

	Pipelines	IMP	SAMSa	MetaTrans	FMAP	MOCAT2	MG-RAST	metagenomics	MetAMOS
	Steps								
Preprocessing	Quality check	FastQC	None	FastQC	None	SolexaQA	DRISEE, kmer profiles, nucleotide histograms	None	FastQC
	Removal of low quality sequences/regions	Trimmomatic	Trimmomatic	Kraken tools	BMTagger	FastX, SolexaQA, custom scripts	SolexaQA	Trimmomatic, Biopython	fastx_toolkit
	Adapter removal	Not specified	Trimmomatic	Kraken tools	None	Usearch	None	Biopython	None
	rRNA removal	SortMeRNA	None	SortMeRNA	None	None	BLAT	rRNASelector	None
	Host sequences removal	bwa	None	None	BMTagger	SOAPAligner2	Bowtie	None	None
	Alignment of paired end reads	None	FLASh	Kraken tools	None	None	None	SeqPrep	None
Assembly	Assembly	IDBA-UD, MEGAHIT	None	None	None	SOAPdenovo	None	None	SOAPdenovo, Newbler, Velvet, Velvet-SC, MetaVelvet, Meta-IDBA, CABOG and Minimus
	Quality control of assembly	MetaQUAST	None	None	None	SOAPdenovo, BWA	None	None	bowtie, bowtie2, Bambus2, several plots
Annotation	Functional annotation	Prokka	MG-RAST	SOAP2 (with in house scripts)	USEARCH, DIAMOND	fetchMG, DIAMOND, perl script	sBLAT	InterProScan	BLAST, MetaPhyler, PHMMER, PhyloSift, PhymmBL, FCP
	Taxonomic annotation	MetaQUAST	MG-RAST	SOAP2 (with in house scripts)	None	fetchMG, mOTU-LG, specl	sBLAT	Qiime	BLAST, MetaPhyler, PHMMER, PhyloSift, PhymmBL, FCP
	Depth of coverage calculation	BEDtools	None	None	None	None	Not specified	None	Repeatoire
	Variant calling	Samtools mpileup, Freebayes, Platypus	None	None	None	None	None	None	None
	Binning	VizBin	None	None	None	None	Not specified	None	None
	Gene calling	MetaQUAST	MG-RAST (FragGeneScan)	FragGeneScan	None	Prodigal, MetaGeneMark	FragGeneScan	rRNAselector, FragGeneScan	MetaGeneMark, FragGeneScan, Glimmer-MG
Results analysis	Taxonomic analysis	Barplots	Barplots	Plots	None	None	phyloseq, rank abundance, rarefaction	Pie chart, barplot, Krona	Krona, heatmaps
	Abundance of pathways	Heatmap, Krona	Barplots	DESeq2, iPath2	KEGG, ShotgunFunctionalizer	None	heatmap, Krona	None	Krona
	Variants analysis	VizBin	None	None	None	None	None	None	Sequence alignment
	Species sequences detection	VizBin	None	None	None	None	None	None	None
	Depth of coverage	VizBin	None	None	None	None	None	None	R
	General sequences information	None	None	None	None	None	Flowchart	None	Plots