

19th International Uttmann Chicago Lymphoma Symposium

**LIVE
Symposium**

APRIL 29-30
2022



THE UNIVERSITY OF
CHICAGO
MEDICINE &
BIOLOGICAL
SCIENCES

Biology of Follicular Lymphoma

R. Kridel, Princess Margaret Cancer Centre, Toronto

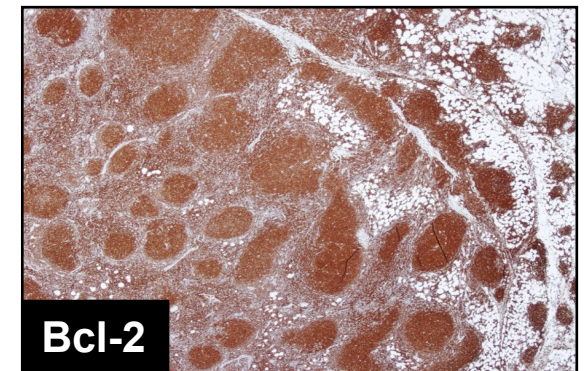
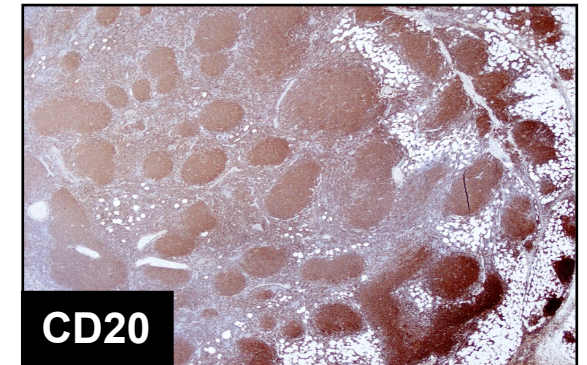
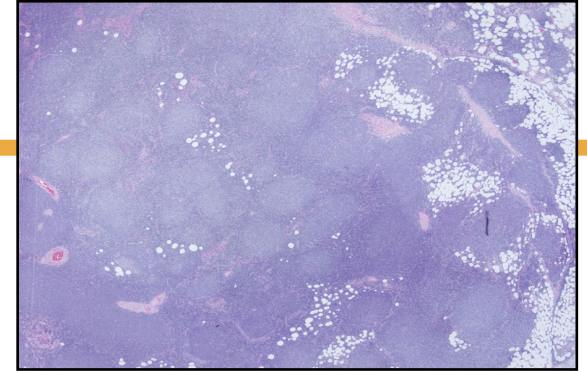


Disclosures

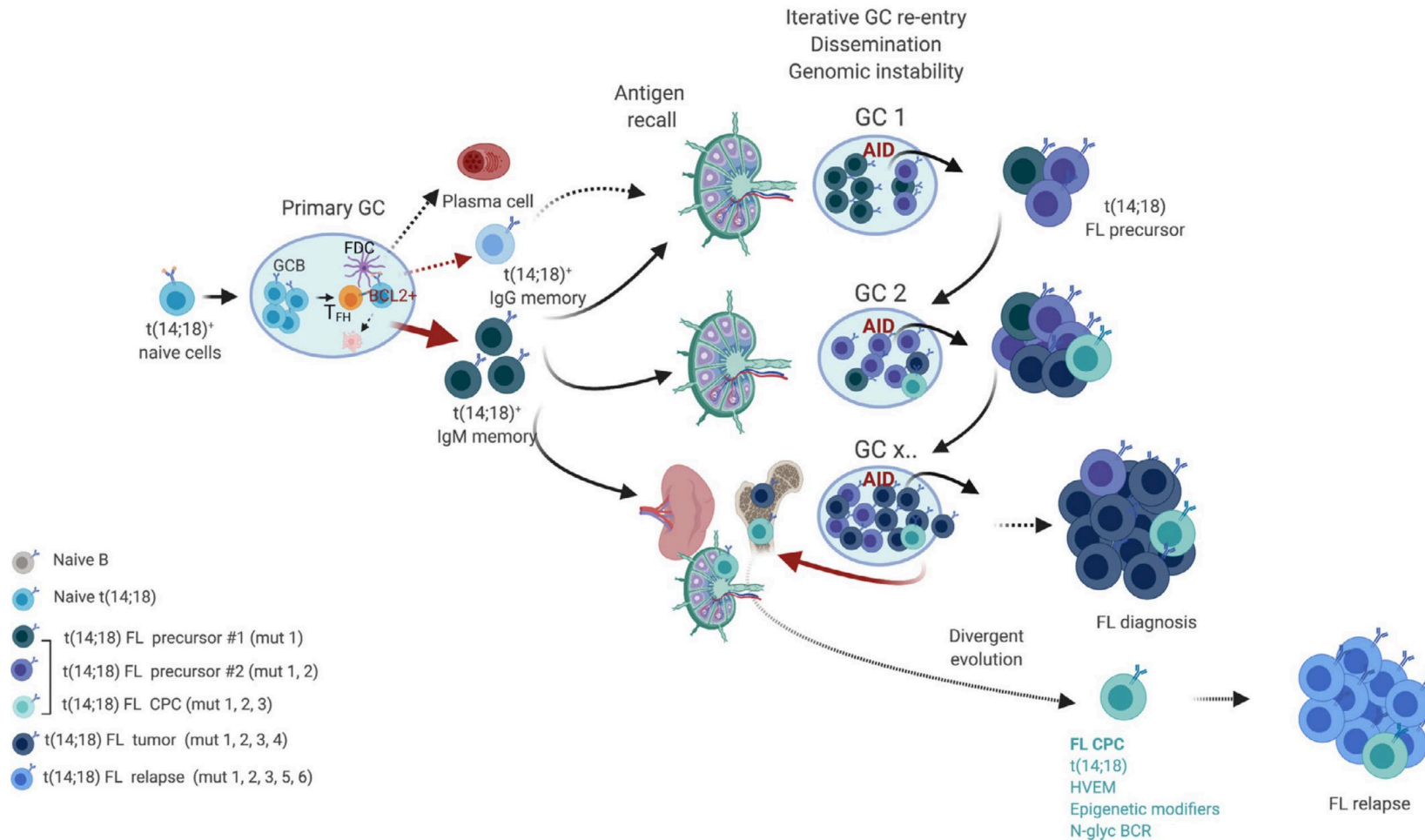
- Research funding from Roche and Abbvie.

