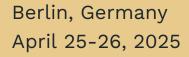
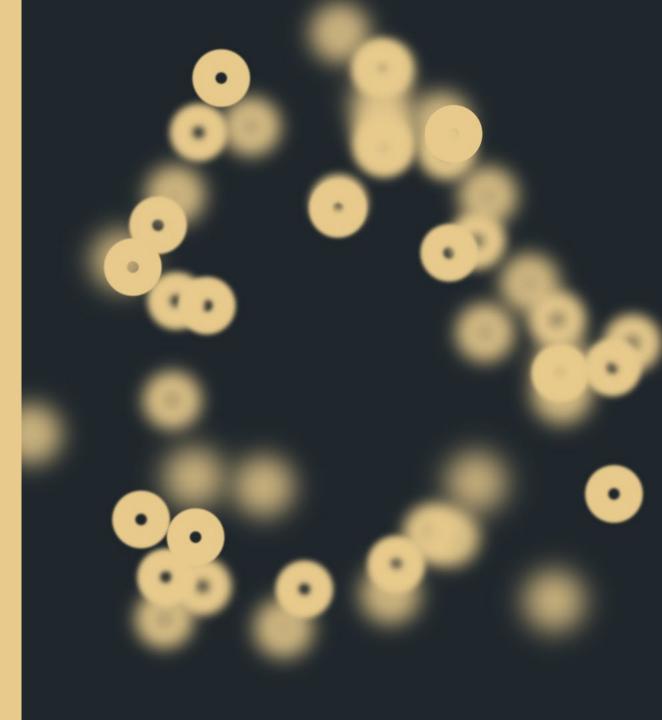


AML and the Bone Marrow Microenvironment

Prof D Bonnet The Francis Crick Institute, London, UK



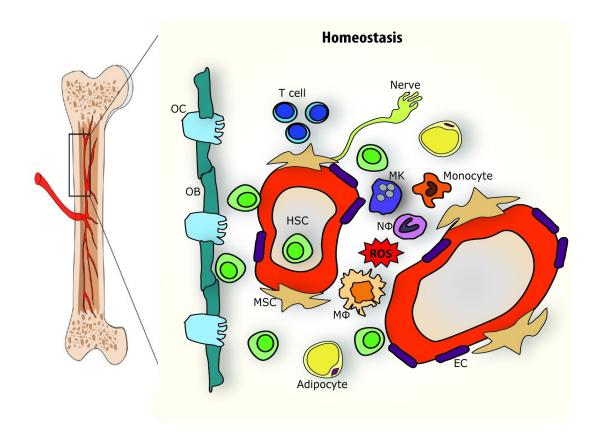


DISCLOSURES OF COMMERCIAL SUPPORT

• Nothing to declare

Bone Marrow Environment (BME): Complex ecosystem

- AML-IC could be maintained *ex vivo* via co-culture with MSC (Griessinger E et al., Stem Cell Trans Med, 2014; Griessinger et al. Cancer Res, 2016)



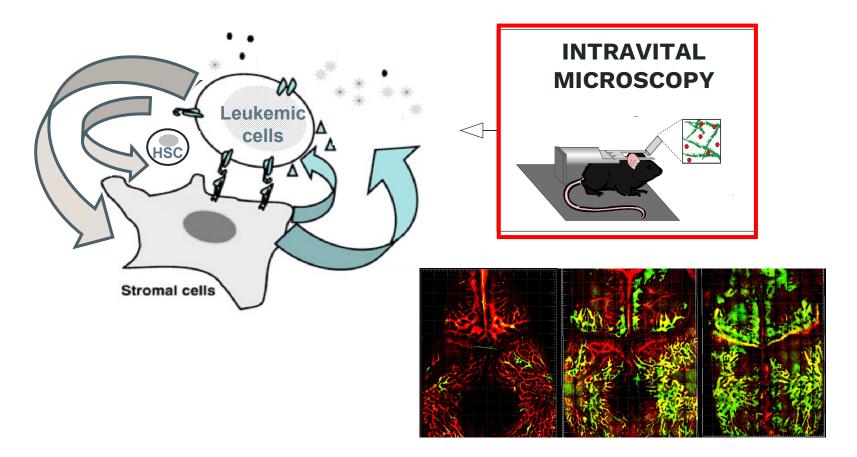
- How malignant cells interact with the BME ?

- What are BME changes during leukaemic evolution: from CH to MDS to AML ?

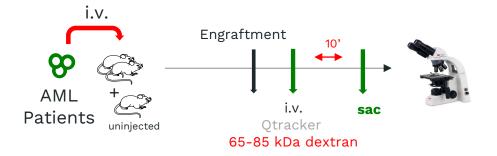
- How is the BME involved in chemoresistance of LSC ?

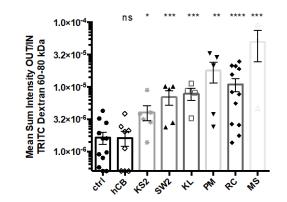
- Can cytotoxic drugs impede BME and potentially promote AML dev/relapse?

