1. 


2. 1.a maps 446748 (89.35%), 1.b maps 464659 (92.93%). The parameters in 1.b are less stringent than in 1.a. 1.a parameters only allow one mismatch in the whole read while 1.b allow one mismatch in the first 12 bases of the read, the remaining bases in the read can have any number of mismatches in the alignment and therefore more reads map.

3. 

4. This requires 3 separate commands:
   bwa aln mm9BWA /projects/sreadgrp/Day5/ILS_R1_small.fastq > ILS_R1_small.sai
   bwa aln mm9BWA /projects/sreadgrp/Day5/ILS_R2_small.fastq > ILS_R2_small.sai
   bwa sampe -a 400 mm9BWA ILS_R1_small.sai ILS_R2_small.sai /projects/sreadgrp/Day5/ILS_R1_small.fastq /projects/sreadgrp/Day5/ILS_R2_small.fastq > outHW4.sam

5. /opt/bedtools/2.22.0/coverageBed -abam out1a.sorted.bam -b YBR118W.bed > test.coveragebed

   If using question 1.a. alignment:
   How many reads overlap this gene? 792
   How many bases of YBR118W have non-zero coverage? 1376

   If using question 1.a. alignment:
   How many reads overlap this gene? 895
   How many bases of YBR118W have non-zero coverage? 1376