

Personal Snapshot

- Molecular Biosciences student at Bellevue College
- Favorite subjects: Biology, Genetics, earth science, biochemistry, and astronomy.
- Career interest: diseases and cancer research.
- Fun activities: hiking, picnicking, gardening, cooking, and cleaning.
- My motivation: learn new things to enhance in personal and professional level.

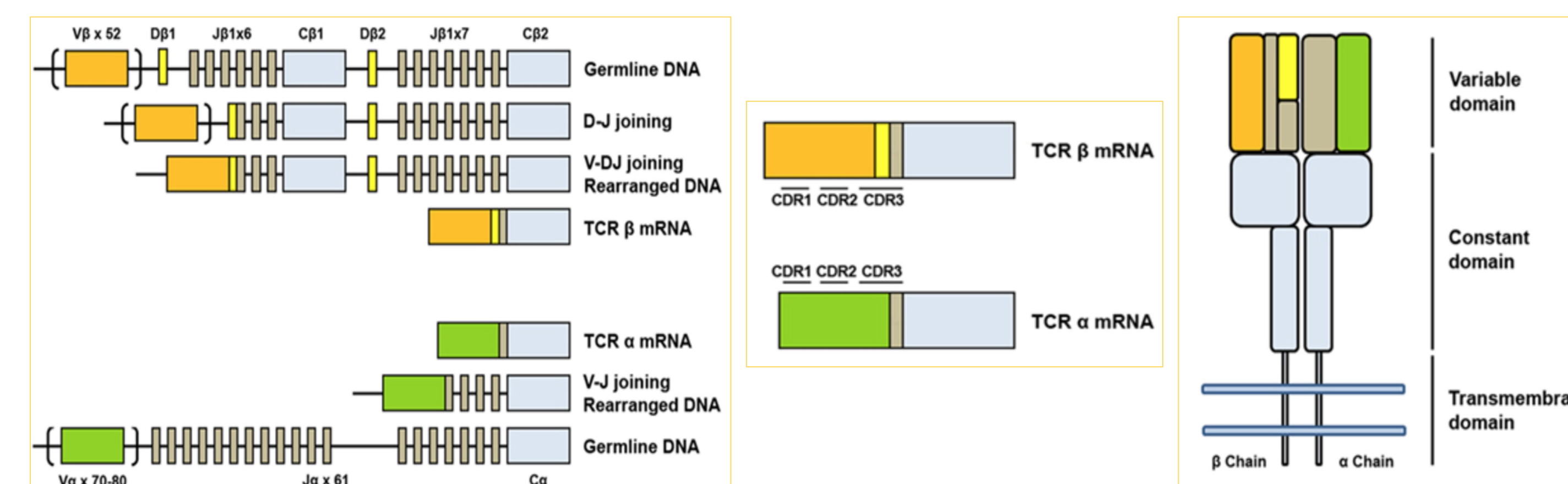
Newell Team



Lab Contributions to Fred Hutch's mission

The objective is to create and utilize innovative techniques to detect and analyze antigen-specific T cells in individuals with cancer or chronic infections. The goal is to identify precise and reliable indicators of human health and illness by focusing on these antigen-specific T cells.

