

SUPPLEMENTARY FIGURE LEGENDS

Supplementary figure S1. Regulation of fatty acid oxidation by PML and predisposition to obesity in *Pml*-KO mice.

(A) Fatty acid oxidation levels in *Pml*-WT and KO transformed (Ras-E1A) MEFs. *, p<0.05; error bars indicate S.D. from triplicates.

(B-C) food intake (B) and activity (C) in *Pml*-WT and KO male mice subjected to a control (LF) or high fat (HF) diet.

(D) Pml immunoreactivity in *Lep*^{Ob/+} (left panels) and *Lep*^{Ob/Ob} liver sections at 3 months of age. Asterisk depicts PML immunoreactivity in macrophages, arrows indicate PML immunoreactivity in hepatocytes.

(E) Representative picture (2 months old animals) of *Pml*-*Lep*^{Ob/Ob} double mutant female mice (Left, *Pml*^{WT}-*Lep*^{Ob/Ob}; right, *Pml*^{KO}-*Lep*^{Ob/Ob}).

(F-J) Body weight (F), Fat mass (G, H) and lean mass (I, J) in *Pml*^{wt} and *Pml*^{ko} *Lep*^{Ob/Ob} mice of the indicated sex and age.

Supplementary figure S2. *Pml* regulates PGC1A and PPAR signaling.

(A) Gene validation from the differentially expressed genes in *Pml*-WT and KO liver extract microarray by real-time PCR (N=7-8) using *36b4/Rplp0* as endogenous control. Error bars represent S.E. p-value indicates statistical significance by two-tailed T-test.

(B) Real-time PCR analysis of *Pdk4* in primary MEFs treated with palmitate and carnitine (P+C; 100μM and 1mM, respectively, N=4) using *Glucuronidase B* as endogenous control. Error bars represent S.D. p-value indicates statistical significance by T-test.

(C) PML over-expression in HEK293 cells shown in Fig. 3B.

(D) Immunofluorescence and confocal imaging of HA-PGC1A and endogenous PML in U2OS cells, in the absence (left) or presence (right) of exogenous Flag-GCN5.

(E) Immunofluorescence and confocal imaging of HA-PGC1A and PML in U2OS cells, arrows indicate areas of co-localization (DAPI staining is shown in blue).

- (F)** Immunofluorescence and confocal imaging of HA-PGC1A, Flag-GCN5 and EGFP-PML in U2OS cells.
- (G)** Co-immunoprecipitation of Flag-PML with HA-PGC1A and GCN5.
- (H)** Western Blot for detection of PGC1A acetylation in PGC1A imunoprecipitates from U2OS cells transfected with empty or PML-expressing vectors and treated with Vehicle or the SIRT1 inhibitor EX527 (10 μ M, 3h).
- (I)** Immunofluorescence and confocal imaging of HA-PGC1A, Flag-SIRT1 and EGFP-PML in U2OS cells, which also express non-tagged GCN5.

Supplementary figure S3. Effect of PML and PPARA on survival upon loss of attachment.

- (A-B)** Cell survival measured by alamar Blue (**A**) and Cell Titer Glo (Promega) (**B**) at the indicated time points in detached MCF10A cells from (**Fig. 4A**).
- (C)** Western blot analysis of PML and HSP90 in MDA-MB-231 and MCF7 breast cancer cells.
- (D)** Cell survival upon 60h detachment in cells from (**C**) treated with vehicle or GW6471 (10 μ M). *p indicates statistical significance (student T test) compared to vehicle-treated cells; #p indicates statistical significance (student T test) compared to GW6471-treated MCF7 cells.
- (E)** Effect of Etomoxir on luminal filling in pBABE-infected MCF10A cells (following the experimental design outlined in **Fig. 5D**; representative images are shown).

Supplementary figure S4. Status of PML in breast cancer specimens.

- (A)** Representative micrographs of PML immunoreactivity in normal breast epithelium, scored as absent (PML 0) or low (PML 1+)
- (B)** Representative pictures of the scoring criteria used in human breast cancer samples. Asterisks depict PML immunoreactive epithelial cells.
- (C)** Correlation analysis between PML mRNA levels and tumor or stromal cell immunoreactivity in breast cancer biopsies (N=88).

Supplementary figure S5. PML expression is elevated in basal breast cancer biopsies. Expression of PML by means of 4 different probes in two independent studies. P value indicates the statistical value of the difference in basal cancers vs. rest of the tumors.

Supplementary figure S6. PML expression is elevated in tumors with mutated *Tp53*.

- (A) Correlation of p53 up-regulation and PML expression in the samples analyzed. p-value reflects chi-square statistical significance in the correlation analysis.
- (B) Heatmap (upper panel) and boxplots (lower panels) depicting PML levels in *p53* WT and mutant (Mu) cancer dataset (Miller et al., 2005). Upper legends in boxplots indicate probe ID (left) and statistical significance (p-value, right).
- (C) Time to recurrence in breast cancer patients from Figures 6-7, excluding those harboring TNBC/basal cancers.

Supplementary figure S7. Association between PML expression and PPAR signaling in breast cancer.

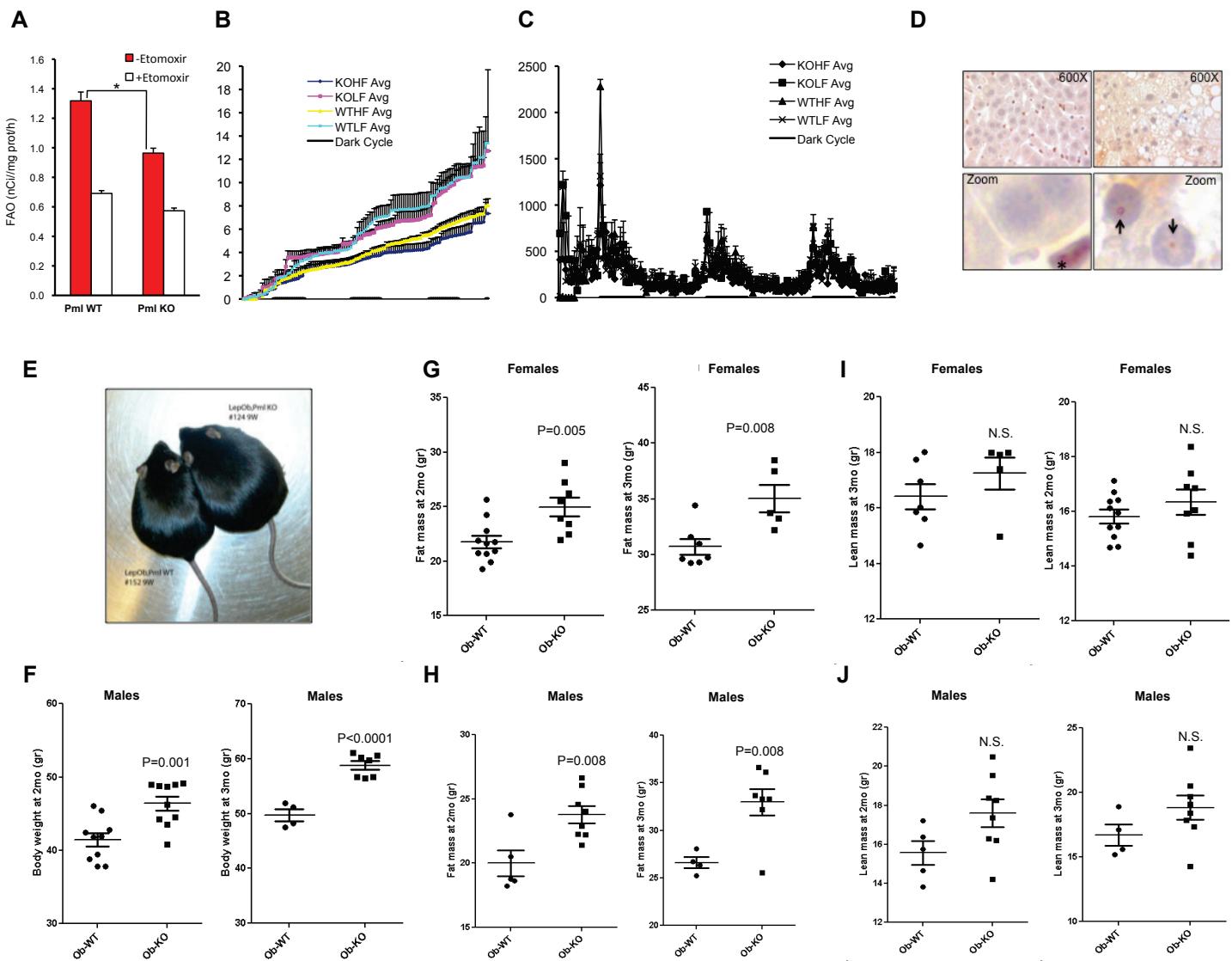
- (A) Heatmap depicting the status of 84 genes down-regulated in *Ppara*-KO mice liver microarray in breast cancers expressing different levels of PML (from Fig. 7C).
- (B) Validation of genes from (A) by Real-Time quantitative PCR (β -ACTIN was used as housekeeping gene, similar results were obtained with GAPDH). p-value was obtained by two-tailed T test.
- (C) GSEA showing significant enrichment of activated PPAR gene signature in PML high (3+) expressing tumors when compared to PML non-expressing tumors (0; upper panel) or the rest of the tumors (0, 1+, 2+; lower panel). The enrichment is represented by Nominal p-value and normalized enrichment score (NES).

