

Supplementary Material

Differential gene expression in porcine oviduct during the oestrous cycle

O. S. Acuña^{A,B,D,E}, *M. Avilés*^{A,D,E}, *R. López-Úbeda*^{C,D,E}, *A. Guillén-Martínez*^{A,D,E}, *C. Soriano-Úbeda*^{C,D,E}, *A. Torrecillas*^F, *P. Coy*^{C,D,E} and *M. J. Izquierdo-Rico*^{A,D,E,G}

^AKey Department of Cell Biology and Histology, Faculty of Medicine, University of Murcia, 30100, Murcia, Spain.

^BKey Faculty of Veterinary, Autonomous University of Sinaloa, Culiacan, 80246, Sinaloa, Mexico.

^CKey Department of Physiology, Veterinary faculty, University of Murcia, 30100, Murcia, Spain.

^DKey International Excellence Campus for Higher Education and Research (Campus Mare Nostrum).

^EKey IMIB-Arrixaca (Institute for Biomedical Research of Murcia).

^FKey Molecular Biology Section, SAI, University of Murcia, 30100, Murcia, Spain.

^GCorresponding author. Email: mjoseir@um.es

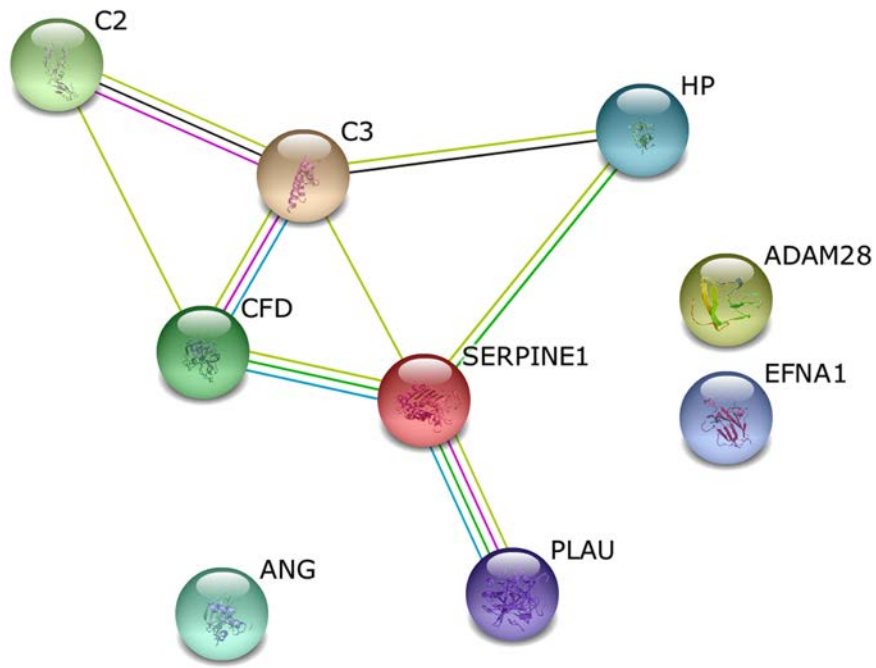


Fig. S1. Network based on genes down-regulated in preovulatory phase versus postovulatory phase.

Table S1. Primer information for the real time RT-PCR amplification of each target gene

Gene symbol	PCR-product (bp)	Melting point (°C)	Primer sequences (Forward/Reverse) (5'-3')	Genbank accession number
<i>CCK</i>	179	93	(F) GCTGCGTCTATCTCGAAGCCAT (R) GACTCGCCGCTACCTTTTG	NM_214237
<i>DAPL1</i>	156	83,5	(F) GGCATCCTCCTGCAGTAAA (R) CGTGTCATTCAGGGCATCCA	NM_001185174
<i>GPX2</i>	167	88.72	(F) TCAACACATTCCGAGGCAGG (R) TCTGACAGTTCTCCTGATGTCC	NM_001115136
<i>MUC1</i>	103	88.43	(F) TCTTACTCGAACCTGGCAGC (R) CCAGCAGGGAAGAACCTCAG	XM_001926883
<i>PEBP4</i>	123	85,2	(F) CGCTGTGCTCTGTAAGGGC (R) TGACAATTGGCTCAGTCCAG	NM_001162888
<i>PLAT</i>	110	87.69	(F) GAGAGCTCTGGTGTGTGCTC (R) CTCTGCAGGTCACCTGTACG	NM_214054
<i>PLAU</i>	145	89.68	(F) AGAGTGCCTACTAGTCCCCG (R) TTCATGGCTGCCTTTGGAGT	NM_213945
<i>SAL1</i>	116	80,5	(F) AGCCTTTAAATTTTCAGAGAAAGGT (R) GGCGAAATTTGTTCTCTCCA	NM_213814
<i>SERPINE1</i>	142	84.96	(F) AGGACCCCTGCCAGGATTAT (R) TGCTAGGTCATGTAGCCCCT	NM_213910
<i>TAC3</i>	81	82,5	(F) AGCAAGGCTAGCGTGGGTG (R) GCCCATAAGACCCACAAAGA	NM_001007196

Table S2.

Primary antibodies				Secondary antibodies		
Gene	[IHC]	[WB]	Reference	[IHC]	[WB]	Reference
GPX2	1:10		Goat Polyclonal to Human GPX2 (LS-C54920, LSBio, Seattle, WA)	1:50		Donkey anti-goat Ig-HRP (sc-2020, Santa Cruz Biotechnology, Inc., Dallas, Texas, USA)
CCK	1:10	1:500	CCK Antibody (C-20) goat polyclonal IgG (sc-21617, Santa Cruz Biotechnology, Inc., Dallas, Texas, USA)	1:50	-	Donkey anti-goat Ig-HRP (sc-2020, Santa Cruz Biotechnology, Inc., Dallas, Texas, USA)
PEBP4	1:10	-	Anti-PEBP4 antibody produced in rabbit (HPA025064, Sigma-Aldrich, España)	1:50	1:20000	Rabbit anti-Goat IgG, HRP (AP106P, Millipore)
TAC3	1:10	-	Neurokinin B Antibody (H-51) rabbit polyclonal IgG (sc-292436, Santa Cruz Biotechnology, Inc., Dallas, Texas, USA)	1:50	-	Goat anti-rabbit IgG-HRP (sc-2004, Santa Cruz Biotechnology, Inc., Dallas, Texas, USA)
MUC1	1:10		Mucin 1 (H-295) rabbit polyclonal (sc-15333, Santa Cruz Biotechnology, Inc., Dallas, Texas, USA)	1:50		Goat anti-rabbit IgG-HRP (sc-2004, Santa Cruz Biotechnology, Inc., Dallas, Texas, USA)

IHC: Immunohistochemical analysis

WB: Western-Blot analysis

Table S3. Genes up-regulated at prepubertal phase versus postovulatory phase in oviduct

Gene	Not detected before in oviduct	Gene name	Genbank accession number	logFC	pdf
DAPL1	*	Death associated protein-like 1	NM_001185174	2.40	0.0001
MUC1		Mucin 1, cell surface associated	XM_001926883	2.18	0.0001
PVALB	*	Parvalbumin	NM_001190157	2.13	0.0001
UPK1B		Uroplakin 1B	NM_001123212	2.01	0.0001
PON3		Paraoxonase 3	NM_001044604	1.99	0.0012
CES1	*	Carboxylesterase 1	NM_214246	1.95	0.0001
FXD3	*	FXD domain containing ion transport regulator 3	NM_214208	1.89	0.0012
MMP7		Matrix metalloproteinase 7 (matrilysin, uterine)	NM_214207	1.83	0.0028
C2		Complement component 2	NM_001101815	1.80	0.0001
ALOX12		Arachidonate 12-lipoxygenase	NM_213931	1.78	0.0038
CXCL16		Chemokine (C-X-C motif) ligand 16	NM_213811	1.77	0.0006
GREB1	*	Protein GREB1-like	XM_005662746	1.75	0.0023
OAS2		2'-5'-oligoadenylate synthetase 2, 69/71kda	NM_001031796	1.75	0.0010
CFB	*	Complement factor B	NM_001101824	1.74	0.0011
GSX2	*	GS homeobox 2-like	XM_003128986	1.63	0.0018
MYOC	*	Myocilin, trabecular meshwork inducible glucocorticoid response	NM_213986	1.62	0.0022
C3		Complement component 3	NM_214009	1.44	0.0089
PSMB8	*	Proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	NM_213935	1.38	0.0018
A	*	Blood group A transferase-like	NM_213799	1.38	0.0042

