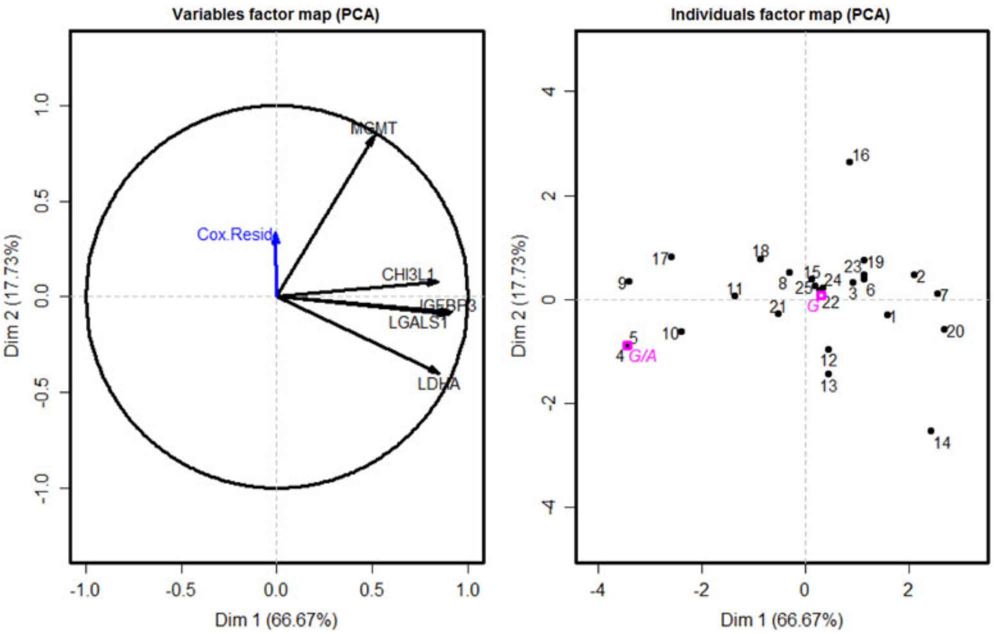

SUPPLEMENTARY FIG. S5. Principal component analysis to identify Gb groups displaying a differential survival time and *IDH1* mutational status. The aim of the PCA analysis was to detect those genes whose expression levels allowed to subset cases in groups that display differential survival and *IDH1* 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.