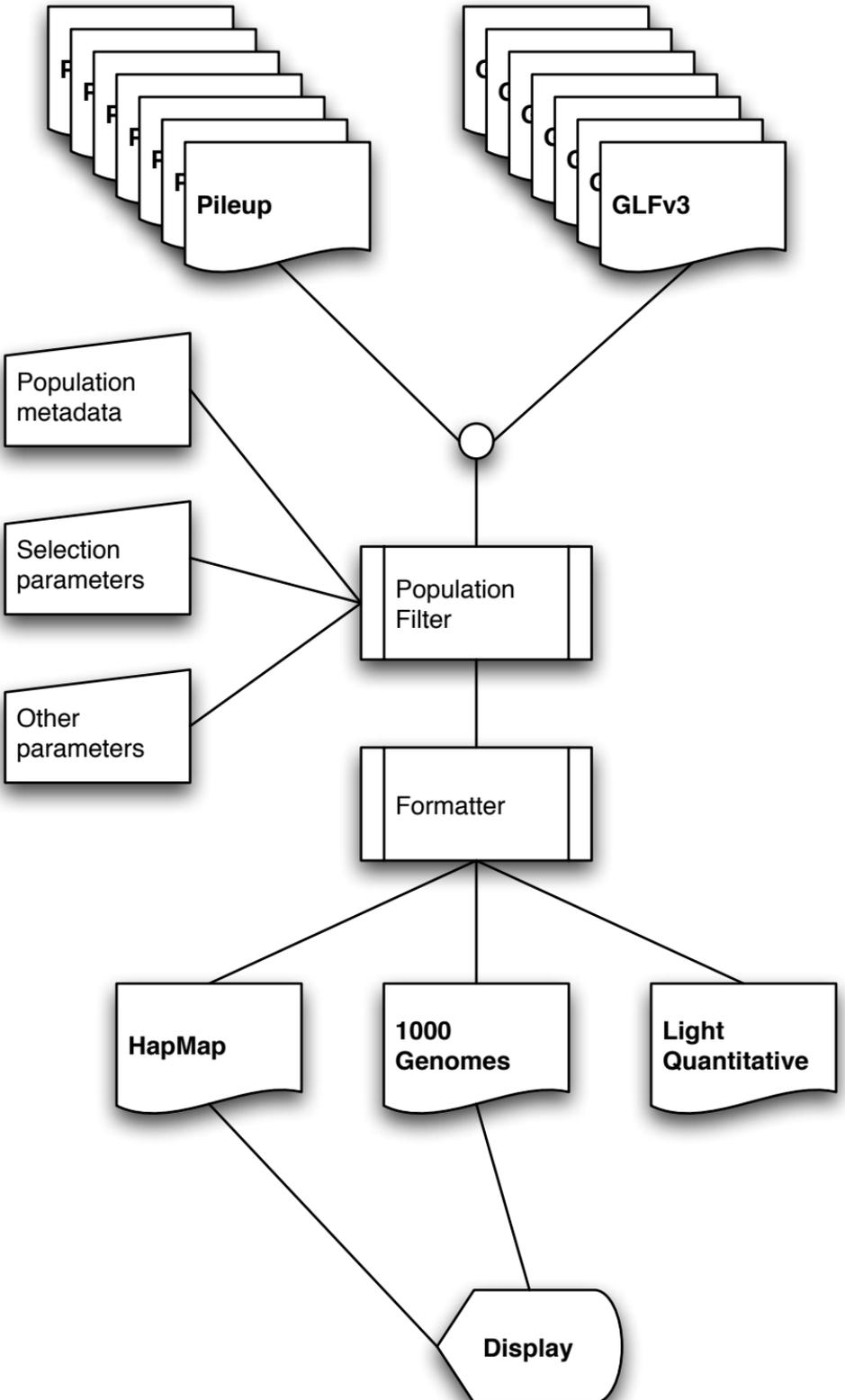
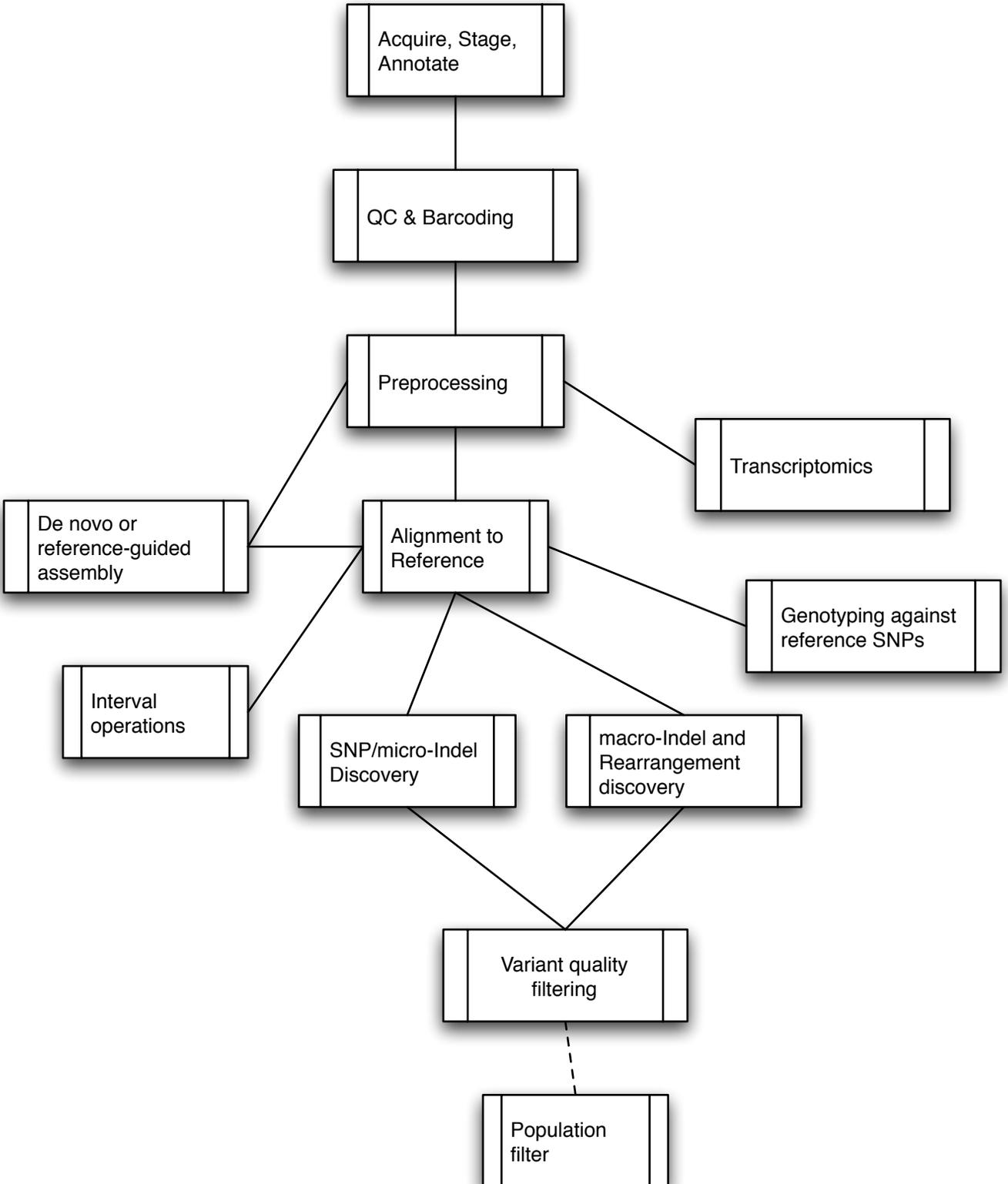