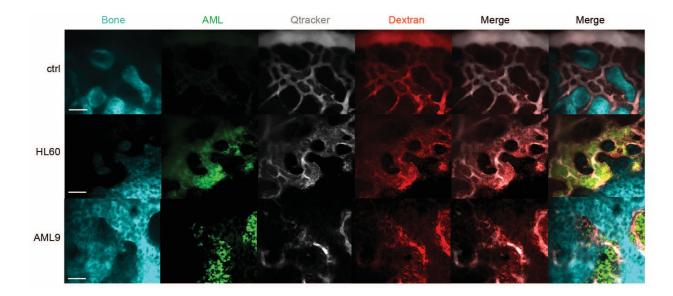
<u>Functional cross-talk between AML and the</u> <u>BM microenvironment</u>



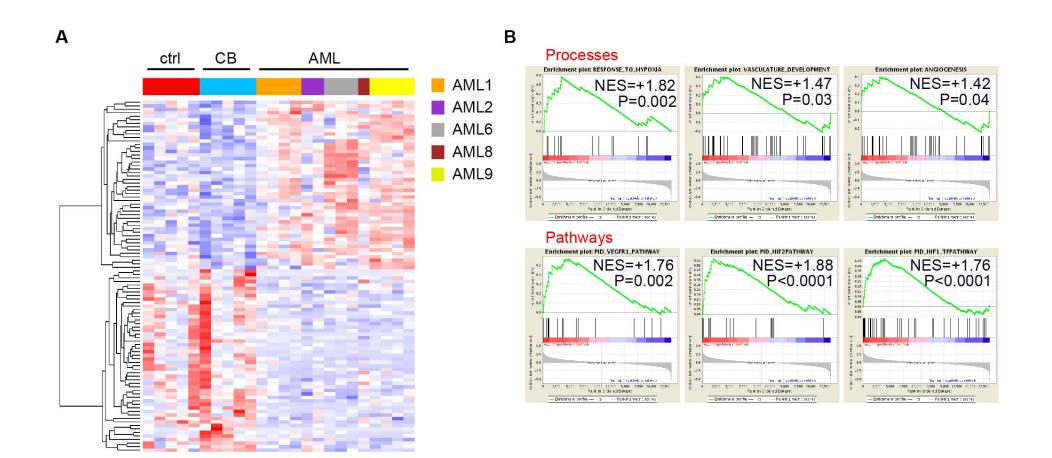
<u>AML-induced toxicity on vessel permeability</u>



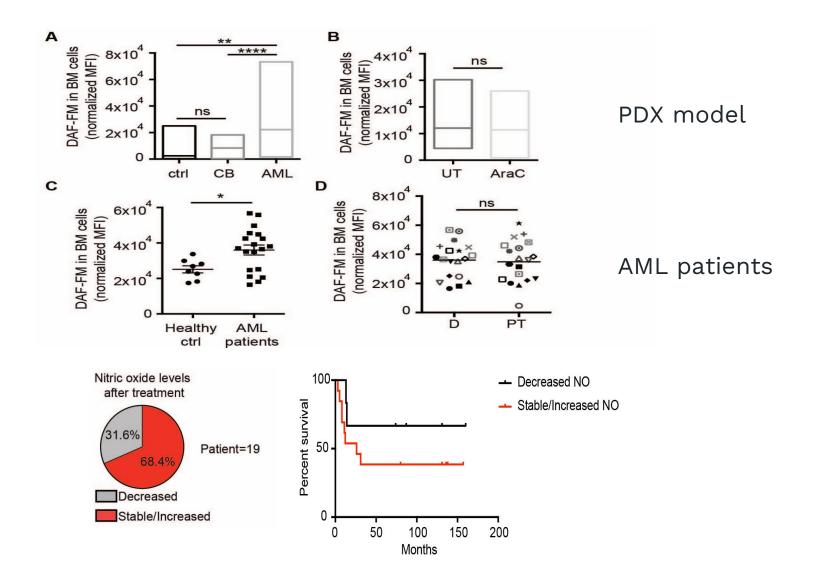




Endothelial cells in contact with AML have altered vascular development, angiogenesis, increase in VEGF-R and HIFs pathways



<u>Upregulation of nitric oxide (NO) pat</u>hway

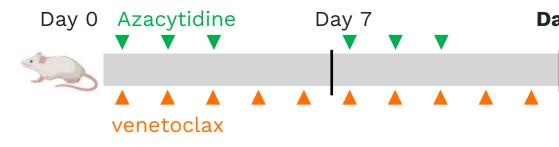


<u>Summary I</u>

- We found several abnormalities in the vascular architecture and function in patient-derived xenografts (PDX), i.e. vascular leakiness.
- We identified an increase in nitric oxide (NO) as major mediator of this phenotype in PDX and in patient-derived BM biopsies.
- Moreover, induction chemotherapy failed to restore normal vascular permeability and NO levels.
- Strikingly, inhibition of NO production reduced vascular permeability, and significantly improved treatment response in PDX.

