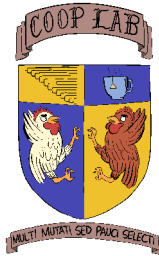


A novel fine-scale human recombination map reveals sex differences



Chenling Antelope, Graham Coop
University of California, Davis



Recombination is an Important Process

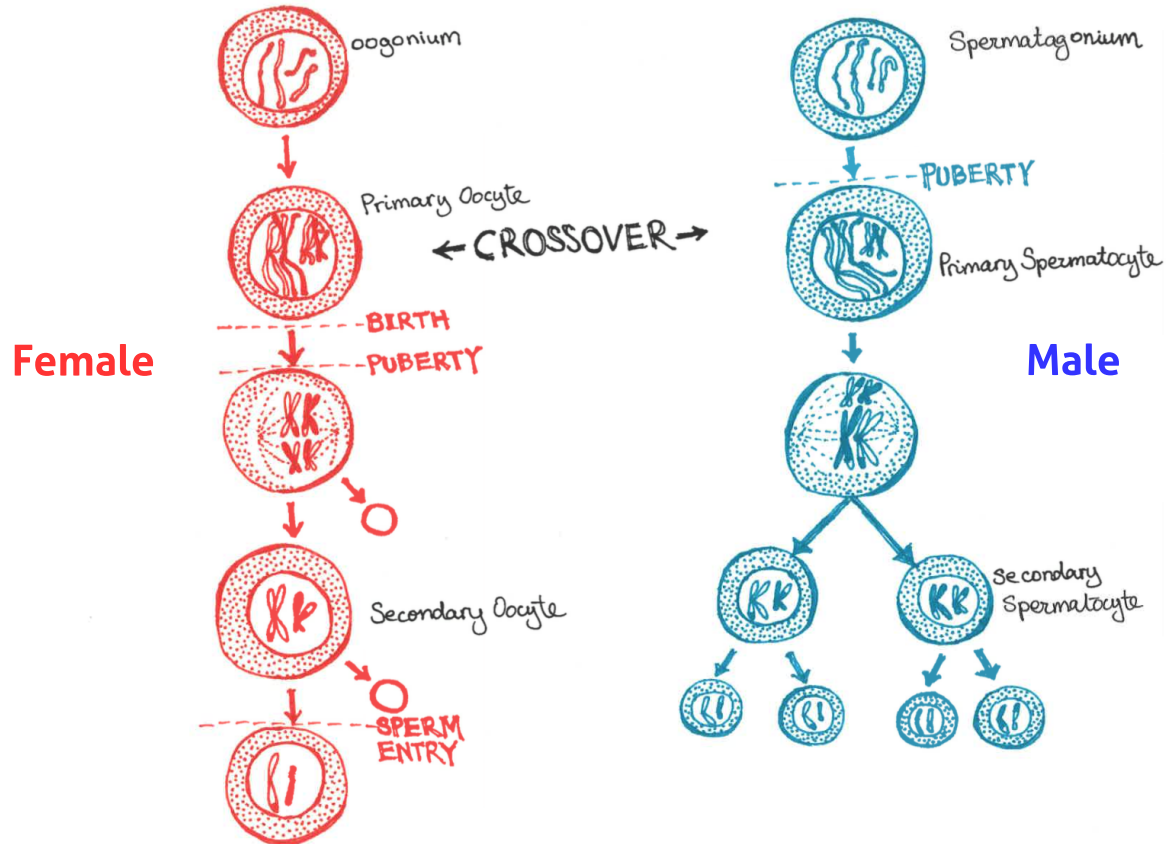
Recombination is a fundamental genetic process

- Increase Genetic Variance
- Breaks up epistatic interactions

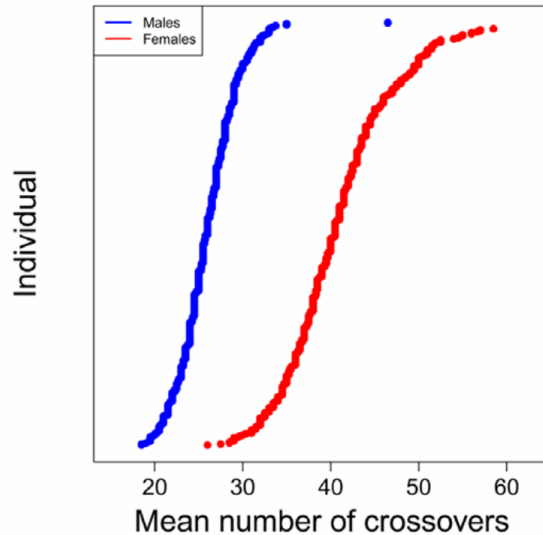
Recombination is a fundamental cellular and molecular process

- Chromosomal segregation
- Hotspots (PRDM9)

Sexual Dimorphism in Human Meiosis

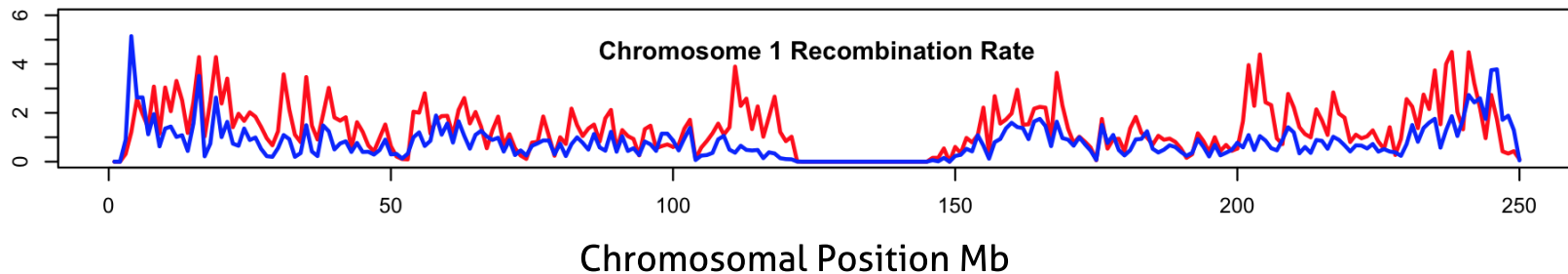


Sexual Dimorphism in Human Recombination Rate



Number of crossovers per individual in the AGRE (Autism Genetic Resource Exchange) pedigree

Fledel-Alon, A. *et al.* Variation in human recombination rates and its genetic determinants. *PloS one* **6**, e20321 (2011). Fledel-Alon, A. *et al.* Variation in human recombination rates and its genetic determinants. *PloS one* **6**, e20321 (2011).



