Procedure to have to merged aligned and sorted file:

1) Align your sample to All\_Bacteria\_1. Result in sample\_1.sam

2) Align your sample to All\_Bacteria\_2. Result in sample\_2.sam

3) Convert sample\_1.sam and sample\_2.sam into sample\_1.bam and sample\_2.bam

4) Merge these two sample bam files into sample\_merged.sam

5) Sort  sample\_merged.bam by readid.  New file is sample\_merged\_sorted.bam

6) Convert sample\_merged\_sorted.bam to sample\_merge\_sorted.sam

Bowtie commands to have to merged aligned and sorted file:

1. bowtie2 --very-sensitive-local -p 2 -1 Staphylococcus\_aureus\_epidermidis.1x.1.fastq Staphylococcus\_aureus\_epidermidis.1x.2.fastq -x M-CAT/All\_Bacteria\_1 –S Staph1.sam
2. bowtie2 --very-sensitive-local -p 2 -1 Staphylococcus\_aureus\_epidermidis.1x.1.fastq Staphylococcus\_aureus\_epidermidis.1x.2.fastq -x M-CAT/All\_Bacteria\_2 -S Staph2.sam
3. samtools view -bS Staph1.sam > Staph1.bam
4. samtools view -bS Staph2.sam > Staph2.bam
5. samtools sort -on Staph1.bam abc > Staph1\_sorted.bam
6. samtools sort -on Staph1.bam abc > Staph1\_sorted.bam
7. samtools cat -o merged.bam Staph1\_sorted.bam Staph2\_sorted.bam