

Additional file 4 - Functional profile of transcripts correlated both to OTF and NL in the mouse ovary ^a

OTF (-) NL (+) ^a	b						Relevant biological or disease role (PMID) ^c	
	RB	RP	RT	ZB	UC	PF		
<i>Cpsf6</i> , cleavage and polyadenylation specific factor 6	■	■					o	Linked to tumor stage in ovarian cancer (18636107)
<i>Ddx17</i> , DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	■						o	Transcriptional co-activator for ER alpha (11250900)
<i>Fubp1</i> , far upstream element (FUSE) binding protein 1	■		■				o	Regulates c-myc transcription (16628215)
<i>Hnrpdl</i> , heterogeneous nuclear ribonucleoprotein D-like	■		■					nrd (§)
<i>Hnrpa2b1</i> , heterogeneous nuclear rnp A2/B1	■						o	Prevents apoptosis in ovarian and other cancers (14633690)
<i>Pabpn1</i> , poly(A) binding protein, nuclear 1 (#)	■	■				■	m	Mutated in oculopharyngeal muscular dystrophy (17110089)
<i>Rbm4</i> , RNA binding motif protein 4	■			■			n	Decreased in the fetal brain in Down's Syndrome (12469345)
<i>Rbm4b</i> , RNA binding motif protein 4B	■			■				nrd (§)
<i>Rbm6</i> , RNA binding motif protein 6	■							Involved in non-small cell lung cancer (11085536)
<i>Rbm12</i> , RNA binding motif protein 12	■							Altered in meibomian cell carcinoma (17889501)
<i>Rbm25</i> , RNA binding motif protein 25	■						o	Stimulates proapoptotic <i>Bcl-x</i> splicing (18663000)
<i>Rbm26</i> , RNA binding motif protein 26	■			■			b	Overexpressed in T-cell lymphomas and leukemia cells (11149944)
<i>Rbm39</i> , RNA binding motif protein 39	■	■	■				o	Coactivates steroid hormone receptors (15694343)
<i>Sfrs2</i> , splicing factor, arginine/serine-rich 2	■	■					o	Expressed in human ovarian cancer (15069551)
<i>Sfrs6</i> , splicing factor, arginine/serine-rich 6	■						o	Upregulates antiangiogenic VEGF isoforms (18843117)
<i>Sfrs7</i> , splicing factor, arginine/serine-rich 7	■			■			e	Involved in GnRH pre-mRNA splicing (16249178)
<i>Sfrs11</i> , splicing factor, arginine/serine-rich 11		■						Modulates alternative splicing of Tau mRNA (16943417)
<i>Sfrs12</i> , splicing factor, arginine/serine-rich 12		■					n	Down-regulated in Alzheimer disease's brain (15456940)
<i>Sfrs18</i> , splicing factor, arginine/serine-rich 18		■						nrd (§)
<i>Stm</i> , SAFB-like, transcription modulator	■		■					Pro-apoptotic effect and inhibition of mRNA synthesis (17630952)
<i>Son</i> , SON DNA binding protein	■						b	Cellular growth factor in leukemogenesis (18952841)
<i>Srrm1</i> , serine/arginine repetitive matrix 1	■	■						Regulates alternative splicing of the CD44 mRNA (16354706)
<i>Tardbp</i> , TAR DNA binding protein	■		■				n	Roles in cystic fibrosis and neurodegenerative disorders (17981595)
<i>Tra2a</i> , transformer 2 alpha homolog (*)	■	■					e	Role in estrogen mediated scavenger receptor splicing (17673517)
<i>Ttc14</i> , tetratricopeptide repeat domain 14	■							nrd (§)
<i>3300001P08Rik</i> , RIKEN cDNA 3300001P08 gene		■					o	Overexpression is associated to cisplatin resistance (10631324)
<i>Arnt</i> , aryl hydrocarbon receptor nuclear translocator			■				o	Binds to HIF-1alpha to recognize VEGF promoter (17208433)
<i>Ccn1l</i> , cyclin L1			■					Oncogene candidate in head and neck cancer (12414649)
<i>Ccn12</i> , cyclin L2 (#)		■						Induces apoptosis in hepatocellular carcinoma cells (14684736)
<i>Dmtf1</i> , cyclin D binding myb-like transcription factor 1			■					Possible tumor suppressor (17237816)
<i>Mll3</i> , myeloid/lymphoid or mixed-lineage leukemia 3			■	■			b	Involved in leukemogenesis and developmental disorders (11718452)
<i>Mll5</i> , myeloid/lymphoid or mixed-lineage leukemia 5			■	■			b	Essential for regulation of hematopoiesis (18952892)
<i>Mycbp2</i> , MYC binding protein 2			■	■	■		m	Plays a key role in neuromuscular development (18255027)
<i>Nfat5</i> , nuclear factor of activated T-cells 5			■					Involved in hyperosmotic stress response (15965902)
<i>Suv420h2</i> , suppressor of variegation 4-20 homolog 2 (*)			■					Implicated in epigenetic dysregulation of breast cancer (16322686)
<i>1810007M14</i> , RIKEN cDNA 1810007M14 gene			■					nrd (§)
<i>2010111H01</i> , RIKEN cDNA 2010111H01 gene			■					Aminopeptidase involved in peptide processing (15687497)
<i>Ece1</i> , endothelin converting enzyme 1			■				o	Modulates prostaglandin-F2 production in pregnancy (16524686)
<i>Luc7l2</i> , LUC7-like 2 (<i>S. cerevisiae</i>)			■					nrd (§)
<i>Zc3h7a</i> , zinc finger CCCH type containing 7 A			■					Increased during macrophage activation (18682727)
<i>Zc3h11a</i> , zinc finger CCCH type containing 11A			■					nrd (§)