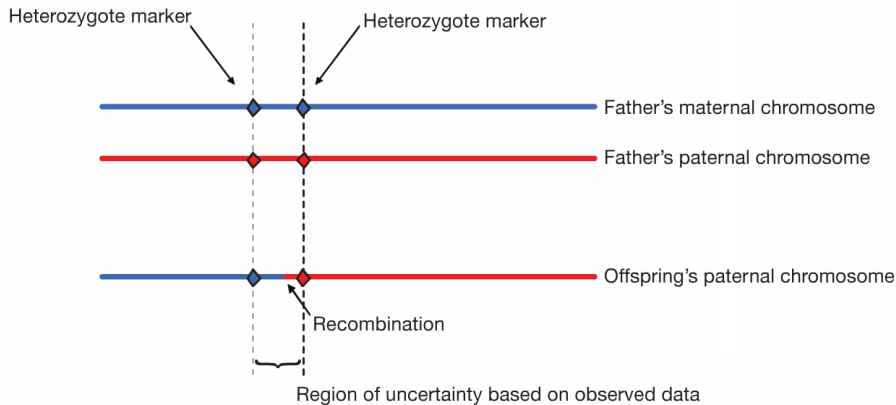
Fine Scale Recombination Rate

Sequence Specificity -> Similar

Fine Scale Chromatin State -> Different

1. New method for inferring sex-specific fine scale recombination rate
2. Amount of fine scale recombination rate sharing
3. Fine-scale recombination rate around genes (as a proxy for chromatin state)
4. Interaction between large scale and fine scale recombination variation

Data & Method



Kong, A, Thorleifsson, G, Gudbjartsson, DF & Masson, G. *Nature* (2010).

3774 Females, 3781 Males

Fledel-Alon, A. *et al.* Variation in human recombination rates and its genetic determinants. *PloS one* **6**, e20321 (2011). Fledel-Alon, A. *et al.* Variation in human recombination rates and its genetic determinants. *PloS one* **6**, e20321 (2011).

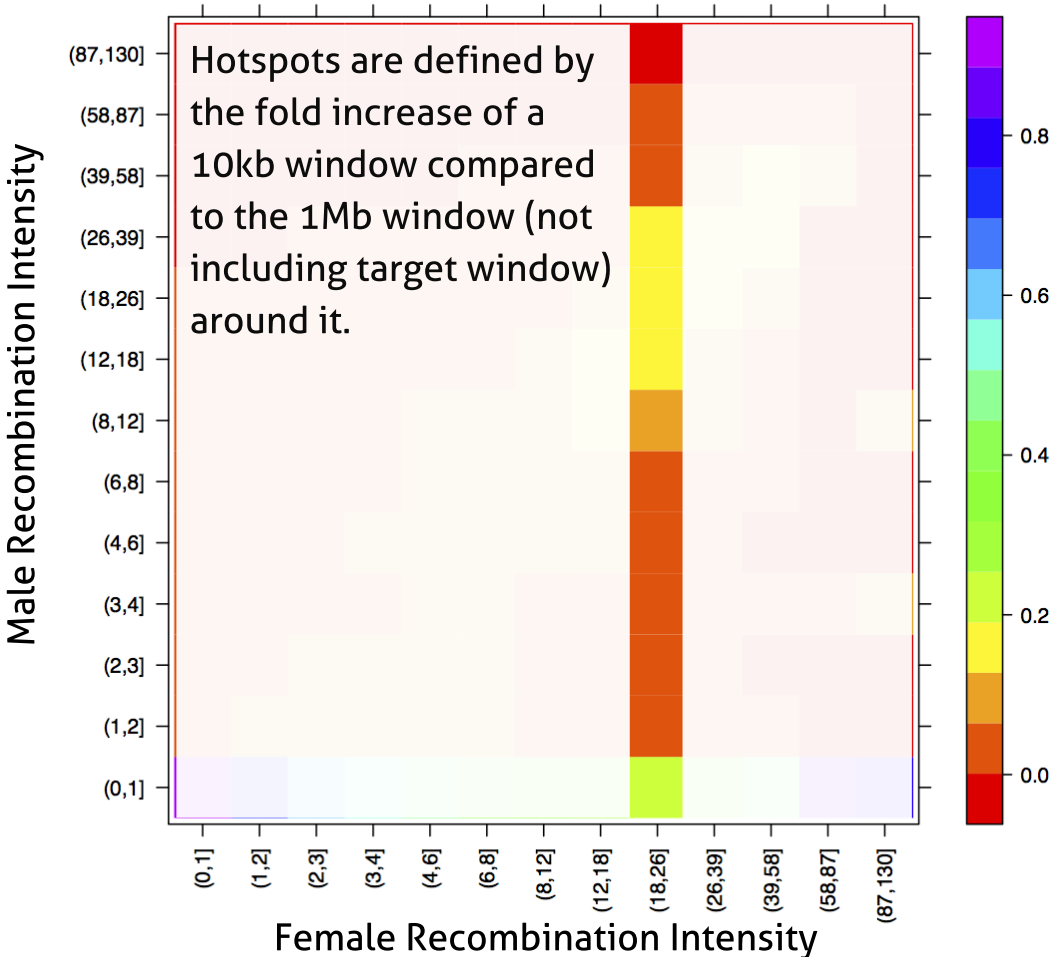
41745 Females, 30184 Males

Kong, A, Thorleifsson, G, Frigge, ML & Masson, G. Common and low-frequency variants associated with genome-wide recombination rate. *Nature* ... (2014).

