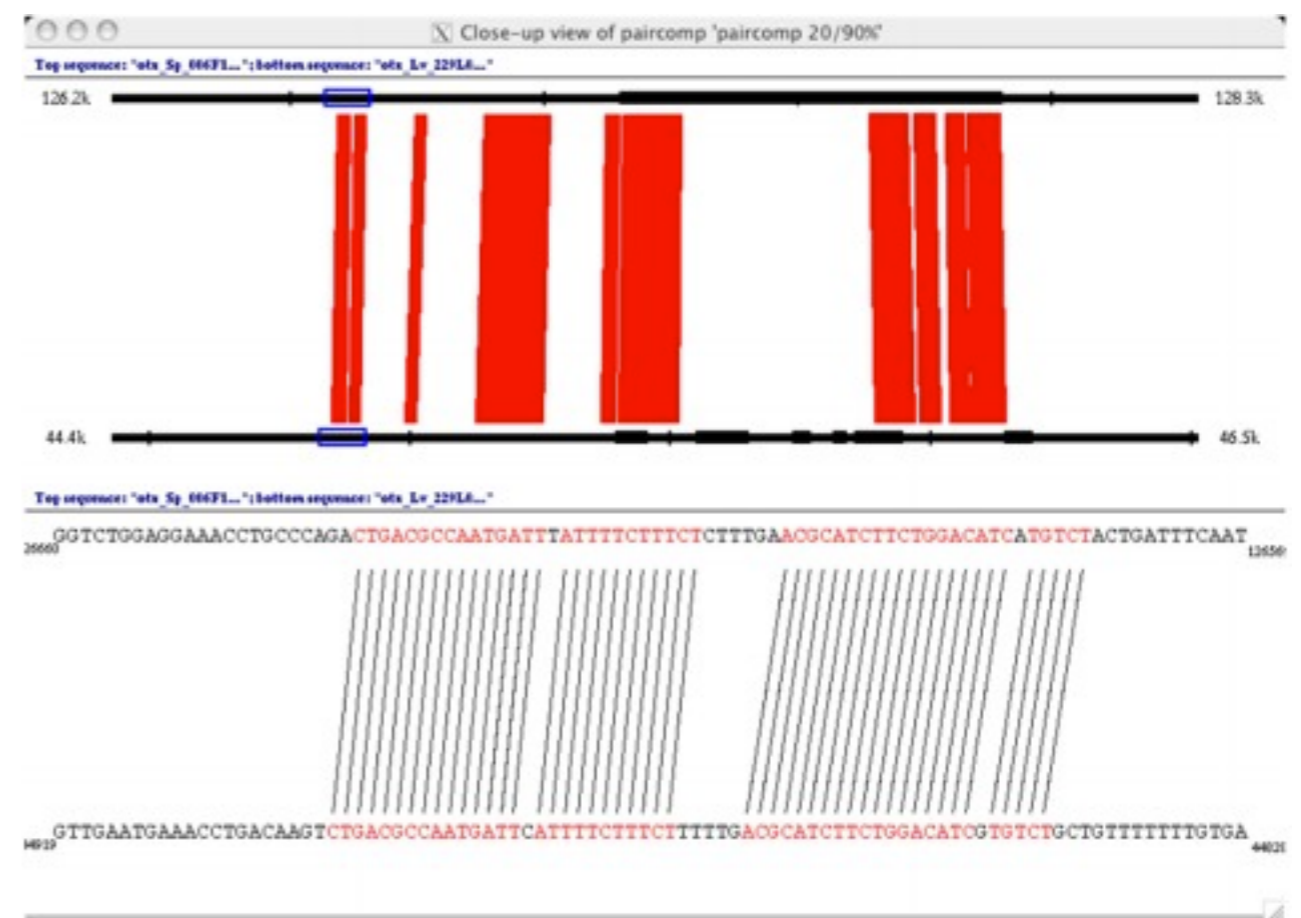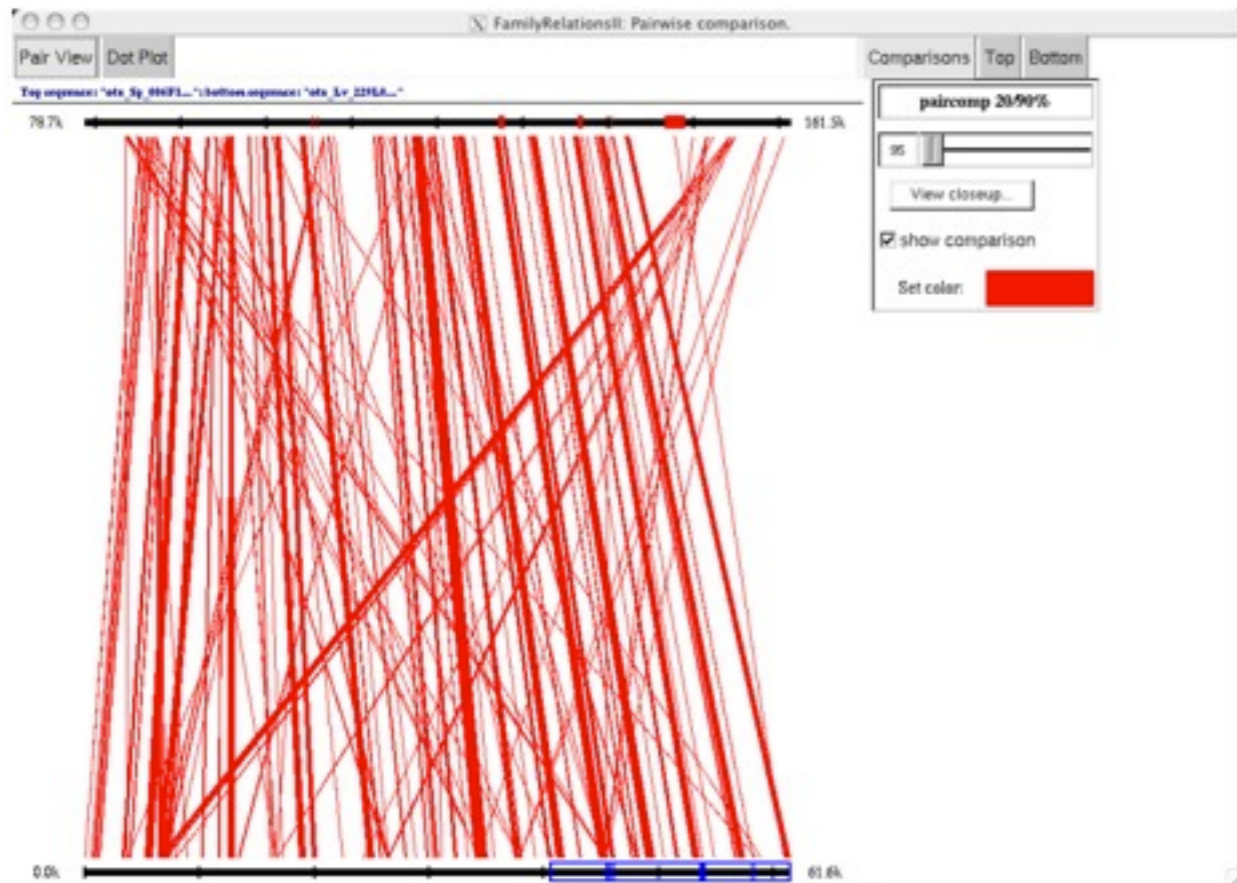Force et al. 1999

Fixed-width window comparisons (seqcomp)
