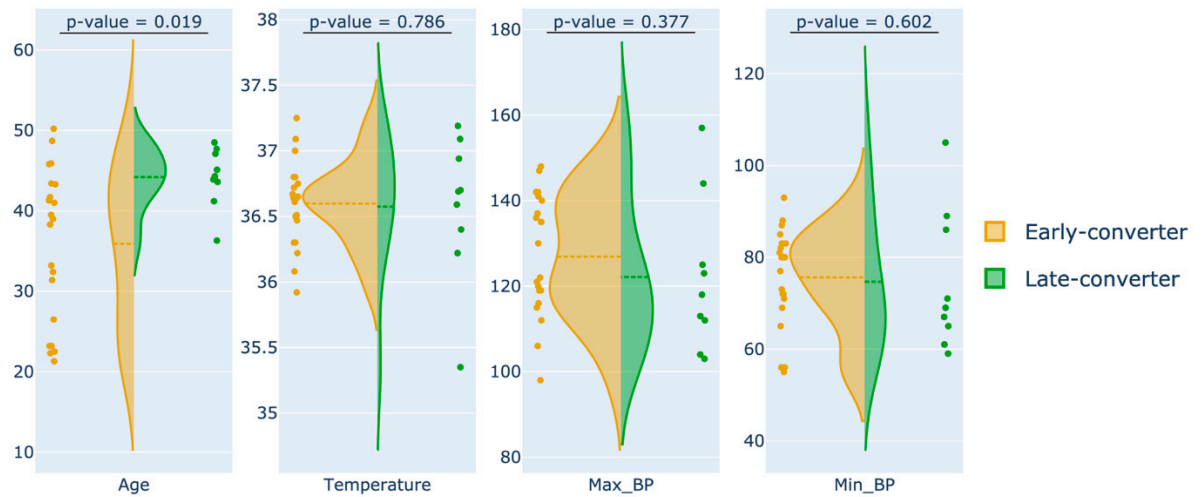


**Table S1. Comparison table of the baseline non-genetic attributes between early and late converters.**

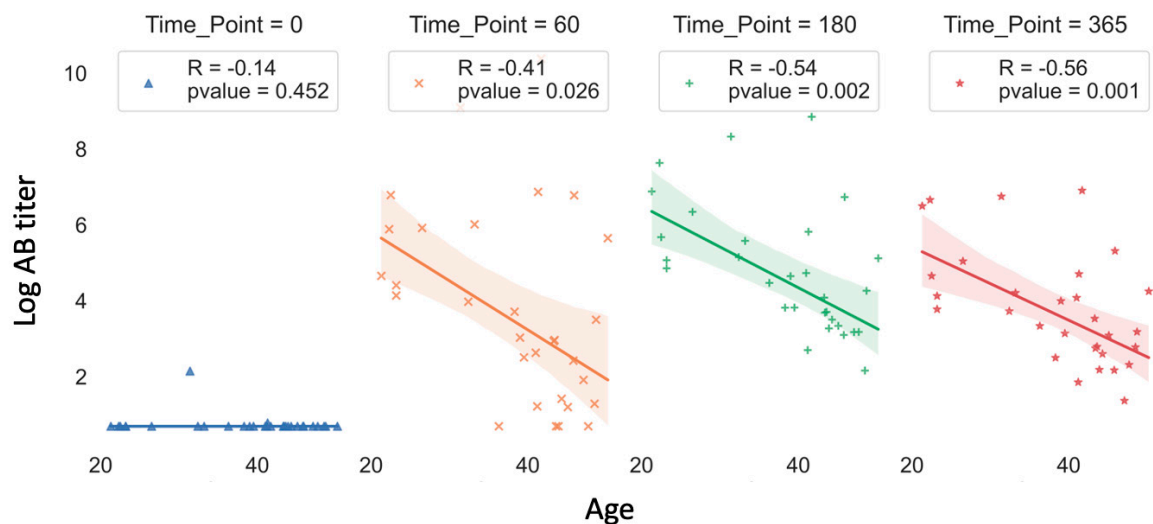
Dataset	Feature	Early-converters (n=21) average (range)	Late-converters (n=9) average (range)
Metadata	Age (years)	35.9 (21.3-50.2)	44.19 (36.3-48.5)
	Temperature ([degree]C)	36.60 (35.92-37.25)	36.57 (35.35-37.19)
	Max BP (mmHg)	126.90 (98-148)	122.11 (103-157)
	Min BP (mmHg)	75.62 (55-93)	74.67 (59-105)
	Female/Male	13/8*	7/2*
CD4+ T cell parameters	B0 (counts)	50790.38 (37866-71140)	50237.89 (29330-87551)
	PPnrB0 (%)	2.71 (2.01-3.45)	3.37 (1.72-5.62)
	PSB0 (%)	2.75 (1.87-3.87)	2.49 (1.40%-4.53%)
	HepBTCRs (counts)	1.02 (0.74-1.36)	0.78 (0.42-1.11)
Cell counts	WBC0 (counts)	6.10 (3.6-9.4)	6.74 (4.3-9.3)
	RBC0 (counts)	4.59 (3.94-5.21)	4.60 (4.14-5.42)
	HGB0 (counts)	13.62 (11.5-15.5)	13.30 (8.1-15.4)
	HCT0 (counts)	40.67 (35.0-46.4)	39.82 (26.2-46.2)
	PLT0 (counts)	243.67 (144.0-351.0)	242.89 (172.0-403.0)
	LYM0 (counts)	34.14 (19.5-47.8)	29.7 (15.3-38.7)
	MON0 (counts)	4.79 (3.2-8.2)	4.13 (2.5-7.4)
	GRA0 (counts)	61.07 (49.0-76.6)	66.17 (57.4-77.3)

