



4th Annual Workshop on Genomics

July 10-11, 2026 • Warsaw, Poland

Co-chairs: Mehmet Samur, Faith Davis, Nikhil Munshi, Felipe Prosper, Marc Raab

Friday, July 10

11:30 - 12:30	REGISTRATION AND LUNCH	
12:30 - 12:45	OPENING REMARKS AND WELCOME <i>Philippe Moreau and Nikhil Munshi</i>	
12:45 - 2:05	SESSION 1: DETERMINANTS OF FUNCTIONAL HIGH-RISK <i>Chairs: Jill Corre and Shaji Kumar</i>	
12:45 - 12:55	How and why do we define functional high-risk?	Philippe Moreau
12:55 - 1:05	Extramedullary disease, PCL and CNS as a functional high-risk features	Saad Usmani
1:05 - 1:15	Can circulating cells and MRD help for dynamic assessment of risk to detect functional high-risk?	Bruno Paiva
1:15 - 1:25	Bone marrow function and risk in MM	Nate Fillmore
1:25 - 1:35	Frailty and risk	Gordon Cook
1:35 - 2:05	Panel discussion	Session faculty + Jens Hillengass and Samir Parekh
2:05 - 2:20	BREAK	
2:20 - 4:00	SESSION 2: GENOMIC DETERMINANTS OF FUNCTIONAL HIGH RISK DISEASE <i>Chairs: Faith Davies and Vincent Rajkumar</i>	
2:20 - 2:30	Can IMS/IMWG CGS detect functional high-risk patients?	Jill Corre
2:30 - 2:40	Can we identify functional high-risk upfront by looking at genomics?	Mehmet Samur
2:40 - 2:50	Co-occurrence of cytogenetic abnormalities and high-risk disease in newly diagnosed and relapsed/refractory multiple myeloma	Niels Weinhold
2:50-3:00	Proteomics-defined HRMM, a new subgroup of MM?	Felix Czernilofsky
3:00 - 3:10	How do you define therapeutic high-risk?	Niccolo Bolli
3:10 - 3:20	How to approach the high-risk myeloma from induction through relapse?	Katja Weisel
3:20 - 4:00	Panel discussion	Session faculty + Wee Joo Chng

4:00 - 4:15

BREAK

4:15 - 6:00

SESSION 3: GENOMIC DETERMINANTS OF ULTRA HIGH-RISK MYELOMA

Chairs: Nikhil Munshi and Herve Avet-Loiseau

4:15 - 4:25	Do we need to define ultra high-risk myeloma?	Suzanne Lentzsch
4:25 - 4:35	What are the potential genomic characteristics of ultra high-risk?	Fancesco Maura
4:35 - 4:45	How much improvement have we made on double-hit patients from double to triple to quadruple treatments?	Martin Kaiser
4:45 - 4:55	Cell proliferation, its regulation and it's role on ultra high-risk MM	Leif Bergsagel
4:55 - 5:05	Biological determinants of ultra high-risk	Masood Shamma
5:05 - 5:15	Do we need to change our therapeutic strategies for ultra high-risk?	Sundar Jagannath
5:15 - 6:00	Panel discussion	Session faculty + Gang An

Saturday, July 11

8:00 - 10:30

SESSION 4: TUMOR MICROENVIRONMENT

Chairs: Noopur Raje and Nizar Bahlis

8:00 - 8:15	Toward a single-cell atlas of high-risk multiple myeloma: Clonal landscape and TME features across risk genotypes	Alessandro Lagana
8:15 - 8:30	Tumor and microenvironment interactions assessed from large-scale single-cell atlas in MM	Chuck Acharya
8:30 - 8:45	Clonal evolution differences between antigen escape mechanisms for BCMA and GPRC5D	Holly Lee
8:45 - 9:00	Effects of HDM/ASCT exposure on microenvironment cells	Mattia D'Agostino
9:00 - 9:15	Genetically-driven immune microenvironment landscapes across myeloma subtypes	Romanos Sklavenitis-Pistofidis
9:15 - 9:30	Immune cell determinants of response and resistance to therapy in MM	Li Ding
9:30 - 9:45	Spatial single cell interactions between MM cells and microenvironment	Manoj Bhasin
9:45 - 10:30	Panel discussion	Session faculty + Mark Bustoros

10:30 - 11:00

BREAK

11:00 - 12:45

SESSION 5: NOVEL THERAPEUTIC VULNERABILITIES

Chairs: Paola Neri and Lawrence Boise

11:00 - 11:15	RNA degraders against MM cells	Domenico Maisano
11:15 - 11:30	The Achilles' heel of RAS/RAF pathway in MM	Constantine Mitsiades
11:30 - 11:45	Epigenetic dependencies in MM	Benjamin Barwick

11:45 - 12:00	Targeting the epitranscriptomic landscape	Eugenio Morelli
12:00 - 12:15	PRKD2-CCR4-NOT-mediated mRNA deadenylation programs oncogenic fitness in multiple myeloma	Raphael Szalat
12:15 - 12:45	Panel discussion	Session faculty + Marta Chesi
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12:45 - 1:30	LUNCH	
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1:30 - 3:15	SESSION 6: PLASMA CELL DYSCRASIAS	
	<i>Chairs: Irene Ghobrial and Gareth Morgan</i>	
1:30 - 1:45	Amyloid proteomics	Anjan Thakurta
1:45 - 2:00	Evolution of WM subclones under treatment pressure	Steven Treon
2:00 - 2:15	Assessing B cell health through single-cell profiling	Matteo Claudio Da Via
2:15 - 2:30	Role of genomics to determine response to treatments	Brian Walker
2:30 - 2:45	CHIP in large-scale cohorts	Adam Sperling
2:45 - 3:15	Panel discussion	Session faculty + Uday Yanamandra
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3:15 - 3:45	BREAK	
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3:45 - 5:30	SESSION 7: NEW APPROACHES TO MM TRANSLATIONAL RESEARCH	
	<i>Chairs: Marc Raab and Felipe Prosper</i>	
3:45 - 4:00	Therapeutic vulnerabilities in high-risk MM	Mariateresa Fulciniti
4:00 - 4:15	Role of N6-methyladenosine (m6A) RNA modification in MM	Jerome Moreaux
4:15 - 4:30	Long read sequencing platforms	Parth Shah
4:30 - 4:45	How do we consistently utilize gene expression risk-stratification in clinic?	Jonathan Keats
4:45 - 5:00	cfDNA based risk stratification	Trevor Pugh
5:00 - 5:30	Panel discussion	Session faculty + Suzanne Trudel
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5:30 - 5:45	CLOSING	
	<i>Nikhil Munshi, Noopur Raje, Faith Davies</i>	

The IMS gratefully acknowledges the following organization for their sponsorship of the 4th Annual Workshop on Genomics:

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