TCR structure



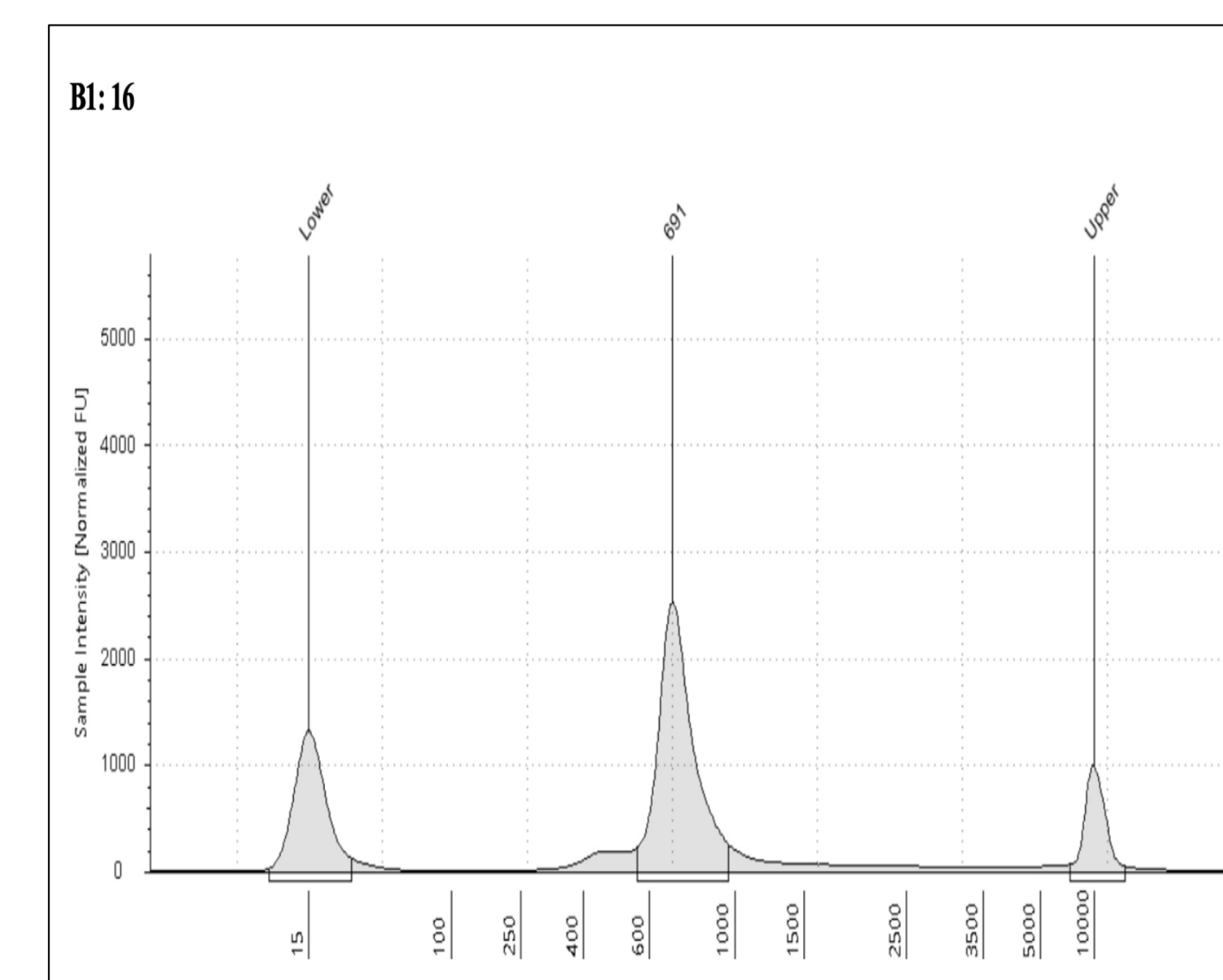
PCR1: to amplify and synthesize cDNA.
PCR2: to amplify and generate TCR library.



Magnetic bead-based to purify amplified libraries.



Qubit: for TCR library quantification and concentration.



Tapestation: to validate the final library cleanliness for sequencing.

My Contributions

Since there are different projects happening in the Lab, I get to exposed to different methods and assays including

Wet lab:

- TCR sequencing
- DNA extraction
- Lanthanide conjugation
- PBMC

Dry lab:

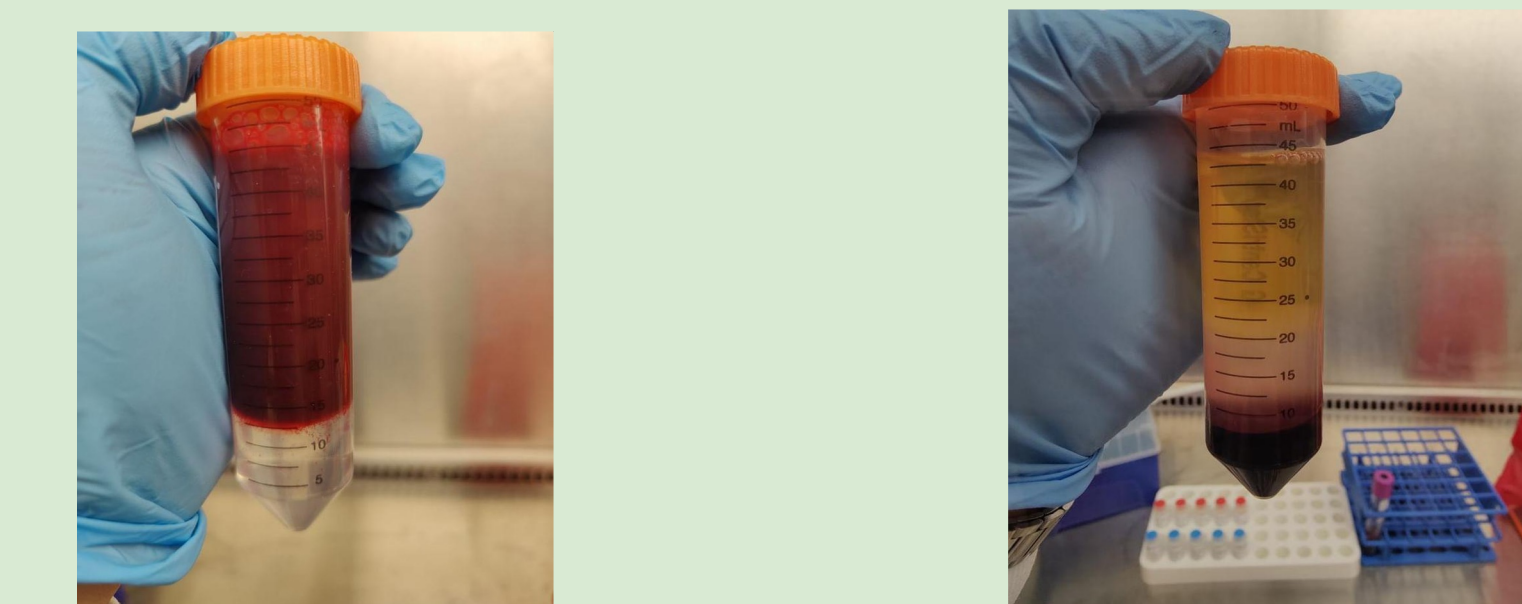
- Data analysis
- Flow-Jo
- Mass cytometry or CyTOF

