Supplementary Data

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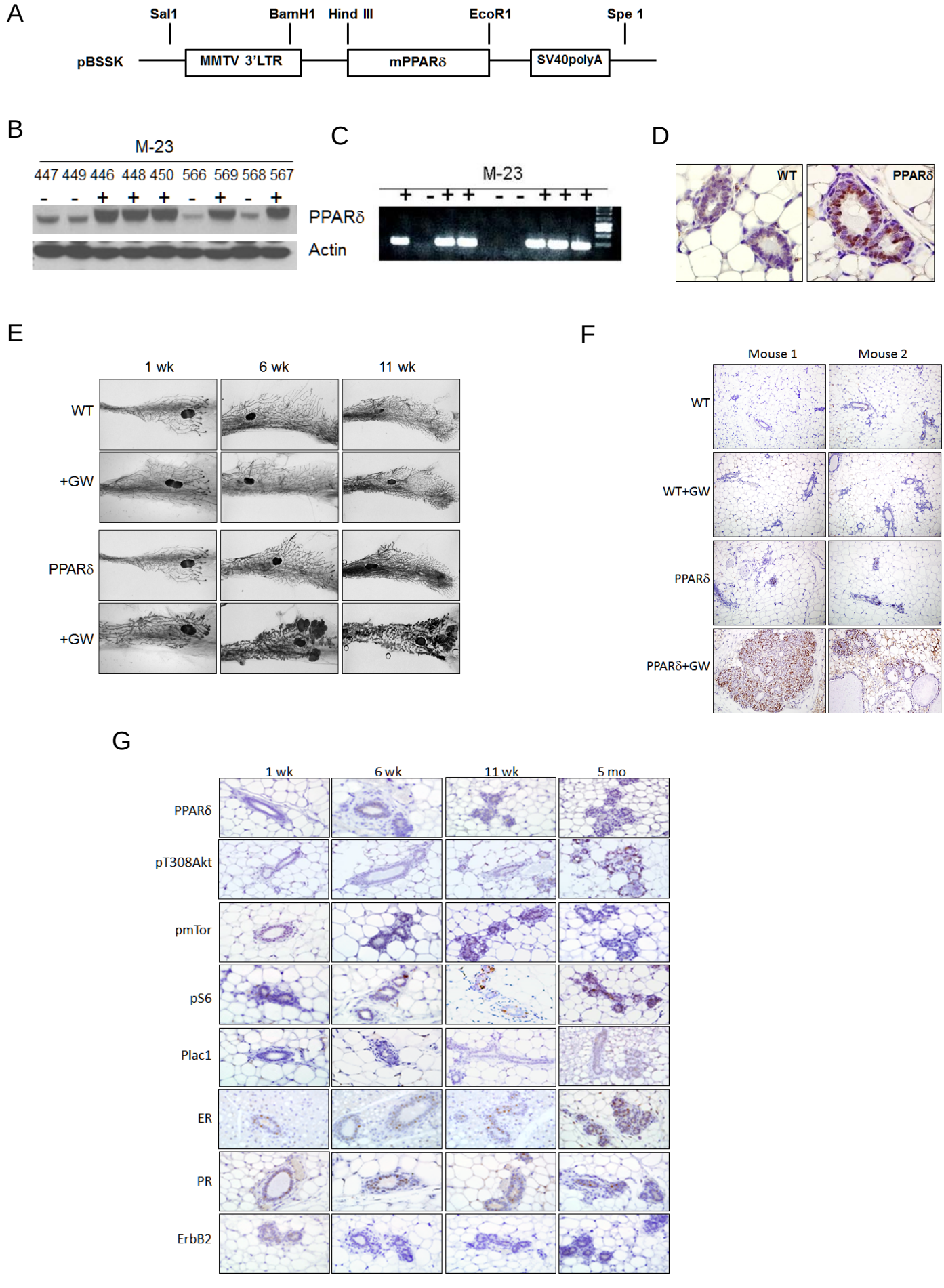
Supplementary Table 6. Gene expression preferentially altered in wild-type mice treated with GW501516 for 11 weeks.

Supplementary Figure 1. Characterization of MMTV-PPARδ transgenic mice. **A**, MMTV-PPARδ construct. **B**, Founder lines identified by PCR of tail genomic DNA. **C**, Western analysis of mammary gland lysates from 5-week-old mice of founder M-23, showing higher PPARδ expression in transgenic (+) vs. wild-type (-) mice. **D**, IHC detection of PPARδ in the mammary gland of 5-week-old wild-type (WT) and transgenic (PPARδ) mice. Magnification, 400X. **E**, Whole mounts of wild-type (WT) and transgenic (PPARδ) mice fed a GW501516 diet (GW) for 1 to 11 weeks. Note the extensive nodules only in PPARδ mice fed the GW501516 diet (PPARδ+GW). Magnification, 10X. **F**, IHC detection of Ki-67 in mammary tissue of 11-week old WT and PPARδ mice fed the GW diet for 6 weeks. Only PPARδ mice fed the GW diet expressed Ki-67. Magnification, 200X.

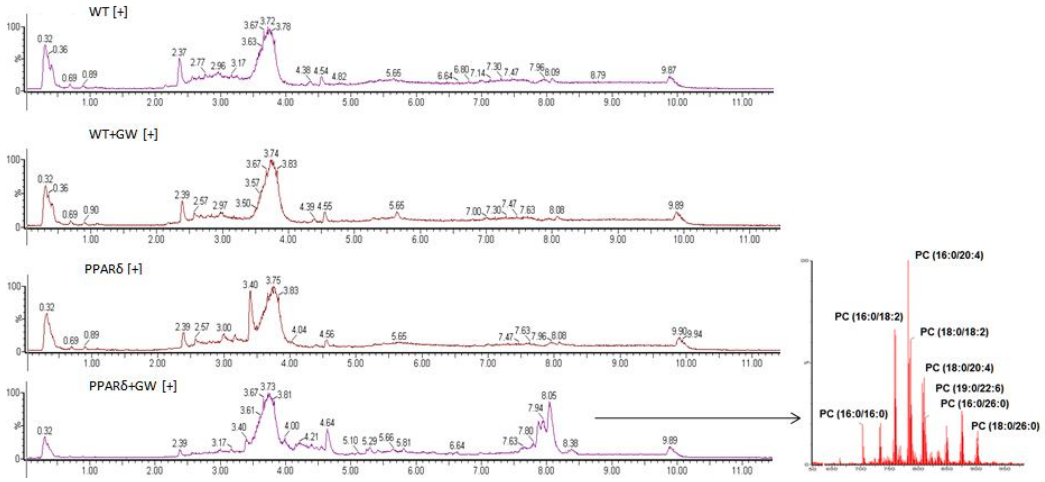
Supplementary Figure 2. **A**, LC-MS profiles of [+] ions from mammary tissue of control and GW501516-treated wild-type (WT) and PPARδ mice. The inset indicates the phosphatidylcholine (PC) profile of the [+] ions in the chromatogram. **B**, total ion chromatogram (TIC) of [-] ions corrected for retention time. As a visualization of the quality control of this correction procedure, an overlay of TIC's from each sample is shown. **C**, TIC of [+] ions corrected for retention time.

Supplementary Figure 3. Signaling pathways associated with PPRE-containing genes activated in MMTV-PPARδ mice treated with GW501516 for 11 weeks. **A**, Signaling pathways determined by Pathway Studio 9.0 based on the gene expression profile in Supplementary Table 4. **B** and **C** are enlargements of the boxed areas in **A**.



