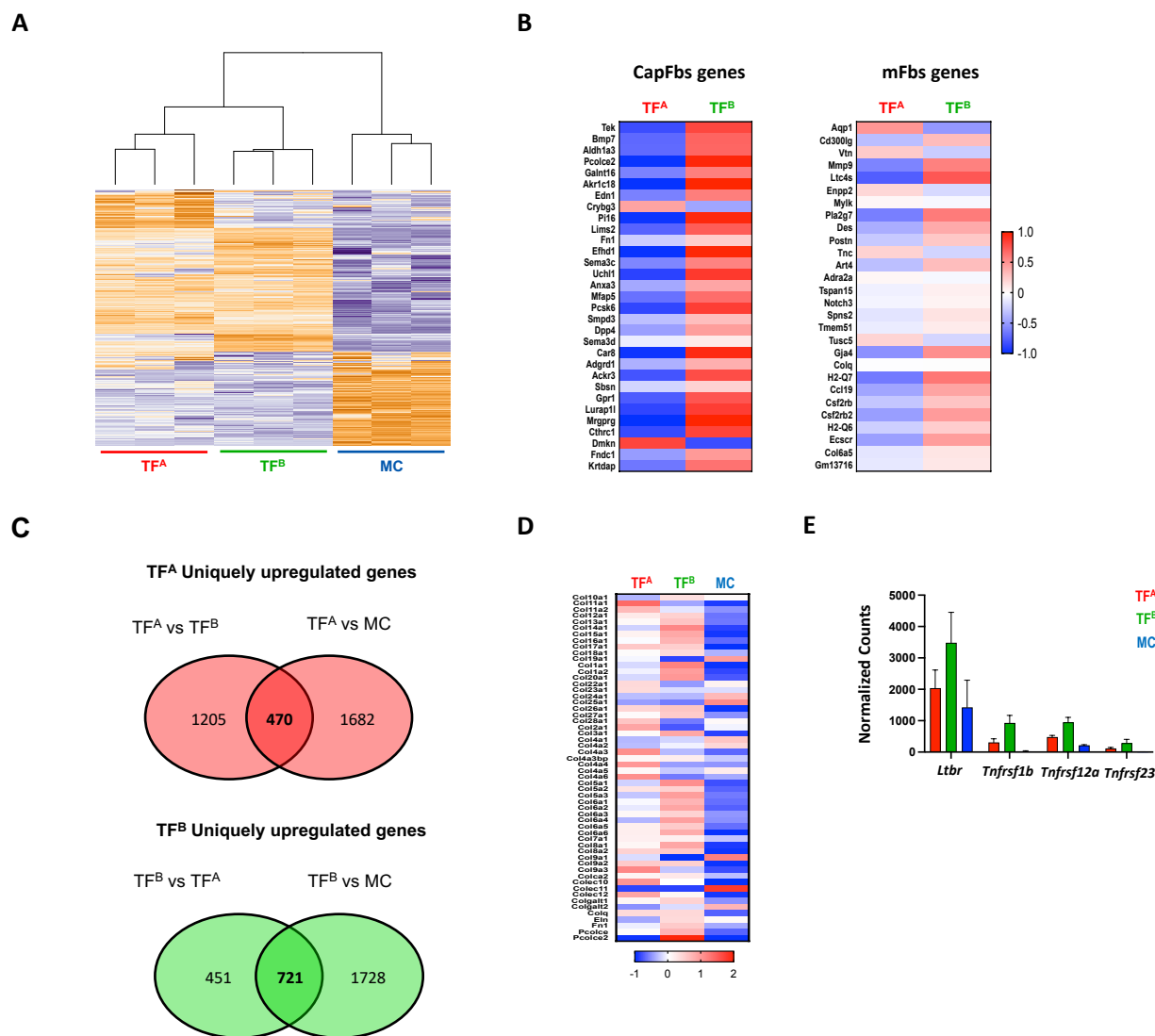


Fig. S1. Gating strategy for flow cytometry analysis of thymic mesenchymal cells. (A) Representative analysis of cells obtained from 1 week-old thymus depicting the gating strategy used to identify TMCs defined as clusters 2 and cluster 3. Numbers in plots indicate the frequency of cells found within each gate.

