S5 Table. Full list of biological pathways with significant p-value (p<0.05) predicted as modulated by 6 miRNAs (bta-miR-133b, bta-miR-205, bta-miR-584, bta-miR-551a, bta-miR-1193 and bta-miR-1225-3p) up-regulated in OECs from non-pregnant compared to pregnant cows.

| Pathways | Number of genes | P-value |
|----------|----------------|---------|
| bta04360 Axon guidance | 70 | 0 |
| bta04014 Ras signaling pathway | 91 | 0 |
| bta04010 MAPK signaling pathway | 105 | 0 |
| bta05212 Pancreatic cancer | 37 | 0.0001 |
| bta04062 Chemokine signaling pathway | 67 | 0.0003 |
| bta05220 Chronic myeloid leukemia | 34 | 0.0005 |
| bta04810 Regulation of actin cytoskeleton | 71 | 0.0008 |
| bta04068 FoxO signaling pathway | 49 | 0.0008 |
| bta05214 Glioma | 33 | 0.0009 |
| bta05200 Pathways in cancer | 155 | 0.001 |
| bta04530 Tight junction | 61 | 0.0011 |
| bta05205 Proteoglycans in cancer | 68 | 0.0014 |
| bta00565 Glycerophospholipid metabolism | 40 | 0.0015 |
| bta04722 Neurotrophin signaling pathway | 45 | 0.0016 |
| bta04072 Phospholipase D signaling pathway | 53 | 0.0018 |
| bta04660 T cell receptor signaling pathway | 40 | 0.0023 |
| bta01522 Endocrine resistance | 36 | 0.0027 |
| bta04921 Oxytocin signaling pathway | 52 | 0.0027 |
| bta04012 ErbB signaling pathway | 33 | 0.0028 |
| bta04514 Cell adhesion molecules (CAMs) | 53 | 0.0035 |
| bta04912 GnRH signaling pathway | 35 | 0.0038 |
| bta04928 Parathyroid hormone synthesis, secretion and action | 38 | 0.0039 |
| bta05215 Prostate cancer | 36 | 0.0046 |
| bta04550 Signal pathways regulating pluripotency of stem cells | 48 | 0.0046 |
| bta04710 Circadian rhythm | 16 | 0.0047 |
| bta04310 Wnt signaling pathway | 53 | 0.0052 |
| bta04611 Platelet activation | 42 | 0.0053 |
| bta05211 Renal cell carcinoma | 28 | 0.0054 |
| bta04925 Aldosterone synthesis and secretion | 35 | 0.0056 |
| bta04020 Calcium signaling pathway | 63 | 0.0061 |
| bta05163 Human cytomegalovirus infection | 74 | 0.0061 |
| bta04934 Cushing syndrome | 51 | 0.0061 |
| bta04071 Sphingolipid signaling pathway | 41 | 0.0072 |
| bta04157 Mitophagy | 26 | 0.0072 |
| bta05225 Hepatocellular carcinoma | 55 | 0.0079 |
| bta04114 Endocytosis | 73 | 0.0082 |
| bta05223 Non-small cell lung cancer | 26 | 0.0083 |
| bta04150 mTOR signaling pathway | 50 | 0.0097 |
| bta04152 AMPK signaling pathway | 41 | 0.0099 |
| bta05224 Breast cancer | 48 | 0.0103 |
| bta04920 Adipocytokine signaling pathway | 27 | 0.0103 |
| bta04261 Adrenergic signaling in cardiomyocytes | 48 | 0.0103 |
| bta04211 Longevity regulating pathway | 32 | 0.0103 |
| bta04024 cAMP signaling pathway | 68 | 0.011 |
| bta04067 Viral protein interaction with cytokine and cytokine receptor | 33 | 0.012 |
| bta05219 Bladder cancer | 18 | 0.0122 |
| bta04919 Thyroid hormone signaling pathway | 39 | 0.0128 |
| bta04668 TNF signaling pathway | 39 | 0.0128 |
| Gene ID  | Pathway Description                                           | Score | P-value |
|---------|---------------------------------------------------------------|-------|---------|
| bta05226 | Gastric cancer                                               | 48    | 0.0135  |
| bta04926 | Relaxin signaling pathway                                     | 42    | 0.0136  |
| bta01100 | Metabolic pathways                                           | 372   | 0.014   |
| bta04130 | SNARE interactions in vesicular transport                    | 15    | 0.0143  |
| bta04961 | Endocrine and other factor-regulated calcium reabsorption    | 20    | 0.0149  |
| bta04390 | Hippo signaling pathway                                       | 48    | 0.0176  |
| bta04931 | Insulin resistance                                           | 36    | 0.0181  |
| bta04015 | Rap1 signaling pathway                                       | 63    | 0.0182  |
| bta05218 | Melanoma                                                     | 26    | 0.0188  |
| bta04728 | Dopaminergic synapse                                          | 42    | 0.0198  |
| bta04520 | Adherens junction                                             | 25    | 0.0204  |
| bta05210 | Colorectal cancer                                             | 30    | 0.0216  |
| bta04371 | Apelin signaling pathway                                     | 43    | 0.0239  |
| bta04659 | Th17 cell differentiation                                    | 36    | 0.0244  |
| bta05160 | Hepatitis C                                                  | 49    | 0.0245  |
| bta04917 | Prolactin signaling pathway                                  | 28    | 0.0255  |
| bta04625 | C-type lectin receptor signaling pathway                     | 34    | 0.0261  |
| bta04022 | cGMP-PKG signaling pathway                                   | 50    | 0.0265  |
| bta04070 | Phosphatidylinositol signaling system                         | 32    | 0.0279  |
| bta04140 | Autophagy                                                     | 43    | 0.0282  |
| bta04922 | Glucagon signaling pathway                                   | 33    | 0.0283  |
| bta04923 | Regulation of lipolysis in adipocytes                        | 21    | 0.0283  |
| bta00310 | Lysine degradation                                            | 23    | 0.0308  |
| bta04911 | Insulin secretion                                             | 28    | 0.0317  |
| bta00561 | Glycerolipid metabolism                                      | 23    | 0.0348  |
| bta05166 | Human T-cell leukemia virus 1 infection                       | 65    | 0.035   |
| bta04510 | Focal adhesion                                               | 56    | 0.0371  |
| bta05202 | Transcriptional misregulation in cancer                      | 54    | 0.0401  |
| bta04933 | AGE-RAGE signaling pathway in diabetic complications          | 32    | 0.0408  |
| bta05412 | Arrhythmogenic right ventricular cardiomyopathy (ARVC)        | 25    | 0.041   |
| bta04713 | Circadian entrainment                                        | 31    | 0.0444  |
| bta05100 | Bacterial invasion of epithelial cells                       | 24    | 0.0447  |
| bta00562 | Inositol phosphate metabolism                                | 24    | 0.0447  |
| bta04370 | VEGF signaling pathway                                       | 20    | 0.0451  |
| bta04910 | Insulin signaling pathway                                    | 41    | 0.0454  |
| bta04340 | Hedgehog signaling pathway                                   | 18    | 0.0475  |
| bta04350 | TGF-beta signaling pathway                                   | 29    | 0.0479  |
| bta04670 | Leukocyte transendothelial migration                          | 34    | 0.0491  |