# Population Filter

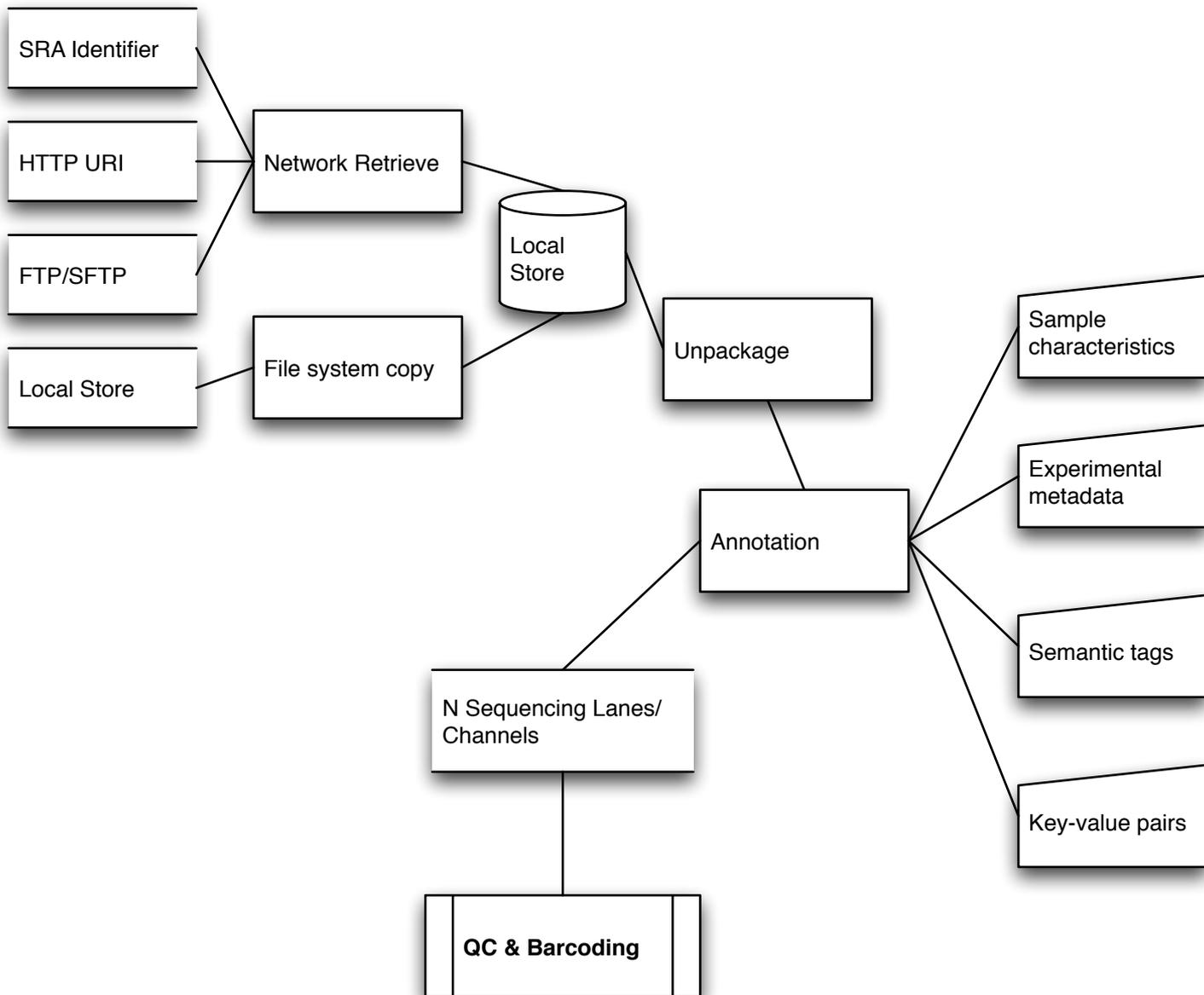
*Outputs from multiple variant detection libraries*