Local alignment     (PipMaker)
Global alignment   (Vista)

FamilyJewels
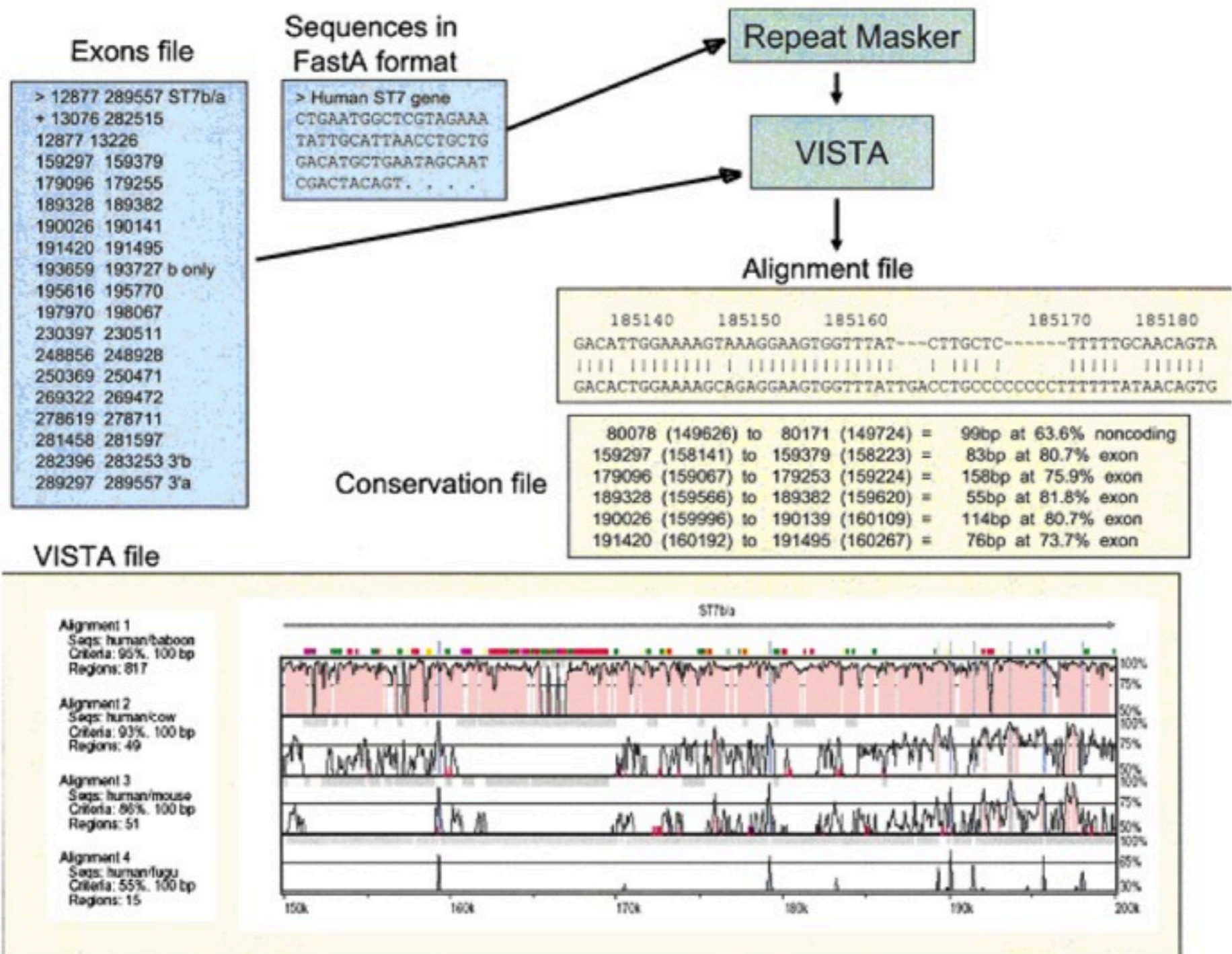