Supplementary Figure 1

A



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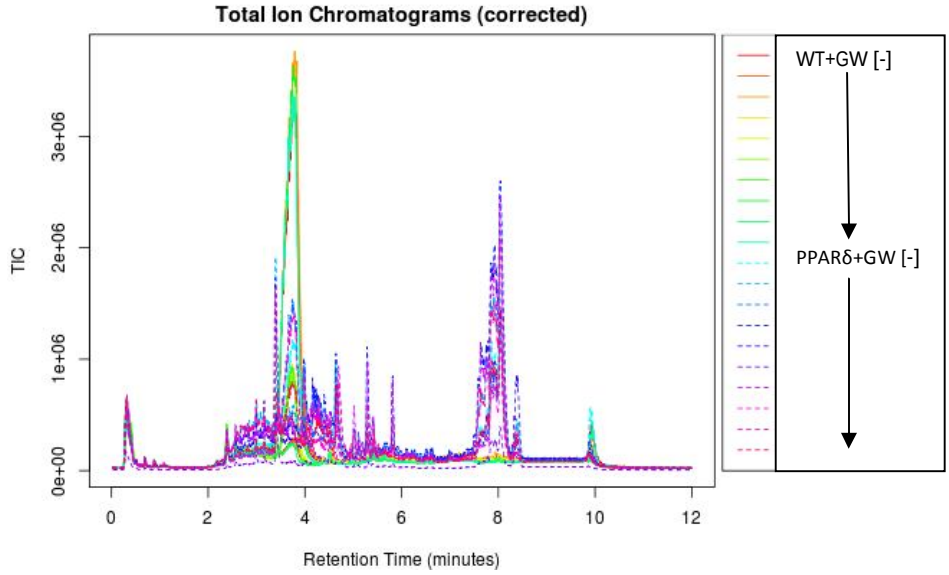

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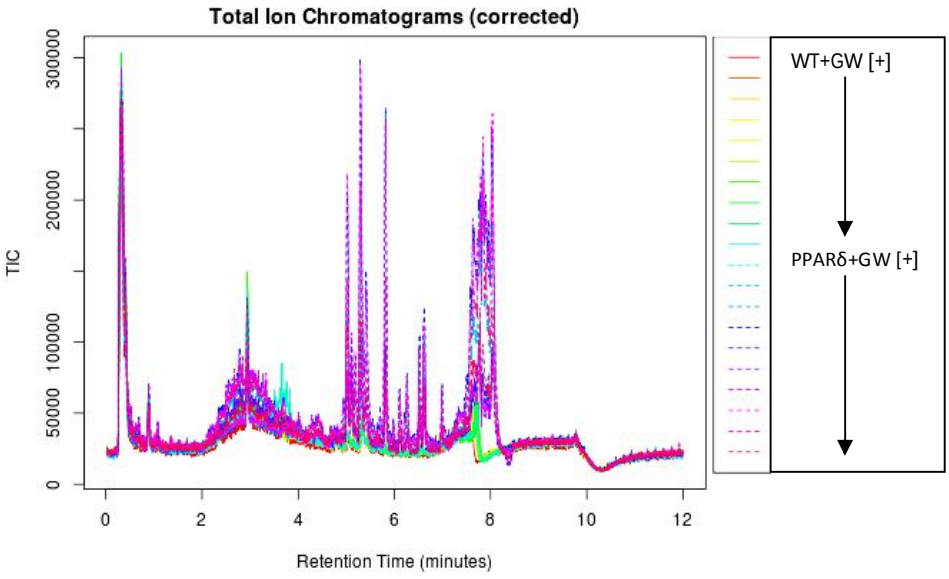
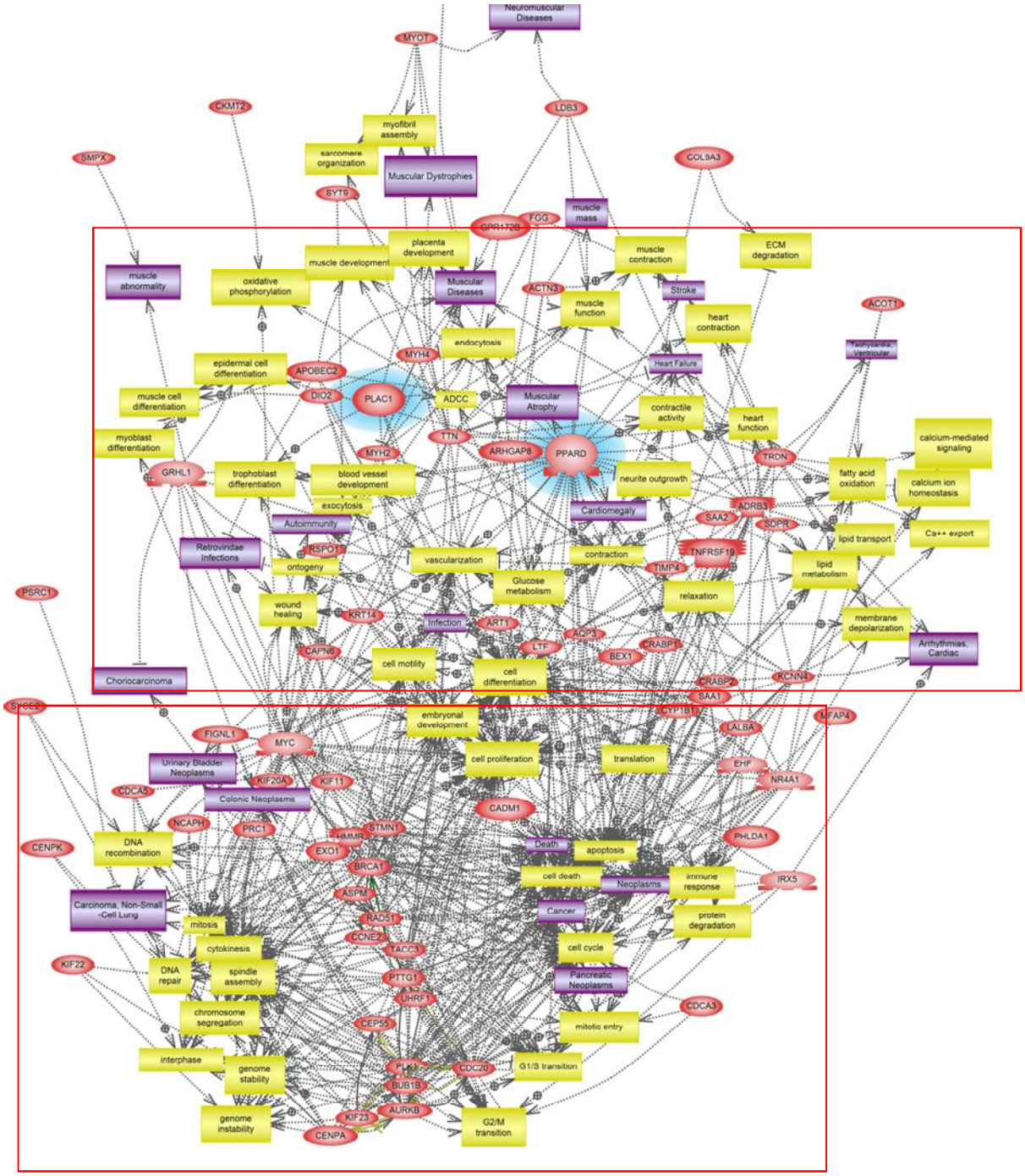


