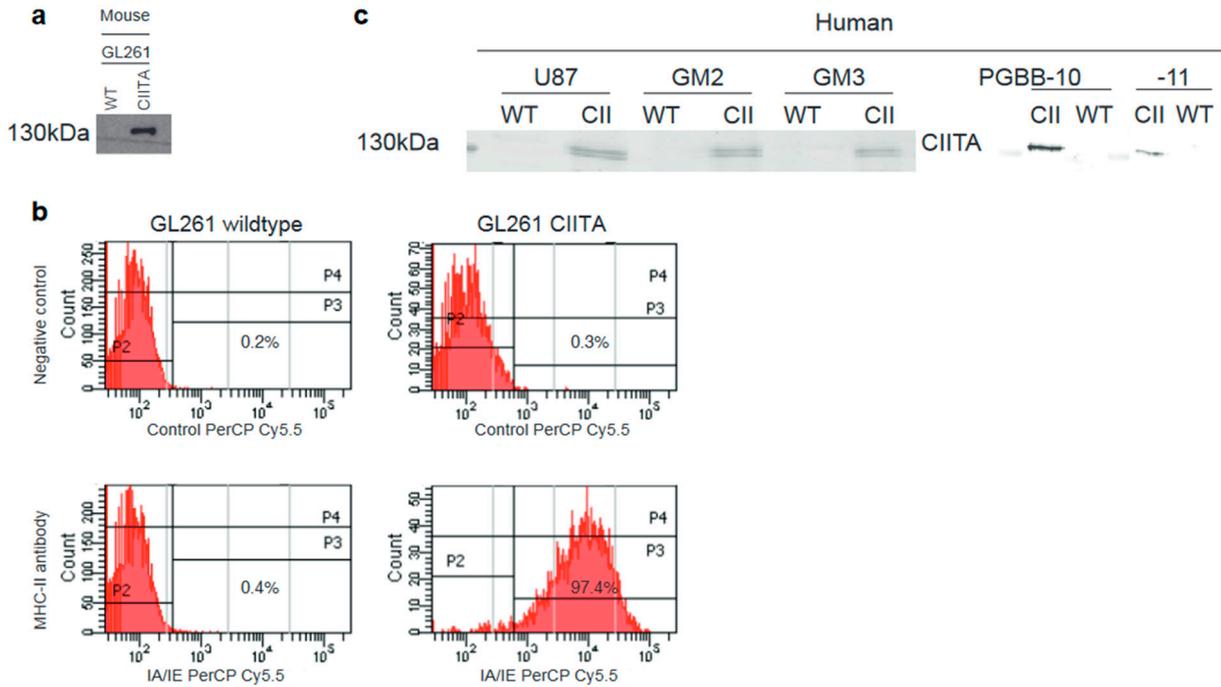


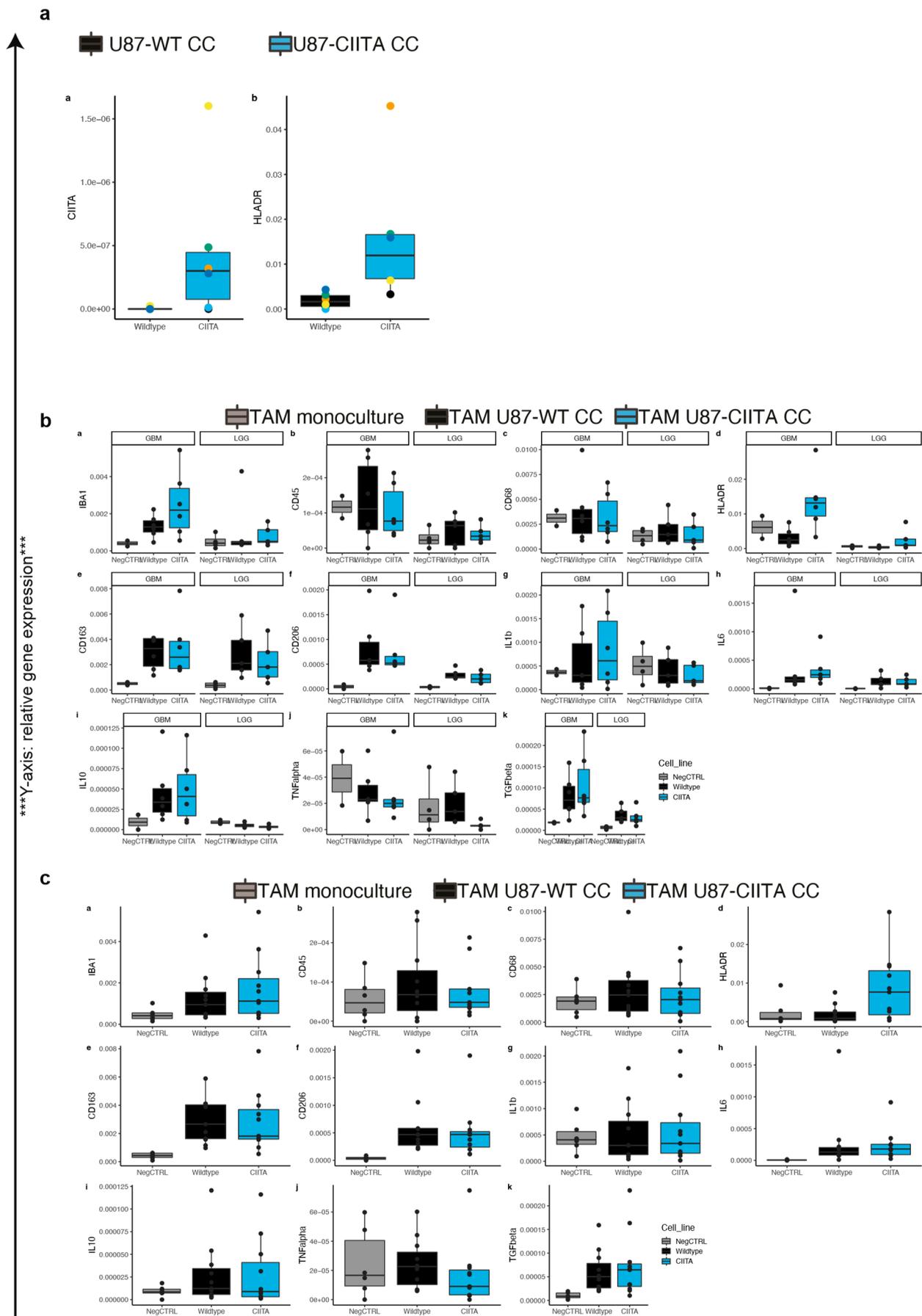
SUPPLEMENTARY FIGURE S1. Western blot results showing CIITA expression in -WT versus -CIITA (a) GL261 murine cells and (c) U87, GM2, GM3, PGB13 