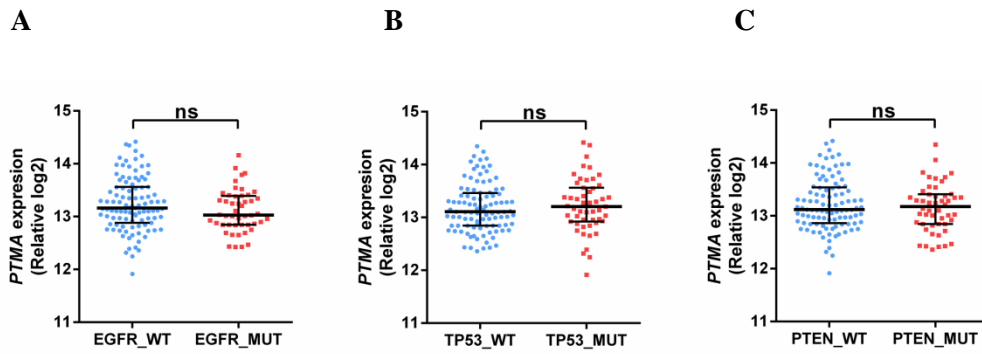
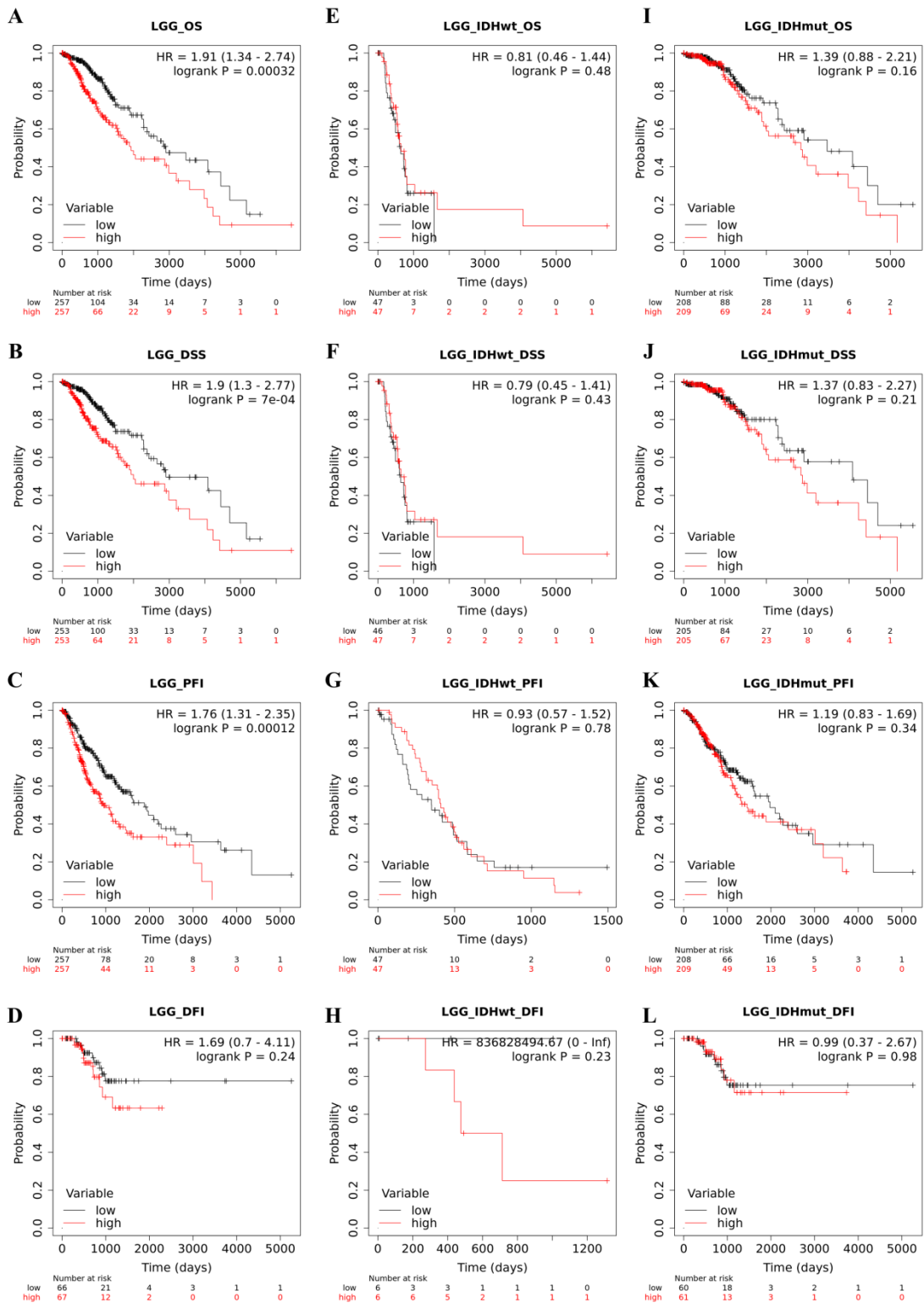


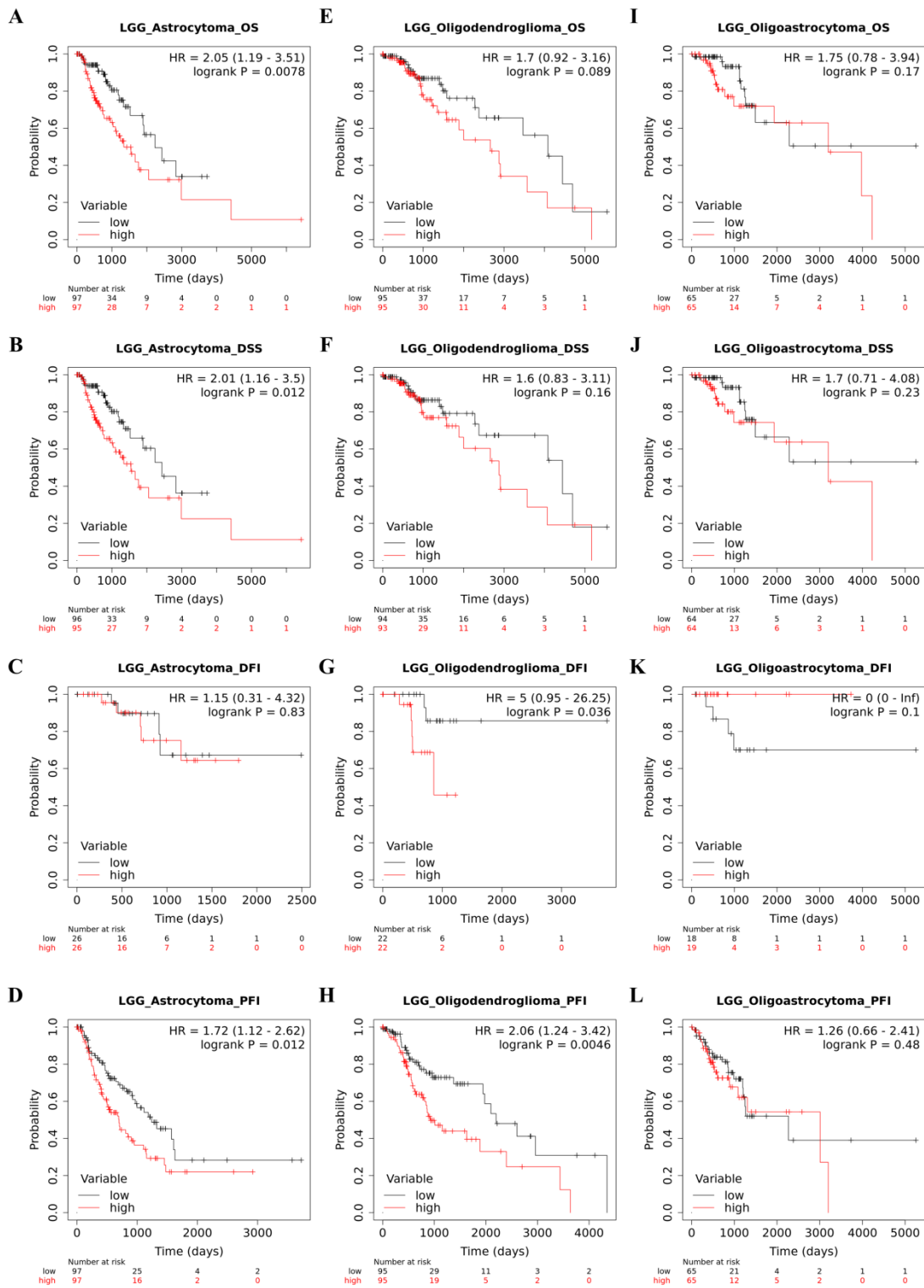
**Supplementary Figure 1:** Association of PTMA expression with age (A) and gender (B) in CGGA dataset and TCGA dataset (C and D) respectively.



