Postgraduate University Interdisciplinary
Doctoral Study of Molecular Biosciences

Doctoral thesis topic defence

Characterisation of the phenotype, transcriptional markers and T cell receptor repertoire of circulating MAIT and γδ T lymphocytes in psoriasis vulgaris

Karakterizacija fenotipa, transkripcijskih biljega i repertoara T staničnih receptora cirkulirajućih MAIT i γδ T limfocita u vulgarnoj psorijazi

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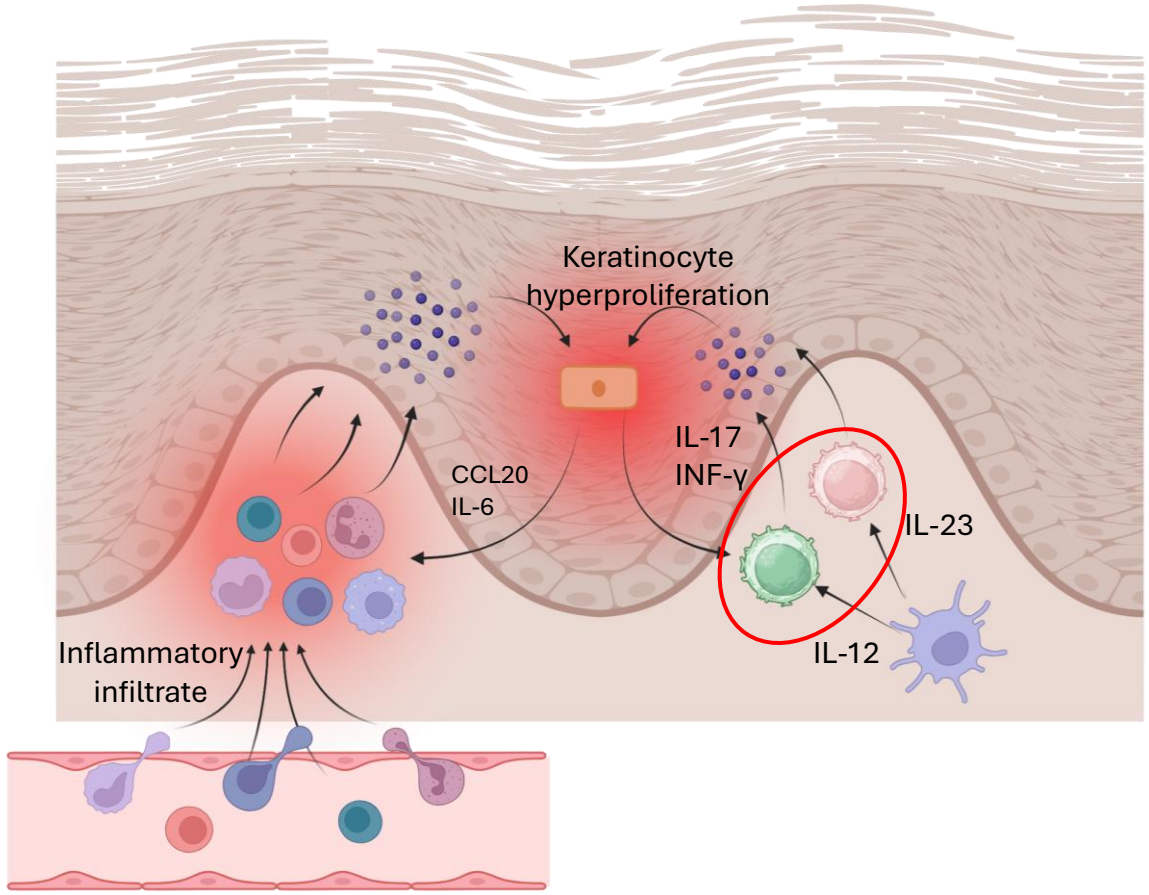
Supervisor 1: Assoc. Prof. Stana Tokić
Supervisor 2: Assoc. Prof. Martin Davey

Osijek, 21st May 2024.

Psoriasis vulgaris

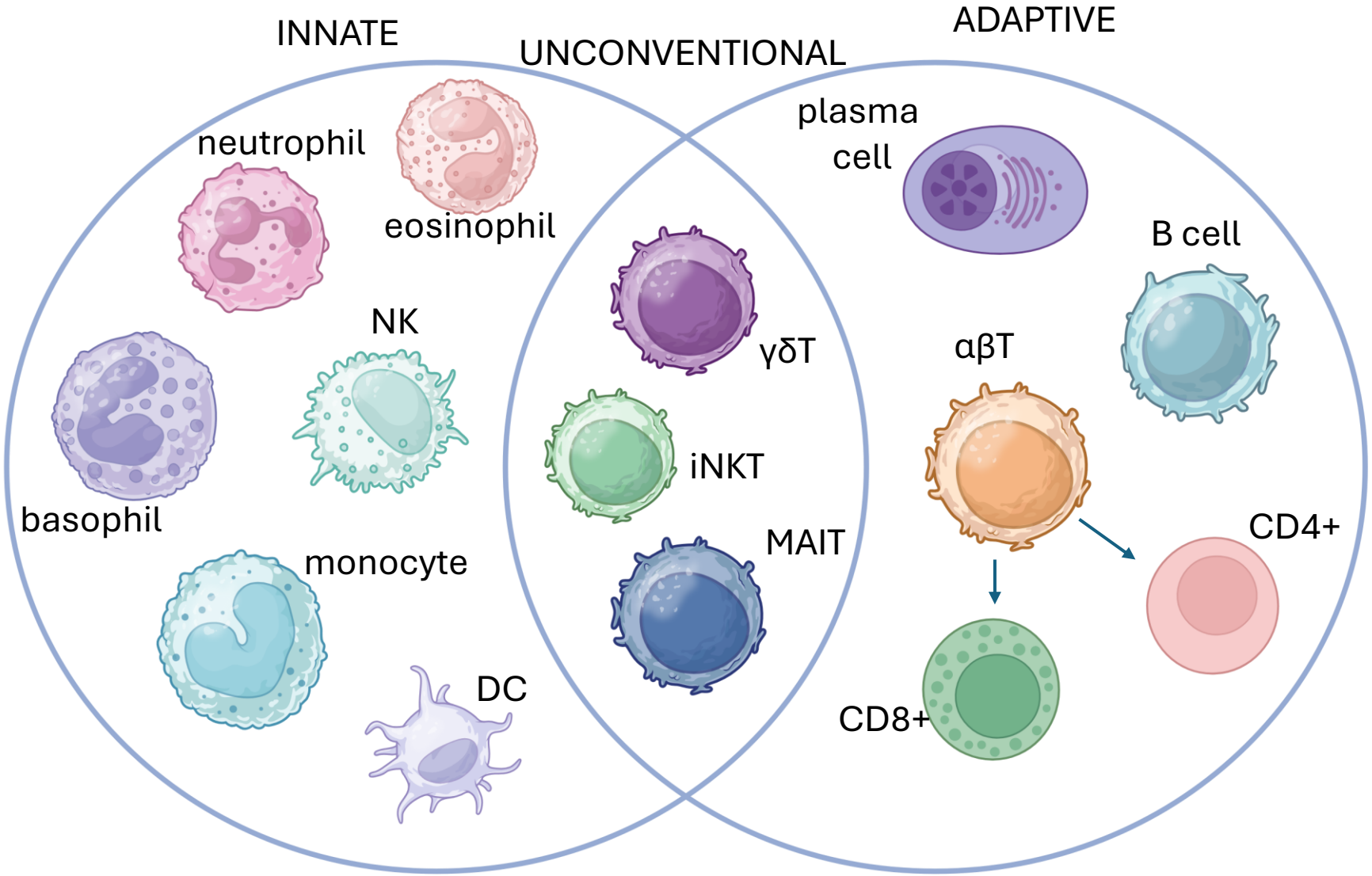
- chronic autoinflammatory disease
- well-defined, raised, erythematous lesions with silvery-white scales
- global prevalence: 2–3%
- genetics and environmental triggers

https://saguaroderm.com/services/medical-dermatology/psoriasis/

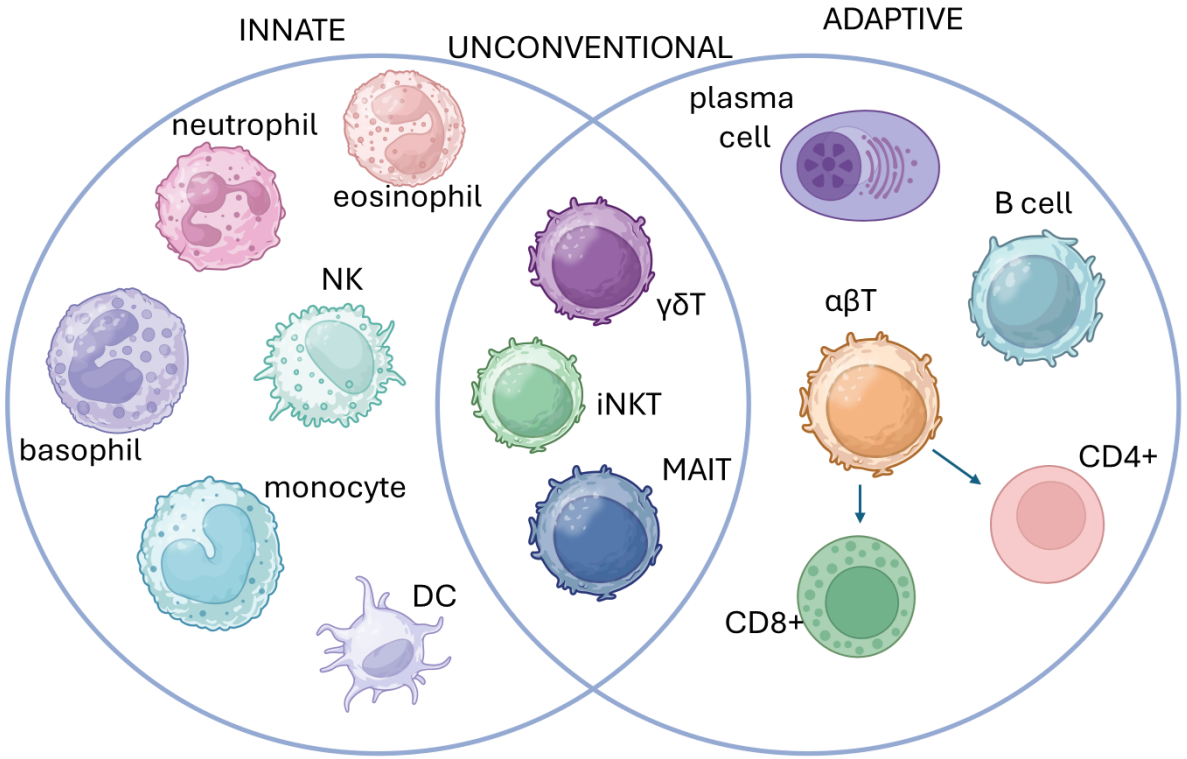


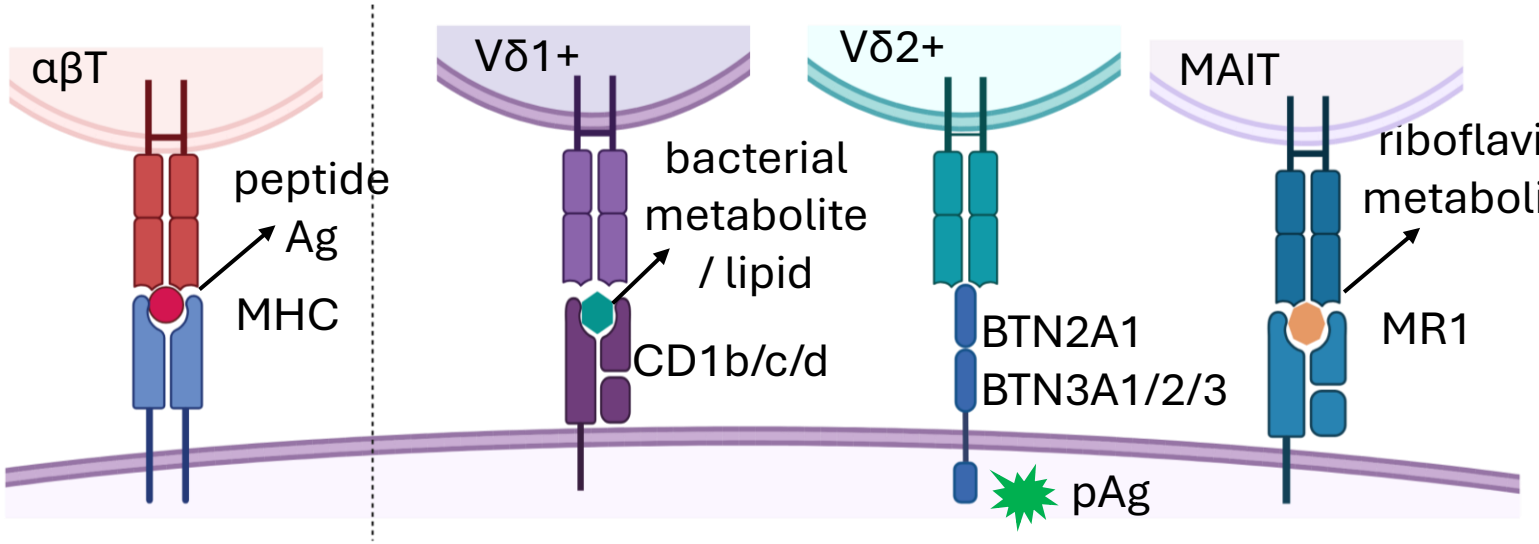
- dysregulation of the immune system and aberrant T cell activation
- multiple comorbidities and other autoimmune disorders
- autoantigens?

What is the role of unconventional T cells in psoriasis vulgaris?


INNATE
UNCONVENTIONAL
ADAPTIVE
neutrophil
eosinophil
plasma cell
B cell
NK
γδT
αβT
basophil
iNKT
CD4+
MAIT
monocyte
DC
CD8+

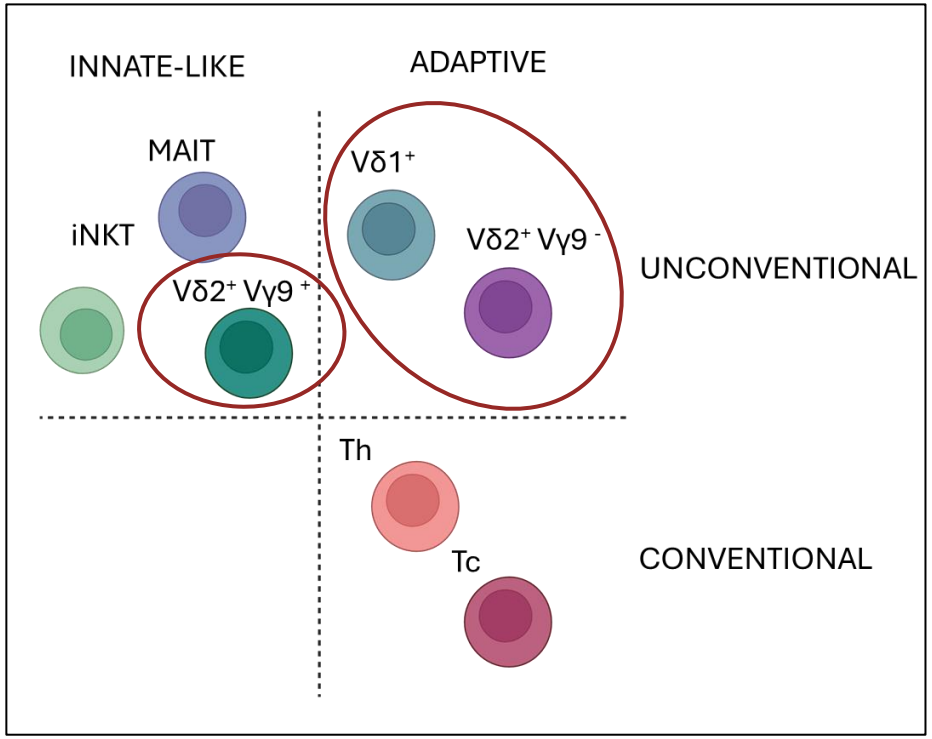
- ~10–30% of the T cell compartment
- enriched in mucosal and epithelial sites → skin, respiratory, digestive, and reproductive tracts
- rapid effector functions
- recognition of non-peptide ligands presented by non-polymorphic antigen presenting molecules
- TCR-independent activation





γδT cells

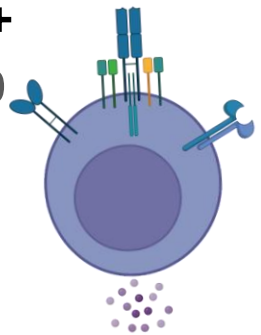
- 1-10% of peripheral T cells
- tissue homeostasis, anti-microbial response, stress surveillance, anti-tumor activity, autoimmunity



Human γδ T cells can be distinguished by δ chain usage:

Vδ2+

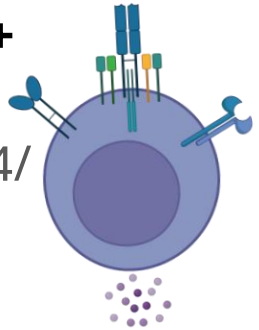
Vγ9



- 50%–90% of the peripheral γδ T
- Vγ9+Vδ2+ / Vγ9-Vδ2 +
- innate-like effector profile

