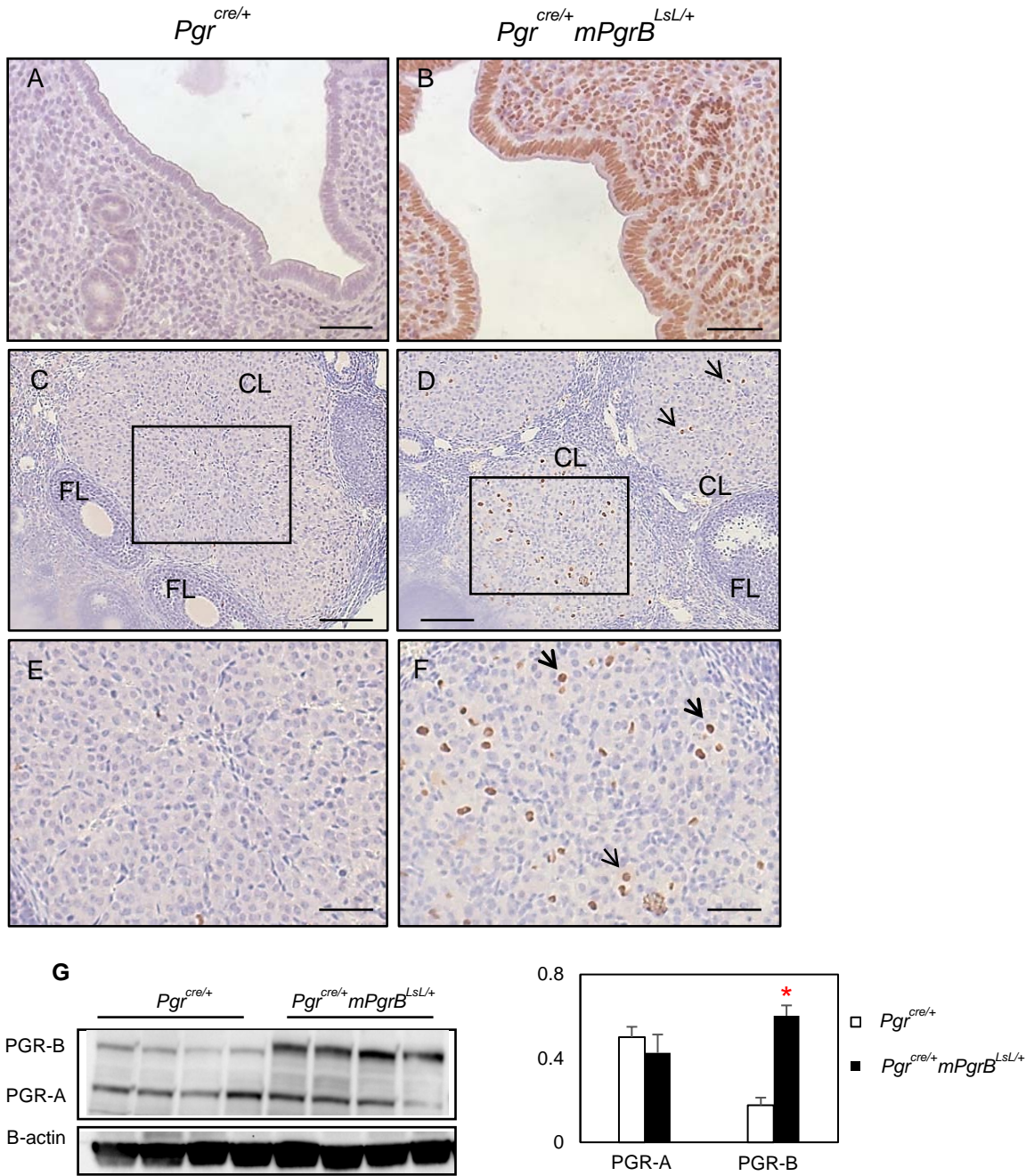
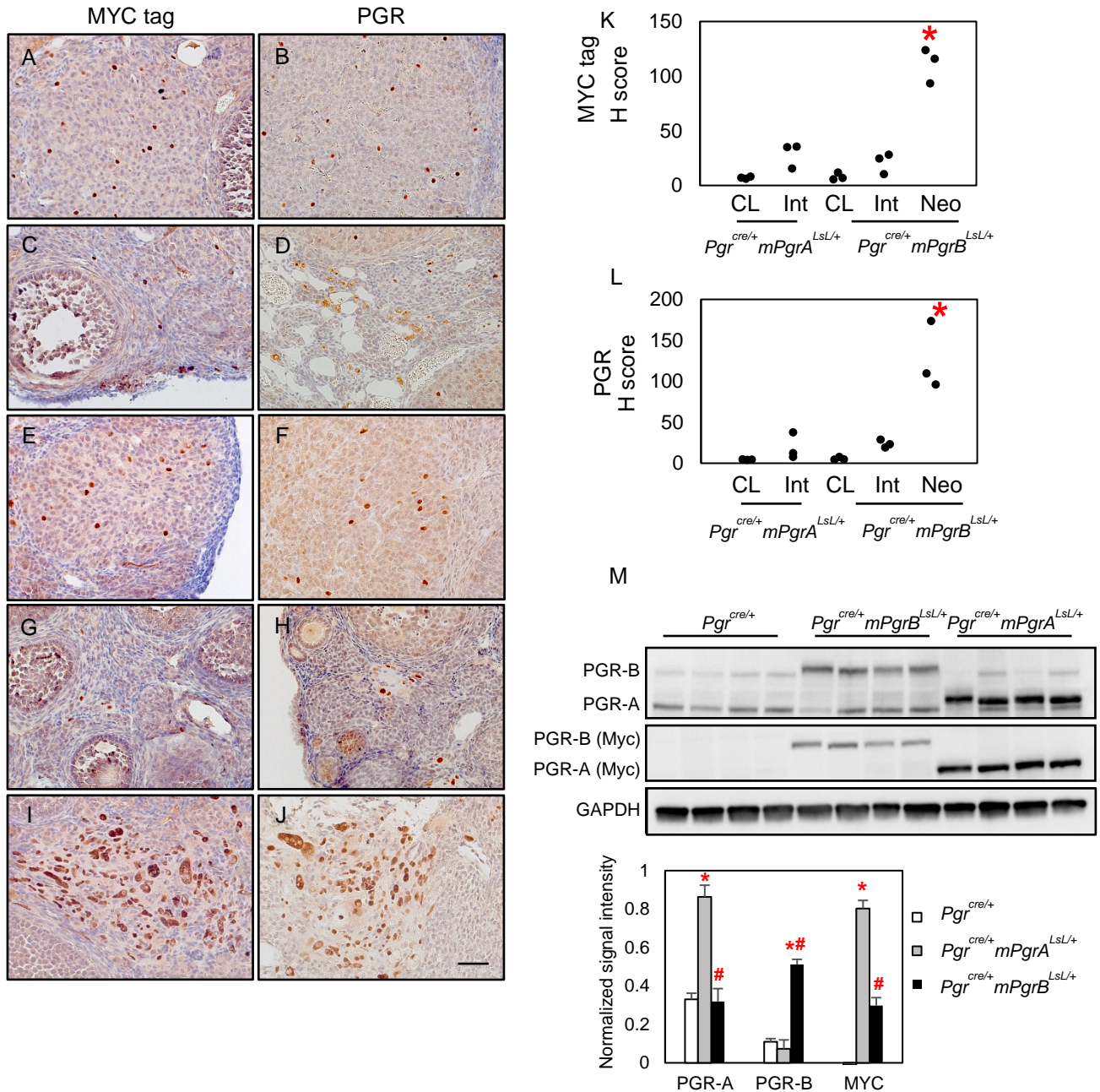


1252
 1253
 1254
 1255
 1256
 1257
 1258
 1259
 1260
 1261
 1262
 1263
 1264
 1265
 1266
 1267
 1268
 1269
 1270
 1271
 1272
 1273
 1274
 1275
 1276
 1277
 1278
 1279
 1280
 1281
 1282
 1283
 1284
 1285
 1286
 1287
 1288
 1289
 1290
 1291
 1292
 1293
 1294
 1295
 1296
 1297
 1298
 1299
 1300
 1301
 1302



