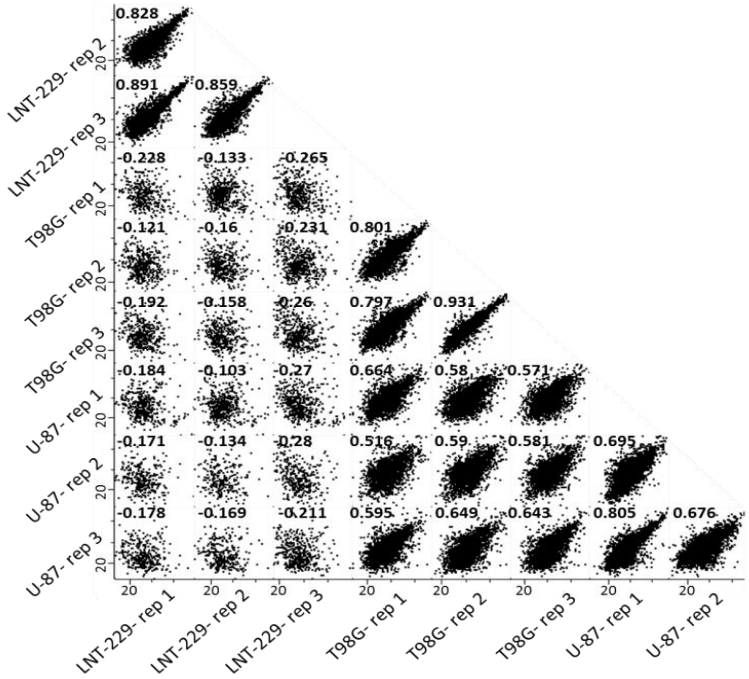
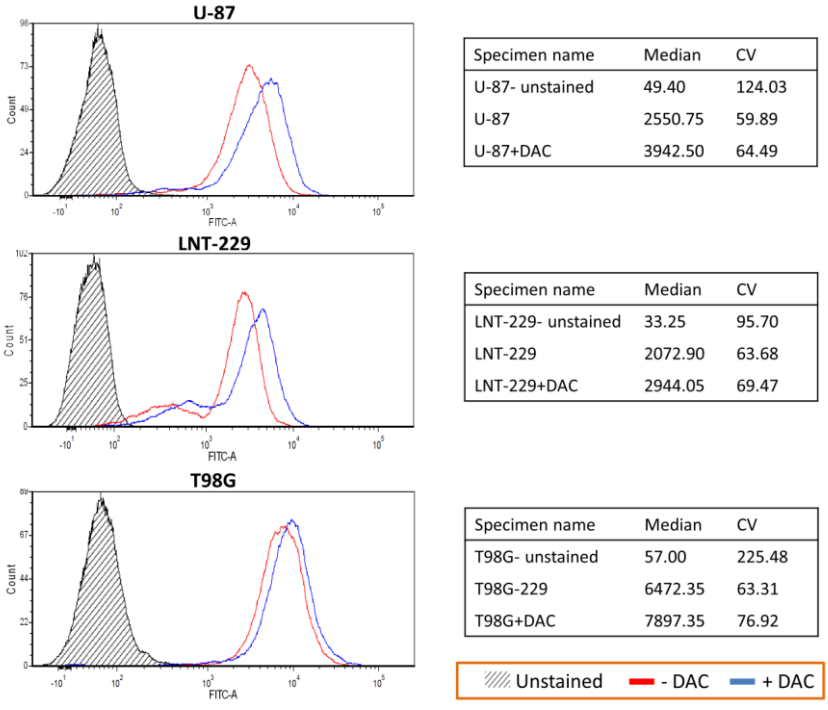


Figure S1. Multi Scatter Plots are displayed as the log2 intensity of the HLA peptides shared between each of the three biological repetitions and in the different cell lines. The insert number in each scatter indicate its Pearson correlation. The U87 and T98G cells share HLA haplotype that is absent from the LNT-229.

A.