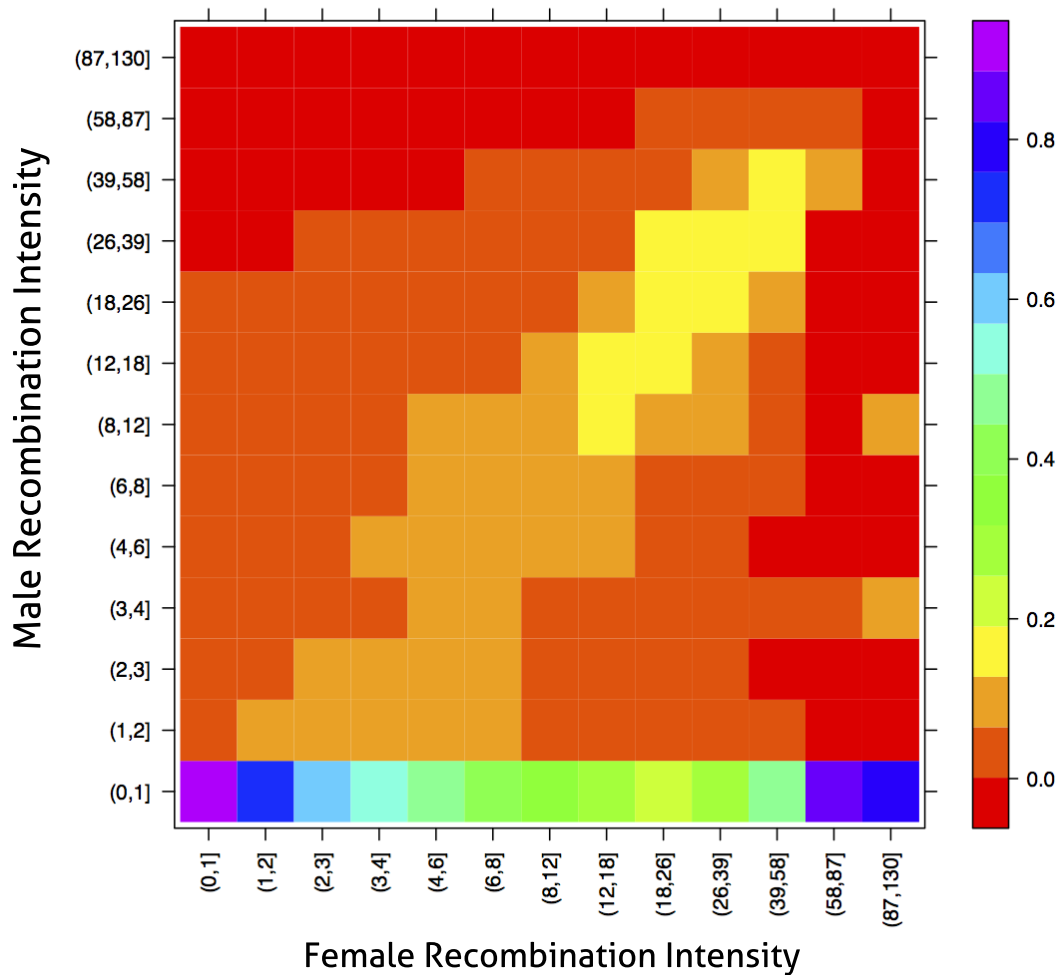
We apply a **Gibbs Sampler Method iteratively** in order to estimate the **position of of a recombination event** and **recombination rates** in genomic windows **simultaneously**.

Male rate and female rate estimated using the same method independently.

