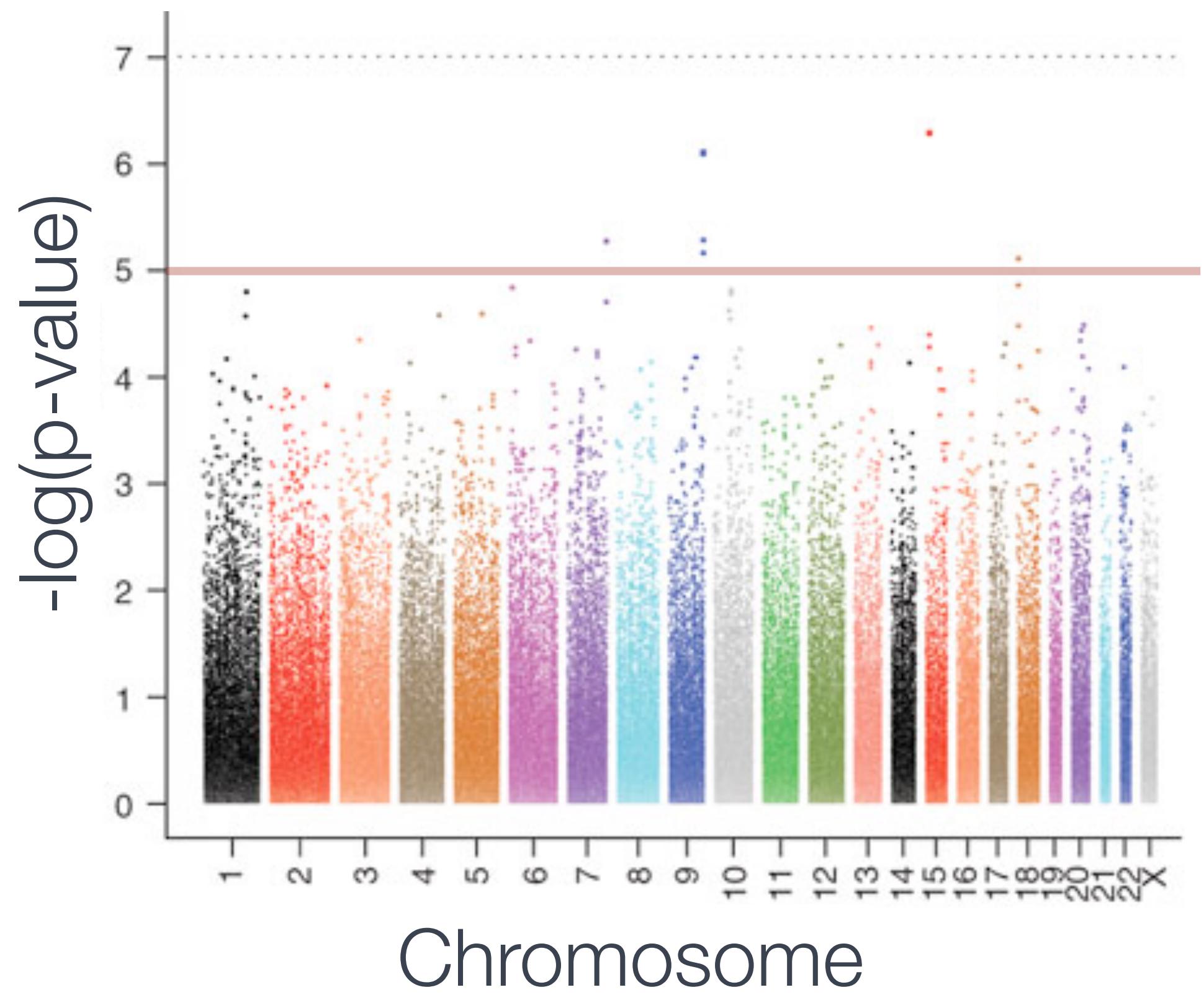


Incorporating signatures into genetic data

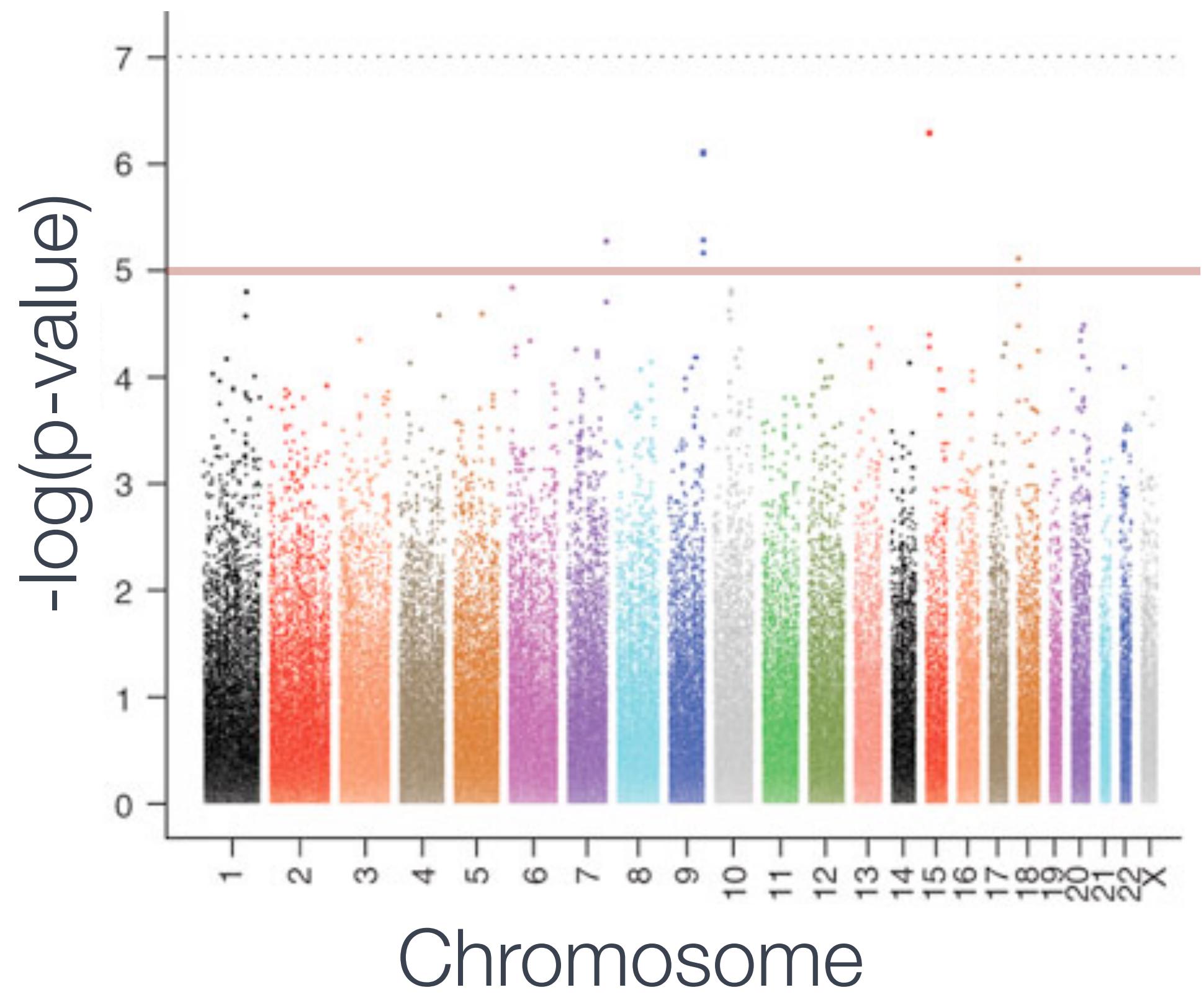
MEDT32/33

I have GWA now what?