Specimen name	Median	CV
U-87- unstained	49.40	124.03
U-87	2550.75	59.89
U-87+DAC	3942.50	64.49

Specimen name	Median	CV
LNT-229- unstained	33.25	95.70
LNT-229	2072.90	63.68
LNT-229+DAC	2944.05	69.47

Specimen name	Median	CV
T98G- unstained	57.00	225.48
T98G-229	6472.35	63.31
T98G+DAC	7897.35	76.92

B.

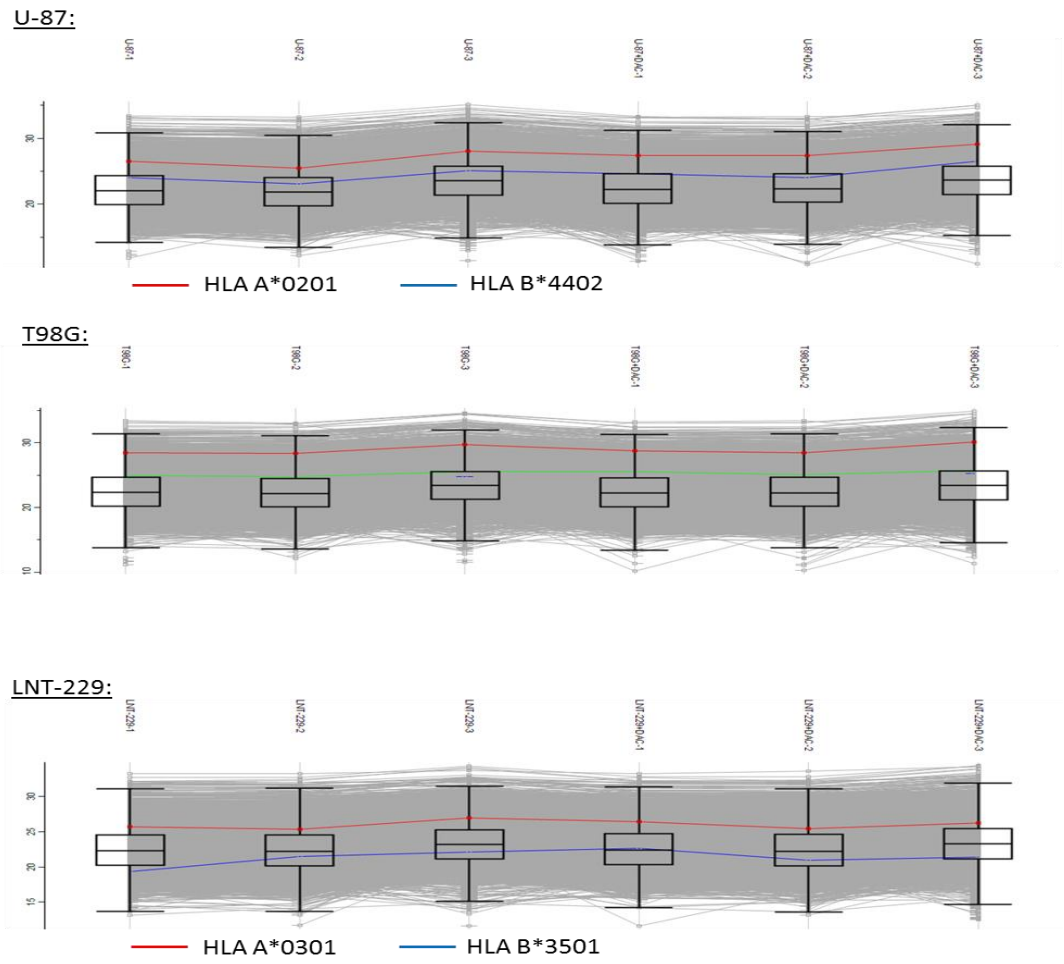


Figure S2.

The HLA class I expression of the three Glioblastoma cell lines before and after treatment with Decitabine as assessed by A) Flow cytometry analysis; B) LFQ values of the individual HLA allotypes present in each cell line from the proteome analyses.

