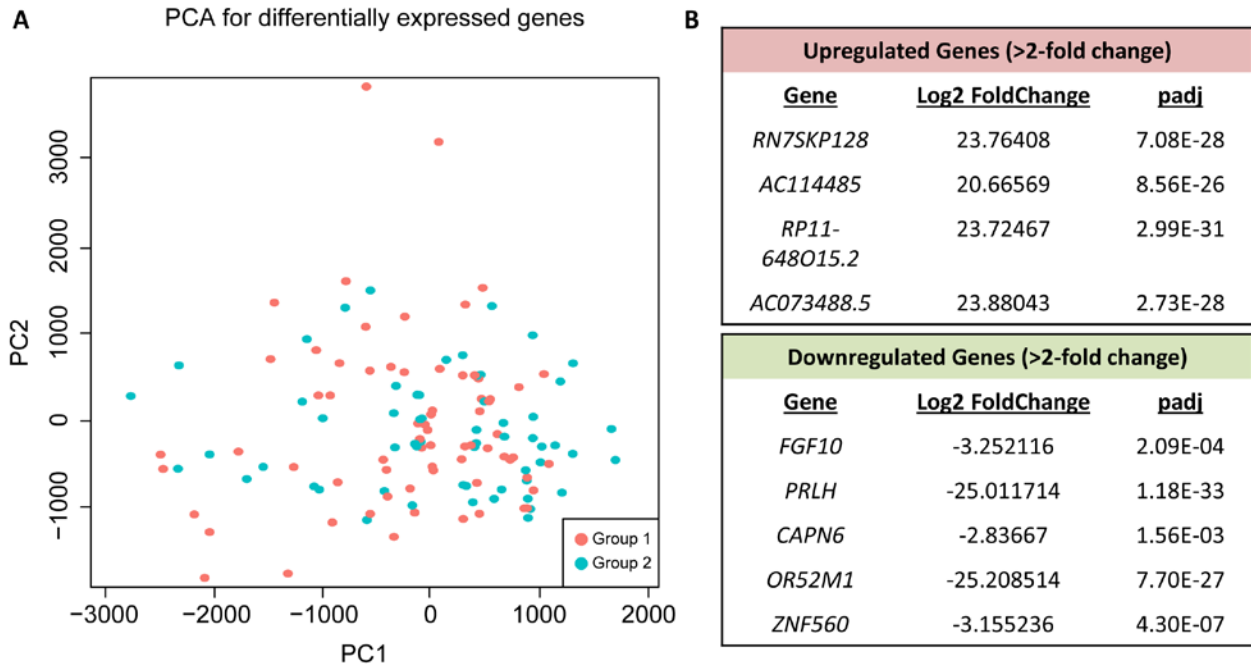
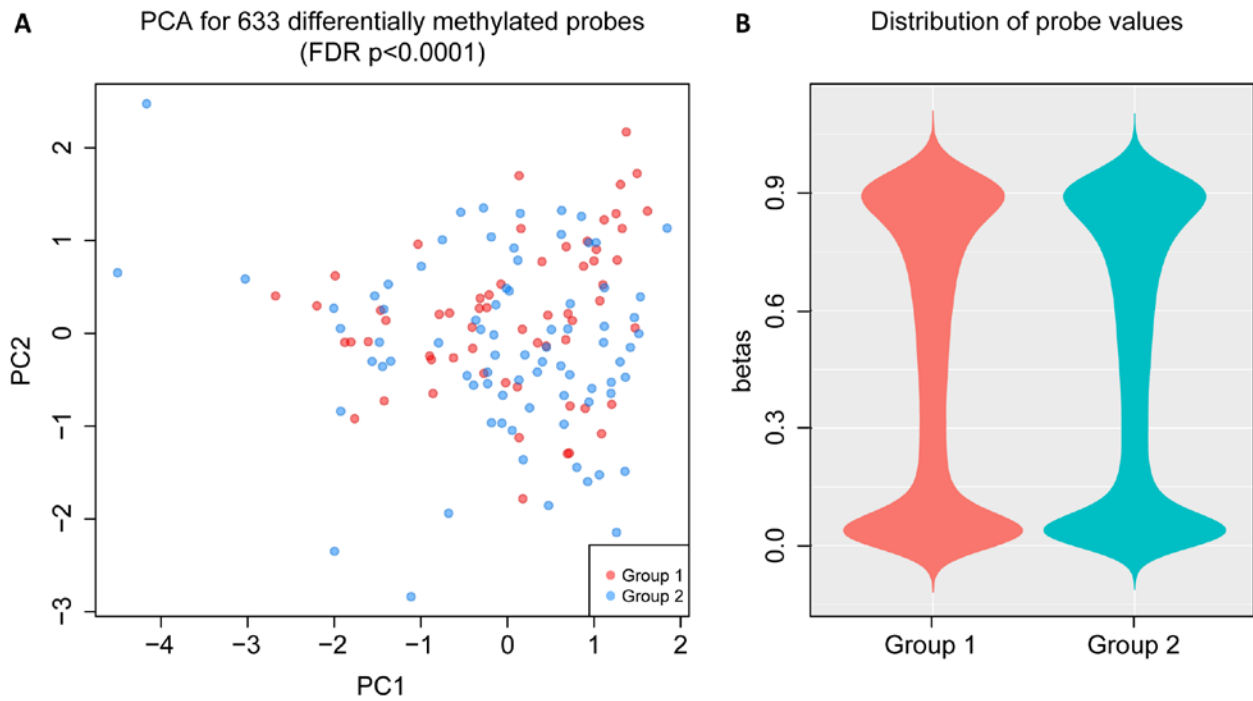


