

# Highlights from IMW 2019

19-20 novembre 2019  
Bologna  
Royal Hotel Carlton

Roberto Ria

## Ruolo del microambiente midollare

*Coordinatore Scientifico*  
Michele CAVO

*Comitato Scientifico*  
Mario BOCCADORO  
Michele CAVO  
Maria Teresa PETRUCCI

## Disclosures for Roberto Ria M.D.



- ✓ **Grant/Research Support:** no disclosure.
- ✓ **Speaker's Bureau:** BMS, CSL Behring, Celgene, Italfarmaco, Janssen Cilag.
- ✓ **Consultant:** BMS, CSL Behring, Celgene, Italfarmaco, Janssen Cilag, Octapharma.
- ✓ **Major Shareholder:** no disclosure.
- ✓ **Other:** no disclosure.

I will be discussing "off-label" uses of the following medications: none

# Dhodapkar Bone marrow microenvironment and MM progression



## Microenvironment

 Growth restricting signals  
 Growth permissive signals



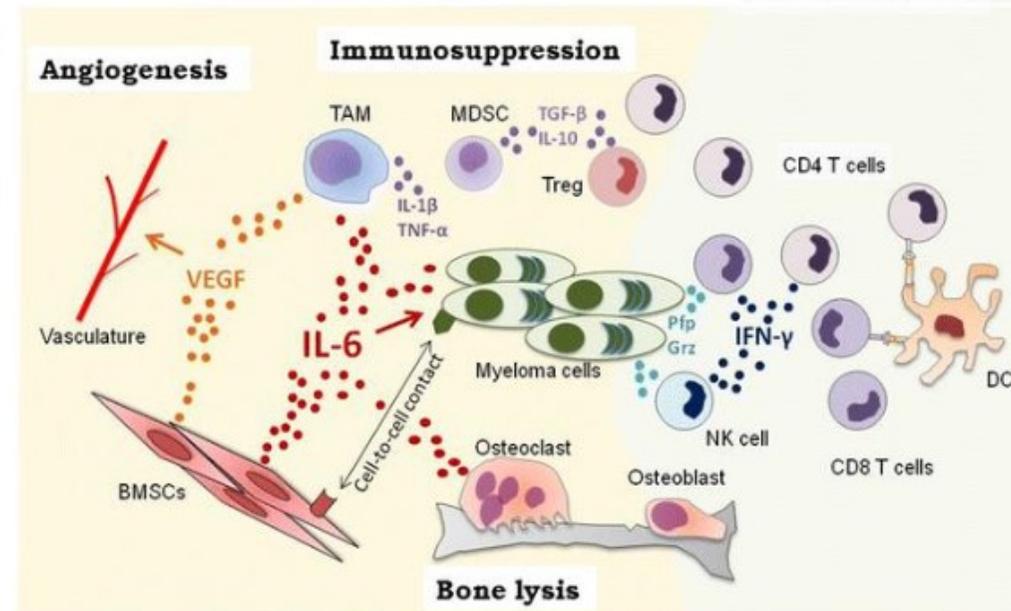
## Paradox:

Many MM genomic alterations originate in MGUS phase.

Yet--Long periods of clinical stability in many MGUS patients.

Tumor supporting

Tumor suppressive



Dhodapkar, Blood 2017  
Guillerey et al. CellMolLifeSci 2016

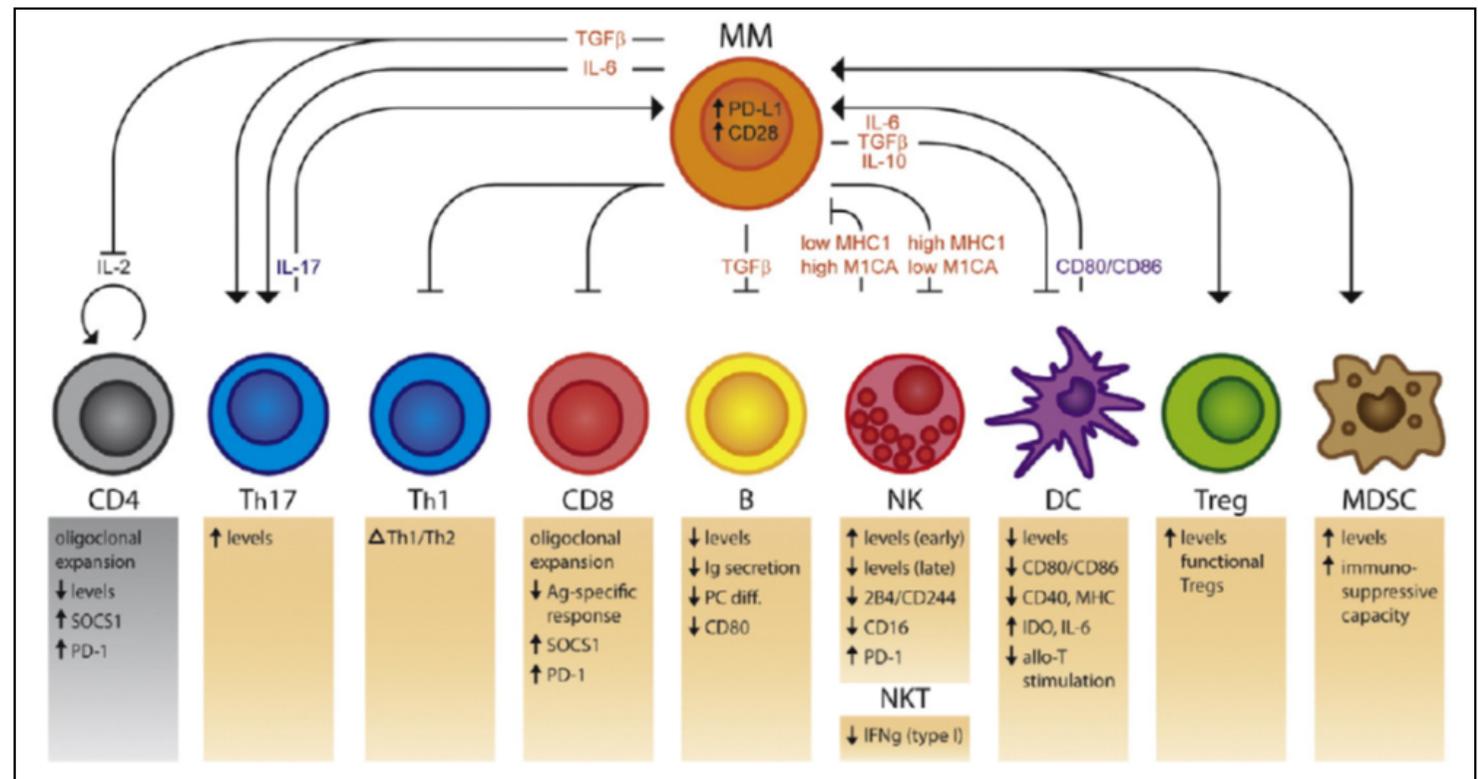
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# THE IMMUNE SYSTEM: Interaction between plasma cells and the host immune system