Supplementary table 1. Differentially expressed genes in *Pml*-WT and KO liver tissue microarray.

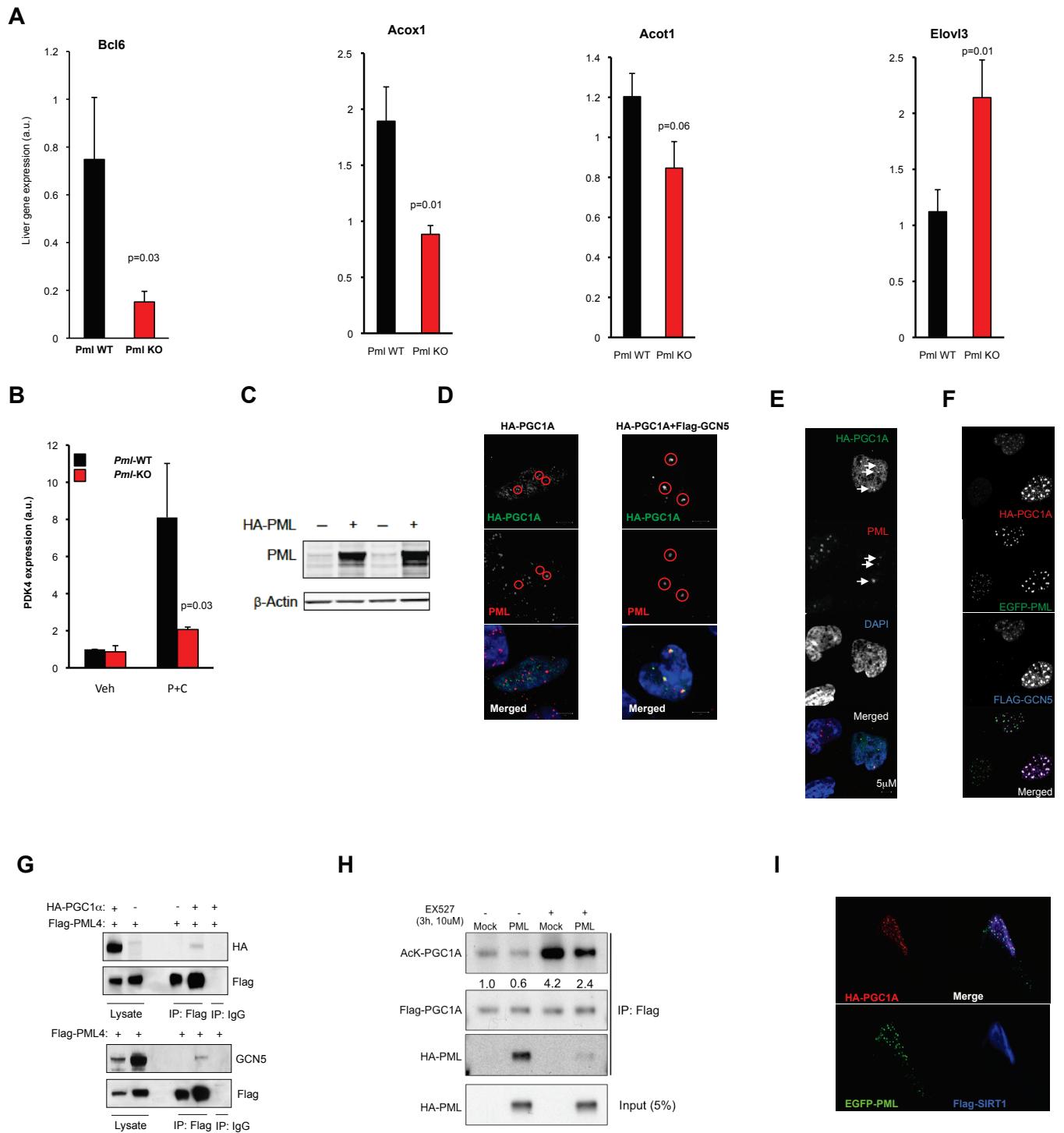
Supplementary table 2. Promoter analysis in lipid metabolism-related genes differentially expressed between *Pml*-WT and KO.

Supplementary table 3. Molecular - histological features and microarray accession numbers of breast cancer biopsies analyzed for this study.

Supplementary Figure S1

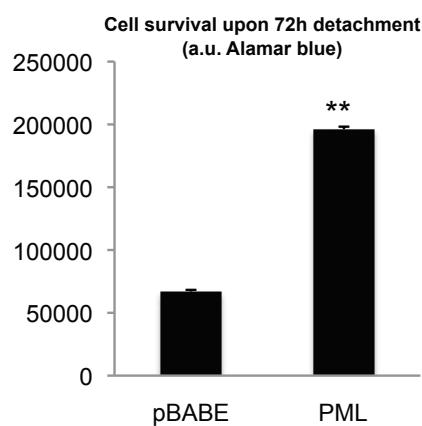


Supplementary Figure S2

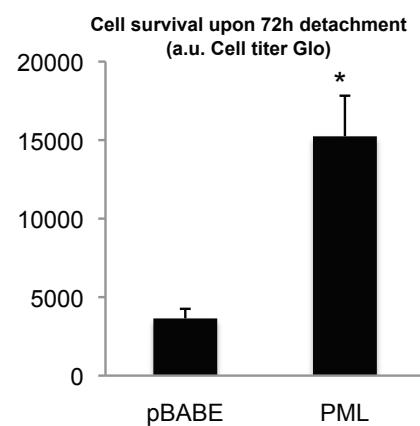


Supplementary Figure S3

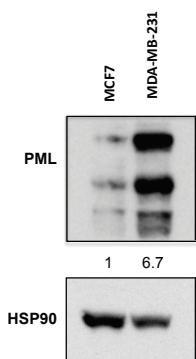
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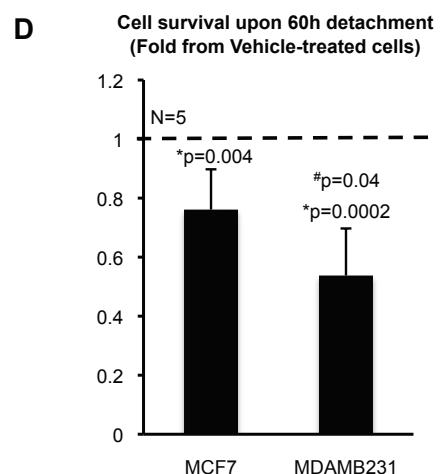
B



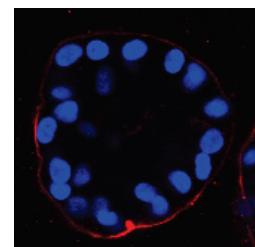
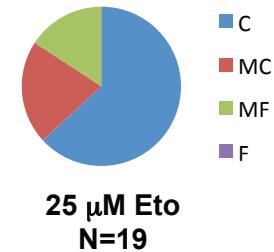
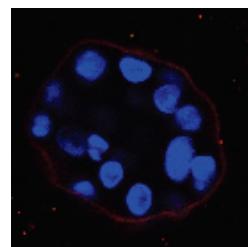
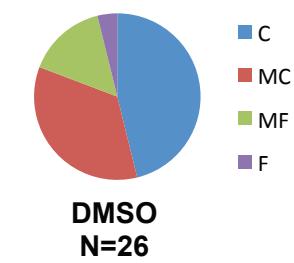
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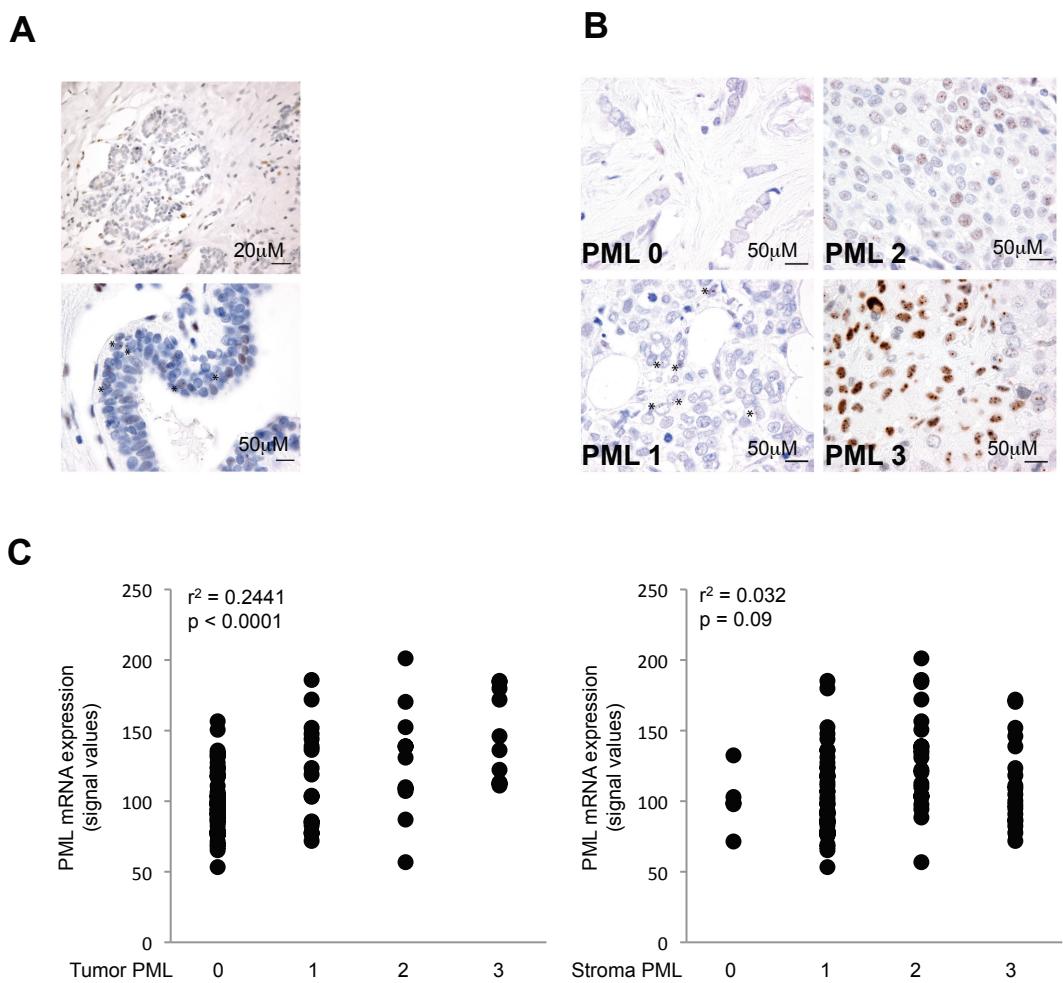
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E

