

Discovering new Alzheimer disease related genes and gene networks through systems biology methods

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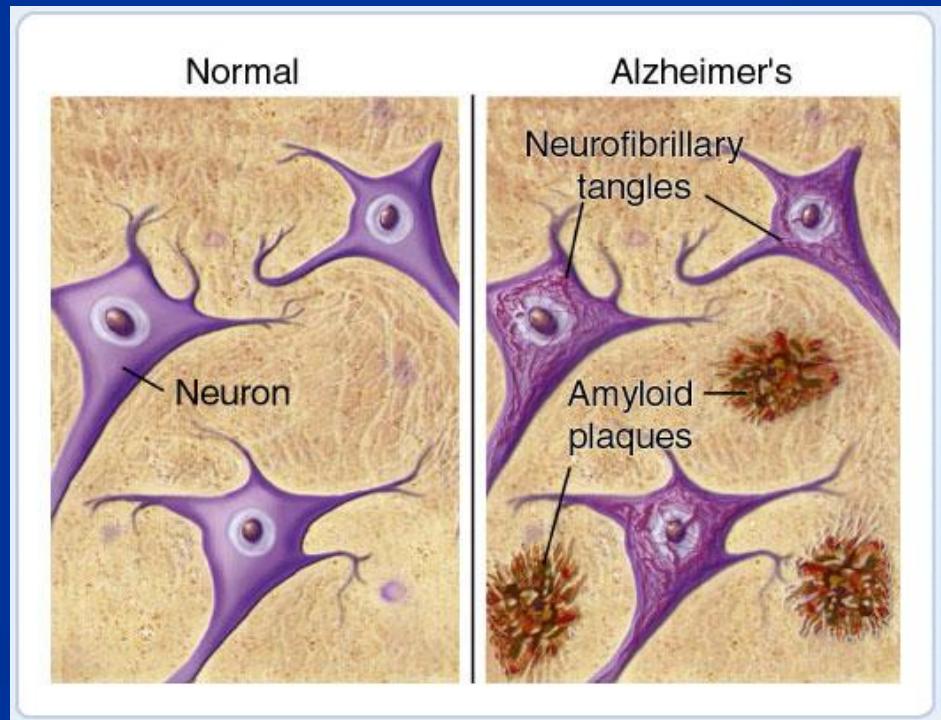
Background of Alzheimer's Disease (AD)



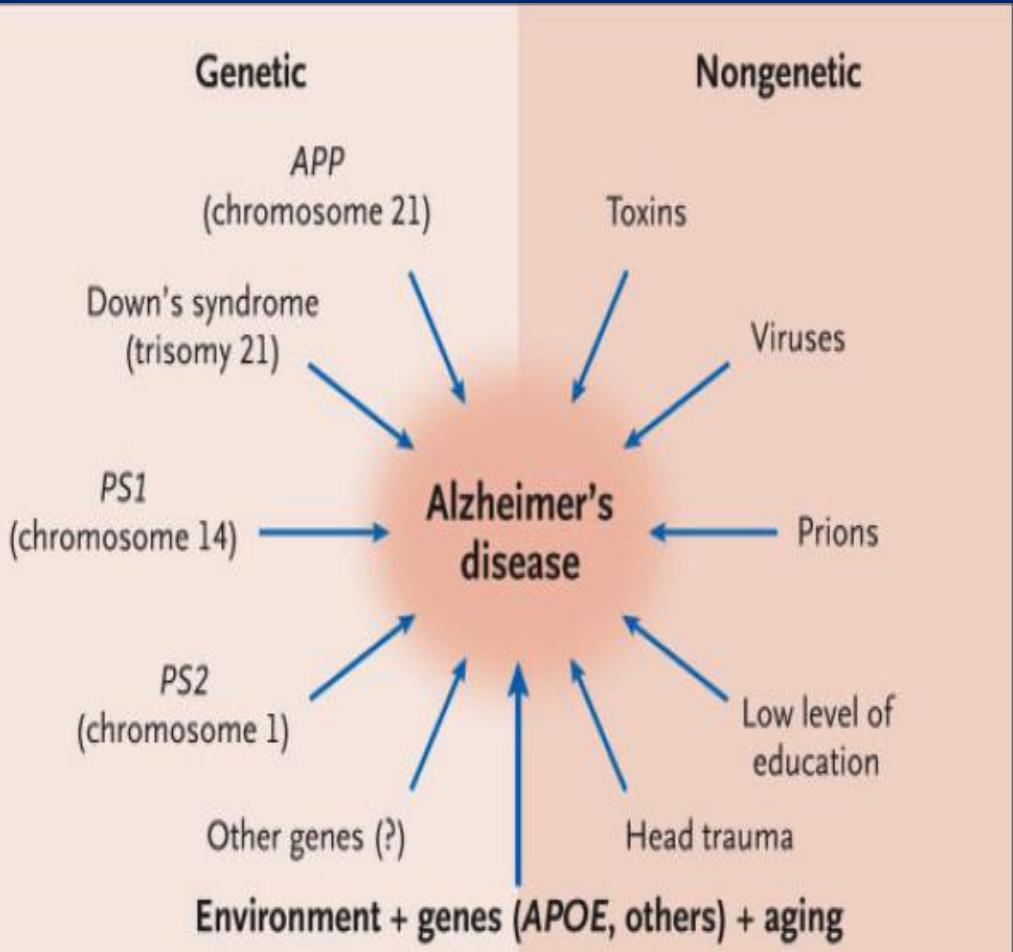
- ◆ One of most common neurodegenerative diseases
- ◆ First described by Alois Alzheimer in 1906 and was named after him
- ◆ There are about 27 million sufferers worldwide
- ◆ AD is predicted to affect 1 in 85 people globally by 2050

Features of Alzheimer's Disease

- ◆ Symptoms: memory loss, cognitive impairment, language breakdown, bodily function loss
- ◆ Neuropathology:
 - Amyloid plaques
 - Neurofibrillary tangles
- ◆ Brain regions:
 - Hippocampus
 - Basal forebrain
 - Cortex



Known causal factors of AD



- ◆ Aging
- ◆ Genetics (APP, APOE, PS1, PS2, etc)
- ◆ Environment (Toxins, Stress, Head trauma, etc)

Several competing hypotheses to explain cause of AD

- ◆ cholinergic hypothesis
- ◆ amyloid hypothesis
- ◆ tau hypothesis
- ◆ myelin hypothesis
- ◆ oxidative stress hypothesis
- ◆ gene mutation hypothesis

Tons of report about AD

alzheimer's disease ... <http://www.ncbi.nlm.nih.gov/sites/entrez>

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[VEGF and central nervous system diseases.]
1. Zhang LY, Fan YY, Liu Z. Zhejiang Da Xue Xue Bao Yi Xue Ban. 2009 Nov;38(6):644-648. Chinese. PMID: 20014493 [PubMed - as supplied by publisher]

Germline humanization of a murine Abeta antibody and crystal structure of the humanized receptor
2. Robert R, Streitsov VA, Newman J, Pearce LA, Wark KL, Dolezal O. Protein Sci. [Epub ahead of print] PMID: 20014445 [PubMed - as supplied by publisher]

Patient death as a censoring event or competing risk event in models of nursing home placement
3. Szychowski JM, Roth DL, Clay OJ, Mittelman M. Stat Med. [Epub ahead of print] PMID: 20014354 [PubMed - as supplied by publisher]

Intracerebral Transplantation of Bone Marrow-Derived Mesenchymal Stem Cells Reduces Amyloid-Beta Deposition and Rescues Memory Deficits in Alzheimer's Disease
4. Mice by Modulation of Immune Responses.
Lee JK, Jin HK, Endo S, Schuchman EH, Carter JE, Bae JS. Stem Cells. [Epub ahead of print] PMID: 20014009 [PubMed - as supplied by publisher]

Memory deficit in patients with subcortical vascular cognitive impairment versus Alzheimer-type dementia: the sensitivity of the 'word list' subtest on the Wechsler Memory Scale-III
5. Suades-Gonzalez E, Jodar-Vicente M, Perdriz-Solas D. Rev Neurol. 2008 Dec 16;49(12):623-629. Spanish. PMID: 20013713 [PubMed - as supplied by publisher]

Freeze-Fracture Electron Microscopy on Domains in Lipid Mono- and Bilayer on Nano-Resolution Scale
6. Desai-Bedjani-Pant S, Chambers D.

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► Coenzyme Q10 effects in neurodegenerative [Neuropsychiatr Dis Treat. 2009]

Most of researches are isolated and separated

Systems Biology:

*An integrative bioinformatic approach
to translate between DNA sequence
polymorphism, gene expression,
phenotype, genotype and disease
susceptibility*

**Systems Genetics is one kind of
Systems Biology**

What is Systems Genetics?

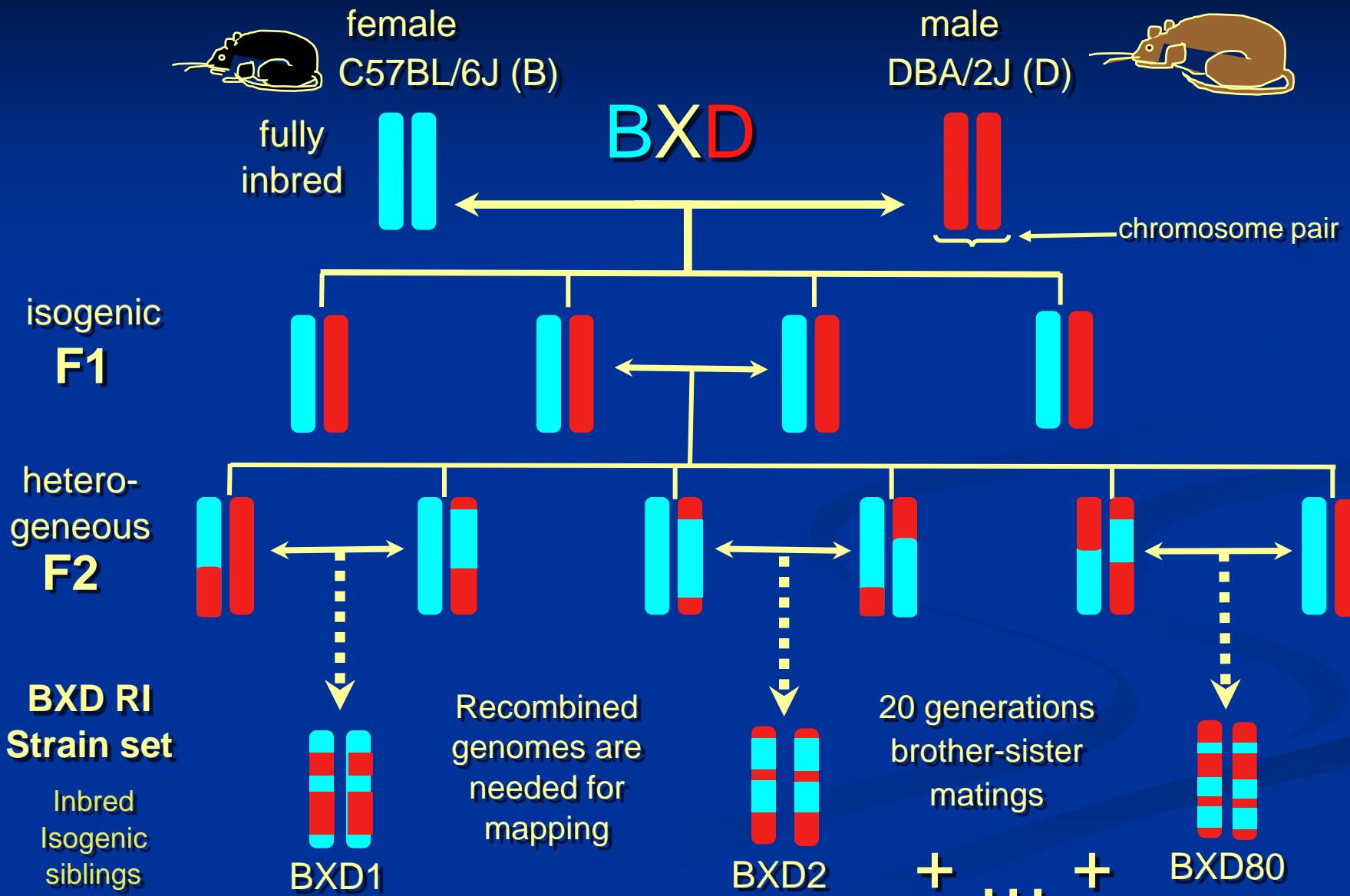
Mendelian Genetics = One gene to one trait
Huntington's disease, albinism, etc.