SERPING1	*	Serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	NM_001123194	1.36	0.0036
SPARC	*	Secreted protein, acidic, cysteine-rich (osteonectin)	NM_001031794	1.31	0.0102
RSAD2		Radical S-adenosyl methionine domain-containing protein 2	NM_213817	1.30	0.0099
DEFB1		Beta-defensin 2	NM_214442	1.29	0.0038
MMRN2	*	Multimerin 2	XM_001927177	1.26	0.0033
TAC3		Tachykinin 3	NM_001007196	1.23	0.0074
SULT2A1	*	Sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA)-preferring, member 1	NM_001037150	1.18	0.0087
PKR	*	Double stranded RNA-dependent protein kinase	NM_214319	1.15	0.0104
ASTN2	*	Astrotactin-2-like	XM_003122097	1.15	0.0066
SQLE	*	Squalene epoxidase	NM_001101026	1.12	0.0097
LGALS9	*	Lectin, galactoside-binding, soluble, 9	NM_213932	1.12	0.0139
RNASE10	*	Ribonuclease, rnase A family, 10 (non-active)	NM_001007111	1.10	0.0129
ID2	*	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	NM_001037965	1.10	0.0091
SLA-DQB1	*	SLA-DQ beta1 domain	NM_001113694	1.09	0.0085
SLA-DRA		MHC class II DR-alpha	NM_001113706	1.08	0.0102
CGA		Glycoprotein hormones, alpha polypeptide	NM_214446	1.07	0.0084
WNT2B	*	Wingless-type MMTV integration site family, member 2B	XM_003125849	1.05	0.0169
IRS1		Insulin receptor substrate 1	NM_001244489	1.05	0.0090
GLTP	*	Glycolipid transfer protein	NM_213822	1.05	0.0347
LDLR		Low density lipoprotein receptor	NM_001206354	1.04	0.0196
SLA-DQA	*	MHC class II histocompatibility antigen SLA-DQA	NM_001114062	1.03	0.0149
MYC		V-myc myelocytomatosis viral oncogene homolog (avian)	NM_001005154	1.03	0.0162
NPSR1	*	Neuropeptide S receptor 1	XM_003134796	1.02	0.0168
PLAT		Plasminogen activator, tissue	NM_214054	1.01	0.0090
STAT1		Signal transducer and activator of transcription 1, 91kda	NM_213769	1.01	0.0315

PDZK1IP1	*	PDZK1 interacting protein 1	NM_001001769	1.00	0.0208
MYH7	*	Myosin, heavy chain 7, cardiac muscle, beta	NM_213855	1.00	0.0361
MX1		Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	NM_214061	0.99	0.0251
PSMB9	*	Proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	NM_001037961	0.99	0.0282
CXCL10		Chemokine (C-X-C motif) ligand 10	NM_001008691	0.99	0.0275
CXCL2	*	Chemokine (C-X-C motif) ligand 2	NM_001001861	0.98	0.0001
HERC5	*	HECT and RLD domain containing E3 ubiquitin protein ligase 5	XM_005667000	0.98	0.0343
IFIT1	*	Interferon-induced protein with tetratricopeptide repeats 1	NM_001244363	0.97	0.0199
SLA-DRB1	*	MHC class II histocompatibility antigen SLA-DRB1	NM_001113695	0.97	0.0222
STMN1		Stathmin 1	NM_001009582	0.94	0.0168
CYP51		Cytochrome P450, family 51, subfamily A, polypeptide 1	NM_214432	0.94	0.0167
ANXA13	*	Annexin A13	XM_005662865	0.93	0.0383
MCM4	*	Minichromosome maintenance complex component 4	XM_003481401	0.92	0.0294
EPHA4	*	EPH receptor A4	NM_001134967	0.91	0.0199
PSMB10	*	Proteasome (prosome, macropain) subunit, beta type, 10	NM_001044565	0.91	0.0298
EPS8L3	*	EPS8-like 3	XM_003125864	0.90	0.0231
GNL3	*	Guanine nucleotide binding protein-like 3 (nucleolar)	XM_001928454	0.90	0.0230
KLF6	*	Kruppel-like factor 6	NM_001134353	0.89	0.0361
COIL	*	Coilin-like	XM_003131625	0.89	0.0362
CDCA7	*	Cell division cycle associated 7	XM_001928628	0.89	0.0345
ID3	*	Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	NM_001243602	0.88	0.0280
IGFBP2		Insulin-like growth factor binding protein 2, 36kda	NM_214003	0.88	0.0493
VCAM1		Vascular cell adhesion molecule 1	NM_213891	0.88	0.0228
MT1A		Metallothionein 1A	NM_001001266	0.87	0.0395

PARP1		Poly (ADP-ribose) polymerase 1	XM_003357641	0.87	0.0283
NEK6	*	NIMA (never in mitosis gene a)-related kinase 6	XM_003122163	0.87	0.0284
NTRK2	*	Neurotrophic tyrosine kinase, receptor, type 2	XM_003130647	0.87	0.0265
WDFY4	*	WDFY family member 4	XM_001926738	0.86	0.0386
NHP2	*	NHP2 ribonucleoprotein	XM_003354180	0.86	0.0283
DDX21	*	DEAD (Asp-Glu-Ala-Asp) box helicase 21	XM_001928772	0.86	0.0369
PTGFR		Prostaglandin F receptor (FP)	FJ750950	0.86	0.0388
ATIC	*	5-aminoimidazole-4-carboxamide Ribonucleotide formyltransferase/IMP cyclohydrolase	NM_001130736	0.85	0.0328
HSP90AA1		90-kda heat shock protein	NM_213973	0.84	0.0469
FKBP10		FK506 binding protein 10, 65 kda	NM_001243807	0.84	0.0484
P311	*	P311 protein	XM_003123844	0.82	0.0412
RPL14	*	Ribosomal protein L14	NM_001097478	0.82	0.0412
LOC780409	*	Chemokine ligand 26-like protein	NM_001078665	0.81	0.0485
IGF2		Insulin-like growth factor 2 (somatomedin A)	NM_213883	0.81	0.0483
HSPE1		Heat shock 10kda protein 1 (chaperonin 10)	NM_214307	0.81	0.0363
STAG2	*	Stromal antigen 2	XM_003360437	0.80	0.0387
NOP14	*	NOP14 nucleolar protein homolog (yeast)	XM_003482333	0.79	0.0468
IGFBP3		Insulin-like growth factor binding protein 3	NM_001005156	0.78	0.0466

Table S4. Genes down-regulated at prepubertal phase versus postovulatory phase in oviduct

