

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

Hassan S. Al-Zahrani<sup>a</sup>, Tarek A. A. Moussa<sup>a,b\*</sup>, Hameed Alsamadany<sup>a</sup>, Rehab M. Hafez<sup>b</sup> and Michael P. Fuller<sup>c</sup>

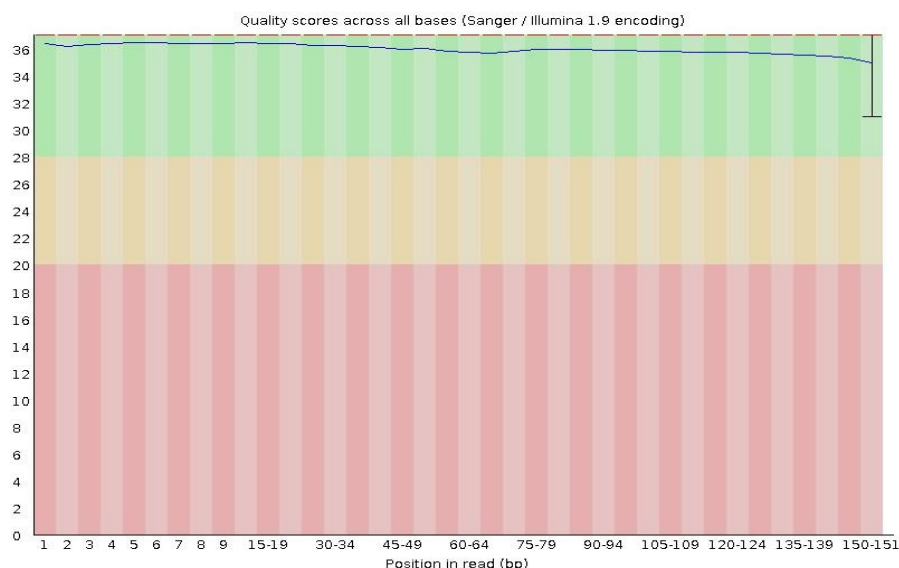
<sup>a</sup> Biological Sciences Department, Faculty of Science, King Abdulaziz University, Jeddah, Saudi Arabia

<sup>b</sup> Botany and Microbiology Department, Faculty of Science, Cairo University, Giza 12613, Egypt

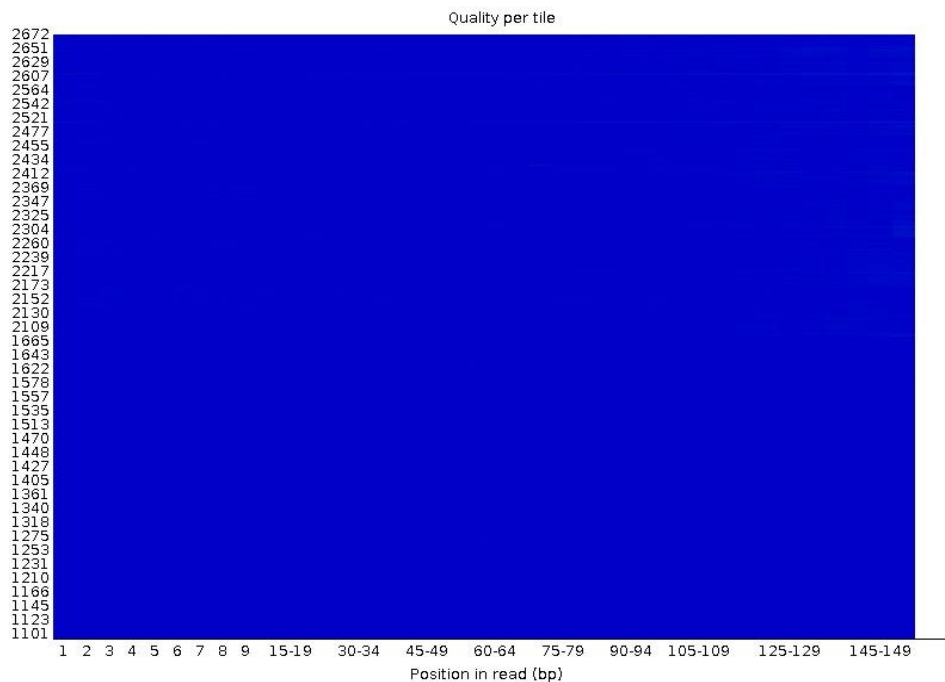
<sup>c</sup> School of Biological and Marine Science, Faculty of Science and Engineering, University of Plymouth, Plymouth, UK

**File S1.1.** Basic statistics of the of the raw data in the cv. super strain B transcriptome under drought stress (fastq 1).

