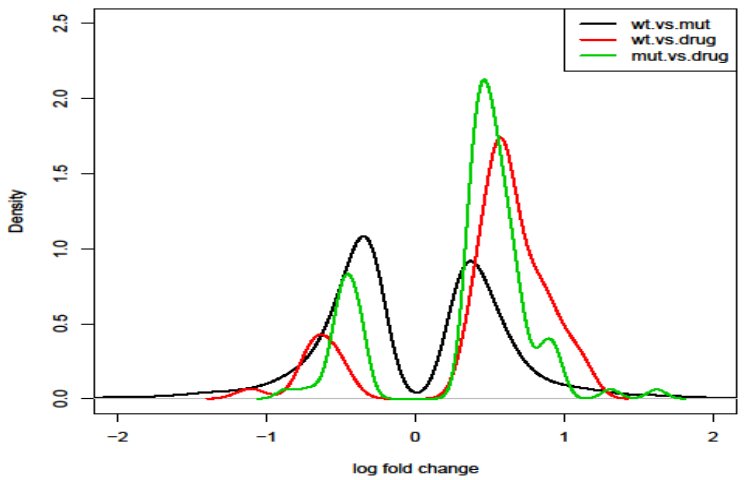
A



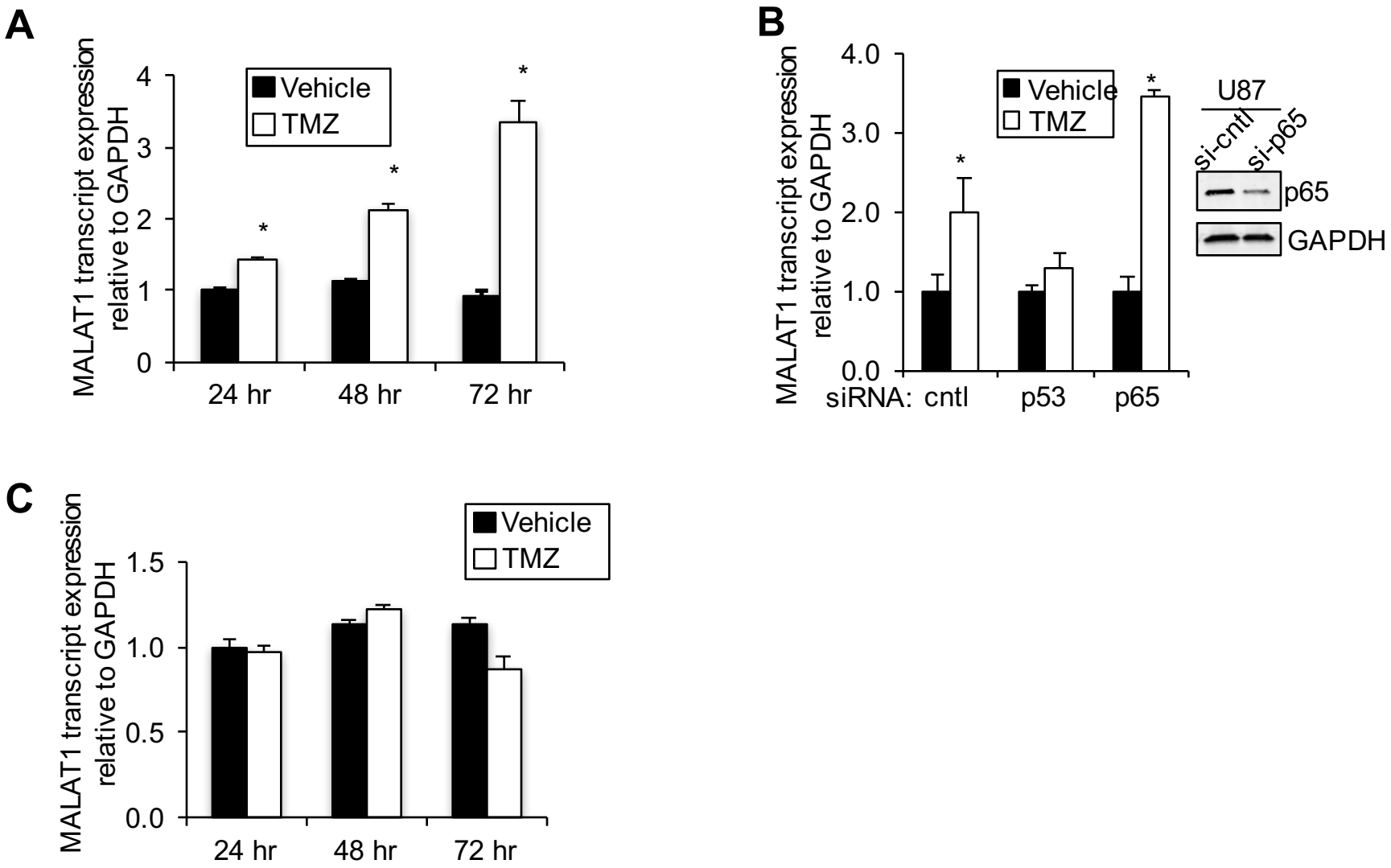
B

CATEGORY	TERM	#	P VALUE	FDR
KEGG_PATHWAY	p53 signaling pathway	10	4.50E-10	2.30E-08
GOTERM_BP_FAT	response to DNA damage stimulus	11	1.40E-05	1.00E-02
GOTERM_BP_FAT	DNA damage response, signal transduction	6	4.80E-05	1.80E-02
GOTERM_BP_FAT	cell cycle	14	9.20E-05	2.30E-02
GOTERM_BP_FAT	cellular response to stress	12	9.80E-05	1.80E-02

