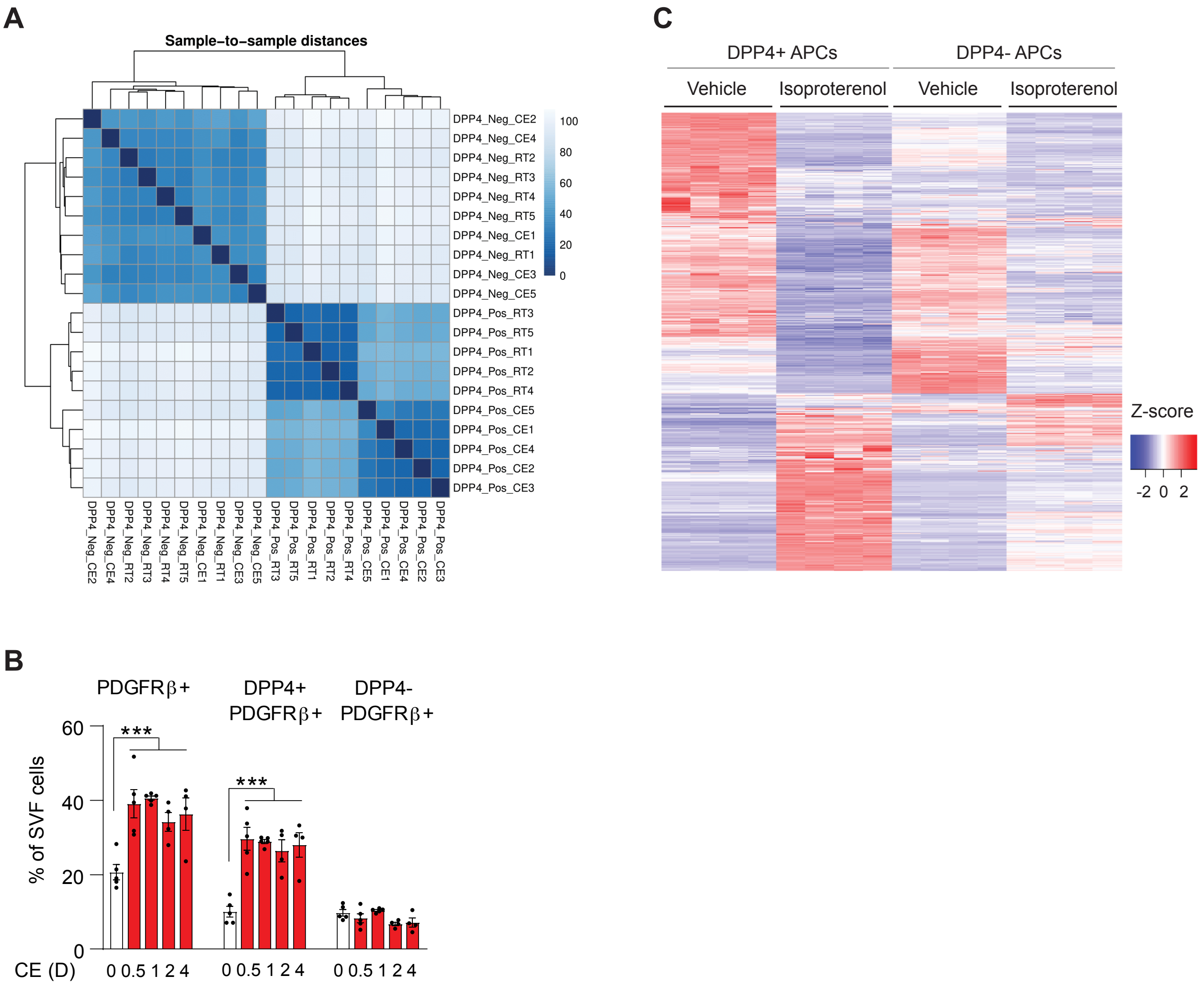

Fig. S2. Transcriptomic analysis of DPP4+ and DPP4- APCs following acute cold exposure or isoproterenol treatment in vitro.

A) Sample clustering analysis based on transcriptomic data obtained by bulk-RNA-seq.

B) The frequencies of total PDGFRβ+ cells, DPP4+ PDGFRβ+ cells DPP4- PDGFRβ+ cells within the stromal vascular fraction (SVF) of iWAT from mice cold exposed (6 ºC) for the indicated numbers of days (D). Mice housed in RT (22 ºC) were used as control ("0"). For 0, 0.5 and 1, n=5 each group; for 2, 4, n=4 each group. Bars represent mean + s.e.m. *** denotes *p*<0.001 by one-way ANOVA.

C) Heat map depicting the change in expression of 4512 genes which are differentially regulated in DPP4+ and DPP4- PDGFRβ+ cells upon treatment with isoproterenol for 4 hours in culture. n=5 for each group. Each sample (n) represents cells pooled from six mice.