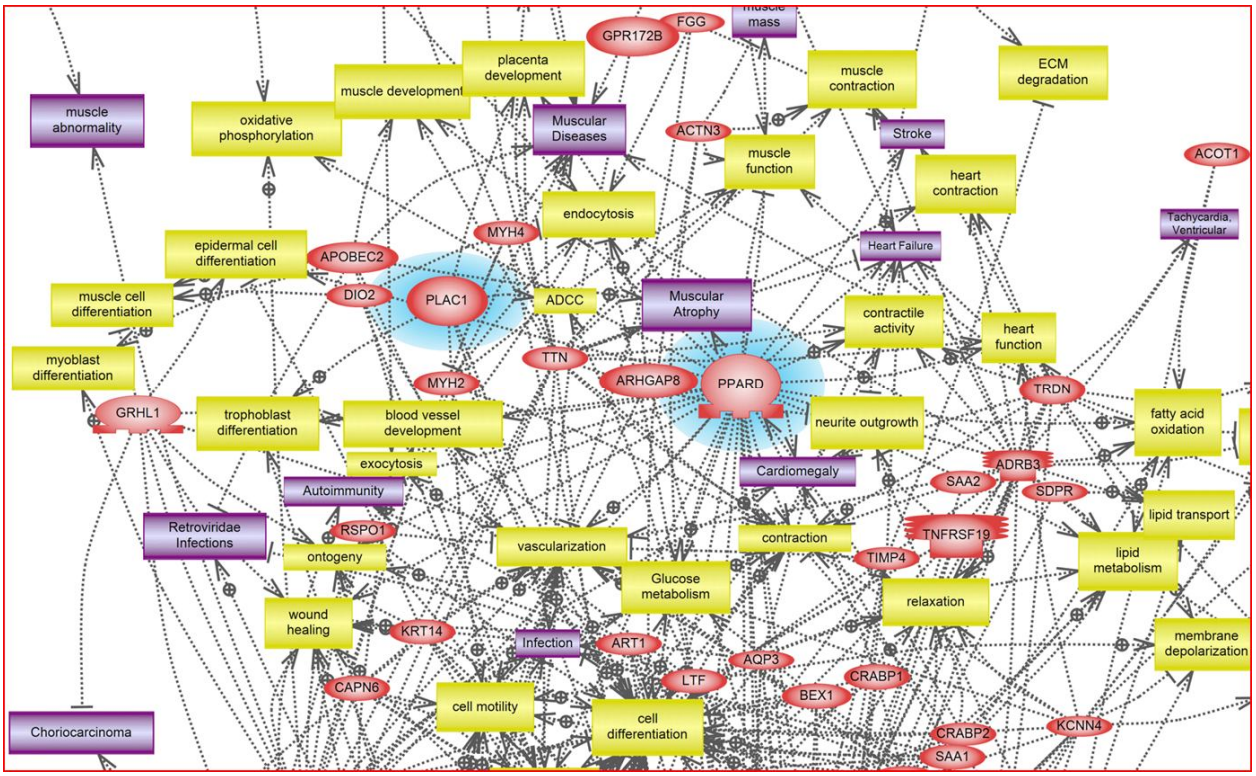
Supplementary Figure 2

A



Supplementary Figure 3A

B



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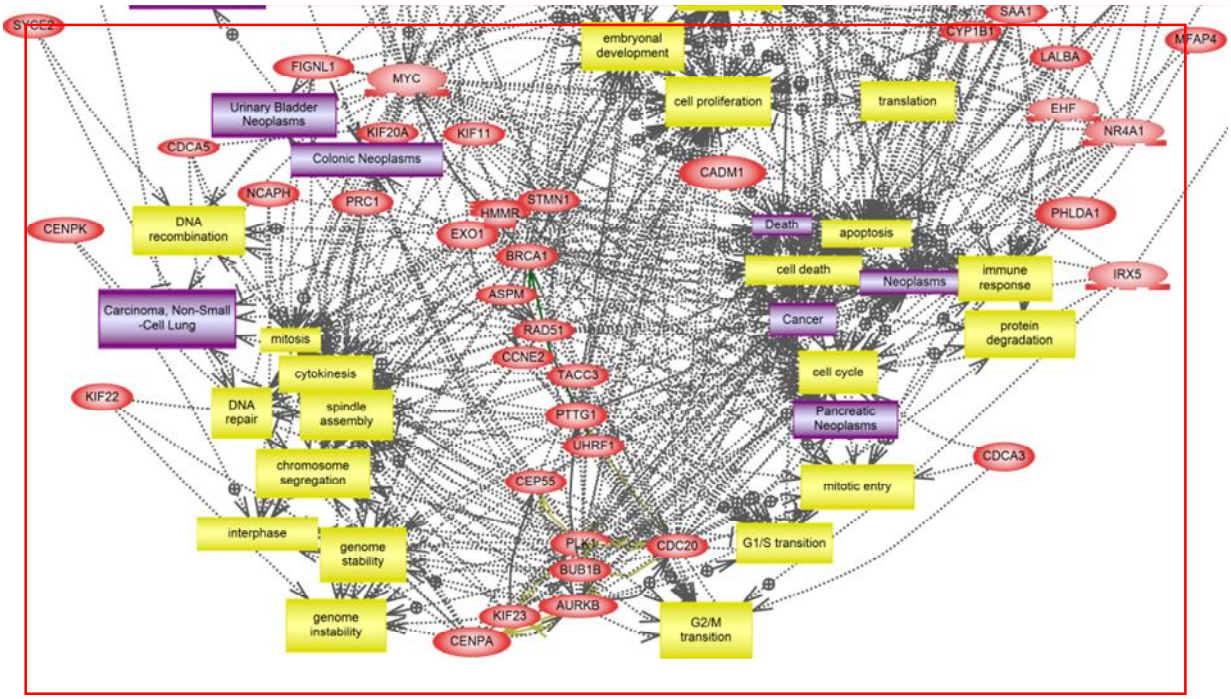

Supplementary Figure 3B,C

Supplementary Table 1. Antibodies for IHC and western blotting.

Antibody	Catalog #	Source	Dilution	
			IHC	WB
Rabbit anti-pSer79AcetylCoA Carboxylase	3661	Cell Signaling		
Rabbit anti-pThr308AKT	sc-16646	Santa Cruz	600	1,000
Sheep anti-pSer473AKT	06-801	Upstate	100	1,000
Rabbit anti-AKT	4685	Cell Signaling		1,000
Mouse anti-PDK1	sc-17765	Santa Cruz	50	1,000
Goat anti-PPARd (K-20)	sc-7197	Santa Cruz	200	500
Rabbit anti-pThr37/46-4EBP	2855	Cell Signaling	60	2,000
Rabbit anti-4EBP	9644	Cell Signaling		1,000
Rabbit anti-pSer2448mTOR	2976	Cell Signaling	50	1,000
Rabbit anti-mTOR	2983	Cell Signaling		1,000
Rabbit anti-p44/42-ERK1/2	4376	Cell Signaling	100	1,000
Rabbit anti-ERK	6182	Cell Signaling		1,000
Rabbit anti-pSer235/236S6	4857	Cell Signaling	200	1,000
Rabbit anti-S6	2317	Cell Signaling		1,000
Rabbit anti-Plac1		Michael Fant, University of South Florida	400	1,000
Mouse anti-Actin	A5441	Sigma		5,000

Supplementary Table 2. List of primers for q-RT-PCR analysis

Gene	Forward Primer (5'→3')	Reverse Primer (5'→3')
Saa2	ACACCAGCAGGATGAAGCTA	GCCAGCTTCCTTCATGTCA
Klk6	GGCTTCCTGTGATAGGTGGT	CTCCGACCAGGCTGATTTAG
Klk11	TAGGGAAGTAAGGCGAAGGA	CAGGTTCCCTGGTTTCTGTAG
Olah	AAGACTGGCTGGGAGAGAAA	TGTAGGATCCGAAACTGTGG
Acsl4	CAGCACCTTCGACTCAGATC	TTGGAGAAGGCAATAATGGA
Slc28a3	GAAATGGGTGGTCTGGAGTT	ATGAGTCCGCCAAAGGATAC
Scnn1g	CCCAGCCAACAGTATTGAGA	GGCGGGCAATAATAGAGAAG
mPlac1	AAGATTGAAGGCTAAGGGACC	CTCCTTTGAAACGTGGCTTTG
Esr1	TGATCAACTGGGCAAAGA	CAGGAGCAGGTCATAGAG
mPPARd	ACGGTAAAGGCAGTCCATCT	GTGGCTGTTCCATGACTGAC

Supplementary Table 3. Gene expression preferentially altered in MMTV-PPARδ mice treated with GW501516 and everolimus. MMTV-PPARδ mice (*δ*) were fed a diet containing 0.005% GW501516 (*GW*) for 6 weeks, and administered either vehicle or 10 mg/kg everolimus (*RAD*) by gavage once daily during weeks 4 through 6. Shown are ≥3-fold changes in gene expression in mammary tissue with a raw score ≥300. Symbols in ***bold*** denote genes containing PPAR response elements.

