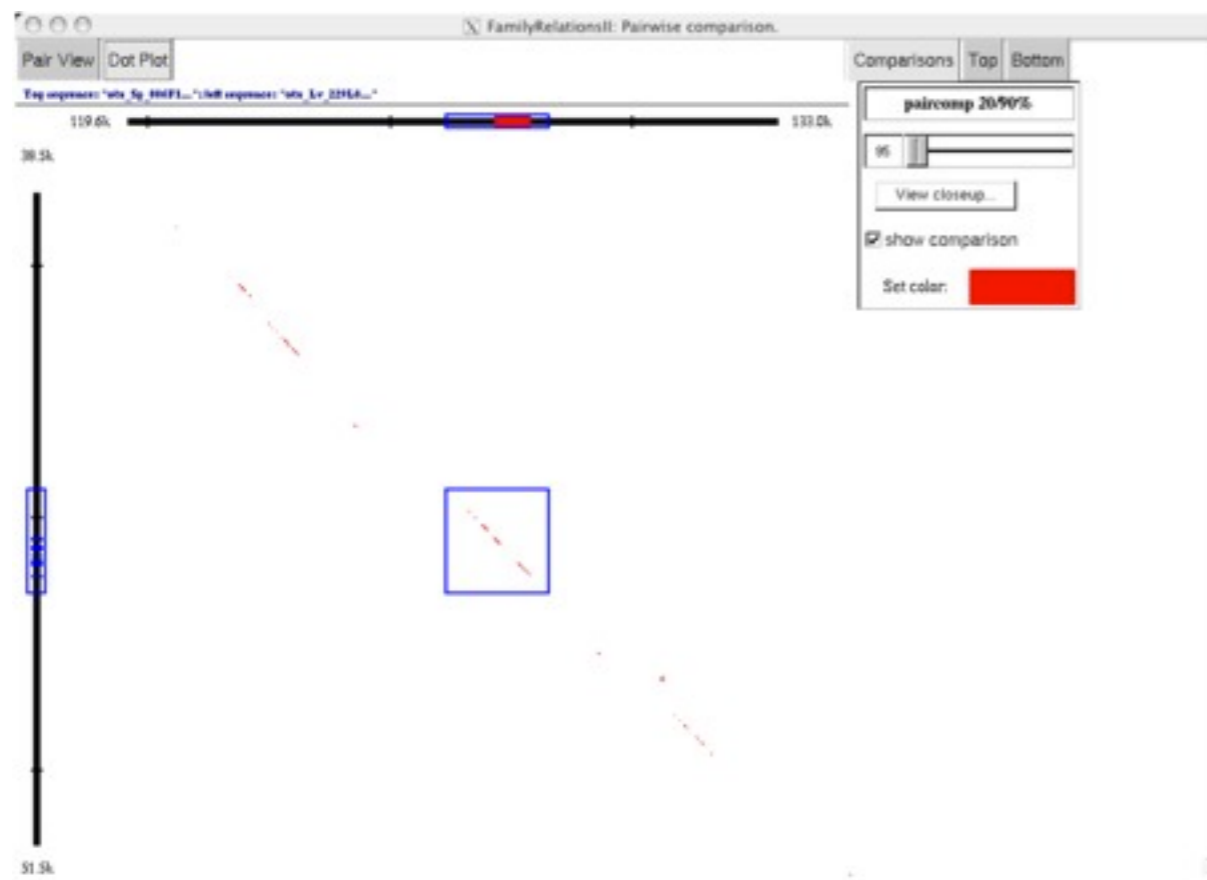
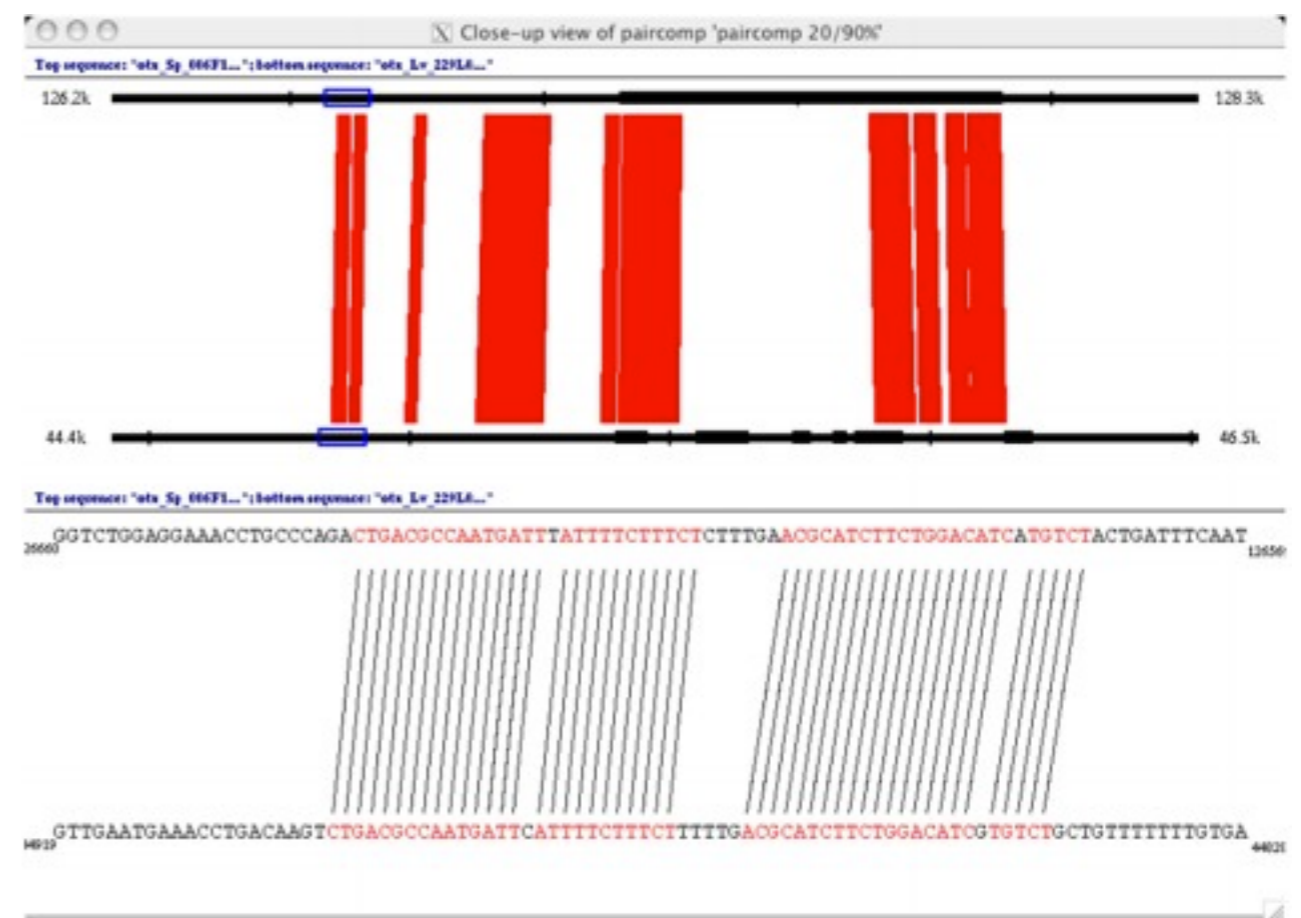