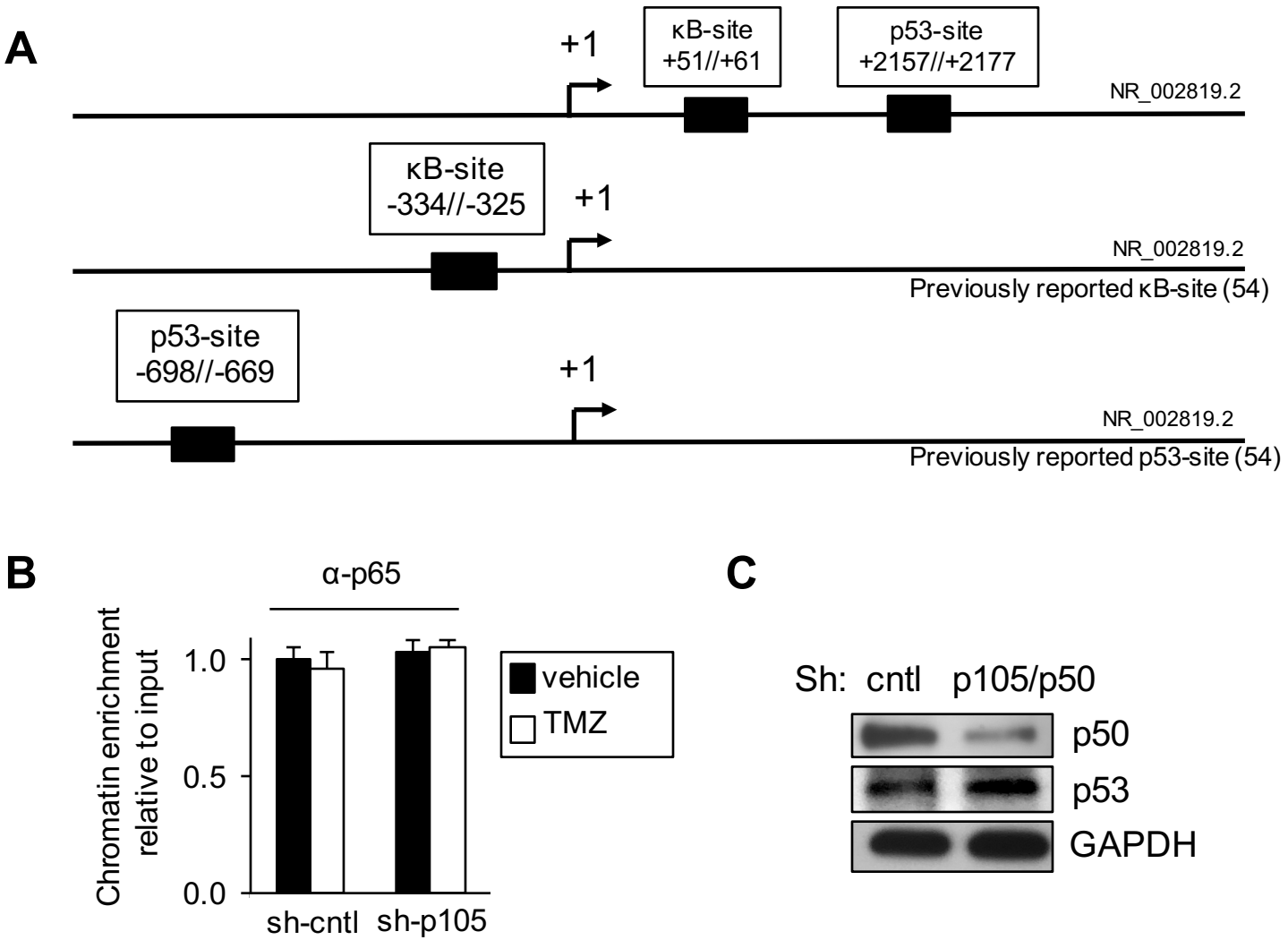
C

CATEGORY	TERM	#	P VALUE	FDR
KEGG_PATHWAY	p53 signaling pathway	7	5.10E-08	1.50E-06
GOTERM_BP_FAT	regulation of apoptosis	13	3.60E-07	1.90E-04
GOTERM_BP_FAT	regulation of programmed cell death	13	4.00E-07	1.10E-04
GOTERM_BP_FAT	regulation of cell death	13	4.20E-07	7.30E-05
GOTERM_BP_FAT	positive regulation of apoptosis	8	9.20E-05	1.20E-02
GOTERM_BP_FAT	positive reuglation of programmed cell death	8	9.70E-05	1.00E-02
