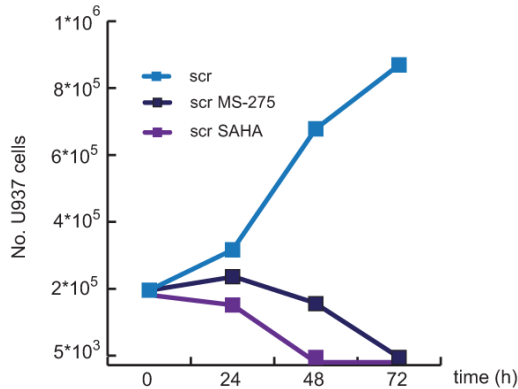


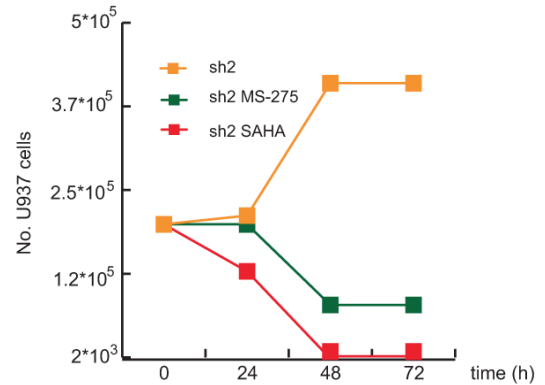
HDAC2 deregulation in tumorigenesis is causally connected to repression of immune modulation and defense escape