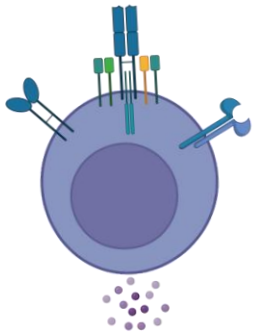
Vδ1+

Vγ2/3/4/5/8/9



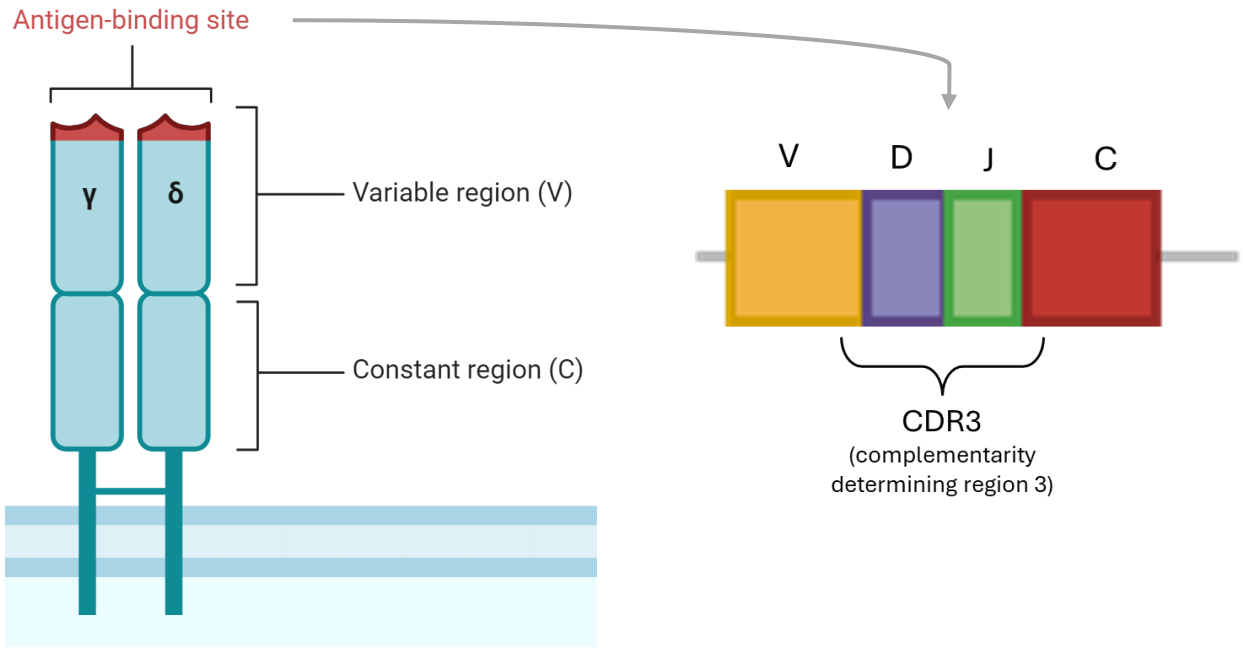
- up to ~ 30% of peripheral γδ T
- epithelial and mucosal sites → gut, skin, spleen, and liver
- adaptive immunobiology

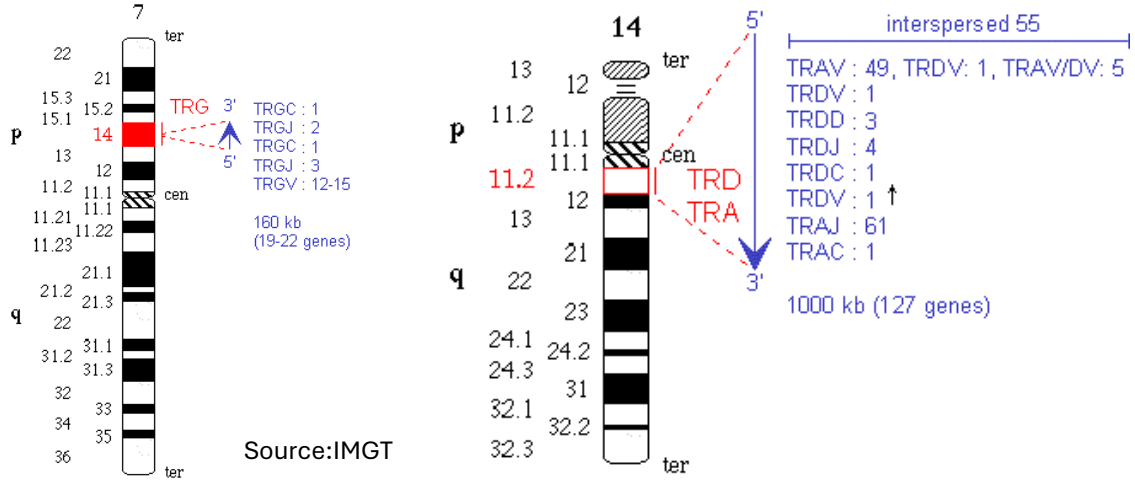
Vδ3+



- <1% peripheral γδ T
- enriched in the liver and gut
- anti-microbial immunity
- ??

γδTCR structure and V(D)J recombination





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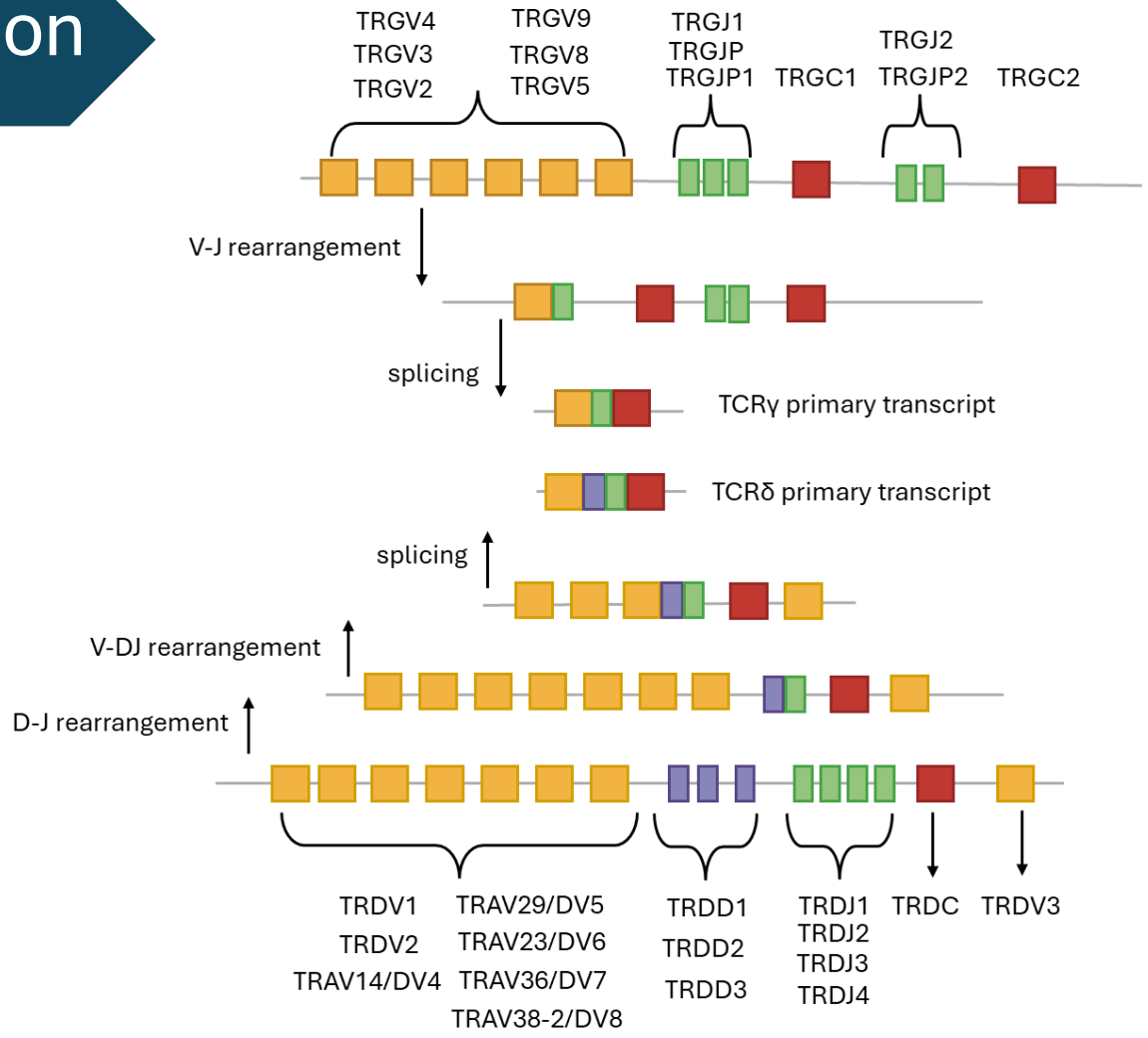
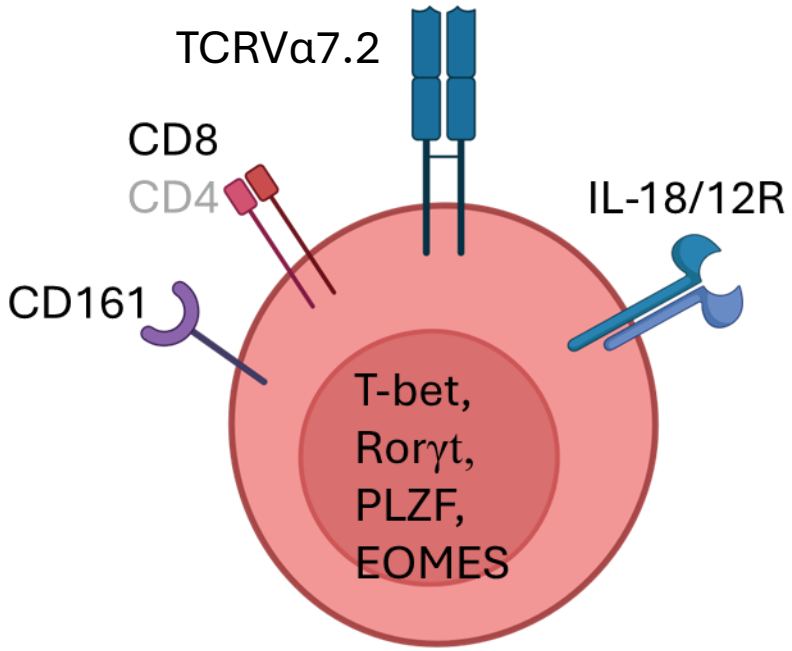


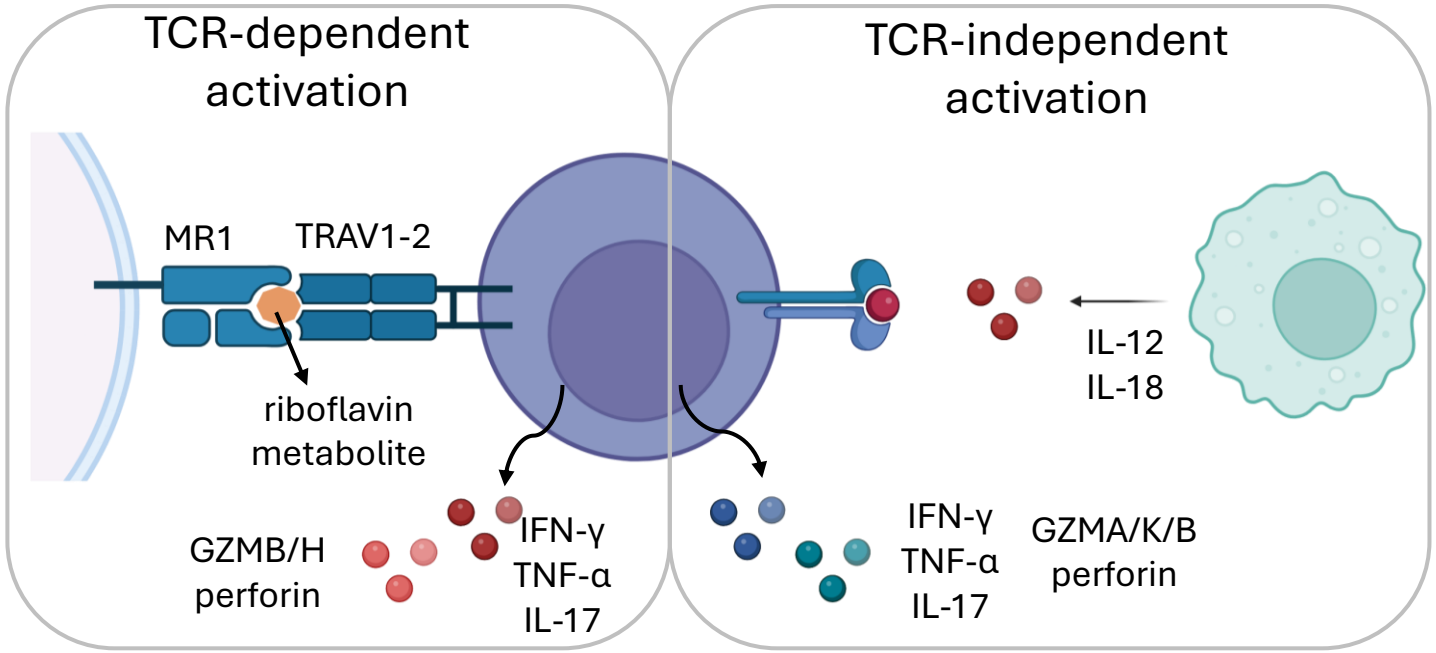
- diversity amplified by junctional diversity → insertion of palindromic sequences and of non-templated nucleotides

MAIT cells

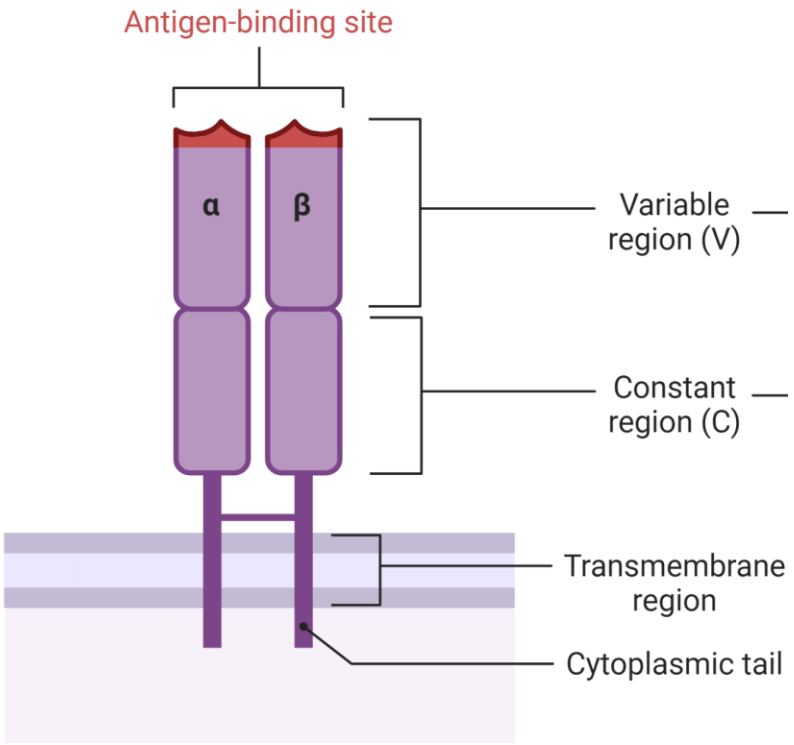
(mucosal-associated invariant T)

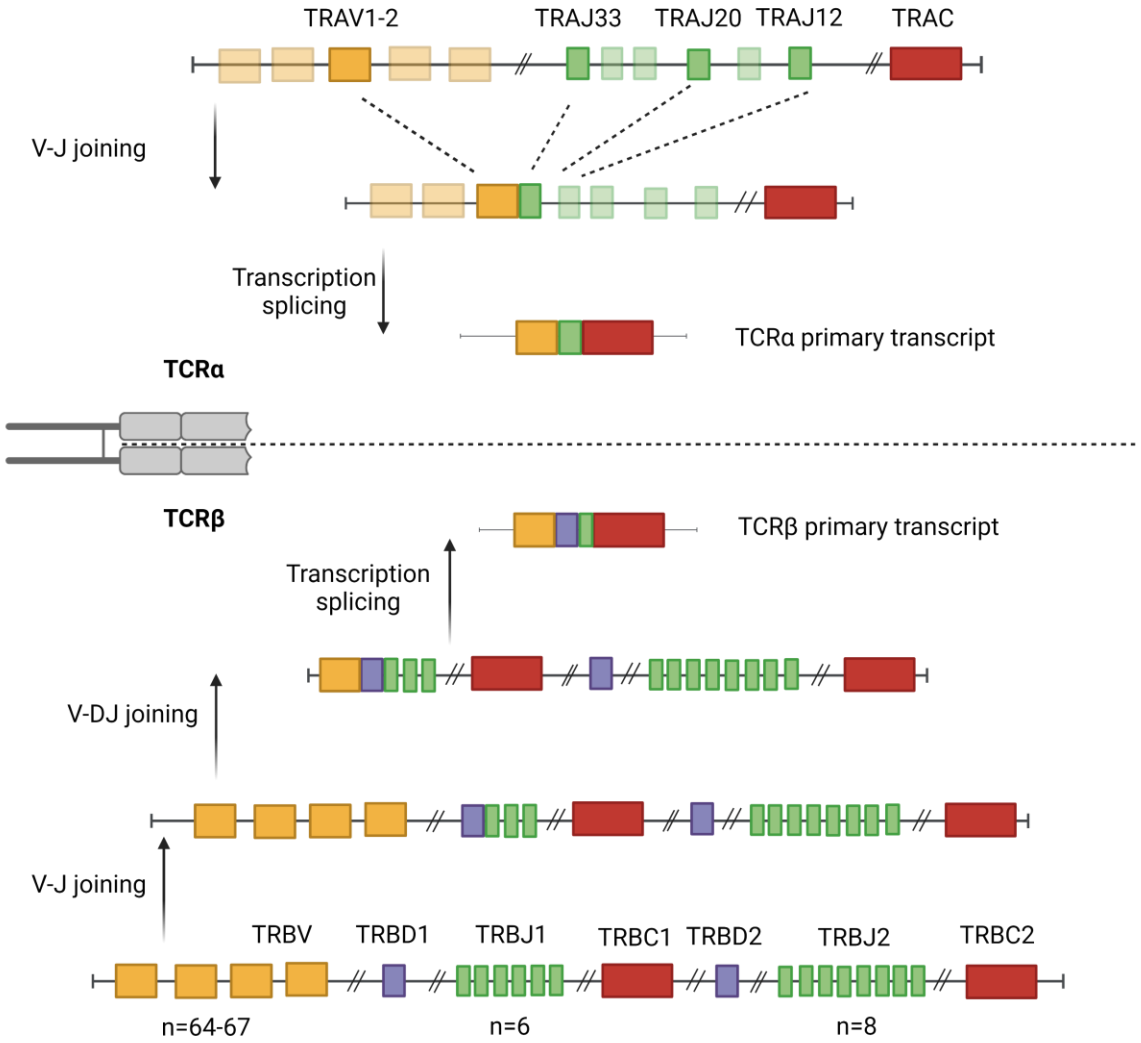
- Up to 5% of peripheral T cells
- subsets based on the CD4 /CD8 expression:
  - CD4−CD8+ → ~80% of total circulating MAIT cells
  - CD4−CD8− → ~ 15% of the total MAIT
  - CD4+CD8− / CD4+CD8+ → < 5%
- identified using MR1 tetramers loaded with the bacterial ligand 5-(2-oxopropylideneamino)-6-D-ribitylaminouracil (5-OP-RU)
- variation in phenotype, function and TCR repertoire





