

Supplemental Table Legends 1-4:

Supplemental Table 1: Normalized Counts for RNA sequencing of 2D vs. 3D planar co-cultures

This table contains the normalized counts for the TRAP RNA sequencing on the 2D and 3D planar co-culture of HUVECs. This includes the counts for all lots included in each culture type, 2D day 1, 3D day 1, 3D day 4, 3D day 8, as well as the input samples which were taken at 3D day 8.

Supplemental Table 2: Normalized counts for RNA sequencing of Fibrin Bead Assay

The normalized counts for the TRAP RNA sequencing on the second type of 3D co-culture assay, the Fibrin Bead Assay. This includes the input and control samples to validate TRAP is effective in this second type of 3D culture.

Supplemental Table 3: Supporting data for main figures

Supplemental Table 3 contains all supporting data for all of the main figures in the manuscript. Each tab represents a single panel on each figure and is clearly labeled as such. The complete list of tabs corresponding to panels on the main figures with their respective titles are listed as follows:

1. Main-2A: DEGs input vs. TRAP: LogFC1 P value <0.05 (Main figure 2A-C)
2. Main-2B: ShinyGO Analysis of DEGs logFC 3- CellTypeSigDB (Main Figure 2B)
3. Main-2C: ShinyGO Analysis of DEGs logFC 3- Biological Processes (Main Figure 2C)
4. Main 3B- set analysis: Set analysis comparing DEGs from each 3D timepoint back to 2D culture to determine shared and unique sets of DEGs.
5. Main 3B- heatmap: Complete list of all DEGs ordered based on set analysis shared/unique categories for heatmap
6. Main- 3C- all DEGs: Metascape GO analysis for each comparison: 2D vs. 3D day 1 upregulated and downregulated DEGs, 2D vs. 3D day 4 upregulated and downregulated DEGs, and 2D vs. 3D day 8 upregulated and downregulated DEGs.
7. Main- 3C topGO DEGS: DEGs that make up Blood Vessel Development and Mitotic Cell Cycle Upregulated and Downregulated bars for figure 3C horizontal barplot.
8. Main- 4A: Set analysis between Blood Vessel Development GO term complete list and Day 1, Day 4, and Day 8 Unique genesets
9. Main- 4A heatmap: Day unique Blood Vessel Development DEGs included in heatmap
10. Main 5A and 5B: NOTCH Signaling Pathway GO Term (GO: 0007219) genes with counts greater than 25 in 2D vs. 3D day 1
11. Main- 6A: DEGs in Day 4 and Day 8 Mitotic Cell Cycle GO term (GO:0000278) shown across all time points for heatmap
12. Main- 6C and 6D: Image J Cell Count Quantifications - SG2M Reporter Quantification in 2D vs. 3D culture- Main Figure 6C-D

13. Main- 7A: 2D vs. All Q 0.01 multivariate analysis in Qlucore Gene List results for Supplemental Figure 5
14. Main- 7B: Metascape Analysis of DEGs from 2D vs. All Q 0.01 multivariate analysis for "*in vitro morphogenesis*" Gene Signature
15. Main- 7C: GO Gene Set

Supplemental Table 4: Supporting data for supplemental figures

This table contains all supporting data for the supplemental figures in the manuscript. Each tab represents a single panel on each figure and is clearly labeled as such. The complete list of tabs corresponding to panels on the supplemental figures with their respective titles are listed as follows:

1. Sup 2B: RiboTag vs. Input from Fibrin Bead Assay DEGs
2. Sup- 2C: ShinyGO analysis-mSig Cell Type- DEGs between TRAP and Input samples- Bead Assay Supplemental Figure 6D
3. Sup- 2D: ShinyGO Analysis-Biological Processes- DEGs between TRAP and Input samples- Bead Assay Supplemental Figure 6D
4. Sup 3A-3B: 2D vs. 3D day 1 DEGs
5. Sup- 3B: ShinyGO Analysis of DEGs logFC 1- Biological Processes Supplemental Figure 2C
6. Sup- 5A-5B: Raw data from Fiji/Image J quantification of proliferation reporter validation