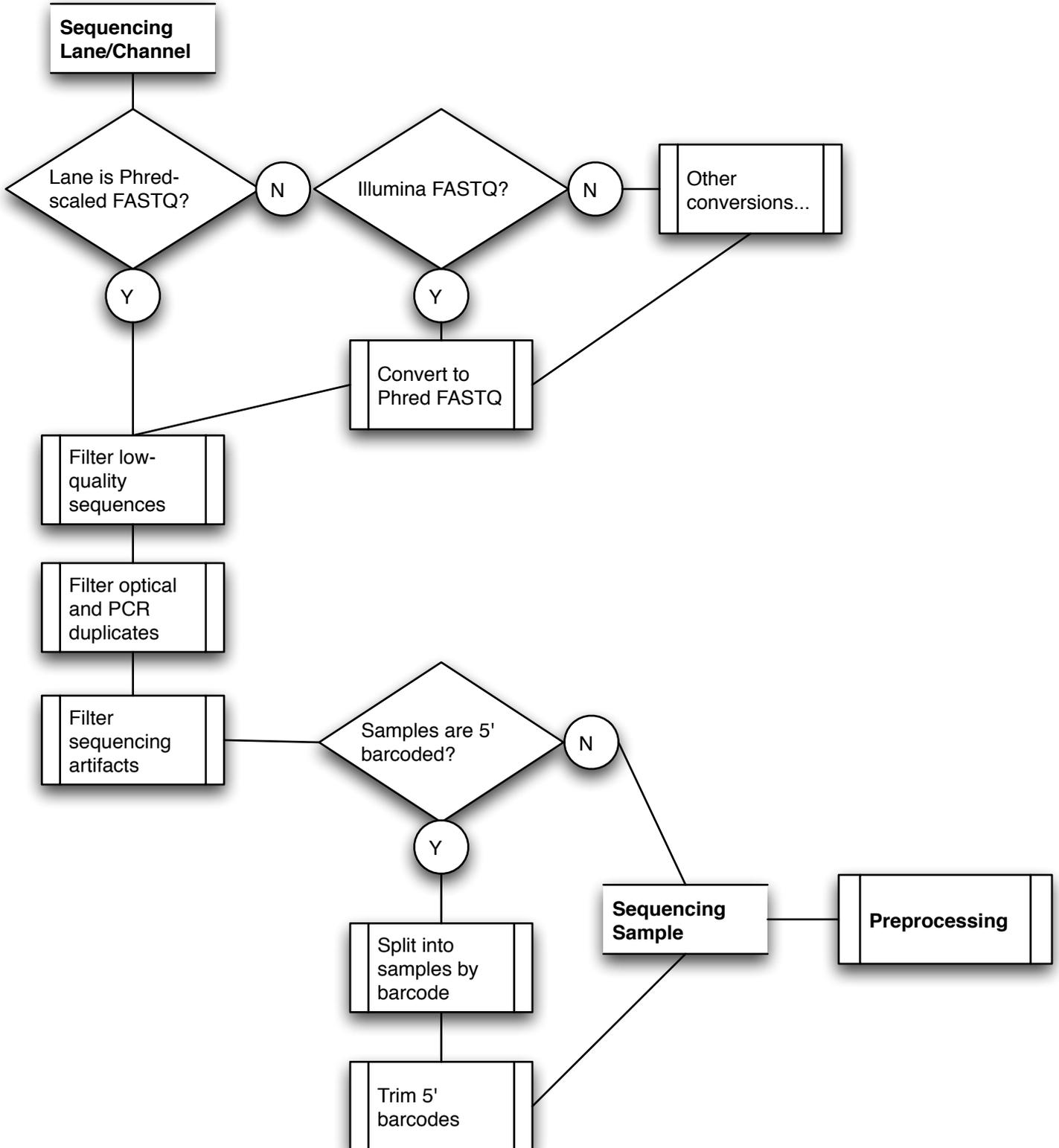
# Overview



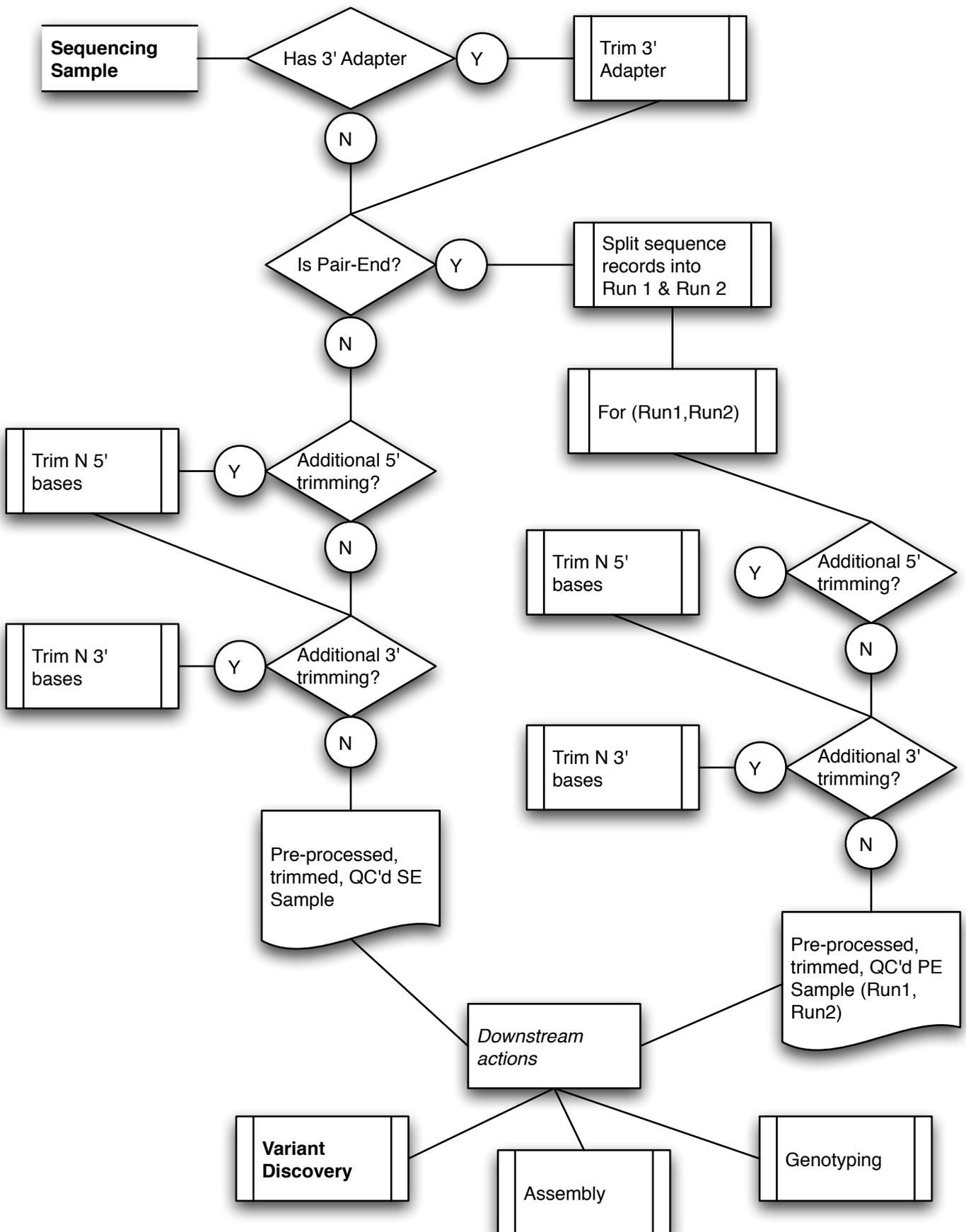
# Acquire, Stage, Annotate



