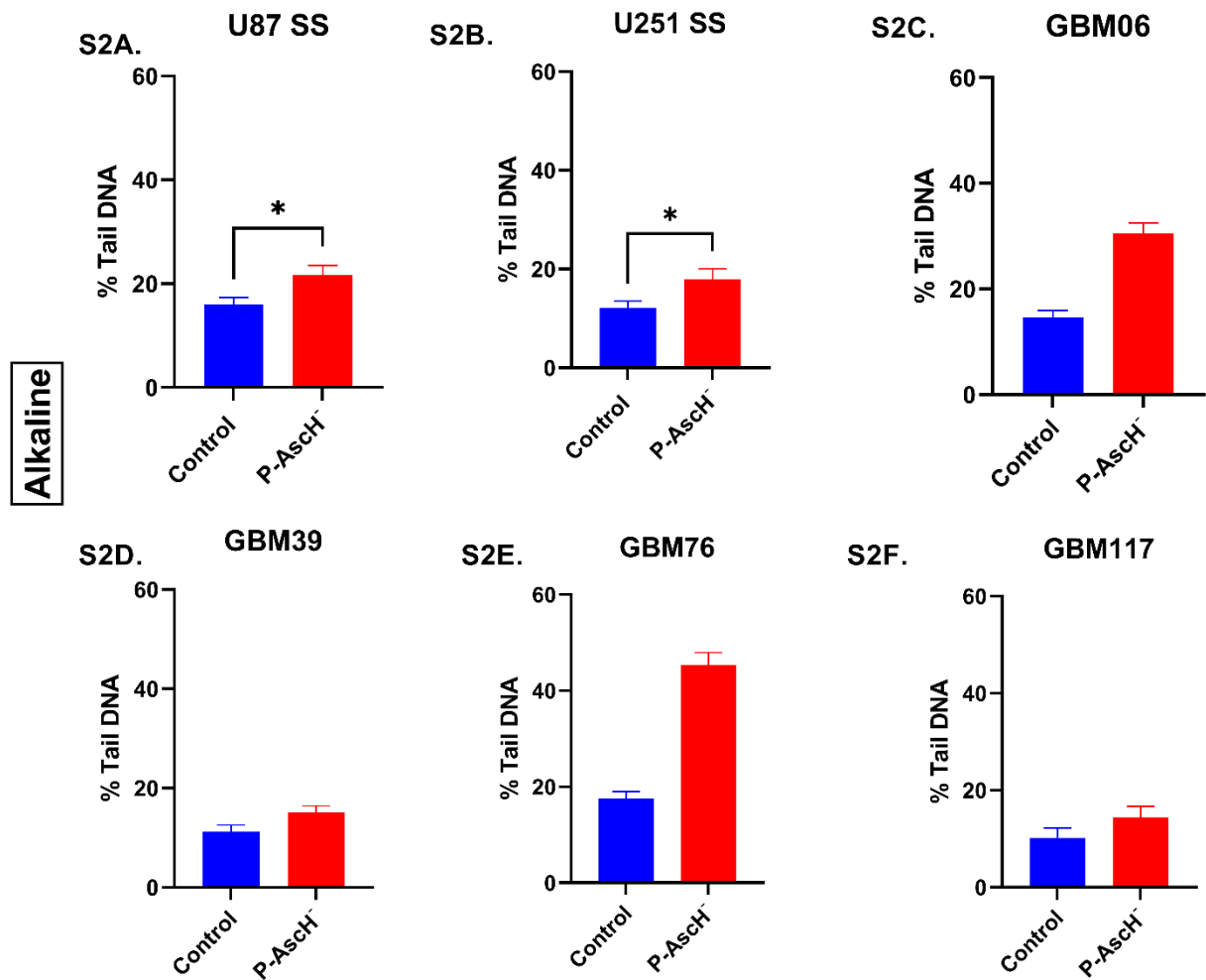
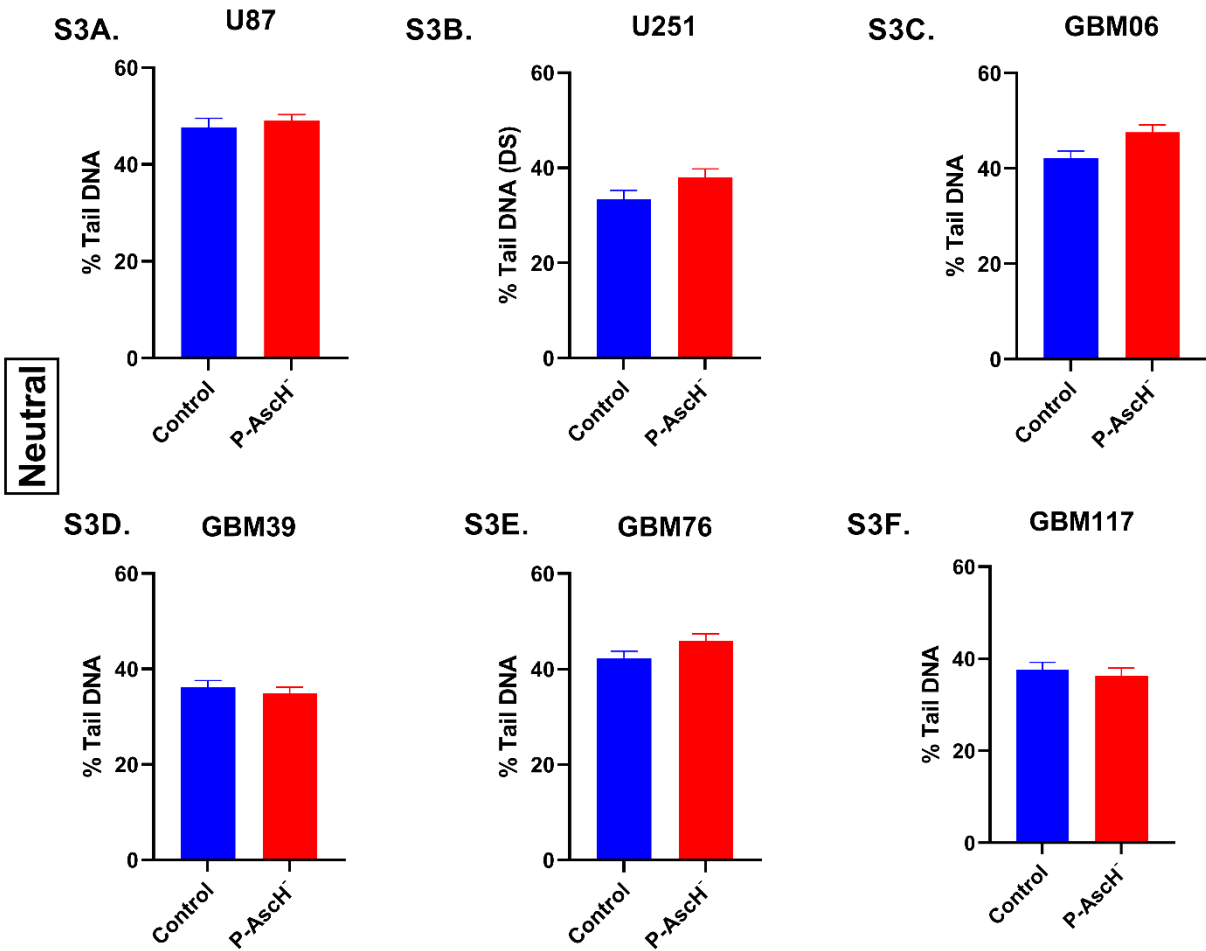