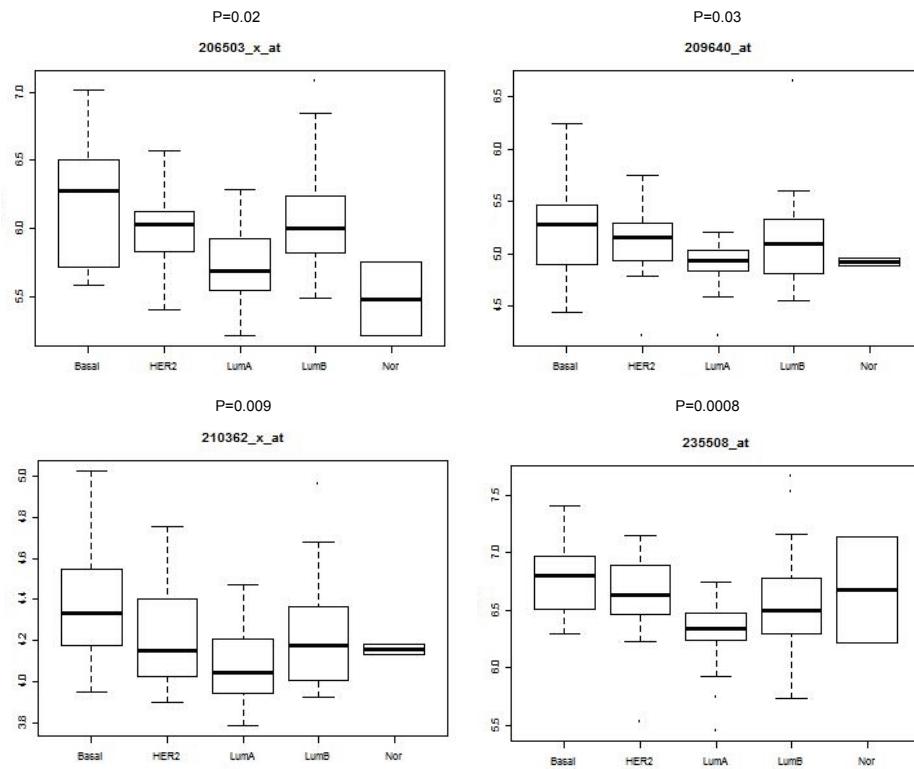


Supplementary Figure S4

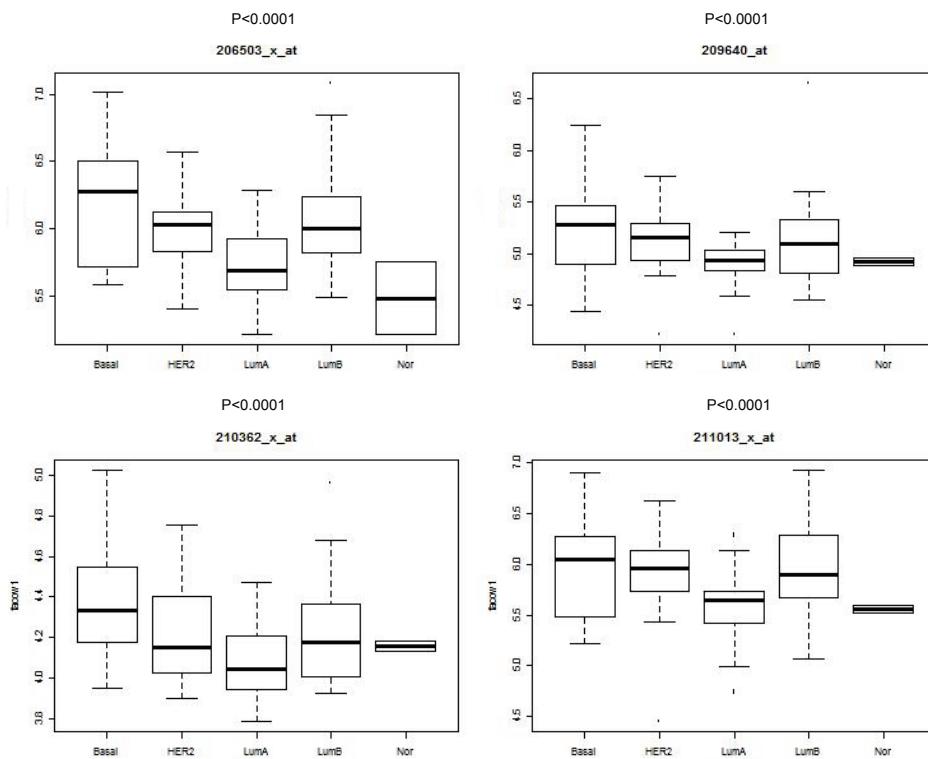


Supplementary Figure S5

From: Dedeurwaerder S, Desmedt C, Calonne E, Singhal SK et al. DNA methylation profiling reveals a predominant immune component in breast cancers. *EMBO Mol Med* 2011 Dec;3(12):726-41. PMID: 21910250

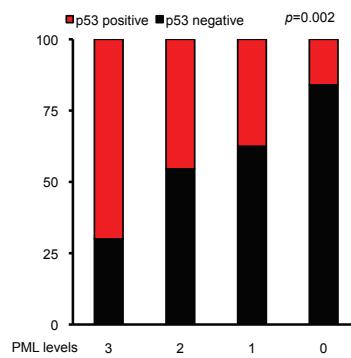


From: Sabatier R, Finetti P, Cervera N, Lambaudie E et al. A gene expression signature identifies two prognostic subgroups of basal breast cancer. *Breast Cancer Res Treat* 2011 Apr;126(2):407-20. PMID: [20490655](#)

