Improving artificial selection, breaking linkage using Correlated Trait mapping.

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The authors declare no conflict of interest.

## Abstract

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## Introduction

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## Material & Methods

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### Genes

We pre-selected genes in the following categories:

Cluster of differentiation: 63  
Interleukines: 43  
Major histocompatibility complex of the mouse: 26  
Angiotensin-converting enzymes: 6  
Estrogen Receptor: 20  
Amyloid precursor protein: 3  
Obesity related: 19  
Natriuretic Peptide: 9  
Cyclin: 35  
Tumor related: 81  
Heat shock proteins: 81

Datasets  
GN111 - Hippocampus mRNA  
GN206 - Hippocampus mRNA  
GN207 - Eye mRNA  
GN239 - Kidney mRNA  
GN318 - Hypothalamus mRNA  
GN469 - Adipose mRNA  
GN709 - Retina mRNA

## Results

1) We discover more regions of interest, which are not found by QTL mapping

2) CTL mapping gives information which loci regulate correlation between different traits

3) CTL allows us to define define groups, and visualize resulting networks using cytoscape

## Conclussion and Discussion

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## Bibliography

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## Additional Files

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### Tables / Table legends

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### Figures / Figure legends

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