

Supplementary Figures

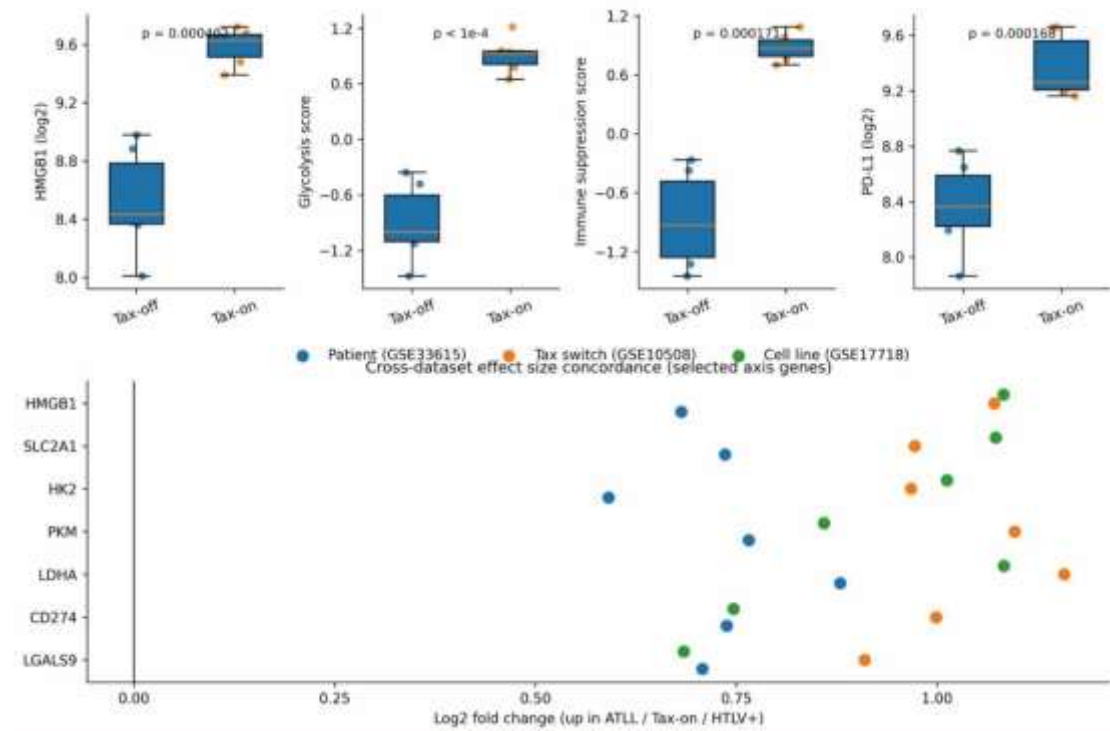


Figure S1 Tax status drives HMGB1 and concordant glycolysis/immune axis changes. Top panels: Tax switch model comparisons (Tax-off n=6, Tax-on n=6). Bottom panel: effect-size concordance for selected genes across cohorts.

