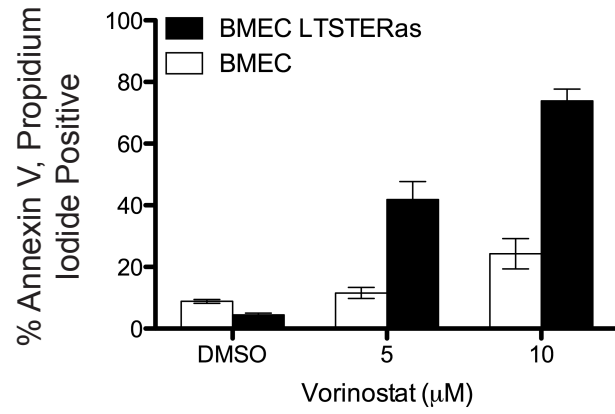
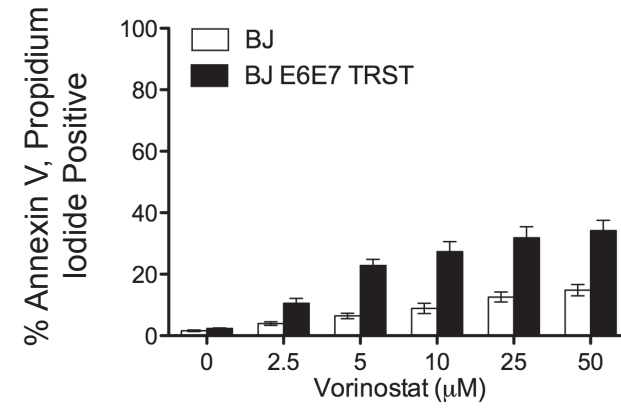
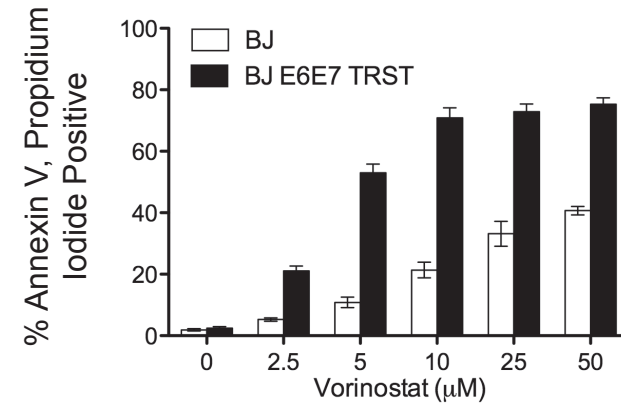


SUPPLEMENTARY FIGURES

Supp. Fig. 1. (A) BMEC and BMEC BJ LTSTERas cells were incubated with vehicle (DMSO) or with 10 or 25 μM vorinostat for 48 hrs, harvested, stained with annexin-V-APC and propidium iodide, and analysed by flow cytometry. The percentage of total cells staining positive for annexin-V-APC binding / PI uptake is shown. Data are presented as mean \pm SEM from three separate experiments. **(B)** BJ and BJ E6E7 TRST cells were incubated with 0, 2.5, 5, 10, 25 and 50 μM vorinostat for 48 and 72 hrs and the percentage of cell death was measured by annexin-V-APC binding and propidium iodide uptake by flow cytometry. Data are presented as mean (% AnnV+/PI+ double positive) \pm SEM of 5 independent experiments.

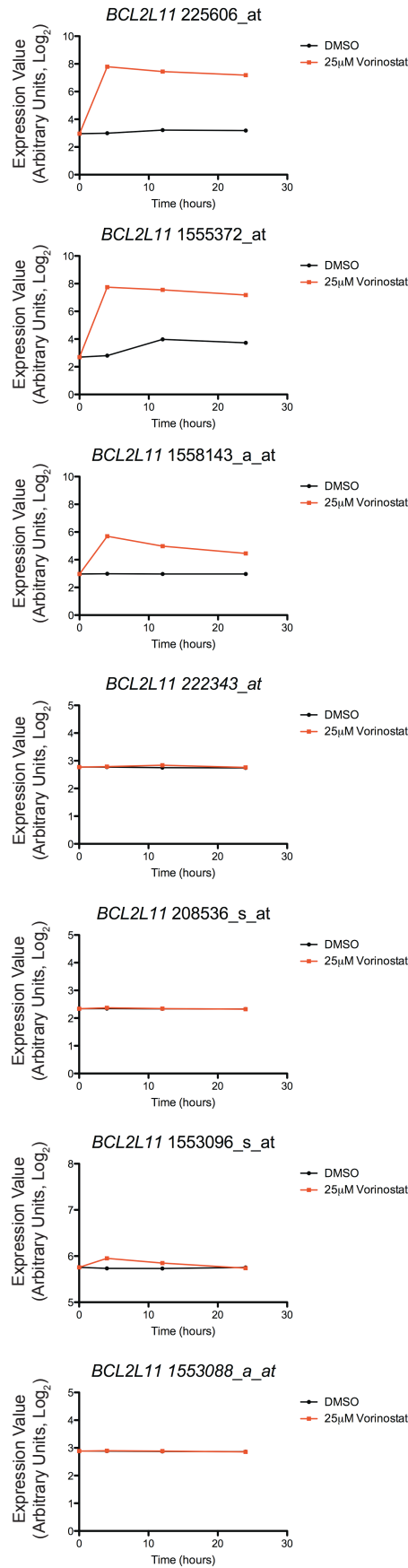
Supp. Fig. 2. Responses of 7 Affymetrix HG U133 plus 2.0 probe sets targeting

