Supplementary Information (16 pages) for:


This file contains the complete list of 275 ORFs (Tables 1-8) that were used for the DNA microarray experiments described in the article. Tables 1-4 are taken from the article while the additional ORFs that were studied are given in Tables 5-8.

Table 1. ORFs whose expression is dramatically (> 5-fold) down-regulated by S°.
Table 2. ORFs whose expression is dramatically (> 5-fold) up-regulated by S°.
Table 3. Highly-expressed S°-independent ORFs.
Table 4. Poorly-expressed S°-independent ORFs.
Table 5. ORFs whose expression is moderately (2 to 5-fold) down-regulated by S°.
Table 6. ORFs whose expression is moderately (2 to 5-fold) up-regulated by S°.
Table 7. Moderately-expressed S°-independent ORFs.
Table 8. ORFs that did not yield PCR products.
Table 1. ORFs whose expression is dramatically (＞5-fold) down-regulated by S°.

<table>
<thead>
<tr>
<th>ORF</th>
<th>ORF Description</th>
<th>Intensity Ratio (log₂ ± SD)</th>
<th>Change in expression (-fold)</th>
</tr>
</thead>
<tbody>
<tr>
<td>577932</td>
<td>[hydrogenase expression/formation regulatory protein, hypF]</td>
<td>5.28 ± 0.89</td>
<td>39.0</td>
</tr>
<tr>
<td>1337916</td>
<td>membrane bound hydrogenase ORF 1, mbh1&lt;sup&gt;d&lt;/sup&gt;</td>
<td>4.14 ± 0.80</td>
<td>17.6</td>
</tr>
<tr>
<td>1251888</td>
<td>hydrogenase II gamma, hydG2</td>
<td>3.78 ± 1.47</td>
<td>13.7</td>
</tr>
<tr>
<td>1338167</td>
<td>membrane bound hydrogenase ORF 2, mbh2&lt;sup&gt;d&lt;/sup&gt;</td>
<td>3.77 ± 1.29</td>
<td>13.6</td>
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<tr>
<td>1339081</td>
<td>membrane bound hydrogenase ORF 5, mbh5&lt;sup&gt;d&lt;/sup&gt;</td>
<td>3.68 ± 1.30</td>
<td>12.8</td>
</tr>
<tr>
<td>1339520</td>
<td>membrane bound hydrogenase ORF 6, mbh6&lt;sup&gt;d&lt;/sup&gt;</td>
<td>3.65 ± 0.77</td>
<td>12.6</td>
</tr>
<tr>
<td>1253842</td>
<td>hydrogenase II alpha, hydL2</td>
<td>3.57 ± 1.45</td>
<td>11.8</td>
</tr>
<tr>
<td>1341399</td>
<td>membrane bound hydrogenase ORF 8 (like cooM, mbh8)&lt;sup&gt;d&lt;/sup&gt;</td>
<td>3.49 ± 0.79</td>
<td>11.2</td>
</tr>
<tr>
<td>1338538</td>
<td>membrane bound hydrogenase ORF 3, mbh3&lt;sup&gt;d&lt;/sup&gt;</td>
<td>3.31 ± 1.66</td>
<td>9.9</td>
</tr>
<tr>
<td>1252601</td>
<td>hydrogenase II delta, hydS2</td>
<td>3.25 ± 1.43</td>
<td>9.5</td>
</tr>
<tr>
<td>1342770</td>
<td>membrane bound hydrogenase ORF 11, mbh11&lt;sup&gt;d&lt;/sup&gt;</td>
<td>3.06 ± 1.22</td>
<td>8.3</td>
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<tr>
<td>866528</td>
<td>hydrogenase I delta, hydS1</td>
<td>2.95 ± 0.66</td>
<td>7.7</td>
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<tr>
<td>1345018</td>
<td>membrane bound hydrogenase ORF 13 (like hydC, cooK, echB, mbh13)&lt;sup&gt;d&lt;/sup&gt;</td>
<td>2.77 ± 0.85</td>
<td>6.8</td>
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<tr>
<td>1345434</td>
<td>membrane bound hydrogenase ORF 14 (like hyeF, echF, cooX, mbh14)&lt;sup&gt;d&lt;/sup&gt;</td>
<td>2.73 ± 1.40</td>
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<tr>
<td>1344050</td>
<td>membrane bound hydrogenase ORF 12, catalytic NiFe subunit, mbh12</td>
<td>2.68 ± 0.59</td>
<td>6.4</td>
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<tr>
<td>864857</td>
<td>hydrogenase I beta, hydB1</td>
<td>2.66 ± 1.08</td>
<td>6.3</td>
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<tr>
<td>1251025</td>
<td>hydrogenase II beta, hydB2</td>
<td>2.65 ± 1.04</td>
<td>6.3</td>
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<tr>
<td>1342256</td>
<td>membrane bound hydrogenase ORF 10, small subunit homolog, mbh10&lt;sup&gt;d&lt;/sup&gt;</td>
<td>2.59 ± 0.87</td>
<td>6.0</td>
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<tr>
<td>ORF</td>
<td>Description</td>
<td>Ratio</td>
<td>Log2</td>
</tr>
<tr>
<td>-------</td>
<td>--------------------------------------------------</td>
<td>--------</td>
<td>-------</td>
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<tr>
<td>51760</td>
<td>[conserved hypothetical protein]</td>
<td>2.59 ± 1.14</td>
<td>6.0</td>
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<tr>
<td>1338785</td>
<td>membrane bound hydrogenase ORF 4, mbh4&lt;sup&gt;d&lt;/sup&gt;</td>
<td>2.54 ± 2.16</td>
<td>5.8</td>
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<tr>
<td>615154</td>
<td>ornithine carbamoyltransferase, argF</td>
<td>2.43 ± 0.49</td>
<td>5.4</td>
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</tbody>
</table>