Supplementary Material

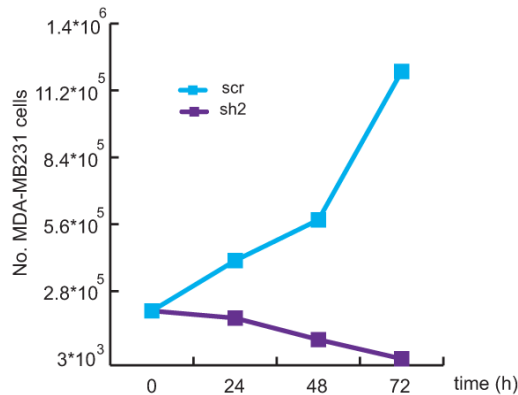
A



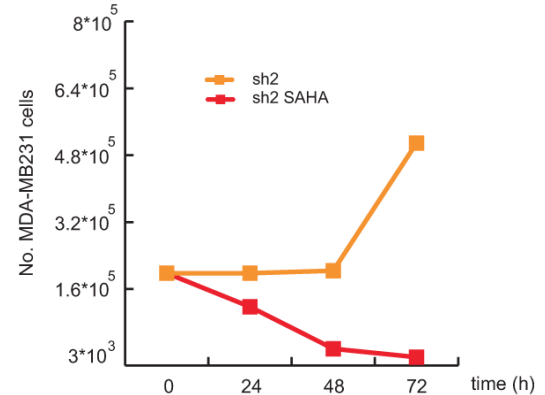
B



C



D



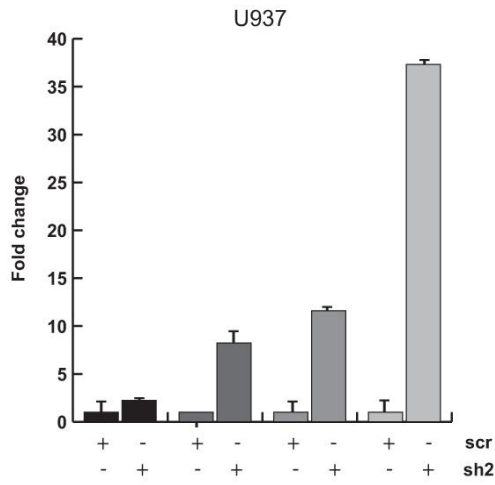
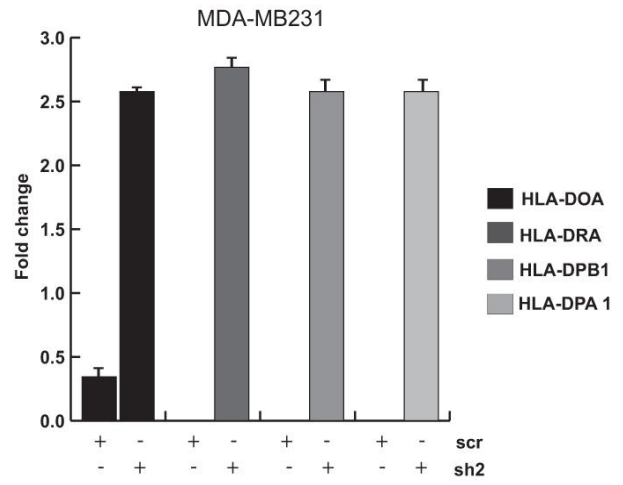
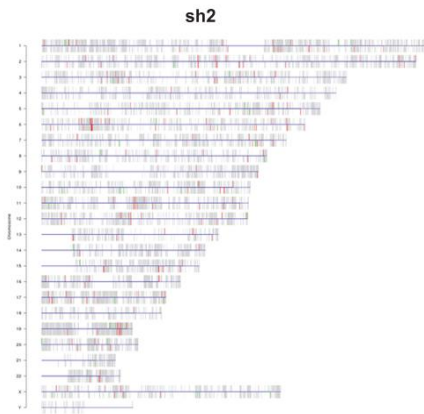
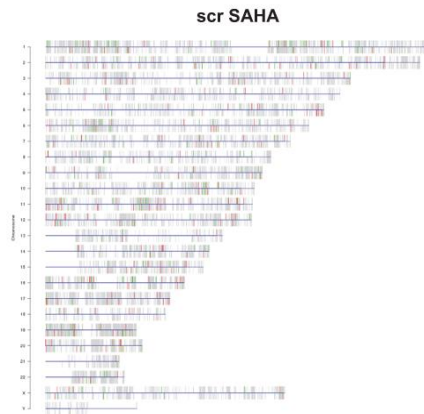
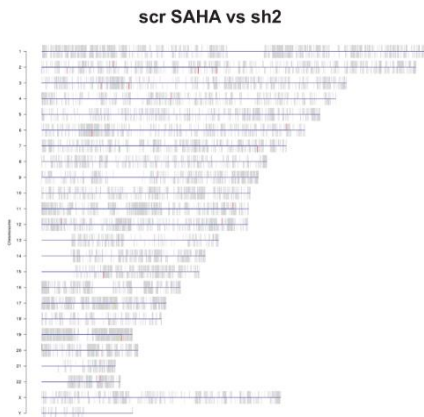
Supplementary figure 1: Proliferation rate in U937 and MDA-MB231 cell lines

A: Proliferation rate of U937 cells comparing scr clone untreated and treated with HDACi SAHA and MS-275 after 24, 48 and 72 hours.

B: Proliferation rate of U937 cells comparing sh2 clone untreated and treated with HDACi SAHA and MS-275 after 24, 48 and 72 hours.

C: Proliferation rate of MDA-MB231 cells comparing scr clone untreated and treated with HDACi SAHA after 24, 48 and 72 hours.

D: Proliferation rate of MDA-MB231 cells comparing sh2 clone untreated and treated with HDACi SAHA after 24, 48 and 72 hours.

A**B****C****D****E**

Supplementary figure 2: Genes involved in MHC class II regions

A: Real-time PCR of *HLA-DOA*, *HLA-DRA*, *HLA-DPB1* and *HLA-DPA1* genes in sh2 and scr U937 clones.

B: Real-time PCR of *HLA-DOA*, *HLA-DRA*, *HLA-DPB1* and *HLA-DPA1* genes in sh2 and scr MDA-MB231 clones.

C: Chromosome localization of the 269 differentially expressed genes upon HDAC2 silencing in U937 cells with FDR <0.01 and fold change >2.

D: Chromosome localization of the differentially expressed genes in common upon 6 and 24 hours SAHA treatment in U937 cells with FDR <0.01 and fold change >2.

E: Chromosome localization of the differentially expressed genes in common upon 6 and 24 hours SAHA treatment in U937 HDAC2-silenced cells with FDR <0.01 and fold change >2.

Supplementary table 1: Gene targets deregulated after HDAC2 knockdown

Validation of chosen gene targets deregulated after HDAC2 knockdown with relative fold changes. Genes downregulated and upregulated upon HDAC2 silencing are highlighted in bold.

Gene name	sh2
HDAC2	0,274047903
ACT18	0.943765278
TERT	0.864237657
EHD2	0.664573191
SNURF	0.002591494
FLJ35767	1.437438268
MMP1	3.369419364
PSD3	1.443929196
ASGR1	1.624504793
EMP1	1.733875127
HLA-DOA	2.233025924
ARGHF10L	1.348635052
C16 ORF45	52.14655352
DEFB1	83.45924706
MBNL2	134.7834921
KLK1	12.52292787
MAGED1	26.8341819
C1ORF54	6.776310582
HLA-DPB1	11.59957466
AGAP2	10.62580325
CD2	1.274118975
MFAP4	2.484576564
MYBPH	2.030028526
HLA-DPA 1	37.31024685
SYTL3	1.2397077
SUCNR1	1.885569072
TYROBP	3.342667836
CAMP	1.9126964
HLA-DRA	8.230613663
RNFT2	6.484520959
TMEM	1.085229372

Supplementary table 2: HLA-DPA1 promoter regions

HLA-DPA1 promoter regions listed on the basis of their relative position on the promoter and motifs for TFs present. The region that presumably recognizes p300 is highlighted in bold.

