

# Highlights from IMS 20th meeting 2023

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Fattori Predittivi  
della Risposta

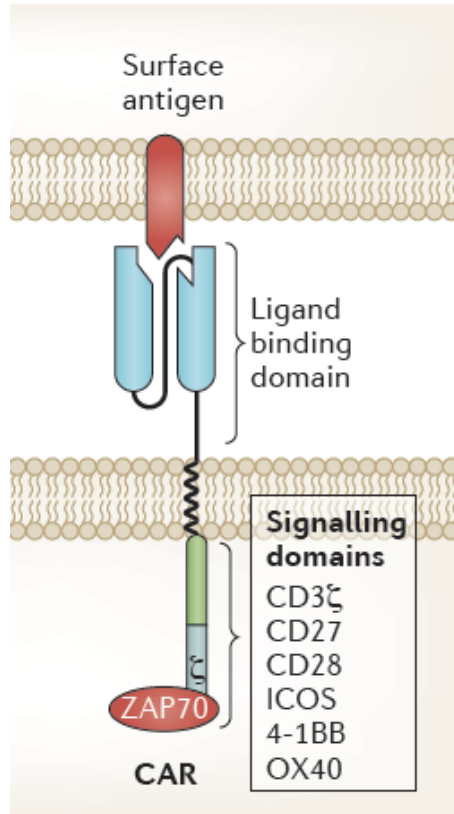
30-31 gennaio 2024

BOLOGNA, Royal Hotel Carlton

## Disclosures of Paola Neri

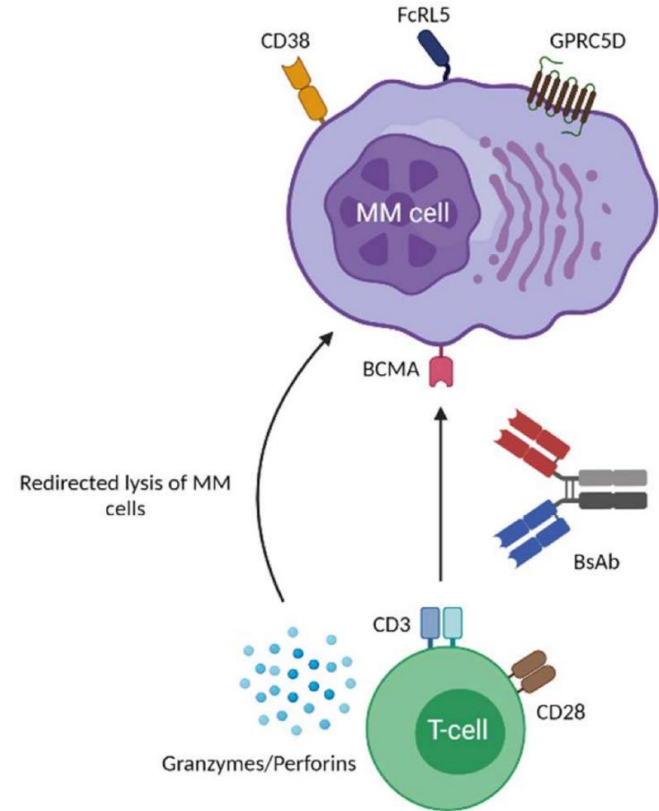
Company name	Research support	Employee	Consultant	Stockholder	Speakers bureau	Advisory board	Other
Sanofi			x			x	
Pfizer						x	
Janssen						x	
BMS			x			x	

# Chimeric Antigen Receptor T cells (CAR-T) and T cell engagers (TCE)



Fesnak A et al. Nat Rev Cancer 2016

- BCMA
- GPRC5D
- FcRH5
- CD38
- SLAMF7
- BCMA+TACI
- BCMA+GPRC5D

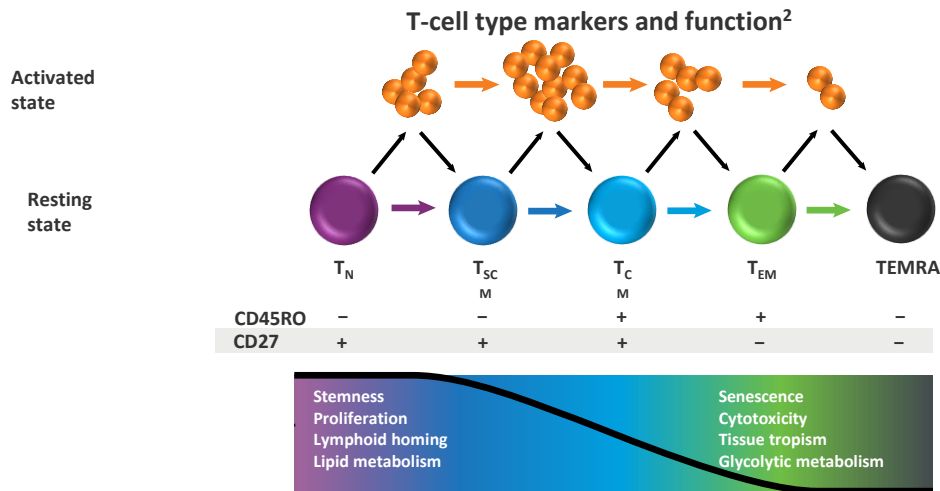


Hosny M et al, Journal of Clinical Medicine 2021

CAR-T and T cell engagers (TCE) have demonstrated unprecedented efficacy in RRMM patients. However, the cellular and molecular predictors of response as well as the mediators of resistance remain elusive.

# T-Cell Phenotypes as a Determinant of Clinical Activity of CAR-T

- As T cells differentiate, proliferation increases before decreasing as memory function and, subsequently, effector function increase.
- Preferential CAR+ CD8 T-cell expansion and enrichment of CAR+ T cells with memory phenotypes have been associated with enhanced CAR-T cell clinical activity<sup>1</sup>.



CAR, chimeric antigen receptor; T<sub>CM</sub>, central memory T cell; T<sub>EM</sub>, effector memory T cell; TEMRA, terminally differentiated T cell; T<sub>N</sub>, naive T cell; T<sub>SCM</sub>, stem cell memory T cell.

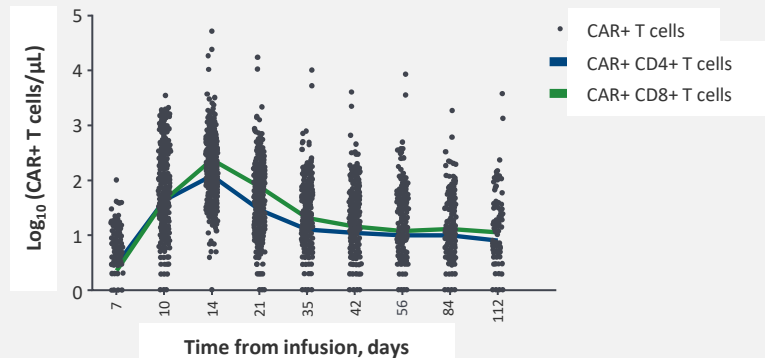
1. Cohen AD et al, J Clin Invest 2019

2. Adapted from Springer Nature: Springer Nature, (2015). Harnessing Stem Cell-Like Memory T Cells for Adoptive Cell Transfer Therapy of Cancer. In: Ascierto, P., Stroncek, D., Wang, E. (eds) Developments in T Cell

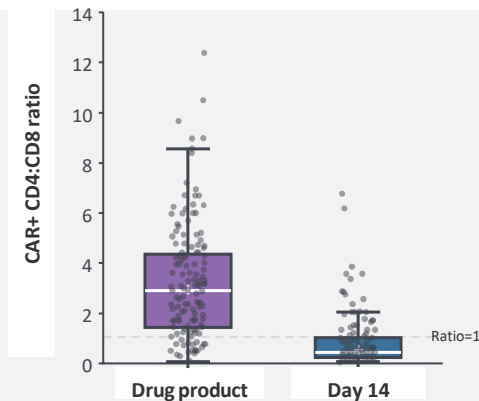
# CARTITUDE-4: Preferential Expansion of CAR+ CD8 T Cells Post Infusion

- Both CAR+ CD4 and CAR+ CD8 T cells expanded after infusion
- Consistent with CARTITUDE-1,<sup>1</sup> in CARTITUDE-4 CAR+ CD8 T cells expanded more than CAR+ CD4 T cells in blood
  - CAR+ CD4:CD8 T cells ratios were lower in blood at  $\sim T_{\max}$  than in drug product ( $P < 0.0001$ )

