

Identification of patient-specific T cell neoantigens through HLA-agnostic genetic screens

Chiara M. Cattaneo^{1,2}, Jos Urbanus^{1,2,‡}, Thomas Battaglia^{1,2,‡}, John B.A.G. Haanen^{1,3}, Emile E. Voest^{1,2,#}, Ton N. Schumacher^{1,2,#,*}, and Wouter Scheper^{1,#,*}

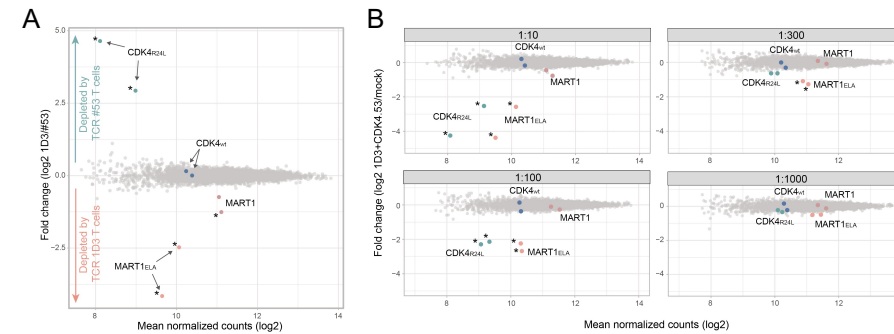
¹Department of Molecular Oncology and Immunology, The Netherlands Cancer Institute, Amsterdam, the Netherlands. ²Oncode Institute, Utrecht, the Netherlands. ³Department of Medical Oncology, The Netherlands Cancer Institute, Amsterdam, The Netherlands. [‡]These authors contributed equally to this work. [#]These authors share senior authorship. ^{*}Correspondence to: w.scheper@nki.nl, t.schumacher@nki.nl

Background

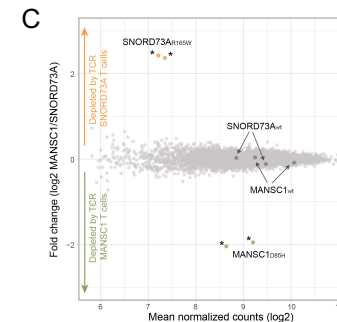
Cancer neoantigens that arise from tumor mutations are drivers of tumor-specific T cell responses, but identification of T cell-recognized neoantigens in individual patients is complicated by their patient-specific nature. Here we develop the first genetic neoantigen discovery platform that allows identification of both CD4+ and CD8+ T cell-recognized neoantigens with high sensitivity and across complete HLA genotypes. This technology should facilitate the development of personalized neoantigen-based cancer immuno-therapies.

Sensitive HLA class I and class II neoantigen discovery technology: validation experiments

(A) An HLA-A*02:01 B cell line was transduced with a library of 4,764 minigenes that included the CDK4_{R24L} neoantigen, its wild-type counterpart, the MART1₂₆₋₃₅ epitope (MART1) and the affinity-enhanced MART1₂₆₋₃₅A27L epitope (MART1-ELA). Library-expressing B cells were co-incubated with donor CD8+ T cells engineered to express a CDK4_{R24L}-specific TCR, or the MART1₂₆₋₃₅-specific TCR 1D3. After 72 hours, minigenes from remaining B cells were amplified and quantified by deep sequencing. Dots represent individual minigenes. (B) CD8+ T cells expressing either the CDK4_{R24L} or 1D3 TCR were diluted 10-, 100-, 300- or 1,000-fold with mock-transduced T cells to simulate T cell pools with low abundance antigen-reactive T cell populations, and were incubated with library-expressing B cells as in (A).

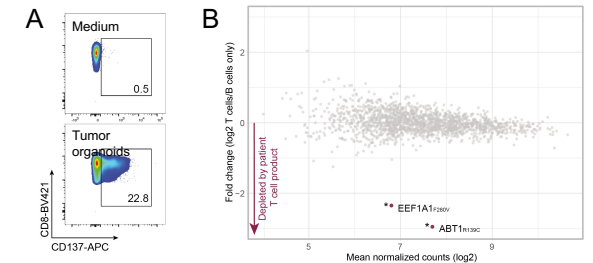


(C) Patient-derived TCRs specific for the MHC class II-restricted MANSC1_{D85H} and SNORD73A_{R165W} neoantigens were expressed in donor CD4+ T cells and used to screen the patient-matched B cell line transduced with the minigene library. In this case, minigenes were subcloned in a vector that couples minigenes to the CD74 signaling motif, to enable processing of minigene products through the HLA class II processing pathway.

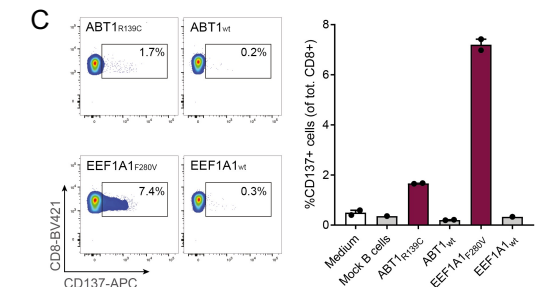


Personalized and HLA-agnostic neoantigen screening of patient T cells

(A) PBMCs from a patient suffering from mismatch repair-deficient colorectal cancer were cocultured with matched tumor organoids for two weeks. Tumor-reactivity of the cell product was then assessed by incubating cultured PBMCs with tumor organoids and analysis of CD137 surface expression. (B) Non-synonymous tumor mutations from a patient suffering from mismatch repair-deficient colorectal cancer were identified by exome and RNA sequencing, and used to design a personalized mutanome minigene library consisting of 1,834 unique minigenes. Patient B cells were immortalized, transduced with the mutanome library, and incubated with patient PBMCs from (A).



(C) Neoantigen hits identified in (B) were validated by expressing EEF1A1_{F280V}, ABT1_{R139C} or the respective wild-type sequences as single minigenes in patient B cells and incubating transduced B cells with organoid-induced patient PBMCs.



Schematic overview of the methodology:

