Supporting Table S3. Assembly statistics for combined Sanger metagenomic libraries using Celera Assembler version 5.4. Assembly parameters used were as follows: utgErrorRate=0.10; ovlErrorRate=0.10; cnsErrorRate=0.10; cgwErrorRate=0.12; utgBubblePopping=0; utgGenomeSize=500000; merSize=15; doFragmentCorrection=0; doExtendClearRanges=1; doResolveSurrogates=1; Unitigger parameter –j = –20.

<p>| | |</p>
<table>
<thead>
<tr>
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<tbody>
<tr>
<td>total num nucleotides</td>
<td>286,258,541</td>
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<tr>
<td>num reads</td>
<td>426,864</td>
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<tr>
<td>num scaffolds</td>
<td>15,008</td>
</tr>
<tr>
<td>scaffold N50</td>
<td>29,346</td>
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<tr>
<td>max scaffold length</td>
<td>2,982,959</td>
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<tr>
<td>num predicted proteins</td>
<td>62,915</td>
</tr>
<tr>
<td>num placed reads</td>
<td>282,583</td>
</tr>
<tr>
<td>% bp placed</td>
<td>69.60%</td>
</tr>
<tr>
<td>% reads placed</td>
<td>66.20%</td>
</tr>
</tbody>
</table>