**Table S1** Spearman correlation between cow’s age and gene expression in females from an *in vivo* group

|  |  |  |
| --- | --- | --- |
| Gene | Spearman correlation (r2) | *P-*value |
| ***ANXA2*** | **−0.91** | **<0.01** |
| *ARL6IP6* | −0.17 | 0.57 |
| *ATP5A1* | −0.10 | 0.73 |
| *BCAP31* | −0.19 | 0.53 |
| *BMP15* | −0.30 | 0.32 |
| *BTG1* | −0.48 | 0.09 |
| ***CD97*** | **−0.59** | **0.04** |
| *CDC20* | 0.06 | 0.85 |
| *CETN3* | 0.39 | 0.19 |
| *CKS2* | −0.36 | 0.22 |
| *CLU* | −0.15 | 0.62 |
| *DDR1* | −0.34 | 0.31 |
| *DNMT3B* | −0.07 | 0.83 |
| *EEF1A1* | −0.02 | 0.95 |
| *F11R* | −0.53 | 0.18 |
| *GDF9* | −0.24 | 0.44 |
| *GJA1* | 0.25 | 0.42 |
| *GOT1* | −0.47 | 0.10 |
| *GTF2F1* | −0.17 | 0.58 |
| *HK1* | −0.33 | 0.26 |
| *HSPA8* | −0.54 | 0.06 |
| *IGF2R* | −0.12 | 0.70 |
| *MSX1* | −0.40 | 0.17 |
| *NOBOX* | −0.37 | 0.22 |
| *PLIN2* | −0.28 | 0.36 |
| *PPA1* | −0.16 | 0.59 |
| *PSEN1* | 0.38 | 0.20 |
| *RPS15* | −0.32 | 0.28 |
| *RPS6KB1* | 0.07 | 0.83 |
| *SERPINE1* | −0.43 | 0.17 |
| *TCF4* | −0.49 | 0.09 |
| *TMIGD1* | −0.38 | 0.40 |
| *TXN* | 0.15 | 0.63 |
| *ZDHHC16* | −0.33 | 0.27 |
| *ZP2* | −0.46 | 0.13 |

In bold: *P* < 0.05.

**Table S2** Scores of oocytes-interacting proteins obtained in the STRING functional network

|  |  |  |
| --- | --- | --- |
| Node 1 | Node 2 | Combined scorea |
| CDC20 | CKS2 | 0.991 |
| DNMT3B | H2AFZ | 0.937 |
| CLU | SERPINE1 | 0.915 |
| HSPA8 | IGF2R | 0.906 |
| GTF2F1 | HSPA8 | 0.901 |
| BMP15 | GDF9 | 0.874 |
| ATP5A1 | PPA1 | 0.836 |
| GDF9 | ZP2 | 0.818 |
| ATP5A1 | RPS15 | 0.758 |
| EEF1A1 | RPS15 | 0.712 |
| CKS2 | H2AFZ | 0.660 |
| ATP5A1 | HSPA8 | 0.646 |
| BMP15 | ZP2 | 0.587 |
| EEF1A1 | HSPA8 | 0.584 |
| HSPA8 | PLIN2 | 0.576 |
| CDC20 | H2AFZ | 0.572 |
| CLU | PSEN1 | 0.518 |
| HSPA8 | TXN | 0.516 |
| ANXA2 | HSPA8 | 0.496 |
| HSPA8 | RPS15 | 0.452 |
| CD97 | F11R | 0.445 |
| GDF9 | GJA1 | 0.440 |
| GOT1 | HK1 | 0.424 |
| DNMT3B | IGF2R | 0.423 |
| ANXA2 | EEF1A1 | 0.401 |

aScores are indicators of confidence. All scores rank from 0 to 1, with 1 being the highest possible confidence.

**Table S3** The main five functional enrichments in the PCOS-interacting proteins network based on the lowest false discovery rate

|  |  |  |  |
| --- | --- | --- | --- |
| #Term ID | Term description | Count in gene set | False discovery rate |
| Biological Process (GO) |  |  |  |
| GO:0050820 | Positive regulation of regulation | 2 of 8 | 0.0030 |
| GO:0001947 | Heart looping | 2 of 8 | 0.0030 |
| GO:0030858 | Positive regulation of epithelial cell differentiation | 2 of 10 | 0.0038 |
| GO:0030326 | Embryonic limb morphogenesis | 2 of 13 | 0.0052 |
| GO:0030509 | BMP signaling pathway | 2 of 15 | 0.0061 |
| Molecular Function (GO) |  |  |  |
| GO:0001786 | Phosphatidylserine binding | 2 of 7 | 0.0039 |
| GO:0030165 | PDZ domain binding | 3 of 16 | 0.00044 |
| GO:0005160 | Transforming growth factor beta receptor binding | 2 of 15 | 0.0092 |
| GO:0005262 | Calcium channel activity | 2 of 22 | 0.0105 |
| GO:0048029 | Monosaccharide binding | 2 of 24 | 0.0105 |
| Cellular Component (GO) |  |  |  |
| GO:0005771 | Multivesicular body | 2 of 17 | 0.0044 |
| GO:0043230 | Extracellular organelle | 3 of 31 | 0.00060 |
| GO:0070062 | Extracellular exosome | 2 of 27 | 0.0087 |
| GO:0062023 | Collagen-containing extracellular matrix | 2 of 34 | 0.0114 |
| GO:0031012 | Extracellular matrix | 3 of 72 | 0.0034 |