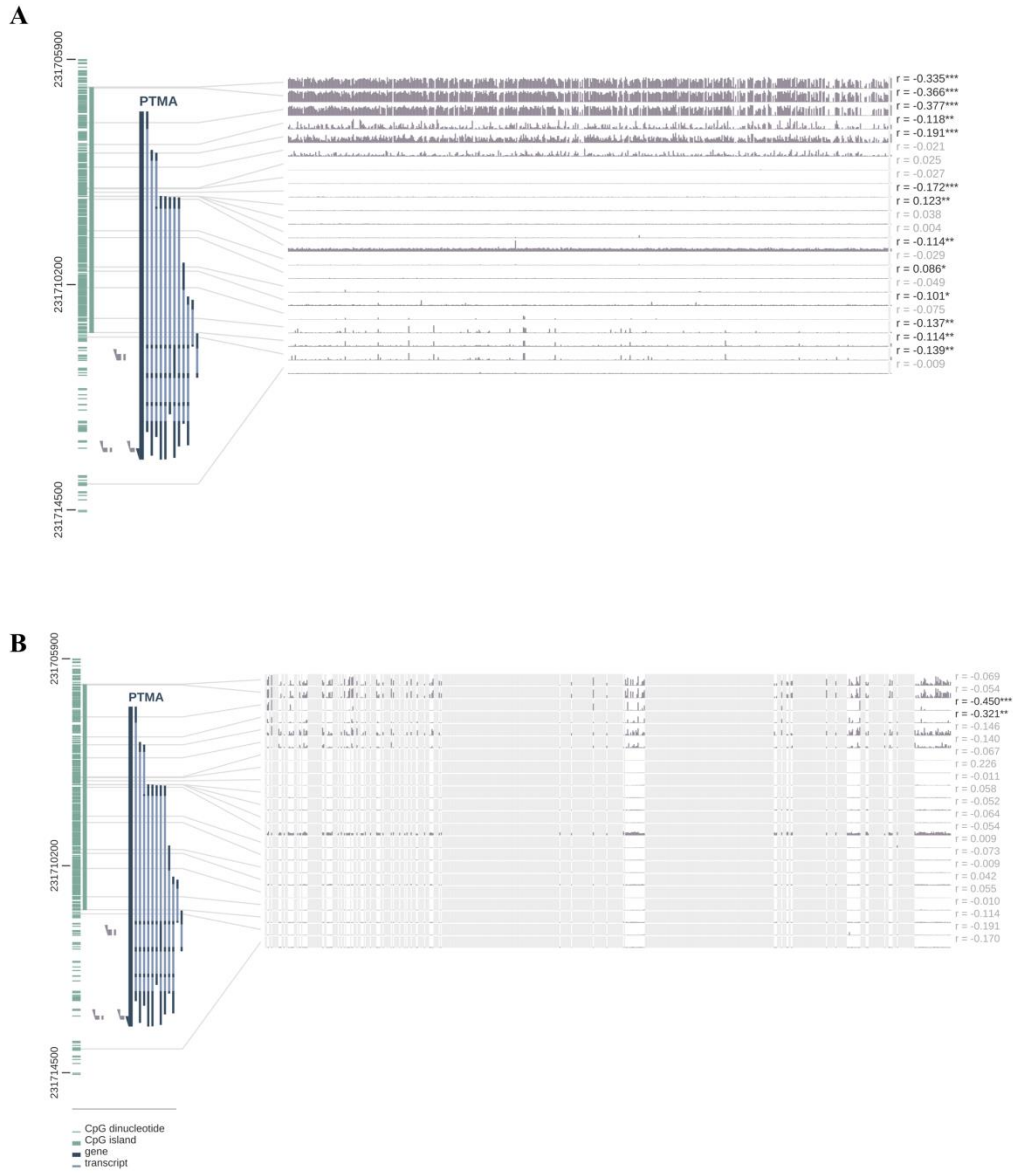
**Supplementary Figure 2:** Association of PTMA expression with molecular signatures in glioma datasets. (A) EGFR mutation status in TCGA-GBM (B) TP53 mutation status in TCGA-GBM (C) PTEN mutation status in TCGA-GBM.