Things I enjoyed

- Having insightful discussions with everyone in the field.
- Exposed to real world experiments and projects that contribute to elimination of cancer and other related diseases.
- Learning lab tricks from everyone.

PBMC

- I also enjoyed PBMC work. They play a crucial role in immunological studies and help us study the immune system in greater details.



The research focuses on:

- Research focuses on how T cells behave in a context of different diseases in individuals.

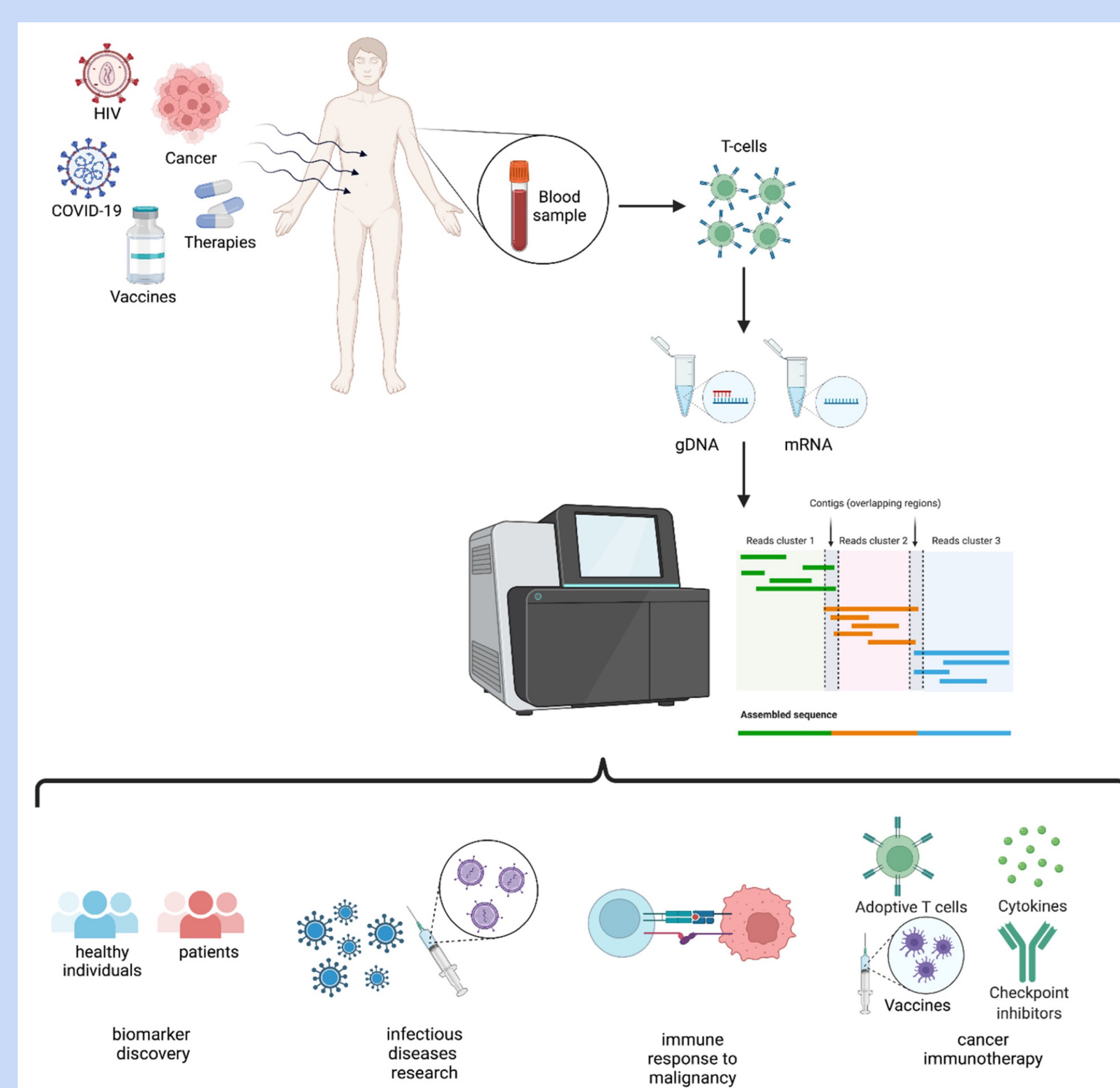
How TCR seq be useful in the research?