Does the drugs treatment impact the bone marrow microenvironment?

Ven/aza treatment induces remodeling of the vascular niche





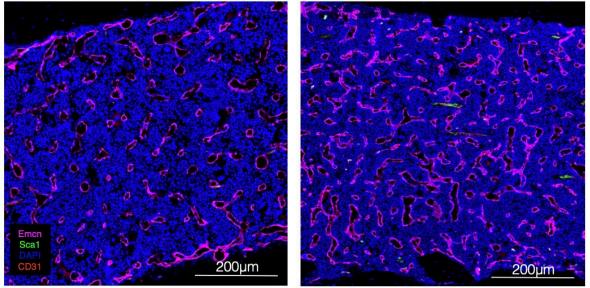
cull mice for:

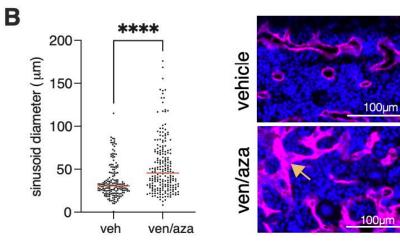
- Immunofluorescent imaging
- Flow cytometry analysis
- scRNAseq



Α



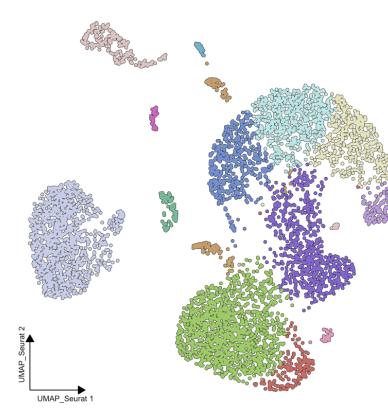


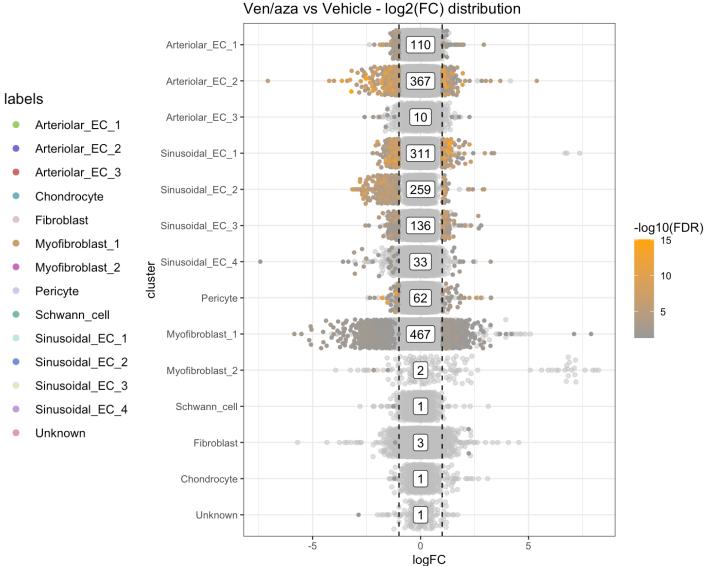




Ven/aza induces transcriptional reprogramming of ECs

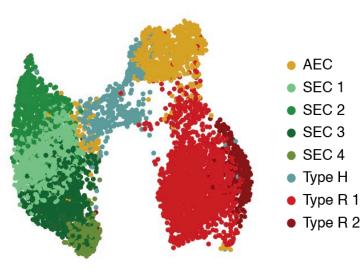




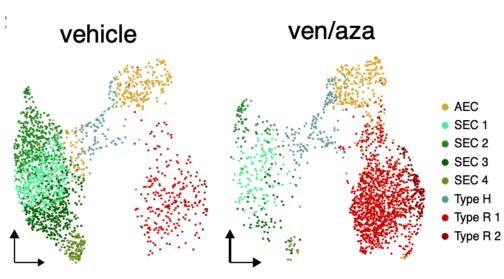


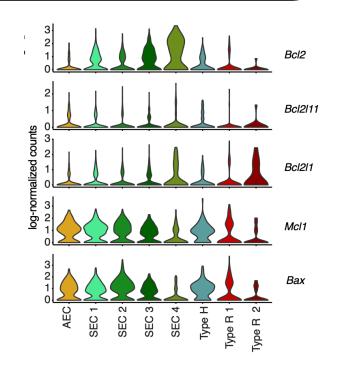
Transcriptional reprogramming in the ECs in response to ven/aza

