

Table S1 Primer sequences used to quantitate (real-time PCR) mRNA steady state levels for LMB receptor. These genes were chosen based upon their significance in LMB reproduction and follicular development. Note that the forward primer is given in the 5' to 3' orientation in relation to the 5' to 3' coding strand (sense) deposited in NCBI GenBank and the reverse primer is 5' to 3' in relation to the complementary strand (antisense).

Gene	Forward 5'-3'	Reverse 5' to 3'	Amplicon (bp)
<i>mPR-alpha</i>	GGG GTC GCT CTC TAC CAA	CAG CAG CCA AAG CAA GTA AG	137
<i>ghr1</i>	AGG GCT CAG ACA CCC AGA	CAG TTT GGG TTT GGA CG	267
<i>lhr</i>	TCA TCC TGC TCT TCA ACG TG	AGC CTT GGT GAA GAT AGC GTA A	299
<i>fshr</i>	CAG TCC TCA TCT TCA CCG ACT T	AGG CGT ACA GGA AGG GGT T	159
<i>18S rRNA</i>	CGG CTA CCA CAT CCA AGG AA	CCT GTA TTG TTA TTT TTC GTC ACT ACC T	86

Footnote: All partial gene sequences used in this study have been submitted to GenBank; NCBI gene accession numbers are as follows: LMB *mPR-α*, (FJ030924), LMB *ghr-1* (FJ030934), LMB *lhr* (FJ751229), and LMB *fshr* (FJ751230). The partial gene fragment cloned for *mPR-α* (463 bp) carried 94% nucleotide similarity to the Atlantic croaker sequence (EU095257; *Micropogonias undulates*). Real-time PCR primers were designed to amplify 137 bp of the LMB *mPR-alpha* transcript. The partial gene fragment cloned for LMB *ghr-1* (267 bp) showed 88% nucleotide similarity to that of the Orange spotted grouper (EF052273; *Epinephelus coioides*). The partial gene fragment cloned for LMB *lhr* (299 base pairs; bp) exhibited 91% nucleotide similarity to the European seabass mRNA (AY642114; *Dicentrarchus labrax*), while that for LMB *fshr* (159 bp) showed 95% nucleotide similarity to the mRNA from European seabass (EU282006; *Dicentrarchus labrax*).

Table S2 Mean fold change of significantly altered mRNA for transcription factors and receptors across ovarian stages based on SAM analysis. Due to the fact that it is not possible to pinpoint at which particular stage a gene significantly changed in expression, the fold changes reported in the table below were determined using a multi-class approach. The fold change is measured in the time course analysis as the difference between the highest and the lowest expression value over all ovarian stages. Duplicate gene titles arise from duplicate probes on the LMB microarray.

Time Series Analysis	LMB Probe ID	Gene Title	Fold Change
PN_CA_eVtg_IVtg_eOM_IOM_OV	UF_Msa_AF_101575	general transcription factor IIF, polypeptide 1, 74kDa	1.661
	UF_Msa_AD_200371	similar to hepatocytic transcription factor hB1F-2	2.545
	UF_Msa_AF_104835	GA-binding protein transcription factor, alpha subunit	2.236
	UF_Msa_AF_106495	general transcription factor IIF, polypeptide 1, 74kDa	2.094
	UF_Msa_AF_106954	general transcription factor IIF, polypeptide 1	2.264
	UF_Msa_AF_102863	immune-related, lectin-like receptor 3	9.181
	UF_Msa_AF_108143	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 2	2.962
	UF_Msa_AF_107775	gamma-aminobutyric acid (GABA) A receptor, beta 3	2.698
	UF_Msa_AF_101384	peroxisome proliferator activated receptor gamma	3.266
	UF_Msa_AD_200114	protein tyrosine phosphatase, receptor type Z, polypeptide 1	3.672
	UF_Msa_AF_103526	protein tyrosine phosphatase, non-receptor type 6	2.823

