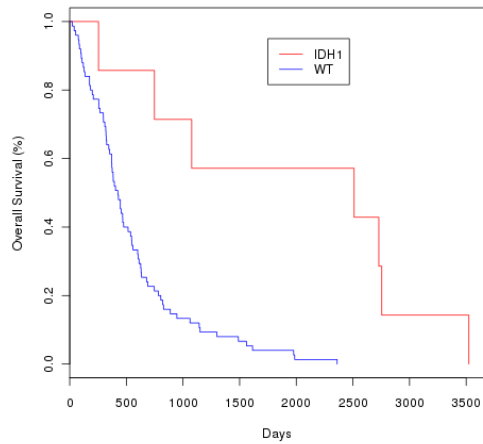
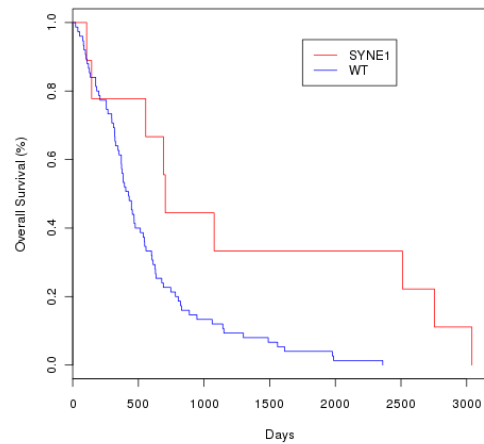


**A**  $\log(\text{Haz. Ratio}) = 1.9757$  Z-Score = 3.245 P-Val = 0.00118



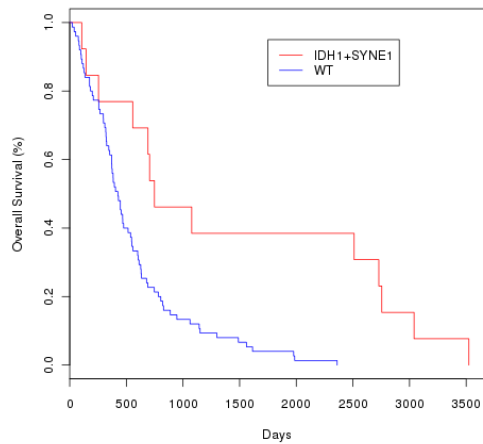
Mutated in IDH1 (*IDH1*) vs wild type for IDH1 and SYNE1 (*WT*)

**B**  $\log(\text{Haz. Ratio}) = 1.1584$  Z-Score = 2.646 P-Val = 0.00814



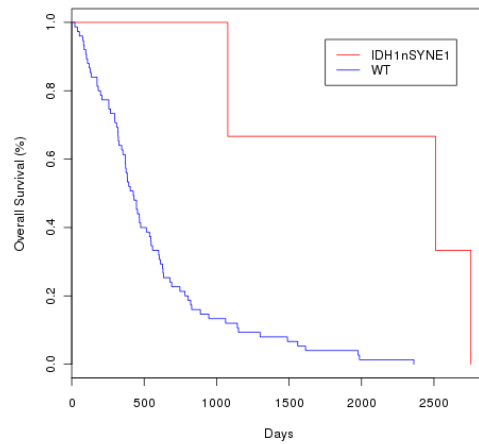
Mutated in SYNE1 (*SYNE1*) vs wild type for IDH1 and SYNE1 (*WT*)

**C**  $\log(\text{Haz. Ratio}) = 1.2637$  Z-Score = 3.267 P-Val = 0.00109



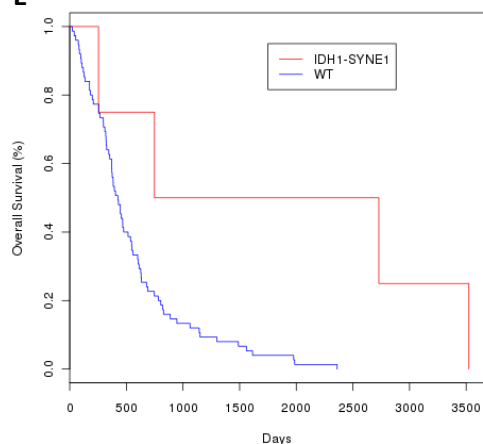
The union of samples mutated in IDH1 and SYNE1 (*IDH1+SYNE1*) vs wild type for IDH1 and SYNE1 (*WT*)