MAIT αβTCR structure and recombination





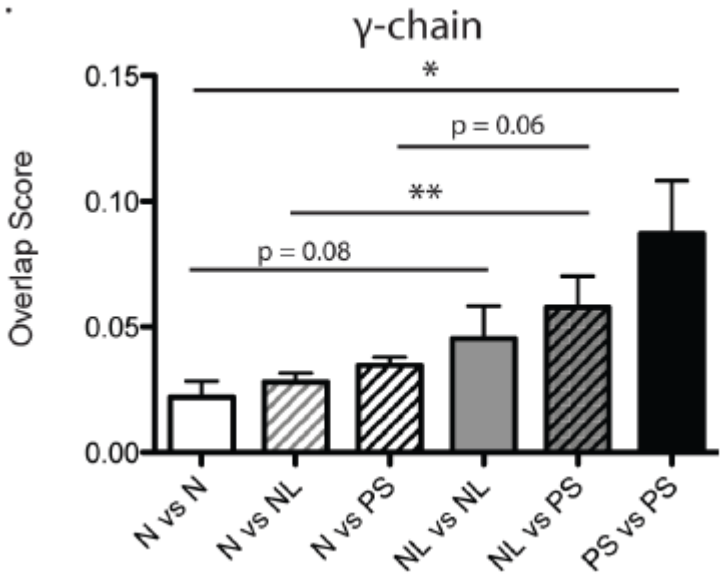
- semi-invariant TCR consisting of an invariantly rearranged TCR α chain (**TRAV1-2** – TRAJ33/20/12), combined with diversely rearranged TCR β chain

T cells in psoriasis

Deep Sequencing of the T-cell Receptor Repertoire Demonstrates Polyclonal T-cell Infiltrates in Psoriasis [version 1; referees: 2 approved]

Jamie L. Harden[1], David Hamm[2], Nicholas Gulati[1], Michelle A. Lowes[3], James G. Krueger[1]

- non-specific polyclonal infiltrate in affected skin and a higher level of shared, public TCRγ clonotypes in patients with psoriasis



Clinically resolved psoriatic lesions contain psoriasis-specific IL-17–producing αβ T cell clones

Tiago R. Matos,[1,2,3] John T. O'Malley,[1] Elizabeth L. Lowry,[1] David Hamm,[4] Ilan R. Kirsch,[4] Harlan S. Robins,[4] Thomas S. Kupper,[1] James G. Krueger,[5] and Rachael A. Clark[1]

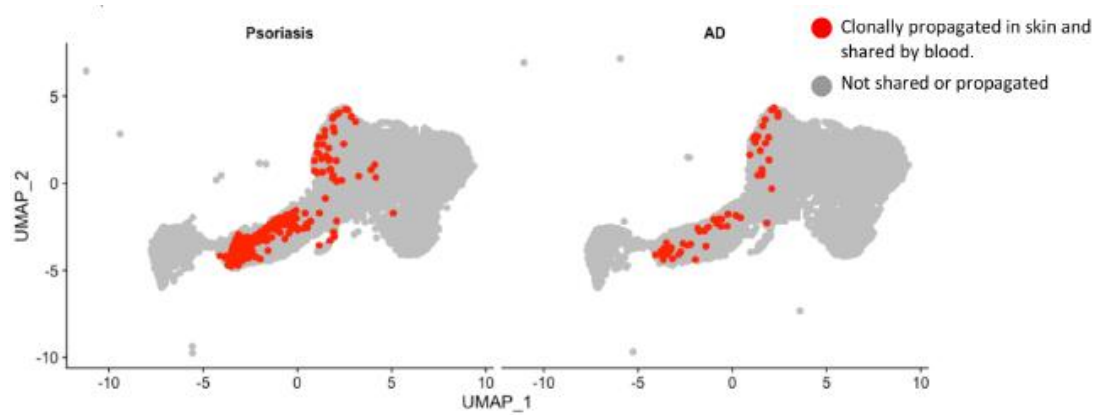
- clinically resolved psoriatic lesions contained oligoclonal populations of T cells that produced IL-17A in both resolved and active psoriatic lesions

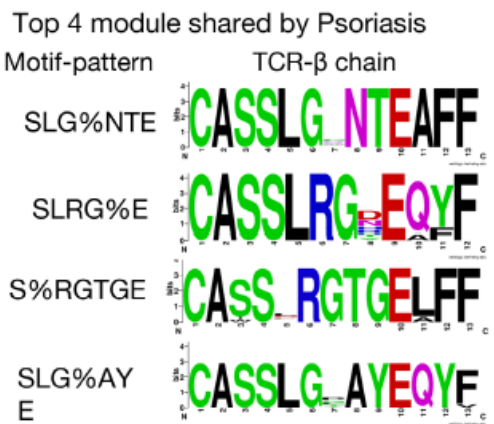
	Shared in patients	Nucleotide sequences identical?	Present in healthy controls?
Shared TCRβ CDR3			
CASSQDLAGGPDTQYF	3, 13	Yes	No
CSARGGNTIYF	1,9	Yes	No
CASSISATGDTEAFF	3, 5	Yes	No
CASSDRYLGGGNSPLHF	12, 14	Yes	No
CASSPQETQYF	3, 4	No	No
CASSLVGQAYEQYF	4, 13	No	No
CASSESNQPQHF	11, 13	No	No
CASSFYNEQFF	3, 13	No	No
CASSLGEKLFF	9, 13	No	No
CASSLGAGQPQHF	8, 13	No	No
CASSEGYEQYF	6, 8	No	No
CASSPGPSYEQYF	10, 12	No	No
CASSPLAGSYNEQFF	3, 10	No	No
CASSATGYGYTF	5, 11	No	No
CASSLGTGELFF	3, 11	No	No
Shared TCRα CDR3			
CALSKAAGNKLTF	1, 3	Similar[A]	No
CALRNTGGFKTIF	1, 3	Similar[A]	No
CIVRVYGGATNKLIF	7, 3	Similar[A]	No
CAVDSGGSNYKLTF	9, 10	No	No

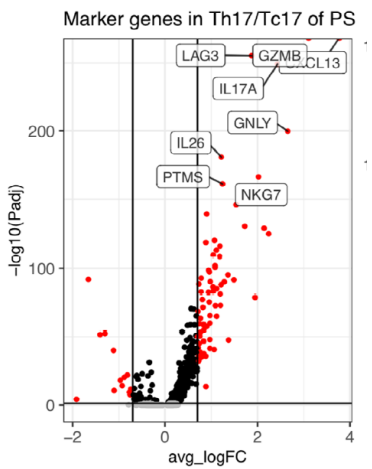
Single-cell profiles reveal distinctive immune response in atopic dermatitis in contrast to psoriasis

Bowen Zhang[1,2] | Lennart M. Roesner[3,4] | Stephan Traidl[3,4] |
Valerie A. C. M. Koeken[1,2,5] | Cheng-Jian Xu[1,2,5] | Thomas Werfel[3,4] | Yang Li[1,2,4,5]

- a systemic involvement of type-3 inflammation in PV circulating cells



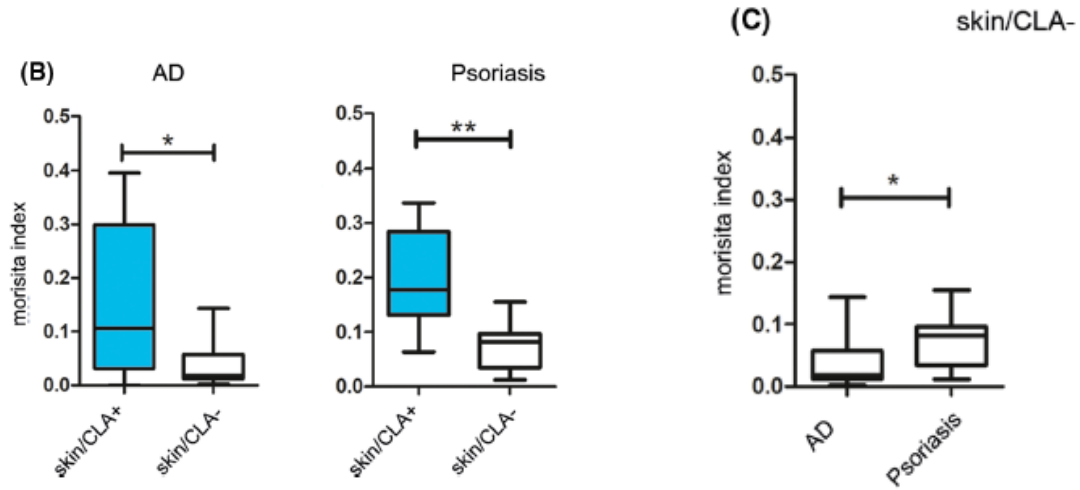


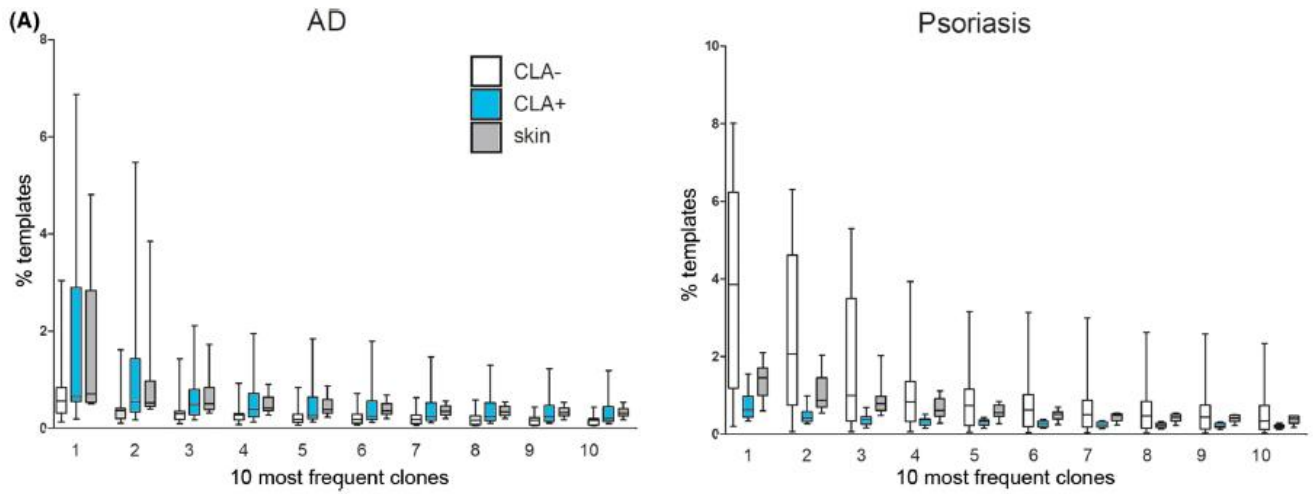


T-cell receptor sequencing specifies psoriasis as a systemic and atopic dermatitis as a skin-focused, allergen-driven disease

Lennart M. Roesner[1,2] | Ahmed K. Farag[1] | Rebecca Pospich[1] | Stephan Traidl[1,2] |
Thomas Werfel[1,2]

- T-cell clones that infiltrate psoriatic skin lesions do not exclusively possess skin-homing ability

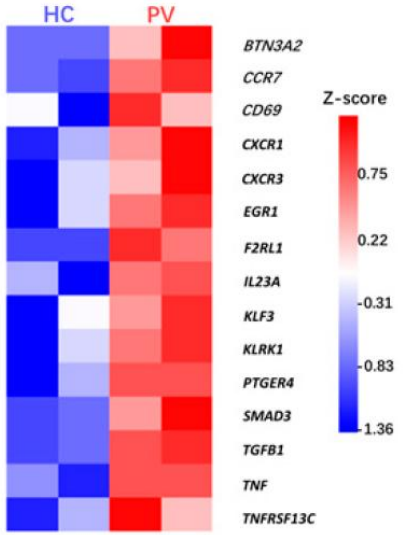




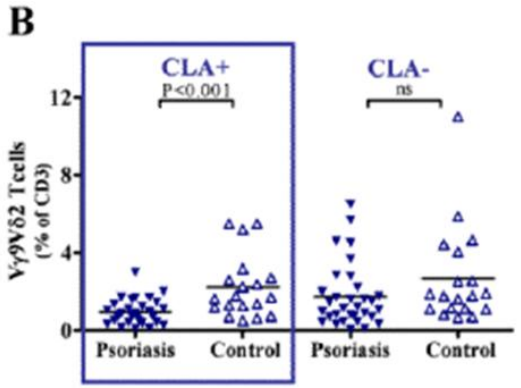
γδT cells in PV

Up-regulation of BTN3A1 on CD14$^+$ cells promotes Vγ9Vδ2 T cell activation in psoriasis

Jiaqing Zhou[a,1], Jingjing Zhang[b,d,1], Lu Tao[a], Kexin Peng[a], Qiaoan Zhang[a], Kexiang Yan[a], Jing Luan[a], Jiewen Pan[a], Xiaohui Su[b,c,d], Jiping Sun[b,c,d], Zhenghua Zhang[a,2], and Lei Shen[b,c,d,2]



- more than 2000 differentially expressed genes (DEGs) in peripheral Vγ9Vδ2 cells of affected individuals compared to healthy controls



Identification of a novel pro-inflammatory human skin-homing Vγ9Vδ2 T cell subset with a potential role in psoriasis

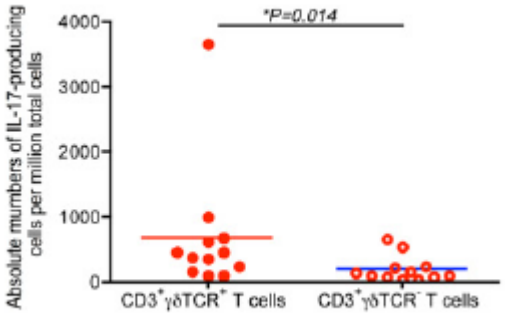
Ute LAGGNER*, Paola DI MEGLIO*, Gayathri K. PERERA*, Christian HUNDHAUSEN*, Katie E. LACY*, Niwa ALI*, Catherine H. SMITH†, Adrian C. HAYDAY‡, Brian J. NICKOLOFF§, and Frank O. NESTLE*

- changes in the distribution of the skin-homing CLA+CCR6+ Vγ9Vδ2
- infiltration into the affected skin

Pivotal Role of Dermal IL-17-Producing γδ T Cells in Skin Inflammation

Yihua Cai,[1,2] Xiaoyan Shen,[1] Chuanlin Ding,[2] Chunjian Qi,[2] Kejia Li,[1] Xia Li,[1] Venkatakrishna R. Jala,[2] Huang-ge Zhang,[2] Tian Wang,[3] Jie Zheng,[1,*] and Jun Yan[2,*]

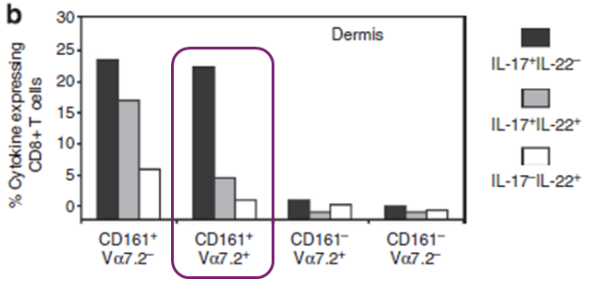
- increased prevalence of γδ T cells in the dermis of psoriatic plaques that expressed higher levels of IL-17



MAIT cells in PV

The IL-17A-Producing CD8$^+$ T-Cell Population in Psoriatic Lesional Skin Comprises Mucosa-Associated Invariant T Cells and Conventional T Cells

Marcel B.M. Teunissen[1], Nataliya G. Yeremenko[2], Dominique L.P. Baeten[2], Saskia Chielie[1], Phyllis I. Spuls[1], Menno A. de Rie[1], Olivier Lantz[3] and Pieter C.M. Res[1]

