

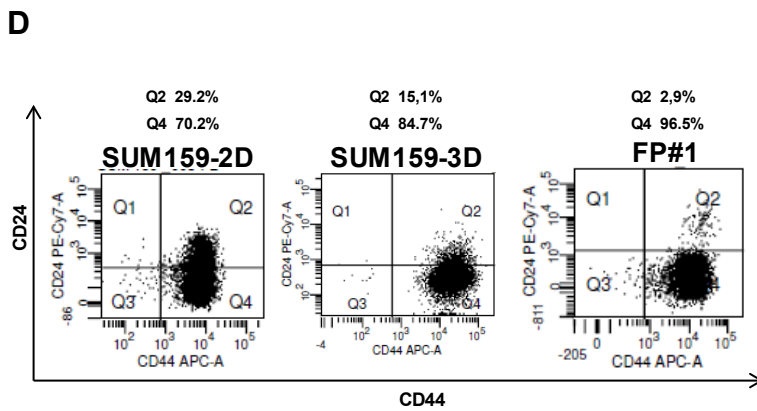
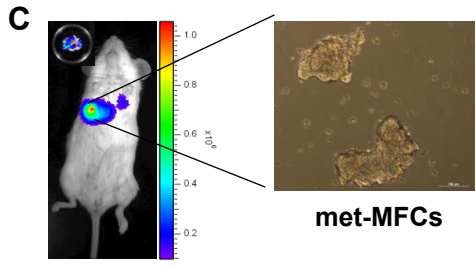
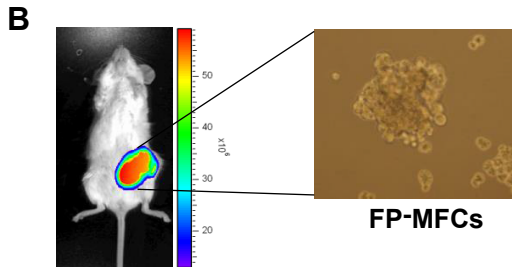
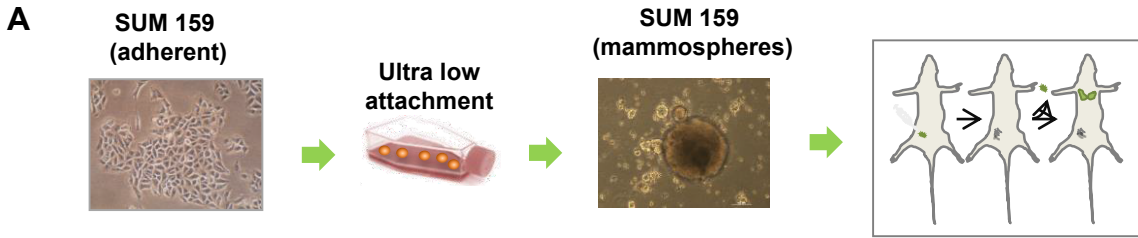
TABLE S1. Mutational analysis for a panel of tumor suppressor genes and oncogenes in the different clones used in the study.

	Gene	CLONE					
		FP#1	LM#1	FP#2	LM#2	SUM159-3D	SUM159-2D
1	AKT1						
2	ALK						
3	AR						
4	BRAF						
5	CDK4						
6	CTNNB1						
7	DDR2						
8	EGFR						
9	ERBB2						
10	ERBB3						
11	ERBB4						
12	ESR1						
13	FGFR2						
14	FGFR3						
15	GNA11						
16	GNAQ						
17	HRAS	G12D (63,60%)	G12D (66,15%)	G12D (66,77%)	G12D (70,16%)	G12D(62,35%)	G12D (55,78%)
18	IDH1						
19	IDH2						
20	JAK1						
21	JAK2						
22	JAK3						
23	KIT						
24	KRAS						
25	MAP2K1						
26	MAP2K2						
27	MET						
28	MTOR						
29	NRAS						
30	PDGFRA						
31	PIK3CA	H1047L (50,03%)	H1047L (66,58%)	H1047L(72,46%)	H1047L (68,16)	H1047L (60,8%)	H1047L (62,61%)
32	PTEN						
33	PTPN11						
34	ROS						
35	RB1						
36	RET						
37	SMAD4						
38	SMARCB1						
39	SMO						
40	SRC						
41	STK11						
42	TP53	V157_R158insL (100%)	V157_R158insL (100%)	V157_R158insL (100%)	V157_R158insL (100%)	V157_R158insL (100%)	V157_R158insL (100%)
43	VHL						

TABLE S2. Analysis of gene copy variation for a panel of oncogenes in the different clones used in the study.

	GENE	CLONE					
		FP#1	LM#1	FP#2	LM#2	SUM159-3D	SUM159-2D
1	ALK						
2	AR						
3	BRAF						
4	CCND1						
5	CDK4						
6	CDK6						
7	EGFR						
8	ERBB2						
9	FGFR1						
10	FGFR2						
11	FGFR3						
12	FGFR4						
13	KIT						
14	KRAS						
15	MET						
16	MYC	52,03 (0,34)	54 (0,32)	86 (0,32)	88,7 (0,37)	79 (0,34)	96 (0,30)
17	MYCN						
18	PDGFRA						
19	PIK3CA						
20	JAK1						

