

Dissecting the Genetic Basis of Thermal Tolerance in a Multi-Parental Population of Fruit Flies.

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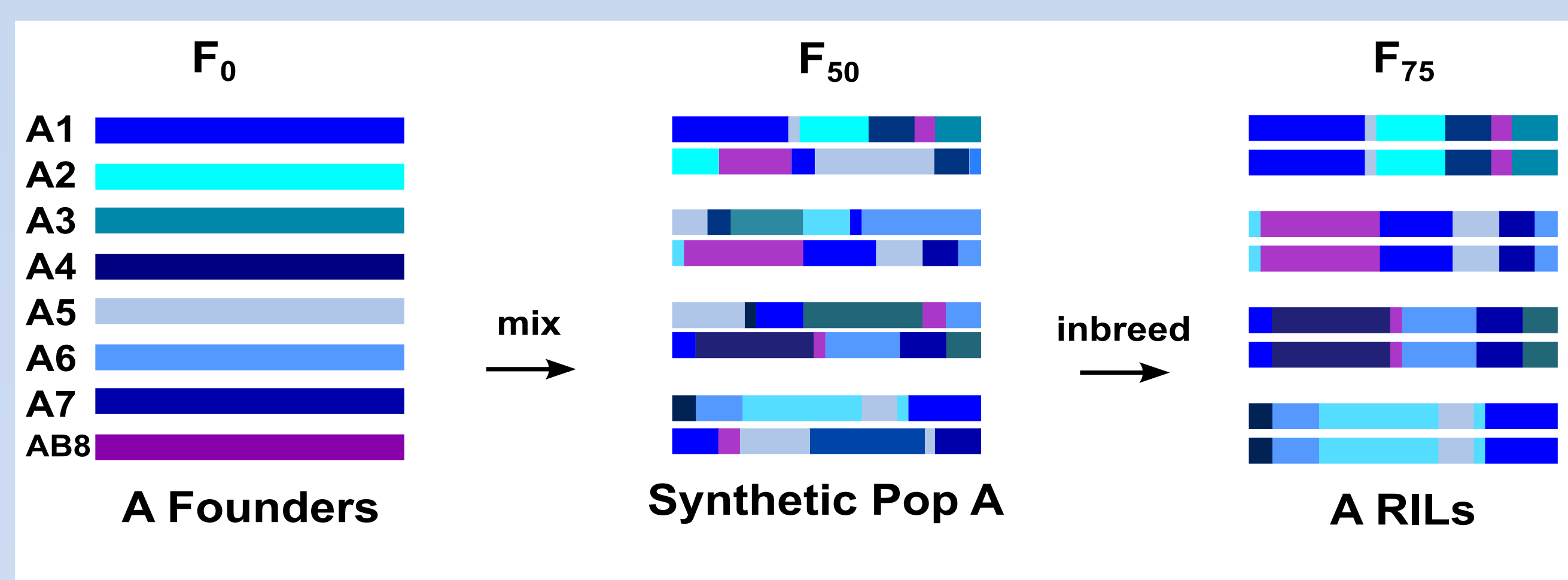


OBJECTIVES

- ❖ Characterize thermal tolerance in the DSPR lines.
- ❖ Identify underlying genetic basis of thermal tolerance in *D. melanogaster*.

