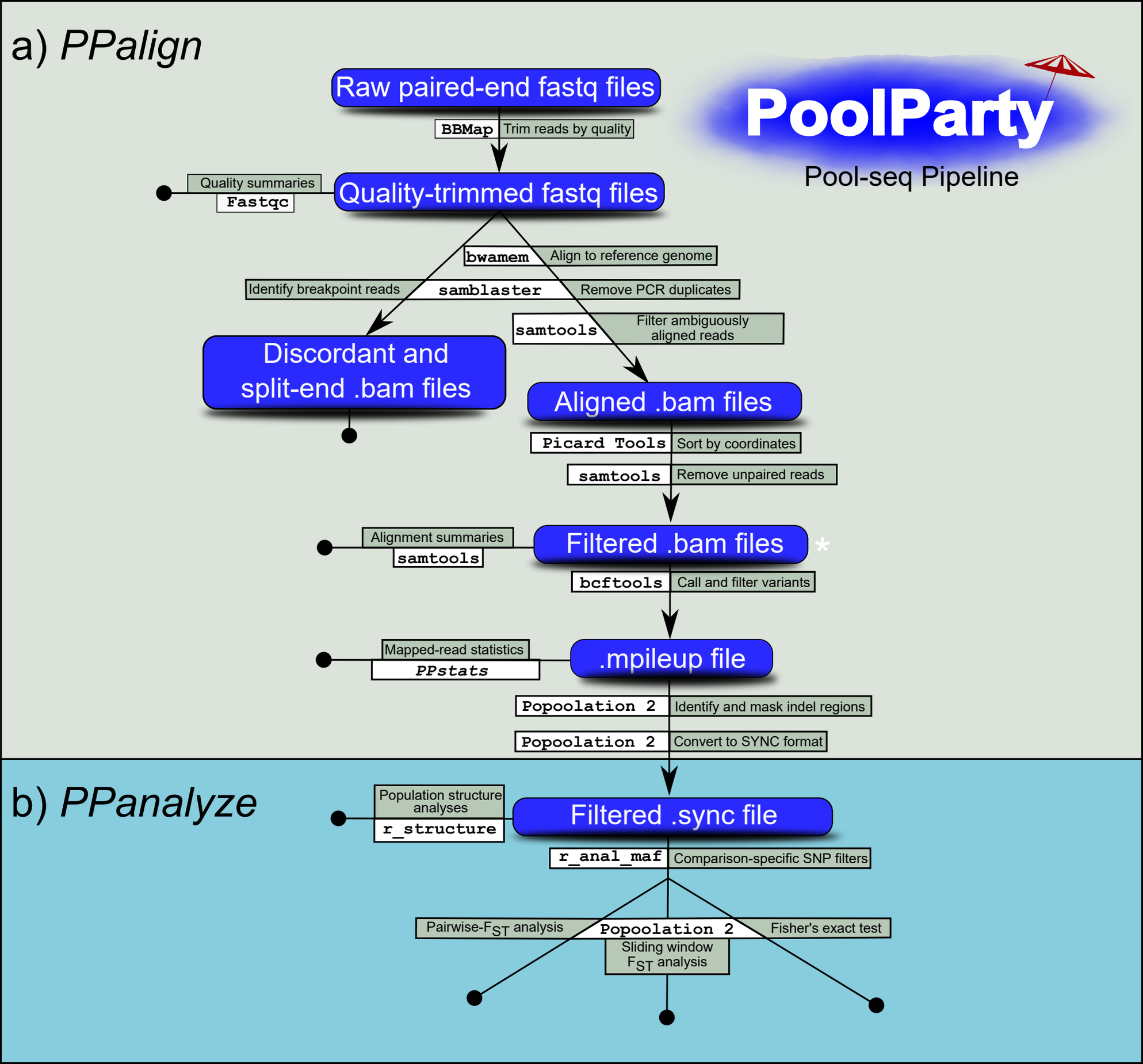
a) PPalign
PoolParty
Pool-seq Pipeline
Raw paired-end fastq files
BBMap
Trim reads by quality
Quality summaries
Fastqc
Quality-trimmed fastq files
bwamem
Align to reference genome
Identify breakpoint reads
samblaster
Remove PCR duplicates
samtools
Filter ambiguously aligned reads
Discordant and split-end .bam files
Aligned .bam files
Picard Tools
Sort by coordinates
samtools
Remove unpaired reads
Alignment summaries
samtools
Filtered .bam files
*
bcftools
Call and filter variants
Mapped-read statistics
PPstats
.mpileup file
Popoolation 2
Identify and mask indel regions
Popoolation 2
Convert to SYNC format
b) PPanalyze
Population structure analyses
r_structure
Filtered .sync file
r_anal_maf
Comparison-specific SNP filters
Pairwise-FST analysis
Popoolation 2
Fisher's exact test
Sliding window FST analysis