CAR+ CD4 and CAR+ CD8 T-cell levels



CAR+ CD4:CD8 T-cell ratio

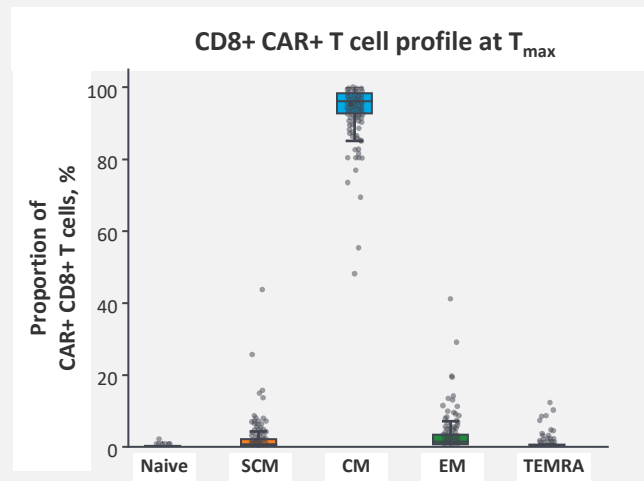
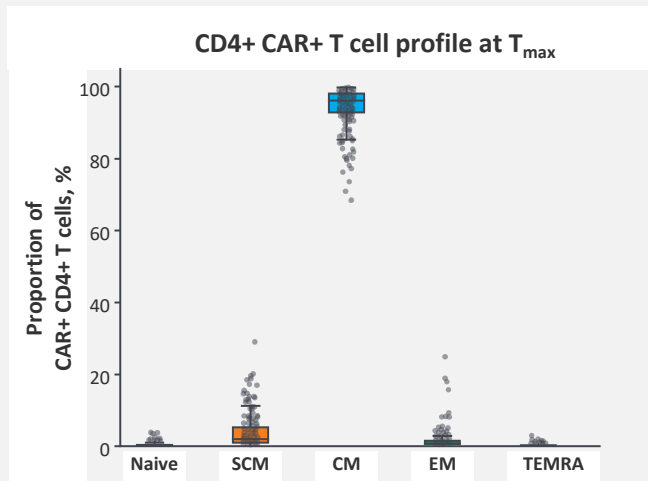


Preferential CAR+ CD8 T-cell expansion has been suggested to be correlated with greater clinical activity<sup>1</sup>



# CARTITUDE-4: CAR+ T Cells at Peak Expansion Primarily Have a Central Memory Phenotype

- T cells with a central memory phenotype were dominant in the CAR+ CD4+ and CD8+ compartments at T<sub>max</sub>

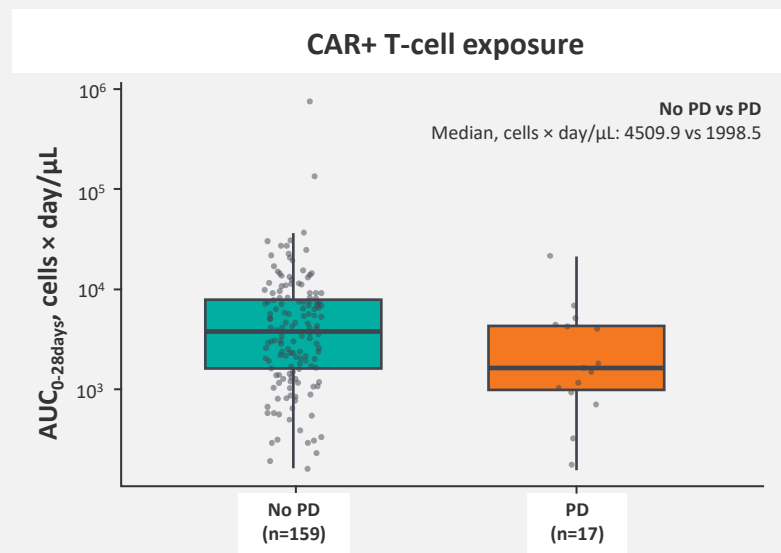
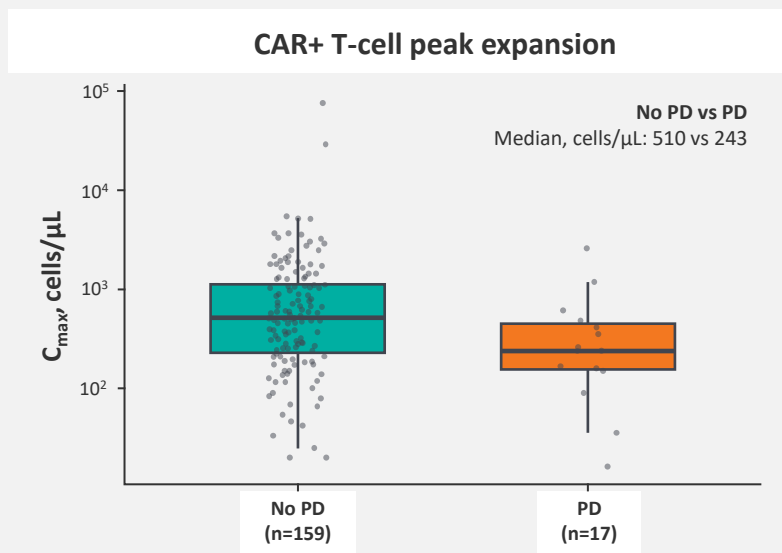


**Enrichment with T cells possessing memory phenotypes is suggested to enhance clinical responses and durations of response<sup>1-3</sup>**



# CARTITUDE-4: CAR-T Cell Expansion and Exposure Are Not Associated With Disease Progression

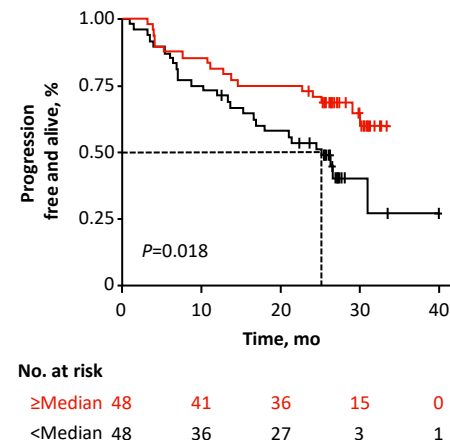
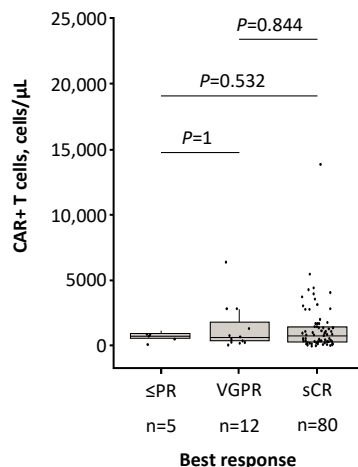
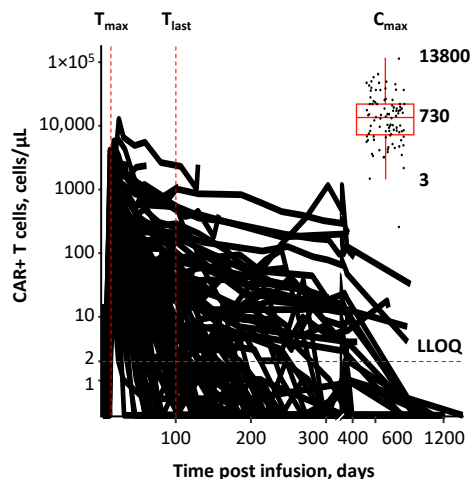
- CAR+ T-cell expansion ( $C_{max}$ ) and exposure ( $AUC_{0-d28}$ ) comparable in patients with progression vs those without



$AUC_{0-d28}$ , area under the curve from day 0 to day 28 post infusion; CAR, chimeric antigen receptor;  $C_{max}$ , maximal concentration; PD, progressive disease.