<sup>a</sup>ORF designation is the end nucleotide number (http://comb5-156.umbi.umd.edu/).

<sup>b</sup>The ORF description is derived either from annotation by homology (given within brackets) or where there is experimental data to support the ORF assignment specifically in <i>P. furiosus</i> (given without brackets).

<sup>c</sup>The intensity ratio is expressed as a log<sub>2</sub> value so that the standard deviation can be given. For ease of comparison between ORFs, the apparent change in the expression level of a given ORF is also indicated.

<sup>d</sup>This work, see text for details.
Table 2. ORFs whose expression is dramatically up-regulated by S°.

<table>
<thead>
<tr>
<th>ORF</th>
<th>ORF Description</th>
<th>Intensity Ratio (log₂ ± SD)</th>
<th>Change in expression (-fold)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1871822</td>
<td>[conserved hypothetical protein, <em>sipA</em>]</td>
<td>5.94 ± 1.43</td>
<td>61.4</td>
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<tr>
<td>1872873</td>
<td>[putative polyferredoxin, <em>sipB</em>]</td>
<td>4.65 ± 1.90</td>
<td>25.1</td>
</tr>
<tr>
<td>1487371</td>
<td>[tryptophan synthase, subunit beta, <em>trpB-1</em>]</td>
<td>2.98 ± 0.69</td>
<td>7.9</td>
</tr>
<tr>
<td>1805557</td>
<td>[conserved hypothetical protein]</td>
<td>2.93 ± 1.29</td>
<td>7.6</td>
</tr>
<tr>
<td>1008251</td>
<td>[aspartokinase II alpha subunit]</td>
<td>2.92 ± 0.89</td>
<td>7.6</td>
</tr>
<tr>
<td>1131551</td>
<td>[NADH oxidase, <em>noxA-2</em>]</td>
<td>2.88 ± 0.39</td>
<td>7.4</td>
</tr>
<tr>
<td>1825269</td>
<td>[thermosome, single subunit]</td>
<td>2.83 ± 1.69</td>
<td>7.1</td>
</tr>
<tr>
<td>900019</td>
<td>[acetolactate synthase]</td>
<td>2.78 ± 1.02</td>
<td>6.9</td>
</tr>
<tr>
<td>65527</td>
<td>[fibrillarin-like pre-rRNA processing protein]</td>
<td>2.70 ± 0.80</td>
<td>6.5</td>
</tr>
<tr>
<td>204761</td>
<td>[oligopeptide transport system permease protein]</td>
<td>2.68 ± 0.45</td>
<td>6.4</td>
</tr>
<tr>
<td>102519</td>
<td>[glutaredoxin-like protein]</td>
<td>2.61 ± 1.72</td>
<td>6.1</td>
</tr>
<tr>
<td>1352206</td>
<td>[NADH dehydrogenase subunit]</td>
<td>2.59 ± 0.59</td>
<td>6.0</td>
</tr>
</tbody>
</table>

aSee Table 1 for details.
bSee text for details.
Table 3. Highly-expressed\textsuperscript{a} S\textdegree-independent ORFs.

