**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 3 – Results of Metascape ontology analyses for differentially expressed mRNAs

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

Microsoft Excel document with results of Metascape ontology analyses for biological processes associated with predicted mRNA targets of differentially expressed miRNAs. 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 multiple spreadsheets, each providing the results of the Metascape ontology enrichment analysis. The spreadsheets are labeled according to the specific comparison made. For comparisons of scNT vs IVF embryos at a specific stage: “scNT vs IVF at stage” (e.g., scNT vs IVF at Mo). For sequential comparisons by stage: “stage A vs stage B for embryo type” (e.g., Oo vs 2c for IVF).

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).

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| **Supplementary file 5 column definitions.** | |
| GroupID | Indicates whether the term is a member of the cluster of terms, or the term that serves as the overall label (summary) |
| Category | Specifies the type of ontology term (biological process, cellular compartment, or molecular function) |
| Term | Accession number for the ontology term |
| Description | Descriptive name of the ontology term |
| LogP | Log10 p value |
| Log(q-value) | Log10 of the false discovery rate-corrected p-value (the q-value) |
| InTerm\_InList | Number of genes within the query set that are annotated by that term/number of genes in the complete list for that term |
| Genes | Gene ID accession numbers for all genes that were annotated with that term |
| Symbols | Gene symbols for all genes that were annotated with that term |

**Discipline:** Developmental Biology

*We usually select based on your department and area*

*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*