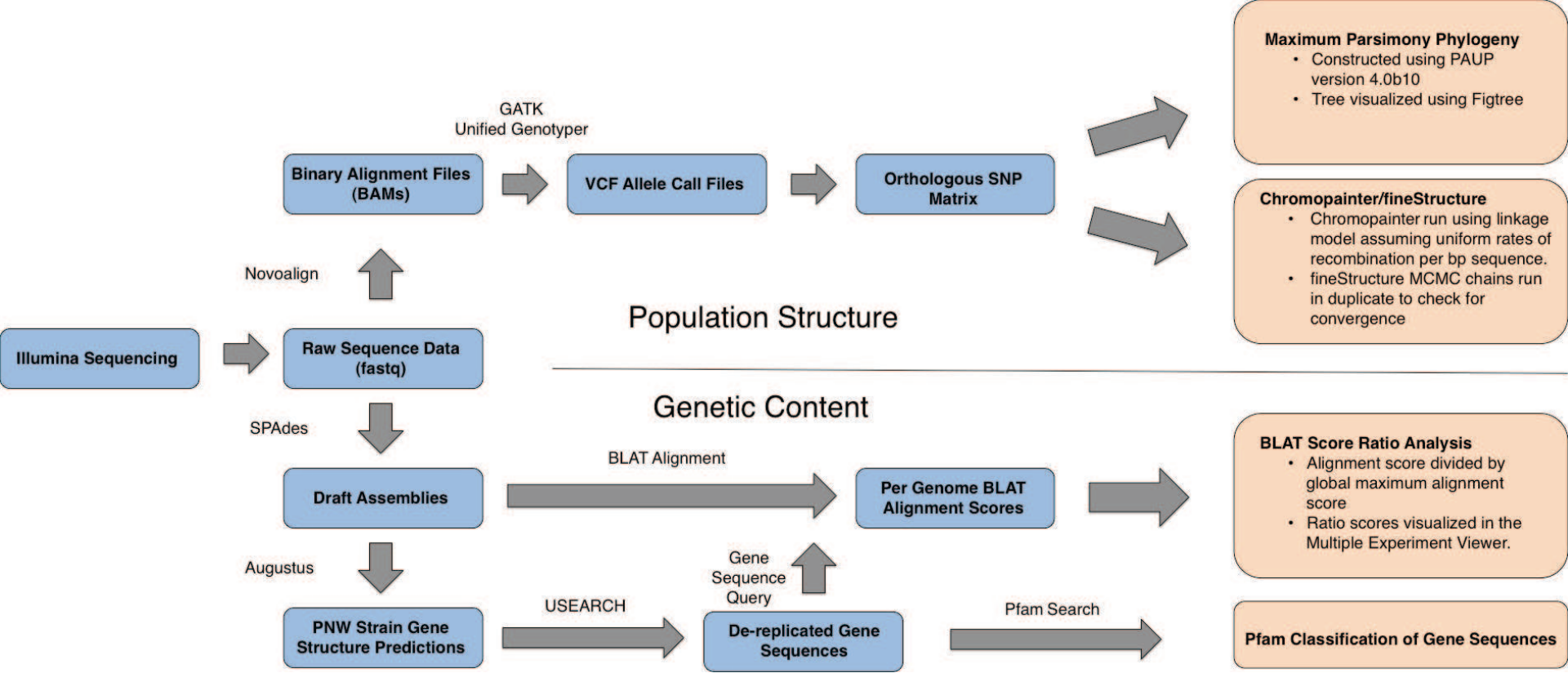
GATK
Unified Genotyper
Binary Alignment Files (BAMs)
VCF Allele Call Files
Orthologous SNP Matrix
Maximum Parsimony Phylogeny
Constructed using PAUP version 4.0b10
Tree visualized using Figtree
Chromopainter/fineStructure
Chromopainter run using linkage model assuming uniform rates of recombination per bp sequence.
fineStructure MCMC chains run in duplicate to check for convergence
Novoalign
Population Structure
Illumina Sequencing
Raw Sequence Data (fastq)
Genetic Content
SPAdes
BLAT Alignment
Draft Assemblies
Per Genome BLAT Alignment Scores
BLAT Score Ratio Analysis
Alignment score divided by global maximum alignment score
Ratio scores visualized in the Multiple Experiment Viewer.
Augustus
Gene Sequence Query
USEARCH
Pfam Search
PNW Strain Gene Structure Predictions
De-replicated Gene Sequences
Pfam Classification of Gene Sequences