<table>
<thead>
<tr>
<th>ORF\textsuperscript{b}</th>
<th>ORF description\textsuperscript{b}</th>
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</thead>
<tbody>
<tr>
<td>49183</td>
<td>phosphoenolpyruvate synthetase, \textit{ppsA}</td>
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<tr>
<td>143318</td>
<td>[conserved hypothetical protein]</td>
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<tr>
<td>232621</td>
<td>enolase (2-phosphoglycerate dehydratase)</td>
</tr>
<tr>
<td>236793</td>
<td>[hexulose-6-phosphate synthase]</td>
</tr>
<tr>
<td>358419</td>
<td>aldehyde ferredoxin oxidoreductase, \textit{aor}</td>
</tr>
<tr>
<td>478142</td>
<td>glyceraldehyde-3-phosphate ferredoxin oxidoreductase, \textit{gor}</td>
</tr>
<tr>
<td>683389</td>
<td>[methylmalonyl-CoA decarboxylase, subunit alpha, \textit{mmdA}]</td>
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<tr>
<td>720985</td>
<td>[alkyl hydroperoxide reductase subunit C]</td>
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<tr>
<td>925374</td>
<td>pyruvate ferredoxin oxidoreductase beta, \textit{porB}</td>
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<tr>
<td>926380</td>
<td>pyruvate ferredoxin oxidoreductase alpha, \textit{porA}</td>
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<tr>
<td>927947</td>
<td>2-ketoisovalerate ferredoxin oxidoreductase beta, \textit{vorB}</td>
</tr>
<tr>
<td>928888</td>
<td>2-ketoisovalerate ferredoxin oxidoreductase subunit alpha, \textit{vorA}</td>
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<tr>
<td>1145403</td>
<td>formaldehyde ferredoxin oxidoreductase, \textit{for}</td>
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<tr>
<td>1208774</td>
<td>[LSU ribosomal protein L10]</td>
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<tr>
<td>1210188</td>
<td>superoxide reductase, \textit{sor}</td>
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<tr>
<td>1210814</td>
<td>[rubrerythrin]</td>
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<tr>
<td>1425928</td>
<td>[ethylene-inducible protein homolog]</td>
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<tr>
<td>1493675</td>
<td>glutamate dehydrogenase, \textit{gdh}</td>
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<tr>
<td>1597902</td>
<td>intracellular protease, \textit{pfpI}</td>
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<tr>
<td>1619038</td>
<td>[putative trehalose synthase]</td>
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</table>