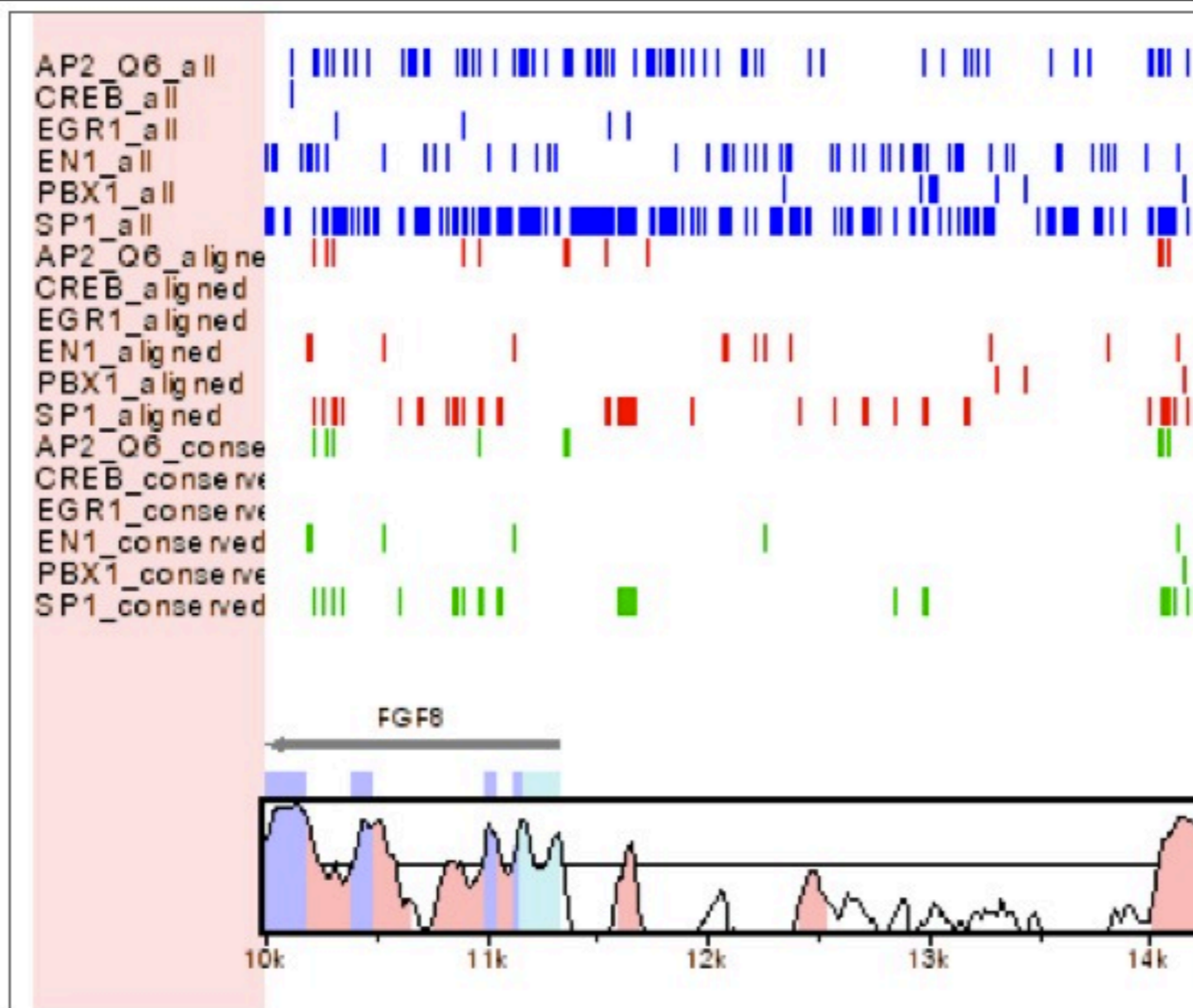http://family.caltech.edu/

PipMaker and MultiPipMaker
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.
