

Data Supplement 1

Table X - Statistical Analysis Data -Comparing Gilbert et al., and current paper

	Christenson et al. mGC	Gilbert et al. 22h vs -2h	
total number of transcripts in array	24128	25200	
number of expressed transcripts (mGC filter Affy Probes & Probes not present in all 18 samples BHPV<0.01 FC >1.5) (Gilbert: pv<0.05 FC >1.5)	2417	689	
number of transcripts with mapped gene symbols	13981	14403	IPA mapping ; HOMOLOG GENE ID
number of unique gene symbols	10221	11452	IPA mapping ; HOMOLOG GENE ID
number of unique gene symbols in both Gilbert et. al. 0 & 1 and Christenson et. al.	8389		
number of significantly LH-regulated unique genes	1532	443	IPA mapping ; HOMOLOG GENE ID
number of common significantly LH-regulated unique genes (Christenson :BHPV<0.01 FC >1.5 ;Gilbert: pv<0.05 FC >1.5)	1418	328	
number of common genes significant in both studies	121		
significance of this observation (Fisher's exact test p-value)	5.40E-19 very significant		
All common genes:			
Pearson -> 0.012962 (0.23521)	no correlation in gene expression		
Spearman -> 0.29489 (6.1375e-168)	no correlation in rank of gene expression		
Significant common genes:			
Pearson -> 0.47293 (4.3137e-008)	moderate correlation in gene expression		
Spearman -> 0.64131 (2.2947e-015)	significant correlation in rank of gene expression		

Table Y - Comparison of marker gene expression (Fold-changes and significance) between this paper and Gilbert et al., 2011.

Gene Symbol	Christenson et. al.				Gilbert et. al.		
	p-value	Benjamini-Hochberg adjusted p-value	Fold-Change	Significant	p-value	Fold-Change	Significant
ADAMTS1	7.85E-05	1.39E-03	4.587	Yes	2.63E-01	1.358	No
CCND2	1.01E-09	8.69E-07	-27.334	Yes	9.89E-03	-1.833	Yes
CYP11A1	3.29E-02	1.21E-01	-9.991	No	2.55E-01	-1.333	No
CYP19A1	3.07E-06	1.34E-04	-18.554	Yes	5.17E-01	-1.241	No
FSHR	1.30E-03	1.16E-02	-3.909	No	5.75E-01	1.169	No
LHCGR	4.38E-06	1.68E-04	-16.782	Yes	9.98E-02	-1.390	No
NR5A1	2.25E-02	9.27E-02	-1.578	No	8.77E-01	-1.051	No
NR5A2	4.11E-01	6.24E-01	-1.597	No	6.30E-01	1.111	No
PCNA	3.46E-05	7.41E-04	-2.690	Yes	6.30E-02	-1.522	No
PTGS2	4.50E-06	1.70E-04	48.708	Yes	8.73E-01	1.030	No
PTX3	1.35E-12	2.02E-08	711.362	Yes	4.61E-01	1.216	No
STAR	5.60E-04	6.07E-03	2.098	Yes	4.45E-03	-2.594	Yes
TIMP1	8.81E-08	1.36E-05	38.276	Yes	2.24E-02	2.309	Yes
HSD3B1	2.75E-01	4.93E-01	-2.182	No	6.21E-01	-1.157	No

The list of 14 cell marker transcripts present in both studies

Significance criteria for differential expression

Christenson et. al; Absolute fold change ≥ 1.5 and Benjamini-Hochberg adjusted p-value ≤ 0.01 .

