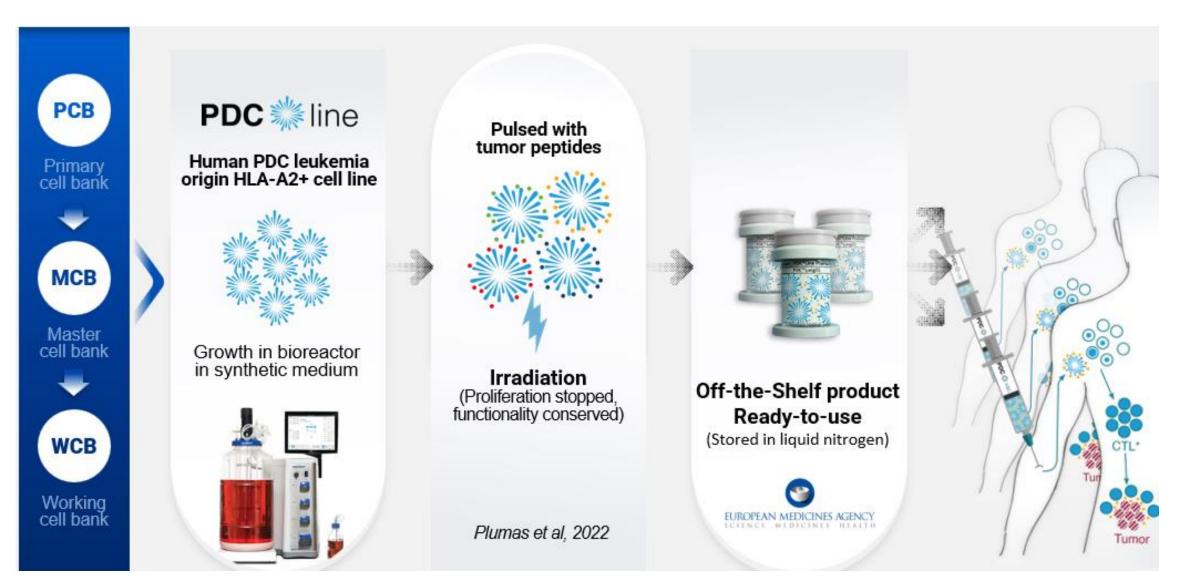
Evaluation of the immune response using TCR repertoire analysis in patients with non-small cell lung cancer treated with a PDC*line cell-based cancer vaccine in combination or not with an anti-PD-1

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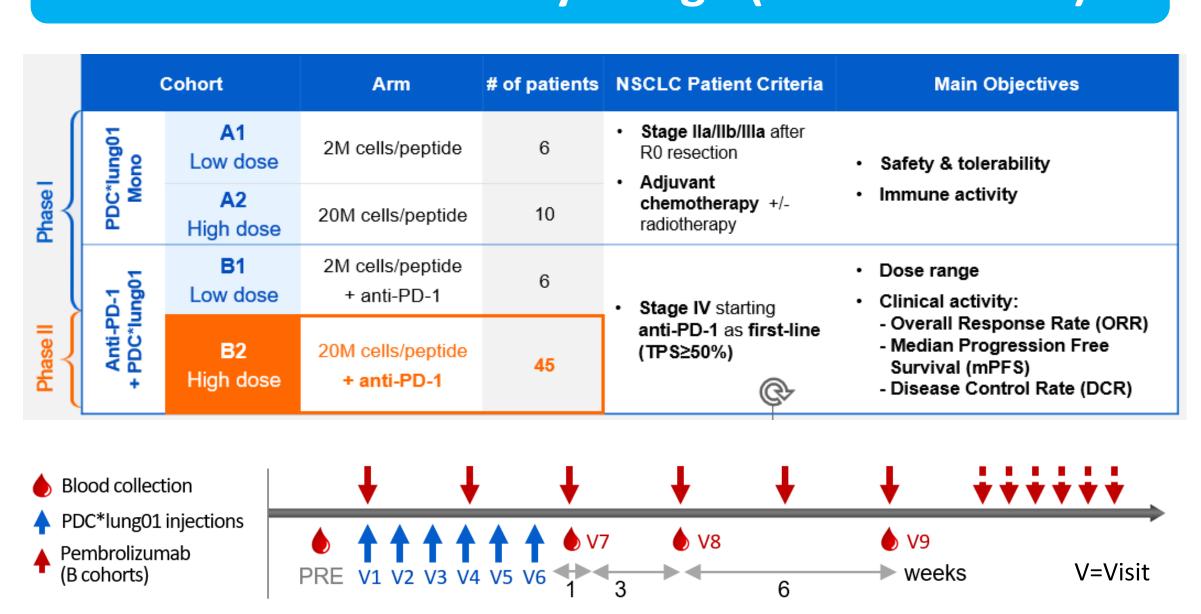
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PDC*lung01 Off-the-shelf plasmacytoid dendritic cell-based product