GOTERM_BP_FAT	positive regulation of cell death	8	9.90E-05	8.70E-03
GOTERM_BP_FAT	induction of apoptosis	7	1.50E-04	1.10E-02
GOTERM_BP_FAT	induction fo programmed cell death	7	1.50E-04	9.70E-03
GOTERM_BP_FAT	response to DNA damage stimulus	7	3.30E-04	1.90E-02
GOTERM_BP_FAT	cellular response to stress	8	4.90E-04	2.50E-02

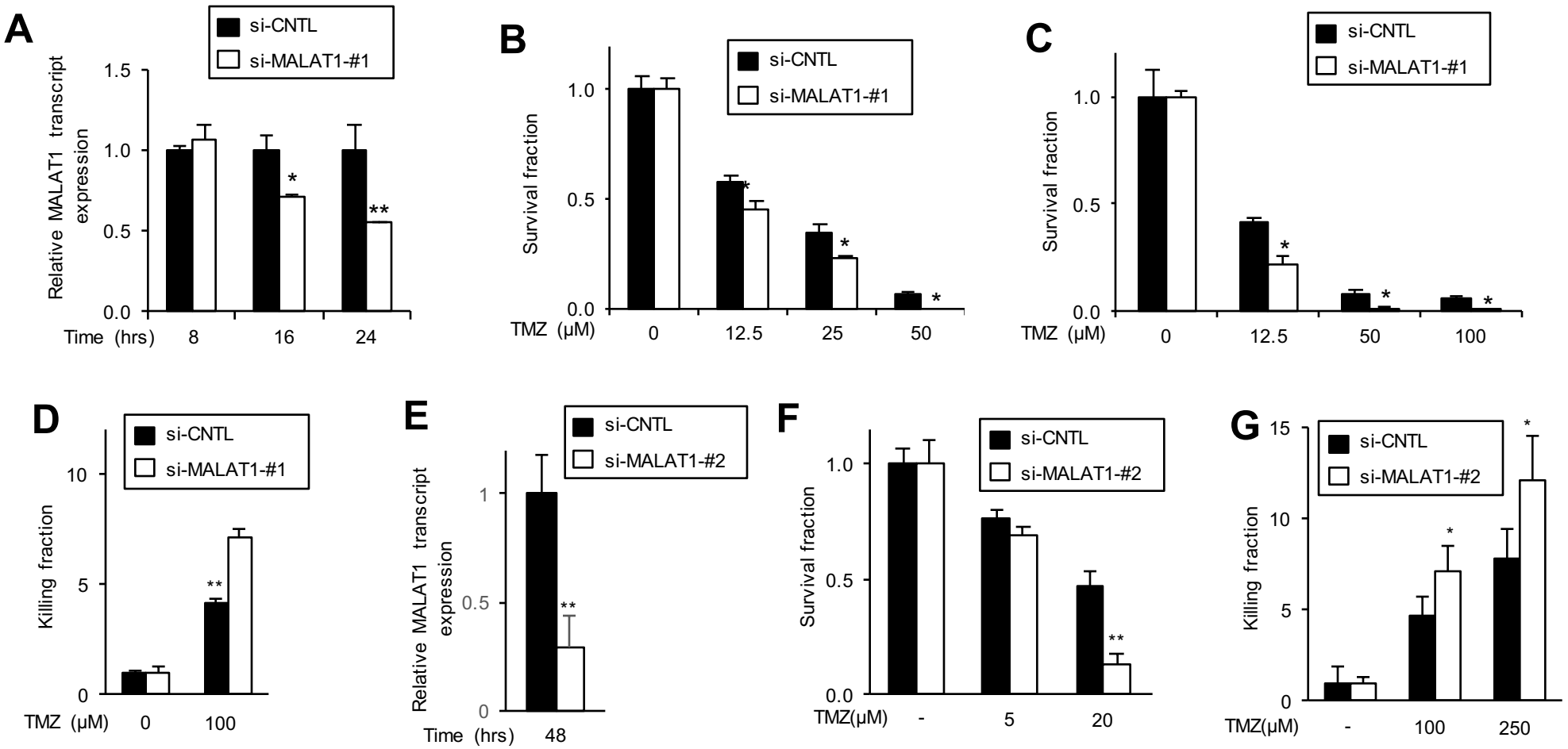
Supplementary Figure 1. p50 dependent gene expression analysis. (**A**) Distribution of dysregulated transcripts. Log-fold change of transcripts from sh-control (wt) and sh-p105 (mut) cells shown. (**B**) Enriched gene ontology pathways among the transcripts significantly altered in sh-p105 cells after treatment with TMZ compared to vehicle. (**C**) Enriched gene ontology pathways among the transcripts significantly altered in sh-control cells after treatment with TMZ compared to vehicle.