BACKGROUND

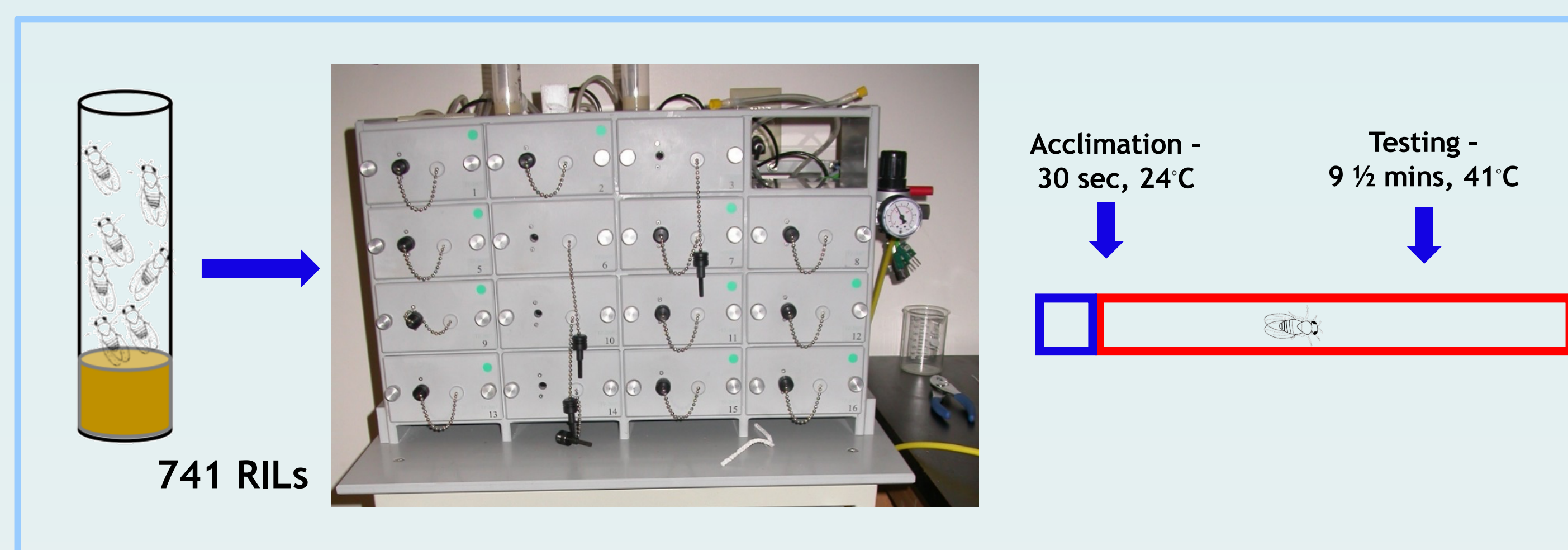
Drosophila Synthetic Population Resource (DSPR)



- ❖ The *Drosophila* Synthetic Population Resource (DSPR) is multi-parental (founders) intercrossed panel of *D. melanogaster* (fruit flies).
- ❖ The population was then mixed for 50 generations, which created a mosaic of synthetic populations.
- ❖ After another 25 generations of full sibling mating, a panel of 800 (population A) recombinant inbred lines (RILs) were generated, whose genomes are a fine-scale mosaic of segments from the parental lines (segment sizes average ~3 cM).