Complex Trait Genetics = Several genes to one trait
Most of phenotypes or human diseases

Systems Genetics = Many genes, gene pathways
and gene networks to many traits
Advanced approach to study human diseases

Systems Genetics requires:
Dense phenotypes and genotypes
Gene expression data
Genetic Reference Populations

How to make genetic reference population



Multiscale integration & cumulative data

environmental responses

disease resistance or susceptibility

structure

physiology

behavior

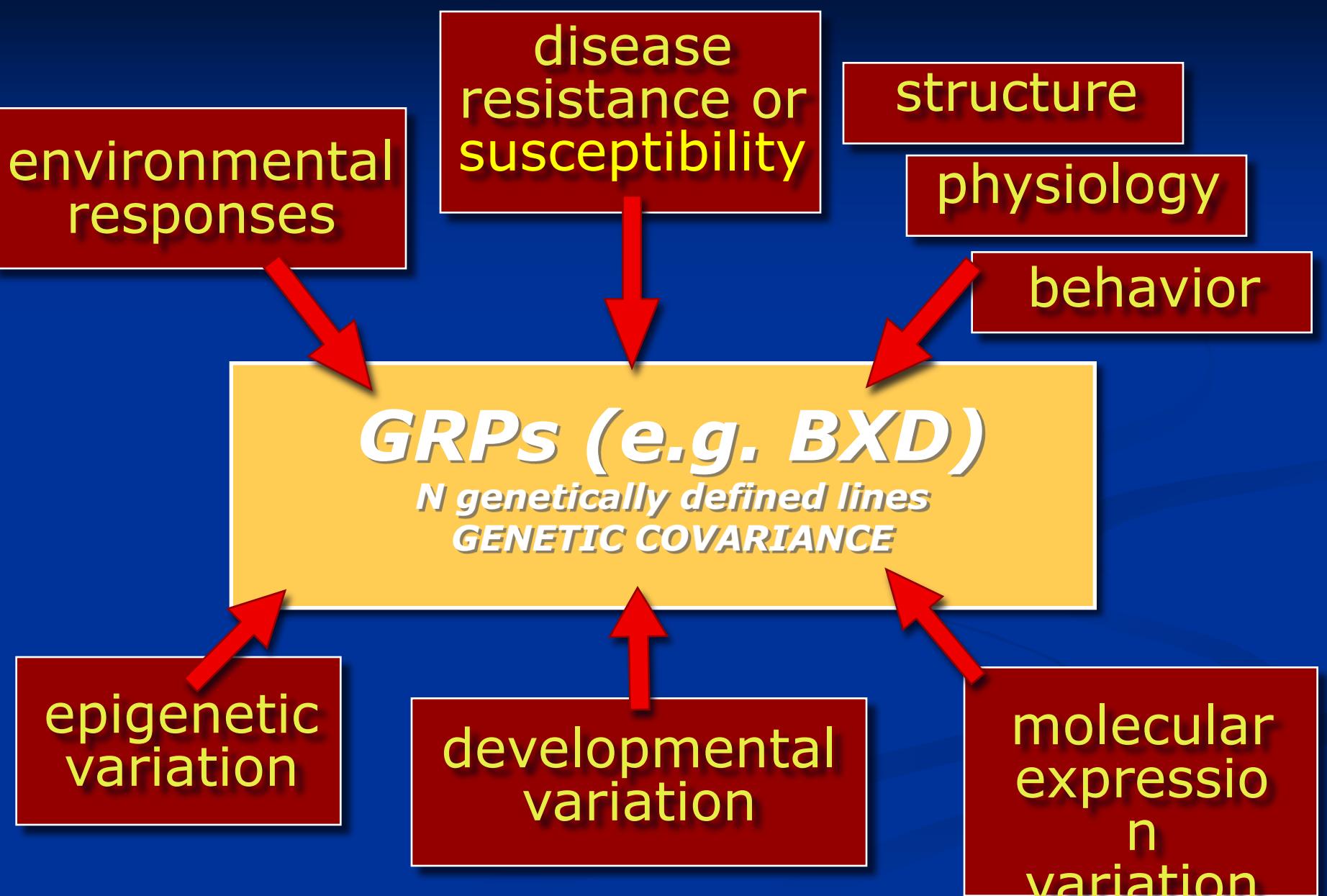
GRPs (e.g. BXD)

N genetically defined lines
GENETIC COVARIANCE

epigenetic variation

developmental variation

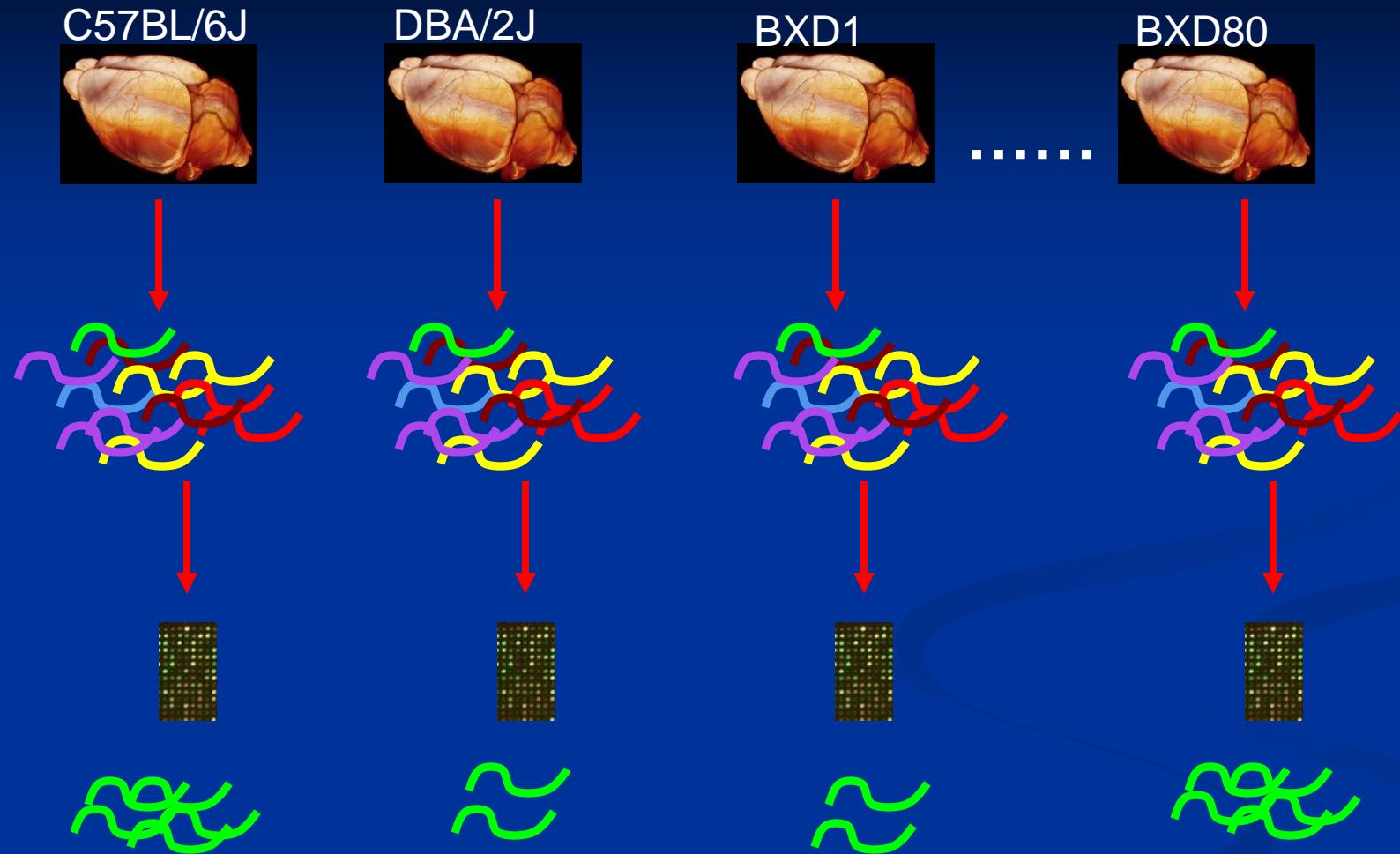
molecular expression variation



Complex (or Quantitative) Traits

- They are determined by multiple gene loci (polygene) and multiple environmental inputs.
- As a result, such traits tend to be normally distributed.
- A quantitative trait locus (QTL) is a site on a chromosome containing a gene or

Gene Expression

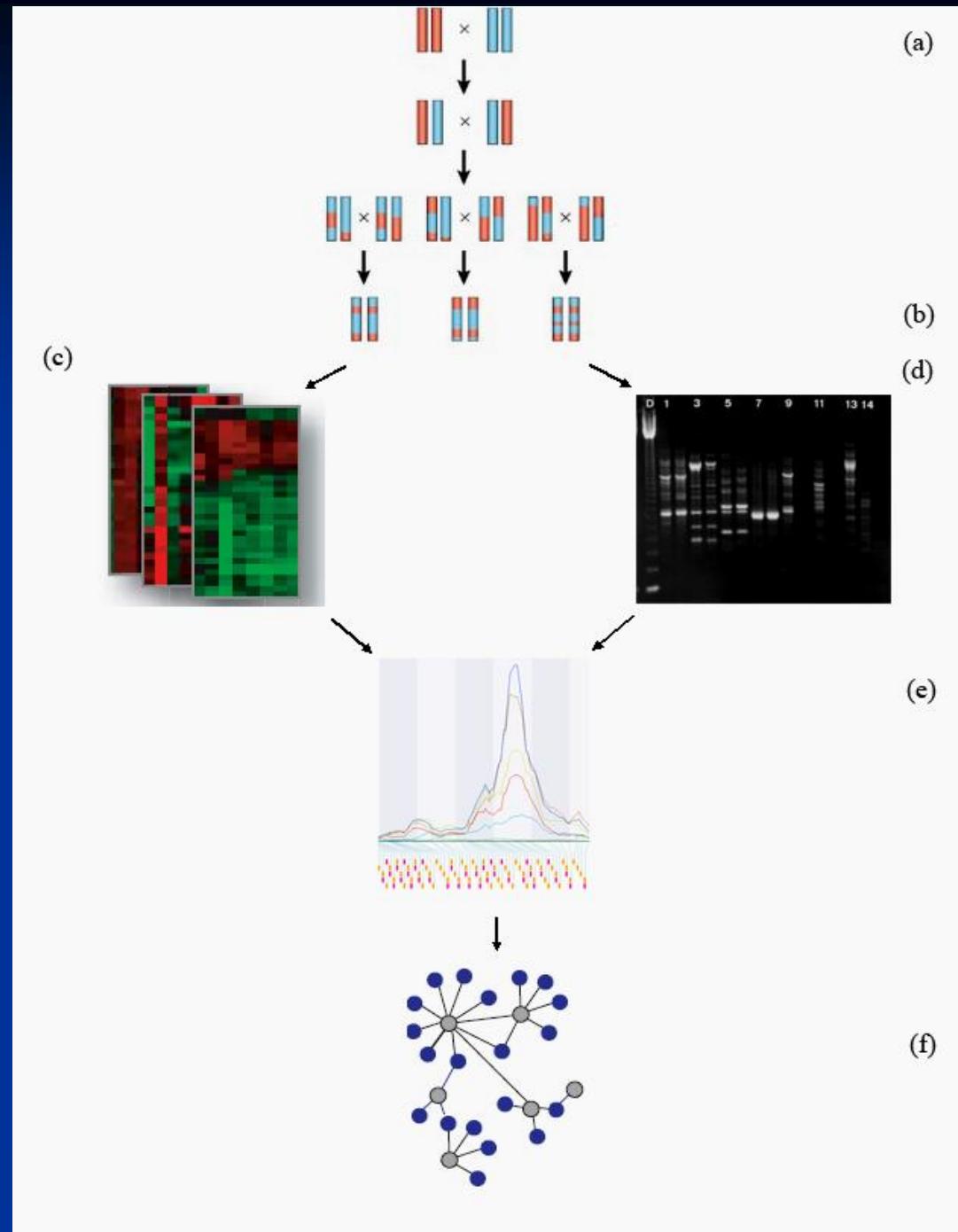


Quantify the amount of specific species of mRNA in each strain

Genetic genomics

Find expression QTL
(eQTL) that control
gene expression level
using linkage analysis

- (a) Inbreeding of animals
- (b) Genetic reference populations (GRP)
- (c) Expression from whole genome microarray
- (d) Genotype
- (e) Transcriptome-QTL mapping
- (f) Gene network building



Collection of AD related genes



ISI Web of KnowledgeSM



There are 366 genes that could be related to AD.