	UF_Msa_AF_103274	nuclear receptor coactivator 7	2.163
	UF_Msa_AD_200291	gamma-aminobutyric acid (GABA) A receptor, gamma 2	2.164
	UF_Msa_AF_104357	NMDA receptor-regulated gene 1a	1.348
	UF_Msa_AF_106812	NMDA receptor-regulated gene 1a	1.381
	UF_Msa_AF_109141	kinase insert domain receptor (a type III receptor tyrosine kinase)	1.668
	UF_Msa_AF_104177	nuclear receptor co-repressor 2	2.740
PN_CA_eVtg_IVtg_eOM_IOM_OV	UF_Msa_AF_109021	basic transcription factor 3	-1.189
	UF_Msa_AF_101486	transcription elongation factor B (SIII), polypeptide 2 (18kD, elongin B)	-2.795
	UF_Msa_AF_104468	cofactor required for Sp1 transcriptional activation, subunit 3	-2.036
	UF_Msa_AF_104235	CCR4-NOT transcription complex, subunit 10	-2.342
	UF_Msa_AD_200191	progesterin and adipoQ receptor family member VII	-2.267
	UF_Msa_AF_104034	parathyroid hormone receptor 2	-2.878
	UF_Msa_AD_200271	estrogen receptor 2a	-3.418
	UF_Msa_AF_109083	progesterin and adipoQ receptor family member VII	-2.354
	UF_Msa_AF_107005	NMDA receptor-regulated gene 1a	-3.284
	UF_Msa_AD_200112	low density lipoprotein receptor	-2.113

PN_CA_eVtg_IVtg_eOM_IOM_AT	UF_Msa_AF_104468	cofactor required for Sp1 transcriptional activation, subunit 3	-3.402
	UF_Msa_AF_107712	transcription factor Dp 1	-2.919
	UF_Msa_AF_104750	SPEN homolog, transcriptional regulator (Drosophila)	-6.177
	UF_Msa_AF_101460	CCR4-NOT transcription complex, subunit 1	-2.306
	UF_Msa_AF_106226	activating transcription factor 4 (tax-responsive enhancer element B67)	-1.220
	UF_Msa_AF_104034	parathyroid hormone receptor 2	-2.878
	UF_Msa_AD_200321	protein tyrosine phosphatase, receptor type Z, polypeptide 1	-8.914
	UF_Msa_AD_200191	progesterin and adipoQ receptor family member VII	-3.756
	UF_Msa_AD_200112	low density lipoprotein receptor	-2.113
	UF_Msa_AF_100542	thyroid hormone receptor associated protein 1 (predicted)	-1.818
	UF_Msa_AF_107005	NMDA receptor-regulated gene 1a	-6.167
	UF_Msa_AF_101308	similar to Protein tyrosine phosphatase, receptor type, B	-5.548
	UF_Msa_AF_101979	protein tyrosine phosphatase, non-receptor type 13	-1.873
	UF_Msa_AD_200271	estrogen receptor 2a	-3.418
	UF_Msa_AF_109083	progesterin and adipoQ receptor family member VII	-2.524

Table S3 Significant gene ontology for BP for ovarian genes by major stages. Class 0 proportions refer to differentially expressed transcripts and Class 1 proportions refer to transcripts not differentially expressed when transitioning from stage to stage. PG = primary growth (PN and CA), SG = secondary growth (eVtg and IVtg), OM = oocyte maturation (eOM and IOM), OV = ovulation, AT = atresia. Appendix 2 presents all the data from the gene ontology analysis.

Stage transition	_GO_Biological_Process Category	Raw_p	Class 0 Proportion	Class 1 Proportion	over/under
PG to SG	GO:0006096; glycolysis	0.016	0.009	0.0011	under
PG to SG	GO:0006811; ion transport	0.019	0.012	0.0034	under
PG to SG	GO:0006821; chloride transport	0.045	0.005	0.0000	under
PG to SG	GO:0008380; RNA splicing	0.023	0.010	0.0204	over
SG to OM	GO:0006468; protein amino acid phosphorylation	0.035	0.031	0.0147	under
SG to OM	GO:0042157; lipoprotein metabolic process	0.001	0.001	0.0110	over
SG to OM	GO:0006810; transport	0.004	0.061	0.0971	over
SG to OM	GO:0006118; electron transport	0.017	0.026	0.0458	over
SG to OM	GO:0006821; chloride transport	0.029	0.002	0.0092	over
SG to OM	GO:0006744; ubiquinone biosynthetic process	0.039	0.004	0.0110	over
SG to OM	GO:0006725; aromatic compound metabolic process	0.040	0.002	0.0073	over
SG to OM	GO:0006839; mitochondrial transport	0.040	0.002	0.0073	over