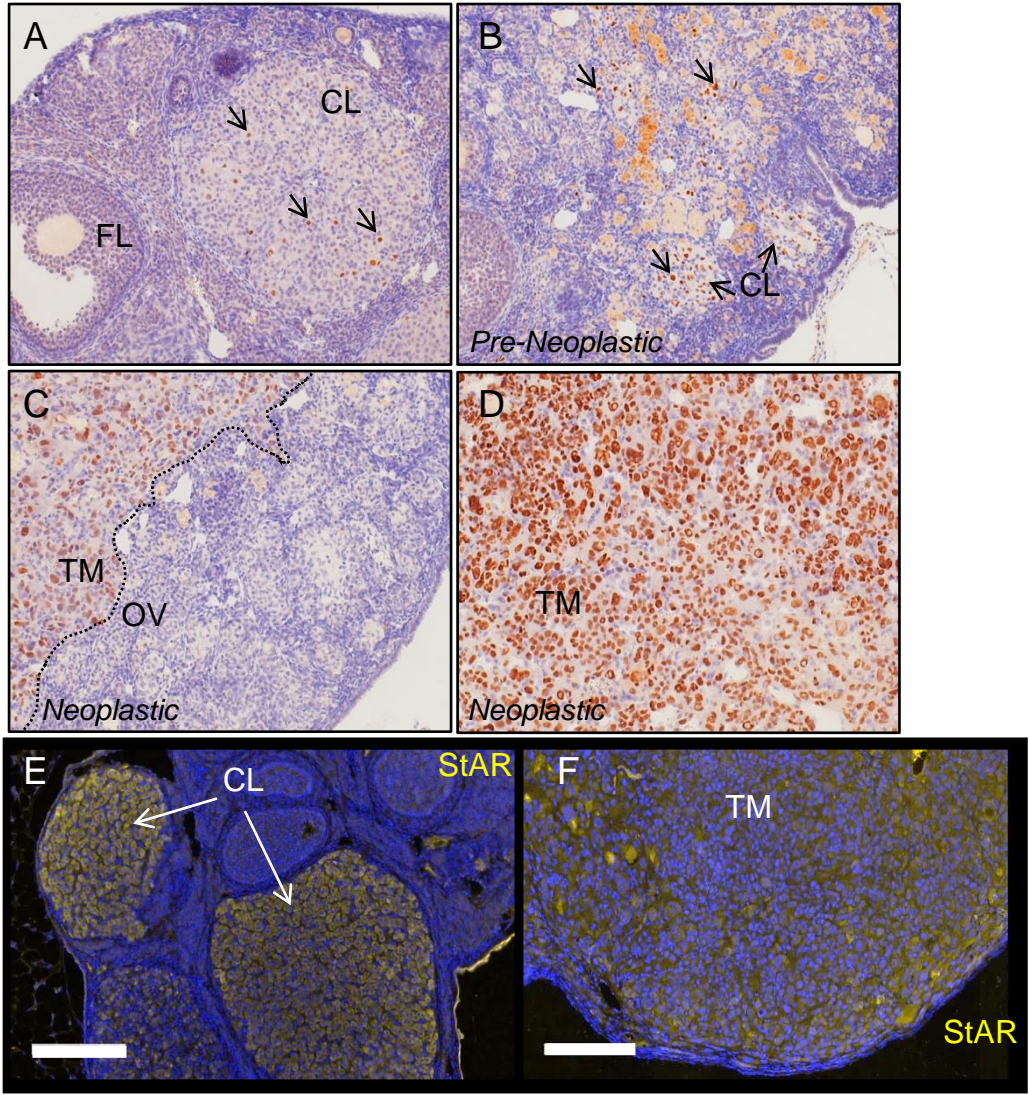
Supplemental Figure 1: Levels of the conditional overexpression allele for *mPgrB* in uterine and ovarian tissue. (A-D) Myc-tag immunohistochemistry of 8-week-old wildtype uterus (A) and ovary (C) compared to $Pgr^{cre/+} mPgrB^{LsL/+}$ mouse uterus (B) and ovary (D). (E-F) High magnification images of corpora lutea from insets in (C-D) in wildtype ovary (E) and $Pgr^{cre/+} mPgrB^{LsL/+}$ ovary (F). (G) Western blot and the associated quantification of PGR levels from whole uterine isolates in wildtype $Pgr^{cre/+}$ and $Pgr^{cre/+} mPgrB^{LsL/+}$ mice. PGRB protein (118 kDa), PGRA protein (90 kDa). C-D 100 μ M scale bar, A-B, E-F 50 μ M scale bar. n=2-4 mice for immunohistochemistry. Each band of the western blot indicates one mouse. Student's t-test used to compare groups. * $p < 0.05$ compared to $Pgr^{cre/+}$. Scale bar means SEM.

1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353



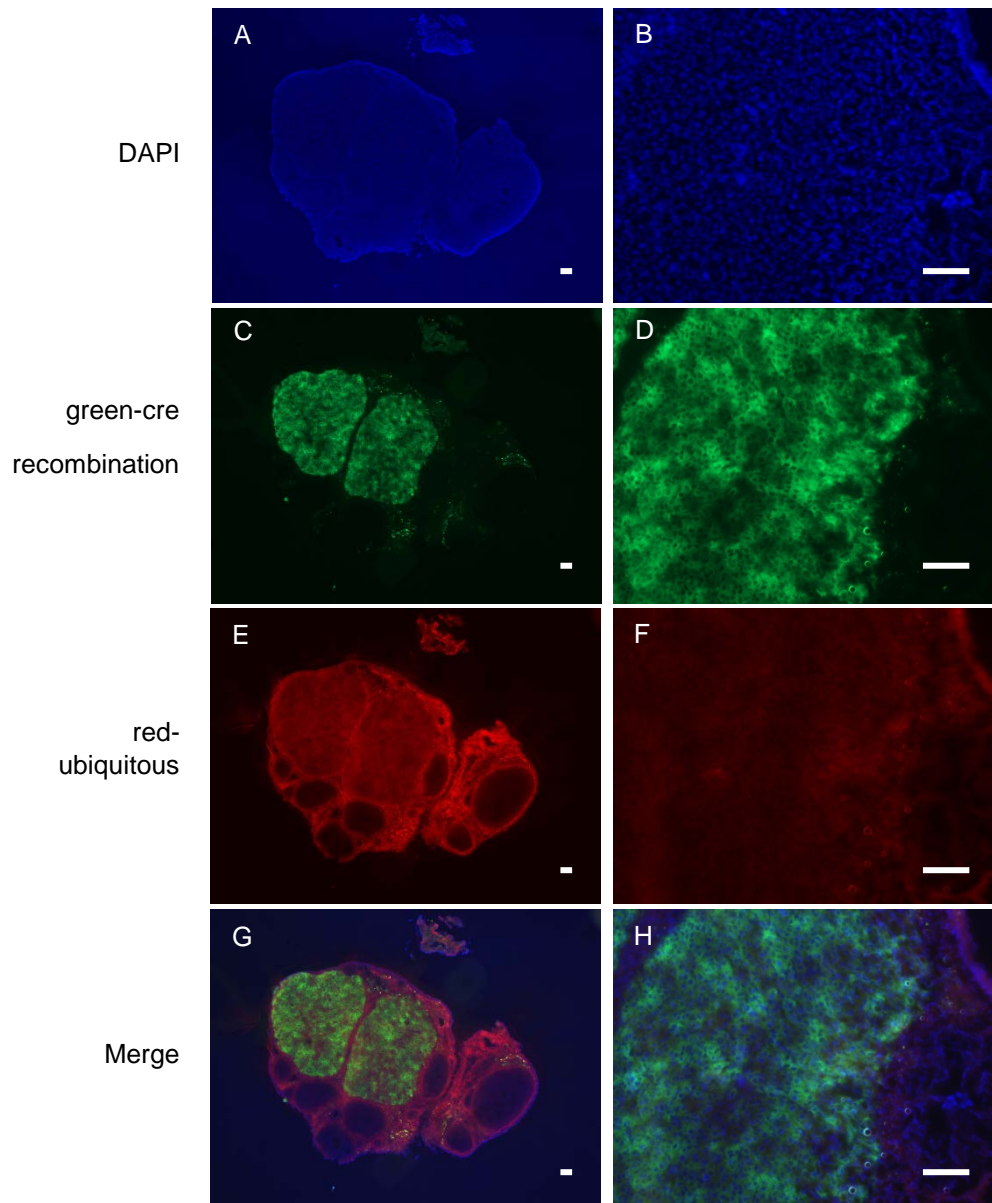
Supplemental Figure 2: PGR transgene levels are comparable in both *Pgr^{cre/+}mPgrA^{LsL/+}* and *Pgr^{cre/+}mPgrB^{LsL/+}* mice at 13 weeks of age. Immunohistochemistry showed MYC tag staining (A, C, E, G, I) and PGR (B, D, F, H, J) in the CL (A, B) and Int (C, D) of *Pgr^{cre/+}mPgrA^{LsL/+}* ovary (A-D), the CL (E, F) and Int (G, H), and Neoplastic tumor (I, J) of *Pgr^{cre/+}mPgrB^{LsL/+}* ovary (E-J). n=3 mice. *p<0.05. CL: Corpus luteum; Int: Interstitial tissues; Neo: 23 week neoplastic stage tumor. H score indices for MYC tag (K) and PGR (L) immunohistochemistry. Western blot of PGR and MYC tag and the associated quantification in whole uterine isolates (M). One-way ANOVA with post hoc Tukey's test was used to compare groups. *p<0.05 compared with *Pgr^{cre/+}* mice. #p<0.05 compared with *Pgr^{cre/+}mPgrA^{LsL/+}* mice. 50 μ M scale bar. n=3 mice for immunohistochemistry. n=4 mice for western blot. Scale bar means SEM.