# Ciltacabtagene Autoleucel: Longer PFS Was Observed in Patients With a Higher Effector to Target Ratio (or CAR+ T cell to sBCMA Ratio)



Variable cilta-cel expansion and persistence<sup>a</sup>

Cilta-cel peak expansion ( $C_{max}$ ) does not associate with best response<sup>b</sup>

Patients with higher effector to target ratio had significantly longer PFS<sup>c</sup>

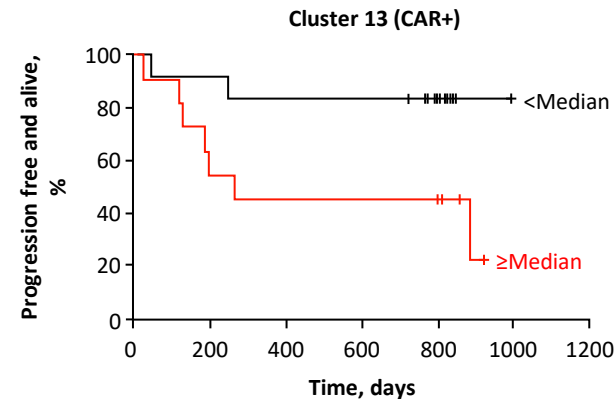
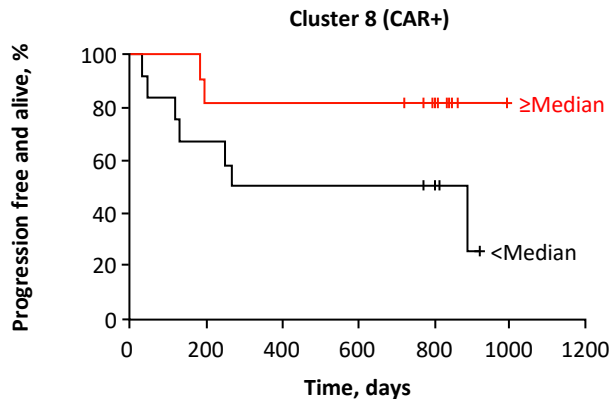
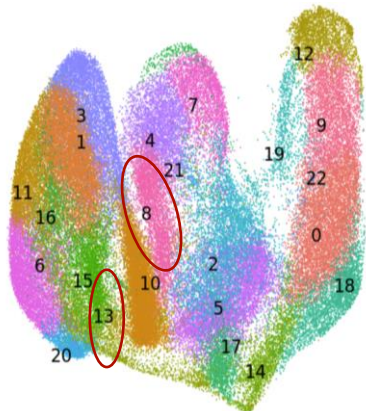
<sup>a</sup> $C_{max}$  was 730 cells/μL (range, 3–13800),  $T_{max}$  was 14 days (range, 10–56), and  $T_{last}$  was 100 days (range, 20–912). <sup>b</sup>P value determined using Wilcoxon test. <sup>c</sup>To assess the significance of effector to target ratio, CAR+ T cells at  $C_{max}$  were normalized to baseline tumor burden utilizing sBCMA. Best response and PFS were assessed by independent review committee.

CAR, chimeric antigen receptor;  $C_{max}$ , maximum observed concentration of CAR+ T cells in blood; LLOQ, lower limit of quantification; PR, partial response; sBCMA, soluble BCMA; sCR, stringent complete response;  $T_{last}$ , actual sampling time (days post infusion) of last measurable concentration of CAR+ T cells; VGPR, very good PR.



# Ciltacabtagene Autoleucel Longer PFS Was Associated With a CAR+CD8+ Stem Cell–Like Phenotype in the Drug Product

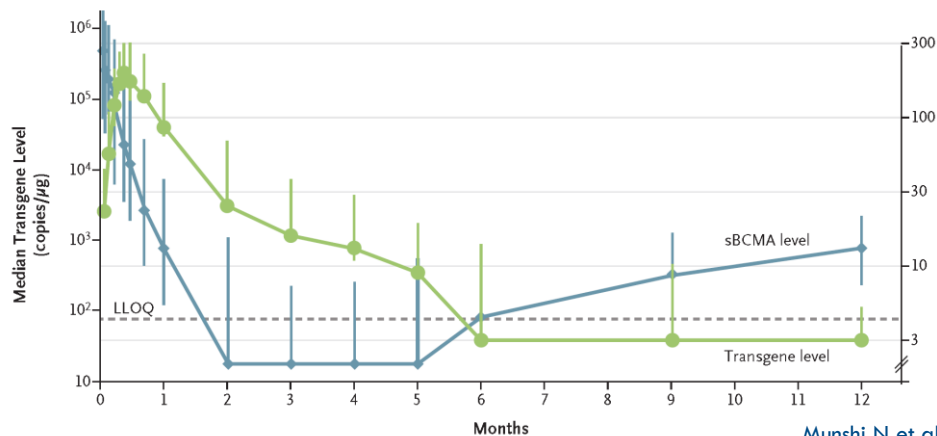
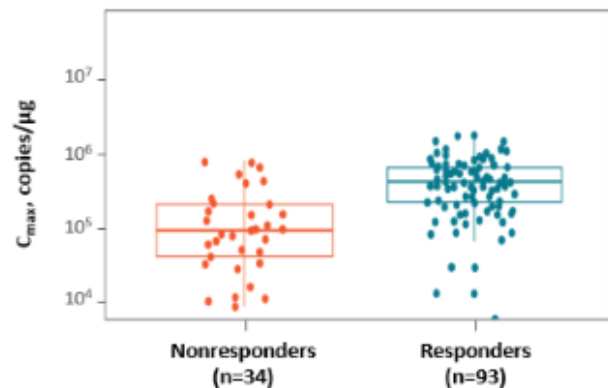
Cluster	Hazard ratio	P value	Marker	Phenotype
8	0.62	0.032	CD8+TCF7+LEF1+CCR7+	CAR+CD8+ stem cell–like T cells with ability to proliferate into T <sub>cm</sub> and T <sub>em</sub>
13	1.62	0.006	CD4+FOXP3+	CAR+CD4+ Treg cell–like phenotype



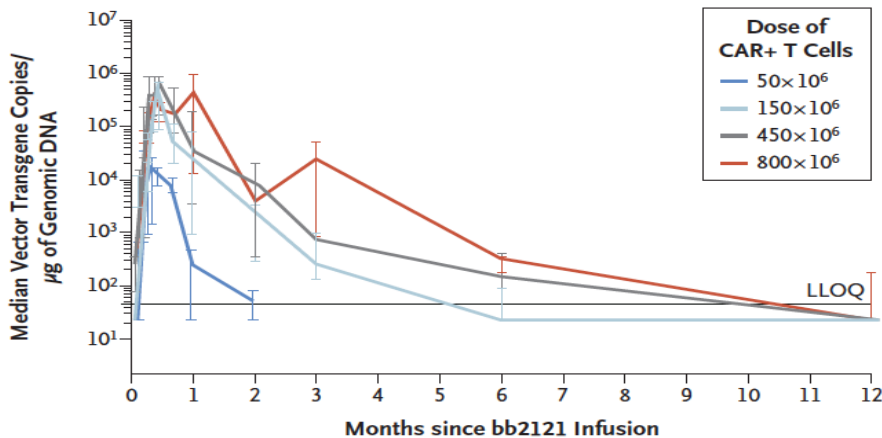
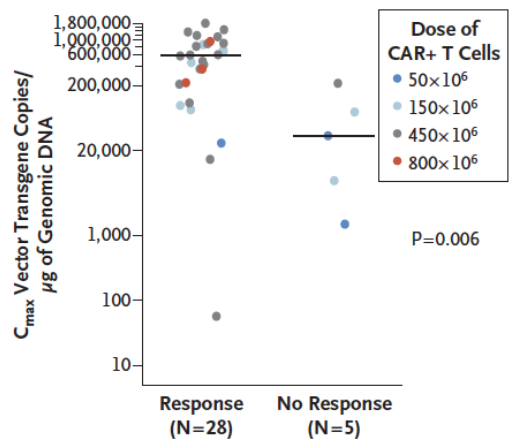
Longer PFS was directly associated with a CAR+CD8+ T-stem cell–like phenotype and inversely correlated with a CAR+CD4+ Treg cell–like phenotype in the drug product