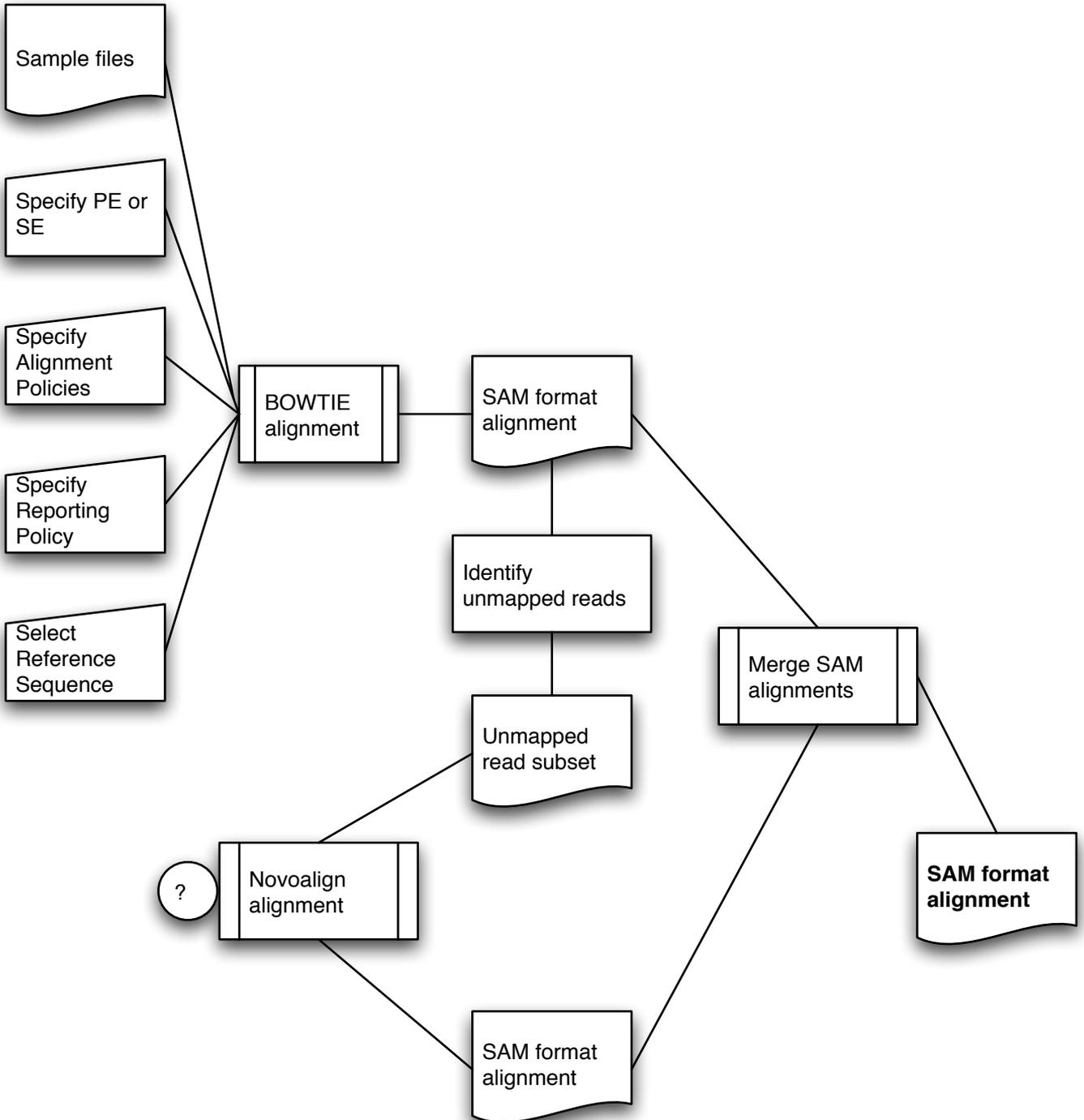
# QC and Barcode Resolution



# Preprocessing

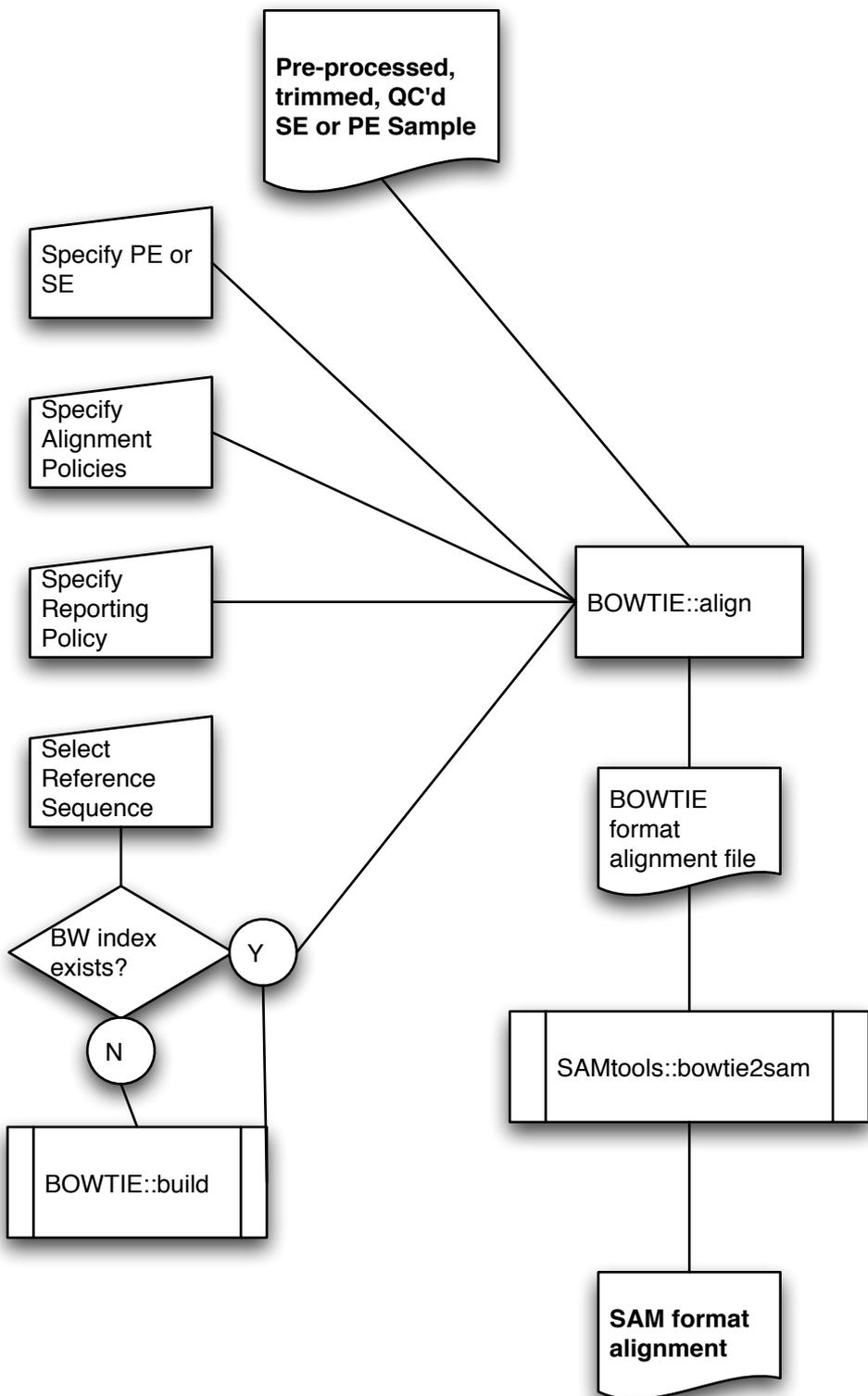