Gilbert et. al. : Absolute fold change ≥ 1.5 and p-value ≤ 0.05

Supplementary Table 1: Primers used for cDNA synthesis and qPCR

Gene		Sequence	Accession nos.
<i>GAPDH</i>	rt	CAGTCTTCTGGGTGGCAGTGATG	NM_001034034
	rev	GCAGGAGGCATTGCTGACAATCT	
<i>STAR</i>	for	AGCGAGATCCTGCCAACATCAAG	NM_174189
	rt	GTTGGCCTTCAACACCTAGCTTC	
<i>CYP11A1</i>	rev	CTGCGAGAGGACCTGGTTGATG	NM_176644
	for	TTGTGAGCGTACGCTGTACCAAG	
<i>HSD3B1</i>	rt	AGGGACACTGGTGTGGAACATC	NM_174343
	rev	GGTCTTTCTTCCAGGTTCTGAC	
<i>CYP17A1</i>	for	AGAGAATCCACTTTCCGCCACATC	NM_174304
	rt	TCAGGGCACAAGTGTACAAGGTG	
<i>CYP19A1</i>	rev	GCATTCCTGACGTCAATGACAGAG	NM_174305
	for	TGTTGGTGGAGGAGAAGGATCTG	
<i>FSHR</i>	rt	AGAGAGAGAGGCTCGGACAGATC	NM_174061
	rev	TTCAGGTTGCCATCCTTGAACAG	
<i>LHCGR</i>	for	TGATGATTGGACACCACCAGTTG	NM_174381
	rt	GAGCATGTTAGAGGTGTCCAGCA	
<i>PCNA</i>	rev	ATGCCGATGAACTGCAACCCAAGTT	NM_001034494
	for	GGATCGGCAGTGCCTGCAATTAATA	
<i>PTGS2</i>	rt	GGGAAGGTTCTGGAAGGCATCAGG	NM_174445
	rev	TCTGGAAGGCATCAGGGTCGATGTA	
<i>NR5A1</i>	for	TCACCAAGCTTCGAGTCATCCCAA	NM_174403
	rt	GGAAGGCGTCGTTGTGCATCTTCT	
<i>NR5A2</i>	rev	GGGAAATCAGCGTTGTCCCATTGA	XM_615597
	for	GCATCCACAAGCTTCCAGATGTTACGA	
<i>CCND2</i>	rt	GAAACCTTTTCTGATTTGGAGCTT	NM_001076372
	rev	CGTGTCCGCGTTATCTTCAGCTCTT	
<i>PTX3</i>	for	GTGAACCTGCAGAGCATGGACTCGT	NM_001076259
	rt	ATGTCTCCATAGAGCGCTTCTAAC	
<i>TIMP1</i>	rev	CTGGTCAATTGAAGCCTTTGATAC	NM_174471
	for	TACAGCACTTGAGTGGCTATCAC	
<i>ADAMTS1</i>	rt	TCACCAGGCTGTGGTTGTTTCAGGA	NM_001101080
	rev	GTCAGCTCCACCTCCTGCCCTGT	
<i>ADAMTS1</i>	for	ACGCAGGTGCATGGTCTTCAAGGA	NM_001101080
	rt	CCCTCCACCAGCTGGAAGTTCTCC	
<i>ADAMTS1</i>	rev	GATGGAGCCCTCCTTTCCGTGAAC	NM_001101080
	for	ATGTGCAAGATGGCAGACCAGACG	
<i>ADAMTS1</i>	rt	CGCCAGGAACATGCACACGGCCCCC	NM_001101080
	rev	CACGGCCCCCAGCAGCTGCAGATGG	
<i>ADAMTS1</i>	for	CGCAGGGCCGTGCCGGACGCCAAC	NM_001101080
	rt	random p(dN) ₆ + oligo-dT p(dT) ₁₅	
<i>ADAMTS1</i>	rev	TGCAGGCTTCCCTCCAGCCGGCCCA	NM_001101080
	for	CCCACTGAGGACCCACGCCGTGCGAC	
<i>ADAMTS1</i>	rt	random p(dN) ₆ + oligo-dT p(dT) ₁₅	NM_001101080
	rev	AGGCTCGGCTGGGGGCTGTGAGCCA	
<i>ADAMTS1</i>	for	CGCAGCTCAGGCCCTGCCGCCATCG	NM_001101080
	rt	random p(dN) ₆ + oligo-dT p(dT) ₁₅	
<i>ADAMTS1</i>	rev	CCGGCCGCCACGGAGAACAAGGTCAG	NM_001101080
	for	CACTGTGCAGTGGGCGCCGCGGGA	

for, forward primer; rev, reverse primer; rt, primer used for cDNA synthesis

Supplementary Table 2. Morphological and physiological data of analyzed follicles.

	n ^a	Diameter ^b [mm]	P4 ^c [ng/ml]	E2 ^d [ng/ml]	E2/P4 ^e
before LH	3	13.8 (1.2)	21.1 (5.1)	89.3 (6.7)	4.9 (1.5)
after LH	3	20.5 (0.9)	212.7 (113.7)	81.2 (1.0)	0.6 (0.2)
p (t-test)		0.010	0.168	0.292	0.049

^a numbers of follicles; ^b mean diameters of follicles; ^c mean antral progesterone (P4) and ^d estrogen (E2) concentrations, and ^e mean E2/P4 ratios; standard errors of means are shown in brackets; LH, luteinizing hormone surge; p values were calculated according to t-test analysis.