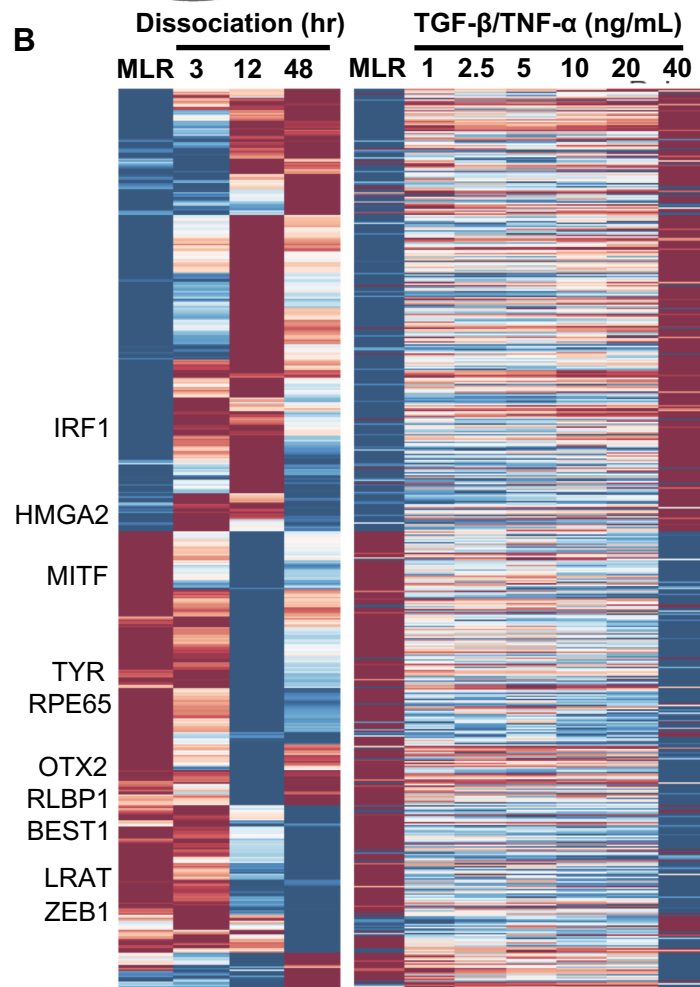
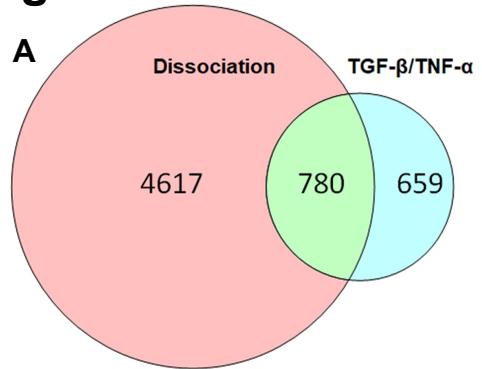
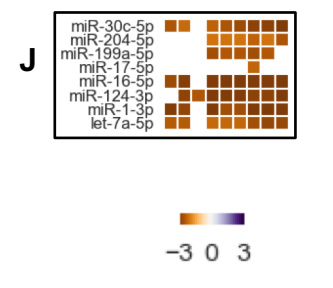
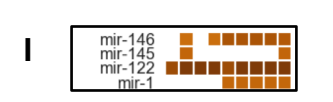
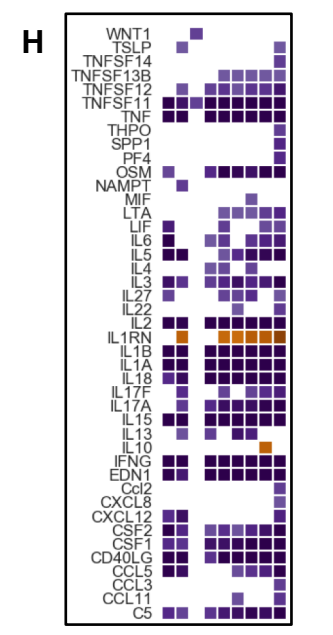