Pathology

- FL grade 1-3A -> classic FL (cFL)
- FL grade 3B -> follicular large B-cell lymphoma (FLBCL)
- t(14;18) in ~85% of cases
- Variations:
 - In-situ follicular B-cell neoplasm
 - Paediatric-type follicular lymphoma
 - Duodenal-type follicular lymphoma
 - Primary cutaneous follicle centre lymphoma

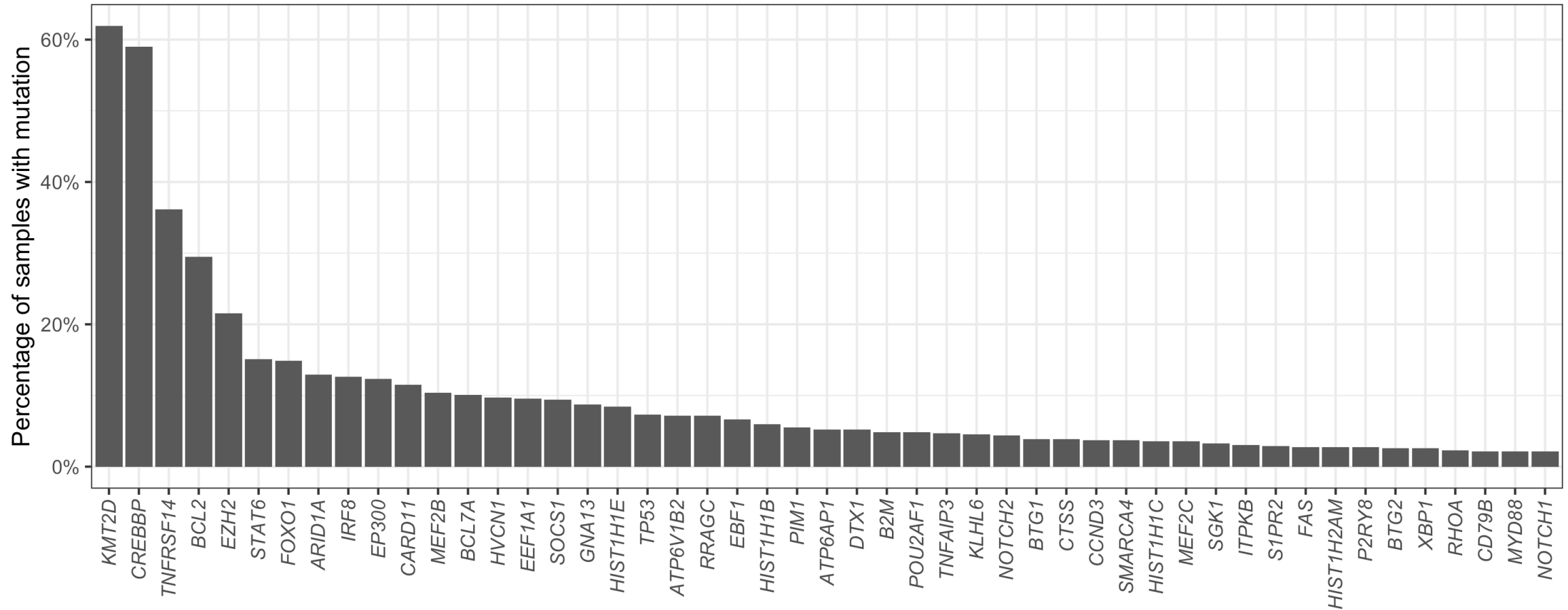