and PGB-14 human (primary) glioblastoma cells. (b) FACS data indicating high IA/IE (MHC-II antibody) after transfection with the CIITA plasmid versus low IA/IE expression in wildtype cells.



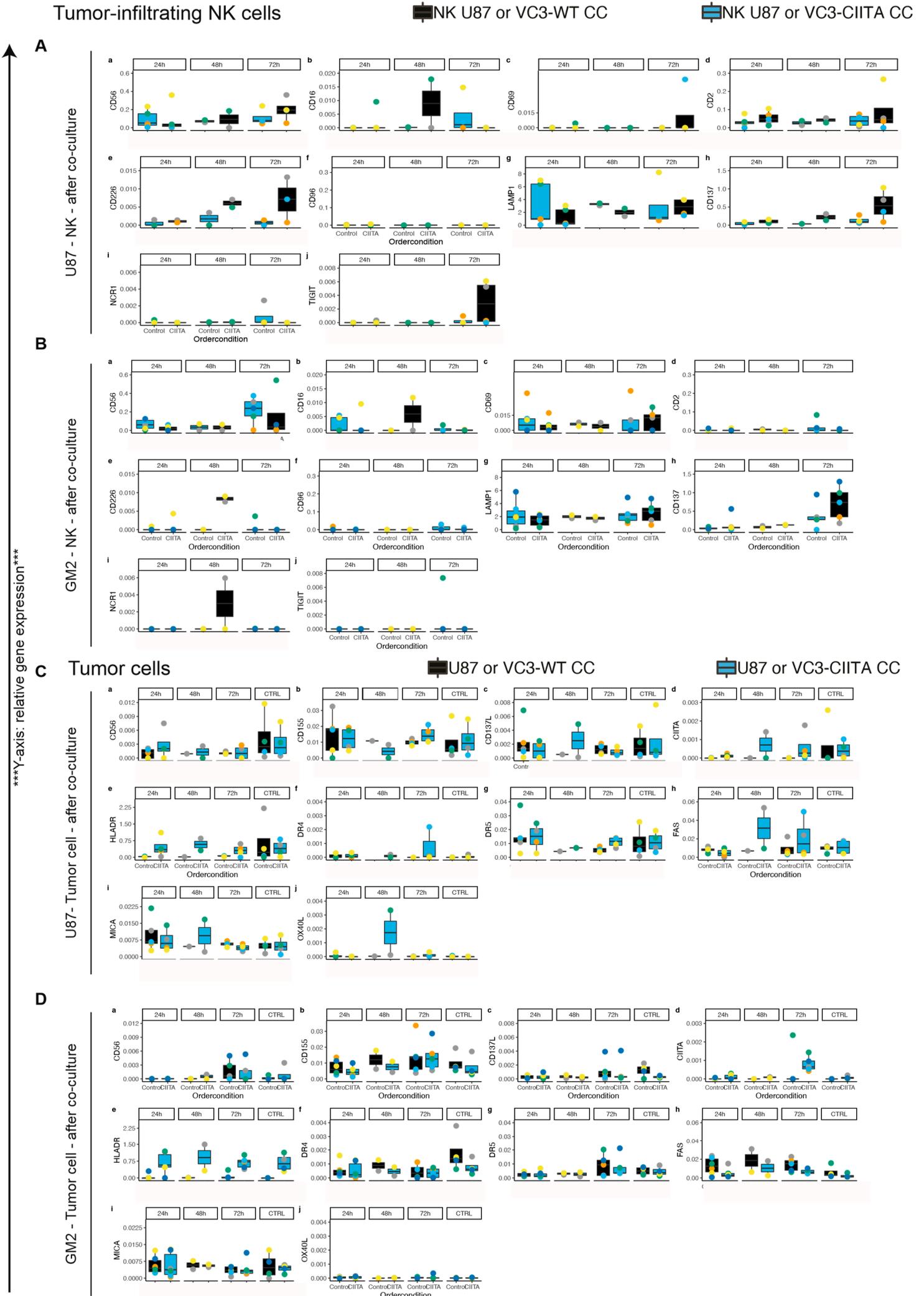
SUPPLEMENTARY TABLE S1. Histopathological diagnosis of glioma used for isolation of tumor-associated myeloid cells, tumor-infiltrating lymphocytes and NK-cells in co-culture experiments.