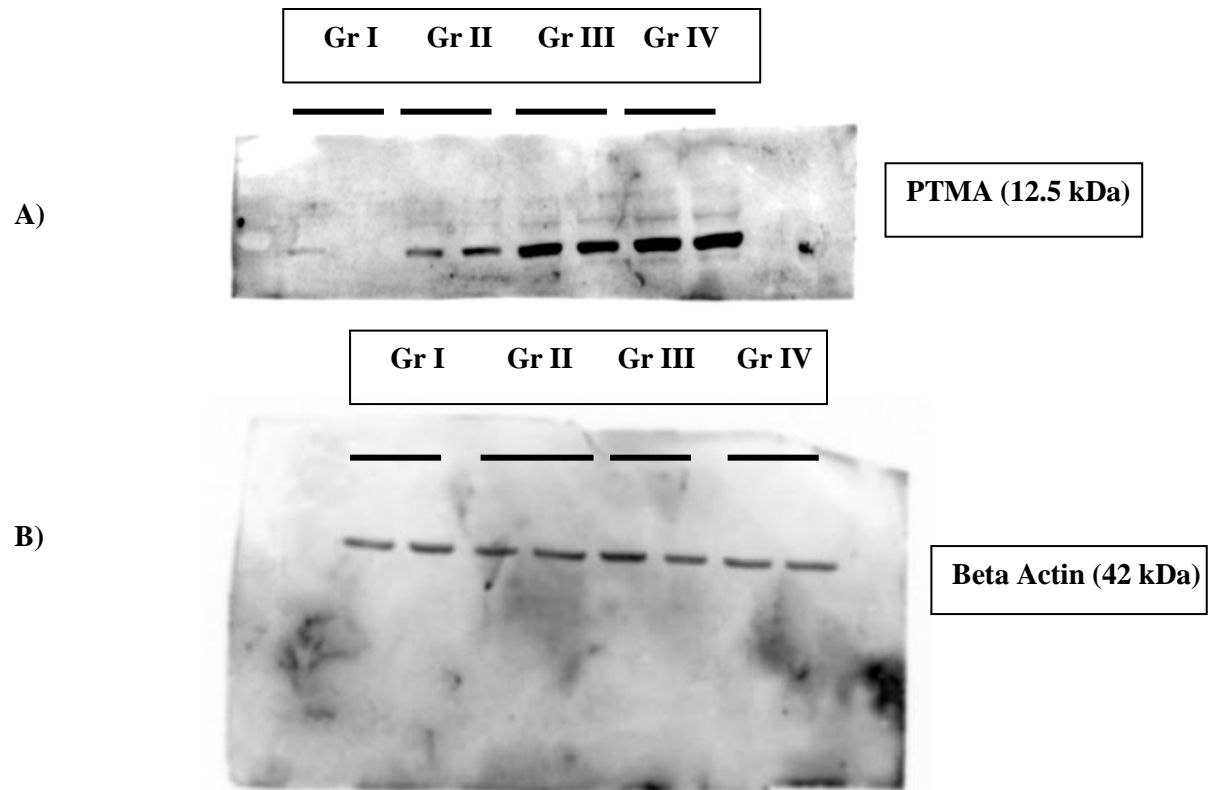
**Supplementary Figure 3:** Kaplan-Meier survival analysis showing overall survival (OS), disease-specific survival (DSS), progression-free interval (PFI), and disease-free interval (DFI), respectively in TCGA\_LGG samples. (A-D) IDH mutant, (E-H) and IDH wild type (I-L). HR represents the hazard ratio.



**Supplementary Figure 4:** Kaplan-Meier survival analysis showing OS, DSS, DFI, and PFI in TCGA\_LGG based in tumor histology. (A-D) Astrocytoma; (E-H) Oligodendroglioma; (I-L) Oligoastrocytoma. HR represents the hazard ratio.



**Supplementary Figure 5:** Correlation of PAXX gene methylation with gene expression in (A) TCGA-LGG and (B) TCGA-GBM dataset from MEXPRESS webserver.



**Supplementary Figure 6:** Raw and uncropped western blot images of glioma tissue lysates (A and B), represented as figure 1E in main article file. Here, figure A and B represents blots for PTMA and beta actin respectively.