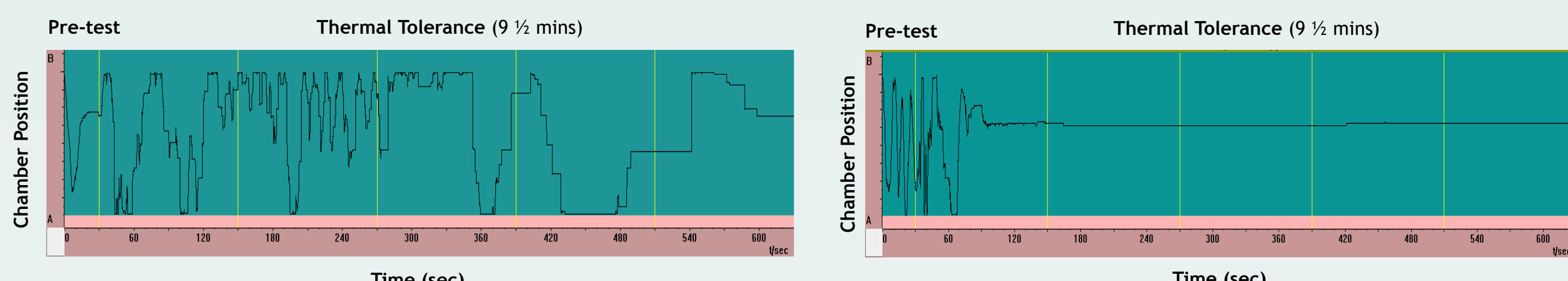
PHENOTYPING

Phenotyping Thermal Tolerance within the Heat Box



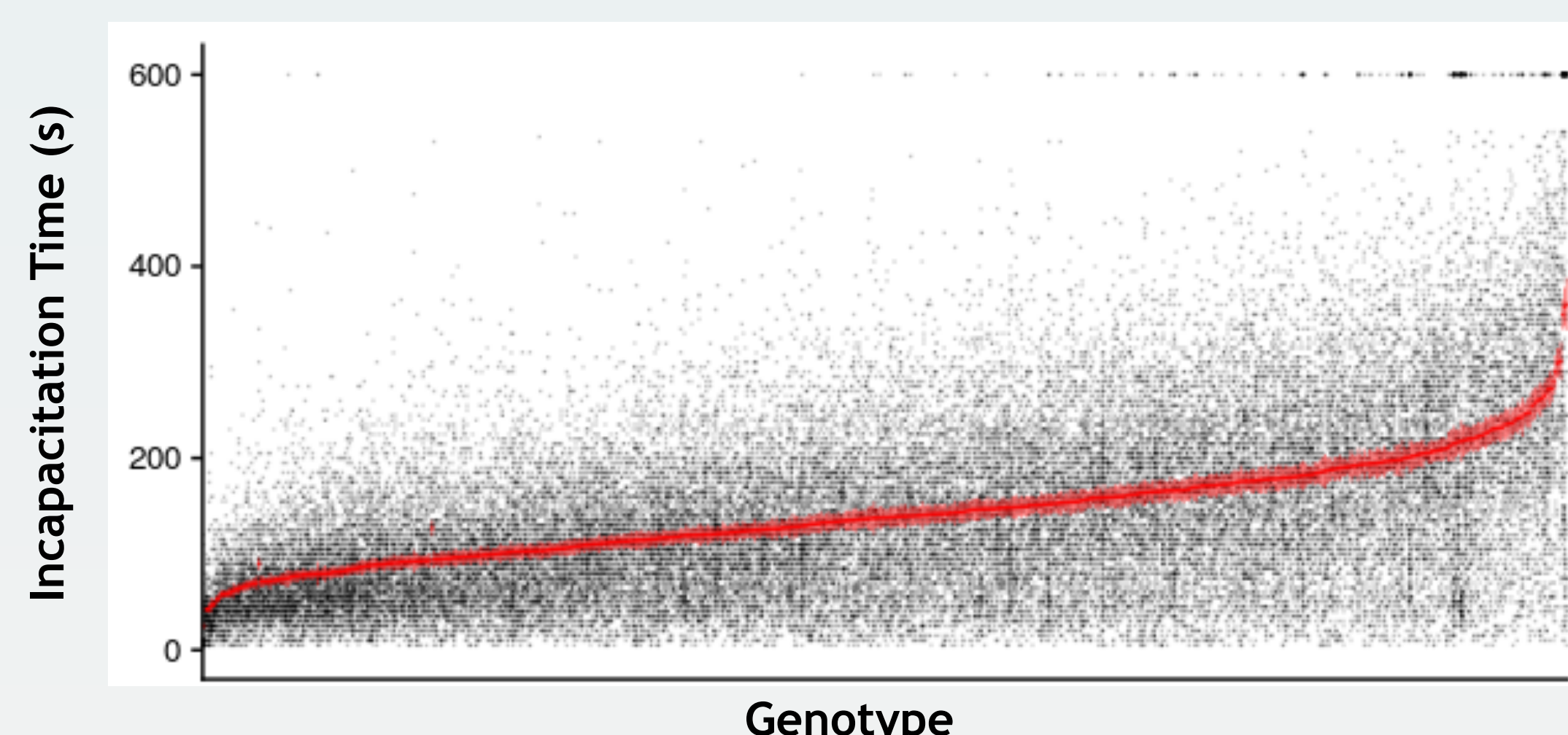
High Thermal Tolerance

Low Thermal Tolerance



- ❖ Position Traces showing the responses of a single fly within the heat box.