Stepwise model of follicular lymphoma pathogenesis



Milpied et al. *Advances in Immunology*, 2021

Mutational landscape



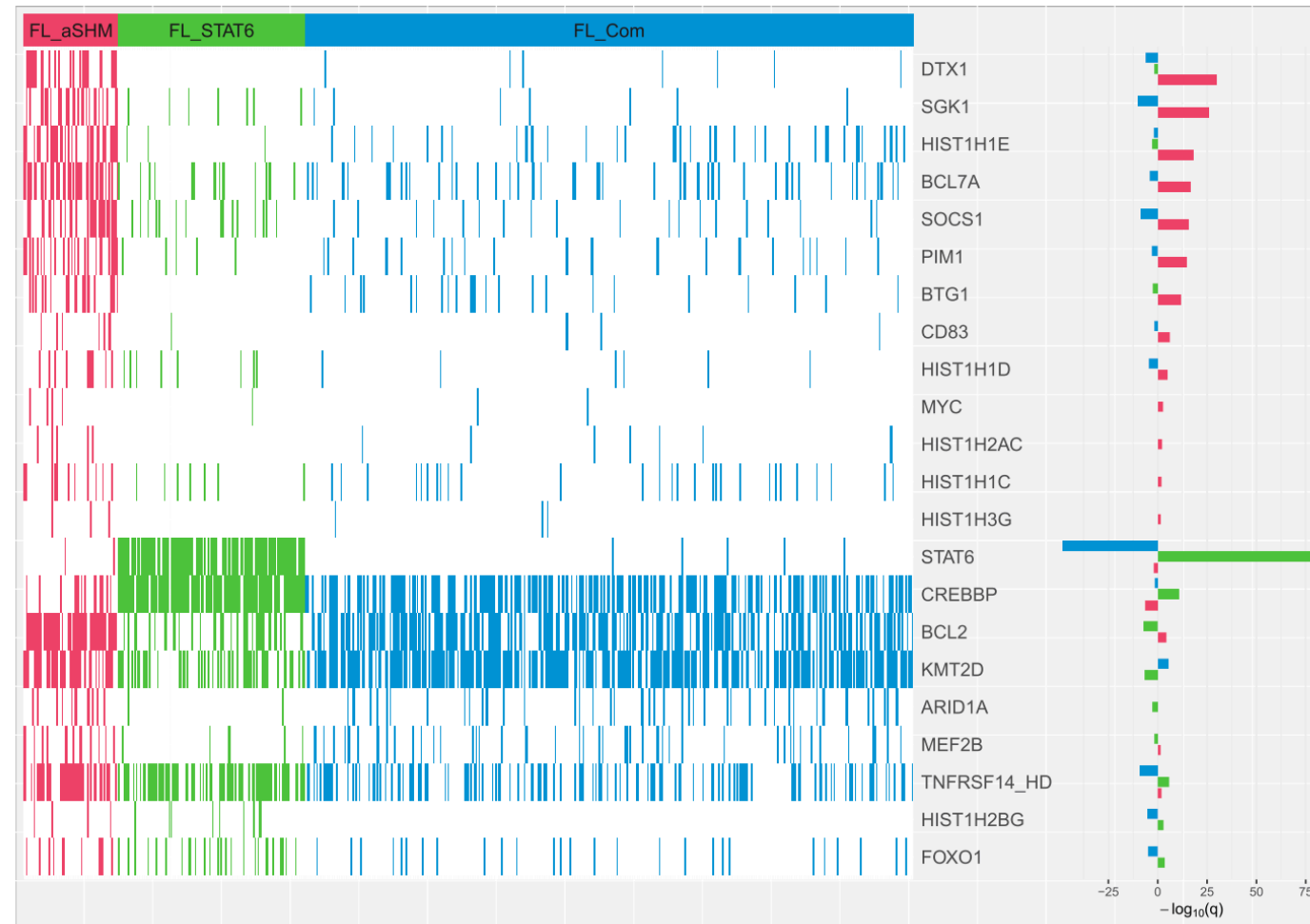
Genetic subtypes in FL

UK Haematological
Malignancy Research
Network

548 pts

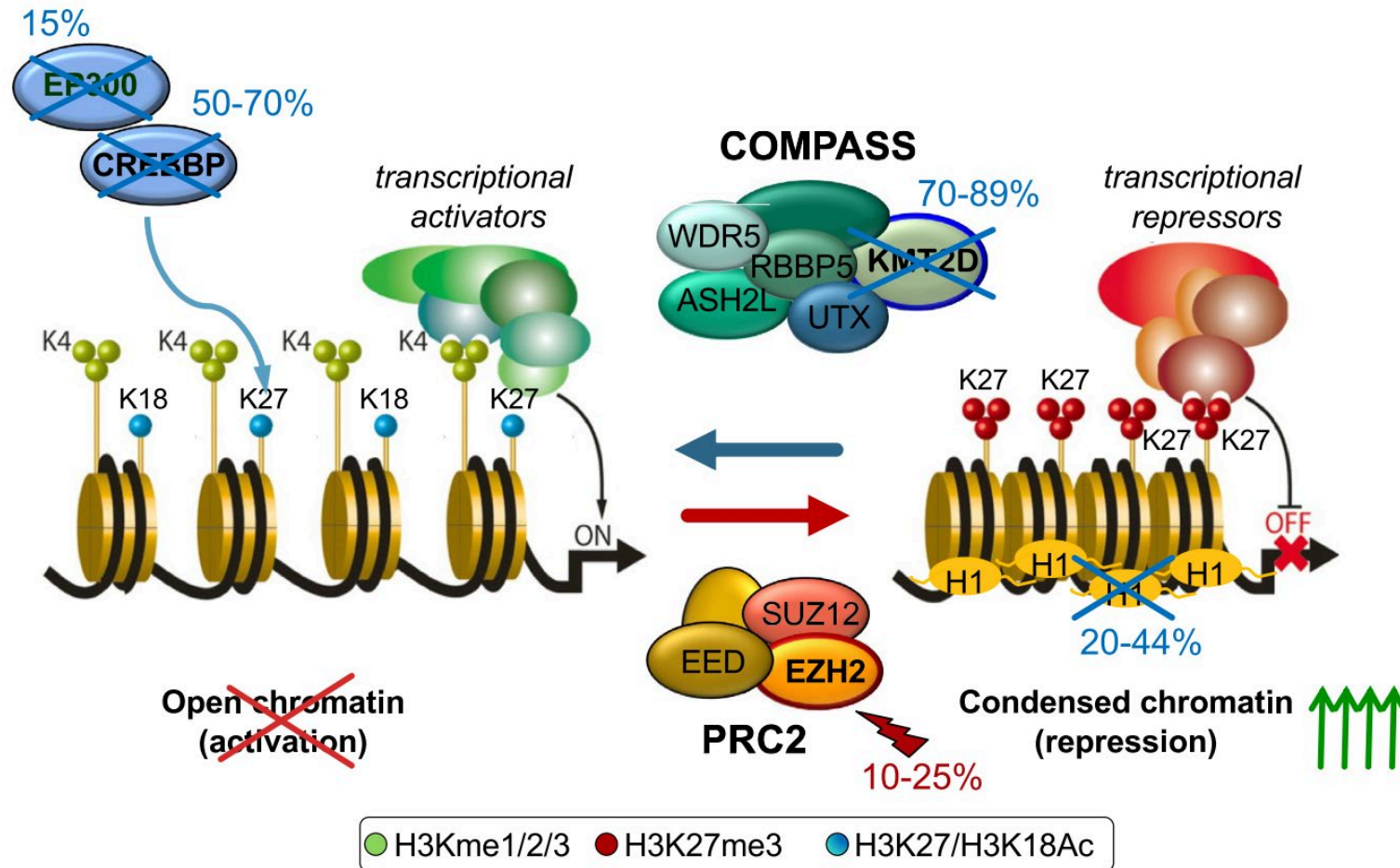
Targeted DNA sequencing
(293-gene panel)

aSHM subgroup associated
with inferior outcome (older
age)

