

## Changes made to parameter settings in Cpipe and Galaxy workflow

Steps	Cpipe	Galaxy
<b>Markduplicates</b>	Remove_duplicates : true  <b>CHANGED TO</b> Remove_duplicates : false (default value)	Remove_duplicates : false
<b>RealignerTargerCreator</b>	--known \$GOLD_STANDARD_IND ELS -S (not specified) --interval_merging (not specified) --mismatchFraction (not specified)  <b>CHANGED TO</b> --known \$db SNP \$1000G \$Mills and 1000G -S strict --interval_merging ALL --mismatchFraction 0.15	--known \$db SNP \$1000G \$Mills and 1000G -S strict --interval_merging ALL --mismatchFraction 0.15
<b>IndelRealigner</b>	--known (not specified)  <b>CHANGED TO</b> --known \$db SNP \$1000G \$Mills and 1000G	--known \$db SNP \$1000G \$Mills and 1000G
<b>BaseRecalibrator</b>	-cov ReadGroupCovariate - cov QualityScoreCovariate - cov CycleCovariate -cov ContextCovariate  <b>CHANGED TO</b> -cov CycleCovariate -cov ContextCovariate	-cov CycleCovariate -cov ContextCovariate
<b>HaplotypeCaller</b>	-dcov 1600 -A AlleleBalance -A Coverage -A FisherStrand -- contamination_fraction_to_fi lter (not specified) --genotyping_mode (not specified) --minPruning (not specified)	-dcov (not specified)  -A (not specified) -- contamination_fraction_to_filte r 0.05 --genotyping_mode DISCOVERY --minPruning 1

Steps	Cpipe	Galaxy
	<p><b>CHANGED TO</b></p> <p>-dcov (removed)</p> <p>-A (removed)</p> <p>contamination_fraction_to_filter 0.05</p> <p>--genotyping_mode DISCOVERY</p> <p>--minPruning 1</p>	