- small effect of individual genes
- Looking at the GWA genes does not provide a coherent, significant pathway?
- combine GWAS with genome-wide expression data
- cluster genes with highly correlated expression.
- GO-enrichment analysis to reveal significant enrichment



Marker approach

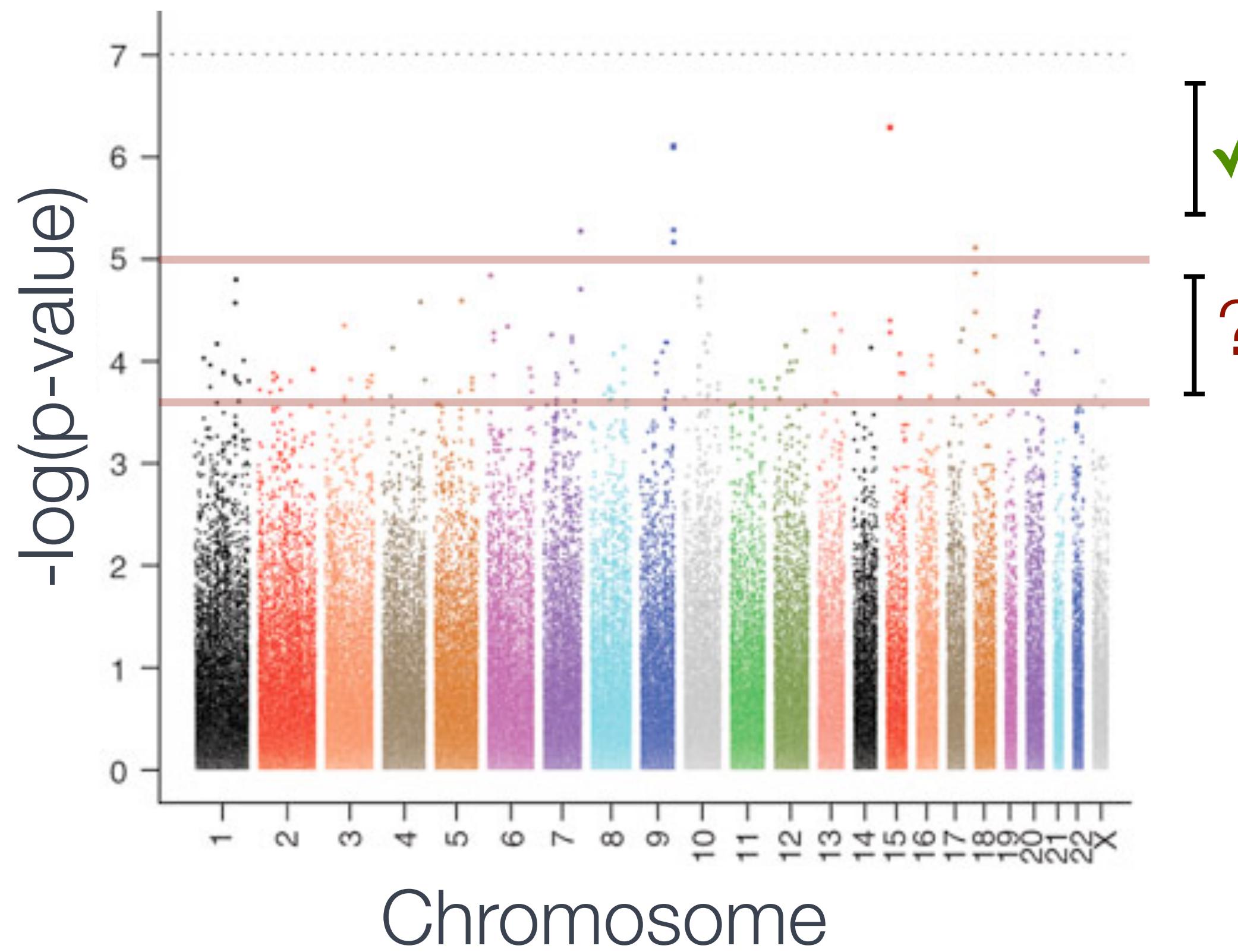


Marker approach

Gene A

Gene B

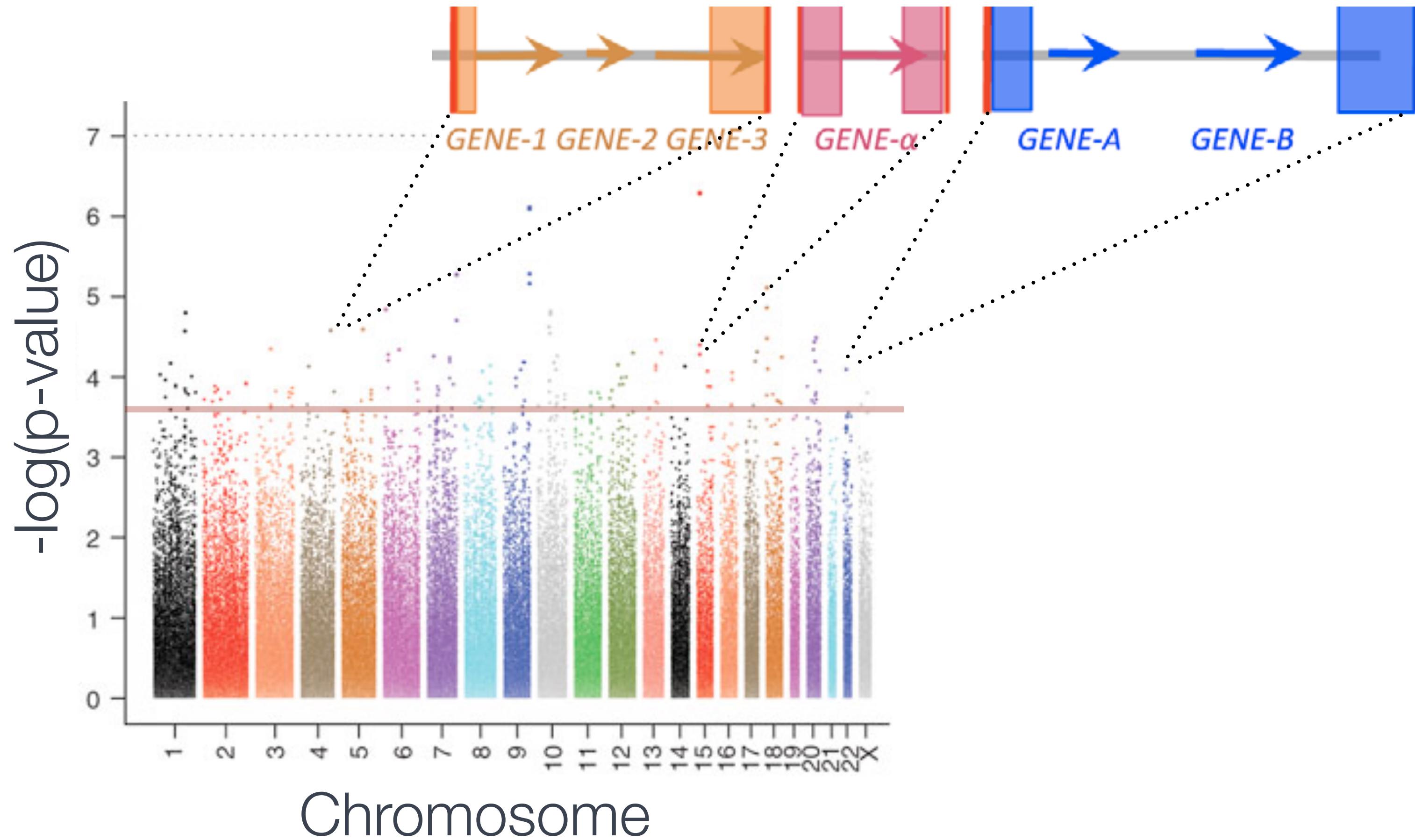
Gene C

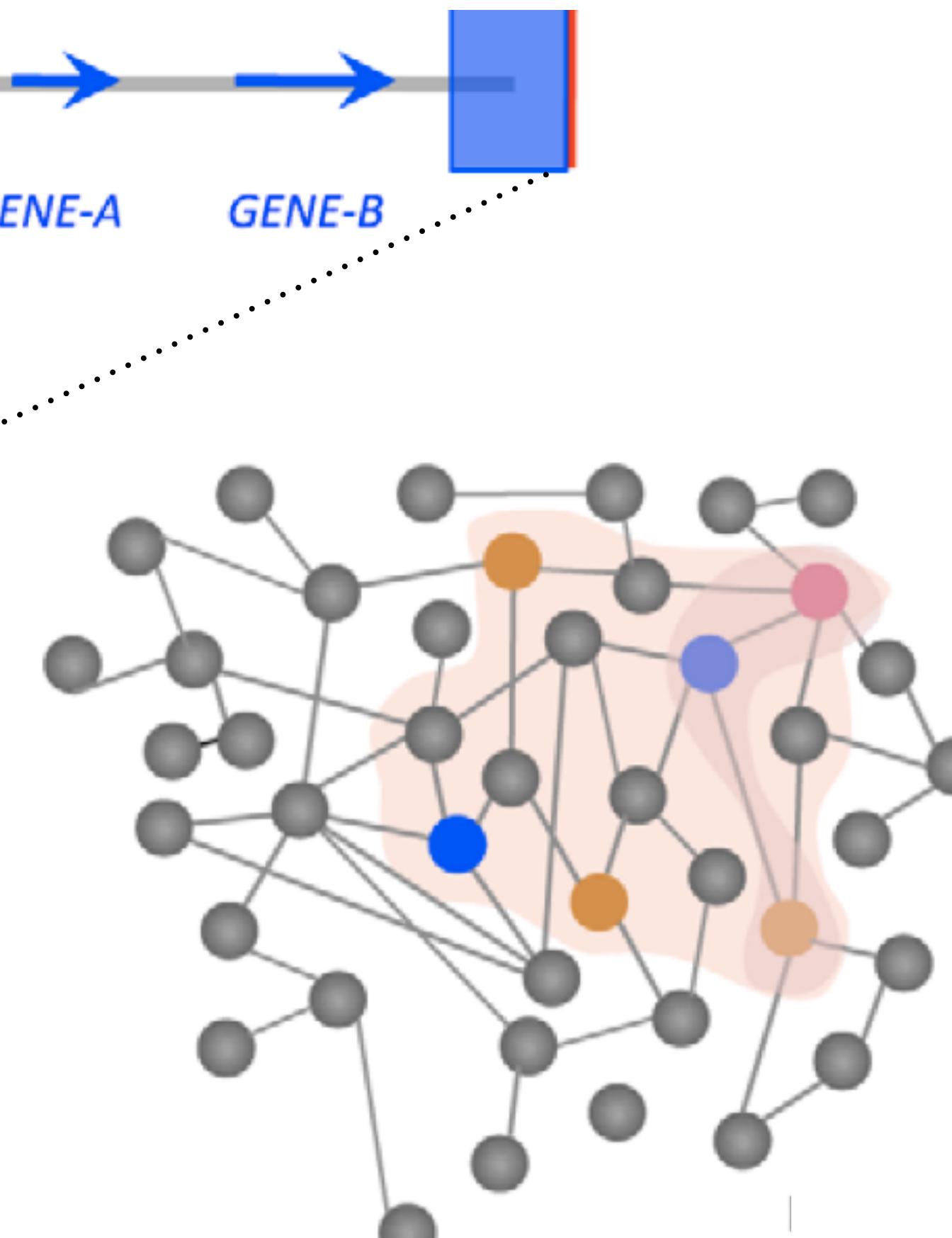
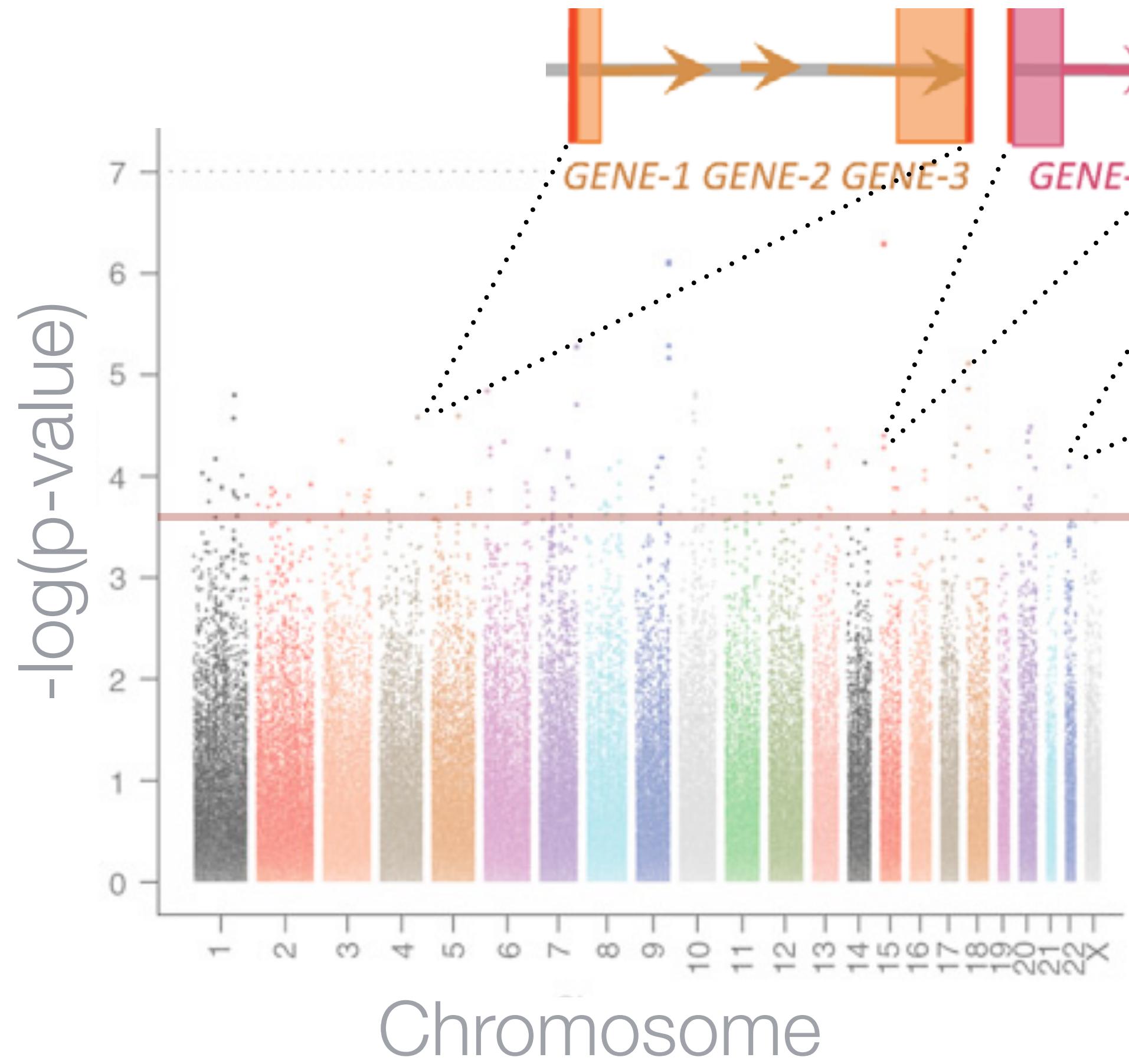


