Table S3. Sequencing and assembly characteristics of Marine Group I (MGI) Thaumarchaeota single amplified genomes (SAGs).

<table>
<thead>
<tr>
<th>SAG</th>
<th>IMG Taxon ID</th>
<th>Station</th>
<th>Assembly size (Mb)</th>
<th>No. of contigs</th>
<th>% Genome recovery</th>
<th>Estimated genome size (Mb)</th>
<th>No. of protein coding genes</th>
<th>%GC</th>
</tr>
</thead>
<tbody>
<tr>
<td>AAA001-A19</td>
<td>2513237067</td>
<td>South Atlantic</td>
<td>0.76</td>
<td>223</td>
<td>33.0</td>
<td>2.30</td>
<td>891</td>
<td>35.7</td>
</tr>
<tr>
<td>AAA007-N19</td>
<td>2513237068</td>
<td></td>
<td>0.89</td>
<td>194</td>
<td>73.4</td>
<td>1.21</td>
<td>1098</td>
<td>35.6</td>
</tr>
<tr>
<td>AAA007-O23</td>
<td>2527291500</td>
<td></td>
<td>1.10</td>
<td>32</td>
<td>94.7</td>
<td>1.17</td>
<td>1354</td>
<td>35.7</td>
</tr>
<tr>
<td>AAA007-C21</td>
<td>2524023106</td>
<td></td>
<td>0.15</td>
<td>24</td>
<td>20.2</td>
<td>0.72</td>
<td>265</td>
<td>34.9</td>
</tr>
<tr>
<td>AAA007-E02</td>
<td>2524023111</td>
<td></td>
<td>0.31</td>
<td>43</td>
<td>31.9</td>
<td>0.96</td>
<td>559</td>
<td>35.3</td>
</tr>
<tr>
<td>AAA007-E15</td>
<td>2524023107</td>
<td></td>
<td>0.26</td>
<td>29</td>
<td>23.4</td>
<td>1.12</td>
<td>468</td>
<td>35.1</td>
</tr>
<tr>
<td>AAA007-G17</td>
<td>2524023108</td>
<td></td>
<td>0.20</td>
<td>31</td>
<td>7.5</td>
<td>2.73</td>
<td>373</td>
<td>35.9</td>
</tr>
<tr>
<td>AAA007-M20</td>
<td>2524023109</td>
<td></td>
<td>0.11</td>
<td>27</td>
<td>7.5</td>
<td>1.44</td>
<td>231</td>
<td>35.4</td>
</tr>
<tr>
<td>AAA007-N23</td>
<td>2524023110</td>
<td></td>
<td>0.08</td>
<td>17</td>
<td>3.2</td>
<td>2.54</td>
<td>155</td>
<td>35.1</td>
</tr>
<tr>
<td>AAA007-E15</td>
<td>2524023112</td>
<td></td>
<td>0.28</td>
<td>33</td>
<td>26.6</td>
<td>1.05</td>
<td>485</td>
<td>35.1</td>
</tr>
<tr>
<td>AAA007-E17</td>
<td>2524023113</td>
<td></td>
<td>0.22</td>
<td>25</td>
<td>9.6</td>
<td>2.27</td>
<td>374</td>
<td>35.4</td>
</tr>
<tr>
<td>AAA007-G03</td>
<td>2524023114</td>
<td></td>
<td>0.36</td>
<td>44</td>
<td>36.2</td>
<td>1.01</td>
<td>660</td>
<td>35.2</td>
</tr>
<tr>
<td>AAA007-M21</td>
<td>2524023115</td>
<td></td>
<td>0.20</td>
<td>18</td>
<td>13.8</td>
<td>1.44</td>
<td>353</td>
<td>33.6</td>
</tr>
<tr>
<td>AAA007-M23</td>
<td>2524023116</td>
<td></td>
<td>0.23</td>
<td>20</td>
<td>12.8</td>
<td>1.77</td>
<td>370</td>
<td>35.2</td>
</tr>
<tr>
<td>AAA007-N07</td>
<td>2524023117</td>
<td></td>
<td>0.16</td>
<td>20</td>
<td>9.6</td>
<td>1.69</td>
<td>293</td>
<td>36.5</td>
</tr>
<tr>
<td>AAA008-O05</td>
<td>2524023118</td>
<td></td>
<td>0.24</td>
<td>24</td>
<td>28.7</td>
<td>0.84</td>
<td>423</td>
<td>35.6</td>
</tr>
<tr>
<td>AAA008-O18</td>
<td>2524023119</td>
<td></td>
<td>0.21</td>
<td>36</td>
<td>22.3</td>
<td>0.93</td>
<td>417</td>
<td>34.1</td>
</tr>
<tr>
<td>AAA008-P02</td>
<td>2524023120</td>
<td></td>
<td>0.30</td>
<td>45</td>
<td>25.5</td>
<td>1.18</td>
<td>574</td>
<td>35.7</td>
</tr>
<tr>
<td>AAA008-P23</td>
<td>2524023121</td>
<td></td>
<td>0.33</td>
