

Step1

extractMtDNAReads
sample1: 00115101162M16BFF2

GATK

extractMtDNAReads
sample2: 00113051204M47BFF2

Step2

convert_cram_to_fastq

Samtools

BWA mem

Align2ShiftedRef

Align2RawRef

Align2RawRef

convert_cram_to_fastq

Align2ShiftedRef

create_input_file_for_variant_calling

Mitoquest

Step3

VarCalling_shifted

VarCalling_raw

Custom script

mitoVCF_merging
id: BIGCS_II

run_all