

1 **Table S1:** Summary of recovered 454-pyrosequencing reads, quality filtering  
 2 and number of OTUs.

	<b>Sample</b>			
	<b>-1</b>	<b>9</b>	<b>18</b>	<b>16</b>
<b>Total 454-reads</b>	19138	43623	27735	31504
<b>Average length (bp)</b>	326	341	343	344
<b>Acceptable length*</b>	13536	32538	20967	23934
<b>Quality filtering:</b>				
<b>More than one N, chimeras, incorrect forward primer, and non-target organisms</b>	1678	3126	2380	2458
<b>Singletons</b>	341	826	619	714
<b>Total filtered reads</b>	11517	28586	17968	20762
<b>OTUs (97% identity)</b>	459	714	599	702
<b>Abundant OTUs**</b>	12	13	16	12
<b>Rare OTUs**</b>	447	701	583	690

3 \* reads with a minimum length of 300 bp and a maximum length of 670 bp;

4 \*\* abundant OTU = number of reads  $\geq 1\%$  of total reads, otherwise it is rare

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