```
Pool 1          Pool 2          ...      Pool 24
Index 1         Index 2                  Index 24

                  Sequencing Library

      MiSeq Run 1                    MiSeq Run 1

Pool 1                  Trim Reads                  Pool 1
Run 1              Trimmomatic v. 0.36              Run 2
FASTQ                                               FASTQ
                        Map Reads
                        BWA v. 0.75

                  De-duplication (PCR &
                        optical)
                     Picard v. 1.127

                          BQSR
                       GATK v. 3.6

                    IN/DEL Realign
                       GATK v. 3.6

Pool 1                                              Pool 1
Run 1                                               Run 2
BAM                                                 BAM

                     Pool 1
                     Merged
                      BAM

                De-duplication (PCR
                       only)
                    GATK v. 3.6

                   IN/DEL Realign
                    GATK v. 3.6

                 Joint Genotyping
                    GATK v. 3.6

                      All
                     Pools
                     VCF
```
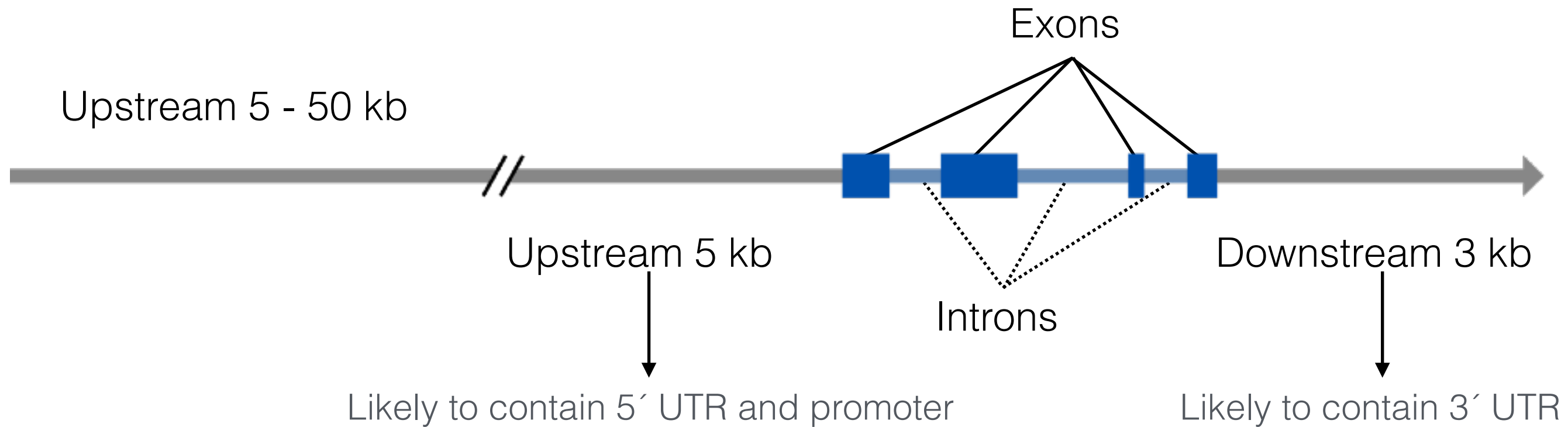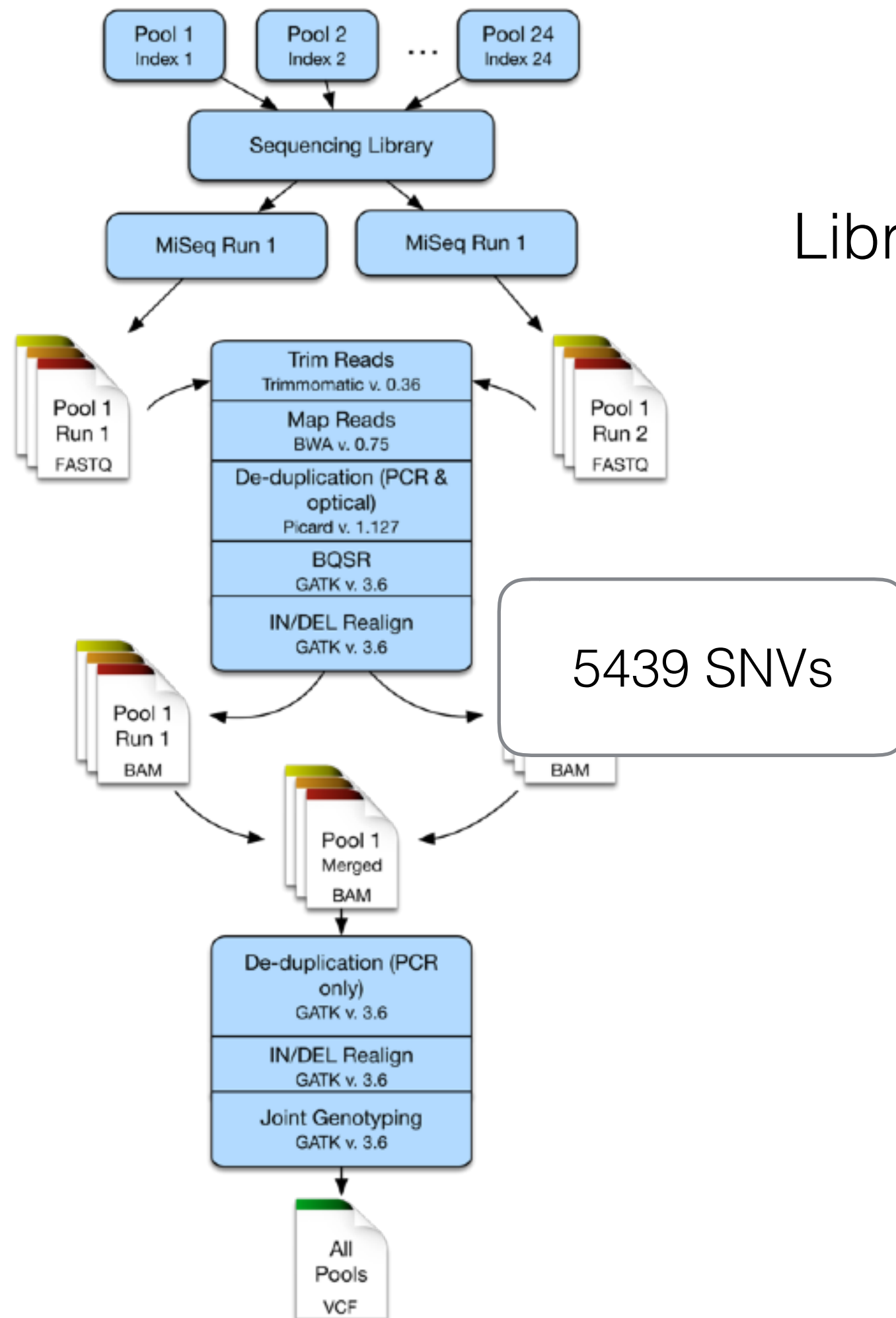
Library sequenced twice

5439 SNVs

Genes & regions

Library sequenced twice

5439 SNVs