Assembly: validation & QC PE metagenomic reads Collect stats SAM files (bbmap.sh, samtools, QC (fastQC) piccard tools) % reads mapped contig coverage Trim adapters & Map reads Filtered reads quality filter (bbmap.sh) (fastq) (bbduk.sh) Contigs Assemble (fasta) (megahit) Collect stats (stats.sh, MetaQUAST)

N50, max, min, mean