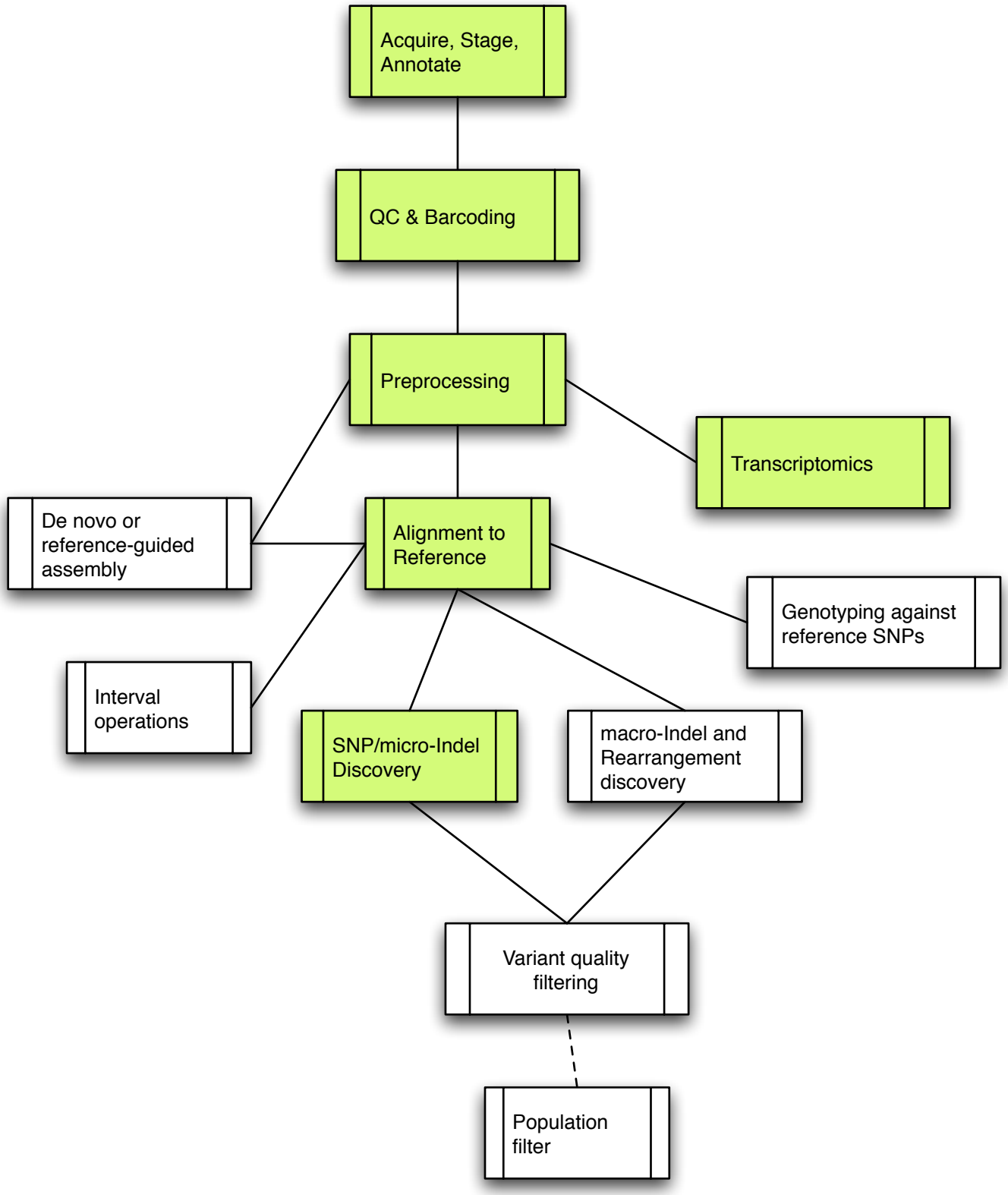
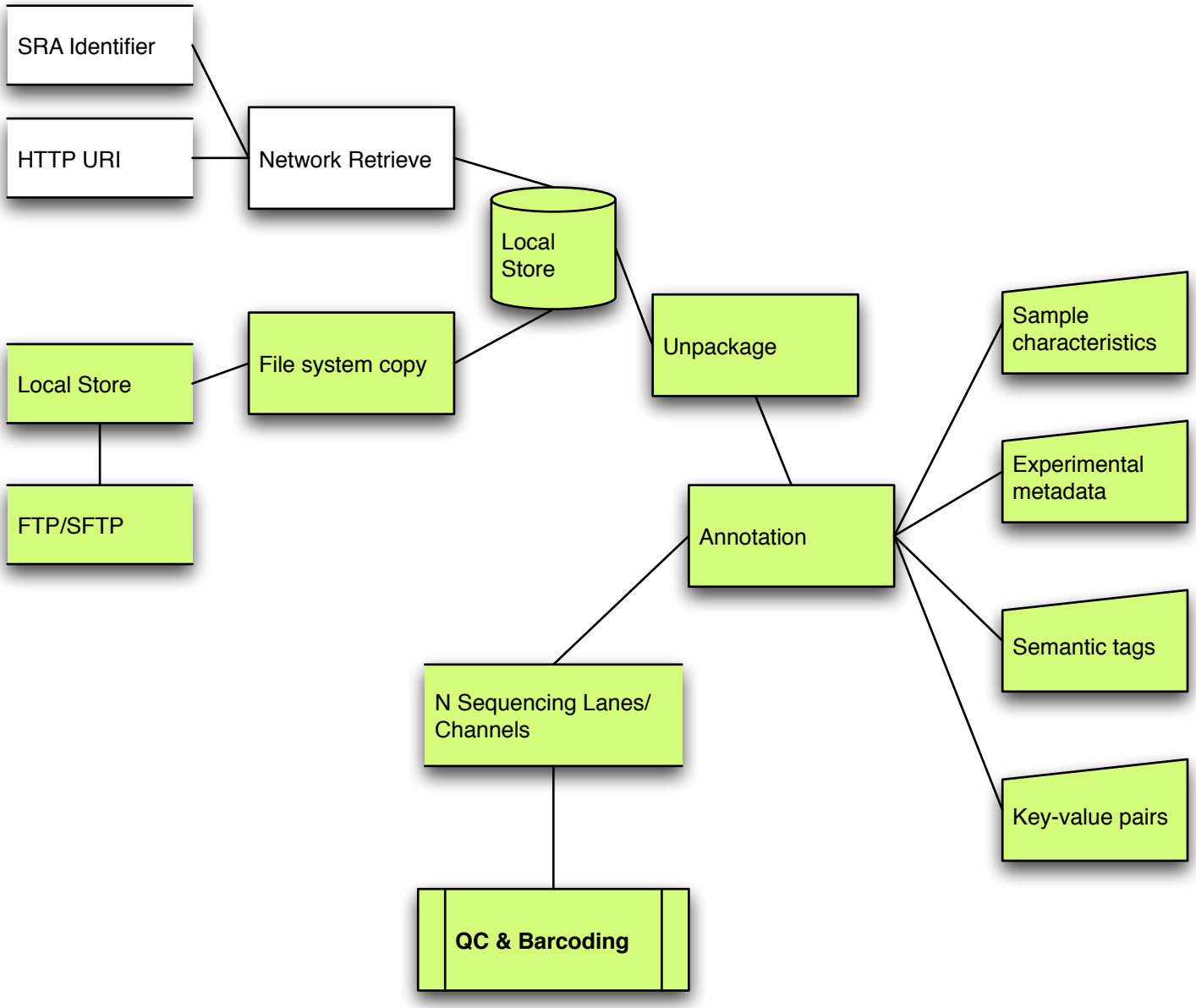