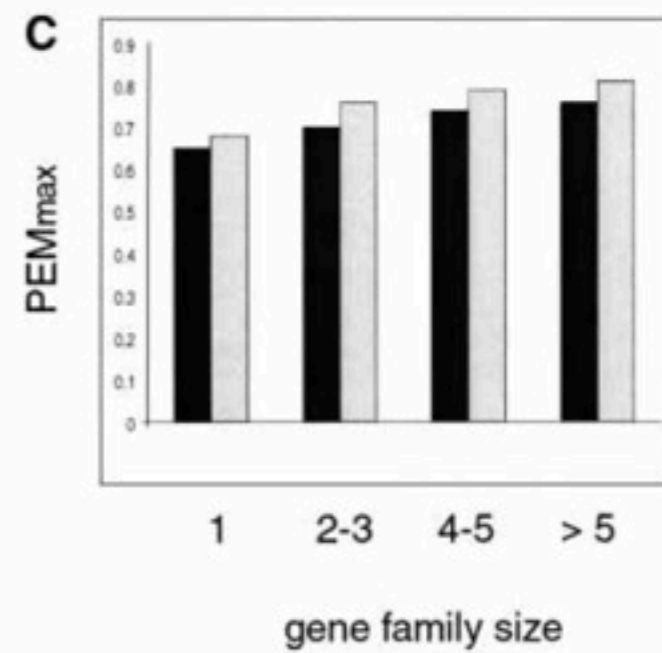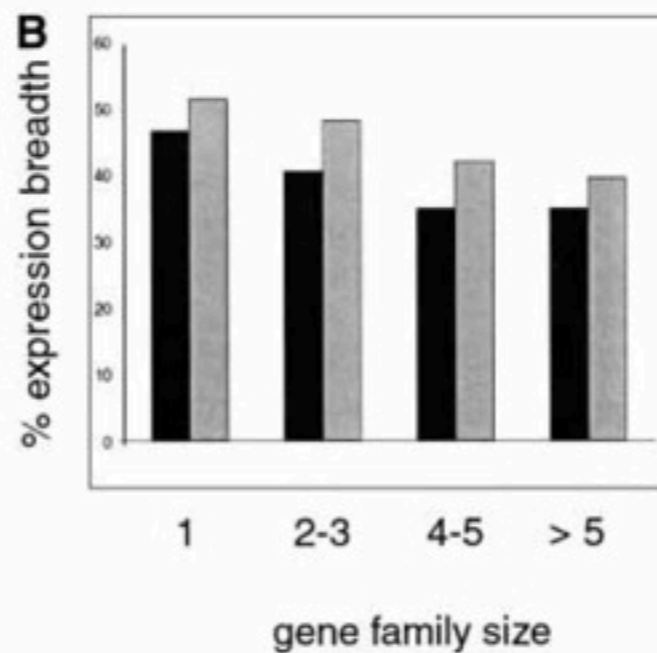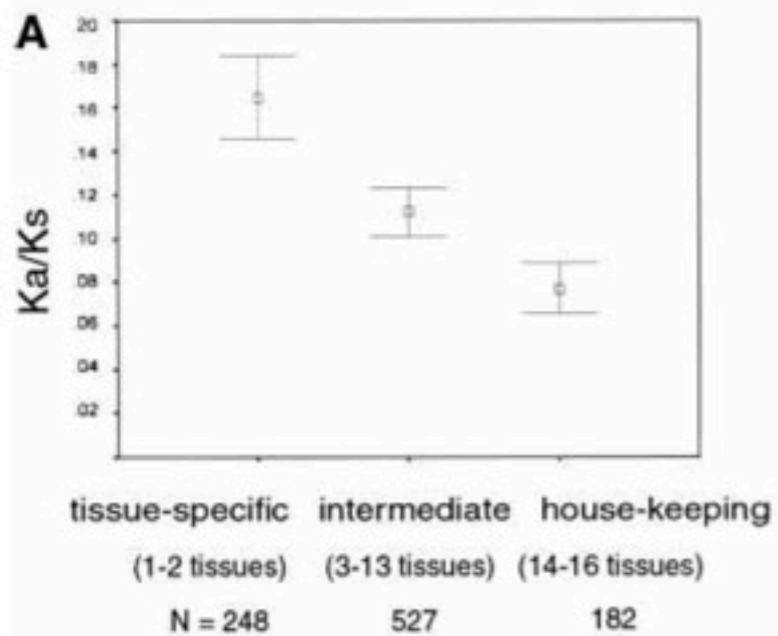