

Genome-wide expression profile of trophoblastic cells during late pregnancy in ewes

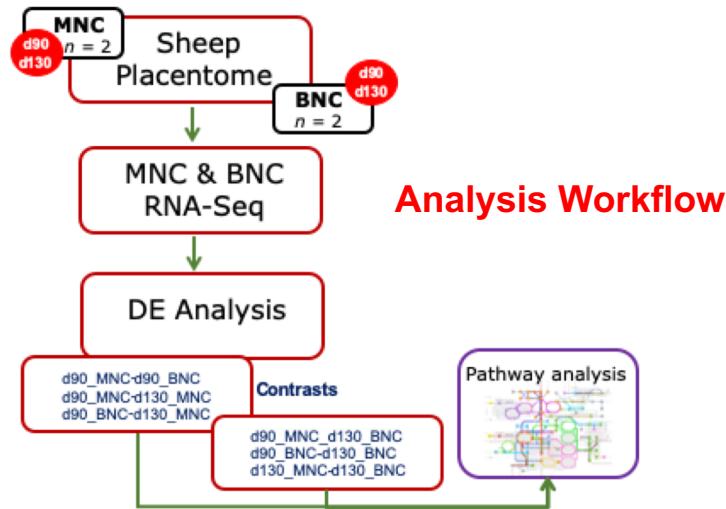
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Introduction

The placenta plays a pivotal role in fetal-maternal communication.

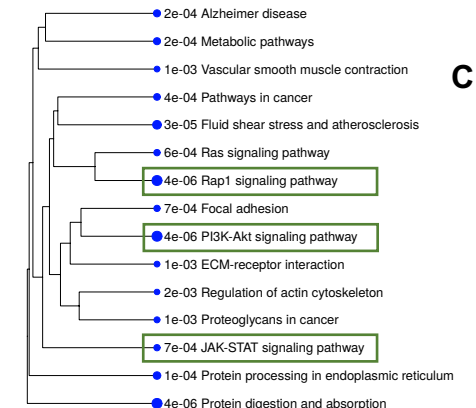
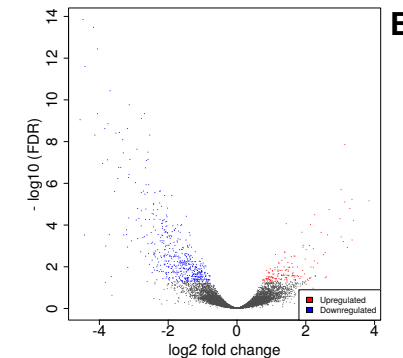
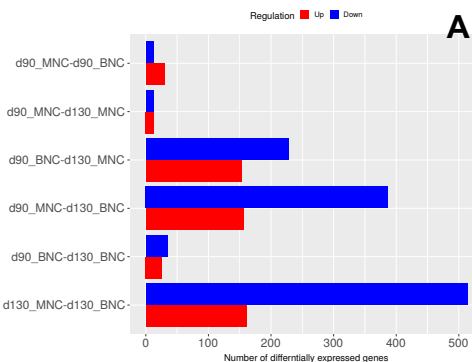
To identify differentially expressed genes (DEG) and regulatory pathways underlying placentation, a genome-wide expression profile analysis of trophoblast mononuclear (MNC) and binuclear (BNC) cells from ovine placentomes on day 90 and 130 of pregnancy was performed.

Material & Methods



Results

Among six pairwise contrasts possible (A), we focused on the one between **MNC** and **BNC** on day 130. Accordingly, we identified 514 upregulated genes and 161 downregulated in BNC (B) (adj.Pval ≤ 0.05). We found nine DE long intergenic noncoding RNAs that have been associated with gene expression regulation *in utero*. We identified the *PLA2G10* gene which is involved in the production of prostaglandins and has been associated with placental blood flow. The functional analysis is shown in (C). Some of these pathways are involved in cell proliferation and differentiation, morphogenesis, and energy metabolism.



Conclusion

These findings suggest an intricate and complex network of gene expression changes between cell types and time points that are essential for the fetal-maternal placenta relationship.