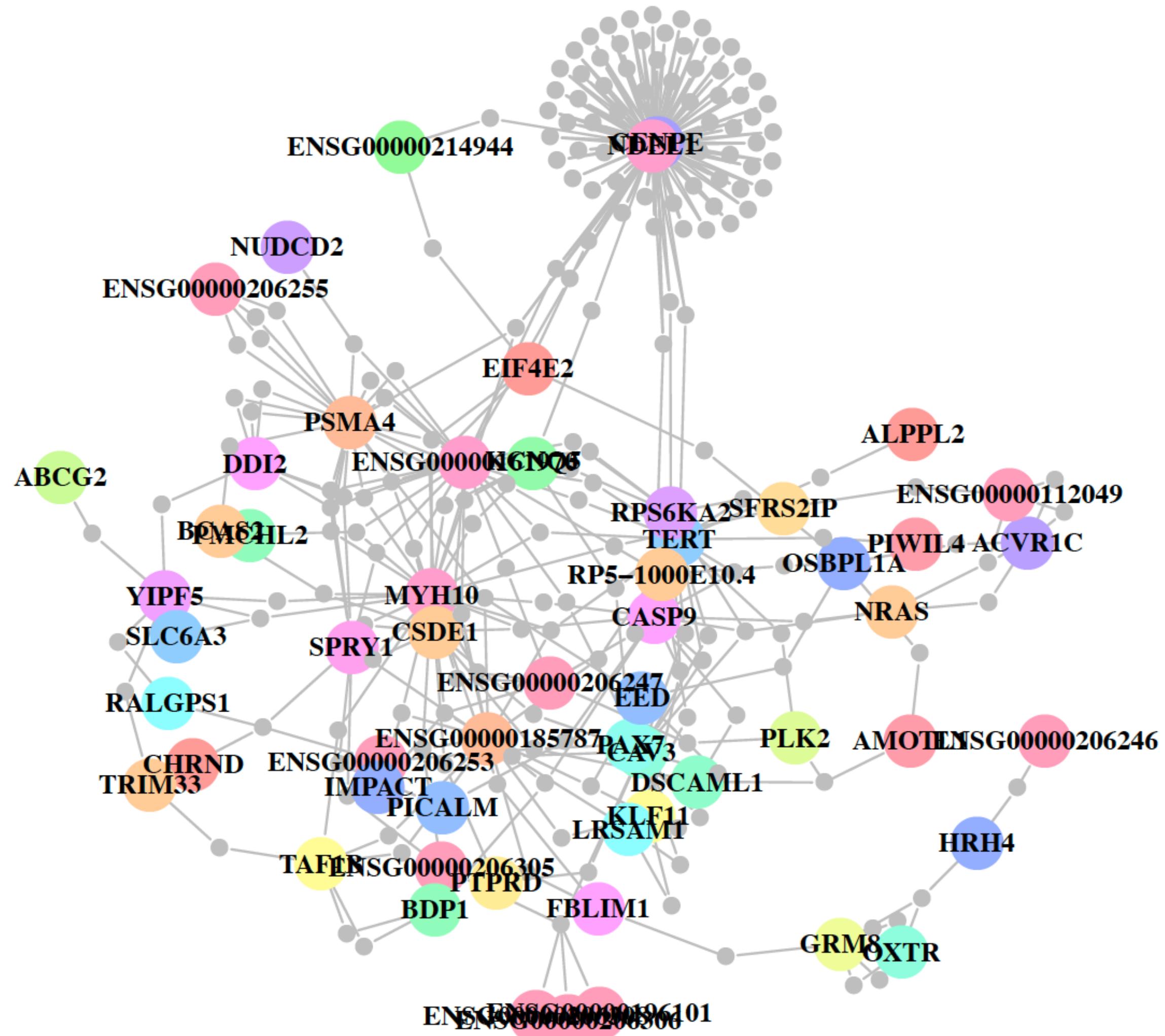
Network approach

Voight et al. Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nat Genet 2009

Rossin et al. PLoS Genet (2011) vol. 7 (1) pp. e1001273

