

*Promoter Analysis: Application to the Interpretation of Mouse Gene Expression Data of Project Normal*

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In this paper we applied promoter analysis to the mouse gene expression data from project normal [1]. We have identified sets of genes that are highly or specifically expressed in each tissue (say liver) in comparison to the other two (testis and kidney). We annotated the promoter regions in mouse genome and developed a mouse promoter database. We analyzed the regulatory regions of co-expressed genes and found sub-sets of genes that may be co-regulated. In each co-regulated sub-set of genes we identified common transcription factor (TF) binding sites and regulatory mechanisms.