Supplementary Figure 1



SF1, Fitting a linear mixed effect model where age and number of TCR sequenced are controlled whilst sequencing run and treatment are fitted as random effects. Controlling for these covariates, responders have an average of 5.7 more large clones (defined by TRA) on day 21 than patients who progress by 6 months. Fitted lines indicate responding large clone counts (dark blue) and those for progressors (ANOVA, F-statistic).

Supplementary Figure 2



Gating strategy to identify CD8+ T-cell subsets from whole PBMCs

Antibody	Clone	Conjugate	Supplier
LIVE/DEAD™ Fixable Near-IR Dead Cell Stain Kit	n/a	n/a	Thermofisher scientific
Mouse anti-human CD3	UCHT1	BV785	Biolegend
Mouse anti-human CD56	5.1H11	BV421	Biolegend
Mouse anti-human CD4	RPA-T4	APC	Biolegend
Mouse anti-human CD8a	RPA-T8	BV510	Biolegend
Mouse anti-human CD45RA	HI100	FITC	Becton Dickinson
Mouse anti-human CD27	M-T271	AF700	Biolegend

Supplementary Figure 3



a, By combining the expression of the lead gene from ICB induced modules (M1:M9) at day 21, baseline monocyte and neutrophil counts, large clones at day 21 and total large clones (sum of those at baseline and at day 21) we can use random forest (RF) to build a model of outcome. We used 5 fold cross-validation (repeated 10 times) to find the best model with optimal parameters tuned.

b, Based on the RF model, we measured the importance for a predictor by the degree of decrease in accuracy removing that predictor (this measure is more robust than directly measuring a predictor by its predictive power). A high score in accuracy indicates a highly informative predictor. We next applied linear discriminant analysis to combine all identified informative predictors. We calculated linear discriminant scores (LD scores) used for patient response prediction. LD scores are a linear combination of predictors (thus with better prediction explanations); the performance (measured by AUC) of each combination was compared to predictors as to ongoing response at six-months.