Supplementary Figure S1

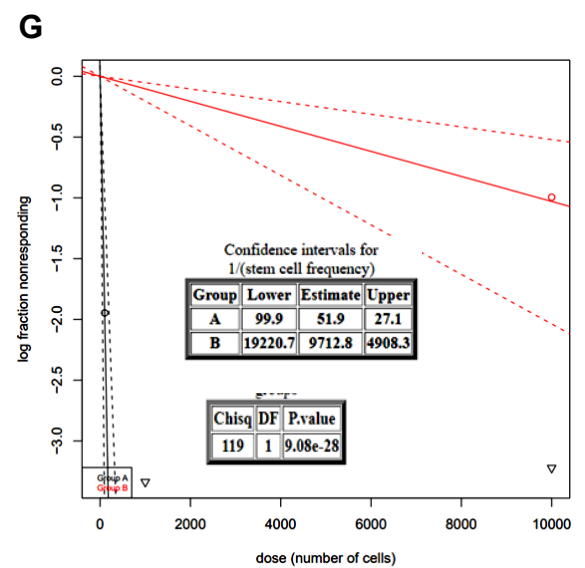
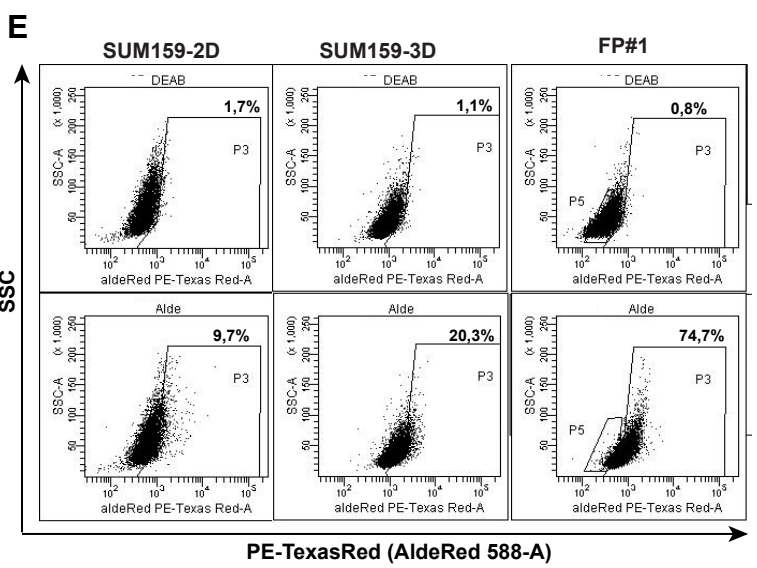


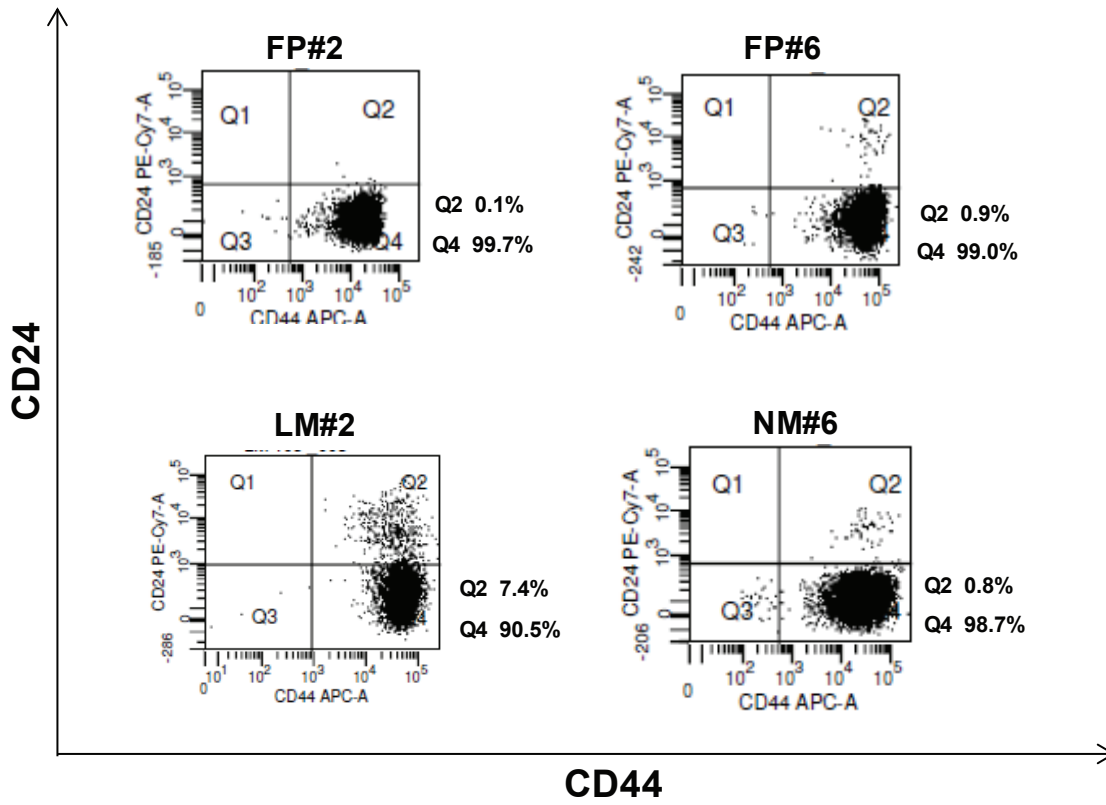
F

Confidence intervals for 1/(stem cell frequency)			
Group	Lower	Estimate	Upper
FP#1	2.21	1.75	1.44
FP#6	1.79	1.54	1.35
SUM159-2D	25.86	18.94	13.91

