

## **BWA MEM**

Purpose: align reads

Input: FASTQ(s)

Output: SAM

## **samblaster**

Purpose: mark duplicates

Input: SAM

Output: SAM

## **samtools view**

Purpose: convert SAM to BAM

Input: SAM

Output: BAM

## **samtools index**

Purpose: index BAM file

Input: BAM

Output: BAI

**Final  
BAM  
file**

## **samtools sort**

Purpose: coordinate sort reads

Input: BAM

Output: BAM

