### S2 Table. Sequences per sample

<table>
<thead>
<tr>
<th>Sample</th>
<th>raw</th>
<th>filtered</th>
<th>denoised</th>
<th>merged</th>
<th>non-chimeric</th>
</tr>
</thead>
<tbody>
<tr>
<td>M1</td>
<td>96442</td>
<td>82180</td>
<td>82180</td>
<td>50857</td>
<td>47987</td>
</tr>
<tr>
<td>M2</td>
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<td>44344</td>
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</tr>
<tr>
<td>M3</td>
<td>91042</td>
<td>81773</td>
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<td>54282</td>
<td>49545</td>
</tr>
<tr>
<td>M5</td>
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<td>46581</td>
<td>44017</td>
</tr>
<tr>
<td>M6</td>
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<td>36876</td>
<td>34870</td>
</tr>
<tr>
<td>C1</td>
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<td>54916</td>
<td>51168</td>
</tr>
<tr>
<td>C2</td>
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<td>117763</td>
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<tr>
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<td>940432</td>
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<td>554745</td>
</tr>
</tbody>
</table>

Note: raw reads were processed using dada2. Samples starting with M were collected at the roots of maize plants and samples starting with C were collected from bulk soil, collected at 30 cm from each plant.