# CAR T cells expansion (Cmax and AUC) correlate with clinical response with Ide-Cel

Ide-cel Peak Exposure in Responders Versus Nonresponders



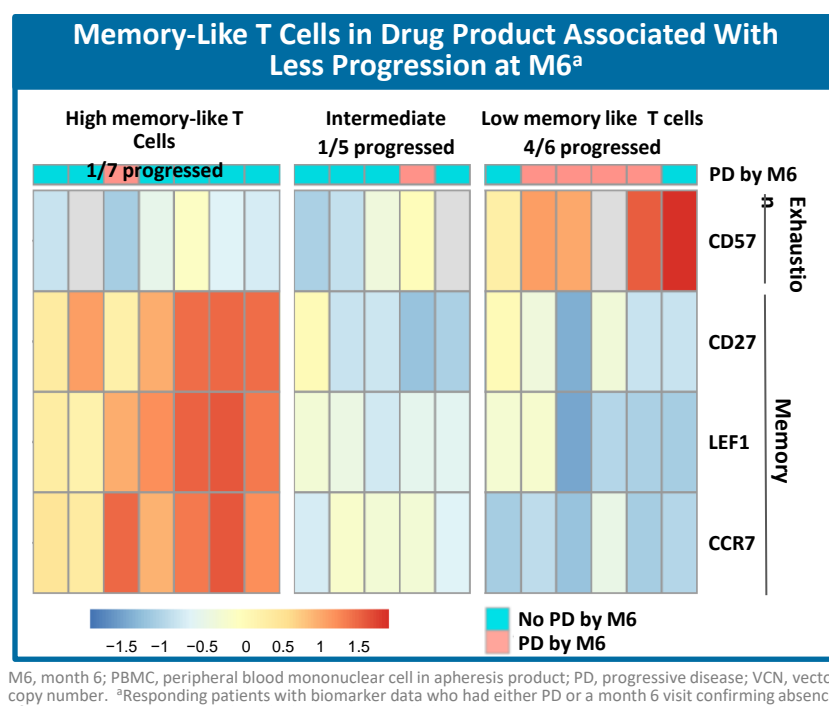
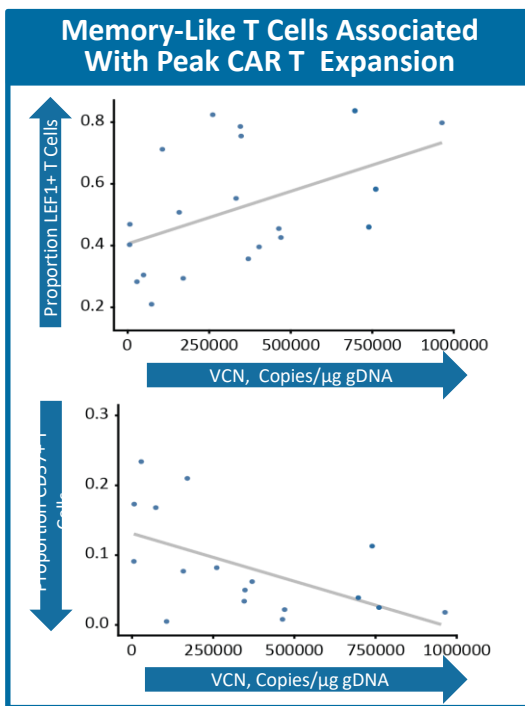
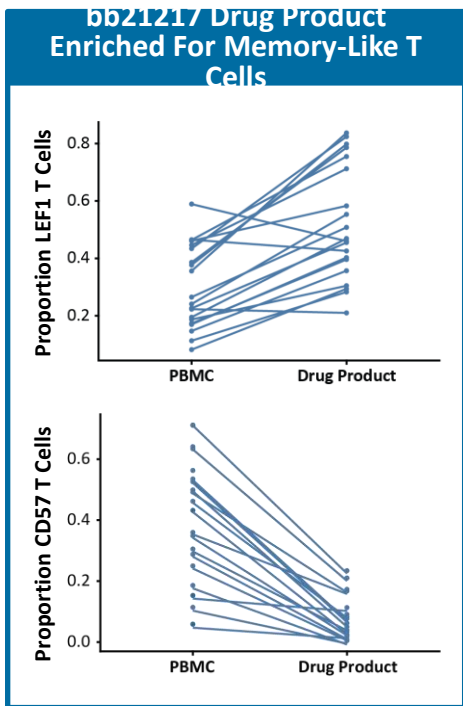
Munshi N et al, NEJM 2021



Raje N et al. N Engl J Med 2019

# Enrichment for Memory-Like T Cells Is Associated With Robust CAR T Expansion and Less Progression by M6

- Patients with a higher proportion of memory-like T cells in bb21217 drug product have significantly better peak expansion.
- A higher proportion of memory-like T cells is associated with numerically less progression by M6.



M6, month 6; PBMC, peripheral blood mononuclear cell in apheresis product; PD, progressive disease; VCN, vector copy number. <sup>a</sup>Responding patients with biomarker data who had either PD or a month 6 visit confirming absence of PD, 1 patient with continued stable disease at M6 included.



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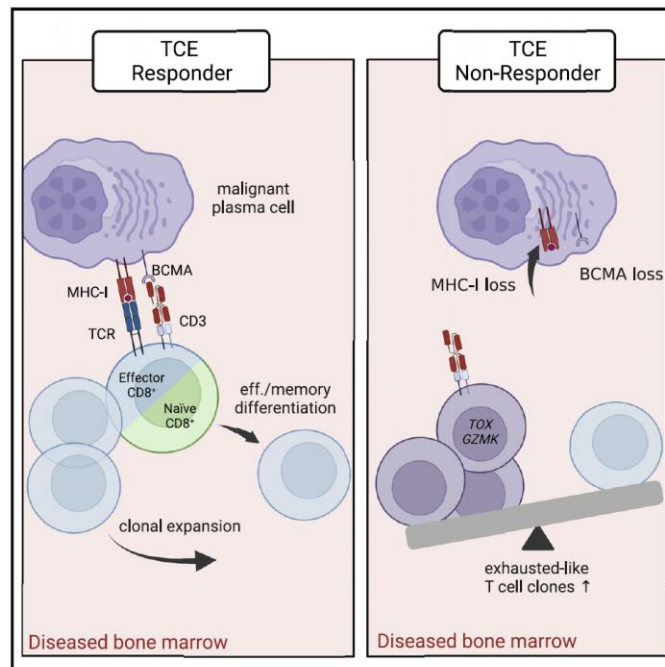
# Cancer Cell

