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; cgwErrorRate=0.12; utgBubblePopping=0; utgGenomeSize=500000; merSize=15; doFragmentCorrection=0; doExtendClearRanges=1; doResolveSurrogates=1; Unitigger parameter –j = –20.

total num nucleotides	286,258,541
num reads	426,864
num scaffolds	15,008
scaffold N50	29,346
max scaffold length	2,982,959
num predicted proteins	62,915
num placed reads	282,583
% bp placed	69.60%
% reads placed	66.20%