The sequenced rat brain transcriptome - Its use in identifying networks predisposing alcohol consumption

Saba, Laura M.

Flink, Stephen C.

Vanderlinden, Lauren A.

Israel, Yedy

Tampier, Lutske

Colombo, Giancarlo

Kiianmaa, Kalervo

Bell, Richard L.

Printz, Morton P.

Flodman, Pamela

Koob, George

Richardson, Heather N.

Lombardo, Joseph

Hoffman, Paula L.

Tabakoff,

© 2015 FEBS. A quantitative genetic approach, which involves correlation of transcriptional networks with the phenotype in a recombinant inbred (RI) population and in selectively bred lines of rats, and determination of coinciding quantitative trait loci for gene expression and the trait of interest, has been applied in the present study. In this analysis, a novel approach was used that combined DNA-Seq data, data from brain exon array analysis of HXB/BXH RI rat strains and six pairs of rat lines selectively bred for high and low alcohol preference, and RNA-Seq data (including rat brain transcriptome reconstruction) to quantify transcript expression levels, generate co-expression modules and identify biological functions that contribute to the predisposition of consuming varying amounts of alcohol. A gene co-expression module was identified in the RI rat

strains that contained both annotated and unannotated transcripts expressed in the brain, and was associated with alcohol consumption