▶ PDC*lung01 (IMP) is a therapeutic cancer vaccine based on an irradiated plasmacytoid dendritic cell line loaded with HLA-A*02:01-restricted peptides (NY-ESO-1, MAGE-A3, MAGE-A4, Multi-MAGE-A, MUC1, Survivin and Melan-A) able to prime and expand peptide-specific CD8+ T cells in vitro and in vivo. PDC*lung01 was shown to expand antitumor CD8+ T-cells from PBMC of patients with melanoma or NSCLC and to be synergistic with anti-Programmed Cell Death (PD)-1 (Pembrolizumab®; Charles, Oncolmmunol 2020; Lenogue, Vaccines 2021; Hannani, Int. J. Mol. Sci. 2023).



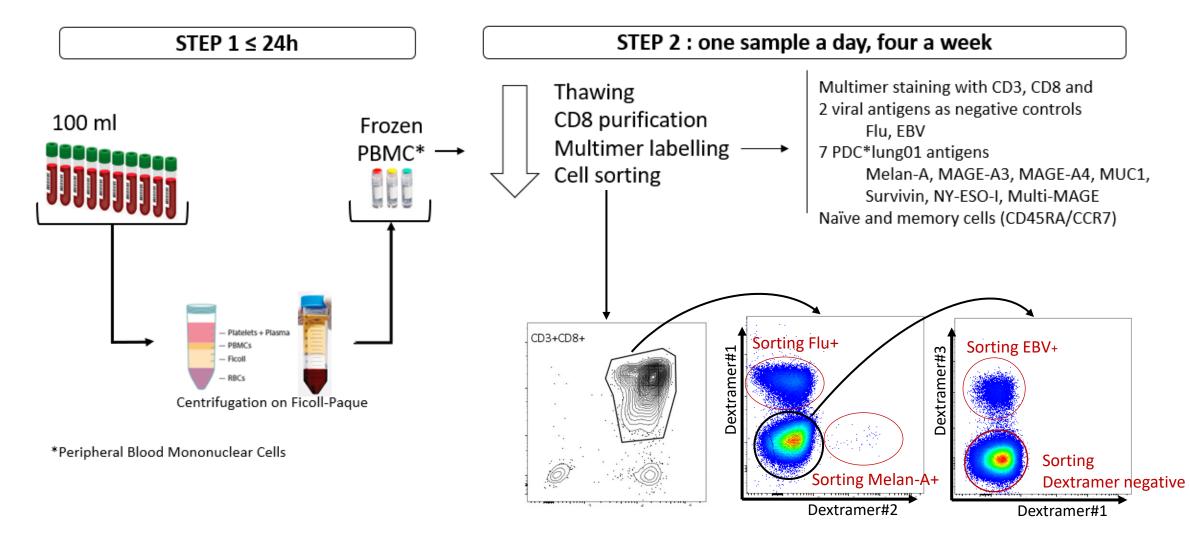
PDC-LUNG-101 study design (NCT03970746)