Gene	Not detected before in oviduct	Gene name	Genbank accession number	logFC.	pfp
SAA2		Serum amyloid A2	NM_001044552	-3.32	0.0049
PLAU		Plasminogen activator, urokinase	NM_213945	-3.09	0.0001
NANOS1	*	Nanos homolog 1 (Drosophila)	XM_001928298	-2.41	0.0001
SAL1	*	Salivary lipocalin	NM_213814	-2.25	0.0001
CITED1	*	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1	NM_001037964	-1.85	0.0001
SULT1E1	*	Sulfotransferase family 1E, estrogen-preferring, member 1	NM_213992	-1.84	0.0001
TGM2	*	Tissue transglutaminase homologue	XM_003359989	-1.81	0.0001
ADM		Adrenomedullin	NM_214107	-1.80	0.0004
SCIN	*	Scinderin	NM_001244731	-1.55	0.0010
LOC100154257	*	Uncharacterized LOC100154257	NM_001243180	-1.54	0.0001
ACP5	*	Acid phosphatase 5, tartrate resistant	NM_214209	-1.50	0.0011
SERPINE1		Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	NM_213910	-1.49	0.0018
LOC100154257	*	uncharacterized LOC100154257, transcript variant X1, mRNA	XM_005663592	-1.44	0.0001
CA14	*	Carbonic anhydrase XIV	XM_001924881	-1.44	0.0012
ATP6V1C2	*	Atpase, H ⁺ transporting, lysosomal 42kda, V1 subunit C2	XM_003125387	-1.37	0.0039
GGT1		Gamma-glutamyltransferase 1	NM_214030	-1.36	0.0027
APOD		Apolipoprotein D	XM_001926063	-1.35	0.0014
LOC396905	*	Acrosin inhibitor	NM_213877	-1.34	0.0032
CYP19A3	*	Cytochrome P450 19A3	NM_214431	-1.33	0.0040

FADS6	*	Fatty acid desaturase domain family, member 6	NM_001244792	-1.32	0.0027
TIMP2		TIMP metallopeptidase inhibitor 2	NM_001145985	-1.32	0.0040
GPX2		Glutathione peroxidase 2 (gastrointestinal)	NM_001115136	-1.27	0.0033
FMO1	*	Flavin containing monooxygenase 1	NM_214064	-1.25	0.0037
PLAC9	*	Placenta-specific 9	NM_001190209	-1.23	0.0037
SLC25A1	*	Solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	NM_001190189	-1.22	0.0038
CYP2C49	*	Cytochrome P450 2C49	NM_214420	-1.22	0.0080
SERPINA1		Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	NM_214395	-1.19	0.0001
RGN	*	Regucalcin (senescence marker protein-30)	NM_001077220	-1.17	0.0039
SRPX	*	Sushi-repeat containing protein, X-linked	XM_001927105	-1.13	0.0096
PROM1	*	Prominin 1	XM_005666536	-1.13	0.0057
PHGDH	*	Phosphoglycerate dehydrogenase	NM_001123162	-1.11	0.0075
KRT5		Keratin 5	XM_003126173	-1.09	0.0099
LOC100510917	*	Glutathione S-transferase A4-like	XM_003128793	-1.08	0.0167
SLC7A7	*	Solute carrier family 7 (amino acid transporter light chain, y+L system), member 7	NM_001110421	-1.07	0.0087
CELA2A	*	Chymotrypsin-like elastase family, member 2A	NM_214109	-1.07	0.0088
HP		Haptoglobin	NM_214000	-1.04	0.0001
CCK	*	Cholecystokinin	NM_214237	-1.03	0.0237
DPT	*	Dermatopontin-like	XM_003125649	-1.03	0.0208
SLC52A3		Riboflavin transporter 2-like	XM_003134352	-1.02	0.0147
TUBB2B	*	Tubulin, beta 2B class iib	NM_001243434	-1.01	0.0106
NAGLU	*	N-acetylglucosaminidase, alpha	XM_003131388	-1.01	0.0109
SEC14L3	*	SEC14-like 3 (<i>S. Cerevisiae</i>), transcript variant 2	XM_003483457	-1.00	0.0159
AKAP12	*	A kinase (PRKA) anchor protein 12	XM_001927265	-1.00	0.0207

RENBP	*	Renin binding protein	NM_213900	-0.99	0.0098
EFHC1	*	EF-hand domain (C-terminal) containing 1	XM_001928760	-0.96	0.0205
HSD11B2		Hydroxysteroid (11-beta) dehydrogenase 2	NM_213913	-0.95	0.0149
HSD11B1		Hydroxysteroid (11-beta) dehydrogenase 1	NM_214248	-0.95	0.0329
GRN	*	Granulin	NM_001044578	-0.95	0.0193
SLC44A4	*	Solute carrier family 44, member 4	NM_001101818	-0.95	0.0211
ABC1		ATP-binding cassette sub-family A member 1-like	XM_003480560	-0.95	0.0168
PHACTR3	*	Phosphatase and actin regulator 3	NM_001110176	-0.94	0.0295
RASGEF1A	*	Rasgef domain family, member 1A	XM_001926447	-0.94	0.0260
RGS2	*	Regulator of G-protein signaling 2, 24kda	NM_001044600	-0.93	0.0269
MARVELD3	*	MARVEL domain containing 3	NM_001243842	-0.93	0.0271
FCGRT	*	Fc fragment of igg, receptor, transporter, alpha	NM_214197	-0.92	0.0284
SIRT3	*	Sirtuin 3	NM_001110057	-0.92	0.0258
TUBB	*	Tubulin, beta class I	NM_001044612	-0.92	0.0001
REEP3	*	Receptor expression-enhancing protein 3-like	XM_001925659	-0.91	0.0419
TMEM45B	*	Transmembrane protein 45B-like	XM_003130073	-0.90	0.0233
IGF1		Insulin-like growth factor 1 (somatomedin C)	NM_214256	-0.90	0.0269
C4H1orf189	*	Chromosome 4 open reading frame, human C1orf189	XM_003125733	-0.90	0.0238
ENPP2	*	Ectonucleotide pyrophosphatase/phosphodiesterase 2	XM_003125510	-0.90	0.0409
FOLR1		Folate receptor 1 (adult)	NM_213830	-0.90	0.0001
PHGK	*	Phosphorylase kinase, gamma 1 (muscle)	NM_001293144	-0.89	0.0295
FAM84A	*	Protein FAM84A-like	XM_003125420	-0.88	0.0267
FUT2		Fucosyltransferase 2 (secretor status included)	NM_214069	-0.87	0.0396
CFLAR	*	CASP8 and FADD-like apoptosis regulator	NM_001001628	-0.87	0.0436
LOC100523871	*	Uncharacterized LOC100523871	XR_297824	-0.87	0.0249
PITPNC1	*	Phosphatidylinositol transfer protein, cytoplasmic 1	NM_001143722	-0.86	0.0339
TSGA10	*	Testis specific, 10	XM_003124906	-0.86	0.0281

DIRAS3	*	DIRAS family, GTP-binding RAS-like 3	NM_001044598	-0.85	0.0409
PGM1	*	Phosphoglucomutase 1	NM_001246318	-0.85	0.0441
EPHX2	*	Epoxide hydrolase 2, cytoplasmic	NM_001001641	-0.85	0.0394
LMAN2	*	Lectin, mannose-binding 2, transcript variant X1, mRNA	XM_005661451	-0.85	0.0399
GREB1L	*	Growth regulation by estrogen in breast cancer-like	XM_005653403	-0.84	0.0276
HEXA	*	Hexosaminidase A (alpha polypeptide)	NM_001123221	-0.83	0.0433
HOOK2	*	Hook homolog 2 (Drosophila)	XM_003123331	-0.82	0.0428
ANXA8		Annexin A8	NM_001243599	-0.79	0.0432
STEAP4	*	STEAP family member 4	NM_001166489	-0.77	0.0484
UPK3A	*	Uroplakin 3A	XM_003125969	-0.63	0.0465

Table S5. Genes up-regulated at preovulatory phase versus postovulatory phase in oviduct

