

Supplemental Table 1: SAHA dose response for prevention of 231-BR brain metastatic colonization^A.

Experiment	Dose (mg/kg)	N	Micrometastases:			Large Metastases ^B :		
			Mean ^C	95% CI	P ^D	Mean	95% CI	P
1	0	5	205	165 to 246		6.78	5.42 to 8.14	
	100	3	140	114 to 167	0.015	2.87	1.11 to 4.63	0.003
	150 ^E	6	152	115 to 189	0.081	3.52	2.27 to 4.76	0.003
2	0	5	72.5	51.8 to 93.2		3.26	2.68 to 3.84	
	100	9	78.3	48.4 to 108.3	NS ^F	2.28	1.26 to 3.29	NS
	150	9	66.6	51.2 to 82.1	NS	1.47	1.03 to 1.90	0.0003

^A231-BR cells (500,000 in Experiment 1; 100,000 in Experiment 2) were injected into the left cardiac ventricle of Balb/c nude mice. SAHA was administered once daily by ip injection starting 3 days post-injection.

^BSize of metastases determined by a 16 mm² ocular grid. Large metastases greater than 300 microns on the longest axis.
per section.

^CMean number of metastases per section counted in 10 step sections from one hemisphere of the brain.

^DA two-factor factorial ANOVA was used to determine significance. All p-values are two-tailed and adjusted for multiple comparisons using Dunnett's method.

^EIn Experiment 1, this group of mice received 200 mg/kg starting 3 days post injection but due to toxicity, the dose was reduced to 150 mg/kg on day 8 post-injection.

^F Not significant.

Supplemental Table 2 – Top genes downregulated in tumor cells from brain metastasis in vorinostat treated mice compared to tumor cells from brain metastasis in vehicle treated mice listed in order of false discovery rate.

Fold difference	Symbol	GeneName
29.33	HES1	hairy and enhancer of split 1, (Drosophila)
9.77	ZNF202	zinc finger protein 202
8.02	MEPCE	methylphosphate capping enzyme
16.02	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein
5.82	HES1	hairy and enhancer of split 1, (Drosophila)
18.74	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila)
4.92	GMEB2	glucocorticoid modulatory element binding protein 2
11.95	KLF2	Kruppel-like factor 2 (lung)
4.95	CTCF	CCCTC-binding factor (zinc finger protein)
7.83	ZNF24	zinc finger protein 24
4.34	MXD4	MAX dimerization protein 4
8.05	FRMD4A	FERM domain containing 4A
4.75	SEMA4C	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C
4.89	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4
4.88	PON2	paraoxonase 2
4.51	CPT1B	carnitine palmitoyltransferase 1B (muscle)
5.47	ZBTB38	zinc finger and BTB domain containing 38
4.04	HEATR6	HEAT repeat containing 6
4.60	SCYL3	SCY1-like 3 (S. cerevisiae)
3.24	TMED1	transmembrane emp24 protein transport domain containing 1
3.25	PAN2	PAN2 polyA specific ribonuclease subunit homolog (S. cerevisiae)
3.07	ZBTB40	zinc finger and BTB domain containing 40
3.84	GOSR1	golgi SNAP receptor complex member 1
5.61	PHF17	PHD finger protein 17
4.93	ZNF274	zinc finger protein 274
5.68	ZNF24	zinc finger protein 24
6.61	SCYL3	SCY1-like 3 (S. cerevisiae)
5.02	ZNF193	zinc finger protein 193
3.60	EIF5	eukaryotic translation initiation factor 5
4.15	RBM22	RNA binding motif protein 22
3.52	HEATR6	HEAT repeat containing 6
3.86	CYTH2	cytohesin 2
4.21	SOX9	SRY (sex determining region Y)-box 9