1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404



Supplemental Figure 3: PGR positive ovarian neoplasia from *Pgr^{cre/+}mPgrB^{LsL/+}* mice consume the entire ovarian bursa and exhibit robust StAR expression levels. Immunohistochemical images of PGR positive cells within corpora lutea (indicated by arrows) from normal *Pgr^{cre/+}mPgrB^{LsL/+}* mouse ovaries at 10 weeks (A) and from pre-neoplastic ovaries (B). (C-D) PGR immunohistochemistry of PGR positive outgrowth of cells occurring in neoplastic ovaries from *Pgr^{cre/+}mPgrB^{LsL/+}* mice. Immunofluorescent staining for steroidogenic acute regulatory protein (StAR) in a wildtype ovary (E) and neoplastic ovarian tumor (F) of *Pgr^{cre/+}mPgrB^{LsL/+}* mice. Blue staining is DAPI, yellow staining represents positive StAR staining. 100 μ M scale bar for A-D. 200 μ M scale bar for E-F. FL=follicle, CL=corpora lutea, OV=ovary, TM=tumor tissue. n=4 mice for A-B images. C-D are representative of individual mouse tumor burden over time. n=3 mice for E-F images.

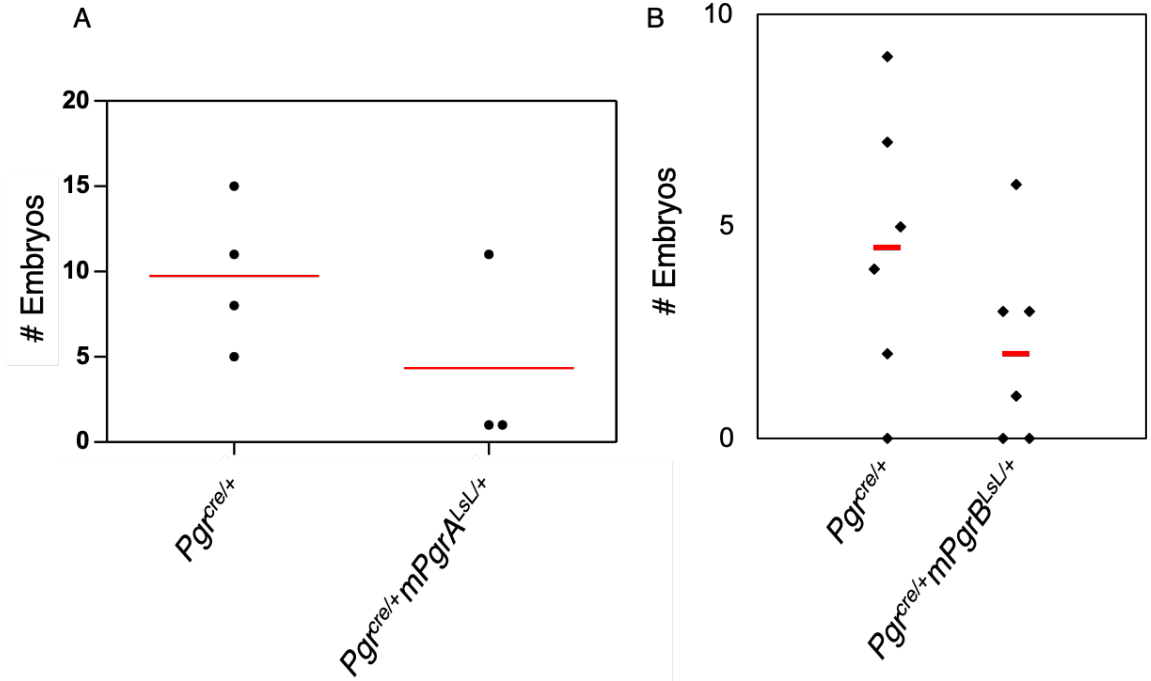
Pgr^{cre/+} Rosa^{mT/mG}



Supplemental Figure 4: Lineage tracing using the *Pgr^{cre/+} Rosa^{mT/mG}* model demonstrates localized Cre recombination to the corpus luteum at 8 weeks of age. DAPI (A, B), positive Cre recombinase activity in green from the *Rosa^{mT/mG}* construct (C, D), ubiquitous red fluorescence from *Rosa^{mT/mG}* model (E, F), and red-green overlay (G, H). *Pgr^{cre/+} Rosa^{mT/mG}* mouse ovary (A, C, E, G) and ovarian corpus luteum (B, D, F, H). 100 μ M scale bar. n=3 mice.

