<table>
<thead>
<tr>
<th>EC number</th>
<th>Enzyme name</th>
<th>Pathway</th>
<th>Nb Sequences</th>
<th>Nb Sites</th>
<th># Distinct Alignment Patterns</th>
<th>Organisms</th>
<th>ML – Cluster / Sister group trypanosomatids</th>
<th>NJ – Cluster / Sister group trypanosomatids</th>
<th>Cluster / Sister group TPEs</th>
<th>Figure</th>
<th>Average genomic coverage</th>
<th>Average contig coverage</th>
<th>Average gene coverage</th>
<th>Genome*</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.1.1.169</td>
<td>2-dehydroquinate 2-reductase</td>
<td>Pantothenate</td>
<td>607</td>
<td>1123</td>
<td>962</td>
<td>All SHTs and Herpetomonas, but not the other RTs.</td>
<td>They group within Firmicutes (BS=98).</td>
<td>They group within Firmicutes and a few other groups of bacteria (BS=95).</td>
<td>-</td>
<td>9</td>
<td>23x</td>
<td>18x</td>
<td>18x</td>
<td>A. deanei</td>
</tr>
<tr>
<td>2.4.2.11</td>
<td>nicotinate phosphoronyltransferase</td>
<td>Nicotinate</td>
<td>630</td>
<td>1050</td>
<td>1010</td>
<td>All SHTs, RTs and TPEs</td>
<td>Trypanosomatid clade (BS=100) clusters within the Gammaproteobacteria (BS=93).</td>
<td>Trypanosomatid clade (BS=97) cluster within the Gammaproteobacteria (BS=91).</td>
<td>ML: Group with Alcaligenaceae (BS=90); NJ: Group with Talyorella and Advenella spp. (BS=99), and with the Alcaligenaceae (low BS).</td>
<td>10</td>
<td>24x</td>
<td>22x</td>
<td>27x</td>
<td>A. desouzai</td>
</tr>
<tr>
<td>4.1.3.40</td>
<td>chorismate lyase</td>
<td>Ubiquinone</td>
<td>217</td>
<td>389</td>
<td>372</td>
<td>SHTs from Strigomonas genus</td>
<td>Strigomonas clade (BS=98) very similar to Pseudomonas, clusters within Gammaproteobacteria (BS=99), although this gene seems to diverge quite fast, making the identification of putative orthologs difficult.</td>
<td>Strigomonas clade (BS=97) clusters within Gammaproteobacteria (low BS).</td>
<td>-</td>
<td>11</td>
<td>28x</td>
<td>14x</td>
<td>14x</td>
<td>S. galati</td>
</tr>
</tbody>
</table>

* Genome, contig, and gene average sequencing coverages were calculated for the organism indicated in the "Genome" column.