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| EA | Description | Code |
| 3A | Script for generating the Bowtie2 index | Bowtie2-build –f sakaigenome.fasta EcoliSakai |
| 3B | Script for both paired end and unpaired alignment using Bowtie2 | Unpaired : bowtie2 -N -x EcoliSakai -U file1.fastq.gz, file2.fastq.gz .sam file  Paired end: bowtie2 -N -x EcoliSakai -1 file.fastq.gz -2 file2.fastq.gz –S .sam file |
| 3C | Script provided by David for index for featureCounts | { printf 'GeneID\tChr\tStart\tEnd\tStrand\n'; (grep -v CDS Sakai.gff  | grep gene| sed -e 's/[^\t]\*gene=//' -e 's/\.[0-9]//'| awk 'BEGIN{OFS="\t"}{print $9, $1,  $4, $5,$7}')} |uniq > exons.saf |
| 3D | featureCounts script | featureCounts –a exons.saf –F SAF –o outputfile.txt .sam file |
| 3E | Script for using blastdb for creation of database | formatdb name.fasta –n databaseName –t title –p F |
| 3F | Script for using matching the probe sequences to the database | blastall -p blastn –m8 –I Agilentprobes.fasta –d SakaiDatabase –v |-o output.txt |