\textsuperscript{a}ORFs displaying average fluorescent intensities >20,000, see Fig. 1B. 
\textsuperscript{b}See Table 1 for details
<table>
<thead>
<tr>
<th>ORF</th>
<th>ORF description</th>
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<td>53135</td>
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<td>349245</td>
<td>[flagella-related protein D, putative]</td>
</tr>
<tr>
<td>350457</td>
<td>[conserved hypothetical protein]</td>
</tr>
<tr>
<td>350944</td>
<td>[flagellin B2 precursor]</td>
</tr>
<tr>
<td>351748</td>
<td>[flagellin B2 precursor]</td>
</tr>
<tr>
<td>373060</td>
<td>[ABC transporter, OppBC family]</td>
</tr>
<tr>
<td>379218</td>
<td>[beta-galactosidase precursor]</td>
</tr>
<tr>
<td>488057</td>
<td>[DNA mismatch repair protein, <em>MutS</em>]</td>
</tr>
<tr>
<td>562899</td>
<td>[molybdopterin converting factor, subunit 1, <em>moaD</em>]</td>
</tr>
<tr>
<td>575520</td>
<td>[NADH oxidase, <em>noxA-4/nitrite reductase</em>]</td>
</tr>
<tr>
<td>637268</td>
<td>[molybdopterin-guanine dinucleotide biosynthesis protein, <em>mobA</em>]</td>
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<tr>
<td>637303</td>
<td>[hydrogenase maturation protease, <em>hycI</em>]</td>
</tr>
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<td>722839</td>
<td>[conserved hypothetical protein]</td>
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<td>738742</td>
<td>[conserved hypothetical protein]</td>
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<tr>
<td>743892</td>
<td>[putative proline depeptidase]</td>
</tr>
<tr>
<td>834030</td>
<td>[conserved hypothetical protein]</td>
</tr>
<tr>
<td>838710</td>
<td>[conserved hypothetical protein]</td>
</tr>
<tr>
<td>880926</td>
<td>[ferric enterobactin transport ATP-binding protein homolog]</td>
</tr>
<tr>
<td>881669</td>
<td>[iron (III) ABC transporter, permease protein, <em>hemU-1</em>]</td>
</tr>
<tr>
<td>882732</td>
<td>[iron (III) ABC transporter ATP-binding protein, <em>hemV-2</em>]</td>
</tr>
<tr>
<td>962748</td>
<td>[alkaline phosphatase IV precursor]</td>
</tr>
<tr>
<td>1012695</td>
<td>[phosphoglycerate kinase]</td>
</tr>
<tr>
<td>1138558</td>
<td>[transcriptional regulator (FurR family)]</td>
</tr>
<tr>
<td>1158892</td>
<td>[dissimilatory sulfate adenylyltransferase]</td>
</tr>
<tr>
<td>1165967</td>
<td>[4-aminobutyrate aminotransferase]</td>
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<tr>
<td>1197174</td>
<td>[putative nucleolar protein II, Nol1-Nop2-sun family]</td>
</tr>
<tr>
<td>1208389</td>
<td>[conserved hypothetical protein]</td>
</tr>
</tbody>
</table>
1417217  [sugar-binding transport ATP-binding protein]
1647980  2-keto acid:ferredoxin oxidoreductase subunit alpha]
1668574  [sarcosine oxidase, alpha subunit, SoxA]
1669077  [putative polyferrodoxin, muhB]
1711295  [molybdenum cofactor biosynthesis protein, moaC]
1873595  [nitrogen reductase, N-terminus]
1873914  [ferrodoxin-family protein]

*ORFs displaying average fluorescent intensities below 2,000, see Fig. 1B.
See Table 1 for details.
Table 5. ORFs whose expression is moderately (2 to 5-fold) down-regulated by S°.

<table>
<thead>
<tr>
<th>ORF</th>
<th>ORF Description</th>
<th>Intensity Ratio (log₂ ± SD)</th>
<th>Change in expression (-fold)</th>
</tr>
</thead>
<tbody>
<tr>
<td>224077</td>
<td>[arginosuccinate synthetase, argG]</td>
<td>-1.63 ± 1.51</td>
<td>3.10</td>
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<tr>
<td>521928</td>
<td>[probable iron (FeIII) ABC transporter]</td>
<td>-1.47 ± 0.47</td>
<td>2.78</td>
</tr>
<tr>
<td>566869</td>
<td>[hydrogenase expression/formation protein, hypC]</td>
<td>-1.17 ± 0.89</td>
<td>2.24</td>
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<tr>
<td>567973</td>
<td>[hydrogenase expression/formation protein, hypD]</td>
<td>-1.32 ± 0.50</td>
<td>2.50</td>
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<td>636092</td>
<td>[hydrogenase expression/formation protein, hypA]</td>
<td>-1.37 ± 0.88</td>
<td>2.58</td>
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<td>685707</td>
<td>carbamate kinase-like carbamoylphosphate synthetase, cpkA</td>
<td>-1.72 ± 1.00</td>
<td>3.29</td>
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<td>700151</td>
<td>not annotated</td>
<td>-2.02 ± 1.29</td>
<td>4.05</td>
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<td>702081</td>
<td>[prismane protein homolog]</td>
<td>-1.45 ± 1.33</td>
<td>2.74</td>
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<td>714814</td>
<td>[conserved hypothetical protein]</td>
<td>-2.11 ± 0.83</td>
<td>4.32</td>
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<td>739367</td>
<td>[probable ferritin, rsgA]</td>
<td>-1.69 ± 0.39</td>
<td>3.22</td>
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<td>825121</td>
<td>[iron-dependent repressor]</td>
<td>-1.65 ± 1.24</td>
<td>3.13</td>
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<tr>
<td>865732</td>
<td>hydrogenase I, gamma, hydG1</td>
<td>-2.28 ± 3.91</td>
<td>4.87</td>
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<td>867811</td>
<td>hydrogenase I, alpha, hydL1</td>
<td>-1.17 ± 1.06</td>
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<td>1092336</td>
<td>[conserved hypothetical protein]</td>
<td>-1.24 ± 0.98</td>
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<td>1148005</td>
<td>beta-mannosidase, BmnA</td>
<td>-1.16 ± 0.80</td>
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<td>1341748</td>
<td>membrane bound hydrogenase ORF 9, mbh9δ</td>
<td>-2.07 ± 0.72</td>
<td>4.20</td>
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<tr>
<td>1418206</td>
<td>[ABC transporter integral membrane protein]</td>
<td>-1.20 ± 0.97</td>
<td>2.30</td>
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<td>1591790</td>
<td>[carbamoyl-phosphate synthase, small subunit, carA]</td>
<td>-1.49 ± 1.55</td>
<td>2.80</td>
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<td>1626630</td>
<td>[probable sulfate transport system permease protein ABC transporter]</td>
<td>-1.33 ± 0.41</td>
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<td>1689568</td>
<td>[archaeal histone A1, hpyA1-2]</td>
<td>-1.47 ± 1.02</td>
<td>2.77</td>
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<tr>
<td>1760272</td>
<td>ferredoxin</td>
<td>-2.00 ± 1.23</td>
<td>4.00</td>
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</table>