Zfp644, zinc finger protein 644
Zfp820, zinc finger protein 820
Zufsp, zinc finger with UFM1-specific peptidase domain
Otud7b, OTU domain containing 7B
Ube2e1, ubiquitin-conjugating enzyme E2E 1
Usp15, ubiquitin specific peptidase 15
Wsb1, WD repeat and SOCS box-containing 1

				■					
				■					
				■					
				■	■				
				■	■				m
				■	■				
				■	■				e

nrd (§)
nrd (§)
nrd (§)
Prevents interleukin-8 mediated inflammation response (18178551)
Upregulated in rat model of cardiac ischemia (15665047)
Involved in cell cycle control (18346885)
Modulates thyroid metabolism (15965468)

OTF (+) NL (-) ^a

BC003993, cDNA sequence BC003993
Lmo1, LIM domain only 1
Sall4, sal-like 4 (*)
Nfia, nuclear factor I/A
Cited1, Cbp/p300-interacting transactivator
Hsp90aa1, heat shock protein 90 a, class A, member 1
Dnajb1, DnaJ (Hsp40) homolog, subfamily B, member 1
P4hb, prolyl 4-hydroxylase, beta polypeptide (#)

	RB	RP	RT	ZB	UC	PF	
		■					
				■			b
			■	■			n
			■				n
			■				o
						■	o
						■	o
						■	o

nrd (§)
Involved in normal and pathological leukemogenesis (15198727)
Implicated in congenital and neurological disorders (16545361)
Regulates CNS development (19058033)
Regulated by FSH in human granulosa cells (16556681)
Overexpressed in ovarian endometriosis (16815388)
Involved in ovarian development in *Drosophila* (18718532)
Participates in procollagen synthesis in the ovary (17495471)

^a The 145 clones correlated with both OTF and NL (see Table 2) were reduced to 96 unique gene identities after merging repeats and excluding unknowns, non-coding, and non-annotated clones. Based on the direction of correlation these 96 genes were further decomposed in sub-lists of 76 OTF(-) NL(+) and 20 OTF(+) NL(-) genes. This table shows the genes in enriched functional domains (56 out of the 96).

^b Functional analysis was done with WebGestalt (<http://bioinfo.vanderbilt.edu/webgestalt>) using the hypergeometric test. Enriched gene ontology (GO) terms and their respective *p* values are as follows: RB= RNA binding (9.4e-16), MP= mRNA processing (1.0e-14), RT=regulation of transcription (6.6e-4), ZB=zinc ion binding (9.3e-4), UC=ubiquitin cycle (3.4e-2), PF=protein folding (1.5e-3). Tissue/organ codes are: o=ovarian; m=muscle; n=neural; b=blood; e=endocrine (non-ovarian).

^c PubMed was queried through GeneCards using "gene symbol/alias" and "ovary/ovarian" when corresponded. The PMIDs for the most informative entries are shown.

[§] Not reported to date. Most of these cases correspond to recently identified genes for which the GO term was inferred from electronic annotation.

At least one of the functional terms did not directly appeared in the GO database but was deduced from the literature.

* Corresponds to *Drosophila* homolog genes.