Contents lists available at ScienceDirect  
 Biochimica et Biophysica Acta  
 ELSEVIER  
 journal homepage: www.elsevier.com/locate/bba  
 BBA  
 REVIEW IN  
 Cancer  
 Review  
 Cellular immunotherapy in multiple myeloma: Lessons from preclinical models  
 M. Binsfeld<sup>a</sup>, K. Fostier<sup>b</sup>, J. Müller<sup>a</sup>, F. Baron<sup>a,c</sup>, R. Schots<sup>b</sup>, Y. Beguin<sup>a,c</sup>, R. Heusschen<sup>a,\*</sup>, J. Caers<sup>a,c,1</sup>



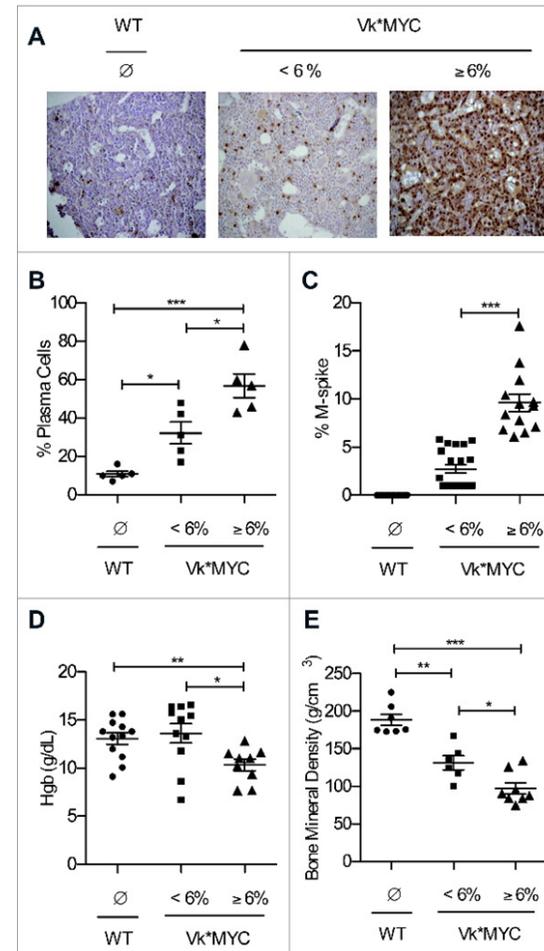
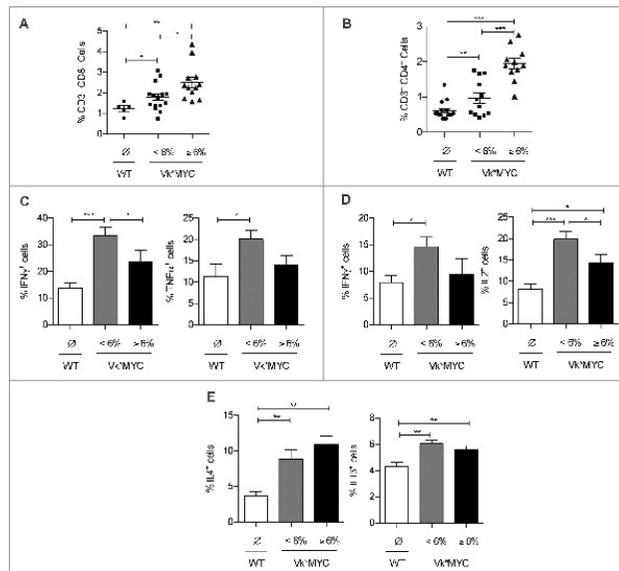
# THE IMMUNE SYSTEM: Role in SMM progression to MM



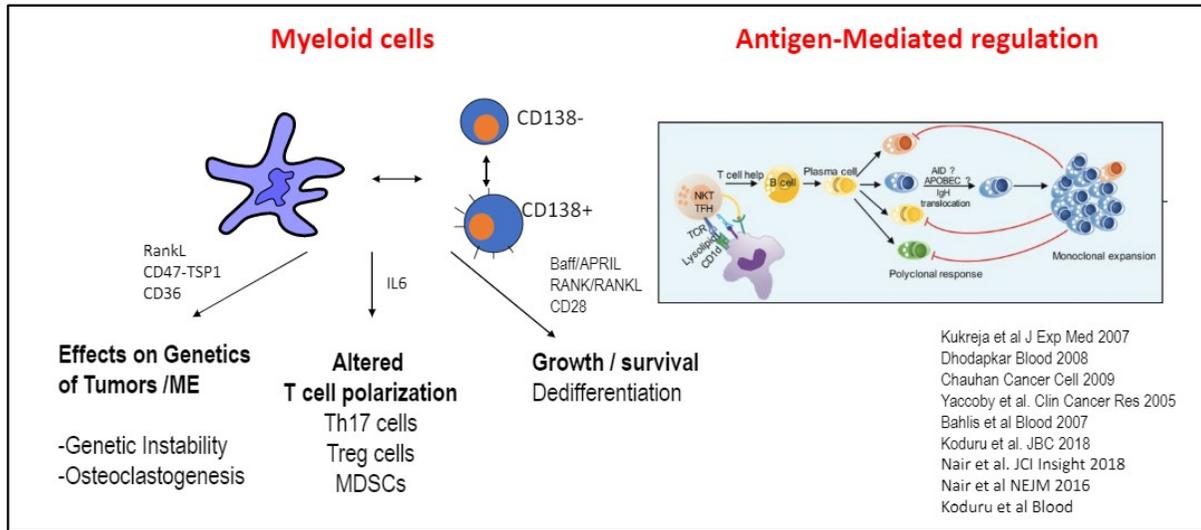
ORIGINAL RESEARCH  
 Oncoimmunology 4(5), e1100850; June 2015; Published with license by Taylor & Francis Group, LLC

**Modifications of the mouse bone marrow microenvironment favor angiogenesis and correlate with disease progression from asymptomatic to symptomatic multiple myeloma**

Arianna Calcinotto<sup>1,2</sup>, Maurizio Ponzoni<sup>1</sup>, Roberto Ria<sup>1</sup>, Matteo Groni<sup>1</sup>, Elena Cattaneo<sup>1</sup>, Isabella Villa<sup>1</sup>, Maria Teresa Sabrina Bertilaccio<sup>3</sup>, Marta Chesi<sup>1</sup>, Alessandro Rubinacci<sup>1</sup>, Giovanni Tononi<sup>4</sup>, P Leif Bergsagel<sup>1</sup>, Angelo Vacca<sup>1</sup>, and Matteo Bellone<sup>1,\*</sup>



