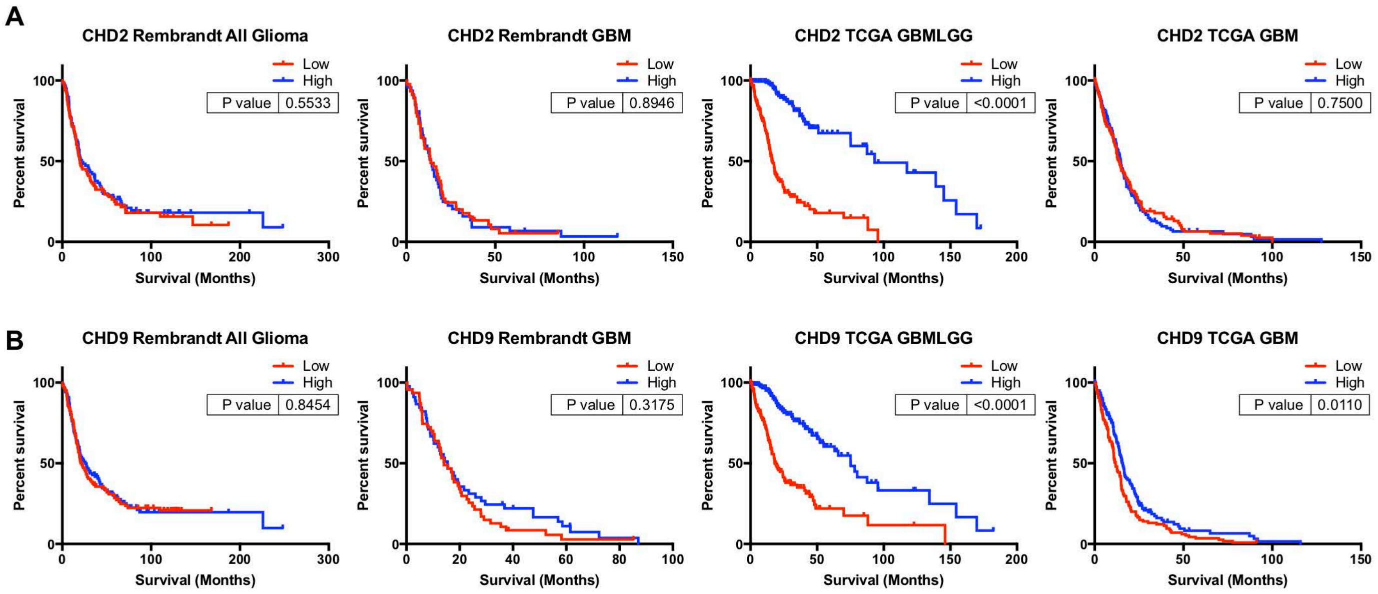
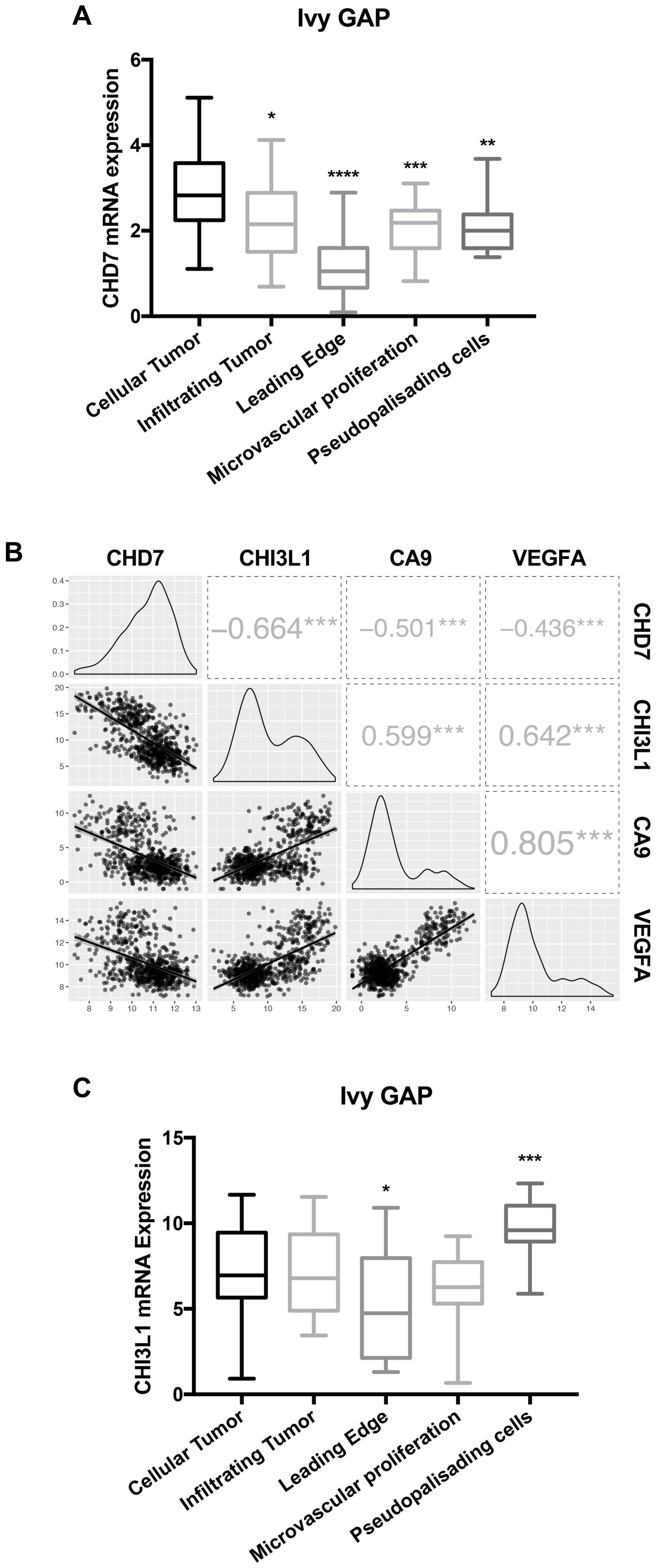