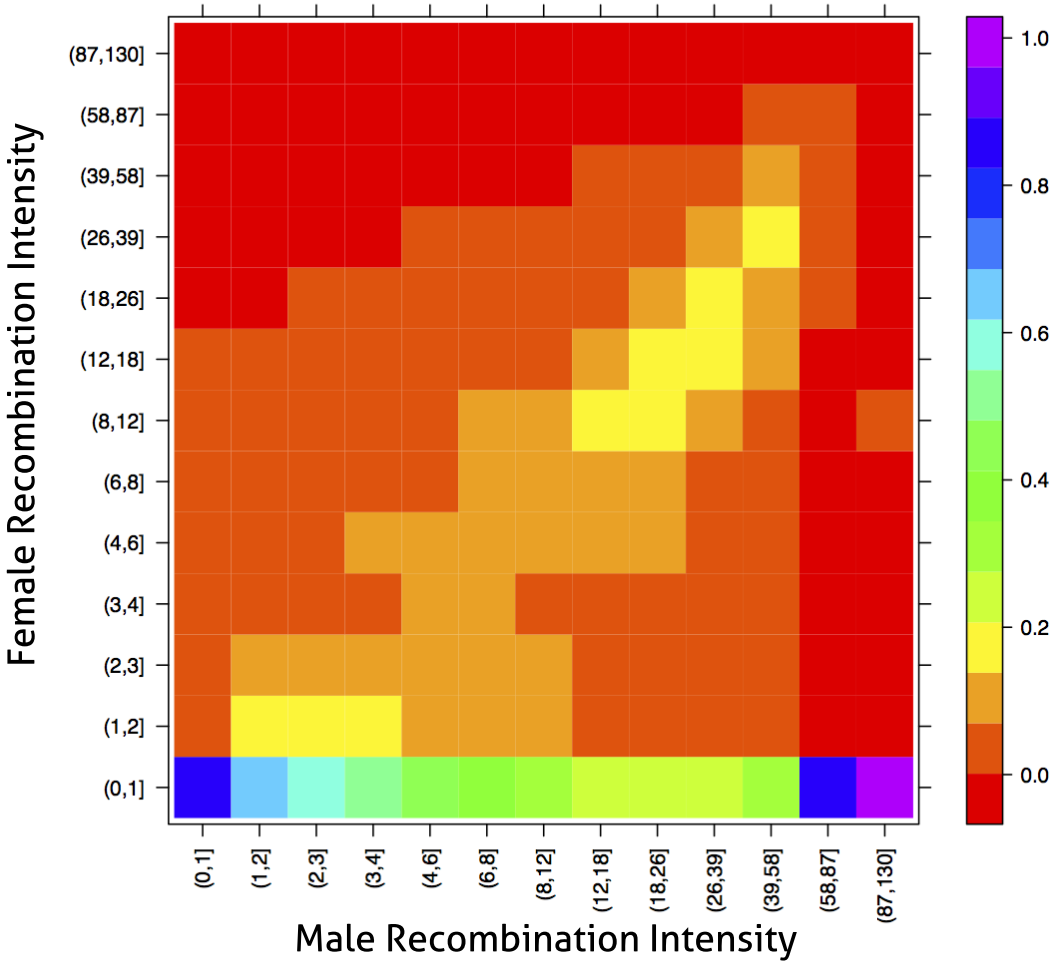
Hotspot Sharing



Hotspot Sharing

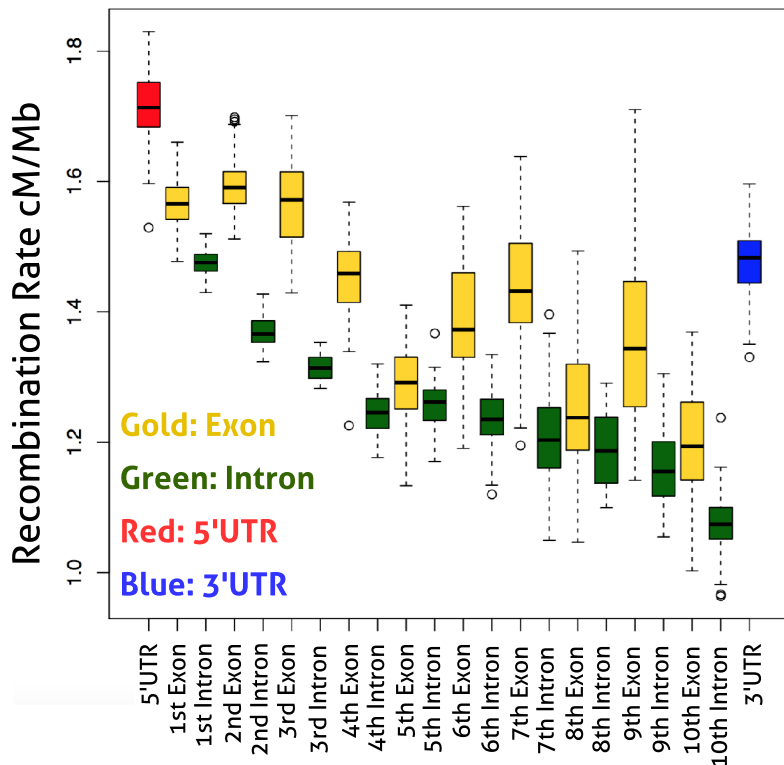


Hotspot Sharing

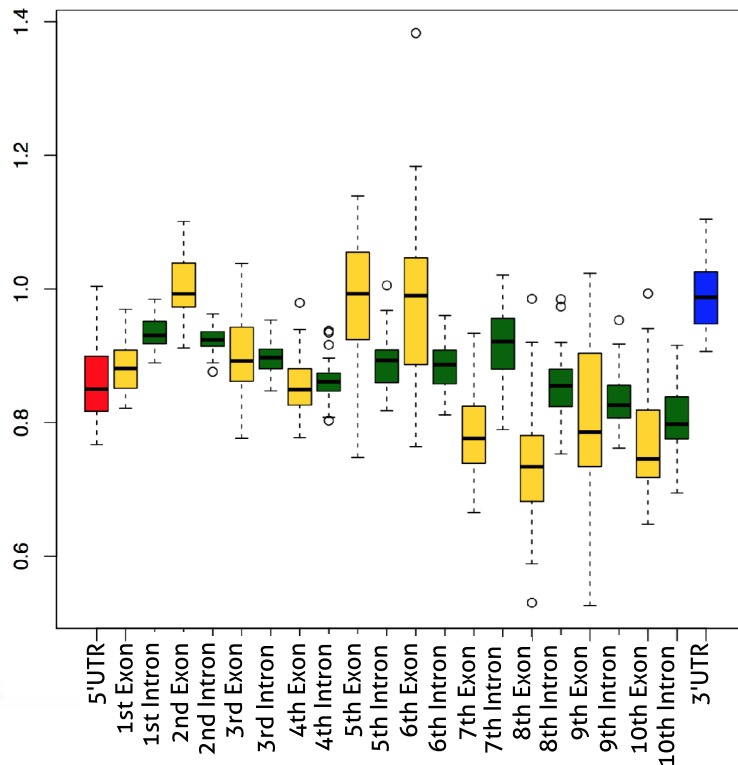


Recombination Rate Along Transcript

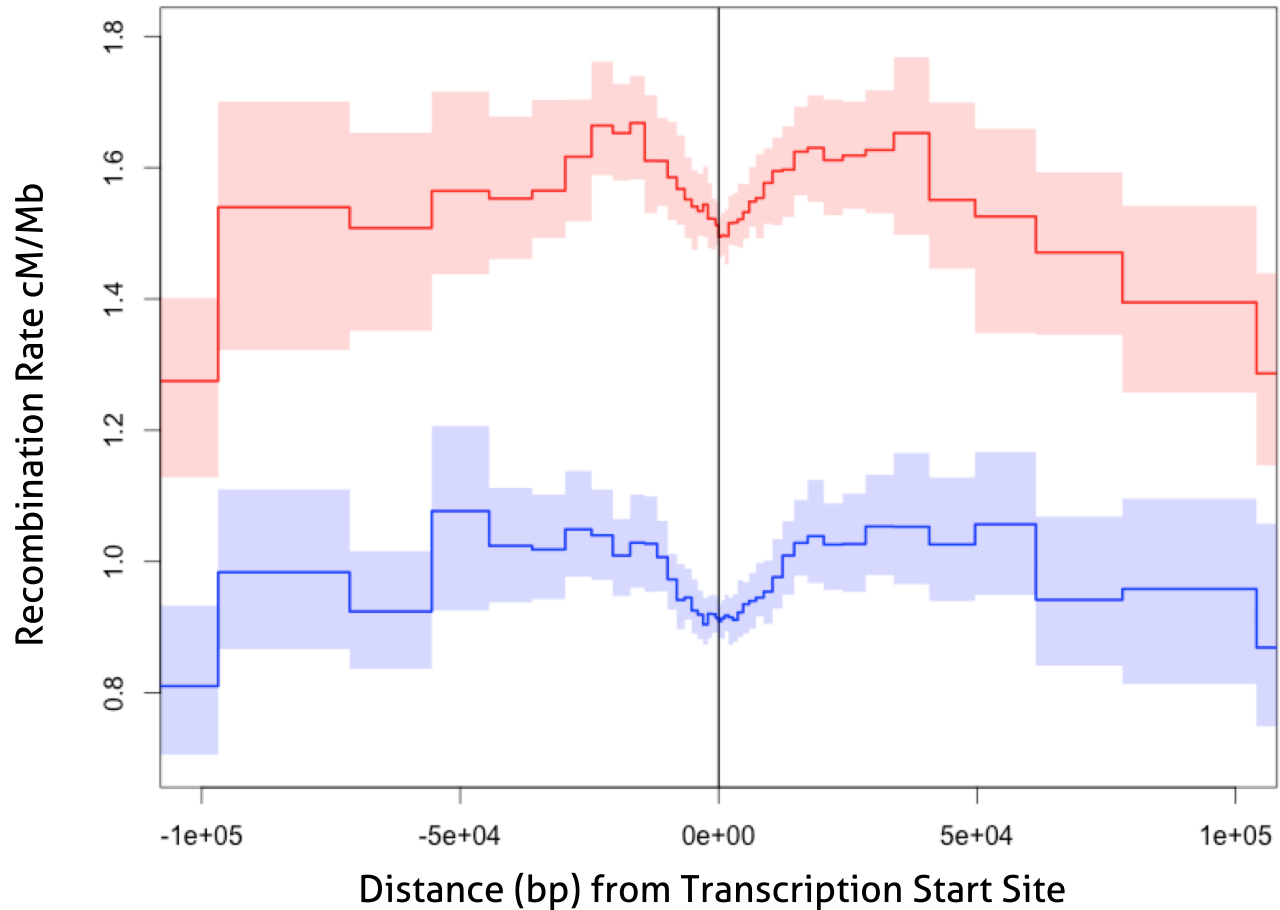
Female



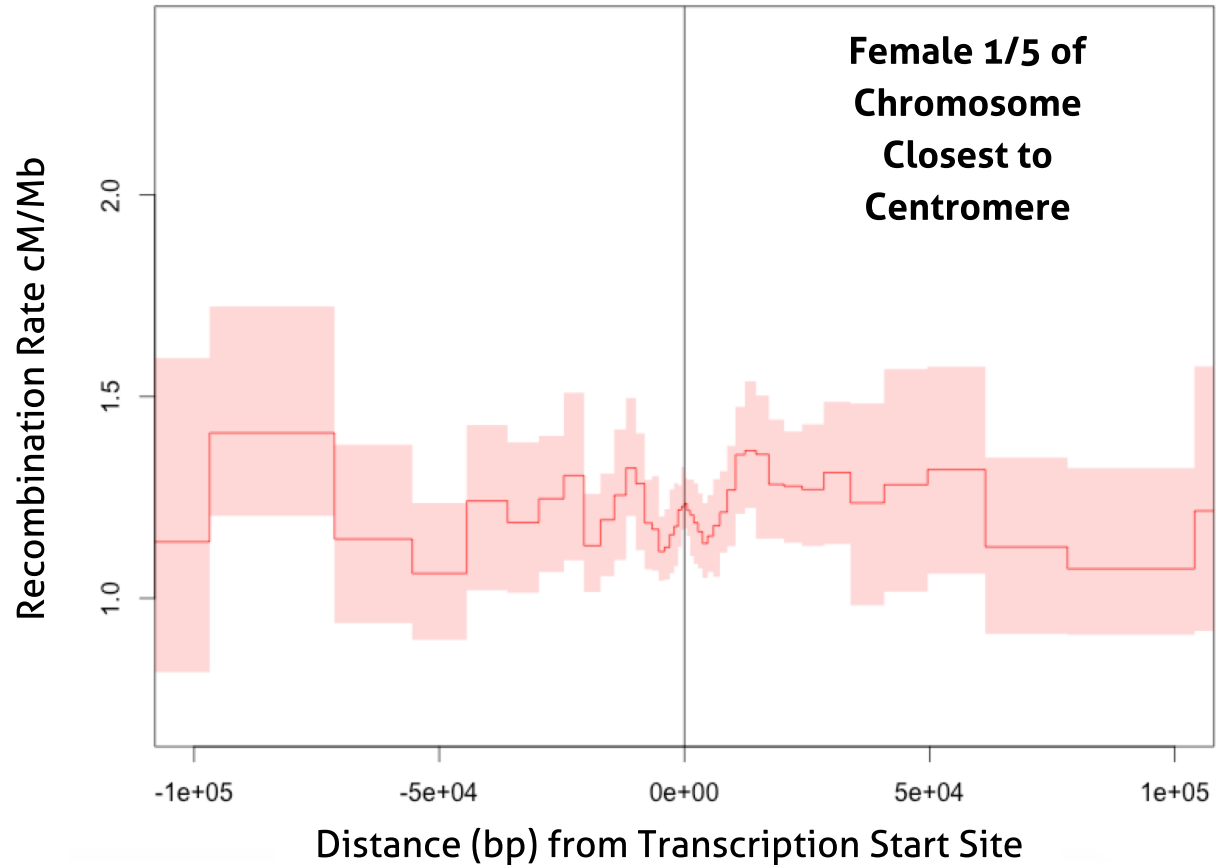
