

Fine-mapping a trans-eQTL hotspot

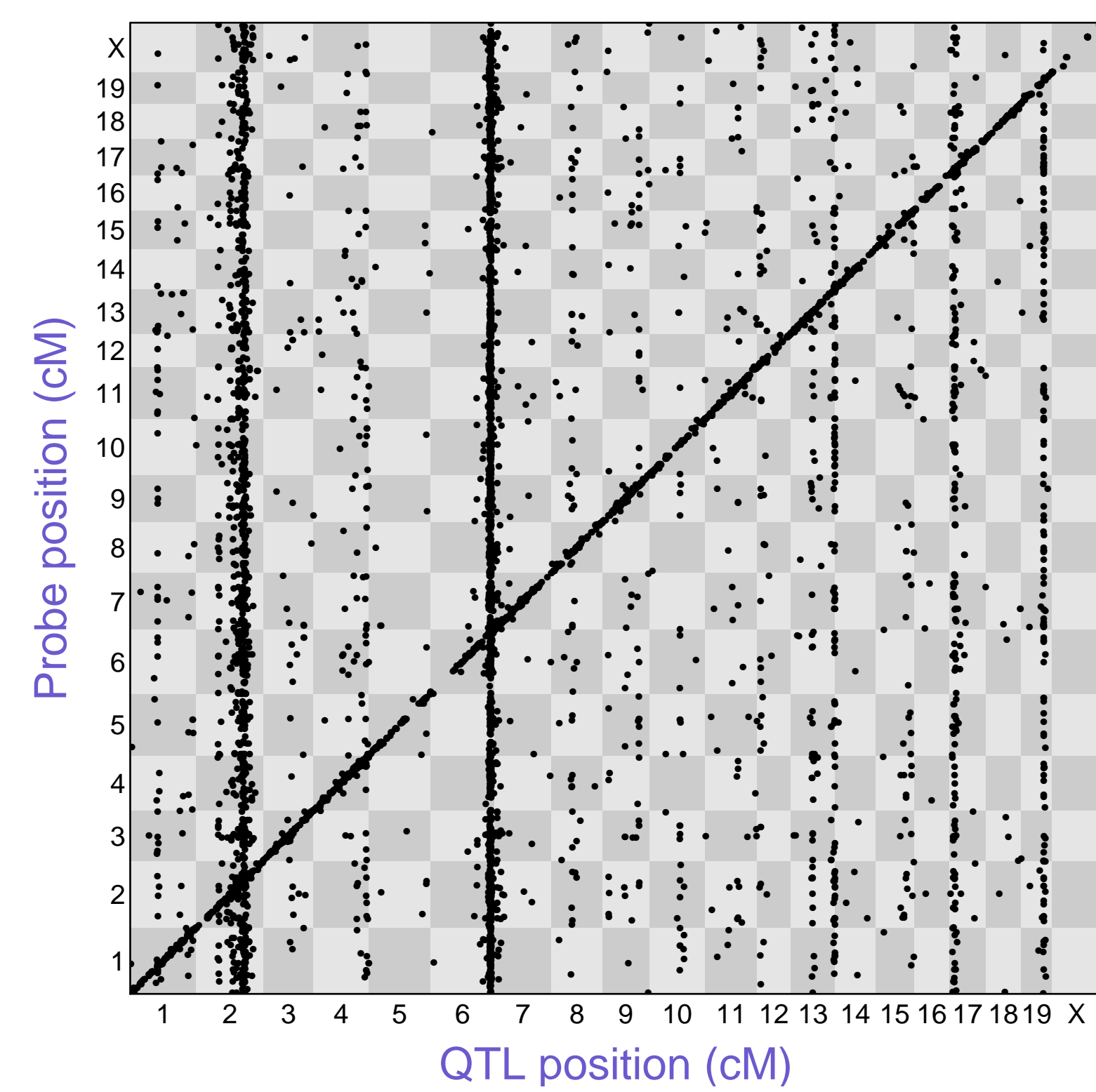