See the original manuscripts [19], [24] for breakdown of features.

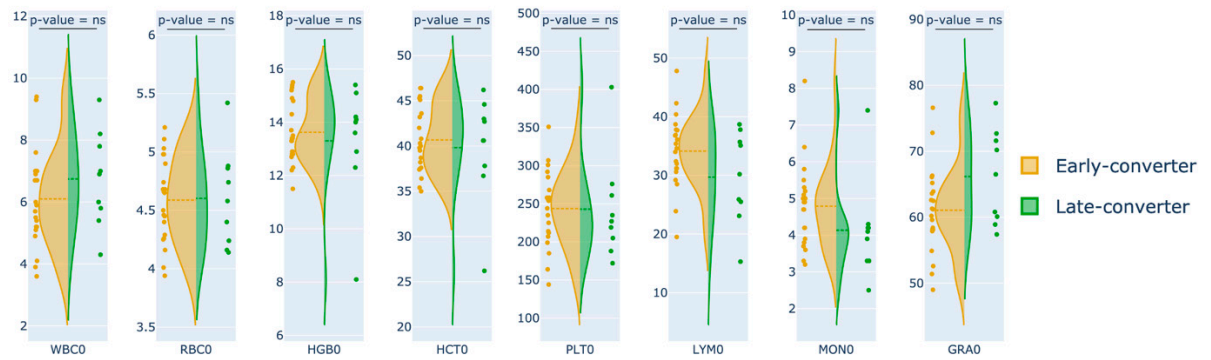
Maximum blood pressure (day 0) (Max BP); minimum blood pressure (day 0) (Min BP); total unique TCR sequences (day 0) (B0); fraction of HBs-Ag-aspecific (day 0) (PPnrB0); fraction of HBs-Ag-specific (day 0) (PSB0); normalised ratio of vaccine-specific TCRs (day 0) (HepBTCRs); white blood cells count (day 0) (WBC0); red blood cells count (day 0) (RBC0); haemoglobin protein count (day 0) (HGB0); hematocrit (day 0) (HCT0); platelets count (day 0) (PLT0); lymphocytes count (day 0) (LYM0); monocytes count (day 0) (MON0); granulocytes count (day 0) (GRA0). \*Number of individuals.