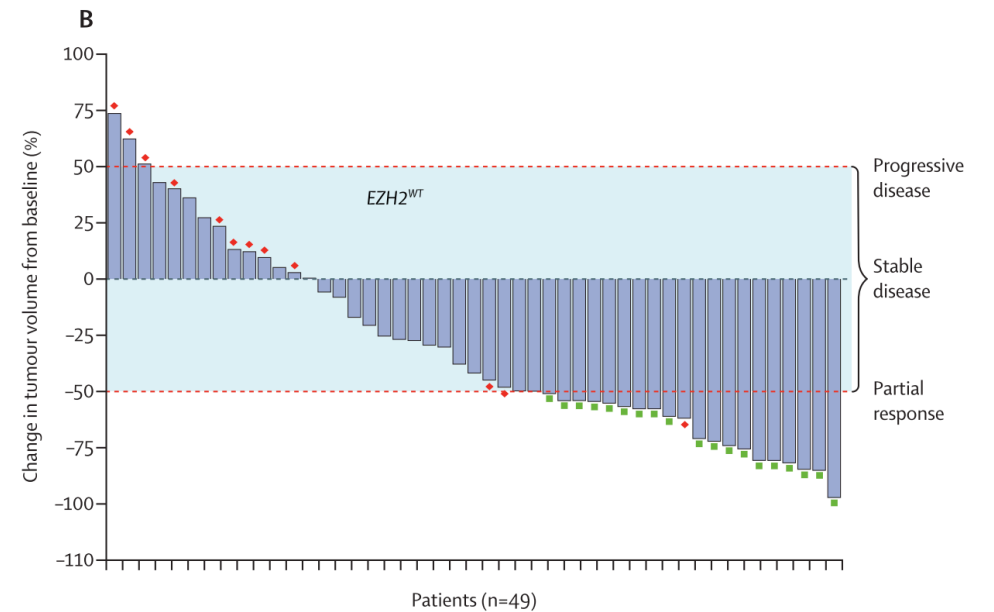
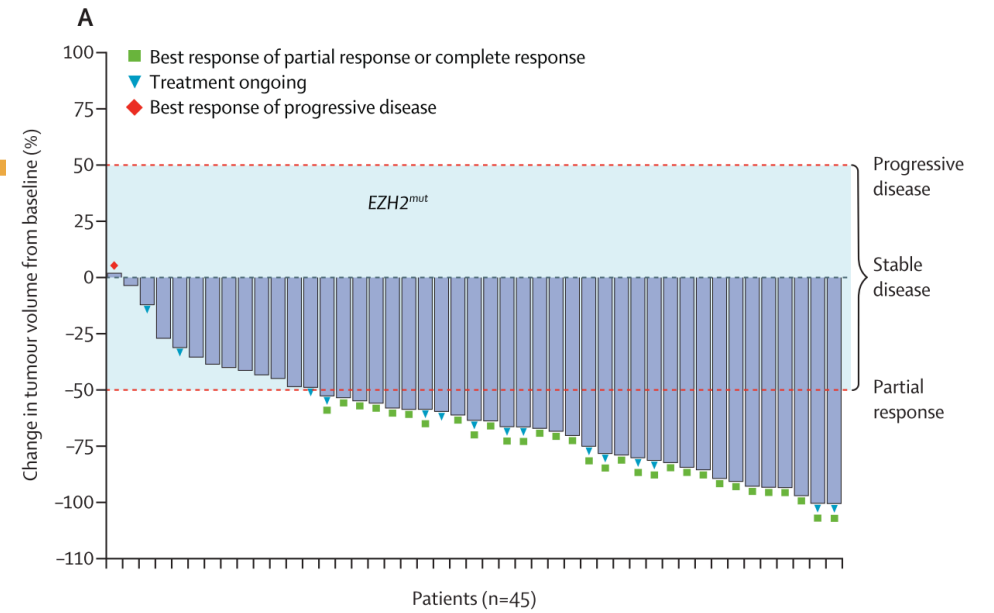
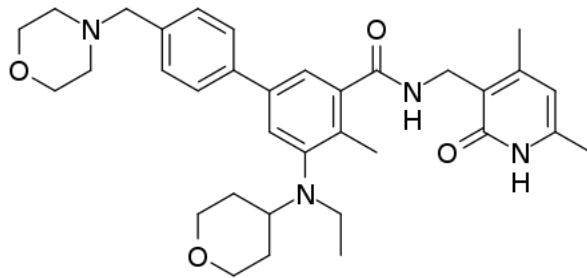
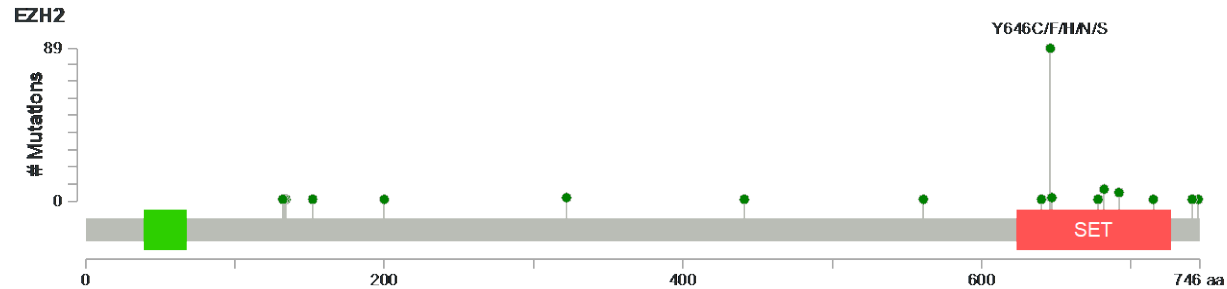