1456

1457



1458

1459

1460

1461

1462

1463

1464

1465

1466

1467

1468

1469

1470

1471

1472

1473

1474

1475

1476

1477

1478

1479

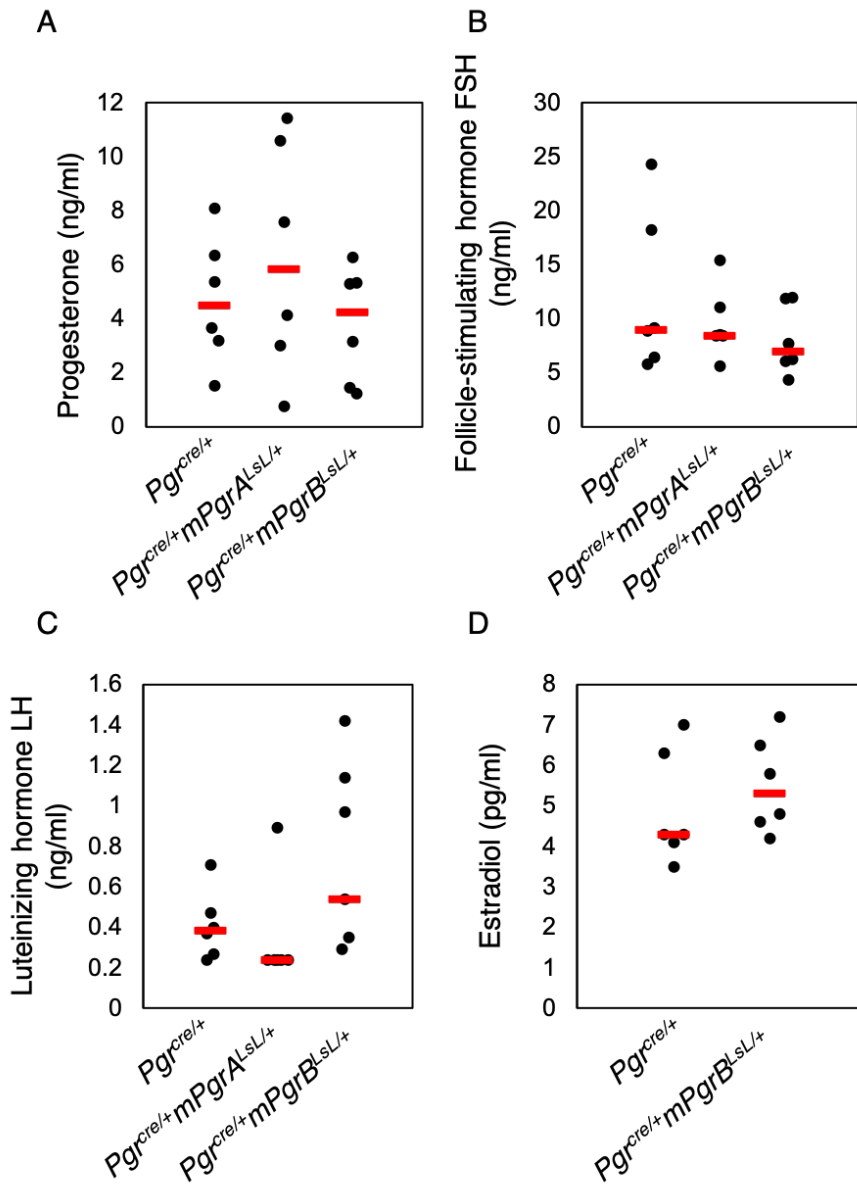
1480

1481

1482

1483

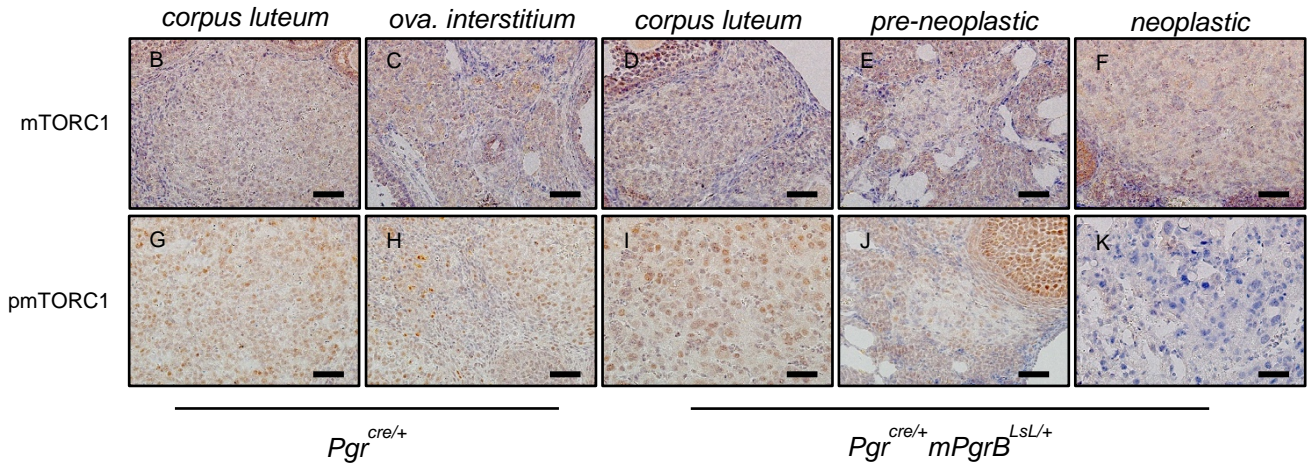
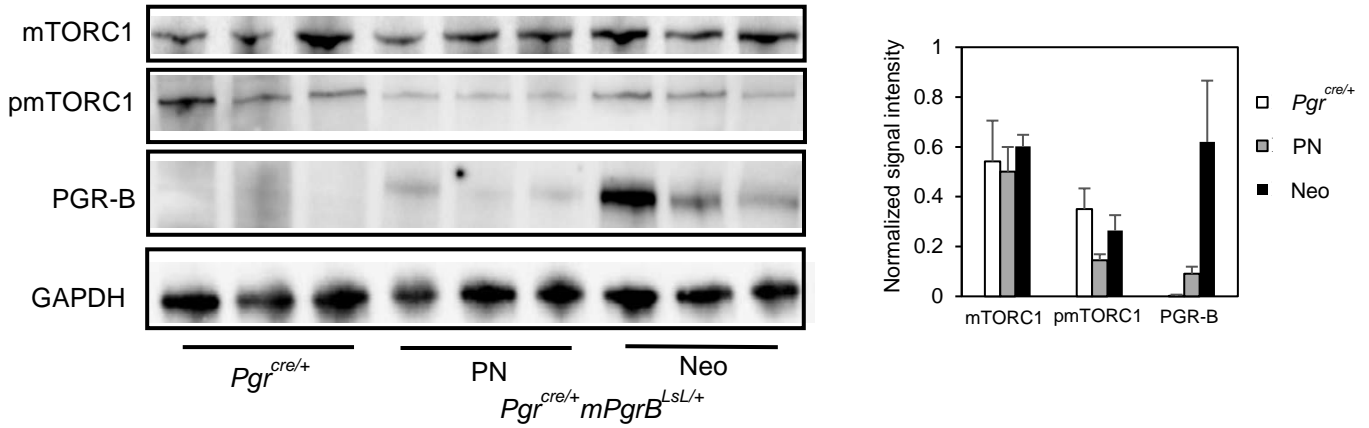
1484
 1485
 1486
 1487
 1488
 1489
 1490
 1491
 1492
 1493
 1494
 1495
 1496
 1497
 1498
 1499
 1500
 1501
 1502
 1503
 1504
 1505
 1506
 1507
 1508
 1509
 1510
 1511
 1512
 1513
 1514
 1515
 1516
 1517
 1518
 1519
 1520
 1521
 1522
 1523
 1524
 1525
 1526
 1527
 1528
 1529
 1530
 1531



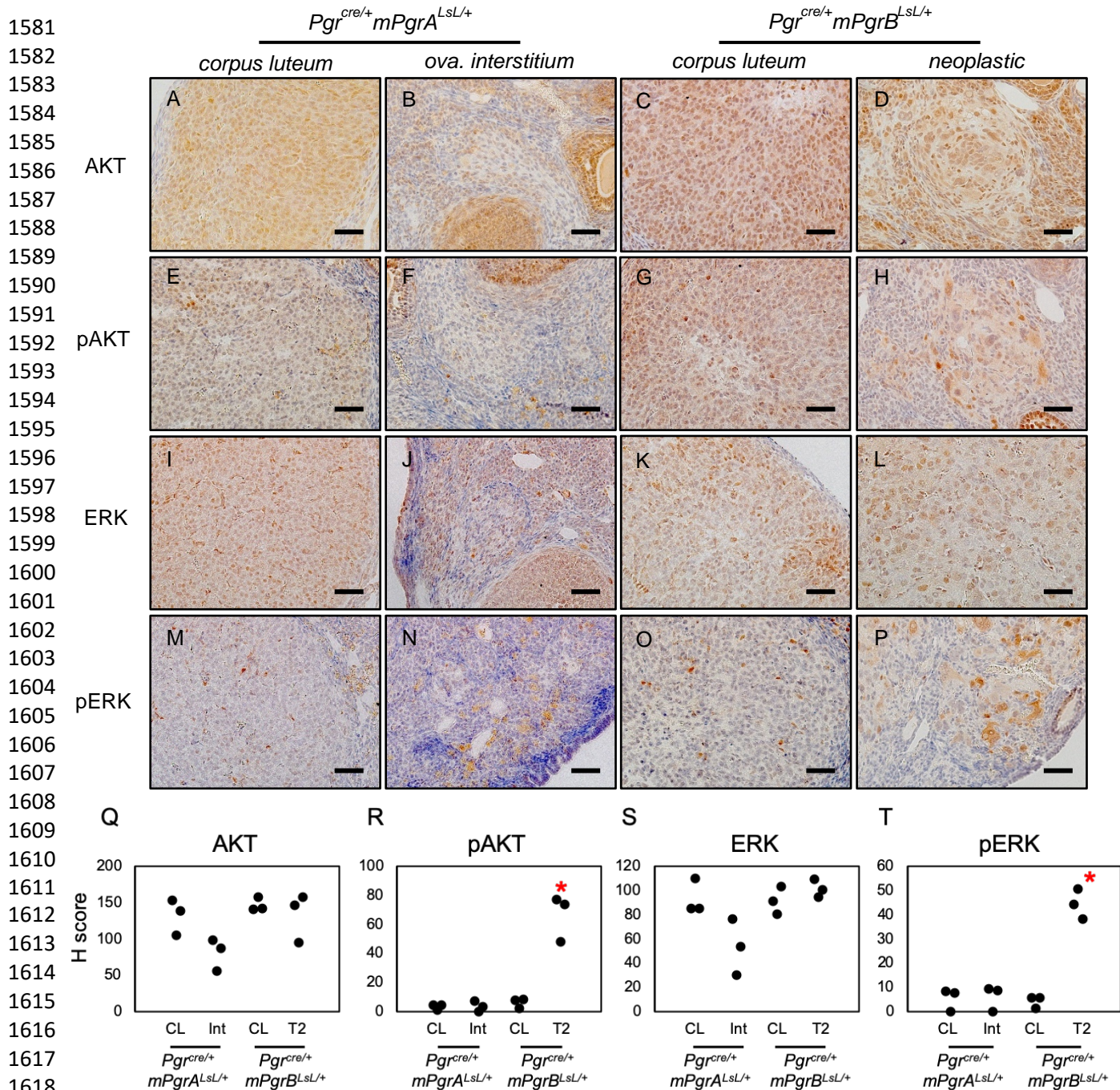
Supplemental Figure 6: Increased ovarian PGR expression does not impair endogenous hormone levels. Serum levels of progesterone (A), follicle-stimulating hormone (FSH) (B), and luteinizing hormone (LH) (C) from 23 week-old *Pgr^{cre/+} mPgrA^{LsL/+}* mice and *Pgr^{cre/+} mPgrB^{LsL/+}* mice at diestrous stage. (D) Serum estradiol levels for *Pgr^{cre/+}* and *Pgr^{cre/+} mPgrB^{LsL/+}* mice. Each dot indicates the serum level from one mouse. The red line indicates median level. n=6 mice. One-way ANOVA with post-hoc Tukey's test was used for progesterone, FSH, and LH analyses. Student's t-test was utilized to compare estradiol levels.