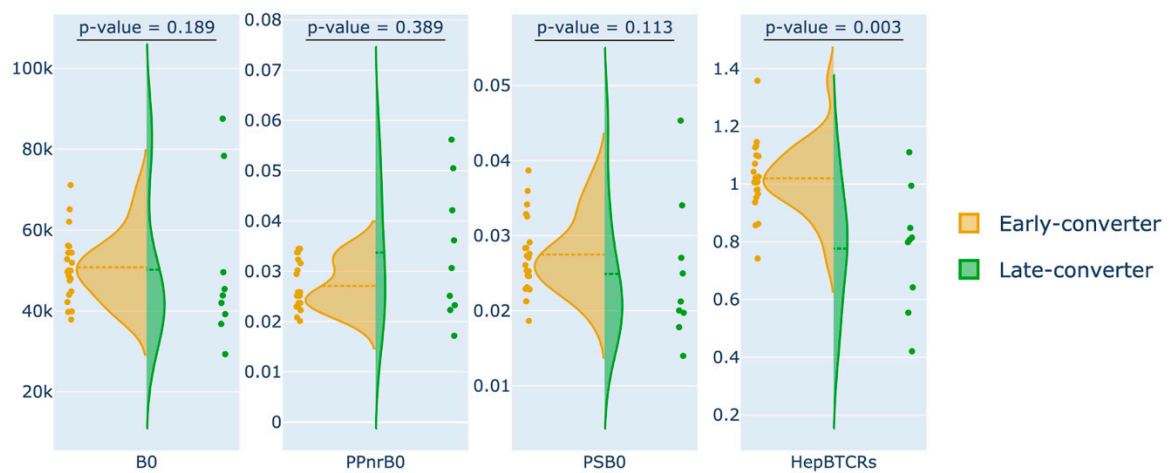
**Figure S1. Metadata distributions reveal age differences.** Metadata feature distributions per class. Age is significantly higher for late converters (p-value = 0.019, two-sided Mann-Whitney U-test).