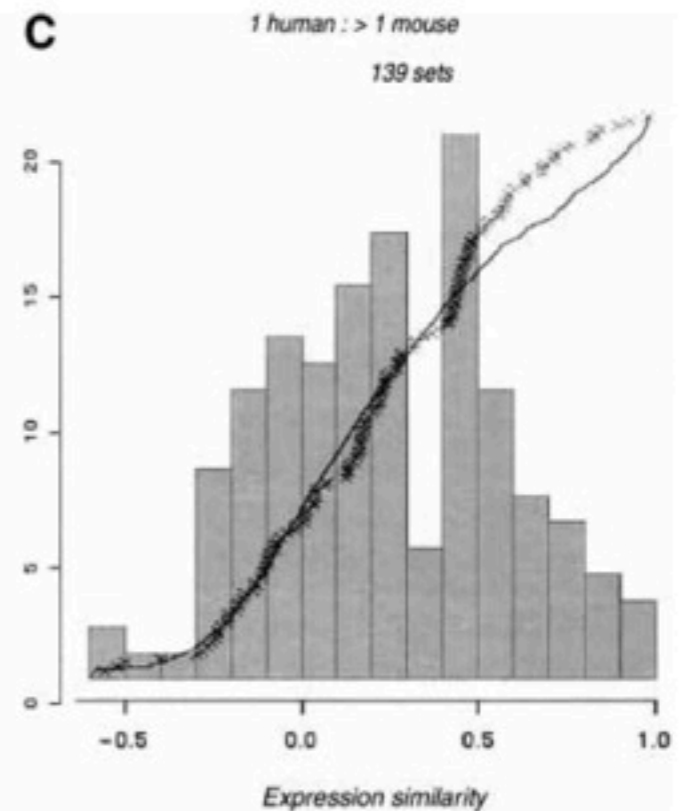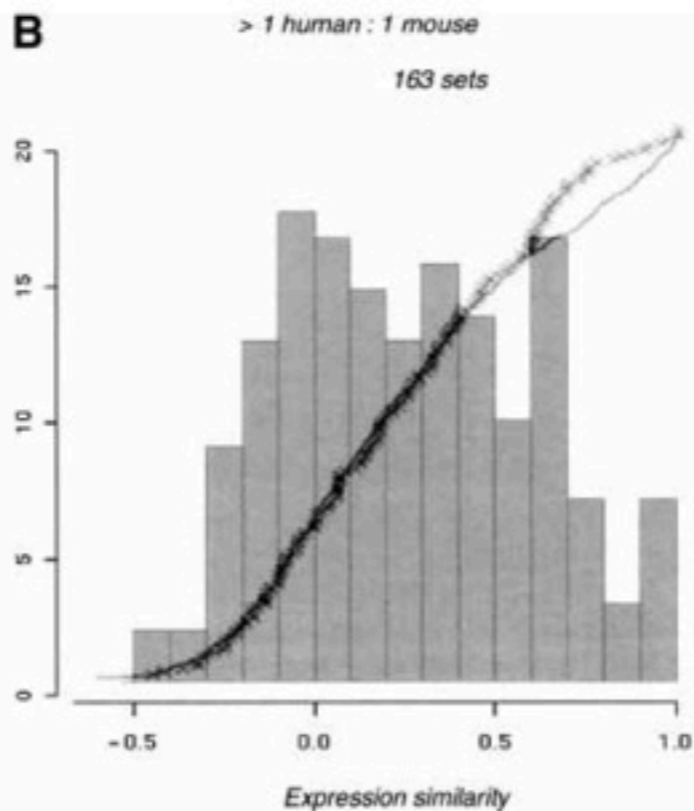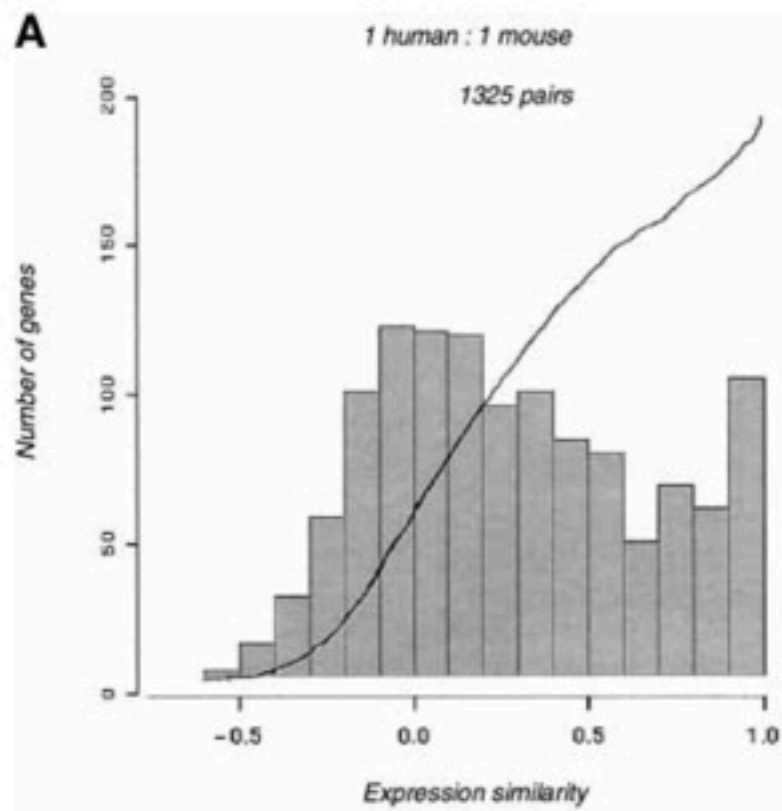