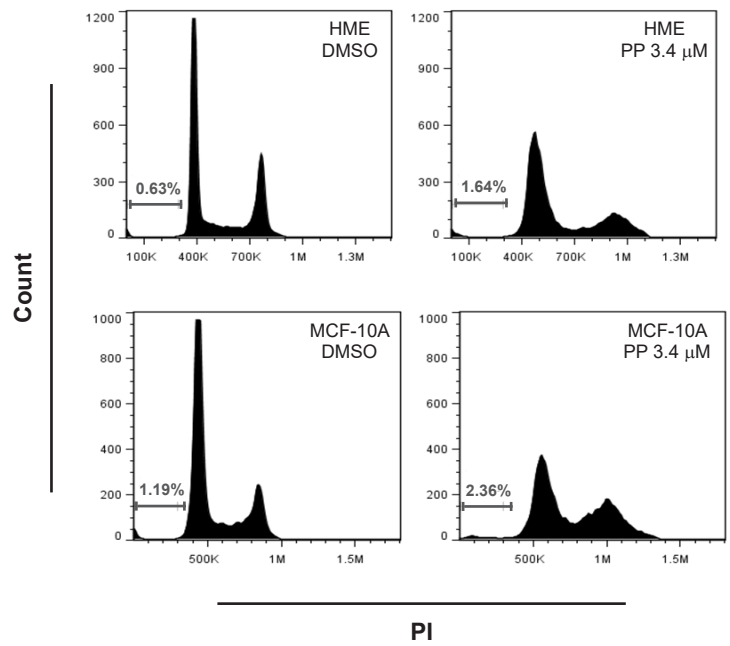
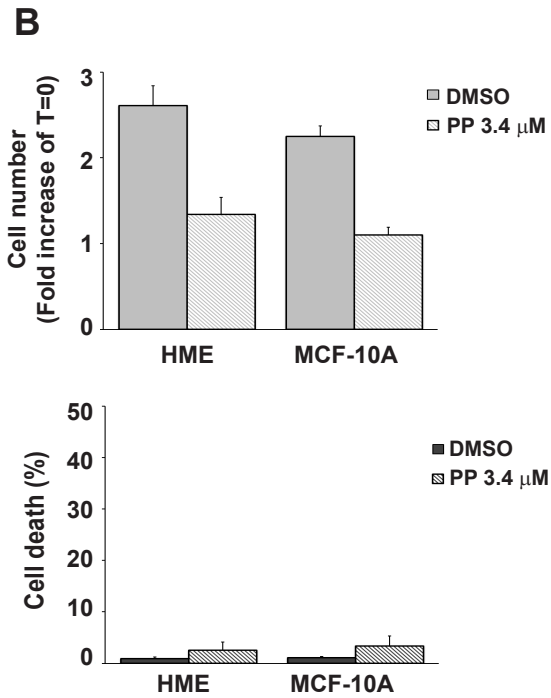
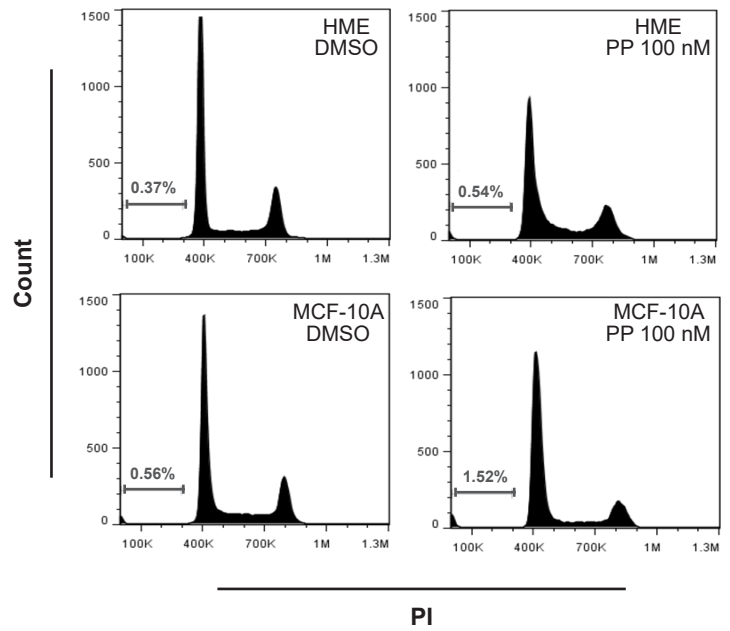
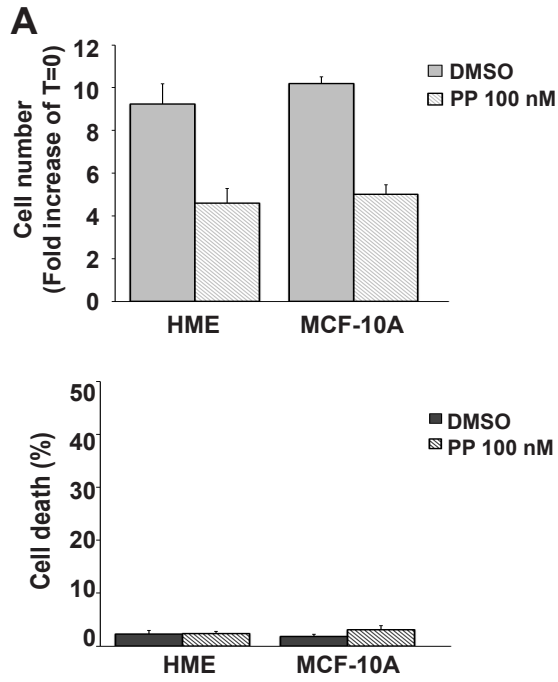
Overall test for differences in SCF between any of the groups		
Chisq	DF	P.Value
319	3	6.58e-69

SCF: stem cell frequencies

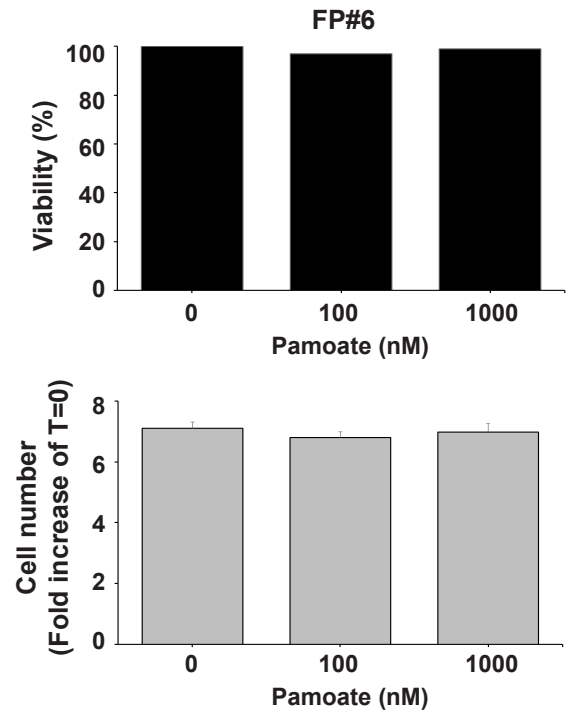
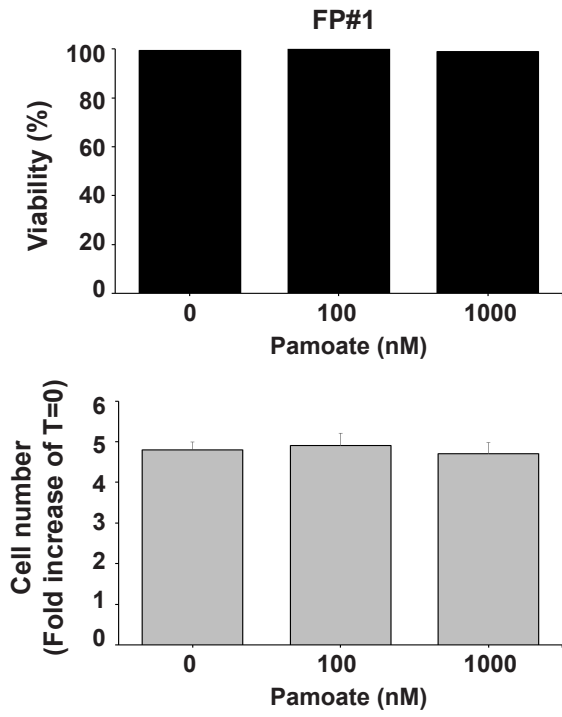




