Supplementary Figure S1. The isolation and culture of MNGCs and SCs from GCTB samples. A. After a quick centrifuge, the raw MNGCs were stained with Hoechst 33342 for 1h and sorted by a flow cytometric cell sorter. The MNGCs were huge and contained high levels of DNA and were thus clearly gated and sorted. A representative TRAP staining of the isolated MNGCs was shown. D. SCs were isolated and a representative microscopic morphology was shown.

Supplementary Figure S2. Gene microarray and pathway analysis. A, A heat map of genes that are up-regulated over 1.5-fold by IL-17A in IL-17RA+SCs. The IL-17RA+SCs were treated with DMSO or 10 ng/ml IL-17A. After 48 hrs of IL-17A treatment, RNAs were isolated from cells and then subjected to gene microarray analysis. IL-17A pathway in IL-17RA-positive stromal cells. B, Software-assisted identification of pathways affected by IL-17A exposure, as revealed by Ingenuity Pathway Analysis. Differentially-expressed proteins showing a +1.5-fold change or greater were selected and entered into IPA software to illustrate potential interactions.

Supplementary Figure S3. Myc and STAT3 inhibitor treatment suppressed IL-17A stimulated cell proliferation and RANKL expression in IL-17RA+SCs. A, The Myc inhibitor 10058-F4 treatment blocked IL-17A stimulated IL-17RA+ SCs proliferation. B, Treatment with the STAT3 inhibitor AG490 blocked IL-17A-induced RANKL mRNA expression in IL-17RA+SCs. The results are expressed as the mean values ± SD. a,b,c,d data not sharing the same letter are significantly different from one another in each group (P < 0.05) by ANOVA and Duncan's multiple range test.