Fresh hippocampus dissection



Gene expression of hippocampus in BXD RI mice

- ◆ There are 29310 genes that present in hippocampus with expression value above 7.
- ◆ 5397 genes have higher expression in hippocampus with expression value above 10.
- ◆ The expression value of top 100 genes in hippocampus is above 14. Some of those genes have been reported to be related to AD directly or indirectly.

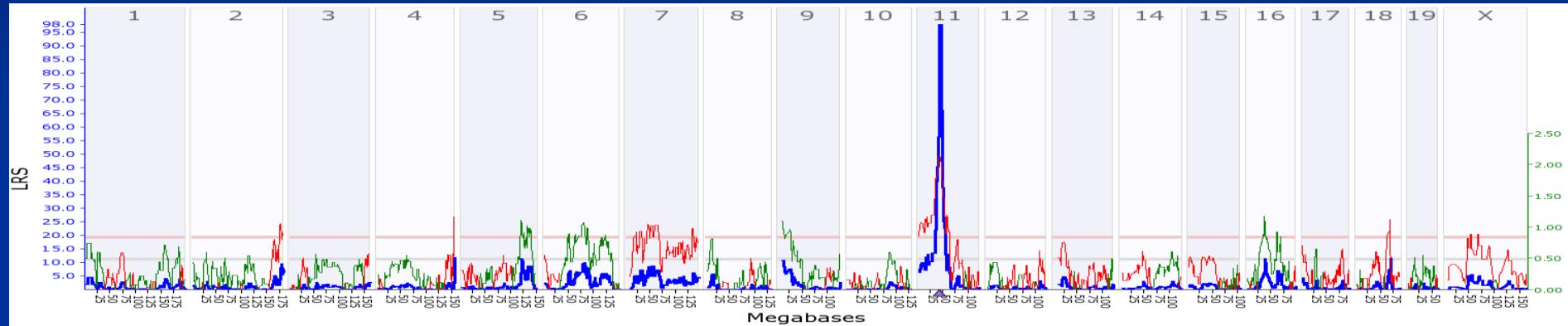
QTL analysis of gene expression in the hippocampus of BXD RI mice

| QTL category | QTL number | Percentage of total probesets | Percentage of total QTL |
|-------------------|------------|-------------------------------|-------------------------|
| significant QTL | 7710 | 26.3 | |
| cis-eQTLs | 3733 | 12.7 | 48.4 |
| trans-eQTLs | 3977 | 13.6 | 51.6 |
| eQTLs with LRS>50 | 1342 | 4.6 | 17.4 |

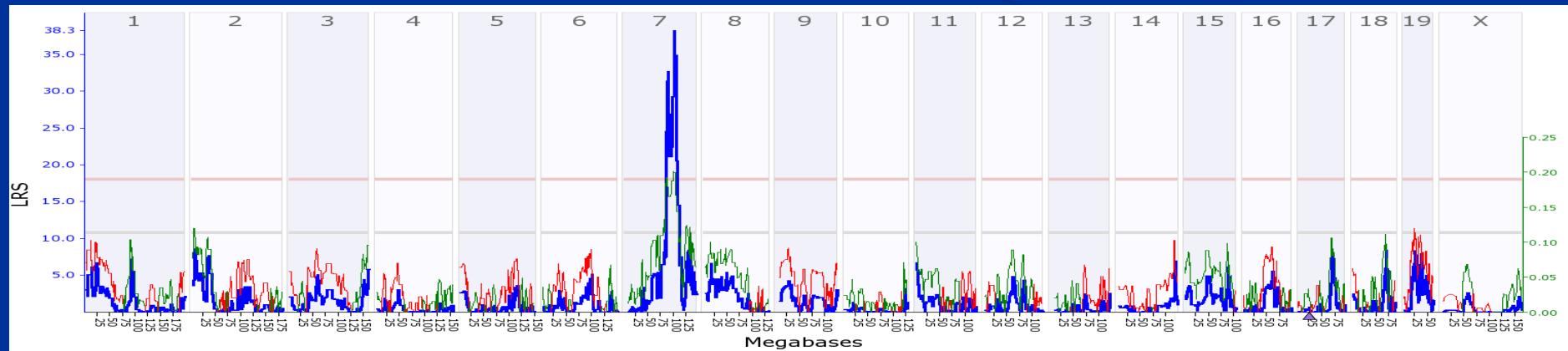
There are total 29310 present probesets

Local vs distant expression linkages

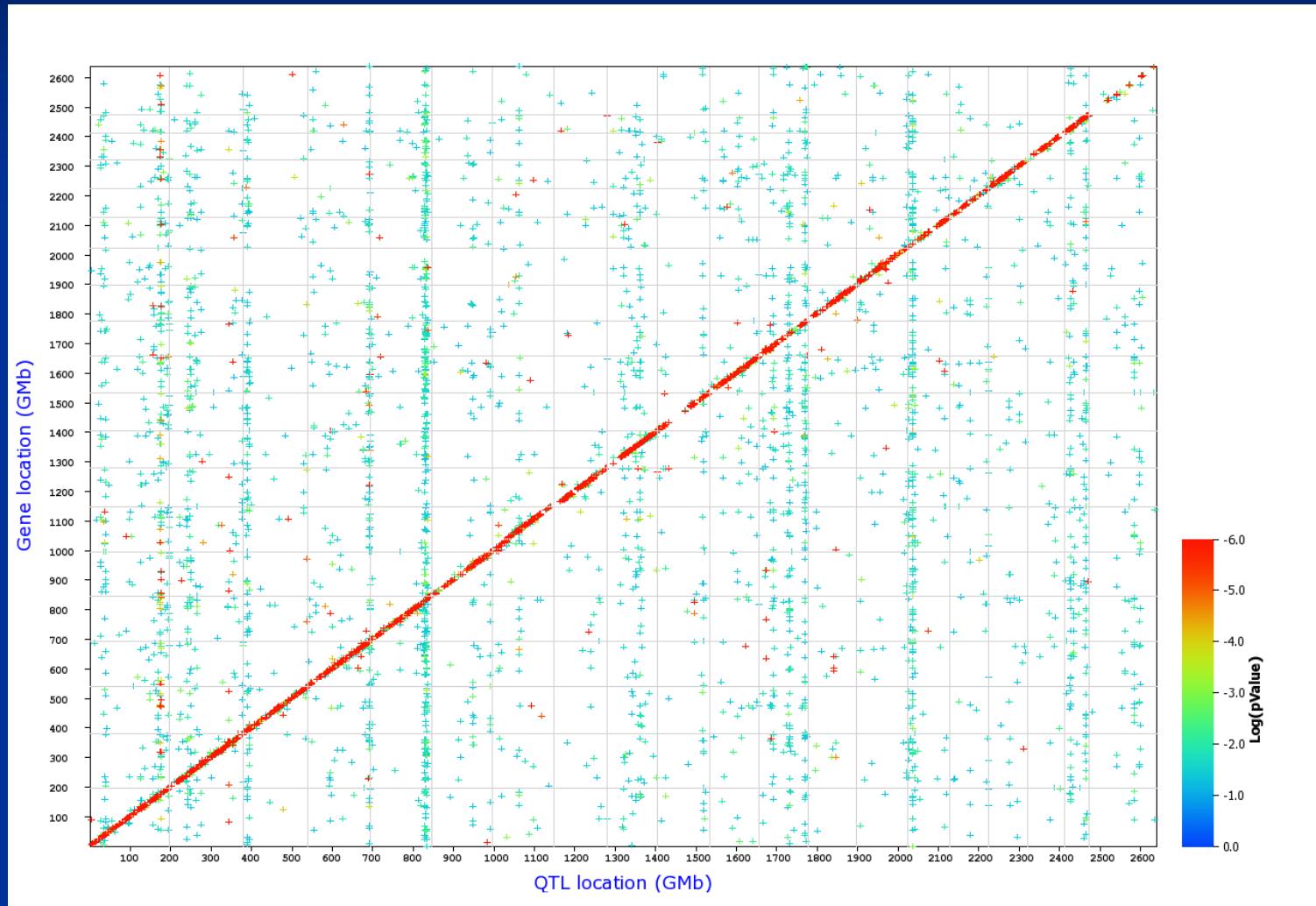
Local linkage or putative cis - modulation (e.g., Pttg1)



Distant linkage or putative trans - modulation (e.g., Axin1)



Distribution of QTLs across the genome



Expression analysis of AD related genes

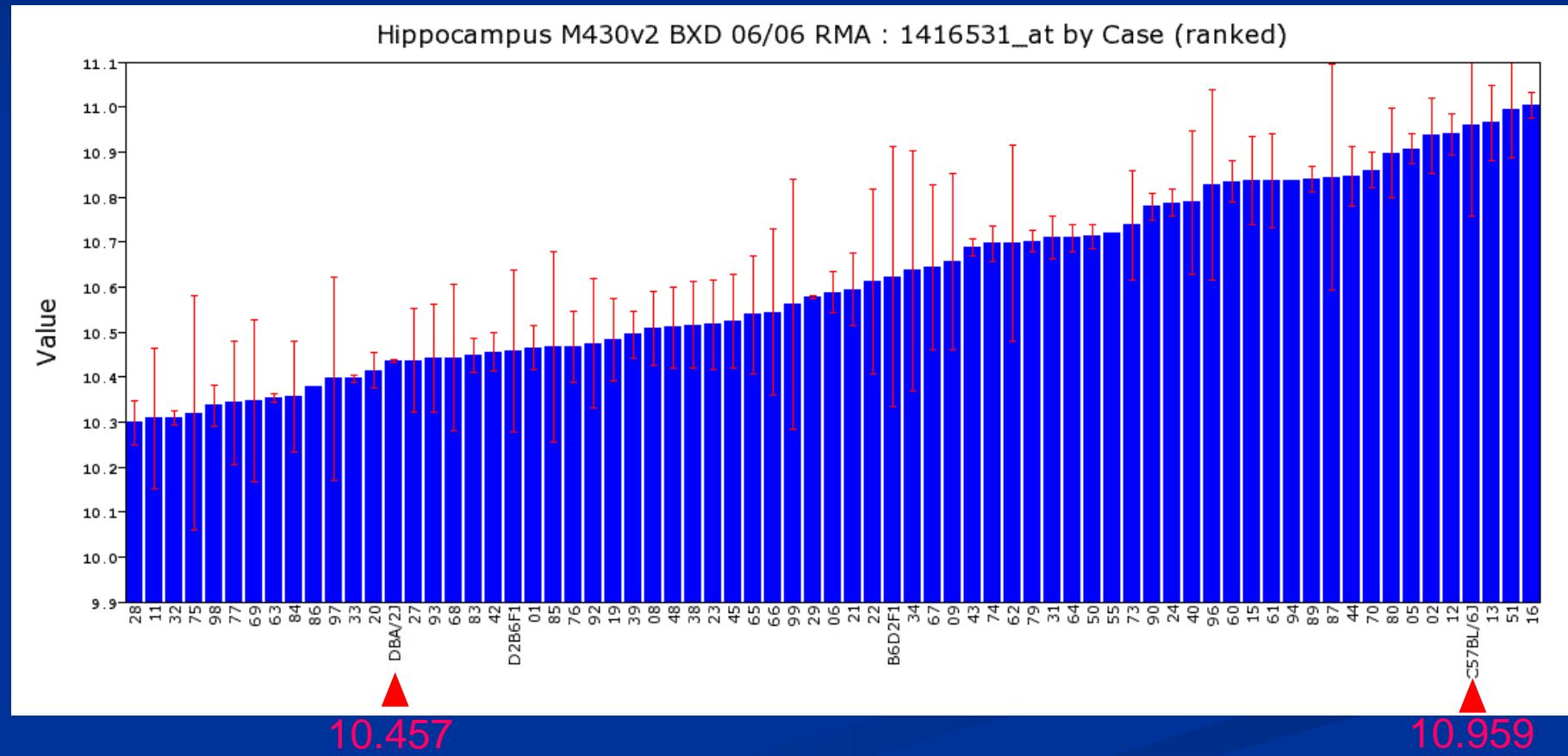
There are total 366 AD related genes found through literature search.