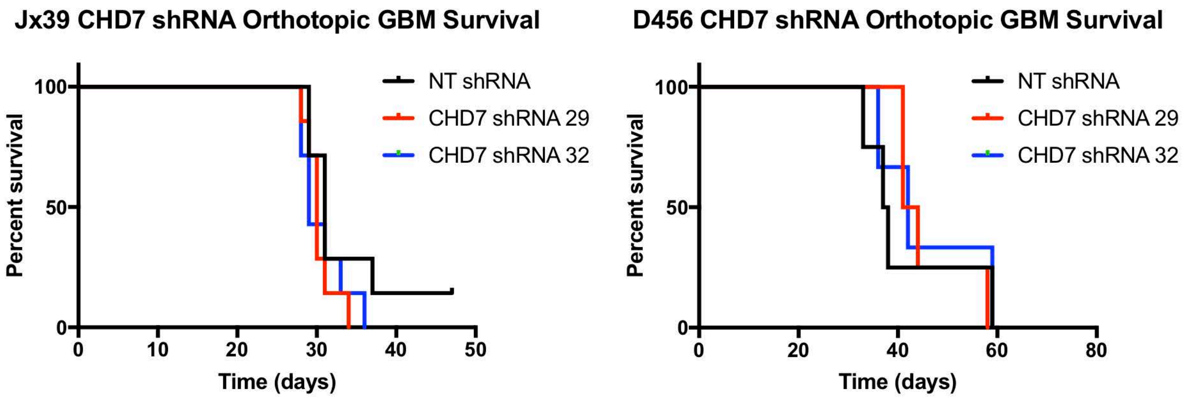