# Alignment to Reference



# BOWTIE Alignment (BWT/Suffix Array)

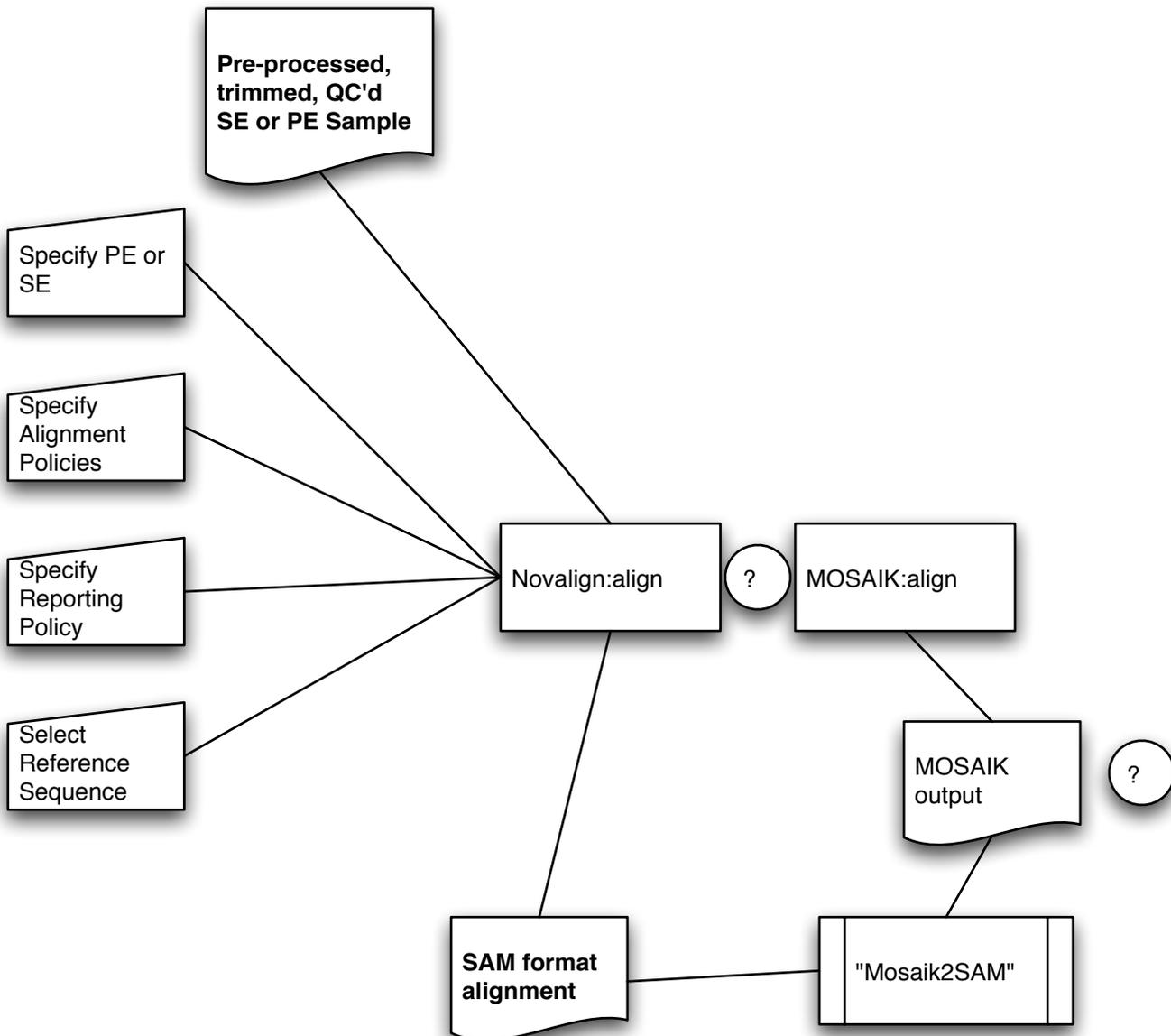