There are 130 genes whose expression are controlled by eQTL

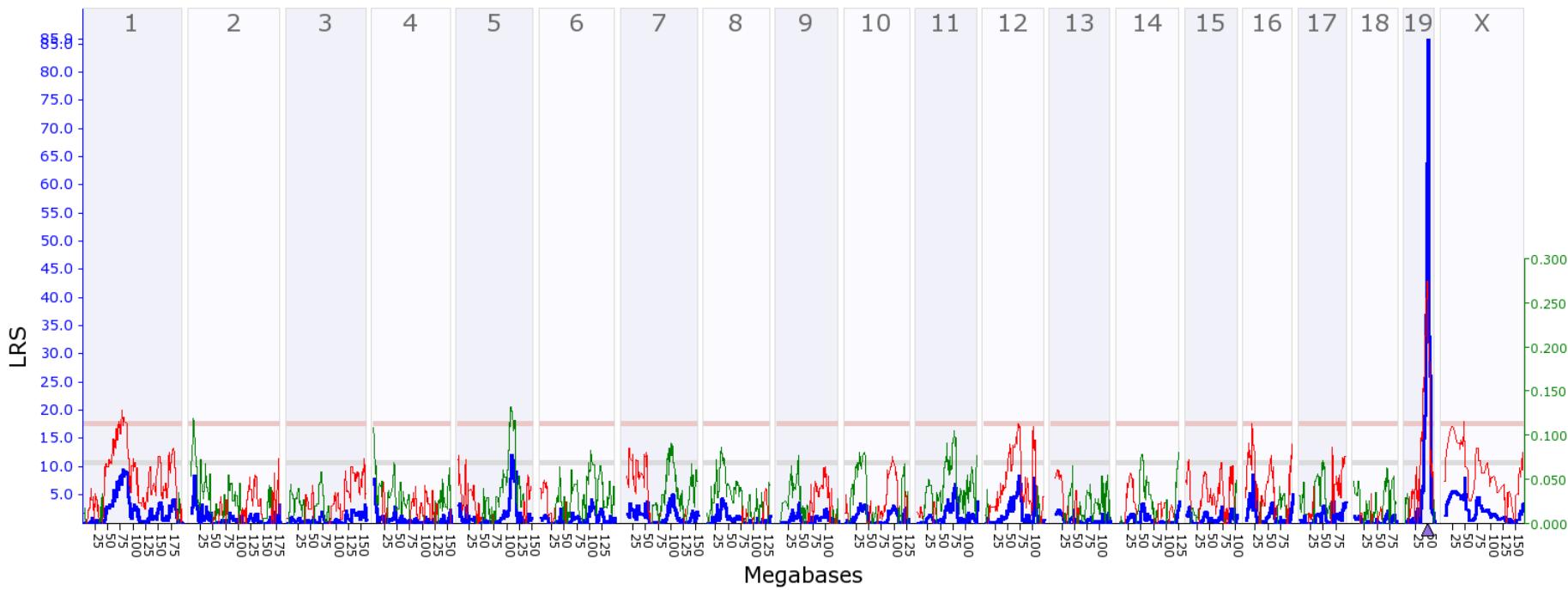
Expression of 64 genes is controlled by local sequence variants (cis-eQTL)

Expression of 66 genes is controlled by other region of the genome (trans-eQTL)

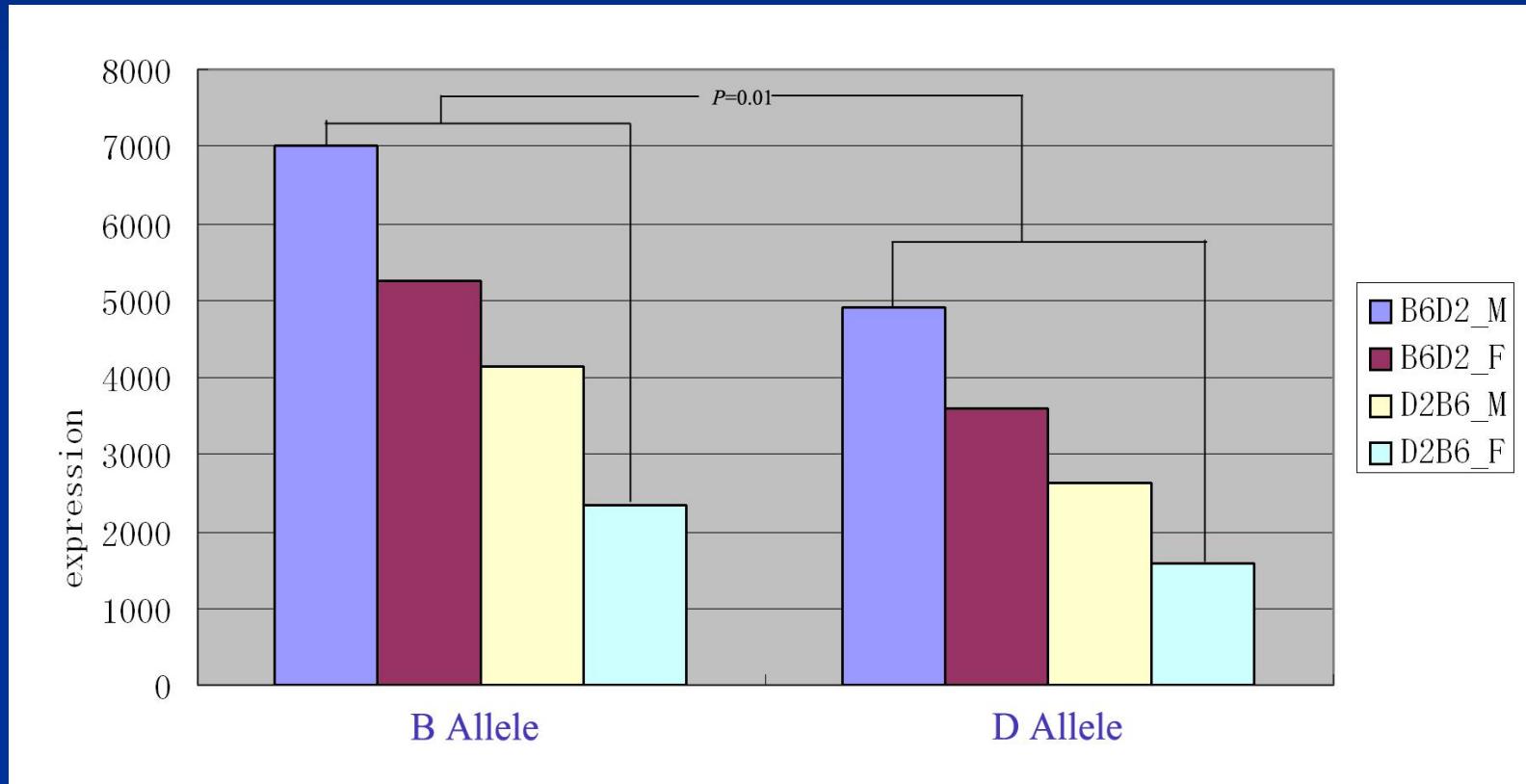
Expression of *Gsto1* gene (Probeset 1416531) in the hippocampus of BXD RI mice



eQTL Mapping for *Gsto1* in Hippocampus of BXD mice

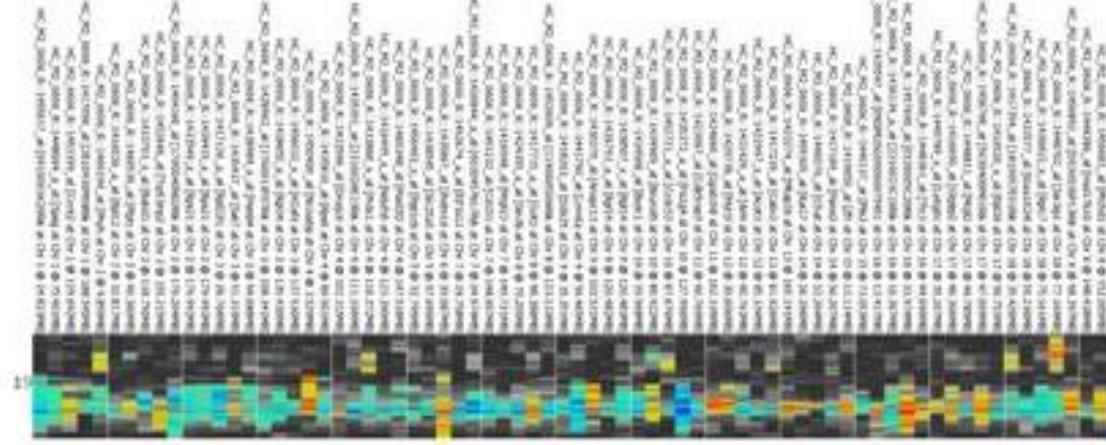


Allele-specific expression assay (ASE) analysis of *GstO1* gene



Downstream gene analysis of Gsto1

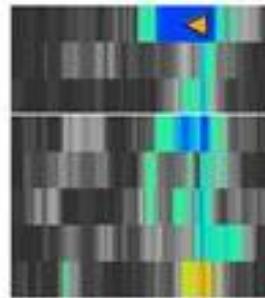
A



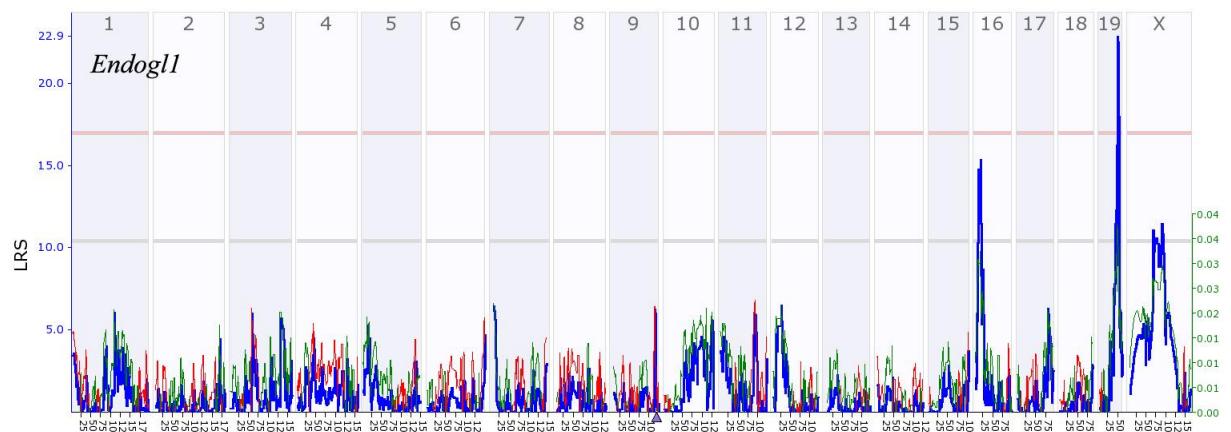
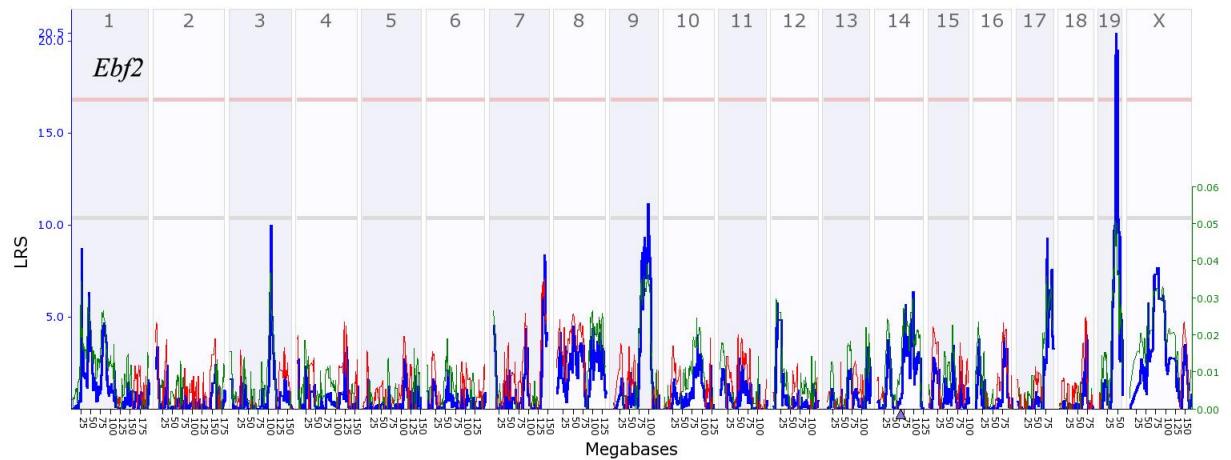
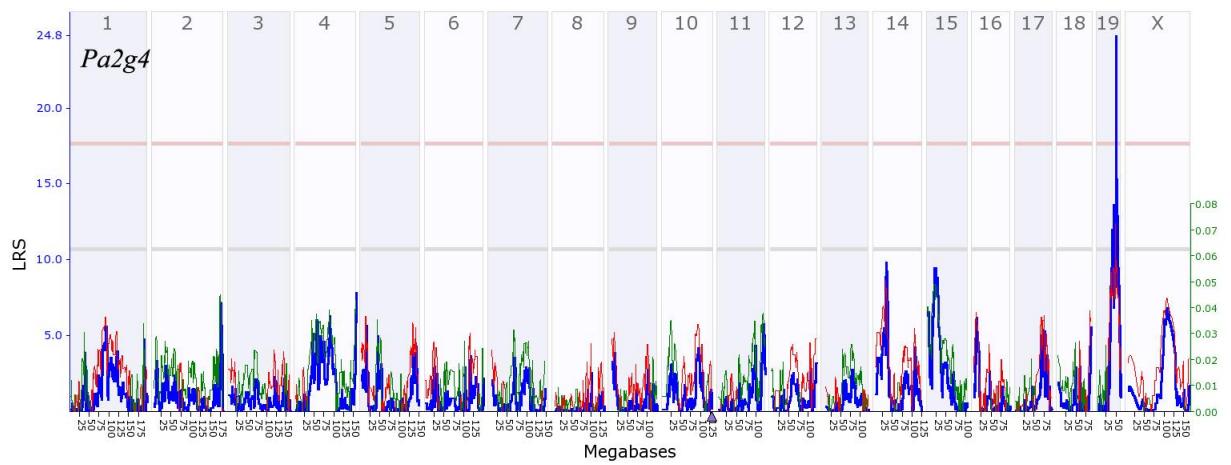
C57BL/6J +
DBA/2J +