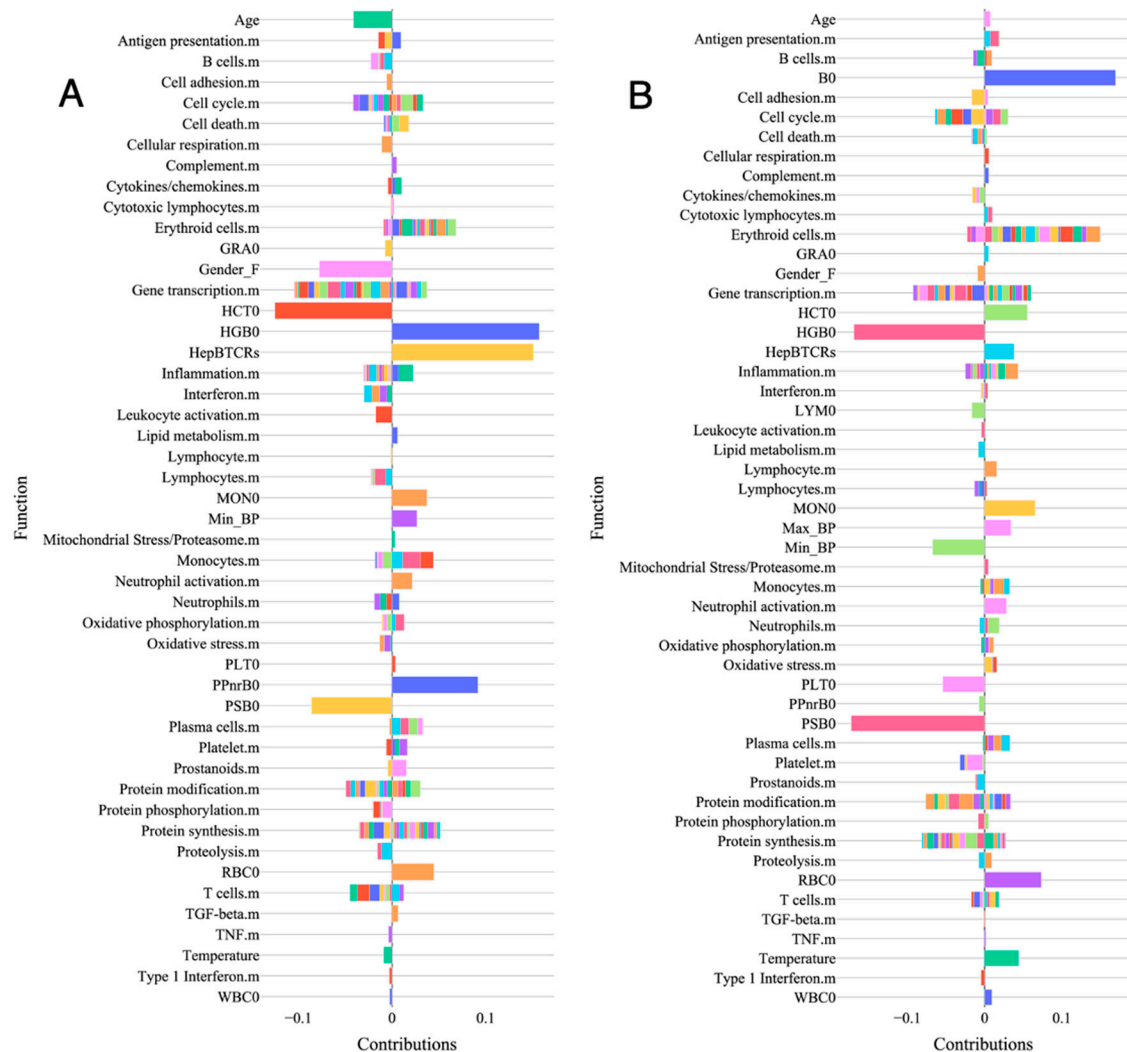
**Figure S2. Longitudinal analysis of AB titers shows anticorrelation with age.** Comparison between age and AB for early and late converters, presented at each timepoint of the study. Time is expressed in days from the first vaccine shot. Antibody (AB).