Gene	Not detected before in oviduct	Gene name	Genbank accession number	logFC.	pdfp
TAC3		Tachykinin 3	NM_001007196	2.78	0.0000
COL1A2		Collagen, type I, alpha 2	NM_001243655	2.42	0.0000
SULT2A1	*	Sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA)-preferring, member 1	NM_001037150	2.31	0.0000
PEG10		Paternally expressed 10	NM_001109944	2.12	0.0022
PON3	*	Paraoxonase 3	NM_001044604	2.06	0.0031
GREB1	*	Protein GREB1-like	XM_003125379	1.93	0.0031
LPPR5	*	Lipid phosphate phosphatase-related protein type 5	NM_001245001	1.93	0.0024
NPSR1	*	Neuropeptide S receptor 1	XM_003134796	1.92	0.0025
LDLR	*	Low density lipoprotein receptor	AK236400	1.85	0.0023
PGR		Progesterone receptor	NM_001166488	1.80	0.0025
SQLE	*	Squalene epoxidase	NM_001101026	1.80	0.0028
LOC100522001		Tumor necrosis factor alpha-induced protein 8-like protein 3-like	XM_005659607	1.78	0.0041
CRELD2	*	Cysteine-rich with EGF-like domain protein 2-like, transcript variant 1	XM_003126783.4	1.74	0.0051
MYH7	*	Myosin, heavy chain 7, cardiac muscle, beta	NM_213855	1.70	0.0060
PVALB	*	Parvalbumin	NM_001190157	1.62	0.0095
UPK1B	*	Uroplakin 1B	NM_001123212	1.61	0.0056
DAPL1	*	Death associated protein-like 1	NM_001185174	1.58	0.0097
RIMS1	*	Regulating synaptic membrane exocytosis 1, transcript variant 1	XM_003353243	1.51	0.0105
LOC100523351	*	Astrotactin-2-like	XM_003122097	1.49	0.0056

NPPB	*	Natriuretic peptide B	NM_213846	1.48	0.0080
SLC5A5		Solute carrier family 5 (sodium iodide symporter), member 5	NM_214410	1.47	0.0096
HSPA5		Heat shock 70kda protein 5 (glucose-regulated protein, 78kda)	XM_001927795	1.48	0.0095
ANPEP	*	Alanyl (membrane) aminopeptidase	NM_214277	1.43	0.0110
SLC2A8	*	Solute carrier family 2 (facilitated glucose transporter), member 8	XM_003480608	1.43	0.0106
ADAMTS19	*	ADAM metallopeptidase with thrombospondin type 1 motif, 19	XM_003123903	1.42	0.0056
CA3		Carbonic anhydrase III, muscle specific	NM_001008688	1.39	0.0076
SPARC	*	Secreted protein, acidic, cysteine-rich (osteonectin)	NM_001031794	1.38	0.0148
CDC20	*	Cell division cycle 20 homolog (S. Cerevisiae)	NM_001123094	1.35	0.0134
CYP51		Cytochrome P450, family 51, subfamily A, polypeptide 1	NM_214432	1.34	0.0139
MSH2		Muts homolog 2, colon cancer, nonpolyposis type 1 (E. Coli)	NM_001195357	1.33	0.0134
ID2	*	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	NM_001037965	1.33	0.0141
DBI	*	Diazepam binding inhibitor (GABA receptor modulator, acyl-coa binding protein)	NM_214119	1.32	0.0224
NGLY1		N-glycanase 1	XM_003132075	1.32	0.0290
VNN2	*	Vanin 2	XM_003121196	1.32	0.0213
LOC100514810	*	PCNA-associated factor	NM_001244997	1.32	0.0109
VCAN	*	Versican	NM_001206429	1.29	0.0135
NANS	*	N-acetylneuraminic acid synthase	NM_001185139	1.29	0.0118
ABHD5	*	Abhydrolase domain containing 5	NM_001012407	1.26	0.0156
PARP1		Poly (ADP-ribose) polymerase 1	XM_003357641	1.26	0.0147
CALR	*	Calreticulin	NM_001174133	1.25	0.0166
RCAN2	*	Regulator of calcineurin 2 (RCAN2), partial mRNA	XM_003482207	1.25	0.0132
YPEL1	*	Protein yippee-like 1-like	XM_003132989	1.23	0.0224
MYH1	*	Myosin, heavy chain 1, skeletal muscle, adult	NM_001104951	1.23	0.0212
UCHL1	*	Ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	NM_213763	1.22	0.0152

IHH	*	Indian hedgehog	NM_001244470	1.20	0.0162
SCARB1		Scavenger receptor class B, member 1	NM_213967	1.20	0.0183
NPM3	*	Nucleoplasmin-3-like	XM_003359343	1.19	0.0333
ST6GALNAC2	*	ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	NM_213784	1.18	0.0185
COL5A2	*	Collagen type V alpha 2	AY368623	1.18	0.0241
DNAJC3	*	Dnaj (Hsp40) homolog, subfamily C, member 3	NM_001190184	1.18	0.0225
CCK	*	Cholecystokinin	NM_214237	1.17	0.0160
ENPEP	*	Glutamyl aminopeptidase (aminopeptidase A)	NM_214017	1.17	0.0202
LOC100153182	*	Sus scrofa EF-hand calcium-binding domain-containing protein 1-like, transcript variant 2	XM_003355061	1.17	0.0148
GUCY1B3	*	Guanylate cyclase 1, soluble, beta 3	NM_001018032	1.17	0.0213
AGXT2	*	Alanine--glyoxylate aminotransferase 2	NM_001244884	1.17	0.0372
LOC100153765	*	Uncharacterized protein c13orf33 homolog	XM_001927721	1.16	0.0328
AQP5		Aquaporin 5	NM_001110424	1.16	0.0245
FBP1		Fructose-1,6-bisphosphatase 1	NM_213979	1.15	0.0282
CD109		CD109 molecule, transcript variant 1	XM_001927545	1.15	0.0243
ASPN	*	Asporin	NM_001243889	1.13	0.0283
S100A11	*	S100 calcium binding protein A11	NM_001004045	1.13	0.0242
TOPOII		Topoisomerase II	NM_213884	1.12	0.0220
POMGNT2	*	Protein O-linked mannose N-acetylglucosaminyltransferase 2 (beta 1,4-)	XM_003132141	1.11	0.0215
S100C	*	S100C gene	AB003363	1.10	0.0275
CD1D		CD1d molecule	NM_001102680	1.10	0.0219
SPP1		Secreted phosphoprotein 1 (osteopontin)	NM_214023	1.09	0.0277
PLAT		Plasminogen activator, tissue	NM_214054	1.08	0.0157
EMILIN1	*	Elastin microfibril interfacier 1	XM_003125303	1.08	0.0267

LRRC59	*	Leucine rich repeat containing 59	NM_001244951	1.08	0.0365
CDK1	*	Cyclin-dependent kinase 1	NM_001159304	1.07	0.0245
SLC17A1	*	Solute carrier family 17 (organic anion transporter), member 1	NM_214344	1.07	0.0469
CDCA3	*	Cell division cycle associated 3	XM_001928347	1.07	0.0323
SERPINH1	*	Serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	NM_001244132	1.06	0.0291
PKIA	*	Protein kinase (camp-dependent, catalytic) inhibitor alpha	NM_214204	1.06	0.0293
CKAP4	*	Cytoskeleton-associated protein 4	NM_001244631	1.05	0.0440
MDH2	*	Malate dehydrogenase 2, NAD (mitochondrial)	NM_001244153	1.04	0.0278
CERCAM	*	Cerebral endothelial cell adhesion molecule, transcript variant X1	XM_001925579	1.03	0.0460
C5		Complement component 5	NM_001001646	1.03	0.0470
IGF1		Insulin-like growth factor 1 (somatomedin C)	NM_214256	1.02	0.0417
PTGS2		Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	NM_214321	1.02	0.0283
SGK1	*	Serum/glucocorticoid regulated kinase 1	NM_001244459	1.00	0.0445
COL4A1	*	Collagen, type IV, alpha 1	XM_003131091	1.00	0.0448
TAOK3	*	TAO kinase 3, transcript variant X2	XM_003483429	1.00	0.0464
LOC100513808	*	Leucine-rich repeat-containing protein 17-like	XM_003130238	0.99	0.0408
INSIG1	*	Insulin induced gene 1	NM_001244521	0.98	0.0465
TUBB	*	Tubulin, beta class I	NM_001044612	0.96	0.0328
NT5DC1	*	5'-nucleotidase domain containing 1	XM_001928200	0.94	0.0446
CYB5B	*	Cytochrome b5 type B (outer mitochondrial membrane)	NM_001159592	0.93	0.0314
HNRNPA3	*	Heterogeneous nuclear ribonucleoprotein A3-like, transcript variant 2	XM_003359565	0.93	0.0375