## The pre-existing T cell landscape determines the response to bispecific T cell engagers in multiple myeloma patients



HEIDELBERG  
UNIVERSITY  
HOSPITAL

### Graphical abstract



### Authors

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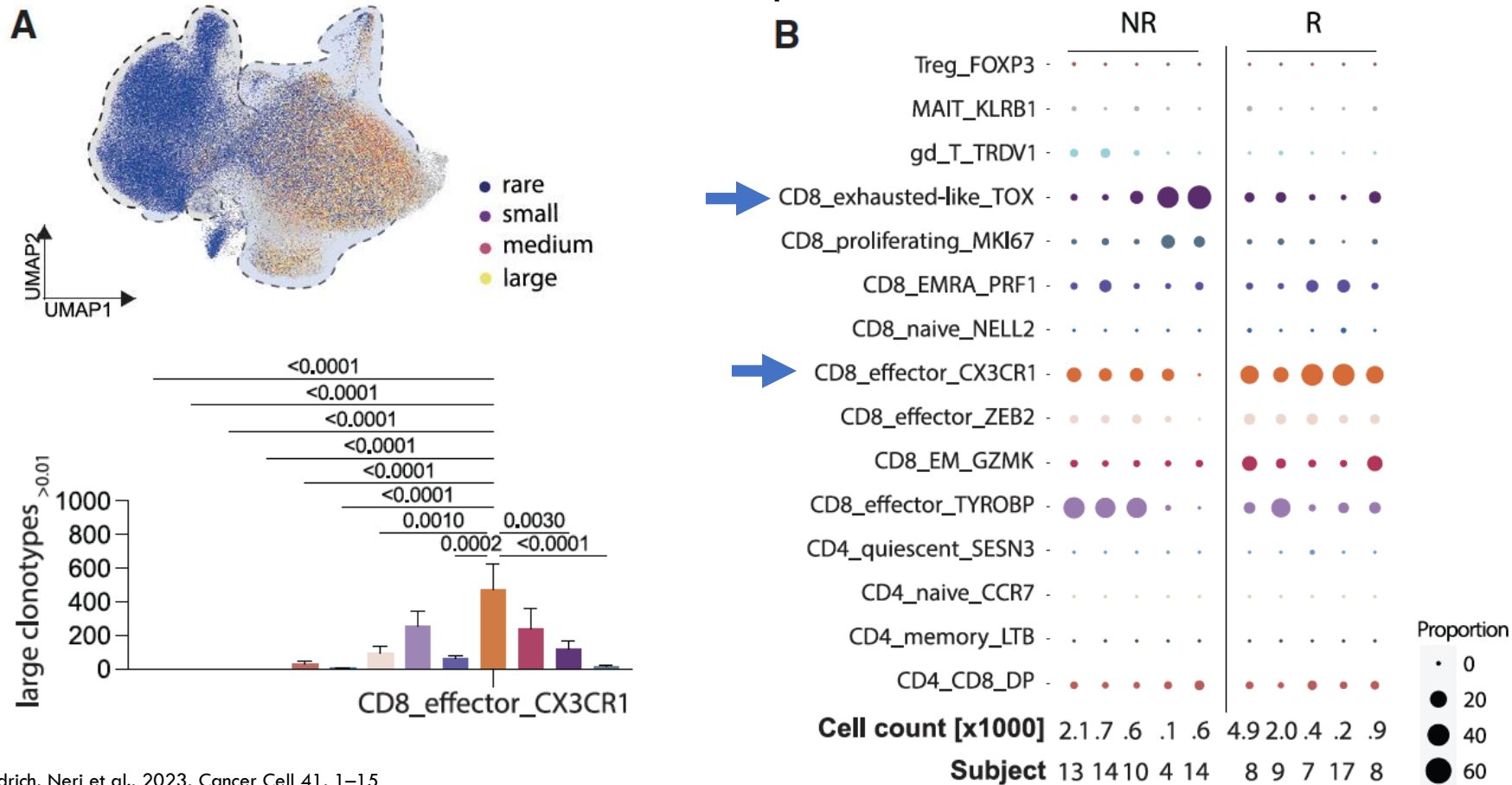
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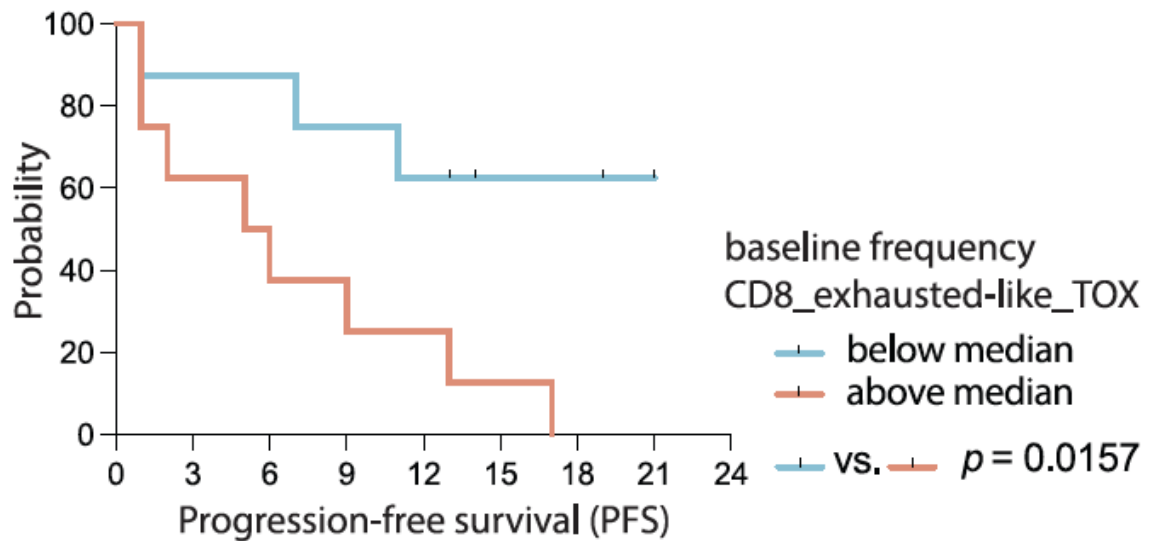
### In brief

Bispecific T cell engagers (TCEs) have shown promise in the treatment of various cancers, but their mode of action in humans is elusive. Providing new insight into immunological mechanisms, Friedrich et al. identify how T cells in multiple myeloma patients respond to TCEs according to their cell state and link inter-individual differences in the immune repertoire to clinical response.

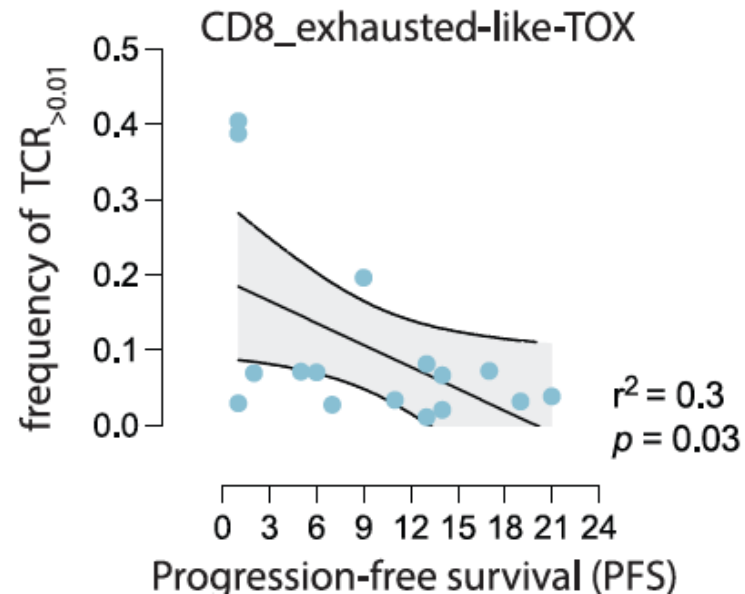
# Abundance of exhausted-like T cell clones is associated with clinical response failure



# Proportion of pre-existing exhausted CD8+ clonotypes pre-therapy is significantly increased in BCMAxCD3 TCE non-responder patients

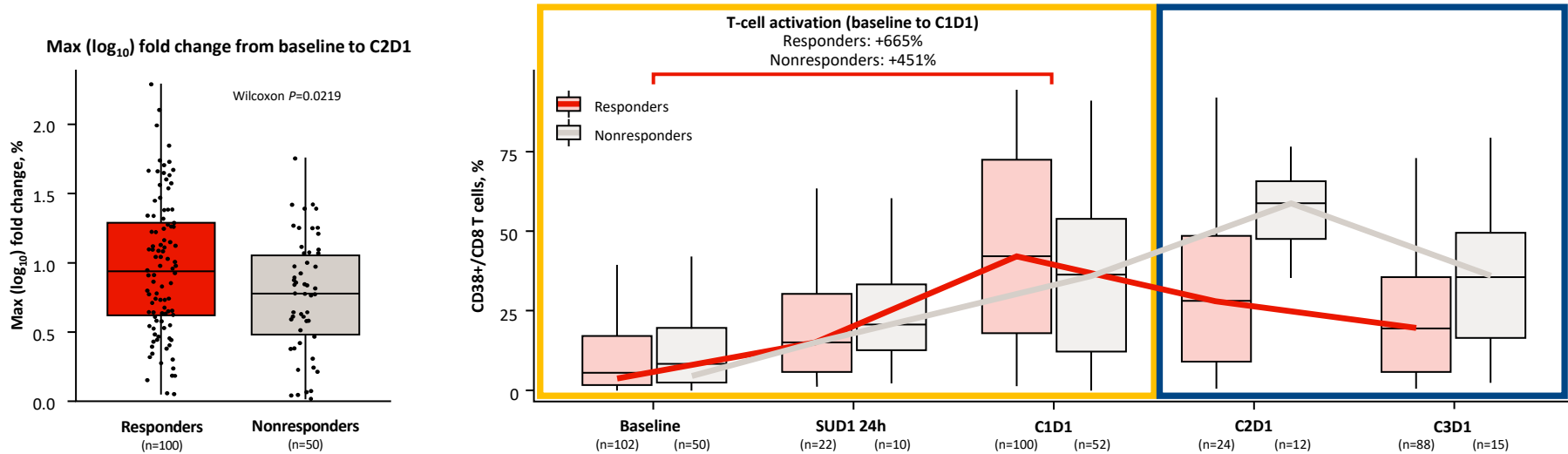


Number at risk (censored)									
—	8	7	7	6	5	4(2)	2(2)	1(4)	median PFS not reached
—	8	5	4	3	3	2	0	0	median PFS 5.5 months