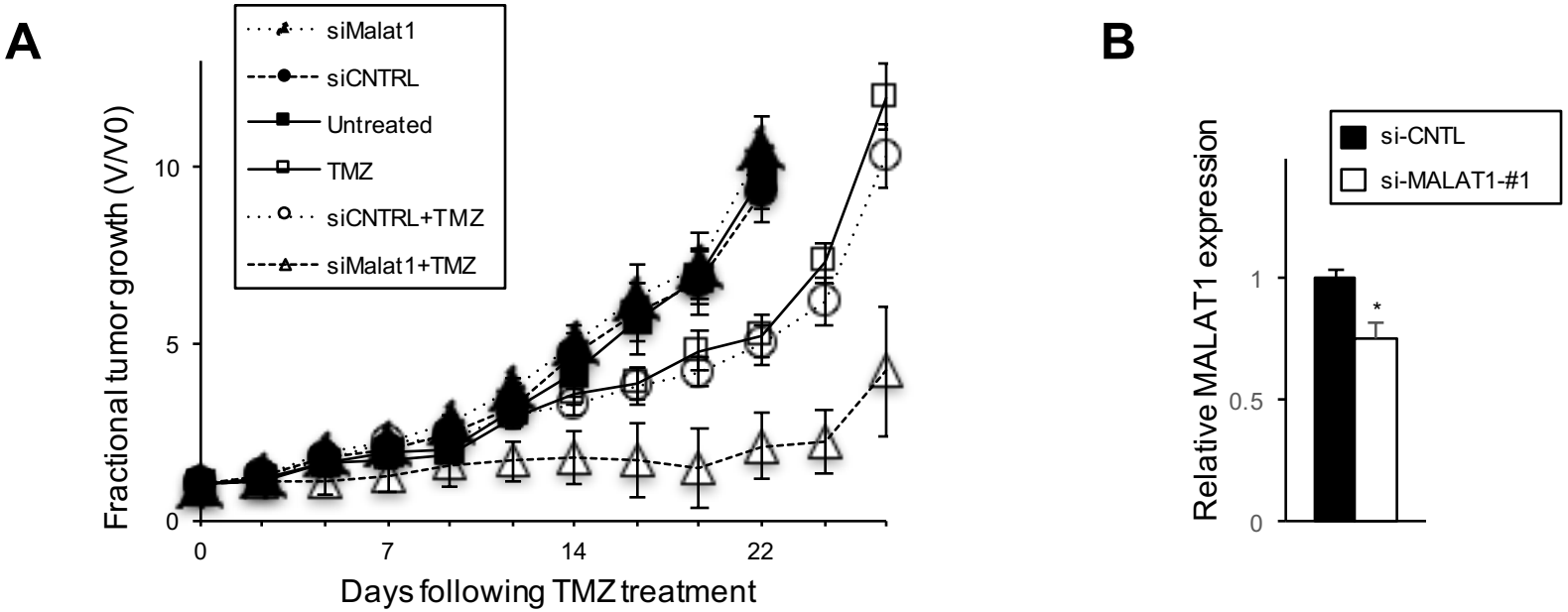
Supplementary Figure 2. MALAT1 is induced by TMZ in a time and dose dependent manner. qPCR analysis of RNA expression. (**A**) A172 cells were treated with 100 μM TMZ or vehicle for the indicated time. (**B**) U87 glioma cells treated with vehicle or 100 μM TMZ transfected with the indicated siRNA. Inset: immunoblot of p65 and GAPDH (loading control). (**C**) MALAT1 expression in U251 GBM cells following treatment with vehicle or TMZ (100μM). Data show mean transcript expression relative to *GAPDH*, ± SD of triplicate samples from 3 separate biological experiments normalized to vehicle. *, $P < 0.05$.



Supplementary Figure 3. (A) Schematic of current and previously identified -κB and p53 binding sites. Top panel: -κB and p53 binding sites identified in the current study. Middle Panel: previously reported -κB site (54). Bottom panel: previously reported p53 binding site (55). (**B**) Quantitative ChIP assay using primers spanning the κB-site in the indicated U87 cells treated as shown. Data represent chromatin enrichment of p65 relative to input DNA after controlling for non-specific binding using anti-histone H1 (positive control) and anti-IgG, normalized to vehicle, ±SD of triplicate samples, repeated with similar results. (**C**) Immunoblot with p50, p53, or GAPDH (loading control) in U87 cells expressing the indicated shRNA construct.