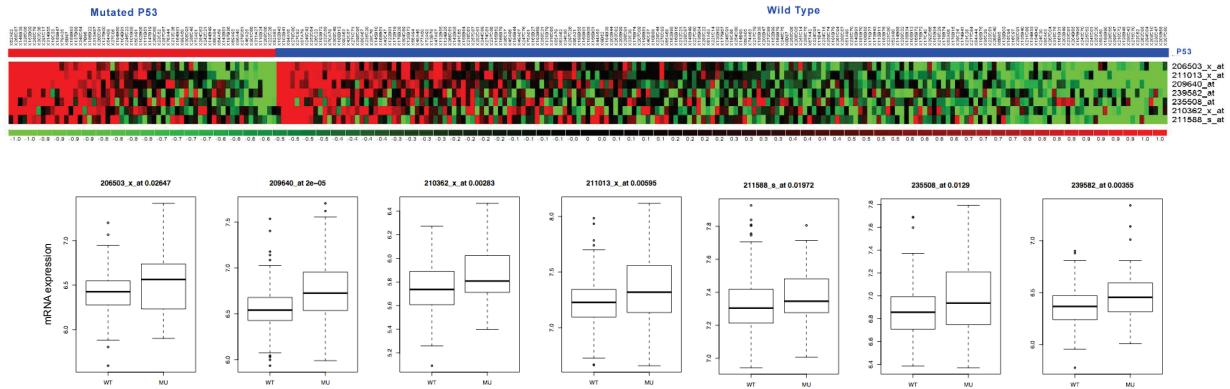


Supplementary Figure S6

A

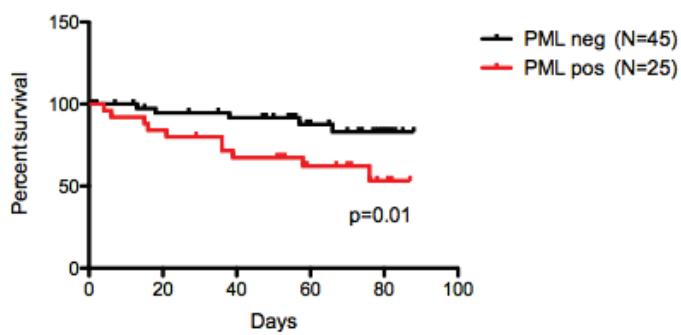


B



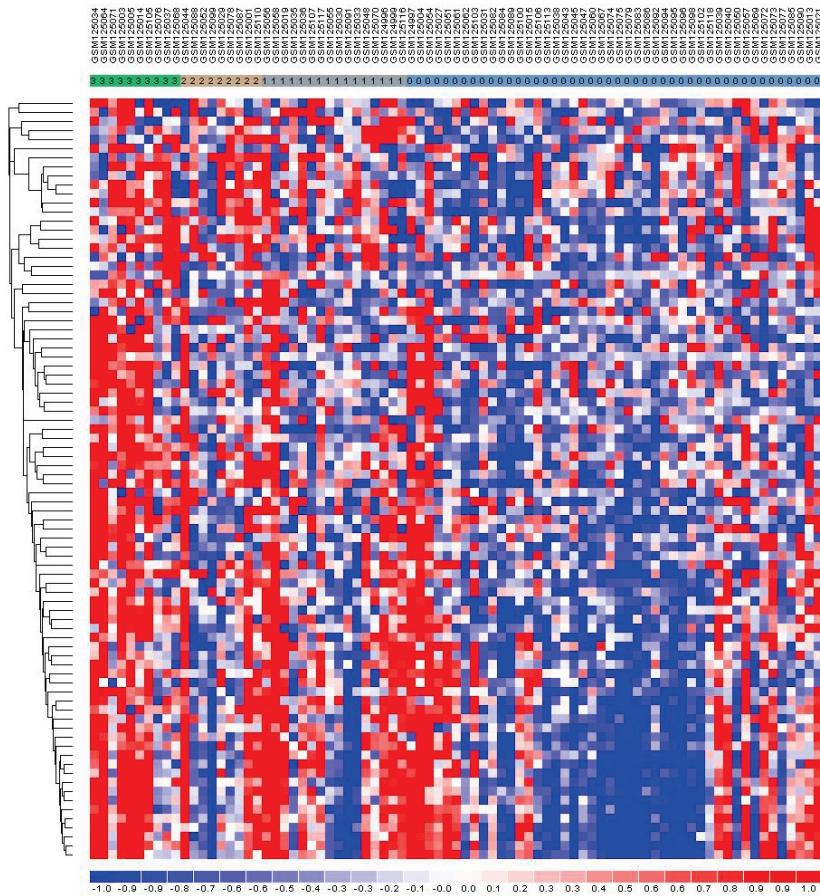
C

Recurrence (excluding TNBC)

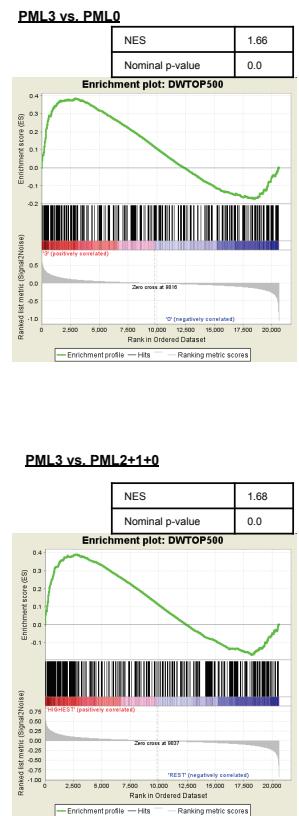


Supplementary Figure S7

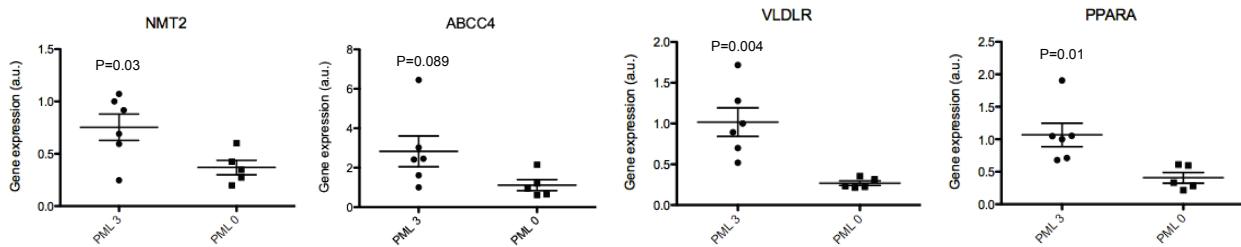
A



C



B



Supplementary Table 1

Probe	Unigene	Gene symbol	Parametric p-value	FDR	Permutation p-value	Geom mean of intensities in class 1-KO	Geom mean of intensities in class 2-WT	Fold-change
1421818 PM at	Mm.347398	Bcl6	0.020	0.208	0.2	73.3	278.2	0.26
1428942 PM at	Mm.147226	Mt2	0.043	0.292	0.3	73.2	268.7	0.27
1422557 PM s at	Mm.192991	Mt1	0.023	0.216	0.2	447.8	1499.2	0.30
1429203 PM at	Mm.205196	2410076I21Rik	0.000	0.013	0.1	14.0	42.2	0.33
1450381 PM a at	Mm.347398	Bcl6	0.010	0.135	0.2	30.8	88.9	0.35
1443147 PM at	Mm.442717	---	0.008	0.132	0.1	20.3	58.6	0.35
1448757 PM at	Mm.392123	Pml	0.000	0.002	0.1	12.4	35.0	0.35
1422925 PM s at	Mm.202331	Acot3	0.007	0.125	0.1	55.2	152.6	0.36
1443422 PM at	Mm.458646	2410089E03Rik	0.000	0.029	0.1	27.9	73.0	0.38
1436736 PM x at	Mm.407415	D0H4S114	0.013	0.164	0.1	97.2	230.7	0.42
1448700 PM at	Mm.439721	G0s2	0.009	0.133	0.1	367.1	857.1	0.43
1460591 PM at	Mm.463262	Esr1	0.000	0.006	0.1	155.1	358.7	0.43
1456156 PM at	Mm.259282	Lepr	0.000	0.014	0.1	19.1	43.0	0.44
AFFX-r2-Bs-phe-5 at	---	---	0.028	0.244	0.2	22.2	49.0	0.45
1425644 PM at	Mm.259282	Lepr	0.001	0.043	0.1	12.0	26.0	0.46
1441115 PM at	---	D18Ert232e	0.036	0.272	0.2	23.9	51.5	0.46
1435465 PM at	Mm.46675	Kbtbd11	0.021	0.208	0.1	18.4	39.3	0.47
1449065 PM at	Mm.1978	Acot1 /// LOC100044830	0.005	0.115	0.1	87.4	186.5	0.47
1444518 PM at	Mm.356689	Acox1	0.001	0.043	0.1	98.4	197.6	0.50
1422685 PM at	Mm.265512	Exoc4	0.000	0.013	0.1	33.1	66.4	0.50
1431213 PM a at	---	LOC433762	0.023	0.216	0.3	29.7	59.3	0.50
1448556 PM at	Mm.10516	Prlr	0.006	0.119	0.1	36.3	71.3	0.51
1450839 PM at	Mm.407415	D0H4S114	0.017	0.201	0.2	180.2	353.8	0.51
1438658 PM a at	Mm.136736	S1pr3	0.003	0.074	0.1	11.5	22.4	0.52
1440230 PM at	Mm.25317	Tsku	0.002	0.056	0.1	44.3	85.6	0.52
1437953 PM at	Mm.211211	Prei4	0.011	0.149	0.1	39.5	76.3	0.52
1422997 PM s at	Mm.1978	Acot1 /// Acot2 /// LOC100044830	0.002	0.056	0.1	97.7	187.8	0.52
1452951 PM at	Mm.458646	2410089E03Rik /// LOC100039599	0.000	0.021	0.1	31.6	60.4	0.52
1441547 PM at	---	---	0.020	0.208	0.2	37.2	71.2	0.52
AFFX-r2-Bs-lys-3 at	---	---	0.025	0.226	0.2	20.1	38.5	0.52
1438294 PM at	Mm.476983	Atxn1	0.020	0.208	0.2	82.7	156.5	0.53
AFFX-PheX-5 at	---	---	0.045	0.293	0.2	24.2	45.3	0.53
1437874 PM s at	Mm.27816	Hexb	0.040	0.284	0.2	99.5	185.3	0.54
AFFX-r2-Bs-lys-M at	---	---	0.009	0.132	0.1	44.1	81.9	0.54
1443471 PM at	Mm.440824	Zbtb20	0.005	0.115	0.1	110.9	205.5	0.54
AFFX-r2-Bs-thr-3 s at	---	---	0.048	0.302	0.2	132.8	246.1	0.54
1443866 PM at	Mm.95780	Lutm1	0.000	0.003	0.1	11.8	21.9	0.54
1456310 PM a at	Mm.10374	2610002J02Rik	0.004	0.102	0.1	19.5	35.6	0.55
1426259 PM at	Mm.255044	Pank3	0.003	0.074	0.1	61.0	111.2	0.55
1455267 PM at	Mm.89989	Esrrg	0.033	0.262	0.1	11.5	20.7	0.56
1451190 PM a at	Mm.29660	Sbk1	0.004	0.098	0.1	203.2	361.2	0.56
1460318 PM at	Mm.17235	Csrp3	0.001	0.043	0.1	90.3	159.4	0.57
1434473 PM at	Mm.25773	Slc16a5	0.004	0.096	0.1	33.5	58.9	0.57
1436120 PM at	Mm.217269	Setdb2	0.043	0.292	0.3	105.4	184.4	0.57
1417904 PM at	Mm.2805	Dclre1a	0.000	0.013	0.1	168.9	294.1	0.57
1419749 PM at	Mm.6979	Trdmt1	0.007	0.125	0.1	16.2	28.2	0.58
1446068 PM at	Mm.188734	Adk	0.020	0.208	0.2	66.3	113.0	0.59
1460180 PM at	Mm.27816	Hexb	0.002	0.068	0.1	57.3	97.5	0.59
1460555 PM at	Mm.217319	Fam65b	0.015	0.182	0.2	18.3	31.1	0.59
1455700 PM at	Mm.255401	Mterfd3	0.001	0.031	0.1	26.3	44.4	0.59
1439478 PM at	---	Acot2	0.014	0.169	0.2	46.2	77.9	0.59
1439293 PM at	Mm.208955	BC031353	0.007	0.125	0.1	148.4	248.4	0.60
1440038 PM at	---	B430007K19Rik	0.004	0.103	0.1	13.4	22.3	0.60
1425853 PM s at	Mm.10516	Prlr	0.002	0.069	0.1	182.7	303.0	0.60
1440284 PM at	Mm.31030	---	0.008	0.132	0.2	24.6	40.9	0.60
1452888 PM at	Mm.284114	1110034G24Rik	0.041	0.289	0.3	75.2	123.9	0.61
1422076 PM at	Mm.475660	Acot4	0.046	0.293	0.3	50.1	81.4	0.62
1447408 PM at	---	---	0.005	0.108	0.1	27.9	44.9	0.62
1437397 PM at	Mm.442298	Prlr	0.023	0.216	0.1	74.4	119.7	0.62
1445640 PM at	---	---	0.000	0.013	0.1	13.3	21.4	0.62
1429383 PM at	Mm.368668	Csnk1q3	0.019	0.208	0.1	80.3	127.4	0.63

