

Supplemental Table S1.

NSN oocytes

<i>Category</i>	<i>Gene name</i>
Cytoplasmic part	<i>Clta, Dnach2, Sort1, Rpl37, Trim63</i>
Transport	<i>Clta, Dnach2, Abcg4, Sort1</i>
Intracellular organelle part	<i>Clta, Dnach2, Sort1, Rpl37</i>
Establishment of localization	<i>Clta, Dnach2, Abcg4, Sort1</i>
Cytoplasm	<i>Clta, Dnach2, Boll, Sort1, Rpl37, Trim63</i>

Supplemental Table S2.

SN oocytes

<i>Category</i>	<i>Gene name</i>
Ribosome	<i>Rpl31, Mrpl23, Rpl23a, Rpl26, Mrpl27, Rpl24, Rpl7, Rpl6, Rps6, Rpl13, Rpl3, Rnaset2b, Rps28, Rpl27, Rpl8, Rpl30, Rpl11, Rpl35a, Rpl27a, Rps19, Rps15a, Rpl36a</i>
Translation	<i>Rpl31, Mrpl23, Rpl23a, Rpl26, Mrpl27, Rpl24, Eef1g, Rpl7, Rpl6, Rps6, Rpl13, Rpl3, Gspt1, Rps28, Rpl27, Rpl8, Rpl30, Zfp3611, Rpl11, Rpl35a, Rpl27a, Rps19, Rps15a, Rpl36a</i>
Ribosomal subunit	<i>Mrpl23, Rpl26, Mrpl27, Rpl7, Rpl8, Rpl11, Rps6, Rps28</i>
Ribonucleoprotein complex	<i>Rpl31, Mrpl23, Rpl23a, Rpl26, Mrpl27, Hnrnpa1, Rpl24, Rpl7, Rpl6, Rps6, Rpl13, Msi2, Pabpc1, Rpl3, Rnaset2b, Rps28, Rpl27, Rpl8, Rpl30, Rpl11, Rpl35a, Rpl27a, Rps19, Rps15a, Rpl36a, Pes1</i>
Biosynthetic process	<i>Rpl31, Ptgs2, Elovl6, Npr2, Cav1, Mrpl23, Zdhhc2, Rpl23a, Igf1, Galnt10, Rpl26, Acaca, Mrpl27, Hsd17b1, Gadd45, Rpl24, Eef1g, Rpl7, Rpl6, St8sia4, Atp5g3, Sh3glb1, Rps6, Apobec1, Rpl13, Ednra, St3gal4, Nme2, Stat5b, Hexb, Rpl3, Gspt1, Rps28, Ak3, Prps2, Chst11, Rpl27, Rpl8, Ddah2, Rpl30, Zfp3611, Rpl11, Rpl35a, Apobec1, Rpl27a, Rps19, Rps15a, Rpl36a, Fabp3, Atp5j</i>
Structure molecular activity	<i>Rpl31, Crygf, Thbs1, Coll1a1, Mrpl23, Rpl23a, Perp, Rpl26, Mrpl27, Omd, Rpl24, Rpl6, Rpl7, Ntng1, Rps6, Rpl13, Thbs4, Rpl3, Tuba1a, RnasetbB, Rps28, Rpl27, Rpl8, Rpl30, Rpl11, Rpl35a, Rpl27A, Rps19, Rps15a, Actg1, Rpl36a, Cryge</i>
Cytosol	<i>Mt1, Ppia, Rpl26, Fmnl1, Psme1, Pgam1, Ngfrap1, Rpl7, Rpl6, Pea15a, Sh3glb1, Rps6, Rpl13, Nisch, Rps28, Rpl27, Rpl8, Zfp3611, Rpl11, Rps19, Rpl36a</i>