Male



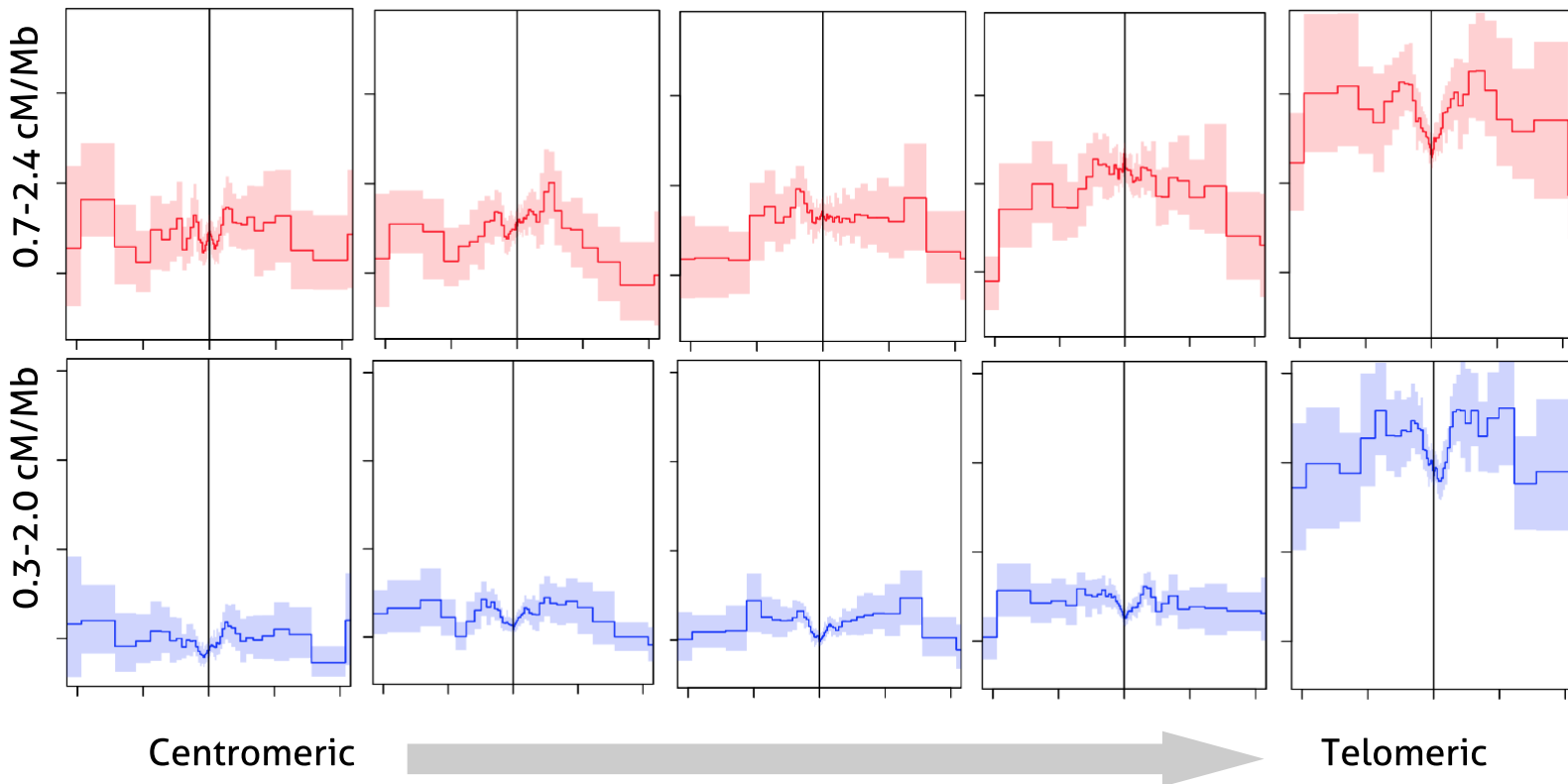
Recombination Rate Near Transcription Start Site



Variation Along Chromosome Arm



Variation Along Chromosome Arm



Conclusions:

- ~50% of recombination hotspots are shared.

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Further questions:

- What mechanisms are causing the recombination patterns we are seeing?

Thanks to



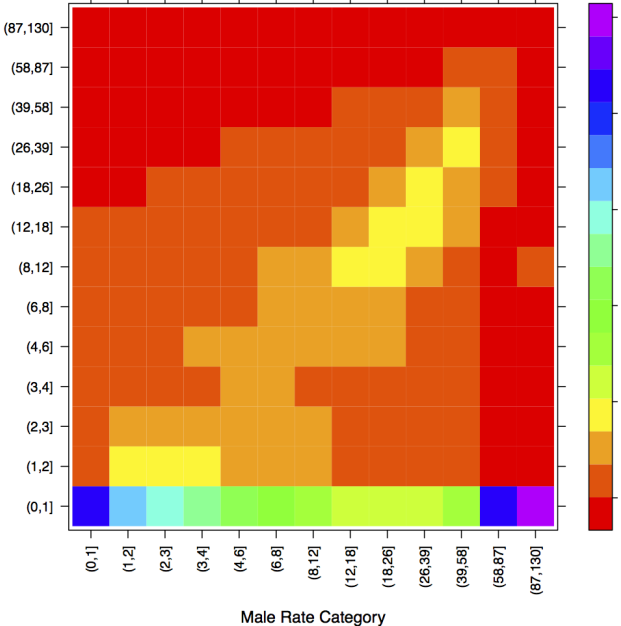
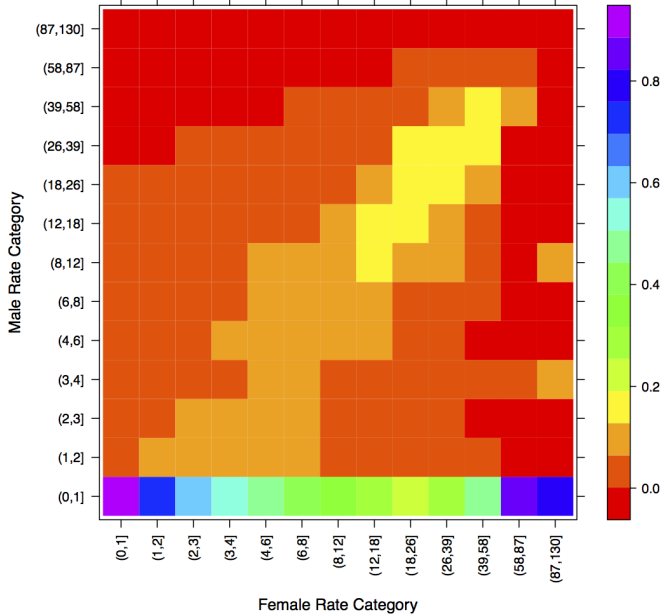
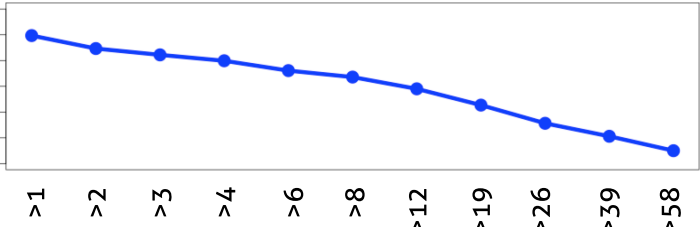
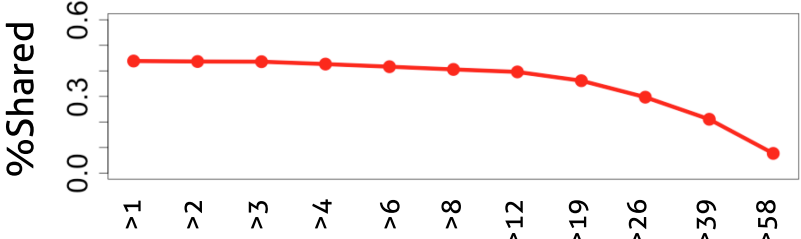
Coop Lab