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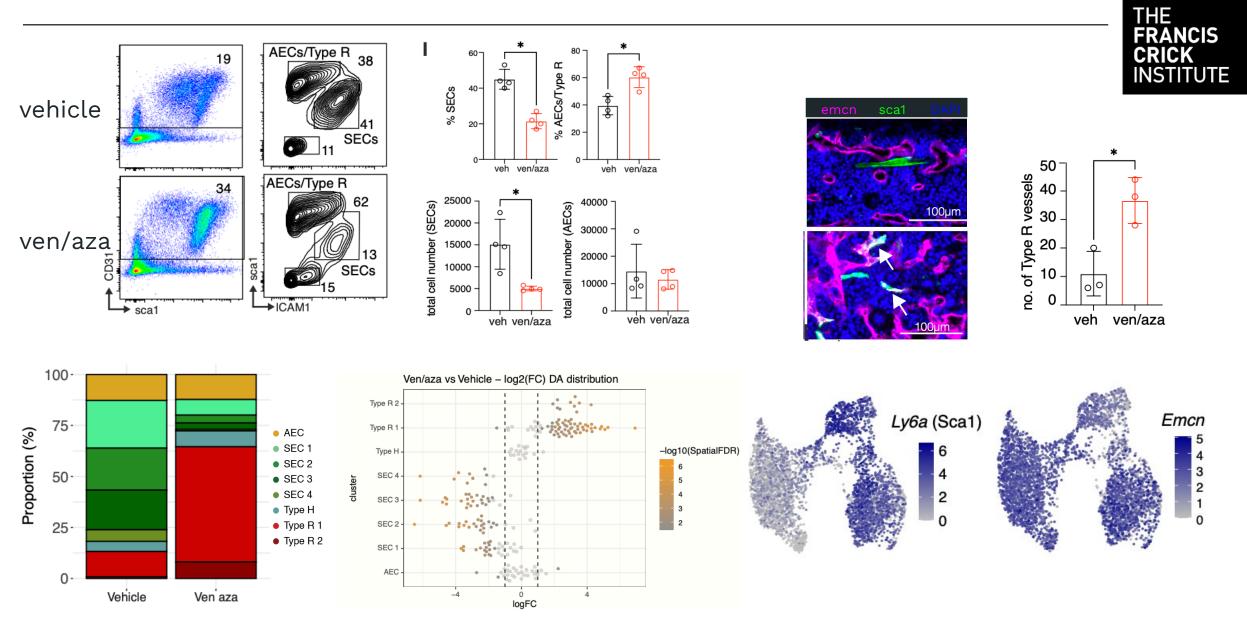


SECs: Sca1^{low}, PDPN⁺, VEGFR3⁺ AECs: Sca1^{high}, PDPN⁻, VEGFR3⁻ Type H: CD31^{high}/Emcn^{high} metaphysis capillary ECs - "**mpECs**" (Kusumbe et al. 2014) Type R: remodelling-associated capillaries -"**rECs**" (Mohanakrishnan et al. 2024)

