

# **Meccanismi di escape immunologico della recidiva post trapianto allogenico**

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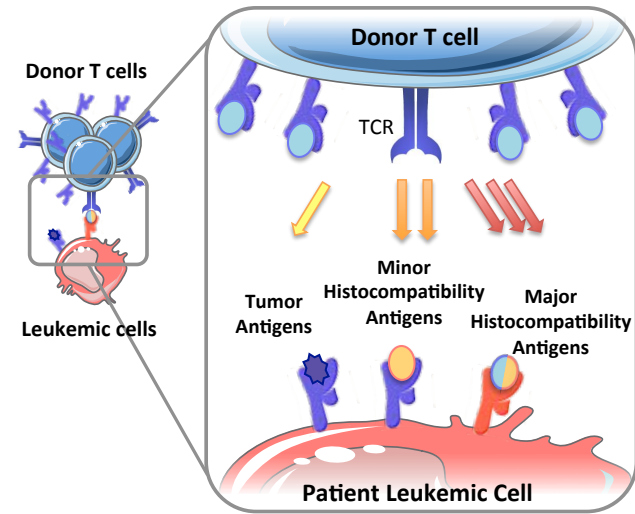
# Disclosures

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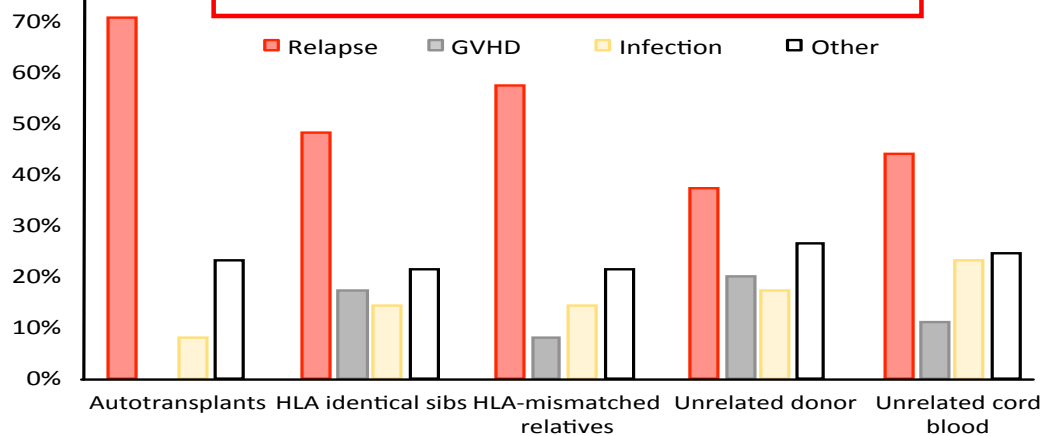
- I have NO following relevant financial relationships to disclose

# Background: HSCT and Relapse

In allogeneic HSCT immune cells from the donor recognize and eliminate residual malignant cells (“**Graft versus Leukemia effect**”)



**Causes of death after HSCT in the US**



*Adapted from Horowitz, Bone Marrow Transplant, 2018*

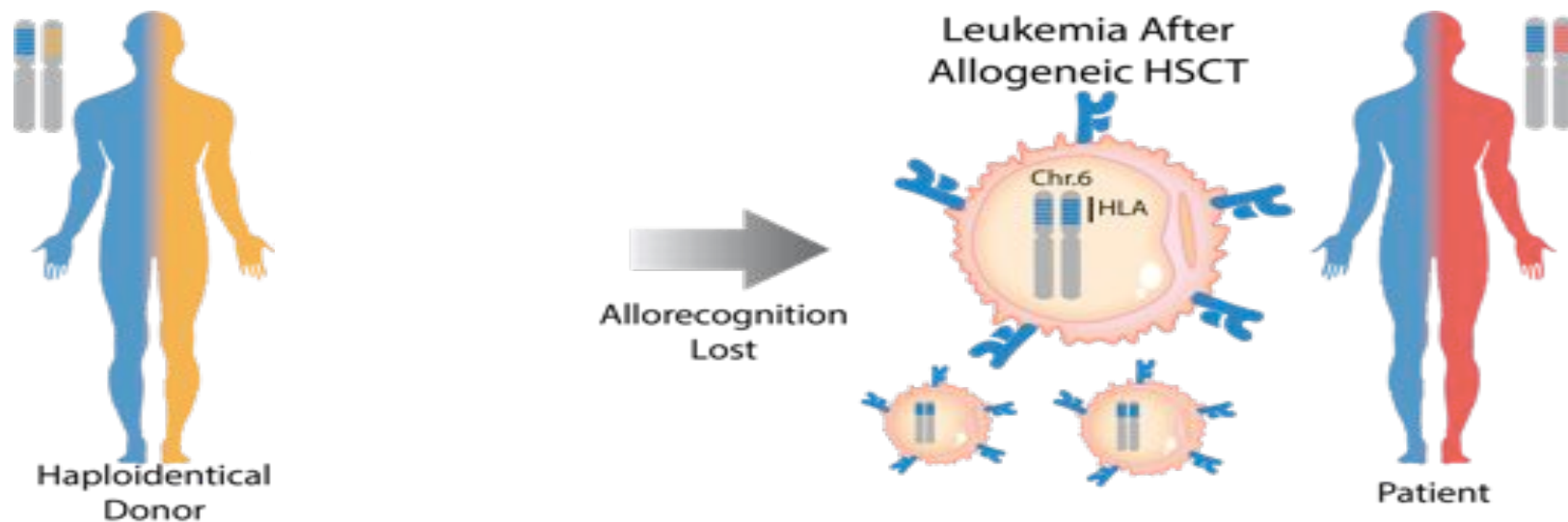
Reappearance of disease after initial remission (**relapse**) represents the most frequent cause of post-transplantation mortality

# Outline of the Talk

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- 1. Genomic HLA loss (10 years later)**
- 2. Novel modalities of relapse (not all in genomics...)**

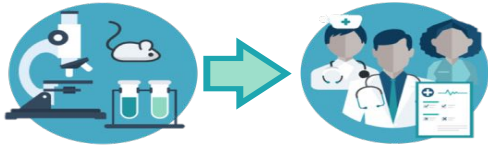
## Molecular Mechanism and Immunological Consequences of HLA Loss



- Loss of the entire HLA complex (both class I and class II)
- Genomic mechanism (irreversible)
- Occurs only in leukemia cells, and rapidly becomes clonally prevalent
- Loss is counterbalanced by duplication of the other haplotype (expression level unchanged)

*Vago, N Engl J Med, 2009; Toffalori, Blood, 2012  
Crucitti, Leukemia, 2015; Ahci and Toffalori, Blood, 2017*

# The HLA loss Timeline



2009

2019

## Confirmation/Epidemiology

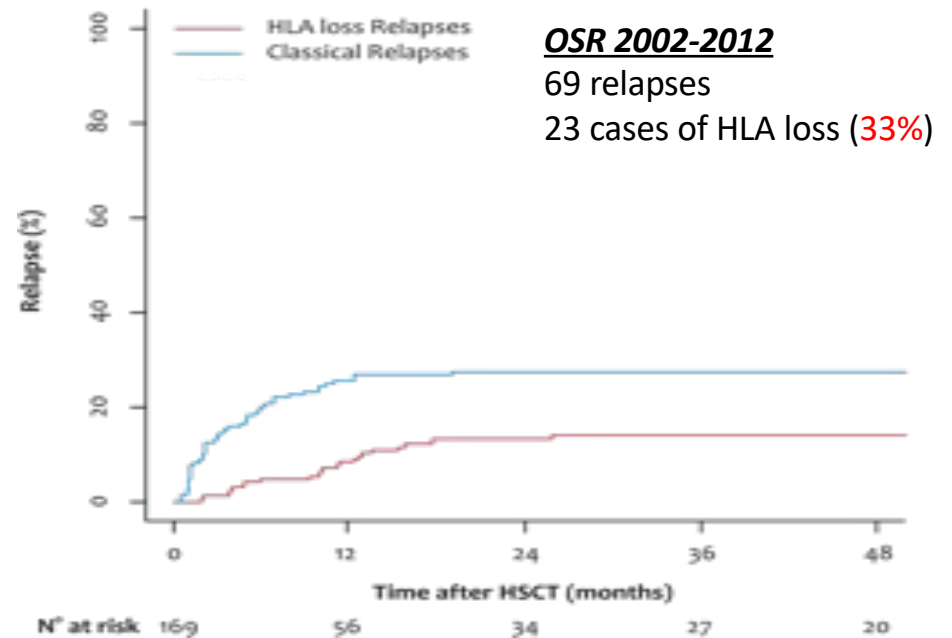
Studies confirming HLA loss relapses in other HSCT settings and addressing the frequency of the event