Supplemental Figure S1. CHD2 and CDH9 Do not Consistently Correlate with Poor Glioma Patient Outcomes. CHD family members **(A)** CHD2 and **(B)** CHD9 which were also downregulated by acidic stress in the initial screen were assessed for correlations with patient outcomes using REMBRANDT or TCGA data. P values for the indicated log rank survival curve comparisons are shown.



Supplemental Figure S2. Levels of CHD7 and a Candidate Target Gene, CH13L1, in Pseudopalisading Cells and Correlations with Hypoxia Target Genes. (A) CHD7 mRNA levels in the Ivy GAP dataset indicate lower levels in pseudopalisading cells in comparions to the more cellular tumor. **(B)** In silico analysis demonstrates expression of CHD7 in TCGA glioma patient samples with correlation coefficients for CHI3L1, CA9 or VEGFA. **(C)** CHI3L1 levels are elevated in pseudopalisading cells in the Ivy GAP dataset. *, $p<0.05$; **, $p<0.01$; ***, $p<0.001$; **** , $p<0.0001$ with ANOVA comparison to cellular tumor



Jx39 CHD7 shRNA Orthotopic GBM Survival

D456 CHD7 shRNA Orthotopic GBM Survival

Supplemental Figure S3. Screen for Chromatin Remodeling Genes Transcriptionally Regulated by Perinecrotic Microenvironments. Jx39 and D456 GBM PDX were transduced with shRNA directed toward CHD7 or random non-targeting sequence and orthotopically implanted into mice. Survival curves generated from mice monitored until they reached a tumor burden that induced neurological signs. CHD7 shRNA did not significantly affect survival of these mice as compared to the non-targeting shRNA.

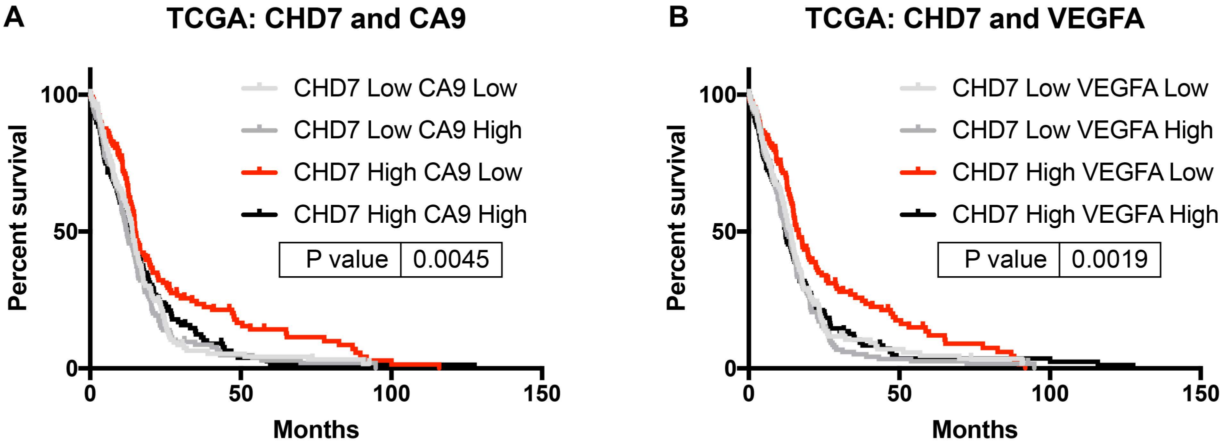


Figure S4. CHD7 Co-Expression with the Hypoxia Target Genes CA9 or VEGF Correlates with Prognosis. In silico analysis demonstrates expression of CHD7 in TCGA GBM patient samples stratified by CHD7 expression (low or high) and co-expressed with **(A)** CA9 or **(B)** VEGFA. P value shown for Log-rank Mantel-Cox test.