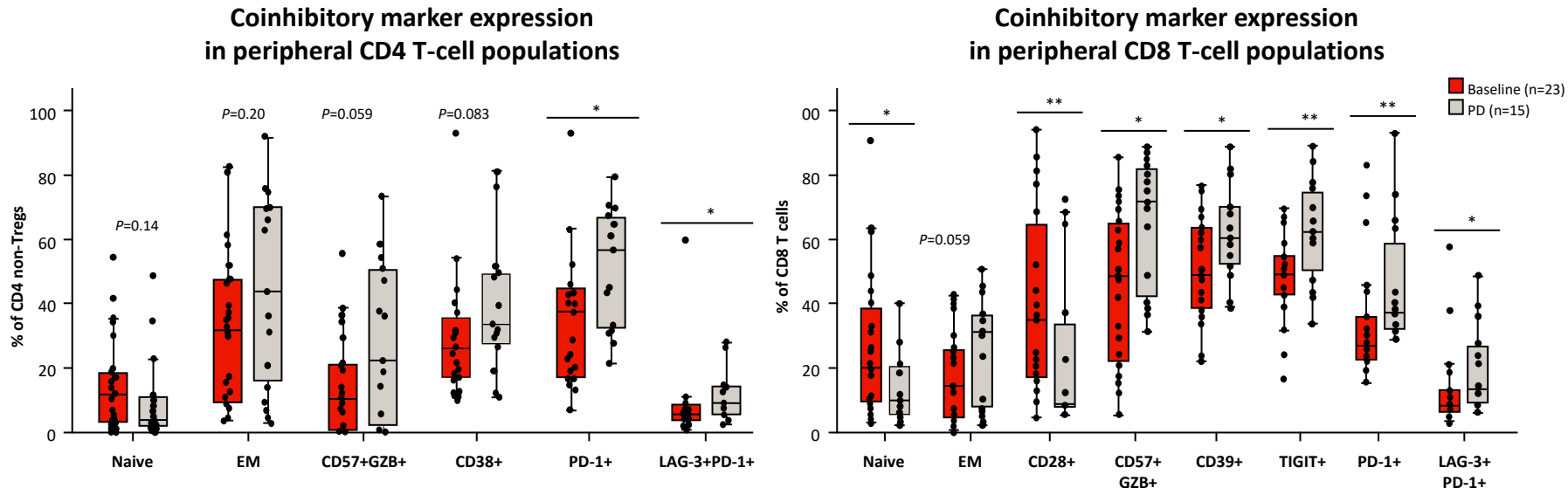
# Response Was Associated With Greater T-Cell Activation in the First Treatment Cycle Compared with Non responders

## Greater early expression of CD38 on CD8 T cells in peripheral blood in responders



- Patients responding to teclistamab exhibited greater, transient T-cell activation early in the first treatment cycle, indicated by a greater maximum fold change in induction of CD38 on CD8 T cells in peripheral blood
- T-cell activation in responders was early, reaching peak CD38 induction on CD8 T cells at C1D1 (orange box), whereas, T-cell activation was delayed in non responders, reaching peak CD38 induction at C2D1 (blue box)

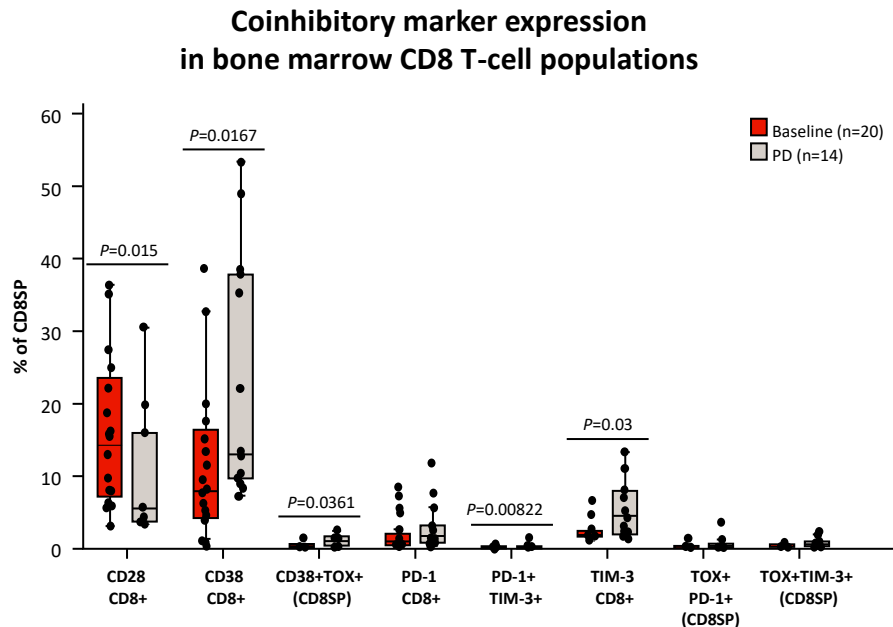
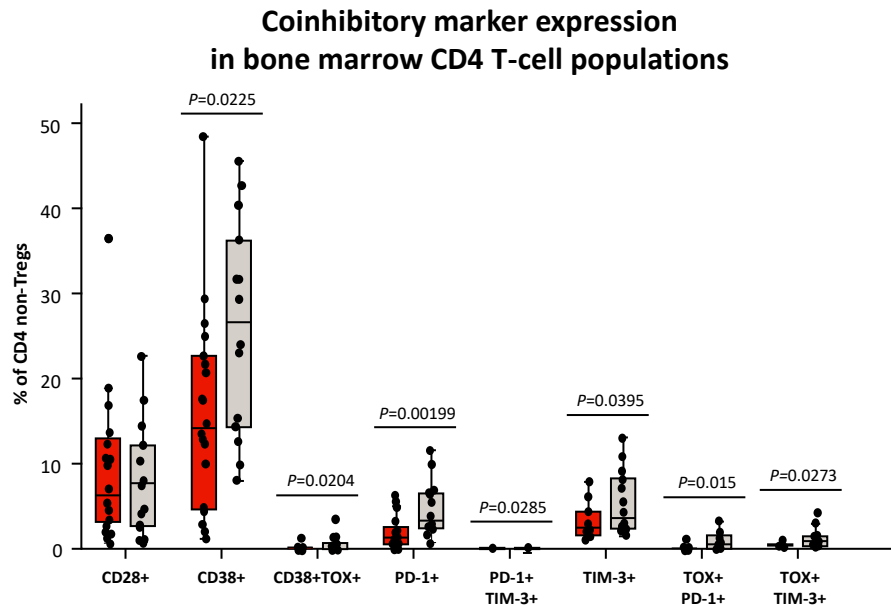
# Relapse Was Associated With Higher Proportions of T Cells Expressing Exhaustion Markers, Checkpoints, at PD vs Baseline in the PB



- CyTOF analysis in peripheral blood showed trends for lower frequencies of naive T cells and higher frequencies of differentiated EM CD4 and CD8 T-cell subsets at relapse vs baseline
- Significantly higher proportions of exhausted T cells at relapse were observed, indicated by increased frequencies of CD4 or CD8 T cells expression and co-expression PD-1, LAG-3, TIGIT, CD39, and CD57/GZB, as well as reduced frequencies of costimulatory CD28 and CD8 T cells



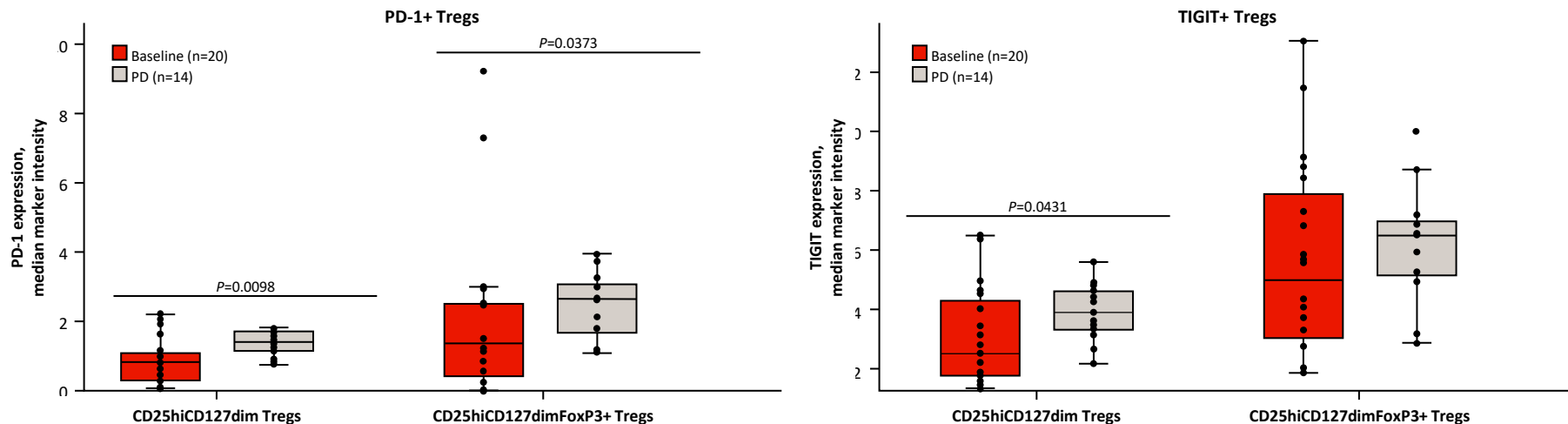
# Relapse Was Associated With Higher Proportions of T Cells Expressing Exhaustion Markers, Checkpoints, at PD vs Baseline in the BM