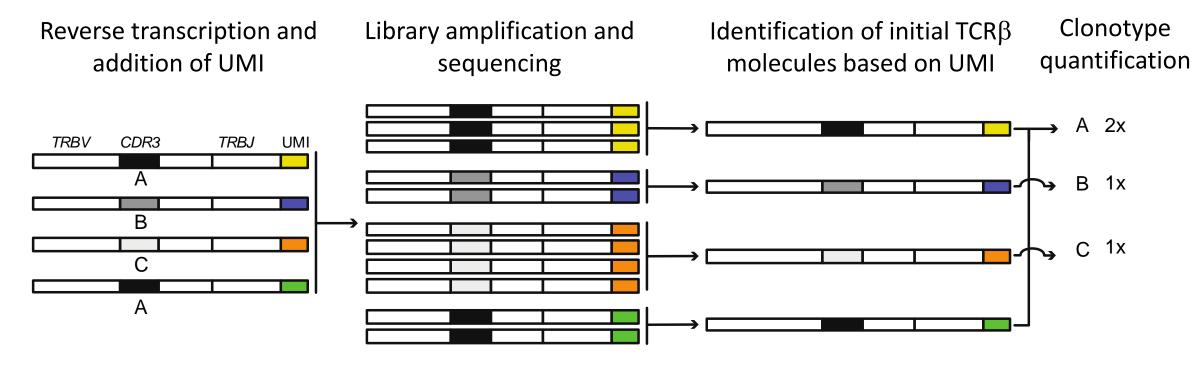
- PDC*lung01 administration schedule: IV+SC every week (6 times)
- Anti-PD-1 administration schedule: IV, every 3 weeks (until progression)

Immunomonitoring assays and qTCRseq

➤ Leukocyte count and peptide-specific CD8+ T were monitored in the bloodstream at different times before and after vaccination. The different populations of interest are sorted based on dextramer staining.



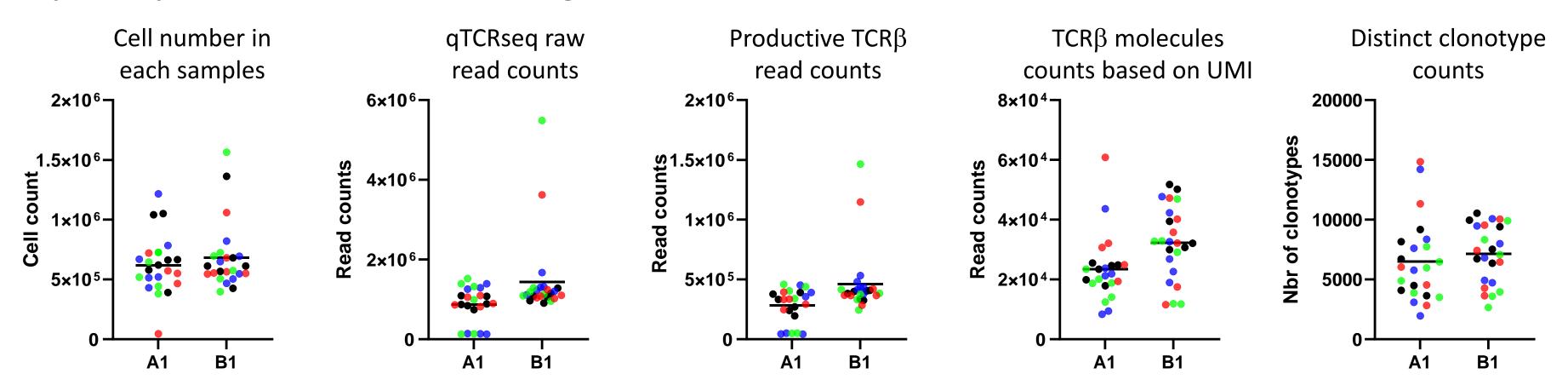
 \triangleright Quantitative TCR sequencing (qTCRseq): RNA was extracted from sorted T CD8+ cells and reverse transcribed to cDNA with the addition of a Unique Molecular Identifier (UMI) on each TCR β molecules. The UMI allows to correct for amplification biases during library preparation or sequence errors introduced during the complete sequencing process and to obtain the absolute quantification of molecules sequenced.