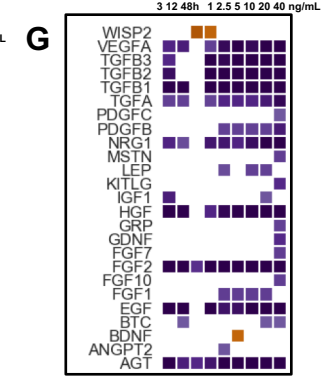
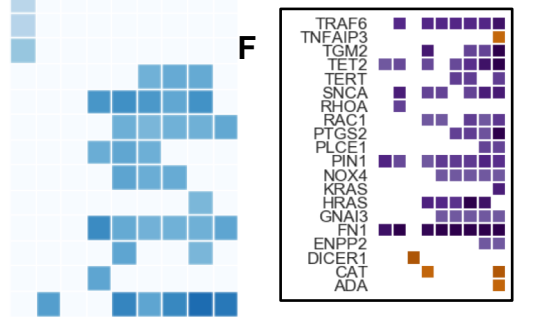
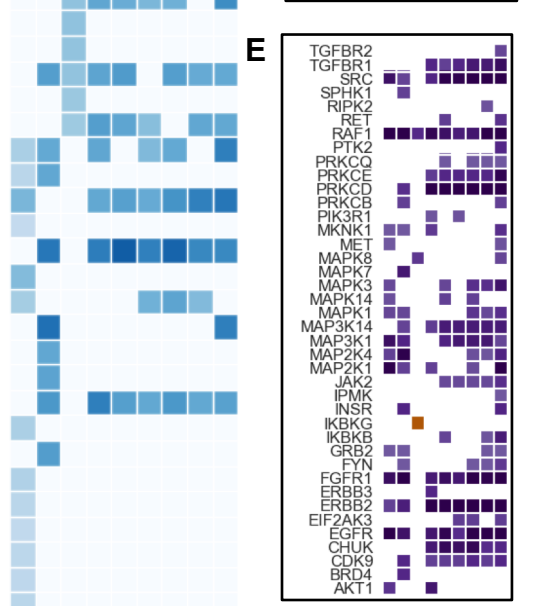
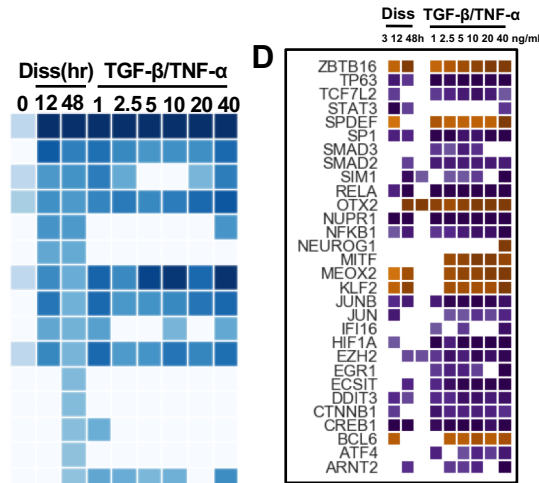
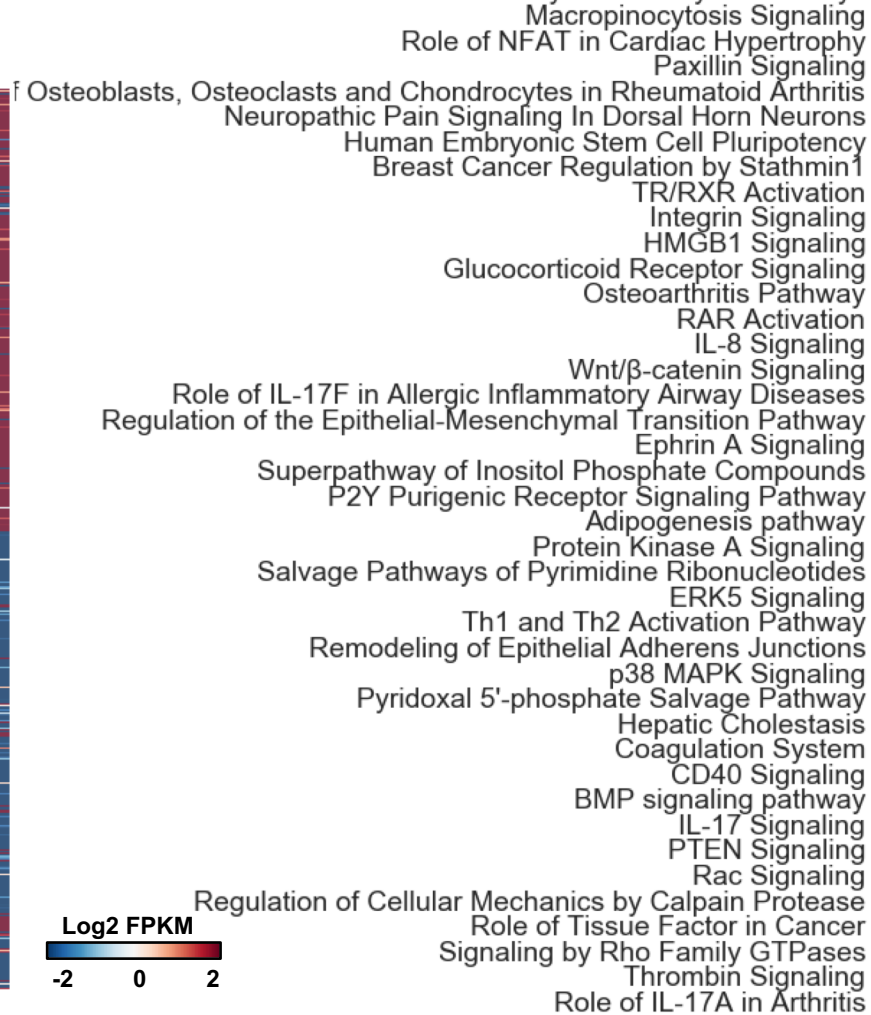


