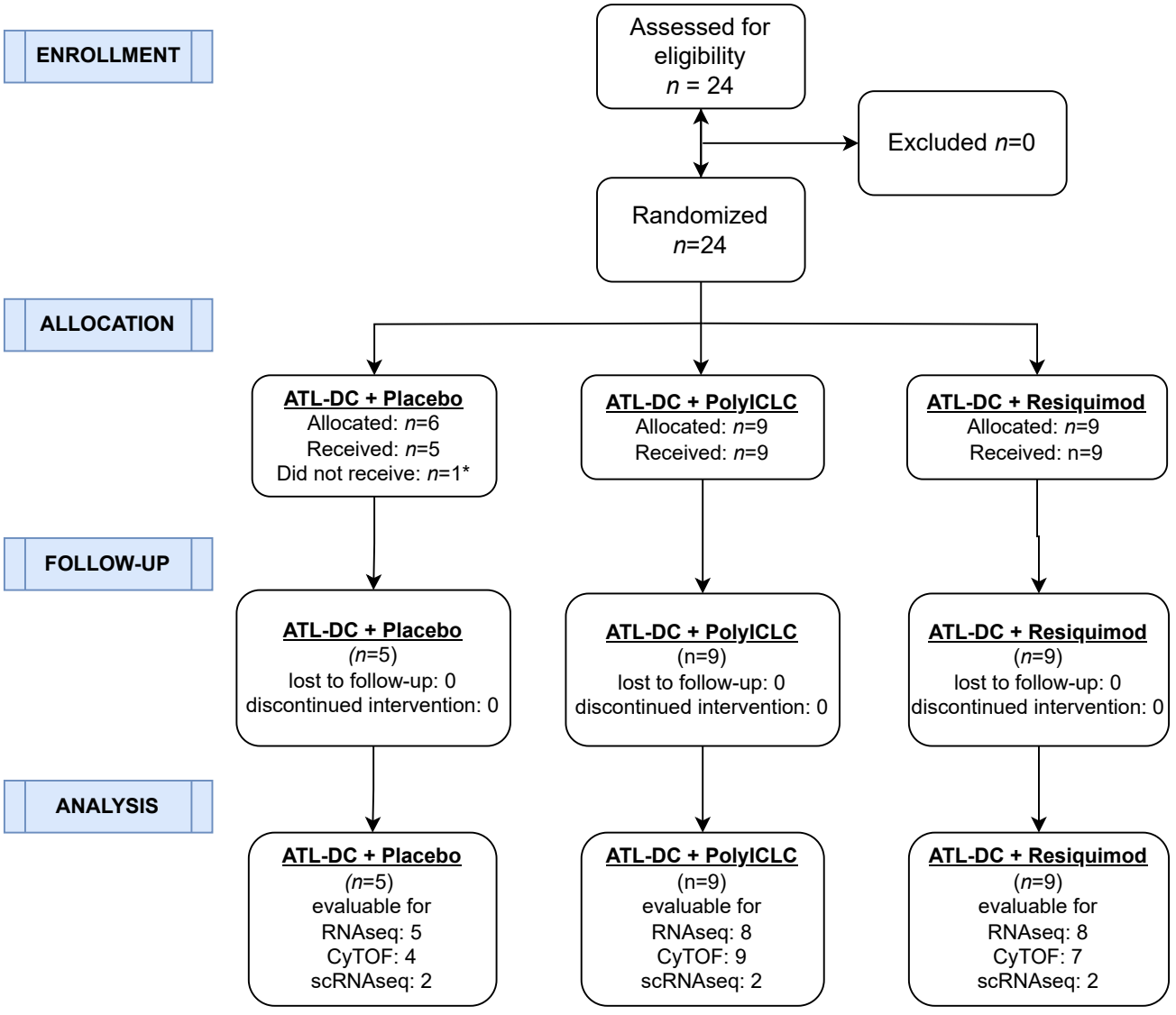
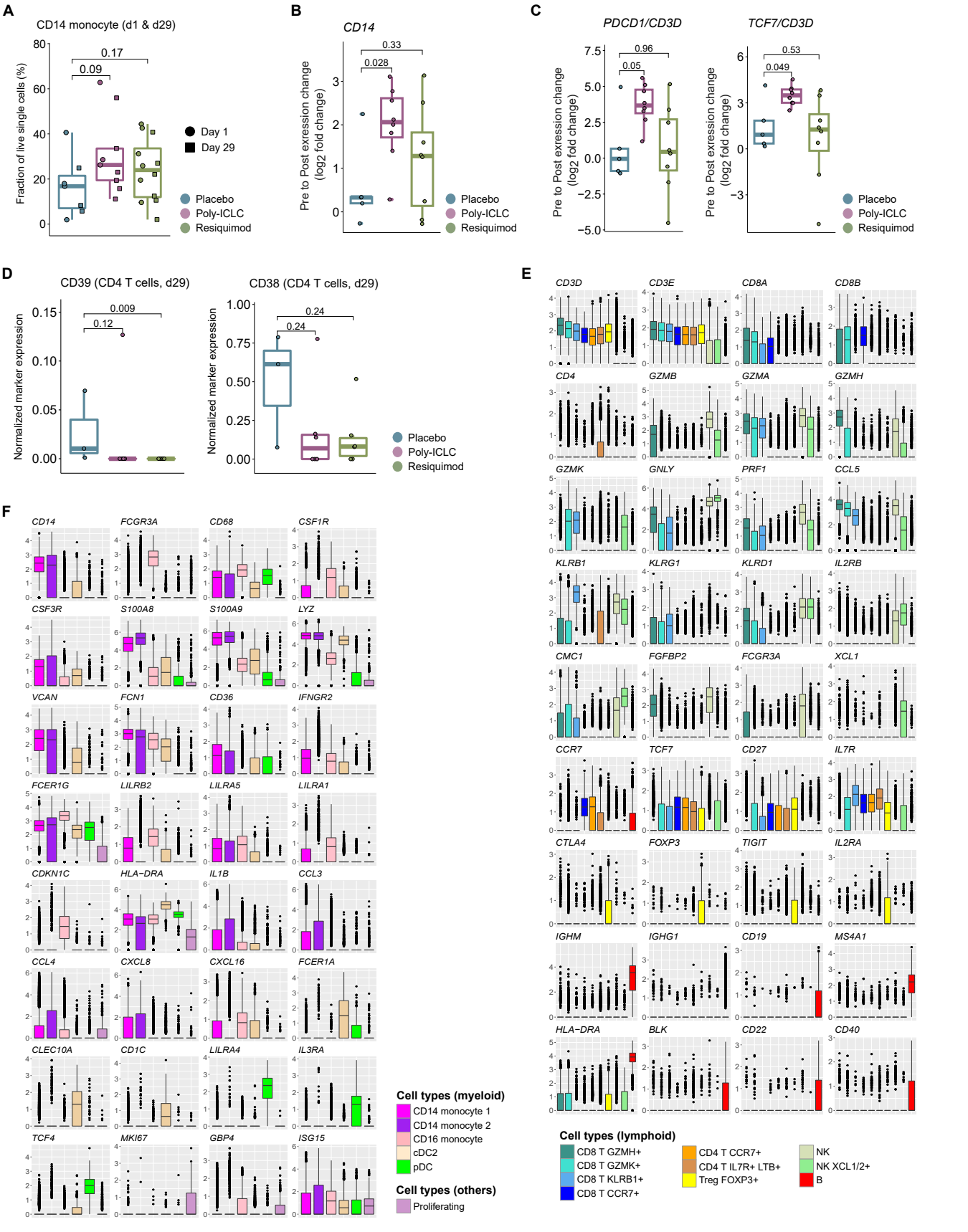
Supplementary Figure 1. CONSORT diagram of clinical trial enrollment.