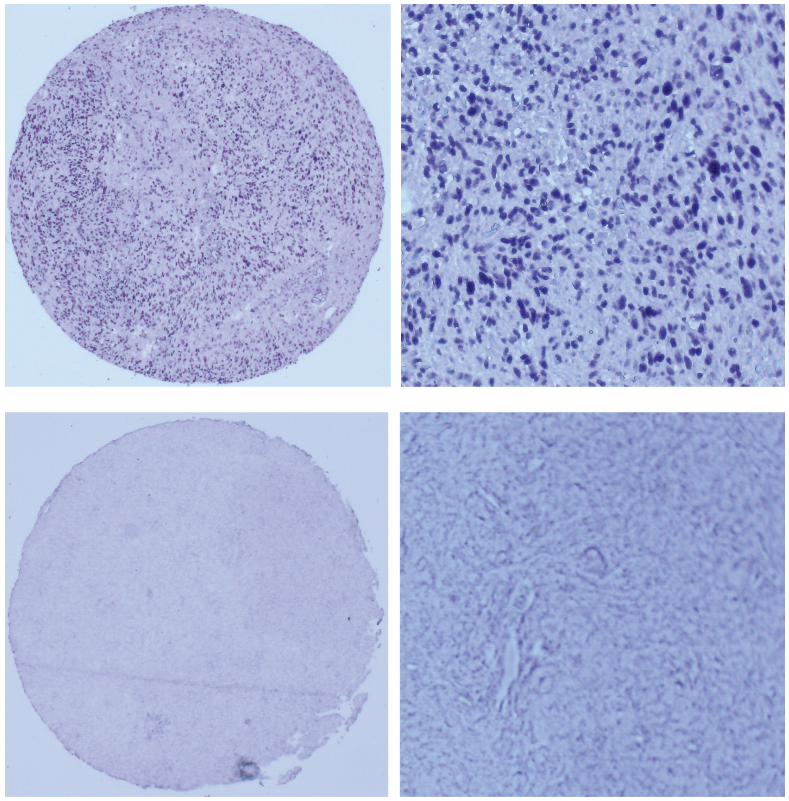
Supplementary Figure 4. Knockdown of MALAT1 with 2 distinct siRNAs decreases cell survival and increases killing following TMZ treatment. (**A**) qPCR analysis of MALAT1 expression, relative to GAPDH, in U87 cells at indicated time following transfection with si-cntl or si-MALAT1-#1. (**B and C**) Clonogenic assays showing survival fraction in (B) U251 glioma cells and (C) A172 glioma cells transfected with si-cntl or si-MALAT1-#1 and treated with TMZ. (**D**) Trypan blue assay showing killing fraction in GBM44 cells transfected with si-MALAT1-#1 and treated with TMZ. (**E**) qPCR analysis of MALAT1 expression, relative to GAPDH, in U87 cells at indicated time following transfection with si-cntl or