Crouch et al. Blood Advances, 2022

Remodeling of epigenetic machinery



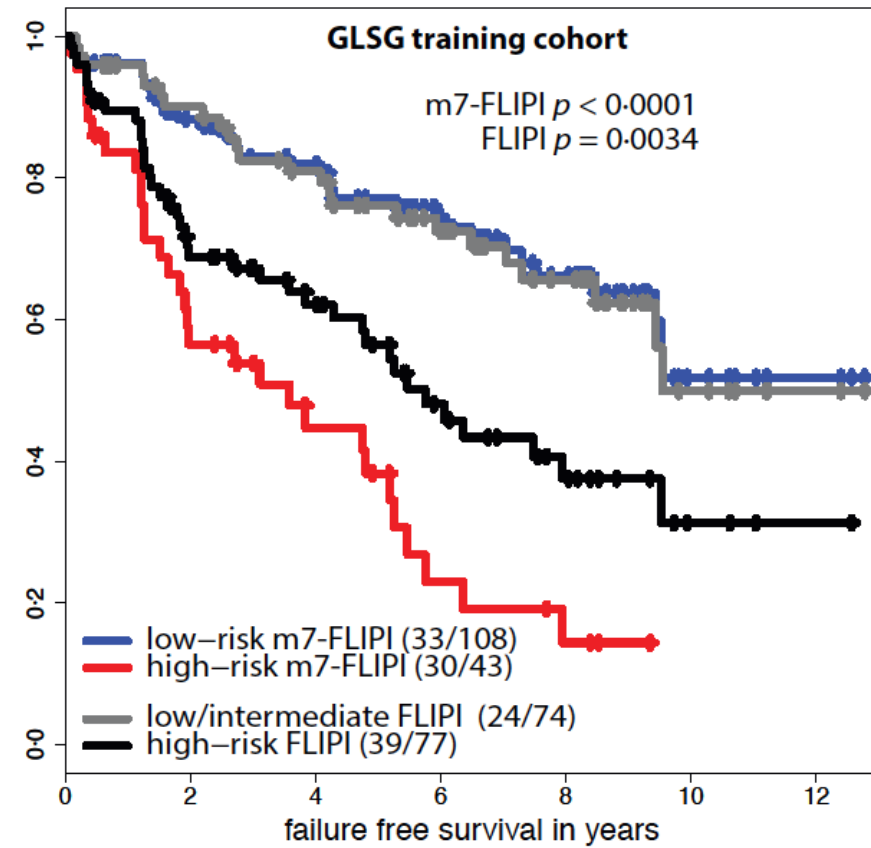
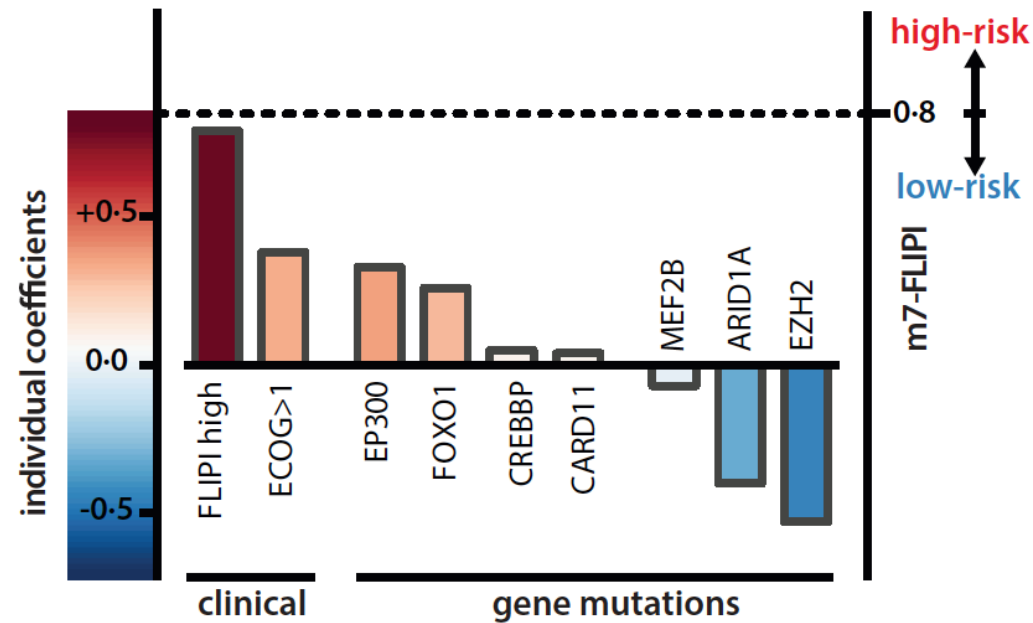
EZH2 – target for therapy