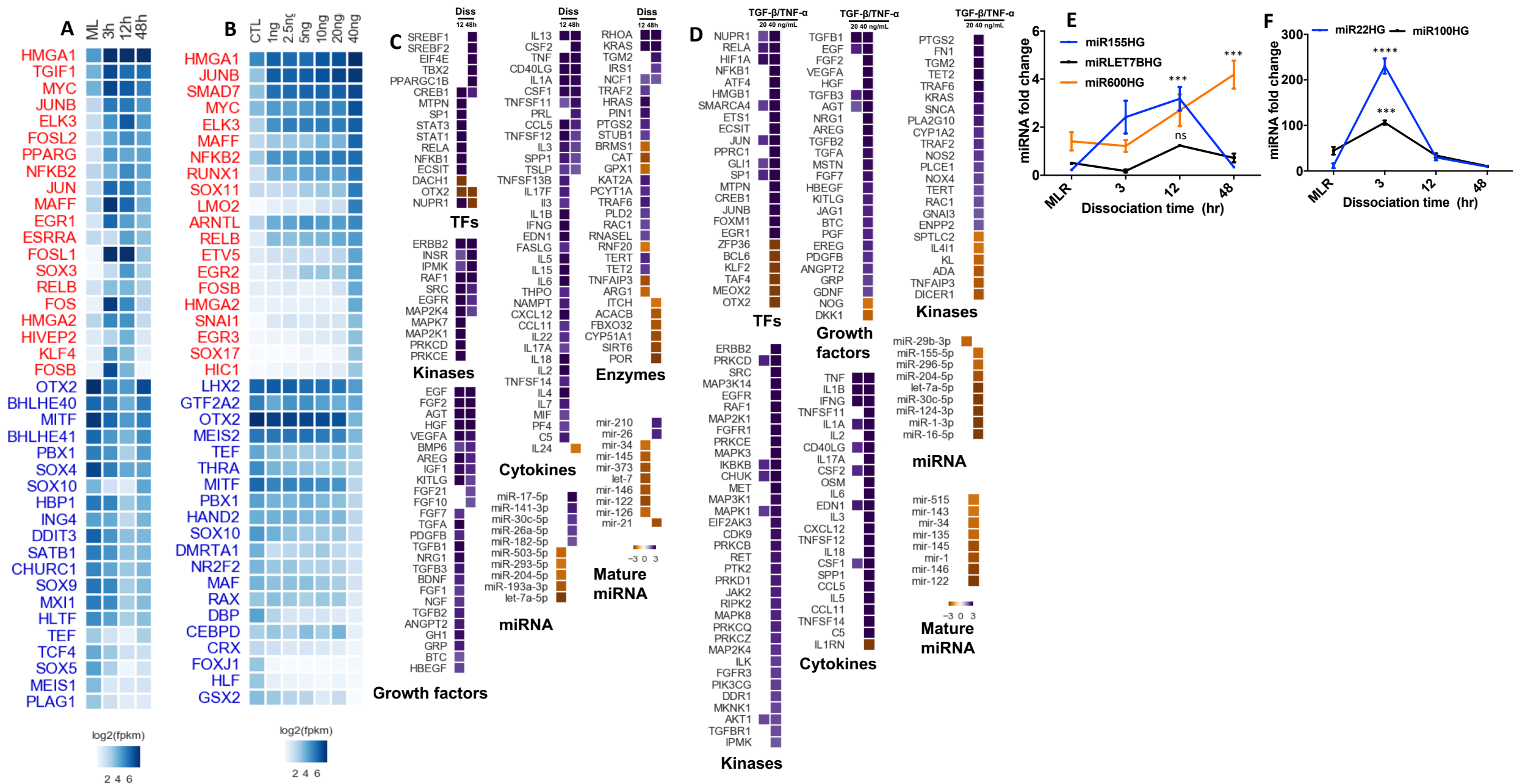
# Figure S1



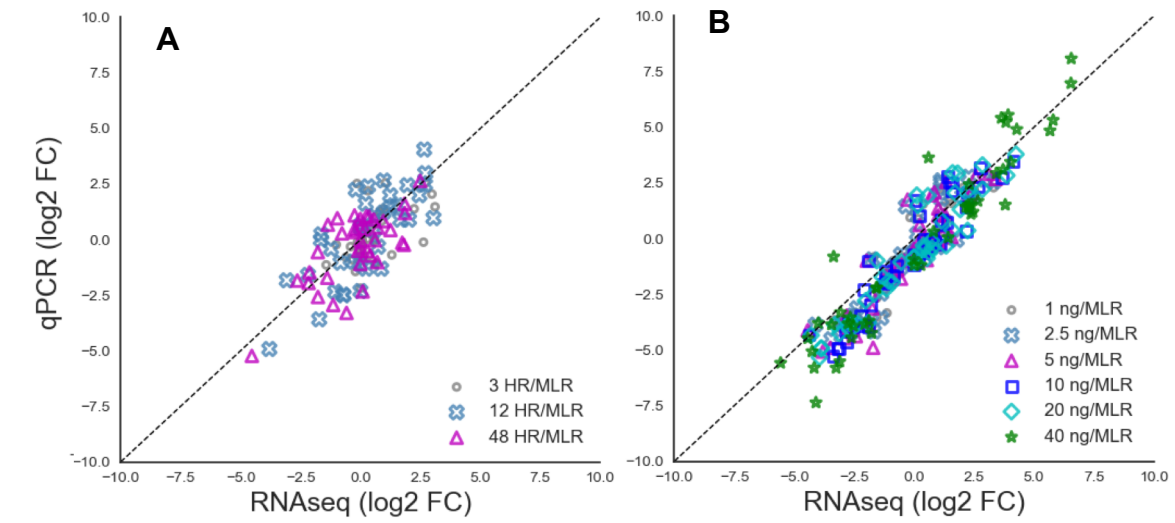
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis



# Figure S2



**Figure S3**



**D**

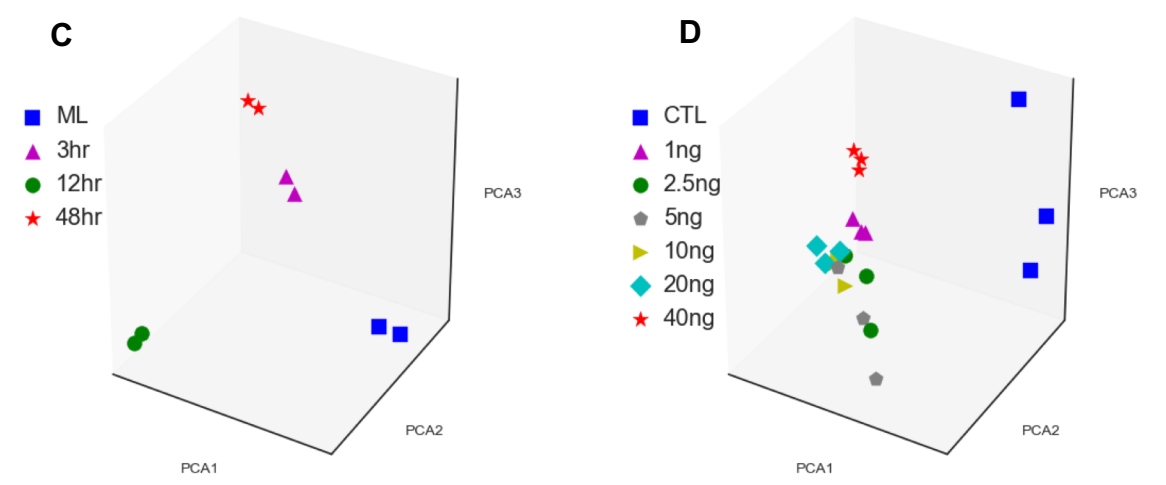


Figure S4

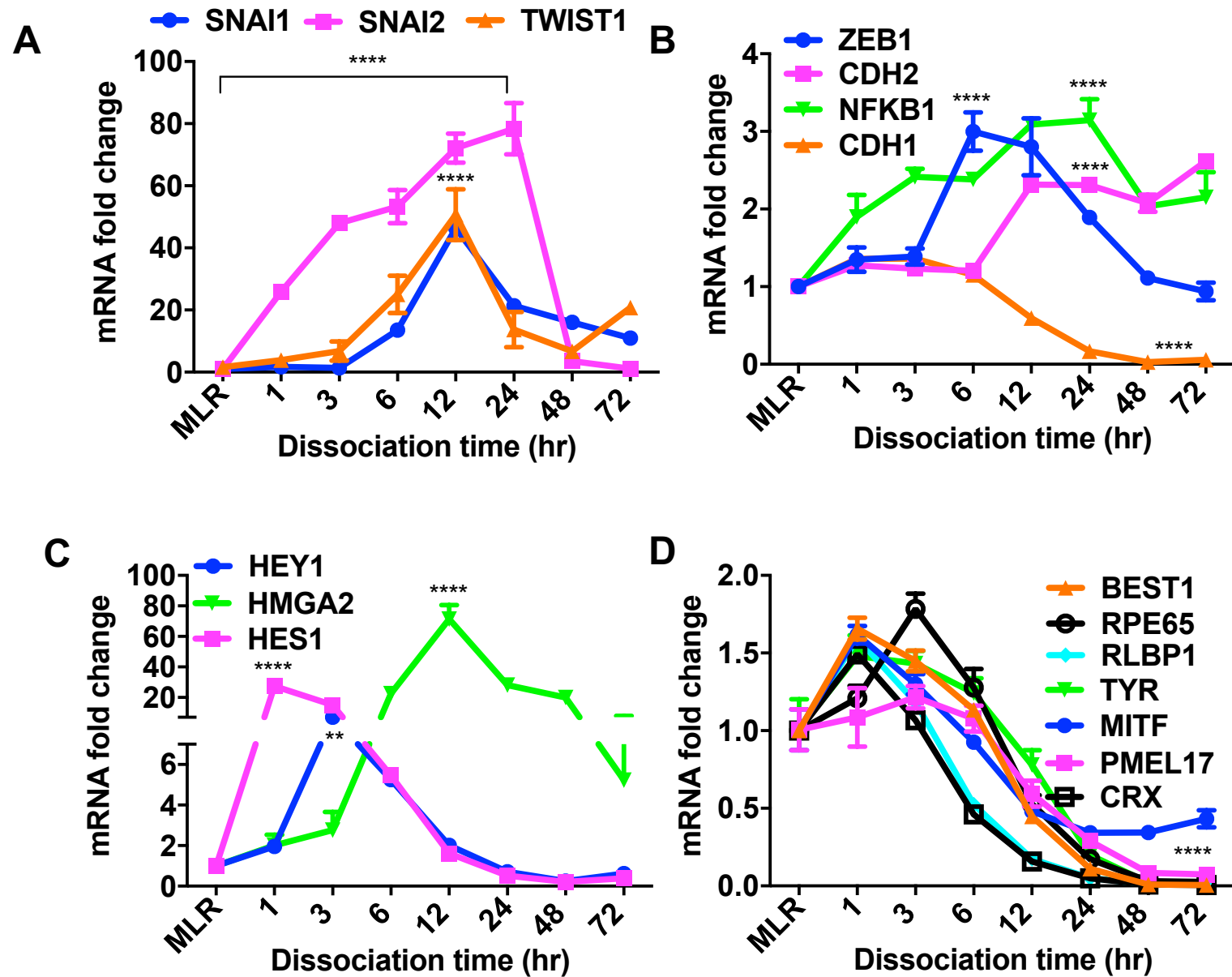
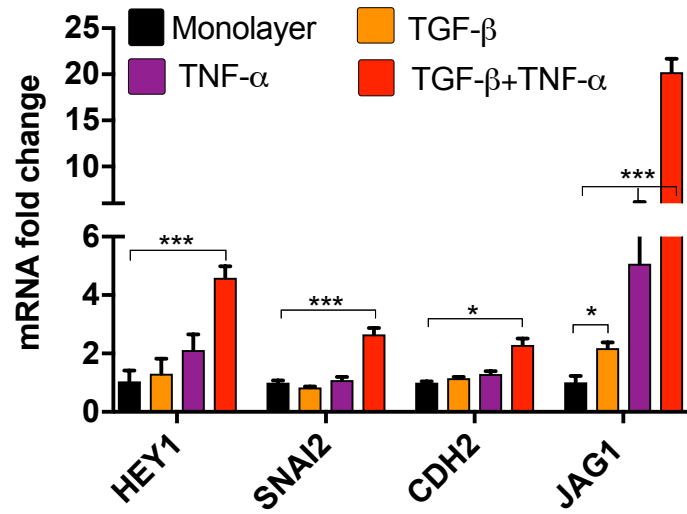
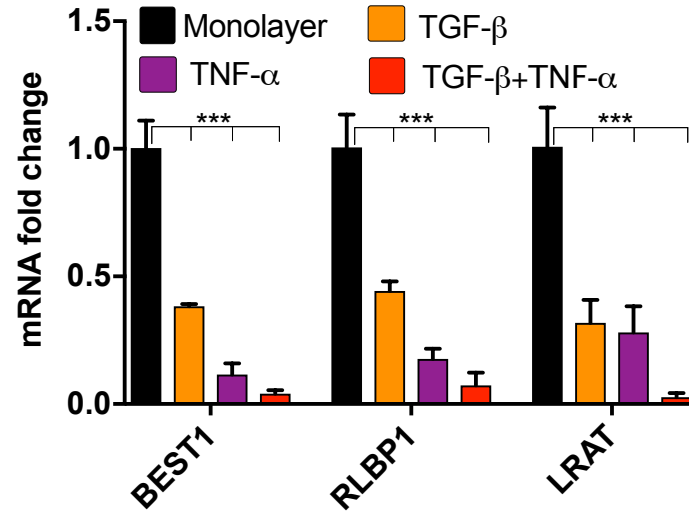