		Raw Score		Ratio
Function	**Gene Symbol**	**δ+GW**	**δ+GW+RAD**	**δ+GW+RAD/δ+GW**
Adhesion/Extracellular Matrix				
contactin 1	**Cntn1**	101	323	3.2
proline arginine-rich end leucine-rich repeat	**Prelp**	654	1811	2.8
cadherin-related family member 1	Cdhr1	424	148	0.3
Differentiation/Development				
keratin 77	**Krt77**	4	354	88.3
loricrin	Lor	13	588	46.5
keratinocyte differentiation associated protein	**Krtdap**	55	594	10.9
keratin 10	**Krt10**	313	2962	9.5
neuronatin	**Nnat**	803	3246	4.0
keratin 15	**Krt15**	151	527	3.5
mesoderm specific transcript	**Mest**	174	518	3.0
keratin 79	**Krt79**	810	264	0.33
lactotransferrin	**Ltf**	4356	1116	0.26
parvalbumin	**Pvalb**	2059	436	0.21
casein alpha s2-like B	Csn1s2b	851	160	0.19
Inflammation/Immune Response				
killer cell lectin-like receptor subfamily A, member 20	Klra20	90	356	3.9
monocyte to macrophage differentiation-associated 2	Mmd2	170	523	3.1
interleukin 1 receptor-like 1	Il1rl1	112	315	2.8
immunoglobulin heavy chain 2 (serum IgA)	Igh-2	6338	1914	0.30
polymeric immunoglobulin receptor	Pigr	621	148	0.24
serum amyloid A 3	Saa3	1553	376	0.24
immunoglobulin lambda chain, variable 1	Igl-V1	311	63	0.20
serum amyloid A 1	**Saa1**	11018	1306	0.12
serum amyloid A 2	**Saa2**	6073	516	0.08
Invasion				
kallikrein related-peptidase 7 (chymotryptic, stratum corneum)	**Klk7**	1031	224	0.22
kallikrein related-peptidase 10	**Klk10**	841	177	0.21
kallikrein related-peptidase 6	**Klk6**	1835	194	0.11
cystatin E/M	**Cst6**	7735	841	0.11
Metabolism				
arginase type II	Arg2	114	425	3.7
vanin 1	**Vnn1**	231	679	2.9
protein phosphatase 1, regulatory (inhibitor) subunit 3A	**Ppp1r3a**	114	36	0.32
enolase 3, beta muscle	**Eno3**	2129	576	0.27
cytochrome c oxidase, subunit VI a, polypeptide 2	**Cox6a2**	657	140	0.21
apolipoprotein B mRNA editing enzyme, catalytic polypeptide 2	**Apobec2**	477	91	0.19
phosphoglycerate mutase 2	**Pgam2**	1106	176	0.16
carbonic anhydrase 6	Car6	1095	122	0.11
creatine kinase, mitochondrial 2	**Ckmt2**	482	55	0.11
Motility				
tropomyosin 1, alpha	**Tpm1**	2141	704	0.33
tropomyosin 2, beta	**Tpm2**	554	183	0.33
actin, alpha 1, skeletal muscle	**Acta1**	7867	2551	0.32
actinin alpha 3	**Actn3**	828	265	0.32
myosin, heavy polypeptide 4, skeletal muscle	**Myh4**	3911	1252	0.32
myozenin 1	**Myoz1**	940	299	0.32
cardiomyopathy associated 5	Cmya5	408	127	0.31
myosin, light polypeptide 1	Myl1	5294	1573	0.30
calsequestrin 1	**Casq1**	504	152	0.30
prosaposin-like 1	Psapl1	801	217	0.27
titin-cap	**Tcap**	474	130	0.27
creatine kinase, muscle	**Ckm**	3124	836	0.27
troponin C2, fast	**Tnnc2**	6563	1621	0.25
ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	Atp2a1	1096	275	0.25
LIM domain binding 3	**Ldb3**	372	85	0.23
myotilin	**Myot**	470	106	0.23
myoglobin	Mb	462	102	0.22
myosin, heavy polypeptide 1, skeletal muscle, adult	**Myh1**	1450	322	0.22
troponin I, skeletal, fast 2	**Tnni2**	3361	739	0.22
titin	**Ttn**	552	121	0.22
myosin light chain, phosphorylatable, fast skeletal muscle	**Mylpf**	5660	1233	0.22
troponin T3, skeletal, fast	**Tnnt3**	2231	478	0.21
small muscle protein, X-linked	**Smpx**	436	72	0.16

Proliferation				
calmodulin 4	**Calm4**	8	566	70.5
amphiregulin	Areg	350	1937	5.5
v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma d	**Mycl1**	87	347	4.0
synuclein, gamma	**Sncg**	1644	4939	3.0
FK506 binding protein 5	Fkbp5	663	1898	2.9
placental specific protein 1	**Plac1**	1098	723	0.66
myeloid leukemia factor 1	Mlf1	344	117	0.34
Receptors				
peroxisome proliferator activator receptor delta	**Ppard**	1736	1368	0.79
Transport				
secretogranin III	Scg3	124	854	6.9
natriuretic peptide receptor 3	**Npr3**	296	1300	4.4
Transcription				
zinc finger and BTB domain containing 16	**Zbtb16**	495	2114	4.3
forkhead box I1	**Foxi1**	196	577	2.9

Supplementary Table 4. Gene expression preferentially altered in MMTV-PPARd mice treated with GW501516 for 11 weeks.
Four week old mice were fed a diet containing 0.005% GW501516 for 11 weeks. Shown are ≥3-fold changes in gene expression in mammary tissue with a raw score ≥300 in GW501516-treated MMTV-PPARδ mice (*δ+GW*) vs. GW501516-treated wild-type littermates (WT+GW). Symbols in ***bold*** denote genes with PPAR response elements.

Gene Name	Gene Symbol	WT	WT+GW	PPARd	PPARd+GW	d+GW/WT+GW
Adhesion						
cell adhesion molecule 1	**Cadm1**	391	501	1175	1267	2.5
Differentiation						
casein alpha s2-like B	Csn1s2b	58	67	95	676	10.1
annexin A8	**Anxa8**	339	246	548	1094	4.4
keratin 14	**Krt14**	683	1329	5433	5323	4.0
Inflammation/Immune Response						
cathelicidin antimicrobial peptide	Camp	40	21	23	420	19.7
serum amyloid A 3	**Saa3**	79	156	178	2838	18.2
S100 calcium binding protein A9 (calgranulin B)	**S100a9**	272	118	183	1657	14.0
serum amyloid A 2	**Saa2**	1626	980	409	12963	13.2
S100 calcium binding protein A8 (calgranulin A)	**S100a8**	431	342	415	4266	12.5
interleukin 1 family, member 9	**Il1f9**	58	61	56	629	10.2
serum amyloid A 1	**Saa1**	2715	1742	730	14810	8.5
interleukin 1 receptor antagonist	Il1rn	84	48	135	330	6.8
interleukin 1 beta	**Il1b**	99	55	224	341	6.3
chemokine (C-C motif) ligand 8	**Ccl8**	1977	1777	2068	7690	4.3
prostaglandin-endoperoxide synthase 2	**Ptgs2**	69	89	83	349	3.9
Fc fragment of IgG binding protein	Fcgbp	2493	1067	353	110	0.1
Invasion						
kallikrein related-peptidase 6	**Klk6**	142	106	101	18338	173.1
kallikrein related-peptidase 7 (chymotryptic, stratum corneum)	**Klk7**	109	116	90	5357	46.1
matrix metallopeptidase 13	Mmp13	10	7	5	319	45.1
kallikrein related-peptidase 10	Klk10	9	32	78	938	29.2
matrix metallopeptidase 12	**Mmp12**	157	157	332	2668	17.0
kallikrein related-peptidase 11	**Klk11**	36	70	164	722	10.3
cystatin E/M	**Cst6**	53	633	120	3899	6.2
Metabolism						
oleoyl-ACP hydrolase	Olah	21	227	237	1361	6.0
acyl-CoA synthetase long-chain family member 4	**Acsl4**	230	336	372	1287	3.8
phospholysine phosphohistidine inorganic pyrophosphate phosphatase	Lhpp	177	157	532	527	3.3
cellular retinoic acid binding protein I	**Crabp1**	225	421	924	1077	2.6
Proliferation						
placental specific protein 1	**Plac1**	31	41	2731	4491	108.9
reprimo, TP53 dependent G2 arrest mediator candidate	Rprm	9	34	896	140	4.1
cyclin B1	**Ccnb1**	132	187	919	536	2.9
cyclin B2	Ccnb2	205	309	1459	798	2.6
Transport						
aquaporin 3	**Aqp3**	61	127	1990	6002	47.3
G protein-coupled receptor 172B	**Gpr172b**	320	510	1380	1482	2.9
solute carrier family 34 (sodium phosphate), member 2	**Slc34a2**	240	494	966	1407	2.8

