PrimerID Workflow

PRE-PROCESSING

R1 FASTQ

R2 FASTQ

PRIMER FILE

REF CDS

Trim 4N
fastx_trimmer

(gaps are okay)

Make Contig
pandaseq
concatenate_fastq.pl

Find PrimerID
filter_fastq_by_primerid_length.pl

(multiple amplicons per sample is okay)

Split by Region
Btrim64

Remove Off-target Reads
bwa mem
SortSam
bamToBed
get_majority_start_stop.pl
intersectBed
graph_coverage.pl

MERGING

Call Consensus for PrimerID Groups
merge_primerid_read_groups.pl

Consensus FASTA

LINKAGE AND SELECTION ANALYSIS

Make Frequency Tables
convert_reads_to_amino_acid.pl

VARIANTS (nuc, codon, aa)

FREQUENCY TABLES (nuc, codon, aa)

Calculate Linkage Disequilibrium
calculate_linkage_disequilibrium.pl
calculate_quasi_cliques.pl

Selection Analysis
HyPhy?

Sample Comparisons
[code from MpileupFrequency.pl]