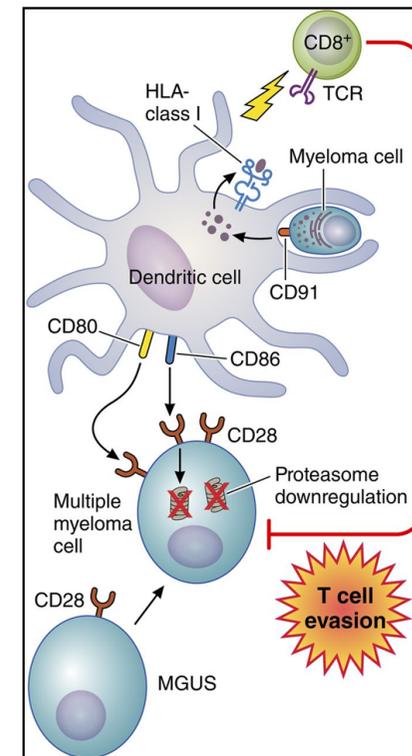
# Dhodapkar The Dark Side: microenvironment-mediated regulation and evolution in MM



LYMPHOID NEOPLASIA **blood** | 2015 • VOLUME 126, NUMBER 12

**Dendritic cells accumulate in the bone marrow of myeloma patients where they protect tumor plasma cells from CD8<sup>+</sup> T-cell killing**

Patrizia Leone,<sup>1</sup> Simona Berardi,<sup>1</sup> Maria Antonia Frassanito,<sup>1</sup> Roberto Ria,<sup>1</sup> Valli De Re,<sup>2</sup> Sebastiano Cicco,<sup>1</sup> Stefano Battaglia,<sup>1</sup> Paolo Ditunno,<sup>3</sup> Franco Dammacco,<sup>1</sup> Angelo Vacca,<sup>1</sup> and Vito Racanelli<sup>1</sup>



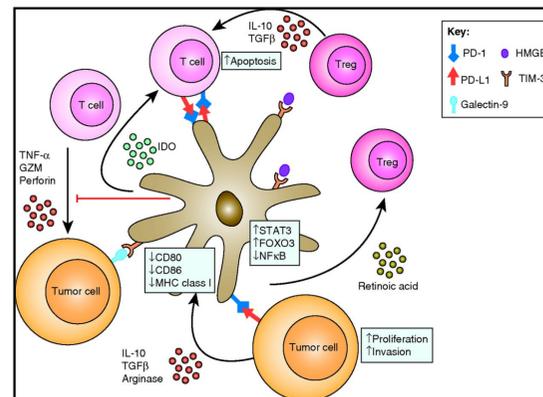
**The Journal of Immunology**

**Tumor-Infiltrating Dendritic Cells in Cancer Pathogenesis**

Jo Marie Tran Janco, Purushottam Lamichhane, Lavakumar Karyampudi and Keith L. Knutson

This information is current as of August 30, 2018.

*J Immunol* 2015; 194:2985-2991; ;  
doi: 10.4049/jimmunol.1403134  
<http://www.jimmunol.org/content/194/7/2985>



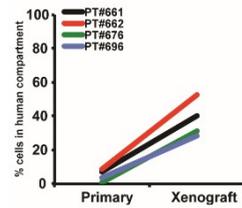
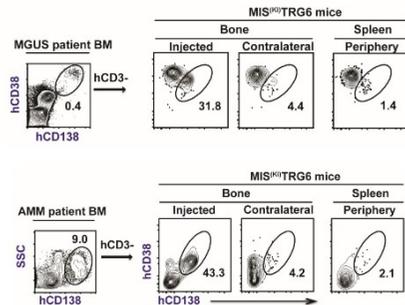
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# Dhodapkar Progressive growth of asymptomatic monoclonal gammopathies in humanized mice

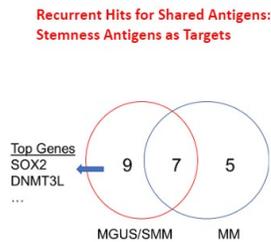


## An Argument for Dominant Role of Microenvironment in Maintaining Stability In Vivo

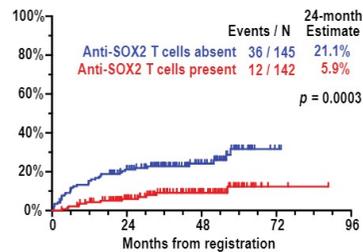


Das et al. Nat Med 2016

## T Cell Immunity Against Stemness Antigens and Risk of Malignant Transformation



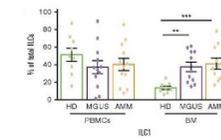
## Prospective Evaluation of Risk- SWOG S0120



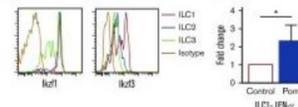
Spisek et al. J Exp Med  
Dhodapkar et al. Blood

## Early Alterations In Both Innate And Adaptive Immunity In The MGUS Marrow

### Innate Lymphoid Cells (ILCs) and ILC Subsets

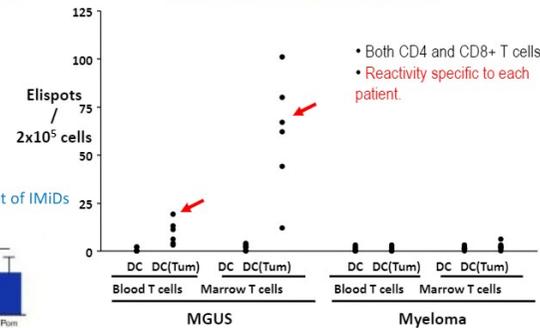


### High Expression of Ikaros/Aiolos in ILCs: target of IMiDs



Bailur et al. Blood Adv 2017;1:2343

### Tumor-specific IFN-γ producing T cells



J Exp Med 198:1753  
PNAS 99:13009

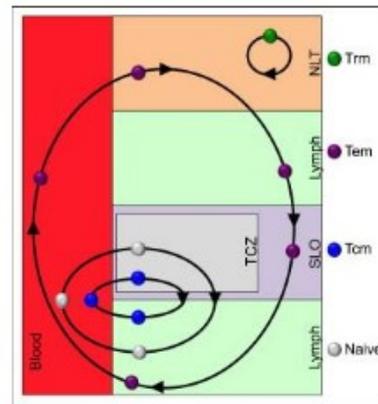
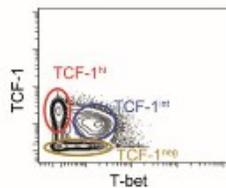
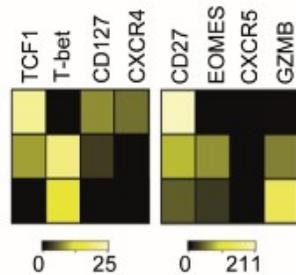
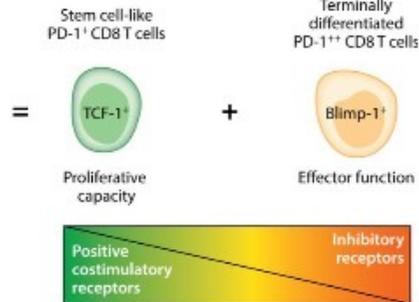
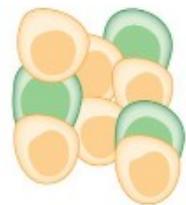
## Implications of Long Premalignant Phase in Human Cancer

- Many of the oncogenic mutations / neoantigens originate during the precursor stages....which last many years.
- How are the memory T cells maintained for so long in spite of getting "exhausted"?
- What are the implications for immune therapies?