***BCL2L11* in BJ and BJ LTSTERas fibroblasts.** Transcriptional responses of *BCL2L11* in BJ and BJ LTSTERas fibroblasts following DMSO- (black) and 25 μM vorinostat-treatment (red). Log₂ transformed expression intensities of seven HG U133 plus 2.0 probe sets corresponding to *BCL2L11* are shown. Probe set IDs are indicated in the title of each panel. Normalized probe set intensity values (Y-axis) are shown, which allows direct comparison of *basal* expression (Time 0hr) and log₂ transcriptional responses over time between cell types (BJ and BJ LTSTERas). Data represent the summarized probe set intensities from three independent microarray time course experiments.

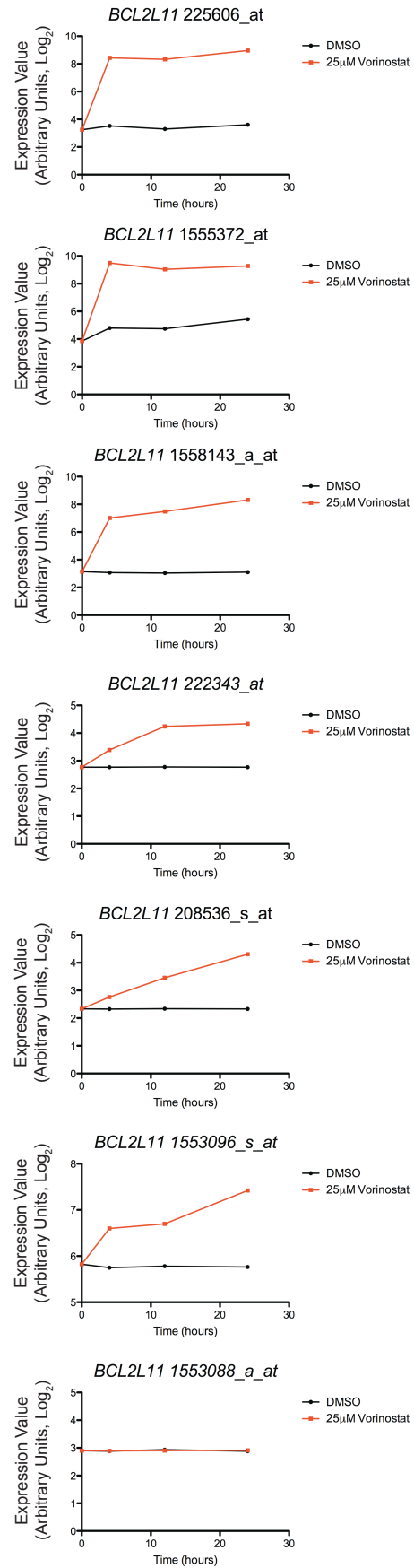
A**B****48 hr****72 hr**

Supplementary Figure 1

BJ



BJ LTSTERas



Supplementary Table 1. Gene Ontology biological process terms over-represented in genes that are induced by vorinostat in BJ LTSTERas cells and repressed in BJ cells $p < 0.05$