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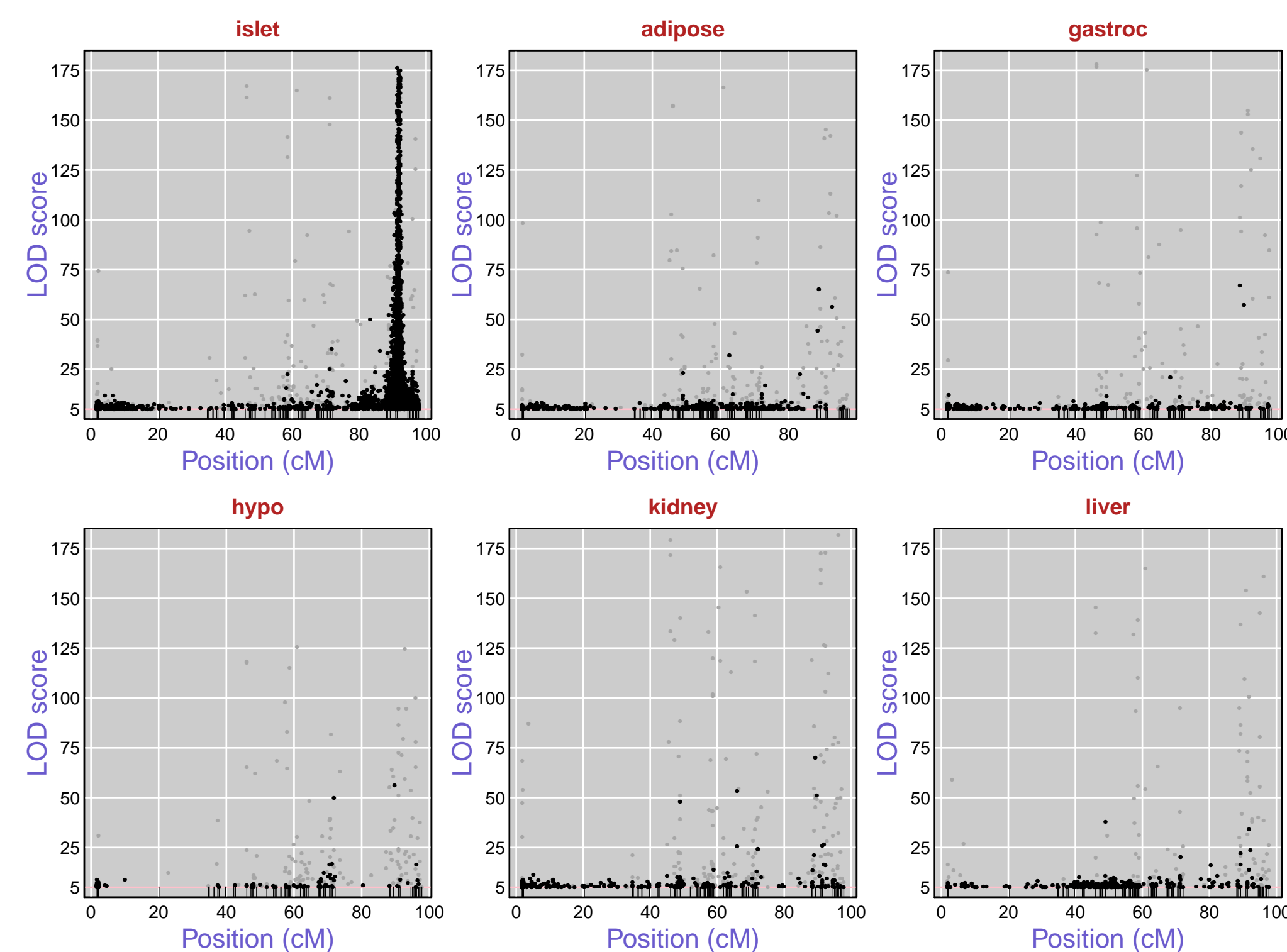
C57BL/6J (B6) × BTBR intercross

