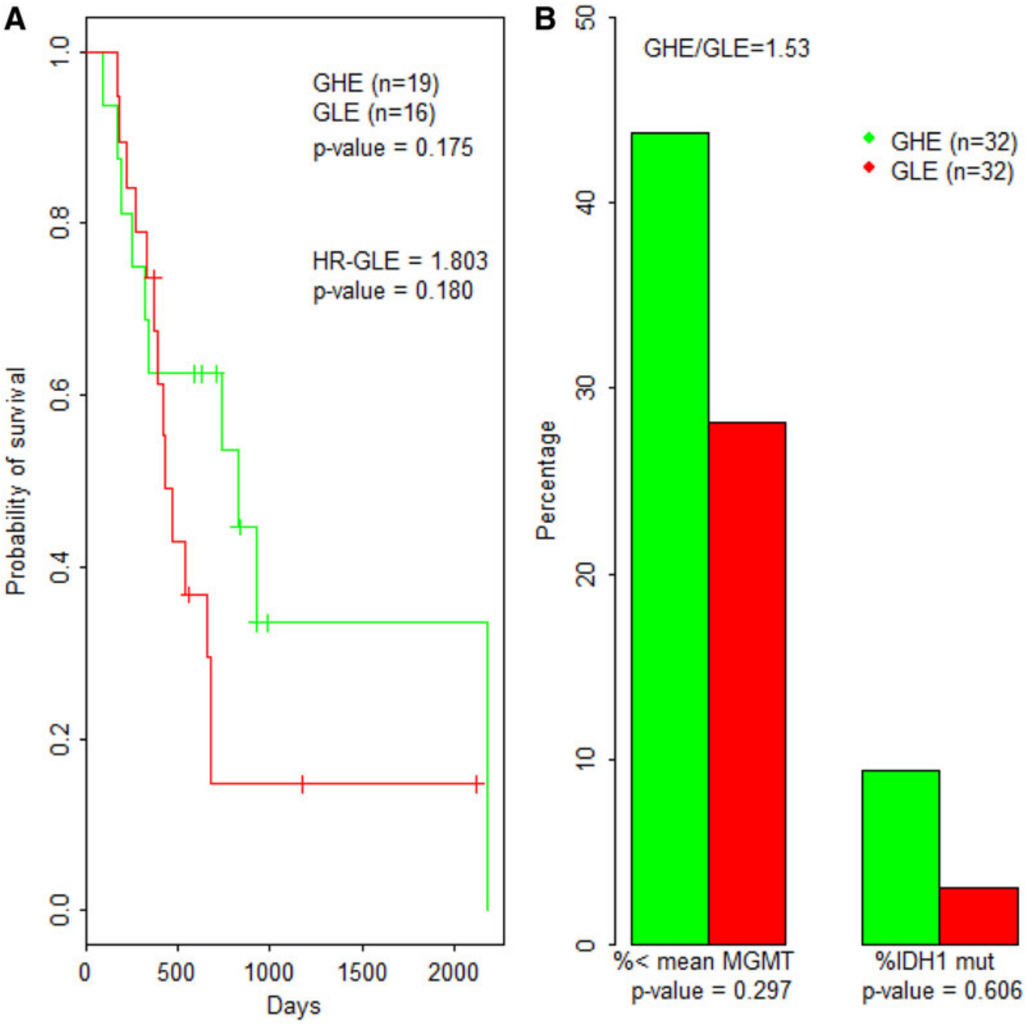
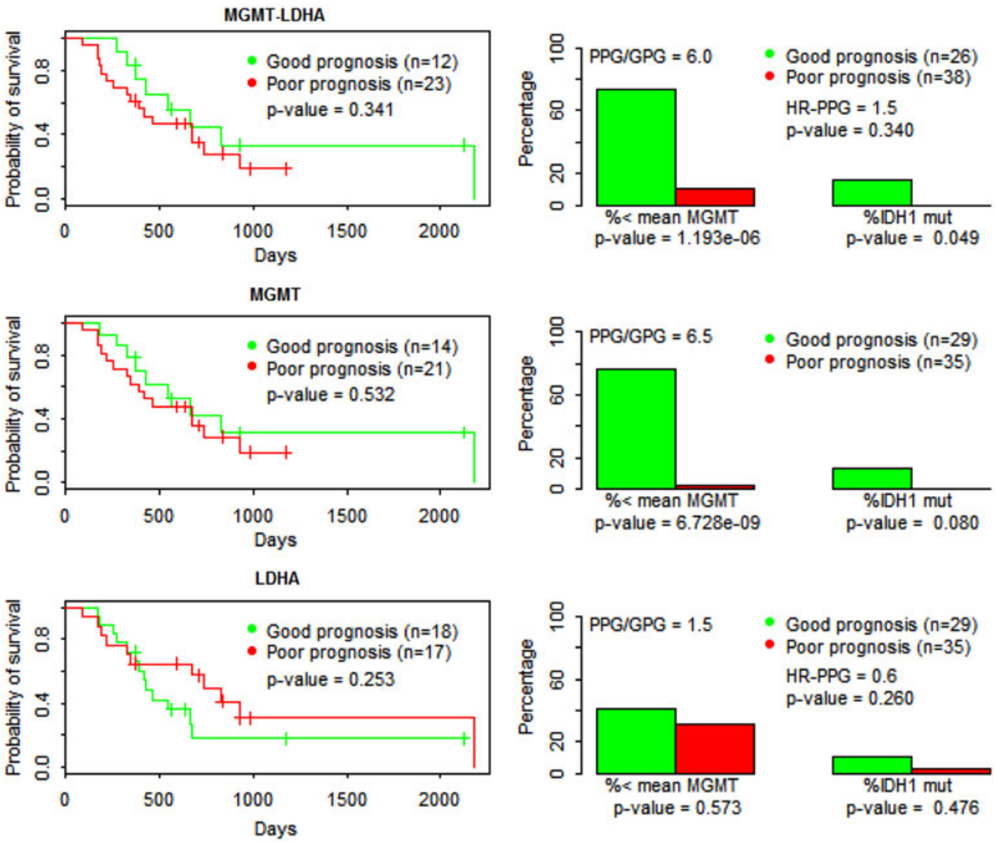
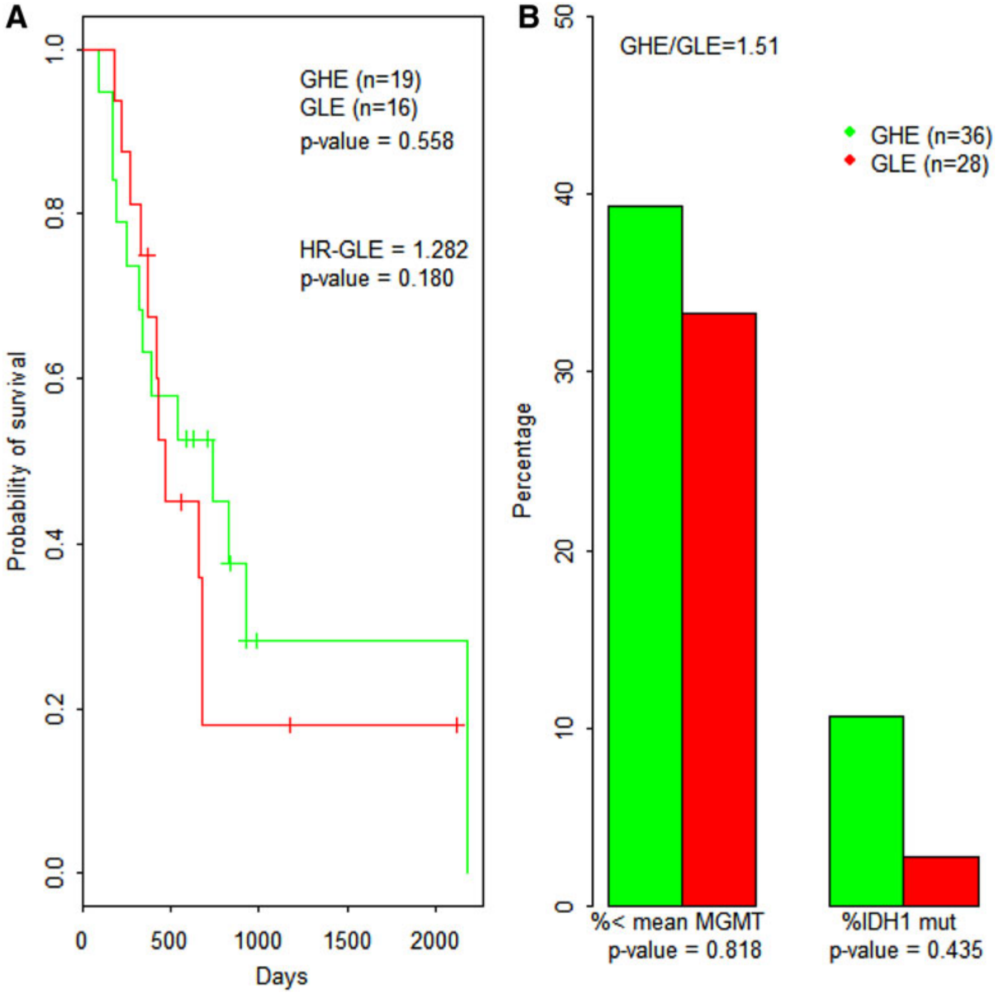


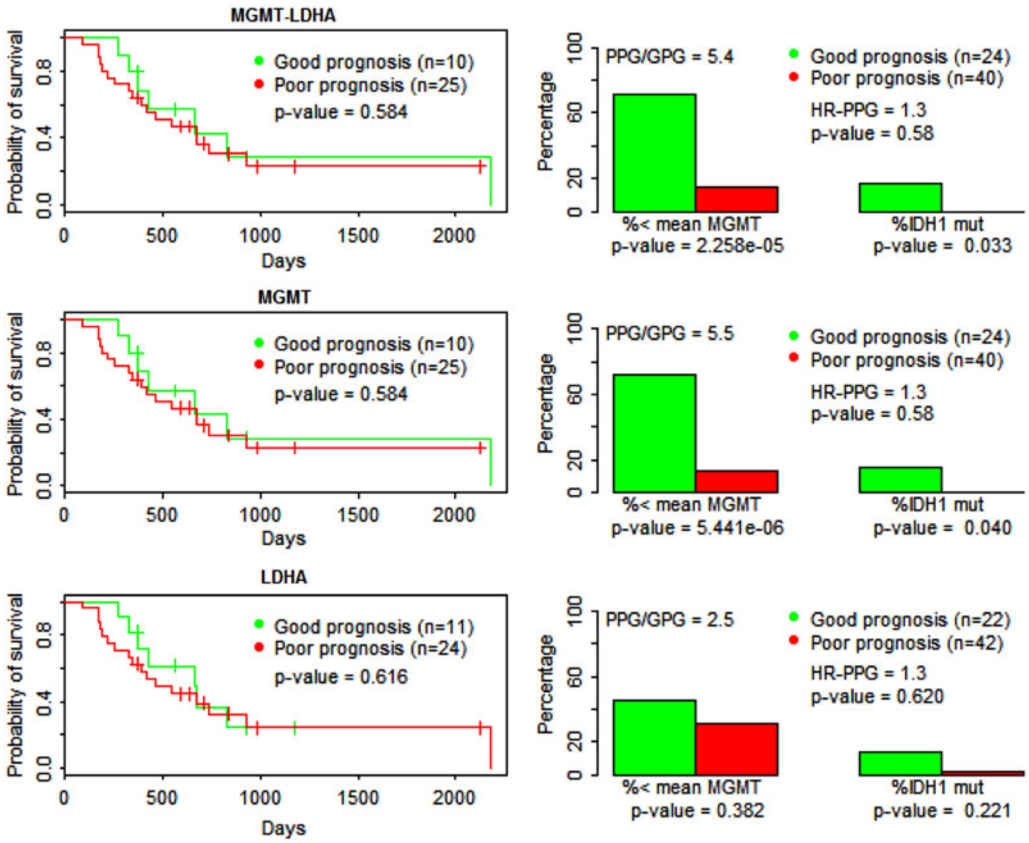
SUPPLEMENTARY FIG. S10. Survival and molecular features of ColSBE based on classification obtained from Equation 2. All cases ($n = 64$) were classified as group of low and high expression (GLE and GHE) using Equation 2. **(A)** Survival curves based on ColSBE as classified by the LDA equation using standardized Ct values for those cases with survival data available. **(B)** This figure summarizes the molecular features based on *MGMT* expression and *IDH1* mutational status (codon 132). The *left-side bars* describe the percentage of cases below the *MGMT* average expression by ColSBE group, while the *right-side bars* provide the percentage of cases showing *IDH1* mutation in each ColSBE group. The GHE/GLE indicates the fold-change between groups for the *MGMT* expression levels. The *p* value denotes the probability that proportions are equal.



