Description of Additional Supplementary Files

Supplementary Data 1 : This data file contains differential gene expression analysis on synovial tissue single cell RNA sequencing data pertaining to figure 2. Sublining fibroblasts for healthy and RA synovial tissues were subset and DEG performed in Seurat.

Supplementary Data 2 : This data file contains differential gene expression analysis on synovial tissue single cell RNA sequencing data pertaining to figure 2. Sublining fibroblasts for healthy and OA synovial tissues were subset and DEG performed in Seurat.

Supplementary Data 3 : XCMS raw data output of the lipidomics analysis of SPE-chloroform fractions versus SPEacetone fractions from the adipocyte conditioned media (ACM). The reversed phase HPLC-MS (negative ion mode) data were collected and converted to mzdata files and analyzed using R software (version 3.4.2) package XCMS (1.52.0), which reported m/z, retention time, fold change, p-value, and intensity for every data point (n=1,884).”

Supplementary Data 4 : This data file contains differential gene expression analysis pertaining to bulk RNA sequencing data displayed in figure 4. DEGs for basal vs 22hrs of stimulation with FCM, cortisol, or FCM+ mifepristone are included in addition to the gene lists derived from the DEG list to create activation scores for cortisol, FCM, and FCM+ mifepristone.

Supplementary Data 5 : This data file contains data on the number of healthy synovial cells from single cell RNA sequencing which map to a given AMP phase 2 defined cell cluster.

Supplementary Data 6 : This data file contains differential gene expression analysis pertaining to adipose tissue single cell RNA sequencing data displayed in figure 6. Each tab displays the differentially expressed genes among the adipose tissue fibroblast clusters as calculated in Seurat.

Supplementary Data 7 : This data file contains differential gene expression analysis pertaining to bulk RNA sequencing data displayed in supplemental figure 13A-D. DEGs for basal vs 22hrs of stimulation with TNF, TGFB, FCM+TNF, FCM+TGFB, as well as DEGs for basal vs 4hrs of stimulation with FCM, cortisol, or FCM+ mifepristone, TNF, TGFB, FCM+TNF, and FCM+TGFB are included.

Supplementary Data 8 : This data file contains a list of pathways identified by fast gene set enrichment analysis (FGSEA) to be significantly enriched in fibroblasts stimulated with TGFB for 22hrs. Bulk RNA sequencing derived differential gene expression was used as input for FGSEA calculations.

Supplementary Data 9 : This data file contains a list of pathways identified by fast gene set enrichment analysis (FGSEA) to be significantly enriched in fibroblasts stimulated with FCM+ TGFB for 22hrs. Bulk RNA sequencing derived differential gene expression was used as input for FGSEA calculations.

Supplementary Data 10 : This data file contains statistical details for the main figures including n, F, t, DF, and exact p values.