Supplementary Table 5. Gene expression preferentially altered in MMTV-PPARδ mice. Shown are ≥3-fold changes in gene expression in mammary tissue with a raw score ≥300 in MMTV-PPARδ mice (*δ*) vs. wild-type littermates (*WT*) at 15 weeks of age. Symbols in ***bold*** denote genes containing PPAR response elements.

		Raw Score		Ratio
Function	**Symbol**	**WT**	**δ**	**δ/WT**
Adhesion/Extracellular Matrix				
tight junction protein 3	Tjp3	365	1626	**4.5**
EMI domain containing 1	Emid1	394	1708	**4.3**
microfibrillar-associated protein 4	**Mfap4**	97	350	**3.6**
desmocollin 2	Dsc2	94	324	**3.4**
collagen, type IX, alpha 3	**Col9a3**	139	450	**3.2**
cell adhesion molecule 1	**Cadm1**	391	1175	**3.0**
cartilage acidic protein 1	**Crtac1**	511	147	**0.29**
fibrinogen gamma chain	**Fgg**	907	181	**0.20**
carcinoembryonic antigen-related cell adhesion molecule 10	Ceacam10	927	115	**0.12**
fibrinogen beta chain	Fgb	497	58	**0.12**
Apoptosis				
BCL2/adenovirus E1B 19kD interacting protein like	Bnipl	63	305	**4.9**
pleckstrin homology-like domain, family A, member 1	**Phlda1**	2352	8397	**3.6**
Iroquois related homeobox 5 (Drosophila)	**Irx5**	648	2258	**3.5**
Iroquois related homeobox 3 (Drosophila)	**Irx3**	1447	4624	**3.2**
Differentiation/Development				
keratin 14	**Krt14**	683	5433	**8.0**
casein alpha s2-like A	Csn1s2a	255	1019	**4.0**
keratin 23	Krt23	131	504	**3.8**
grainyhead-like 1 (Drosophila)	**Grhl1**	593	2275	**3.8**
hairy/enhancer-of-split related with YRPW motif 1	Hey1	1114	346	**0.31**
lactotransferrin	**Ltf**	6590	901	**0.14**
lactalbumin, alpha	**Lalba**	2426	322	**0.13**
DNA Repair				
RAD51 homolog (S. cerevisiae)	**Rad51**	88	459	**5.2**
excision repair cross-complementing rodent repair deficiency complementation group 6-like	Ercc6l	72	307	**4.3**
DNA-damage-inducible transcript 4-like	Ddit4l	137	495	**3.6**
breast cancer 1	**Brca1**	68	331	**4.9**
fidgetin-like 1	**Fignl1**	176	770	**4.4**
exonuclease 1	**Exo1**	46	335	**7.2**
ubiquitin-like, containing PHD and RING finger domains, 1	**Uhrf1**	246	985	**4.0**
synaptonemal complex central element protein 2	**Syce2**	306	1202	**3.9**
denticleless homolog (Drosophila)	Dtl	130	501	**3.8**
ADP-ribosyltransferase 1	**Art1**	90	308	**3.4**
high mobility group box 2	Hmgb2	946	3081	**3.3**
Inflammation/Immune Response				
peptidylprolyl isomerase (cyclophilin) like 5	Ppil5	43	438	**10.3**
tumor necrosis factor receptor superfamily, member 19	**Tnfrsf19**	43	400	**9.4**
ectodysplasin-A receptor	Edar	32	303	**9.4**
WAP four-disulfide core domain 12	Wfdc12	131	703	**5.4**
serum amyloid A 1	**Saa1**	3209	861	**0.27**
immunoglobulin heavy chain 6 (heavy chain of IgM)	Igh-6	3888	1022	**0.26**
serum amyloid A 2	**Saa2**	1626	409	**0.25**
immunoglobulin kappa chain variable 28 (V28)	Igk-V28	527	81	**0.15**
Fc fragment of IgG binding protein	Fcgbp	2493	353	**0.14**
immunoglobulin heavy constant gamma 1 (G1m marker)	Ighg1	3663	484	**0.13**
Invasion				
calpain 6	**Capn6**	32	331	**10.3**
Rho GTPase activating protein 8	**Arhgap8**	224	876	**3.9**
tissue inhibitor of metalloproteinase 4	**Timp4**	4348	1253	**0.29**
Ion Channel				
potassium channel tetramerisation domain containing 14	Kctd14	49	595	**12.1**
potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	**Kcnn4**	1230	5036	**4.1**
potassium channel, subfamily K, member 1	Kcnk1	1044	3241	**3.1**
Metabolism				
calcitonin/calcitonin-related polypeptide, alpha	Calca	35	5293	**153.1**
acyl-CoA thioesterase 1	**Acot1**	1321	7933	**6.0**
cellular retinoic acid binding protein II	**Crabp2**	255	1115	**4.4**
creatine kinase, mitochondrial 2	**Ckmt2**	197	836	**4.3**
deiodinase, iodothyronine, type II	**Dio2**	79	321	**4.1**
ELOVL family member 7, elongation of long chain fatty acids (yeast)	Elovl7	285	1056	**3.7**
cellular retinoic acid binding protein I	**Crabp1**	195	734	**3.8**
carbonic anhydrase 2	**Car2**	1145	4116	**3.6**
inositol (myo)-1(or 4)-monophosphatase 2	Impa2	118	418	**3.5**
phosphoglycerate mutase 2	**Pgam2**	592	1912	**3.2**
apolipoprotein B mRNA editing enzyme, catalytic polypeptide 2	**Apobec2**	398	1221	**3.1**
cytochrome P450, family 1, subfamily b, polypeptide 1	**Cyp1b1**	1564	4711	**3.0**
phospholysine phosphohistidine inorganic pyrophosphate phosphatase	Lhpp	177	532	**3.0**
cholecystokinin	Cck	1372	403	**0.29**