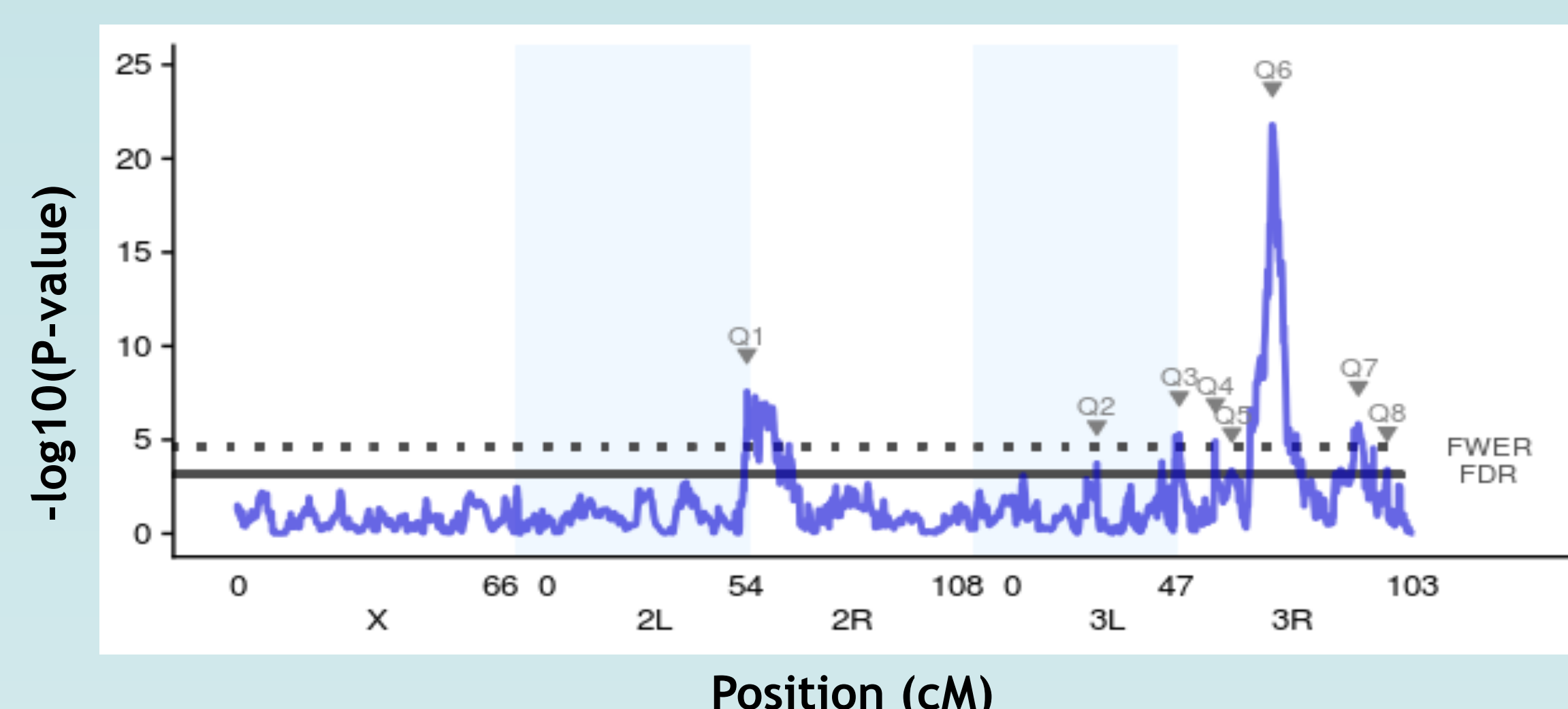
Phenotypic Variation in 39,392 Individuals



- ❖ Incapacitation time of 741 RILs (39,392 individuals), ordered from minimum to maximum. For each RIL we measured at least 40 female flies. Black dots represent individuals within a RIL and red bars represent SEM.