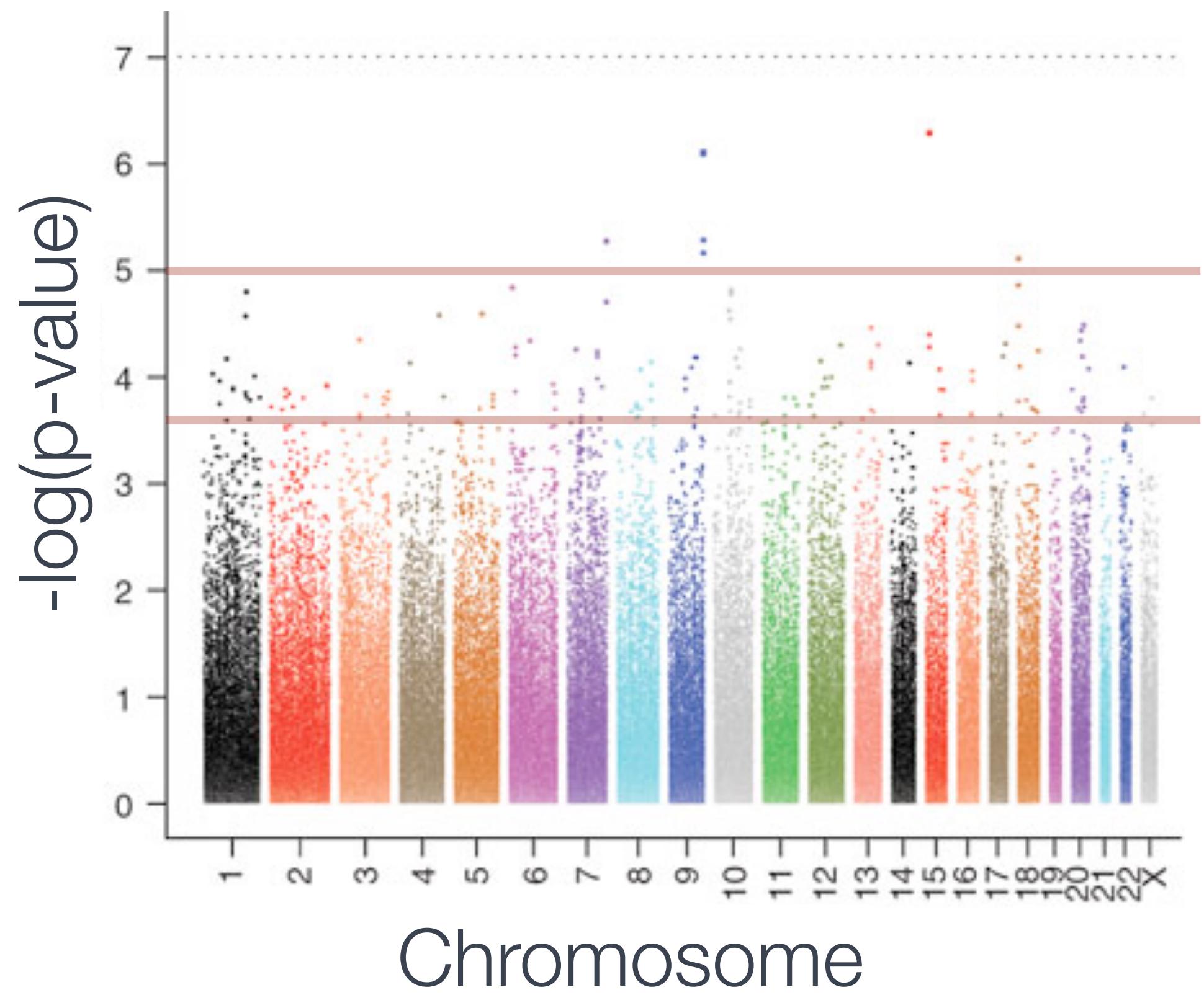




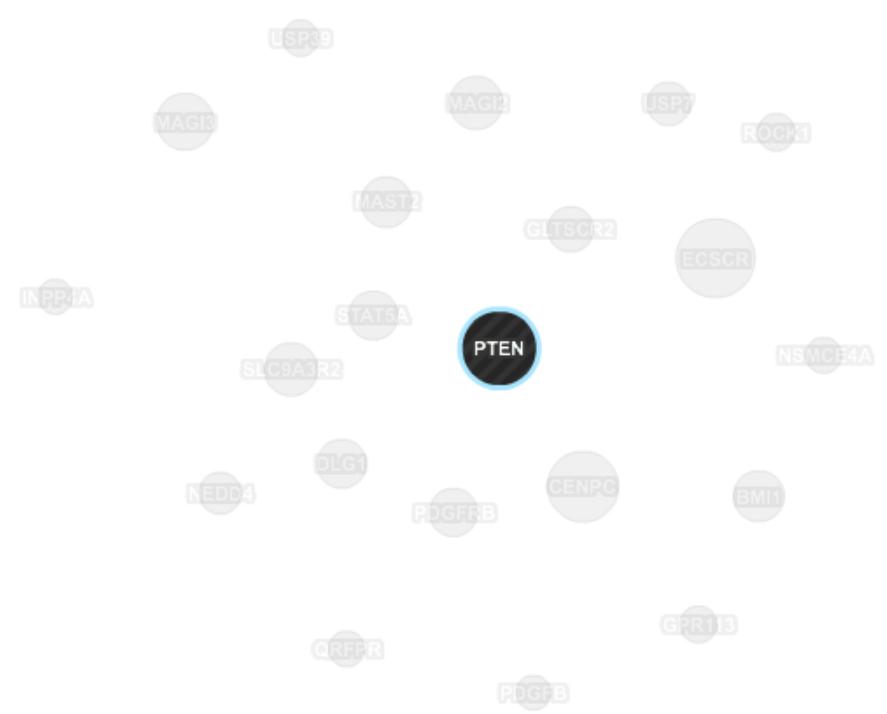


Sample results

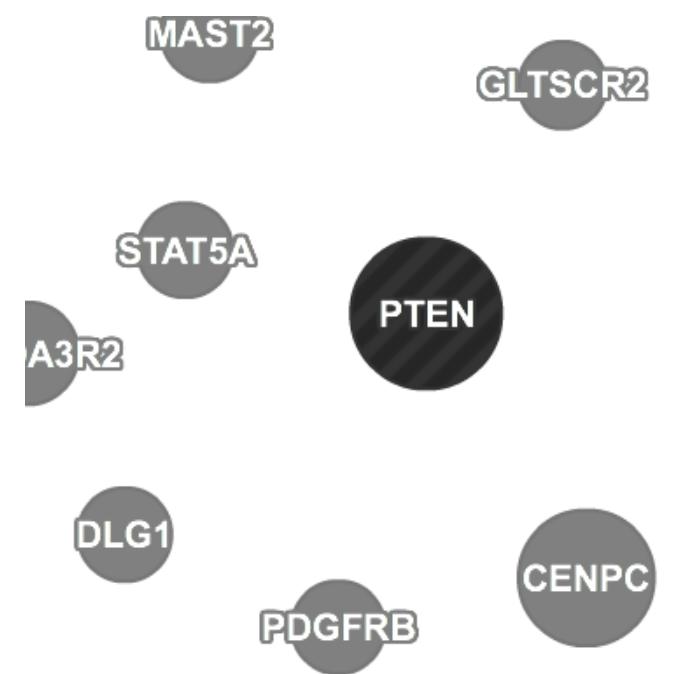
Lung cancer survival study. Data courtesy of David Christiani and Mike Wang