Patiënt	Histopathology	Experiment
PGB1	Glioblastoma WHO grade IV	TIL experiment
PGB2	Glioblastoma WHO grade IV	TIL experiment
PGB3	Glioblastoma WHO grade IV	TAM experiment
PGB4	Glioblastoma WHO grade IV	TAM experiment
PGB5	Glioblastoma WHO grade IV	TAM experiment
PGB6	Glioblastoma WHO grade IV	TAM experiment
PGB7	Glioblastoma WHO grade IV	TAM experiment
PGB8	Glioblastoma WHO grade IV	TAM experiment
PGB9	Diffuse astrocytoma WHO II	TAM experiment
PGB10	Diffuse low grade glioma WHO II	TAM experiment
PGB11	Gemistocytair astrocytoom WHO II	TAM experiment
PGB12	Diffuse astrocytoma WHO II	TAM experiment
PGB13	Glioblastoma WHO grade IV	NK-cell experiment
PGB14	Anaplastic oligodendroglioma WHO grade III	NK-cell experiment
PGB15	Glioblastoma WHO grade IV	NK-cell experiment
PGB16	Glioblastoma WHO grade IV	NK-cell experiment
PGB17	Low grade glioma WHO grade II	NK-cell experiment

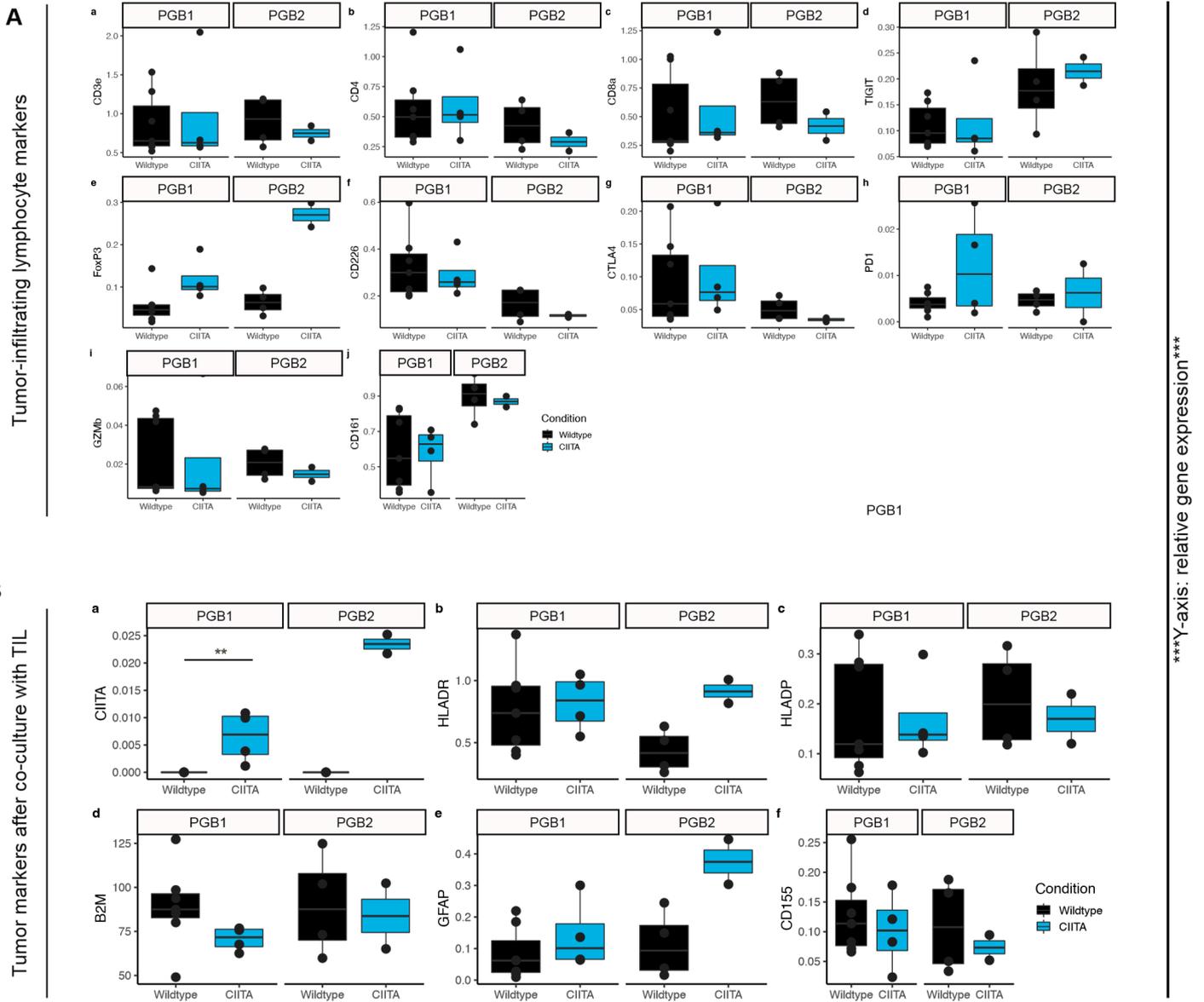
SUPPLEMENTARY FIGURE S2. (a) CIITA and HLA-DR expression in U87-WT and U87-CIITA cells after co-culture with TAM. (b) TAM relative gene expression after co-culture differentiating between glioblastoma-derived (GBM) versus low-grade glioma derived (LGG) TAM. (c) TAM gene expression. Each bar represents the mean \pm SD relative gene expression with separate data points.



SUPPLEMENTARY FIGURE S3. (A) RT-qPCR analyzed relative gene expression of NK-cell related genes after co-culture with U87 (NK-cell markers (A) or tumor cell markers (B) or GM2 NK (C) versus tumor (D). Each bar represents the mean \pm SD relative gene expression with separate data points.



SUPPLEMENTARY FIGURE S4. (A) RT-qPCR analyzed relative gene expression of tumor-infiltrating lymphocytes. TIL-related genes (A) or tumor related genes \ (B) Each bar represents the mean \pm SD relative gene expression with separate data points.



SUPPLEMENTARY TABLE S2. Primers pairs for tested genes.