Approximate ungapped alignment



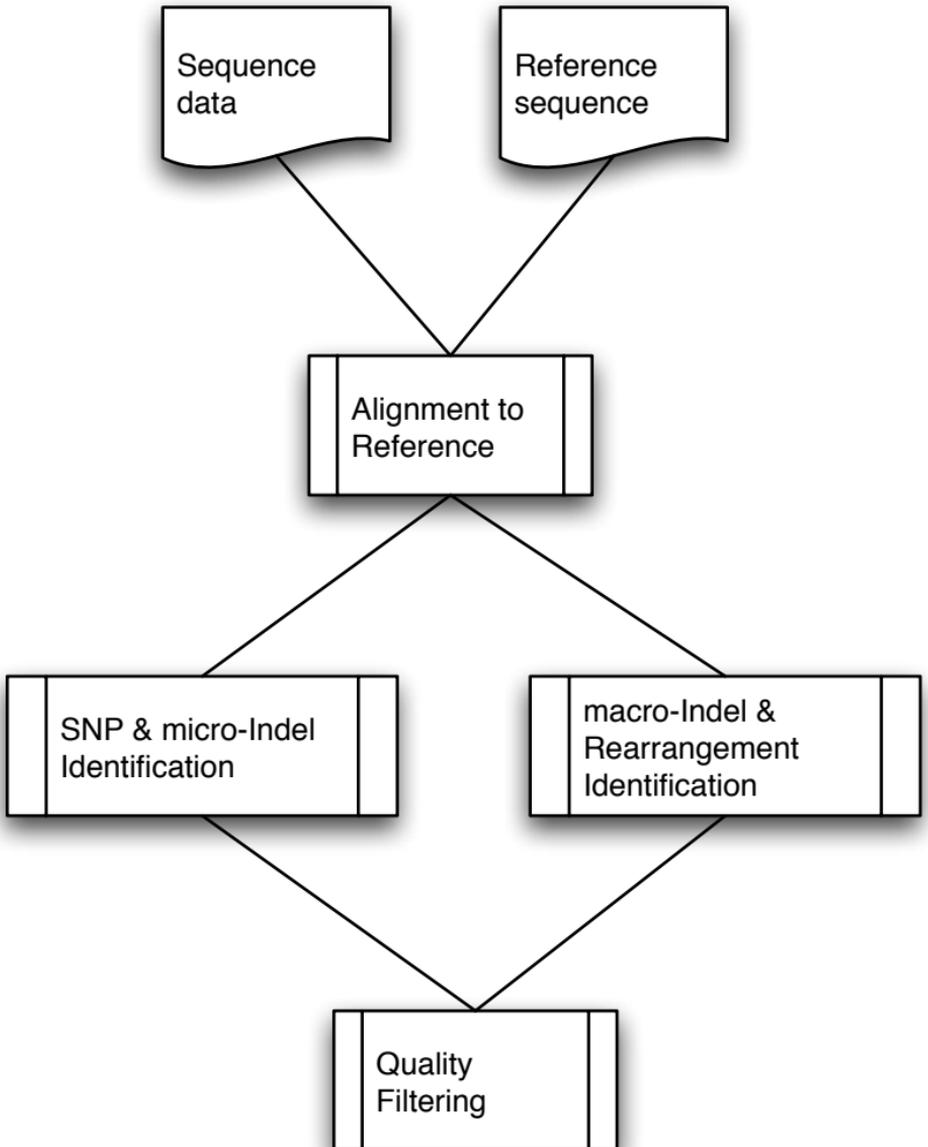
# Noalign Alignment (Needleman-Wunsch)