Mitosis				
spindle and kinetochore associated complex subunit 1	Ska1	31	371	**12.0**
budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	Bub1	74	769	**10.4**
centromere protein F	Cenpf	40	418	**10.3**
maternal embryonic leucine zipper kinase	Melk	56	577	**10.3**
kinesin family member 11	**Kif11**	79	630	**8.0**
kinesin family member 2C	Kif2c	76	569	**7.5**
ect2 oncogene	Ect2	98	727	**7.4**
cyclin B1	Ccnb1	145	1013	**7.0**
asp (abnormal spindle)-like, microcephaly associated (Drosophila)	**Aspm**	61	419	**6.9**
non-SMC condensin I complex, subunit G	Ncapg	78	526	**6.8**
budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	**Bub1b**	85	561	**6.6**
shugoshin-like 1 (S. pombe)	Sgol1	52	338	**6.5**
kinesin family member 20A	**Kif20a**	61	379	**6.2**
centromere protein E	Cenpe	49	302	**6.2**
aurora kinase B	**Aurkb**	78	465	**5.9**
proline/serine-rich coiled-coil 1	**Psrc1**	62	363	**5.9**
protein regulator of cytokinesis 1	**Prc1**	120	688	**5.7**
polo-like kinase 1 (Drosophila)	**Plk1**	76	424	**5.6**
centrosomal protein 55	**Cep55**	187	971	**5.2**
kinesin family member C1	Kifc1	63	319	**5.1**
SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Spc25	215	1066	**5.0**
kinesin family member 22	**Kif22**	552	2664	**4.8**
Zwilch, kinetochore associated, homolog (Drosophila)	Zwilch	85	401	**4.7**
calmodulin-like 3	Calml3	250	1149	**4.6**
kinesin family member 23	**Kif23**	115	521	**4.5**
non-SMC condensin I complex, subunit H	**Ncaph**	292	1301	**4.5**
transforming, acidic coiled-coil containing protein 3	**Tacc3**	114	490	**4.3**
aurora kinase A	Aurka	94	390	**4.1**
centromere protein A	**Cenpa**	390	1566	**4.0**
centromere protein K	**Cenpk**	152	532	**3.5**
inner centromere protein	Incenp	384	1284	**3.3**
stathmin 1	**Stmn1**	2042	6681	**3.3**
centromere protein N	Cenpn	102	329	**3.2**
pituitary tumor-transforming gene 1	**Pttg1**	852	2669	**3.1**
coiled-coil domain containing 99	Ccdc99	137	425	**3.1**
Motility				
myosin, light chain 10, regulatory	Myl10	70	2069	**29.7**
hyaluronan mediated motility receptor (RHAMM)	**Hmmr**	115	726	**6.3**
titin	**Ttn**	217	944	**4.4**
small muscle protein, X-linked	**Smpx**	233	938	**4.0**
myomesin 2	Myom2	78	301	**3.9**
myosin VC	Myo5c	117	389	**3.3**
myotilin	**Myot**	282	909	**3.2**
myosin, heavy polypeptide 4, skeletal muscle	**Myh4**	2018	6339	**3.1**
myosin, heavy polypeptide 2, skeletal muscle, adult	**Myh2**	195	597	**3.1**
actinin alpha 3	**Actn3**	589	1787	**3.0**
triadin	**Trdn**	212	642	**3.0**
myoglobin	Mb	416	1258	**3.0**
LIM domain binding 3	**Ldb3**	331	1001	**3.0**
Proliferation				
reprimo, TP53 dependent G2 arrest mediator candidate	Rprm	9	896	**103.8**
placental specific protein 1	**Plac1**	31	2731	**87.1**
R-spondin homolog (Xenopus laevis)	**Rspo1**	222	3838	**17.3**
Shc SH2-domain binding protein 1	Shcbp1	115	970	**8.4**
syntaxin 19	**Stx19**	44	351	**7.9**
antigen identified by monoclonal antibody Ki 67	Mki67	200	1469	**7.3**
cyclin B2	Ccnb2	205	1459	**7.1**
cyclin A2	Ccna2	309	2170	**7.0**
shisa homolog 2 (Xenopus laevis)	Shisa2	220	1434	**6.5**
cell division cycle 20 homolog (S. cerevisiae)	**Cdc20**	437	2781	**6.4**
X-linked myotubular myopathy gene 1	Mtm1	297	1907	**6.4**
brain expressed gene 1	**Bex1**	243	1554	**6.4**
brain expressed gene 4	Bex4	62	351	**5.7**
cell division cycle associated 5	**Cdca5**	245	1384	**5.6**
cell division cycle associated 3	**Cdca3**	151	831	**5.5**
cyclin-dependent kinase 1	Cdk1	522	2623	**5.0**
DBF4 homolog (S. cerevisiae)	Dbf4	254	1057	**4.2**
CDC28 protein kinase regulatory subunit 2	Cks2	623	2628	**4.2**
cyclin E2	**Ccne2**	177	585	**3.3**
ribosomal protein L3-like	**Rpl3l**	80	260	**3.3**
myeloid leukemia factor 1	Mlf1	188	595	**3.2**
cell division cycle 25 homolog A (S. pombe)	Cdc25a	312	958	**3.1**
thymidine kinase 1	Tk1	166	506	**3.1**
S-phase kinase-associated protein 2 (p45)	Skp2	187	565	**3.0**
minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	Mcm2	217	652	**3.0**
serum deprivation response	**Sdpr**	6603	2180	**0.33**

Protein Folding				
ankyrin repeat and SOCs box-containing 5	Asb5	128	457	**3.6**
Receptors				
peroxisome proliferator activator receptor delta	**Ppard**	0	2586	**NA**
nuclear receptor subfamily 4, group A, member 1	**Nr4a1**	428	2506	**5.9**
glutamate receptor, ionotropic, delta 1	**Grid1**	32	155	**4.9**
thyroid hormone receptor interactor 13	Trip13	184	686	**3.7**
adrenergic receptor, beta 3	**Adrb3**	516	173	**0.33**
RNA Splicing				
epithelial splicing regulatory protein 2	Esrp2	172	612	**3.6**
Transport				
aquaporin 3	**Aqp3**	87	2386	**27.3**
ATPase, H+ transporting, lysosomal V1 subunit C2	Atp6v1c2	164	2984	**18.2**
synaptotagmin IX	**Syt9**	42	565	**13.6**
major urinary protein 1 (Slc25A19)	Mup1	1025	4316	**4.2**
G protein-coupled receptor 172B	**Gpr172b**	382	1599	**4.2**
solute carrier family 34 (sodium phosphate), member 2	Slc34a2	240	966	**4.0**
major urinary protein 5	Mup5	289	1118	**3.9**
Transcription				
E2F transcription factor 8	E2f8	62	468	**7.6**
helicase, lymphoid specific	Hells	266	1276	**4.8**
ets homologous factor	**Ehf**	656	2576	**3.9**
transcription factor AP-2, alpha	**Tcfap2a**	162	509	**3.1**
myelocytomatosis oncogene	**Myc**	923	2727	**3.0**

Mitosis				
spindle and kinetochore associated complex subunit 1	Ska1	31	371	**12.0**
budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	Bub1	74	769	**10.4**
centromere protein F	Cenpf	40	418	**10.3**
maternal embryonic leucine zipper kinase	Melk	56	577	**10.3**
kinesin family member 11	**Kif11**	79	630	**8.0**
kinesin family member 2C	Kif2c	76	569	**7.5**
ect2 oncogene	Ect2	98	727	**7.4**
cyclin B1	Ccnb1	145	1013	**7.0**
asp (abnormal spindle)-like, microcephaly associated (Drosophila)	**Aspm**	61	419	**6.9**
non-SMC condensin I complex, subunit G	Ncapg	78	526	**6.8**
budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	**Bub1b**	85	561	**6.6**
shugoshin-like 1 (S. pombe)	Sgol1	52	338	**6.5**
kinesin family member 20A	**Kif20a**	61	379	**6.2**
centromere protein E	Cenpe	49	302	**6.2**
aurora kinase B	**Aurkb**	78	465	**5.9**
proline/serine-rich coiled-coil 1	**Psrc1**	62	363	**5.9**
protein regulator of cytokinesis 1	**Prc1**	120	688	**5.7**
polo-like kinase 1 (Drosophila)	**Plk1**	76	424	**5.6**
centrosomal protein 55	**Cep55**	187	971	**5.2**
kinesin family member C1	Kifc1	63	319	**5.1**
SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Spc25	215	1066	**5.0**
kinesin family member 22	**Kif22**	552	2664	**4.8**
Zwilch, kinetochore associated, homolog (Drosophila)	Zwilch	85	401	**4.7**
calmodulin-like 3	Calml3	250	1149	**4.6**
kinesin family member 23	**Kif23**	115	521	**4.5**
non-SMC condensin I complex, subunit H	**Ncaph**	292	1301	**4.5**
transforming, acidic coiled-coil containing protein 3	**Tacc3**	114	490	**4.3**
aurora kinase A	Aurka	94	390	**4.1**
centromere protein A	**Cenpa**	390	1566	**4.0**
centromere protein K	**Cenpk**	152	532	**3.5**
inner centromere protein	Incenp	384	1284	**3.3**
stathmin 1	**Stmn1**	2042	6681	**3.3**
centromere protein N	Cenpn	102	329	**3.2**
pituitary tumor-transforming gene 1	**Pttg1**	852	2669	**3.1**
coiled-coil domain containing 99	Ccdc99	137	425	**3.1**
Motility				
myosin, light chain 10, regulatory	Myl10	70	2069	**29.7**
hyaluronan mediated motility receptor (RHAMM)	**Hmmr**	115	726	**6.3**
titin	**Ttn**	217	944	**4.4**
small muscle protein, X-linked	**Smpx**	233	938	**4.0**
myomesin 2	Myom2	78	301	**3.9**
myosin VC	Myo5c	117	389	**3.3**
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R-spondin homolog (Xenopus laevis)	**Rspo1**	222	3838	**17.3**
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E2F transcription factor 8	E2f8	62	468	**7.6**
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transcription factor AP-2, alpha	**Tcfap2a**	162	509	**3.1**
myelocytomatosis oncogene	**Myc**	923	2727	**3.0**

