SUPPLEMENTARY FIG. S9. Principal component analysis to identify Gb groups displaying a differential survival time and IDH1 mutational status. The aim of the PCA analysis was to detect those genes whose expression levels allowed to subset cases in groups that display differential survival and *IDH1* mutation status' features. Both genes (*left side*) and cases (*right side*) can be plotted in the space defined by the two first components (Dim1 and 2 in the plots), which are the components accumulating the highest amount of variability in the dataset. In addition, the supplementary variables (the Cox's residuals, *blue arrow*, and the *IDH1* mutation status, G and G/A *pink colored*) can be depicted. On the *left side*, each *arrow* corresponds to a gene and as more parallel is to a component, the higher the correlation with that component is. A high correlation of *MGMT* values with both positive values of the second component and the Cox's residuals is observed, which means that high *MGMT* values are expected to correspond to a high probability of death. To a lower extent, the *LDHA* expression values are also correlated to the Cox's residuals, but to the negative values, which would indicate a higher chance of survival. In contrast, the rest of genes showed almost a null correlation with Cox's residuals. On the *right side*, the centroid of patients harboring the G/A mutation of *IDH1* gene falls in the area delimited by negative values of both components. Cases are denoted as *points* and its associated number. Considering this feature and the higher survival expected from cases displaying negative values of the second component, a −0.5 value from the second component was set as the threshold to split cases in two groups displaying the highest difference in survival.