# Dhodapkar Attrition of "stem-like" and marrow-resident memory T cells and accumulation of terminal effector T cells from MGUS to MM



CD8 T cell exhaustion



"Stem Like" T Cells  
Replicative Potential



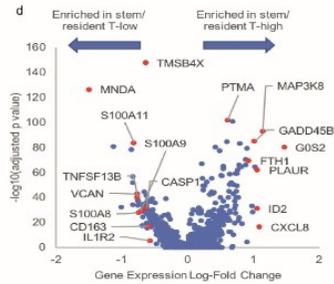
Terminal Effectors



Kini Bailur et al. JCI Insight 2019  
 Im et al Nature 2016  
 Boddupalli et al. JCI  
 Boddupalli et al. JCI Insight

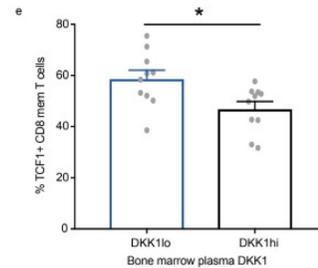
## Dhodapkar

Enrichment of stem-like/marrow-resident T cells is associated with myeloid signature of TLR-mediated activation and correlates inversely with bone marrow Dkk-1 levels



Gene Set ID	Description	Nominal p-value	PMID
GSE2706 (shown above)	Genes down-regulated in unstimulated vs LPS-stimulated dendritic cells	p<0.001	15995707
GSE22886	Genes down-regulated in unstimulated vs LPS-stimulated dendritic cells	p<0.001	15789058
GSE9988	Genes up-regulated in monocytes treated with anti-TREM1 and LPS vs monocytes treated with control IgG	p<0.001	18292579
GSE2706	Genes down-regulated in comparison of unstimulated vs R848-stimulated dendritic cells.	p<0.001	15995707

Bone marrow plasma Dkk1 levels



Kini Bailur et al. JCI Insight 2019

- Hierarchy of T cell exhaustion is established early in premalignancy.
- Immune response to stemness antigens as a predictor of risk of malignancy.
- Attrition of memory T cells with stem-like and tissue-residence signatures in the tumor bed with disease progression may underlie loss of immune surveillance.
- Retention or attrition of such cells in situ in turn depends on local signals in the tumor bed which change with clonal evolution and therapy.

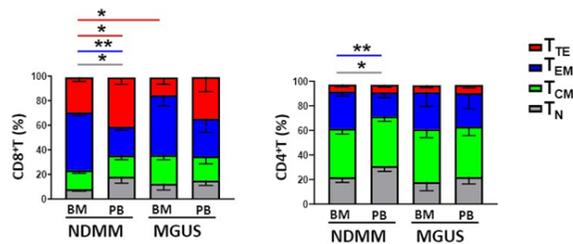
### Potential Clinical Implications:

- Biology of resident and stem-like cells may determine durability / curative potential of T cell redirection in MM.
- Functional aspects of immune microenvironment may also impact durability of preventive approaches.

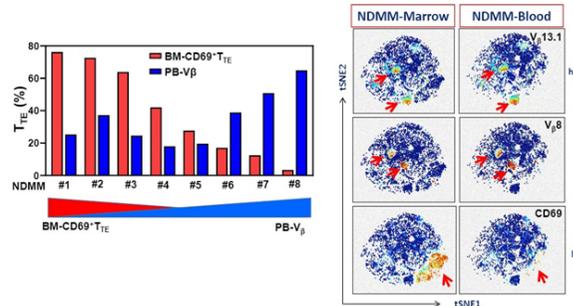
# Bryant T-cells



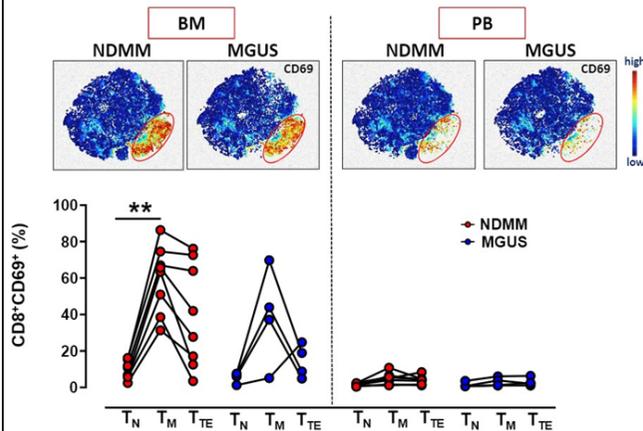
## CD8<sup>+</sup>T<sub>TE</sub> Accumulate in the Marrow in NDMM



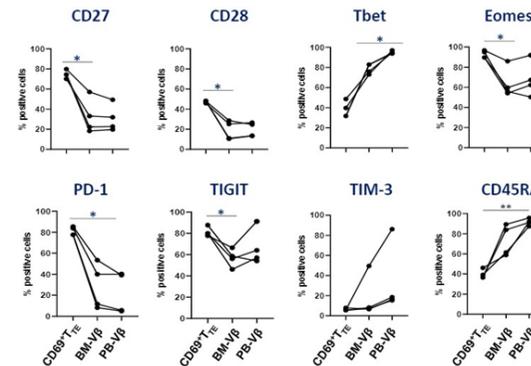
## Inverse Relationship Between CD69<sup>+</sup>T<sub>TE</sub> and Clonally Expanded T<sub>TE</sub> in NDMM



## CD69<sup>+</sup>T<sub>TE</sub> Accumulate in the Marrow of NDMM



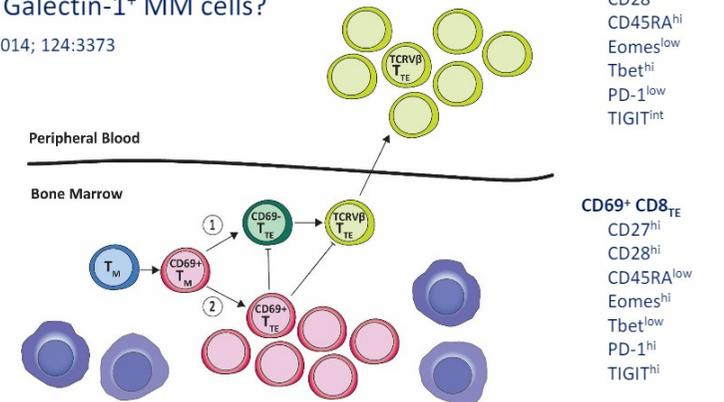
## CD69<sup>+</sup>T<sub>TE</sub> and Clonally Expanded T<sub>TE</sub> Are Phenotypically Different



## Exhausted CD69<sup>+</sup> CD8 T<sub>TE</sub> cells accumulate at the expense of clonally expanded CD8<sub>TE</sub>

- Failure of CD8 T<sub>M</sub> to down-regulate CD69<sup>+</sup>
- Role of Galectin-1<sup>+</sup> MM cells?