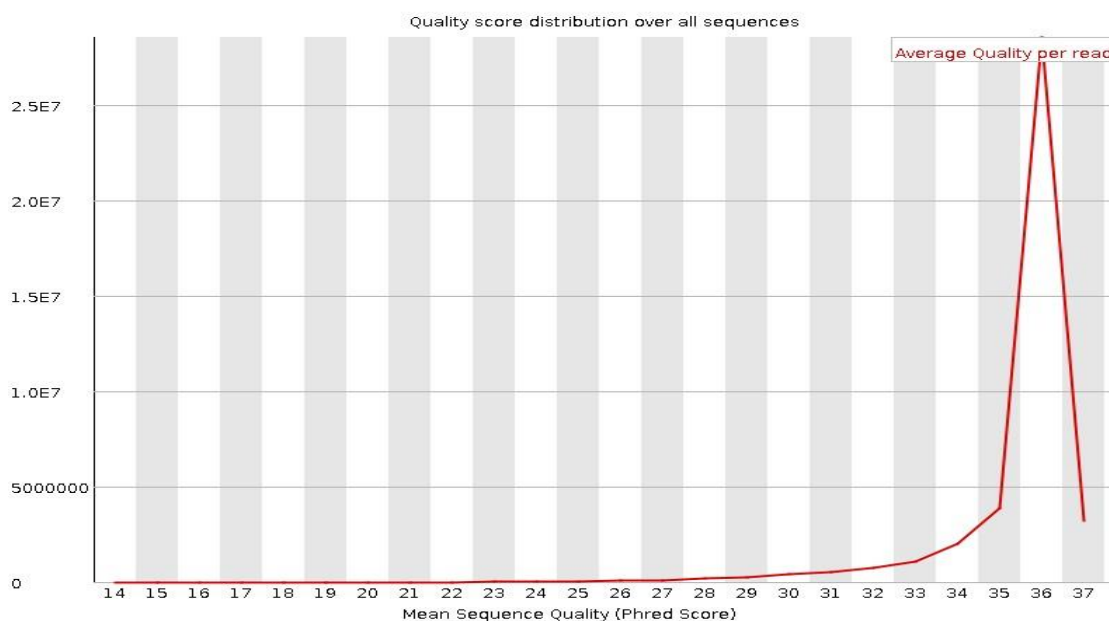
Measure	Value
Filename	1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	41779729
Sequences flagged as poor quality	0
Sequence length	151
%GC	44



