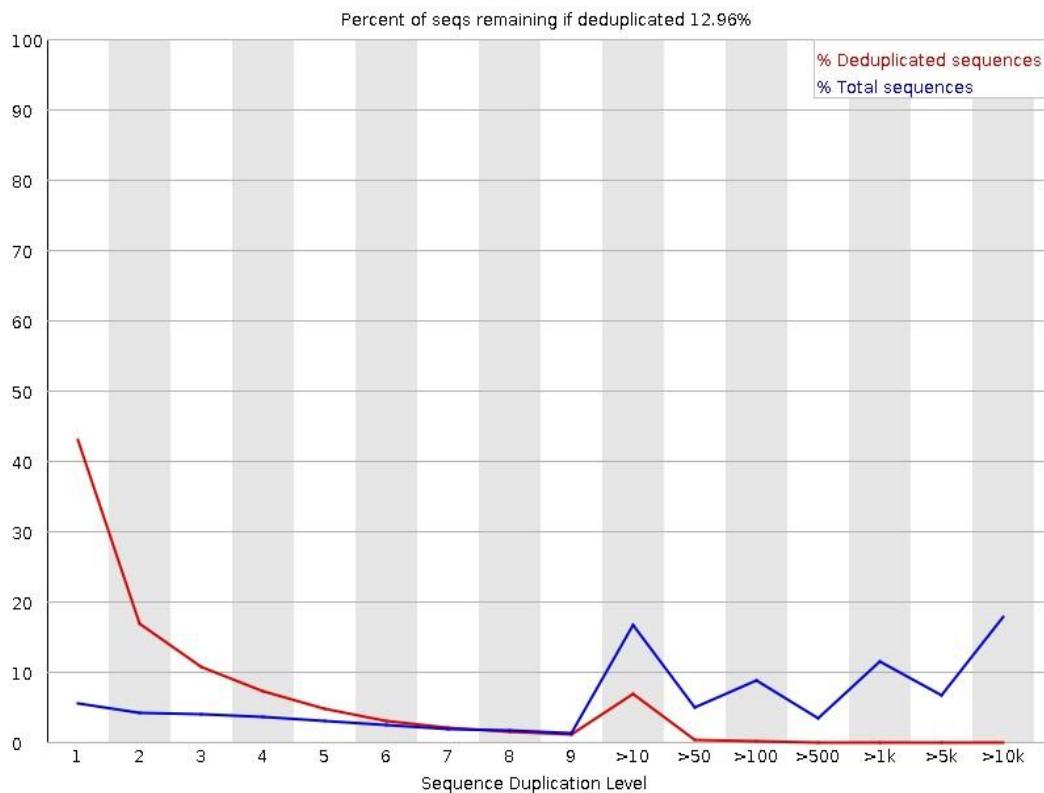
File S3.6. Summary of per sequence GC content of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).



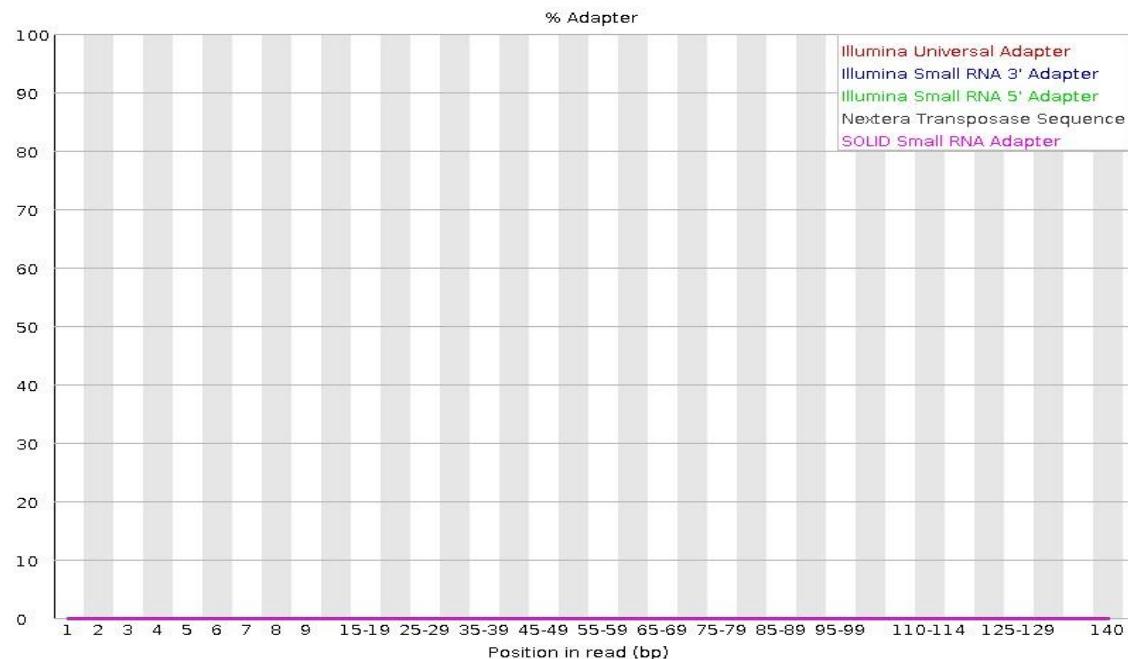
File S3.7. Per base N content plot of the trimmed data in the cv. super strain B transcriptome under drought stress (fastq 1).