Gene	Primers sequence		Gene	Primers sequence	
	General Forward	Reverse		TIL Forward	Reverse
CIITA	GCTGGAGAAGAAGAGAT	CCGATATTGGCATAAG	FoxP3	CTCAGCTTAGACTGCAGAGGAAC	TTATATGGGGTGTAGTCCAGCA
GFAP	TGGAGCTCAATGACCGCTTT	CCAGAAAGCGACCTTCTC	CTLA4	GGCACCTCCAGTGGAATCA	TCAGCACACACTACCACTT
GAPDH	TGCCACCAACTGCTTAGC	GGCATGGAAGTGTGTCATGA	PD1	ACGAGGGACAATAGGAGCCAG	GCCCATCCGCTAGGAAAGAC
RNA-polymerase II	GTTTTCCGTGCTGTGATGGG	TCATTGTTGCTGCTTTGGA	CD161	TGCCATGGACCAACAAGCAA	CCAAGTGAACCTGACAGA
E2Ubi	CTGAAGAGAATCCACAAGGAATTGA	CTCCAACAGGACCTGCTGAAC	NK-cells		
TBP	CAGCTTCGGAGAGTTCTGGG	TATATTCGGCTTTCGGGCA	CD56	ACTTATCGACCATTGGAGCGC	AGCTCACAAGGTTCTGCGCT
TAM			CD155	AAAGAGGGACCTCCAGTGA	GTGGATCCTGGGAAGAGCTG
IBA1	AGACGTTCACTACCTGACTT	GGCCTGTTGGCTTTTCTTTTCTC	CD137L	GAGCTTTCCGCCAGCAT	GTCAGTACACAGCTCAGGG
CD45	GCAGCTAGCAAGTGGTTTGTC	AAACAGCATGCGTCTTTTCTC	DR4	GTCTGTTGTCATCGGCTC	TGTGAGCAATGCTCCAGCC
CD68	CTTCTCTCAATCCCTATGGACA	GAAGGACACATTGTACTCCACC	DR5	TCCTGAGATGTGCCGGAAGT	CCACTGTGCTTTGTACTCTGATTC
HLA-DR	CCCAGGGAAGACCACCTTT	CACCCTGCAGTCGTAACCGT	FAS	GAACACTGTGACCTTGCAC	AAGACAAAGCCACCCCAAGT
CD163	TTTGCAACTTGTAGTCCCTTAC	TCCCGCTACACTTGTTTTAC	MICA	GCTGGCATCTTCCCTTTTGC	CTGCACAGATCCATCCAGG
CD206	TGCAGAAGCAAACCAACTGTAA	CAGGCCTTAAGCCAACGAAACT	OX40L	TCTGCCTGCACTTCTCTGC	CCTCCTTTTGGGAAGTGAGGA
IL-1b	TTTGAGTCTGCCAGTTCCC	TCAGTTATATCCTGGCCGCC	CD16	GACAGCGGCTCCTACTTCT	ATGGTTGACACTGCCAAACCT
IL-6	TGCAATAACCAACCCCTGACC	TGCGCAGAAATGAGATGAGTTG	CD69	TGCATCCGGAGATGGACAA	CACACAGGACAGGAACCTTGG
IL-10	GGCGCTGTCAATCGATTTCTTC	CACTCATGGCTTTGTAGATGCC	CD2	GGCAGCCTCTTGTATGGTCTT	CTGTGGGCTCTTGTCTCCAG
TNF-alpha	TGGAGAAGGGTGACCGACTC	TCACAGGGCAATGATCCCAA	CD96	GACCTCCAGTGGGACAGATAC	CATGAAGTGTGAGCCTGCAC
TGF-beta	CAATTCCTGGCGATACCTCAG	GCACAACTCCGGTGACATCAA	LAMP1	GTAACGCTCATGATGCCAC	CTGCTTGTTCACAGCGGTGC
Beta-2-microglobulin	GTGCTCGCGTACTCTCTCT	TCAATGTCCGATGGATGAAA	CD137	ACGCTCCGTTTCTCTGTTGT	GAAATCGGCAGCTACAGCCA
TIL			NCR1	CATCTATCGGGTTGGGAGC	CGAGATCACTTCGGGTCCAG
CD3e	TATCAGTTGGCGTTTGGGGG	TCCAGGATACTGAGGGCATGT	TIGIT	TGGGACGTACACTGGGAGAA	TGGCTCCAAGCAATGGAATCT
CD4	TGCTAGTGACTCGGGACAG	CCAGCACAATCAGGGCCATTG	CD226	TTAGAGCGACGACACTCAC	TGCCAAAGCACTCTTCCACA
CD8a	ACTTGTGGGTCTCTCTCT	GTCTCCCGATTTGACCACAG	Granzyme B	TGGGGGACCCAGAGATTAATA	TTTCGTCCATAGGAGACAATGC

SUPPLEMENTARY FIGURE S5. (a) RNA sequencing data showing HLA-I and -II expression in human glioblastoma cell lines. (b) Survival curve of patients with high (>0%) and no (0%) CIITA expression. (c) Survival curve of patients with high (>0%) or no (0%) HLA-DRa expression. (d) Survival curve from TGCA database patients with highest 90 and lowest 10th percentile and (e) highest 75 and lowest 25th percentile. (f) Caspase 3/7 apoptose assay in NK cell co-culture experiments. (g) Percentage of cells in apoptosis per time point, GM2-WT versus -CIITA.