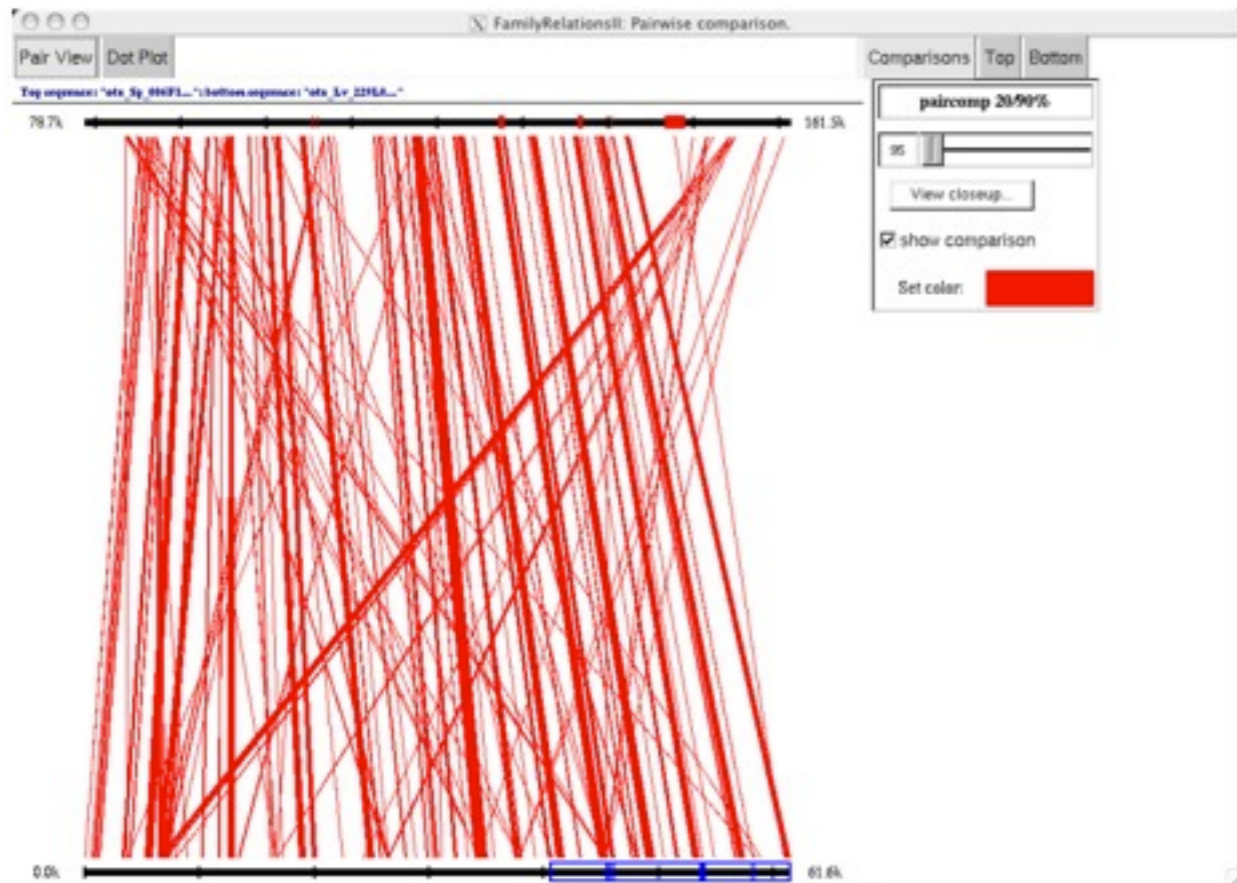