<td>48</td>
<td>24.5</td>
<td>1.35</td>
<td>615</td>
<td>34.7</td>
</tr>
<tr>
<td>AAA288-I14</td>
<td>2513237066</td>
<td>North Pacific</td>
<td>1.06</td>
<td>150</td>
<td>78.7</td>
<td>1.35</td>
<td>1404</td>
<td>35.3</td>
</tr>
<tr>
<td>AAA288-I14</td>
<td>2513237065</td>
<td></td>
<td>0.68</td>
<td>253</td>
<td>55.3</td>
<td>1.23</td>
<td>796</td>
<td>35.8</td>
</tr>
<tr>
<td>AAA288-C17</td>
<td>2524023122</td>
<td></td>
<td>0.39</td>
<td>51</td>
<td>27.7</td>
<td>1.39</td>
<td>681</td>
<td>34.9</td>
</tr>
<tr>
<td>AAA288-D03</td>
<td>2524023123</td>
<td></td>
<td>0.26</td>
<td>42</td>
<td>11.7</td>
<td>2.26</td>
<td>518</td>
<td>34.6</td>
</tr>
<tr>
<td>AAA288-D22</td>
<td>2524023124</td>
<td></td>
<td>0.39</td>
<td>46</td>
<td>42.6</td>
<td>0.92</td>
<td>704</td>
<td>35.2</td>
</tr>
<tr>
<td>AAA288-E09</td>
<td>2524023125</td>
<td></td>
<td>0.31</td>
<td>46</td>
<td>27.7</td>
<td>1.13</td>
<td>547</td>
<td>35.3</td>
</tr>
<tr>
<td>AAA288-G05</td>
<td>2524023126</td>
<td></td>
<td>0.55</td>
<td>49</td>
<td>37.2</td>
<td>1.47</td>
<td>926</td>
<td>35.7</td>
</tr>
<tr>
<td>AAA288-K02</td>
<td>2524023127</td>
<td></td>
<td>0.43</td>
<td>70</td>
<td>31.9</td>
<td>1.36</td>
<td>761</td>
<td>35.6</td>
</tr>
<tr>
<td>AAA288-K05</td>
<td>2524023128</td>
<td></td>
<td>0.29</td>
<td>35</td>
<td>27.7</td>
<td>1.04</td>
<td>487</td>
<td>35.4</td>
</tr>
<tr>
<td>AAA288-K20</td>
<td>2524023097</td>
<td></td>
<td>0.37</td>
<td>54</td>
<td>24.5</td>
<td>1.52</td>
<td>685</td>
<td>35.5</td>
</tr>
<tr>
<td>AAA288-M04</td>
<td>2524023098</td>
<td></td>
<td>0.32</td>
<td>49</td>
<td>25.5</td>
<td>1.25</td>
<td>608</td>
<td>35.6</td>
</tr>
<tr>
<td>AAA288-M23</td>
<td>2524023099</td>
<td></td>
<td>0.28</td>
<td>48</td>
<td>20.2</td>
<td>1.39</td>
<td>529</td>
<td>34.5</td>
</tr>
<tr>
<td>AAA288-N15</td>
<td>2524023100</td>
<td></td>
<td>0.14</td>
<td>27</td>
<td>17.0</td>
<td>0.85</td>
<td>300</td>
<td>35.3</td>
</tr>
<tr>
<td>AAA288-N23</td>
<td>2524023101</td>
<td></td>
<td>0.31</td>
<td>39</td>
<td>27.7</td>
<td>1.12</td>
<td>539</td>
<td>34.3</td>
</tr>
<tr>
<td>AAA288-O17</td>
<td>2524023102</td>
<td></td>
<td>0.03</td>
<td>9</td>
<td>2.1</td>
<td>1.55</td>
<td>80</td>
<td>34.5</td>
</tr>
<tr>
<td>AAA288-O22</td>
<td>2524023103</td>
<td></td>
<td>0.25</td>
<td>38</td>
<td>17.0</td>
<td>1.48</td>
<td>466</td>
<td>34.3</td>
</tr>
<tr>
<td>AAA288-P02</td>
<td>2524023104</td>
<td></td>
<td>0.65</td>
<td>58</td>
<td>34.0</td>
<td>1.91</td>
<td>1069</td>
<td>35.06</td>
</tr>
<tr>
<td>AAA288-P18</td>
<td>2524023105</td>
<td></td>
<td>0.43</td>
<td>73</td>
<td>39.4</td>
<td>1.10</td>
<td>793</td>
<td>35.68</td>
</tr>
</tbody>
</table>

1SAGs in bold are genomes with larger assembly sizes; all other SAGs were derived from Nextera-prepared sequence libraries and had smaller genome assembly sizes.

2Genome recovery estimates based on 94 conserved single copy genes (CSCG) present within 98% of 155 archaeal genomes from IMG.

3Number of protein coding sequences determined after removing contigs <2 kbp.