SUPPLEMENTARY FIG. S11. Survival and molecular features of ColSBE based on classification obtained from Equations 6–8. All cases ($n = 64$) were classified as group of good and poor prognosis (GPG and PPG) using Equations 6–8. *Left plots* are survival curves based on LDA functions fitted with either *MGMT-LDHA*, *MGMT*, or *LDHA* expression values. All samples having survival data available were used ($n = 35$). 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 ($n = 64$) and the percentage of cases showing *IDH1* mutation in each group (GPG and PPG). The p value denotes the probability that proportions are equal.



SUPPLEMENTARY FIG. S12. Survival and molecular features of ColSBE based on classification obtained from microarrays experiments for the 42 training cases. The test cases ($n = 22$) were classified as group of low and high expression (GLE and GHE) using Equation 2. In contrast, the original ColSBE label obtained from microarrays data was set to the training cases ($n = 42$). **(A)** Survival curves based on ColSBE as classified by the LDA equation using standardized Ct values for those cases with survival data available. **(B)** This figure summarizes the molecular features based on *MGMT* expression and *IDH1* mutational status (codon 132). The *left-side bars* describe the percentage of cases below the *MGMT* average expression by ColSBE group, while the *right-side bars* provide the percentage of cases showing *IDH1* mutation in each ColSBE group. The GHE/GLE indicates the fold-change between groups for the *MGMT* expression levels. The p value denotes the probability that proportions are equal.



SUPPLEMENTARY FIG. S13. Survival and molecular features of ColSBE based on classification obtained from microarrays experiments for the 25 training cases. The test cases ($n = 39$) were classified as group of good and poor prognosis (GPG and PPG) using Equations 6–8, while the original label obtained from Supplementary Figure S9 above was set to the training cases ($n = 25$). *Left plots* are survival curves based on LDA functions fitted with either *MGMT-LDHA*, *MGMT,* or *LDHA* expression values. All samples having survival data available were used (n = 35). 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 ($n = 64$) and the percentage of cases showing *IDH1* mutation in each group (GPG and PPG). The p value denotes the probability that proportions are equal.