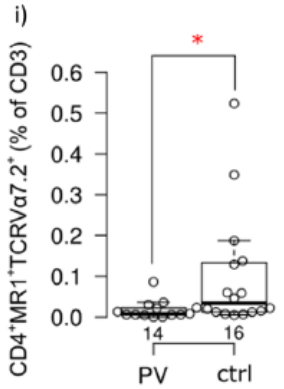


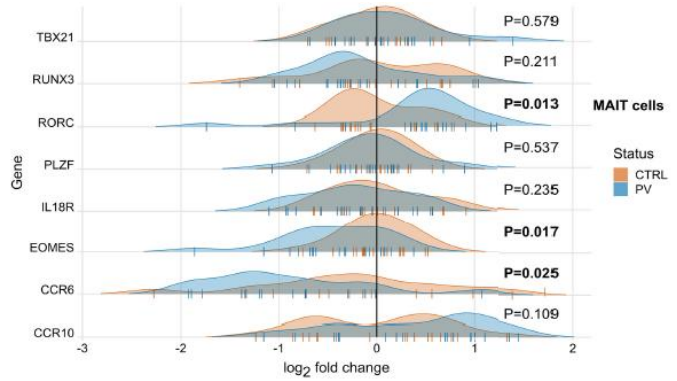
- IL-17A expression in TCR-Va7.2+CD161+ cells within the psoriatic plaque–derived CD8+ lymphocytes

Differential Skewing of Circulating MR1-Restricted and γδ T Cells in Human Psoriasis Vulgaris

Vera Plužarić[1,2†], Mario Štefanić[3†], Martina Mihalj[2,4], Maja Tolušić Levak[2,5], Ivanka Muršić[2], Ljubica Glavaš-Obrovac[1], Martin Petrek[6], Peter Balogh[7] and Stana Tokić[1*]*

- decrease in the proportion of CD4+ MR1-tet+TCRVα7.2+ cells
- altered expression of the EOMES, CCR6, and RORγt

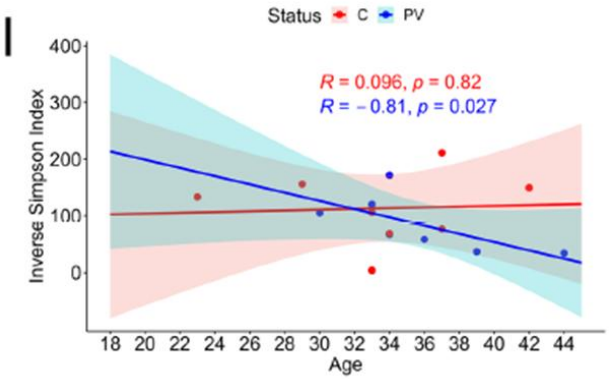


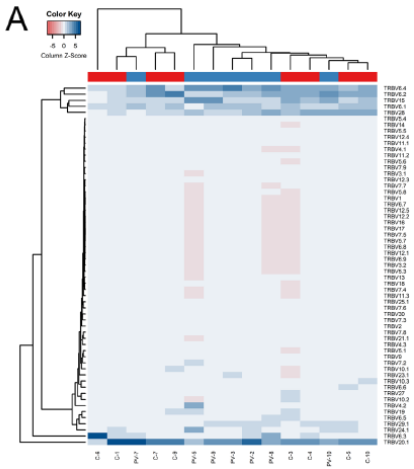


Characterization of the TCRβ repertoire of peripheral MR1-restricted MAIT cells in psoriasis vulgaris patients

Maja Jirouš Drulak[1✉], Zvonimir Grgić[2], Vera Plužarić[2,3], Marija Šola[3], Teuta Opačak-Bernardi[1], Barbara Viljetić[1], Kristina Glavaš[4], Maja Tolušić-Levak[3,5], Vlatka Periša[6,7], Martina Mihalj[3,8], Mario Štefanić[9✉] & Stana Tokić[2✉]

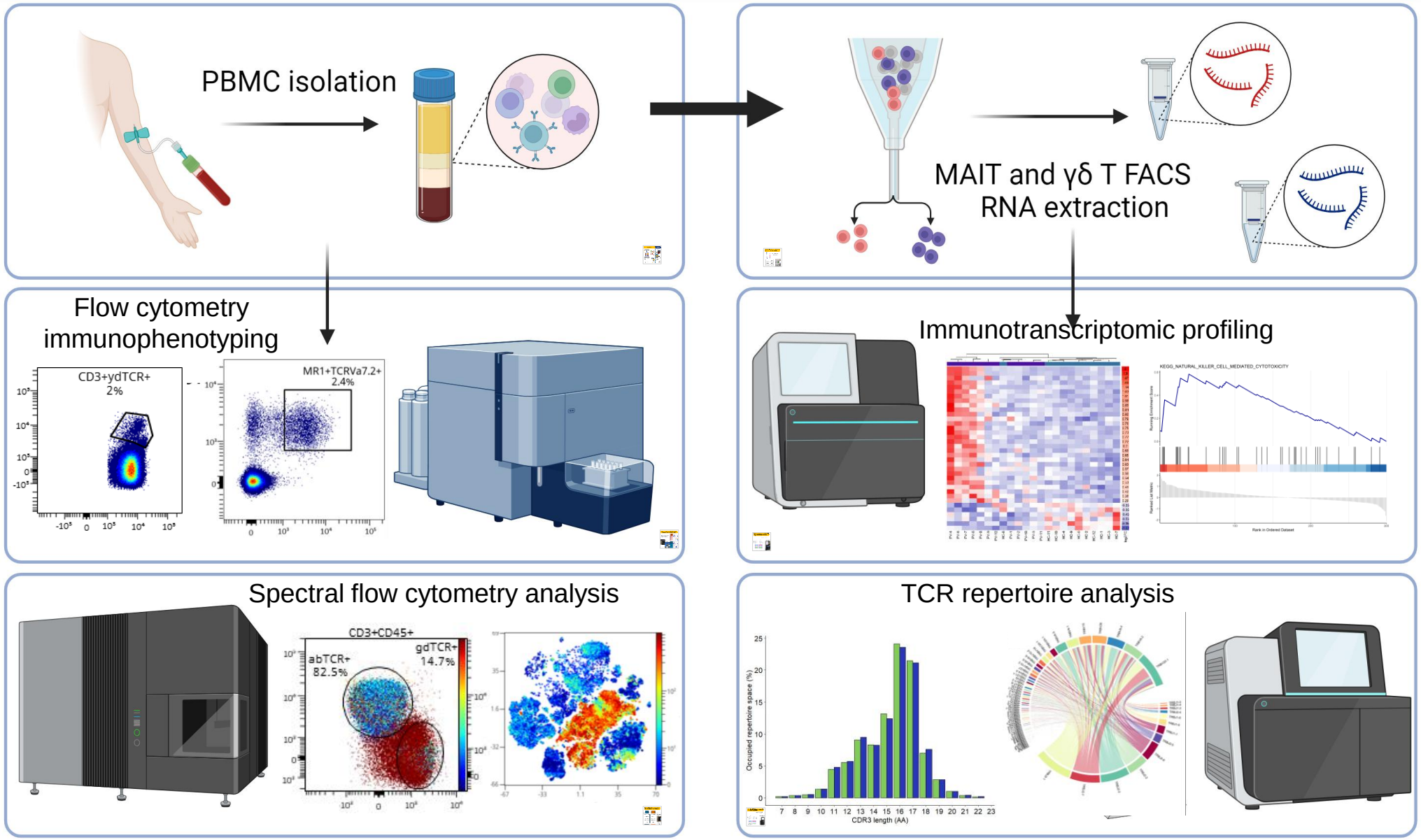
- high diversity in TCRβ clonotypic variants
- hyperexpanded clonotypes increasing with age of PV but not healthy individuals





Hypothesis

- The **peripheral proportions**, **phenotype and gene expression** of immune markers related to activation, differentiation, migration and effector capacity, as well as the **clonal repertoire of T cell receptors** of circulating MAIT and γδ T lymphocytes in patients with psoriasis vulgaris **differ significantly from the healthy controls, and correlate with anthropometric and biochemical characteristics and indicators of disease severity**.

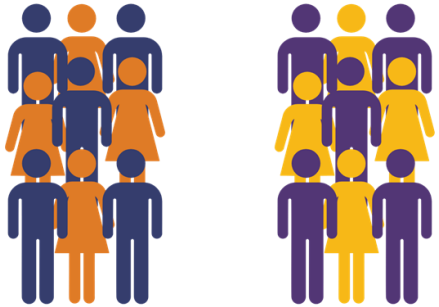

PBMC isolation
MAIT and γδ T FACS
RNA extraction
Flow cytometry
immunophenotyping
CD3+ydTCR+
2%
MR1+TCRVa7.2+
2.4%
Immunotranscriptomic profiling
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY
Spectral flow cytometry analysis
CD3+CD45+
abTCR+
82.5%
gdTCR+
14.7%
TCR repertoire analysis
Occupied repertoire space (%)
CDR3 length (AA)

Sample collection

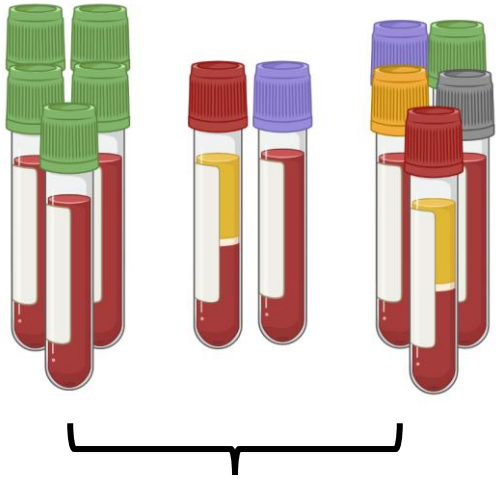
Department of Dermatology and Venereology Clinical Hospital Centre Osijek

Therapy-naive PV patients

Healthy control participants



- Psoriasis Area and Severity Index (PASI)
- Dermatology Life Quality Index (DLQI)
- anthropometric and demographic characteristics
- Exclusion criteria:
  - autoimmune or inflammatory diseases
  - malignancies
  - allergic reactions (6 weeks prior to sampling)



PBMC isolation

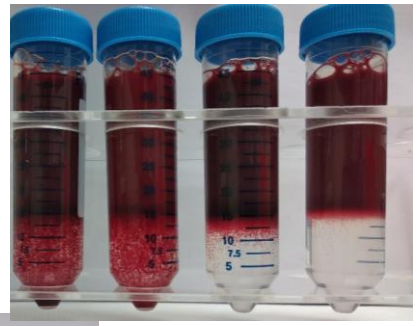
haematological and biochemical lab tests

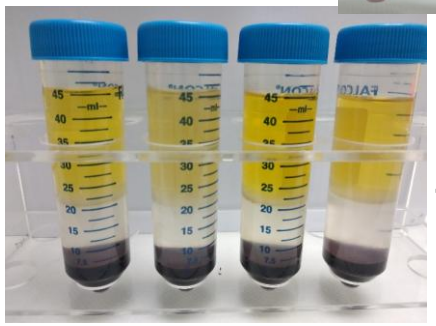
anti-CMV IgM/IgG, HBsAg, anti-HBs, anti-HCV, Mtb markers

PBMC isolation

20 ml heparinised blood

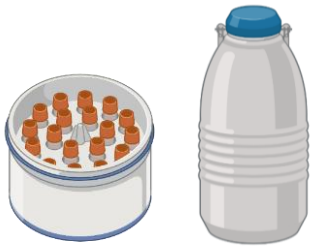
Lymphoprep medium density gradient centrifugation





Cell counting

Cryopreservation (10% DMSO in FBS) -80, 48h, Mr. Frosty liquid nitrogen



Analysis of the frequencies of MAIT and γδ T lymphocyte populations and subpopulations by flow cytometry

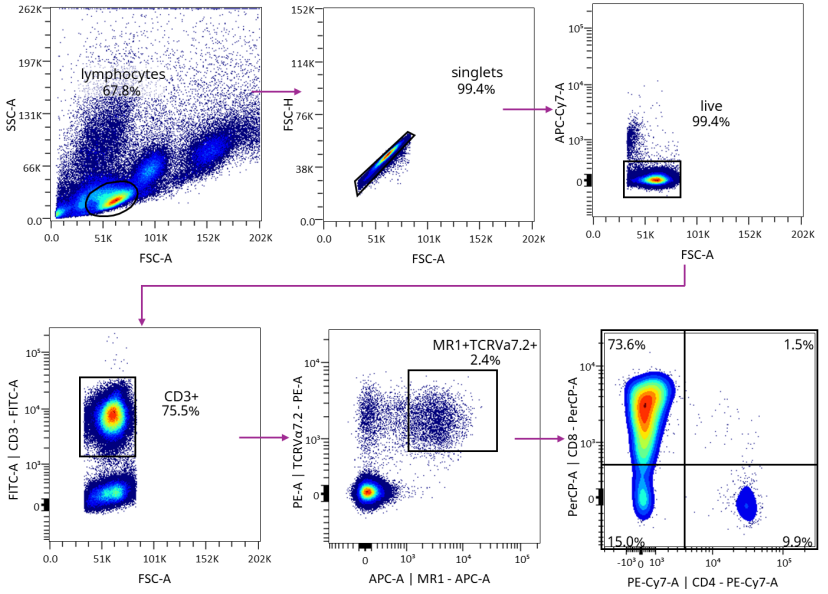
- to determine the relative frequency of peripheral MAIT and γδ T lymphocyte subpopulations
- a minimum of 90 subjects (60 PV + 30 HC)

BD FACS Canto II flow cytometer

Szentágothai Research Centre in Pécs

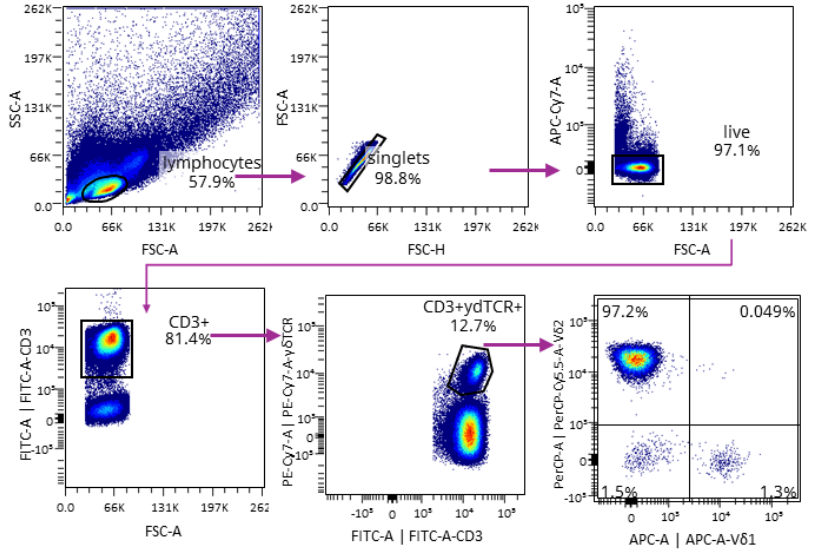
MAIT

CD3
CD4
CD8
TCRVα7.2
5-OP-RU-MR1 tetramer



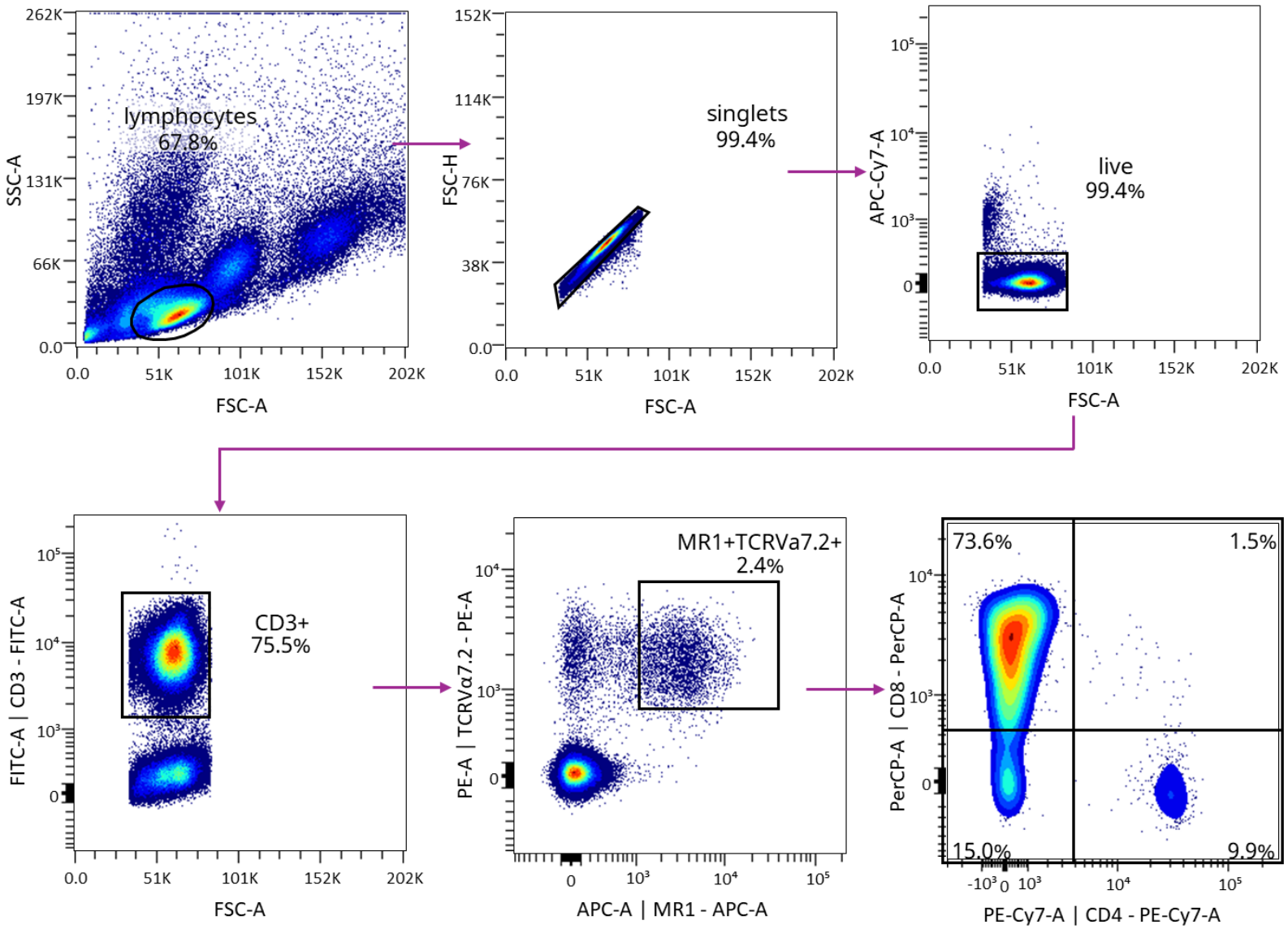
γδ T

CD3
TCRγδ
Vδ1
Vδ2



MAIT

CD3
CD4
CD8
TCRVα7.2
5-OP-RU-MR1
tetramer



Analysis of the frequencies of MAIT and γδ T lymphocyte populations and subpopulations by flow cytometry

