Pipeline Description & Flow	Programs	File Types
Quality Check	FastQC	input: .fastq output: .fastqc
Clean Data	Trimmomatic	input: .fastq output: .fastq
Quality Check	FastQC	input: .fastq output: .fastqc
Index Reference Genome	BWA	input: .fasta output: .fasta
Map Data to Reference	BWA	input: .fastq output: .sam
Convert .SAM to .BAM	SAMTools	input: .sam output: .bam
Summarize Count Data	SAMTools	input: .bam output: .txt