Supplementary Figure 1. CONSORT diagram of clinical trial enrollment.

Supplementary Figure 2

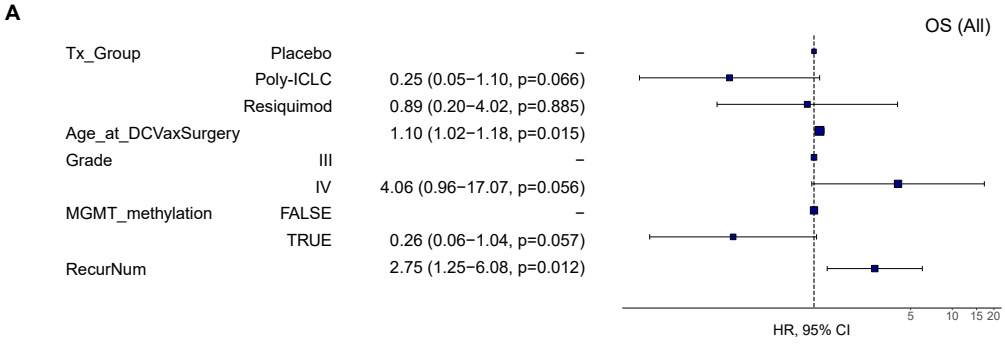


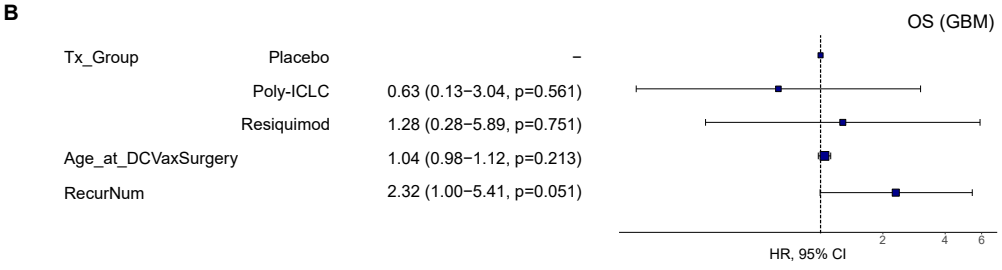
Supplementary Figure 2. CyTOF and single cell transcriptomics of patient PBMCs before and after ATL-DC vaccine with or without adjuvant TLR agonist.
A, Comparison of CD14+ monocyte fraction in post-treatment PBMCs of patients from indicated treatment groups. P values, two-sided Wilcoxon rank sum test.
B, Differential gene expression (pre vs. post-treatment fold change, in $\log_2$) of *CD14* transcript across treatment groups (P values, two-sided Welch t test).
C, Differential gene expression (pre vs. post-treatment fold change, in $\log_2$) of *PDCD1* transcript across treatment groups (P values, two-sided Welch t test) after adjusting for the change in *CD3D* transcript expression in the same sample pair. The values approximate the changes of *PDCD1* transcript per T cell.
D, Normalized expression of indicated markers in CD4 T cell populations within the PBMC samples of patients from indicated treatment groups. P values, two-sided Wilcoxon rank sum test.
E, F, Boxplots showing marker gene expressions in lymphoid cell populations (**E**) or myeloid and proliferative cell populations (**F**).

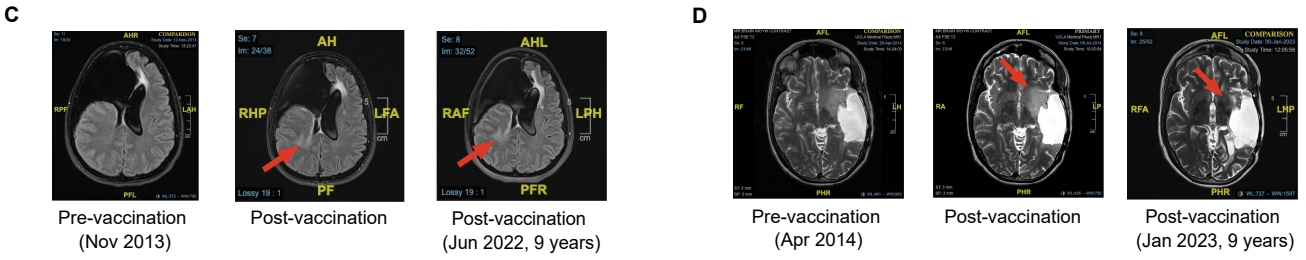
The number of sample pairs analyzed by CyTOF in **A** and **D** are: ATL-DC+placebo, 4 pairs; ATL-DC+poly-ICLC, 9 pairs; ATL-DC+resiquimod, 7 pairs.
The number of sample pairs analyzed by RNAseq in panels B and C are: ATL-DC +placebo, 5 pairs; ATL-DC+poly-ICLC, 8 pairs; ATL-DC+resiquimod, 8 pairs.

The rectangular box in each boxplot represents the interquartile range (IQR), spanning from the first quartile (25^{th} percentile, bottom of box) to the third quartile (75^{th} percentile top of box). Inside the box, the median (50^{th} percentile) is marked. The whiskers (shown as lines extending from the box) extend to the largest and smallest non-outlier values within 1.5 times the IQR, while outliers lie beyond the whiskers.

Supplementary Figure 3







Pre-vaccination (Nov 2013) | Post-vaccination | Post-vaccination (Jun 2022, 9 years)