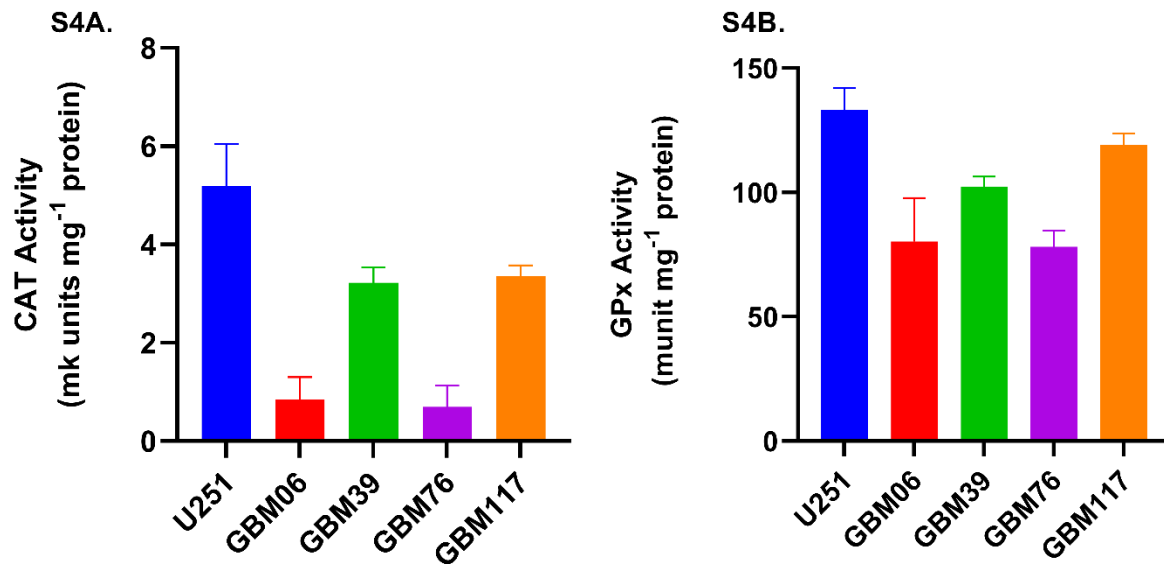
**Figure S1. The effect of P-AscH<sup>+</sup> on response to standard of care (SOC) therapy in GBM cell lines.** Data shown in classical, mesenchymal, and proneural GBM cells. Data are representing 3 replicates in each cell line (n = 3), GBM39 (n = 2). Error bars represent standard error of the mean (SEM).