m7-FLIPI

151 patients GLSG – R-CHOP

107 patients BC Cancer – R-CVP +/- maintenance



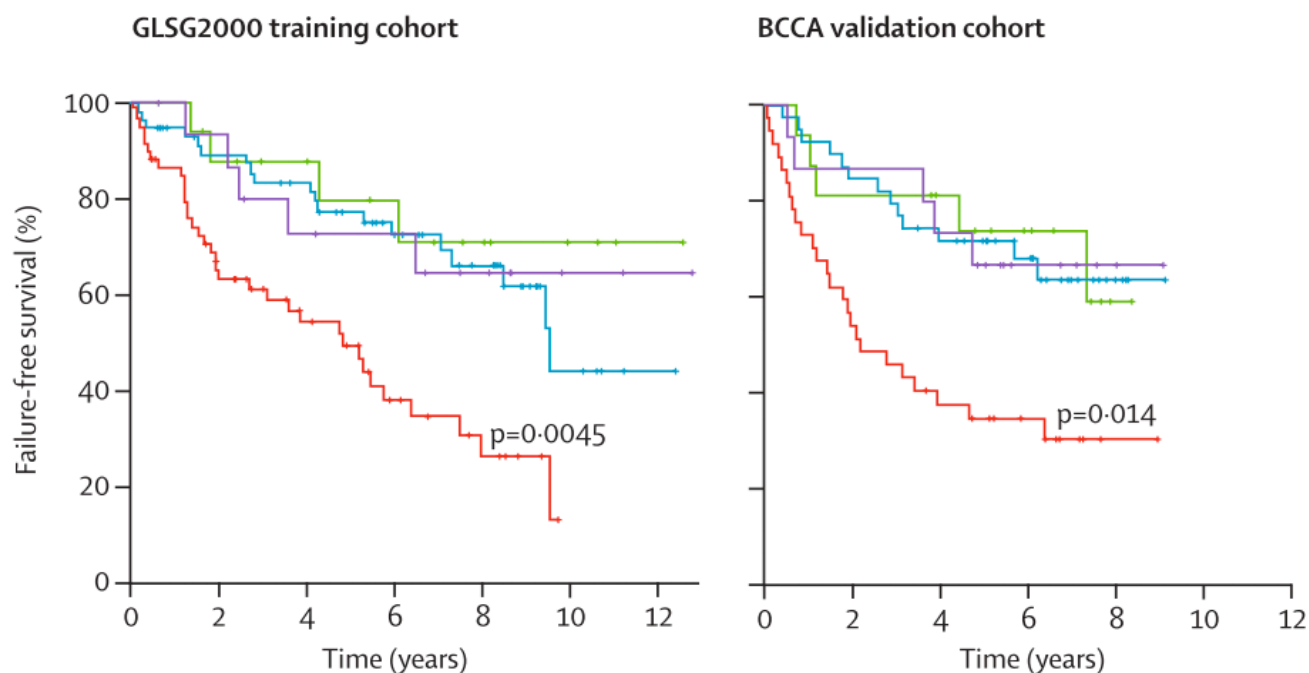
Pastore et al. Lancet Oncol 2015

EZH2 mutations – predictive and prognostic implications

~20% of all FLs

Predictive biomarker for response to tazemetostat

Prognostic biomarker for immunochemotherapy



Patients at risk

EZH2 mut, FLIPI low/int	16	14	10	9	6	2	1	15	13	11	5	2
EZH2 wt, FLIPI low/int	58	47	41	28	19	5	1	39	33	27	19	4
EZH2 mut, FLIPI high	17	14	12	9	6	3	1	16	13	11	7	1
EZH2 wt, FLIPI high	60	34	23	12	6	37	20	13	8	1

— EZH2 mutated
 — EZH2 wild-type

} FLIPI low/int

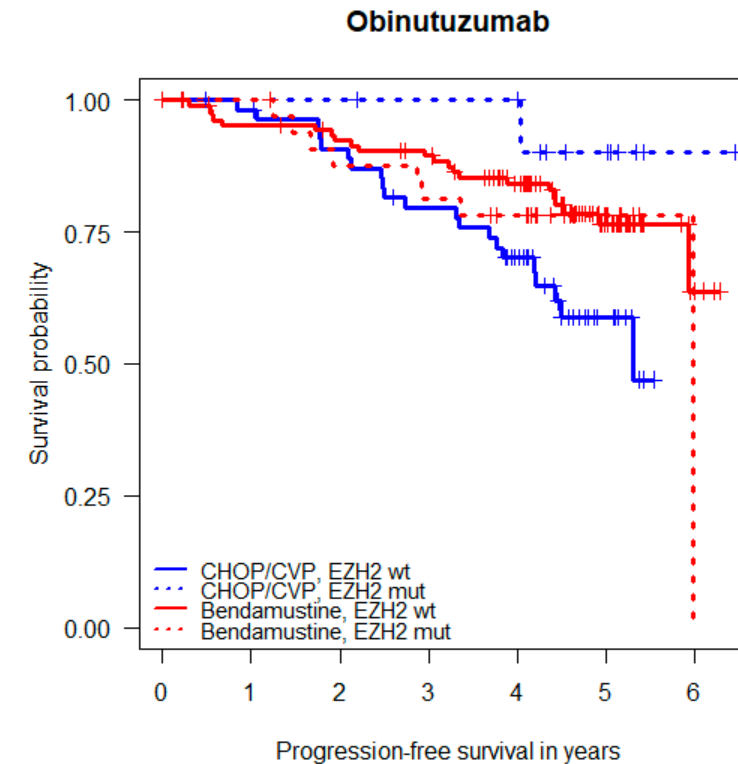
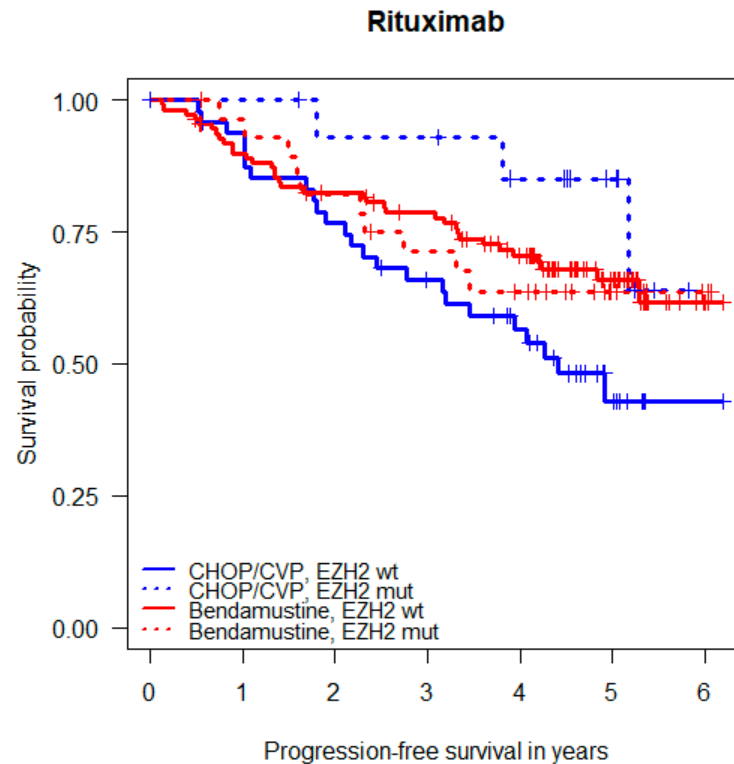
— EZH2 mutated
 — EZH2 wild-type

