

Additional Data File 2 - the transcriptional response to HDACi

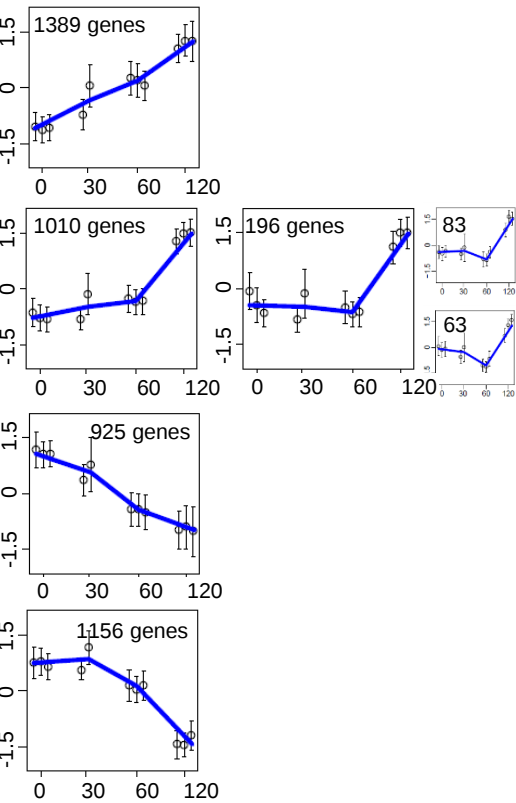
Significant genes were identified by ANOVA (fold change >1.5, FDR<10%) and clustered by SOTA. Clusters were combined as shown to represent rapid or delayed up- and down-regulation. For each cluster the top significant ontological terms (enrichment score >2) are shown.

A Responses to 1mM VPA

B Responses to 0.5 and 12.5µM SAHA

A

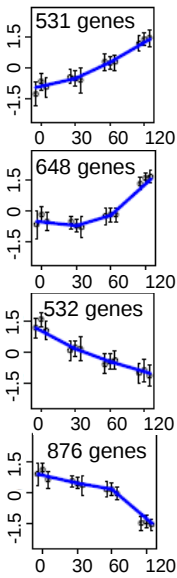
5mM VPA



Category	Term	Count	P-value	Fold Enrichment
GOBP	regulation of transcription	138	4.1 x10 ⁻⁴	1.3
	positive regulation of transcription	38	2.7 x10 ⁻³	1.7
GOBP	pattern specification process	28	7.8 x10 ⁻⁶	2.6
GOBP	multicellular organism reproduction	35	9.8 x10 ⁻⁴	1.8
GOBP	endocytosis	21	4.8 x10 ⁻⁴	2.4
GOMF	ligand-dependent nuclear receptor activity	8	6.6 x10 ⁻³	3.6
SMRT	ZnF C2H2	76	3.5 x10 ⁻²¹	3.3
GOBP	regulation of transcription	119	2.8 x10 ⁻¹³	1.9
GOMF	cytokine activity	31	5.8 x10 ⁻¹⁶	6.5
GOBP	defense response	36	2.1 x10 ⁻⁶	2.4
GOMF	growth factor activity	14	1.6 x10 ⁻⁴	3.6
GOBP	regulation of transcription	126	1.8 x10 ⁻⁷	1.5
GOBP	defense response	30	1.9 x10 ⁻²	1.5
GOCC	histone acetyltransferase complex	10	6.6 x10 ⁻⁶	7.4
GOBP	taxis	20	6.5 x10 ⁻⁷	4.0
GOMF	glucuronosyltransferase activity	6	5.2 x10 ⁻⁴	8.6

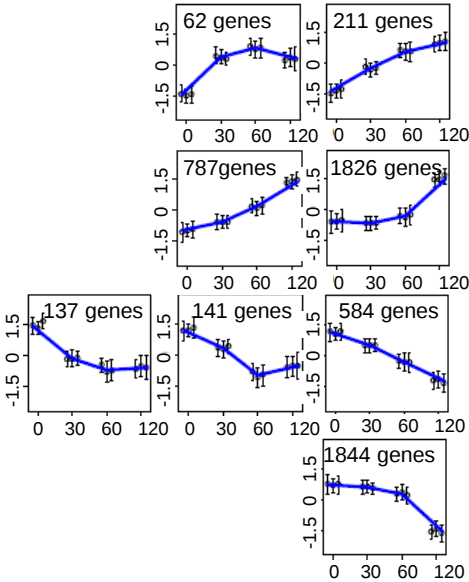
B

0.5µM SAHA



Category Term		Count	P-Value	FE
GOBP	regulation of transcription	65	1 x10 ⁻³	1.5
GOMF	phospholipid binding	10	2.3 x10 ⁻³	3.5
GOCC	Golgi apparatus	23	1.9 x10 ⁻³	2.0
GOMF	glucose transmembrane transporter activity	3	2.4 x10 ⁻²	12.4
GOBP	pattern specification process	22	1.6 x10 ⁻⁷	4.0
GOMF	steroid hormone receptor activity	7	3.8 x10 ⁻⁴	7.2
GOMF	DNA binding	74	2.2 x10 ⁻⁵	1.6
GOBP	regulation of transcription	77	6.3 x10 ⁻⁴	1.4
GOBP	sensory organ development	15	2.9 x10 ⁻⁴	3.2
GOBP	cell fate commitment	12	1.4 x10 ⁻⁴	4.2
GOMF	cytokine activity	27	9.2 x10 ⁻¹⁷	8.4
GOBP	regulation of transcription	72	6.2 x10 ⁻⁸	1.8
GOBP	transcription	94	2.4 x10 ⁻¹⁰	1.9
GOBP	defense response	28	1.3 x10 ⁻³	1.9
GOMF	transcription regulator activity	51	1.9 x10 ⁻³	1.5
GOCC	histone acetyltransferase complex	7	4.2 x10 ⁻⁴	7.1
GOBP	chromatin modification	16	2.1 x10 ⁻³	2.5

12.5µM SAHA



Category Term		Count	P-Value	FE
GOMF	transcription repressor activity	9	3.8 x10 ⁻³	3.5
GOBP	regulation of transcription	36	7.5 x10 ⁻⁴	1.7
GOBP	pattern specification process	37	4.7 x10 ⁻⁵	2.1
GOCC	anchored to membrane	32	1.5 x10 ⁻⁵	2.3
GOBP	cell motility	38	3.8 x10 ⁻⁴	1.8
GOBP	ossification	19	6.3 x10 ⁻⁴	2.5
GOCC	intrinsic to plasma membrane	110	3.8 x10 ⁻⁵	1.5
GOBP	Wnt receptor signaling pathway	21	5.5 x10 ⁻⁴	2.3
GOBP	endocytosis	30	3.7 x10 ⁻⁴	2.0
GOMF	transcription repressor activity	36	1.2 x10 ⁻³	1.8
GOBP	regulation of transcription	133	2.9 x10 ⁻²²	2.2
GOMF	cytokine activity	30	2.6 x10 ⁻¹⁵	6.4
GOBP	regulation of transcription	201	9 x10 ⁻¹⁴	1.6
GOMF	glucuronosyltransferase activity	8	4.4 x10 ⁻⁵	7.7
GOCC	integral to plasma membrane	74	1.3 x10 ⁻⁴	1.6
GOBP	defense response	45	4.3 x10 ⁻³	1.5
GOMF	C-C chemokine receptor activity	7	5.6 x10 ⁻⁵	9.3
GOCC	histone acetyltransferase complex	10	1.4 x10 ⁻⁴	5.0
GOBP	chromatin modification	23	1.1 x10 ⁻²	1.8