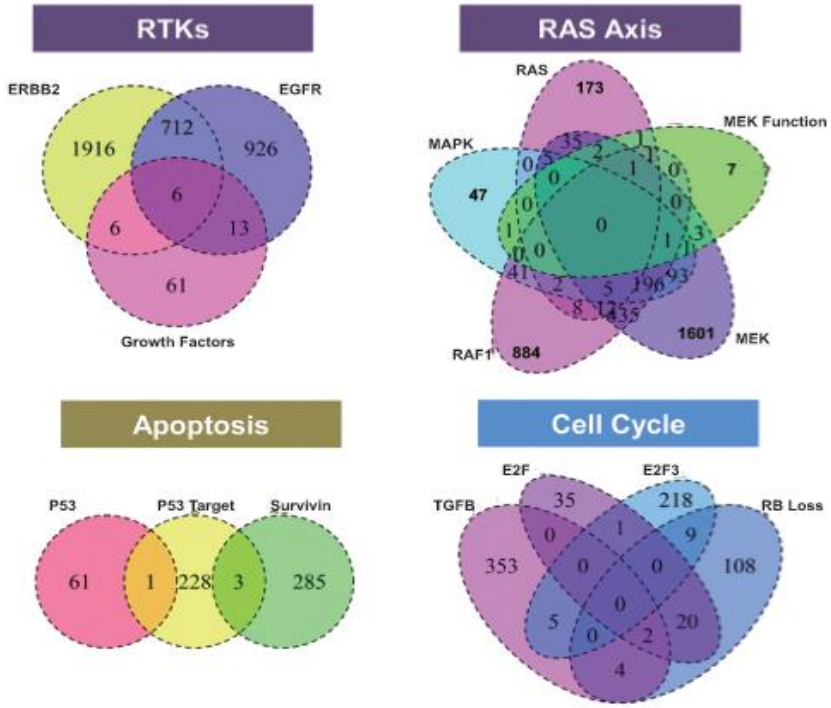
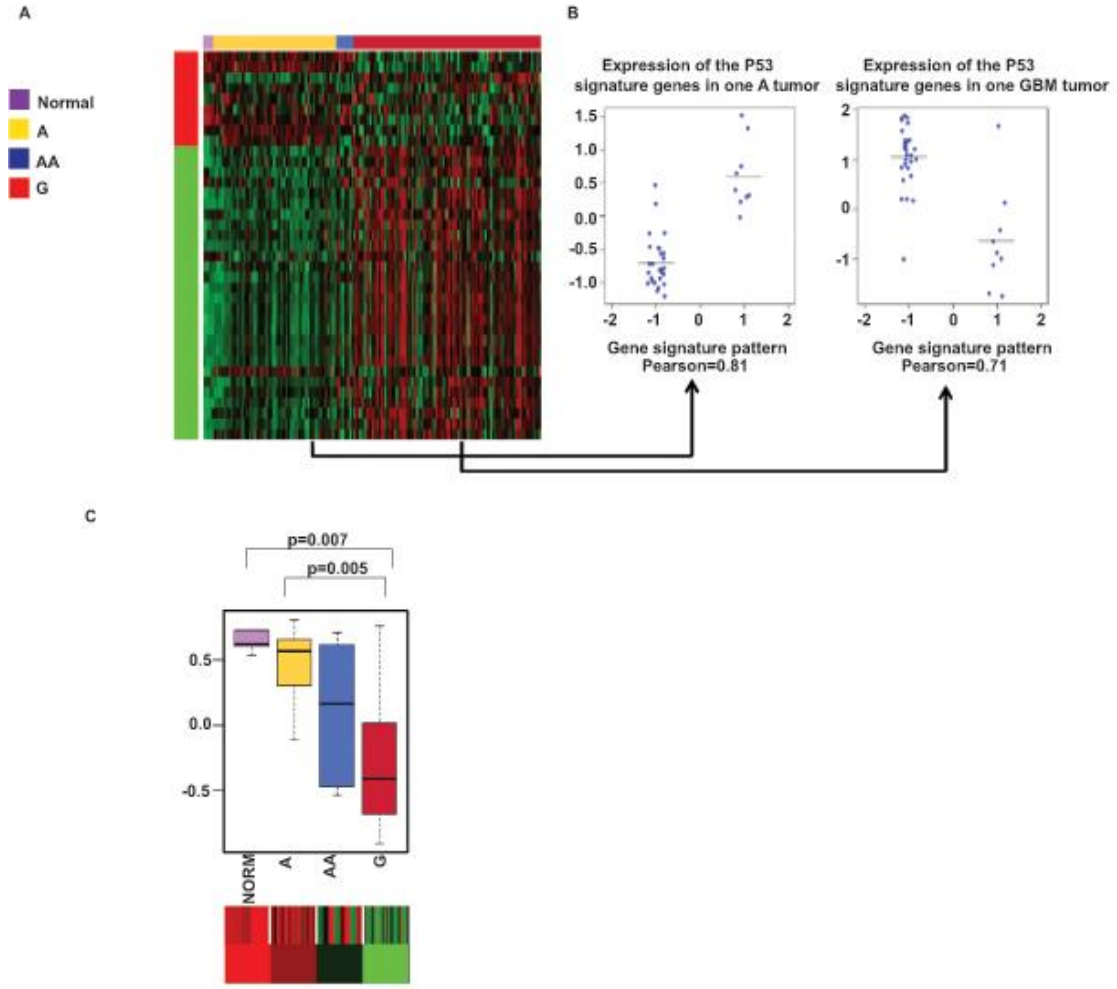
Epigenetic suppression of EGFR signaling in G-CIMP+ glioblastomas