Figure S5

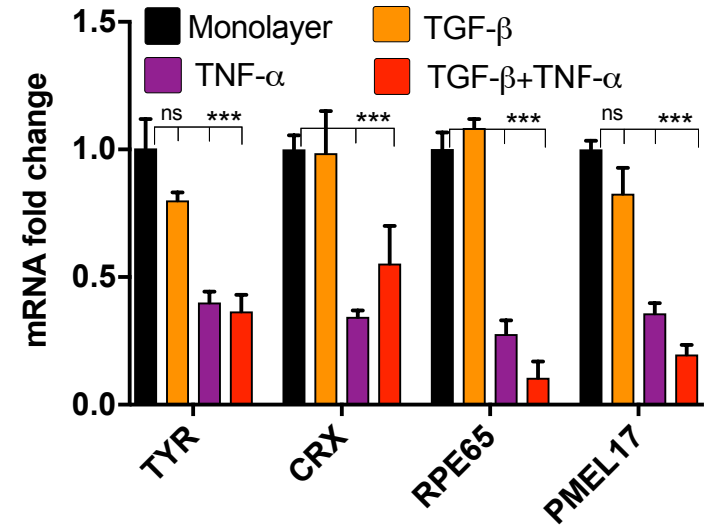
**A**



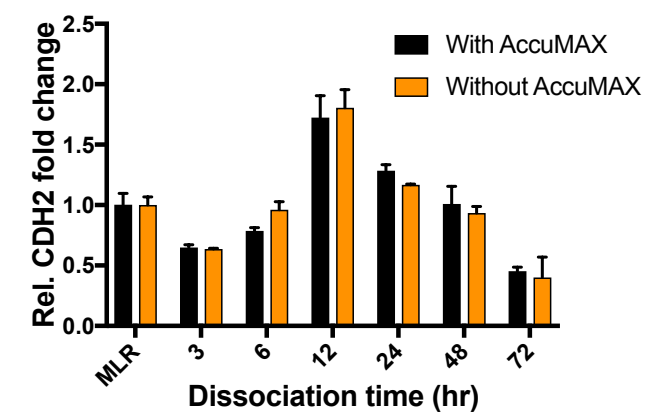
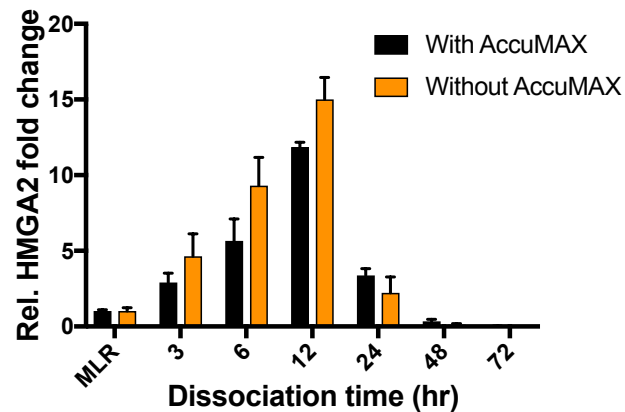
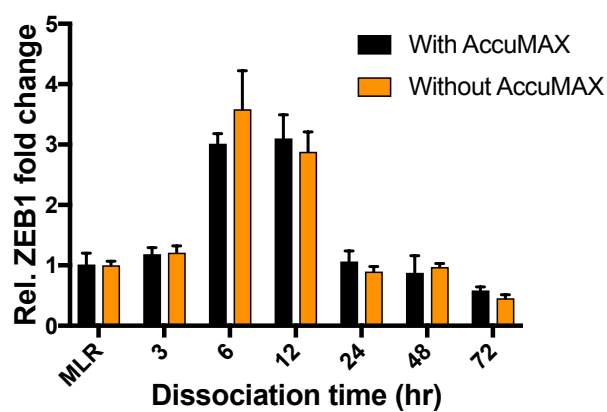