Supplementary Table 6. Gene expression preferentially altered in wild-type mice treated with GW501516 for 11 weeks. Mice (*WT*) at 4 weeks of age were fed a diet containing 0.005% GW501516 for 11 weeks. Shown are ≥3-fold changes in gene expression in mammary tissue with a score ≥300. Scores for similarly treated MMTV-PPARδ mice (δ) are shown for comparison. Symbols in ***bold*** denote genes containing PPAR response elements.

		Score		Ratio	Score		Ratio
Function	**Symbol**	**WT**	**WT+GW**	**WT+GW/WT**	d	d+GW	δ+GW/δ
Adhesion/Extracellular Matrix							
leupaxin	Lpxn	674	201	**0.30**	453	670	1.5
cartilage acidic protein 1	**Crtac1**	511	118	**0.23**	147	73	0.49
fibrinogen beta chain	Fgb	497	69	**0.14**	58	60	1.0
Differentiation/Development							
loricrin	Lor	120	2215	**18.4**	118	117	1.0
parvalbumin	**Pvalb**	1648	13592	**8.2**	4107	3129	0.76
casein alpha s2-like A	Csn1s2a	255	2034	**8.0**	1019	2625	2.6
SET and MYND domain containing 1	Smyd1	76	597	**7.8**	79	68	0.86
SPEG complex locus	**Speg**	91	594	**6.5**	142	92	0.64
late cornified envelope 1A1	Lce1a1	194	977	**5.0**	142	167	1.2
DNA Repair							
ADP-ribosyltransferase 1	**Art1**	90	2142	**23.8**	308	214	0.70
DNA-damage-inducible transcript 4-like	Ddit4l	137	2224	**16.2**	495	327	0.66
Inflammation/Immune Response							
tumor necrosis factor receptor superfamily, member 19	**Tnfrsf19**	43	342	**8.0**	400	70	0.17
leucine rich repeat containing 20	Lrrc20	140	570	**4.1**	184	176	1.0
polymeric immunoglobulin receptor	Pigr	195	796	**4.1**	586	1416	2.4
monocyte to macrophage differentiation-associated 2	Mmd2	133	525	**3.9**	115	158	1.4
chemokine (C-X-C motif) ligand 15	Cxcl15	524	1635	**3.1**	648	1313	2.0
interleukin 27 receptor, alpha	**Il27ra**	538	173	**0.3**	332	439	1.3
CD28 antigen	**Cd28**	323	80	**0.25**	223	284	1.3
CD52 antigen	**Cd52**	4775	1131	**0.24**	3934	4099	1.0
chemokine (C-C motif) ligand 5	Ccl5	3089	707	**0.23**	2552	2857	1.1
interleukin 2 receptor, gamma chain	**Il2rg**	484	109	**0.22**	306	437	1.4
immunoglobulin heavy chain 6 (heavy chain of IgM)	Igh-6	3888	813	**0.21**	1022	2754	2.7
CD3 antigen, gamma polypeptide	Cd3g	907	161	**0.18**	742	762	1.0
immunoglobulin kappa chain variable 28 (V28)	Igk-V28	527	91	**0.17**	81	165	2.0
T-cell receptor beta-2 joining region	tcrb-j	2048	334	**0.16**	1424	1671	1.2
CD3 antigen, epsilon polypeptide	Cd3e	364	55	**0.15**	256	325	1.3
lymphocyte protein tyrosine kinase	**Lck**	1206	179	**0.15**	886	1041	1.2
lymphotoxin B	**Ltb**	2802	390	**0.14**	2176	2381	1.1
immunoglobulin heavy constant gamma 1 (G1m marker)	Ighg1	3663	508	**0.14**	484	1167	2.4
chemokine (C-C motif) receptor 6	Ccr6	463	52	**0.11**	324	350	1.1
interleukin 7 receptor	Il7r	879	93	**0.11**	561	1058	1.9
interleukin 4 induced 1	**Il4i1**	383	38	**0.10**	245	280	1.1
linker for activation of T cells	**Lat**	510	49	**0.10**	369	400	1.1
chemokine (C-C motif) ligand 21A	Ccl21a	3750	308	**0.08**	1775	3017	1.7
CD3 antigen, delta polypeptide	Cd3d	1261	100	**0.08**	901	865	1.0
CD5 antigen	Cd5	320	22	**0.07**	192	226	1.2
CD79B antigen	**Cd79b**	1388	81	**0.06**	739	679	0.92
chemokine (C-C motif) receptor 7	**Ccr7**	456	20	**0.04**	256	310	1.2
complement receptor 2	**Cr2**	391	13	**0.03**	180	215	1.2
CD8 antigen, beta chain 1	Cd8b1	340	10	**0.03**	194	244	1.3
chemokine (C-C motif) ligand 19	Ccl19	1995	54	**0.03**	1213	1422	1.2
immunoglobulin heavy variable V14-2	Ighv14-2	1331	32	**0.02**	618	451	0.73
Invasion							
leucine rich repeat containing 2	Lrrc2	11	540	**47.4**	58	41	0.71
cystatin E/M	**Cst6**	53	633	**12.1**	120	3899	32.5
tissue inhibitor of metalloproteinase 4	**Timp4**	4348	1341	**0.31**	1253	834	0.67
Ion Channel							
calcium channel, voltage-dependent, gamma subunit 1	**Cacng1**	13	362	**27.5**	75	54	0.72
potassium voltage-gated channel, shaker-related subfamily, member 7	Kcna7	1484	6226	**4.2**	1724	1434	0.83
Metabolism							
calcitonin/calcitonin-related polypeptide, alpha	Calca	35	1315	**38.1**	5293	18	0.00
creatine kinase, mitochondrial 2	**Ckmt2**	197	5344	**27.2**	836	397	0.48
protein phosphatase 1, regulatory (inhibitor) subunit 3A	**Ppp1r3a**	30	627	**21.0**	114	66	0.57
apolipoprotein B mRNA editing enzyme, catalytic polypeptide 2	**Apobec2**	398	6907	**17.3**	1221	793	0.65
cytochrome c oxidase, subunit VI a, polypeptide 2	**Cox6a2**	396	6569	**16.6**	1136	841	0.74
aspartate-beta-hydroxylase	**Asph**	92	1447	**15.7**	224	178	0.79
phosphoglycerate mutase 2	**Pgam2**	592	8511	**14.4**	1912	1426	0.75
phosphorylase kinase, gamma-subunit 1	**Phkg1**	64	465	**7.3**	70	67	1.0
phosphofructokinase, muscle	**Pfkm**	654	3302	**5.0**	801	567	0.71
acyl-CoA thioesterase 1	**Acot1**	1321	5814	**4.4**	7933	5664	0.71
pyridoxal-dependent decarboxylase domain containing 1	Pdxdc1	80	300	**3.7**	185	423	2.3
cytochrome P450, family 1, subfamily b, polypeptide 1	**Cyp1b1**	347	1285	**3.7**	1547	1021	0.66
Motility							
myogenic factor 6	Myf6	21	944	**45.2**	118	87	0.74
myosin, light polypeptide 2, regulatory, cardiac, slow	Myl2	20	796	**40.4**	15	22	1.4
myomesin 2	Myom2	78	2452	**31.5**	301	176	0.58
myozenin 2	Myoz2	25	748	**29.7**	94	39	0.42
muscle-related coiled-coil protein	Murc	19	480	**25.9**	66	35	0.53
myotilin	**Myot**	282	7162	**25.4**	909	736	0.81
sarcoglycan, gamma (dystrophin-associated glycoprotein)	Sgcg	37	1002	**26.8**	124	80	0.64
titin	**Ttn**	217	5659	**26.1**	944	467	0.49
smoothelin-like 1	Smtnl1	43	1106	**26.0**	105	67	0.63