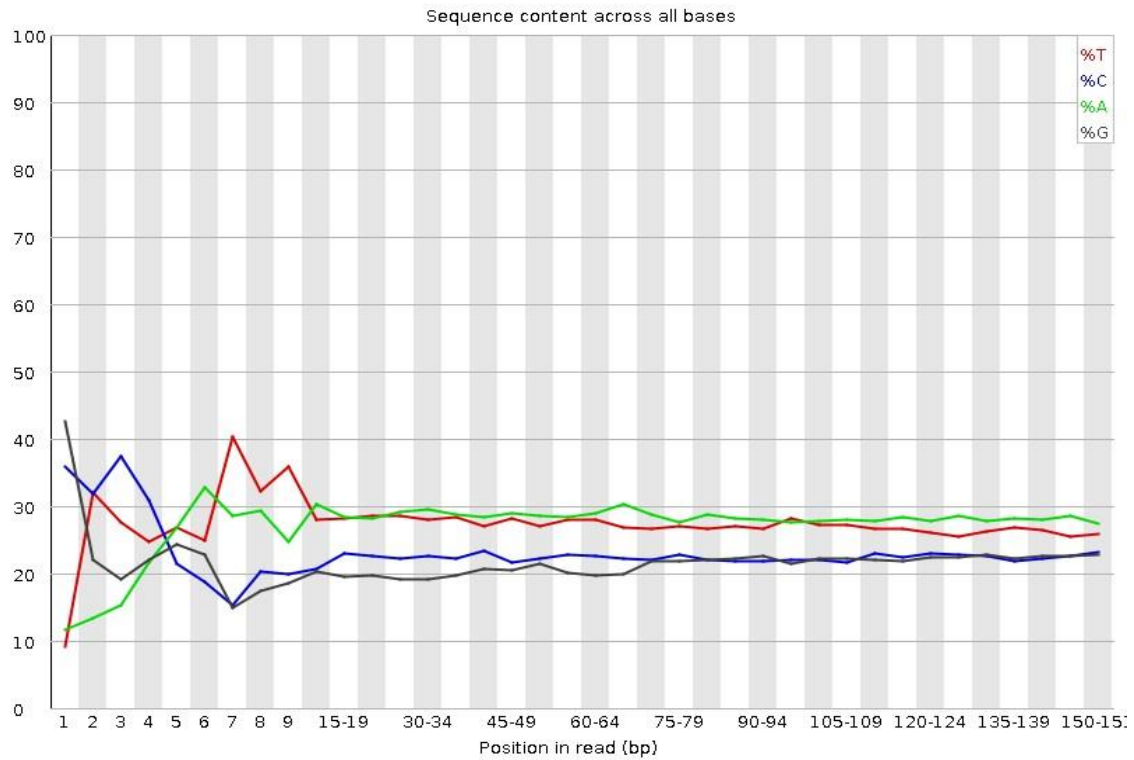
**File S1.2.** Summary of per base sequence quality of the raw data in the cv. super strain B transcriptome under drought stress (fastq 1).



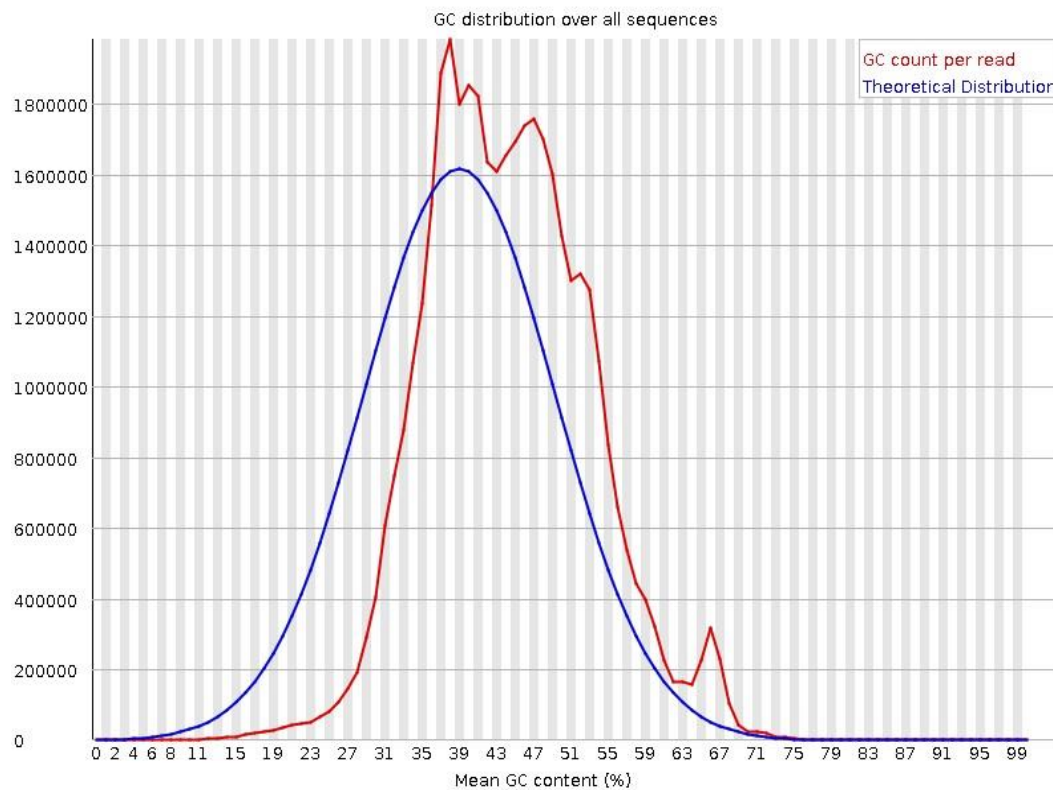
**File S1.3.** Summary of per tile sequence quality of the raw data in the cv. super strain B transcriptome under drought stress (fastq 1).



