

**INPUT FILES:**  
BAM  
VCF  
SEQZ (SEQUENZA), BAM (FACETS, ASCAT) Other CNA output (CNVkit)  
BED



**PROCESSES:**

	input:	output:	tool:	
Variant annotation	vcf	maf	VEP/ANNOVAR/SnpEff (bash)	K
Phasing	vcf, bam	phased vcf	WhatsHAP	A
Joint sc analyses	vcf, bam tsv.gz (barcode)	mtx (sparse matrix)	Vartrix/ Others (bash)	G
Cohort summary	annotated maf	maftools plots	maftools (R)	Az
CNA QC	annotated maf, CNA calls	CNAqc object	CNAqc [+ CNA caller] (R/bash)	L
Pile-up (multisample)	bam, vcf	maf	Platypus (bash)	V
Joint table (multisample)	maf	maf	in-house script (R)	V
Subclonal deconvolution	maf/ annotated maf	MOBSTERh (single sample) VIBER/Pyclone (multisample)	MOBSTERh/VIBER/PYCLONE (R)	E,G
Clone tree buiding	VIBER/Pyclone object	ctree object	ctree	E
Signature inference	SpareSig, SigProfiler Basilica	vcf	specific tool object	Az