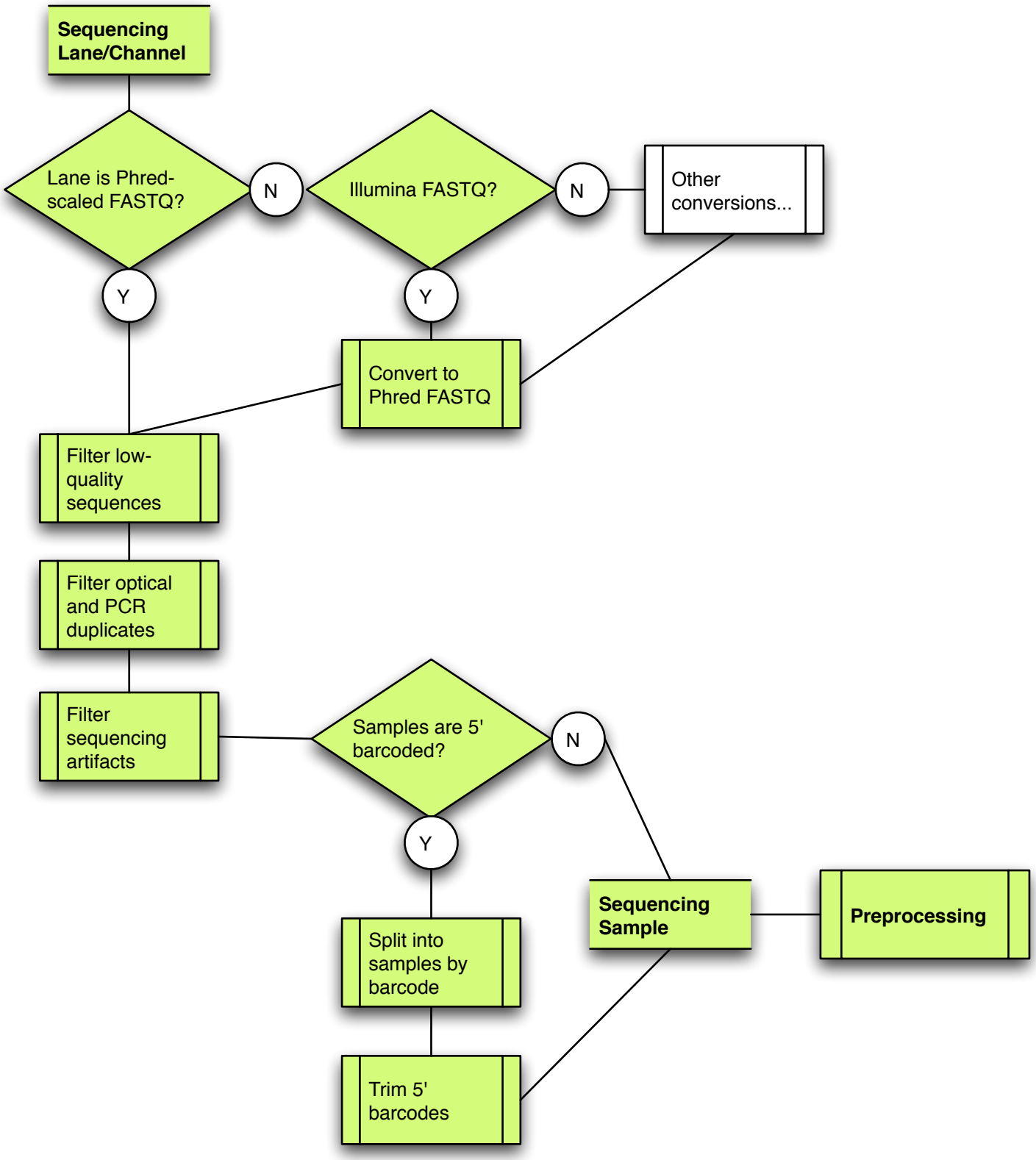
Overview