Gene	Rel. Position	X	Sequence	Factor.name	ABS.Start	ABS.End	Strand
HLA-DPA1	797	(-)	ggcccGCGGGgc	AP-2	33048748	33048759	-
HLA-DPA1	1112	(-)	gggGAGGGg	CKROX	33048436	33048444	-
HLA-DPA1	30	(-)	gtaattATTATtta	FOXJ2	33042412	33042425	-
HLA-DPA1	1045	(+)	ccaGGAAGcgct	GABP	33048500	33048511	-
HLA-DPA1	12	(-)	CGTGG	Kid3	33049540	33049544	-
HLA-DPA1	445	(+)	CCACC	Kid3	33049107	33049111	-
HLA-DPA1	525	(+)	CCACC	Kid3	33049027	33049031	-
HLA-DPA1	585	(-)	GGTGG	Kid3	33041866	33041870	-
HLA-DPA1	748	(-)	GGTGG	Kid3	33041703	33041707	-
HLA-DPA1	868	(+)	CCACG	Kid3	33041583	33041587	-
HLA-DPA1	994	(+)	CCACG	Kid3	33048558	33048562	-
HLA-DPA1	995	(+)	CCACC	Kid3	33041456	33041460	-
HLA-DPA1	1112	(-)	ggggaGGGGGcgg a	KROX	33048431	33048444	-
HLA-DPA1	122	(-)	ttttgTGACcttctc	LXR alpha	33042319	33042333	-
HLA-DPA1	167	(-)	ttttcTGACctccc	LXR alpha	33049375	33049389	-
HLA-DPA1	211	(+)	gctgaGGTCAcctcc	LXR alpha	33049331	33049345	-
HLA-DPA1	701	(-)	tatagTGACCaaaaa	LXR alpha	33041740	33041754	-
HLA-DPA1	852	(+)	tcagGGTCAtgggc	LXR alpha	33048690	33048704	-
HLA-DPA1	860	(-)	tctctTGACCacgct	LXR alpha	33041581	33041595	-
HLA-DPA1	1112	(+)	gGGGAGgg	MAZ	33048437	33048444	-
HLA-DPA1	983	(-)	ccggaACTCCccca	p300	33048560	33048573	-
HLA-DPA1	573	(+)	tttttCACCCc	Pax-4	33048972	33048983	-
HLA-DPA1	746	(-)	gGGGTGgggctc	Pax-4	33041698	33041709	-
HLA-	1050	(-)	gcctcagttctcatCAC	Pax-5	33041378	33041405	-

DPA1			TGttcctgtg				
HLA-DPA1	574	(+)	ttttTCACCccacat	SREBP	33048968	33048982	-
HLA-DPA1	574	(+)	ttttCACCCca	SREBP	33048971	33048982	-
HLA-DPA1	796	(+)	gaaGGTGTaact	TBX5	33041648	33041659	-
HLA-DPA1	1008	(-)	aaGCGCGcgaact	ZF5	33048536	33048548	-

Supplementary table 3: *HLA-DPA1* promoter regions

HLA-DRA promoter regions listed on the basis of their relative position on the promoter and motifs for TFs present. The region that presumably recognizes p300 is highlighted in bold.

Gene	Rel Position	X	Sequence	Factor.name	ABS.Start	ABS.End	Strand
HLA-DRA	329	(+)	cCAATCt	HOXA7	32406947	32406953	+
HLA-DRA	789	(-)	aGATTGg	HOXA7	32407407	32407413	+
HLA-DRA	95	(-)	GGTGG	Kid3	32406713	32406717	+
HLA-DRA	98	(-)	GGTGG	Kid3	32406716	32406720	+
HLA-DRA	190	(+)	CCACC	Kid3	32406808	32406812	+
HLA-DRA	13	(+)	cacgaGGTCAggagt	LXR alpha	32406631	32406645	+
HLA-DRA	284	(-)	ttcatTGACctgaat	LXR alpha	32406902	32406916	+
HLA-DRA	1061	(-)	gcctcACTCCgag	p300	32407679	32407692	+
HLA-DRA	892	(+)	atgAACGGa	v-Myb	32407510	32407518	+