SUPPLEMENTARY MATERIAL



Supplementary Figure 1. Differentially expressed genes do not predict poor survival group of paired initial/recurrent glioblastoma. A) Principle component analysis of significantly differentially expressed genes of TCGA dataset comparing regions of relatively poor (Group 1) and better (Group 2) survival. B) Only nine differentially expressed genes identified in group 1 relative to group 2 (>2-fold change; adjusted p-value<0.05).



Supplementary Figure 2. Differentially methylated probes are not of diagnostic utility to predict poor survival group of paired initial/recurrent glioblastoma. A) Principle component analysis of highest ranked differentially methylated genes of TCGA dataset comparing regions of relatively poor (Group 1) and better (Group 2) survival. B) Violin plots showing overlapping distribution of probe values for Group 1 versus Group 2.

Pathway	B-H adj. p-value	Genes	Pathway ID
Cell Cycle	0.006628077	ATM, CCNA1, CCND2, CDK6, CDKN1C, FKBPL, HIST1H3I, HIST1H4L, HSPA2, MDC1, NUP98, PSMB8, PSMB9, RAB1B, TUBB	R-HSA-1640170
p53 signaling pathway	0.006628077	APAF1, ATM, CCND2, CDK6, IGFBP3, PTEN	hsa04115
Antigen processing and presentation	0.006628077	HSPA1A, HSPA1L, HSPA2, TAP1, TAP2, TAPBP	hsa04612
Legionellosis	0.013984079	APAF1, HSPA1A, HSPA1L, HSPA2, RAB1B	hsa05134
Cellular responses to stress	0.022219649	ATM, CCNA1, CDK6, HIST1H3I, HIST1H4L, HSPA1A, HSPA1L, HSPA2, NUP98, PSMB8, PSMB9	R-HSA-2262752
Regulation of HSF1-mediated heat shock response	0.02632611	ATM, HSPA1A, HSPA1L, HSPA2, NUP98	R-HSA-3371453
Attenuation phase	0.02632611	HSPA1A, HSPA1L, HSPA2	R-HSA-3371568
Cell Cycle, Mitotic	0.02632611	CCNA1, CCND2, CDK6, CDKN1C, FKBPL, HIST1H3I, HIST1H4L, NUP98, PSMB8, PSMB9, RAB1B, TUBB	R-HSA-69278
Transcriptional regulation by RUNX1	0.031795388	CCND2, CDK6, ESR1, GATA3, HIST1H3I, HIST1H4L, PSMB8, PSMB9	R-HSA-8878171
ER-Phagosome pathway	0.038987293	PSMB8, PSMB9, TAP1, TAP2, TAPBP	R-HSA-1236974
Generic Transcription Pathway	0.038987293	APAF1, ATM, BRD2, CCNA1, CCND2, CDK6, ESR1, GATA3, HIST1H3I, HIST1H4L, IGFBP3, MDC1, NOTCH4, PSMB8, PSMB9, PTEN, THRB, ZNF311	R-HSA-212436
Cellular response to heat stress	0.040462015	ATM, HSPA1A, HSPA1L, HSPA2, NUP98	R-HSA-3371556
Cellular responses to external stimuli	0.040462015	ATM, CCNA1, CDK6, HIST1H3I, HIST1H4L, HSPA1A, HSPA1L, HSPA2, NUP98, PSMB8, PSMB9	R-HSA-8953897
Direct p53 effectors	0.040462015	APAF1, BCL2, CAV1, IGFBP3, PTEN, TAP1	p53downstream pathway
Hepatitis B	0.044881948	APAF1, ATF6B, BCL2, CCNA1, CDK6, PTEN	hsa05161
Mitotic G1-G1/S phases	0.047027426	CCNA1, CCND2, CDK6, CDKN1C, PSMB8, PSMB9	R-HSA-453279

Supplementary Table 1. Significantly impacted biologic pathways as determined by differentially methylated genes comparing regions of poor versus better survival groups.