1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580

A

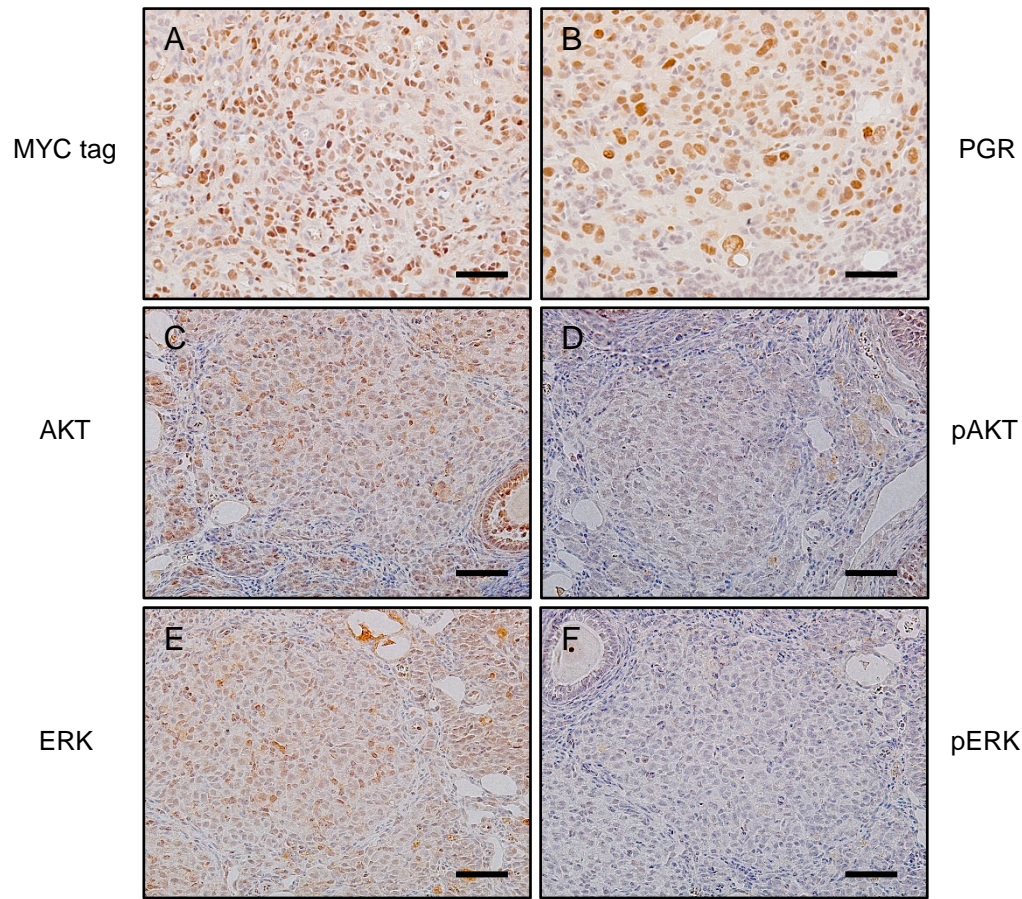


Supplemental Figure 7: Phosphorylated mTORC1 protein levels are slightly reduced in neoplasia of the *Pgr^{cre/+} mPgrB^{LsL/+}* ovary. Western blot of mTORC1, pmTORC1, PGRB and GAPDH in the *Pgr^{cre/+}*, and *Pgr^{cre/+} mPgrB^{LsL/+}* ovaries at different stages with the associated quantification (A). Immunohistochemistry of mTORC1 (B-F) and pmTORC1 (G-K) staining in the corpus luteum (B, G) and ovarian interstitium (C, H) of the *Pgr^{cre/+}* ovary (B, C, G, H), the corpus luteum (D, I), pre-neoplastic (E, J), and neoplastic tumor (F, K) of *Pgr^{cre/+} mPgrB^{LsL/+}* ovary (D-F, I-K). 50 μm scale bar. n=3 mice. Scale bar means SEM. One-way ANOVA with post-hoc Tukey's test used to determine significance.



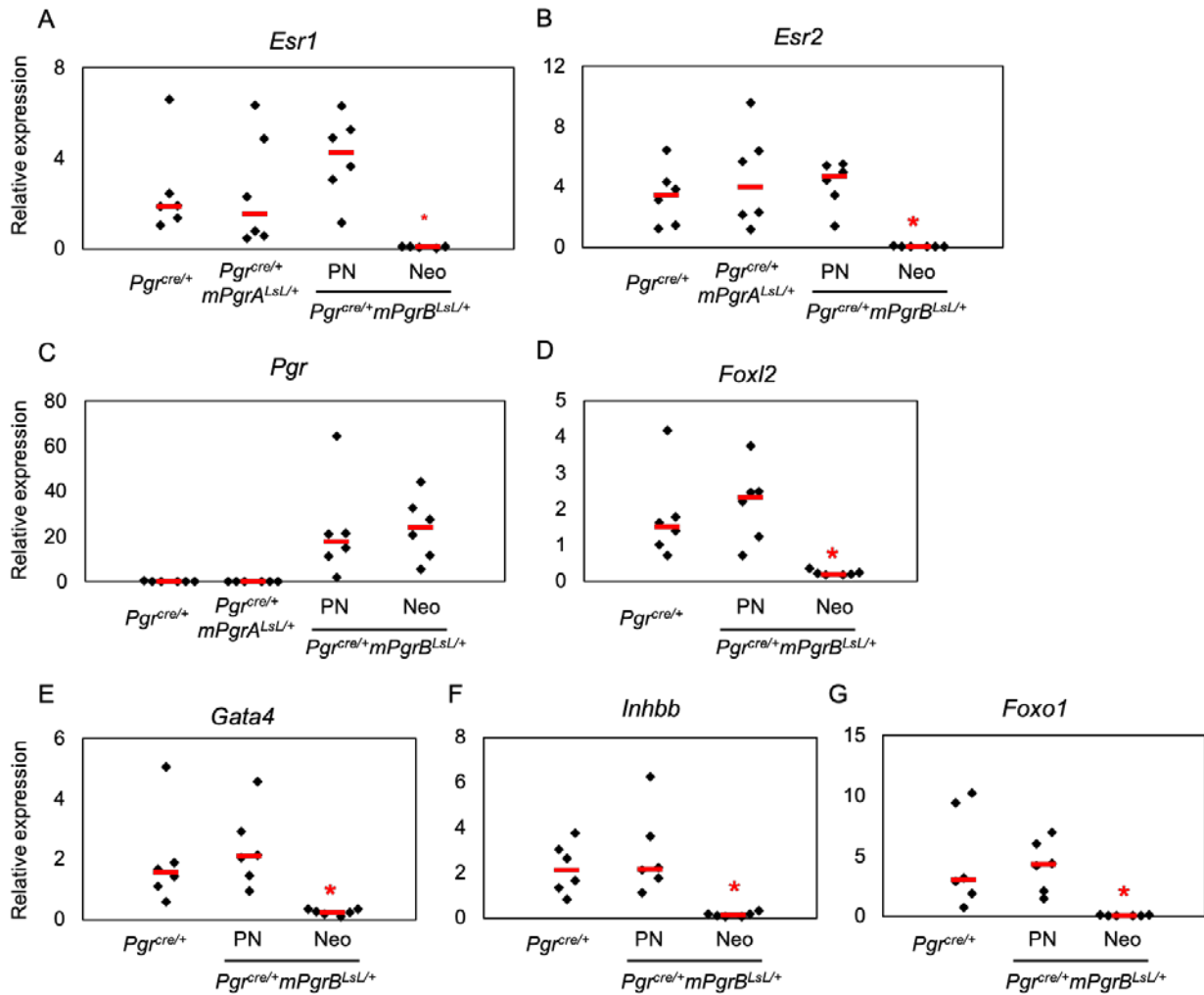
1620 Supplemental Figure 8: pAKT and pERK expression in the $Pgr^{cre/+} mPgrA^{LsL/+}$ ovaries were comparable
 1621 to the corpus luteum of $Pgr^{cre/+} mPgrB^{LsL/+}$ ovary, but much lower than the tumor tissues of
 1622 $Pgr^{cre/+} mPgrB^{LsL/+}$ ovary at 23 weeks neoplastic. Immunohistochemistry showed AKT (A-D), pAKT (E-
 1623 H), ERK (I-L) and pERK (M-P) in the CL (A, E, I, M) and Int (B, F, J, N) of $Pgr^{cre/+} mPgrA^{LsL/+}$ ovary
 1624 compared to CL (C, G, K O) and neoplastic ovary (D, H L P) of $Pgr^{cre/+} mPgrB^{LsL/+}$ mice. H score of AKT
 1625 (Q), pAKT (R), ERK (S) and pERK (T). n=3 mice. CL: Corpus luteum; Int: Interstitial tissues; T2:
 1626 neoplastic (23wks). One-way ANOVA with post-hoc Tukey's test for significance. *p<0.05 compared to
 1627 CL. 50 μ M scale bar.
 1628

1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676



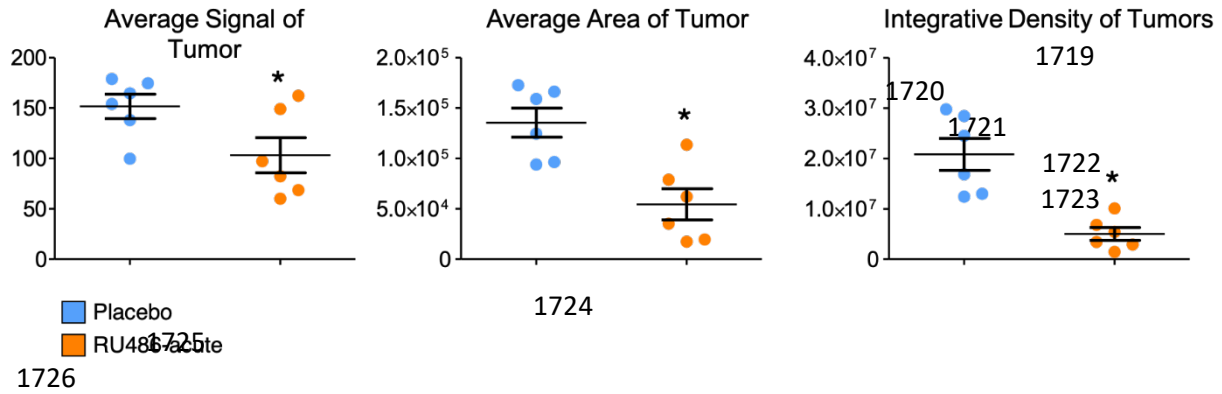
Supplemental Figure 9: pAKT and pERK were not activated in the *Pgr^{cre/+}mPgrA^{LSL/+}* ovaries with neoplasia. Immunohistochemistry of MYC tagged PGRA (A), PGR (B), AKT (C), pAKT (D), ERK (E) and pERK (F) in the *Pgr^{cre/+}mPgrA^{LSL/+}* ovary. n=1 mouse. 50 μ M scale bar.