Force et al. 1999

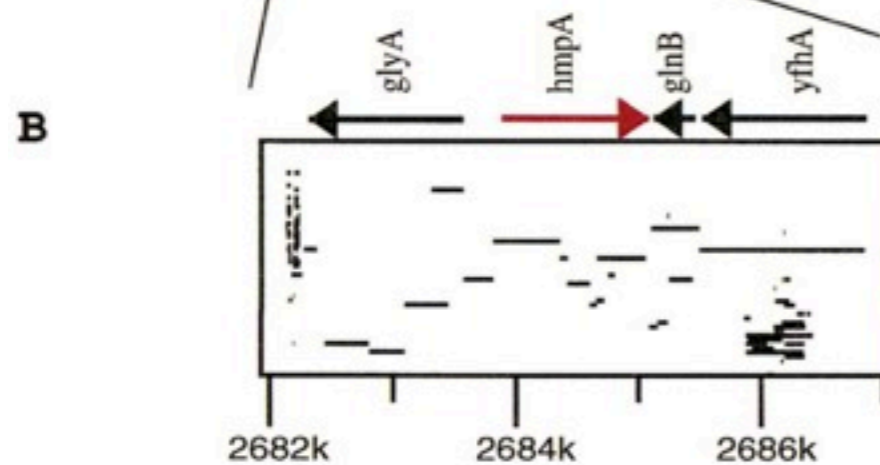
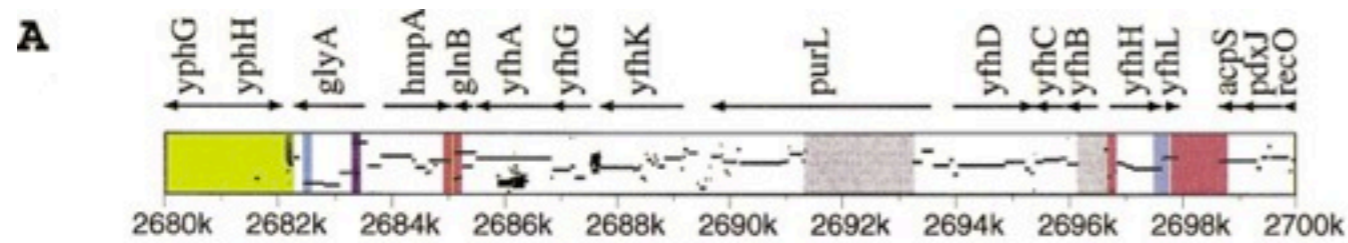
Fixed-width window comparisons (seqcomp)

Local alignment (PipMaker)

Global alignment (Vista)



FamilyJewels  
<http://family.caltech.edu/>



**C**

```

250 . . . . . : glyA < +1 . . . :
2683554 AAAATTTTGGCCTTTATAGGCGGTCCTGTTGGACAACGGCGAACAGTAT
      ||||| ||-||| | ||||:||||-|| |||| |||||
252 AAAATTTGTG CCTGAAAAGGCAGTCC GTGGGACTTCGGCCAACAGTAT

300 . . . . . : .PurR:
2683604 AACCGAATCATTGTGCGATAACAGGTCTTGACAAAGGAATTTACGCAAAC
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
300 AACCGAATCATTCTTCGATAACAGGTCTTGACAAAGGTTTTTACGCAAAC

350 . . . . . :
2683654 GATTACCTTCAGGCTACGCAAGGCTTTGGAGAATAAAGAGCTTGCAACCG
      ||||| ||| :|:| :|:| ||| ||| :|:|:|:| | :|:| :
350 GATTACCTATGCGTCAGATAAAGGTTTCTGAACGAGAGCCTGACGAATT

400 . MetR . . . : . MetR . . . :
2683704 GAAACGGATTTCTTTTCAGGTTTGTGATGCAAATTTTCACTTCATCACA
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
400 TCAACGGATTTCTTTTCAGCTTTGTGATGCAGATTTTTCAGTTGTTACC

450 . . . . . : promoter: . . . :
2683754 TTCTTTCTGAAAAACACCAAAGAACCATTACATTGCAGGGCTATTTTTT
      |:| :| |||:| | :||| ||||| ||||| ||||| -
450 TCCATAACGTAAAGCAGAGAAGATCCATTTACAATGCAAGGGTATTTTT

500 . . . +1 : >hmpA : . . . :
2683804 ATAAGATGCATTTGAGATACATCAATTAAGATGCAAAAAAGGAAGACCA
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
499 ATAAGATGCATTTGATATACATCATTAGATTTTACATAAAGGAAGCAGG
  
```

PipMaker and MultiPipMaker  
[http://www.bx.psu.edu/miller\\_lab/](http://www.bx.psu.edu/miller_lab/)