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).

Sequence	Count	Percentage	Source
GCCTTATGTGATAGATGCCTTTAAAAATCTAAGTGCTGGGGTTATGA	331079	0.8058601211193797	No Hit
GCCGTCTTCTGCTTAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	307690	0.7489303177405452	No Hit
CCCATTAGTTATAATGATGCCTTATGTGATAGATGCCTTTAAAAAT	139482	0.3395050166696569	No Hit
GCCTCACTTAGTTACAGTTATGGATAATTGGGATATTCTTGGTATAG	104123	0.25343973308881923	No Hit
GCCTCTTAAAAATCTAAGTGCTGGGGTTATGAGTAGGGATGAGCATAA	101559	0.24719884994446367	No Hit
CTTATGTGATAGATGCCTTTAAAAATCTAAGTGCTGGGGTTATGAGT	91963	0.22384178494710183	No Hit
GGGGTTATGAGTAGGGATGAGCATAAACCAACAACTCTCAAAGAAGATGG	89410	0.21762767626241397	No Hit
GCCCATAACAATAGGAAATATCAGAAATCCAATAAGAATCAGCAATTCA	86690	0.21100708259913503	No Hit
GGGAAGCTATACTATAGGTGGCTATCTATCCCTACCAAGGTTATATT	74359	0.18099291331167475	No Hit
GGAAGCTATACTATAGGTGGCTATCTATCCCTACCAAGGCTTATATTG	67693	0.16476759075306552	No Hit
GGGCTATTGATATTAAACAAATATCCAGCAAAGGTTTCCAGGAGATGT	66741	0.1624503829709179	No Hit
GTGGCTATCTATCCCTACCAAGGCTTATATTGAAGTATAACCAATGAGA	60497	0.14725222604683208	No Hit
GCTGGGGTTATGAGTAGGGATGAGCATAAACCAACAACTCTCAAAGAAGA	58493	0.14237440630373985	No Hit
GCCCGTTTCAGGTGGCCTCAGCGTACGGCGGGACCTCTGAGAATTGGGA	57581	0.14015456019311104	No Hit
CAATAGGATTGTAGCCCAGGATGAGTCCCTCAGCGTGACGCAGTAAC	56414	0.13731403342654983	No Hit
GCAGTAGTTATAAGGAATATATCCCATTAGTTATAATGATGCC	55741	0.1356759233032459	No Hit
CCAGGAGATGTTGAACTCTACCAATTGGAGCTTCTAGCTGTCTAGC	53679	0.13065692913645138	No Hit
GATGCCCTATGTGATAGATGCCTTTAAAAATCTAAGTGCTGGGGTTA	50511	0.12294588475216185	No Hit
GGGATATTCTTGGTATAGTTGGATTAAATCATTAATAGCATGATG	48586	0.11826035431031925	No Hit
GCCGTCTTCTGCTTGAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	48045	0.11694353770302739	No Hit
GGCAGTTCCAGAACGTGTATCACATCTAGGCATGGAATTCTATGCCAG	45850	0.11160081597843283	No Hit
GTGATAGATGCCCTTTAAAATCTAAGTGCTGGGGTTATGAGTAGGGA	43883	0.10681305578149548	No Hit
GTCCTTACAAGTCCGCTCTGGGAGCTTGATTGATAATTCTGTATAAG	43826	0.10667431539958118	No Hit
GGCGTGGTAGAATTACTGGCACTCCAATGATTCCATATAACGCCATAAT	42577	0.10363419720640643	No Hit
GTAGTTATAAGGAATATATCCCATTAGTTATAATGATGCC	42108	0.10249263160784841	No Hit
AGGAGATGTTGAACTCTACCAATTGGAGCTTCTAGCTGTCTAGCAG	41943	0.10209101471283333	No Hit