## MOSAIK Alignment (Smith-Waterman)

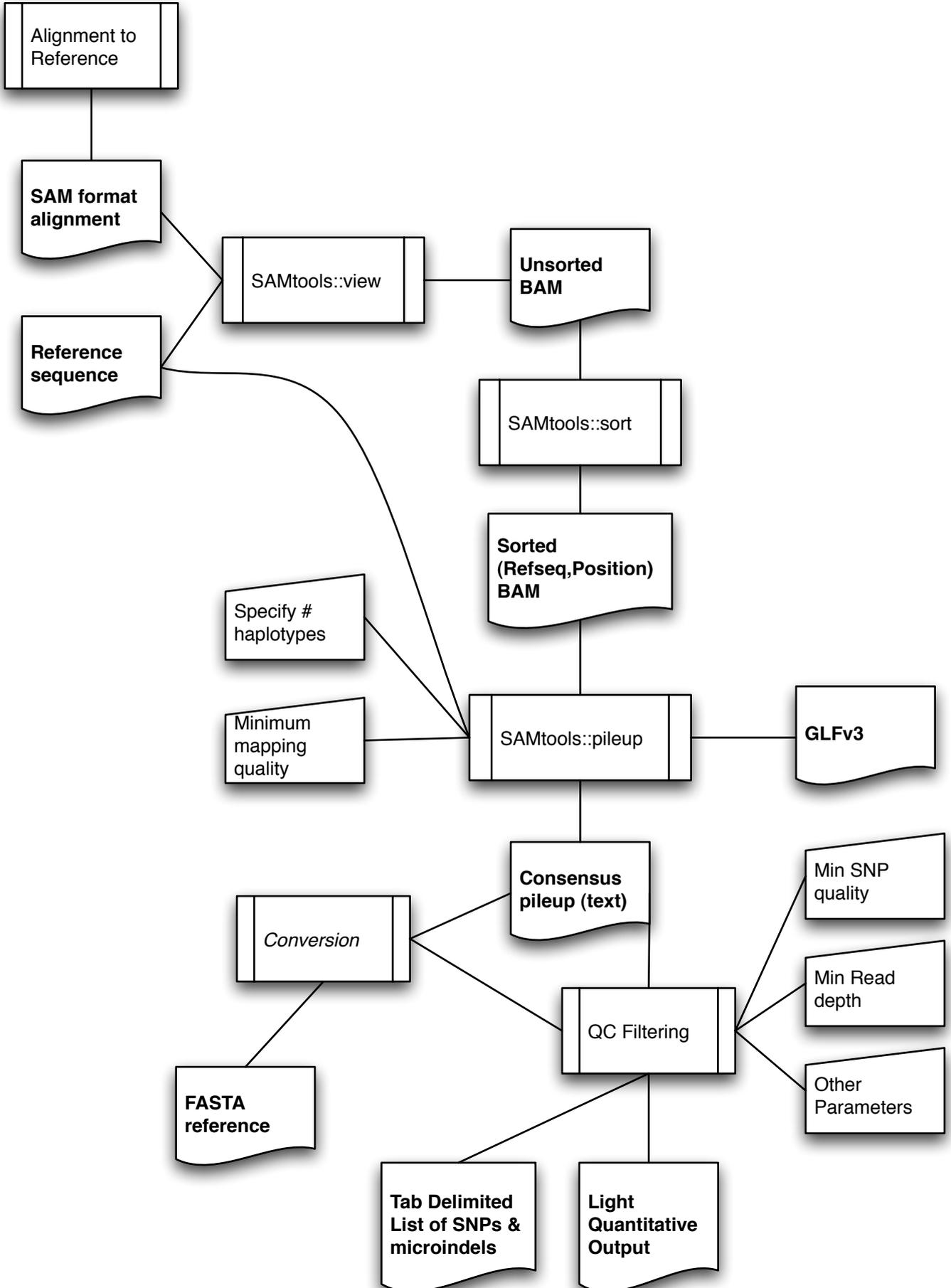
Sensitive gapped alignment



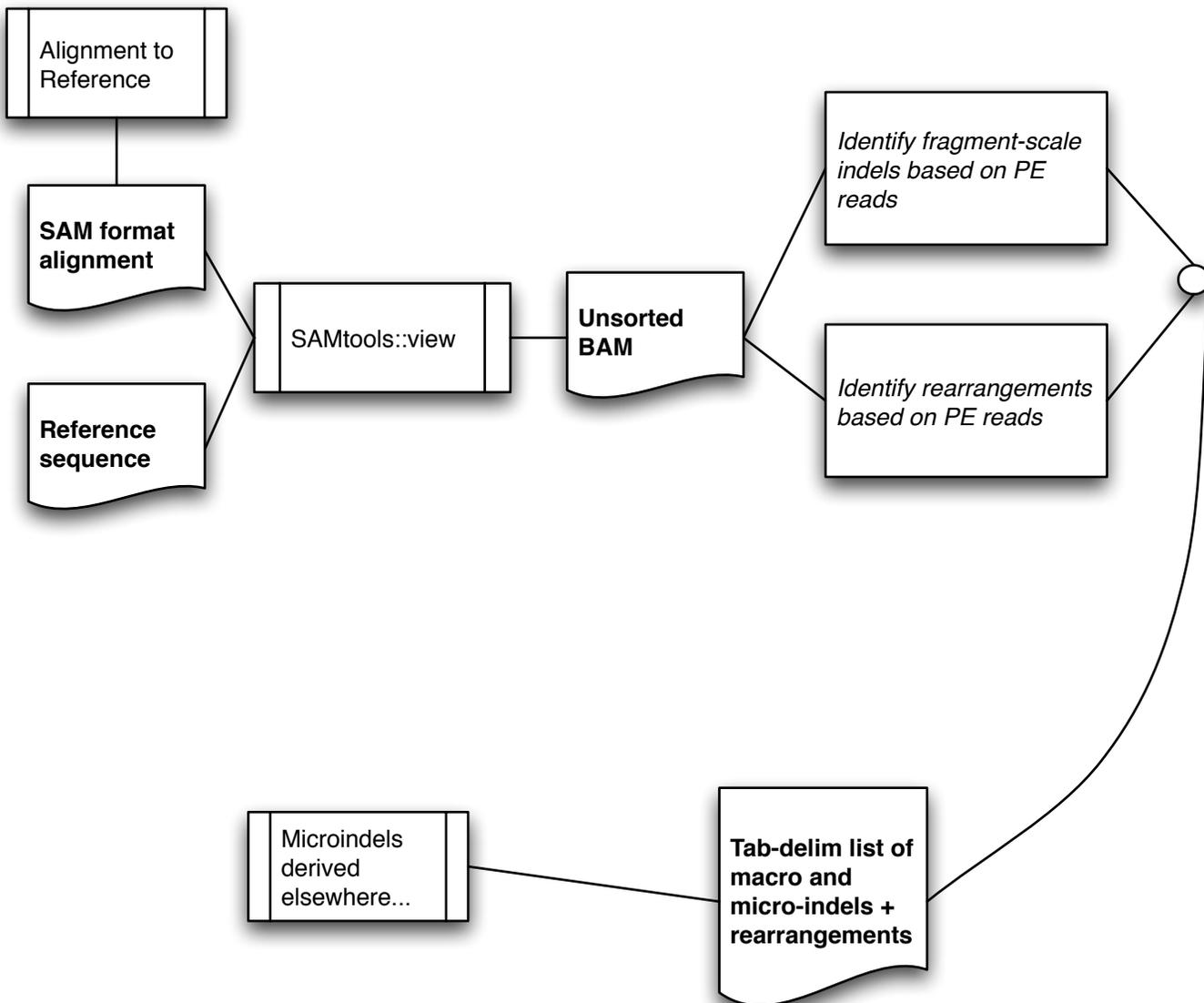
# Variant Discovery



# SNP & micro-Indel Discovery



# macro-Indel and Rearrangement Discovery



# Transcriptomics