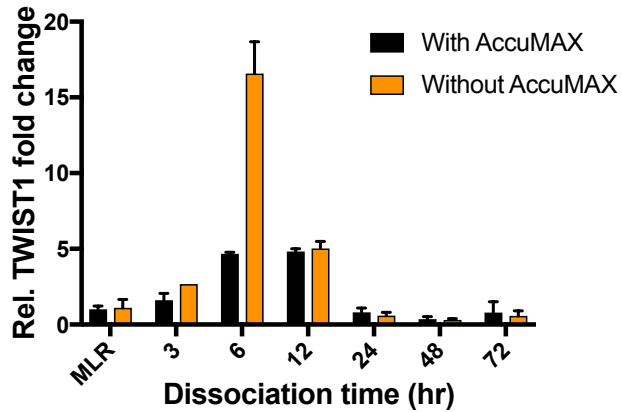
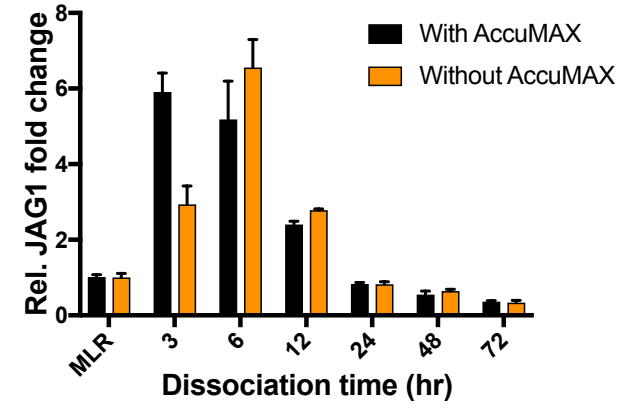
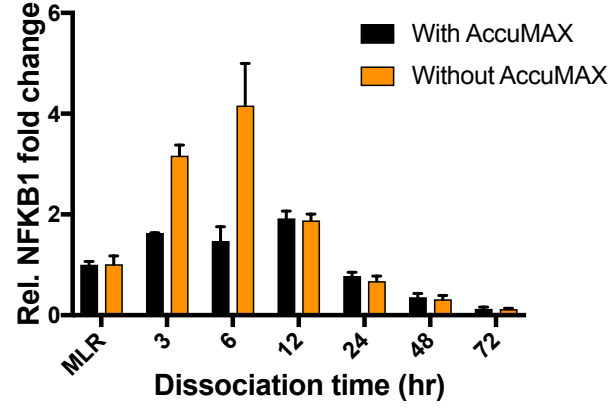
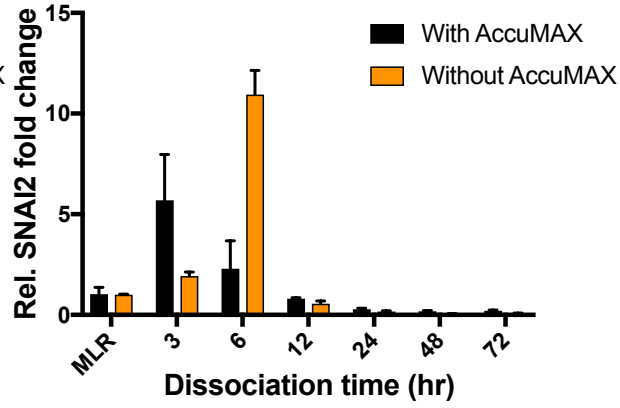
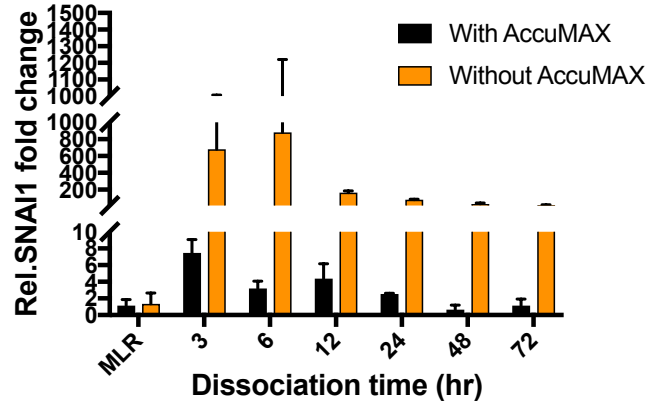
**B**



