Given data: # RNA-seq data from two house mouse (Mus musculus) tissues (Heart, Liver) across

# tow sampling times (ZT0, ZT12), with 1 biological replicates for each tissue and sampling time,

# resulting in a total of 16 paired-end FASTQ files.

Pipeline override log file of hisat2 bamstat merges make 1 file name issue as wait is used  
  
