PoolParty base.sh Raw paired-end fastg files **PoolParty** Popoolations Trim reads by quality Pool-seg Pipeline Quality-trimmed fastq files Alian to reference genome BWA-MEM Samblaster Remove PCR Duplicates Samtools aligned reads Discordant and split-end .bam files Aligned .bam files Picard Tools Sort by coordinates Samtools Removed unpaired reads Read Alignment Statistics Filtered .bam files Samtools Samtools Combined BAM files Coverage Statistics .mpileup file PP Stats.sh Popoolations 2 Identify In-del regions Popoolations 2 Convert to SYNC format Calculate allele Allele frequency table In-del filtered .sync file Cochran-Mantel-Haenszel test PP AF.R Popoolations 2 Genetic-distance PP NJ.R calculation, boostrapping Pairwise-FST analysis Popoolations 2 Fisher's Exact Test Sliding Window FST analysis FFT results LocalScore.R Local score analysis