cleaned aDNA reads (FASTQ file)
align FASTQ sample to MT reference fasta (BWA and optionally CircularMapper)
aligned reads (BAM file)
sort, MD-tag and index aligned BAM file (SAMtools)
aligned, MD-tagged, indexed reads (BAM file)
estimate endogenous deamination (contDeam)
estimate contamination and call the mtDNA consensus sequence (schmutzi)
endogenous (unfiltered) consensus sequence (FASTA) and log file
schmutzi pipeline
quality-filtering of consensus sequence (log2fasta)
Database containing raw genomic data
filtered consensus sequence (FASTA)
quality-filtering of consensus equence (ANGSD -dofasta -trim -minQ)
ANGSD pipeline
cleaned aDNA reads (BAM file)
create index file (BAI) after checking that BAM is sorted (SAMtools)
index file of BAM reads (BAI)
isolate MT chromosome (SAMtools - only required if whole genome data used)
MT chromosme reads (BAM)
call the mtDNA (unfiltered) consensus sequence (ANGSD -dofasta)
unfiltered consensus sequence (FASTA)