**Single Cell RNA sequencing in the Placenta Literature Search**

Date of Search: 2/28/19

Pubmed terms: “Placenta” + “Single Cell RNA Sequencing”

“Placenta” + “Single Cell Transcriptomics”

Year Range: 2019-2014 (Don’t bother going beyond this -single cell RNA sequencing wasn’t really feasible before this time)

Number of Hits: 25 (PubMed)  
Number of Hits that are actually what we are looking for: 4

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| --- | --- | --- | --- | --- | --- | --- |
| Citation | Number of Samples Included | Number of Cells Measured | Brief Description of Population | Timepoint Measured | Main Findings | Is Data Publicly Available |
| (Pavličev et al., 2017) | 2 | 87 single cell transcriptomes | Fresh term placenta from normal pregnancies: C section in the absence of labor | Term | To study these, we inferred the cell-cell interactome by assessing the gene expression of receptor-ligand pairs across cell types. We find a highly cell-type-specific expression of G-protein-coupled receptors, implying that ligand-receptor profiles could be a reliable tool for cell type identification. Furthermore, we find that uterine decidual cells represent a cell-cell interaction hub with a large number of potential incoming and outgoing signals | YES  [GSE87726](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE87726) |
| (Liu et al., 2018) | 8 embryos | 1471 cells | 8 weeks placenta and 24 weeks placenta  \*no information about sample population | First and Second Trimesters | New subtypes of cells of the known cytotrophoblast cells (CTBs), extravillous trophoblast cells (EVTs), Hofbauer cells, and mesenchymal stromal cells were identified and cell-type-specific gene signatures were defined. Functionally, this study revealed many previously unknown functions of the human placenta. | YES  [GSE89497](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE89497) |
| (Suryawanshi et al., 2018) | Placental villi: 8  Maternal decidua: 6 | 1524 stromal cells of decidua | Freshly collected first-trimester | First Trimester | Here, we report single-cell RNA sequencing of 14,341 and 6754 cells from first-trimester human placental villous and decidual tissues, respectively. Further detailed analysis revealed proliferating subpopulations, enrichment of cell type-specific transcription factors, and putative intercellular communication in the fetomaternal microenvironment. | No |
| (Tsang et al., 2017) | 4 samples  2 male, 2 female babies | 24,000 nonmarker selected cells | Cesarean section-delivered placentas | Full-term and early preeclamptic | Through integrative analysis with maternal plasma cell-free RNA, we resolved the longitudinal cellular dynamics of hematopoietic and placental cells in pregnancy progression. Furthermore, we were able to noninvasively uncover the cellular dysfunction of extravillous trophoblasts in early preeclamptic placentas. | YES  [Whole-tissue expression](http://portals.broadinstitute.org/genome_bio/human_lincrnas/?q=lincRNA_catalog) |
| (Sun et al., 2019) | Unknown | 1465 trophoblast cells; 7245 cells for sexual dimorphism analysis | Unknown | First trimester | We identified five major cell types (trophoblasts, stromal cells, hofbauer cells, antigen presenting cells and endothelial cells) with unique crosstalk at the maternal-fetal interface. We identified seven unique trophoblast subclusters…we analyzed sex differences in each cell type and identified differences in immune cell function. TGFβ1, β-estradiol, and dihydrotestosterone emerge as upstream regulators of sexually dimorphic genes in a cell type specific manner. Thus, the fetal contribution at the maternal-fetal interface is cell and sex specific. | No |
| (Vento-Tormo et al., 2019) | 11 decidua and 5 placentas from 6-14 gestational weeks & 6 matched peripheral blood mononuclear cells | 70,000 single cell transcriptome | First-trimester | First trimester | We use single-cell transcriptomics to comprehensively resolve the cell states that are involved in maternal-fetal communication in the decidual, during the early pregnancy when the placenta is established. We then used a computational framework to predict cell-type-specific ligand-receptor complexes and present a new database of the curated complexes. By integrating these predictions with spatial in situ analysis, we construct a detailed molecular and cellular map of the human decidual-placental interface | Yes  [E-MTAB-6701](http://www.ebi.ac.uk/microarray-as/aer/result?queryFor=Experiment&eAccession=E-MTAB-6701) (for droplet-based data), [E-MTAB-6678](http://www.ebi.ac.uk/microarray-as/aer/result?queryFor=Experiment&eAccession=E-MTAB-6678) (for Smart-seq2 data) and [E-MTAB-7304](http://www.ebi.ac.uk/microarray-as/aer/result?queryFor=Experiment&eAccession=E-MTAB-7304) (for the whole-genome sequencing data). |

Works Cited

Liu, Y., Fan, X., Wang, R., Lu, X., Dang, Y.-L., Wang, H., Lin, H.-Y., Zhu, C., Ge, H., Cross, J.C., et al. (2018). Single-cell RNA-seq reveals the diversity of trophoblast subtypes and patterns of differentiation in the human placenta. Cell Res. *28*, 819–832.

Pavličev, M., Wagner, G.P., Chavan, A.R., Owens, K., Maziarz, J., Dunn-Fletcher, C., Kallapur, S.G., Muglia, L., and Jones, H. (2017). Single-cell transcriptomics of the human placenta: inferring the cell communication network of the maternal-fetal interface. Genome Res. *27*, 349–361.

Sun, T., Gonzalez, T.L., Deng, N., DiPentino, R., Clark, E.L., Lee, B., Tang, J., Wang, Y., Stripp, B.R., Yao, C., et al. (2019). The maternal-fetal interface of successful pregnancies and impact of fetal sex using single cell sequencing. BioRxiv.

Suryawanshi, H., Morozov, P., Straus, A., Sahasrabudhe, N., Max, K.E.A., Garzia, A., Kustagi, M., Tuschl, T., and Williams, Z. (2018). A single-cell survey of the human first-trimester placenta and decidua. Sci. Adv. *4*, eaau4788.

Tsang, J.C.H., Vong, J.S.L., Ji, L., Poon, L.C.Y., Jiang, P., Lui, K.O., Ni, Y.-B., To, K.F., Cheng, Y.K.Y., Chiu, R.W.K., et al. (2017). Integrative single-cell and cell-free plasma RNA transcriptomics elucidates placental cellular dynamics. Proc. Natl. Acad. Sci. U. S. A. *114*, E7786–E7795.

Vento-Tormo, R., Efremova, M., Botting, R.A. *et al.* Single-cell reconstruction of the early maternal–fetal interface in humans. *Nature* **563,**347–353 (2018).