Assembling approach

SOLiD Reads Cleaning
During the library preparation, some contaminants could be introduced due to the non-perfect efficiency of the 'RNA enrichment' phase. SOLiD RNA-seqs were cleaned by contaminants using an implementation of PASS program that removes all sequences that map onto a collection of contaminants. The contaminants resulted less than 1% of the total sequences in all analyzed samples.

The collection of contaminants includes:

(3) Collection of E. Coli strain genomes.
(4) GtRNAdb a database of transfer RNA genes detected in genomic sequence (http://gtrnadb.ucsc.edu/).
(5) RDP database (http://rdp.cme.msu.edu/seqmatch/seqmatch_intro.jsp).

De novo assembling
The version of SATRAP pipeline was 0.1, while Velvet assembly 1.2.10 and Oases 0.2.8.

The SATRAP pipeline run with the following parameters:
```
bin/satrap -step 1 2 3 4 \n-kmer_set 31 29 27 25 \n-reads_path SAMPLE_DIR/ \n-file_esten.csfastq \n-velvet_path velvet_1.2.10_path/ \noases_path oases_0.2.8_path/ \n-q 28 -t1 5 -t2 0
```

For details about setting please, see the SATRAP manual at http://satrap.cribi.unipd.it.

STATISTICS

<table>
<thead>
<tr>
<th>Developmental Phase</th>
<th>N50</th>
<th>Size (bases)</th>
<th>Contig number</th>
</tr>
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<tbody>
<tr>
<td>TO</td>
<td>549</td>
<td>57,459,032</td>
<td>149067</td>
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<tr>
<td>MC</td>
<td>562</td>
<td>64,451,533</td>
<td>166584</td>
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<tr>
<td>Pre-TO</td>
<td>515</td>
<td>65,460,907</td>
<td>176885</td>
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Table S1: De novo transcriptome assembly statistics obtained using the SATRAP pipeline.