

Supplementary Figure 1.

(A) Kaplan Meier analysis of OS for the SurVaxM treated cohort stratified as LT (OS $\geq$ 18 mo; blue) and ST (OS<18 mo; red) survivors. Significant p-value reported from the log rank test (n=33, p<0.0001). (B) Kaplan Meier analysis of OS for the SurVaxM treated cohort stratified by molecular subtype⁵ as determined by gene set variation analysis. A non-significant p-value is reported from the log rank test (n=33, p=0.45).

Supplementary Figure 2.

(A) Occurrence of CNAs for individual genes across all chromosomes as a percentage of each OS class (blue=LT; red=ST) in a genome-wide stacked bar plot. Commonly altered genes in GBM are highlighted in black text and gene CNAs enriched in at least 3 LT or ST samples are highlighted in gold text. (B) Oncoprint of copy number alterations for genes altered in at least 3 samples and uniquely enriched in either LT or ST tumors (HETLOSS=heterozygous loss; HOMDEL=homozygous deletion). Rows are grouped by indicated chromosome locations for each gene. Annotations denote OS class, OS in months from initial SurVaxM dose, assigned molecular subtype⁵, and methylation status of *MGMT*. Row-wise frequency of gene alterations are indicated by percentages and vertical bar plot.

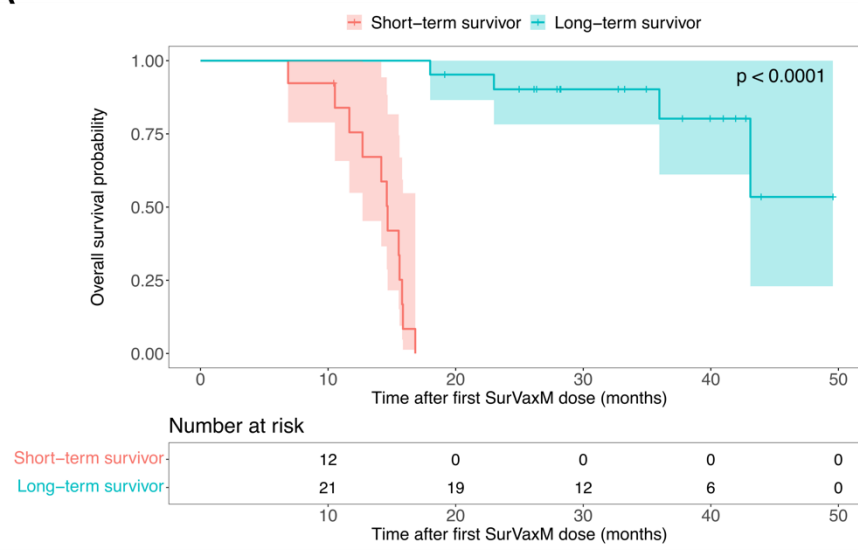
Supplementary Figure 3.

(A) Principal components plot of PC1 (18.73% of variation) and PC2 (12.87% of variation) for all RNA-seq analyzed tumor samples (n=33) with molecular subtype⁵ indicated by color (classical=red, mesenchymal=blue, proneural=green, or IDH1 mutant=orange). (B) Boxplots of DESeq2 normalized expression counts and statistics (LFC=log₂ fold change; adj.p=FDR adjusted

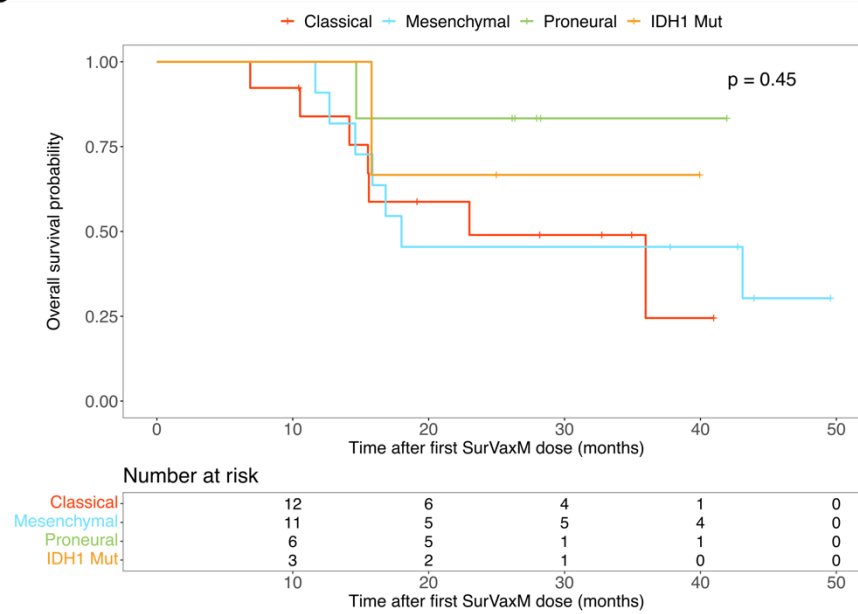
p-value) for all differentially expressed genes between LT (n=20, blue) and ST (n=13, red) OS classes. Boxplots represent median and interquartile range. **(C)** Correlation plot of B cell and endothelial transcriptomic GSVA signature scores for molecularly profiled GBM samples colored by OS class (n=33; ST=red, blue=LT, grey=95% CI; Pearson correlation). **(D)** Kaplan Meier analysis of molecularly profiled GBM samples stratified by high (positive GSVA score; red) or low (negative GSVA score; green) endothelial expression signature (n=33, log rank test).