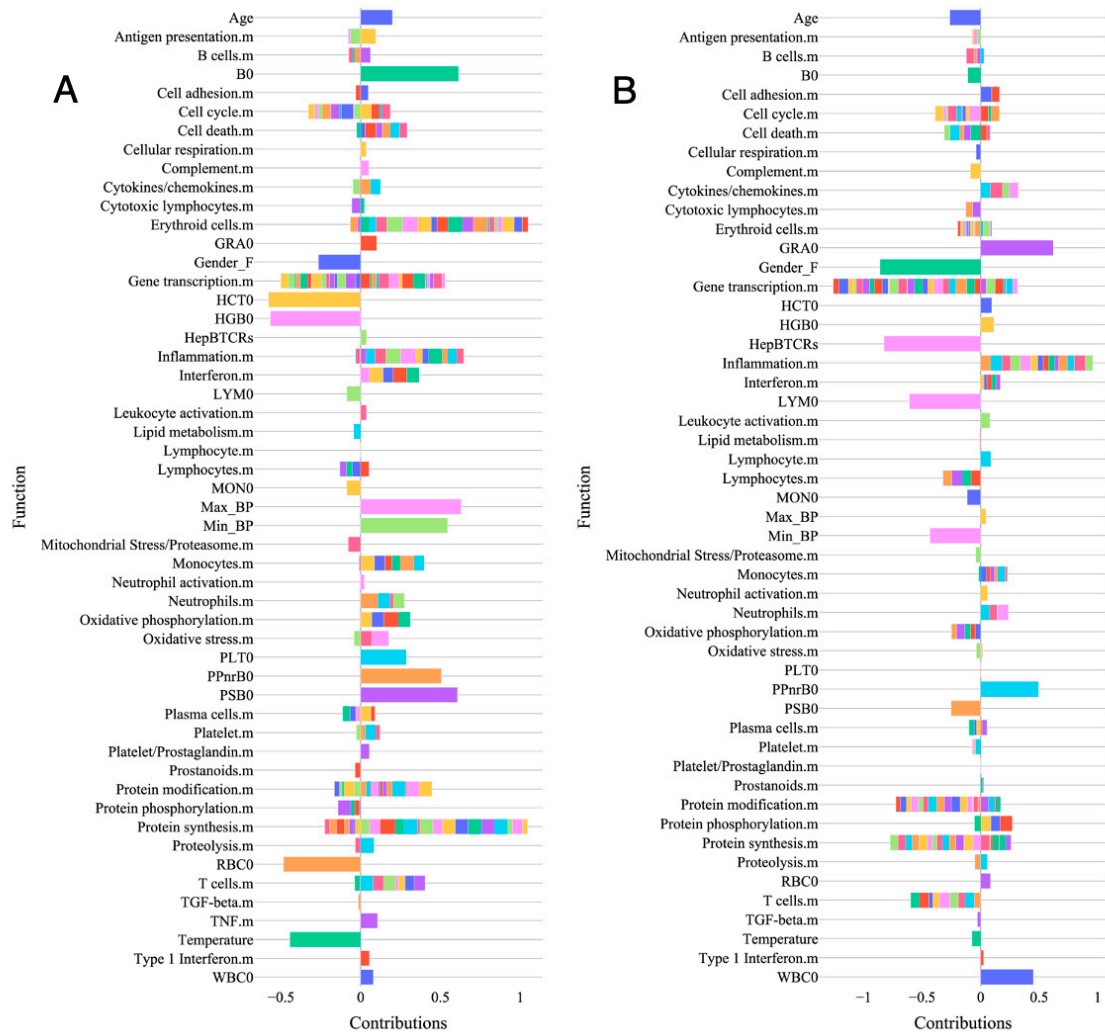
**Figure S3. Cell counts distributions reveal class differences.** Cell counts feature distributions per class. Granulocytes and monocytes appear in lower quantities, respectively, for early and late converters. However, possible outliers lead to non-significant differences.



**Figure S4. CD4+ T cell parameters reveal class differences.** Pre-vaccination TCR data feature distribution per class. HepBTCRs are significantly elevated in early vaccine responses (p-value = 0.003, two-sided Mann-Whitney U-test). T-Cell Receptor (TCR).



**Figure S5. MCCA reveals distinct contributions of the metadata and expression.** Visualisations of the loadings to the first (A) and second (B) dimensions of the MCCA projection. Coefficients were stacked by function, with null-values and modules without associated functionality being omitted. Multi-view Canonical Correlation Analysis (MCCA).