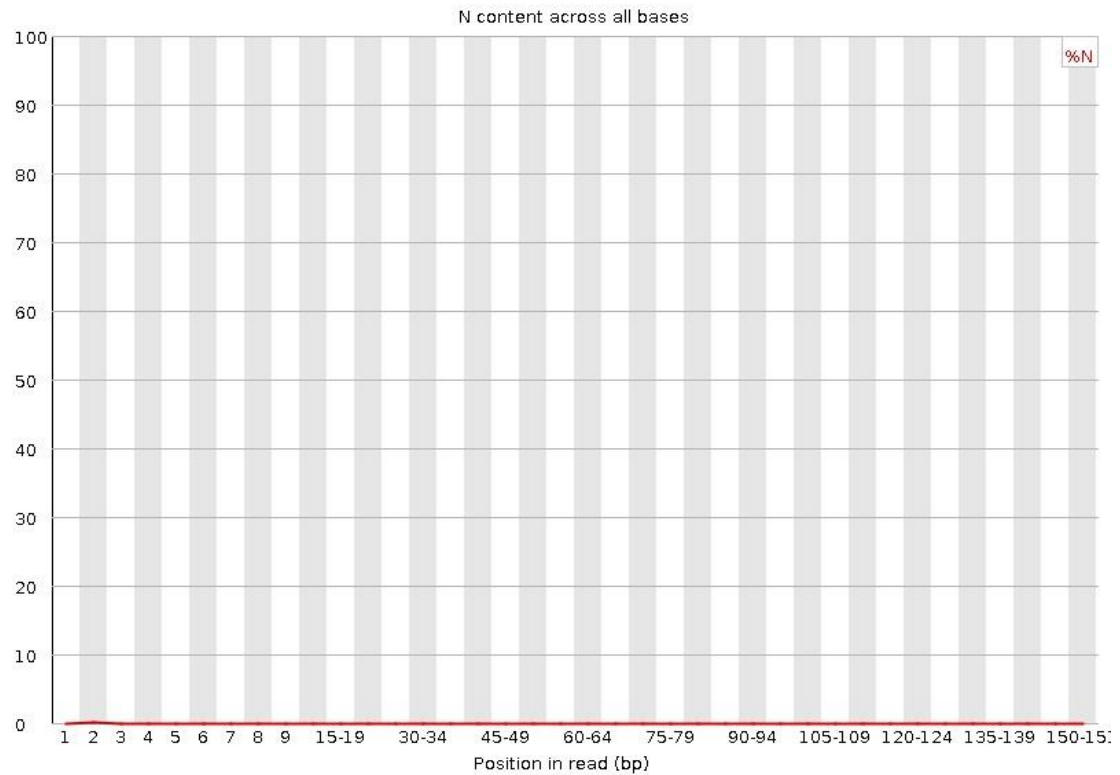
**File S1.4.** Summary of per sequence quality scores of the raw data in the cv. super strain B transcriptome under drought stress (fastq 1).