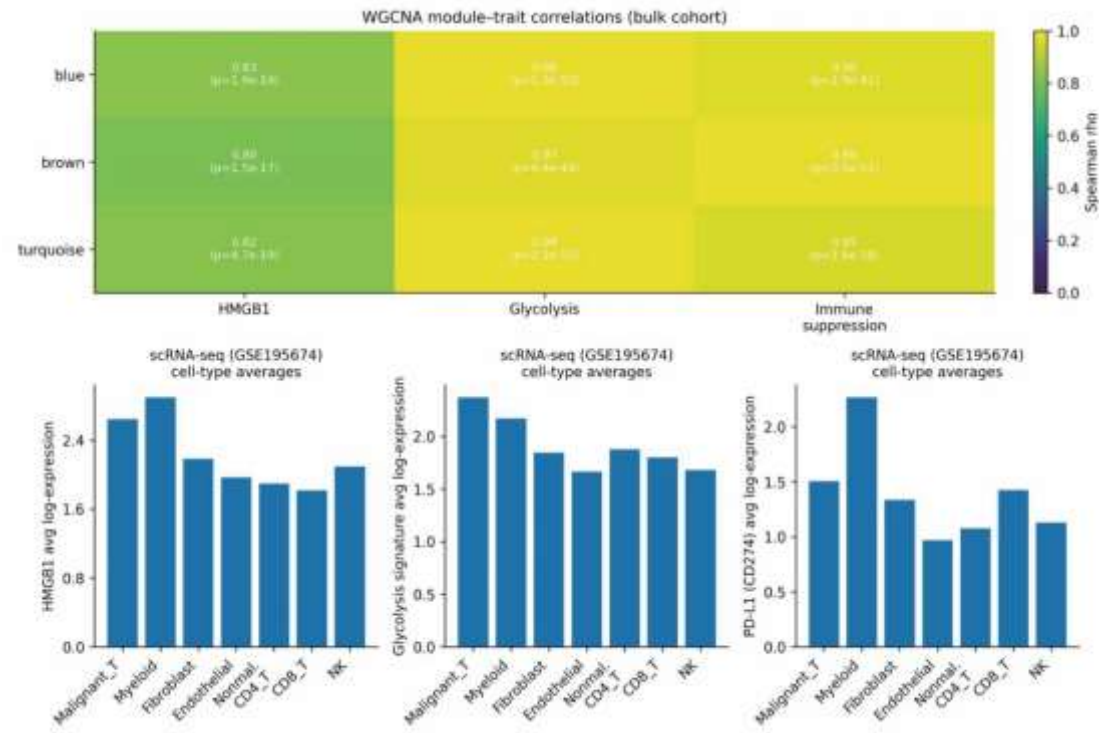


Figure S2 Network integration and cell-type context. Top: WGCNA module–trait correlations in the bulk ATLL cohort. Bottom: scRNA-seq cell-type average expression for HMGB1, glycolysis signature, and PD-L1.

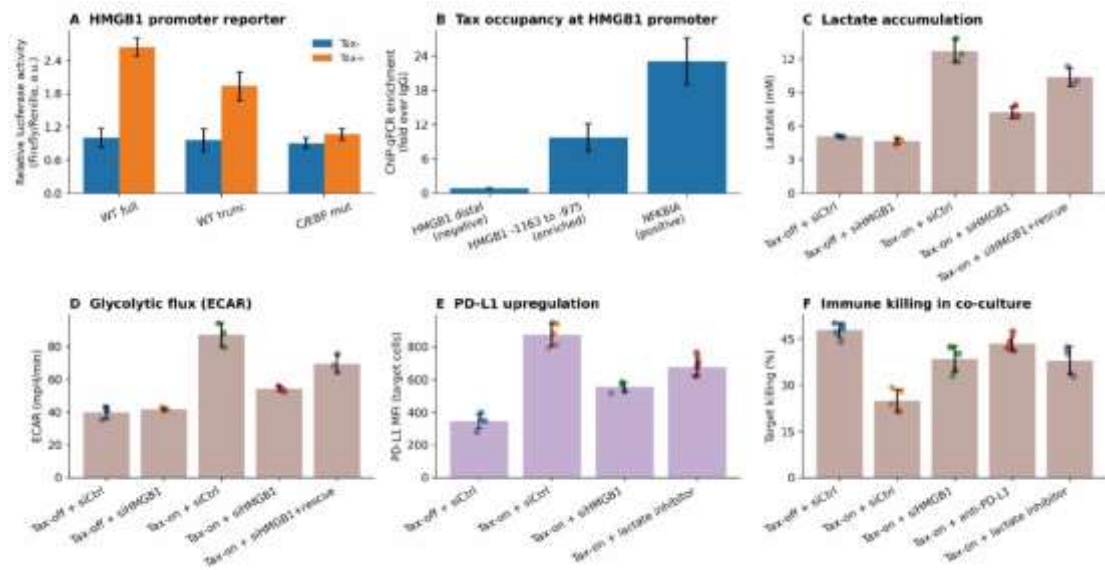


Figure S3 Functional validation of the Tax–HMGB1–glycolysis–PD-L1 axis. (A) HMGB1 promoter luciferase activity in Tax-off/on conditions and after mutation of the C/EBP motif. (B) ChIP–qPCR enrichment at the HMGB1 promoter interval (–1163 to –975), a distal negative-control region, and a positive-control promoter. (C–D) Lactate concentration and ECAR across Tax/HMGB1 perturbations (n=3 independent experiments). (E) PD-L1 surface expression (MFI) on target cells (n=5 donors). (F) Target-cell killing in donor-matched cytotoxic co-cultures (n=5 donors).