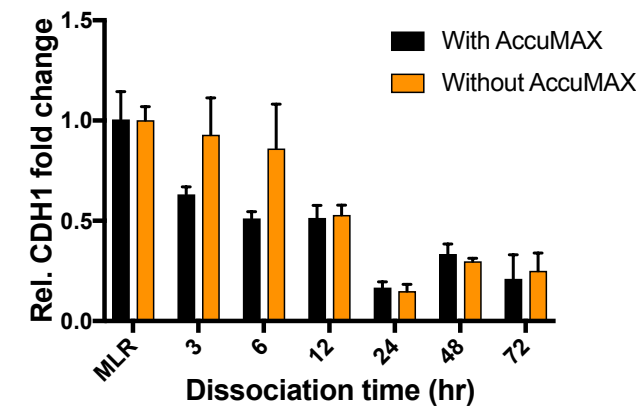
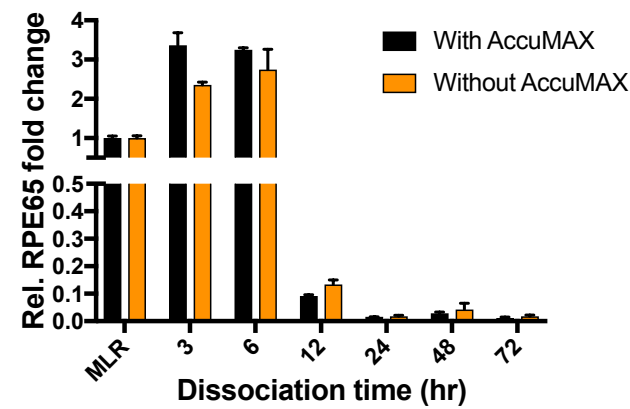
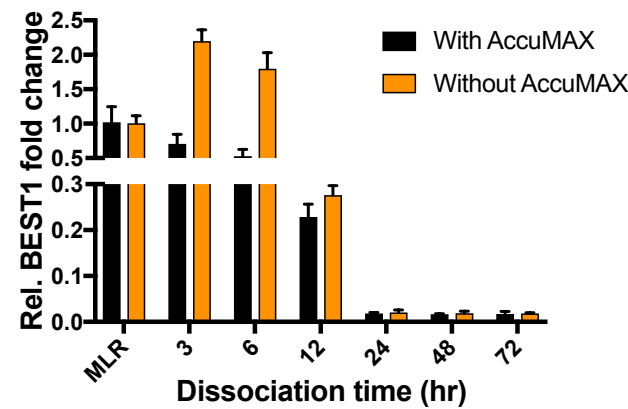
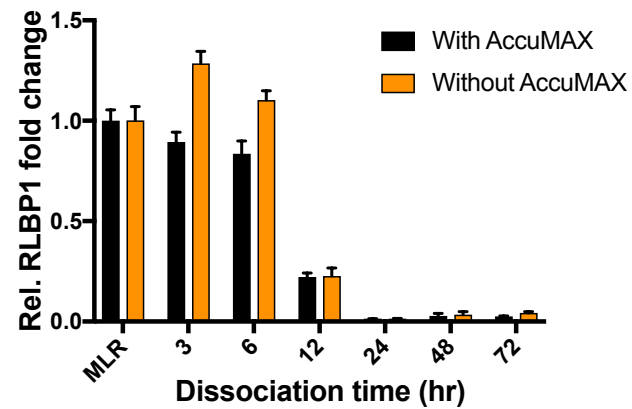
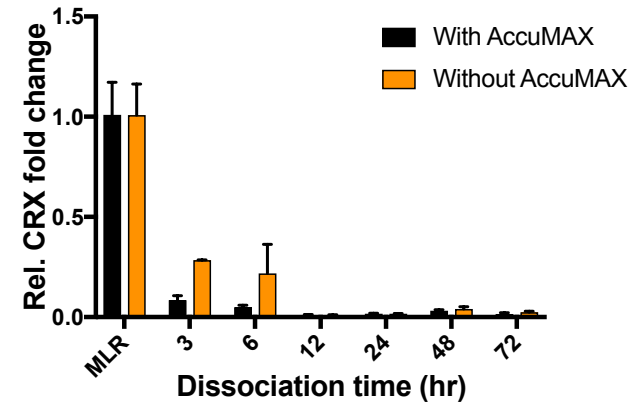
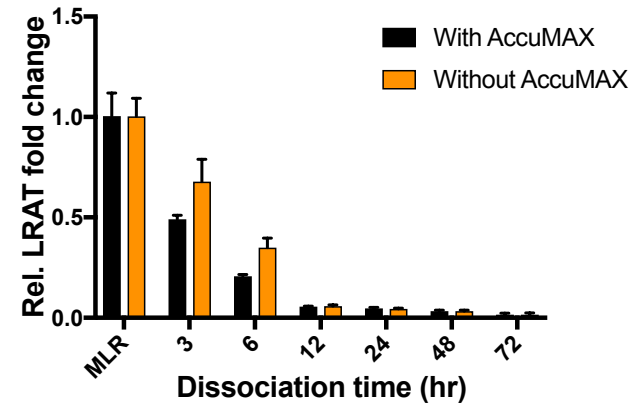
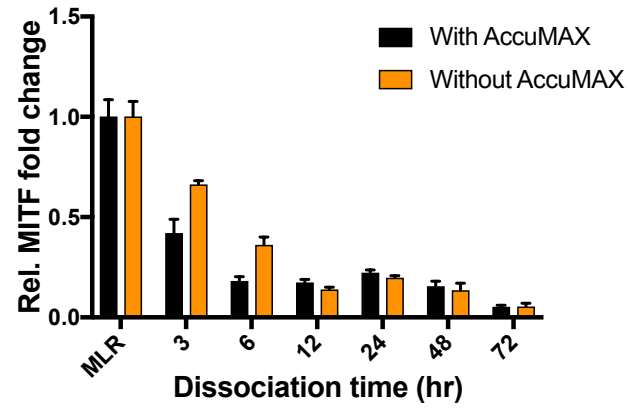
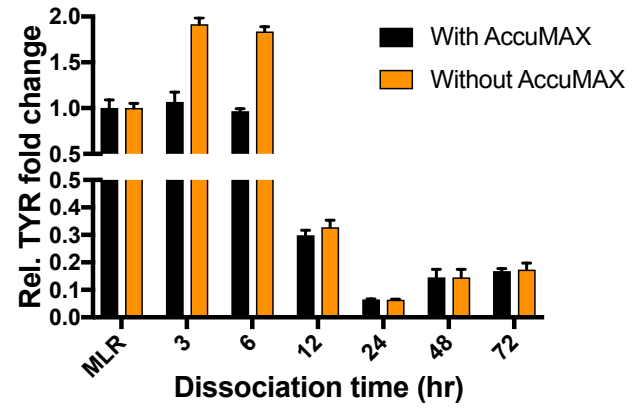
**C**