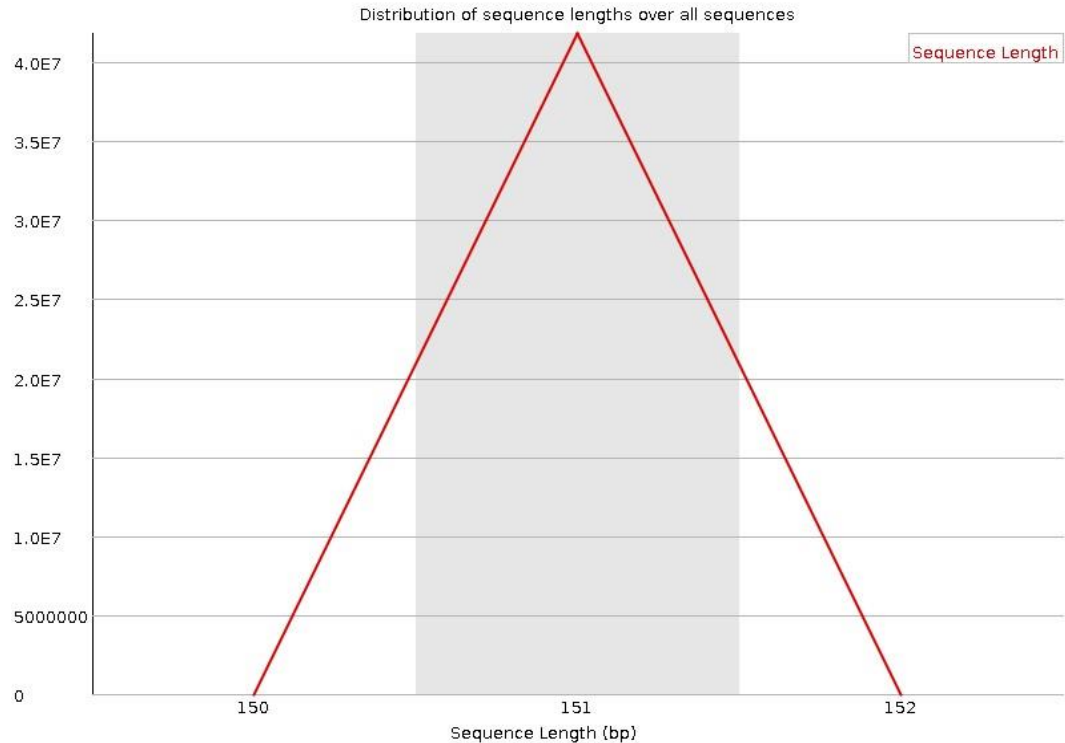
**File S1.5.** Summary of per base sequence content of the raw data in the cv. super strain B transcriptome under drought stress (fastq 1).



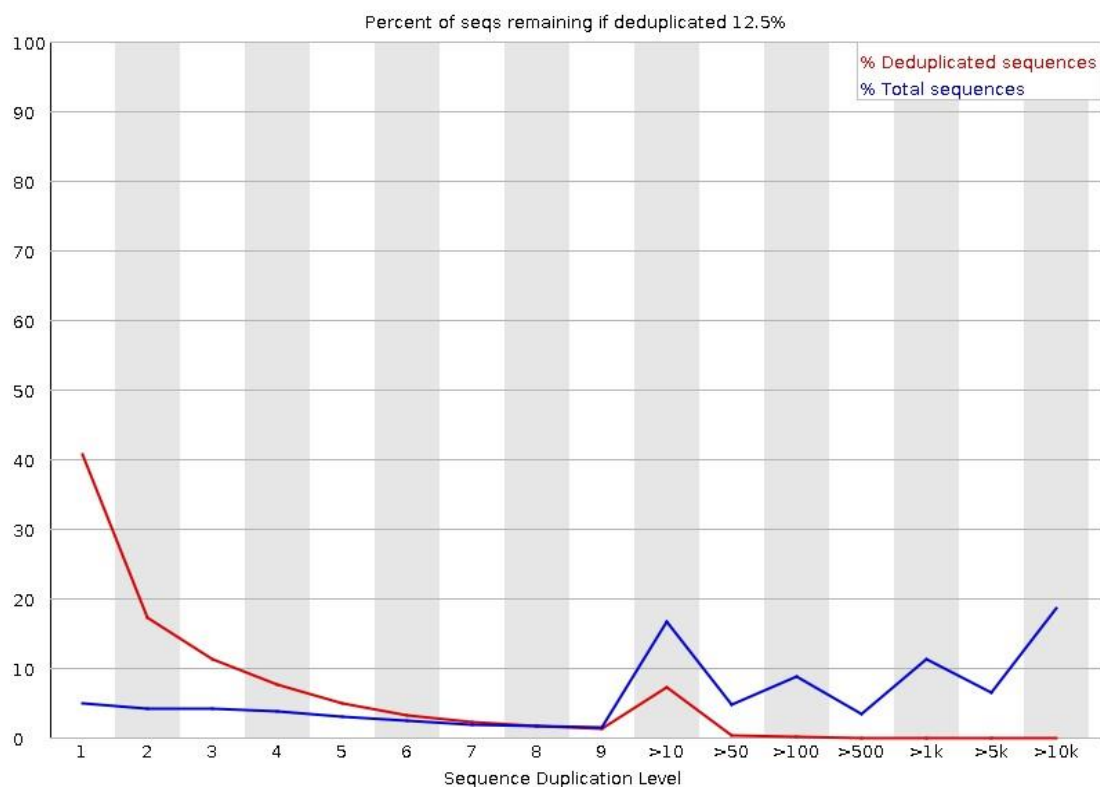
**File S1.6.** Summary of per sequence GC content of the raw data in the cv. super strain B transcriptome under drought stress (fastq 1).