1457770	PM at	Mm.270647	Slc39a14	0.030	0.252	0.2	20.0	31.7	0.63
1429656	PM at	Mm.26659	Rhobtb1	0.046	0.293	0.2	100.2	156.9	0.64
1439331	PM at	---	4932439E07Rik	0.024	0.221	0.2	43.6	67.2	0.65
1422230	PM s at	Mm.389848	Cyp2a4 /// Cyp2a5 /// LOC100047711	0.035	0.272	0.2	2936.7	4523.8	0.65
1454799	PM at	Mm.271911	Agpat9	0.003	0.074	0.1	121.7	187.0	0.65
1437066	PM at	Mm.136238	Zbtb20	0.001	0.043	0.1	154.7	237.8	0.65
1460011	PM at	Mm.255246	Cyp2b6	0.046	0.295	0.1	19.9	30.3	0.66
1417769	PM at	Mm.18472	Psmc6	0.003	0.074	0.1	42.9	64.3	0.67
1436221	PM at	Mm.101743	Ildr2	0.031	0.254	0.2	69.9	104.7	0.67
1421382	PM at	---	Prlr	0.040	0.284	0.3	241.6	361.2	0.67
1426452	PM a at	Mm.389966	Rab30	0.044	0.293	0.1	54.2	80.3	0.68
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1455905	PM at	Mm.237103	2610507B11Rik	0.011	0.149	0.1	47.7	69.4	0.69
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1435092	PM at	Mm.12723	Arl4a	0.030	0.252	0.1	50.2	72.0	0.70
1448502	PM at	Mm.29161	Slc16a7	0.021	0.208	0.2	240.5	344.9	0.70
1441413	PM at	---	---	0.025	0.226	0.2	278.2	398.0	0.70
1447839	PM x at	Mm.1408	Adm	0.048	0.302	0.2	19.1	27.0	0.71
1439397	PM at	Mm.4938	Fmn1	0.039	0.284	0.3	8.0	11.2	0.71
1449025	PM at	Mm.426079	Ifit3	0.001	0.043	0.1	52.2	72.7	0.72
1418129	PM at	Mm.133370	Dhcr24	0.037	0.279	0.3	503.8	697.8	0.72
1425312	PM s at	Mm.229207	Cpsf4l	0.006	0.115	0.1	68.6	93.1	0.74
1458279	PM at	Mm.450309	---	0.036	0.272	0.2	20.9	28.1	0.75
1430996	PM at	Mm.272548	Etnk1	0.040	0.284	0.2	17.8	23.8	0.75
1444396	PM at	Mm.293605	Trp53inp2	0.039	0.284	0.2	44.7	57.4	0.78
1422823	PM at	Mm.235346	Eps8 /// LOC632638	0.029	0.244	0.1	12.7	15.7	0.80
1416936	PM at	Mm.6826	Aatk	0.040	0.284	0.2	15.1	18.8	0.80
1428547	PM at	Mm.244235	Nt5e	0.028	0.244	0.1	22.4	27.2	0.83
1438941	PM x at	Mm.274335	Ampd2	0.038	0.283	0.2	164.7	128.0	1.29
1455940	PM x at	Mm.335454	Wdr6	0.010	0.135	0.1	220.3	165.0	1.33
1452769	PM at	Mm.156771	Rnf145	0.009	0.132	0.1	409.2	299.6	1.37
1452975	PM at	Mm.29125	Agxt2l1	0.020	0.208	0.1	1816.1	1326.4	1.37
1444296	PM a at	Mm.297023	Serpina4-ps1	0.009	0.133	0.1	809.0	577.4	1.40
1416256	PM a at	Mm.273538	Tubb5	0.031	0.252	0.2	493.4	350.5	1.41
1451903	PM at	Mm.105278	Kynu	0.042	0.290	0.2	31.5	22.3	1.41
1448092	PM x at	Mm.297023	Serpina4-ps1	0.009	0.132	0.1	1120.6	785.1	1.43
1438619	PM x at	Mm.399660	Zdhhc14	0.022	0.212	0.2	110.4	76.3	1.45
1451803	PM a at	Mm.15607	Vegfb	0.000	0.029	0.1	66.9	46.0	1.45
1448261	PM at	Mm.35605	Cdh1	0.033	0.262	0.1	209.4	143.7	1.46
1458356	PM at	Mm.396244	---	0.046	0.293	0.2	53.2	36.1	1.47
1415904	PM at	Mm.1514	Lpl	0.025	0.226	0.2	147.7	99.3	1.49
1437094	PM x at	Mm.79127	Dnaic1	0.013	0.163	0.1	32.7	21.9	1.49
1418209	PM a at	Mm.271744	Pfn2	0.019	0.208	0.2	72.2	47.9	1.51
1416066	PM at	Mm.210676	Cdg	0.032	0.260	0.2	238.9	158.7	1.51
1449385	PM at	Mm.26719	Hsd17b6	0.000	0.029	0.1	3484.3	2288.2	1.52
1418492	PM at	Mm.25760	Grem2	0.006	0.119	0.1	188.7	119.2	1.58
1445108	PM at	---	---	0.014	0.169	0.2	19.3	12.1	1.60
1435216	PM a at	Mm.330116	Odf2	0.006	0.119	0.1	32.6	20.0	1.63
1432075	PM a at	Mm.42257	Tekt1	0.020	0.208	0.2	28.4	17.3	1.64
1437140	PM at	Mm.440423	4930412F15Rik	0.024	0.221	0.2	49.6	29.7	1.67
1422947	PM at	Mm.144300	---	0.026	0.226	0.2	20.1	11.6	1.73
1427347	PM s at	Mm.469917	Tubb2a	0.002	0.056	0.1	188.7	109.1	1.73
1422735	PM at	Mm.44235	Foxq1	0.031	0.252	0.2	62.8	36.3	1.73
1437754	PM at	Mm.332837	Kpn47	0.012	0.159	0.2	15.7	8.4	1.88
1420722	PM at	Mm.21806	Elov13	0.007	0.125	0.1	1092.4	580.0	1.88
1418210	PM at	Mm.271744	Pfn2	0.000	0.026	0.1	54.2	27.7	1.95
1444297	PM at	Mm.297023	Serpina4-ps1	0.001	0.043	0.1	467.9	239.4	1.95
1428294	PM at	Mm.17519	Zfp259	0.009	0.132	0.1	123.4	63.0	1.96
1423600	PM a at	Mm.2215	Tcof1	0.044	0.293	0.3	54.8	27.8	1.97
1445633	PM at	---	---	0.038	0.283	0.3	62.7	28.1	2.23
1457282	PM x at	Mm.284306	Tubgcp5	0.006	0.115	0.2	67.8	29.9	2.27
1448724	PM at	Mm.4592	Cish	0.010	0.135	0.1	126.2	52.7	2.39
1427820	PM at	Mm.466733	---	0.002	0.056	0.1	215.3	71.0	3.03