} FLIPI high

EZH2 mutations – prognostic implications based on chemo

EZH2 mutated FL: better outcome with CVP/CHOP backbone

EZH2 wild-type FL: better outcome with bendamustine backbone



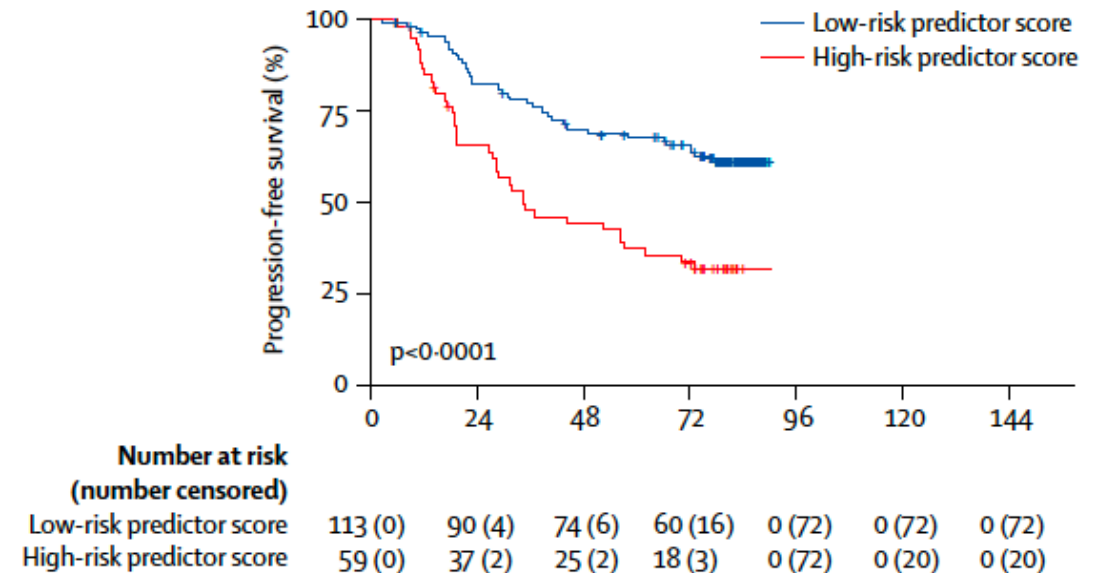
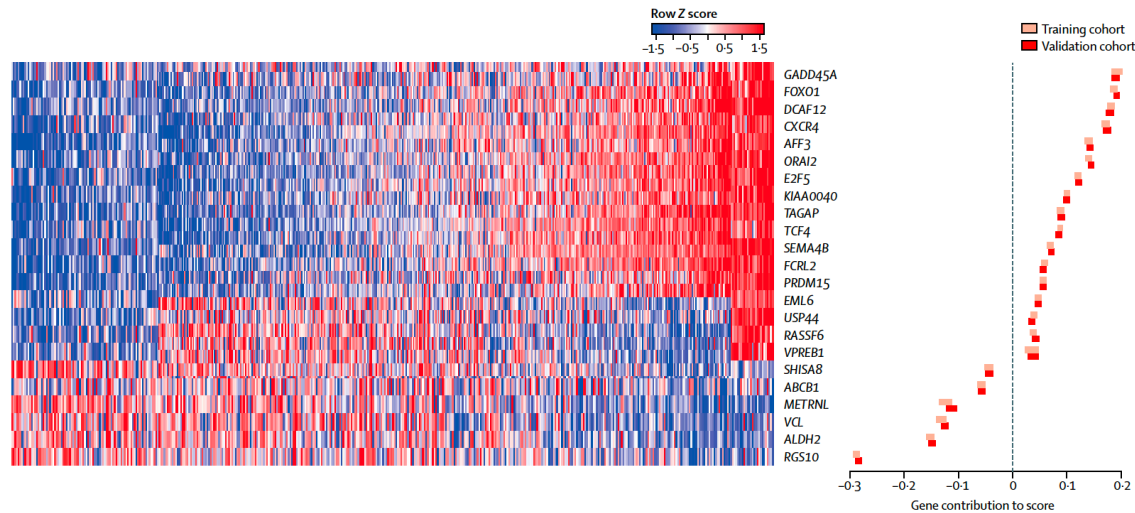
Jurinovic et al, ASH, 2019

23 gene signature

Trained in samples from PRIMA trial.

