

Table S1. List of software and commands used in this study

Software	Commands	Version	Analysis	Citation
ABYSS	<pre>\$abyss-pe name=\$SRA_ID k=\$kmer in=\$file1.fastq.gz \$file2.fastq.gz</pre>	2.1.5	Assembly	[1]
MEGAHIT	<pre>\$megahit -1 \$file1.fastq.gz -2 \$file2.fastq.gz -o "megahit/\${sra}" -- out-prefix "\${sra}"</pre>	1.2.9	Assembly	[2]
Ray Meta	<pre>\$mpiexec -n 10 Ray -k \$kmer -p \$file1.fastq.gz \$file2.fastq.gz -o "\${sra}"</pre>	2.3.1	Assembly	[3]
SPAdes	<pre>\$spades.py -1 \$file1.fastq.gz -2 \$file2.fastq.gz -o "\${sra}"</pre>	3.14.1	Assembly	[4]
metaSPAdes	<pre>\$metaspades.py -1 \$file1.fastq.gz -2 \$file2.fastq.gz -o "\${sra}"</pre>	3.14.1	Assembly	[5]
Velvet	<pre>\$velveth "velvet\${kmer}/\${sra}" \$kmer -short -separate -fastq \$file1.fastq.gz \$file2.fastq.gz \$velvetg "velvet\${kmer}/\${sra}" -read_trkg yes</pre>	1.2.10	Assembly	[6]
MetaVelvet	<pre>\$velveth "metavelvet\${kmer}/\${sra}" \$kmer -short - separate -fastq \$file1.fastq.gz \$file2.fastq.gz \$velvetg "metavelvet\${kmer}/\${sra}" -read_trkg yes</pre>	1.2.01	Assembly	[7]

	<pre>\$meta-velvetg "metavelvet\${kmer}/\${s ra}"</pre>			
Trinity	<pre>\$Trinity --seqType fq --max_memory 10G -- left \$file1.fastq.gz --right \$file2.fastq.gz -- no_bowtie</pre>	2.11.0	Assembly	[8]
MetaQUAST	<pre>\$metaquast.py *contig.fasta -o \$Output_Directory -r MN908947.3.fasta -- fast --silent</pre>			[9]
BWA	<pre>\$bwa mem MN908947.3.fasta \$file1.fastq.gz \$file2.fastq.gz >out.sam</pre>		Alignment of short reads	[10]
Minimap2	<pre>\$minimap2 -ax asm5 MN908947.3.fasta \$input.fasta >out.sam</pre>		Alignment of contigs	[11]
Picard	<pre>\$java -jar picard.jar MarkDuplicates I=\$file.sorted.bam O=\$file.dupsMarked.bam M=\$file.marked_dup_met rics.txt</pre>		Duplicate read marking	[12]
Bedtools	<pre>\$bedtools intersect -a \$file1.bed -b \$file2.bed \$bedtools makewindows -g MN908947.3.sizes.txt - w 50 \$bedtools bamtobed -i \$file.bam > \$file.bed</pre>		Analysis of bed file	[13]
Samtools	<pre>\$samtools sort \$file.bam -o \$file.sorted.bam \$samtools index \$file.bam</pre>		Analysis of sam/bam file	[14]

bcftools	<pre>\$bcftools mpileup -f MN908947.3.fasta \$file.sorted.bam > \$file.raw.vcf \$bcftools call -c -v - -ploidy 1 -O v -o \$file.call.vcf \$file.raw.vcf</pre>		Variant calling	[14]
SRA Toolkit	<pre>\$fastq-dump --split- files --outdir \$Output_Directory -- gzip \$SRA_ID</pre>		Download SRA files	[15]
R		3.5.2	Visualization and statistics	[16]

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