myosin, heavy polypeptide 8, skeletal muscle, perinatal	**Myh8**	36	882	**24.7**	135	90	0.67
myosin, heavy polypeptide 2, skeletal muscle, adult	**Myh2**	195	4517	**23.2**	597	187	0.31
small muscle protein, X-linked	**Smpx**	233	5309	**22.8**	938	531	0.57
LIM domain binding 3	**Ldb3**	224	4982	**22.3**	590	425	0.72
popeye domain containing 3	Popdc3	18	403	**22.3**	87	64	0.74
troponin I, skeletal, fast 2	**Tnni2**	41	890	**21.9**	121	86	0.71
cysteine and glycine-rich protein 3	**Csrp3**	87	1724	**19.9**	217	151	0.70
triadin	**Trdn**	153	3035	**19.8**	499	365	0.73
caveolin 3	**Cav3**	22	430	**19.4**	62	58	0.93
myosin, light polypeptide 3	**Myl3**	25	483	**19.2**	59	53	0.90
myomesin 1	Myom1	170	3204	**18.9**	469	346	0.74
sarcolipin	Sln	36	644	**18.0**	146	42	0.29
actinin alpha 2	**Actn2**	101	2056	**20.3**	257	147	0.57
synaptophysin-like 2	Sypl2	35	711	**20.2**	92	81	0.89
troponin C, cardiac/slow skeletal	**Tnnc1**	23	373	**16.5**	36	76	2.1
SH3-binding domain glutamic acid-rich protein	Sh3bgr	168	2706	**16.1**	457	294	0.64
titin-cap	**Tcap**	425	6819	**16.0**	1251	712	0.57
myoglobin	Mb	416	6489	**15.6**	1258	732	0.58
myosin, heavy polypeptide 6, cardiac muscle, alpha	**Myh6**	51	801	**15.6**	120	103	0.86
tropomodulin 4	**Tmod4**	220	3402	**15.4**	576	535	0.93
myozenin 1	**Myoz1**	550	8477	**15.4**	1472	1342	0.91
cardiomyopathy associated 5	Cmya5	311	4760	**15.3**	832	616	0.74
taxilin beta	Txlnb	183	2753	**15.1**	222	209	0.94
myosin, heavy polypeptide 1, skeletal muscle, adult	**Myh1**	822	12194	**14.8**	1734	1816	1.0
actinin alpha 3	**Actn3**	589	8734	**14.8**	1787	1624	0.91
ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	Atp2a1	861	11786	**13.7**	1969	1718	0.87
myosin binding protein H	**Mybph**	111	1500	**13.5**	158	133	0.84
PDZ and LIM domain 5	**Pdlim5**	384	5112	**13.3**	819	640	0.78
calsequestrin 1	**Casq1**	374	4979	**13.3**	919	648	0.71
troponin T3, skeletal, fast	**Tnnt3**	1554	16137	**10.4**	4393	3925	0.89
myosin, light polypeptide kinase 2, skeletal muscle	**Mylk2**	87	893	**10.2**	119	92	0.77
myosin, heavy polypeptide 4, skeletal muscle	**Myh4**	2018	19402	**9.6**	6339	5177	0.82
troponin I, skeletal, fast 2	**Tnni2**	2197	18307	**8.3**	6095	4698	0.77
troponin T1, skeletal, slow	**Tnnt1**	49	395	**8.0**	55	34	0.63
actin, alpha, cardiac muscle 1	**Actc1**	463	2291	**5.0**	707	643	0.91
creatine kinase, muscle	**Ckm**	2080	14207	**6.8**	5540	5226	0.94
myosin, light polypeptide 1	Myl1	3185	15349	**4.8**	7526	6061	0.81
myosin light chain, phosphorylatable, fast skeletal muscle	**Mylpf**	2783	17675	**6.4**	7623	6172	0.81
actin, alpha 1, skeletal muscle	**Acta1**	5136	18951	**3.7**	10566	10658	1.0
troponin C2, fast	**Tnnc2**	4306	14733	**3.4**	9804	8161	0.83
X-linked myotubular myopathy gene 1	Mtm1	297	1411	**4.8**	1907	686	0.36
PDZ and LIM domain 3	Pdlim3	1027	3723	**3.6**	1491	719	0.48
SAM domain, SH3 domain and nuclear localization signals, 1	Samsn1	341	72	**0.21**	192	314	1.6
Proliferation							
ribosomal protein L3-like	**Rpl3l**	80	2016	**25.4**	260	194	0.75
myeloid leukemia factor 1	Mlf1	188	3446	**18.3**	595	473	0.80
R-spondin homolog (Xenopus laevis)	**Rspo1**	222	2610	**11.7**	3838	226	0.06
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phosphodiesterase 4D interacting protein (myomegalin)	**Pde4dip**	778	4056	**5.2**	963	795	0.83
profilin 2	**Pfn2**	717	2661	**3.7**	1315	779	0.59
sel-1 suppressor of lin-12-like 3 (C. elegans)	Sel1l3	107	396	**3.7**	131	142	1.1
transforming growth factor, beta 2	Tgfb2	176	547	**3.1**	417	356	0.85
Protein Folding							
ankyrin repeat and SOCS box-containing 11	Asb11	55	1169	**21.2**	156	106	0.68
ankyrin repeat and SOCs box-containing 5	Asb5	128	2557	**19.9**	457	278	0.61
ankyrin repeat and SOCS box-containing 12	**Asb12**	17	325	**19.1**	47	35	0.75
Transport							
aquaporin 4	**Aqp4**	42	910	**21.9**	92	73	0.80
ATPase, H+ transporting, lysosomal V1 subunit C2	**Atp6v1c2**	164	1228	**7.5**	2984	2392	0.80
ATP-binding cassette, sub-family B (MDR/TAP), member 4	Abcb4	84	497	**5.9**	116	94	0.81
Transcription							
paired-like homeodomain transcription factor 2	**Pitx2**	12	332	**27.4**	32	21	0.66
ISL1 transcription factor, LIM/homeodomain	**Isl1**	15	346	**23.7**	40	21	0.53
ets homologous factor	**Ehf**	656	2216	**3.4**	2576	1686	0.65
putative homeodomain transcription factor 2	Phtf2	481	1467	**3.0**	504	511	1.0
LIM homeobox protein 8	**Lhx8**	136	409	**3.0**	165	161	1.0
Spi-B transcription factor (Spi-1/PU.1 related)	**Spib**	934	27	**0.03**	525	780	1.5
Unknown							
submaxillary gland androgen regulated protein 2	Smr2	133	2011	**15.1**	314	282	0.90