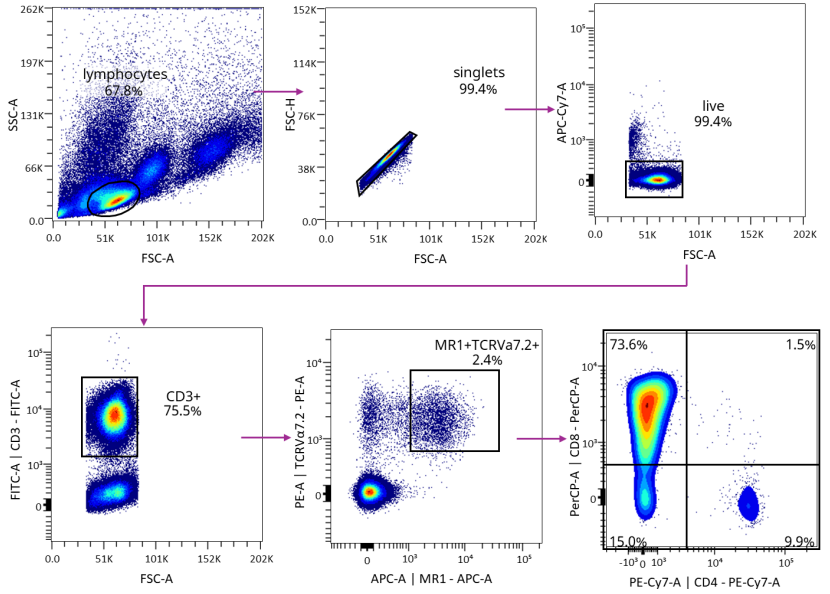
- to determine the relative frequency of peripheral MAIT and γδ T lymphocyte subpopulations
- 90 subjects (60 PV + 30 HC)

BD FACS Canto II flow cytometer

Szentágothai Research Centre in Pécs

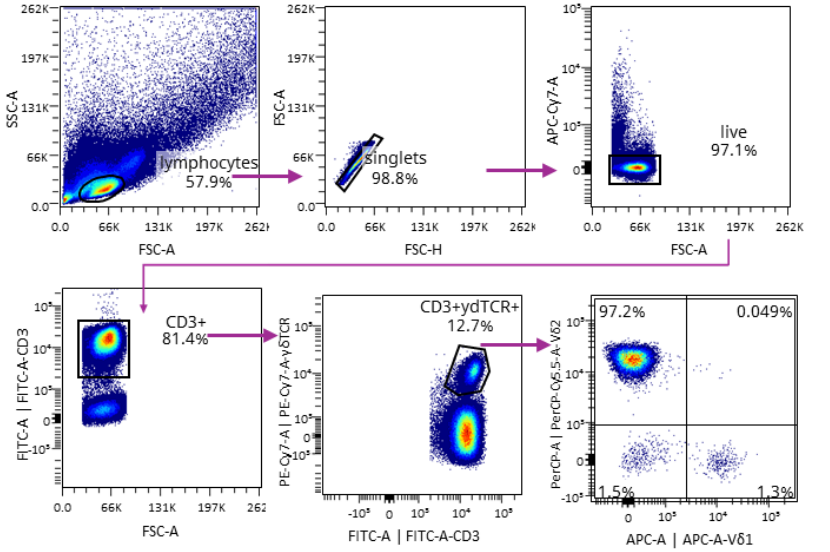
MAIT

CD3
CD4
CD8
TCRVα7.2
5-OP-RU-MR1 tetramer



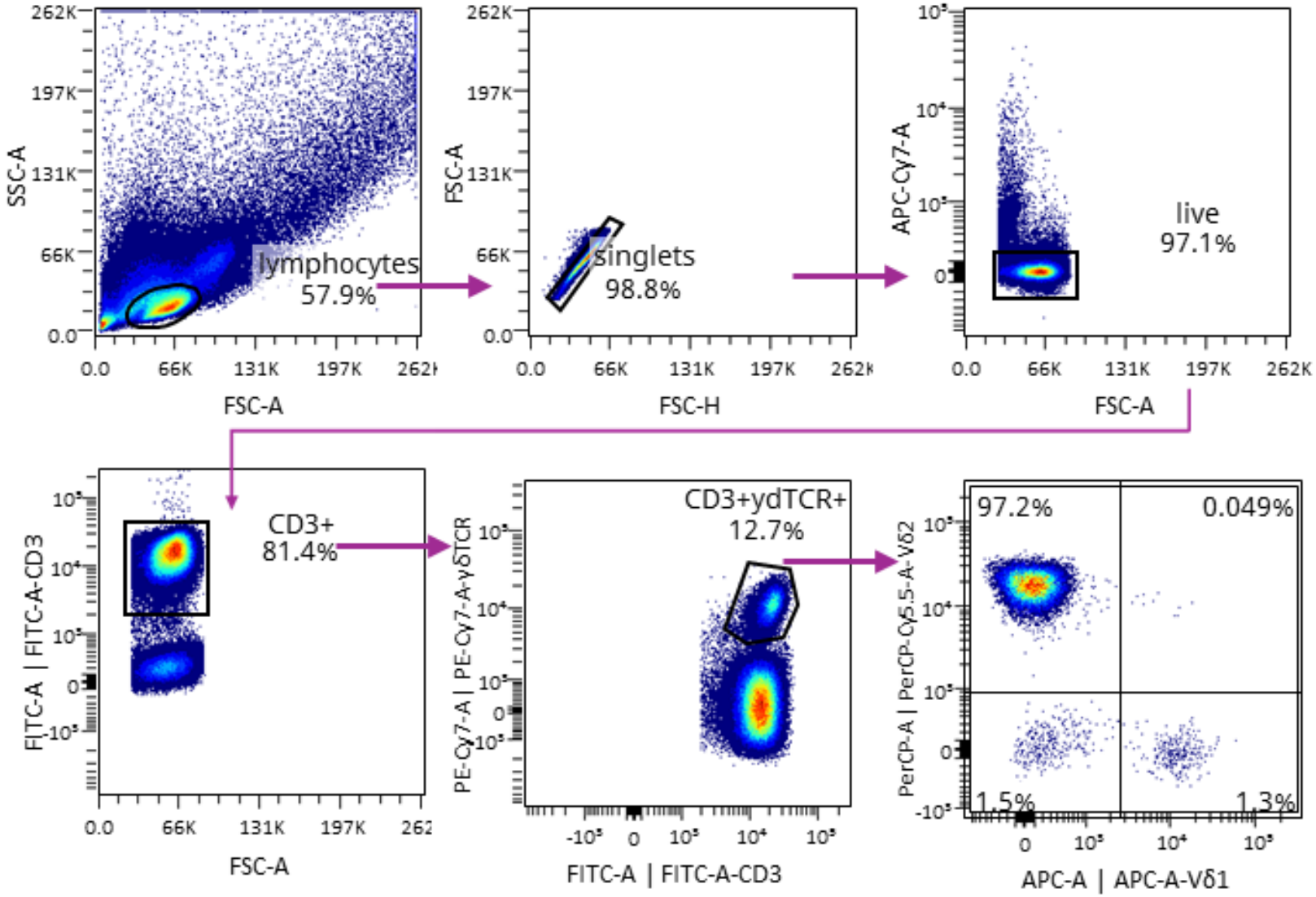
γδ T

CD3
TCRγδ
Vδ1
Vδ2



γδ T

CD3
TCRγδ
Vδ1
Vδ2



Single-cell analysis of surface and intracellular markers of MAIT and γδ T lymphocytes by spectral flow cytometry

Surface panel

- live/dead, CD3, CD45, CD4, CD8
- αβTCR, TCRVa7.2, MR1-tet, CD161
- γδTCR, Vδ1, Vδ2, Vδ3, Vγ9
- CD25, CD69, HLA-DR, CD38, CD28
- CD127, CD27, CD45RA
- CD11a, CD103, CCR7, CCR6
- CXCR3, CXCR5, CX3CR1, CD57, PD-1
- CD16, CD56, CD94
- CLA

Intracellular panel

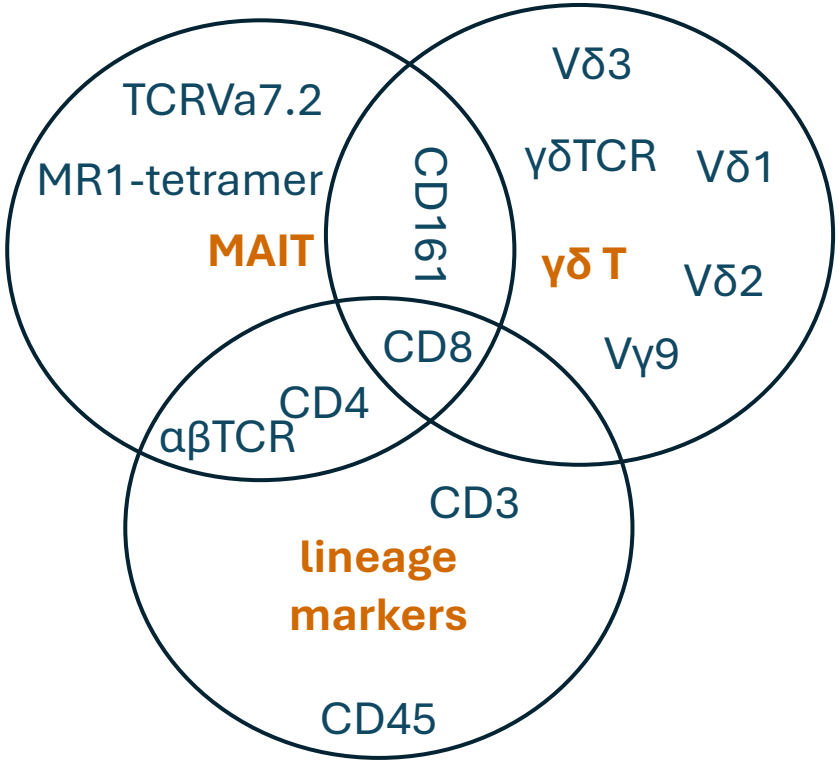
- CD3, CD4, CD8a, αβTCR
- γδTCR, Vδ1, Vδ2, Vδ3
- CD16, CD56,
- CD11a, CX3CR1, PD-1
- CD27, CD28, CD45RA, CD127
- T-bet, EOMES, TOX, BLIMP-1
- GzmA, GzmB, GzmK, granulysin, perforin
- Ki67

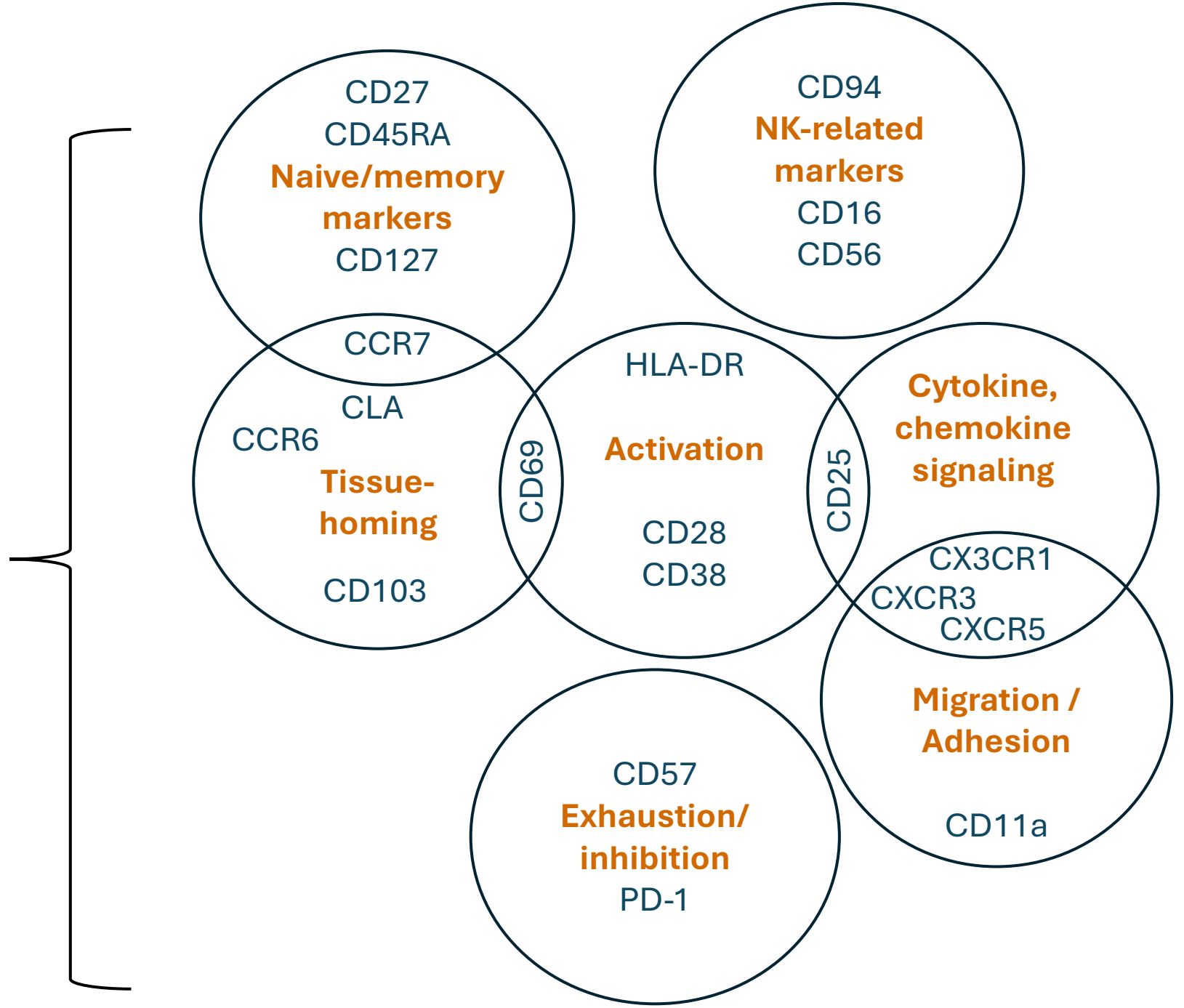
- 25 samples (15 PV + 10 HC)
- Spectral analyser Sony ID7000 at University of Warwick Medical School

- OMIQ platform for analysis

Dotmatics OMIQ

Surface panel





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- CD11a, CD103, CCR7, CCR6
- CXCR3, CXCR5, CX3CR1, CD57, PD-1
- CD16, CD56, CD94
- CLA

Intracellular panel

- CD3, CD4, CD8a, αβTCR
- γδTCR, Vδ1, Vδ2, Vδ3
- CD16, CD56,
- CD11a, CX3CR1, PD-1
- CD27, CD28, CD45RA, CD127
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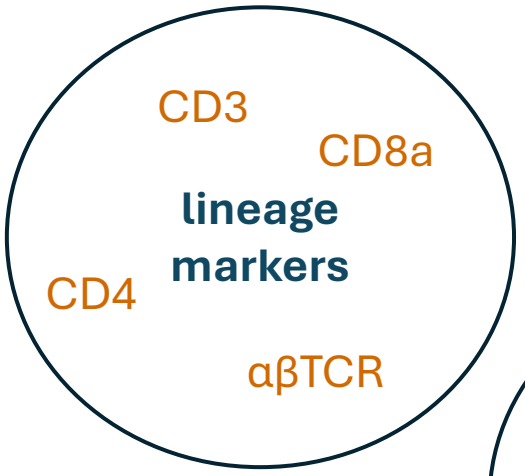
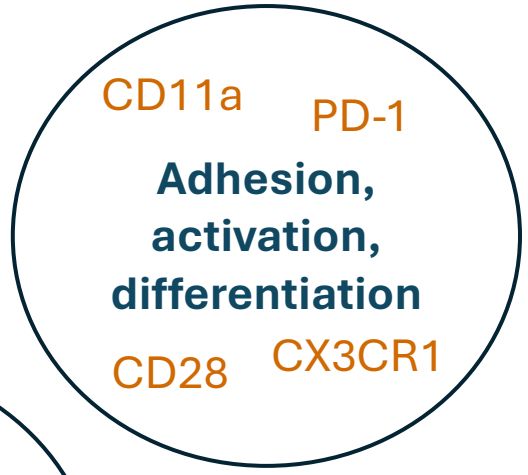
Dotmatics OMIQ

