

Isoform switching and exon skipping induced by the DNA methylation inhibitor 5-aza-2'-deoxycytidine

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Supplementary Tables:

Supplementary Table S1. Detailed annotation results of all differentially expressed genes after 5-Aza-CdR treatment.

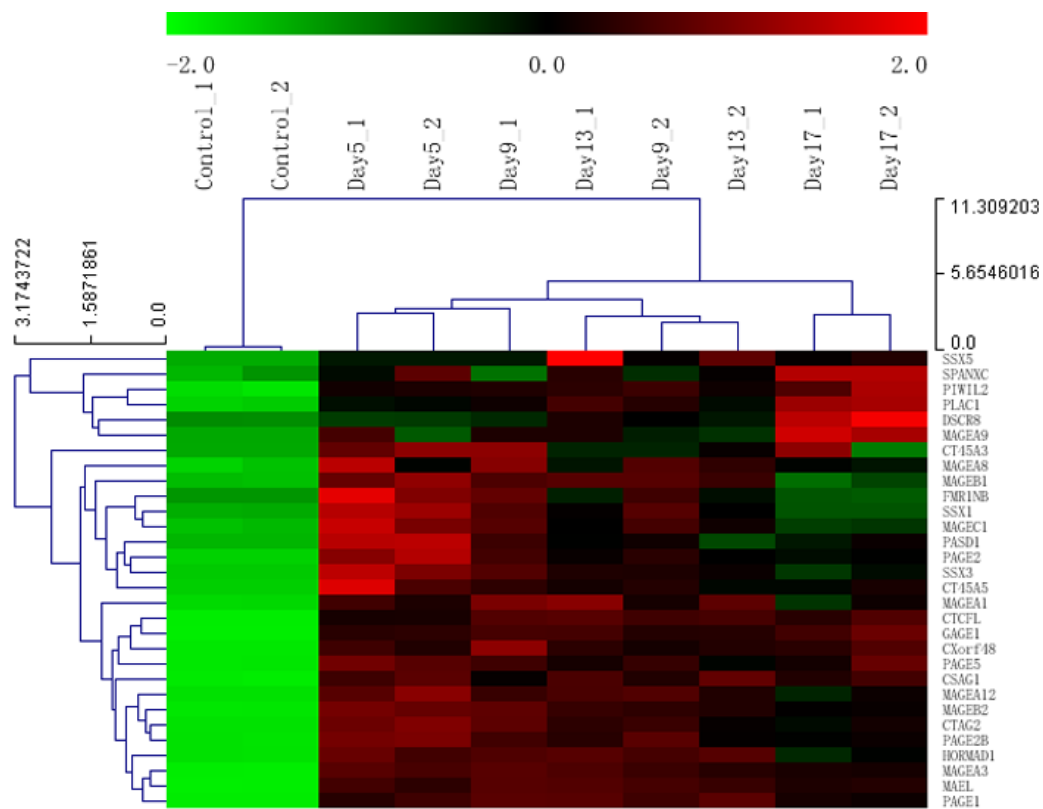
Day5	Total	Up	Down
lncRNA	150	112	38
sense intronic	6	5	1
pseudogene	101	92	9
sense overlapping	3	3	0
processed transcript	16	15	1
antisense	92	75	17
miRNA	2	1	1
protein coding	940	882	58
misc_RNA	5	4	1

Day9	Total	Up	Down
polymorphic pseudogene	1	1	0
lncRNA	158	110	48
sense intronic	7	4	3
pseudogene	105	87	18
sense overlapping	6	4	2
processed transcript	16	15	1
antisense	82	62	20
miRNA	3	1	2
protein coding	961	856	105
misc_RNA	5	4	1