*Villalobos, Blood, 2010*

*Waterhouse, Biol Blood Marrow Transplant, 2011*

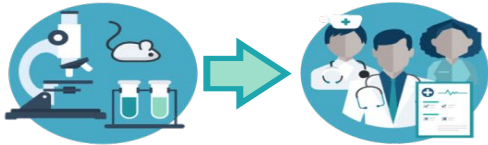
*Toffalori, Blood, 2012*

*McCurdy, Leukemia, 2016*



*Crucitti, Leukemia, 2015*

# The HLA loss Timeline



2009

2019

## Routine Diagnosis

Development and industrial validation of fast and reliable molecular assays amenable to routine laboratory practice

*Ahci and Toffalori, Blood, 2018*

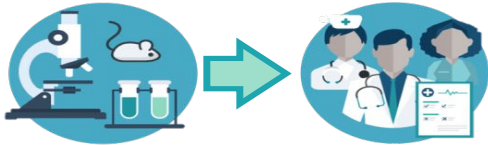
**HLA-KMR<sup>®</sup> ASSAYS**  
DETECTION OF HLA  
LOSS BY QPCR

**GENDX**

personalizing diagnostics

- Fast and sensitive qPCR assay
- 10 unique markers
- Most frequent allele groups of HLA-A, -C and -DPB1
- Applicable with KMRtrack protocol
- Fully integrated with KMReengine

# The HLA loss Timeline



2009

2019

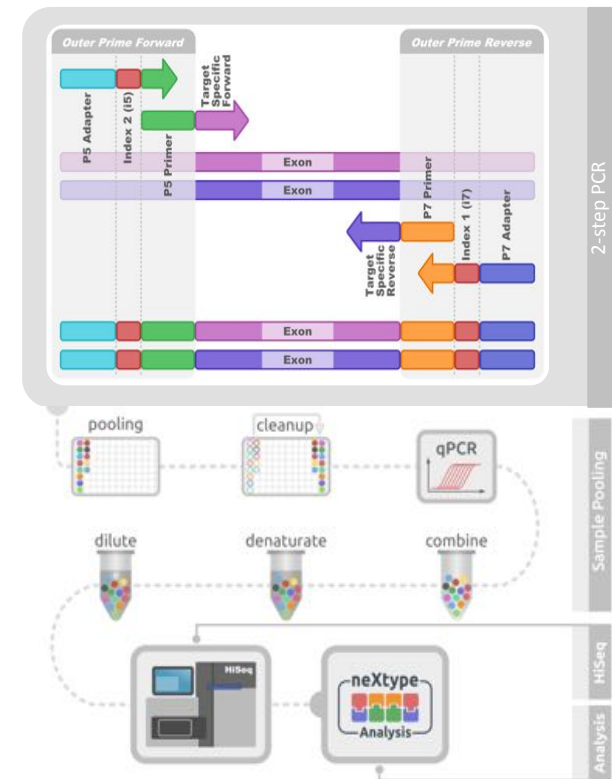
## Routine Diagnosis

Development and industrial validation of fast and reliable molecular assays amenable to routine laboratory practice

*Ahci and Toffalori, Blood, 2018*

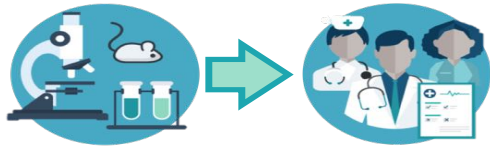
Adaptation of an HLA NGS typing pipeline to the analysis of HLA loss in up to 48 samples in a single run

*with DKMS*





# The HLA loss Timeline

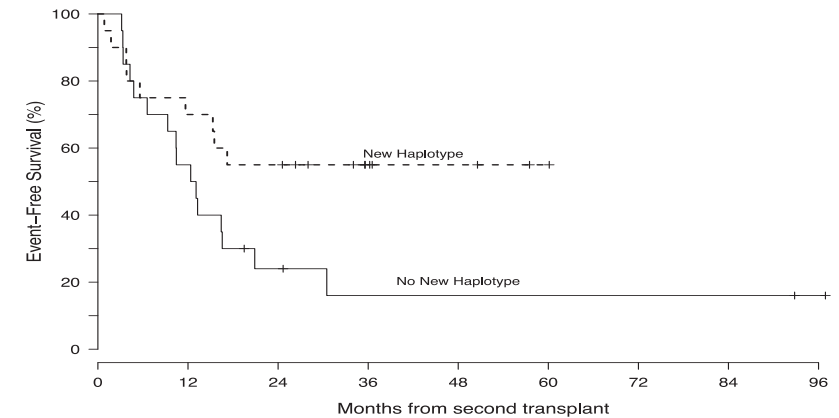
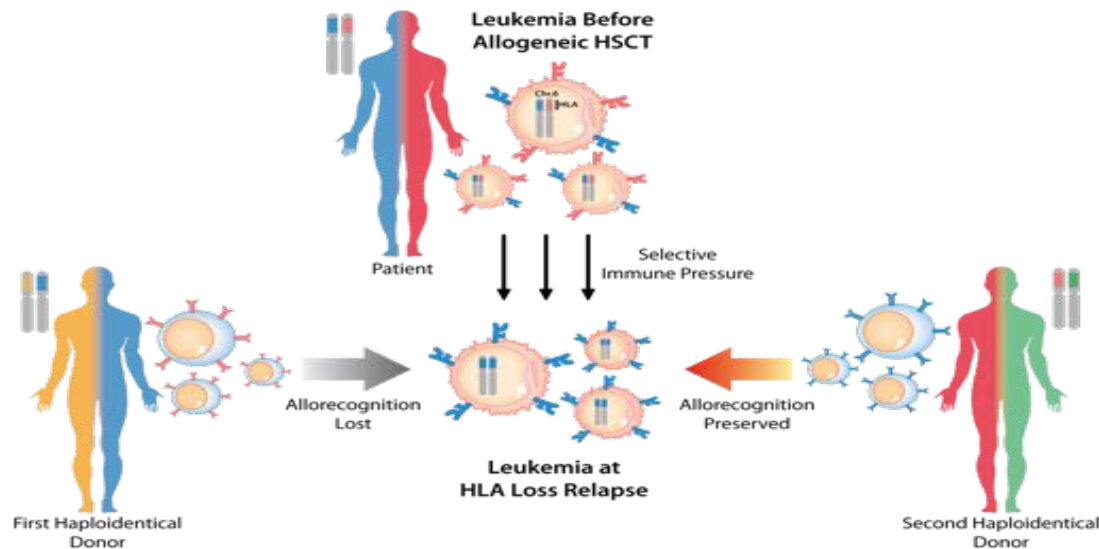