Huminiecki and Wolfe 2004
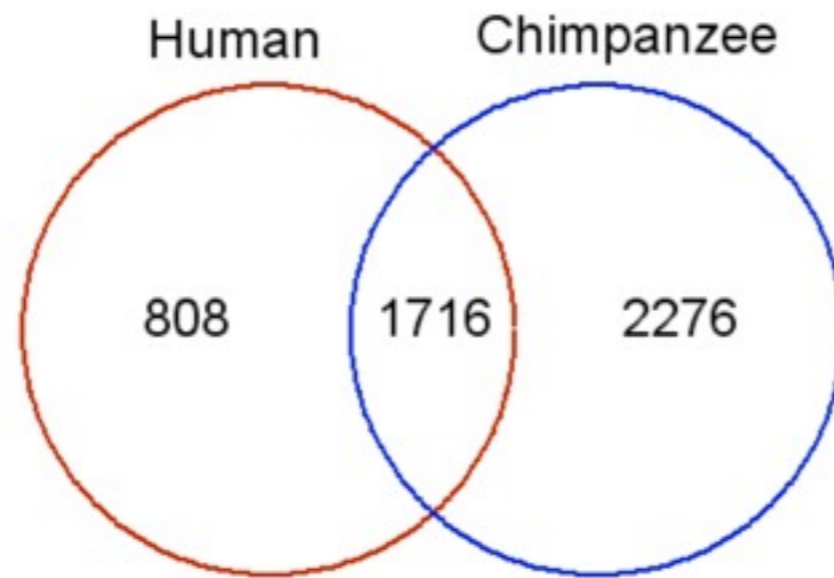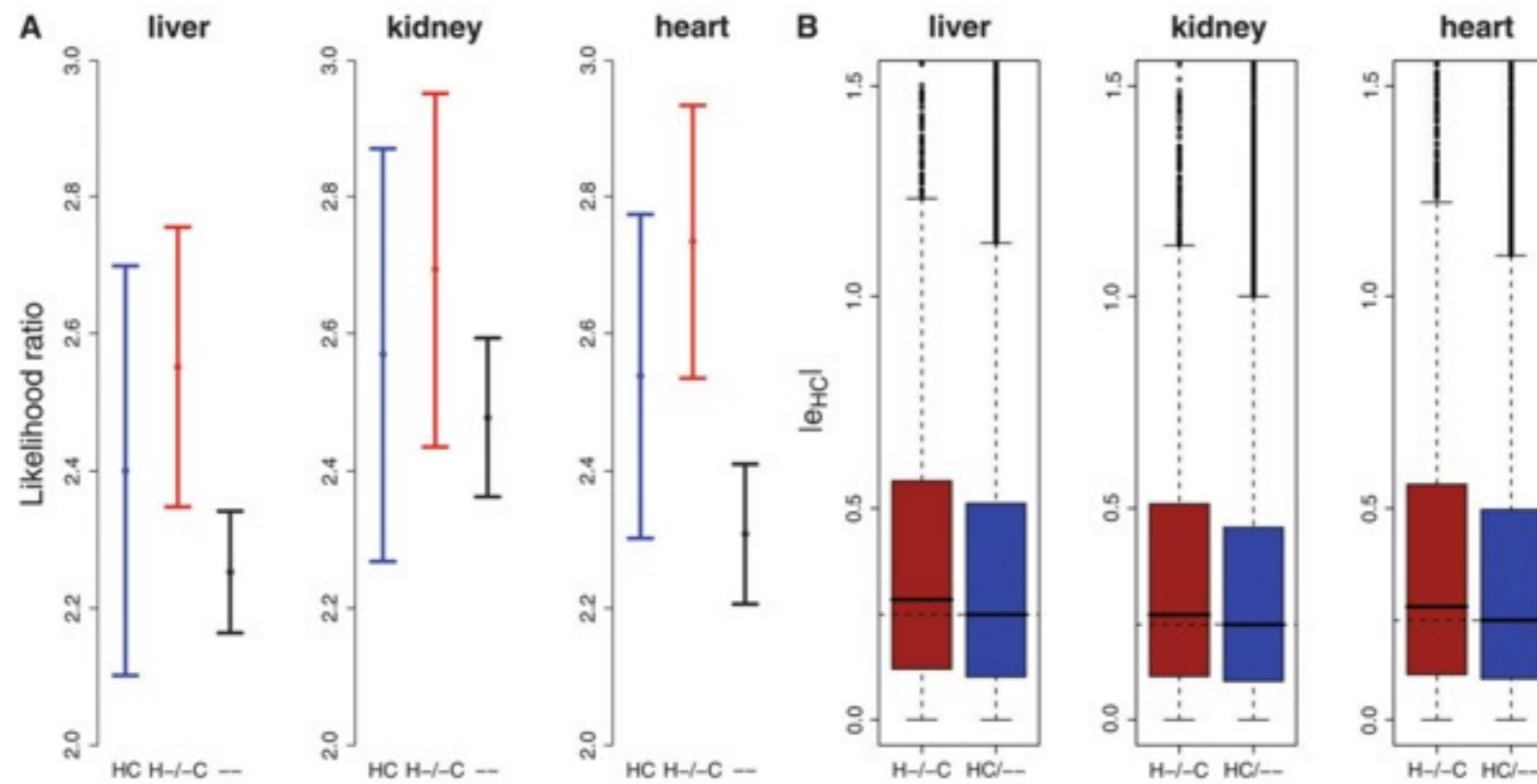