

```
(rseqc) [ssm9301@quser23 op_assign_2]$ infer_experiment.py -r /projects/e31265/ssm9301/op_assign_2/ge
ncode.v41.bed12 -i 13_hr_Aligned.sortedByCoord.out.bam
[E::idx_find_and_load] Could not retrieve index file for '13_hr_Aligned.sortedByCoord.out.bam'
Reading reference gene model /projects/e31265/ssm9301/op_assign_2/gencode.v41.bed12 ... Done
Loading SAM/BAM file ... Total 200000 usable reads were sampled

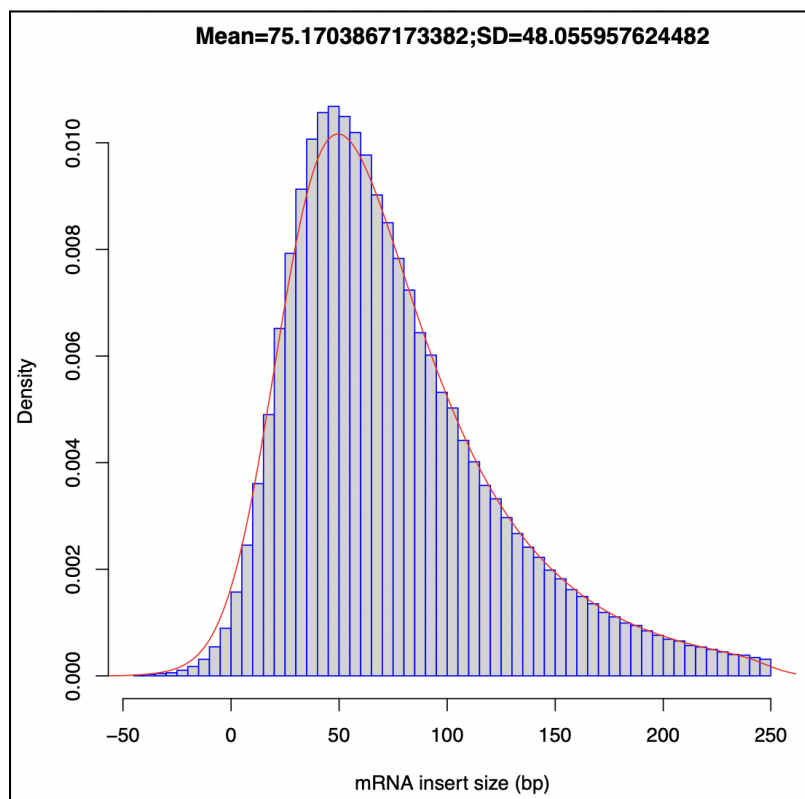
This is PairEnd Data
Fraction of reads failed to determine: 0.1522
Fraction of reads explained by "1++,1--,2+-,2-+": 0.0256
Fraction of reads explained by "1+-,1-+,2++,2--": 0.8222
```

13hr infer_experiment results

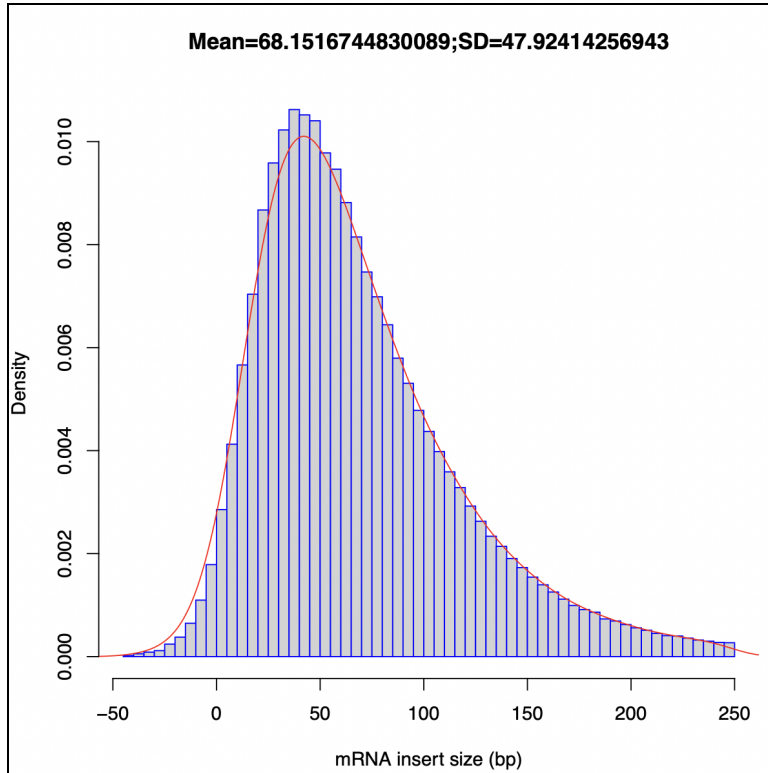
```
(rseqc) [ssm9301@quser23 op_assign_2]$ infer_experiment.py -r /projects/e31265/ssm9301/op_assign_2/ge
ncode.v41.bed12 -i 25_hr_Aligned.sortedByCoord.out.bam
[E::idx_find_and_load] Could not retrieve index file for '25_hr_Aligned.sortedByCoord.out.bam'
Reading reference gene model /projects/e31265/ssm9301/op_assign_2/gencode.v41.bed12 ... Done
Loading SAM/BAM file ... Total 200000 usable reads were sampled

This is PairEnd Data
Fraction of reads failed to determine: 0.1428
Fraction of reads explained by "1++,1--,2+-,2-+": 0.0235
Fraction of reads explained by "1+-,1-+,2++,2--": 0.8337
```