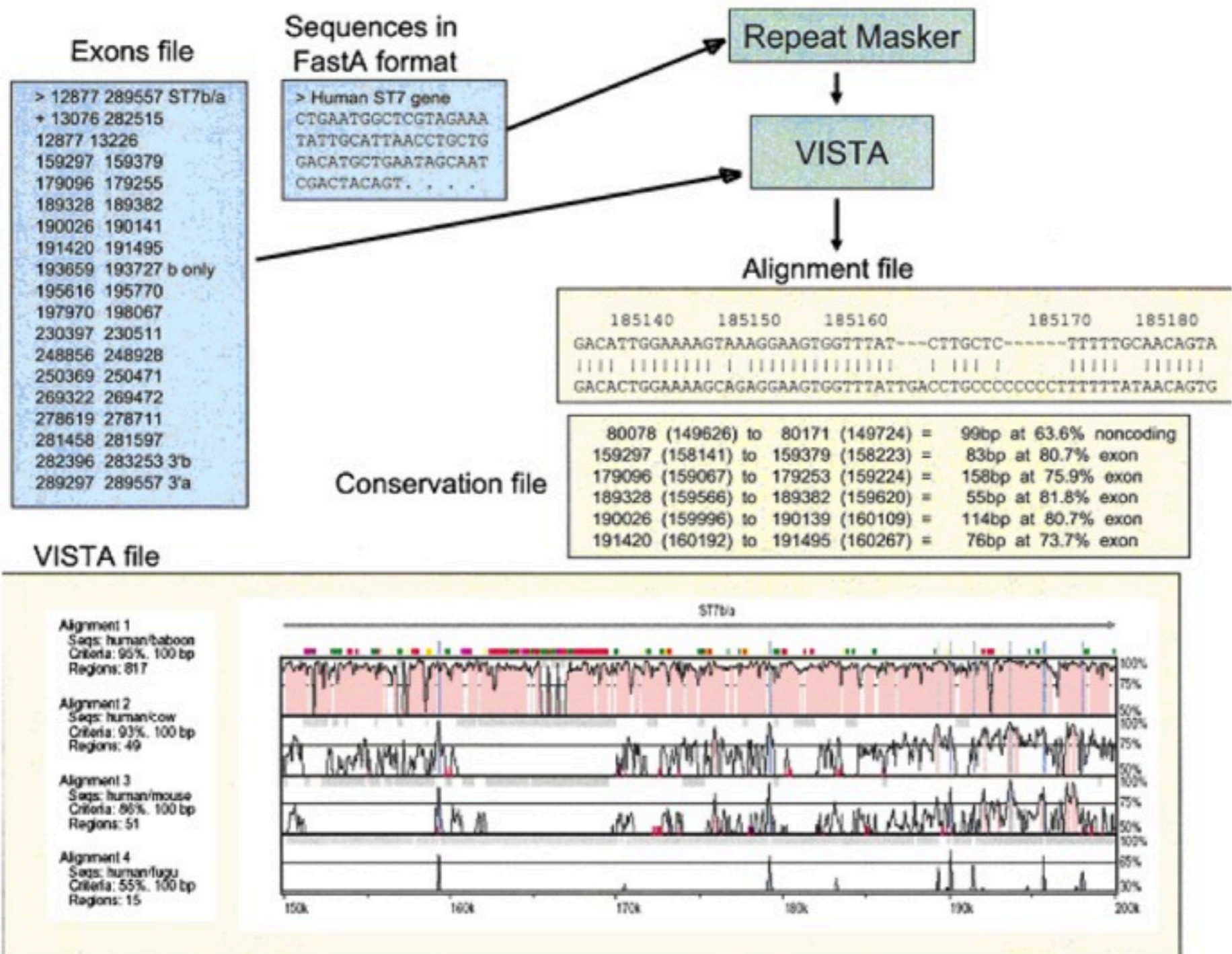
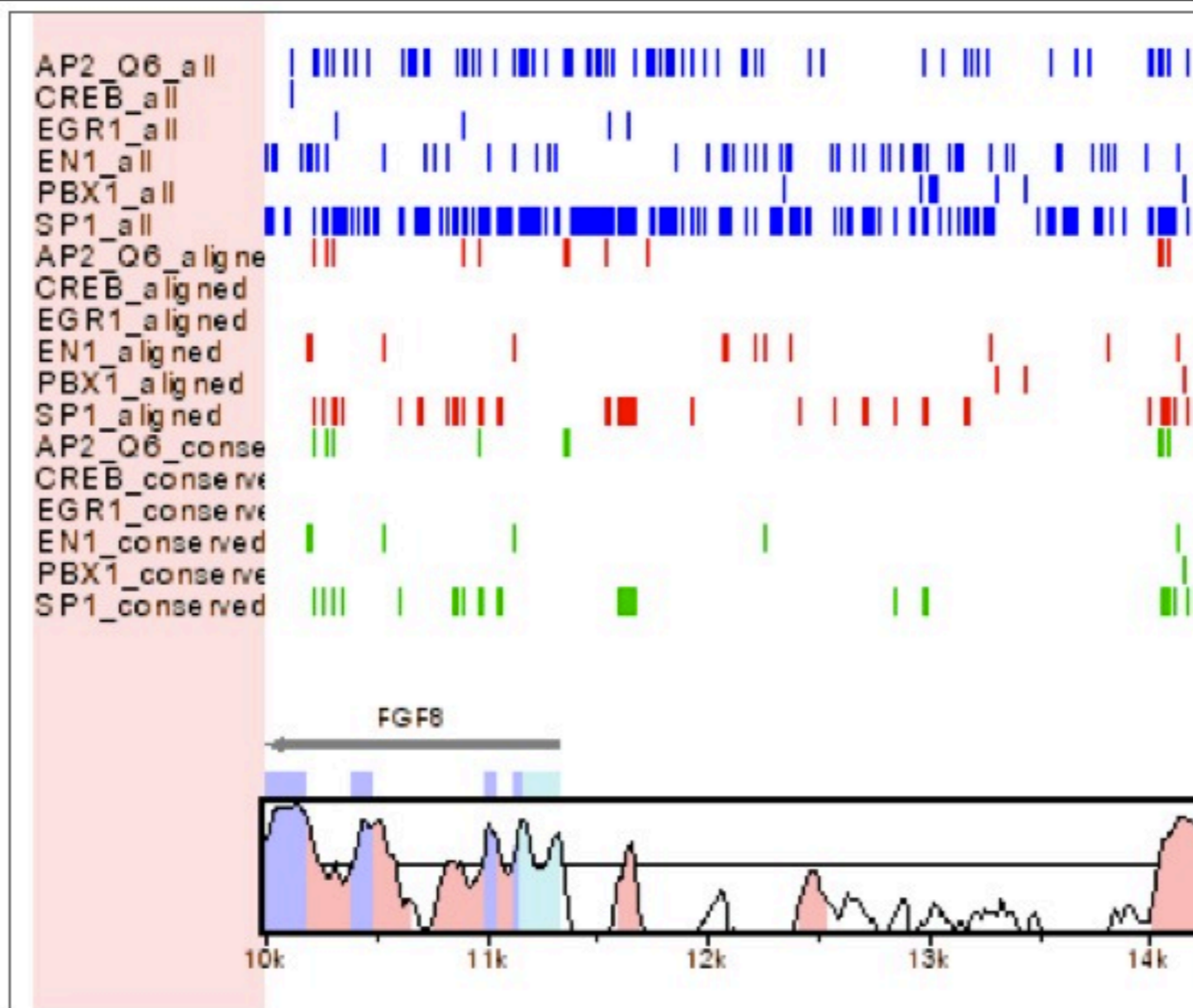


Fig. 1. mVISTA input and output diagram

**mVISTA**  
Align and compare your sequences from multiple species

VISTA  
<http://genome.lbl.gov/vista/index.shtml>





### **rVISTA**

Locate regulatory sequences in your data using comparative sequence analysis and transcription factor binding site search.

