

**S2 Table: CLC Genomics workbench bioinformatics workflow parameters**

**Step 1: Initial trimming parameters**

**Quality trimming**

Ambiguous trim	yes
Ambiguous limit	2
Quality limit	0.05
Quality Trim	yes

Sequence to Trim	Strand	Action	Mismatch	Gapcost	Cutoff	Sequence
TruSeq-adapter-1	Both	Remove adapter	2	3	10	GGGGTAGTGGATCCTCCTAGGCCAGTTGGGTTATTCTAGAAGCAGATGTGTTGGCTGTTCTGAAACTCTGAAAA
TruSeq-adapter-3	Both	Remove adapter	2	3	10	CAACAGCCGGTCAAACATCTGGAGGGTAAGCCATAAACACCTCAACAGAAAA
PCR-primer-1	Both	Remove adapter	2	3	10	CGATAACTTCGTATAATGTATGCTATACGAAGTTATTACG
PCR-primer-2	Both	Remove adapter	2	3	10	GCATAACTTCGTATAGCATAATTATACGAAGTTATTACGA
Nextera-primer-adapter-1	Both	Remove adapter	2	3	10	GATCGGAAGAGCACACGTCTGAACTCCAGTCAC
Nextera-primer-adapter-2	Both	Remove adapter	2	3	10	GATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT
Nextera-junction-adapter-1	Both	Remove adapter	2	3	10	CTGTCTTTATACACATCTAGATGTGTATAAGAGACAG
SmartSeq-adapter-1	Both	Remove adapter	2	3	10	AATGATACGGCGACCACCGAGATCTACACTTCGCTACAGGACGCTGTTCCGTTCTATGGG
SmartSeq-adapter-2	Both	Remove adapter	2	3	10	ACACTTCGCTACAGGACGCTGTTCCGTTCTATGGG
SmartSeq-adapter-3	Both	Remove adapter	2	3	10	CAGACGTGTGCTCTCCGATCT
5'PolyG	Plus	Remove adapter	2	3	-	G <sup>150</sup>
3'PolyG	Minus	Remove adapter	2	3	-	C <sup>150</sup>
PCR-20mer	Plus	Remove adapter	2	3	10	GACCATCTAGCGACCTCCCA

**Filtering on length**

Max nr of nt in reads	1000
Min nr of nt in reads	20
Short reads discarded	yes

**Step 2: Map to host parameters**

Input host genomes/scaffolds downloaded from NCBI: *Myotis brandtii* assembly no. GCF\_00412655.1

Masking mode	no
Mismatch cost	2
Insertion cost	3
Deletion cost	3
Length fraction	0.7
Similarity fraction	0.9
Global alignment	no
Color error cost	3
Auto detect paired distances	yes
Non-specific match handling	Map randomly

**Outputs:**

Report	produced
Read mapping	Host NGS reads
Unmapped reads	Non-host NGS reads

**Remove PhiX sequencing control**

Same parameters as mapping to host

**Step 3: CLC de novo assembly**

**Map reads to contigs**

Mapping mode	Map reads back to contigs (slow)
Update contigs	yes

**Mapping options**

Mismatch cost	2
Insertion cost	3
Deletion cost	3
Length fraction	0.5
Similarity fraction	0.8
Alignment mode	local
Color space error cost	3
Create list of unmapped reads	yes

**Graph parameters**

Automatic bubble size	yes
Bubble size	50
Automatic word size	yes
Word size	20

**Contig length**

minimum contig length	200
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**Paired reads**

Perform scaffolding	yes
Autodetect paired distances	yes

**Outputs:**

Report	yes
Assembly with Mapping	NGS contig output
Unmapped reads	Left over reads not included in the assembly