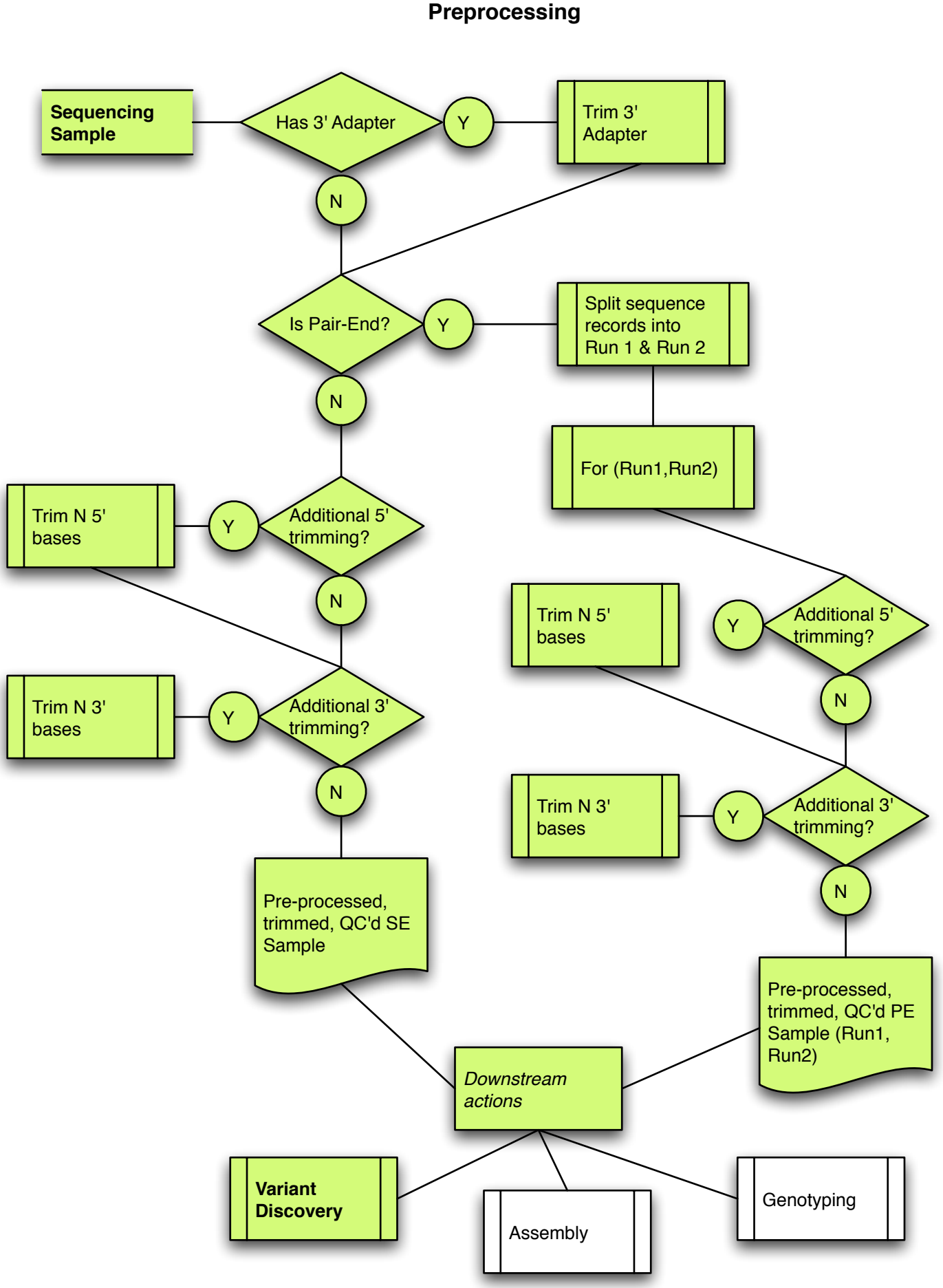

Acquire, Stage, Annotate
QC & Barcoding
Preprocessing
Transcriptomics
De novo or reference-guided assembly
Alignment to Reference
Genotyping against reference SNPs
Interval operations
SNP/micro-Indel Discovery
macro-Indel and Rearrangement discovery
Variant quality filtering
Population filter