Table S6. Genes down-regulated at preovulatory phase versus postovulatory phase in oviduct

Gene	Not detected before in oviduct	Gene name	Genbank accession number	logFC.	pfp
HP		Haptoglobin	NM_214000	-2.56	0.0000
PLAU		Plasminogen activator, urokinase	NM_213945	-2.09	0.0000
SAL1	*	Salivary lipocalin	NM_213814	-2.02	0.0010
FMO1	*	Flavin containing monooxygenase 1	NM_214064	-1.89	0.0008
ACP5	*	Acid phosphatase 5, tartrate resistant	NM_214209	-1.87	0.0014
MT-III	*	Metallothionein-III	NM_214056	-1.67	0.0009
UPK3A	*	Uroplakin 3A	XM_003125969	-1.66	0.0059
NANOS1	*	Nanos homolog 1	XM_001928298	-1.65	0.0013
GNMT	*	Glycine N-methyltransferase	NM_001110419	-1.63	0.0032
SULT1E1	*	Sulfotransferase family 1E, estrogen-preferring, member 1	NM_213992	-1.45	0.0058
GRB7	*	Growth factor receptor-bound protein 7	XM_003131502	-1.41	0.0067
GPT2	*	Glutamic pyruvate transaminase (alanine aminotransferase) 2	XM_005664462	-1.39	0.0068
SERPINE1		Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	NM_213910	-1.37	0.0053
swc3		Swine workshop cluster 3 antigen precursor	AJ544724	-1.32	0.0068
LOC102162525	*	Uncharacterized LOC102162525 (LOC102162525)	XR_306596	-1.29	0.0081
CDO1	*	Cysteine dioxygenase, type I	NM_001167643	-1.26	0.0096
STEAP4	*	STEAP family member 4	HQ533145	-1.23	0.0132
RGN	*	Regucalcin (senescence marker protein-30)	NM_001077220	-1.21	0.0119
LOC102164901	*	Uncharacterized LOC102164901 (LOC102164901)	XR_305592	-1.18	0.0127
ABCG1	*	ATP-binding cassette, sub-family G (WHITE), member 1	XM_003483364	-1.18	0.0094

SLC27A3	*	Solute carrier family 27 (fatty acid transporter), member 3	XM_001929591	-1.17	0.0123
LOC100523871	*	Hypothetical protein LOC100523871	XM_003133986	-1.15	0.0119
C3		Complement component 3	NM_214009	-1.13	0.0187
FERMT1	*	Fermitin family member 1	XM_001927818	-1.12	0.0289
AKAP13	*	A kinase (PRKA) anchor protein 13	XM_001926474	-1.11	0.0149
FAM134B	*	Fat deposition protein	JX854456	-1.07	0.0287
ANG		Angiogenin	NM_001044573	-1.07	0.0362
LOC100620153	*	Zinc finger protein 184-like, transcript variant 1	XM_003356561	-1.06	0.0217
PDK4	*	Pyruvate dehydrogenase kinase, isozyme 4	NM_001159306	-1.05	0.0362
ALDOC	*	Aldolase C, fructose-bisphosphate	NM_001243928	-1.03	0.0311
NDRG2	*	NDRG family member 2	NM_001078683	-1.02	0.0305
LOC396905	*	Acrosin inhibitor	NM_213877	-1.02	0.0307
KLF6	*	Kruppel-like factor 6	NM_001134353	-1.02	0.0470
GLRX	*	Glutaredoxin (thioltransferase)	NM_214233	-1.02	0.0310
USP32	*	Ubiquitin specific peptidase 32	XM_003483052	-1.02	0.0381
FOXO1	*	Forkhead box O1	NM_214014	-1.00	0.0429
CFLAR	*	CASP8 and FADD-like apoptosis regulator	NM_001001628	-0.99	0.0385
TGM2	*	Transglutaminase 2	XM_003359989	-0.98	0.0379
TMEM45B	*	Transmembrane protein 45B-like	XM_003130073	-0.98	0.0452
CFD	*	Complement factor D	Z49058	-0.97	0.0472
PPARGC1A		Peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	NM_213963	-0.95	0.0475
MARVELD3	*	MARVEL domain containing 3	NM_001243841	-0.95	0.0426
BCAM	*	Basal cell adhesion molecule-like	XM_003481884	-0.93	0.0496
GPR125	*	G protein-coupled receptor 125	XM_003128880	-0.93	0.0383
EFTUD2		Elongation factor Tu GTP binding domain containing 2	XM_003131332	-0.93	0.0495
IGSF8	*	Immunoglobulin superfamily, member 8	XM_003481424	-0.92	0.0435
EFNA1		Ephrin-A1	NM_001123110	-0.92	0.0499

ATP2C2	*	Atpase, Ca ⁺⁺ transporting, type 2C, member 2	XM_003126826	-0.92	0.0441
HSPB1		Heat shock 27kDa protein 1	NM_001007518	-0.91	0.0498
ADAM28	*	ADAM metallopeptidase domain 28	XM_001924176	-0.90	0.0475
C2		Complement component 2	NM_001101815	-0.88	0.0468

Table S7. Genes up-regulated at luteal phase versus postovulatory phase in oviduct

Gene	Not detected before in oviduct	Gene name	Genbank accession number	logFC.	pfp
DAPL1	*	Death associated protein-like 1	NM_001185174	2.76	0.0001
MMP7		Matrix metalloproteinase 7	NM_214207	2.22	0.0001
IL24	*	Interleukin 24, transcript variant X1	XM_005667545	2.16	0.0350
MUC1		Mucin 1, cell surface associated	XM_001926883	1.93	0.0012
CXCL16		Chemokine (C-X-C motif) ligand 16	NM_213811	1.91	0.0011
KIT	*	V-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	NM_001044525	1.87	0.0082
CES1	*	Carboxylesterase 1	NM_214246	1.56	0.0167
C3		Complement component 3	NM_214009	1.46	0.0258
NGLY1		N-glycanase 1	XM_003132075	1.40	0.0348
KIRREL	*	Kin of IRRE like (Drosophila)	XM_003125691	1.36	0.0200
UPK1B	*	Uroplakin 1B	NM_001123212	1.34	0.0252
MYC		V-myc myelocytomatosis viral oncogene homolog	NM_001005154	1.33	0.0245
FABP5		Fatty acid binding protein 5	NM_001039746	1.24	0.0311
LYZ		Lysozyme	NM_214392	1.22	0.0379
PDZK1IP1	*	PDZK1 interacting protein 1	NM_001001769	1.20	0.0353

Table S8. Genes down-regulated at luteal phase versus postovulatory phase in oviduct