si-MALAT1-#2. (**F**) Clonogenic assay in U87 cells showing survival fraction in transfected with si-cntl or si-MALAT1-#2 and treated with TMZ. (**G**) Trypan blue assay showing killing fraction in U87 cells transfected with si-MALAT1-#2 for 24 hours and treated with TMZ. *, $p < 0.05$, **, $p < 0.01$.



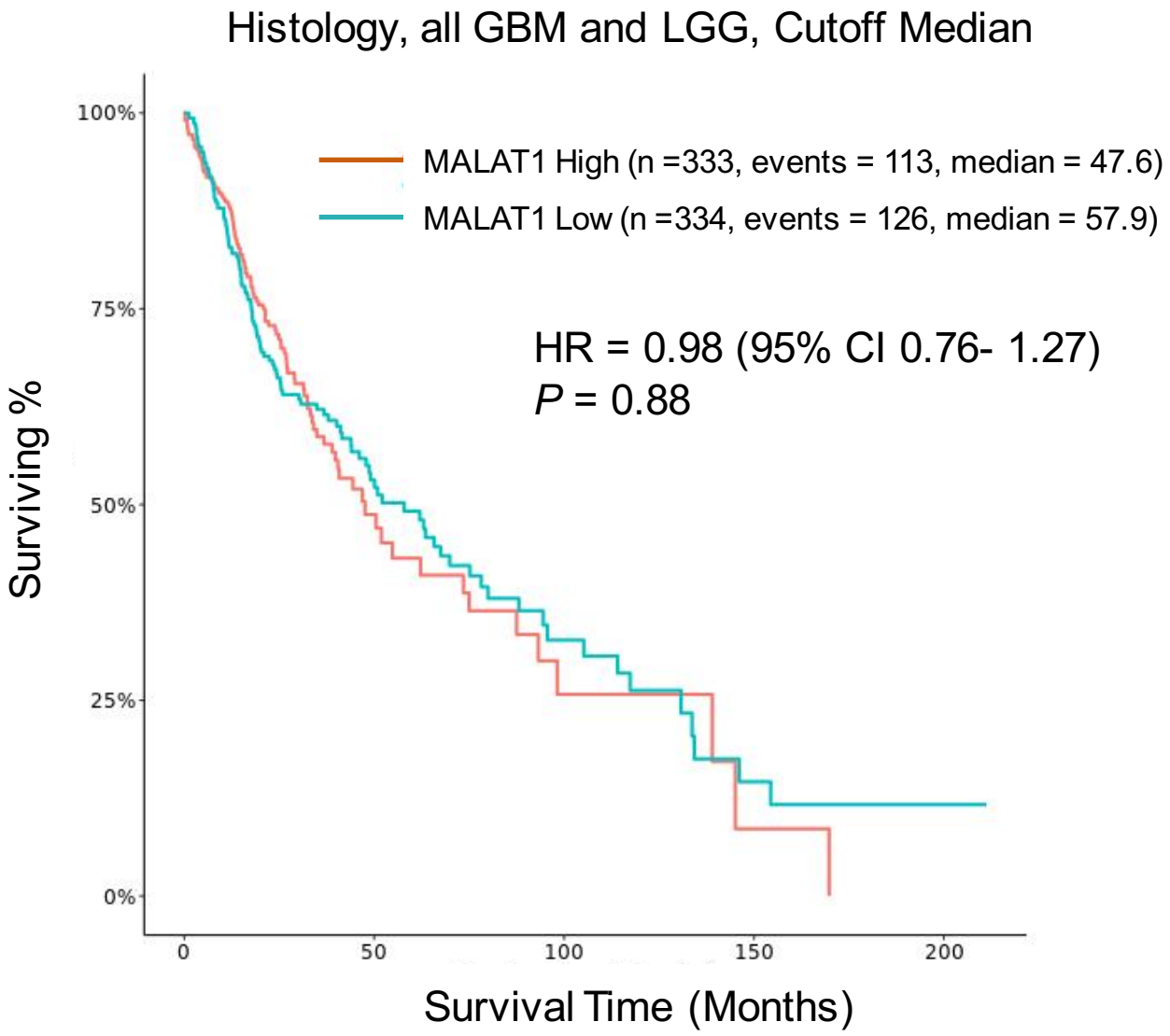
Supplementary Figure 5. (**A**) Relative growth of hindlimb U87 xenografts in mice (n=6 mice per group) following treatment with TMZ (days 4, 7, and 10) and/or the indicated NP. $p < 0.01$, Log-rank: TMZ + NP-si-MALAT1-#1 vs. TMZ + NP-si-cntl or NP-si MALAT1-#1 alone. (**B**) qPCR analysis of MALAT1 expression in xenograft tissue 4 days following treatment with NP with si-cntl or si-MALAT1-#1. *, $p < 0.05$.