### **GenomeVISTA**

Compare your sequences against whole-genome assemblies.

### **wgVISTA**

Align pair of sequences up to 10Mb long (finished or draft) including microbial whole-genome assemblies.

### **VISTA Browser**

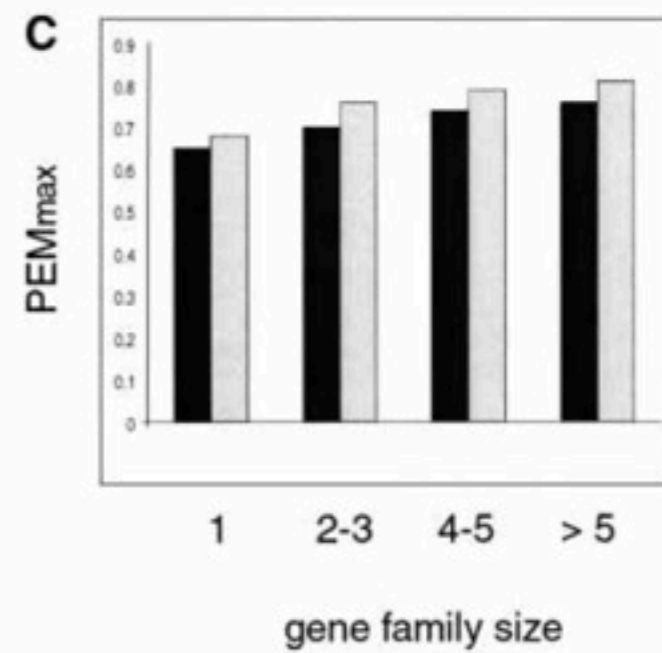
