



SUPPLEMENTARY FIG. S6. Survival and molecular features of LDA functions and IDH1 mutational status based on 271 TCGA cases. *Left plots* are survival curves based on classification provided by the *IDH1* status and by the LDA functions fitted with *CoISBE*, *MGMT-LDHA*, *MGMT*, or *LDHA* expression values (Equations 1–4). The discriminant scores for classification were computed by multiplying standardized values from TCGA data by the discriminant coefficients obtained from our training RT-PCR data ($n=35$, Equations 1–4). The cut-off to classify in one of two groups was set to zero. The p value indicates the probability that curves are equal. Plots on the *right* depict the percentage of cases showing an *MGMT* expression below the average of all cases and the percentage of cases showing *IDH1* mutation in each group. The p value denotes the probability that proportions are equal.