Acquire, Stage, Annotate

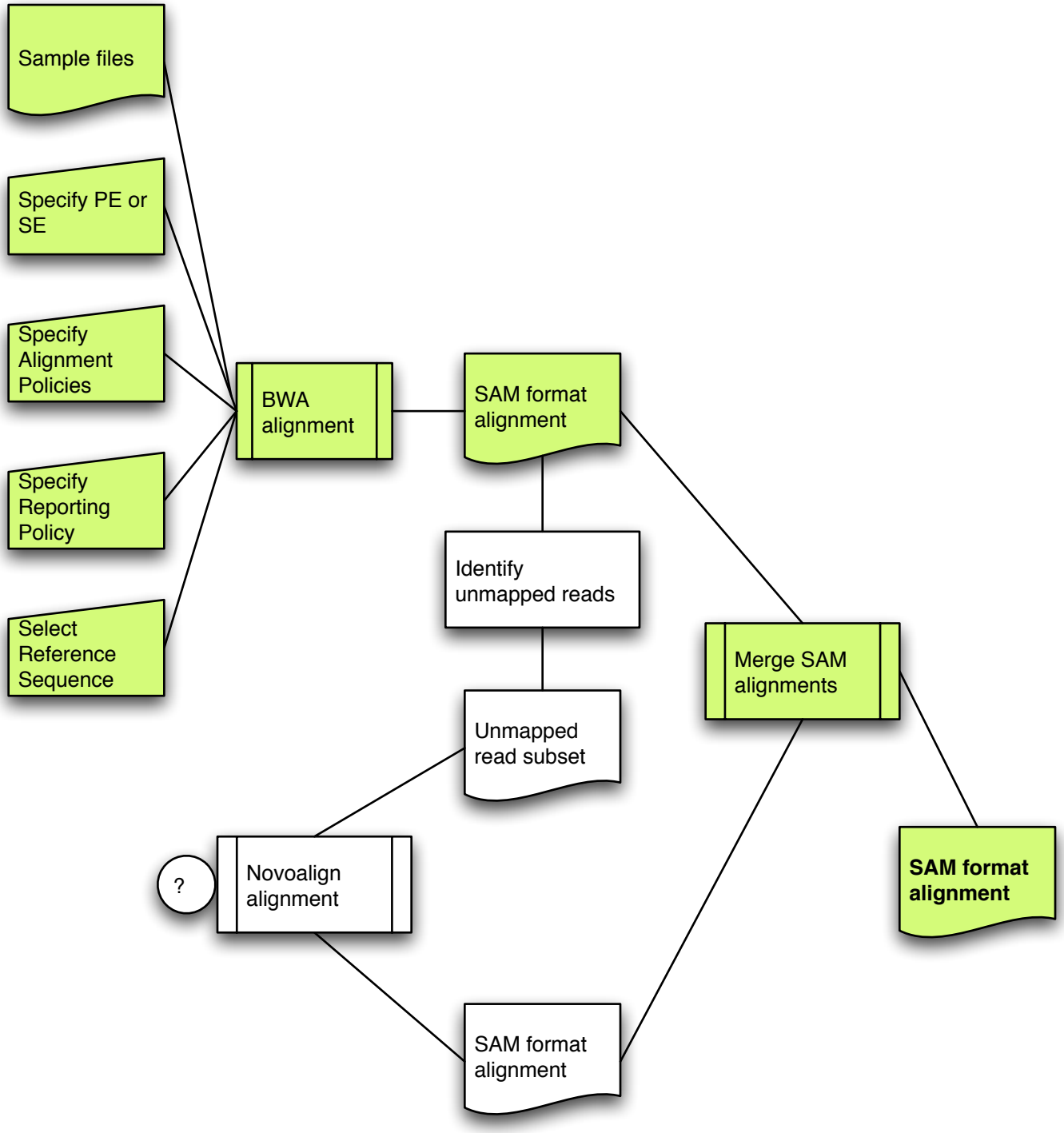


QC and Barcode Resolution



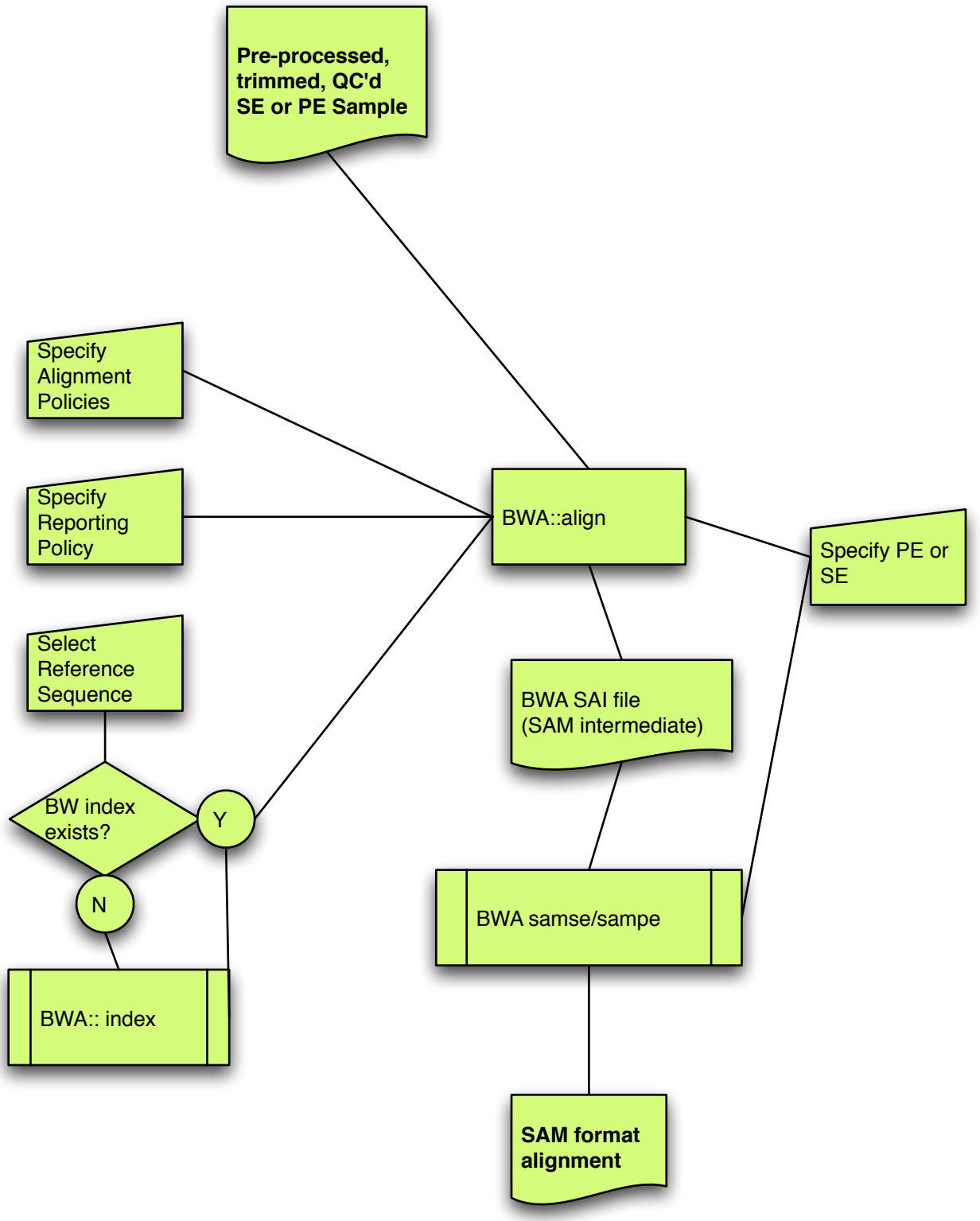

Preprocessing
Sequencing Sample
Has 3' Adapter
Y
Trim 3' Adapter
N
Is Pair-End?
Y
Split sequence records into Run 1 & Run 2
N
For (Run1,Run2)
Trim N 5' bases
Y
Additional 5' trimming?
N
Trim N 5' bases
Y
Additional 5' trimming?
N
Trim N 3' bases
Y