**Figure S6**



# Figure S7



**Figure S1. Transcriptomic profiling shows commonality between enzymatic dissociation and TGF- $\beta$ /TNF- $\alpha$  induced RPE EMT.**

(A) Venn diagram represents the genes that shares the common number of genes between dissociation (3-48 hr) and TGF- $\beta$ /TNF- $\alpha$  (1-40 ng/mL) induced EMT-RPE. (B) Hierarchical clustering of  $\log_2$ -transformed ratios and average abundances of differentially expressed genes showing significant differences across time point after enzymatic dissociation and TGF- $\beta$ /TNF- $\alpha$  induced RPE-EMT. (C) Top canonical pathways were predicted based on the highly enriched genes that changed in abundance (activated or inhibited) during enzymatic dissociation and TGF- $\beta$ /TNF- $\alpha$  induced EMT were plotted based on p-value. (D-J) Heatmaps of IPA generated upstream regulator analysis from common genes that altered from both RPE-EMT. IPA uses activation Z-score as a statistical measure of the match between expected relationship direction and observed changes in gene expression regulator including (D) transcription regulators (E) kinases (F) enzymes (G) growth factors (H) cytokines (I-J) miRNAs.

**Figure S2. Top transcription factors and upstream regulators of enzymatic dissociation and TGF- $\beta$ /TNF- $\alpha$  induced RPE-EMT.**

Heat maps of top 20 transcription factors that up-regulated (EMT) and down-regulated (RPE) during enzymatic dissociation induced (A) and TGF- $\beta$ /TNF- $\alpha$  (B) induced RPE-EMT. (C) Heatmaps of IPA generated upstream regulators identified from dissociation (C) and TGF- $\beta$ /TNF- $\alpha$  (D) induced RPE-EMT. (E-F) Expression ratios for miRNA were plotted against  $\log_2$  fold change value from the RNA-seq analysis of dissociation induced RPE-EMT.

**Figure S3. Correlation of RPE EMT gene expression ratios between RNA-seq and qRT PCR.**

The expression ratios were plotted against  $\log_2$  fold change value from RNA-seq (x-axis) and qRT PCR was performed using the amplified cDNA from each RNAseq sample (y-axis). Statistically significant Pearson correlation is shown between the gene expression levels analyzed by qRT PCR and RNA-seq (A) Dissociation/Monolayer (39 genes), (B) TGF-B/TNF-A/Monolayer (54 genes). Principal Components Analysis (PCA) of gene expression data from dissociation (C) and TGF-



$\beta$ /TNF- $\alpha$  treatment (D) were significantly correlated. Only genes with statistically significant changes at FDR of 5% ( $q < 0.05$ ) were included in analysis.

**Figure S4. Validation of dissociation induced RPE-EMT in hiPS (IMR90.4) RPE cells.**

Differential expression of key EMT associated genes (A-C) and RPE specific genes (D) were measured by qRT PCR after enzymatic dissociation of monolayers (MLR) into single cells.

**Figure S5. Validation of TGF- $\beta$ /TNF- $\alpha$  induced RPE-EMT in hiPS (IMR90.4) RPE cells.**

Differential expression of key EMT associated genes (A-B) and RPE specific genes (C) were measured by qRT PCR after enzymatic dissociation of monolayers (MLR) into single cells.

**Figure S6. Enzyme-free dissociation induced RPE-EMT.** Differential expression of EMT-associated factor due to the physical (using cell scraper) dissociation.

**Figure S7. Enzyme-free dissociation induced RPE-EMT.** Differential expression of RPE-associated factor due to the physical (using cell scraper) dissociation.

**Dataset S01.** List of genes that enriched during dissociation induced RPE-EMT

**Dataset S02.** List of genes that enriched during TGF- $\beta$ /TNF- $\alpha$  RPE EMT induced RPE-EMT

**Dataset S03.** List of genes that altered from both dissociation and TGF- $\beta$ /TNF- $\alpha$  induced RPE-EMT

**Dataset S04.** List of canonical pathways that enriched during dissociation induced RPE EMT

**Dataset S05.** List of canonical pathways that enriched during TGF- $\beta$ /TNF- $\alpha$  RPE EMT

**Dataset S06.** List of canonical pathways that enriched in common from dissociation and TGF- $\beta$ /TNF- $\alpha$  induced RPE-EMT

**Dataset S07.** Upstream regulator analysis of enzymatic dissociation induced RPE EMT

**Dataset S08.** Upstream regulator analysis of TGF- $\beta$ /TNF- $\alpha$  induced RPE EMT

**Dataset S09.** Upstream regulators that enriched in common from dissociation and TGF- $\beta$ /TNF- $\alpha$  induced RPE-EMT.