Fine-mapping a trans-eQTL hotspot

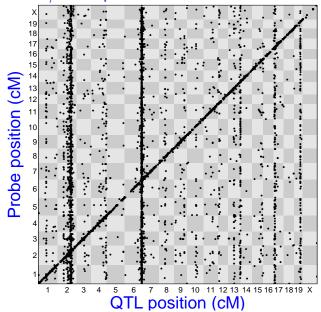
Jianan Tian

Department of Statistics, UW-Madison

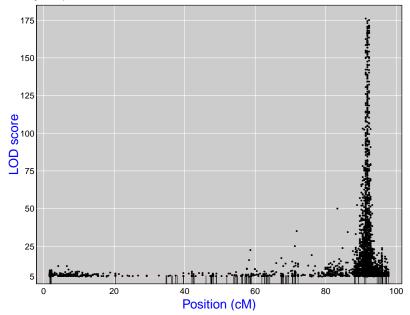
C57BL/6J (B6) x BTBR intercross

- Collaboration with Alan Attie
- $ightharpoonup \sim 500$ mice, all leptin knockouts
- ▶ Genotypes at ~ 2000 markers
- ► Gene expression microarray on 6 tissues
 - islet, adipose, gastrocnemius, hypothalamus, kidney, liver
- Numerous clinical phenotypes