2009

2019

## Therapy

Criterion for AVOIDING DLI and selection of a second haplo donor

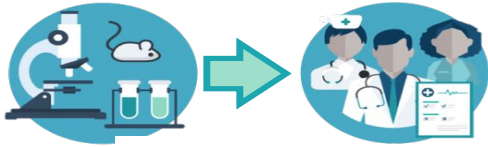


No. at risk	0	12	24	36	48	60	72	84	96
No New Haplotype	20	14	11	5	3	1	0	0	0
New Haplotype	20	14	11	5	3	1	0	0	0

*Vago and Ciceri, BBMT, 2017*

*Imus, BBMT, 2017*

# The HLA loss Timeline



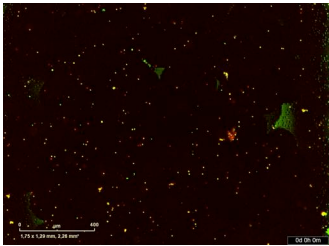
2009

2019

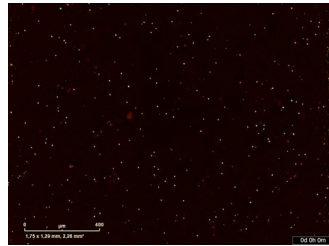
## Therapy

Rationale for non HLA-restricted cancer immunotherapy approaches  
(bispecific antibodies, CAR T cells)

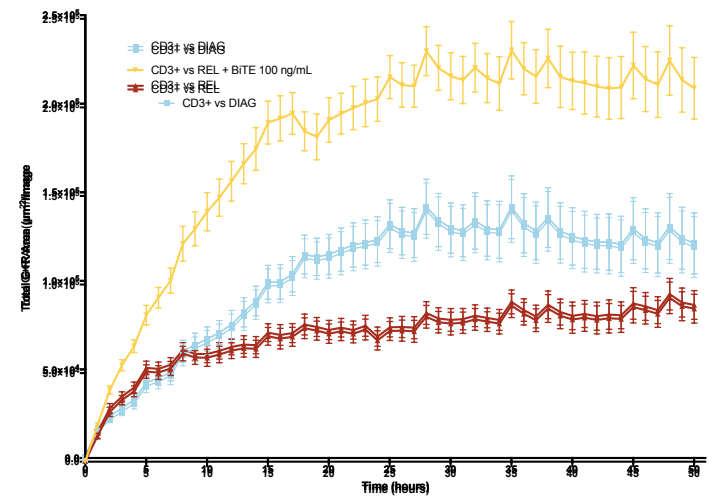
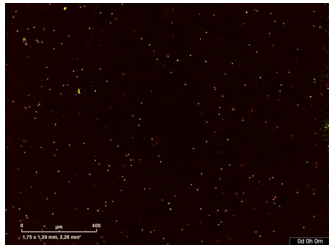
### vs Diagnosis



### vs HLA loss relapse

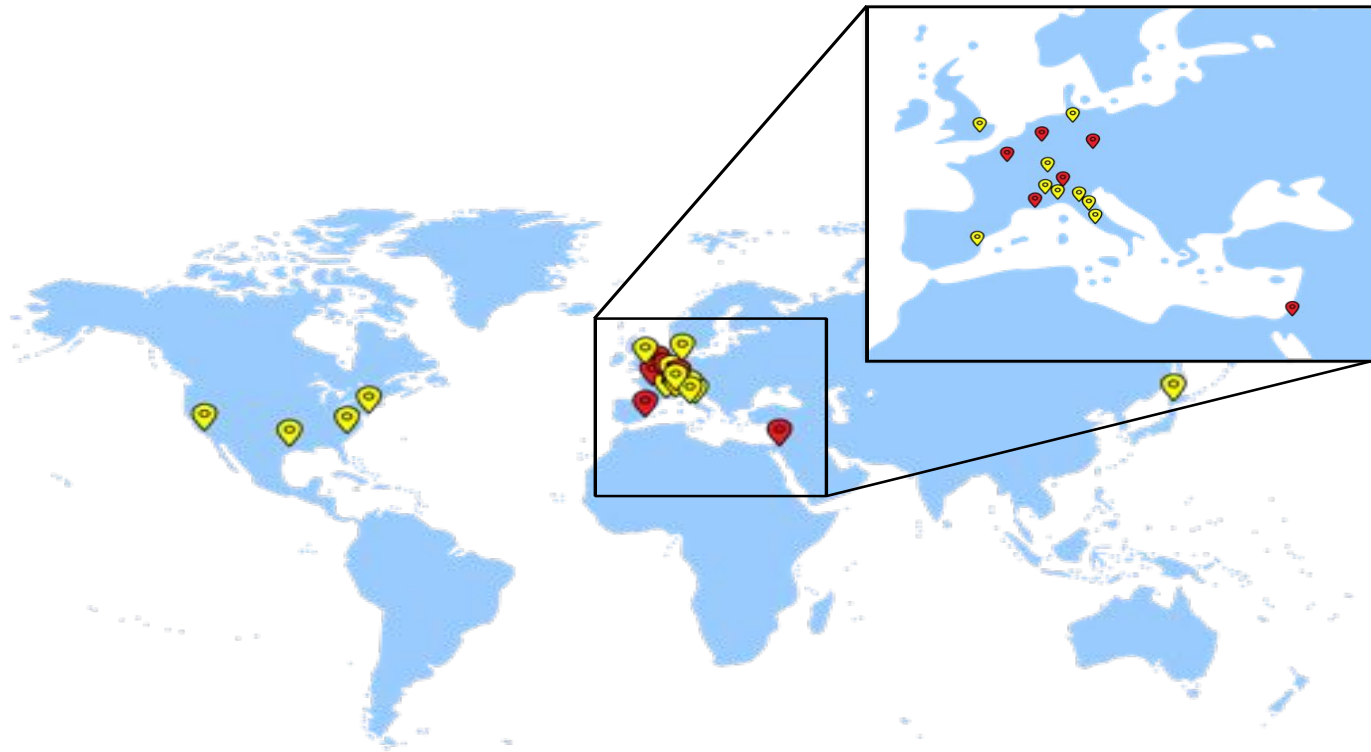


### vs HLA loss relapse + antiCD3/CD33 BiTE



*With M. Subklewe*

# The HLALOSS Transcan Project



**Aim:** addressing the frequency and risk factors of HLA loss in different HSCT settings

More than 20 centers from Europe, US, Japan

More than 1000 patient and donor samples (>600 relapses) characterized by an ad hoc optimized NGS pipeline

**TRANSCAN-2**

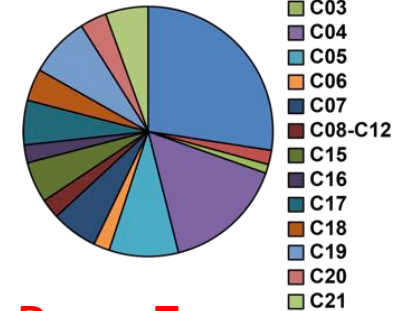
ERA-NET: Aligning national/regional translational cancer research programmes and activities



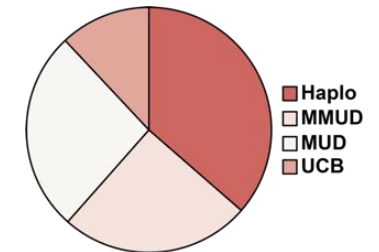
# Patient and Transplant Characteristics