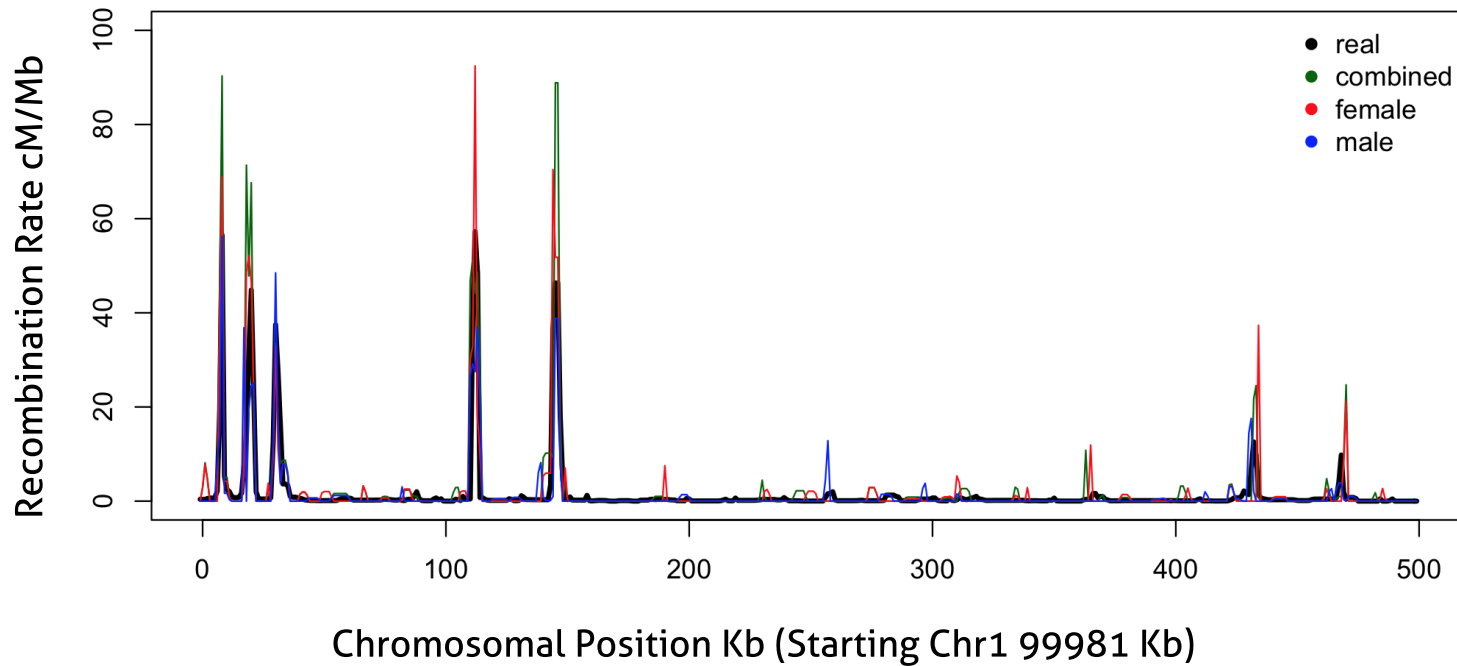
Molly Przeworski

I will be moving to UC Berkeley next year to start my PhD in the Computational Biology Graduate Group!