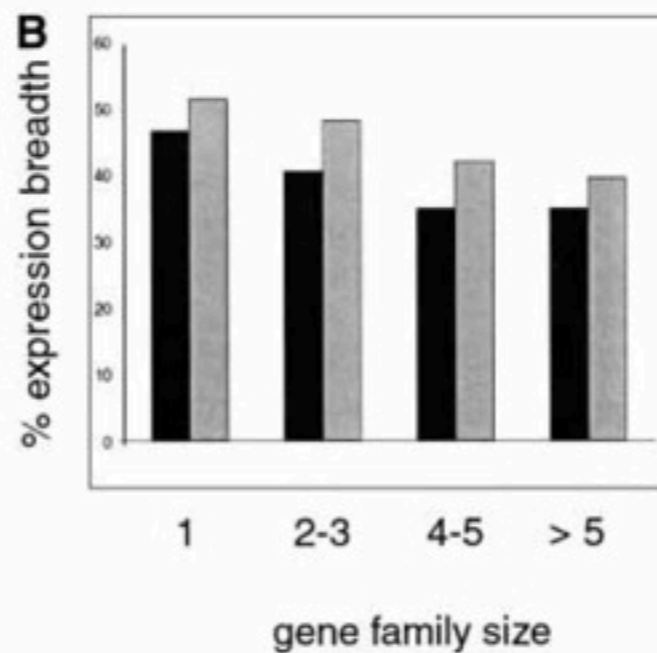
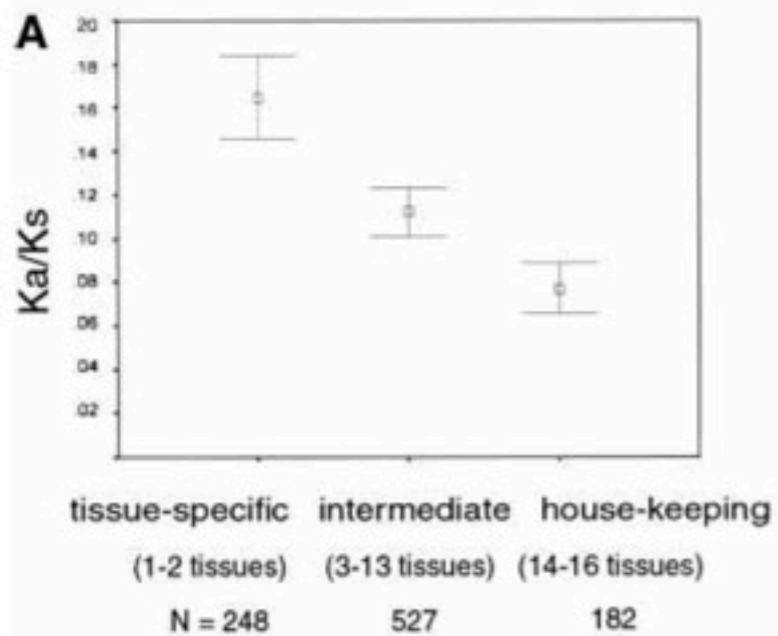
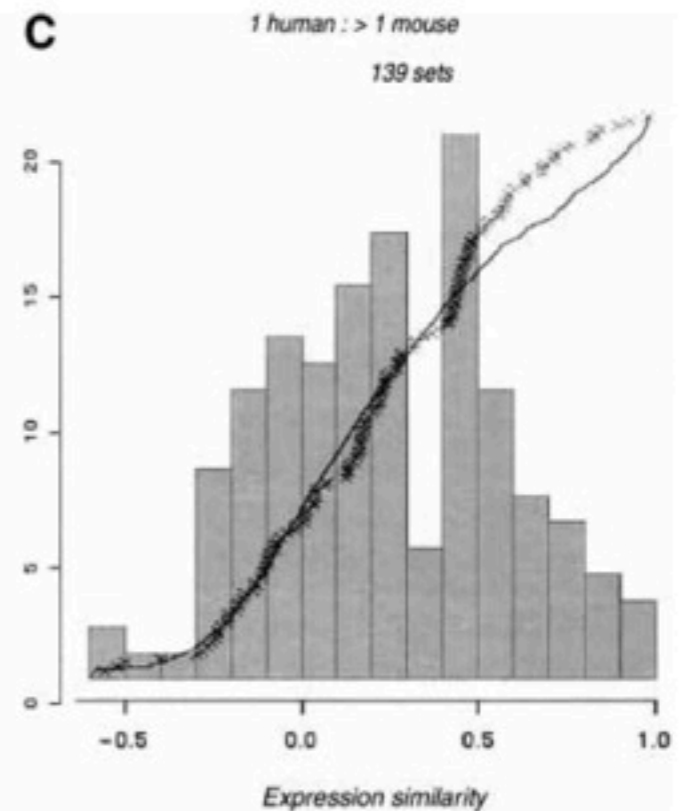
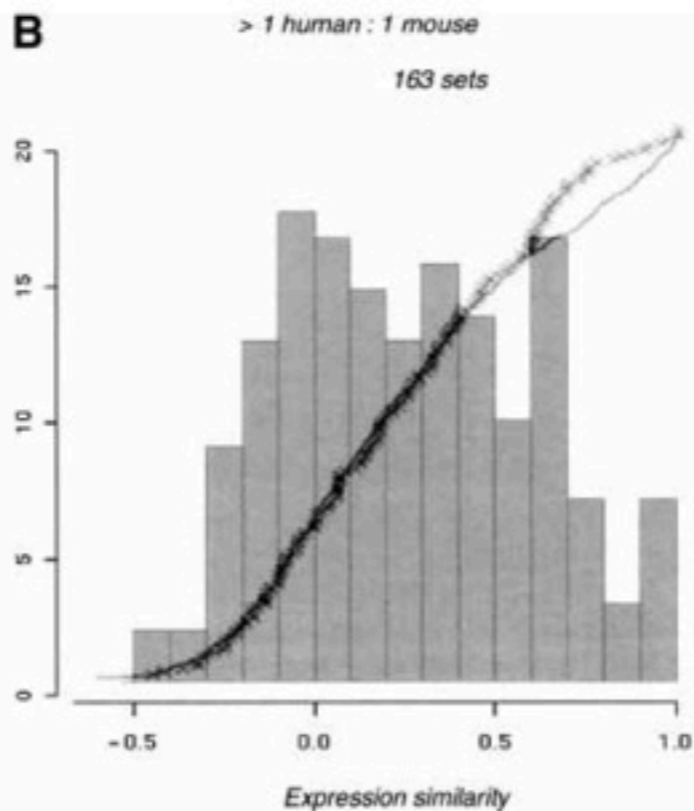
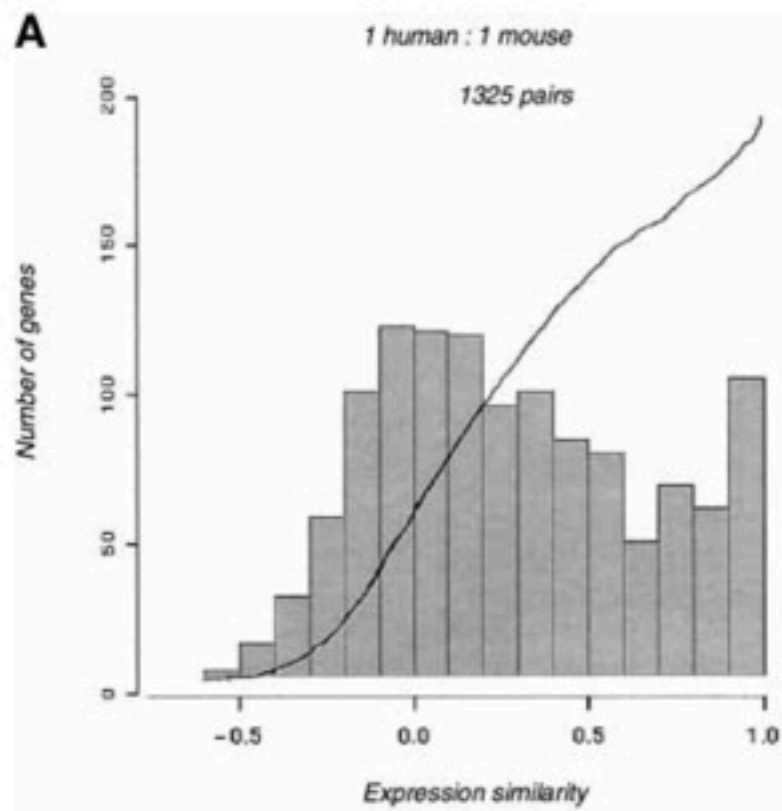
Examine pre-computed pairwise and multiple alignments of whole genome assemblies.