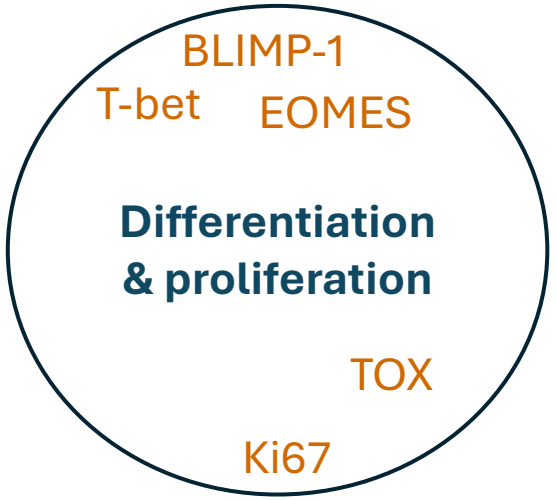
Intracellular panel

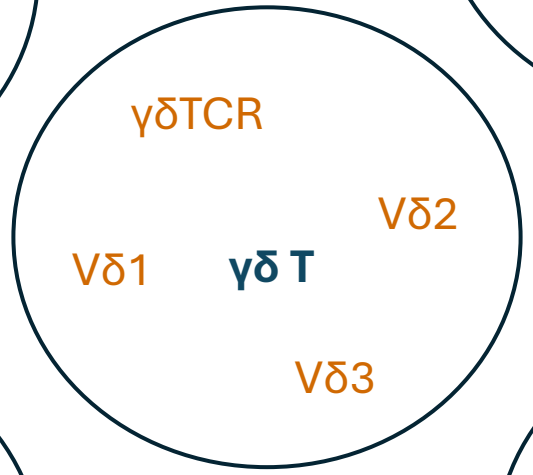
Surface markers

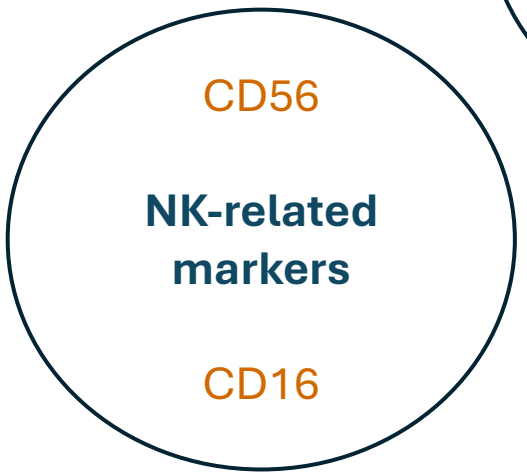
Intracellular markers

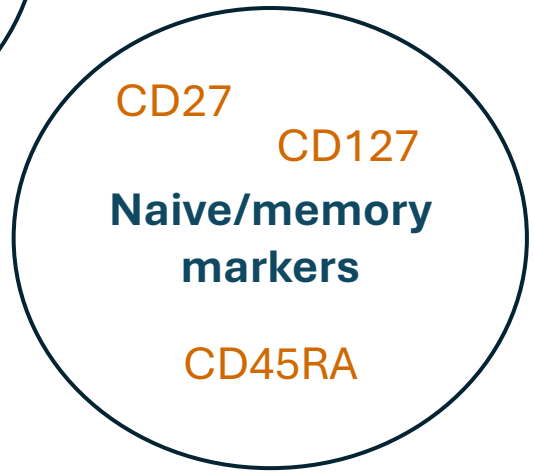


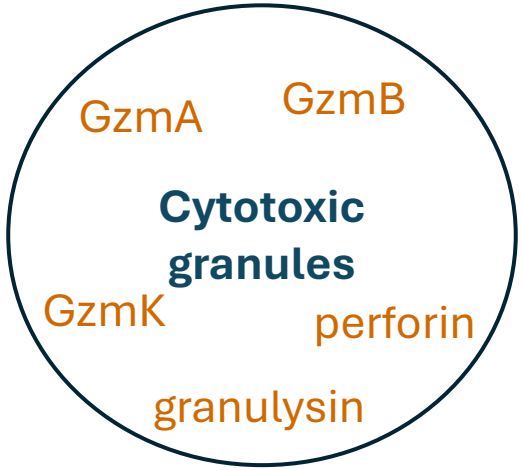




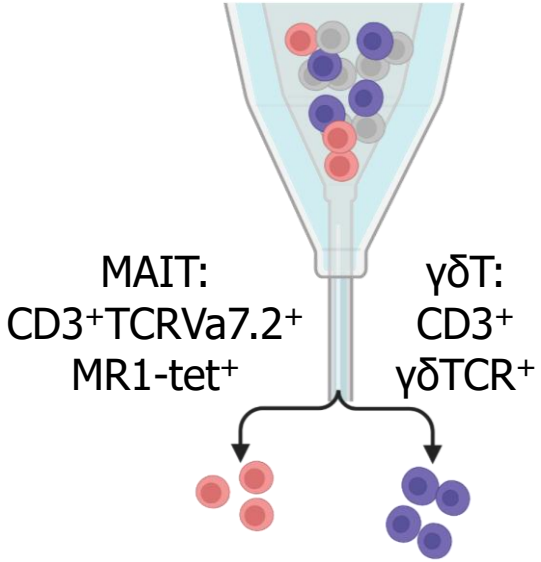






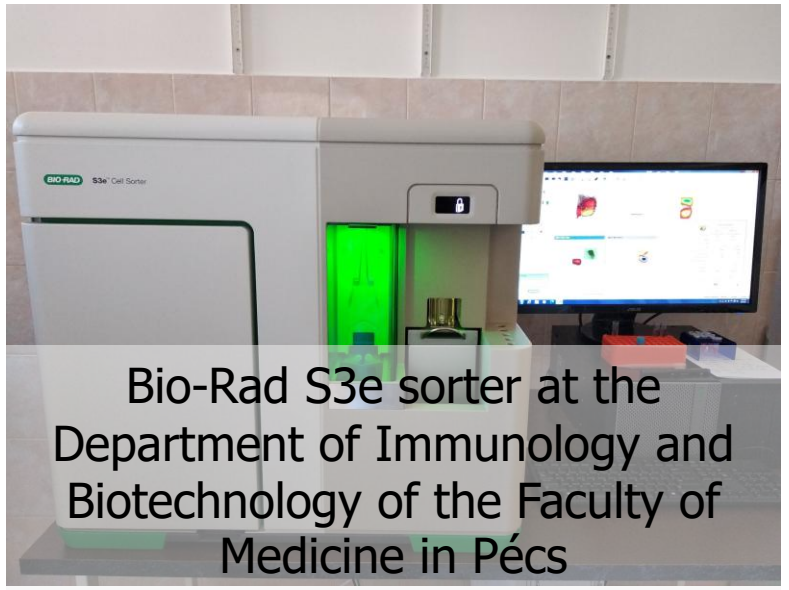


Fluorescence-activated cell sorting of peripheral MAIT and γδ T lymphocytes and total RNA extraction



- Cells directly sorted into TRIzol™ reagent
- total RNA extraction - Direct-zol commercial kit

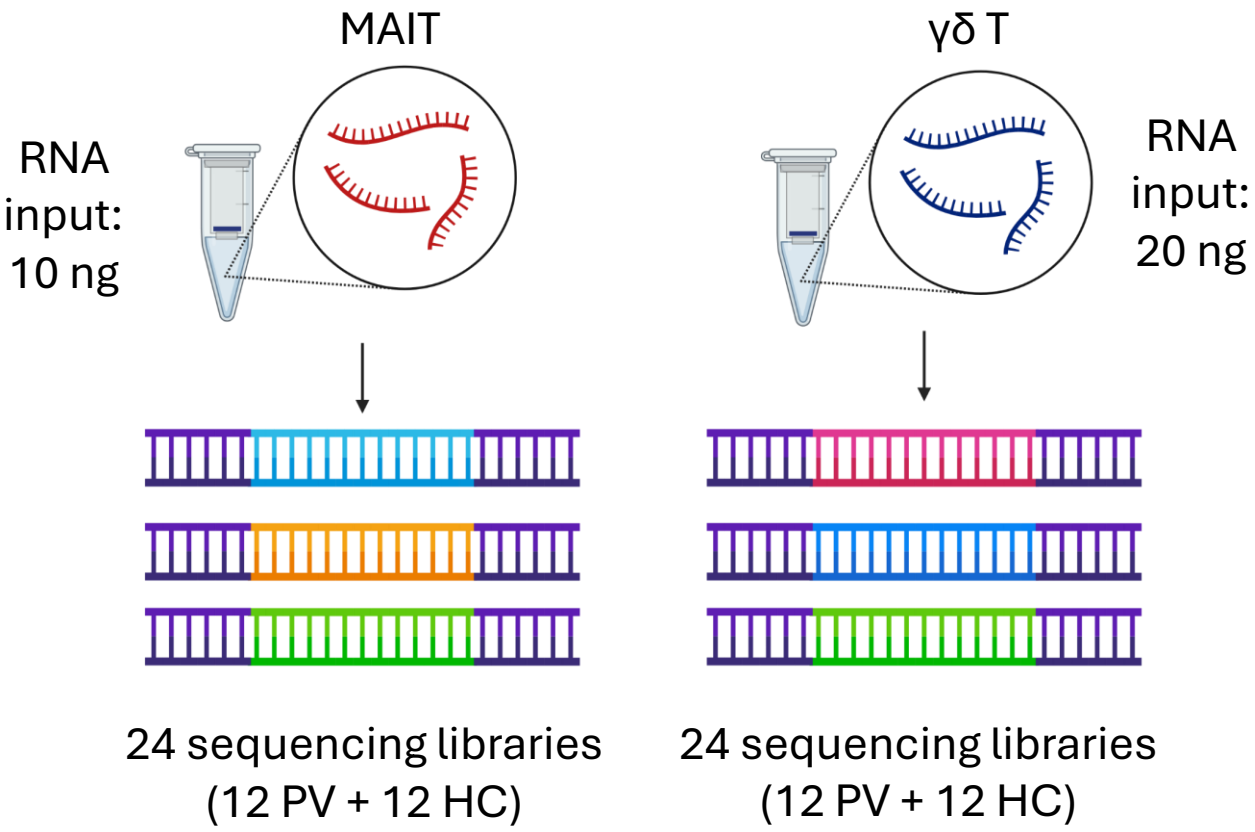
	Me (Q1, Q3)
PBMC input (x10⁶)	12.9 (10.6, 15.9)
Sorted γδT	140760 (71220,249827)
γδT extracted RNA (ng)	106 (51,197)
Sorted MAIT	37198 (12166, 69199)
MAIT extracted RNA (ng)	45 (27-75)



Bio-Rad S3e sorter at the Department of Immunology and Biotechnology of the Faculty of Medicine in Pécs

Immunotranscriptomic profiling analysis of MAIT and γδ T lymphocytes by RNA sequencing

- Immune Response Panel (Illumina)
- 395 immunologically relevant genes



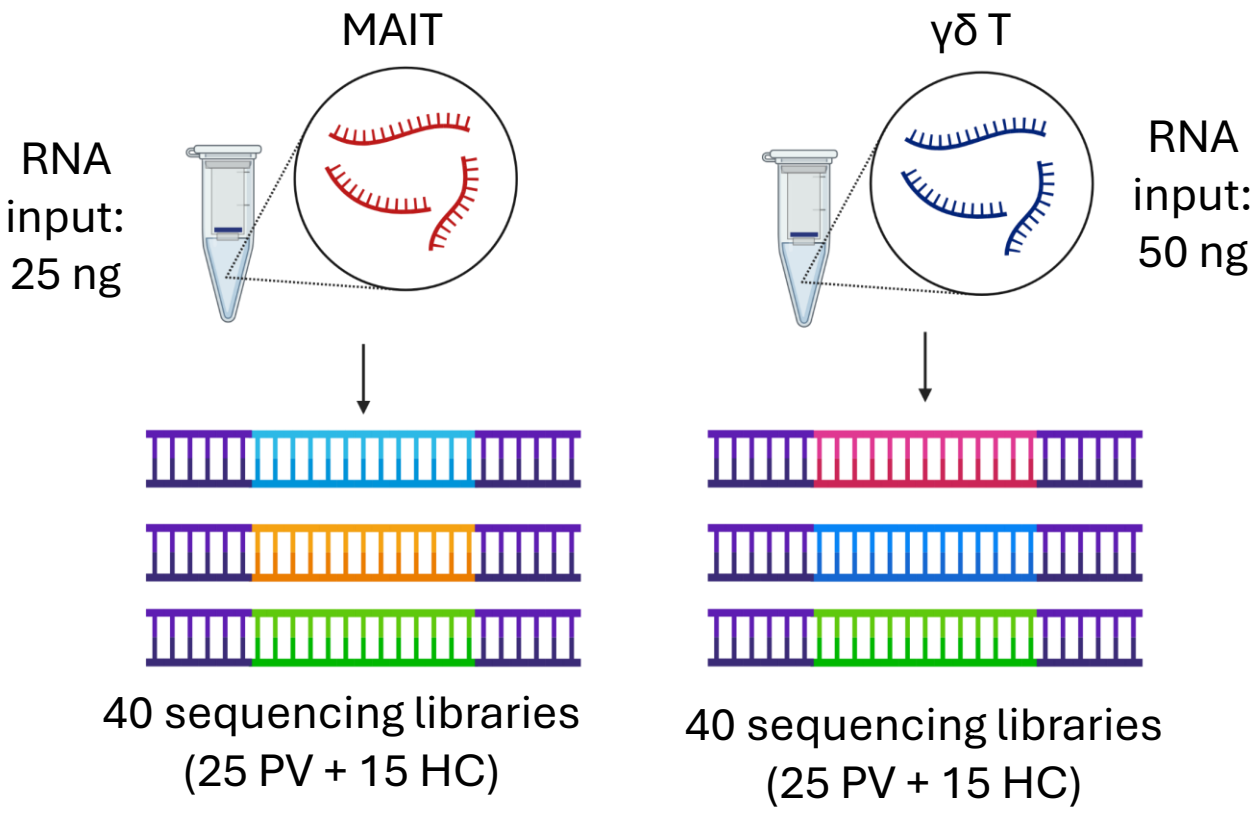
Miniseq Illumina sequencer, Faculty of Medicine Osijek

Bioinformatic analysis

STAR	featureCounts	DEseq2	clusterProfiler
RNA-seq aligner hg38 genome reference	Measure gene expression in RNA-Seq experiments from SAM or BAM files	Test for differential expression by use of negative binomial generalized linear models	Statistical analysis and visualisation of functional profiles for genes and gene clusters

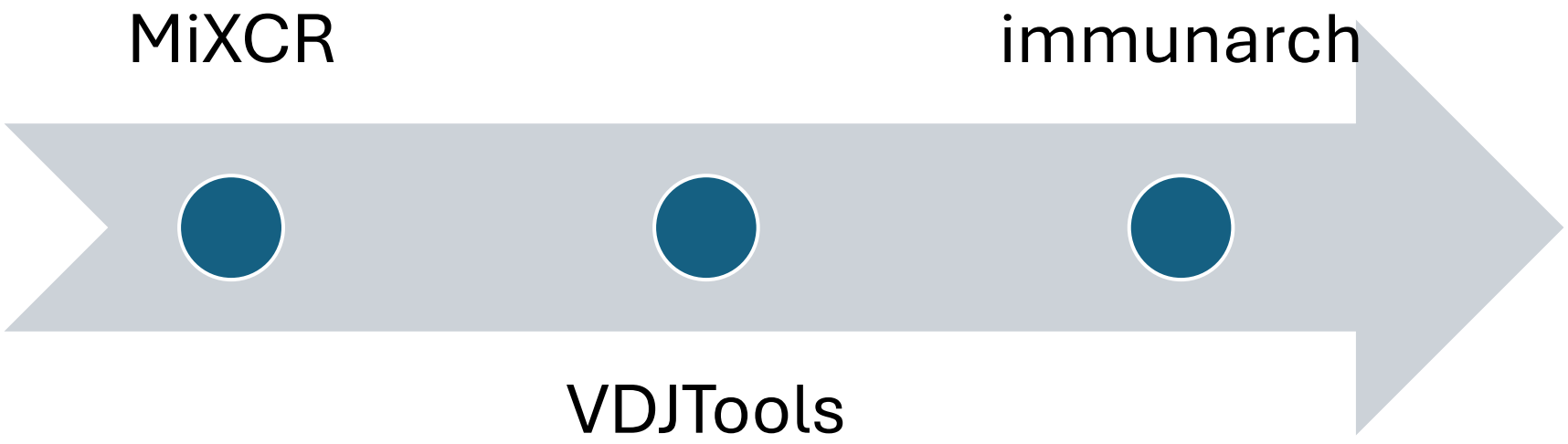
The analysis of T-cell receptor repertoires of MAIT and γδ T lymphocytes

- Archer® Immunoverse™-HS TCR kit
- simultaneous sequencing of the CDR3 regions of α-, β-, γ-, and δ-chains