Additional 3' trimming?
N
Trim N 3' bases
Y
Additional 3' trimming?
N
Pre-processed, trimmed, QC'd SE Sample
Pre-processed, trimmed, QC'd PE Sample (Run1, Run2)
Downstream actions
Variant Discovery
Assembly
Genotyping

Alignment to Reference



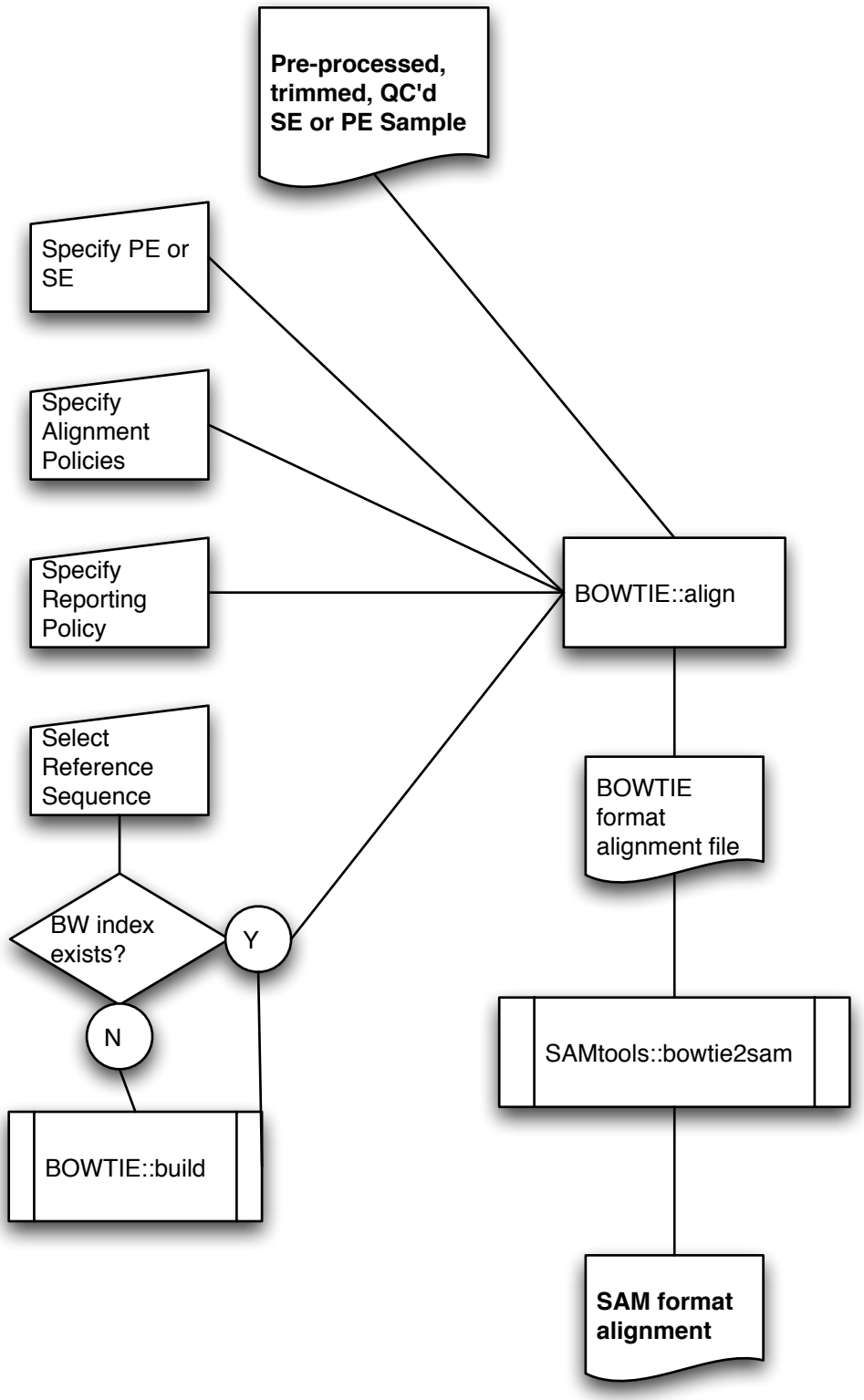
BWA Alignment (BWT/Suffix Array)

Approximate ungapped alignment



BOWTIE Alignment (BWT/Suffix Array)