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

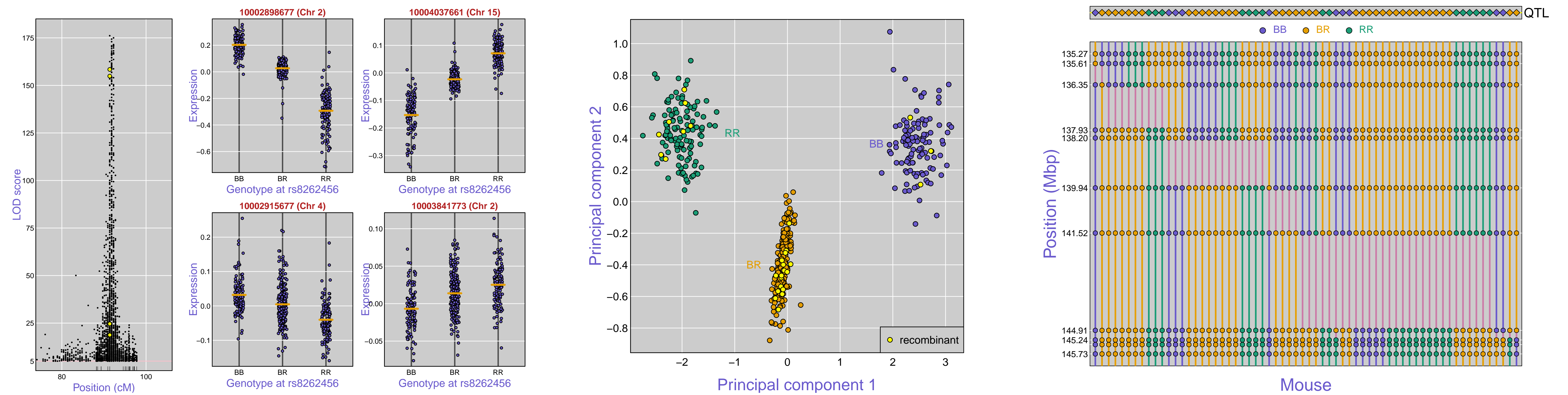
Islet eQTL: cis/trans plot



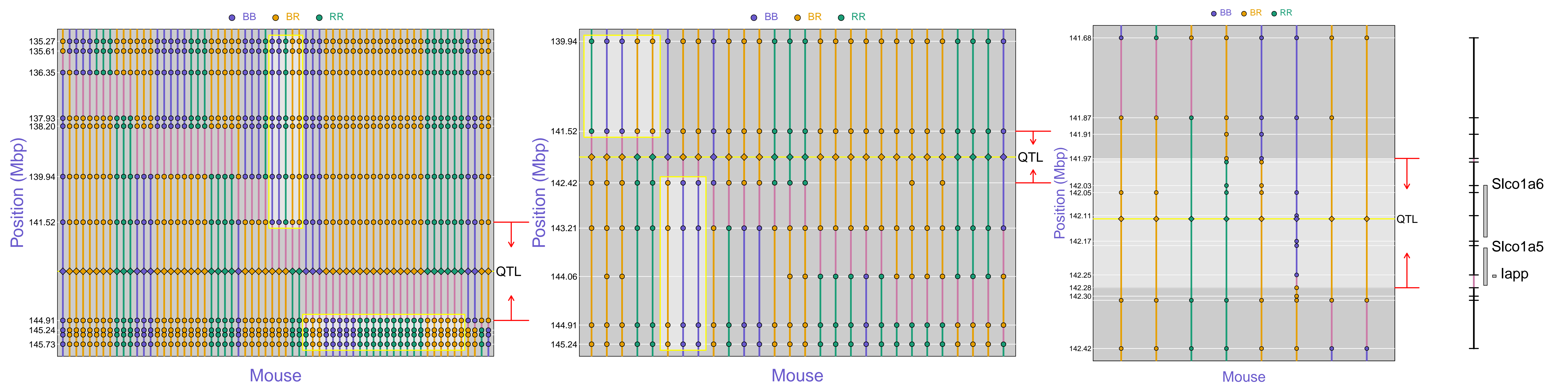
All six tissues, chr 6: trans-eQTL



From expression pattern to QTL genotype



Fine-mapping with the help of recombinant mice



Summary

- Islet-specific trans-eQTL band affecting ~ 2500 transcripts
- We use the expression pattern of non-recombinant mice to infer the QTL genotypes of recombinant mice
- Adding markers targeting the crossovers reduced the QTL interval
 - Interval: 13 Mpb → 3.39 Mbp → 0.31 Mbp
 - Protein Coding Gene: 87 → 23 → 3

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