What is TCR seq?

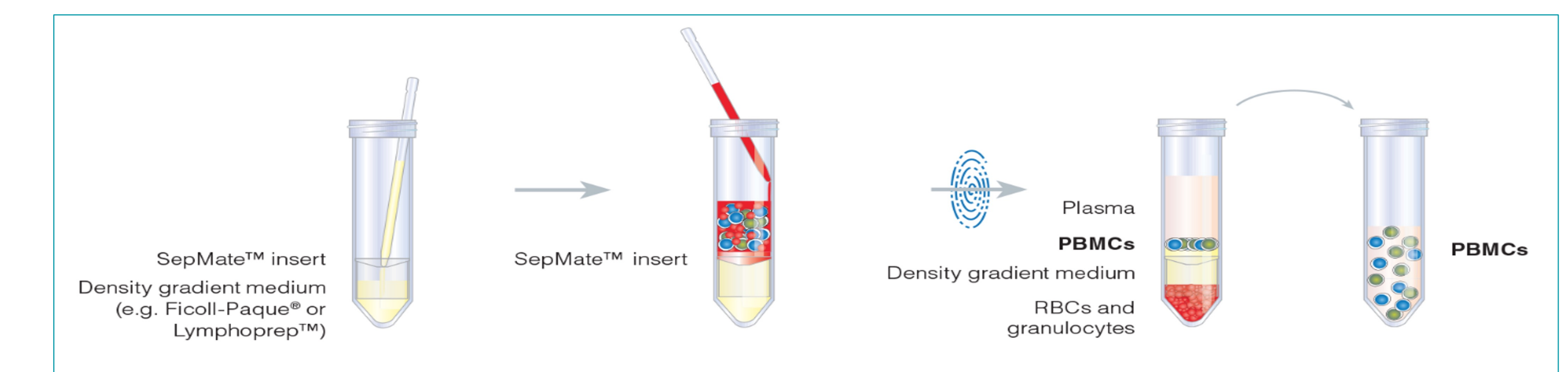
- A tool for analyzing the diversity and specificity of T-cell receptors.

Method

- Sample collection: blood from consented donor.
- T cells isolation achieved through PBMC isolation and extraction.
- Genetic material extraction: mRNA.
- cDNA synthesis by SMARTer kit and QC.
- PCR amplification: multiple PCR.
- Purification: magnetic beads to remove impurity (primer, enzyme), and tapestation..



- Sequencing using sequencing machine.
- Data generation: sequencing generates raw reads that assembled into contig (TCR seq).
- Data can be used: biomarker, infectious disease research, immune response to malignancy, and cancer treatment.



Acknowledgements

I would like to thank everyone in the Newell lab for their invaluable guidance and support throughout the program. I learned many new skills and techniques, which have significantly enhanced my understanding and capabilities in the lab. Not only was I exposed to wet lab procedures, but I also gained experience in the computational aspects of the research, such as data analysis methods.

Special thanks to Michelle, my mentor, whose expertise and patience were instrumental in my learning process.

I am deeply grateful to Dr. Mary Grace for making the LabLaunch program possible and for her continued support and encouragement. This opportunity has been instrumental in my professional and personal development, and I look forward to applying these skills in my future endeavors.

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