1677
 1678
 1679
 1680
 1681
 1682
 1683
 1684
 1685
 1686
 1687
 1688
 1689
 1690
 1691
 1692
 1693
 1694
 1695
 1696
 1697
 1698
 1699
 1700
 1701
 1702
 1703
 1704
 1705
 1706
 1707
 1708
 1709
 1710
 1711
 1712
 1713
 1714
 1715
 1716
 1717



Supplemental Figure 10: Message levels of estrogen and progesterone receptors and granulosa cell markers decrease in advanced PGR-driven neoplasia. Relative message levels for (A) *Esr1*, (B) *Esr2*, (C) *Pgr*, and granulosa cell markers (D) *Foxl2*, (E) *Gata4*, (F) *Inhbb*, and (G) *Foxo1* in $Pgr^{cre/+}$ control ovarian tissue compared to $Pgr^{cre/+}mPgrA^{LsL/+}$ ovaries and $Pgr^{cre/+}mPgrB^{LsL/+}$ pre-neoplastic (PN) and neoplastic (Neo) ovarian tissue. One-way ANOVA with post-hoc Tukey's test used to compare groups. * $p < 0.05$ compared to $Pgr^{cre/+}$. n=6 mice.

1718



1727

1728 Supplemental Figure 11: *Pgr^{cre/+}mPgrB^{LsL/+}* tumors exhibit decreased density and size after acute RU486
1729 treatment. (A-C) ImageJ analysis on tumor frames exhibiting the greatest tumor diameter taken from the
1730 final week of treatment. (A) Reports average signal output or lightened areas in tumor images in RU486
1731 vs placebo groups. (B) Depicts average areas of tumor as a function of the measurement tool used in the
1732 ImageJ software platform of RU486 versus placebo treated tumors. (C) Average integrative density (cell
1733 signal multiplied by cell area) for the ultrasound frames from RU486 versus placebo treated
1734 *Pgr^{cre/+}mPgrB^{LsL/+}* ovarian tumors. Student's t-test utilized to determine significance. *p<0.05. Error bars
1735 represent ±SEM. n=6 mice.

1736

1737

1738

1739

1740

1741

1742

1743

1744

1745

1746

1747

1748

1749

1750

1751

1752

1753

1754

1755

1756

1757

1758

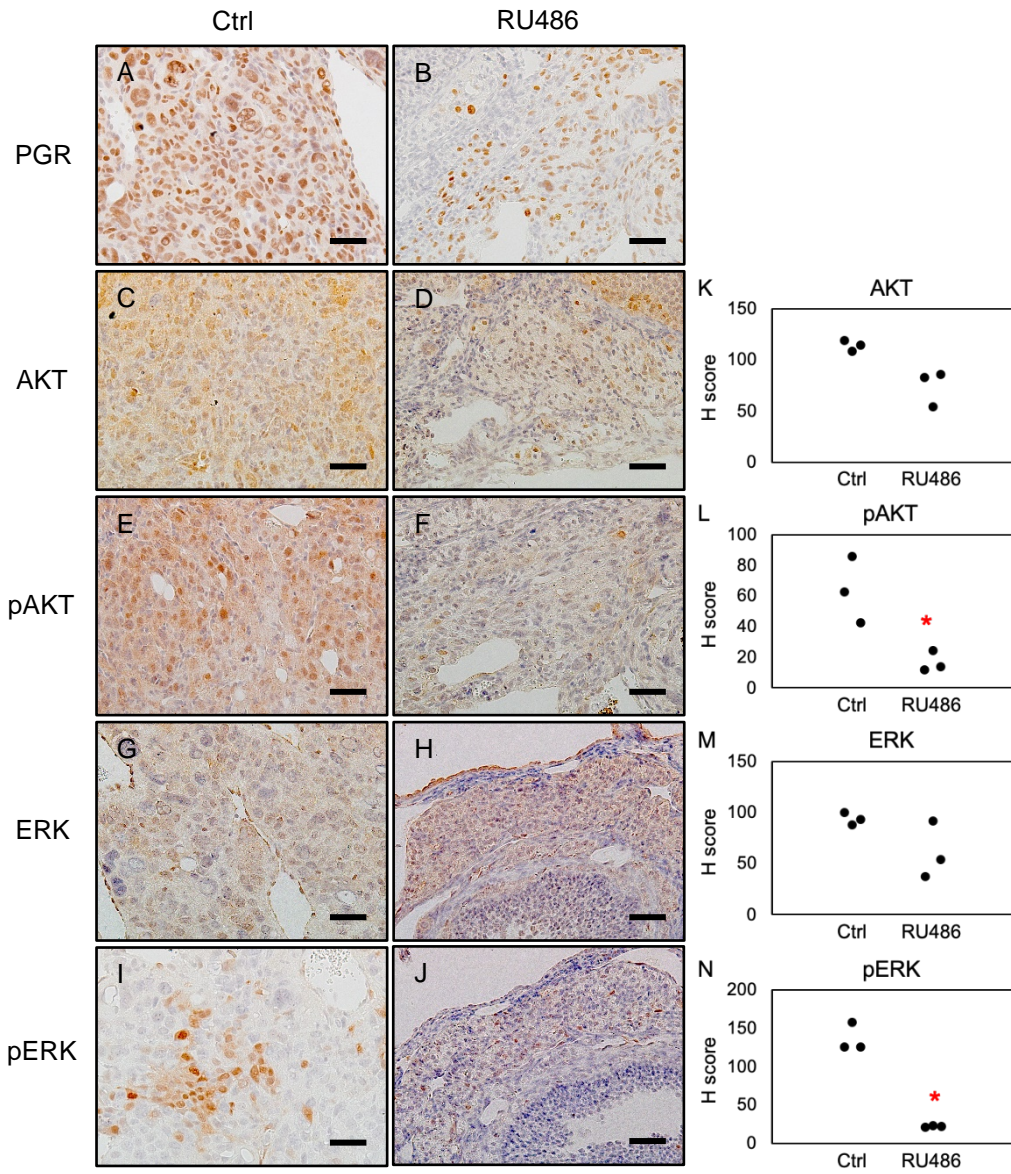
1759

1760

1761

1762

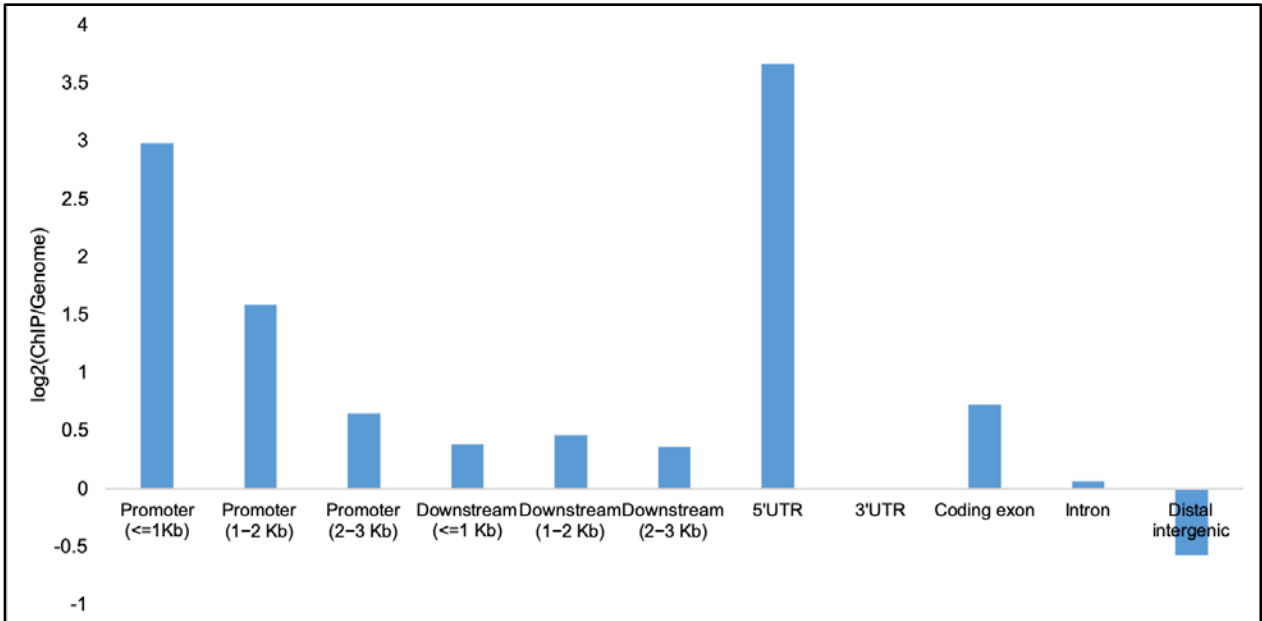
1763
 1764
 1765
 1766
 1767
 1768
 1769
 1770
 1771
 1772
 1773
 1774
 1775
 1776
 1777
 1778
 1779
 1780
 1781
 1782
 1783
 1784
 1785
 1786
 1787
 1788
 1789
 1790
 1791
 1792
 1793
 1794
 1795
 1796
 1797
 1798
 1799
 1800
 1801
 1802
 1803
 1804
 1805
 1806
 1807
 1808
 1809
 1810



