**Integrated regulatory network reveals novel candidate regulators in the development of negative energy balance in cattle**

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**Supplementary Material S7** *A summary and some selected GO terms of the integrated regulatory modules.*

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| Cluster | Regulators | Target genes | Selected GO Terms (P.value) |
| 0 | FOXM1 | 43 | positive regulation of cell cycle phase transition (0.004) |
| KLF7 | 43 | positive regulation of cell cycle process (0.000) |
| SOX5 | 43 | positive regulation of cytokinesis (0.0008) |
| bta-mir-19a | 7 | cell cycle process (0.0003) |
| 8 |  |  |  |
| bta-mir-2346 | 10 | positive regulation of brown fat cell differentiation (0.034), regulation of brown fat cell differentiation (0.036) |
| bta-let-7d | 11 | - |
| XBP1 | 51 | - |
| GRHL1 | 44 | - |
| TFE3 | 29 | - |
| 18 | bta-mir-193b | 5 | cellular response to glucose starvation (0.040), negative regulation of cellular response to oxidative stress (0.040), pathway-restricted SMAD protein phosphorylation (0.040), response to sterol (0.040), negative regulation of response to oxidative stress (0.040), positive regulation of glucose import (0.043), positive regulation of glucose transport (0.044), regulation of cellular response to oxidative stress (0.046), activation of MAPKK activity (0.046) |
| bta-mir-1277 | 3 | - |
| 88 | XBP1 | 63 | - |
| ZNF219 | 61 | - |
| bta-mir-1468 | 5 | ADP biosynthetic process (0.028), GTP metabolic process (0.049) |
| bta-mir-132 | 11 | - |
| bta-mir-10b | 7 | regulation of leukotriene production involved in inflammatory response (0.033), short-chain fatty acid biosynthetic process (0.044) |
| bta-mir-182 | 10 | - |
| bta-mir-26b | 12 | - |
| bta-mir-30d | 6 | positive regulation of leukotriene production involved in inflammatory response (0.029) |
| 110 | CREB3L4 | 35 | DNA metabolic process (0.003) |
| SMAD4 | 30 | DNA metabolic process (0.0005), nucleic acid metabolic process (0.038) |
| bta-mir-2346 | 5 | regulation of unsaturated fatty acid biosynthetic process (0.018), positive regulation of insulin receptor signaling pathway (0.029), white fat cell differentiation (0.029), negative regulation of cellular response to oxidative stress (0.039), negative regulation of TOR signaling (0.042) |
| bta-mir-487b | 4 | behavioral response to starvation (0.018), regulation of unsaturated fatty acid biosynthetic process (0.018), cellular response to stress (0.029), regulation of steroid biosynthetic process (0.046) |
| bta-mir-543 | 5 | behavioral response to starvation (0.009), hepatocyte apoptotic process (0.019), response to stress (0.021), negative regulation of TOR signaling (0.026),activation of MAPKK activity (0.031), cellular glucose homeostasis (0.031), negative regulation of I-kappaB kinase/NF-kappaB signaling (0.032), negative regulation of Wnt signaling pathway (0.050), regulation of cellular ketone metabolic process (0.047), regulation of steroid metabolic process (0.038), regulation of carbohydrate metabolic process (0.050)  |
| 143 | bta-mir-24-2 | 2 | regulation of steroid biosynthetic process (0.035), negative regulation of lipid metabolic process (0.042), regulation of steroid metabolic process (0.047), negative regulation of canonical Wnt signaling pathway (0.049), regulation of ketone biosynthetic process (0.015) |
| bta-mir-326 | 4 | - |
| ZNF239 | 12 |  |
| 145 | TFEB | 16 | - |
| ZNF219 | 20 | - |
| bta-mir-127 | 1 | - |
| bta-mir-143 | 2 | - |
| bta-mir-23a | 4 | negative regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress (0.027), regulation of immunoglobulin secretion (0.048) |