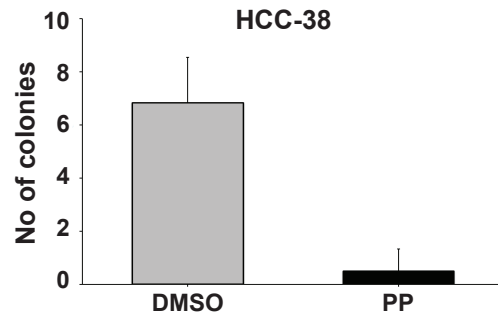
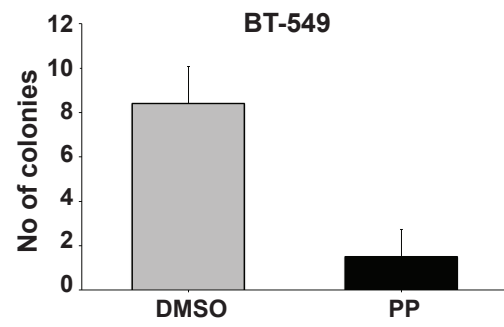
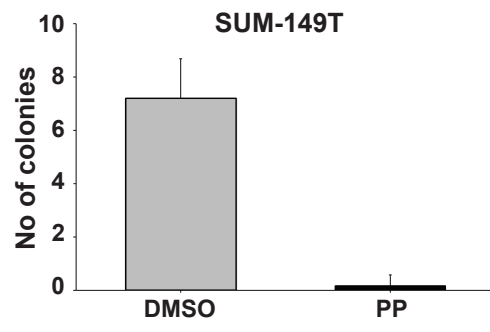
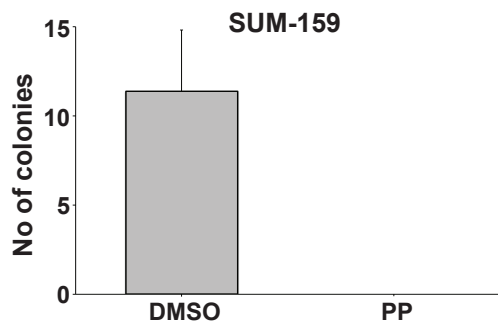
Supplementary Figure S3



