

Supplementary Data 1

1. ATAC-seq DCA: Detailed information on regions with differential chromatin accessibility and associated predicted target genes.
2. ATAC-seq Unique Regions by Cell: Detailed information on regions with differential chromatin accessibility stratified by cell line.
3. ATAC-seq Target Genes by Cell: Detailed information on regions with differential chromatin accessibility and associated predicted target genes stratified by cell line.

Supplementary Data 2

1. RNA-seq DGE: Detailed information on differential gene expression between experimental conditions (stromal co-culture).
2. RNA-seq DGE Annotation: Functional annotation of the genes differentially expressed between experimental conditions (stromal co-culture).
3. RNA-seq Discordant by Cell: Differentially expressed genes with limited agreement between the three cell lines (transcripts with discordant behavior in response to stromal co-culture, transcripts outside Bland-Altman limits of agreement, n = 4083 transcripts, 6.73% of all transcripts).
4. RNA-seq Discordant Annotation: Functional annotation of the differentially expressed genes with limited agreement between the three cell lines.

Supplementary Data 3

1. Target Gene Annotation: Functional annotation of the predicted target genes.

Supplementary Software 1

R and Stata code to calculate the S ASI as a summary measure of adverse stromal interactions as well as example data and documentation