

<https://doi.org/10.7124/bc.000B8D>

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PILOT MULTI-COMPARTMENT TRANSCRIPTOMIC PROFILING OF THE FETAL-MATERNAL INTERFACE IN INTRAUTERINE GROWTH RESTRICTION

Background. Intrauterine growth restriction (IUGR) is associated with impaired placental function and increased perinatal risk. The fetal-maternal interface includes placental villi, decidua, amnion and maternal immune cells; therefore, multi-compartment transcriptomics may provide a broader view of IUGR. **Aim.** To establish a targeted transcriptomic workflow for IUGR and compare expression across amnion, decidua, placental villi and maternal blood mononuclear cells. **Materials and Methods.** Samples were obtained from one control and one severe IUGR pregnancy. For each case, amnion, decidua, trophoblast-enriched placental villi and maternal blood mononuclear fraction were collected. The IUGR case showed fetal growth below the 3rd percentile, oligohydramnios, pathological uterine artery blood flow, growth restriction from 24 weeks and delivery at 35 weeks. Targeted sequencing used Ion Torrent S5 / AmpliSeq Transcriptome. Analysis included count processing, normalization, PCA, sample distances and exploratory DESeq2-based batch-aware expression comparison with log2 fold-change shrinkage. Further samples are stored. **Results.** PCA demonstrated strong separation between biological compartments; the first two principal components explained 77% of total variance. Sample-distance analysis confirmed compartment-specific clustering. Exploratory batch-aware IUGR-control comparison highlighted the genes of interest including HLA-C, HLA-DMB, TAS2R43, PSMD5, SMN2 and MRPS21. Because the current study includes one biological case per condition, adjusted *p*-values were not interpreted as confirmatory evidence. Functional enrichment and RT-qPCR validation are planned after cohort expansion. **Conclusion.** Multi-compartment transcriptomic profiling of the fetal-maternal interface in IUGR is feasible. At this pilot stage, the principal result is compartment-specific transcriptomic separation rather than definitive IUGR-control discrimination. Cohort expansion will allow replicated tissue-specific comparisons, functional analysis, candidate validation and integration with systems-level models of placental pathology. **Funding.** Research was partially supported by ALT Ukraine LLC and CHEMLABORREACTIV LLC.

Keywords: placenta, IUGR, transcriptome, NGS.

Received: 06.07.2026; Accepted: 08.09.2026; Published: 29.09.2026

Citation: Rodriguez R.R., Gukovsky R.V., Martsenyuk O.P., Zahorodnia O.S., Koziaruk A.A., Obolenska M.Yu. (2026) Pilot multi-compartment transcriptomic profiling of the fetal-maternal interface in intrauterine growth restriction. *Biopolymers & Cell*, Special issue(42), 82. <https://doi.org/10.7124/bc.000B8D>

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