SG to OM	GO:0015986; ATP synthesis coupled proton transport	0.042	0.007	0.0165	over
OM to OV	GO:0006869; lipid transport	0.001	0.004	0.0206	over
OM to OV	GO:0042157; lipoprotein metabolic process	0.001	0.001	0.0129	over
OM to OV	GO:0009968; negative regulation of signal transduction	0.002	0.012	0.0334	over
OM to OV	GO:0006821; chloride transport	0.007	0.002	0.0129	over
OM to OV	GO:0006879; cellular iron ion homeostasis	0.022	0.010	0.0257	over
OM to OV	GO:0007420; brain development	0.034	0.004	0.0129	over
OM to OV	GO:0006118; electron transport	0.038	0.027	0.0463	over
OM to OV	GO:0006826; iron ion transport	0.042	0.010	0.0231	over
OM to AT	GO:0007596; blood coagulation	0.007	0.005	0.0000	under
OM to AT	GO:0006413; translational initiation	0.008	0.008	0.0014	under
OM to AT	GO:0016055; Wnt receptor signaling pathway	0.013	0.004	0.0000	under
OM to AT	GO:0042157; lipoprotein metabolic process	0.013	0.004	0.0000	under
OM to AT	GO:0042221; response to chemical stimulus	0.013	0.004	0.0000	under
OM to AT	GO:0008284; positive regulation of cell proliferation	0.022	0.007	0.0014	under
OM to AT	GO:0006869; lipid transport	0.033	0.008	0.0021	under
OM to AT	GO:0006826; iron ion transport	0.037	0.015	0.0071	under

OM to AT	GO:0008283; cell proliferation	0.014	0.002	0.0085	over
OM to AT	GO:0045039; protein import into mitochondrial inner membrane	0.020	0.000	0.0043	over
OM to AT	GO:0006839; mitochondrial transport	0.036	0.001	0.0050	over
OM to AT	GO:0007219; Notch signaling pathway	0.043	0.000	0.0036	over

Table S4 Gene set enrichment analysis for the major stages in ovarian development. A gene set is shown here if it is altered greater than 20% and the number of members measured in the pathway is greater than 10. Provided in this table are the number of members within a pathway and extended pathway, number of member measured and present on the LMB microarray, normalized enrichment scores, overall change in the pathway (medium fold change) and p-value. No pathway met these criteria for SG to OM transition. The complete list of pathways identified by GSEA is given in appendix 2.

Stage Transition	Name	Expanded # of Entities	# of Measured Entities	Normalized ES	Median change	p-value
PG to SG	MPL -> SPI1 signaling	34	11	1.729	1.226	0.0000
PG to SG	T-cell receptor -> ATF/CREB signaling	189	16	1.775	1.229	0.0000
PG to SG	FibronectinR -> CTNNB signaling	38	10	1.764	1.703	0.0000
PG to SG	AGER -> NF-kB signaling	34	12	1.674	1.226	0.0041
PG to SG	FibronectinR -> NF-kB signaling	58	14	1.734	1.293	0.0044
PG to SG	T-cell receptor -> NF-kB signaling	176	13	1.822	1.416	0.0045
PG to SG	EGFR/ERBB2 -> HIF1A signaling	66	13	1.638	1.229	0.0136
PG to SG	ICAM2 -> CTNNB/FOXO/STAT3 signaling	29	10	1.778	1.561	0.0138
PG to SG	IL7R -> FOXO/NF-kB signaling	36	10	1.693	1.469	0.0142
PG to SG	B-cell receptor -> NF-kB signaling	50	11	1.549	1.261	0.0167
PG to SG	T-cell receptor -> NFATC signaling	172	10	1.638	1.469	0.0184

PG to SG	PTAFR -> NF-kB signaling	63	16	1.599	1.261	0.0213
PG to SG	T-cell receptor -> AP-1 signaling	180	15	1.649	1.261	0.0231
PG to SG	GDNF -> HSF1 signaling	64	16	1.623	1.226	0.0250
PG to SG	Notch -> NF-kB signaling	33	10	1.609	1.261	0.0284
PG to SG	AdenosineR -> NF-kB signaling	49	10	1.501	1.261	0.0327
PG to SG	VEGFR -> CTNNB signaling	27	10	1.489	1.261	0.0498
OM to OV	ICAM2 -> CTNNB/FOXO/STAT3 signaling	29	10	-1.923	-1.530	0.0000
OM to OV	T-cell receptor -> NFATC signaling	172	10	-1.876	-1.530	0.0000
OM to OV	TLR1/2/6 -> NF-kB signaling	39	12	-1.655	-1.390	0.0000
OM to OV	T-cell receptor -> ATF/CREB signaling	189	16	-1.810	-1.402	0.0044
OM to OV	FibronectinR -> CTNNB signaling	38	10	-1.792	-1.496	0.0046
OM to OV	T-cell receptor -> NF-kB signaling	176	13	-1.719	-1.474	0.0047
OM to OV	Sphingolipid metabolism	164	27	-1.631	-1.399	0.0049
OM to OV	T-cell receptor -> CREBBP signaling	176	11	-1.744	-1.541	0.0088
OM to OV	IL7R -> FOXO/NF-kB signaling	36	10	-1.549	-1.474	0.0226
OM to OV	ErythropoietinR -> NF-kB signaling	48	10	-1.551	-1.368	0.0233
OM to OV	NK Cell Activation	523	74	-1.458	-1.236	0.0280