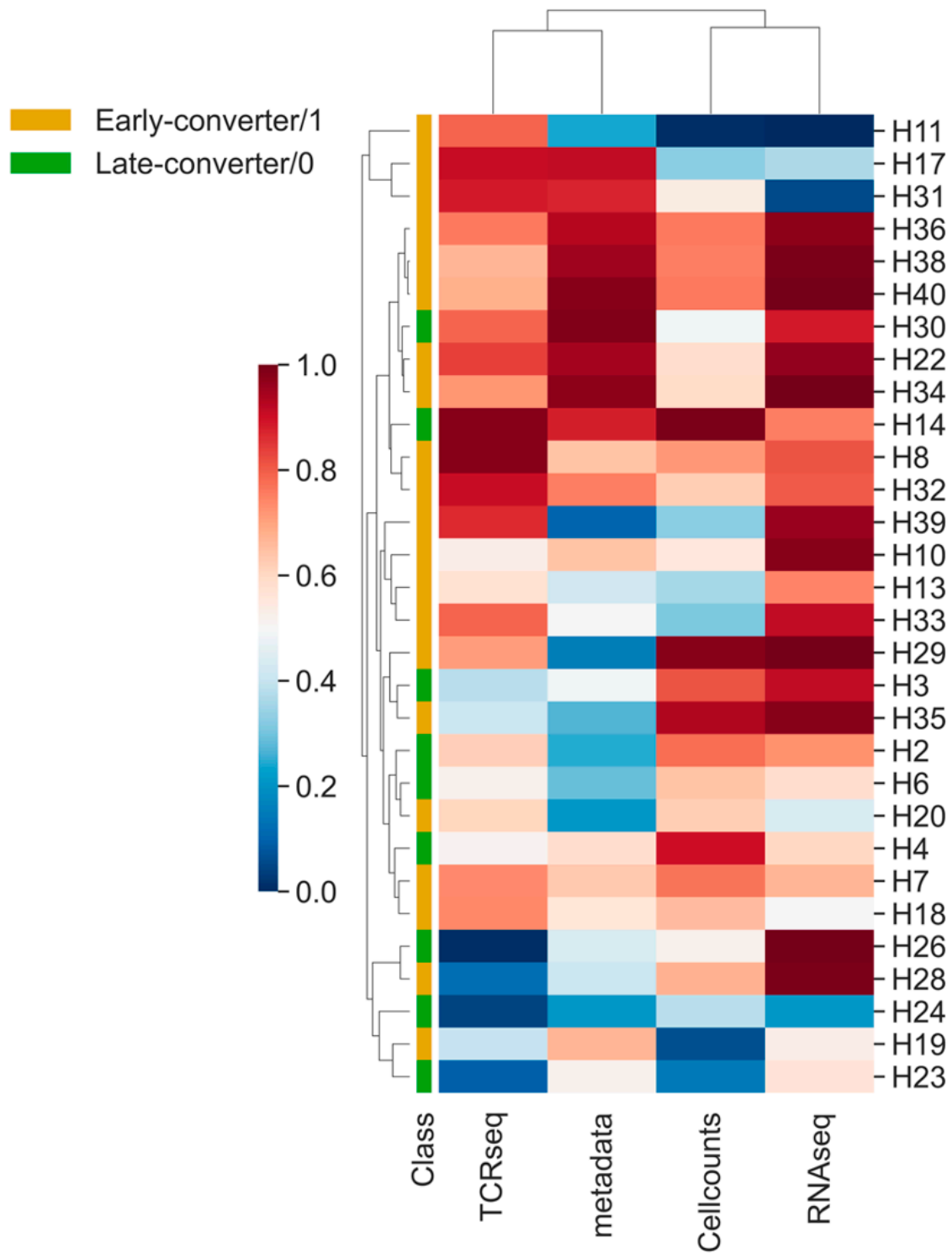


**Figure S6. GroupPCA components support MCCA findings and offer better interpretability.** Visualisations of the loadings to the first (A) and second (B) dimensions of the GroupPCA projection. Coefficients were stacked by function, with null-values and modules without associated functionality being omitted. Principal Component Analysis (PCA).

**Table S2. Performance table for the evaluation in terms of AUC and accuracy of a LR trained on single modality data.**

View	Cell counts	TCR-seq	Metadata	RNA-seq
Accuracy	0.506±0.044	0.708±0.067	0.598±0.058	0.440±0.018
AUC	0.430±0.038	0.731±0.040	0.588±0.028	0.611±0.009

Area Under Curve (AUC); Logistic Regression (LR).



**Figure S7. Unimodal predicted probabilities show layer to layer difference in predictive power.** Predicted probabilities attributed to each patient of the cohort, per single data modality of a LOOCV LR. Leave-One-Out Cross-Validation (LOOCV).