**Digital Commons – Data Fields**

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**Title of Your Dataset or Journal article:**

Mapping transcriptional changes associated with the maternal-to-embryonic transition in bovine embryos to small non-coding RNA profiles in both in vitro-fertilized and scNT cattle embryos. Supplementary File 2 – Results of DESeq2 analyses for annotated mRNAs

**Description (short description of your dataset; indicate it is supporting an article):**

Microsoft Excel document with results of DESeq2 differential expression analysis comparing scNT vs IVF embryos at each developmental stage and sequential comparisons of developmental stage for both IVF and scNT embryos. This data set is supporting material for a dissertation and a forthcoming journal article.

**Comments**:(*anything you need people to know right up front – special software they will need to use your data? Order of download or use? This information appears on the front of the Digital Commons page, with the title, the Journal title, authors, etc. so it’s a good place to show users important information*)

This file includes three spreadsheets providing results of DESeq2 analyses for mRNAs. For each spreadsheet, the pairwise comparisons are noted with the two naming conventions. First, for sequential comparisons by stage: “embryo type: sample A vs. sample B” (e.g., IVF: Oo vs 2c). Second, for comparisons of scNT vs IVF embryos at a specific stage: “scNT vs IVF: stage” (e.g., scNT vs IVF: Mo).

Abbreviations are: for embryo type, *in vitro* fertilized(IVF) or somatic cell nuclear transfer (NT); and for developmental stage, fibroblasts (Fb), oocytes (Oo), 2-cell stage embryo (2c), 8-cell stage embryo (8c), morula stage embryo (Mo), blastocyst stage embryo (Bl), blastocyst derived cells (BSCs).

For each comparison, results of the DESeq2 analyses are provided as outlined below:

|  |  |
| --- | --- |
| **Supplementary file 2 column definitions.** | |
| ID | Ensemble transcript accession ID |
| baseMean | The mean of normalized counts of all samples, normalizing for sequencing depth |
| Log2FoldChange | Average log2 fold change calculated for comparison indicated in the top row name |
| lfcSE | Log2 standard error of the calculated average log2 fold change |
| stat | Wald statistic |
| P-value | Wald test unadjusted P-value |
| Padj | False discovery rate adjusted P-value using the Benjamini-Hochberg method |

**Discipline:** Developmental Biology

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*You can see a list of disciplines here:* [*http://network.bepress.com/*](http://network.bepress.com/)

*At the bottom of the page, you can click and drill down through the subsequent pages to see additional breakdown*.

**Keywords:**

Transcriptome, mRNA, maternal-to-embryonic transition, embryonic genome activation, somatic cell nuclear transfer, microRNA

**Journal:** TBD

*If applicable, name of journal in which your article is appearing that your dataset is supporting*

**Volume, Issue, Date (year is fine that is all you have):** TBD

*For journal issue*

**Embargo:** 12/31/2020

*Date that you want the data to be made public. If immediate, enter today’s date*