### **VISTA-Point**

Access complete data and visual presentation of pairwise and multiple alignments of whole genome assemblies.

### **Whole Genome rVISTA**

Identify transcription factor binding sites that are conserved between species and over-represented in upstream regions of groups of genes.



Huminiecki and Wolfe 2004  
Inference from microarray expression

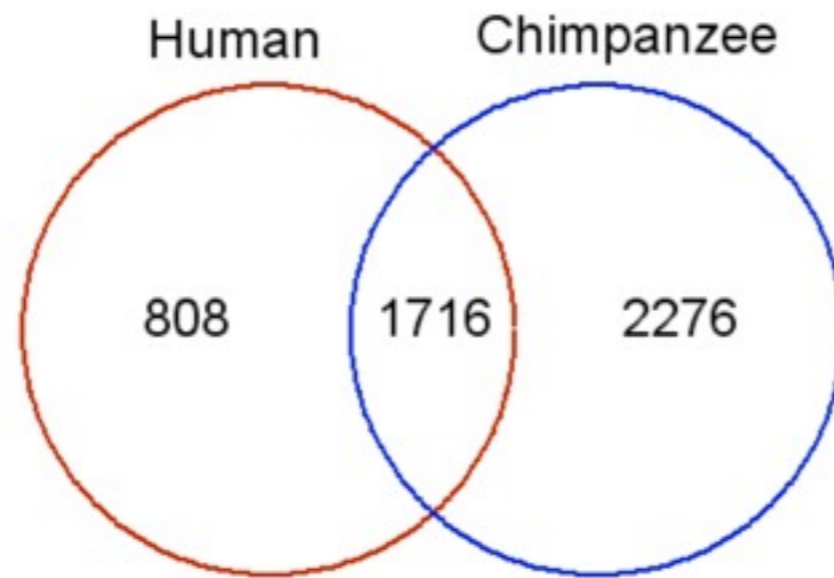
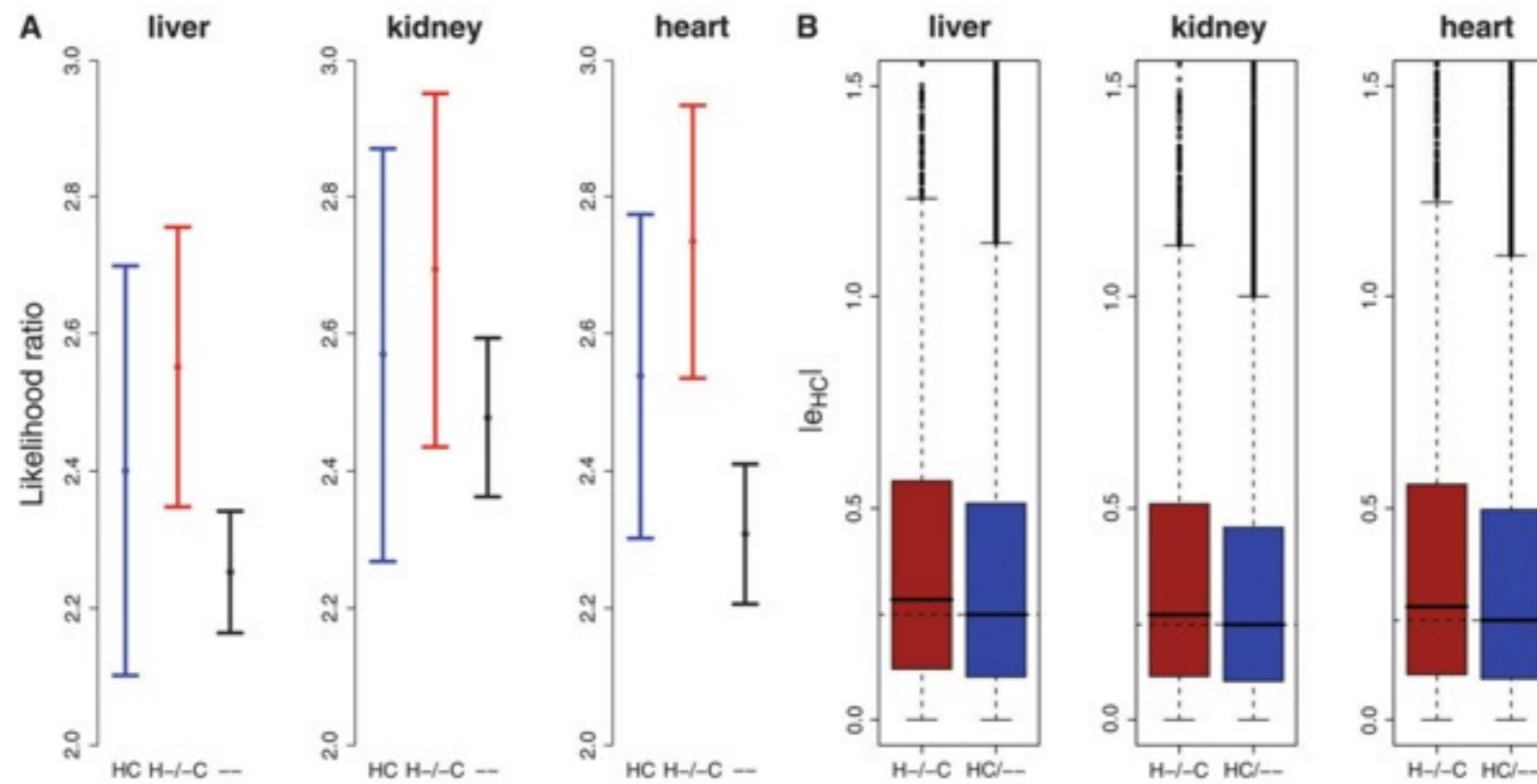
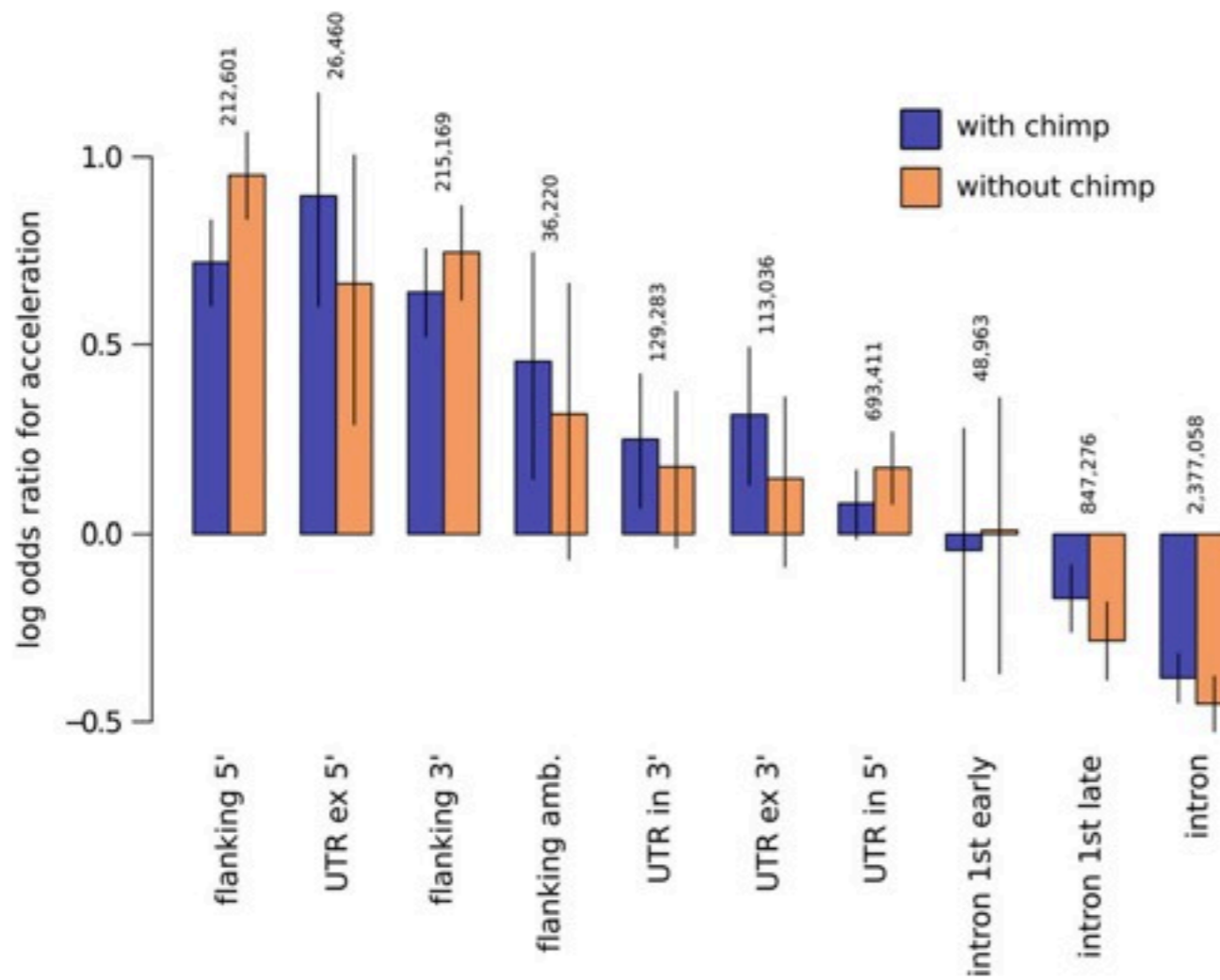
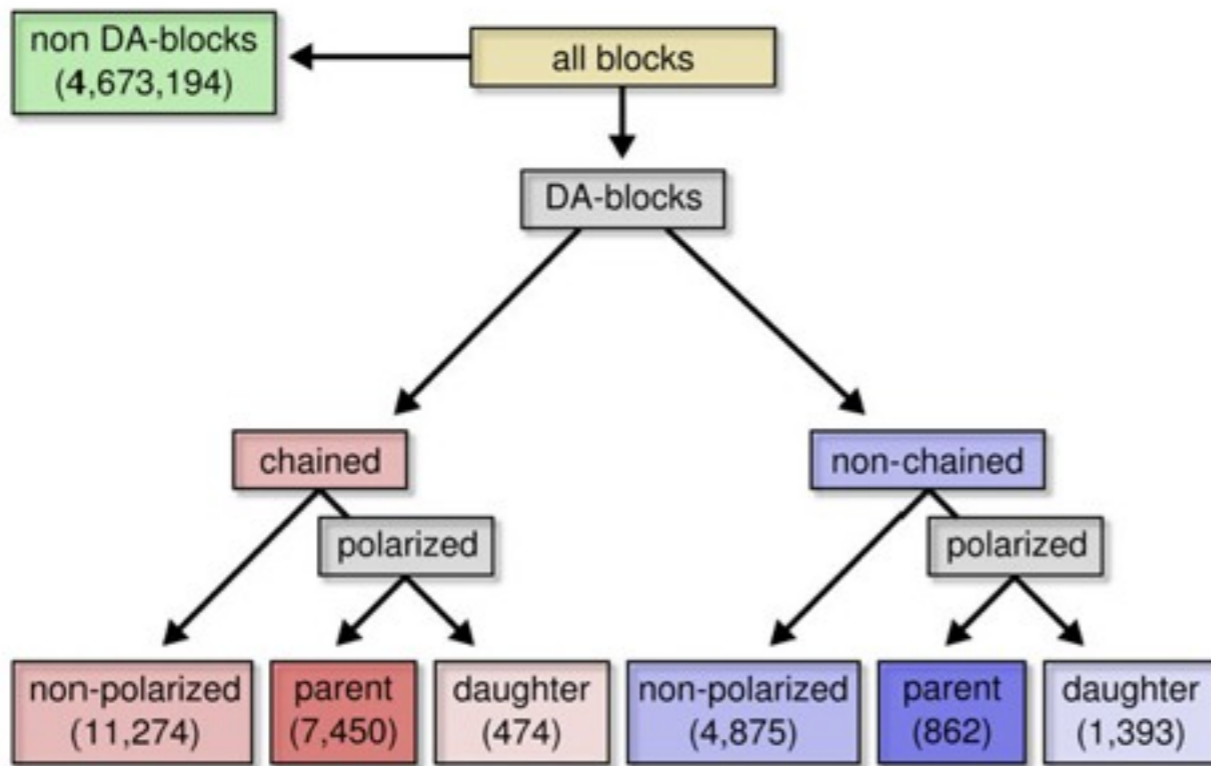


FIGURE S1.—A Venn diagram of the numbers of genes within segmental duplications in human and chimpanzee.



Blekhman et al. 2009  
Inference from microarray expression





Kostka et al. 2010  
examine non-coding sequences