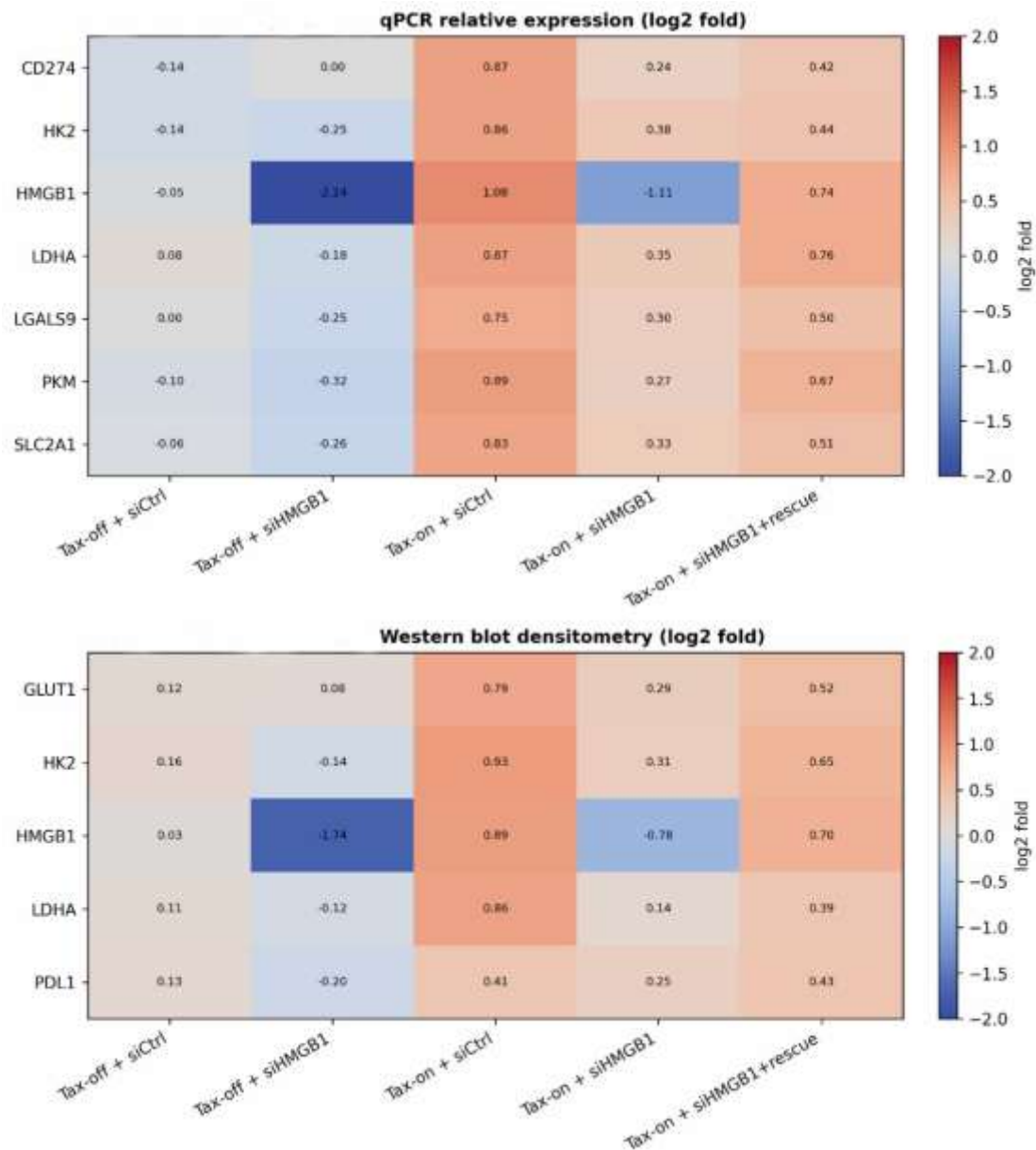


Figure S4. Effects of HMGB1 silencing on glycolysis- and immune-related gene expression under Tax activation. (A) Heatmap showing relative mRNA expression levels (log2 fold change) of CD274, HK2, HMGB1, LDHA, LGALS9, PKM, and SLC2A1 measured by qPCR under the indicated conditions. (B) Heatmap showing protein expression changes (log2 fold change) determined by Western blot densitometry for GLUT1, HK2, HMGB1, LDHA, and PDL1 under the indicated conditions. Color scale represents log2 fold change relative to the control condition.