Supplemental Figure 12: Chronic RU486 treatment suppresses pAKT and pERK levels in the *Pgr^{cre/+}mPgrB^{LsL/+}* ovarian tumor tissue. Immunohistochemistry of PGR (A, B), AKT (C, D), pAKT (E, F), ERK (G, H), and pERK (I, J) in the control (Ctrl) (A, C, E, G, I) and RU486 treated (B, D, F, H, J) *Pgr^{cre/+}mPgrB^{LsL/+}* ovaries. H score of AKT (K), pAKT (L), ERK (M), and pERK (N). Ctrl: age comparable *Pgr^{cre/+}mPgrB^{LsL/+}* ovaries without treatment. RU486: RU486 pellet treated. n=3 mice. Student's t-test used to compare groups. *p<0.05. 50 μm scale bar.

1811

A



1812

B

			1813
1		Nuclear Receptor	1814
2		ATF/JUN	1816
3		GATA	1818
4		CEBP	1820
5		HNF1	1822
6		ETS	1824
7		STAT	1826
8		RUNX	1828
9		SP1/KLF	1830

1832

1833

1834

1835

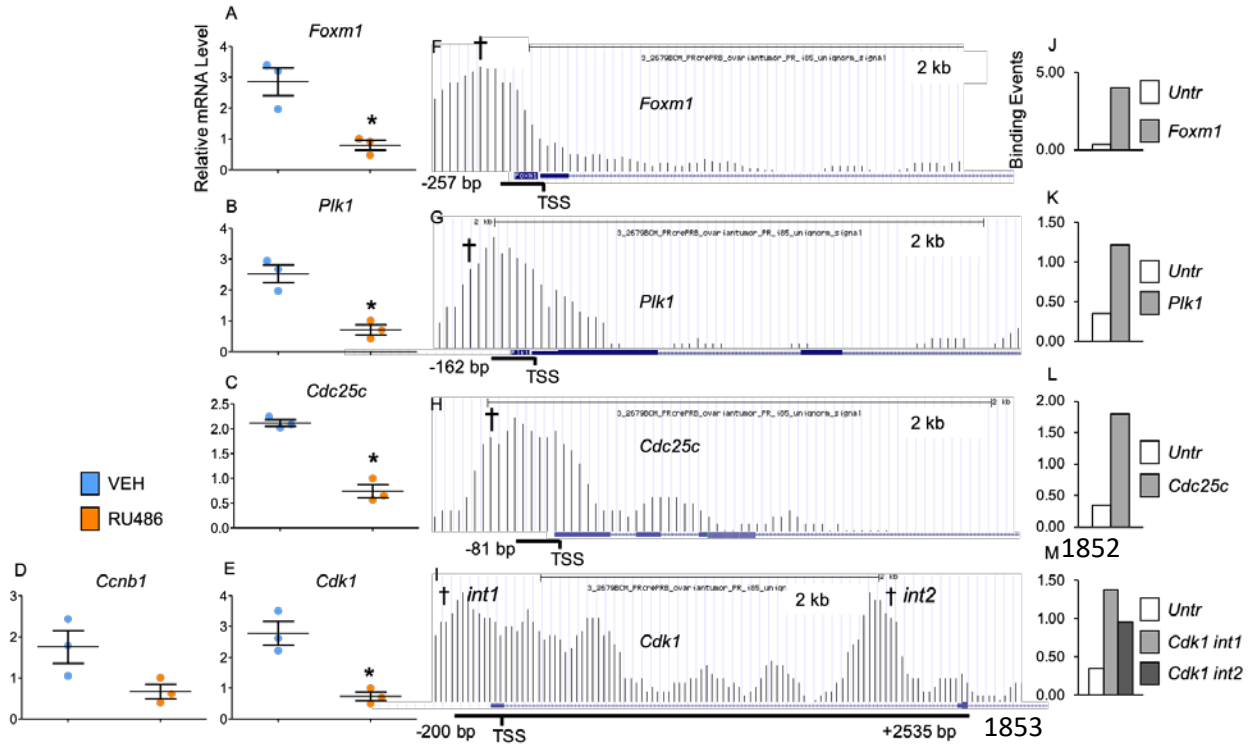
1836

1837

1838

Supplemental Figure 13: PGR ChIP-seq is enriched at promoter regions and binds to hormone receptor binding sequences. (A) Enrichment distribution of PGR binding on the genome compared to normal expected enrichment. Data is equivalent to the natural log of PGR chip binding/basal genome binding. (B) Top binding of known motifs by PGR in the ovarian tumor ChIP-Seq.

1839
 1840
 1841
 1842
 1843
 1844
 1845
 1846
 1847
 1848
 1849
 1850
 1851



1854
 1855
 1856
 1857
 1858
 1859
 1860
 1861
 1862
 1863
 1864
 1865
 1866
 1867
 1868
 1869
 1870
 1871
 1872
 1873
 1874
 1875
 1876
 1877
 1878

Supplemental Figure 14: PGRB promotes the cell cycle through direct regulation of genes necessary for the G2/M transition. Relative message levels for (A) *Foxm1*, (B) *Plk1*, (C) *Cdc25c*, (D) *Ccnb1*, and (E) *Cdk1*. (F-I) Graphical description of the PGR binding events for (F) *Foxm1*, (G) *Plk1*, (H) *Cdc25c*, and (I) *Cdk1* with validated binding intervals indicated by † and distances reported from transcription start site (TSS). (J-M) ChIP-qPCR validation results of binding events indicated with † described in (F-I) for *Foxm1* (J), *Plk1* (K), *Cdc25c* (L), and *Cdk1* (M). Y-axis represents the number of binding events detected per 1000 cells in the untranslated region versus interval of interest. Error bars indicate the standard deviation of averaged binding occurrences. Student's t-test was used to determine significance. *denotes significance with a p-value ≤ 0.05.

1879
1880
1881
1882
1883
1884
1885
1886
1887
1888

Age	Unilateral	Bilateral
23 weeks	2	0
28 weeks	4	2
33 weeks	7	1

Supplemental Table 1: Bilateral and unilateral tumors occur in *Pgr^{cre/+}mPgrB^{LsL/+}* mice. n=16 mice.