Supplementary Figure 2



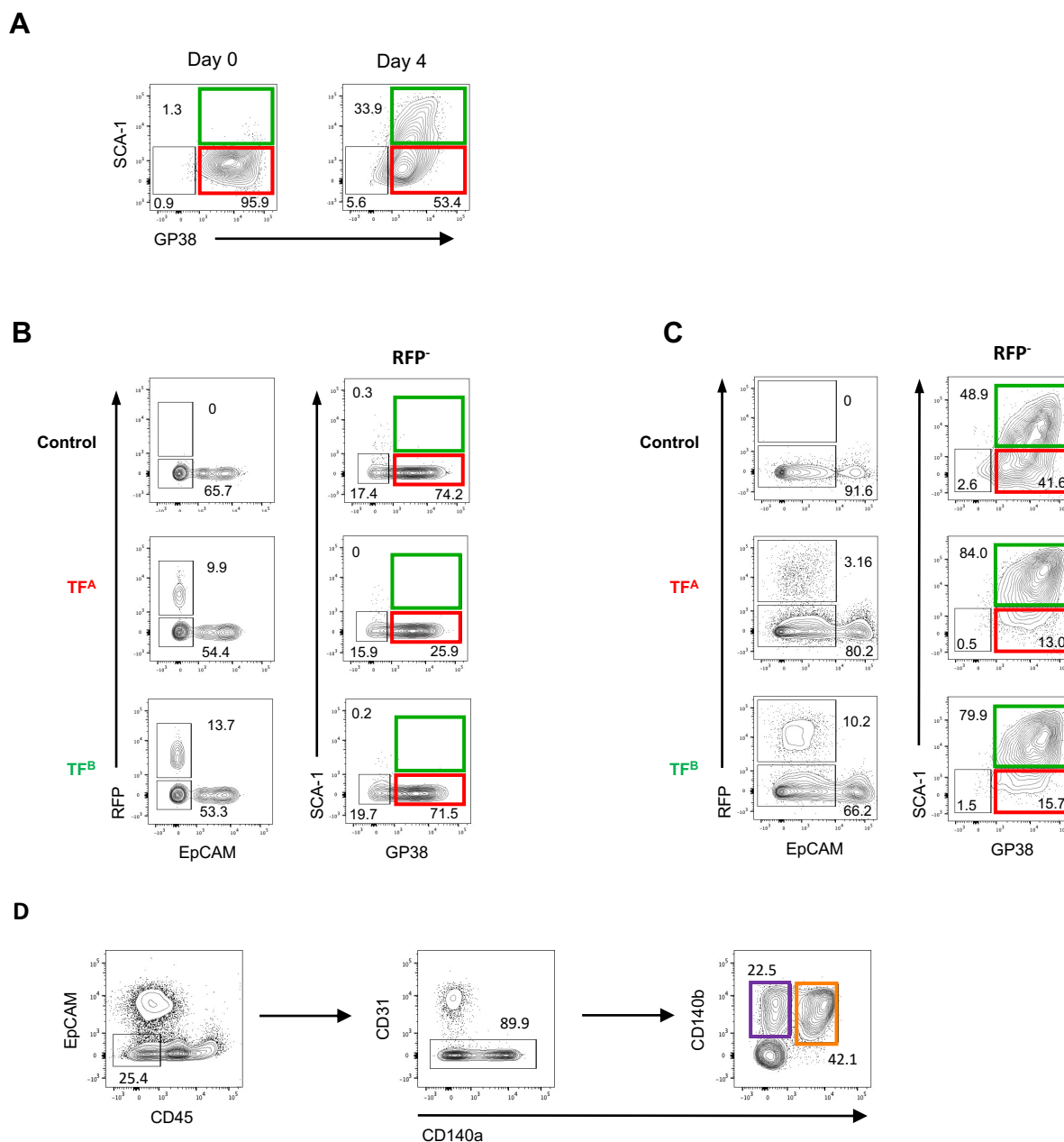


Fig. S3. Precursor-Product relationship between TF subsets. (A) Flow cytometry analysis of the expression pattern of GP38 and SCA-1 at day 0 and after 4 days in culture, from TMCs obtained from fetal thymic organ cultures (FTOC) established with thymic lobes collected from E14 C57BL/6 mice. (B) Flow cytometry analysis of day 0 (input) and day 7 (output) RTOC established by combining cells obtained from disaggregated E14 thymus cells from C57BL/6 mice alone (Control) or co-cultured with either TF^A or TF^B cells isolated from Post-natal day P1-P3 Actin-RFP C57BL/6 mice. (C) Representative analysis of cells obtained from 1 week-old thymus depicting the gating strategy used to identify TMCs defined as clusters 2 and cluster 3 in *RAG2*^{-/-} *I12rg*^{-/-}. Numbers in plots indicate the frequency of cells found within each gate.

Table S1. Total normalized counts for all detected genes in the RNAseq analysis of populations TF^A, TF^B and MC.

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Table S2. Total normalized counts and deviation to the mean expression value obtained for genes used as phenotypic markers of populations TF^A, TF^B and MC and for genes previously associated with pericyte and fibroblast cells.

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Table S3. Total normalized counts and deviation to the mean expression value obtained for genes previously associated with capsular fibroblast cells in our TF^A and TF^B cell populations.

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Table S4. Total normalized counts and deviation to the mean expression value obtained for genes previously associated with medullar fibroblast cells in our TF^A and TF^B cell populations.

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Table S5. Total normalized counts of the uniquely upregulated genes of population TF^A in relation to populations TF^B and MC.

[Click here to download Table S5](#)

Table S6. Total normalized counts of the uniquely upregulated genes of population TF^B in relation to populations TF^A and MC.

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Table S7. Total normalized counts of the gene ontology analysis of the uniquely upregulated genes of population TF^A.

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Table S8. Total normalized counts of the gene ontology analysis of the uniquely upregulated genes of population TF^B.

[Click here to download Table S8](#)

Table S9. Total normalized counts and deviation to the mean expression value obtained for collagen and ECM associated genes in our TF^A and TF^B cell populations.

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