5.51	PARVA	parvin, alpha
3.17	TRIM68	tripartite motif-containing 68
6.19	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17
3.78	HMG2L1	high-mobility group protein 2-like 1
3.28	CALML4	calmodulin-like 4
2.62	CUL7	cullin 7
3.01	WDR6	WD repeat domain 6
3.80	LOC791120	hypothetical LOC791120
2.66	PATZ1	POZ (BTB) and AT hook containing zinc finger 1
3.51	RAD52	RAD52 homolog (S. cerevisiae)
3.77	PPP1R10	protein phosphatase 1, regulatory (inhibitor) subunit 10
2.84	RBM4B	RNA binding motif protein 4B
4.57	PHF15	PHD finger protein 15
3.37	WIPF2	WAS/WASL interacting protein family, member 2
2.59	TRIM27	tripartite motif-containing 27
3.78	DLG5	discs, large homolog 5 (Drosophila)
6.62	DUSP4	dual specificity phosphatase 4
4.16	PCBP2	poly(rC) binding protein 2
3.92	SF1	splicing factor 1
4.15	ERMAP	erythroblast membrane-associated protein (Scianna blood group)
4.48	FCGBP	Fc fragment of IgG binding protein
2.98	PRDX2	peroxiredoxin 2
4.78	INTS6	integrator complex subunit 6
4.16	ZFP64	zinc finger protein 64 homolog (mouse)
8.44	PRDM10	PR domain containing 10
2.90	RHOBTB2	Rho-related BTB domain containing 2
2.92	RBM5	RNA binding motif protein 5
3.54	JRK	jerky homolog (mouse)
2.54	CTGLF1	centaurin, gamma-like family, member 1
2.98	GMEB2	glucocorticoid modulatory element binding protein 2

Supplemental Table 3 – Top genes upregulated in tumor cells from brain metastasis in vorinostat treated mice compared to tumor cells from brain metastasis in vehicle treated mice listed in order of false discovery rate.

Fold difference	Symbol	GeneName
8.81	AVPI1	arginine vasopressin-induced 1
14.90	STC1	stanniocalcin 1
12.80	NRG1	neuregulin 1
3.72	MAP3K9	mitogen-activated protein kinase kinase kinase 9
14.49	TUFT1	tuftelin 1
78.80	HBE1	hemoglobin, epsilon 1
11.86	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
5.85	CXCR4	chemokine (C-X-C motif) receptor 4
4.05	CLP1	CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)
4.00	GATA2	GATA binding protein 2
3.15	SNRPA1	small nuclear ribonucleoprotein polypeptide A'
18.86	HBA1	hemoglobin, alpha 1
4.94	PECI	peroxisomal D3,D2-enoyl-CoA isomerase
4.54	EFNA1	ephrin-A1
4.00	TBPL1	TBP-like 1
13.35	PTCH1	patched homolog 1 (Drosophila)
6.32	GPRC5A	G protein-coupled receptor, family C, group 5, member A
4.12	DAD1	defender against cell death 1
4.87	MID1	midline 1 (Opitz/BBB syndrome)
5.99	KIAA1609	KIAA1609
4.69	PRPS1	phosphoribosyl pyrophosphate synthetase 1
3.24	GLRX	glutaredoxin (thioltransferase)
3.36	BZW2	basic leucine zipper and W2 domains 2
3.66	RNF24	ring finger protein 24
4.67	CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7
5.69	SPATA2L	spermatogenesis associated 2-like
2.72	CSRP2	cysteine and glycine-rich protein 2
3.04	COPS2	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)
4.68	ZSCAN16	zinc finger and SCAN domain containing 16
3.31	JARID2	jumonji, AT rich interactive domain 2
2.95	GPN3	GPN-loop GTPase 3
2.89	ARID3B	AT rich interactive domain 3B (BRIGHT-like)
2.54	NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21
4.69	TTR	transthyretin

2.44	LIMS1	LIM and senescent cell antigen-like domains 1
2.76	DUSP14	dual specificity phosphatase 14
4.09	KIAA1609	KIAA1609
3.15	PVT1	Pvt1 oncogene homolog (mouse)
3.77	LIMA1	LIM domain and actin binding 1
4.67	SKP1	S-phase kinase-associated protein 1
2.70	BRP44	brain protein 44
3.23	ATG4A	ATG4 autophagy related 4 homolog A (<i>S. cerevisiae</i>)
2.86	EHD1	EH-domain containing 1
3.46	LMCD1	LIM and cysteine-rich domains 1
4.73	SEC31A	SEC31 homolog A (<i>S. cerevisiae</i>)
3.74	FAM129A	family with sequence similarity 129, member A
3.07	CYCS	cytochrome c, somatic
2.58	TJP1	tight junction protein 1 (zona occludens 1)
3.32	ADA	adenosine deaminase
4.80	DAAM1	dishevelled associated activator of morphogenesis 1
3.27	ELOVL5	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)
2.73	SPCS1	signal peptidase complex subunit 1 homolog (<i>S. cerevisiae</i>)
3.37	MEGF9	multiple EGF-like-domains 9
