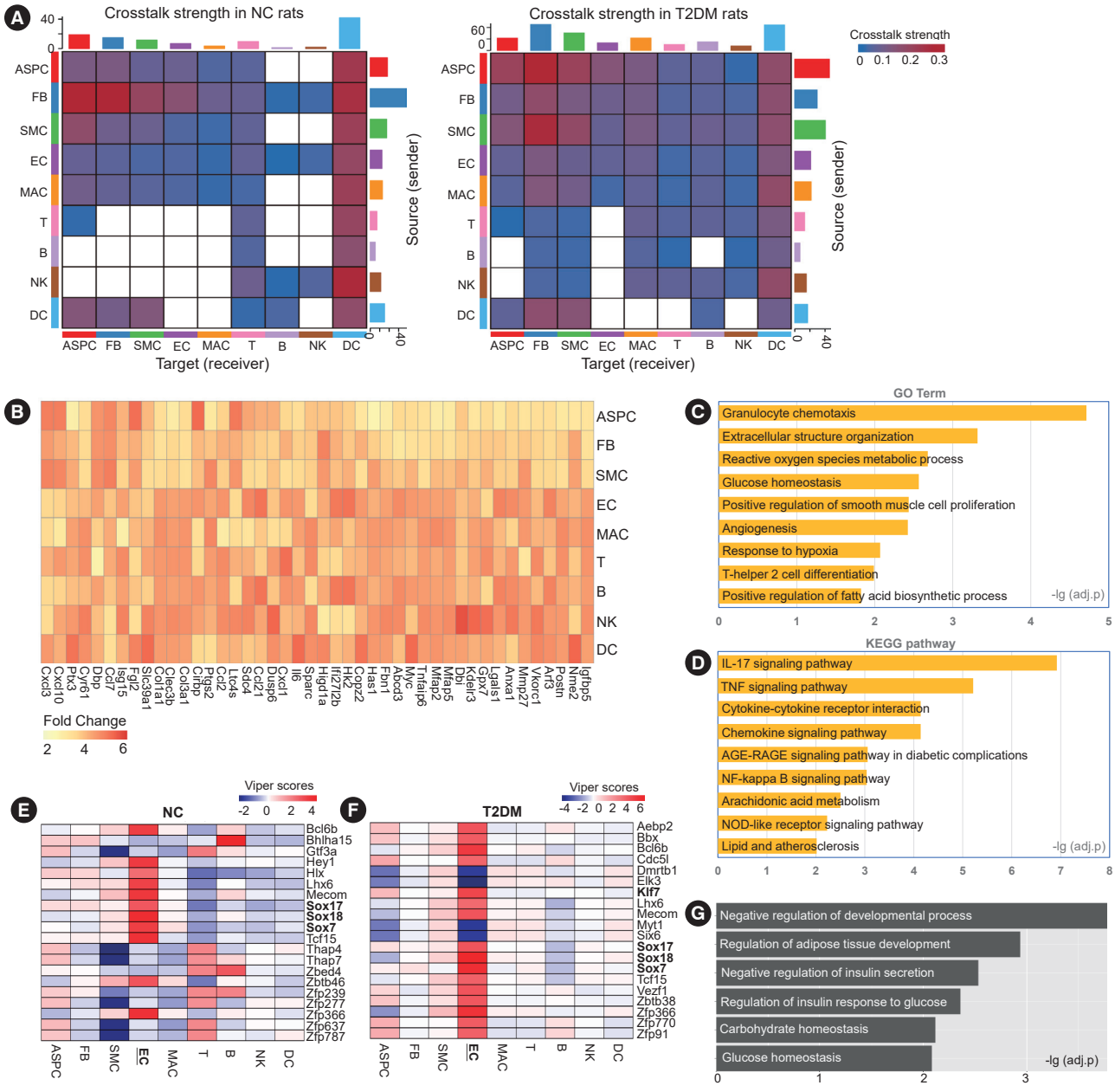

Supplementary Fig. 3. Crosstalk strength between different cell types, conserved responses and transcription factor (TF) activity in brown adipose tissue (BAT) stromal vascular fraction (SVF) of type 2 diabetes mellitus (T2DM) rats. (A) Heatmap of the crosstalk strength between various cell types in the BAT SVF of normal rats (NC) (left panel) and T2DM rats (right panel). The top (right) bar indicates the sum of crosstalk strength in corresponding column (row) in the heatmap. Crosstalk strength: the number/probability of crosstalks among different cell populations calculated by Cellchat. (B-D) Heatmap of fold changes in the expression levels of 44 significantly upregulated genes in all nine cell types of BAT in T2DM rats compared to the NC (B) and their enrichment analysis in the Gene Ontology (GO) Term (C) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway (D). (E, F) Heatmap of viper scores of the top 20 highly active TFs in each cell type of BAT SVF in NC rats (E) and T2DM rats (F). Viper scores: evaluation of TF activity according to virtual inference of protein-activity by enriched regulon analysis. (G) Functional enrichment analysis of the target genes regulated by the TF *Klf7* in endothelial cells (ECs). ASPC, adipose stem/progenitor cell; FB, fibroblast; SMC, smooth muscle cell; MAC, macrophage; NK, natural killer; DC, dendritic cell; IL, interleukin; TNF, tumor necrosis factor; AGE-RAGE, advanced glycation end products-receptor for advanced glycation end products; NF, nuclear factor; NOD, ncleotide oligomerization domain.