Workflow

Base calls from the sequencer

FASTQ files with base calls

SAM with standard alignment

VCF digests variants

Annotate VCF with Gene Data (Optional)
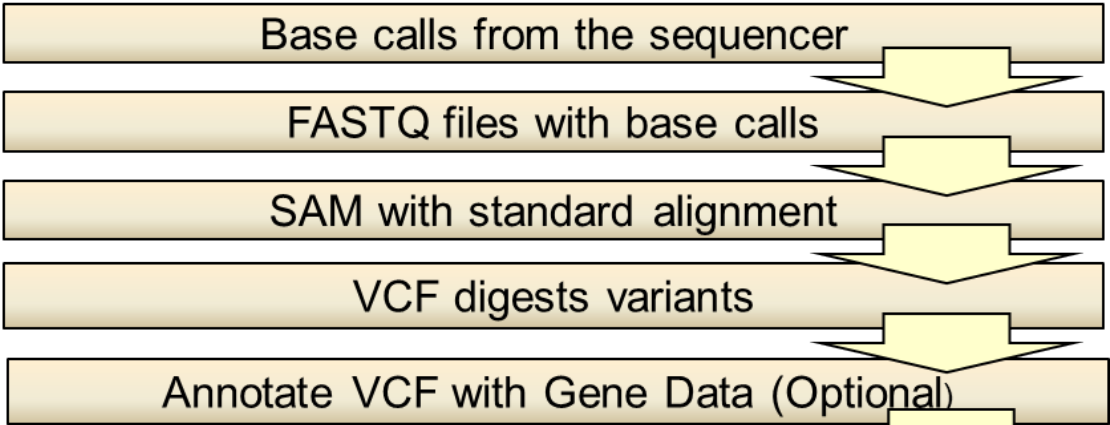
i2b2 Workbench

File   Search   Window   Help   Run

Bulk Loader Status   Genomics Import ⊠   Import Data

Import NGS Variant Data

Analysis details
Information related to the NGS data

Specify input file:	nes\CEUExon\ANNOVAR\CEU.exon.20 Browse
Input file format:	VCF-ANNOVAR
VCF mapping file:	ANNOVAR\CEU.exon.2010_03.map.txt Browse
I2B2 Patient number:	
I2B2 Encounter number:	
Date of encounter:	
Reference genome version:	hg18

Submit

Progress Bar:

Sample details
Information related to the sample

Sample ID:	
Sample Type:	TISSUE
Anatomical Source:	Pericardium
Collection Method:	BIOPSY
Additive:	UNKNOWN

Sample Pathology
Information related to the sample pathology

Pathology:	TUMOR
Tumor Grade	UNKNOWN
Tumor Stage	UNKNOWN

Sequence Ontology enabled i2b2 file