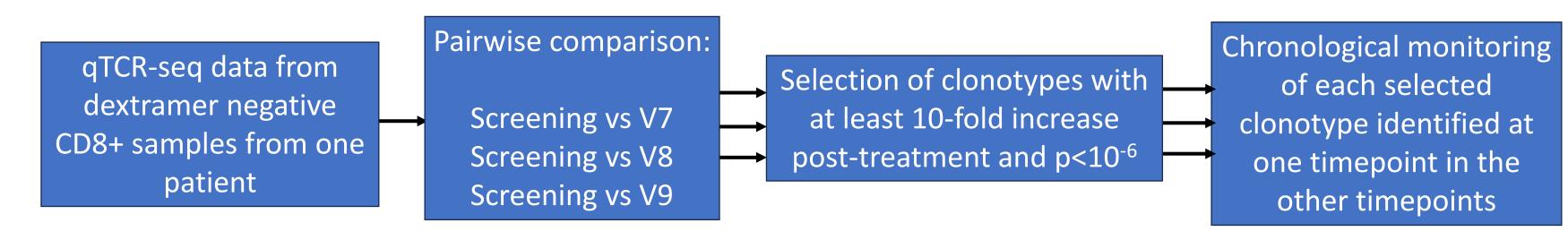
> qTCRseq was performed on samples from patients of cohort A1 and B1

TCR repertoire analysis from dextramer-negative CD8+ cell population

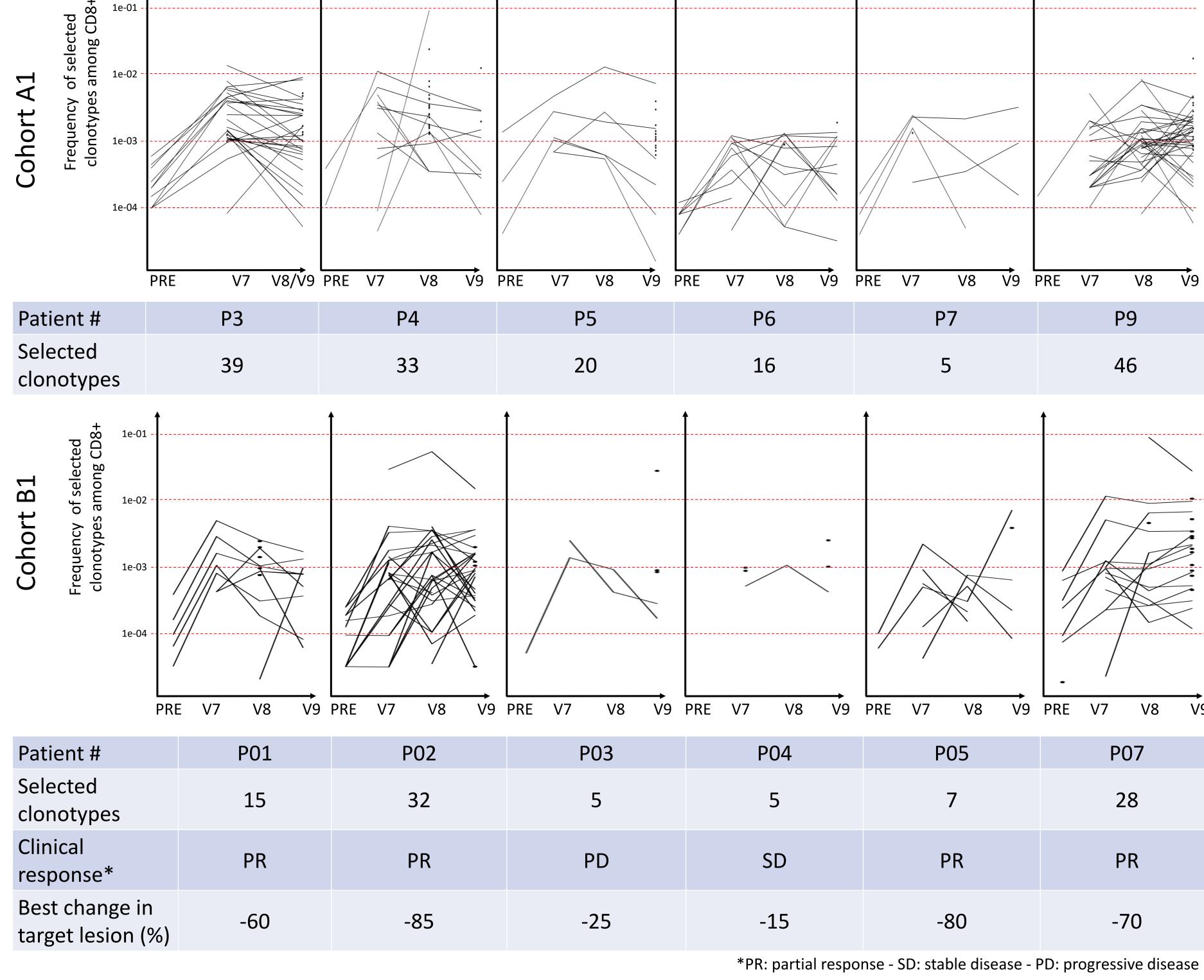
> qTCRseq metrics overview : screening - V7 - V8 - V9