**Figure S2. Single-strand DNA damage following P-Asch<sup>-</sup> treatment in GBM cells.** Single strand DNA damage as % Tail DNA following an alkaline comet assay in GBM cells treated with 20 pmol/cell P-Asch<sup>-</sup> for 1 hour. Data are representing 3 replicates in each cell line (n = 3). Error bars represent standard error of the mean (SEM).



**Figure S3. Double-strand DNA damage following P-AsCH<sup>-</sup> treatment in GBM cells.** Double strand DNA damage as % Tail DNA following a neutral comet assay in GBM cells treated with 20 pmol/cell P-AsCH<sup>-</sup> for 1 hour. Data are representing 3 replicates in each cell line (n = 3). Error bars represent standard error of the mean (SEM).



**Figure S4. Catalase and glutathione peroxidase (GPx) enzyme activities in GBM cells. S4A.** Catalase activity (mk units per mg protein) in GBM cells. **S4B.** GPx1 activity (munit per mg protein) in GBM cells. Data are representing 3 replicates in each cell line (n = 3). Error bars represent standard error of the mean (SEM).

**Table S1. Hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) removal capacities among GBM cell lines of different subtypes.** H<sub>2</sub>O<sub>2</sub> removal rates (10<sup>-12</sup> s<sup>-1</sup> cell<sup>-1</sup> L) in GBM cells ± the standard deviation. Data are representing 3 replicates in each cell line (n = 3).

Cell Line	Subtype	Avg. H <sub>2</sub> O <sub>2</sub> Removal Rate kcell (10 <sup>-12</sup> s <sup>-1</sup> cell <sup>-1</sup> L)	± SD
GBM 06	Classical	3.68	± 1.5
GBM 76	Classical	5.2	± 1.9
GBM 39	Mesenchymal	1.76	± 0.9
U87	Mesenchymal	5.66	± 2.1
U251	Mesenchymal	11.7	± 4.0
GBM85	Proneural	23.6	± 5.1
GBM117	Proneural	18.0	± 2.5