

Read Mapping

Details

- Reads mapped with Burrows-Wheeler Aligner (BWA) version 0.6.1. BWA aln and BWA sampe were used.
- Reads were mapped to NC_012920.

Refine Read Mappings

Details

- Mappings were refined using the Genome Analysis Toolkit (GATK) version 2.5-2.
- First, we realigned reads around indels using RealignerTargetCreator and IndelRealigner
- Second, we performed base recalibration using BaseRecalibrator and PrintReads

Joint-call variants

Details

- Called variants for all samples concurrently using FreeBayes, version 1.0.2, with settings: -p 1 -F 0.6.

Annotate variants

Details

- Annotate variants based on previously observed variants. Downloaded and used variant information from MITOMAP. Included: variant frequency, source, locus name, etc. for each known variant.
- Determined mitochondrial haplogroup using Phy-Mer, version 1.0, and selecting the most probable haplogroup for each sample.