	Total (n=425)	Haplo (n=155)	MMUD (n=110)	MUD (n=111)	UCB (n=49)	P
<b>Male/Female Ratio</b>	1.14	0.96	1.15	1.31	1.45	0.5
<b>Median Age (range)</b>	51 (16-77)	49 (16-72)	56 (17-77)	55 (22-75)	34 (16-67)	<0.001
<b>Diagnosis</b>						<0.001
AML	317	122	74	93	28	
ALL	47	9	12	5	21	
MDS or MPN	61	24	24	13	0	
<b>Disease status</b>						<0.001
CR	192	50	56	51	35	
Active Disease	233	105	54	60	14	
<b>Cytogenetic risk</b>						0.41
Favourable	16	4	7	5	0	
Intermediate	209	80	55	59	15	
Adverse	160	60	39	43	18	
<b>Chemorefractory Disease</b>						<0.001
Yes	164	85	24	30	25	
No	257	70	82	81	24	
<b>Hyperleukocytosis at Diagnosis</b>						0.057
Yes	74	36	14	12	12	
No	268	96	61	79	32	
<b>Previous Allogeneic HSCT</b>						<0.001
Yes	47	37	4	4	2	
No	378	118	106	107	47	
<b>Stem Cell Source</b>						0.008
PB	331	127	103	101	/	
BM	45	28	7	10	/	
<b>Conditioning Intensity</b>						0.005
MAC	259	75	70	74	40	
RIC	136	61	32	34	9	
<b>ATG Use</b>						<0.001
Yes	295	88	70	93	44	
No	117	65	31	17	4	
<b>Median infused CD3+ (x10e5/Kg), range</b>	2350 (3-9995)	2560 (20-9995)	2550 (3-7950)	2000 (21-6300)	53 (40-70)	0.09
<b>Number of GvL mismatches</b>						<0.001
1	71	5	27	38	1	
2	52	3	31	14	4	
3	38	9	22	0	7	
4	36	27	3	0	6	
5	69	55	3	0	11	
6	47	42	1	0	4	
>6	6	1	0	0	5	

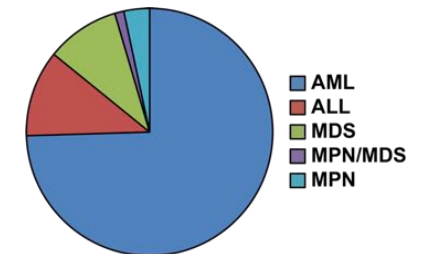
## Centers



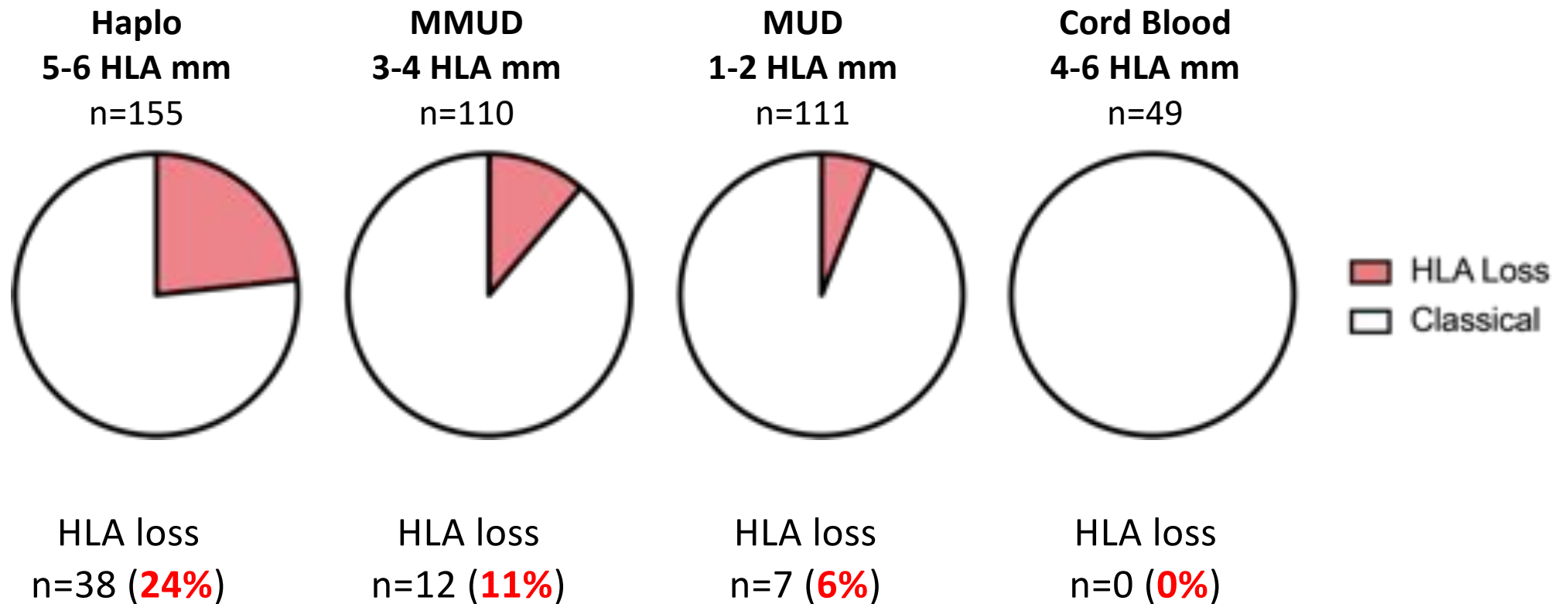
## Donor Types



## Diseases



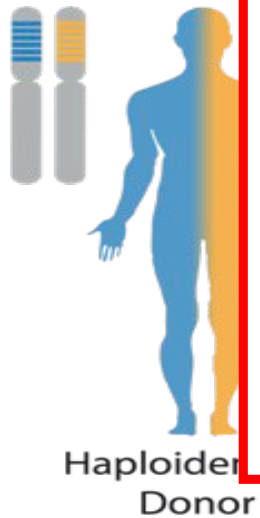
# Results: Incidence of HLA Loss



# An Immunogenetic Perspective

## Haploidentical HSCT

## Unrelated Cord Blood HSCT



**An HSCT dogma shifting**

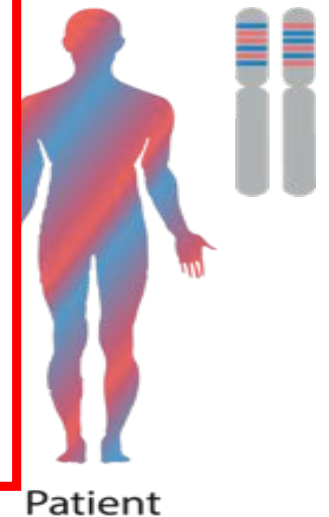
HLA matching as a “conditio sine qua non” (1970-1990)

↓

Incompatibilities no longer a barrier (1990-present)

↓

The future: Exploiting mismatches to improve outcome?