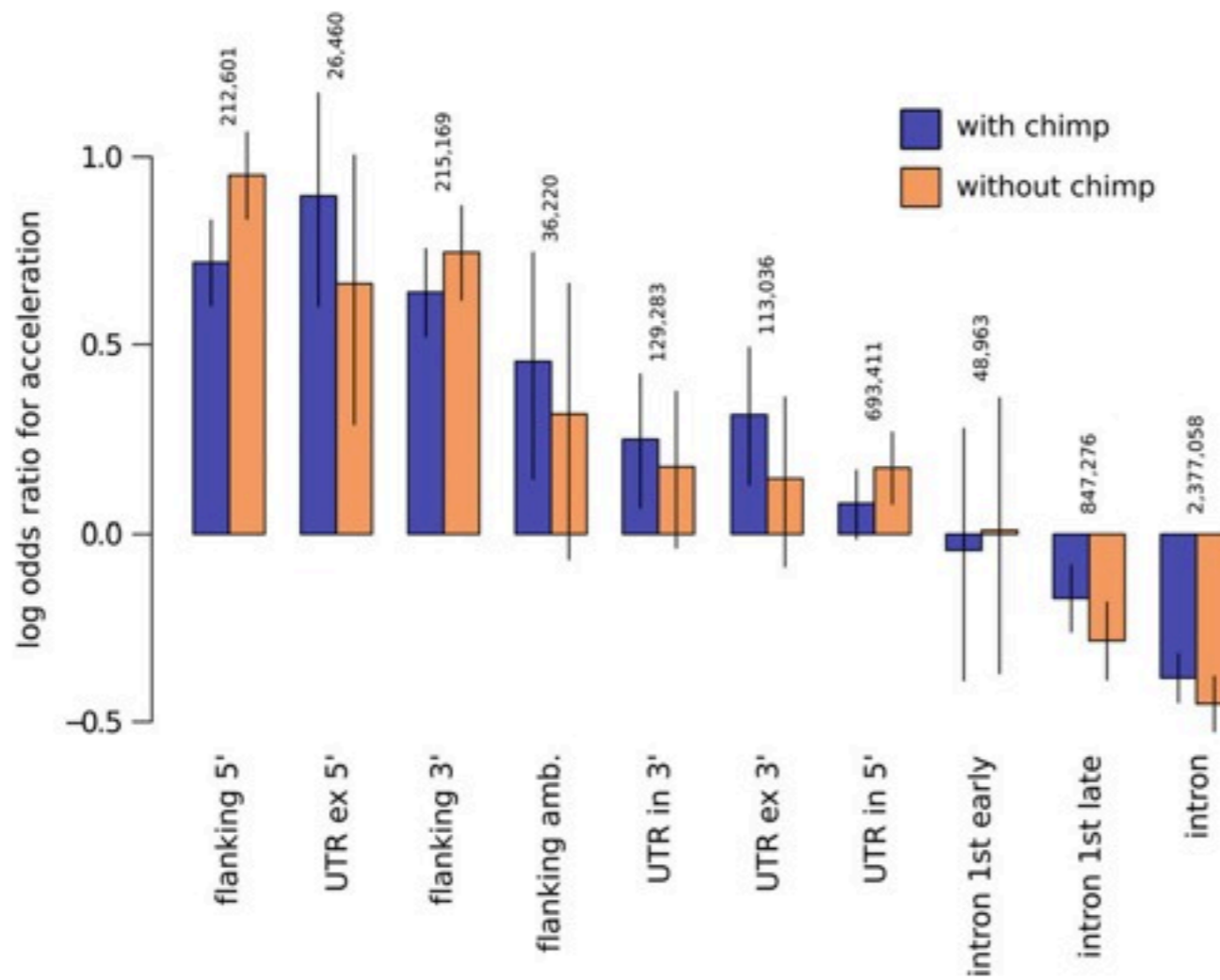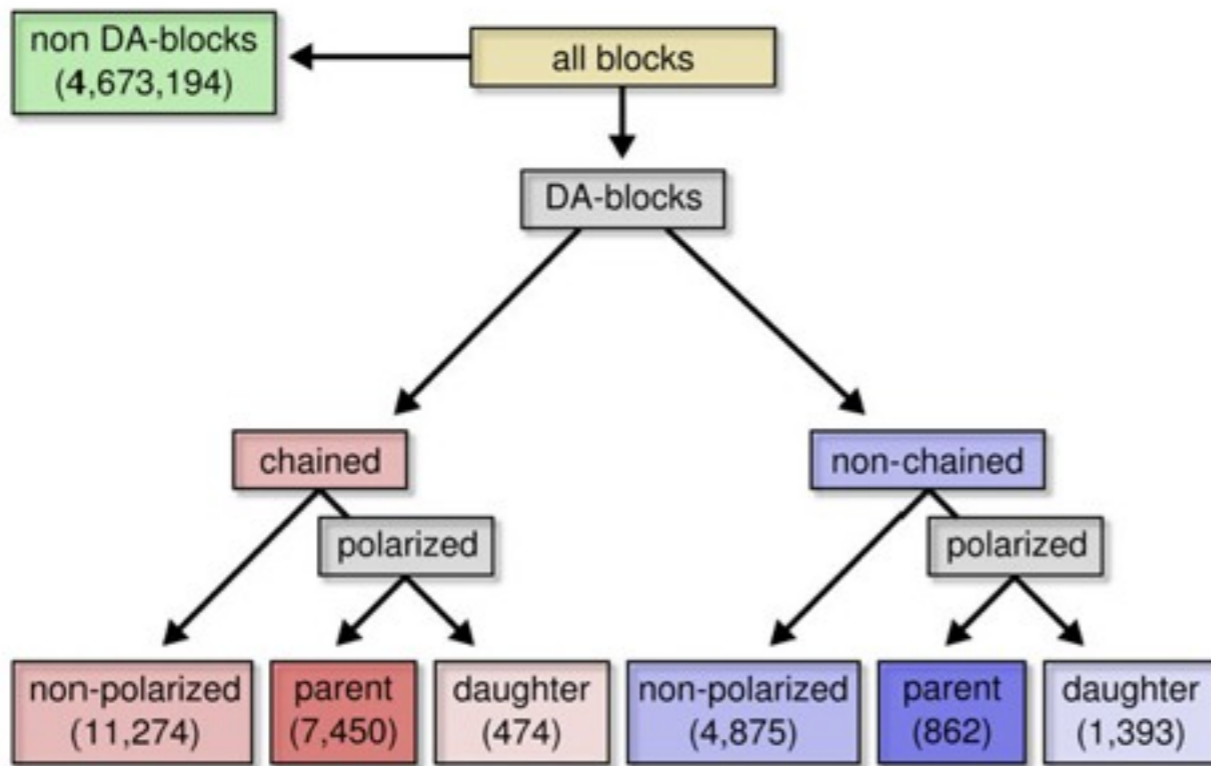Inference from microarray expression

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

8

Kostka et al. 2010
examine non-coding sequences