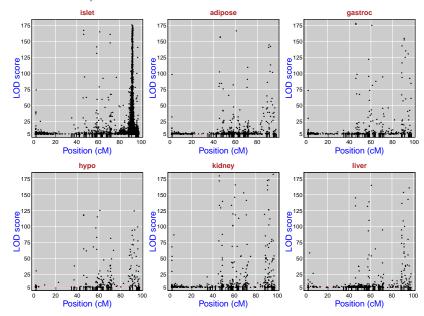
Islet eQTL: cis/trans plot



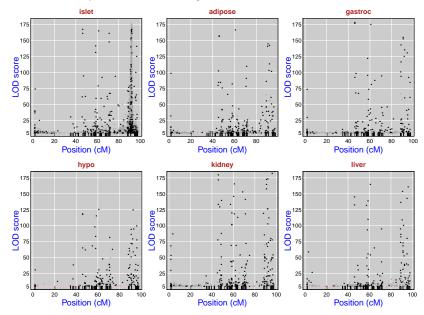
Islet eQTL, chr 6



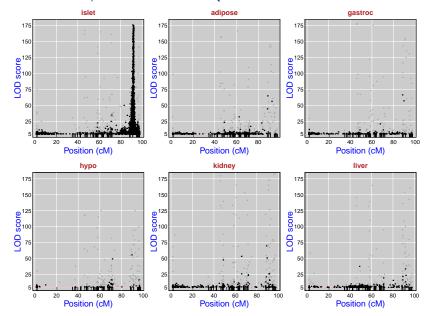
All six tissues, chr 6



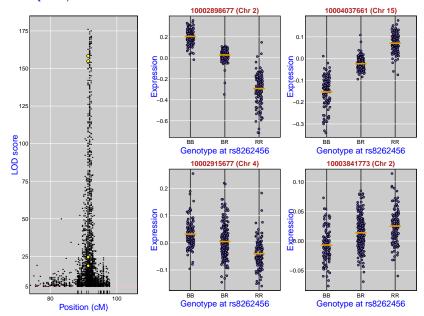
All six tissues, chr 6: cis-eQTL



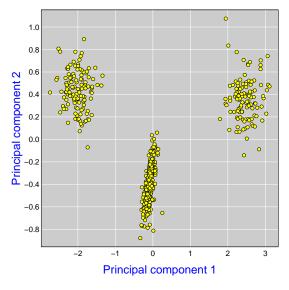
All six tissues, chr 6: trans-eQTL



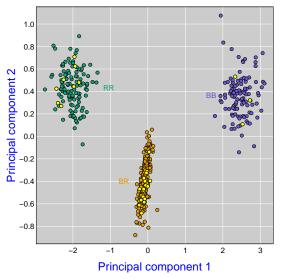
Islet eQTL, chr 6



From expression pattern to QTL genotype

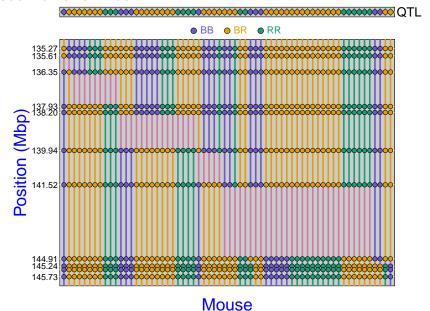


From expression pattern to QTL genotype

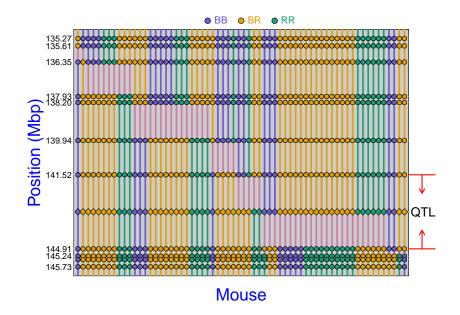


Non-recombinant: mice with the same genotype in the region yellow = recombinant mice in the region

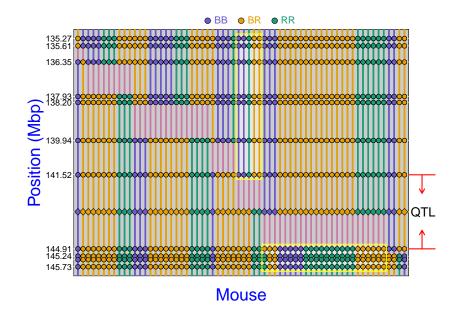
Recombinant mice



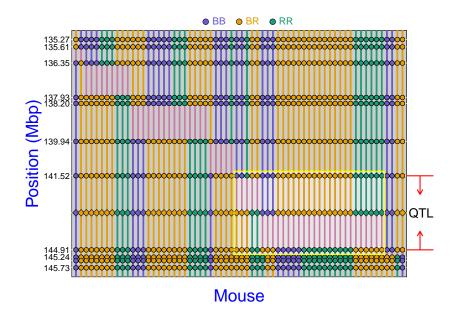
Recombinant mice (3.39 Mbp)



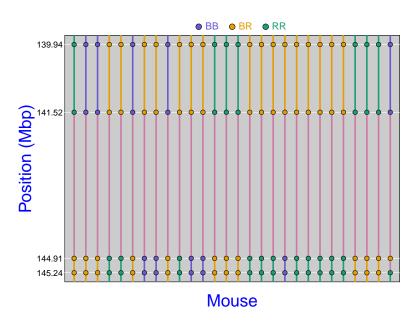
Recombinant mice (3.39 Mbp)



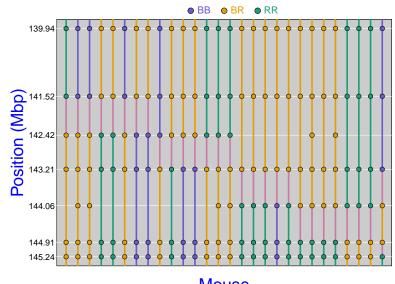
Recombinant mice (3.39 Mbp)



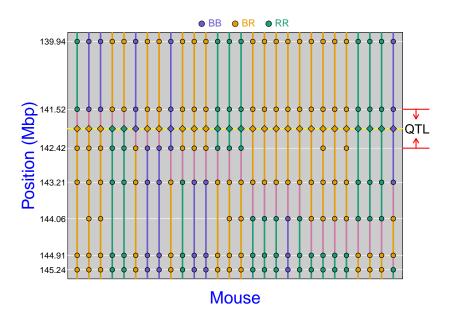
Close up



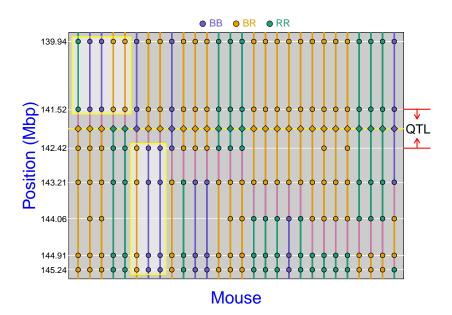
New genotypes: 3 more markers



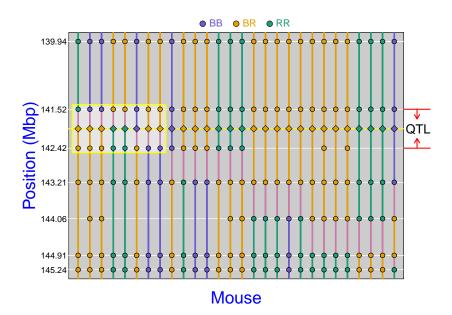
New genotypes: 3 more markers (0.90 Mbp)