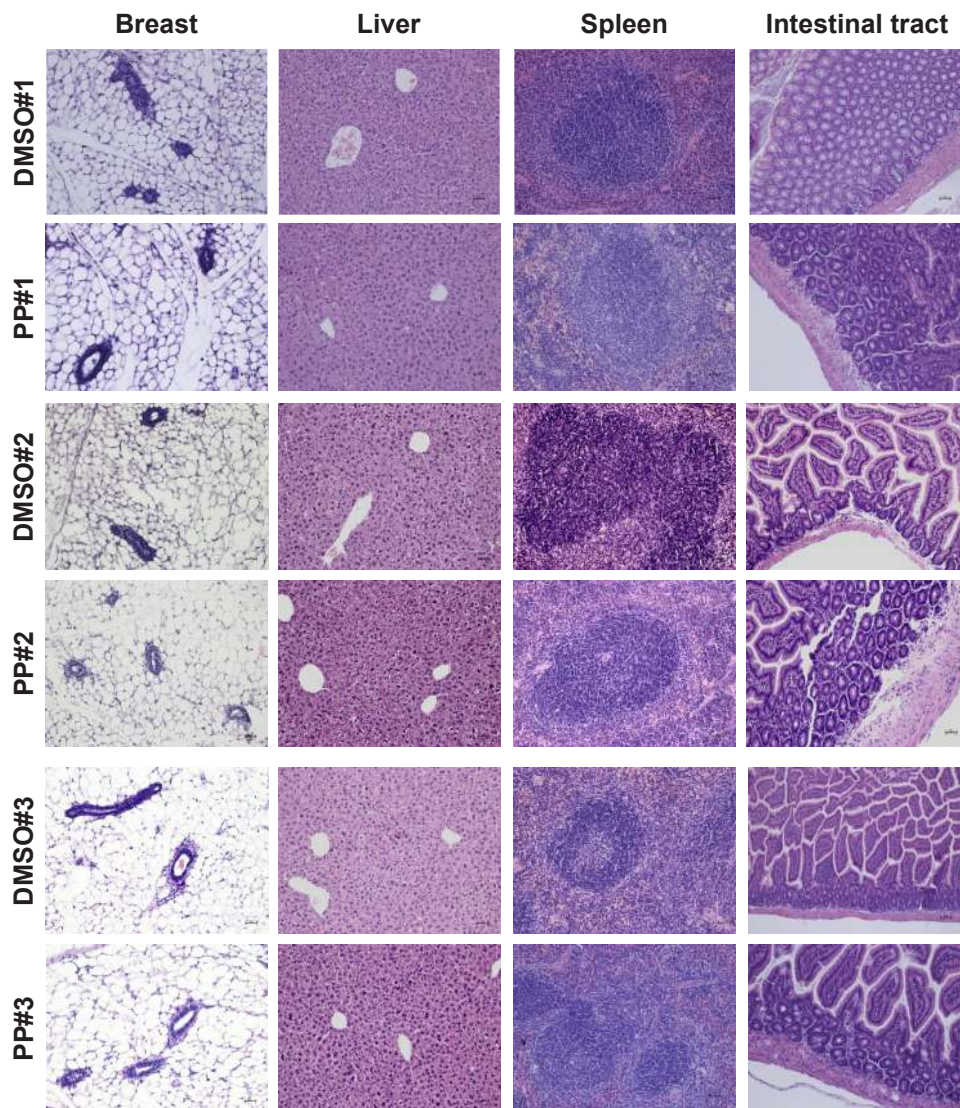
Supplementary Figure S4



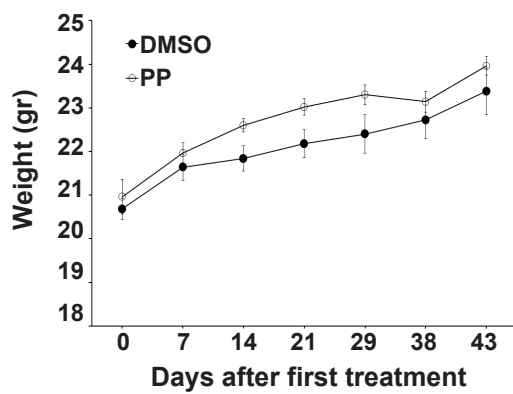
Supplementary Figure S5



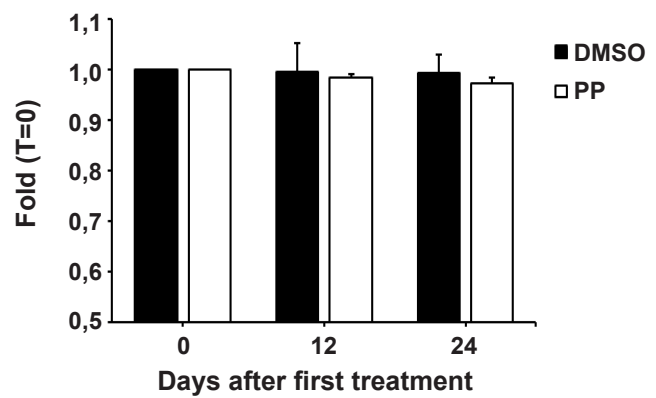
A

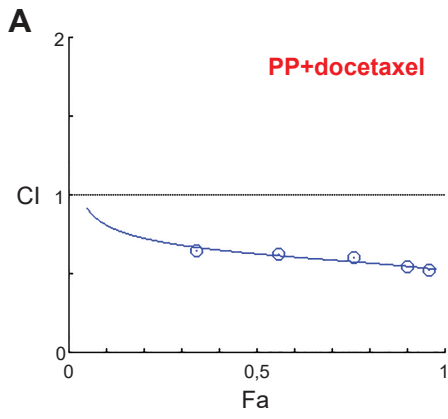


B



C



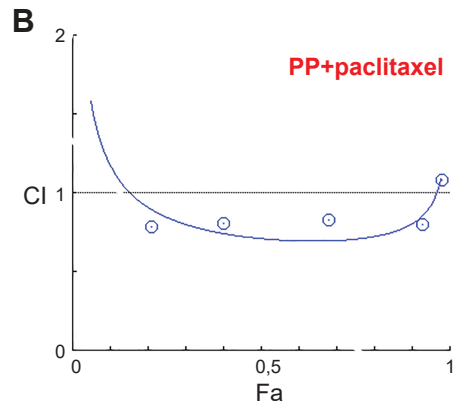


CI values for actual experimental points:

Fa	CI Value
0.34	0.64938
0.56	0.62332
0.76	0.60718
0.9	0.54471
0.96	0.52292

CI values at:

Combo	lc50	lc75	lc90	lc95
	0.62875	0.57989	0.54950	0.53685



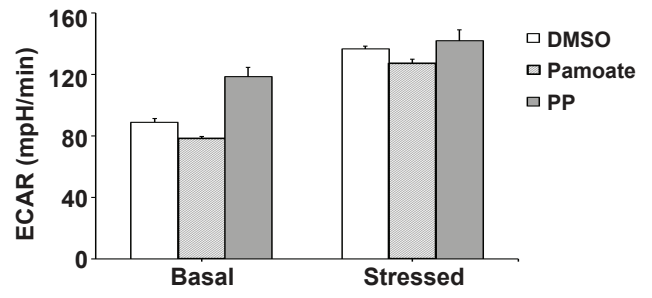
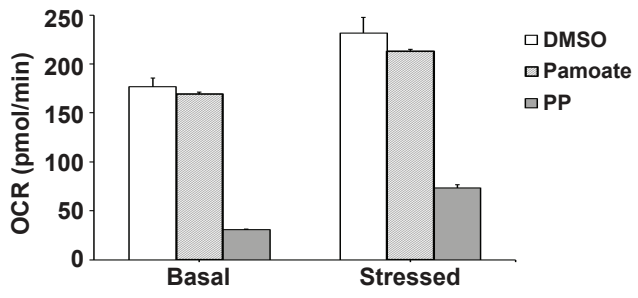
CI values for actual experimental points:

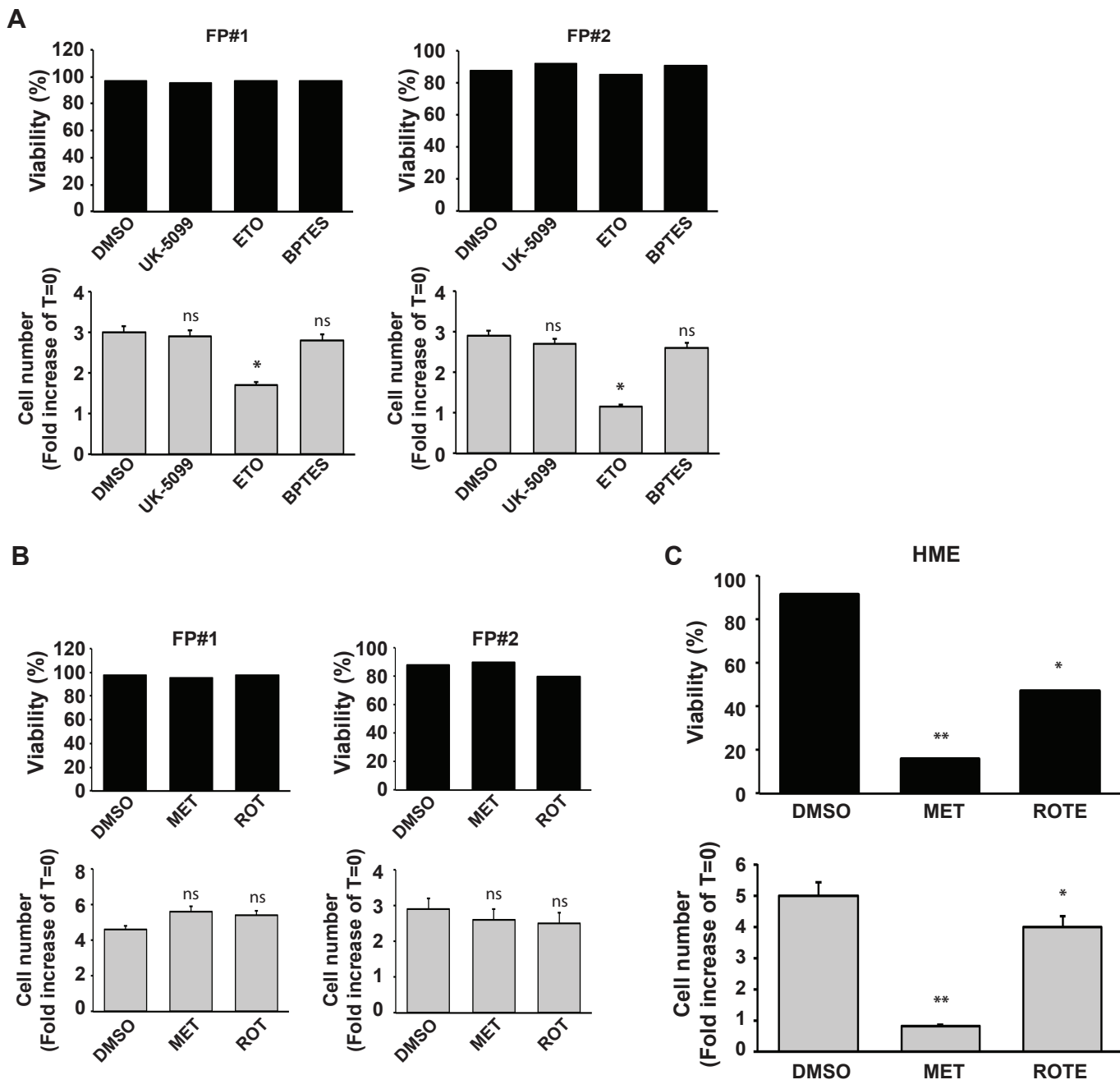
Fa	CI Value
0.21	0.78323
0.4	0.80978
0.68	0.82927
0.93	0.80307
0.98	1.08277

CI values at:

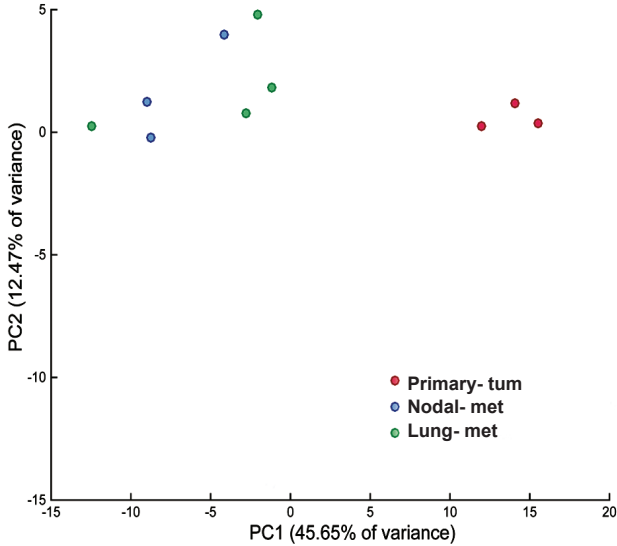
Combo	lc50	lc75	lc90	lc95
	0.71151	0.70826	0.80646	0.92617