Supplementary Table 2

Matrix name	Yes (sites/Kb)	No (sites/Kb)	Yes/No	P-value	Matched promoters p-value	From	To
V\$BACH2_01	0.1944	0	inf	7.11E-06	6.47E-06	-400	100
V\$NFAT_Q4_01	1.2442	0.4808	2.588	1.03E-05	0.002	-500	-200
V\$AP1_Q4_01	0.4277	0.0801	5.3377	6.76E-05	2.52E-05	-200	100
V\$ZIC3_01	0.972	0.4167	2.3329	3.52E-04	0.0119	-300	0
V\$LUN1_01	0.2333	0.024	9.7049	3.73E-04	3.28E-04	-500	-200
V\$AP1_Q2_01	0.1944	0.016	12.131	6.49E-04	6.06E-04	-400	100
V\$IPF1_Q4_01	0.5055	0.1683	3.0039	0.0014	0.0802	-500	-100
V\$DBP_Q6	0.7776	0.3365	2.3107	0.0014	4.80E-04	-400	-100
V\$CRX_Q4	0.3111	0.0681	4.567	0.0015	0.0045	-500	-200
V\$FXR_Q3	0.3111	0.0681	4.567	0.0015	0.0076	-500	-200
V\$MAZ_Q6	0.5443	0.1923	2.8306	0.0015	0.0112	-300	0
V\$BCL6_Q3	0.972	0.4688	2.0737	0.0015	0.0048	-300	0
V\$CKROX_Q2	0.4666	0.1482	3.1475	0.0015	0.0199	-200	100
V\$EBF_Q6	0.8554	0.3966	2.1566	0.0018	0.0192	-400	-100
V\$SREBP_Q6	1.3997	0.7973	1.7557	0.0023	0.0575	-300	0
V\$HNF4ALPHA_Q6	1.0109	0.5208	1.941	0.0027	0.0157	-500	-200
V\$NKX25_Q5	1.4386	0.8373	1.7181	0.0027	3.42E-04	-500	-200
V\$CEBP_Q2_01	1.0887	0.5809	1.874	0.003	0.0167	-500	-100
V\$TAXCREB_01	0.5832	0.2364	2.4673	0.0032	0.0015	-300	0
V\$E2F_Q6_01	0.1944	0.028	6.9321	0.0032	0.0031	-500	100
V\$HMGIY_Q6	0.6999	0.3125	2.2396	0.0032	8.81E-04	-500	-200
V\$SREBP_Q3	2.1385	1.4022	1.5251	0.0034	0.0506	-300	0
V\$NFY_Q6_01	0.4277	0.1482	2.8852	0.0041	0.0041	-200	100
V\$CEBPDELTA_Q6	0.3111	0.0841	3.6971	0.0041	0.0034	-500	0
V\$STAT1_01	0.2333	0.0481	4.8524	0.0046	0.0147	-500	-100
V\$SMAD3_Q6	1.2831	0.7492	1.7126	0.0046	0.0988	-300	0
V\$PAX5_Q2	0.1944	0.0321	6.0656	0.0048	0.0205	-400	-100
V\$ETF_Q6	3.8882	2.9087	1.3368	0.0049	0.2762	-400	0
V\$AP2_Q6	0.2722	0.0681	3.9961	0.0051	0.0098	-400	100
V\$DR4_Q2	0.3888	0.1322	2.9409	0.0054	0.1418	-200	100
V\$TCF11_01	0.8943	0.4728	1.8916	0.006	0.0073	-200	100
V\$AP2ALPHA_01	0.2333	0.0521	4.4792	0.0062	0.0358	-200	100
V\$HNF3_Q6_01	0.2333	0.0521	4.4792	0.0062	0.0455	-400	0
V\$HNF3B_01	0.6221	0.2845	2.187	0.0064	0.0135	-200	100
V\$PPARA_01	0.2722	0.0721	3.7741	0.0066	0.0126	-200	100
V\$ZF5_B	0.2722	0.0721	3.7741	0.0066	0.0404	-200	100
V\$NFY_01	0.661	0.3125	2.1152	0.0067	0.0032	-200	100
V\$MAF_Q6_01	0.1944	0.0361	5.3916	0.0069	0.0067	-400	-100
V\$E2F_03	0.1944	0.0361	5.3916	0.0069	0.0275	-400	100
V\$AP2_Q6_01	0.1944	0.0361	5.3916	0.0069	0.0046	-500	-200
V\$NF1_Q6_01	0.1944	0.0361	5.3916	0.0069	0.0275	-300	100
V\$DR1_Q3	0.3111	0.0962	3.235	0.0079	0.017	-400	0
V\$CEBPA_01	0.2333	0.0561	4.1592	0.0081	0.0057	-400	-100

Supplementary Table 3

Sample name	GEO accession fd	TNM Stage	Stage group	Time of followup	Event	Type of recurrence	p53 IHC	Array profile subtype	Tumor grade	ER IHC	PR IHC	HER2 IHC	PML IHC	PML mRNA (array a.u.)
B1	GSM125026	T2 N0	IIA	80	0	None	n	ER LG	I	p	p	n		117.16
B10	GSM125033	T2 N0	IIA	82	0	None	n	HER	II	p	p	p	1	185.89
B11	GSM125034	T1c N0	I	75	0	None	p	TN	III	n	n	p	3	179.9
B12	GSM125035	T2 N2a	IIIA	36	1	Local	n	ER HG	II	p	p	n	1	118.88
B13	GSM125036	T2 N0	IIA	52	0	None	n	ER HG	III	p	n	p	1	85.68
B14	GSM125037	T2 N0	IIA	81	0	None	p	HER	II	n	n	p	3	112.48
B15	GSM125038	T2 N0	IIA	59	0	None	n	ER LG	II	p	p	n	0	98.13
B16	GSM125039	T1c N1a	IIA	1	0	None	n	HER	III	p	p	p	0	124.05
B17	GSM125040	T1c N3	IIIC	83	0	None	n	HER	II	p	p	p	0	91.21
B18	GSM125041	T1c N2a	IIIA	85	0	None	u	ER LG	II	p	n	n		125.1
B19	GSM125042	T2 N2a	IIIA	11	0	None	n	ER HG	II	p	p	n		119.46
B2	GSM125027	T1b N0	I	78	0	None	n	ER HG	III	p	p	p	0	85.09
B20	GSM125043	T1b N0	I	2	0	None	n	ER LG	I	p	p	n	0	110.88
B21	GSM125044	T2 N0	IIA	18	1	Distant	p	TN	III	n	n	n	2	56.79
B22	GSM125045	T2 N0	IIIA	70	0	None	n	ER LG	I	p	p	p	0	65.28
B23	GSM125046	T1c N2a	IIIA	83	0	None	n	ER HG	II	p	p	n		201.1
B24	GSM125047	T2 N2a	IIIA	74	0	None	n	ER LG	I	p	n	n	0	127.24
B25	GSM125048	T1c N0	I	87	0	None	p	HER	III	n	n	p	1	123.51
B26	GSM125049	T1c N0	I	86	0	None	n	ER HG	I	p	p	n		67.4
B28	GSM125050	T3 N2a	IIIA	1	0	None	n	HER	II	p	p	n	0	106.58
B29		T2 N1mi	IIB	58	1	Local	n	ER LG	I	p	p	n	2	138.64
B3	GSM125028	T1c N0	I	78	0	None	n	ER LG	I	p	p	n		77.91
B30	GSM125051	T2 N2a	IIIA	80	0	None	n	ER HG	III	p	p	n	0	134.05
B31	GSM125052	T1b N0	I	78	0	None	n	ER LG	II	p	p	n	2	107.23
B33	GSM125054	T1c N0	I	56	0	None	n	TN/BRCA1	III	n	n	n	0	86.17
B34	GSM125055	T2 N1a	IIB	70	0	None	n	ER LG	I	p	p	n	1	82.82
B35	GSM125056	T2 N1a	IIB	83	0	None	n	TN	III	n	n	n	1	138.8
B36		T2 N1mi	IIB	16	0	None	n	ER LG	I	p	p	n		99.05
B37	GSM125057	T4 N1a	IIIB	14	1	Distant	n	HER	III	n	n	n	0	87.28
B38	GSM125058	T2 N0	IIA	75	0	None	p	TN	III	n	n	n	1	144.07
B39	GSM125059	T2 N0	IIA	77	0	None	n	ER LG	II	p	n	n		110.7
B4	GSM125029	T1c N1a	IIA	51	0	None	n	HER	III	p	p	p	2	109.89
B40	GSM125060	T1c N0	I	15	0	None	n	ER LG	I	p	p	n	0	150.61
B41	GSM125061	T1c N3	IIIC	73	0	None	n	ER HG	III	p	p	n	0	99
B43	GSM125062	T2 N0	IIA	60	0	None	n	ER HG	II	p	p	n	0	78.38
B44	GSM125063	T1c N2a	IIIA	85	0	None	n	ER HG	III	p	p	n		122.46
B45	GSM125064	T1c N0	I	77	0	None	p	TN	III	n	n	n	3	146.1
B47	GSM125065	T2 N2a	IIIA	81	0	None	n	ER HG	II	p	p	n		79.26
B5	GSM125030	T2 N1a	IIB	6	1	Distant	n	ER LG	II	p	p	n	1	151.99
B50	GSM125103	T1c N2a	IIIA	0	0	None	n	ER HG	III	p	n	n	0	90.88
B51	GSM125066	T2 N1a	IIB	50	1	Distant	p	HER	III	n	n	p		141.34
B52	GSM125067	T1c N0	I	81	0	None	n	ER LG	I	p	p	n	0	120.54
B53	GSM125068	T1c N0	I	57	0	None	n	HER	III	n	n	n	3	184.34
B54	GSM125069	T1c N2a	IIIA	48	0	None	n	HER	II	p	p	p	0	135.88
B55	GSM125070	T2 N2a	IIIA	58	0	None	p	HER	III	n	n	p	1	172.01
B57	GSM125071	T1c N0	I	21	1	Distant	p	TN	III	n	n	n	3	136.13
B61	GSM125072	T2 N1a	IIB	66	1	Distant	n	HER	II	p	p	p	0	77.99
B63	GSM125073	T2 N0	IIA	77	0	None	p	HER	III	n	n	p	0	103.53
B65	GSM125074	T1c N1a	IIA	82	0	None	n	ER LG	I	p	p	n	0	102.96
B66	GSM125075	T1c N0	I	35	0	None	n	ER LG	I	p	p	n	0	82.41
B67	GSM125076	T1c N0	I	71	0	None	n	ER HG	III	p	p	p	3	171.93
B68	GSM125077	T2 N2a	IIIA	38	1	Distant	n	HER	II	p	p	p	0	75.85
B7	GSM125031	T1b N0	I	85	0	None	n	ER HG	II	p	p	n	0	97.76
B70	GSM125078	T2 N3	IIIC	36	1	Distant	n	HER	II	p	p	p	2	170.37
B71	GSM125079	T1c N1a	IIA	55	0	None	n	ER LG	I	p	p	n	0	69.32
B72	GSM125080	T2 N1a	IIB	2	1	Distant	n	ER HG	III	p	p	n		125.99