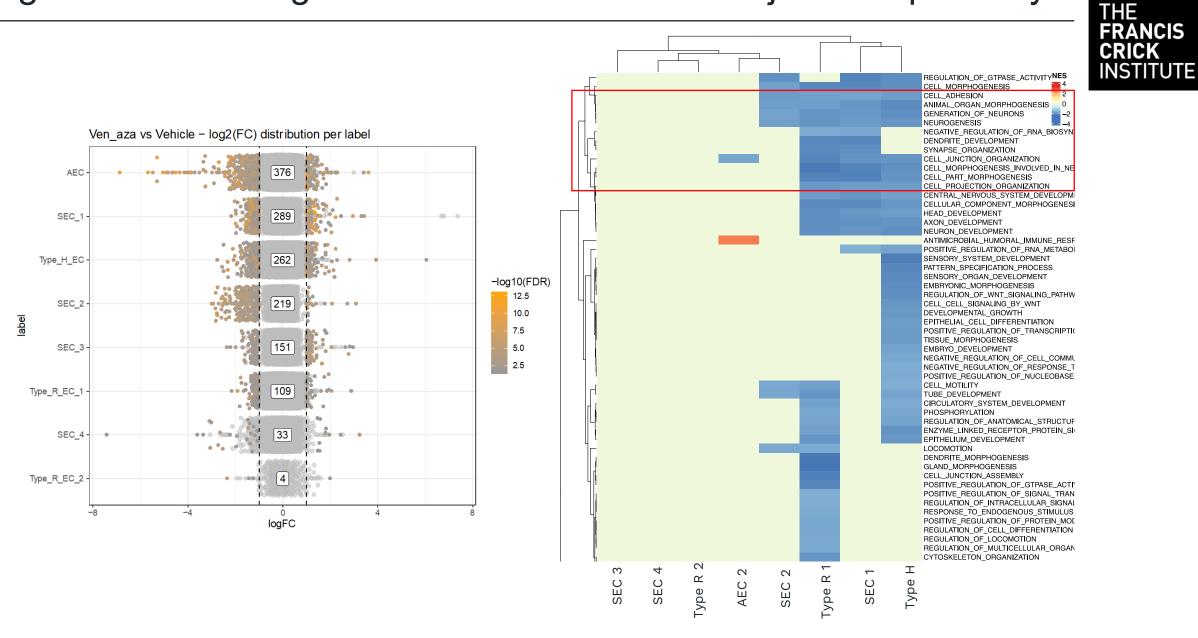




Expansion of novel Type R vessels in response to ven/aza



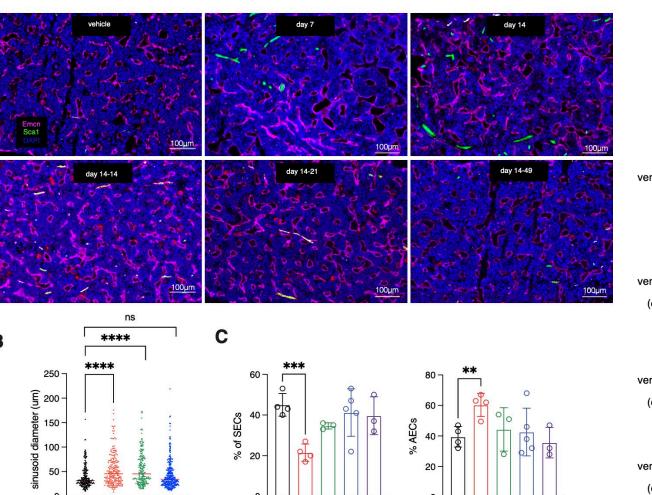
Significant downregulation of cell adhesion/cell junction pathways



Dilation of sinusoids is reversed after three weeks post treatment

othe start other others

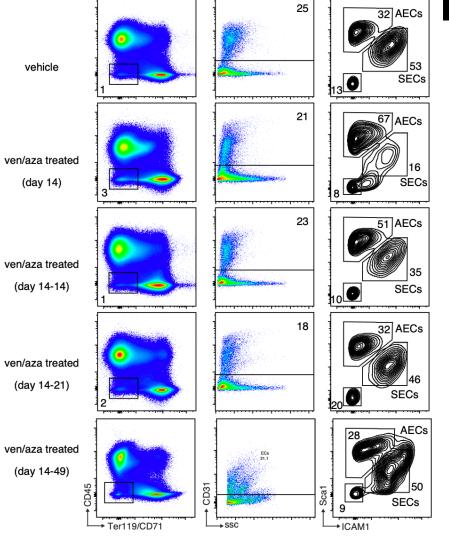
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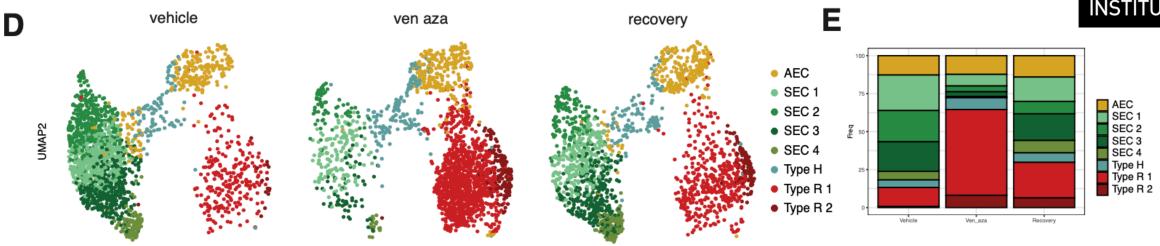
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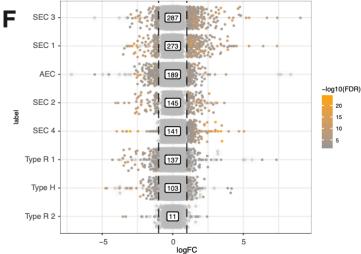
Cell type composition is partially recovered 7 weeks post therapy

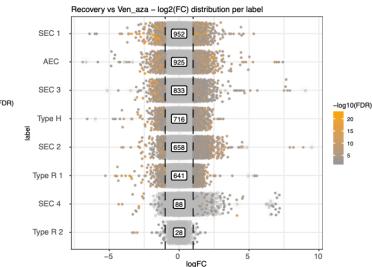
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UMAP1