Apoptotic mitochondrial changes	<i>Bbc3, Casp7, Sh3glb1</i>
Induction of apoptosis	<i>Bok, Bbc3, Gpx1, Perp, Nr4a1, Casp7, Ngfrap1, Sh3glb1, Dap</i>
Regulation of apoptosis	<i>Bok, Bbc3, Gpx1, Perp, Igf1, Nr4a1, Snai2, Casp7, Ngfrap1, Pea15a, Sh3glb1, Stat5b, Cln8, Vegfa, Dap</i>
Apoptotic mitochondrial changes	<i>Bbc3, Casp7, Sh3glb1</i>
Induction of apoptosis	<i>Bok, Bbc3, Gpx1, Perp, Nr4a1, Casp7, Ngfrap1, Sh3glb1, Dap</i>
Regulation of developmental process	<i>Bok, Thbs1, Id1, Cav1, Bbc3, Jun, Gpx1, Perp, Gja1, Igf1, Inhba, Nr4a1, Snai2, Casp7, Ngfrap1, Pea15a, Sh3glb1, Mgp, Socs2, Stat5b, Rhob, Fst, Lect1, Bex1, Cln8, Vegfa, Dap, Maff</i>
Female gonad development; female sex differentiation	<i>Nr5a1, Stat5b, Fst, Vegfa</i>
Development of primary female sexual characteristics	<i>Nr5a1, Stat5b, Fst, Vegfa</i>
Ovulation cycle	<i>Nr5a1, Stat5b, Vegfa</i>
Gonad development	<i>Nr5a1, Stat5b, Fst, Vegfa</i>
Angiogenesis	<i>Egfl7, Thbs1, Id1, Gpx1, Cyr61, Ednra, Rhob, Lect1, Vegfb, Vegfa</i>
Vasculature development	<i>Egfl7, Thbs1, Id1, Gpx1, Cyr61, Ednra, Rhob, Lect1, Vegfb, Vegfa, Cav1, Gja1, Cited1, Zfp361l</i>
Blood vessel development	<i>Egfl7, Thbs1, Id1, Gpx1, Cyr61, Ednra, Rhob, Lect1, Vegfb, Vegfa, Cav1, Gja1, Cited1, Zfp361l</i>
Regulation of angiogenesis	<i>Thbs1, Id1, Rhob, Lect1</i>
Growth	<i>Ptgs2, Bbc3, Cd81, Gpx1, Gja1, Igf1, Inhbb, Inhba, Crim1, Cyr61, Socs2,</i>
Regulation of developmental process	<i>Thbs1, Cav1, Gpx1, Igf1, Inhba, Snai2, Stat5b, Fst, Lect1, Bex1, Cln8, Vegfa, Bok, Id1, Bbc3, Jun, Perp, Gja1, Nr4a1, Casp7, Ngfrap1, Pea15a, Sh3glb1, Mgp, Socs2, Stat5b, Rhob, Dap, Maff</i>
Tissue development	<i>Ptgs2, Coll1a1, Jun, Gpx1, Gja1, Churc1, Inhba, Mef2c, Nr5a1, Mgp, Sost, Fst, Lect1, Phex, Vegfa, Maff</i>
Regulation of epidermis development	<i>Inhba, Maff, Fst</i>

Supplemental Table S3.

NSN oocytes	
BiP	<i>GI:2598562</i>
Heat shock protein 8	<i>GI:13242237</i>
Peptidyl arginine deiminase, egg and embryo abunda	<i>GI:119372294</i>
Type II keratin subunit protein	<i>GI:4159806</i>
Aldolase A, fructose-bisphosphate	<i>GI: 6671539</i>
Y box binding protein 1	<i>GI:92373398</i>
Astacin-like metalloendopeptidase	<i>GI:27369754</i>
Zona pellucida glycoprotein 2	<i>GI:6756081</i>
Unnamed protein product	<i>GI:12846758</i>
Mitochondrial aldehyde dehydrogenase 2	<i>GI:6753036</i>
Transducin-like enhancer protein 6	<i>GI:16716583</i>
Tumor rejection antigen gp96	<i>GI:6755863</i>
Ubiquitin carboxyl-terminal esterase L1	<i>GI:61098212</i>
Heat shock protein 1, alpha	<i>GI:6754254</i>
Put. beta-actin	<i>GI:49868</i>
Unnamed protein product	<i>GI:26344672</i>
Heat shock protein 105	<i>GI:114145505</i>
Hydroxyacyl-Coenzyme A dehydrogenase type II	<i>GI:61888838</i>
Clathrin, heavy polypeptide (Hc)	<i>GI:51491845</i>
	<i>GI:6671664</i>

Acetyl-Coenzyme A acetyltransferase 1 precursor	<i>GI:21450129</i>
Glycogenin 1	<i>GI:7305121</i>
Keratin 15	<i>GI:6680602</i>

Supplemental Table S4.

SN oocytes	
Heat shock 70kDa protein 4	<i>GI:2495342</i>
Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	<i>GI:9507245</i>
Pyruvate kinase	<i>GI:551295</i>
Superoxide dismutase 1	<i>GI:45597447</i>
NACHT, leucine rich repeat and PYD containing 5	<i>GI: 7106379</i>
Hypothetical protein LOC66991	<i>GI:33468985</i>

Supplemental Table S5.

	<i>Total number of modifications</i>		<i>% of modifications</i>	
	<i>NSN</i>	<i>SN</i>	<i>NSN</i>	<i>SN</i>
Total modified	66	23	9.8	6.8
Acetylation	16	7	2.4	2.1
Methylation	39	10	5.8	2.9
Deimination	11	6	1.6	1.8
Unmodified	605	316	90.2	93.2
Total identified	671	339	100	100

Legend Supplemental Tables

Table S1. List of genes over expressed in NSN compared to SN antral oocytes grouped according to the main GO biological process categories to which they belong.

Table S2. List of genes overexpressed in SN compared to NSN antral oocytes grouped according to the main GO biological process categories to which they belong.

Table S3. List of proteins upregulated in NSN compared to SN antral oocytes.

Table S4. List of proteins upregulated in SN compared to NSN antral oocytes.

Table S5. Number of unmodified and modified peptides in NSN and SN oocytes.