B73	GSM125081	T2 N1a	IIB	76	0	None	p	ER LG	III	p	p	n			100.81
B74	GSM125082	T2 N1a	IIB	88	0	None	n	ER HG	III	p	p	n	0		71.44
B75	GSM125083	T1c N2a	IIIA	47	0	None	n	ER LG	I	p	p	n	0		97.6
B76	GSM125084	T1c N1a	IIA	83	0	None	n	ER HG	I	p	p	n	0		94.31
B77	GSM125085	T1c N0	I	54	0	None	p	HER	III	p	p	p	0		118.3
B78	GSM125086	T1c N0	I	79	0	None	n	ER LG	I	p	n	n	0		88.45
B79	GSM125087	T2 N2a	IIIA	15	1	Distant	p	HER	II	n	n	p	2		138.96
B88	GSM125032	T1b N0	I	73	0	None	n	ER LG	I	p	p	n			106.57
B80	GSM125088	T2 N2a	IIIA	76	1	Distant	p	ER HG	III	p	p	n	2		152.44
B81	GSM125089	T2 N1a	IIB	18	1	Distant	n	ER HG	III	p	p	n	0		104.79
B82		T1c N1mi	IIIA	12	0	None	n	ER LG	II	p	p	n	0		117.19
B84	GSM125090	T2 N3	IIIC	7	0	None	n	HER	III	p	p	p	0		117.58
B85	GSM125091	T1c N0	I	76	0	None	n	ER LG	II	p	p	n	1		103.87
B86	GSM125092	T1c N1a	IIA	81	0	None	n	ER LG	I	p	p	n	0		67.69
B88	GSM125093	T2 N0	IIIA	83	0	None	n	ER LG	I	p	p	n			97.78
B89	GSM125094	T1c N2a	IIIA	54	0	None	n	ER LG	I	p	p	n	0		76.17
B90	GSM125095	T1c N0	I	79	0	None	n	ER LG	I	p	p	n	0		90.33
B91	GSM125096	T1c N0	I	74	0	None	n	ER LG	I	p	p	n	0		79.07
B93	GSM125097	T1b N0	I	81	0	None	n	ER LG	I	p	n	n			78.82
B94	GSM125098	T1b N0	I	81	0	None	n	ER LG	I	p	p	n	0		97.87
B95	GSM125099	T2 N0	IIA	76	0	None	n	ER LG	II	p	p	n	2		108.96
B96	GSM125100	T1c N0	I	65	0	None	n	ER HG	II	p	p	n	0		92.15
B97	GSM125101	T1c N0	I	83	0	None	n	ER LG	I	p	p	n			119.98
B98	GSM125102	T1c N0	I	35	0	None	n	ER LG	II	p	p	n	0		103.06
C114	GSM124995	T1b N0	I	38	0	None	p	TN	III	n	n	n			103.42
C115	GSM124996	T2 N0	IIA	29	0	None	p	HER	III	n	n	p	1		71.84
C116	GSM124997	T2 N0	IIIA	60	0	None	p	TN	III	n	n	n	0		93.38
C118	GSM124998	T2 N1a	IIB	62	0	None	p	TN	III	n	n	n			98.68
C119	GSM124999	T2 N1a	IIB	16	1	Distant	p	HER	III	n	n	p	1		77.15
C120	GSM125000	T1c N1a	IIA	64	0	None	n	TN	III	n	n	u			82.03
C121	GSM125001	T2 N0	IIIA	67	0	None	n	HER	III	n	n	p	2		201.18
C122	GSM125002	T2 N1a	IIB	27	1	Distant	n	HER	II	n	n	p			105.43
C123	GSM125003	T2 N1a	IIB	48	1	Distant	p	TN	III	n	n	n	3		113.27
C124		Recurrence					n	TN	III	n	n	n	1		147.72
C125	GSM125004	T2 N0	IIA	62	0	None	p	TN	III	n	n	n	0		94.89
C126	GSM125005	T2 N2a	IIIA	24	1	Distant	p	TN	III	n	n	n	3		185.26
C128	GSM125006	T1c N0	I	52	0	None	u	TN	II	n	n	n			80.2
C130	GSM125007	T2 N3 M1	IV	2	1	Distant	n	TN	III	n	n	n			122.54
C131	GSM125008	T2 N0	IIA	53	0	None	n	TN/ BRCA2	III	n	n	n			89.37
C132	GSM125009	T1b N0	I	54	0	None	p	TN	III	n	n	n			99.39
C133	GSM125010	T1b N0	I	51	0	None	p	TN	III	n	n	n			82.52
C134	GSM125011	T2 N0	IIA	48	0	None	p	TN	III	n	n	n			109.72
C135	GSM125012	T1b N0	I	52	0	None	p	TN	III	n	n	n			127.21
C136	GSM125013	T2 N2a	IIIA	50	0	None	p	HER	III	n	n	p	0		100.68
C138	GSM125014	T2 N0	IIA	50	0	None	n	TN	III	n	n	n	3		111.07
C139	GSM125015	T2 N0	IIIA	40	0	None	n	ER HG	II	n	n	n	0		77.26
C140	GSM125016	T2 N0	IIIA	49	0	None	n	TN	III	n	n	n			72.04
C141	GSM125017	T1c N0	I	53	0	None	p	TN	III	n	n	n			57.76
C142	GSM125018	T1c N0	I	50	0	None	p	TN	III	n	n	n			54.78
C143	GSM125019	T1c N0	I	35	1	Distant	p	TN	III	n	n	n	1		136.33
C144	GSM125020	T2 N0	IIA	50	0	None	p	TN	III	n	n	n			126.65
C145	GSM125021	T2 N1a	IIB	13	1	Local	p	HER	III	n	n	p	0		97.36
C146	GSM125022	T1c N0	I	25	0	None	n	TN	II	n	n	n			105.54
C147	GSM125023	T2 N0	IIA	1	0	None	p	TN/ BRCA1	III	n	n	u			203.81
C148	GSM125024	T2 N0	IIA	36	0	None	p	TN	III	n	n	n			238.62
C149	GSM125025	T2 N0	IIA	39	0	None	n	TN	III	n	n	n			158.85
C156	GSM125105	T3 N3	IIIC	51	0	None	p	TN	III	n	n	p	3		122.24
C158	GSM125106	T2 N1a	IIB	57	1	Distant	n	ER HG	I	p	n	n	0		123.44
C160		T1c N1mi	IIIA	56	0	None	n	ER LG	I	p	p	n	0		131.15
C161	GSM125107	T3 N2a	IIIA	59	0	None	n	ER HG	II	p	p	n	1		103.11
C162	GSM125108	T2 N1a	IIB	69	0	None	p	ER HG	III	p	p	n			103.58
C163	GSM125109	T2 N1a	IIB	71	0	None	u	HER	III	p	p	p			162.34
C165	GSM125110	T3 N3	IIIC	39	1	Distant	p	HER	III	n	n	p	2		130.87
C169	GSM125111	T2 N1a	IIB	0	0	None	n	ER LG	I	p	p	n			93.99

Carracedo et al., uncut film scans

Fig 1C

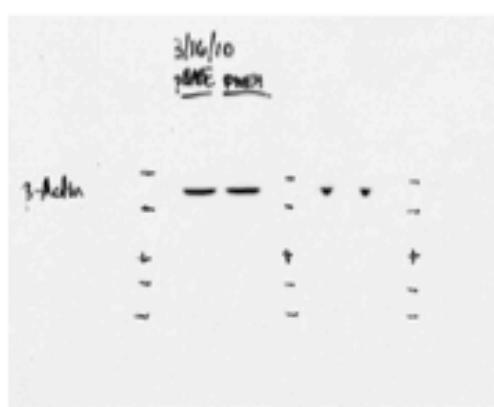
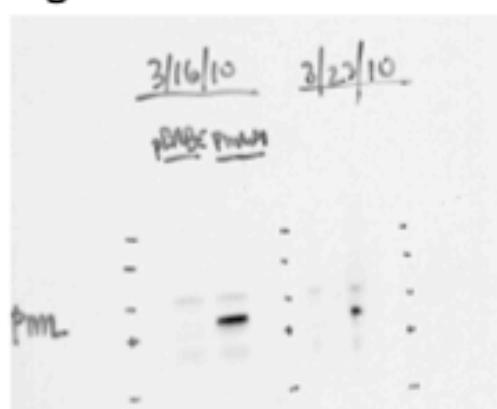