- CyTOF analysis in bone marrow showed that compared with baseline, patients who relapsed had lower CD28 expression on CD8 T cells and significantly higher proportions of CD4 and CD8 T cells expressing and co-expressing checkpoints as well as T-cell exhaustion markers

# Relapse Was Associated With Higher Expression of Coinhibitory Receptors on Treg Populations at PD vs Baseline

## Higher expression of PD-1 and TIGIT on Tregs at relapse than baseline



- CyTOF analysis in bone marrow showed that expression of PD-1 and TIGIT, which contributes to immune suppressive potential, was significantly higher at PD compared with baseline across CD25hiCD127dim and/or CD25hiCD127dimFoxP3+ Tregs in patients who relapsed

# Talquetamab (MonumentAL-1): Greater T-cell Activation in Responders vs Non responders in Cycle 1

## Longitudinal data

Parameter, <sup>a</sup> median (%)	QW		Q2W	
	R	NR	R	NR
CD38+/CD8+ T cells	8.41	0.64	7.32	0.79
LAG-3+/CD8+ T cells	5.63	0.56	6.12	0.57
PD-1+/CD8+ T cells	2.16	0.25	2.26	0.36
PD-1+LAG-3+/CD8+ T cells	9	0.77	11.5	0.78
PD-1+TIM-3+/CD8+ T cells	9.75	0.9	12.52	0.95
TIM-3+/CD8+ T cells	5.94	0.65	8.64	0.81



- Peak induction of expression of markers on CD8+ T cells in cycle 1 = activation

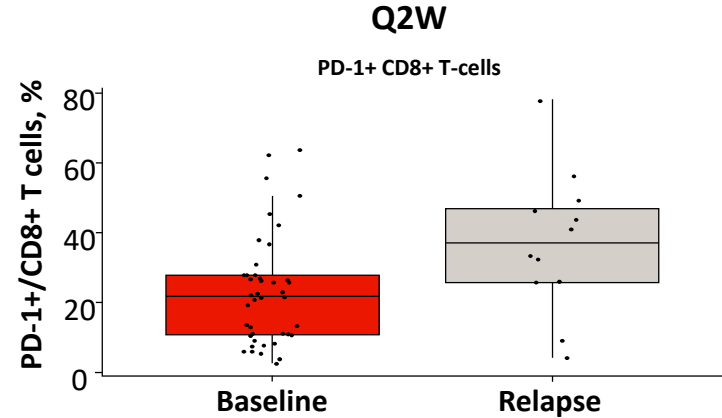
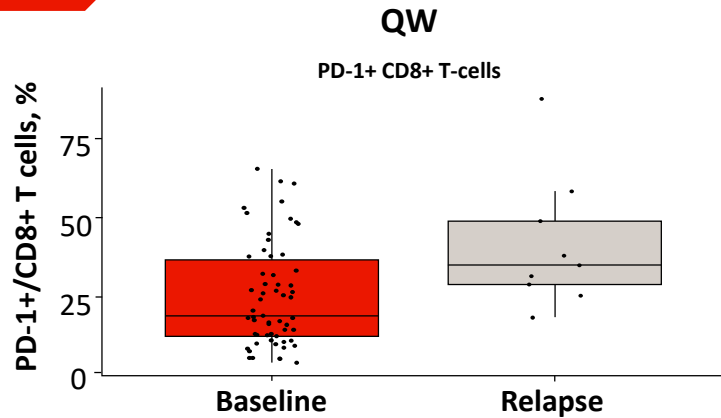
Max-fold change was measured at cycle 1 and corresponds with T-cell activation, indicated by maximum induction of markers at any point in cycle 1 relative to baseline.

<sup>a</sup>Evaluated using flow cytometry.

NR, nonresponders; Q2W, every other week; QW, weekly, R, responders

# MonumentAL-1: Exhausted T-cell Phenotype at Relapse

Relapse data



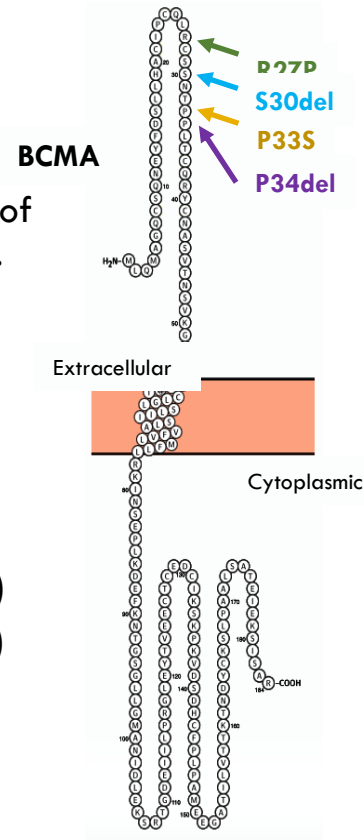
- Patients who relapsed had significantly higher frequencies of PD-1-expression CD8+ T cells compared with baseline across cohorts
- Across cohorts, higher frequencies of LAG-3-, TIM-3-, and PD-1/LAG-3-expressing CD8+ T cells and lower counts of CD3+ T cells were also observed in patients who relapsed compared with baseline (data not shown)

# Antigen escape is a tumor intrinsic mechanism of resistance to targeted immunotherapies: BCMA

By combining bulk WGS and scCNV analysis in 18 RRMM patients we assessed the mechanisms of MM antigen escape to targeted immunotherapies and reported antigen drifting/loss in ~ 30%<sup>1</sup>.

- 5 distinct genomic mechanisms leading to BCMA antigen escape:

Diploid 16p	Focal biallelic loss of <i>TNFRSF17</i>	
Subclone (<1%) with <i>TNFRSF17</i> biallelic loss		Clonal <i>TNFRSF17</i> biallelic loss
Diploid 16p	16p monoallelic loss + mut. <i>TNFRSF17</i> c.R27P point mutation	
	16p monoallelic loss + mut. <i>TNFRSF17</i> in-frame deletion (p.Ser30del)	
	16p monoallelic loss + mut. <i>TNFRSF17</i> in-frame deletion (p.Pro34del)	



# Antigen escape is a tumor intrinsic mechanism of resistance to targeted immunotherapies: GPRC5D

## GPRC5D biallelic loss

- Post TCE:

Clonal convergence → 5 cases of MM relapse with biallelic genomic events on GPRC5D (biallelic deletions or monoallelic deletion and mutations) <sup>1,2</sup>.