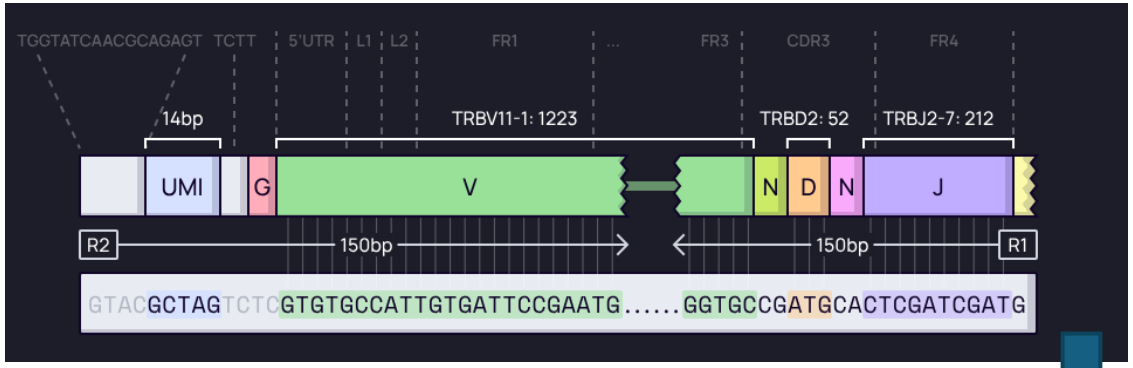


NextSeq 550 Illumina platform

Bioinformatic pipeline

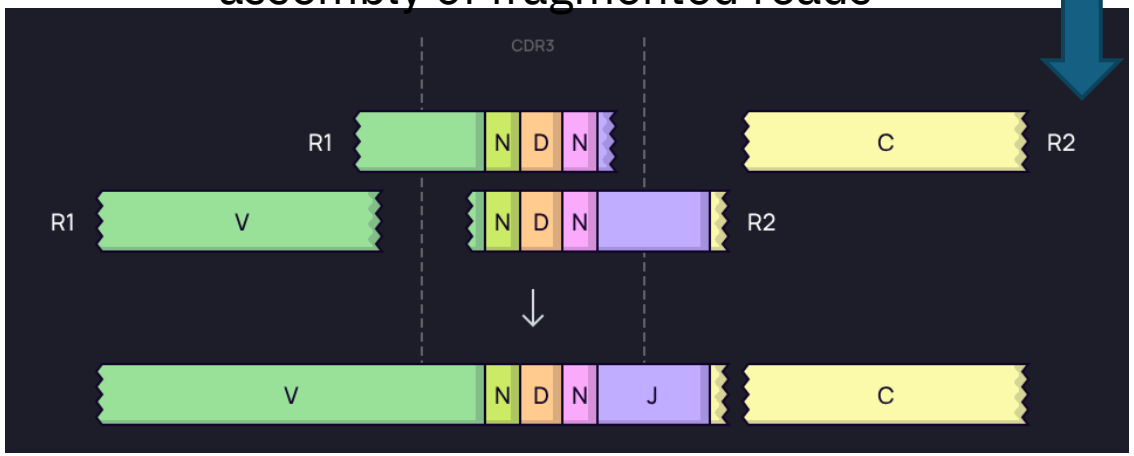


sequence alignment to the human genome

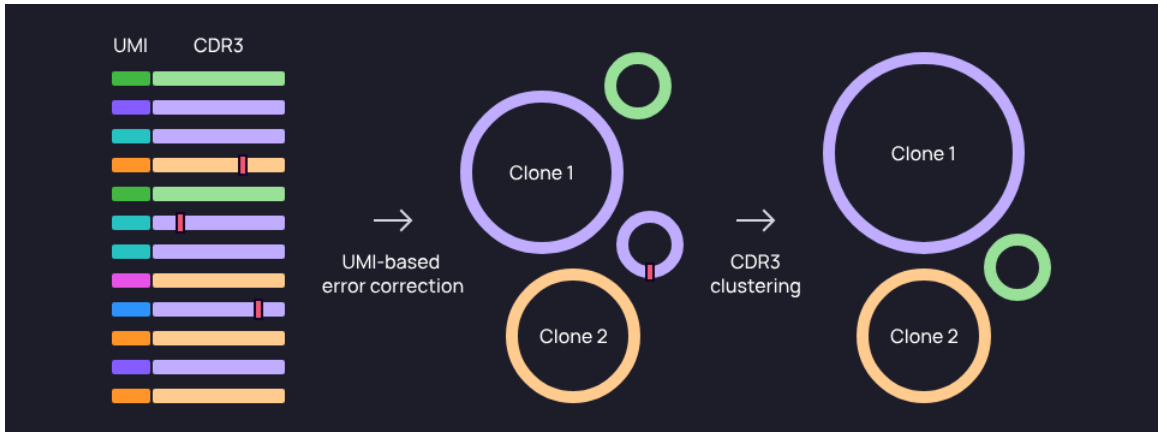


error correction & barcode based sorting

assembly of fragmented reads



clonotype assembly



cloneId	cloneCount	cloneFraction	clonalSequence	clonalSequenceQuality	allVHitsWithScore	allDHitsWithScore	allJHitsWithScore	allCHitsWithScore	allVAlignments	allDAlignments	allJAlignments	allCAlignment
0	25802	0.14206194081211287	TGTGCCACCAGCAGAGATGGAGGGTTTGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV15*00(1069.5)	TRBD2*00(30)	TRBJ2-6*00(248)	TRBC2*00(106.5)	327|345|364|4			
1	4568	0.025150722642807984	TGCAGTGCTATCGAGGGTAGGGCCACTGAAGCTTTCTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(967.8)	TRBD2*00(25)	TRBJ1-1*00(217.4)	TRBC1*00(105.6)	321|331|355|0|10||50.0	27|32|48|12|		
2	2796	0.015394356503785272	TGTGCCAGCAGTGACGGCGGAGGGGGCGGTGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1089.3)	TRBD1*00(40)	TRBJ2-1*00(202.5)	TRBC2*00(104.1)	327|342|364|0|15||75.			
3	2655	0.014618031658637303	TGTGCCAGCAGTGCGTTGGGTGGGTCTGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV2*00(1050.2)		TRBJ2-6*00(258.1)	TRBC2*00(106.3)	330|343|367|4			
4	2522	0.013885753611321404	TGTGCCAGCAGTGAGGCTAGCGGGAACACCGGGGAGCTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1083.7)	TRBD2*00(35)	TRBJ2-2*00(246.3)	TRBC2*00(102.7)	327|341|364|0|14||70.			
6	2450	0.013489332415691672	TGCAGTGCTAGGGGGACTAGCGAGTTCTACGAGCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(977.5)	TRBD2*00(50)	TRBJ2-7*00(217.6)	TRBC2*00(105.4)	321|332|355|0|11||55.			
7	2174	0.011969717825189264	TGTGCCAGCAGTGAAGCTAGCGGGGGGGCAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-1*00(1092.6)	TRBD2*00(39)	TRBJ2-3*00(222.3)	TRBC2*00(103.2)	327|344|364|0|17||85.			
8	2126	0.011705437026841018	TGTGCCAGTAGTCCCGTGGGACGGGAGCCCAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV28*00(1051.8)	TRBD2*00(30)	TRBJ2-1*00(218)	TRBC2*00(106)	327|339|364|0|12|SC335T|44.0			
9	2105	0.011589814177563662	TGCAGTGCTGCTACAGGGGGCGATTCCTACGAGCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(975.2)	TRBD1*00(50)	TRBJ2-7*00(227.2)	TRBC2*00(104.5)	321|330|355|0|9||45.6			
10	1891	0.010411562284927735	TGTGCCAGCAGTTATACTAGCGGAGAGGGCACAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-2*00(1063.7),TRBV6-3*00(1063.7)	TRBD2*00(40)	TRBJ2-3*00(237.7)	TRBC				
11	1864	0.010262904335856847	TGTGCCAGCAGTGAATTGGCGGGAGCTTCAGACGAGCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-1*00(1077.4)	TRBD2*00(35)	TRBJ2-7*00(206.9)	TRBC2*00(105.5)	327|342|364|0|15||75.			
12	1847	0.010169304886441844	TGCAGCGTTGAAGAGCAGGCGGGGGGGGCCTACGAGCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV29-1*00(1065.4)	TRBD2*00(29),TRBD1*00(25)	TRBJ2-7*00(221.9)	TRBC2*00(103.3)	321|			
13	1824	0.01004267033723331	TGCAGCGTTGAAGAAGGGACAGGGGGCAATCAGCCCCAGCATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV29-1*00(1080)	TRBD1*00(50)	TRBJ1-5*00(237.7)	TRBC1*00(106.7)	321|335|355|0|14||70.			
14	1817	0.010004129387474192	TGTGCCAGCAGTGAACTAGCGGGAGGGTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-1*00(1083)	TRBD2*00(60)	TRBJ2-1*00(227.7)	TRBC2*00(105.1)	327|342|364|0|15||75.			
15	1799	0.009905024088809936	TGCAGTGCTAGCGCTCTCAGCGATTCCTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(953.7)		TRBJ2-1*00(242.6)	TRBC2*00(105.4)	321|339|355|0|18|SA332CSA334(			
16	1587	0.00873778389538885	TGCGCCAGCAGTGGGACAGAATATGAAAAACTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV10-2*00(1072.4)	TRBD1*00(30)	TRBJ1-4*00(222.5)	TRBC1*00(105.9)	327|340|364|0|13||65.0	13|19|36|13|		
17	1385	0.007625602202339986	TGTGCCAGCAGTGACTCGACGGGAGGGCCAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1111.9)	TRBD2*00(45)	TRBJ2-3*00(222.3)	TRBC2*00(103.5)	327|346|364|0|19||95.			
18	1352	0.007443909153475568	TGTGCCAGCAGTTTTTAGGGACGGATTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV28*00(1080.7)	TRBD1*00(25),TRBD2*00(25)	TRBJ2-1*00(227.8)	TRBC2*00(106)	327|			
19	1346	0.007410874053682038	TGTGCCAGCAGCTTGGGGGGCGACTTATCTAGCACAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV7-8*00(942.5)	TRBD1*00(35)	TRBJ2-3*00(251.8)	TRBC2*00(103.4)	330|			
20	1313	0.007229181004817619	TGTGCCAGCAGTGACTCAACTAGCGGGGGCAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1102.6)	TRBD2*00(45)	TRBJ2-3*00(221.9)	TRBC2*00(102.3)	327|344|364|0|17||85.			
21	1298	0.007146593255333792	TGTGCCAGCAGTGACTCGACTAGCGGGAGCAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1113.7)	TRBD2*00(50)	TRBJ2-1*00(217.6)	TRBC2*00(103.4)	327|346|364|0|19||95.			
22	1269	0.006986923606331728	TGTGCCAGTAGCCGTGCCGGTGAGGTTTCACCCCTCCACTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV19*00(1066.1)		TRBJ1-6*00(201)	TRBC1*00(105.6)	327|338|364|0|11||55.0		29|4	
23	1263	0.006953888506538197	TGTGCCAGCAGTTTGGGACAGCTCTCTGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV28*00(1067)	TRBD1*00(35)	TRBJ2-6*00(260.9)	TRBC2*00(107)	327|341|364|4			
24	1215	0.006689607708189952	TGCAGCGTGAGGGAGACAGGGGATACCGGGGAGCTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV29-1*00(1059.3)	TRBD1*00(40)	TRBJ2-2*00(226.5)	TRBC2*00(102.8)	321|329|355|0|8||40.6			
25	1175	0.006469373709566414	TGTGCCAGCAGGGACACTAGTGAAACCGGGGAGCTGTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV2*00(1053.9)	TRBD1*00(25),TRBD2*00(25)	TRBJ2-2*00(226.5)	TRBC2*00(103.9)	330|			
27	958	0.005274604267033724	TGTGCCATCAGTGAGGAGGAAGCGGGAGCTAGGGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV10-3*00(1060.8)	TRBD2*00(40)	TRBJ2-1*00(196.8)	TRBC2*00(103.4)	327|342|364|0|15||75.			
28	958	0.005274604267033724	TGTGCCAGCAGTGCGGGACTAGCGGACCAAGAGACCCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-3*00(1063.8),TRBV6-2*00(1063.4)	TRBD2*00(60)	TRBJ2-5*00(236.9)	TRBC2*00(104.8)	327|			
29	953	0.005247075017205781	TGTGCCAGCAGTGAAGACAGCTCTGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-1*00(1087.1)		TRBJ2-6*00(272.8)	TRBC2*00(106.2)	327|343|364|0|16||80.0			
31	874	0.004812112869924294	TGCGCCAGCAGTTCTAGCGAGACCGGGGAGCTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV10-1*00(1109.4)	TRBD2*00(30)	TRBJ2-2*00(226.6)	TRBC2*00(104.6)	327|339|364|0|12||60.0	20|26|48|13|		
32	869	0.004784583620096352	TGTGCCACCAGCCCAGAAAGCTCTGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV15*00(1045.5)		TRBJ2-6*00(273.4)	TRBC2*00(106.2)	327|339|364|0|12||60.0			
33	834	0.004591878871300757	TGTGCCACCAGCAGAGATTCGTCCGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV15*00(1071.3)		TRBJ2-6*00(243.3)	TRBC2*00(105.9)	327|345|364|0|18||90.0			
34	789	0.004344115622849277	TGTGCCAGAAGCGCAGGGTCGCTATACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV5-3*00(1095.9)	TRBD1*00(25),TRBD2*00(25)	TRBJ2-1*00(228.4)	TRBC2*00(106.6)	327|			
35	767	0.004222986923686332	TGTGCCAGCAGTGCAACAGGGAACACTGAAGCTTTCTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1114.9)	TRBD1*00(25)	TRBJ1-1*00(232.1)	TRBC1*00(104.7)	327|340|364|0|13||65.0	15|20|36|15|		
36	763	0.004200963523743978	TGCAGTGCTAGGAGTGGACAGGGGGTTACGAGCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(984)		TRBD1*00(50)	TRBJ2-7*00(212.3)	TRBC2*00(104.2)	321|336|355|0|15||75.			
37	749	0.004123881624422574	TGTGCCAGCAGTTACCAAACAGGCTCTGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-5*00(1073.8)		TRBJ2-6*00(267.9)	TRBC2*00(105.7)	327|342|364|4			
38	739	0.004068823124569855	TGTGCCAGCAGTGAGACTAGCGGTAGCACAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1085.3)	TRBD2*00(45)	TRBJ2-3*00(247.1)	TRBC2*00(102.8)	327|341|364|0|14||70.			
39	664	0.003655884377150723	TGCAGCGTTGAATTGCGGGAGGGCTTAGAGCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV29-1*00(1093.8)	TRBD2*00(50)	TRBJ2-7*00(194.6)	TRBC2*00(101.9)	321|333|355|0|12||60.0	23|33|48|14|		
40	655	0.003606331727460427	TGTGCCAGCAGTGTGTCTAGCGGGGTTGGCGATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1075.5)	TRBD2*00(40)	TRBJ2-1*00(207.2)	TRBC2*00(103.8)	327|340|364|0|13||65.			
41	642	0.003534755677907777	TGTGCCAGCAGCAGGGGTAGCAGGGGACTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV15*00(1053.3)	TRBD1*00(30)	TRBJ2-1*00(233)	TRBC2*00(105.3)	327|341|364|0|14||70.0	16|2		
42	624	0.003435650378527185	TGTGCCAGCAGTGACGGGGGCGACACCGGGGAGCTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1081.3)	TRBD1*00(35)	TRBJ2-2*00(237.1)	TRBC2*00(103.2)	327|342|364|0|15||75.			
43	608	0.00334755677907777	TGTGCCACCAGTGATGGCAGGGTGGACACCGGGGAGCTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV24-1*00(1096.1)	TRBD1*00(25)	TRBJ2-2*00(236.9)	TRBC2*00(105.6)	327|342|365|0|15||75.			
44	588	0.003237439779766013	TGCAGTGCTAGGGACCGGGAGCGAGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(974.6)	TRBD1*00(30),TRBD2*00(30)	TRBJ2-1*00(197.3)	TRBC2*00(105.1)	321|332|355|0|11||55.			
45	585	0.003220922229896963	TGTGCCACCAGCAGAGCCTCCGGAGGGTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV15*00(1062.1)	TRBD2*00(30)	TRBJ2-1*00(228.2)	TRBC2*00(104.5)	327|343|364|0|16||80.			
46	584	0.003215416379903676	TGCAGTGCTAGGCTAGCGGGGGGATAGAGACCCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(884)		TRBD2*00(60)	TRBJ2-5*00(217.2)	TRBC2*00(103.8)	321|		
47	569	0.003132828630419821	TGCAGTGCTAGAGGAGGCGGGGGCAAAGAGACCCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(946.3)	TRBD1*00(30)	TRBJ2-5*00(222.8)	TRBC2*00(106.2)	321|334|355|0|13||65.			
48	563	0.003099793530626290 3	TGCAGTGCTAGAGATGTGGCTAGCGGAGACACAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(939.7)	TRBD2*00(35)	TRBJ2-3*00(231.1)	TRBC2*00(103.2)	321|			
49	560	0.003083275980729525 3	TGTGCCAGCAGTTCAGGGGGCGCGGACACCGGGGAGCTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-2*00(1054.8),TRBV6-3*00(1054.8)	TRBD1*00(35)	TRBJ2-2*00(245.6)	TRBC2*00(102.2)	327|			
50	556	0.003061252580867171	TGCAGTGCTAGGGGGGGGGCAAGCGAGTCCTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(818)	TRBD1*00(30)	TRBJ2-1*00(243.7)	TRBC2*00(105.9)	321|			
51	517	0.002846524432209224	TGTGCCAGCAGCTTAGTGTGGCGGGAAGGGACACAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV11-2*00(1058.1)	TRBD2*00(30)	TRBJ2-3*00(242.5)	TRBC2*00(103.7)	330|			
52	517	0.002846524432209224	TGTGCCAGCAGCCAAAAGGGGGACGCCTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-2*00(1059.1),TRBV6-3*00(1059.1)	TRBD1*00(30)	TRBJ2-1*00(237.8)	TRBC2*00(104.6)	327|			
53	506	0.002785960082587749 7	TGTGCCAGCAGCCCAAGCGGGGGAAGCTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-2*00(1061),TRBV6-3*00(1061)	TRBD2*00(30)	TRBJ2-1*00(233.5)	TRBC2*00(104.8)	327|			
54	498	0.002741913282863042	TGTGCCACCAGCAGCAGCTCATCCCCTGAAAAACTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV15*00(1056.6)		TRBJ1-4*00(217.5)	TRBC1*00(105.1)	327|341|364|0|14||70.0			
55	494	0.002719889883006883	TGTGCCACAGCAGTGAACTCTCTGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-1*00(1096.8)		TRBJ2-6*00(262.6)	TRBC2*00(106.7)	327|342|364|0|15||75.0			

