Genes probably positively regulated by SIM2 and ETS2

Genes probably negatively regulated by SIM2 and ETS2

Promoter sites of putative target genes of SIM2 and ETS2 were analyzed for similarity and transcription factor search by GENEDOC and Promoter Scan tool

Involvement of putative target genes of SIM2 and ETS2 in various biological pathways was analyzed by Panther and KEGG pathway tool

Retrieval of all known promoter sequence from EPD and TRED

Search for consensus sequence of SIM2 and ETS2 binding in those promoter sequence by a Perl program ‘Consensus-Finder’

464 genes those have SIM2 and ETS2 binding site in their promoter sequence were identified

Expression profiles of those 464 genes in different tissue were retrieved by GNF SymAtlas

Tissue-specific differential expression pattern (fold change) of each of these mRNAs were calculated separately by comparing the median value of expression

Gene set I
Genes overexpressed at the sites of overexpression of SIM2 and ETS2

Gene set II
Genes underexpressed at the sites of underexpression of SIM2 and ETS2

Gene set III
Genes overexpressed at the sites of underexpression of SIM2 and ETS2

Gene set IV
Genes underexpressed at the sites of overexpression of SIM2 and ETS2