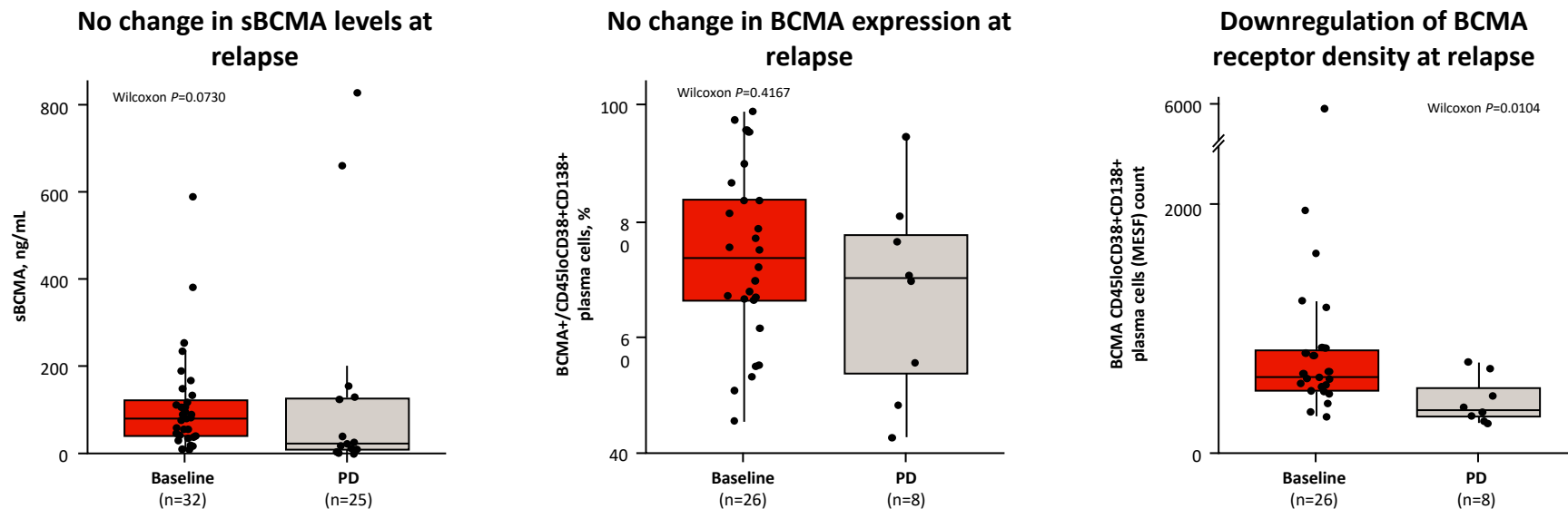
Epigenetic silencing: 2 patients with loss of chromatin accessibility at GPRC5D gene locus<sup>2</sup>.

- Post anti-GPRC5D CAR T:

GPRC5D loss or reduction of surface antigen expression in 6/6 patients post anti-GPRC5D CAR T<sup>3,4</sup>.

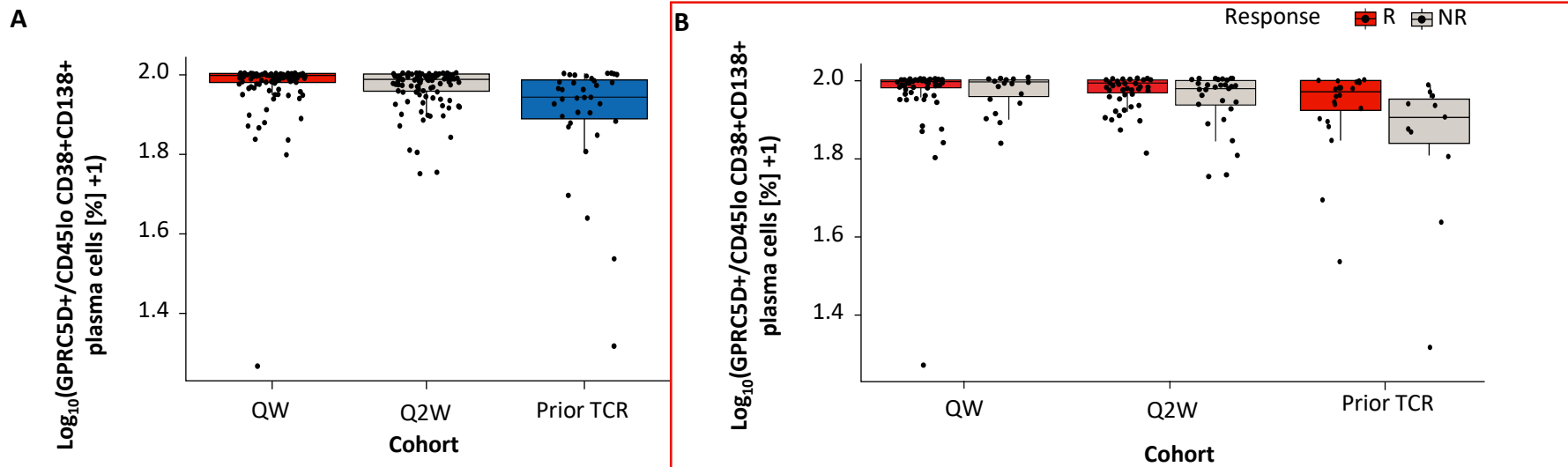
1. Lee H et al. Nat Med. 2023;29:2295-2306
2. Derrien J et al. Nat Cancer 2023; 4: 1536-1543
3. Mailankody S et al N Engl J Med 2022; 387:1196-1206
4. Mi X et al. N Engl J Med 2023; 389:1435-1437

# Majestic 1: No change in BCMA Expression but Reduction of BCMA Receptor Density Was Observed at Relapse in Patients Initially Responding to Teclistamab



- Among patients who initially responded to teclistamab then progressed and had evaluable samples at either baseline or disease progression (PD; small n), there were no significant changes in sBCMA levels or frequency of BCMA+ plasma cells in bone marrow at PD relative to baseline; however, reduction in BCMA receptor density was observed at PD
  - Similar results were observed in patients with matched baseline and PD samples

# MonumenTAL-5: High GPRC5D Expression at Baseline but No Correlation with Response



- GPRC5D was highly expressed on multiple myeloma cells in each cohort; generally, no correlations were observed between baseline GPRC5D expression and response
  - A trend of lower GPRC5D expression in non responders vs responders was observed in the prior TCR cohort
- Additional analyses showed that GPRC5D remained highly expressed at relapse in QW and Q2W cohorts, suggesting that downregulation of GPRC5D was not a mechanism at relapse (Supplement)



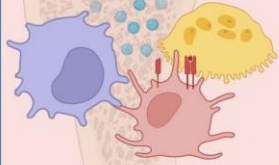
# Summary

## B. Mechanisms of Resistance

### Tumor microenvironment

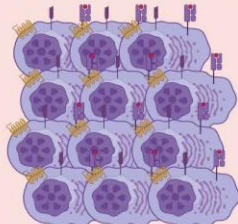
#### Immunosuppressive cells & cytokines

Osteoclasts, tumor associated macrophages, plasmacytoid DC, myeloid-derived suppressor cells  
IL-6, IL-10, TGF- $\beta$ , IDO



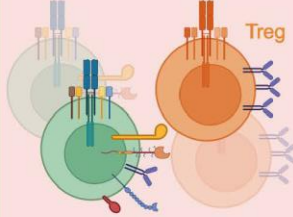
### Tumor intrinsic

**Tumor Biology**  
BMPC >50-60%  
High risk cytogenetics  
R-ISS stage III  
Extramedullary disease

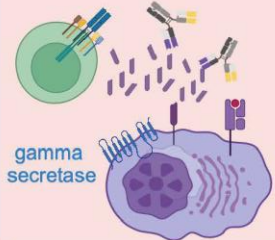


### T cell dysfunction

**T cell exhaustion**  
Checkpoint receptor expression  
CD4+ regulatory T cells (Treg)  
Lack of clonotypic expansion



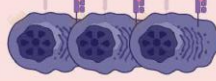
### Soluble BCMA sink



### MHC downregulation

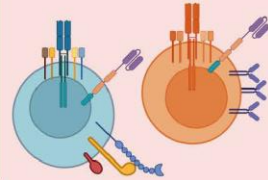


### Target antigen loss



### CAR T exhaustion

Terminal differentiation  
Treg in CAR T product  
Lack of persistence



Immune fitness and T-cell function influence response to CAR-T and TCE

NR: Reduced population of  $T_{SCM}$ ,  $T_{CM}$

NR: Expansion of T reg and/or exhausted T cells  $T_{EX}$  (CD57<sup>+</sup>, TOX<sup>+</sup>, CD28<sup>-</sup>, PDCD1<sup>+</sup>, TIGIT<sup>+</sup>, LAG3<sup>+</sup>)

Antigen escape (biallelic loss, monoallelic loss coupled with extracellular domain mutations) is a mechanism of resistance (more frequent post TCE)

NR: Loss of MHC I surface protein expression on MM cells  
Composition of myeloid/DC compartment (immunosuppressive environment)

Primary resistance to T-cell based therapies

→ High serum soluble BCMA

→ High disease burden and EMD

Defining plasma cells genomic alterations coupled with the immune profiling will help to identify patients with the highest likelihood of respond to these therapies and individualize therapeutics.