Recovery vs Vehicle - log2(FC) distribution per label





Partial recovery at the transcriptional level

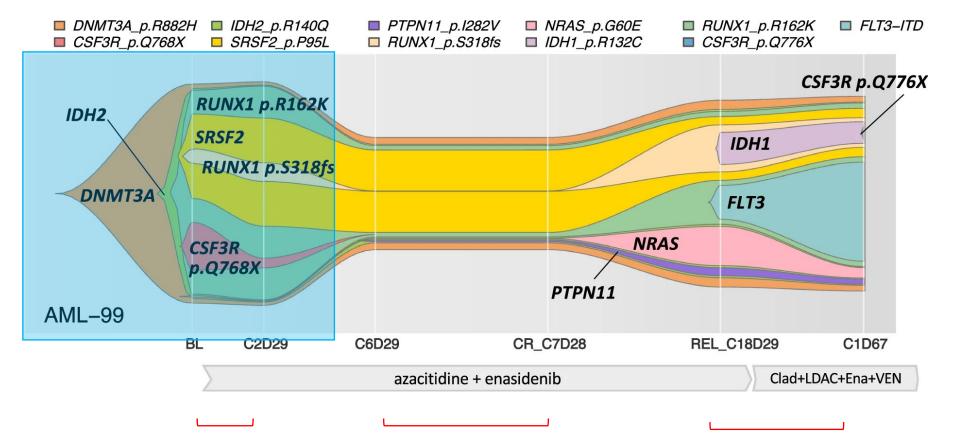


- Venetoclax and azacitidine combinational therapy selectively targets the bone marrow vascular network
- SECs express highest Bcl2 amongst all vascular niche cell types and are most sensitive to therapy
- Damage to the vasculature is partially reversed after three weeks off treatment

Can cytotoxic drugs impede BME and potentially promote AML dev/relapse?



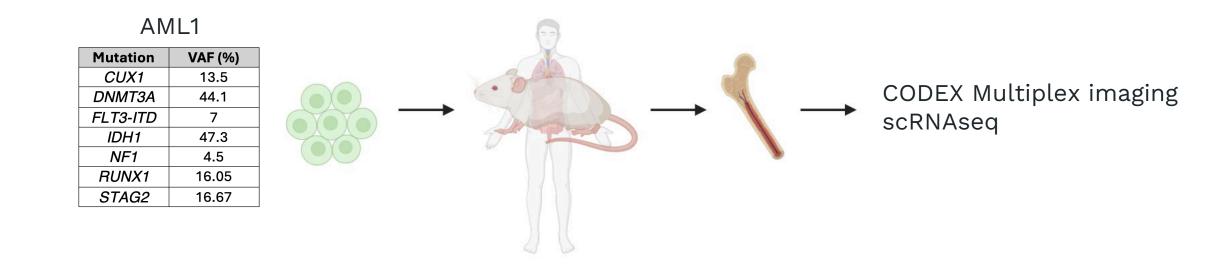
Adapted from Morita et al Nature Comms. 2020



What role does the BME play at each of these stages of disease?

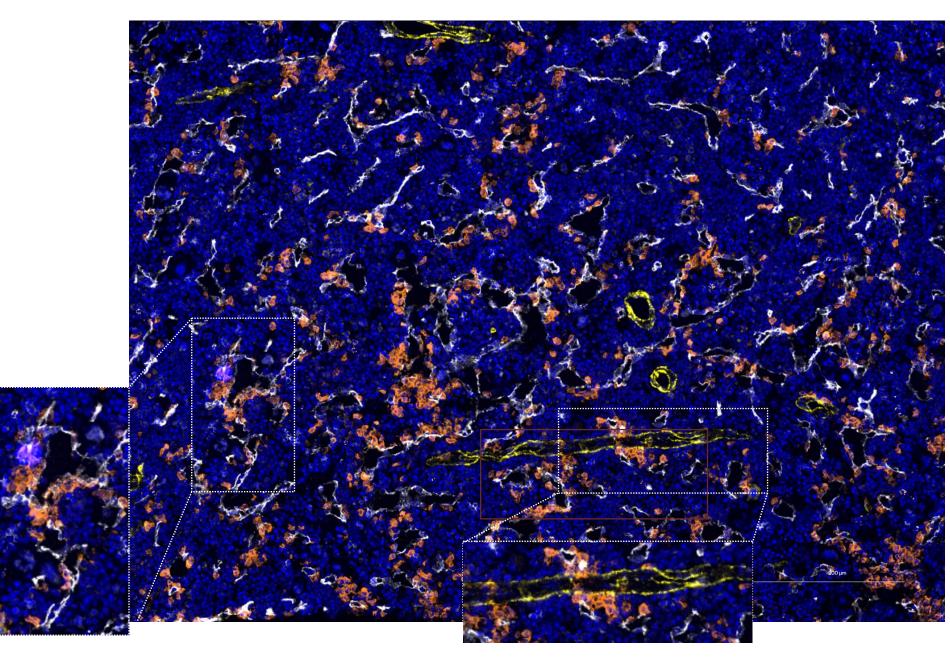
Could different subclones present in an AML patients communicate with the BME differently ?





