S7 Table. Genes and 5'-3'-UTRs displaying decreased expression in 2011ecpR1 versus Rm2011 wild type growing in MOPS medium (P-value ≤ 0.05 and M ≥ 0.7 or ≤ −0.7).

<table>
<thead>
<tr>
<th>Gene ID</th>
<th>Name</th>
<th>Description</th>
<th>M value</th>
<th>Region</th>
</tr>
</thead>
<tbody>
<tr>
<td>SMc00999</td>
<td>Type IV pilus assembly PhZ-like protein</td>
<td></td>
<td>-0.79</td>
<td>CDS</td>
</tr>
<tr>
<td>SMc01410</td>
<td>Putative lipoprotein transmembrane</td>
<td></td>
<td>-0.76</td>
<td>5'UTR</td>
</tr>
<tr>
<td>SMc01167</td>
<td>dnaA</td>
<td>Chromosomal replication initiator</td>
<td>-0.74</td>
<td>5'UTR</td>
</tr>
<tr>
<td>SMc02833</td>
<td>mepA</td>
<td>Putative murein endopeptidase transmembrane protein</td>
<td>-0.67</td>
<td>5'UTR</td>
</tr>
</tbody>
</table>

**Cellular processes and signaling (4)**

<table>
<thead>
<tr>
<th>Gene ID</th>
<th>Name</th>
<th>Description</th>
<th>M value</th>
<th>Region</th>
</tr>
</thead>
<tbody>
<tr>
<td>SMb21438</td>
<td>TRAP-type transporter, periplasmic solute-binding</td>
<td></td>
<td>-1.30</td>
<td>CDS</td>
</tr>
<tr>
<td>SMc02450</td>
<td>argJ</td>
<td>Probable Arginine biosynthesis bifunctional protein</td>
<td>-0.84</td>
<td>CDS</td>
</tr>
<tr>
<td>SMc04239</td>
<td>Hypothetical protein</td>
<td></td>
<td>-0.83</td>
<td>5'UTR</td>
</tr>
<tr>
<td>SMc04028</td>
<td>gbB</td>
<td>Probable glutamate synthase NADPH large chain</td>
<td>-0.80</td>
<td>5'UTR</td>
</tr>
<tr>
<td>SMb21635</td>
<td>paaZ</td>
<td>Aldehyde dehydrogenase (NAD+)</td>
<td>-0.76</td>
<td>CDS</td>
</tr>
<tr>
<td>SMc04294</td>
<td>Putative peptide ABC transporter</td>
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<td>-0.73</td>
<td>CDS</td>
</tr>
<tr>
<td>SMc01118</td>
<td>Putative peptidase</td>
<td></td>
<td>-0.68</td>
<td>CDS</td>
</tr>
</tbody>
</table>

**Metabolism (7)**

<table>
<thead>
<tr>
<th>Gene ID</th>
<th>Name</th>
<th>Description</th>
<th>M value</th>
<th>Region</th>
</tr>
</thead>
<tbody>
<tr>
<td>SMb20162</td>
<td>Probable transcriptional regulator</td>
<td></td>
<td>-1.28</td>
<td>5'UTR</td>
</tr>
<tr>
<td>SMb21601</td>
<td>Putative transcriptional regulator</td>
<td></td>
<td>-0.77</td>
<td>5'UTR</td>
</tr>
</tbody>
</table>

**Information storage and processing (2)**

<table>
<thead>
<tr>
<th>Gene ID</th>
<th>Name</th>
<th>Description</th>
<th>M value</th>
<th>Region</th>
</tr>
</thead>
<tbody>
<tr>
<td>SMb20273</td>
<td>Hypothetical protein</td>
<td></td>
<td>-1.05</td>
<td>5'UTR</td>
</tr>
<tr>
<td>SMb21456</td>
<td>Hypothetical protein</td>
<td></td>
<td>-0.99</td>
<td>CDS</td>
</tr>
<tr>
<td>SMb21413</td>
<td>Hypothetical protein</td>
<td></td>
<td>-0.83</td>
<td>CDS</td>
</tr>
<tr>
<td>SMa0604</td>
<td>Conserved hypothetical protein</td>
<td></td>
<td>-0.79</td>
<td>5'UTR</td>
</tr>
<tr>
<td>SMb20010</td>
<td>Predicted hydrolase or acyltransferase</td>
<td></td>
<td>-0.71</td>
<td>CDS</td>
</tr>
</tbody>
</table>

**Poorly characterized (5)**

<table>
<thead>
<tr>
<th>Gene ID</th>
<th>Name</th>
<th>Description</th>
<th>M value</th>
<th>Region</th>
</tr>
</thead>
<tbody>
<tr>
<td>SMb20162</td>
<td>Probable transcriptional regulator</td>
<td></td>
<td>-1.28</td>
<td>5'UTR</td>
</tr>
<tr>
<td>SMb21601</td>
<td>Putative transcriptional regulator</td>
<td></td>
<td>-0.77</td>
<td>5'UTR</td>
</tr>
</tbody>
</table>

The M value represents the log₂ ratio of transcript levels.
Cell cycle related candidates are denoted in bold and experimentally confirmed targets are underlined.