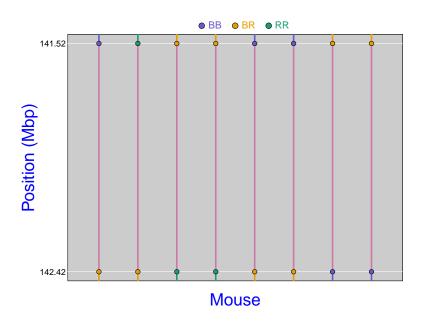
New genotypes: 3 more markers (0.90 Mbp)



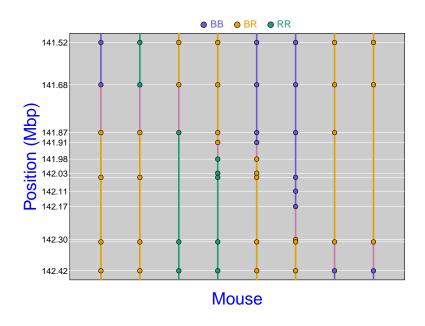
New genotypes: 3 more markers (0.90 Mbp)



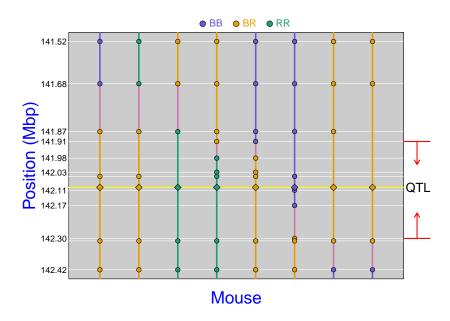
Closer up



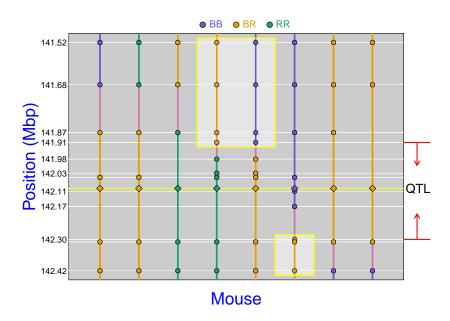
New genotypes: 10 more markers



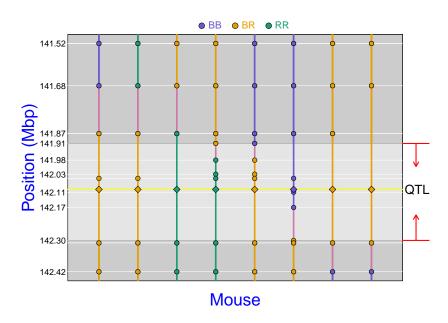
New genotypes: 10 more markers (0.39 Mbp)



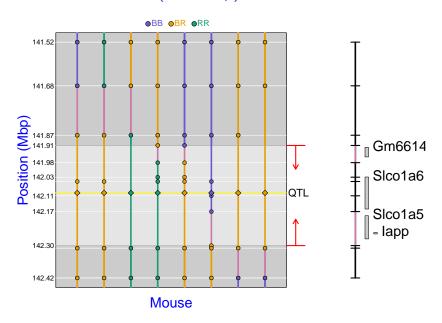
New genotypes: 10 more markers (0.39 Mbp)



New genotypes: 10 more markers (0.39 Mbp)



Genes in the interval (0.39Mbp)



Summary

- ▶ Islet-specific trans-eQTL band affecting \sim 2500 transcripts
- ightharpoonup Expression pattern of non-recombinant mice ightharpoonup QTL genotypes of recombinant mice
- Adding markers targeting the crossovers reduced the QTL interval
 - ▶ Interval: $13\text{Mpb} \rightarrow 3.39\text{Mbp} \rightarrow 0.39\text{Mbp}$
 - ▶ Protein Coding Gene: 87 → 23 → 4

Acknowledgements

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