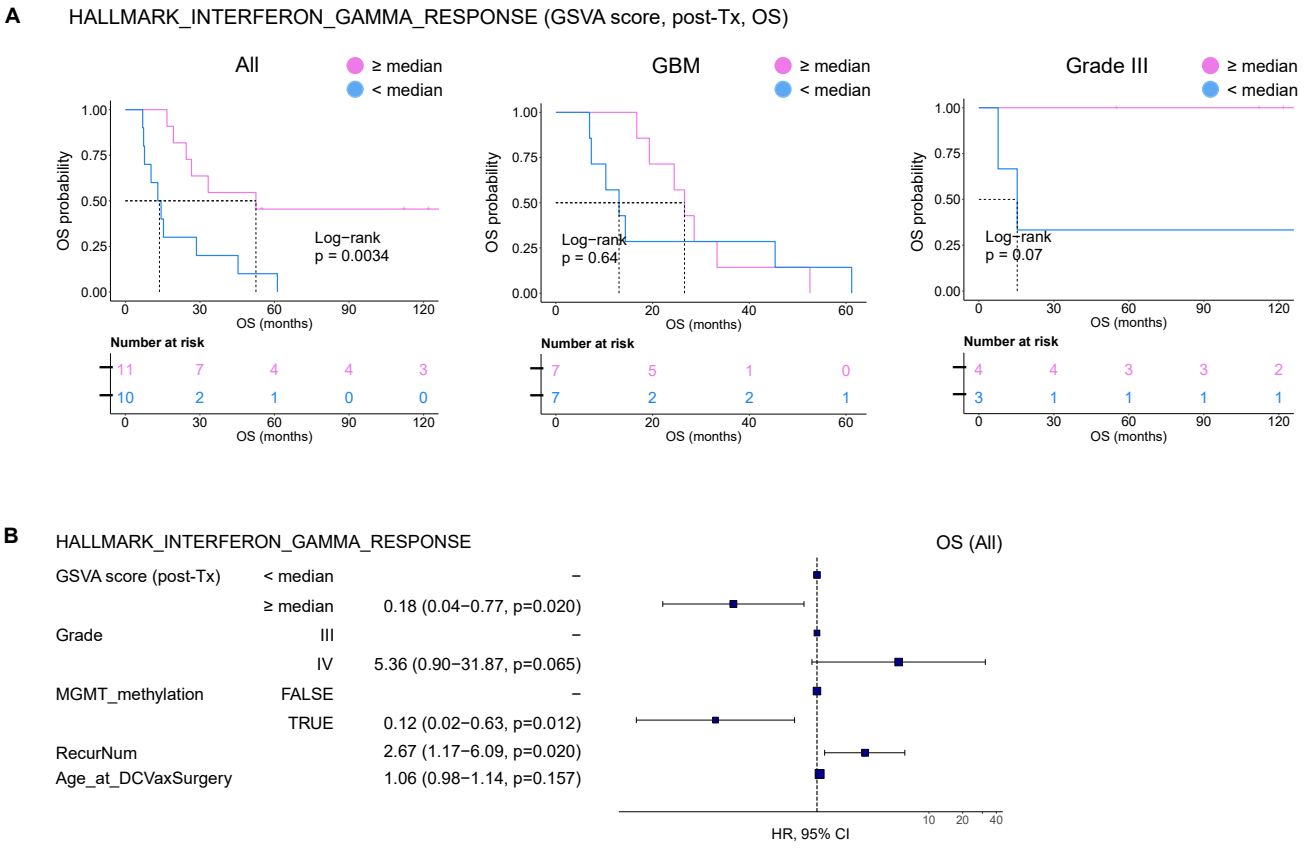
Pre-vaccination (Apr 2014) | Post-vaccination | Post-vaccination (Jan 2023, 9 years)

Supplementary Figure 3. The association between combined ATL-DC vaccine and TLR agonist and patient survival.

A, B, Multivariate Cox proportional hazards analysis assessing the hazard ratios of death in TLR agonist treatment groups against placebo in all patients (**A**) or GBM subset (**B**) after adjusting for other clinical covariates (Tx_Group=treatment group, RecurNum=number of recurrences prior to ATL-DC treatment; the CoxPH model did not converge when MGMT_methylation was included). In the forest plot, the squares are the hazard ratio (HR) estimates, the error bars are 95% confidence interval (CI) of the HR, the P value of each covariate is based on its Wald statistics, the P values are not adjusted. In (**A**), the sample distribution in each covariate is Tx_Group: placebo=5, poly-ICLC=9, resiquimod=9; Grade: III=8, IV=15; MGMT_methylation: True=8, False=15. In (**B**), Tx_Group: placebo=4, poly-ICLC=5, resiquimod=6.

C, D, Representative contrast-enhanced MR imaging of patients treated with ATL-DC + poly-ICLC showing initial increase of T2/FLAIR MRI signal (red arrows), which either persists (**C**) or regresses (**D**) over time. Both patients have significantly longer PFS and OS than the rest of the patients in the cohort.

Supplementary Figure 4



Supplementary Figure 4. The association between IFN pathway activation and overall survival after ATL-DC vaccine and TLR agonist therapy.
A, Kaplan-Meier overall survival curves of all patients (left), GBM (center), and Grade III glioma subsets (right) stratified by their HALLMARK_INTERFERON_GAMMA_RESPONSE GSVA scores in their post-treatment PBMCs. P values, log-rank test.
B, Multivariate Cox proportional hazards analysis assessing hazard ratios of death in patients with high HALLMARK_INTERFERON_GAMMA_RESPONSE GSVA score after adjusting for other clinical covariates. In the forest plot, the squares are the hazard ratio (HR) estimates, the error bars are 95% confidence interval (CI) of the HR, the P value of each covariate is based on its Wald statistics, the P values are not adjusted. T the sample distribution in each covariate is GSVA score (post-Tx): <median=10, ≥median=11; Grade: III=7, IV=14; MGMT_methylation: True=7, False=14.