**Genome-wide Linkage Scan**  
(4,793 expression phenotypes in 1,065 sibpairs from 45 pedigrees)

- t>4: 1,681 expression phenotypes  
  (70 proximal, 1,574 distal, 37 both)

**QTDT: confirmation and fine mapping**  
(all members of 45 pedigrees)

- Proximal: 100 phenotypes with informative genotypes tested:  
  63 phenotypes with P≤0.001

- Distal: 1,517 phenotypes (linkage peaks < 20 Mb  
  & transcripts identified by RNA-Seq)  
  103 phenotypes with P<0.001; 518 with P<0.01;  
  917 with P<0.05.

**Population Association**  
(n=86) Of 63 phenotypes:  
47 with P<0.005

**Differential Allelic Expression**  
Of 63 phenotypes, 43 showed DAE  
(RNA-Seq; P<0.01, chi-square)

**Population Association**  
(n=86) Of 917 phenotypes: 58 with P<0.005; 318 P<0.05

- **siRNA**  
  (expression of 13 target genes changed significantly (P<0.05, t-test) following knockdown of their regulators. Cells: B-cells (n=4 to 6); Fibroblasts (n=2))

- **Metabolic Perturbation**  
  (expression of 4 target genes changed significantly, P<0.005, after addition of insulin that changed expression of INSR. Cells: Fibroblasts (n=4))