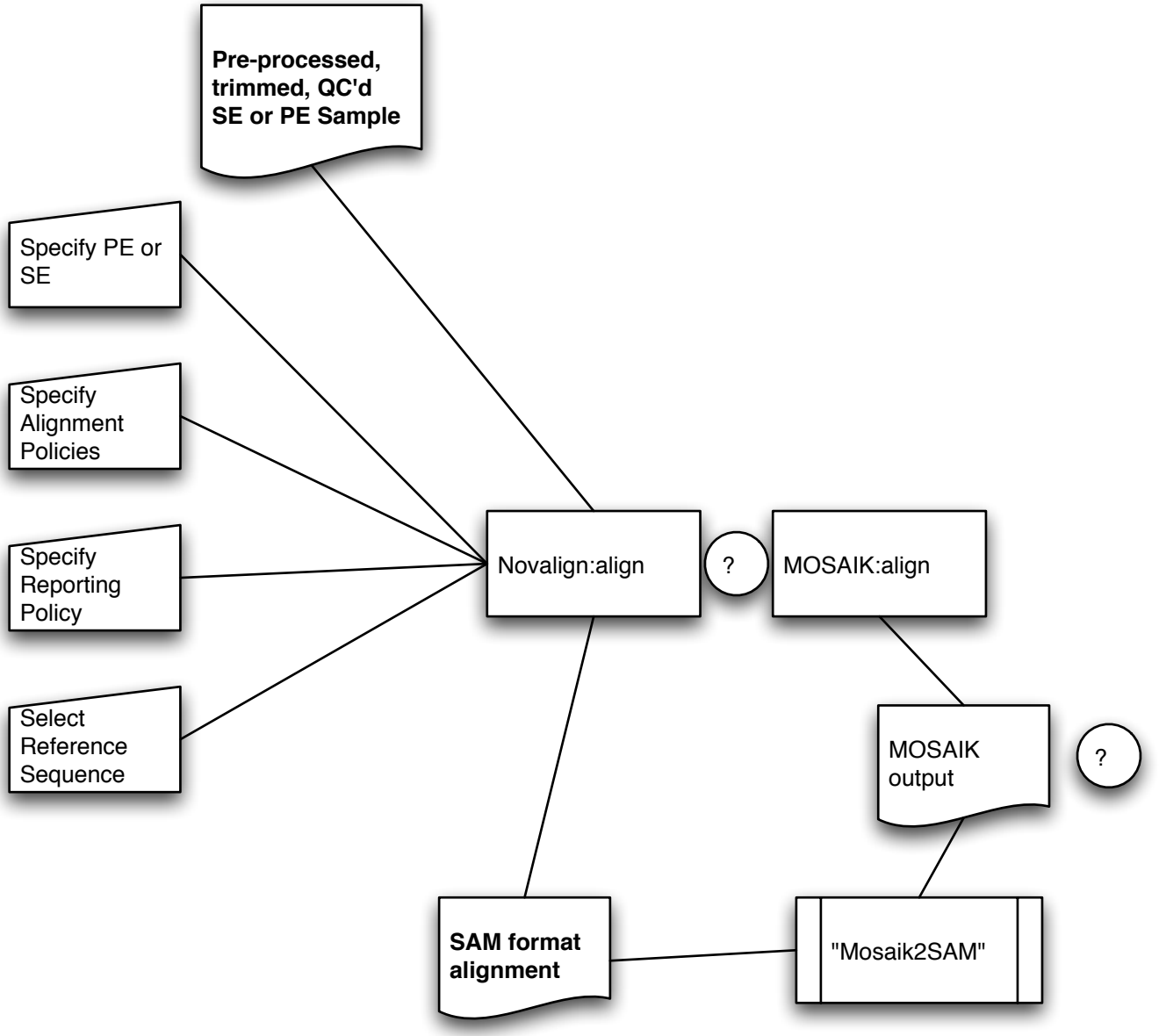
Approximate ungapped alignment



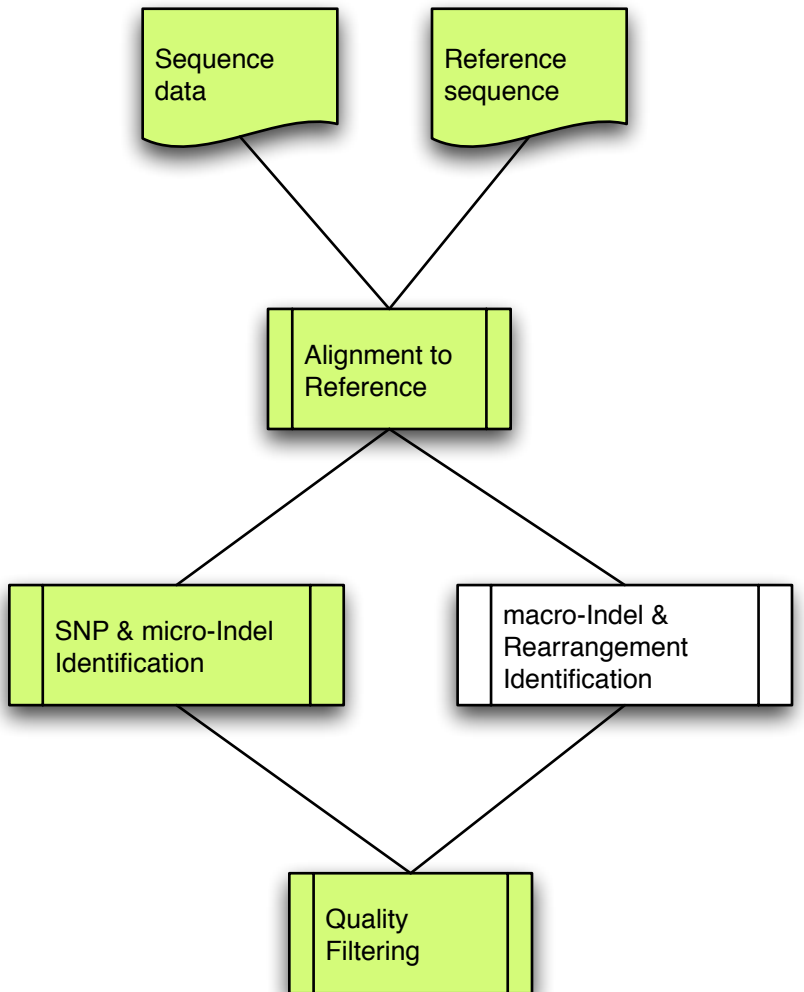
Novalign Alignment (Needleman-Wunsch)

MOSAIK Alignment (Smith-Waterman)