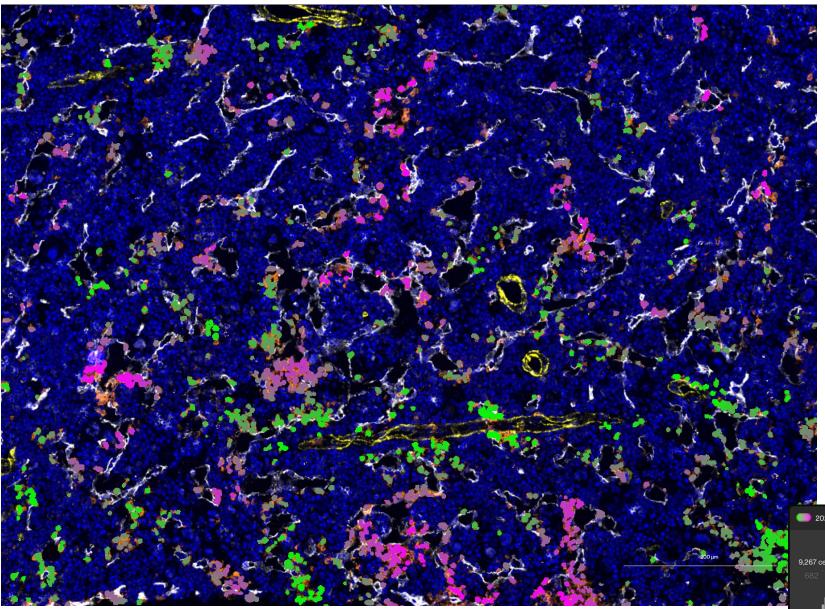
- NSG-SGM3 kit ^{w41/w41} humanized mice allows high engraftment of patient derived cells without irradiation
- mCD45-,hCD45-,Ter119-,CD71- cells were FACs sorted for scRNAseq analysis of the BMN cells

AML blasts localize to either the SECs or AECs



Emcn hCD45 Sma1 DAPI

AML cells localize to either the SECs or AECs





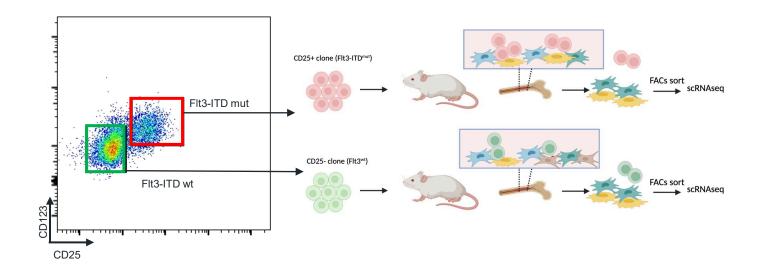
FACs based approach in the isolation of distinct AML subclones

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Marker	fluorophore	
CD34	FITC	
CD38	BUV737	
CD45ra	APC-e780	
ILRaP	AF350	
CD97	PE	
CD82	PE-Cy7	
CD135	BV711	
CD93	BUV661	
CD117	APC	
CD45	PacO	
CD200	BV650	
CD25	BV421	
CD33	PE-Cy5	
viability	Sytox blue	

de Boer et al. Cancer Cell 2018

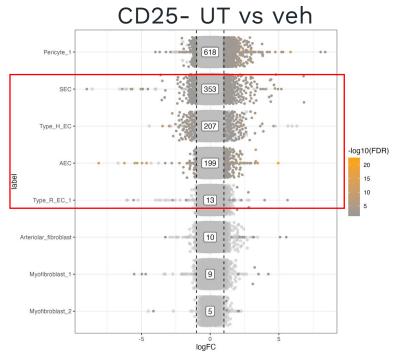
Mutation	VAF (%)	CD25+	CD25-
CUX1	13.5	ns*	ns*
DNMT3A	44.1	45%	45%
FLT3-ITD	7	36%	0
IDH1	47.3	50%	50%
NF1	4.5	ns*	ns*
RUNX1	16.05	ns*	ns*
STAG2	16.67	ns*	ns*