Blood. 2014; 124:3373



# T-cells



#FP-078

## Activated and Bone-marrow Resident Treg Alterations Underlie Malignant Transformation from MGUS to Multiple Myeloma

**Authors:** Slavica Vuckovic et al (Australia)

*The use of mass cytometry revealed two discrete subsets of CD39-Treg which are discordant in MGUS and NDMM patients. These subsets may be permissive of plasma cell growth and thus play a role in malignant transformation from MGUS to myeloma, which warrants further study. Understanding the regulatory properties of these Treg subsets may have diagnostic and prognostic significance in MGUS and MM, including the definition of risk in smoldering MM, as well as therapeutic implications.*

**FP-078 Activated and Bone-marrow Resident Treg Alterations Underlie Malignant Transformation from MGUS to Multiple Myeloma**  
Slavica Vuckovic, Christian Bryant, Felix Marsh-Wakefield, Annabel Krutts, Helen McGuire, Shihong Yang, Barbara Fazakas de St. Groth, Najat Nassif, Scott N. Byrne, John Gibson, Christina Brown, Stephen Larsen, Derek McCulloch, Richard Boyle, Georgina Clark, Douglas Jorlun, Phillipa Joy Ho

Institute of Haematology, Royal Prince Alfred Hospital, Sydney, NSW, Australia; Faculty of Medicine and Health, University of Sydney, Sydney, NSW, Australia; School of Life Sciences, University of Technology Sydney, Sydney, NSW, Australia; \*Research Facility for Human Systems Biology, University of Sydney, NSW, Australia; \*ANZAC Research Institute, Concord Repatriation General Hospital, Concord, NSW, Australia

**Abstract**  
Multiple Myeloma (MM) is preceded by the premalignant, clonal plasma cell disorder monoclonal gammopathy of undetermined significance (MGUS). Altered immune surveillance during malignant transformation from MGUS to myeloma may involve changes in the regulatory T cell (Treg) compartment which are permissive to myeloma immune escape. To address this hypothesis, we used mass cytometry and unsupervised clustering algorithm Flow Self-organizing Map (FlowSOM) to interrogate at high resolution the heterogeneity within the Treg (CD39<sup>+</sup>CD127<sup>low</sup>) cell compartment, in matched bone marrow (BM) and peripheral blood (PB) of MGUS and newly diagnosed (NDMM) patients. Both mass cytometry and flow cytometry confirmed a trend toward prevalence of CD39<sup>+</sup> Treg within the Treg compartment in BM and PB of NDMM patients compared to CD39<sup>+</sup> Treg in MGUS patients. FlowSOM clustering which displayed Treg in 25 molecularly suggested Treg heterogeneity in both MGUS and NDMM patients, and discovered two subsets which emerged within CD39<sup>+</sup> Treg of NDMM patients but were negligible or absent in CD39<sup>+</sup> Treg of MGUS patients. One subset resembled activated Treg based on CD49d, CD49e and CD226 expression and was found in both BM and PB; another subset resembled BM-resident Treg based on its tissue-resident CD69<sup>+</sup>CD226<sup>+</sup>CD84<sup>+</sup> phenotype and restricted location within the BM. Both subsets co-expressed PD-1 and TIGIT, but PD-1 was expressed at higher levels on BM-resident Treg than on activated Treg. Within BM, both subsets had limited Perforin and Granzyme B production, whilst activated Treg in PB acquired high Perforin and Granzyme B production. In conclusion, the use of mass cytometry revealed two discrete subsets of CD39<sup>+</sup> Treg which are discordant in MGUS and NDMM patients. These subsets may be permissive of plasma cell growth and thus play a role in malignant transformation from MGUS to myeloma, which warrants further study. Understanding the regulatory properties of these Treg subsets may have diagnostic and prognostic significance in MGUS and MM, including the definition of risk in smoldering MM, as well as therapeutic implications.

**Introduction & Background**  
The underlying immunological mechanism preventing malignant plasma cell expansion in MGUS compared to the permissive expansion of malignant plasma cells in MM patients remains under active investigation. However, an accepted concept has been that the immune system in MM patients is tipped in favor of myeloma growth by initiating immunosuppressive mechanisms mediated by different regulatory immune cells, particularly Treg.  
We considered that in a growth permissive BM environment, myeloma cells may change pre-existing heterogeneity within the Treg compartment by inducing discrete Treg subsets which facilitate its progression.

**Methods & Materials**  
Paired BM and PB of MGUS (n = 4) and NDMM (n = 6) patients, recruited at the Royal Prince Alfred Hospital, Sydney, NSW, Australia were processed by Mass cytometry (CyTOF 2; Histo Fluidigm, Toronto, Canada). Data were analyzed using FlowJo, 10.6.2; unsupervised clustering algorithm Flow self-organizing map (FlowSOM), and visualized by dimensionality reduction algorithm t-SNE.

**Results**  
**A** Heatmap of median signal intensity of CD39 expression on Treg in matched BM and PB from MGUS and NDMM patients. **B** Frequency of CD39<sup>+</sup> Treg in BM and PB of MGUS and NDMM patients. **C** Representative t-SNE plots of BM and PB from individual MGUS and NDMM patients. **D** Representative t-SNE plots of PD-1 vs. TIGIT expression in activated CD39<sup>+</sup> Treg and BM-resident CD39<sup>+</sup> Treg in matched BM and PB of individual MGUS and NDMM patients.

**High levels of PD-1 expression on BM-resident CD39<sup>+</sup> Treg in NDMM**

**Figure 1. (A)** Heatmap of median signal intensity of CD39 expression on Treg in matched BM and PB from MGUS and NDMM patients. **(B)** Frequency of CD39<sup>+</sup> Treg in BM and PB of MGUS and NDMM patients. **(C)** Representative t-SNE plots of BM and PB from individual MGUS and NDMM patients. **(D)** Representative t-SNE plots of PD-1 vs. TIGIT expression in activated CD39<sup>+</sup> Treg and BM-resident CD39<sup>+</sup> Treg in matched BM and PB of individual MGUS and NDMM patients.