Quantitative Trait Loci (QTL) Mapping

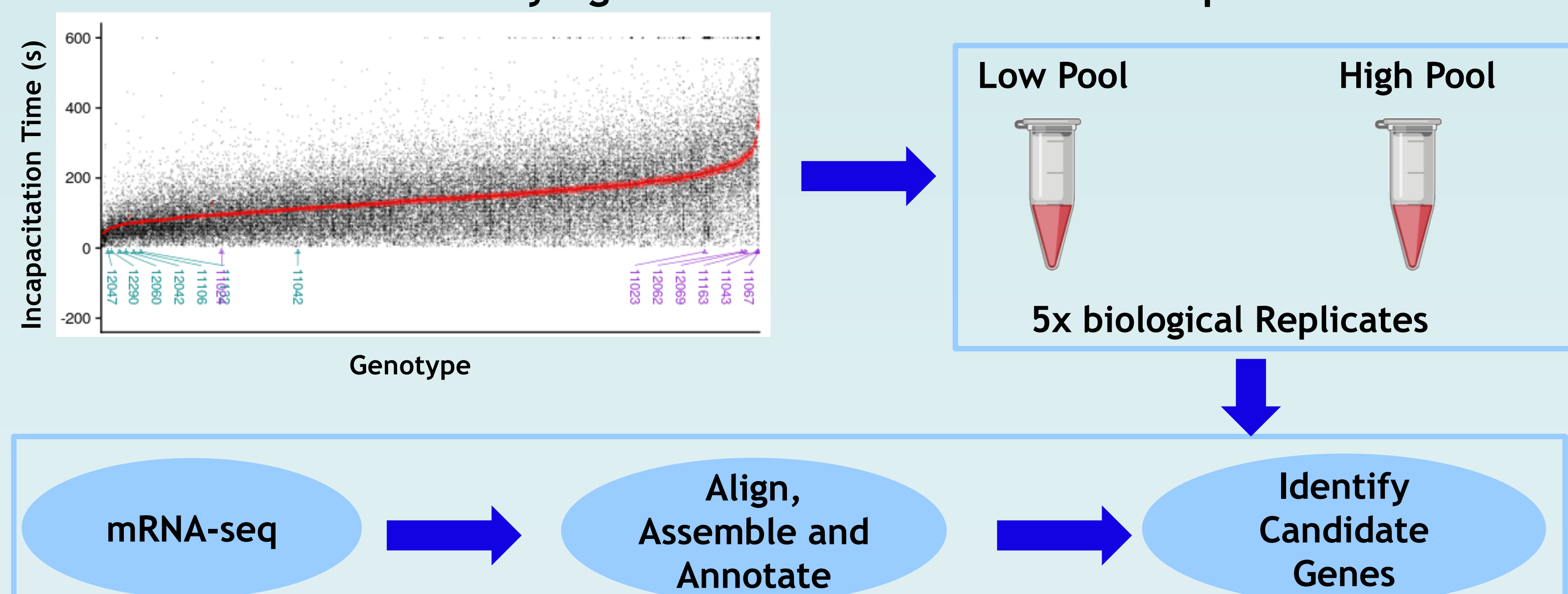
Several QTLs Influence Thermal Tolerance



