

EDGE Trimming	<ul style="list-style-type: none"> - Trim Quality Level: 30 - Average Quality Cutoff: 30 - Minimum Read Length: 50 - "N" Base Cutoff: 2 - Low complexity Filter Ratio: 0.85 - Adapter FASTA: None - Cut #bp from 5' end: 0 - Cut #bp from 3' end: 0
CLC Trimming	<ul style="list-style-type: none"> - Ambiguous limit: 2 - Quality limit: 0.001 - Remove 5' terminal nucleotides: 0 - Remove 3' terminal nucleotides: 0 - Maximum number of nucleotides in reads: 1000 - Minimum number of nucleotides in reads: 50 - Discard short reads
EDGE Assembly	<ul style="list-style-type: none"> - Assembler: SPAdes - Minimum Kmer Length: 31 - Maximum Kmer Length: 121 - Step size: 20 - Minimum Contig Length: 200 - Validation Aligner: Bowtie 2
CLC Assembly	<ul style="list-style-type: none"> - Mapping mode: Map reads back to contigs (slow) - Update Contigs - Mismatch cost: 2 - Insertion cost: 3 - Deletion cost: 3 - Colospace error cost: 3 - Length fraction: 0.5 - Similarity fraction: 0.8 - Colospace alignment - Alignment mode: global - Match mode: random - Bubble size: Automatic - Word size: 64 - Minimum contig length: 200 - Perform scaffolding - Auto-detect paired distances
PhageTerm	Paired reads -s: 20 -d: 20 -m: 250
Contamination Check	<ul style="list-style-type: none"> - Must be less than 5% of reads mapping to host
VF/AR/Integrase Presence	

PHACTS	--classes: classes_lifestyle --replicates: 20 --exclude: None --num_cases: 50 --percent: 1 --variables: 600 --short: 0
High Quality Genome	<ul style="list-style-type: none">- 90% of reads must map back to final genome- 100X coverage for complete genomes- ~400X coverage for finished genomes