**Conclusion & References**  
One of the challenges in the field of plasma cell dyscrasias and myeloma is to understand which factors keep MGUS clinically stable, and what critical events allow permissive expansion of malignant plasma cells to lead to the progression of clinical MM.  
Our data suggest the compelling possibility that MGUS and NDMM patients can be distinguished based on the presence of activated CD39<sup>+</sup> Treg and BM-resident CD39<sup>+</sup> Treg.  
Emergence of activated CD39<sup>+</sup> Treg and BM-resident CD39<sup>+</sup> Treg may represent necessary early changes in normal physiological Treg biology induced by malignant myeloma cells to allow progression from MGUS to clinical MM.  
These changes in the Treg compartment of NDMM patients have real potential to improve our understanding of the clinical stability in MGUS and disease progression into MM, to further advance clinical diagnosis, prognosis, and therapeutic implications for MM.

1. Akashi-Watanabe E, Kishida A, Mochizuki M, Yang S, Rostoff C, Farnas A, de Groot D, Nawa A, Ryan J, Ghossein, Rana C, Lerner, M, Kuroki H, Nakai R, Clark D, Ho A, Durrant J, Mass Caregiver Gateway, Two Clusters of CD39<sup>+</sup> Treg within Bone Marrow of Multiple Myeloma Patients. *Front Immunol* 2019; 10:2185. doi: 10.3389/fimm.2019.0185

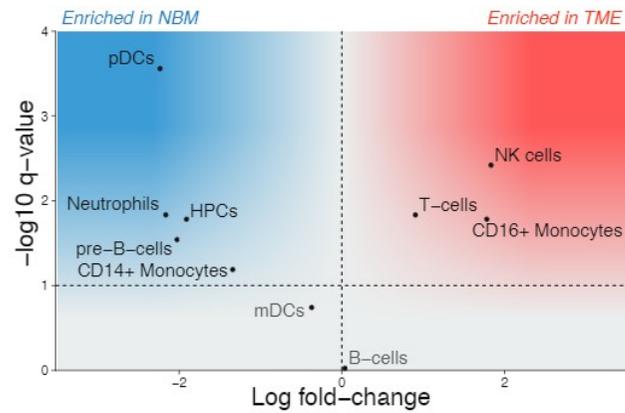
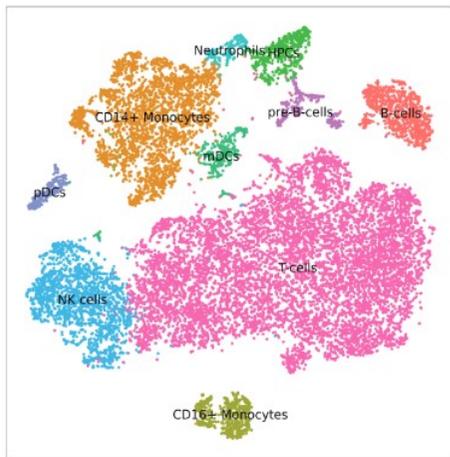
Author contact: Slavica.Vuckovic@health.nsw.gov.au

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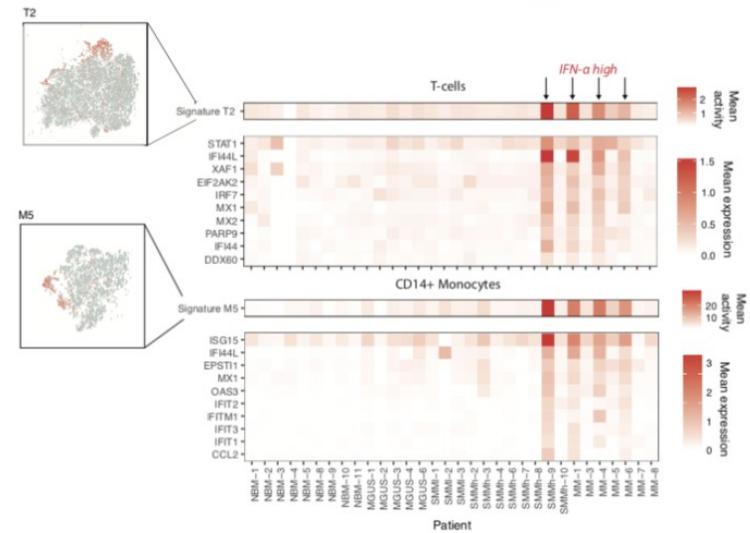
19-20 novembre 2019 Bologna



## Compositional changes in MM bone marrow microenvironment



## Individual Patients Show Upregulation of IFN type-1 Regulated Genes Across Different Cell Types

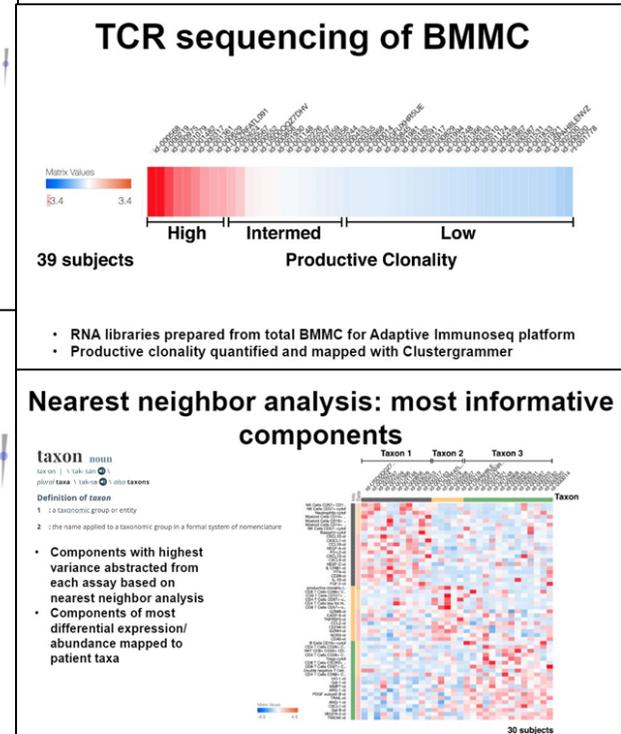
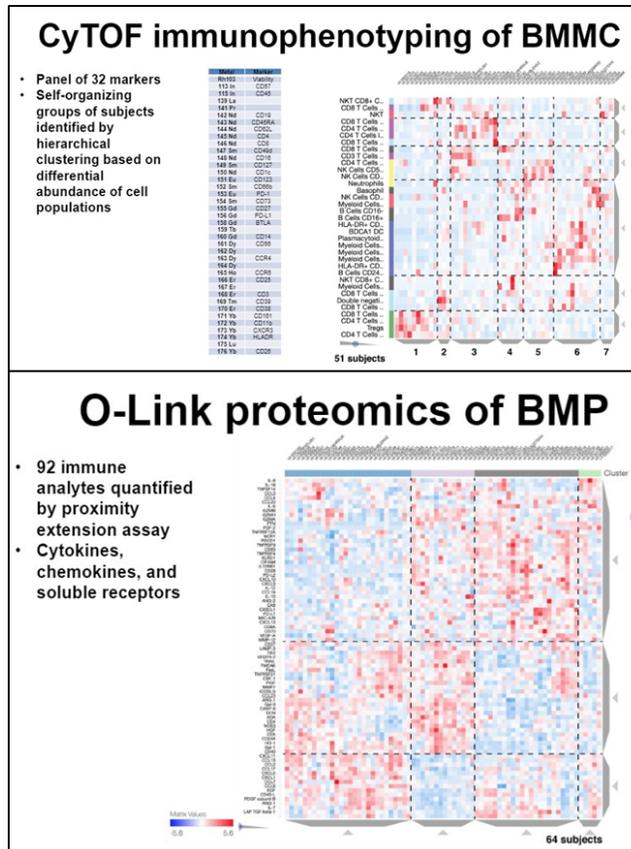