Supplementary Figure S8

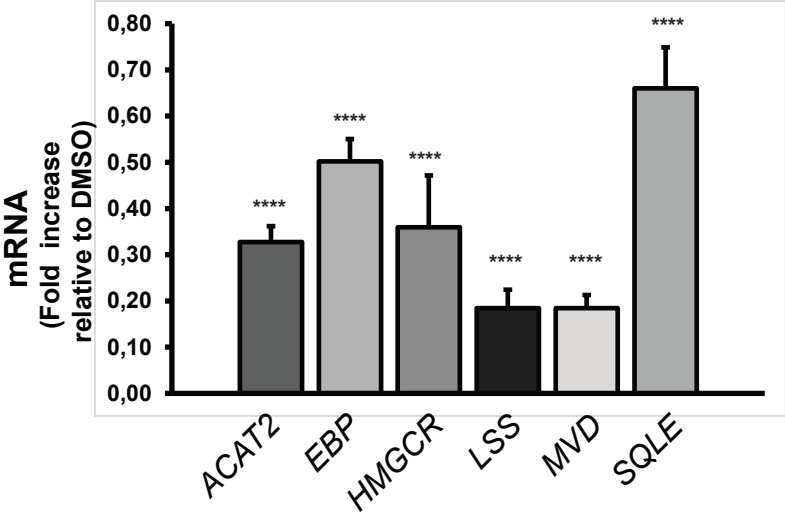




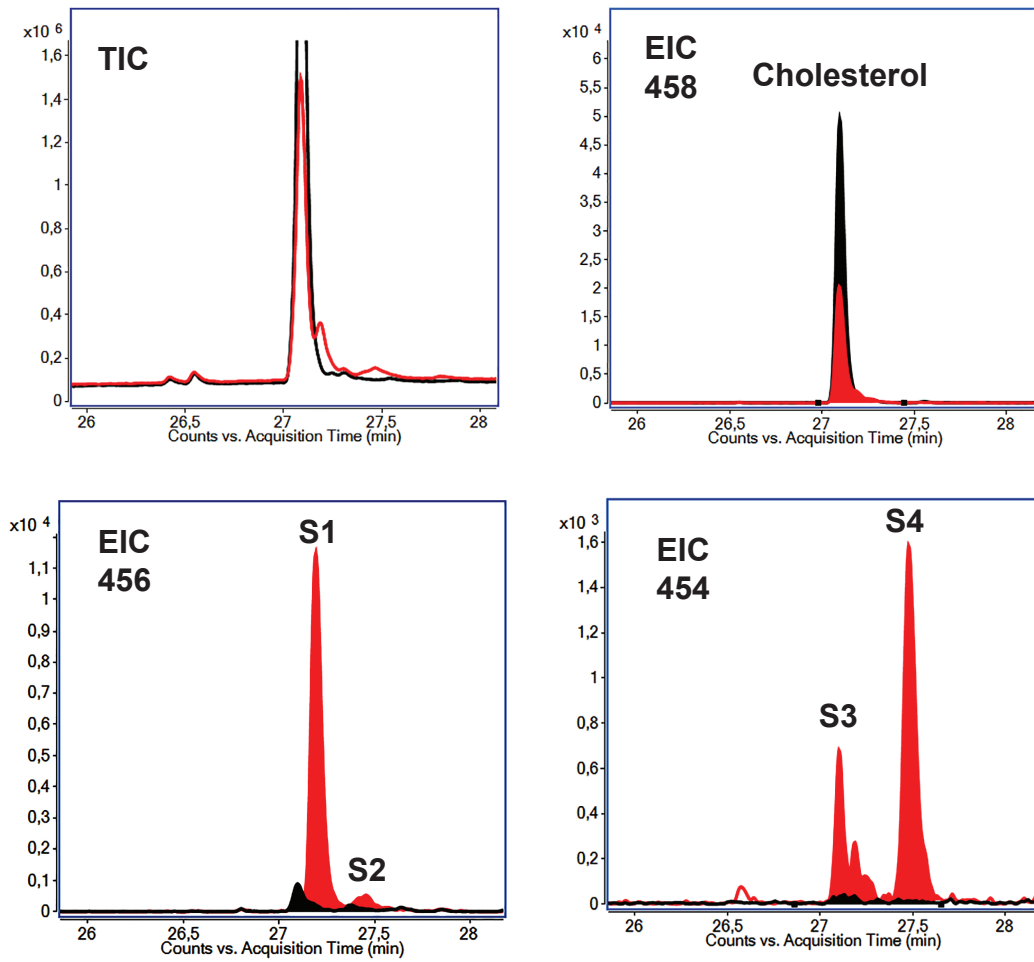
A



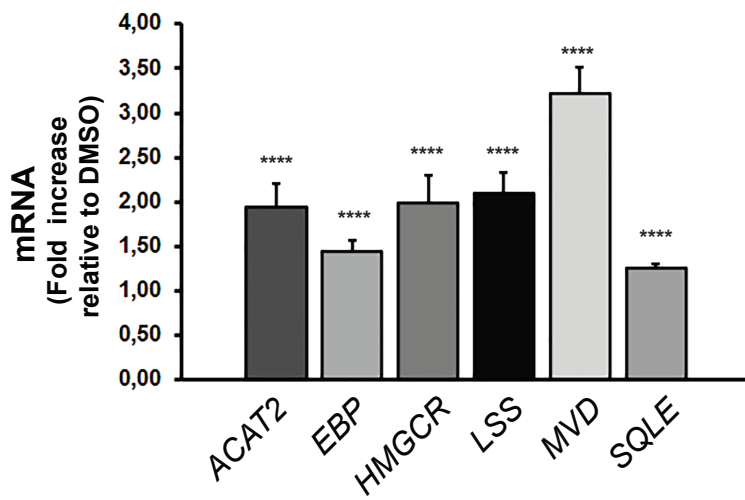
B

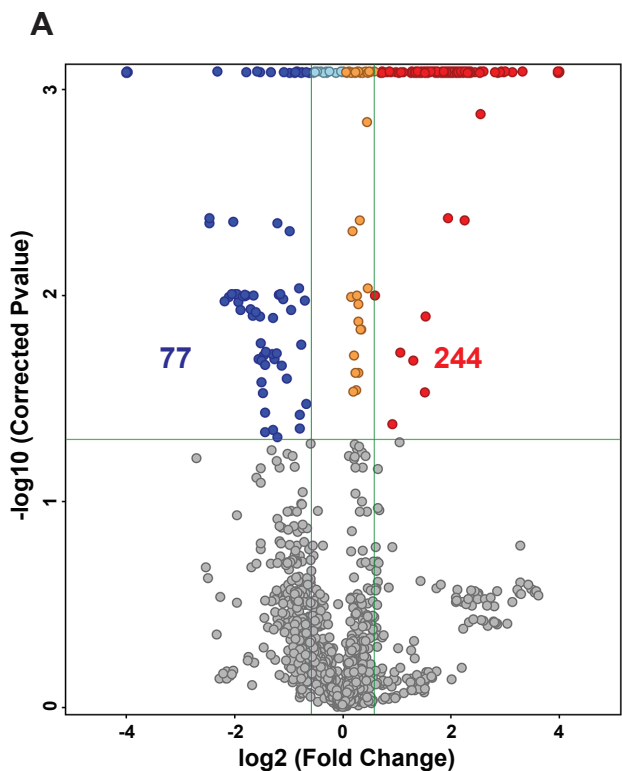


A



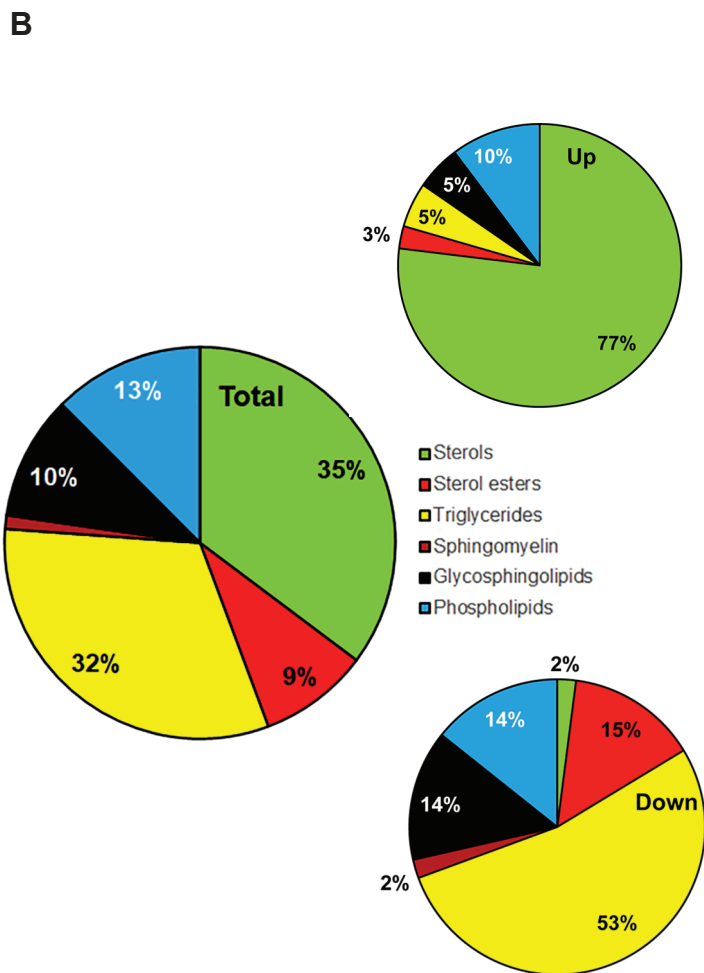
B





Color by p-value fold change cut-offs

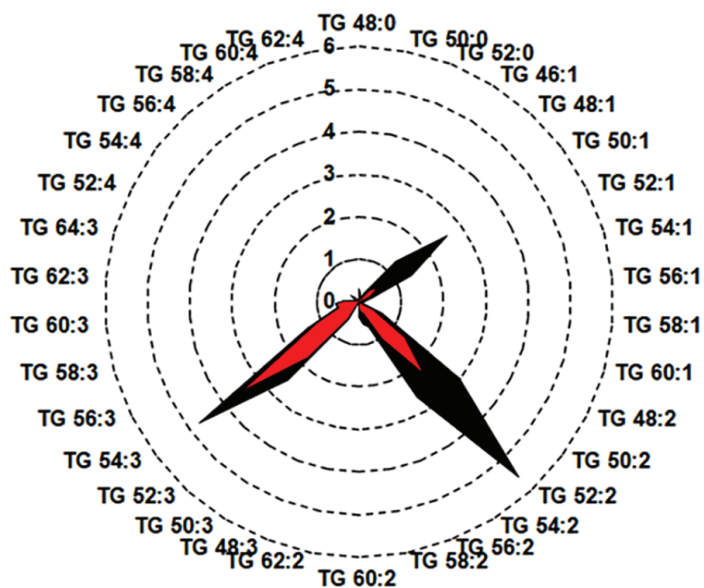