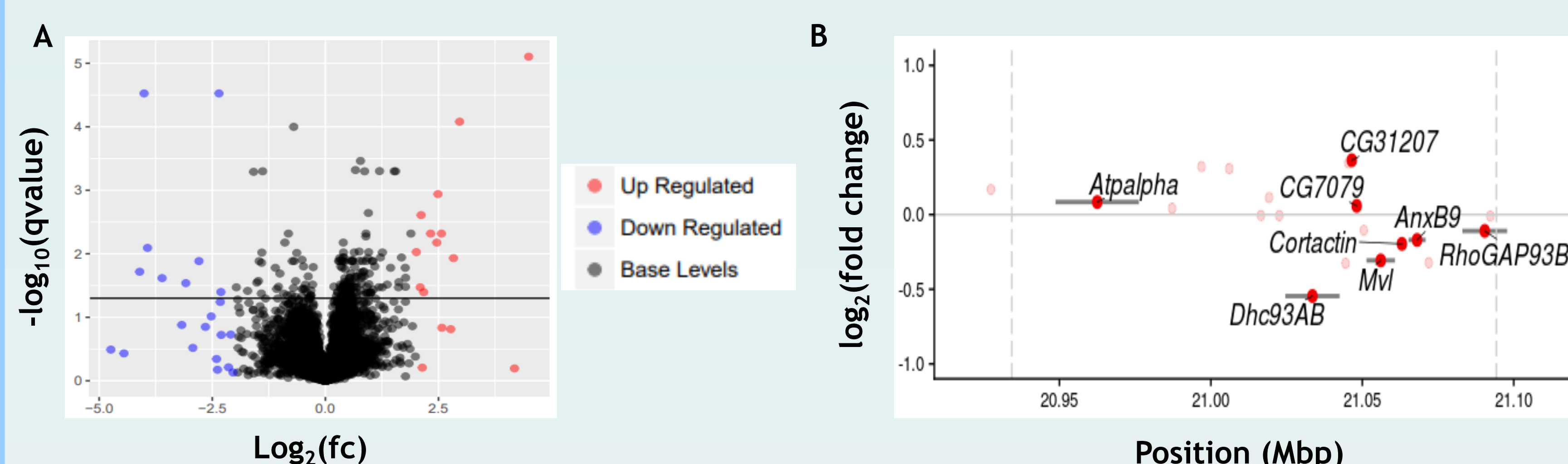
- ❖ QTL of phenotypic traits of 741 RILs. Blue line represents QTLs. Solid black line represents the false discovery rate (FDR) and black dotted line family-wise error rate (FWER). Any QTL passing the threshold is influencing thermal tolerance in the DSPR.

IDENTIFYING CANDIDATE GENES

Identifying Candidate Genes via RNA-seq



Candidate Genes in Thermal Tolerance



- ❖ A) Volcano plot showing the 2 fold change difference of gene expression in bottom and top cohorts of thermal tolerance. A total of 184 genes were significantly differentially expressed. Every dot represents a gene: black dots are base levels expression, red are up-regulated genes, and blue are down-regulated. Any point that passes the threshold of .05, is considered significant, and are candidate genes that are influencing the traits.
- ❖ B) QTL6 BCI region (vertical lines) showing differentially expressed genes. Brightly colored red dots represents significant differentially expressed genes (labeled). Any dot above the horizontal line is up-regulated, whereas those below are down-regulated.

CONCLUSIONS

- ❖ There is a wide phenotypic variation in thermal tolerance in the DSPR RILs.
- ❖ There are several significant QTL that influence thermal tolerance.
- ❖ There are several candidate genes that are differentially expressed within QTL regions.

FUTURE PLANS

- ❖ Fine map regions under QTL peaks.
- ❖ Validate candidate genes.

REFERENCES

- ❖ King, E.G., et al., 2012. *Properties and power of the Drosophila Synthetic Population Resource for the routine dissection of complex traits*. Genetics 191(3): 935 – 949.
- ❖ King, et al., 2012. *Genetic dissection of a model complex trait using the Drosophila Synthetic Population Resource*. Genome Research 22(8): 1558-1566.

ACKNOWLEDGEMENT

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