# Cho High dimensional profiling of the immune microenvironment in SMM



## Immune Microenvironment in Smoldering MM

- Current risk models in SMM are based on tumor-intrinsic factors
  - M-spike/sFLC ratio, velocity, reciprocal depression
  - Cytogenetic/FISH risk factors
- Immune microenvironment of plasma cell dyscrasias is significantly altered
  - Innate *and* adaptive cellular components eg pDCs, myeloid cells, T cells (Chauhan *et al*/Cancer Cell 2009; Bailur *et al*, JCI Insight 2019)
- Hypothesis: are there distinguishing features in the IME of SMM that relate to disease state/ progression?

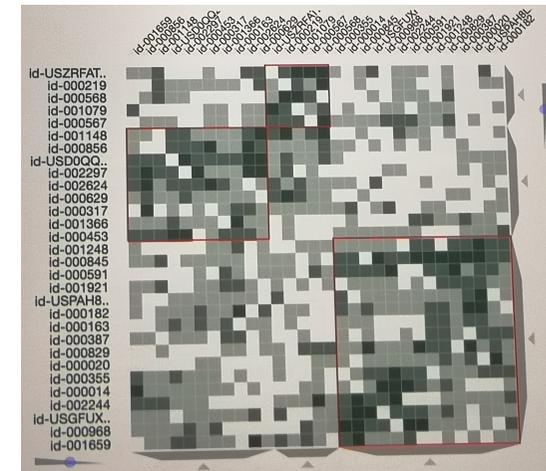


# Cho

## High dimensional profiling of the immune microenvironment in SMM



	Taxon 1	Taxon 2	Taxon 3
<b>Cellular (CyTOF)</b>	NK cells Monocytes Neutrophils Basophils	Effector CD4/8 T cells CD8 TEMRA	Central memory/naïve CD4/CD8 T cells Double neg T cells Treg cells CD16+ B cells NK/T cells
<b>Proteomic (O-Link)</b>	Angiogenesis: VEGFA/C Chemotaxis: CCL19, CXCL1, CXCL9, CXCL13, CXCL19 Inflammation: IL-10: IL-12Rbeta1 Co-stimulation (T cell): CD28 Immune checkpoint: PD-L2 Survival/proliferation: FGF-2, PTN	Apoptosis: Casp-8, Granzyme B/H, NOS-3 Co-stimulatory (APC): OX40L, CD40 Leukocyte activation: CCL2, SLAMF4 (CD244)	Apoptosis: Gal-1, HO-1, TRAIL, TWEAK Angiogenesis: ANG-1, MMP7, PDGFbeta Immunosuppression: ARG-1, Gal-9
<b>Clonality (TCR Seq)</b>	Intermediate	High	Low



### Integrative immune analysis

- Nearest neighbor analysis across high dimensional platforms identify distinct taxa of subjects in SMM
- Taxa share characteristics that may be associated with different states in the immune microenvironment
- Further refinement of NNA may improve precision of taxa definitions
  - Inclusion of tumor-specific data eg GEP
  - Comparison to established risk models
  - Prospective/retrospective analysis *with outcome data*
  - Identification of rational targets for therapeutic intervention

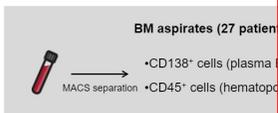
# Zavidij Single-cell RNA sequencing reveals compromised immune microenvironment in precursor stages of MM



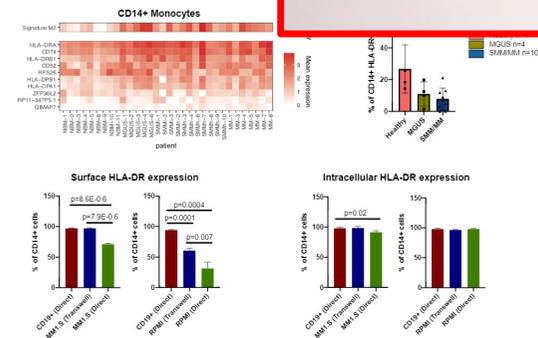
## From MGUS to Myeloma: Dissecting the Path

To better understand changes occurring by MM progression we aim to analyze transcriptional alterations at different stages of disease:

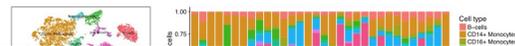
- Examine the characteristics of the immune microenvironment at different stages of MM progression
- Determine the transcriptional alterations in the immune microenvironment at different stages of MM progression



## Compromised Antigen Presentation



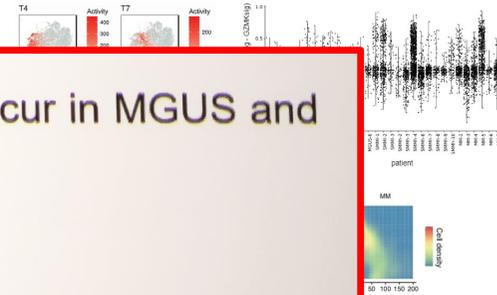
## Compositional Changes in MM Bone Marrow Microenvironment



• Changes in the tumor immune microenvironment already occur in MGUS and include:

- upregulation of interferon type-1 signaling
- skewed differentiation of CD8+ T cells
- suppressive CD14+ monocytes with compromised antigen presentation