B

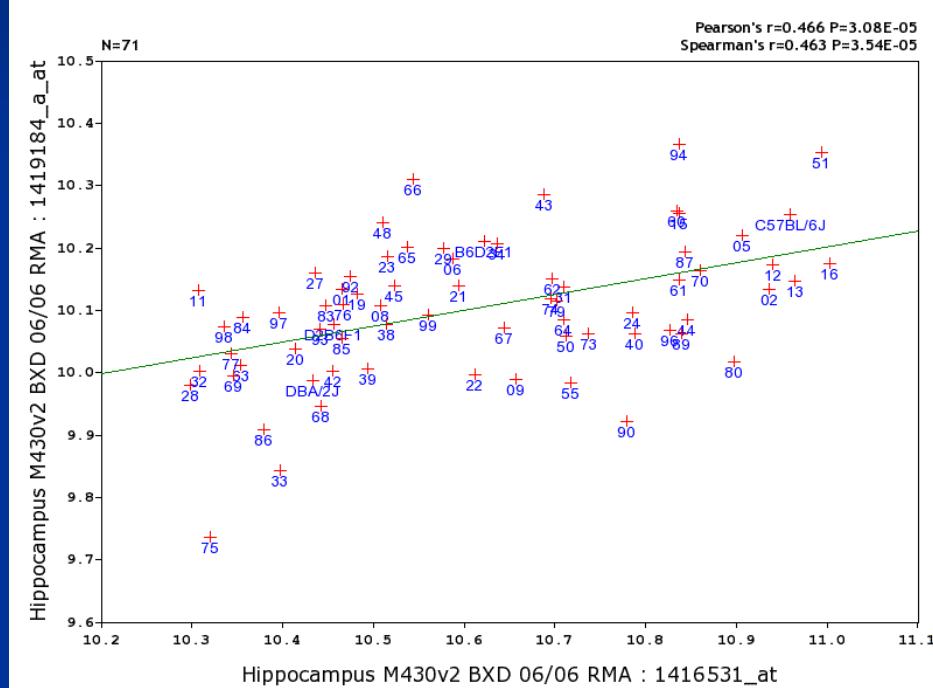
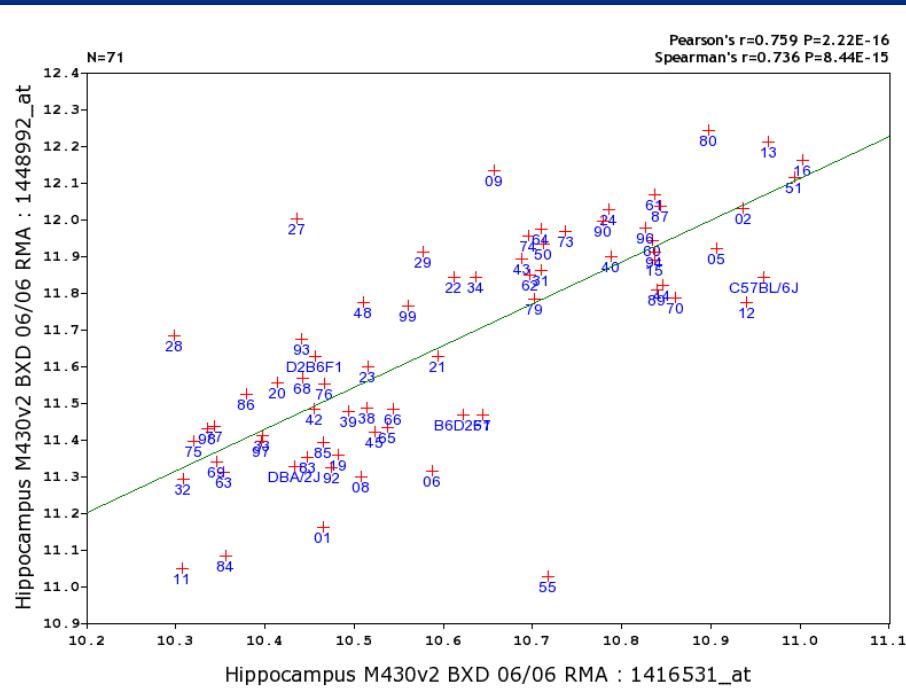
HC_M2_0606_R::1416531_at [Gsto1 at Chr 19 @ 47.939MB]
HC_M2_0606_R::1417189_at [Psme2 at Chr 14 @ 56.207MB]
HC_M2_0606_R::1416948_at [Mirpl23 at Chr 7 @ 149.721MB]
HC_M2_0606_R::1426844_a_at [6030457N17Rik at Chr 7 @ 34.974MB]
HC_M2_0606_R::1456462_x_at [Ppp1cb at Chr 5 @ 32.795MB]
HC_M2_0606_R::1460348_at [Mad2l2 at Chr 4 @ 147.518MB]
HC_M2_0606_R::1428962_at [1700013F07Rik at Chr 3 @ 108.341MB]
HC_M2_0606_R::1460536_at [Ptprj at Chr 2 @ 90.360MB]



Chrome 19



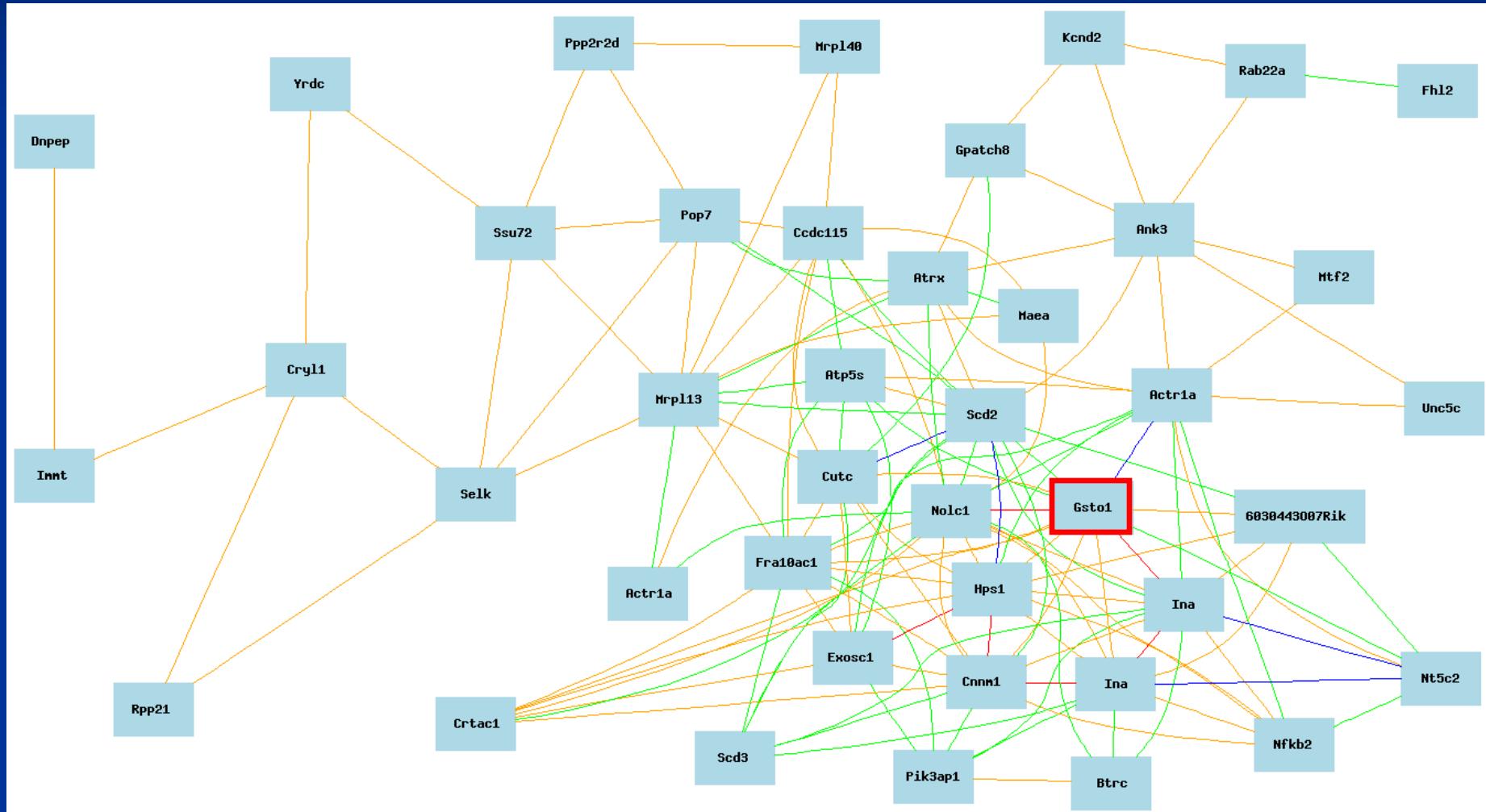
Correlation plot



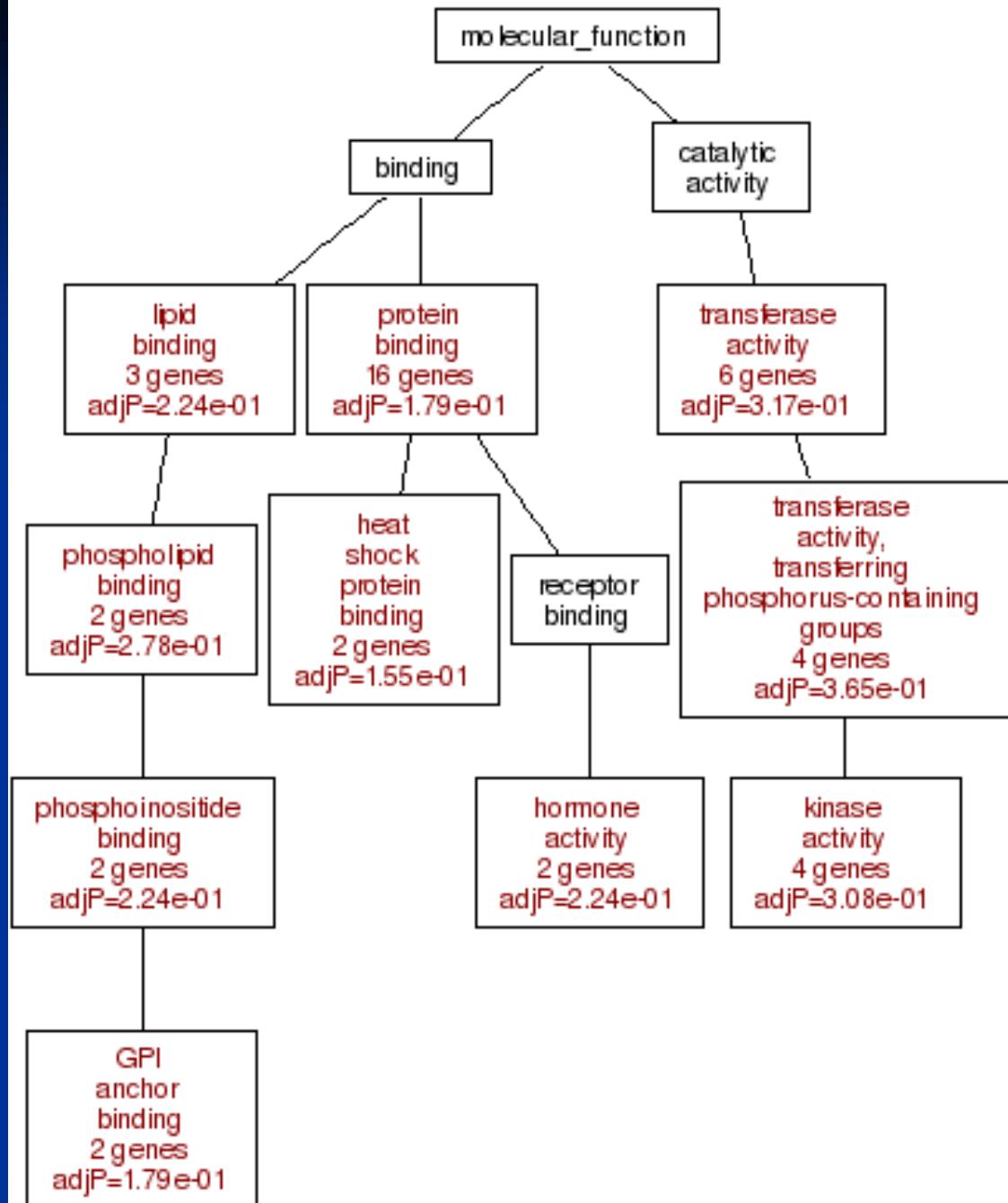
Gstol1&Ina

Gstol1&Fhl2

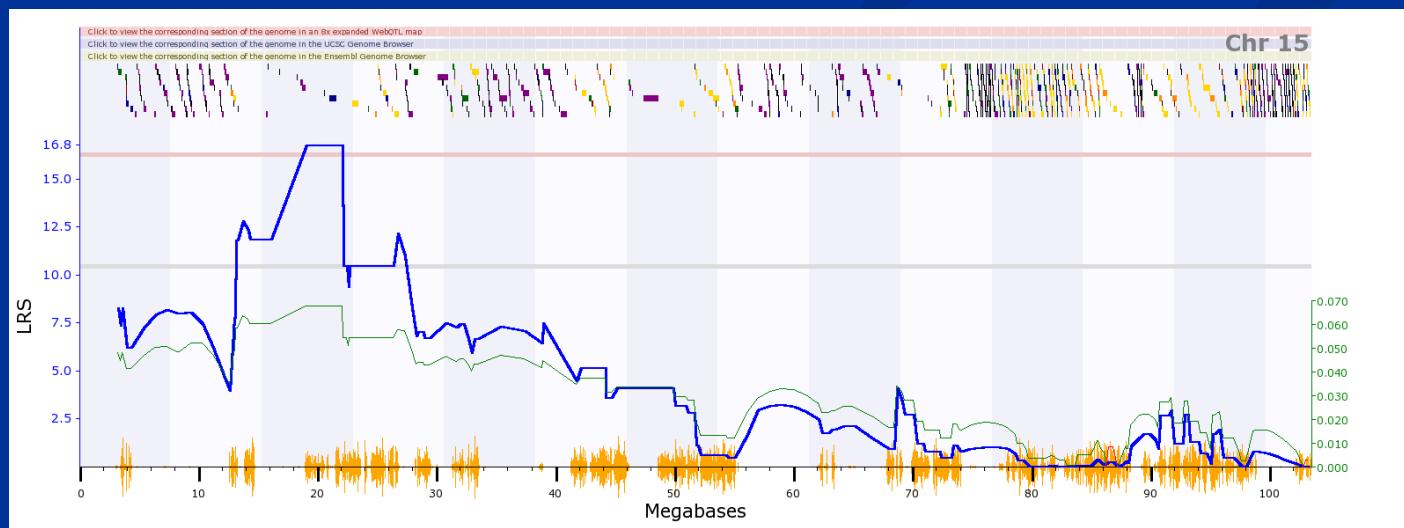
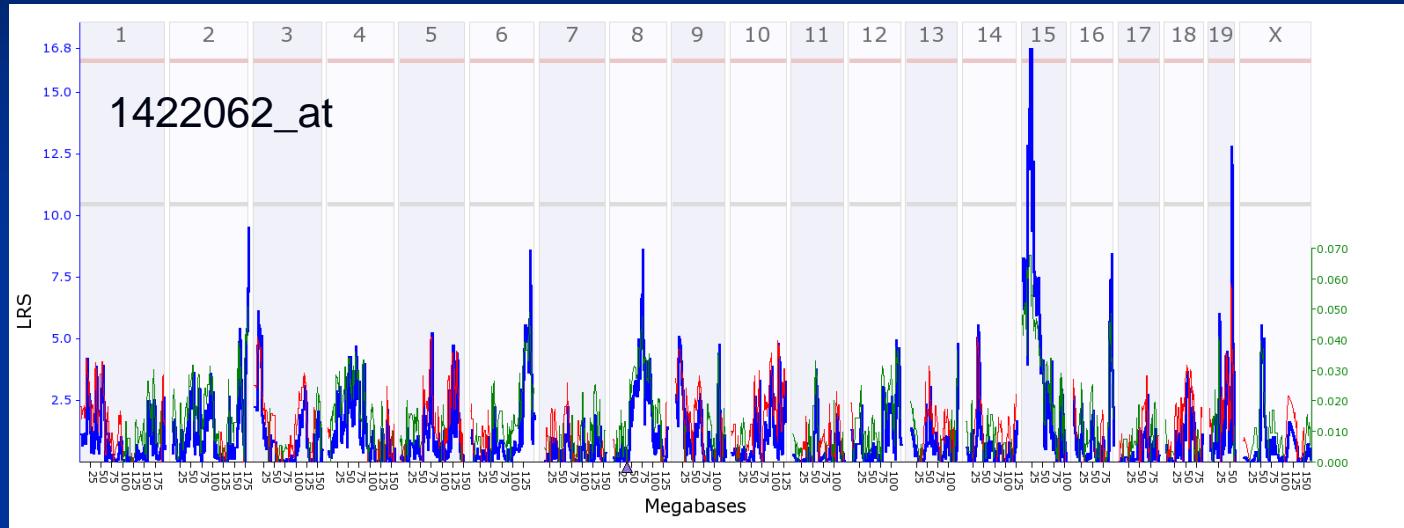
Gene Network of Gstol1



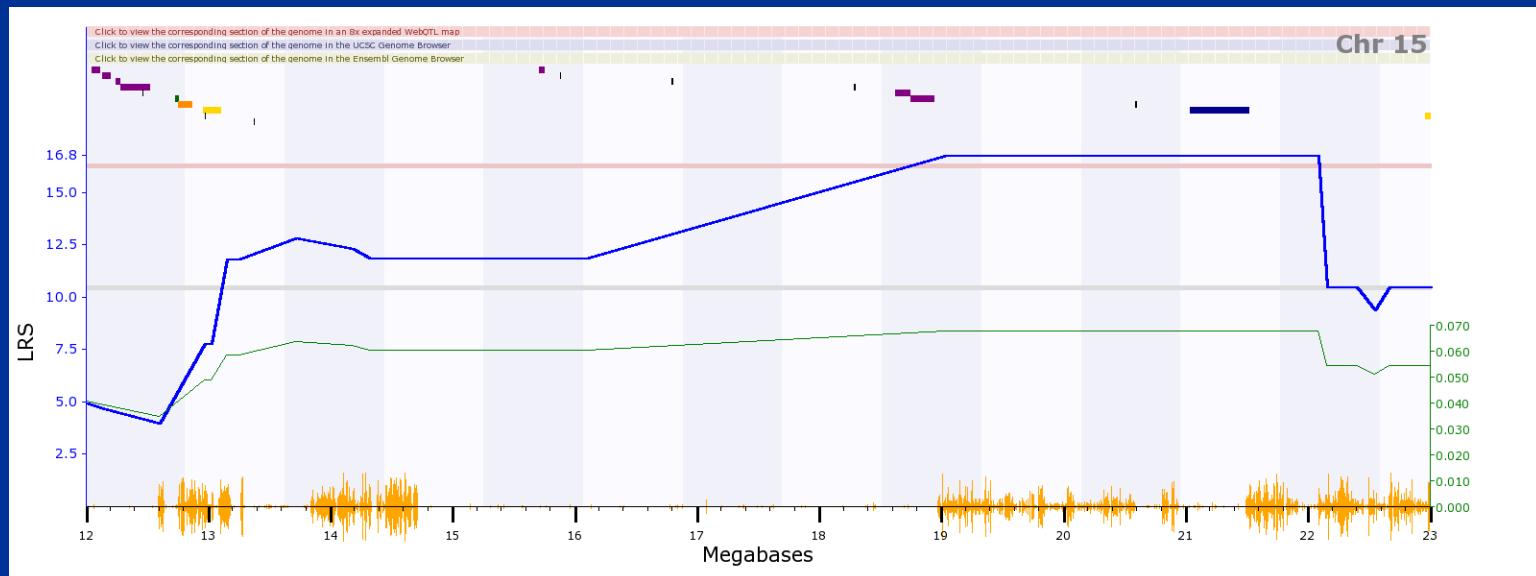
Gene ontology analysis for the top 500 genes whose expression is high significantly correlated with Gsto1 gene



Expression QTL analysis of macrophage scavenger receptor 1 (*Msrl*) gene



The location of Msr1 expression QTL



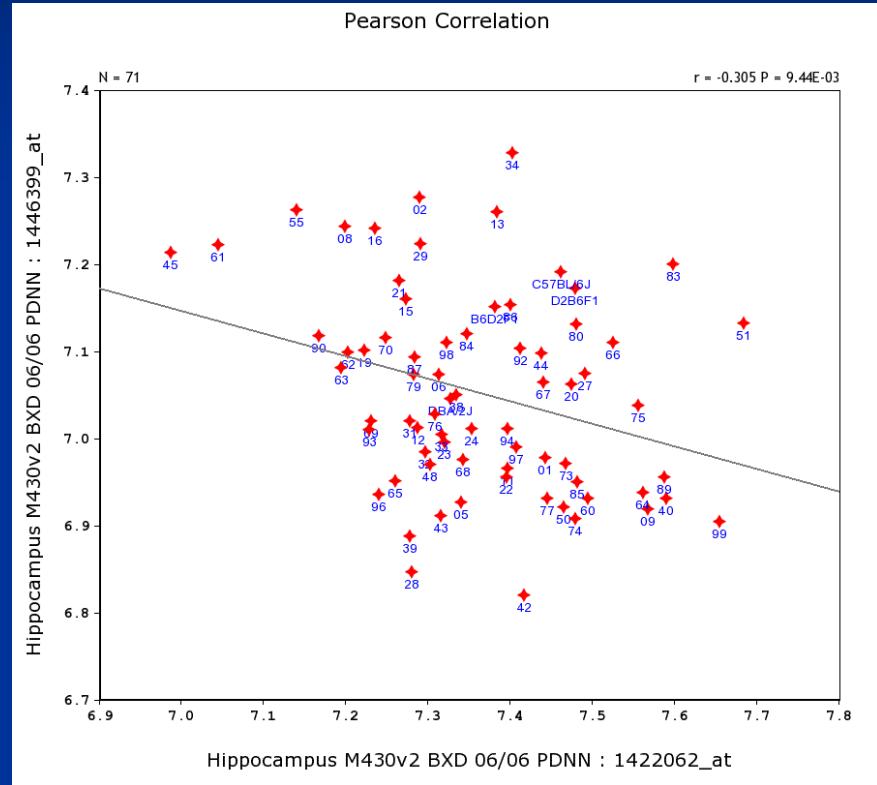
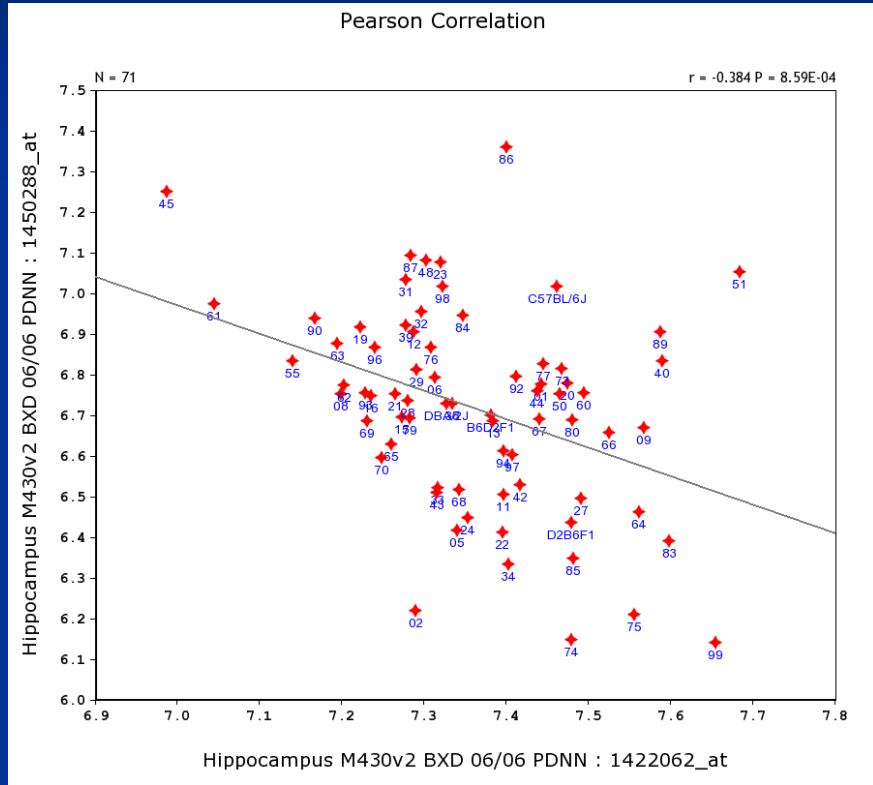
Candidate genes that regulate the expression of *Msrl1*