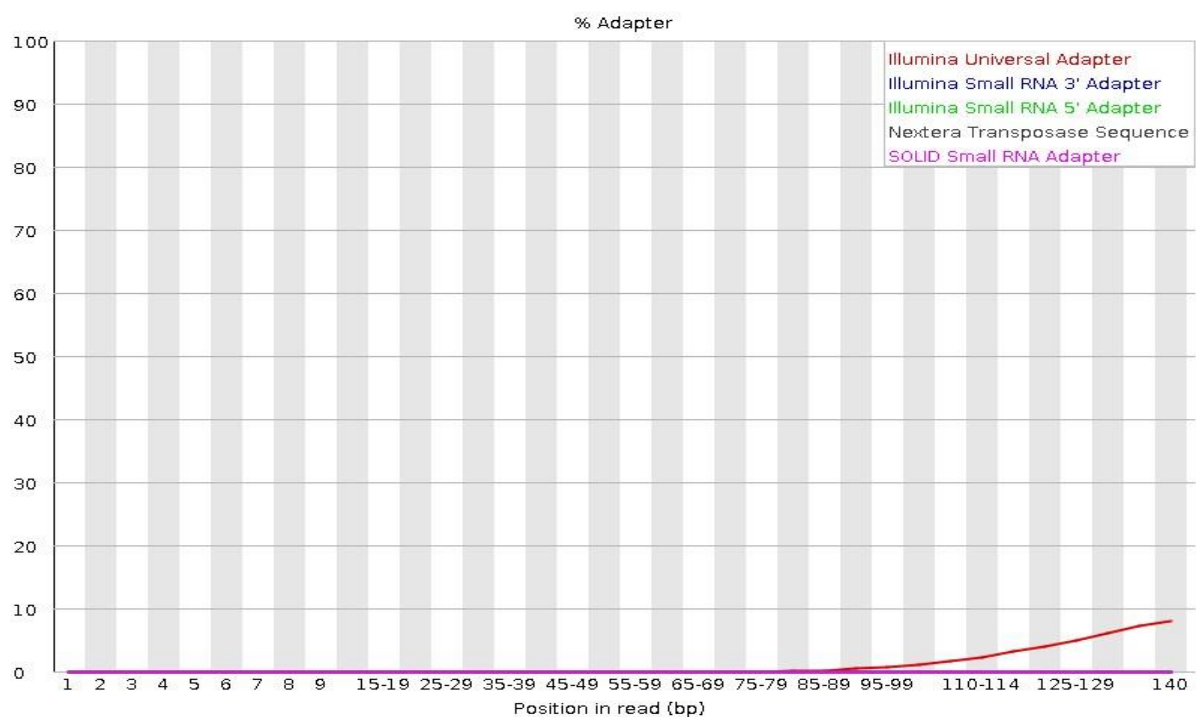
**File S1.7.** Per base N content plot of the raw data in the cv. super strain B transcriptome under drought stress (fastq 1).