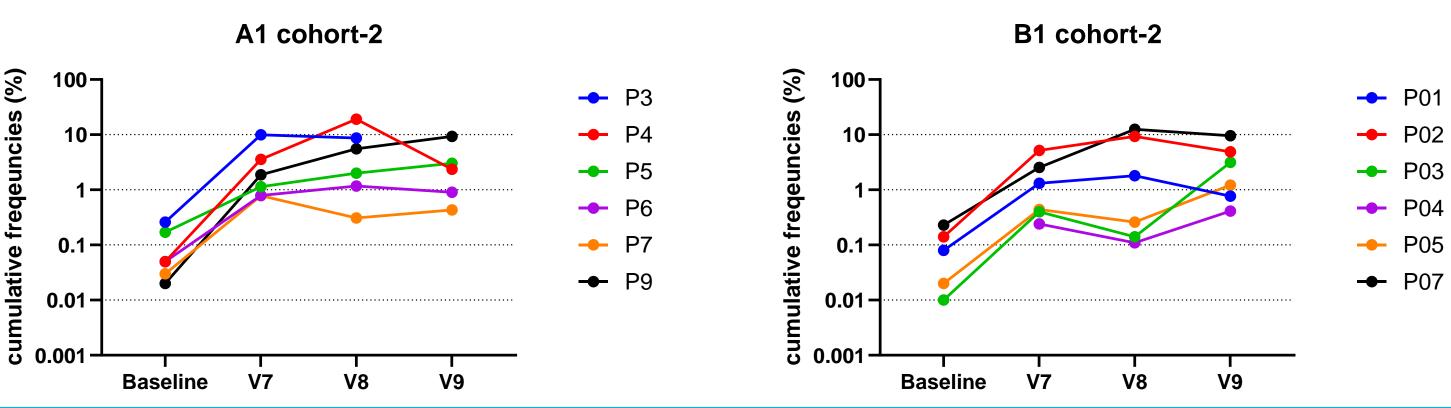
> Analysis strategy to identify clonotypes that increase in the blood after vaccination (selected clonotypes):



Frequencies of selected clonotypes within T CD8+ cell population: lines correspond to frequency variation of selected clonotypes detected at more than one timepoint during monitoring, and dots represent clonotypes identified at a single timepoint.



> Cumulative frequencies of selected clonotypes in each patients: the individual frequencies of each selected clonotype were added together for each timepoints



Conclusion

- > The data generated by qTCRseq are comparable between the two cohorts and the different timepoints
- > The analysis strategy revealed polyclonal amplifications of unknown specificity in the T CD8+ population during treatment with anti-tumour vaccines and immunomodulation
- > The response is dynamic: the identity and number of selected clones are variable between patients and timepoints
- ➤ The cumulative frequencies of selected clonotypes range between 0.1% and 10% of total T CD8+ population and the expansion is still observed 10 weeks post-treatment
- ➤ Similar polyclonal amplifications were observed after treatment in stage IV patients treated with anti-PD1+PDC*lung01 in cohort B1, and in stage IIa to IIIa patients treated only with PDC*lung01 in the adjuvant setting in cohort A1.