| Index | Gene Symbol | Mb Start (mm9) | Gene Length (Kb) | SNP Count | SNP Density (SNP/Kb) | Gene Description |
|-------|---------------|-------------------|------------------|-----------|-------------------------|---------------------------------|
| 1 | Zfr | 12.05 | 67.60 | 3 | 0.04 | zinc finger RNA binding protein |
| 2 | Mtmmr12 | 12.13 | 67.15 | 4 | 0.06 | myotubularin related protein 12 |
| 3 | Golph3 | 12.25 | 29.77 | 1 | 0.03 | golgi phosphoprotein 3 |
| 4 | Pdzd2 | 12.29 | 235.50 | 5 | 0.02 | PDZ domain containing 2 |
| 5 | 5033430J17Rik | 12.47 | 1.21 | 0 | 0.00 | RIKEN cDNA 5033430J17 gene |
| 6 | 6030458C11Rik | 12.74 | 16.23 | 6 | 0.37 | RIKEN cDNA 6030458C11 gene |
| 7 | Rnasen | 12.75 | 110.48 | 343 | 3.10 | ribonuclease III, nuclear |
| 8 | Cdh6 | 12.96 | 139.44 | 230 | 1.65 | cadherin 6 |
| 9 | B130021B11Rik | 12.98 | 0.05 | 0 | 0.00 | RIKEN cDNA B130021B11 gene |
| 10 | LOC239338 | 13.38 | 0.04 | 0 | 0.00 | similar to CDK105 |
| 11 | 4930557F08Rik | 15.71 | 43.43 | 3 | 0.07 | RIKEN cDNA 4930557F08 gene |
| 12 | EG239341 | 15.89 | 0.05 | 0 | 0.00 | predicted gene, EG239341 |
| 13 | Cdh9 | 16.80 | 0.05 | 0 | 0.00 | cadherin 9 |
| 14 | 4921515E04Rik | 18.29 | 10.85 | 0 | 0.00 | RIKEN cDNA 4921515E04 gene |
| 15 | C030047K22Rik | 18.63 | 121.09 | 10 | 0.08 | RIKEN cDNA C030047K22 gene |
| 16 | Cdh10 | 18.75 | 193.91 | 3 | 0.02 | cadherin 10 |
| 17 | Acot10 | 20.59 | 1.54 | 0 | 0.00 | acyl-CoA thioesterase 10 |
| 18 | Cdh12 | 21.04 | 478.08 | 93 | 0.19 | cadherin 12 |
| 19 | Cdh18 | 22.97 | 437.96 | 968 | 2.21 | cadherin 18 |

Selection of candidate genes that regulate the expression of *Msr1*

| Index | Gene Symbol | Correlation P value | Mean Expression | Max LRS | Max LRS Location (Chr: Mb) |
|-------|---------------|---------------------|-----------------|---------|----------------------------|
| 1 | Zfr | 0.000647488 | 7.00 | 11 | Chr5: 133.538653 |
| 2 | Mtmmr12 | #N/A | #N/A | #N/A | #N/A |
| 3 | Golph3 | 1.2211E-07 | 8.00 | 11.9 | Chr9: 81.753446 |
| 4 | Pdzd2 | #N/A | #N/A | #N/A | #N/A |
| 5 | 5033430J17Rik | 3.3522E-05 | 6.56 | 18 | Chr6: 140.066609 |
| 6 | 6030458C11Rik | 0.000127752 | 5.53 | 10.1 | Chr2: 180.825581 |
| 7 | Rnasen | #N/A | #N/A | #N/A | #N/A |
| 8 | Cdh6 | 0.000859319 | 7.90 | 111.7 | Chr15: 12.972088 |
| 9 | B130021B11Rik | #N/A | #N/A | #N/A | #N/A |
| 10 | LOC239338 | #N/A | #N/A | #N/A | #N/A |
| 11 | 4930557F08Rik | #N/A | #N/A | #N/A | #N/A |
| 12 | EG239341 | #N/A | #N/A | #N/A | #N/A |
| 13 | Cdh9 | #N/A | #N/A | #N/A | #N/A |
| 14 | 4921515E04Rik | #N/A | #N/A | #N/A | #N/A |
| 15 | C030047K22Rik | #N/A | #N/A | #N/A | #N/A |
| 16 | Cdh10 | 3.2451E-10 | 8.20 | 10.9 | ChrX: 112.637353 |
| 17 | Acot10 | #N/A | #N/A | #N/A | #N/A |
| 18 | Cdh12 | #N/A | #N/A | #N/A | #N/A |
| 19 | Cdh18 | #N/A | #N/A | #N/A | #N/A |

Correlation plot



Msr1&Cdh6

Msr1&Cdh10

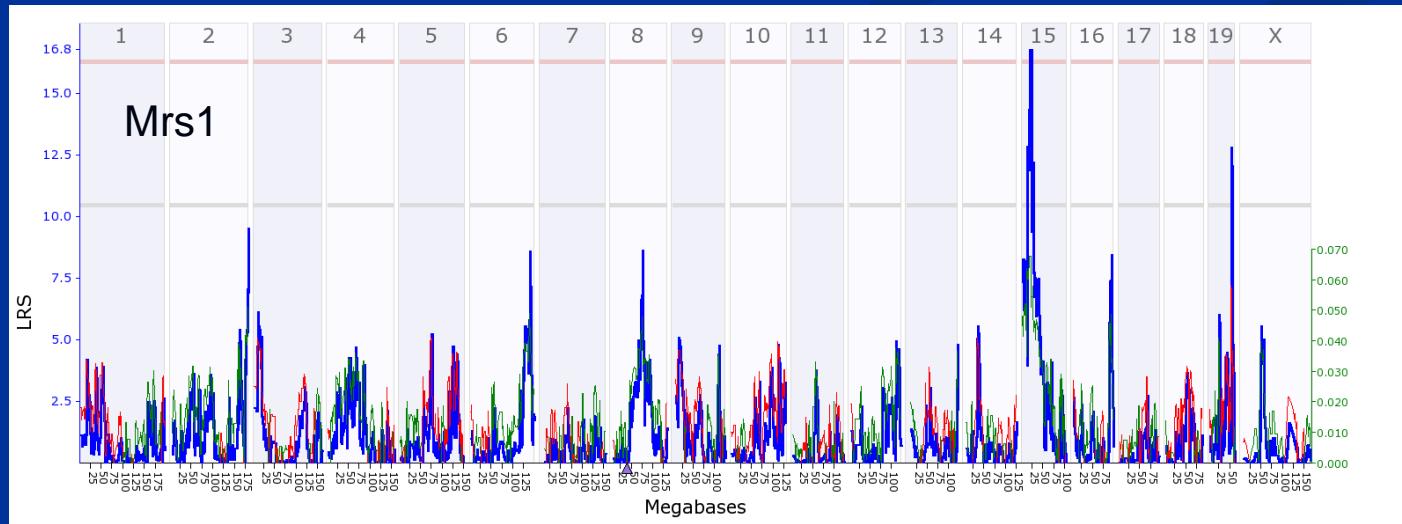
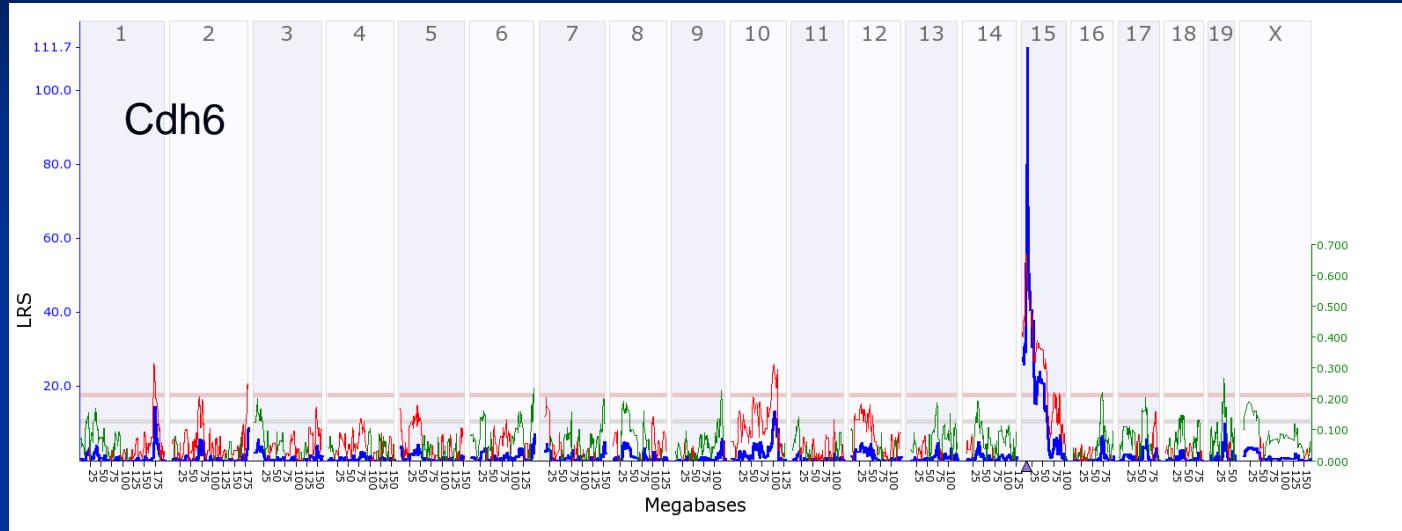
Polymorphism analysis of candidate genes that regulate the expression of *Msrl1*

| chromosome | position | B6 allele | D2 allele | gene | exon |
|------------|----------|-----------|-----------|---------------|------|
| 15 | 12747846 | C | T | 6030458C11Rik | 4 |
| 15 | 12747971 | C | T | 6030458C11Rik | 4 |
| 15 | 12751199 | A | G | 6030458C11Rik | 3 |
| 15 | 12754260 | T | G | 6030458C11Rik | 1 |
| 15 | 12971132 | T | C | Cdh6 | 10 |

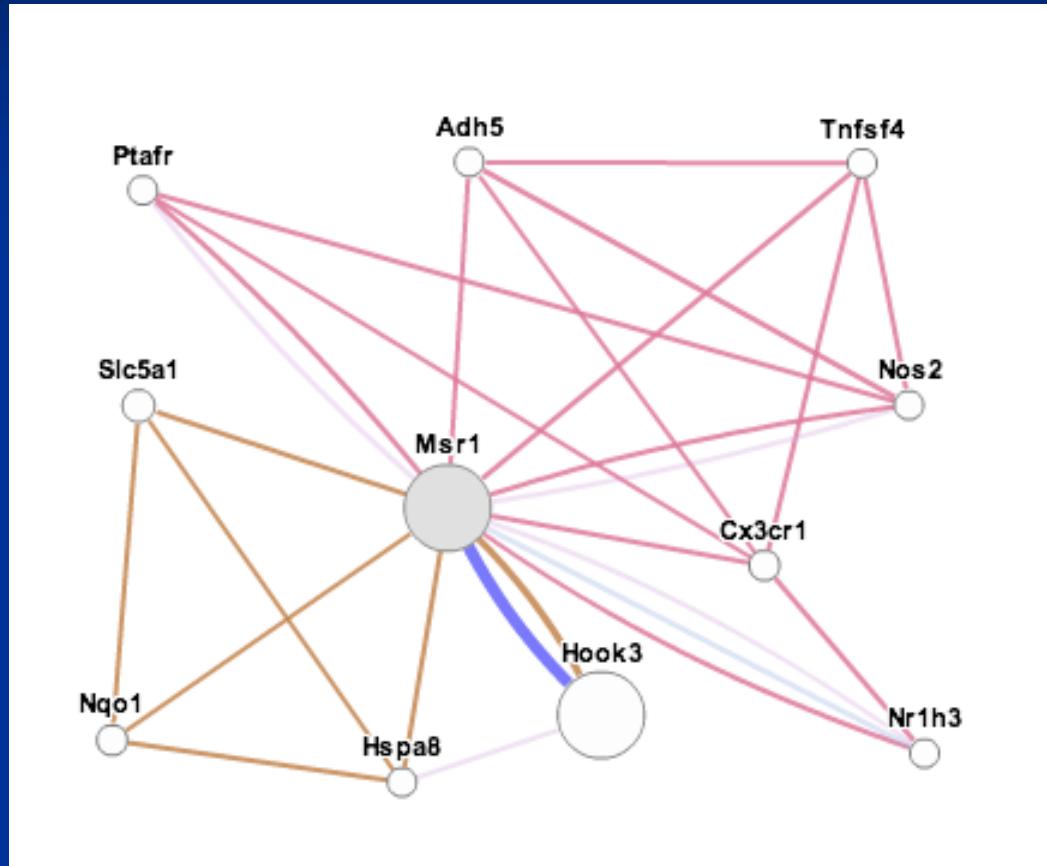
Candidate genes that regulate the expression of *Msr1*

