Table 4. ABPP-MudPIT data for SAHA-BPyne-treated ovarian cancer cell lines.

	Spectral counts							
OVCAR3 Results for Targeted Proteins	SAHA-BPyne				SAHA			
IPI00013774 - Histone deacetylase 1	10	14	25	18	7	9	2	8
IPI00289601 - Histone deacetylase 2	23	27	31	19	10	11	5	10
IPI00006187 - Histone deacetylase 3	5	4	10	2	0	0	0	0
IPI00005711 - Histone deacetylase 6	0	2	8	3	0	0	0	3
IPI00008531 - CoREST protein	3	0	0	0	0	0	0	0
IPI00439194 - Methyl-CpG binding protein 3	10	11	3	5	0	0	0	0
IPI00012773 - Metastasis-associated protein MTA1	4	7	9	4	4	8	3	0
IPI00171798 - Metastasis associated protein MTA2	3	6	6	7	0	2	7	0
IPI00103554 - Transcriptional repressor p66 beta	4	3	2	0	0	0	0	0

	Spectral counts					
SKOV3 Results for Targeted Proteins	SAHA-BPyne			SAHA		
IPI00013774 - Histone deacetylase 1	23	31	18	5	0	0
IPI00289601 - Histone deacetylase 2	21	30	20	6	2	3
IPI00006187 - Histone deacetylase 3	3	2	4	3	0	0
IPI00005711 - Histone deacetylase 6	7	5	5	0	0	2
IPI00008531 - CoREST protein	0	0	2	0	0	0
IPI00439194 - Methyl-CpG binding protein 3	2	6	5	0	0	0
IPI00012773 - Metastasis-associated protein MTA1	5	3	0	0	0	0
IPI00171798 - Metastasis associated protein MTA2	7	5	7	2	0	2
IPI00103554 - Transcriptional repressor p66 beta	2	3	0	0	0	0

Spectral counts are shown for HDAC and HDAC-associated proteins from individual proteomic samples. Averages for these data can be found in Table 2. Unshaded boxes show proteins that had i) an average of at least three spectral counts in SAHA-BPyne-treated samples, and ii) at least a two-fold increase in average spectral counts in SAHA-BPyne-treated versus control samples. Shaded boxes show data for relevant proteins that did not meet this criterion. n = 3-4 experiments per cell line.