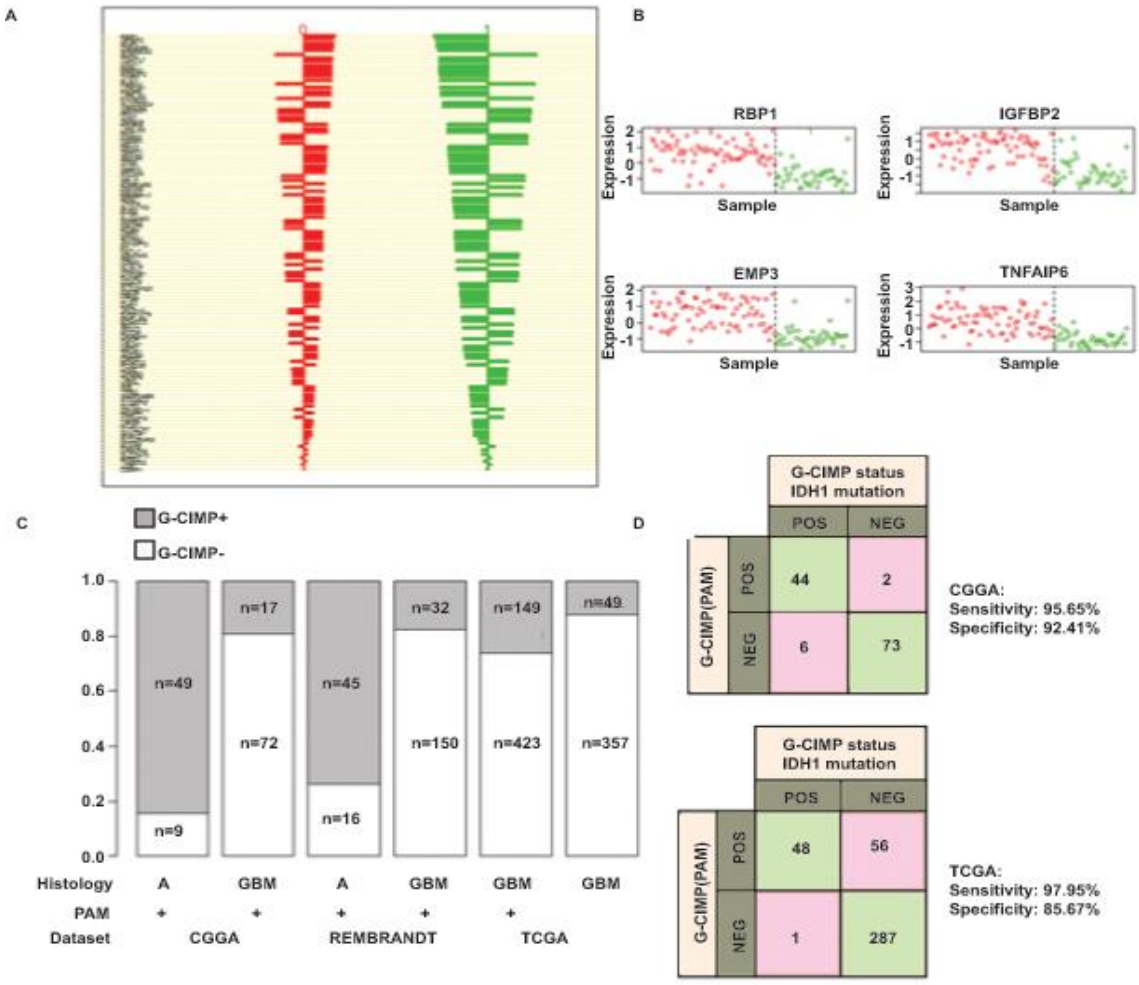
Supplementary Material



Supplemental Figure 1: Venn diagram of the overlap in signature gene list.



Supplemental Figure 2: Schema depicting the derivation of the pathway activity score. (A) Heat map of the expression pattern of the p53 gene signature in the CGGA. Lavender = normal brain, yellow = grade II astrocytoma (A), blue = grade III astrocytoma (AA), red = glioblastoma (G). (B) Activity score is defined as the following manner: Each gene in the signature that was over-expressed was assigned the value of +1; genes that were under-expressed were assigned -1. The normalized expression values of the signature genes in the clinical specimen are then plotted against these assigned values, and Pearson Correlation Coefficient was calculated as the pathway activity. The correlation ranged from -1 (denting low pathway activity) to +1 (denoting high pathway activity). (C) The pathway activity values (top) were averaged and displayed as a heat map (bottom).



Supplemental Figure 3: PAM classification of G-CIMP status. (A) Plot of the centroids for the G-CIMP classifier genes [1] using the CGGA dataset. (B) Expression level of the top four classifier genes and determination of threshold for G-CIMP status. (C) Proportion of glioblastomas classified as G-CIMP+ and G-CIMP- based on the mRNA classifiers. (D) Sensitivity and specificity of G-CIMP status determination by PAM. In the CGGA, IDH1 mutation was used as the gold standard for defining G-CIMP+ status [7]. In the TCGA, hierarchical clustering of methylation was used as the gold standard for G-CIMP+ status [22]. The PPV and NPV for the CGCG dataset was 88 and 97.33% respectively. The PPV and NPV for the TCGA dataset was 97.95 and 83.67%, respectively.

Table S1

	#NORM	#A	#AA	#GBM	#Unique Human Genes
CGGA	5	58	8	89	19416
REMBRANDT	28	61	45	182	18599
TCGA	10	n/a	n/a	406	17814

Supplemental References

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