| Index | Gene Symbol | Correlation P value | Mean Expression | Max LRS | Max LRS Location (Chr: Mb) | non-synonymous mutation |
|-------|---------------|---------------------|-----------------|--------------|----------------------------|-------------------------|
| 1 | Zfr | 0.000647488 | 7.00 | 11 | Chr5: 133.538653 | |
| 2 | Mtmmr12 | #N/A | #N/A | #N/A | #N/A | |
| 3 | Golph3 | 1.2211E-07 | 8.00 | 11.9 | Chr9: 81.753446 | |
| 4 | Pdzd2 | #N/A | #N/A | #N/A | #N/A | |
| 5 | 5033430J17Rik | 3.3522E-05 | 6.56 | 18 | Chr6: 140.066609 | |
| 6 | 6030458C11Rik | 0.000127752 | 5.53 | 10.1 | Chr2: 180.825581 | yes |
| 7 | Rnasen | #N/A | #N/A | #N/A | #N/A | |
| 8 | Cdh6 | 0.000859319 | 7.90 | 111.7 | Chr15: 12.972088 | yes |
| 9 | B130021B11Rik | #N/A | #N/A | #N/A | #N/A | |
| 10 | LOC239338 | #N/A | #N/A | #N/A | #N/A | |
| 11 | 4930557F08Rik | #N/A | #N/A | #N/A | #N/A | |
| 12 | EG239341 | #N/A | #N/A | #N/A | #N/A | |
| 13 | Cdh9 | #N/A | #N/A | #N/A | #N/A | |
| 14 | 4921515E04Rik | #N/A | #N/A | #N/A | #N/A | |
| 15 | C030047K22Rik | #N/A | #N/A | #N/A | #N/A | |
| 16 | Cdh10 | 3.2451E-10 | 8.20 | 10.9 | ChrX: 112.637353 | |
| 17 | Acot10 | #N/A | #N/A | #N/A | #N/A | |
| 18 | Cdh12 | #N/A | #N/A | #N/A | #N/A | |
| 19 | Cdh18 | #N/A | #N/A | #N/A | #N/A | |

Cadherin 6 (*Cdh6*) QTL Mapping



Known working partner of *Msr1* gene

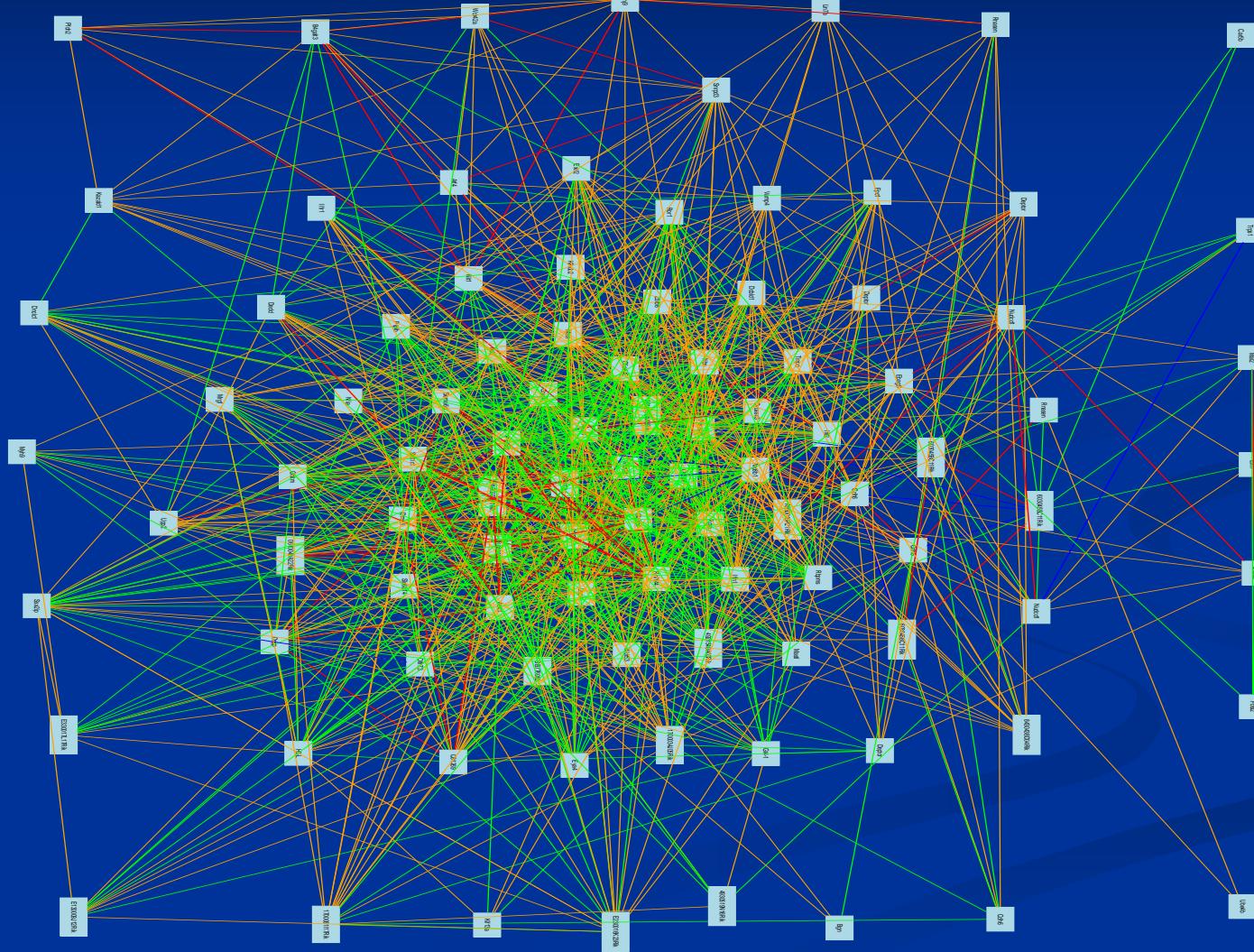


<http://genemania.org>

Confirmed working partner of *Msr1* gene in our expression data

| Index | Gene Symbol | Gene Description | Correlation P value |
|-------|---------------|---|---------------------|
| 1 | Msr1 | macrophage scavenger receptor 1 Gene | 0 |
| 2 | Hook3 | hook homolog 3 (<i>Drosophila</i>)(curated) | 0.002039967 |
| 3 | Slc5a1 | solute carrier family 5 (sodium/glucose cotransporter), member 1 Gene | 1.1373E-07 |
| 4 | Nqo1 | NAD(P)H dehydrogenase, quinone 1 Gene | #N/A |
| 5 | Cx3cr1 | chemokine (C-X3-C) receptor 1 Gene | 0.002811294 |
| 7 | Hspa8 | heat shock protein 8 Gene | 3.58904E-06 |
| 8 | Nr1h3 | nuclear receptor subfamily 1, group H, member 3 Gene | 2.12208E-07 |
| 9 | Ptafr | platelet-activating factor receptor Gene | 4.20329E-05 |
| 10 | Adh5 | alcohol dehydrogenase 5 (class III), chi polypeptide Gene | 1.53053E-09 |
| 11 | Tnfsf4 | tumor necrosis factor (ligand) superfamily, member 4 Gene | 0.002117561 |

Gene Network of *Msr1*



Top 30 working partners of *Msr1* gene

| Record | Symbol | Description | Location (Chr, Mb) | Mean Expr | Sample p(r) |
|--------------|---------------|--|--------------------|-----------|-------------|
| 1422062_at | Msr1 | macrophage scavenger receptor 1 | Chr8: 40.691029 | 7.40 | 0 |
| 1439437_x_at | Cpe | carboxypeptidase E | Chr8: 67.071407 | 8.87 | 0 |
| 1419222_at | Tbxa2r | thromboxane A2 receptor | Chr10: 80.797325 | 8.37 | 0 |
| 1426121_at | Mrgpra3 | MAS-related GPR, member A3 | Chr7: 54.844713 | 8.26 | 0 |
| 1447668_x_at | Efemp2 | epidermal growth factor-containing fibulin-like extracellular matrix protein 2 | Chr19: 5.481717 | 7.83 | 0 |
| 1418989_at | Ctse | cathepsin E | Chr1: 133.571532 | 7.69 | 0 |
| 1442869_at | A930013K19 | hypothetical protein A930013K19 | Chr5: 35.429889 | 7.57 | 0 |
| 1447300_at | Vwa5a | von Willebrand factor A domain containing 5A | Chr9: 39.398309 | 7.55 | 0 |
| 1431634_at | 4930455C13Rik | RIKEN cDNA 4930455C13 | Chr10: 21.044230 | 7.25 | 0 |
| 1450670_at | Dbh | dopamine beta-hydroxylase (dopamine beta-monoxygenase, dopamine to norepinephrine) | Chr2: 27.037106 | 7.19 | 0 |
| 1418765_at | Timd2 | T-cell immunoglobulin and mucin domain containing 2 | Chr11: 46.490707 | 7.10 | 0 |
| 1430398_at | 4921517O11Rik | RIKEN cDNA 4921517O11 gene | Chr18: 22.331255 | 7.06 | 0 |
| 1416396_at | Snx4 | sorting nexin 4 | Chr16: 33.299890 | 7.51 | 2.22045E-16 |
| 1426507_at | Il1f5 | interleukin 1 family, member 5 (delta) | Chr2: 24.138353 | 7.32 | 2.22045E-16 |
| 1422963_at | Sprr2i | small proline-rich protein 2I | Chr3: 92.212874 | 7.20 | 2.22045E-16 |
| 1431750_at | Ush2a | usherin basement membrane protein (Usher syndrome 2A, retinitis pigmentosa and hearing loss) | Chr1: 190.180888 | 7.13 | 2.22045E-16 |
| 1449924_at | Prg3 | proteoglycan 3 | Chr2: 84.829551 | 7.11 | 2.22045E-16 |
| 1420206_at | 5730494M16Rik | RIKEN cDNA 5730494M16 | Chr18: 25.297204 | 7.07 | 2.22045E-16 |
| 1459044_at | AU015558 | ESTs | Chr7: 37.901095 | 7.03 | 2.22045E-16 |
| 1421608_at | Il20 | interleukin 20 | Chr1: 132.803773 | 8.13 | 4.44089E-16 |
| 1445961_at | BG071636 | BG071636 | Chr17: 53.427689 | 8.00 | 4.44089E-16 |
| 1441962_at | Alox5 | arachidonate 5-lipoxygenase (leukotriene synthesis) | Chr6: 116.360136 | 7.80 | 4.44089E-16 |
| 1443828_x_at | 5031400M07Rik | 5031400M07Rik (putative protein processing and translation related) | Chr9: 24.953623 | 7.68 | 4.44089E-16 |
| 1447518_at | Tpx2 | targeting protein of Xklp2 (spindle pole microtubule-associated) | Chr2: 152.719414 | 7.50 | 4.44089E-16 |
| 1457629_at | Atmin | ATM interactor (ATM/ATR-substrate Chk2-interacting Zn2+-finger protein) | Chr8: 119.481822 | 7.05 | 4.44089E-16 |
| 1451292_at | Zfp212 | Zinc finger protein 212 | Chr6: 47.882108 | 9.59 | 6.66134E-16 |
| 1417805_at | Xpnpep2 | X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound | ChrX: 45.489257 | 7.49 | 6.66134E-16 |
| 1433189_at | 4933433N18Rik | RIKEN cDNA 4933433N18 gene | Chr13: 50.760886 | 7.37 | 6.66134E-16 |
| 1443599_at | A930031F18Rik | ESTs | Chr3: 89.158425 | 7.78 | 8.88178E-16 |
| 1421338_at | Elf4 | E74-like factor 4 (ets domain transcription factor) | ChrX: 45.765520 | 7.27 | 8.88178E-16 |

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