Gene	Not detected before in oviduct	Gene name	Genbank accession number	logFC.	pfp
SAA2		Serum amyloid A2	NM_001044552	-3.15	0.0050
PLAU		Plasminogen activator, urokinase	NM_213945	-2.68	0.0001
CCK	*	Cholecystokinin	NM_214237	-2.41	0.0010
PEBP4	*	Phosphatidylethanolamine-binding protein 4	NM_001162888	-1.86	0.0007
LMO1	*	LIM domain only 1 (rhombotin 1)	NM_001113055	-1.82	0.0001
NANOS1	*	Nanos homolog 1-like	XM_001928298	-1.79	0.0011
KIF2C	*	Kinesin family member 2C	XM_003128056	-1.77	0.0008
SMPDL3B	*	Sphingomyelin phosphodiesterase, acid-like 3B	XM_003127737	-1.75	0.0006
LOC102159397	*	Uncharacterized LOC102159397	XR_303376	-1.71	0.0009
CITED1	*	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1	NM_001037964	-1.55	0.0009
CDHR1	*	Cadherin-related family member 1, transcript variant X1	XM_003133094	-1.54	0.0008
MMAA	*	Methylmalonic aciduria (cobalamin deficiency) cbla type	XM_003129165	-1.53	0.0101
LOC102162254	*	Uncharacterized LOC102162254	XR_303875	-1.52	0.0010
MYH7	*	Myosin, heavy chain 7, cardiac muscle, beta	NM_213855	-1.50	0.0043
CCL28	*	Chemokine (C-C motif) ligand 28	NM_001024695	-1.48	0.0035
LOC100510917	*	Glutathione S-transferase A4-like	XM_003128793	-1.47	0.0042
KIAA1324	*	KIAA1324 ortholog, transcript variant X3, mRNA	XM_005663592	-1.46	0.0033
CDH16	*	Cadherin 16, KSP-cadherin	XM_003362154	-1.45	0.0055
SLC35F3	*	solute carrier family 35, member F3, transcript variant X1	XM_001927867	-1.44	0.0027
PROM1	*	Prominin 1	XM_003482346	-1.42	0.0056

SERPINA1		Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	NM_214395	-1.41	0.0050
DEFB1		Defensin, beta 1	NM_213838	-1.40	0.0044
RASGEF1A	*	RasGEF domain family, member 1A	XM_001926447	-1.35	0.0100
CREB3L4	*	Camp responsive element binding protein 3-like 4	NM_001123102	-1.35	0.0208
ATP6V1C2	*	Atpase, H ⁺ transporting, lysosomal 42kda, V1 subunit C2	XM_003125387	-1.34	0.0055
TNNI3	*	Troponin I type 3 (cardiac)	NM_001098599	-1.33	0.0044
PEX6	*	Peroxisomal biogenesis factor 6	NM_001110426	-1.33	0.0064
CCL23	*	Chemokine (C-C motif) ligand 23	XM_003131712	-1.33	0.0056
SYT13	*	Synaptotagmin XIII	XM_003122846	-1.31	0.0091
DMBT1		Deleted in malignant brain tumors 1	NM_001048188	-1.31	0.0072
PHGDH	*	Phosphoglycerate dehydrogenase	NM_001123162	-1.29	0.0054
DDC	*	Dopa decarboxylase (aromatic L-amino acid decarboxylase)	NM_213854	-1.27	0.0090
GGT1		Gamma-glutamyltransferase 1	NM_214030	-1.26	0.0068
SERPINE1		Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	NM_213910	-1.26	0.0060
FUT2		Fucosyltransferase 2 (secretor status included)	NM_214069	-1.26	0.0049
IHH	*	Indian hedgehog	NM_001244470	-1.25	0.0077
TMEM229B	*	Transmembrane protein 229B	XM_005656338	-1.22	0.0076
GSTA1		Glutathione S-transferase alpha 1	NM_214389	-1.21	0.0104
BPI	*	Bactericidal/permeability-increasing protein	NM_001159307	-1.21	0.0115
CD109	*	CD109 molecule, transcript variant 1	XM_001927545	-1.21	0.0455
MUC4		Mucin 4, cell surface associated	NM_001206344	-1.20	0.0133
SAL1	*	Salivary lipocalin	NM_213814	-1.19	0.0138
LOC100515246	*	Tumor protein D53-like	XM_003121221	-1.19	0.0136
COL27A1	*	Collagen, type XXVII, alpha 1	XM_003122091	-1.18	0.0483

GPD1	*	Glycerol-3-phosphate dehydrogenase 1 (soluble)	NM_001190240	-1.18	0.0088
CRELD2	*	Cysteine-rich with EGF-like domains 2	XM_003126783	-1.16	0.0431
SLC44A4	*	Solute carrier family 44, member 4	NM_001101818	-1.14	0.0163
GPC3	*	Glypican 3	XM_003135399	-1.10	0.0195
TRPM6		Transient receptor potential cation channel, subfamily M, member 6	XM_005652699	-1.09	0.0203
CLCN4	*	Chloride channel, voltage-sensitive 4	XM_001925227	-1.08	0.0301
LOC100623233	*	PCNA-associated factor	XM_005659500	-1.08	0.0383
SUCO	*	SUN domain containing ossification factor	XM_003357538	-1.08	0.0285
LOC100524885	*	Glycerophosphodiester phosphodiesterase domain-containing protein 4-like	XM_005667151	-1.07	0.0256
PHACTR3	*	Phosphatase and actin regulator 3	NM_001110176	-1.06	0.0342
LPAR3		Lysophosphatidic acid receptor 3	NM_001162402	-1.05	0.0289
LOC100153765	*	Uncharacterized protein c13orf33 homolog	XM_001927721	-1.05	0.0495
WNT2	*	Wingless-type MMTV integration site family member 2	XM_003134756	-1.05	0.0441
TGM2	*	Tissue transglutaminase homologue	XM_003359989	-1.04	0.0152
RAB37	*	RAB37, member RAS oncogene family	XM_003131228	-1.04	0.0209
COL1A2		Collagen, type I, alpha 2	NM_001243655	-1.02	0.0453
GSTA2	*	Glutathione S-transferase alpha 2	NM_213850	-1.02	0.0346
IGF1		Insulin-like growth factor 1 (somatomedin C)	NM_214256	-1.01	0.0266
SAT1	*	Spermidine/spermine N1-acetyltransferase 1	NM_214358	-1.01	0.0231
GPX2		Glutathione peroxidase 2 (gastrointestinal)	NM_001115136	-0.98	0.0361

Table S9. Representative functional terms from enriched DAVID annotation of genes up-regulated at prepuber phase versus postovulatory phase in oviduct

Gene ontology term	No. of genes	Genes	Fold enrichment	P value
GO:0005615 extracellular space	18	<i>PLAT, LDLR, C3, CXCL2, MMP7, SERPING1, IGF2, MMRN2, TAC3, WNT2B, CXCL10, VCAM1, CXCL16, C2, IGFBP2, IGFBP3, MYOC, PON3</i>	5.09	0.0000
GO:0010033 response to organic substance	15	<i>CGA, HSP90AA1, LDLR, CFB, IGF2, STAT1, IRS1, ID2, SQLE, CXCL16, HSPE1, ID3, PARP1, IGFBP2, MYC</i>	4.47	0.0000
GO:0006955 immune response	13	<i>PSMB10, C3, CFB, CXCL2, RSAD2, SERPING1, OAS2, PSMB8, CXCL10, PSMB9, CXCL16, C2, DEFB1</i>	4.05	0.0001
GO:0009611 response to wounding	10	<i>PLAT, KLF6, C3, CFB, CXCL2, SERPING1, IGF2, ID3, C2, CXCL10</i>	4.05	0.0006
GO:0006952 defense response	11	<i>C3, CFB, CXCL16, CXCL2, RSAD2, SERPING1, IGF2, C2, MX1, DEFB1, CXCL10</i>	3.84	0.0004
GO:0042127 regulation of cell proliferation	13	<i>MMP7, IGF2, SPARC, STAT1, IRS1, CXCL10, VCAM1, CDCA7, ID2, IGFBP3, MYC, GNL3, ALOX12</i>	3.55	0.0002
Secreted	23	<i>PLAT, MUC1, CGA, CFB, C3, CXCL2, MMP7, IGF2, SERPING1, SPARC, LGALS9, MMRN2, CXCL10, TAC3, WNT2B, RNASE10, CXCL16, C2, IGFBP2, DEFB1, IGFBP3, MYOC, PON3</i>	3.40	0.0000
GO:0006508 proteolysis	10	<i>PLAT, PSMB10, C3, CFB, HERC5, MMP7, SERPING1, C2, PSMB8, PSMB9</i>	2.04	0.0497
GO:0007186 G-protein coupled receptor protein signaling pathway	10	<i>CGA, C3, CXCL16, CXCL2, IGF2, NPSR1, PTGFR, DEFB1, CXCL10, TAC3</i>	1.91	0.0689
GO:0007166 cell surface receptor linked signal transduction	16	<i>PLAT, CGA, C3, CXCL2, IGF2, PTGFR, STAT1, IRS1, TAC3, WNT2B, CXCL10, EPHA4, CXCL16, NTRK2, NPSR1, DEFB1</i>	1.85	0.0184
GO:0031974 membrane-	16	<i>CES1, MYH7, SERPING1, IGF2, SPARC, STAT1, MCM4, COIL, NOP14, HSPE1, DDX21,</i>	1.67	0.0430

enclosed lumen

FKBP10, PARP1, NHP2, MYC, GNL3

Table S10. Representative functional terms from enriched DAVID annotation of genes down-regulated at prepuber phase versus postovulatory phase in oviduct

