**Input files:**

Read\_1.fastq, Read\_2.fastq, hg19.fa (reference genome)

Adaptor\_file (eventually, we will have this file); else use option “2”

bait.bed

target.bed

dbsnp\_137.hg19.vcf

dbsnp\_137.hg19.vcf.idx

Mills\_and\_1000G\_gold\_standard.indels.hg19.vcf

Mills\_and\_1000G\_gold\_standard.indels.hg19.vcf.idx

1000G\_phase1.indels.hg19.vcf

1000G\_phase1.indels.hg19.vcf.idx

hapmap\_3.3.hg19.vcf

hapmap\_3.3.hg19.vcf.idx

1000G\_omni2.5.hg19.vcf

1000G\_omni2.5.hg19.vcf.idx