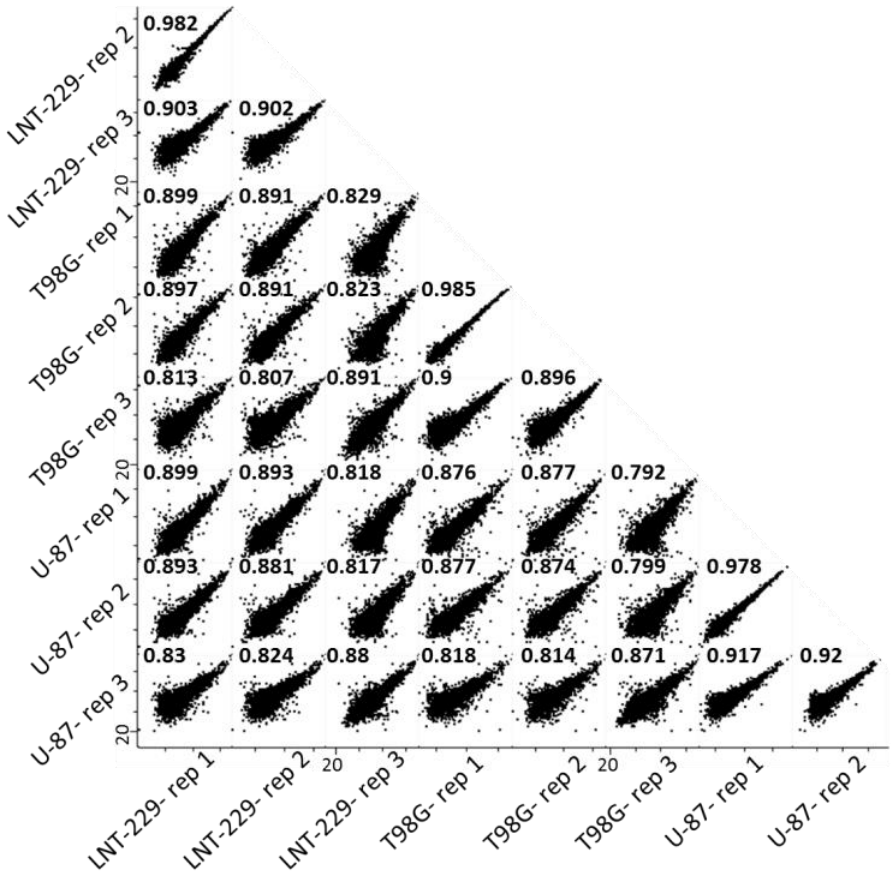


Figure S3. Multi Scatter Plots are displayed as the LFQ intensities of the proteins shared between each of the three biological repetitions in the different cell lines. The insert number in each scatter indicate its Pearson correlation. Repetitions 1 and 2 were performed with in-solution trypsin digests, while repetition 3 was performed by in-gel digests of the proteins resolved by SDS-PAGE (see Methods).