## MM Patients Show Significant Skewing of Cytotoxic T Cells to the Effector State



# Mesenchymal stromal cells

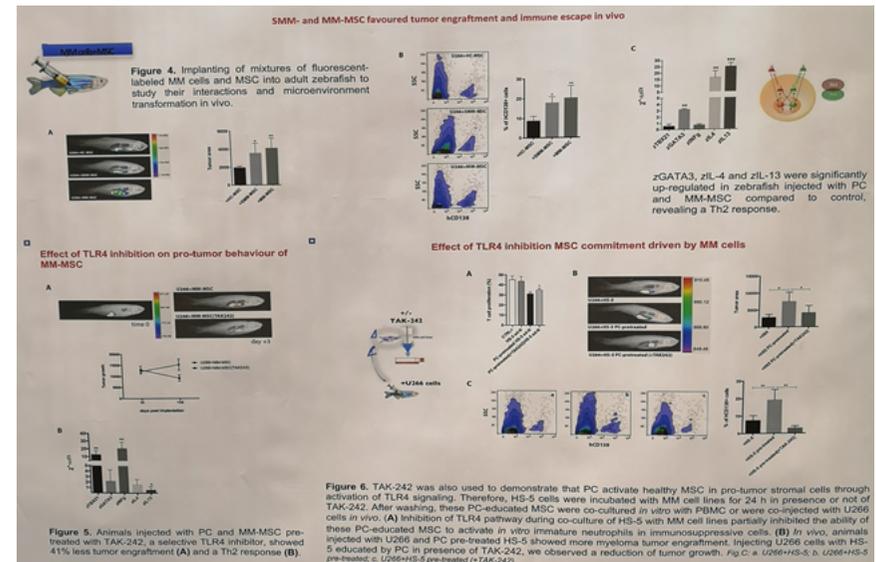
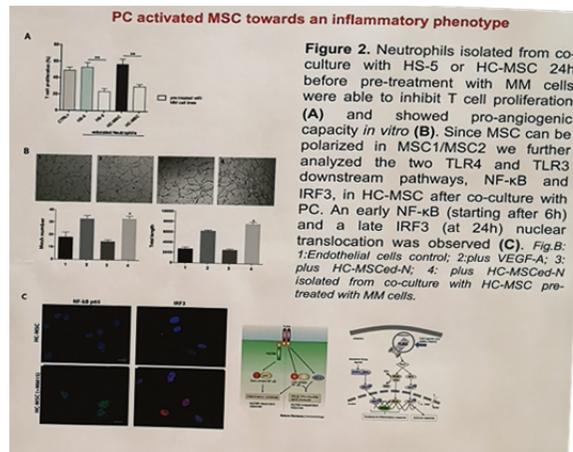
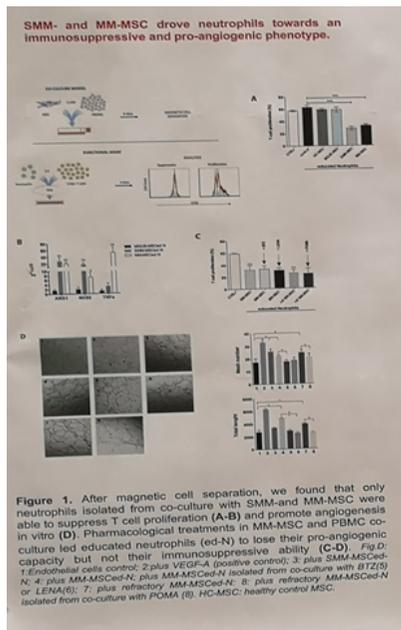


#FP-062

**TLR4 signaling drives mesenchymal stromal cells (MSC) commitment to promote tumor microenvironment transformation in multiple myeloma**

**Authors:** Giallongo C., et al (Catania, Italy)

*TLR4 signaling plays a key role in MSC transformation by inducing a protumor phenotype associated with a permissive microenvironment that circumvents the immune response and allows a better tumor engraftment.*



# Angiogenic cytokines

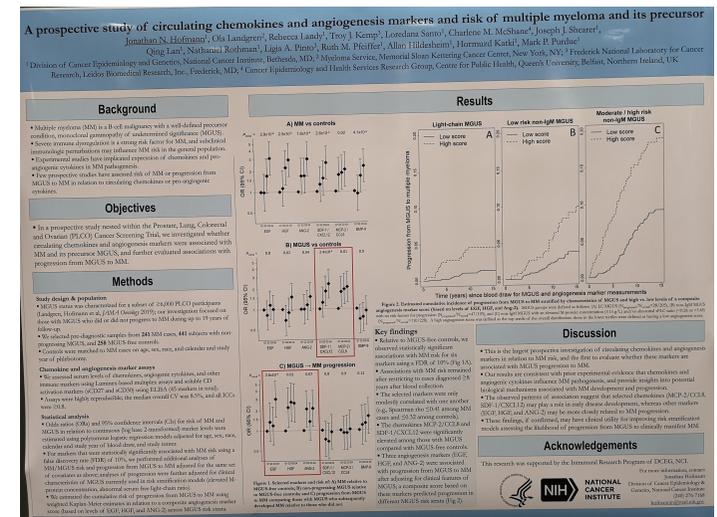


#FP-064

## A prospective study of circulating chemokines and angiogenesis markers and risk of multiple myeloma and its precursor

**Authors:** Jonathan Hofmann, et al (USA, Ireland)

*Our prospective findings provide new insights into mechanisms involved in MM development and suggest that systemic angiogenesis markers could potentially improve risk stratification models for MGUS patients.*



# Highlights from IMW 2019

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## #FP-058

### **A New 'Vicious Cycle': Bidirectional Interactions Between Myeloma Cells and Adipocytes**

**Authors:** Heather Fairfield Campbell, Mariah Farrell, Carolyne Falank, Amel Dudakovic, Samantha Costa, Victoria DeMambro, Jessica Pettitt, Andre J. van Wijnen, Michelle McDonald, Michaela Reagan (USA, Australia)

*MM-adipocytes exhibit a "senescent-like" phenotype in vitro that may explain their support of MM cells.*

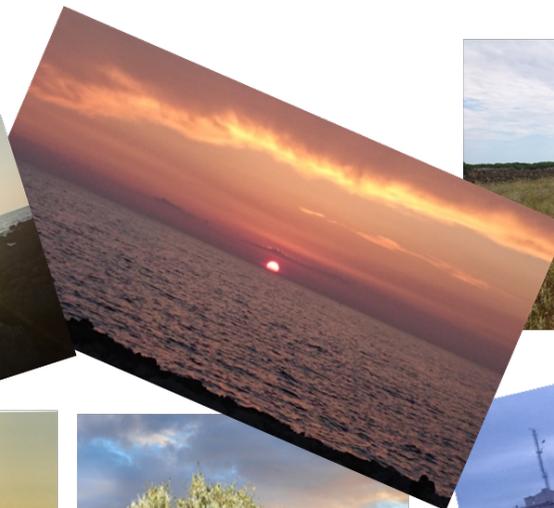
## #FP-054

### **Excessive abdominal fat content indicates poor prognosis in patients with newly diagnosed multiple myeloma**

**Authors:** Li Bao, Yutong Wang (China)

*NDMM patients had higher abdominal fat content but lower adipokine levels than healthy people. Excessive subcutaneous fat might be a predictive factor for high tumor burden and poor treatment response. Visceral fat content may be correlated with high-risk cytogenetic abnormalities.*

Thanks for your attention



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