Gene ontology term	No. of genes	Genes	Fold enrichment	P value
GO:0007565 female pregnancy	6	<i>ADM, GRN, HSD11B2, FCGRT, SULT1E1, PLAU</i>	13.42	0.0001
GO:0048878 chemical homeostasis	11	<i>CCK, SAA2, ADM, HEXA, SERPINE1, EPHX2, TGM2, IGF1, RGN, HP, UPK3A</i>	5.28	0.0000
GO:0042592 homeostatic process	13	<i>GPX2, CCK, SAA2, ADM, HEXA, SERPINE1, EPHX2, TGM2, RGN, IGF1, ACP5, HP, UPK3A</i>	4.26	0.0000
GO:0009611 response to wounding	8	<i>ANXA8, SAA2, ADM, SERPINE1, EPHX2, IGF1, SERPINA1, PLAU</i>	3.71	0.0049
GO:0008289 lipid binding	7	<i>ANXA8, APOD, SCIN, HSD11B2, PITPNC1, SULT1E1, SEC14L3</i>	3.67	0.0106
GO:0042127 regulation of cell proliferation	10	<i>KRT5, ADM, GRN, SCIN, SERPINE1, TGM2, IGF1, TIMP2, PLAU, DPT</i>	3.13	0.0370
GO:0005615 extracellular space	9	<i>PROM1, CCK, SAA2, APOD, ADM, GRN, IGF1, HP, SERPINA1</i>	3.00	0.0085
GO:0055114 oxidation reduction	7	<i>GPX2, STEAP4, FMO1, HSD11B1, PHGDH, HSD11B2, FADS6</i>	2.69	0.0410
Secreted	16	<i>CCK, ENPP2, IGF1, HP, TIMP2, PLAC9, ADM, SAA2, APOD, FOLR1, GRN, SERPINE1, SERPINA1, CELA2A, PLAU, DPT</i>	2.68	0.0006

Table S11. Representative functional terms from enriched DAVID annotation of genes up-regulated at preovulatory phase versus postovulatory phase in oviduct

Gene ontology term	No. of genes	Genes	Fold enrichment	P value
GO:0006928 cell motion	11	<i>PLAT, TUBB, CCK, PTGS2, MSH2, IGF1, VCAN, SCARB1, ENPEP, CERCAM, VNN2</i>	4.75	0.0001
GO:0009719 response to endogenous stimulus	8	<i>SLC2A8, PTGS2, LDLR, MSH2, FBP1, PARP1, IHH, SPP1</i>	4.05	0.0032
GO:0044421 extracellular region part	20	<i>PLAT, ASPN, ADAMTS19, CCK, COL4A1, LDLR, C5, CD109, IGF1, SPARC, CALR, COL5A2, TAC3, EMILIN1, COL1A2, NPPB, VCAN, PON3, SPP1, IHH</i>	3.80	0.0000
GO:0010033 response to organic substance	13	<i>SLC2A8, LDLR, ID2, PTGS2, MSH2, SQLE, FBP1, SCARB1, DNAJC3, PARP1, SERPINH1, IHH, SPP1</i>	3.70	0.0001
Secreted	19	<i>PLAT, ASPN, ADAMTS19, CCK, COL4A1, CRELD2, C5, IGF1, SPARC, CALR, COL5A2, TAC3, EMILIN1, COL1A2, NPPB, VCAN, PON3, SPP1, IHH</i>	2.74	0.0001
GO:0005783 endoplasmic reticulum	13	<i>SGK1, CRELD2, PTGS2, SQLE, CKAP4, INSIG1, LRRC59, AQP5, HSPA5, CERCAM, DNAJC3, CALR, SERPINH1</i>	2.47	0.0049
GO:0031982 vesicle	9	<i>PLAT, SLC2A8, LDLR, IGF1, ANPEP, ENPEP, HSPA5, SPARC, SPP1</i>	2.45	0.0273
GO:0042802 identical protein binding	8	<i>MSH2, COL1A2, S100A11, FBP1, MYH7, PARP1, PON3, EMILIN1</i>	2.42	0.0431
GO:0042981 regulation of apoptosis	9	<i>CDK1, TUBB, CCK, PTGS2, MSH2, IGF1, HSPA5, CALR, IHH</i>	2.29	0.0380
GO:0000267 cell fraction	13	<i>PTGS2, SQLE, SLC17A1, CKAP4, LRRC59, FBP1, ANPEP, SCARB1, CYB5B, CALR, PKIA, PON3, TAC3</i>	2.19	0.0124
GO:0006508 proteolysis	11	<i>PLAT, CDK1, PEG10, ADAMTS19, C5, UCHL1, ANPEP, CDC20, ENPEP, CDCA3, IHH</i>	2.14	0.0280
GO:0042995 cell	8	<i>CCK, PVALB, UCHL1, S100A11, AQP5, SCARB1,</i>	2.10	0.0811

projection			<i>ENPEP, SPP1</i>		
GO:0042127 regulation of cell proliferation	8		<i>PGR, ID2, PTGS2, S100A11, IGF1, SPARC, CALR, IHH</i>	2.08	0.0825
GO:0005829 cytosol	14		<i>CDK1, SULT2A1, UCHL1, ABHD5, FBP1, CDC20, ANPEP, CALR, TUBB, NANS, ID2, GUCY1B3, HSPA5, CDCA3</i>	1.92	0.0242
GO:0005509 calcium ion binding	9		<i>CRELD2, LDLR, PVALB, S100A11, VCAN, ENPEP, HSPA5, SPARC, CALR</i>	1.90	0.0931
GO:0043233 organelle lumen	18		<i>CDK1, MYH1, PTGS2, UCHL1, IGF1, ANPEP, MYH7, CDC20, SPARC, CERCAM, CALR, SERPINH1, HNRNPA3, LRRC59, NPM3, HSPA5, PARP1, MDH2</i>	1.81	0.0149
GO:0031974 membrane-enclosed lumen	18		<i>CDK1, MYH1, PTGS2, UCHL1, IGF1, ANPEP, MYH7, CDC20, SPARC, CERCAM, CALR, SERPINH1, HNRNPA3, LRRC59, NPM3, HSPA5, PARP1, MDH2</i>	1.77	0.0178

Table S12. Representative functional terms from enriched DAVID annotation of genes down-regulated at preovulatory phase versus postovulatory phase in oviduct