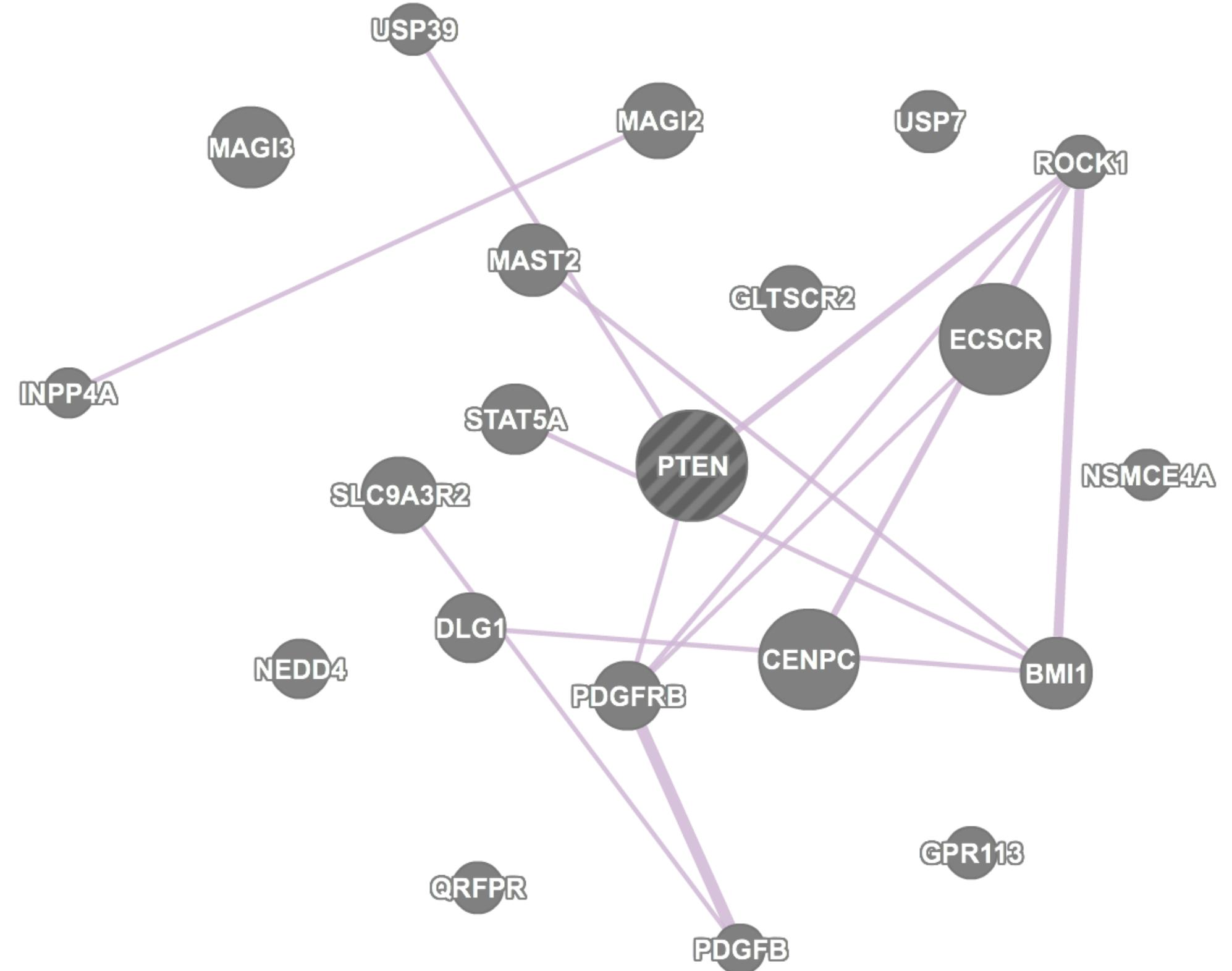
Functional approach



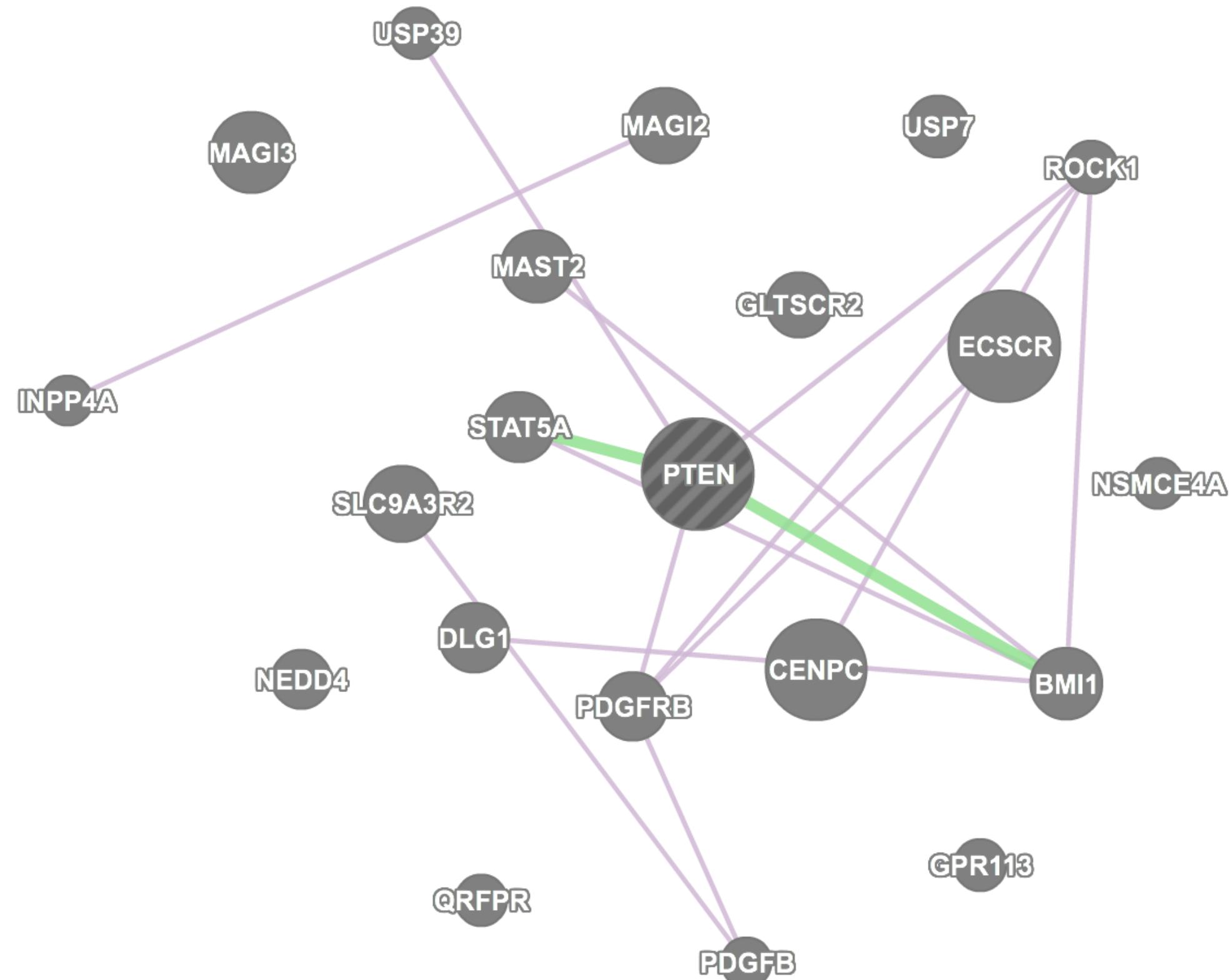
seed gene



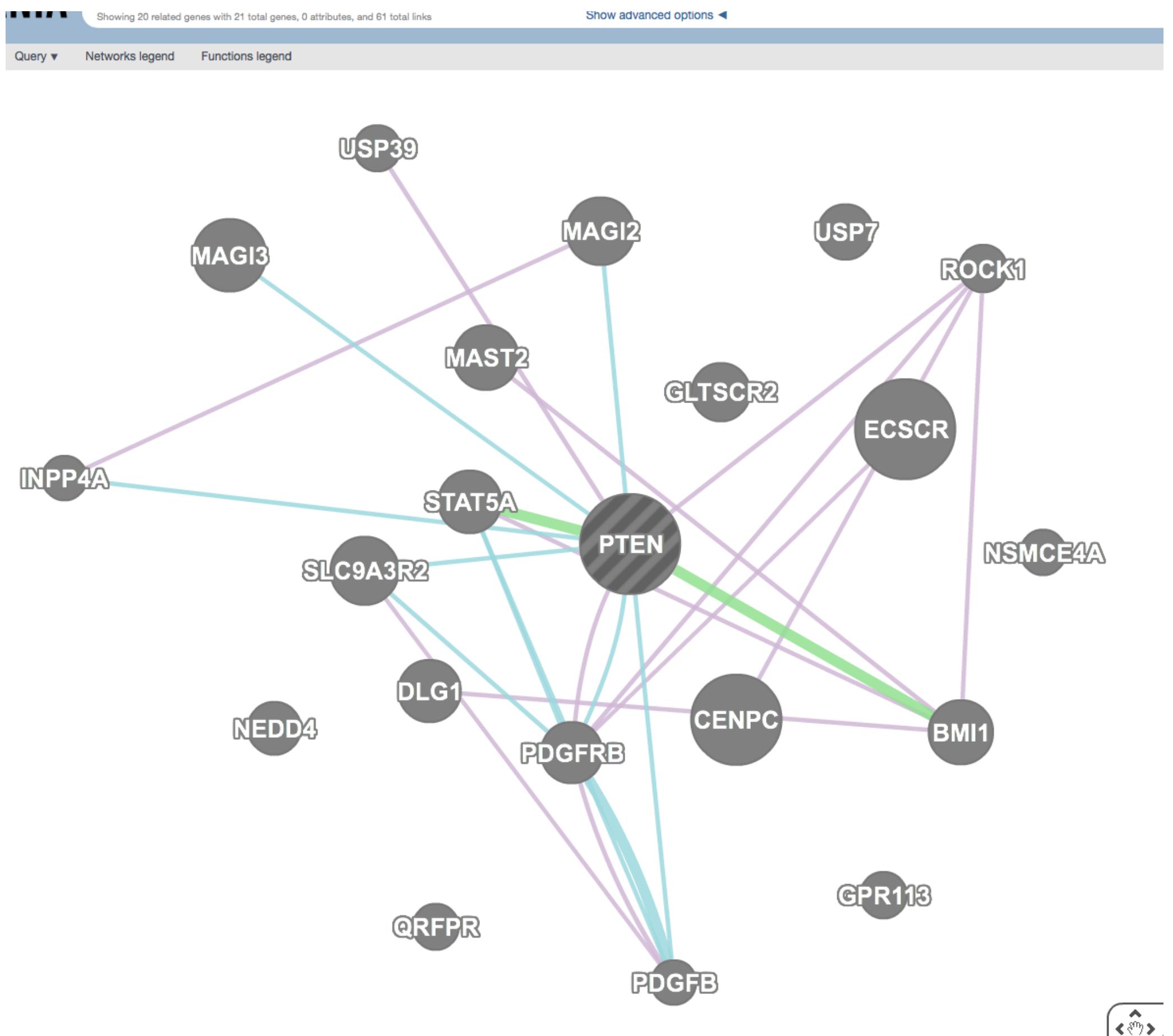
Gene neighbourhood



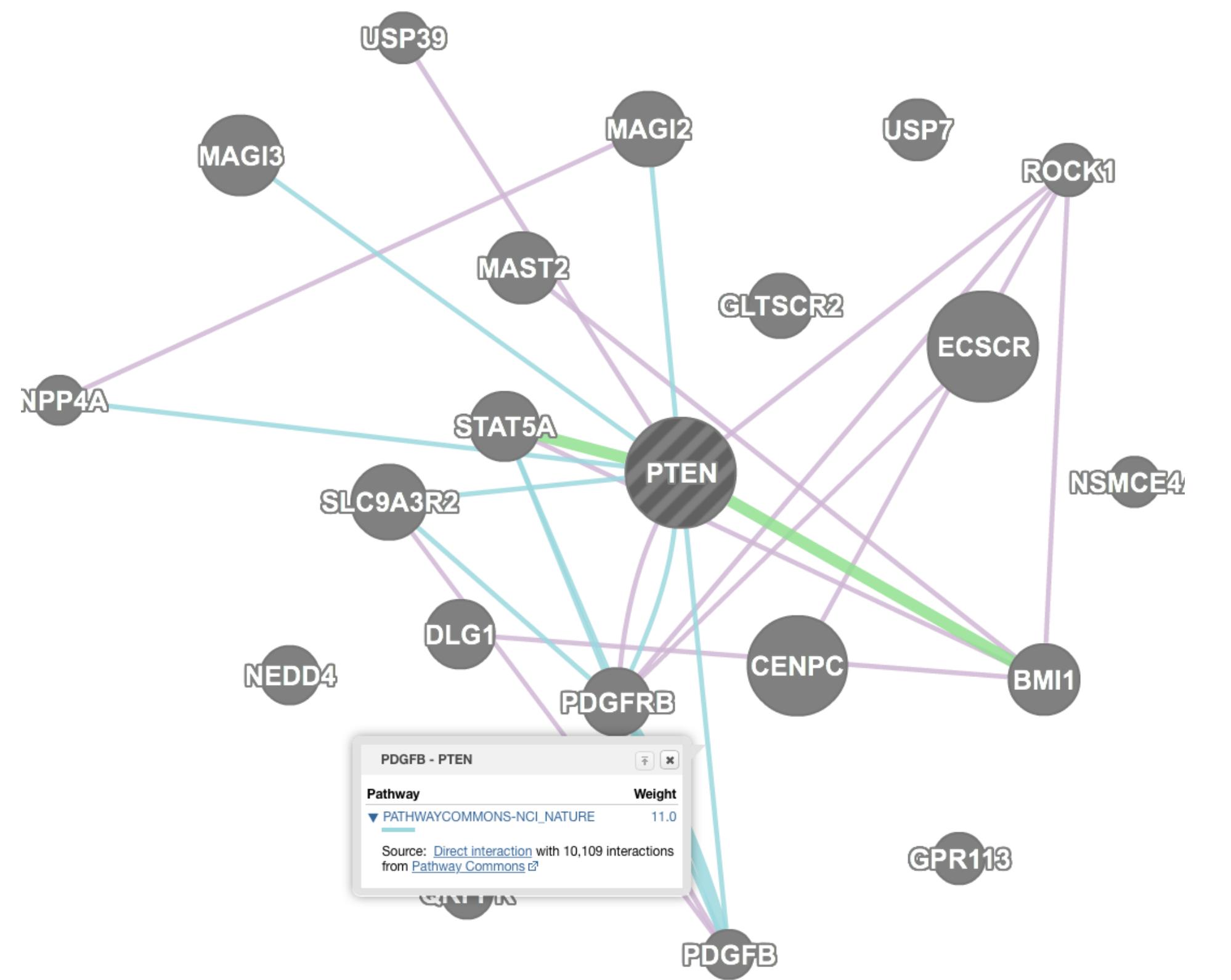