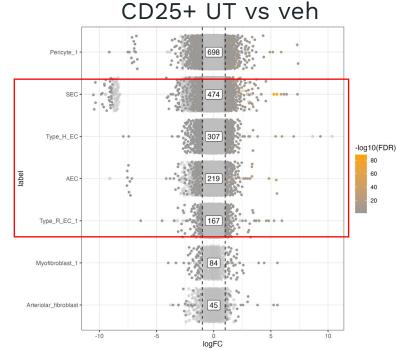


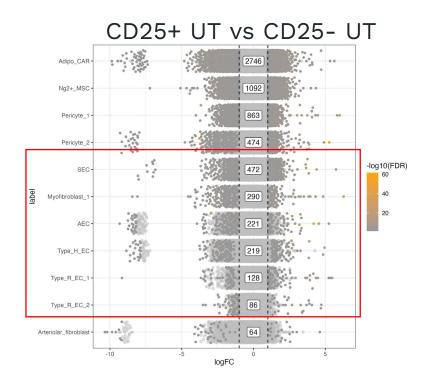


Significant differential gene expression in the presence of AML



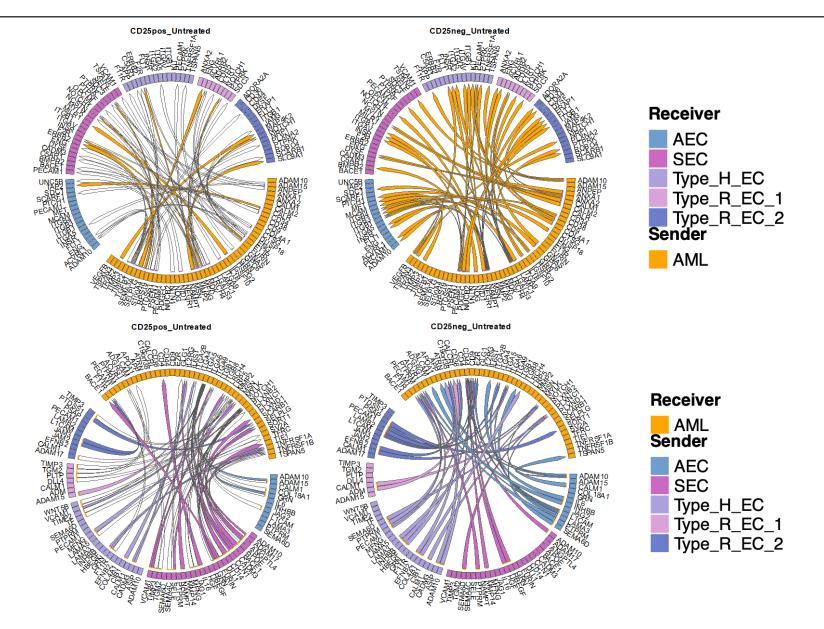








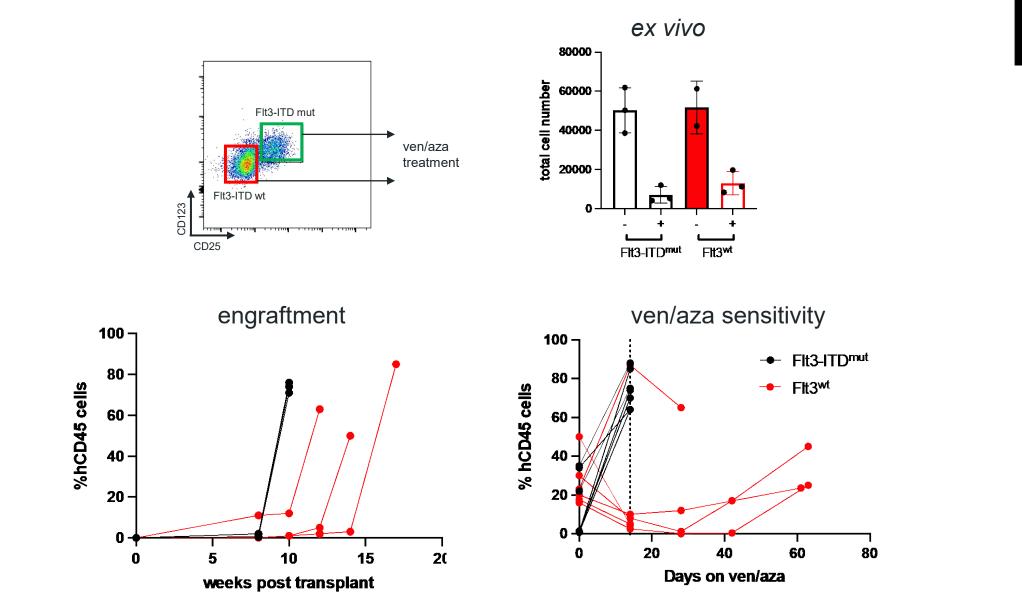
Differential preference in EC interaction between subclones



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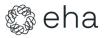
AML1 contains a FLT3-ITD ven/aza resistant subclone







- AML1 contains two distinct genetic subclones that can be separated by the expression of CD25.
- CD25+ subclone is resistant to ven/aza whereas CD25- subclone is sensitive
- We show that CD25+ subclone communicate more with SECs and CD25- subclone with AEC
- Does cross-talk between SECs and the CD25+ subclone contribute to resistance to ven/aza therapy?
- What interactions between the CD25+ and SECs are present following ven/aza treatment?



ACKNOWLEDGMENTS

Haematopoietic Stem Cell Lab

Thanks for your attention !!



Scientific Technical Platforms

Flow cytometry Advanced sequencing Bioinformatic/Biostatistic

Clinical collaborators:

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Manuel Garcia-Albornoz Marion Piganeau Aneesh Sharma Alexander Waclawiczek **Diana Passaro** Jenny Huang

Anna Song

Henry Wood









the Ray Kendall leukaemia fund



Questions related to t-AML?

- 1. Is the bone marrow microenvironment (BMME) the hidden catalyst in malignant haematopoiesis?
- 2. Genome-wide DNA damage in HSCs after cytotoxic therapies are driving the initiation and progression to t-MN: What about the long-term toxicities/effects of the BMME?