**File S1.8.** Sequence length distribution plot of quality scores of the raw data in the cv. super strain B transcriptome under drought stress (fastq 1).



**File S1.9.** Sequences duplicated levels vs total sequences percentage of the raw data in the cv. super strain B transcriptome under drought stress (fastq 1).



**File S1.10.** Adapter content percentages of the raw data in the cv. super strain B transcriptome under drought stress (fastq 1).

**File S1.11.** Summary of overrepresented sequences of the raw data in the cv. super strain B transcriptome under drought stress (fastq 1).

Sequence	Count	Percentage	Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGAATCCATCTCGTAT	520605	1.2460707918904883	TruSeq Adapter, Index 19 (97% over 40bp)
GCCTTATGTGATAGATGCCTCTTTAAAATATCTAAGTGCTGGGGTTATGA	340661	0.8153738862212342	No Hit
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGAATCCATCGCGTAT	263803	0.6314138610137945	TruSeq Adapter, Index 19 (97% over 40bp)
CCCATTTTTAGTTATAATGATGCCTTATGTGATAGATGCCTCTTTAAAAT	148312	0.35498554813507766	No Hit
GCCTCACTTAGTTACAGTTTTATGGATAATTGGGATATTCTTTGGTATAG	107293	0.25680635697756676	No Hit
GCCTCTTTAAAATATCTAAGTGCTGGGGTTATGAGTAGGGATGAGCATAA	103505	0.24773975915449334	No Hit
CTTATGTGATAGATGCCTCTTTAAAATATCTAAGTGCTGGGGTTATGAGT	98627	0.23606424062731476	No Hit
GGGGTTATGAGTAGGGATGAGCATAAACCAACAACCTCTCAAAGAAGATGG	90524	0.21666966772331148	No Hit
GCCCATAACAATAGGAAATATCAGAAATCCAATAAGAATCAGCAATTGAG	89794	0.214922408903131	No Hit
GGGAAGCTATACTATATAGGTGGCTATCTATCCCTACCAAGGCTTATATT	76509	0.18312469188107944	No Hit
GGGCTATTGATATTTAACAAATATCCAGCAAAGGTTTTCCAGGAGATGT	69370	0.16603745802180767	No Hit
GGAAGCTATACTATATAGGTGGCTATCTATCCCTACCAAGGCTTATATTG	68605	0.16420642651846784	No Hit
GTGGCTATCTATCCCTACCAAGGCTTATATTGAAGTATAAACCAATGAGA	62016	0.1484356205374142	No Hit
GCCCGTTTCAGGTGGTCCTCAGCGTACGGCGGGACCTCTGAGAATTGGGA	60120	0.14389753461541122	No Hit
GCTGGGGTTATGAGTAGGGATGAGCATAAACCAACAACCTCTCAAAGAAGA	60002	0.1436151009979026	No Hit
CCAGGAGATGTTGGAACCTCTACCAATTGGAGCTTTCTTAGCTGTCTTAGC	57026	0.13649202942412575	No Hit
GCAGTAGTTTATAAGGAATATATCCATTTTTAGTTATAATGATGCCTTA	56759	0.13585296352688164	No Hit
GATGCCTTATGTGATAGATGCCTCTTTAAAATATCTAAGTGCTGGGGTTA	51324	0.12284426258485305	No Hit
GGGATATTCTTTGGTATAGTTGGGATTTTAATATCATTAATAGCATGATG	50262	0.12030236002727543	No Hit
GGCAGTTTCCAGAAACGTGTATCACATCTAGGCATGGAATCTTATGCCAG	48105	0.1151395692394271	No Hit
CTCGGCAATAGGATTGTAGCCCAGGATGAGTCCCTCAGCGTGACGCAGTA	45431	0.10873933624605367	No Hit
GTCCTTACAAGTCCGCTCCTCGGGGAGCTTGATTGATAATTCTGTATAAG	45288	0.10839706499771697	No Hit
GGCGTGGTAGAATTACTGGCACTCCAATGATTCCATATAACGGCCATAAT	44775	0.10716919681312438	No Hit
GTAGTTTATAAGGAATATATCCATTTTTAGTTATAATGATGCCTTATGT	43012	0.10294944708712687	No Hit