**D**  $\log(\text{Haz. Ratio}) = 2.456$  Z-Score = 2.404 P-Val = 0.0162



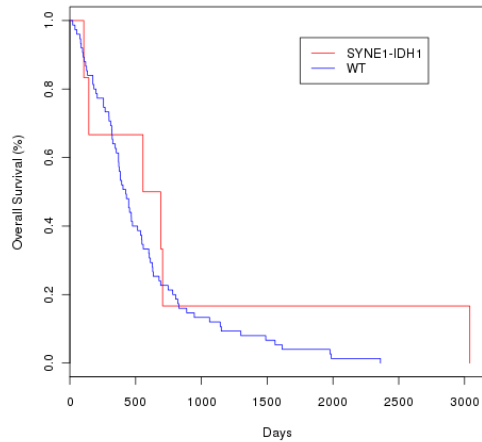
The intersection of samples mutated in IDH1 and SYNE1 (*IDH1nSYNE1*) vs wild type for IDH1 and SYNE1 (*WT*)

**E**  $\log(\text{Haz. Ratio}) = 1.6884$  Z-Score = 2.295 P-Val = 0.0217



Samples mutated in IDH1 and not SYNE1 (*IDH1-SYNE1*) vs wild type for IDH1 and SYNE1 (*WT*)

**F**  $\log(\text{Haz. Ratio}) = 0.5607$  Z-Score = 1.194 P-Val = 0.233



Samples mutated in SYNE1 and not IDH1 (*SYNE1-IDH1*) vs wild type for IDH1 and SYNE1 (*WT*)

**Supplementary Figure 1:** Because IDH1 mutation status has been associated with increased survival among glioblastoma (GBM) patients<sup>1</sup>, and our results show significant mutation-mutation co-occurrence between IDH1 and SYNE mutation status (Fisher's exact p-value, 0.001), we did survival analysis to determine whether or not SYNE1 mutation is also associated with increased survival among GBM patients. Survival for patients with IDH1 mutation and SYNE1 mutation are similar (Supplementary Figures 1A and 1B, respectively), relative to patients with wild type IDH1 and SYNE1. However, Supplementary Figures 1E shows that patients with IDH1 mutation and wild-type SYNE1 have increased survival, while patients with SYNE1 mutation and wild-type IDH1 do not have increased survival (Supplementary Figures 1F). The survival analysis from Supplementary Figures 1A-1F suggests that any apparent increased survival for patients harboring SYNE1 mutation probably does not arise from a mutant SYNE1-specific phenotype.

| Hugo symbol | Substitution site  | Cancer type   |
|-------------|--|---|
| TP53        | A347, R273, P278, F270, H179, N235, P177, R282, C176, R248, C238, Y220, P278, C141, E258, A276, C135, I195, K164, G245, M133, H178, H193, R158, V216, V272, R273, R156, Y220, D281, G244, G105, V173, G266, L130, R175, R175, L130 | Many cancer types   |
| MSH6        | T1219  | Melanoma, adenocarcinoma  |
| RB1         | R661   | Transitional cell carcinoma, small cell carcinoma, leiomyosarcoma |
| NF1         | R977   | Neurofibroma  |
| IDH1        | R132   | Leukemia, GBM, adenocarcinoma                                     |

**Supplementary Table 1.** Genes (*Hugo Symbol*) whose mutation status was correlated with the drastic over- and under-expression of other genes and that were mutated at a specific site that is annotated in the COSMIC database (<http://www.sanger.ac.uk/genetics/CGP/cosmic/>), the *Substitution site*, and the different *Cancer type[s]* those site-specific mutations occur.

1) Parsons *et al.* *An Integrated Genomic Analysis of Human Glioblastoma Multiforme*. *Science* **2008** 321: 1807