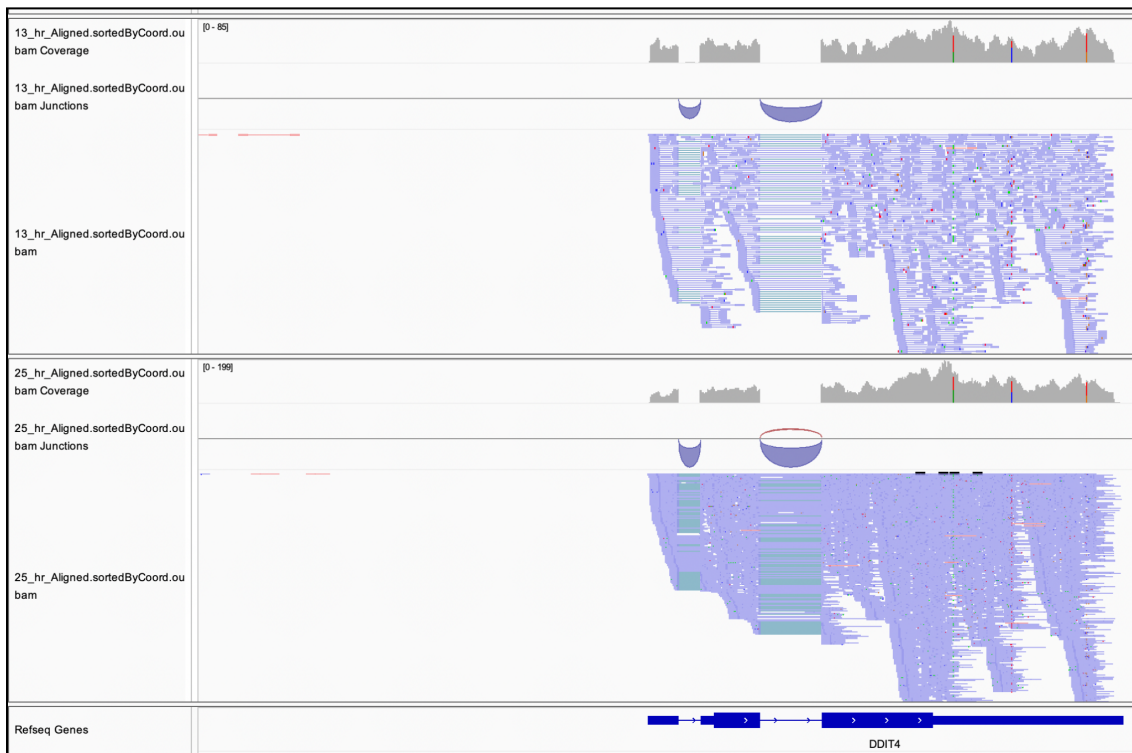
25hr infer_experiment results



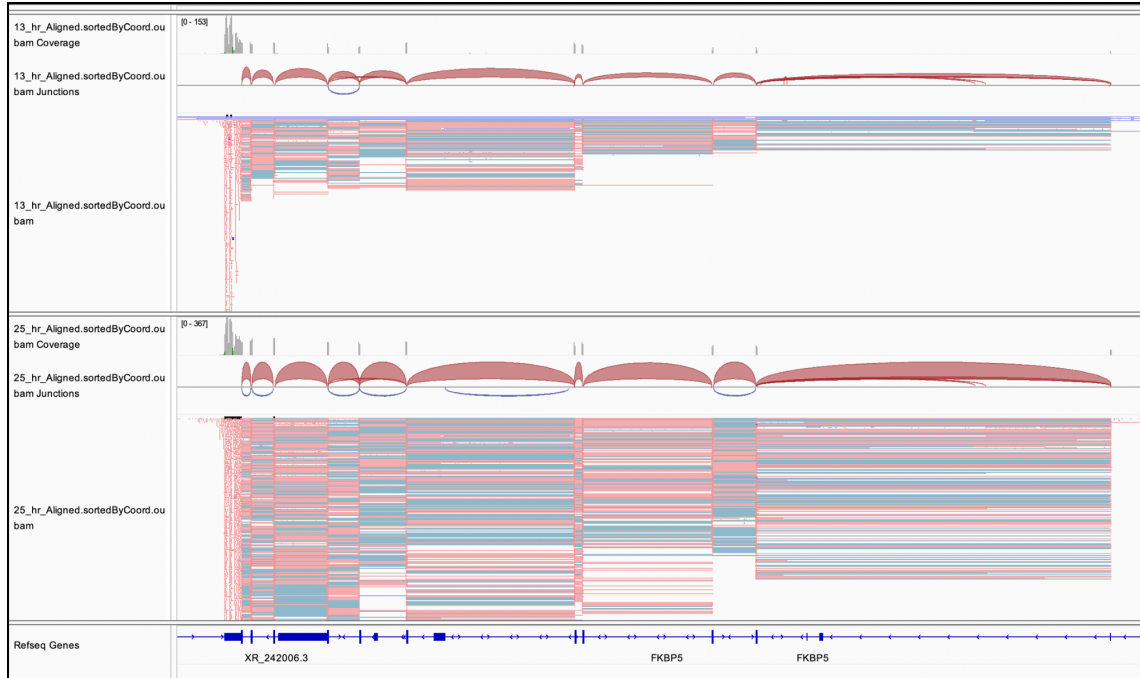
13hr inner_distance data



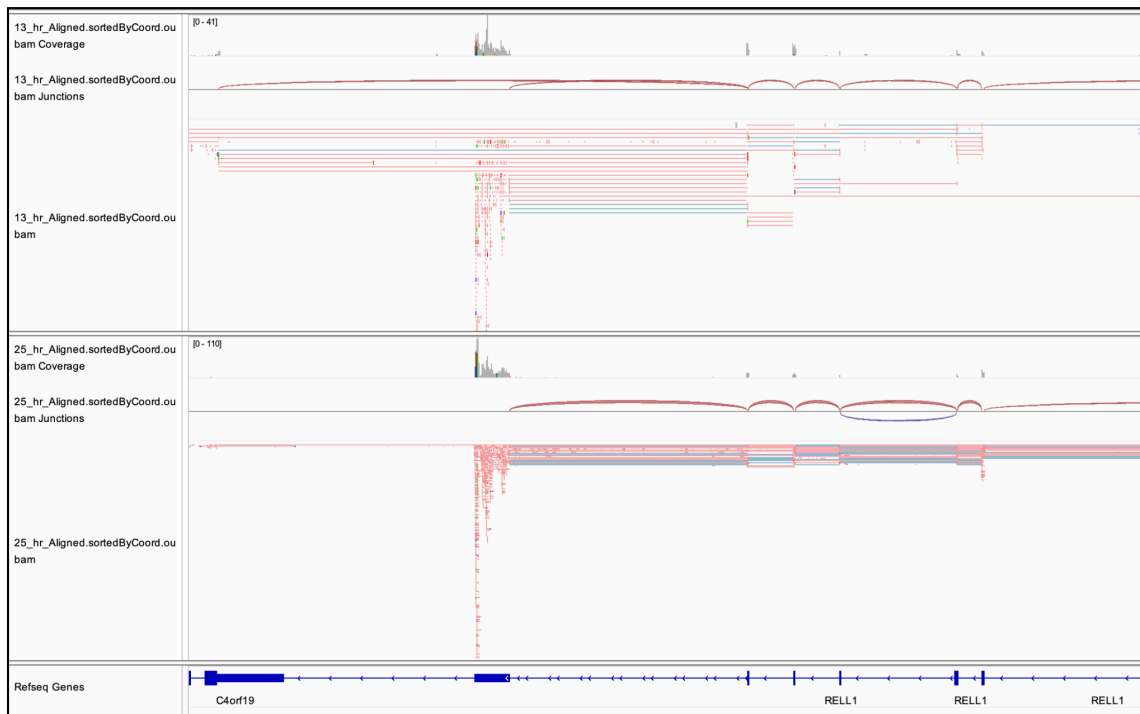
25hr inner_distance results



DDIT4



FKBP5



REL1

It seems like the levels of expression between the two conditions are different as their samples appear to be different. It seems like there is a greater density of paired end readings and thicker junctions in the 25hr sample compared to the 13hr sample, so the expression must be different.