Hotspot Sharing

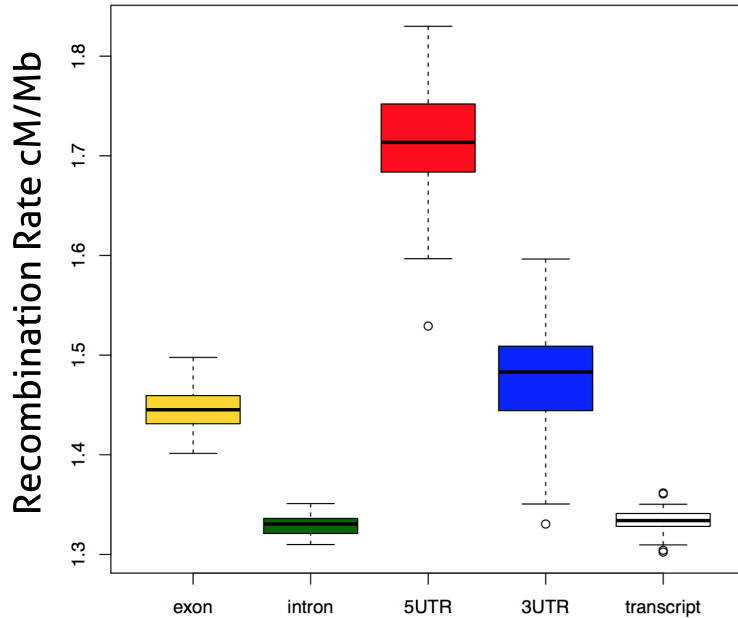


Simulation Using HapMap

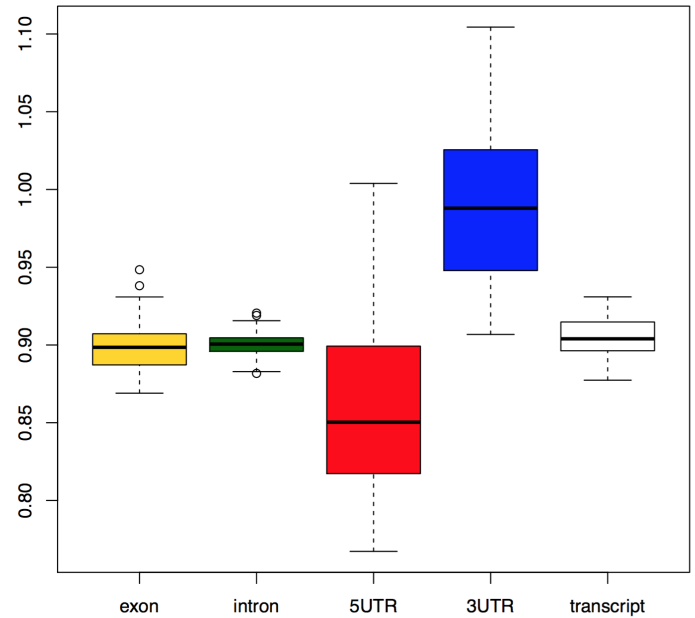


Recombination Rate in Annotation Categories

Female

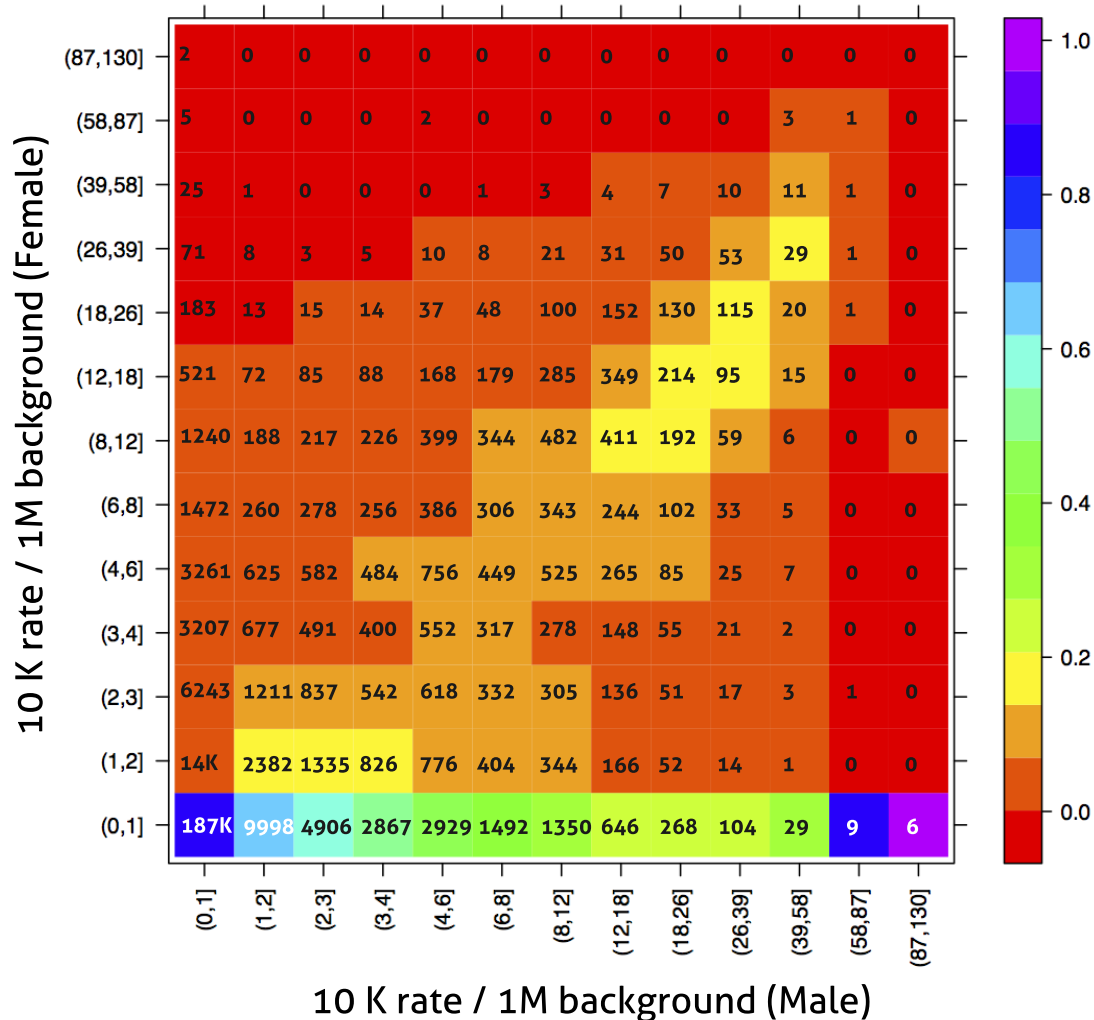


Male



10 K rate / 1M background (Male)

Hotspot Counts



Correlation Between Expression and Recombination