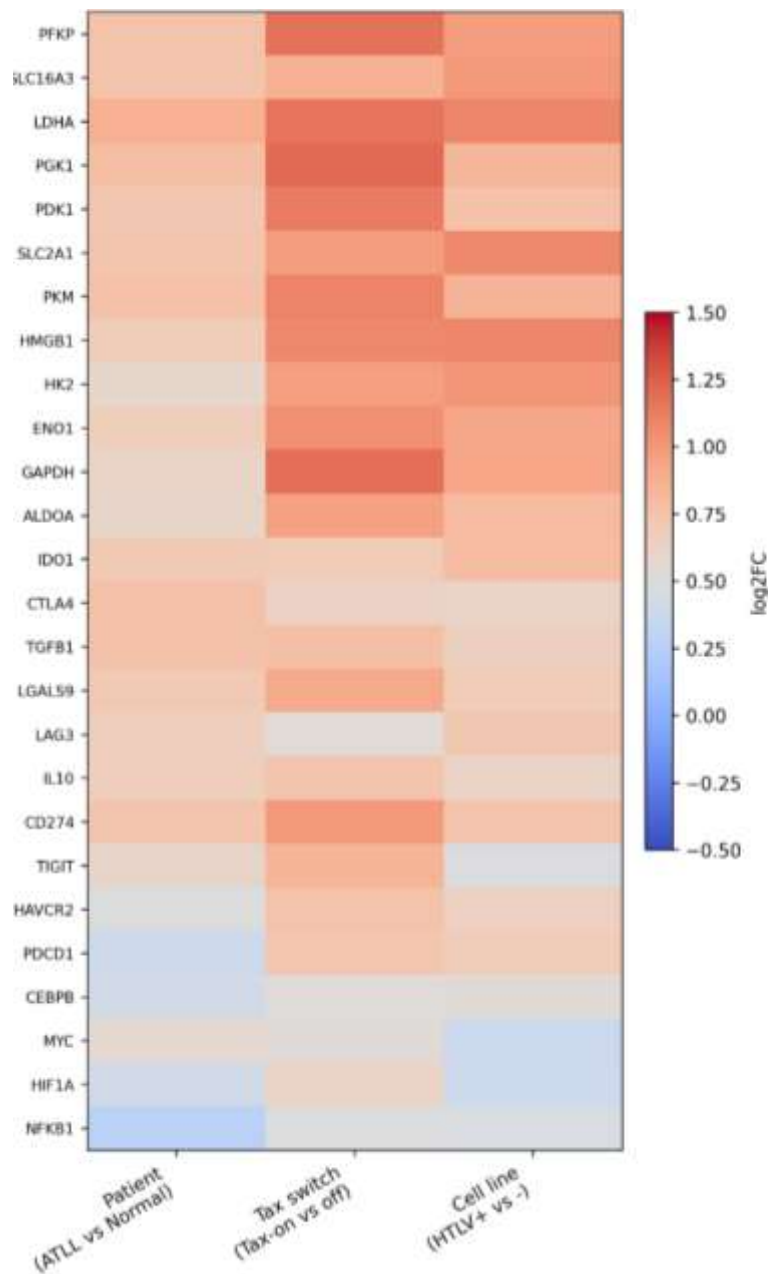


Figure S5. Differential log₂ fold-change concordance across datasets. Heatmap showing log₂ fold changes of 26 genes across three independent datasets, including patient samples (ATLL vs. normal), a Tax-switch model (Tax-on vs. Tax-off), and HTLV-1 cell line comparisons. Genes include glycolysis-related genes (e.g., PKFP, LDHA, PKM), immune checkpoint molecules (e.g., CD274, CTLA4, LAG3, TIGIT), and transcriptional regulators (e.g., MYC, HIF1A, NFKB1). Color scale represents log₂ fold-change values, with red indicating upregulation and blue indicating downregulation.