*see Table 1 for details*
<table>
<thead>
<tr>
<th>ORF</th>
<th>ORF description</th>
<th>Intensity Ratio (log₂ ± SD)</th>
<th>Change in expression (-fold)</th>
</tr>
</thead>
<tbody>
<tr>
<td>9230</td>
<td>thiamine biosynthesis protein, <em>thiF</em></td>
<td>1.02 ± 0.58</td>
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<td>66216</td>
<td>[Nop58/Nop56 related protein]</td>
<td>2.02 ± 0.75</td>
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<td>1.43 ± 1.59</td>
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<td>1.69 ± 1.81</td>
<td>3.22</td>
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<td>not annotated</td>
<td>1.00 ± 1.09</td>
<td>2.00</td>
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<td>97550</td>
<td>[molybdenum cofactor biosynthesis protein, <em>moaA</em>]</td>
<td>2.16 ± 0.84</td>
<td>4.46</td>
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<td>105386</td>
<td>[bacteriochlorophyll synthase, 43 kDa subunit, <em>chlP-I</em>]</td>
<td>2.13 ± 0.52</td>
<td>4.38</td>
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<td>120590</td>
<td>[probable multiple sugar transport protein]</td>
<td>1.05 ± 0.74</td>
<td>2.07</td>
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<td>126676</td>
<td>[probable aspartate aminotransferase]</td>
<td>1.27 ± 0.26</td>
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<td>221932</td>
<td>[glutamate synthase (NADPH) subunit alpha]</td>
<td>1.31 ± 0.69</td>
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<td>228606</td>
<td>DNA-directed DNA polymerase</td>
<td>1.35 ± 0.40</td>
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<td>245558</td>
<td>[conserved hypothetical protein]</td>
<td>1.52 ± 1.24</td>
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<tr>
<td>334012</td>
<td>[similar to acylaminoacyl-peptidase]</td>
<td>2.08 ± 0.94</td>
<td>4.22</td>
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<td>471039</td>
<td>[carboxypeptidase 1]</td>
<td>1.84 ± 0.63</td>
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<td>517476</td>
<td>[reverse gyrase, <em>rgy</em>]</td>
<td>1.37 ± 0.67</td>
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<td>518483</td>
<td>[conserved hypothetical protein]</td>
<td>1.36 ± 1.06</td>
<td>2.56</td>
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<td>636814</td>
<td>[nucleotide-binding protein, Mrp/Nbp35 family]</td>
<td>1.51 ± 0.61</td>
<td>2.85</td>
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<tr>
<td>747589</td>
<td>[thioredoxin peroxidase]</td>
<td>1.18 ± 1.94</td>
<td>2.27</td>
</tr>
<tr>
<td>757388</td>
<td>[NDP-sugar dehydrogenase]</td>
<td>1.31 ± 0.58</td>
<td>2.49</td>
</tr>
<tr>
<td>863522</td>
<td>[leucyl-tRNA synthetase]</td>
<td>1.51 ± 0.56</td>
<td>2.85</td>
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<tr>
<td>903832</td>
<td>[3-isopropylmalate dehydratase large subunit, <em>leuC</em>]</td>
<td>2.05 ± 1.34</td>
<td>4.15</td>
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<td>Expression</td>
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<td>Ratio</td>
<td>Fold Change</td>
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*aSee Table 1 for details.*
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<td>477397</td>
<td>[hydrolase rel. to 2-haloalkanoic acid dehalogenase]</td>
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*Table 7. Moderately-expressed S°-independent ORFs*
13