- Failed to pass both cut-offs
- Passed both cut-offs and down-regulated
- Passed both cut-offs and up-regulated
- Failed to pass fold change cut-off and up-regulated
- Failed to pass fold change cut-off and down-regulated

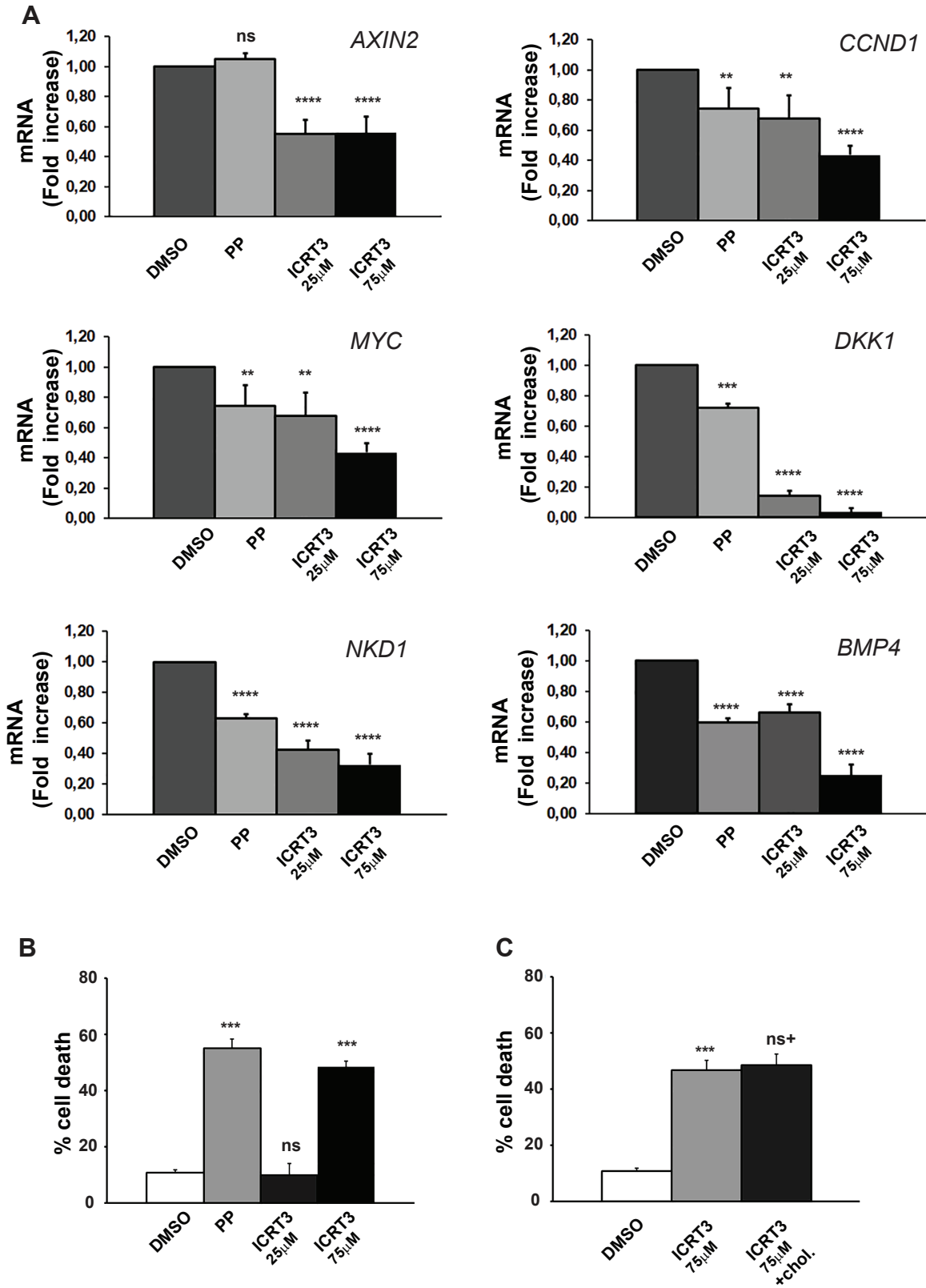


C

TG abundance (nmol/mg protein)

■ DMSO ■ PP





Supplementary Figure S14