GO Accession	GO Term	Count	% Total	EASE
GO:0008632	apoptotic program	5	4.10%	0.002357186
GO:0006260	DNA replication	7	5.74%	0.003200373
GO:0006281	DNA repair	7	5.74%	0.007455047
GO:0006259	DNA metabolic process	12	9.84%	0.008019879
GO:0051348	negative regulation of transferase activity	4	3.28%	0.008217799
GO:0043086	negative regulation of catalytic activity	4	3.28%	0.018768446
GO:0051338	regulation of transferase activity	6	4.92%	0.020159042
GO:0043549	regulation of kinase activity	6	4.92%	0.02288518
GO:0012501	programmed cell death	11	9.02%	0.030193479
GO:0032944	regulation of mononuclear cell proliferation	3	2.46%	0.036431565
GO:0006915	apoptosis	11	9.02%	0.039420601
GO:0050670	regulation of lymphocyte proliferation	3	2.46%	0.040215216
GO:0000079	regulation of cyclin-dependent protein kinase activity	3	2.46%	0.046767451
GO:0045786	negative regulation of progression through cell cycle	5	4.10%	0.047478569

Supplementary Table 2. Gene Ontology biological process terms over-represented in genes that are induced by vorinostat in BJ LTSTERas cells and unchanged in BJ cells $p < 0.05$

GO Accession	GO Term	Count	% Total	EASE
GO:0006888	ER to Golgi vesicle-mediated transport	11	1.14%	0.00100352
GO:0007242	intracellular signaling cascade	94	9.70%	0.003099069
GO:0007264	small GTPase mediated signal transduction	36	3.72%	0.008681954
GO:0008202	steroid metabolic process	17	1.75%	0.012314798
GO:0012502	induction of programmed cell death	20	2.06%	0.013021849
GO:0048193	Golgi vesicle transport	12	1.24%	0.016068731
GO:0043068	positive regulation of programmed cell death	22	2.27%	0.017216584
GO:0019395	fatty acid oxidation	6	0.62%	0.018710224
GO:0043065	positive regulation of apoptosis	22	2.27%	0.019439932
GO:0009064	glutamine family amino acid metabolic process	7	0.72%	0.020396763
GO:0008632	apoptotic program	10	1.03%	0.020999991
GO:0044270	nitrogen compound catabolic process	9	0.93%	0.022263713
GO:0007050	cell cycle arrest	10	1.03%	0.024224036
GO:0006796	phosphate metabolic process	60	6.19%	0.024523132
GO:0015031	protein transport	45	4.64%	0.030712213
GO:0016192	vesicle-mediated transport	35	3.61%	0.031563249
GO:0006464	protein modification process	102	10.53%	0.032839207
GO:0019752	carboxylic acid metabolic process	38	3.92%	0.033383507
GO:0043412	biopolymer modification	104	10.73%	0.034038177
GO:0008610	lipid biosynthetic process	21	2.17%	0.041103783
GO:0006694	steroid biosynthetic process	9	0.93%	0.041936958
GO:0009112	nucleobase metabolic process	4	0.41%	0.04217483
GO:0008206	bile acid metabolic process	4	0.41%	0.044311172
GO:0016310	phosphorylation	50	5.16%	0.046115052
GO:0009615	response to virus	10	1.03%	0.0461995

Supplementary Table 3. Gene Ontology biological process terms over-represented in genes that are hyper-induced by vorinostat in BJ LTSTERas cells $p < 0.05$

GO Accession	GO Term	Count	% Total	EASE
GO:0007242	intracellular signaling cascade	62	11.25%	6.66E-04
GO:0051649	establishment of cellular localization	40	7.26%	0.001875616
GO:0007264	small GTPase mediated signal transduction	24	4.36%	0.006047776
GO:0046907	intracellular transport	32	5.81%	0.006758283
GO:0006796	phosphate metabolic process	40	7.26%	0.007820526
GO:0007243	protein kinase cascade	21	3.81%	0.009972866
GO:0016310	phosphorylation	34	6.17%	0.011188195
GO:0045184	establishment of protein localization	32	5.81%	0.012453905
GO:0043281	regulation of caspase activity	6	1.09%	0.01772116
GO:0015031	protein transport	29	5.26%	0.024455607
GO:0016197	endosome transport	5	0.91%	0.028691201
GO:0008632	apoptotic program	7	1.27%	0.028917113
GO:0044271	nitrogen compound biosynthetic process	8	1.45%	0.033181677
GO:0051336	regulation of hydrolase activity	11	2.00%	0.038027413
GO:0016049	cell growth	11	2.00%	0.039229982
GO:0016192	vesicle-mediated transport	22	3.99%	0.042628943
GO:0007005	mitochondrion organization and biogenesis	7	1.27%	0.043408298
GO:0009890	negative regulation of biosynthetic process	5	0.91%	0.047297269
GO:0007010	cytoskeleton organization and biogenesis	22	3.99%	0.047360603
GO:0008361	regulation of cell size	11	2.00%	0.047726012