order	TOOL	Funtion	Dependencies other than bash, grep, awk, sed	Input	Output
1.000	Megamap2.sh	Invoke quickmap2.sh and pass maplist.txt information along	quickmap2.sh	maplist.txt	{pased to quickmap2.sh}
1.010	quickmap2.sh	Invoke BWA and samtools commands to map reads against references in unsupervised mode	Megamap2.sh	{passed from Megamap2.sh}	indexes, .dict, .fai, package (.log, .sam, .bam, .bai, .Mpileup.txt, DepthOfCoverage.txt, ContigLengthNumreads.txt)
2.000	Sam2rebuildSam.sh	Retain only lines of sam file for index and ectopic site related reads		.sam	.Rebuild.sam
3.000	Sam2dedupFasta.sh	Retain only unique sequences from a mapped set of reads		.sam	.dedup.fa
4.000	TheFinisher2.sh	Invokes most of the scripts downstream of Megamap2/quickmap2	many		
4.010	Megaparse2.1.sh	Generates xy coordinates for easy graphing of mutation data	pileup2baseindel.pl	*pileup.txt	newCounts.txt, perThousand.txt, perThousandEctopicOnly.txt
4.011	pileup2base.pl	tabulates mismatches on a position and per base level but does not include indels	perl	*pileup.txt{passed from Megaparse2.1.sh}	
4.020	NewSummaryStatsEct.sh	Generates sum and percentage data for mutations instead of based on position		parsed1.txt, .pileup.txt	NewMutationSummaryStatsECT.txt
4.030	InsertedBasesPerThousand.sh	Compiles information on how many bases are inserted t a given location		parsed1.txt	InsertedBasesPerThousand.txt, InsertedBasesPerThousandECT.txt, InsertedBasesByPosition.txt, InsertedBasesByPositionECT.txt
4.040	Megapaf2.sh	Generates paf files for use with ALVIS and other scripts –WARNING– zero based numbering by sam2paf	misc, k8	.sam	.paf
4.041	k8	no clue what this is…related to java in some way			
4.042	misc	no clue what this is…related to java or minimap or paftools in some way			
4.050	paf2circos2.1.sh	Generates input for circos plots and summaries for microhomology –WARNING– zero based numbering		.paf	Circos.newCounts.tsv, Circos.newThickness.tsv, Circos.newRenamed.tsv, MicroHomology.txt
4.060	MegaPafChunks2.sh	Determines the mean and deviation of template chunks and provides a histogram –WARNING– zero based numbering		.paf	.chunklengths.txt
4.070	MegaAlvis2.sh	Runs ALVIS on all paf files in a folder of package files	ALVIS of choice	.paf	svg images
4.071	Alvis.jar	Draw reads with Original Color scheme but added mods to scale reads and annotate chunks	java	.paf	svg images
4.072	AlvisBR.jar	Draw reads with Blue-red colors, scale reads and annotate chunks	java	.paf	svg images

4.073	AlvisYB.jar	Draw reads with Yellow-blue colors, scale reads and annotate chunks	java	.paf	svg images
4.080	BrokenEnds.sh	Identifes the base position numbers at the break points of template switching -WARNING- zero based numbering		.paf	BrokenEnds.txt
4.090	Pub2Circos2.1.sh	Generates input for circos plots but ignoring ectopic to ectopic linkages		.paf	CircosSimplifiedCounts.txt, CircosSimplifiedThickness.tsv
4.100	getMicroHomPaf.sh	extracts paf file information only for reads that have microhomology -WARNING- zero based numbering		Microhomology.txt, .paf	MicroHomologyPartialPafData.txt
4.110	BaseChangeCounter.sh	Compiles information on transitions and transversions at mismatch sites	pileup2base.pl	pileup.txt	MutationTypes.txt
4.111	pileup2baseindel.pl	tabulates mutations on a position and level but only accurate for use with indels	perl	*pileup.txt{passed from BaseChangeCounter.sh}	
4.120	BreakpointBases.sh	Identifes the individual ACGT bases at the break points of template switching		BrokenEnds.txt	CountedBrokenBases.txt
4.130	OverlapEnds.sh	Generates sets of coordinates for overlapping chunks where there is microhomology - One based numbering!		.paf	OverlappingEnds.txt
5.000	Pacbio2SnapgeneNames.sh	Renames css data so it is compatible with snapgene		.fa	.fa