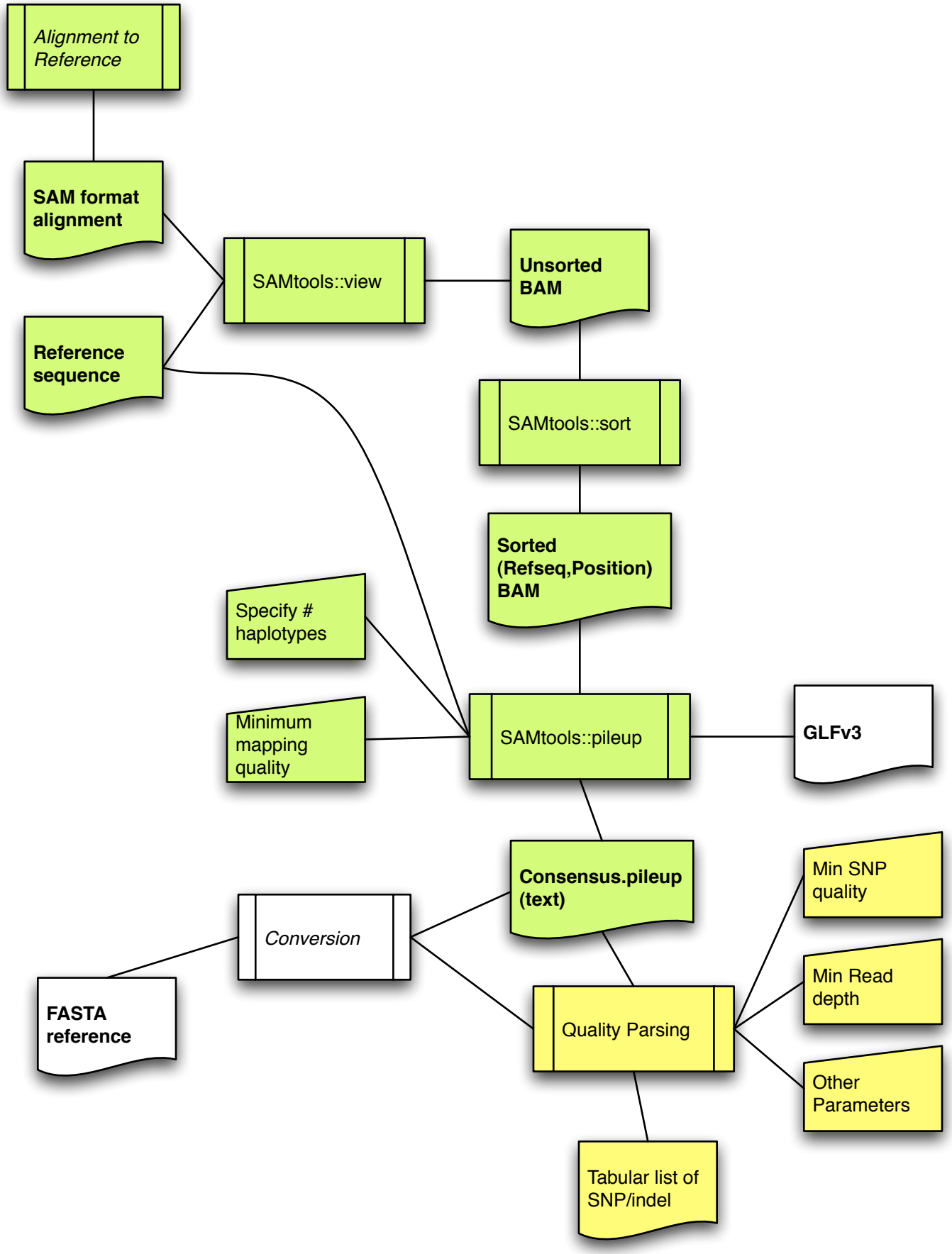
Sensitive gapped alignment



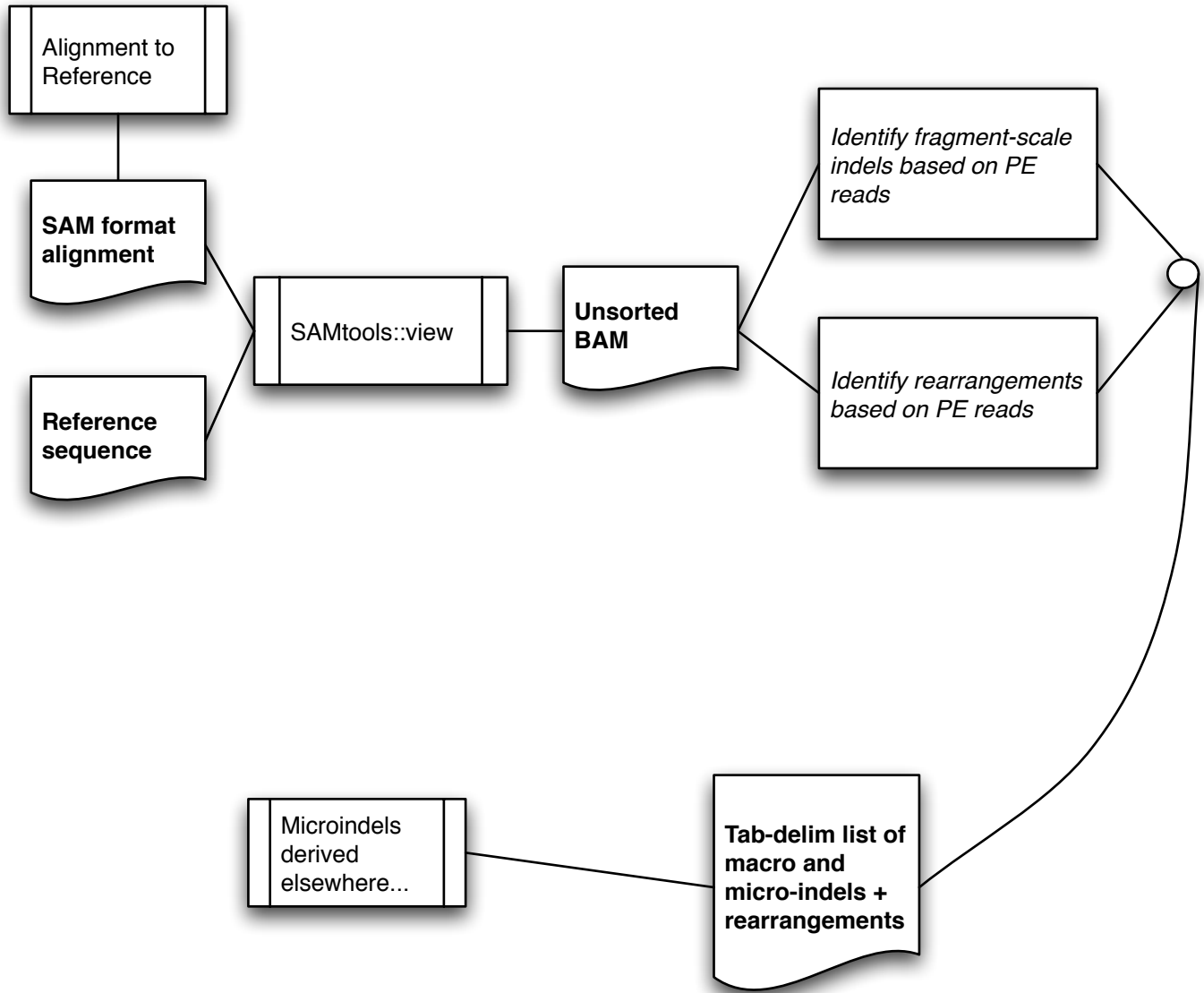
Variant Discovery



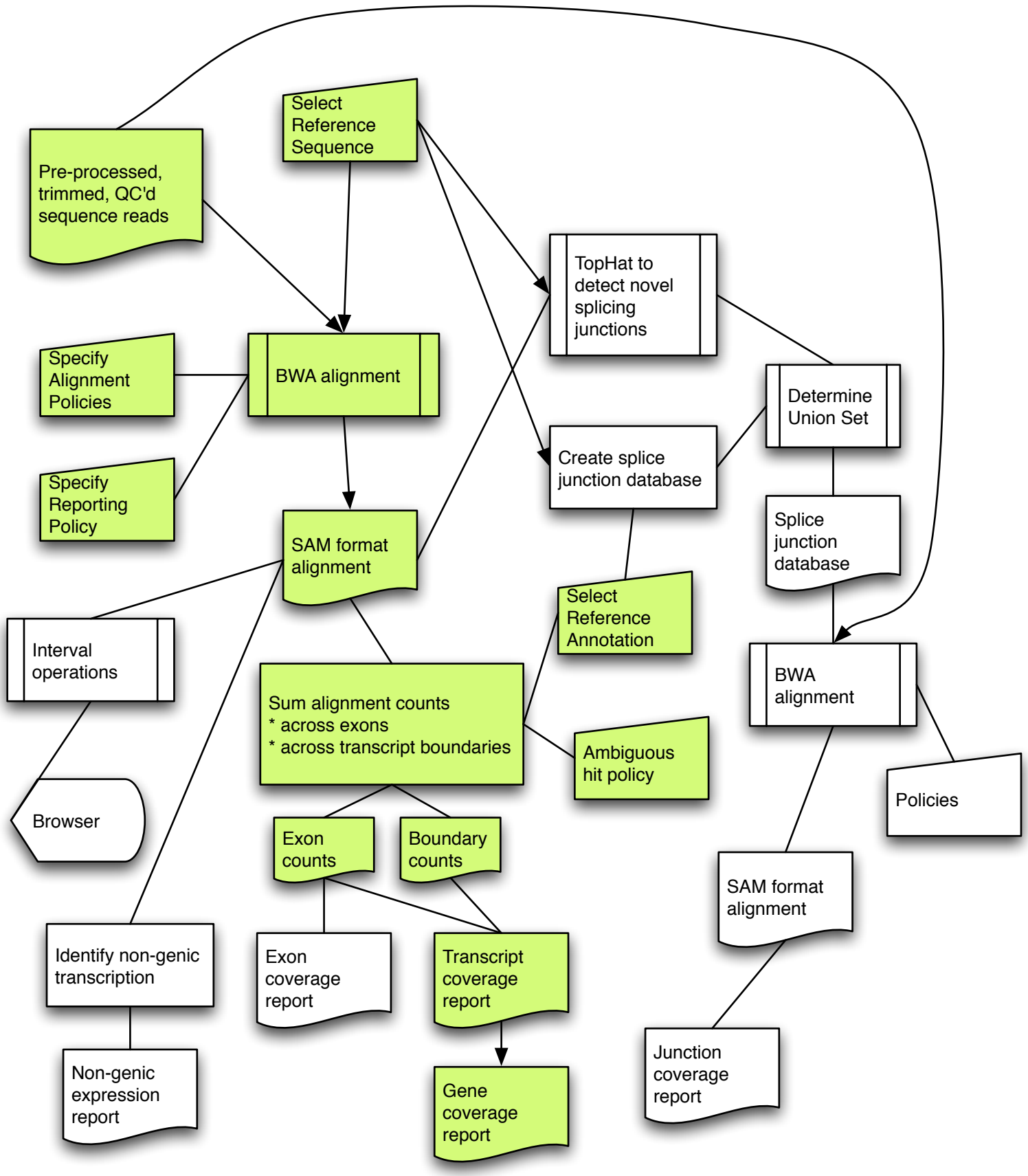
SNP & micro-Indel Discovery



macro-Indel and Rearrangement Discovery



Transcriptomics



Population Filter

Outputs from multiple variant detection libraries