Supplementary Figure 1

A

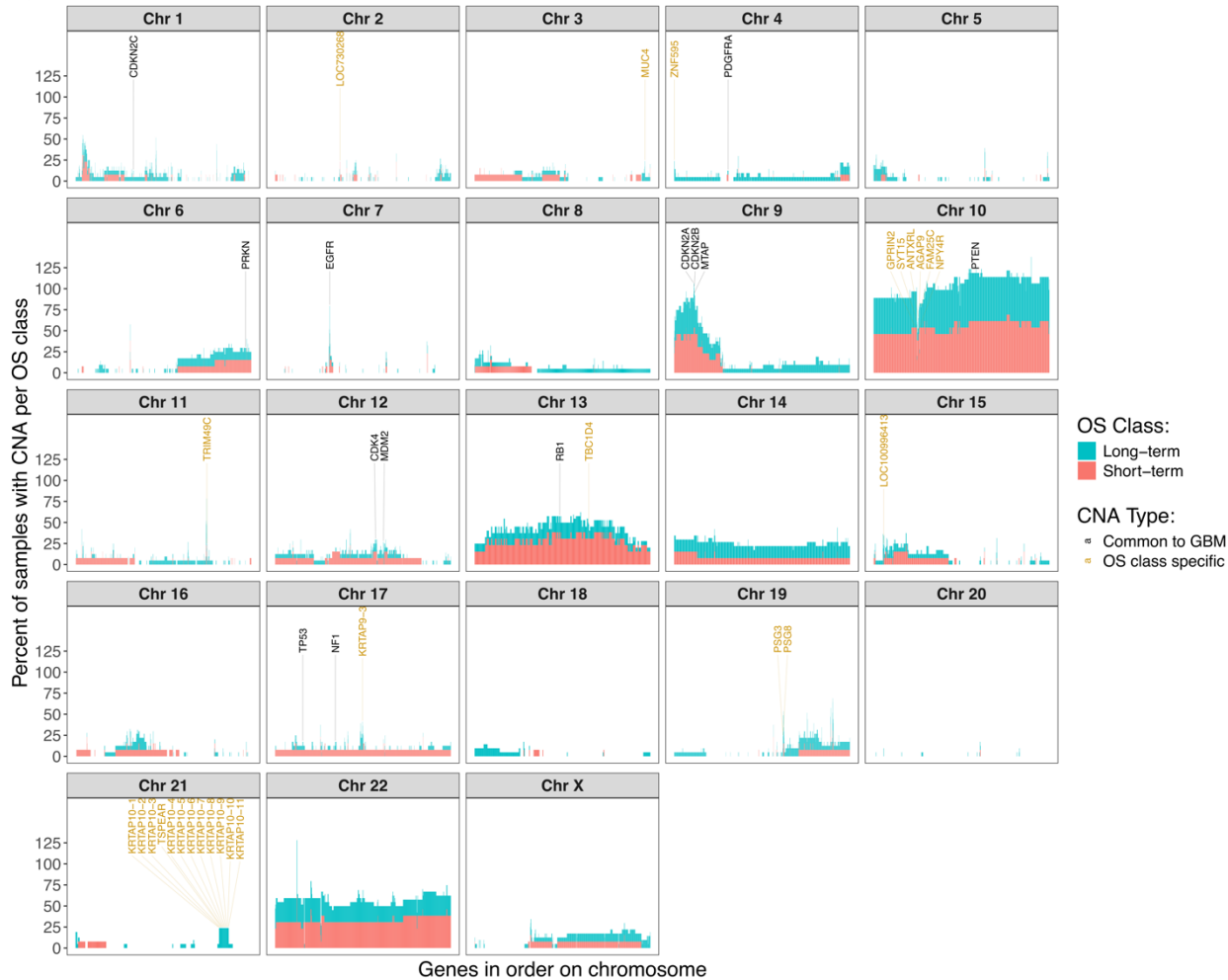


B

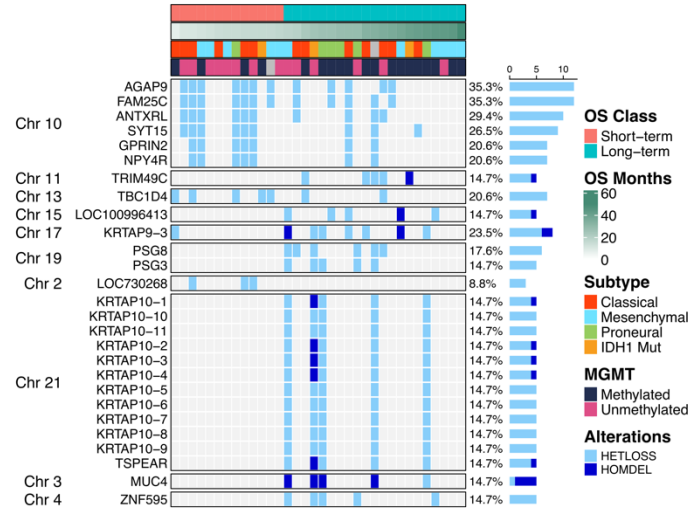


Supplementary Figure 2

A



B



Supplementary Figure 3