OM to OV	FibronectinR -> NF-kB signaling	58	14	-1.570	-1.357	0.0313
OM to OV	Notch -> NF-kB signaling	33	10	-1.530	-1.298	0.0320
OM to OV	ThrombinR -> NF-kB signaling	32	11	-1.550	-1.474	0.0359
OM to OV	AdrenergicRb -> STAT3 signaling	75	13	-1.514	-1.368	0.0417
OM to AT	Gap Junction Regulation	639	57	-1.946	-2.074	0.0000
OM to AT	Skeletal Myogenesis Control	569	69	-1.825	-1.565	0.0000
OM to AT	Actin Cytoskeleton Regulation	473	86	-1.830	-1.454	0.0000
OM to AT	Guanylate Cyclase Pathway	1219	198	-1.763	-1.327	0.0000
OM to AT	Translation Control	984	213	1.288	1.207	0.0000
OM to AT	Respiratory chain and oxidative phosphorylation	118	42	1.516	1.486	0.0000
OM to AT	ROS metabolism	74	14	1.880	1.680	0.0000
OM to AT	T-cell receptor -> AP-1 signaling	180	15	-1.640	-1.576	0.0036
OM to AT	ICAM2 -> CTNNB/FOXO/STAT3 signaling	29	10	-1.677	-2.930	0.0036
OM to AT	T-cell receptor -> ATF/CREB signaling	189	16	-1.543	-1.409	0.0037
OM to AT	Gonadotrope Cell Activation	698	102	-1.490	-1.324	0.0053
OM to AT	EphrinR -> actin signaling	216	42	-1.604	-1.217	0.0058
OM to AT	Focal Adhesion Regulation	308	45	-1.587	-1.343	0.0059

OM to AT	UrokinaseR -> ELK-SRF signaling	58	13	-1.574	-1.474	0.0068
OM to AT	ERBB2/3 -> EP300/ETS/ETV/SP1 signaling	63	13	-1.616	-1.474	0.0104
OM to AT	T-cell receptor -> NFATC signaling	172	10	-1.635	-1.474	0.0105
OM to AT	VEGFR -> CTNNB signaling	27	10	-1.576	-2.305	0.0109
OM to AT	Adherens Junction Regulation	692	51	-1.559	-1.517	0.0142
OM to AT	EGFR/ERBB2 -> HIF1A signaling	66	13	-1.562	-1.474	0.0179
OM to AT	PTAFR -> NF-kB signaling	63	16	-1.598	-1.474	0.0181
OM to AT	Mannose metabolism	73	18	1.702	1.371	0.0192
OM to AT	SerotoninR1 -> FOS signaling	109	19	-1.543	-1.343	0.0196
OM to AT	FSHR -> FOXO1A signaling	54	14	-1.622	-1.474	0.0211
OM to AT	CholinergicRm -> CREB/ELK-SRF signaling	107	18	-1.599	-1.343	0.0230
OM to AT	T-cell receptor -> CREBBP signaling	176	11	-1.503	-2.164	0.0251
OM to AT	GFR -> NCOR2 signaling	130	18	-1.621	-1.474	0.0264
OM to AT	GRM1/5 -> CREB signaling	110	13	-1.594	-2.074	0.0276
OM to AT	AdrenergicRb -> STAT3 signaling	75	13	-1.494	-1.474	0.0285
OM to AT	T-cell receptor -> NF-kB signaling	176	13	-1.527	-1.531	0.0289
OM to AT	FibronectinR -> CTNNB signaling	38	10	-1.526	-1.890	0.0320

OM to AT	VasopressinR1 -> MEF/MYOD/NFATC/MYOG signaling	119	23	-1.504	-1.447	0.0325
OM to AT	Mast Cell Activation	529	83	-1.418	-1.300	0.0392
OM to AT	GNRHR -> ELK-SRF signaling	77	13	-1.499	-2.056	0.0473
OM to AT	GFR -> AP-1/CREB/CREBBP/ELK- SRF/MYC signaling	156	26	-1.496	-1.454	0.0497
OM to AT	NK Cell Activation	523	74	-1.389	-1.301	0.0500