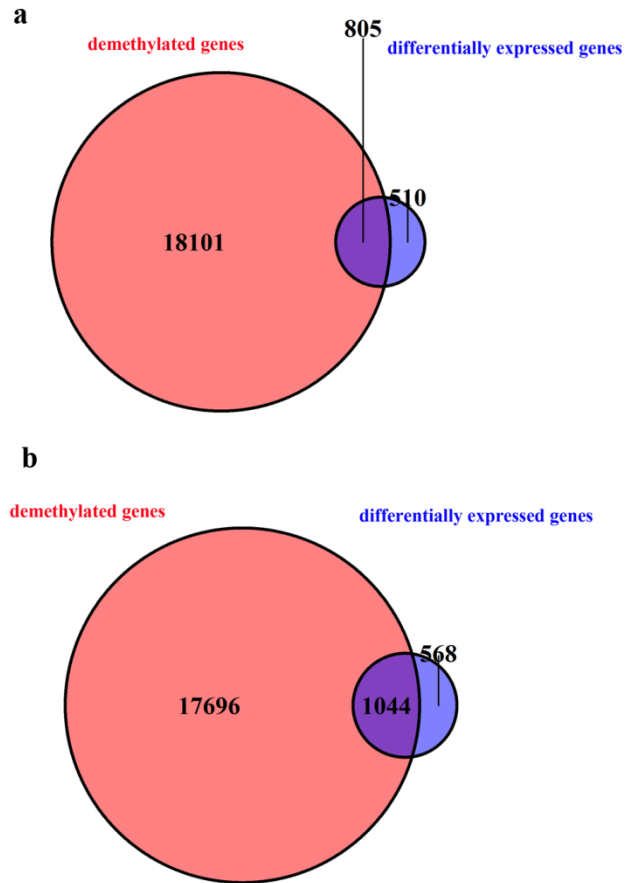
Day13	Total	Up	Down
polymorphic pseudogene	1	1	0
lncRNA	165	111	54
sense intronic	3	3	0
pseudogene	102	84	18
sense overlapping	8	5	3
processed transcript	14	12	2
antisense	72	59	13
TR_V_gene0	1	1	0
miRNA	1	1	0
protein coding	1022	894	128
misc_RNA	4	3	1

Day17	Total	Up	Down
polymorphic pseudogene	2	2	0
lncRNA	186	127	59
sense intronic	4	2	2
pseudogene	113	95	18
snRNA	1	1	0
sense overlapping	6	3	3
processed transcript	16	14	2
antisense	94	79	15
protein coding	1187	1044	143
miRNA	1	1	0
misc_RNA	2	2	0

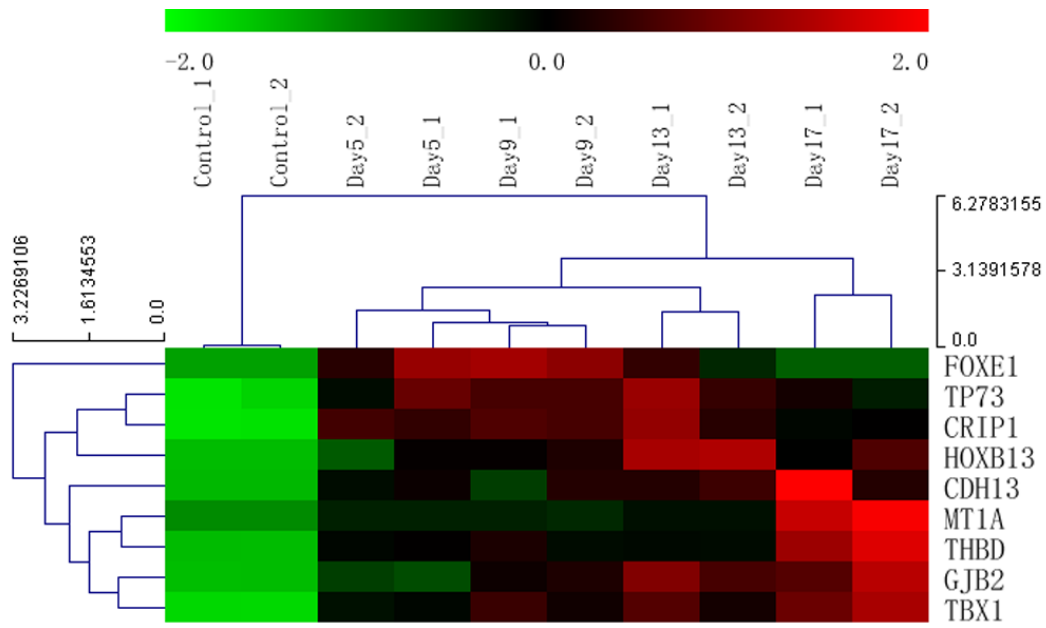
Supplementary Figures



Supplementary Figure S1. Hierarchical clustering of differentially expressed tumor associated antigens after 5-Aza-CdR treatment.



Supplementary Figure S2. Comparison of whole-genome DNA methylation levels with gene expression changes after 5-Aza-CdR treatment. (a) 5-Aza-CdR treatment for 5 days. (b) 5-Aza-CdR treatment for 17 days.



Supplementary Figure S3. Hierarchical clustering of 9 differentially expressed genes which marked with PcG (*EZH2*) and reported to be hypermethylated in cancer.