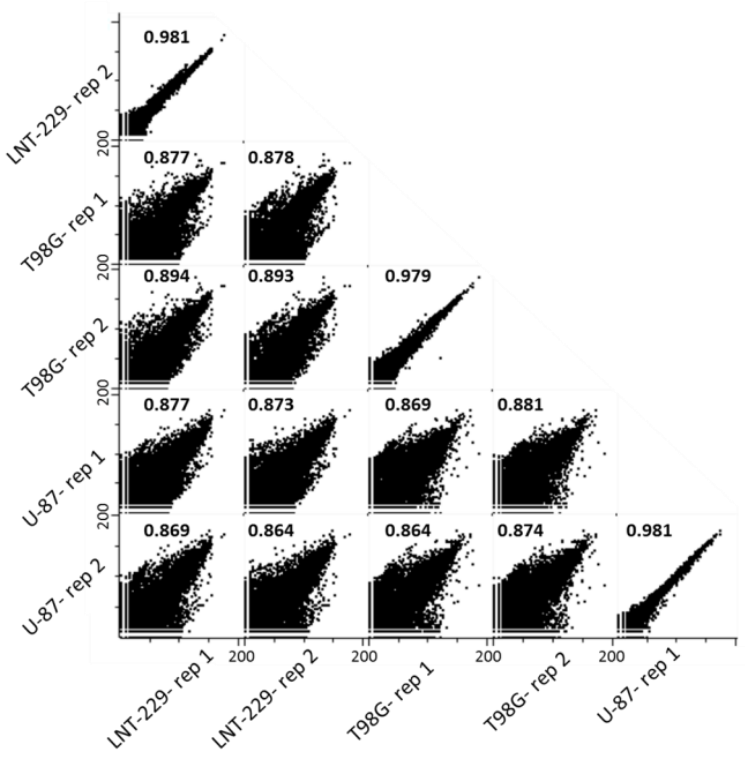


Figure S4. Multi Scatter Plots are displayed as levels of the transcripts shared between each of the two biological repetitions in the different cell lines. The insert number in each scatter indicate its Pearson correlation.

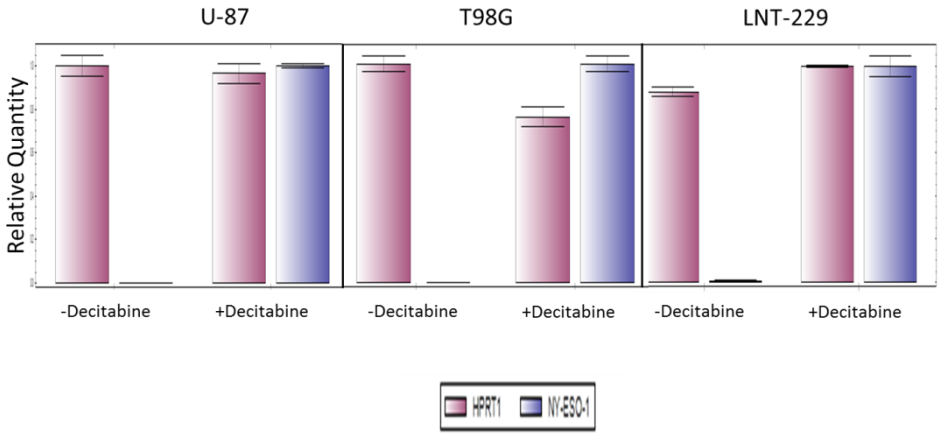


Figure S5. RT-qPCR analyses on the NY-ESO-1 and HPRT1 transcripts of the three Glioblastoma cell lines, before and after treatment with Decitabine. The HPRT1 gene was used as a control.

Table S1. MaxQuant Peptides output table containing the HLA peptides sequences, lengths, masses, proteins IDs and gene names, charge states, identification scores, intensities and normalized log(FC) in each of the samples. It includes also the best HLA type present in the particular cell line and associated with each peptide according to NetMHC. It also indicates if the HLA peptide was significantly affected by Decitabine, whether it was upregulated or down-regulated, and if the source protein of the peptide is defined as a tumor antigen and as a CTA.

Table S2. MaxQuant Protein Group output table listing the proteins IDs, protein and gene names, identification scores and LFQ and iBAQ intensities in the different samples. It also indicates if the protein was significantly affected by Decitabine, whether it was upregulated or down-regulated according to the LFQ values, and if the protein is defined as a tumor antigen and as a CTA.

Table S3. The table lists the genes IDs and their transcript, gene length and position, and the transcript intensities in each of the samples. It also indicates if the transcript was significantly affected by Decitabine, whether it was upregulated or down-regulated, and if the gene is defined as a tumor antigen and as a CTA.

Table S4. Listings of the Tumor Antigens proteins and gene names, with their CTA scores according to the BioGPS data base. It also indicates if each of these tumor antigens' HLA peptides, proteins and transcripts were detected and upregulated following the treatment with Decitabine.