Gene ontology term	No. of genes	Genes	Fold enrichment	P value
GO:0004175 endopeptidase activity	7	<i>ADAM28, CFLAR, SERPINE1, HP, C2, CFD, PLAU</i>	6.92	0.0004
GO:0048878 chemical homeostasis	7	<i>SERPINE1, TGM2, RGN, HP, UPK3A, PPARGC1A, ABCG1</i>	4.87	0.0024
GO:0042592 homeostatic process	10	<i>ANG, SERPINE1, TGM2, ACP5, RGN, HP, UPK3A, PPARGC1A, ABCG1, GLRX</i>	4.74	0.0001
GO:0009611 response to wounding	7	<i>KLF6, C3, SERPINE1, C2, CDO1, CFD, PLAU</i>	4.70	0.0029
GO:0010033 response to organic substance	7	<i>ANG, ALDOC, HSPB1, ACP5, FOXO1, CDO1, ABCG1</i>	3.46	0.0127
GO:0043933 macromolecular complex subunit organization	6	<i>ANG, ALDOC, TGM2, GNMT, PPARGC1A, ABCG1</i>	3.01	0.0426
GO:0008219 cell death	6	<i>CFLAR, ANG, ALDOC, TGM2, AKAP13, HSPB1</i>	2.97	0.0446
GO:0006508 proteolysis	8	<i>ADAM28, CFLAR, C3, HP, C2, CFD, USP32, PLAU</i>	2.70	0.0223
Secreted	9	<i>ADAM28, C3, ANG, EFNA1, SERPINE1, HP, C2, CFD, PLAU</i>	2.38	0.0278
GO:0005829 cytosol	9	<i>AKAP13, ACP5, FOXO1, NDRG2, SULT1E1, GNMT, CDO1, PPARGC1A, GLRX</i>	2.28	0.0336

Table S13. Representative functional terms from enriched DAVID annotation of genes up-regulated at luteal phase versus postovulatory phase in oviduct

Gene ontology term	No. of genes	Genes	Fold enrichment	P value
GO:0030335 positive regulation of cell migration	2	<i>CXCL16, KIT</i>	21.71	0.0823
GO:0005615 extracellular space	6	<i>C3, CXCL16, MMP7, LYZ, KIT, IL24</i>	9.33	0.0002
GO:0008219 cell death	5	<i>DAPL1, LYZ, KIT, IL24, MYC</i>	6.72	0.0038
GO:0012501 programmed cell death	4	<i>DAPL1, KIT, IL24, MYC</i>	6.33	0.0187
Secreted	5	<i>MUC1, C3, CXCL16, MMP7, IL24</i>	3.80	0.0290

Table S14. Representative functional terms from enriched DAVID annotation of genes down-regulated at luteal phase versus postovulatory phase in oviduct

Gene ontology term	No. of genes	Genes	Fold enrichment	P value
GO:0032101 regulation of response to external stimulus	6	<i>GPX2, CCK, SAA2, SERPINE1, TGM2, PLAU</i>	11.60	0.0001
GO:0006874 cellular calcium ion homeostasis	6	<i>CCL23, SAA2, TGM2, LPAR3, TNNI3, CCL28</i>	10.08	0.0003
GO:0001568 blood vessel development	6	<i>COL1A2, TGM2, TNNI3, CITED1, PLAU, IHH</i>	7.53	0.0010
GO:0044421 extracellular region part	15	<i>CCK, CD109, IGF1, CCL28, MUC4, PROM1, WNT2, GPC3, CCL23, SAA2, SMPDL3B, COL27A1, COL1A2, SERPINA1, IHH</i>	4.34	0.0000
GO:0042592 homeostatic process	10	<i>GPX2, CCK, CCL23, SAA2, SERPINE1, TGM2, LPAR3, IGF1, TNNI3, CCL28</i>	4.09	0.0005
Secreted	19	<i>CCK, CRELD2, IGF1, CCL28, MUC4, WNT2, BPI, CCL23, GPC3, SMPDL3B, SAA2, COL27A1, SERPINE1, COL1A2, SERPINA1, DEFB1, PLAU, DMBT1, IHH</i>	3.93	0.0000
GO:0006952 defense response	7	<i>BPI, CCK, CCL23, SAA2, SERPINA1, DEFB1, DMBT1</i>	3.50	0.0125
GO:0042127 regulation of cell proliferation	8	<i>WNT2, CCL23, GPC3, SERPINE1, TGM2, IGF1, PLAU, IHH</i>	3.13	0.0113

Table S15. Peptides identified by proteomic analysis

Peptides that have been manually validated are shown in yellow.

Protein	Peptides	Z	SCORE	SPI	INTENSITY	M/Z
CCK	MIKNLQSLDPSHRISDRDYMGW	3	9.81	78.8	1127704	947.57
	DRDYMGWMDFGRRSAEEYE	3	9.64	79.4	1950993	863.65
	ALLARYIQQARKAPSGRVSM	3	9.54	83.4	966778	771.37
	QQARKAPSGRVSMIKNLQSLDPS	3	9.12	89.5	3291151	870.06
	ARKAPSGRVSMIKNLQSLD	3	8.09	76.4	1559137	717.47
	MIKNLQSLDPSHRISDRDYMGW	3	8.05	75.7	1056966	946.69
TAC3	Peptides	Z	SCORE	SPI	INTENSITY	M/Z
	QLPSSLLRRLCDSRSISLDGLL	3	11.14	78.7	7418445	861.91
	DGLLKMLSKASVGAKESS	3	11.01	70.5	290098	639.83
	FVGLMGKRNIQPGTPVDGNQENAPSL	3	10.33	86.7	1916329	972.23
	LKMLSKASVGAKESSLPQKRDM	3	9.18	94.3	188880	829.26
	MGKRNIQPGTPVDGNQENAPSLGTFK	3	9.18	79.0	4076579	977.62
	NIQPGTPVDGNQENAPSLGTFKYPPS	3	9.00	84.1	328200	936.89
	RSISLDGLLKMLSKASVGAKESS	3	8.90	72.7	294408	851.17
	LKMLSKASVGAKESSLPQKRDM	3	8.67	92.5	3392038	807.23
	MPGGGHSKKDSNLYQLPSSLLRRLCDS	3	8.58	85.9	2887793	1013.79
	MPGGGHSKKDSNLYQL	3	7.94	94.1	61348	609.71
	SSLPQKRDMHDFVGLMGK	3	7.26	82.9	127230	758.69
PEBP4	Peptides	Z	SCORE	SPI	INTENSITY	M/Z
	AVLCKGLKVFYPELGNLGCMMVPECN	3	10.41	92.7	9299434	937.89
	VLCKGLKVFYPELGNLGCMMVVP	3	10.26	77.8	215149	799.58
	KITSWTEPIVKFPGALDGATYILV	3	9.67	92.7	174609	874.30
	LKMLSKASVGAKESSLPQKRDM	3	9.18	94.3	188880	829.26

	SGFHRYQFFVYLQQEK SIS	3	8.80	79.3	48034	841.69
	YPELGNL GCMVVPECNNYRQKIT	3	8.72	79.6	115722	885.96
GPX2	Peptides	Z	SCORE	SPI	INTENSITY	M/Z
	MAYIAKSFYDLSAISLDGEKV	3	12.94	80.5	10471960	833.68
	MAYIAKSFYDLSAISLDGEKV	3	10.63	78.7	9366103	833.10
	PYPYDDPFSLMTDPKFIIWSPVRR	3	10.42	76.9	2297451	1013.40
	ILNSLKYVRPGGGFQPT	3	9.68	93.6	187851	669.30
	YIAKSFYDLSAISLDGEKVD FNTFRGR	3	9.47	97.0	469076	1091.91
	GEKVD FNTFRGRAVLIENVASLUGTTTR	3	8.63	77.2	11158818	1010.86
	LGFPCNQFGHQENCQNEEILNS	3	8.34	86.9	499106	887.13
	KITSWTEPIVKFPGALDGATYILV	3	8.28	83.6	293062	1235.51
	FAYLKDKLPYPYDDPFSLM	3	8.21	82.1	173572	801.24
MUC1	Peptides	Z	SCORE	SPI	INTENSITY	M/Z
	RDAYHPMSEYPTYHTHGRYVPPG	3	12.07	86.1	405237	943.22
	TRDAYHPMSEYPTYHTHGRYVPPGSTKRNP YEQVSAGNGGGSLSYSNLAA	6	9.79	84.0	9790590	937.11
	KQTNKNLALSLSQFLQVYKEDGL	3	8.78	84.5	912668	935.06
	HPMSEYPTYHTHG	2	8.14	78.5	548694	858.07