532443 [probable glutamate aminotransferase]
540820 [aspartate transaminase]
549216 [conserved hypothetical protein]
551149 indolepyruvate ferredoxin oxidoreductase alpha, iorA
551790 indolepyruvate ferredoxin oxidoreductase beta, iorB
561253 methionine aminopeptidase, MAP, Peptidase M
562615 [molybdenum cofactor biosynthesis protein, moeA-1]
619035 [IAA-amino acid hydrolase homolog 1 precursor]
619484 [aspartate carbamoyltransferase, catalytic subunit, pyrB]
621560 [conserved hypothetical protein]
626147 [hydrogenase expression/formation protein, hypE]
631178 [alcohol dehydrogenase]
674979 [putative nucleolar protein IV (NoI1-NoP2-sun family)]
699847 [conserved hypothetical protein, possible thioredoxin/glutaredoxin]
748043 [2-keto acid:ferredoxin oxidoreductase subunit beta]
748906 [2-keto acid:ferredoxin oxidoreductase subunit alpha]
750669 [non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase]
796206 [conserved hypothetical protein]
817300 [2-keto acid:ferredoxin oxidoreductase subunit alpha]
927581 pyruvate ferredoxin oxidoreductase, delta, porD
930085 2-ketovalerate ferredoxin oxidoreductase, delta, vorD
981072 [malate oxidoreductase (malic enzyme)]
988026 [conserved hypothetical protein]
989258 [alkyl hydroperoxide reductase]
991757 [conserved hypothetical protein]
998565 [adenylate kinase, adk]
1019818 [putative aminotransferase]
1020852 [SSU ribosomal protein S8E]
1035285 [conserved hypothetical protein]
1093579 [conserved hypothetical protein]
1104585 [ribulose-1,5-bisphosphate carboxylase (RUBISCO)]
rubredoxin
ferredoxin NADPH oxidoreductase, beta
[aminomethyl transferase]
[conserved hypothetical protein]
[sn-glycerol-1-phosphate dehydrogenase]
[endo/exonuclease, fen-1]
[glutaredoxin/thioredoxin-like protein]
[formate dehydrogenase alpha chain]
[transcriptional regulatory protein, AsnC family]
[ferripyochelin binding protein]
leucine responce protein, lrpA
[imidazoleglycerol-phosphate synthase, cyclase subunit, hisF]
[acetylornithine aminotransferase, argD-1]
[tryptophane synthase, subunit beta, trpB-2]
[carbamoyl-phosphate synthase large chain, carB]
[transcriptional regulatory protein, AsnC family]
[probable sugar-binding transport ATP-binding protein]
[possible fumarate hydratase (fumarase) beta subunit]
[2-keto acid:ferredoxin oxidoreductase subunit alpha]
[molybdenum cofactor biosynthesis protein, moeA-2]
ADP-dependent phosphofructokinase, pfk
[centromere binding protein homolog/pseudouridine synthase]
[adenylate kinase (ATP-AMP transphosphorylase)]
1671649  [preprotein translocase, secY]
1693216  [conserved hypothetical protein]
1716363  [conserved hypothetical protein]
1751962  [DNA repair helicase putative]
1782299  [putative sugar transport ATP-hydrolyzing]
1783837  amylopullulanase
1808382  [agmatinase, speB]
1813313  [4-hydroxybenzoate octaprenyltransferase, putative]
1819997  [probable multiple sugar-binding transport ATP-binding protein]
1828270  [L-aspartate oxidase (quinolinate synthetase)]
1889236  [L-asparaginase]

^ORFs displaying average fluorescent intensities between 2,000 and 20,000, see Fig. 1B.
See Table 1 for details.
Table 8. ORFs that did not yield PCR products.

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*aSee Table 1 for details.*