Anti-sense probe

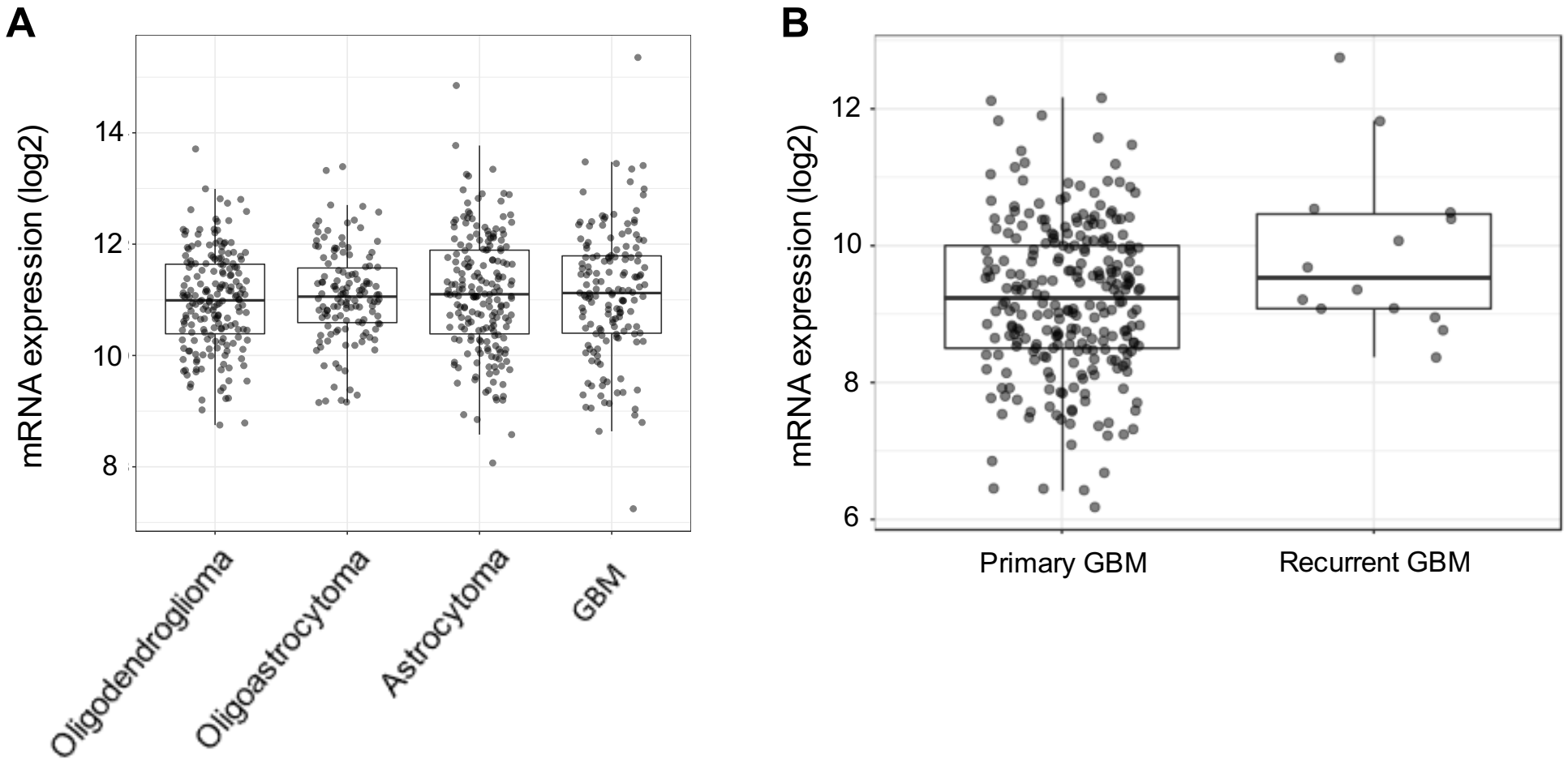
Sense probe



Supplementary Figure 6. Verification of MALAT1 in-situ hybridization using the sense and anti-sense probes as shown.



Supplementary Figure 7. Kaplan Meier survival curves from combined GBM and LGG tumors from TCGA based on MALAT1 RNA seq expression level divided using median expression cut off.



Supplementary Figure 8. MALAT1 mRNA expression. Comparison of expression between (**A**) different grades of glioma in TCGA database gliomas and (**B**) primary and recurrent glioma in Ivy database gliomas. Differences in MALAT1 expression among subtypes were assessed by Turkey's honest significant difference (HSD) test and no statistical significance demonstrated. In the box-plots, the horizontal line indicates the median, boundaries of the box indicate the first and third quartiles, and whiskers indicate confidence intervals (95%). p value > 0.05 between different grades in TCGA and $p < 0.05$ for primary versus recurrent GBM.