\*\*Carrageenan Inflammation Area Using high resolution ultrasound\*\* The data is organized as follow: There are 6 columns, column A describe the code assigned to each individual animal. Column B represent treatment: 0=No stretch, 1= stretch. Column C refers to the time for the treatment: from 24h to 96h. Column D refers to the batch or group of samples. Column E correspond to the weight of the tissue at the time of euthanasia in mg. Column F represent the ultrasound area of the inflammatory lesion per each sample.

\*\*Neutrophils and macrophage subpopulation.\*\*Analysis was performed using Flow cytometry. The data set is organized as follow:

\*For the neutrophils data:\* There are 9 columns, column A indicates the code assigned to each individual animal. Column B represent treatment: 0=No stretch, 1= stretch. Column C refers to the time for the treatment: from 24h to 96h. Column D refers to the batch or group of samples. Column E indicates the type of cell. Column F is the total cell count per each sample. Column G represent the percentage of live cells per sample. Column H describes the relative number of CD45+ cells (leukocytes). Column I describe the relative number of neutrophils. \*For the macrophages:\* There are 8 columns, column A indicates the code assigned to each individual animal. Column B represent treatment: 0=No stretch, 1= stretch. Column C refers to the time for the treatment: from 48h to 96h. Column D refers to the batch or group of samples. Column E indicates the relative number of CD45+ cells (leukocytes). Column F describe the relative number of F4/80+ cells (macrophages) . Column G describe the relative number of M1 macrophages. Column H describes the relative number of M2 macrophages.

\*\*Single cell and bulk library preparation and sequencing\*\* Data set organization is as follow: For each of the cell populations: classic dendritic cells 1 (cDC1), classic dendritic cells 2 (cDC2), Endothelial cells (EC), Fibroblasts (FB), inflammatory dendritic cells (iDC), M1 macrophages (M1), M2c macrophages (M2c), Mast cells (MC), Monocytes (Mo), T helper cells 1 (Th1), T helper cells 2 (Th2), M2a macrophages (M2a), M2b macrophages (M2b); the data include 7 columns; column A include the total list of analyzed genes. Column B is the statistical significance p value, Column C represent the logarithmic of average expression or log 2FC per each gene. Column D is the actual Fold change expression per each gene. Column E is the gene expression for the Stretch sample (pct.1). Column F is the gene expression for the No stretch sample (pct.2). Column G is the adjusted p value.

\*\*Cell clustering analysis\*\* The data set is organized as follow: There are 3 columns: column A represent each cluster. Column B represent the cluster designation. Column C represent the markers used to designate each cluster.

\*\*LC-MS/MS\*\* Data set was organized as follow: There are 5 columns describing the data: Column A describe the total list of lipid mediators analyzed. Column B describe the average of each lipid mediator in No Stretch samples at 48h. Column C describe the average of each lipid mediator in Stretch samples at 48h. Column D describe the average of each lipid mediator in No Stretch samples at 96h. Column E describe the average of each lipid mediator in Stretch samples at 96h.