1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924

1925

Ingenuity Canonical Pathways	-log(p-value)	z-score	Molecules
Acute Phase Response Signaling	3.3	2.694	MAP2K6,IL6ST, FN1,APOH,PIK3R1,HRAS,SERPINA3,CP,FGG,MBL2,JUN,NFKBIA,ITIH4,RBP2,MRAS,AKT3, FGB,OSMR,LBP,TNFRSF1B,IL1RAP,C3,RRAS,IL6R,SERPINF1,MAPK8,C5,FOS,IL18,HP,APOA1,RRAS2,TF,PTPN11,CRP,PIK3CB,FGA,A2M
IL-8 Signaling	6.12	1.697	PRKD1,RND2,RRAS,FGFR1,RAC1,HBEGF,FGFR2,MMP2,MYL9,BCL2L1,ARRB2,CCND2,RHOQ,PTPN11,IRS1,PIK3R6,MAPK10,ANGPT2,PTK2B,PDGFC,EIF4EBP1,BCL2,JUN,KL,AKT3,FLT1,RHOC,MAPK8,IRAK3,CSTB,PLD4,ITGB2,FOS,RRAS2,PIK3CB,KDR,IRAK4,PRKCB
PI3K/AKT Signaling	1.28	2.236	TSC1,GAB2,JAK1,YWHAH,RRAS,PPP2R2A,PIK3R1,HRAS,MDM2,CCND1,EIF4EBP1,BCL2,BCL2L1,RRAS2,NFKBIA,FOXO1,PPM1L,MRAS,AKT3,PIK3CB,GSK3B,ITGA4,THEM4
CXCR4 Signaling	5.35	1.441	PIK3R1,HRAS,GNA14,BCAR1,FGFR3,GNB1,ROCK2,JUN,RHOB,KL,ADCY5,MRAS,AKT3,PRKD1,GNG12,RND2,ADCY2,PAK6,RRAS,RHOC,CXCR4,MYL9,FGFR1,RAC1,ADCY6,MAPK8,FGFR2,ITPR1,MYL9,ADCY9,FOS,RRAS2,RHOQ,PAK3,PTPN11,IRS1,ITPR3,LYN,MAPK10,PIK3R6,PIK3CB,ELMO1,PRKCB
Cyclins and Cell Cycle Regulation	2.22	1.604	CCNE2,HDAC4,HDAC2,HDAC8,PPP2R2A,WEE1,CCND1,CDK1,SKP2,E2F6,CCNE1,CDKN2D,CCND2,PPM1L,E2F7,E2F5,TGFB2,GSK3B,E2F8
Macropinocytosis Signaling	4.68	1.606	RRAS,PDGFA,FGFR1,PIK3R1,RAC1,HRAS,FGFR2,RAB34,PDGFC,CSF1R,ITGB3,FGFR3,ITGB2,RRAS2,PTPN11,CSF1,KL,IRS1,PIK3R6,MRAS,CD14,PIK3CB,PDGFD,PRKD1,PRKCB
Ephrin Receptor Signaling	2.49	1.177	RAP1B,FYN,RAPGEF1,ITSN1,PDGFA,PTPN13,HRAS,EPHA4,LIMK2,GNA14,BCAR1,PDGFC,GRINA,ROCK2,GNB1,EPHB6,VEGFA,EFNB2,EFNA5,MRAS,AKT3,GNG12,ITGA4,GRIN2B,NGEF,PAK6,RRAS,CXCR4,ARHGEF15,CREBBP,RAC1,ATF2,RRAS2,PTPN11,PAK3,PDGFD

1926

1927

1928 Supplemental Table 2: Canonical pathways are altered in 23-week-old neoplastic *Pgr^{cre/+}mPgrB^{LsL/+}*
 1929 mouse ovaries. Ingenuity Pathway Analysis was utilized to obtain the list of top canonical pathways from
 1930 the RNA microarray performed on 23-week-old, neoplastic *Pgr^{cre/+}mPgrB^{LsL/+}* mouse ovarian tumor
 1931 tissue.

1932

1933

1934

1935

1936

1937

1938

1939

1940

1941

1942

1943

1944

1945

1946

1947

1948

1949

1950

1951

1952

1953

1954

1955

1956

Ingenuity Canonical Pathways	-log(p-value)	Ratio	Molecules
Mitotic Roles of Polo-Like Kinase	5.93E00	2.3E-01	KIF23,PRC1,CDC20,KIF11,CDC25C,PLK3,CDC7,RAD21,STAG2,PLK4,PLK1,CDK1,CCNB1,FBXO5
Role of BRCA1 in DNA Damage Response	4.81E00	1.87E-01	FANCC,BRE,E2F1,BARD1,SMARCE1,FANCM,BRIP1,BLM,TOPBP1,FANCA,RBL1,RAD51,RFC4,PLK1
Cell Cycle Control of Chromosomal Replication	4.62E00	3.08E-01	CDC7,MCM2,ORC6,MCM6,CDT1,DBF4,MCM5,CDC6
Hereditary Breast Cancer Signaling	4.03E00	1.4E-01	FANCC,PALB2,MRAS,E2F1,BARD1,SMARCE1,FANCM,H2AFX,CDC25C,BLM,PMS2,CCND1,FANCA,RAD51,RFC4,CDK1,CCNB1
Estrogen-mediated S-phase Entry	3.94E00	2.92E-01	CCNE1,CCND1,SKP2,E2F1,CCNA2,RBL1,CDK1
Pancreatic Adenocarcinoma Signaling	3.85E00	1.47E-01	TGFA,HBEGF,TGFB3,NOTCH1,BIRC5,E2F1,RALGDS,RELA,SMAD3,CCND1,CCNE1,ERBB2,MDM2,BCL2L1,RAD51
Cell Cycle: G1/S Checkpoint Regulation	3.18E00	1.67E-01	TGFB3,CCNE1,CDKN2D,SMAD3,CCND1,SKP2,E2F1,MDM2,RBL1,MAX

1957

1958

1959

Supplemental Table 3: PGR causes many changes in multiple canonical pathways involved in cell proliferation and cancer. Top canonical pathway list for differentially regulated genes between placebo and RU486 acute treatment in the RNA microarray.

1960

1961

1962

1963

1964

1965

1966

1967

1968

1969

1970

1971

1972

1973

1974

1975

1976

1977

1978

1979

1980

1981

1982

1983

1984

1985

1986

1987

1988

1989

1990

1991

1992
1993

Categories	p-Value	# Mols
Embryonic Development, Organismal Survival	1.35E-10	28
Cell Cycle	8.44E-08	19
Cell Cycle, DNA Replication, Recombination, and Repair	3.67E-07	15
DNA Replication, Recombination, and Repair	6.22E-07	17
Cell Cycle, Cellular Assembly and Organization, DNA Replication, Recombination, and Repair	7.47E-07	7
Cancer, Organismal Injury and Abnormalities, Respiratory Disease	2.55E-06	27
Cell Death and Survival	2.69E-06	120
Cellular Assembly and Organization	3.33E-06	7
Cellular Compromise, DNA Replication, Recombination, and Repair	6.79E-06	10
Cancer, Organismal Injury and Abnormalities	6.86E-06	48

1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031

Supplemental Table 4: PGR transcriptionally controls multiple canonical pathways involved in cell proliferation and cancer. Top biological function gene list from Ingenuity Pathway Analysis for the tumor microarray overlapped with the PGR ovarian tumor ChIP-seq analysis. #Mols=number of molecules, p-Value=p-value based on the Ingenuity Pathway Analysis algorithm for analyzing enrichment in a pathway.

2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077

Gene Name (species)	SYBR Primer Sequence
<i>Cdc25c</i> F (Mus musculus)	TTGCAAAGCGTAGCACATCTG
<i>Cdc25c</i> R (Mus musculus)	AAGGACCCGCGTCAATCA
<i>Plk1</i> F (Mus musculus)	CCCGCTGGCGAAAGAAATTC
<i>Plk1</i> R (Mus musculus)	CATTTGGCGAAGCCTCCTTTA
<i>Ptgs1</i> F (Mus musculus)	TTGCACATCCATCCACTCCC
<i>Ptgs1</i> R (Mus musculus)	AATTCGGAAGCCAGGTCCAG
<i>Ptgs2</i> F (Mus musculus)	TTCAACACACTCTATCACTGGC
<i>Ptgs2</i> R (Mus musculus)	AGAAGCGTTTGCGGTACTION
<i>Gata4</i> F (Mus musculus)	CCCTACCCAGCCTACATGG
<i>Gata4</i> R (Mus musculus)	ACATATCGAGATTGGGGTGTCT
<i>Foxl2</i> F (Mus musculus)	ACAACACCCGGAGAAACCAGAC
<i>Foxl2</i> R (Mus musculus)	CGTAGAACGGGAACCTGGCTA
<i>Inhbb</i> F (Mus musculus)	CTTCGTCTCTAATGAAGGAACC
<i>Inhbb</i> R (Mus musculus)	CTCCACCACATTCCACCTGTC
<i>Foxo1</i> F (Mus musculus)	AGTGGATGGTGAAGAGCGTG
<i>Foxo1</i> R (Mus musculus)	GAAGGGACAGATTGTGGCGA
<i>Pgr</i> F (Mus musculus)	CTCCGGGACCGAACAGAGT
<i>Pgr</i> R (Mus musculus)	ACAACAACCCTTTGGTAGCAG
<i>Esr1</i> F (Mus musculus)	AAGTGTACGAAGTGGGCATGA
<i>Esr1</i> R (Mus musculus)	CTCTCTGACGCTTGTGCTTCAA
<i>Esr2</i> F (Mus musculus)	CTGTTACTAGTCCAAGCGCCA
<i>Esr2</i> R (Mus musculus)	CCCAGATGCATAATCACTGCA
Gene Name (species)	Applied Biosystems Taqman Cat #
<i>Hand2</i> (Mus musculus)	Mm00439247_m1
<i>Ccnd1</i> (Mus musculus)	Mm00432359_m1
<i>Foxm1</i> (Mus musculus)	Mm00514924_m1
<i>Cdk1</i> (Mus musculus)	Mm00772471_m1
<i>Ccnb1</i> (Mus musculus)	Mm00838401_g1

Supplemental Table 5: Complete list of SYBR primer sequences and Applied Biosystems Taqman probe catalog numbers.