Donor

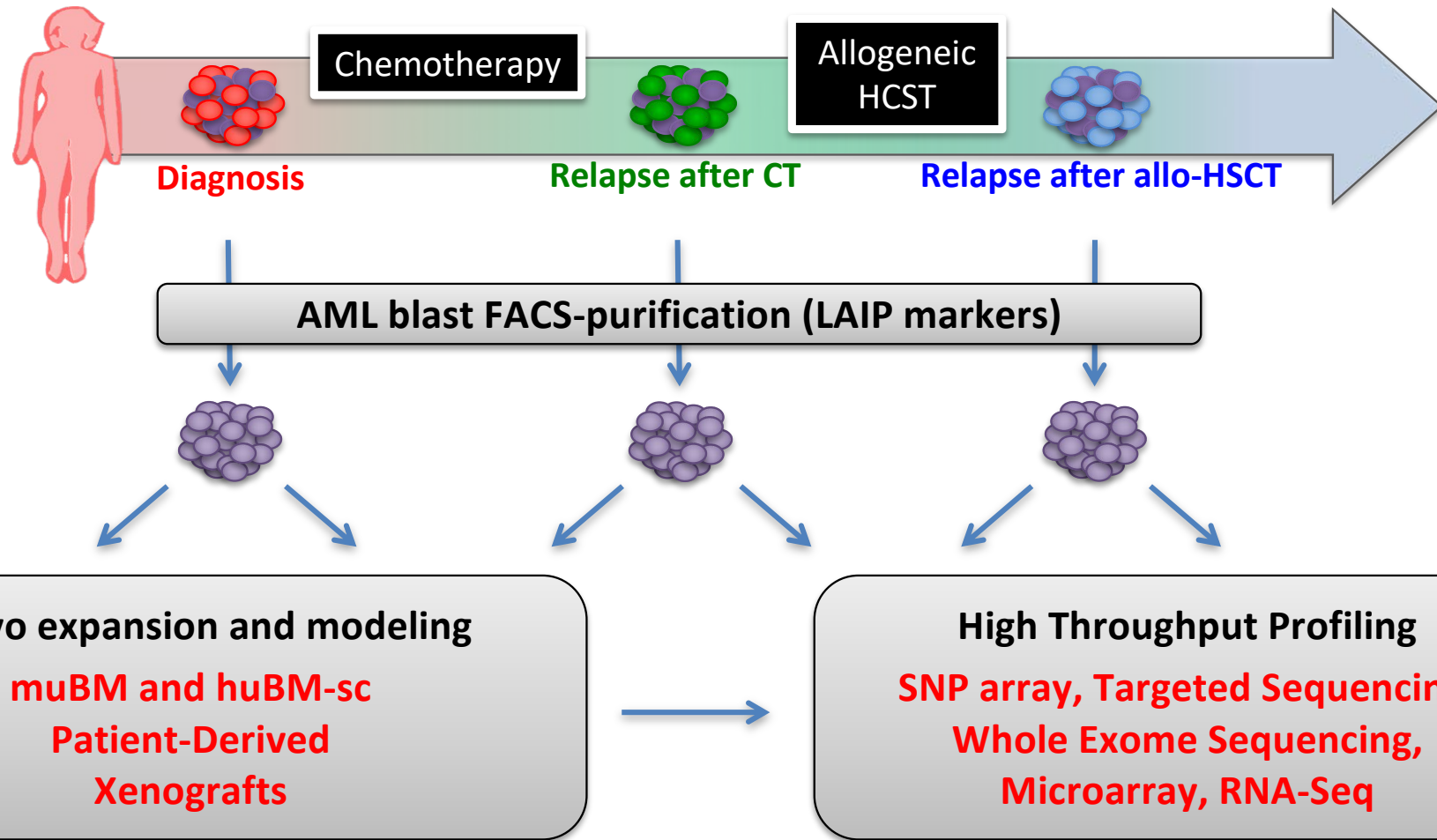
Patient

# Outline of the Talk

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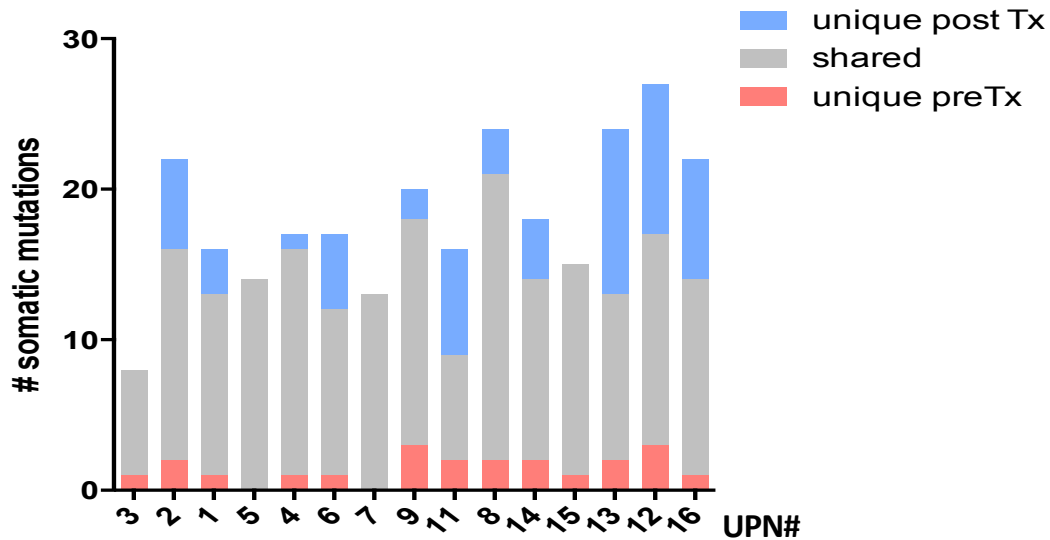
1. Genomic HLA loss (10 years later, becoming an evergreen?)
- 2. Novel modalities of relapse (it's not all in genomics...)**

# Seeking New Mechanisms of AML Immune Evasion



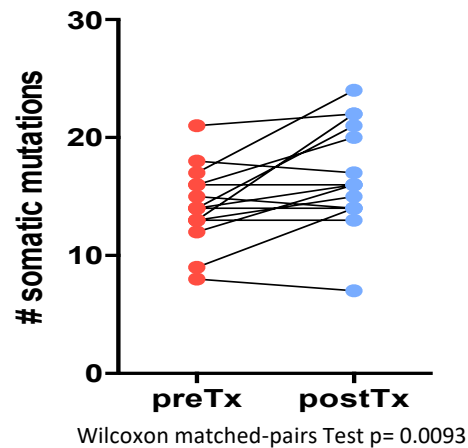


# Mutational Landscape of Relapsed AML



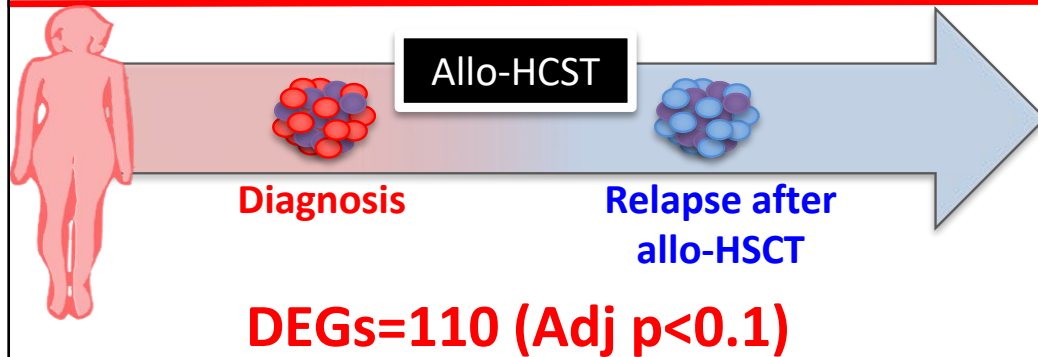
Average coverage for tumor sample: 120X

		UPN#7	UPN#11	UPN#6	UPN#5	UPN#13	UPN#4	UPN#3	UPN#15	UPN#14	UPN#2	UPN#12	UPN#1	UPN#9	UPN#8
tumor suppressor	WT1														
	BRCA1														
myeloid TFs	CBFA2T3														
other TFs or repressor	GFI1B														
	UBTF														
	TRIM13														
	TRIM15														
	ZHX3														
	ZBTB42														
	FOXB1														
RAS pathway	KRAS														
	RIT2														
Ser-Thre kinase pathway	CCND3														
protein phosphatase	PTPN9														
ion channel or transporter	GRIN3B														
	STXBP1														
	SCN3A														
ubiquitin pathway	UBE3B														
RNA splicing	SUGP1														