MiXCR

cloneId	cloneCount	cloneFraction	clonalSequence	clonalSequenceQuality	allVHitsWithScore	allDHitsWithScore	allJHitsWithScore	allCHitsWithScore	allVAlignments	allDAlignments	allJAlignments	allCAlignment
0	25802	0.14206194081211287	TGTGCCACCAGCAGAGATGGAGGGTTTGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV15*00(1069.5)	TRBD2*00(30)	TRBJ2-6*00(248)	TRBC2*00(106.5)	327|345|364|6			
1	4568	0.025150722642807984	TGCAGTGCTATCGAGGGTAGGGCCACTGAAGCTTTCTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(967.8)	TRBD2*00(25)	TRBJ1-1*00(217.4)	TRBC1*00(105.6)	321|331|355|0|10||50.0	27|32|48|12|1		
2	2796	0.015394356503785272	TGTGCCAGCAGTGACGGCGGAGGGGGCGGTGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1089.3)	TRBD1*00(40)	TRBJ2-1*00(202.5)	TRBC2*00(104.1)	327|342|364|0|15||75.			
3	2655	0.014618031658637303	TGTGCCAGCAGTGCGTTGGGTGGGTCTGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV2*00(1050.2)		TRBJ2-6*00(258.1)	TRBC2*00(106.3)	330|343|367|6			
4	2522	0.01388575361321404	TGTGCCAGCAGTGAGGCTAGCGGGAACACCGGGGAGCTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1083.7)	TRBD2*00(35)	TRBJ2-2*00(246.3)	TRBC2*00(102.7)	327|341|364|0|14||70.			
6	2450	0.013489332415691672	TGCAGTGCTAGGGGGACTAGCGAGTTCTACGAGCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(977.5)	TRBD2*00(50)	TRBJ2-7*00(217.6)	TRBC2*00(105.4)	321|332|355|0|11||55.			
7	2174	0.011969717825189264	TGTGCCAGCAGTGAAGCTAGCGGGGGGGCAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-1*00(1092.6)	TRBD2*00(39)	TRBJ2-3*00(222.3)	TRBC2*00(103.2)	327|344|364|0|17||85.			
8	2126	0.011705437026841018	TGTGCCAGTAGTCCCGTGGGACGGGAGCCCAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV28*00(1051.8)	TRBD2*00(30)	TRBJ2-1*00(218)	TRBC2*00(106)	327|339|364|0|12|SC335T|44.0			
9	2105	0.011589814177563662	TGCAGTGCTGCTACAGGGGGCGATTCCTACGAGCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(975.2)	TRBD1*00(50)	TRBJ2-7*00(227.2)	TRBC2*00(104.5)	321|330|355|0|9||45.6			
10	1891	0.010411562284927735	TGTGCCAGCAGTTATACTAGCGGAGAGGGCACAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-2*00(1063.7),TRBV6-3*00(1063.7)	TRBD2*00(40)	TRBJ2-3*00(237.7)	TRBC2				
11	1864	0.010262904335856847	TGTGCCAGCAGTGAATTGGCGGGAGCTTCAGACGAGCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-1*00(1077.4)	TRBD2*00(35)	TRBJ2-7*00(206.9)	TRBC2*00(105.5)	327|342|364|0|15||75.			
12	1847	0.010169304886441844	TGCAGCGTTGAAGAGCAGGCGGGGGGGGCCTACGAGCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV29-1*00(1065.4)	TRBD2*00(29),TRBD1*00(25)	TRBJ2-7*00(221.9)	TRBC2*00(103.3)	321|3			
13	1824	0.01004267033723331	TGCAGCGTTGAAGAAGGGACAGGGGGCAATCAGCCCCAGCATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV29-1*00(1080)	TRBD1*00(50)	TRBJ1-5*00(237.7)	TRBC1*00(106.7)	321|335|355|0|14||70.			
14	1817	0.010004129387474192	TGTGCCAGCAGTGAACTAGCGGGAGGGTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-1*00(1083)	TRBD2*00(60)	TRBJ2-1*00(227.7)	TRBC2*00(105.1)	327|342|364|0|15||75.			
15	1799	0.0099050240880936	TGCAGTGCTAGCGCTCTCAGCGATTCCTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(953.7)	TRBJ2-1*00(242.6)	TRBC2*00(105.4)	321|339|355|0|18|SA332CSA334(				
16	1587	0.00873778389538885	TGCGCCAGCAGTGGGACAGAATATGAAAAACTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV10-2*00(1072.4)	TRBD1*00(30)	TRBJ1-4*00(222.5)	TRBC1*00(105.9)	327|340|364|0|13||65.0	13|19|36|13|1		
17	1385	0.007625602202339986	TGTGCCAGCAGTGACTCGACGGGAGGGCCAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1111.9)	TRBD2*00(45)	TRBJ2-3*00(222.3)	TRBC2*00(103.5)	327|346|364|0|19||95.			
18	1352	0.007443909153475568	TGTGCCAGCAGTTTTTTAGGGACGGATTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV28*00(1080.7)	TRBD1*00(25),TRBD2*00(25)	TRBJ2-1*00(227.8)	TRBC2*00(106)	327|3			
19	1346	0.007410874053682038	TGTGCCAGCAGCTTGGGGGGCGACTTATCTAGCACAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV7-8*00(942.5)	TRBD1*00(35)	TRBJ2-3*00(251.8)	TRBC2*00(103.1)	330|3			
20	1313	0.007229181004817619	TGTGCCAGCAGTGACTCAACTAGCGGGGCAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1102.6)	TRBD2*00(45)	TRBJ2-3*00(221.9)	TRBC2*00(102.3)	327|344|364|0|17||85.			
21	1298	0.007146593255333792	TGTGCCAGCAGTGACTCGACTAGCGGGAGCAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1113.7)	TRBD2*00(50)	TRBJ2-1*00(217.6)	TRBC2*00(103.4)	327|346|364|0|19||95.			
22	1269	0.006986923606331728	TGTGCCAGTAGCCGTGCCGGTGAGGTTTCACCCCTCCACTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV19*00(1066.1)	TRBJ1-6*00(201)	TRBC1*00(105.6)	327|338|364|0|11||55.0	29|4			
23	1263	0.006953888506538197	TGTGCCAGCAGTTTGGGACAGCTCTCTGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV28*00(1067)	TRBD1*00(35)	TRBJ2-6*00(260.9)	TRBC2*00(107)	327|341|364|6			
24	1215	0.006689607708189952	TGCAGCGTGAGGGAGACAGGGGATACCGGGGAGCTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV29-1*00(1059.3)	TRBD1*00(40)	TRBJ2-2*00(226.5)	TRBC2*00(102.8)	321|329|355|0|8||40.6			
25	1175	0.006469373709566414	TGTGCCAGCAGGGACACTAGTGAAACCGGGGAGCTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV2*00(1053.9)	TRBD1*00(25),TRBD2*00(25)	TRBJ2-2*00(226.5)	TRBC2*00(103.9)	330|3			
27	958	0.005274604267033724	TGTGCCATCAGTGAGGAGGAAGCGGGAGCTAGGGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV10-3*00(1060.8)	TRBD2*00(40)	TRBJ2-1*00(196.8)	TRBC2*00(103.4)	327|342|364|0|15||75.			
28	958	0.005274604267033724	TGTGCCAGCAGTGCGGGACTAGCGGACCAAGAGACCCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-3*00(1063.8),TRBV6-2*00(1063.4)	TRBD2*00(60)	TRBJ2-5*00(236.9)	TRBC2*00(104.8)	327|3			
29	953	0.005247075017205781	TGTGCCAGCAGTGAAGACAGCTCTGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-1*00(1087.1)	TRBJ2-6*00(272.8)	TRBC2*00(106.2)	327|343|364|0|16||80.0				
31	874	0.004812112869924294	TGCGCCAGCAGTTCTAGCGAGACCGGGGAGCTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV10-1*00(1109.4)	TRBD2*00(30)	TRBJ2-2*00(226.6)	TRBC2*00(104.6)	327|339|364|0|12||60.0	20|26|48|13|1		
32	869	0.004784583620096352	TGTGCCACCAGCCCAGAAAGCTCTGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV15*00(1045.5)	TRBJ2-6*00(273.4)	TRBC2*00(106.2)	327|339|364|0|12||60.0				
33	834	0.004591878871300757	TGTGCCACCAGCAGAGATTCGTCCGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV15*00(1071.3)	TRBJ2-6*00(243.3)	TRBC2*00(105.9)	327|345|364|0|18||90.0				
34	789	0.004344115622849277	TGTGCCAGAAGCGCAGGGTCGCTATACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV5-3*00(1095.9)	TRBD1*00(25),TRBD2*00(25)	TRBJ2-1*00(228.4)	TRBC2*00(106.6)	327|3			
35	767	0.004222986923606332	TGTGCCAGCAGTGCAACAGGGAACACTGAAGCTTTCTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1114.9)	TRBD1*00(25)	TRBJ1-1*00(232.1)	TRBC1*00(104.7)	327|340|364|0|13||65.0	15|20|36|15|2		
36	763	0.004200963523743978	TGCAGTGCTAGAGATGGACAGGGGGTTTACGAGCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(984)	TRBD1*00(50)	TRBJ2-7*00(212.3)	TRBC2*00(104.2)	321|336|355|0|15||75.			
37	749	0.00412388162422574	TGTGCCAGCAGTTACCAAACAGGCTCTGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-5*00(1073.8)	TRBJ2-6*00(267.9)	TRBC2*00(105.7)	327|342|364|6				
38	739	0.004068823124569855	TGTGCCAGCAGTGAGACTAGCGGTAGCACAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1085.3)	TRBD2*00(45)	TRBJ2-3*00(247.1)	TRBC2*00(102.8)	327|341|364|0|14||70.			
39	664	0.003655884377150723	TGCAGCGTTGAATTGCGGGAGGGCTTAGAGCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV29-1*00(1093.8)	TRBD2*00(50)	TRBJ2-7*00(194.6)	TRBC2*00(101.9)	321|333|355|0|12||60.0	23|33|48|14|2		
40	655	0.003606331727460427	TGTGCCAGCAGTGTGTCTAGCGGGGTTGGCGATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1075.5)	TRBD2*00(40)	TRBJ2-1*00(207.2)	TRBC2*00(103.8)	327|340|364|0|13||65.			
41	642	0.003534755677907777	TGTGCCACCAGCAGGGTAGCAGGGGACTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV15*00(1053.3)	TRBD1*00(30)	TRBJ2-1*00(233)	TRBC2*00(105.3)	327|341|364|0|14||70.0	16|2		
42	624	0.003435650378527185	TGTGCCAGCAGTGACGGGGGCGACACCGGGGAGCTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-4*00(1081.3)	TRBD1*00(35)	TRBJ2-2*00(237.1)	TRBC2*00(103.2)	327|342|364|0|15||75.			
43	608	0.00334755677907777	TGTGCCACCAGTGATGGCAGGGTGGACACCGGGGAGCTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV24-1*00(1096.1)	TRBD1*00(25)	TRBJ2-2*00(236.9)	TRBC2*00(105.6)	327|342|365|0|15||75.			
44	588	0.0032374397797660013	TGCAGTGCTAGGGACCGGGAGCGAGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(974.6)	TRBD1*00(30),TRBD2*00(30)	TRBJ2-1*00(197.3)	TRBC2*00(105.1)	321|332|355|0|11||55.			
45	585	0.0032209222298692363	TGTGCCACCAGCAGAGCCTCCGGAGGGTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV15*00(1062.1)	TRBD2*00(30)	TRBJ2-1*00(228.2)	TRBC2*00(104.5)	327|343|364|0|16||80.			
46	584	0.0032154163799036476	TGCAGTGCTAGCTCGGGGACTAGCGGGGGGATAGAGACCCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(884)	TRBD2*00(60)	TRBJ2-5*00(217.2)	TRBC2*00(103.8)	321|3			
47	569	0.003132828630419821	TGCAGTGCTAGAGGAGGCGGGGGCAAAGAGACCCAGTACTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(946.3)	TRBD1*00(30)	TRBJ2-5*00(222.8)	TRBC2*00(106.2)	321|334|355|0|13||65.			
48	563	0.0030997935306262903	TGCAGTGCTAGAGATGTGGCTAGCGGAGACACAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(939.7)	TRBD2*00(35)	TRBJ2-3*00(231.1)	TRBC2*00(103.2)	321|3			
49	560	0.0030832759807295253	TGTGCCAGCAGTTCAGGGGGCGCGGACACCGGGGAGCTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-2*00(1054.8),TRBV6-3*00(1054.8)	TRBD1*00(35)	TRBJ2-2*00(245.6)	TRBC2*00(102.2)	327|3			
50	556	0.003061252580867171	TGCAGTGCTAGGGGGGGGGCAAGCGAGTCCTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV20-1*00(818)	TRBD1*00(30)	TRBJ1-1*00(243.7)	TRBC2*00(105.9)	321|3			
51	517	0.0028465244322092224	TGTGCCAGCAGCTTAGTGTGGCGGGAAGGGAGCACAGATACGCAGTATTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV11-2*00(1058.1)	TRBD2*00(30)	TRBJ2-3*00(242.5)	TRBC2*00(103.7)	330|3			
52	517	0.0028465244322092224	TGTGCCAGCAGCCAAAAGGGGACGCCTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-2*00(1059.1),TRBV6-3*00(1059.1)	TRBD1*00(30)	TRBJ2-1*00(237.8)	TRBC2*00(104.6)	327|3			
53	506	0.0027859600825877497	TGTGCCAGCAGCCCAAGCGGGGGAAGCTACAATGAGCAGTTCTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-2*00(1061),TRBV6-3*00(1061)	TRBD2*00(30)	TRBJ2-1*00(233.5)	TRBC2*00(104.8)	327|3			
54	498	0.00274191328286304 2	TGTGCCACCAGCAGCAGCTCATCCCCTGAAAAACTGTTTTTT	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV15*00(1056.6)	TRBJ1-4*00(217.5)	TRBC1*00(105.1)	327|341|364|0|14||70.0				
55	494	0.0027198898830006883	TGTGCCAGCAGTGAACTCTCTGGGGCCAACGTCCTGACTTTC	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TRBV6-1*00(1096.8)	TRBJ2-6*00(262.6)	TRBC2*00(106.7)	327|342|364|0|15||75.0				

VDJTools

Pre-processing
- frequency-based correction to eliminate erroneous clonotypes
- filtering non-functional clonotypes

Basic repertoire characteristics
- read counts
- number of clonotypes
- CDR3 length
- NDN size, convergence

Diversity estimation
- diversity indices: Chao1, Efron-Thisted, D50, Shannon-Wiener, Simpson

V(D)J segment usage
- the frequency of associated reads for each of V/J segments present in sample
- spectratype

Overlap analysis
- clonotype sharing for a pair of samples
- Jaccard index, Morisita-Horn index

Shared (public) clonotypes analysis
- Clonotypes with the same AA sequences

immunarch

Relative abundance analysis

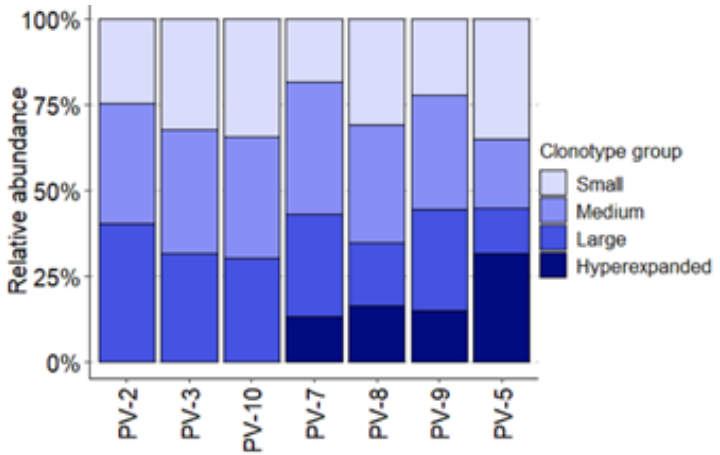
- the proportion of the repertoire occupied by the clones of a given size

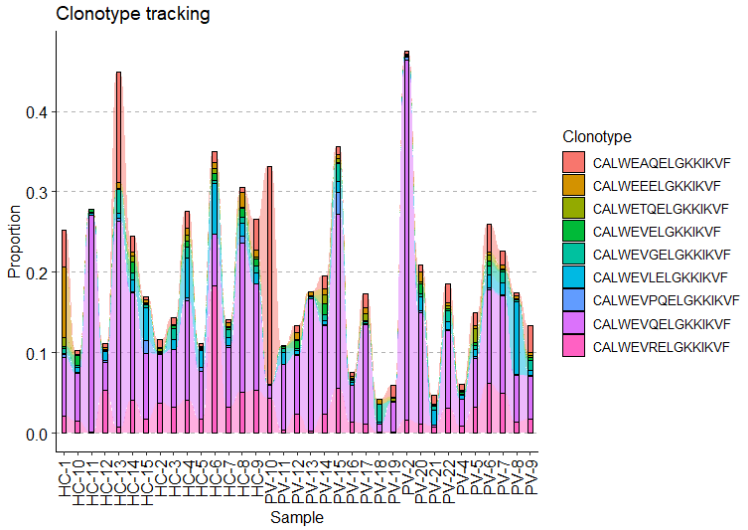
Tracking of clonotypes

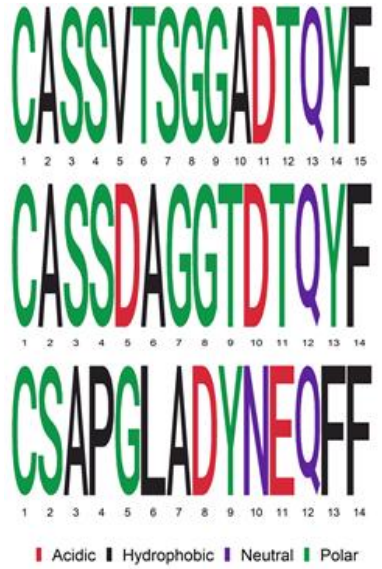
- segment usage
- The most frequent
- Public

Sequence motif visualisation

- Position probability matrix







Research contribution

New insights into the role of MAIT and γδ T lymphocytes in psoriasis

- characterise the molecular mechanisms shaping their phenotype and function
- a detailed characterisation of MAIT and γδ T lymphocytes at the subpopulation level
- a description of the previously unknown repertoire of T cell receptors of these lymphocyte populations in psoriasis

Thank you for your attention!

Discussion

Funding:
Croatian Science Foundation, „NGS analysis of MAIT and γδ T cell transcriptome: phenotype, function and TCR repertoire in the etiology of Psoriasis vulgaris” (UIP-2019-04-3494, PI: Assoc. Prof. Stana Tokić).

HrZZ
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