

Nitty Gritty part

1. Paired-End Sequencing.
2. Randomly sample read numbers to a common size.
3. bwa aln for genome mapping: -n Read-Len/20.
4. Check mappability among samples.
5. Bam file has to be sorted and indexed.
6. TEMP_Insertion.sh \
 -i *.bwa-aln.sorted.bam \
 -o TEMP_OUTDIR \
 -r Transposon-consensus_FA \
 -t UCSC.RepeatMask.bed \
 -m READ_LEN/20 \

***.insertion.refined.bp.summary**