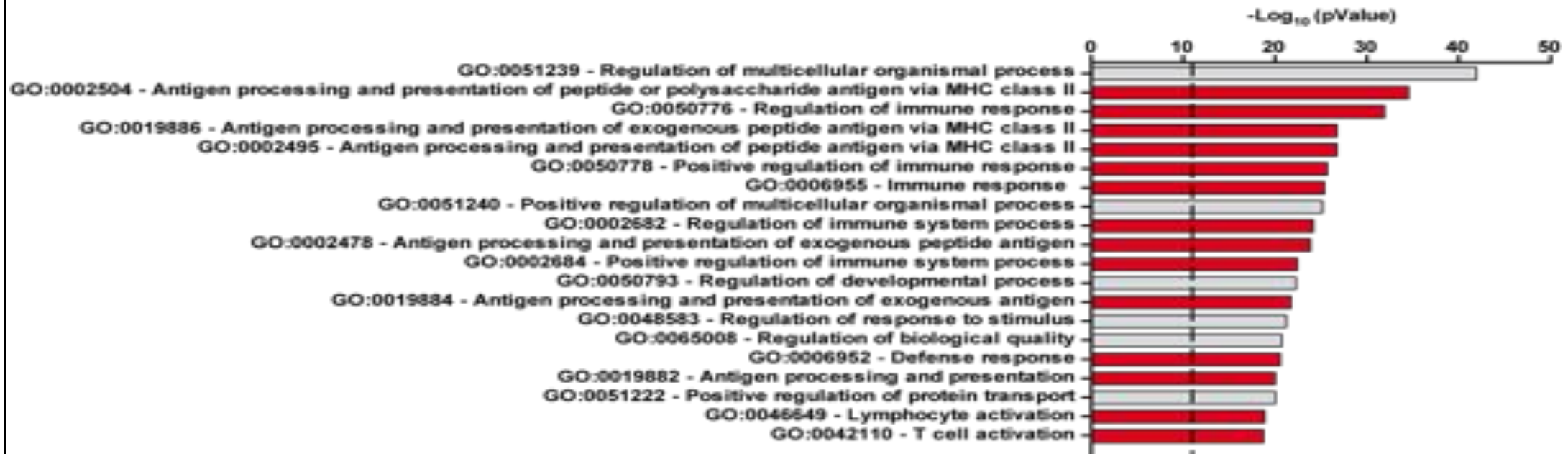


+ other 30 SNV unclassified

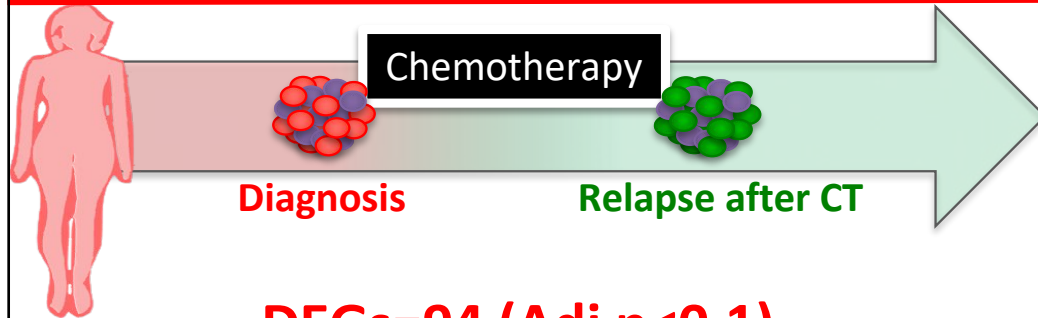
# Deregulation of Immune Processes after Allo-HSCT