Fig 1D

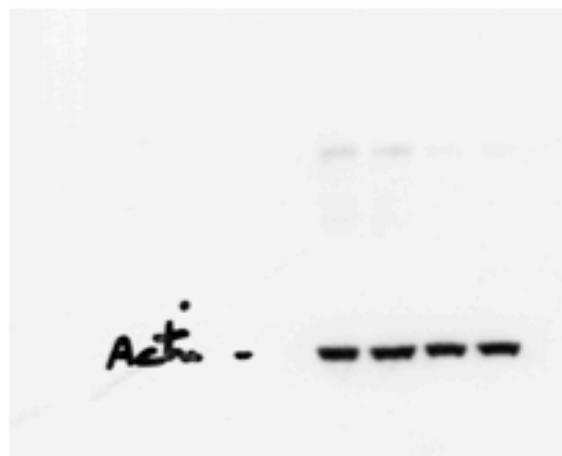


Fig 3C

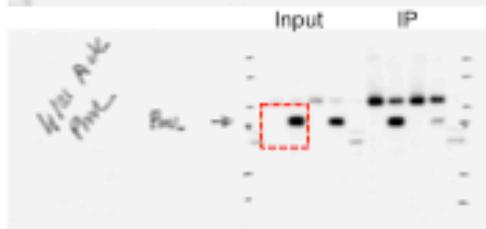
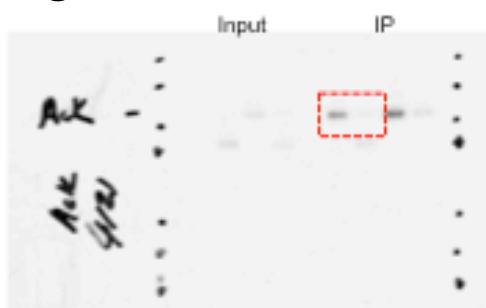


Fig 3D

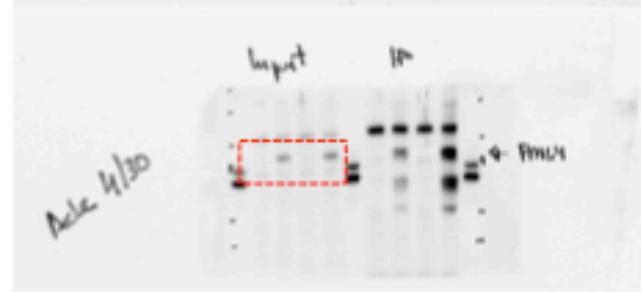
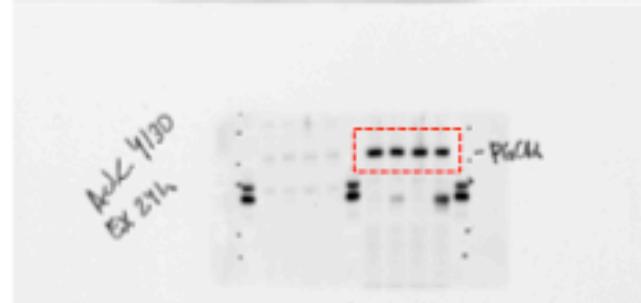
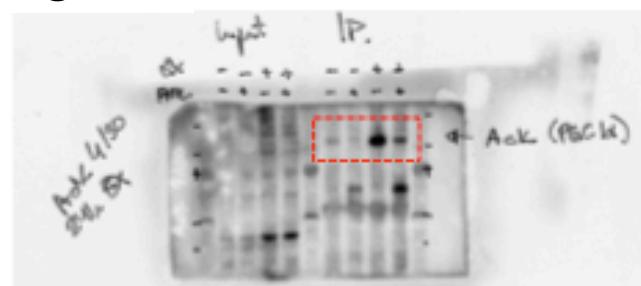


Fig 4A

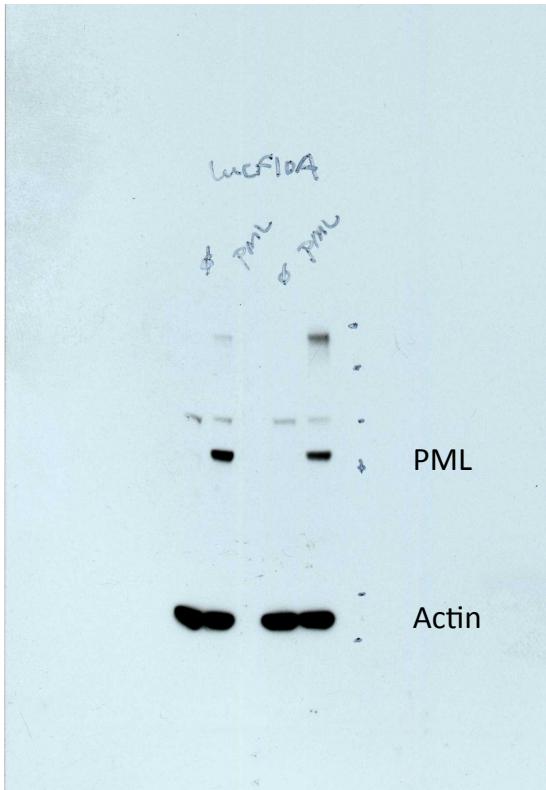


Fig S2C

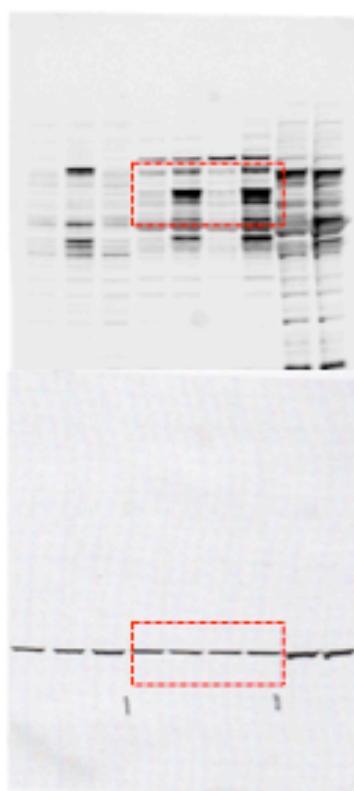


Fig S2G

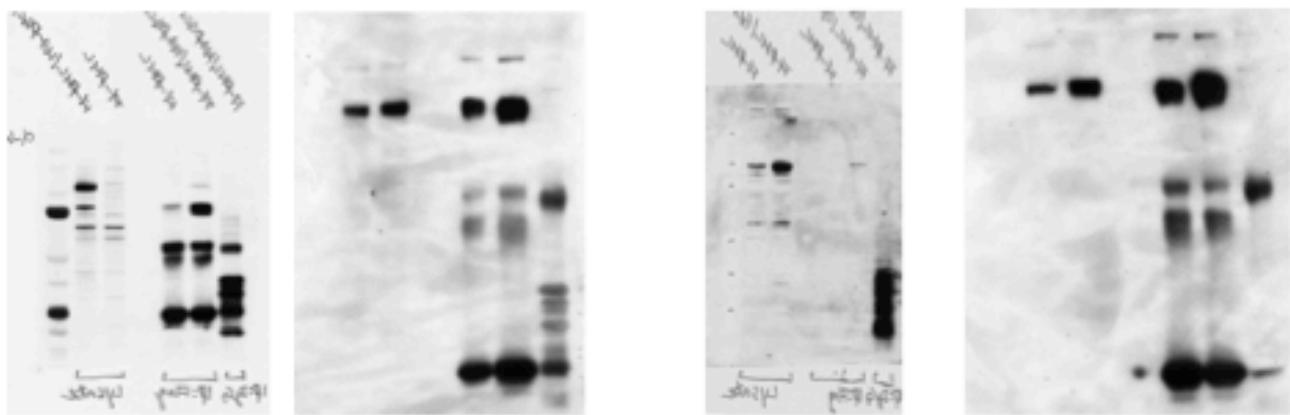


Fig S2G

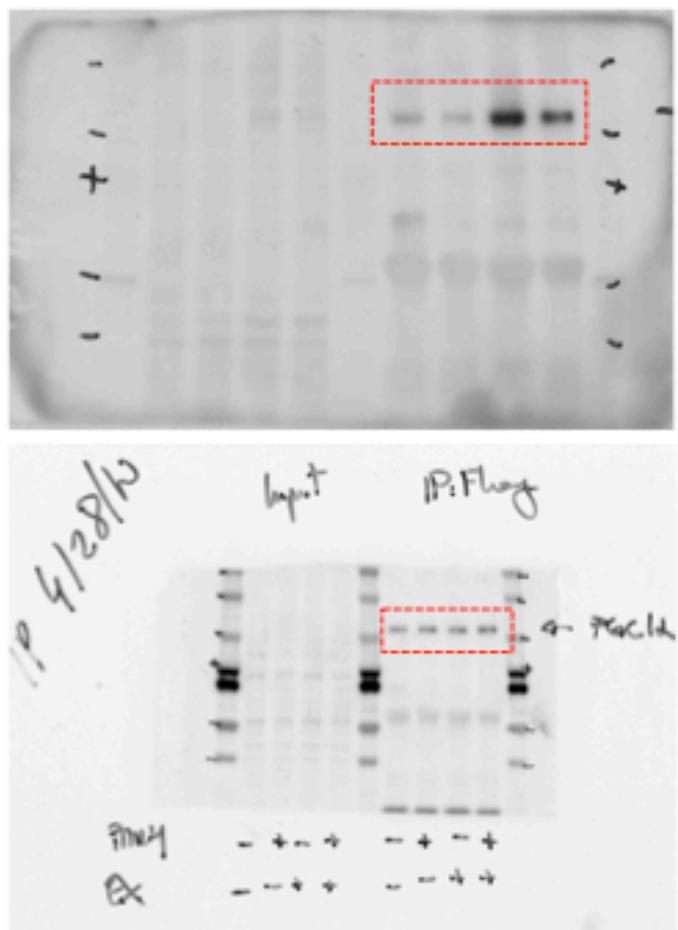


Fig S3C

