

GATK4 Pipeline



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graph TD; A([GATK4 Pipeline]) --> B[/Input Fastq Data (Single End)/]; B --> C[Quality Control (FastQC)]; C --> D[Mapping To Reference Genome (BWA)]; D --> E[Variance Calling (GATK HaplotypeCaller)]; E --> F[Variance Filtering]; F --> G[Variance Annotation (Annovar)]; G --> H[/Output Variant Data/]; H --> I[Output Analysis Report];
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The diagram illustrates the GATK4 Pipeline workflow. It begins with the 'GATK4 Pipeline' title, followed by 'Input Fastq Data (Single End)'. The process then moves through 'Quality Control (FastQC)', 'Mapping To Reference Genome (BWA)', and 'Variance Calling (GATK HaplotypeCaller)'. After 'Variance Calling', the workflow branches into 'Variance Filtering' and 'Variance Annotation (Annovar)'. The final steps are 'Output Variant Data' and 'Output Analysis Report'.

Input Fastq Data
(Single End)

Quality Control (FastQC)

Mapping To Reference Genome (BWA)

Variance Calling (GATK HaplotypeCaller)

Variance Filtering

Variance Annotation (Annovar)

Output Variant
Data

Output Analysis Report