co-expression

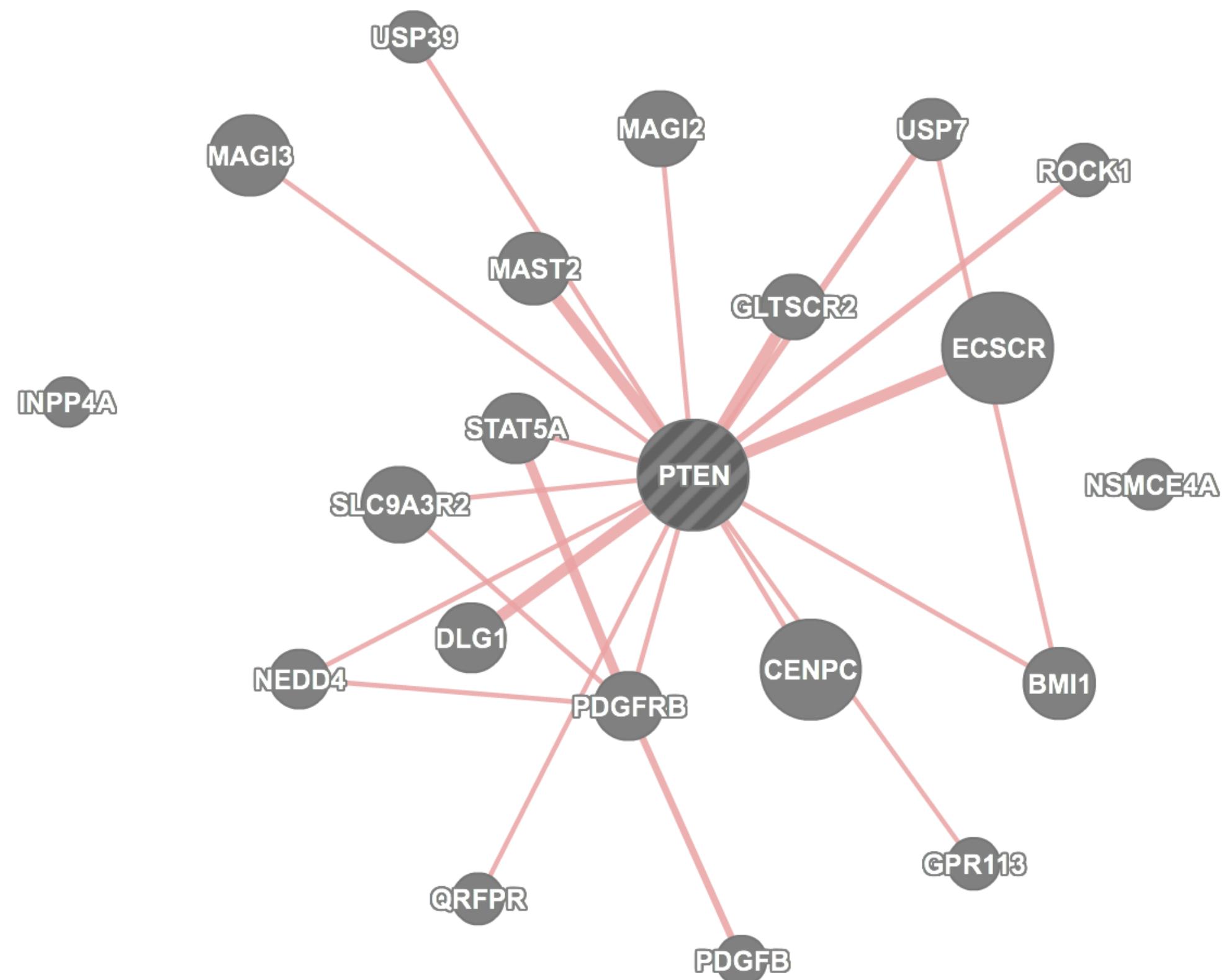


Genetic interactions



Known Pathways





Physical interactions



genemania.org

Gene List

- Download spreadsheet list of SCHZ genes
- Go to genemania.org site
- combine GWAS with genome-wide expression data
 - (Upload network and expand it from 20- 50 genes)
- cluster genes with highly correlated expression.
- perform GO-enrichment analysis to reveal significant enrichment