**62%** (18/29) of the BP  
( $p\text{Value} < 0.05$ ) are involved in  
**immune related processes**

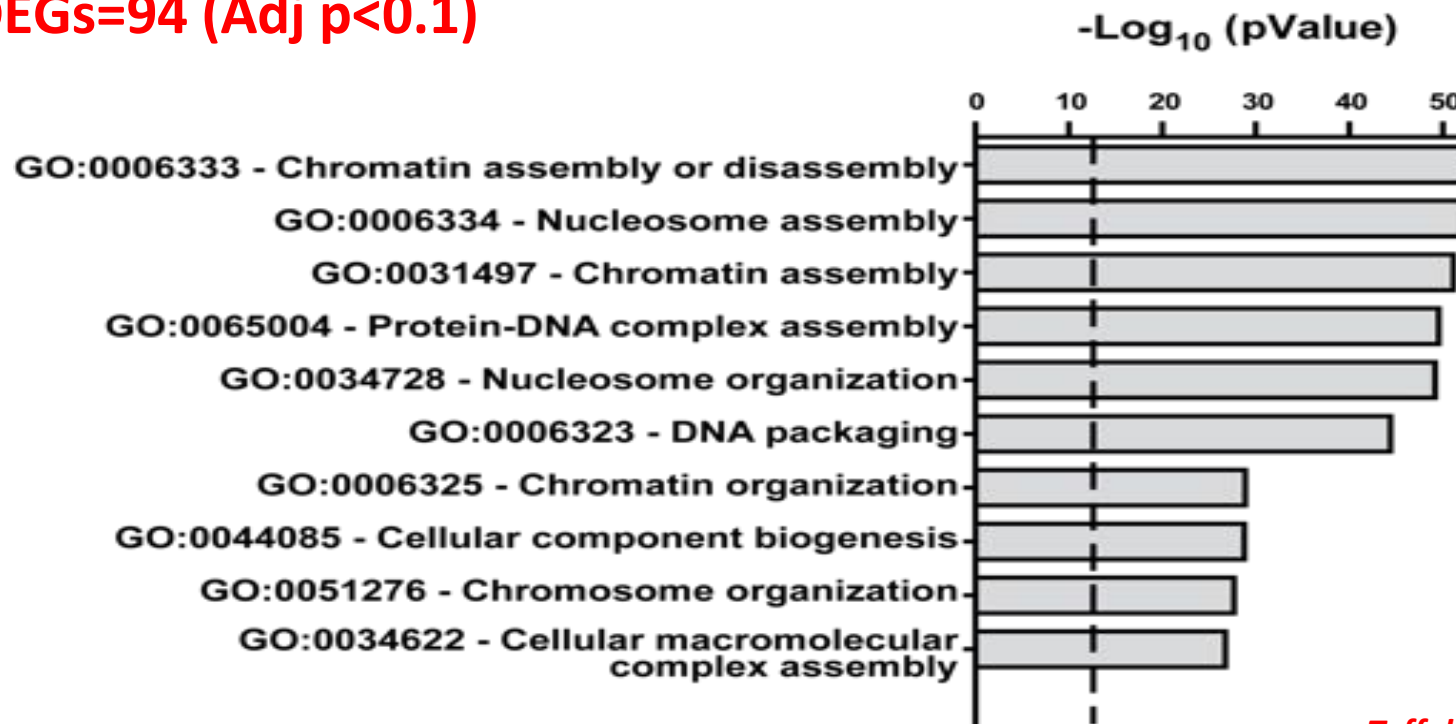


# Deregulation of Immune Processes after Allo-HSCT

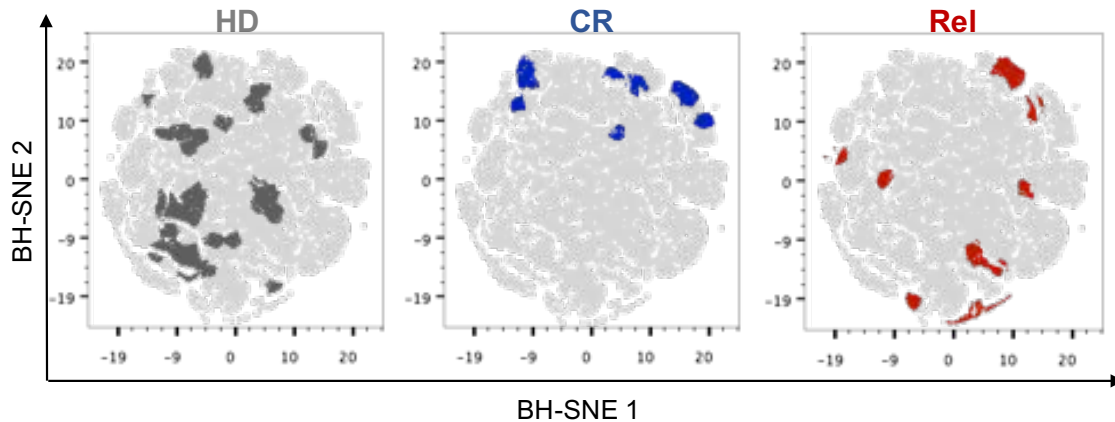


**DEGs=94 (Adj p<0.1)**

No significant enrichment for immune-related processes

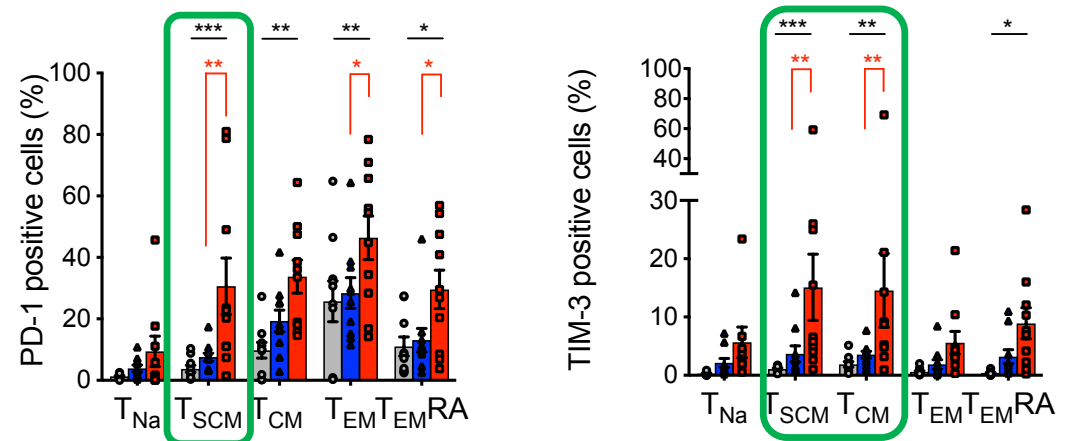


# Exhaustion of Early-Differentiated Tumor-Specific T Cells in the Bone Marrow Anticipates Relapse

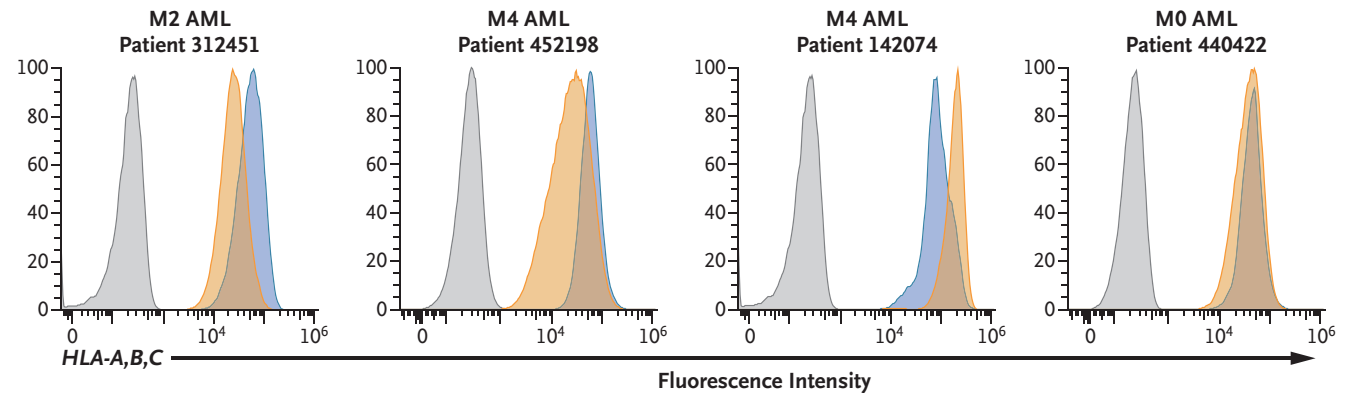
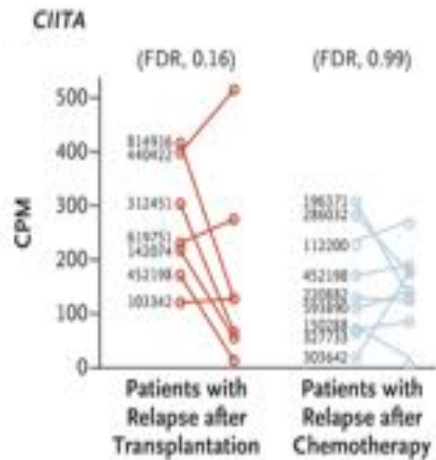
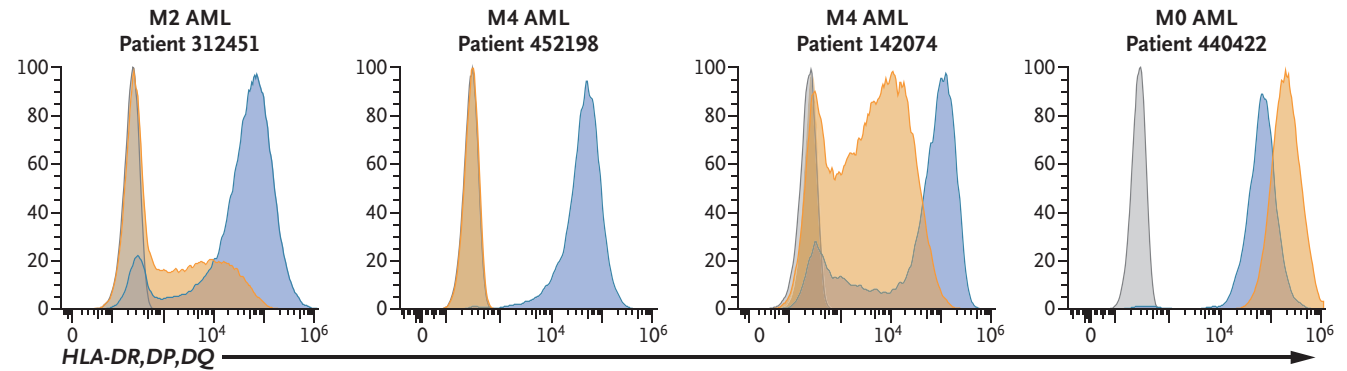
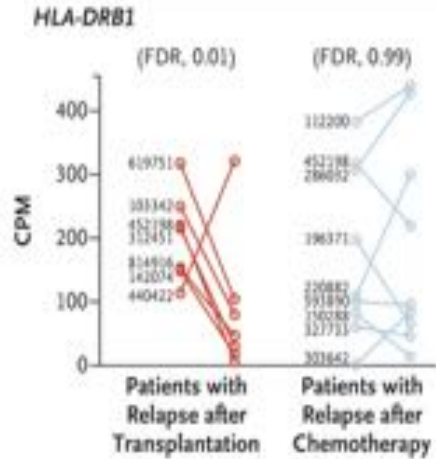


Phenotypic features of T cells infiltrating the bone marrow of relapsing patients are unique

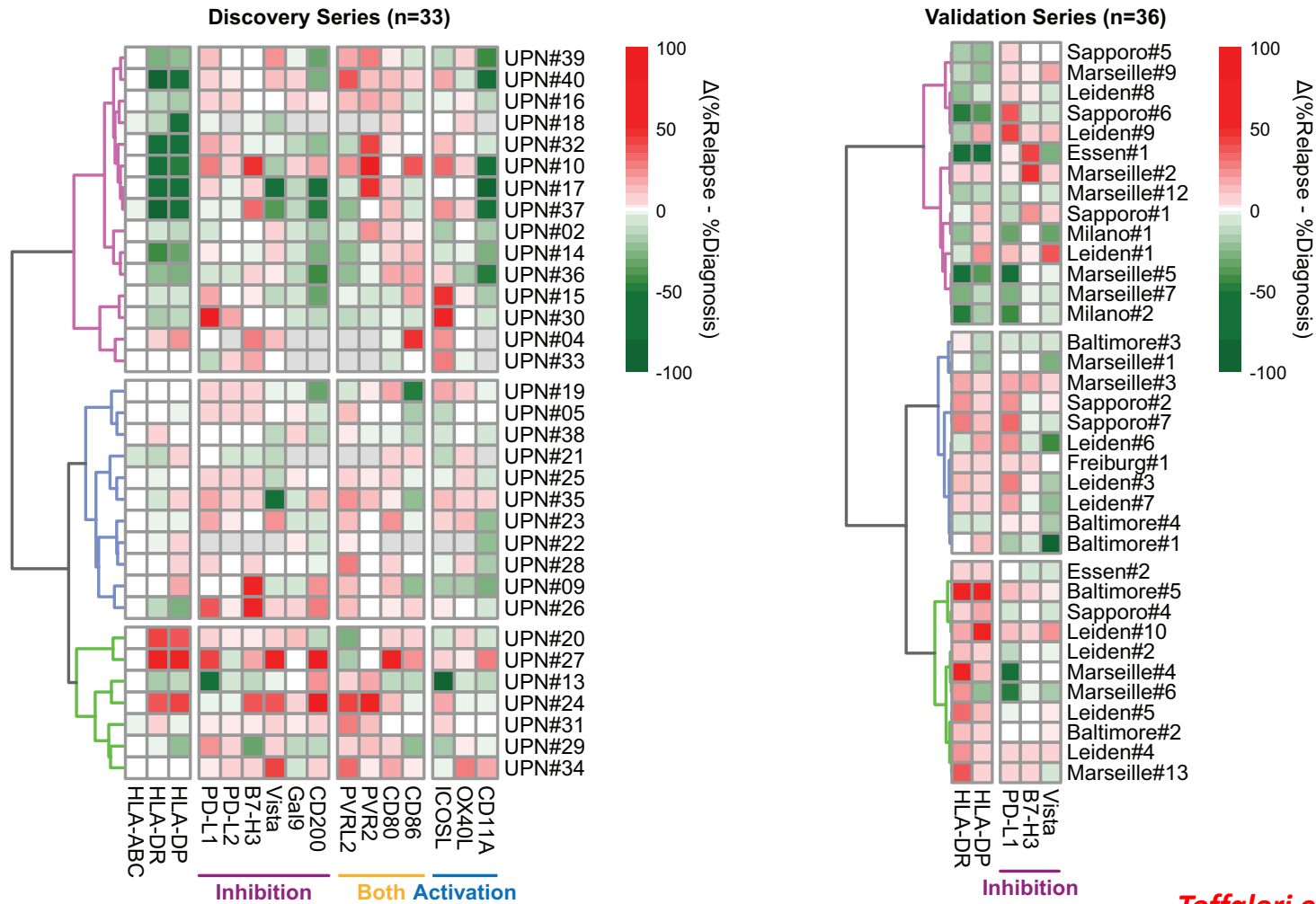
In relapsing patients, T cell exhaustion encompasses not only effectors, but also early differentiated  $T_{SCM}$  and  $T_{CM}$



# Downregulation of Molecules Involved in HLA class II Presentation



# Deregulation of Cohinibitory Ligands and of HLA class II Molecules Are Largely Non-Overlapping

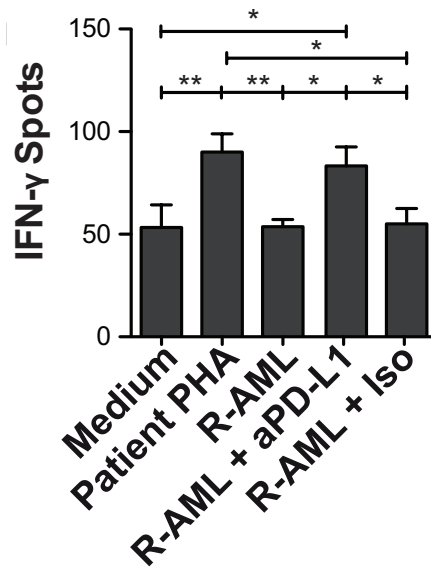


# Deregulation of Cohinibitory Ligands and of HLA Class II Molecules: Therapeutic Implications

**Upregulation of Inhibitory Ligands**  
(mostly IFN-regulated genes)



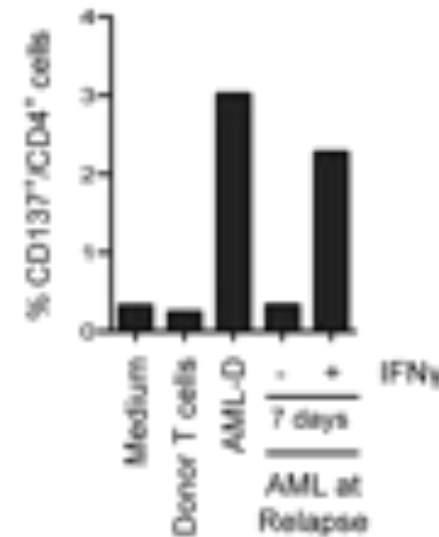
**Worsened by inflammatory signals,  
bypassed through checkpoint blockade**



**Downregulation of HLA class II molecules**  
(also IFN-regulated genes)

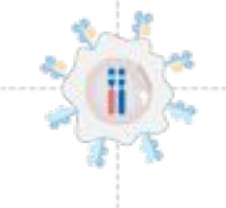
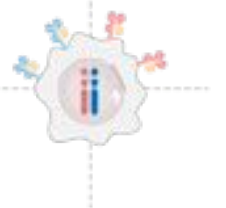
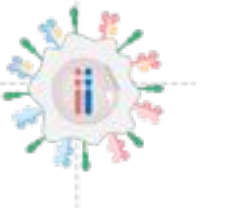


**Recovered though  
inflammatory signals**



*Toffalori et al, Nat Medicine, 2019*

# Post-Transplantation Relapse Modalities: A Recap

	Genomic HLA haplotype loss ("HLA loss")	Downregulation of HLA class II molecules	Upregulation of inhibitory molecules
			
<b>Molecules involved</b>	Incompatible HLAs (both class I and class II)	Compatible and incompatible class II HLAs	PD-L1, B7-H3, PVR, PVRL2
<b>Molecular mechanism</b>	Genomic (CN-LOH)	Epigenetic	Epigenetic
<b>Type of transplants</b>	Mainly HLA-incompatible (haplo>unrelated>cord)	HLA-matched and incompatible	HLA-matched and incompatible
<b>Frequency</b>	~30% in haploidentical, 5-15% in unrelated	30-40% overall	~20% (difficult to address due to complex pattern)
<b>Detection method</b>	HLA typing of sorted blasts, HLA-KMR, HLA-NGS	Flow cytometry, RNA-seq of sorted blasts	Flow cytometry, RNA-seq of sorted blasts
<b>Therapy</b>	No donor lymphocyte infusions, re-transplant or non HLA-restricted immunotherapies	Induction of IFN- $\gamma$ release through leukemia cross-recognition or inflammatory microenvironment (GvHD?)	Immune checkpoint blockade (combinatorial?)

Relapse therapy should be **personalized** and **guided by immunobiology**



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