Genes associated with outcome identified initially using Affymetrix microarrays.

Transposed to NanoString platform.



Huet et al, Lancet Oncol, 2018

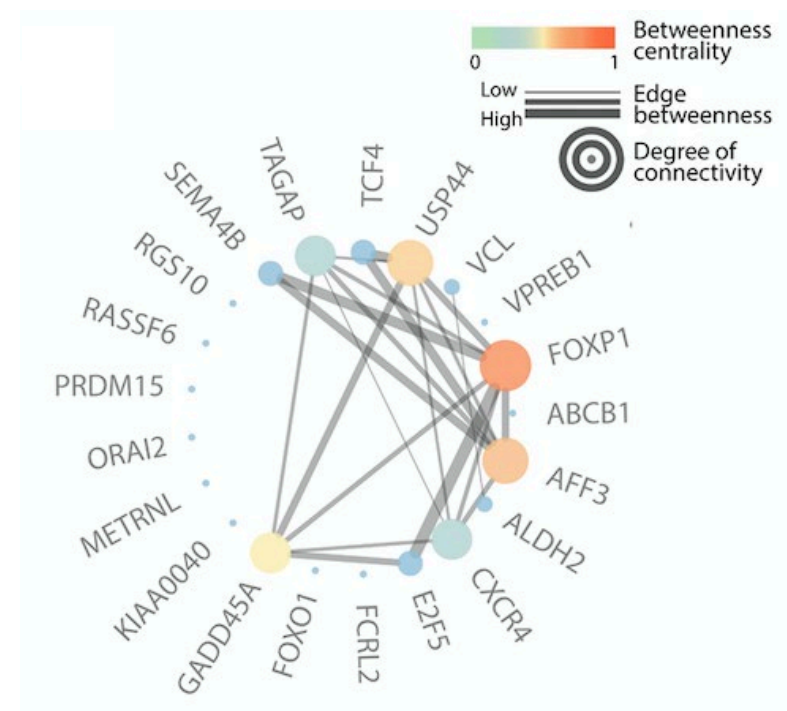
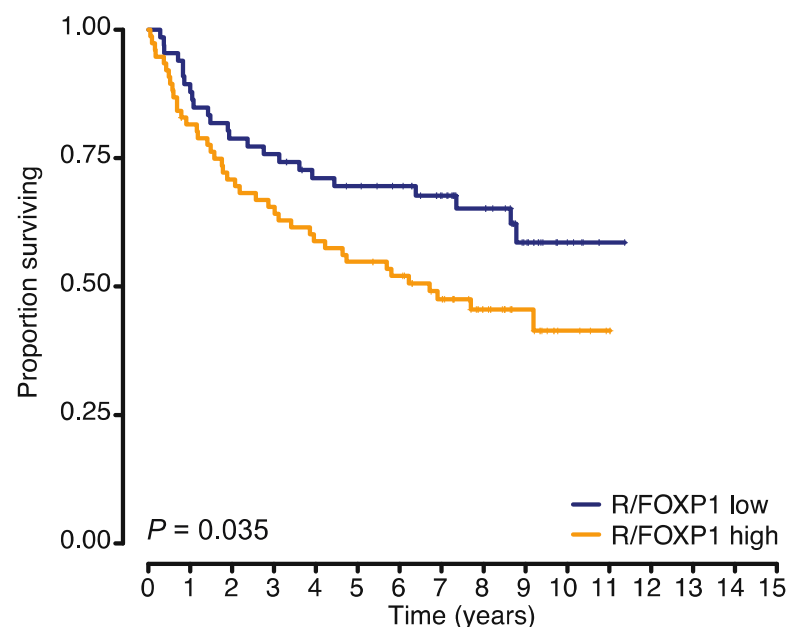
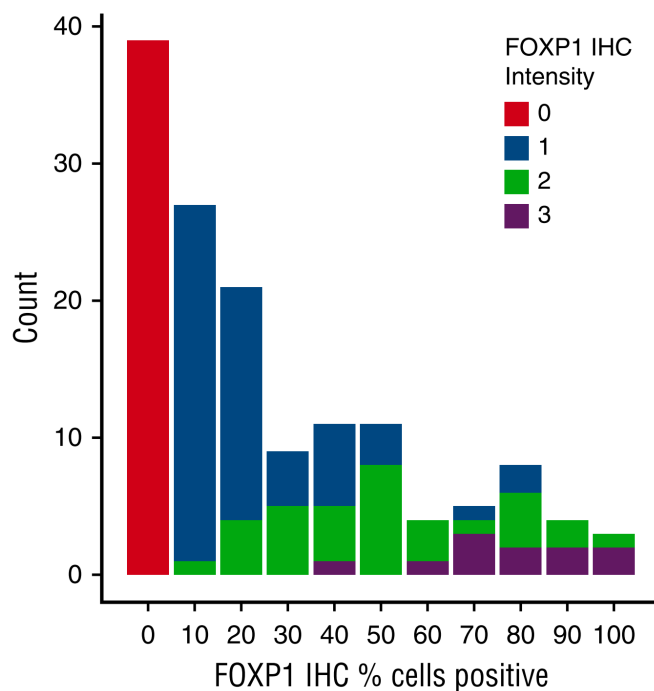
FOXP1 expression

FOXP1 expression downregulated in *EZH2* and *MEF2B*-mutated FL

FOXP1 expression high in a subset of FL cases (*EZH2* and/or *MEF2B*-wildtype FL)

High FOXP1 expression associated with shorter FFS

High FOXP1 expression associated with 23 genes signature



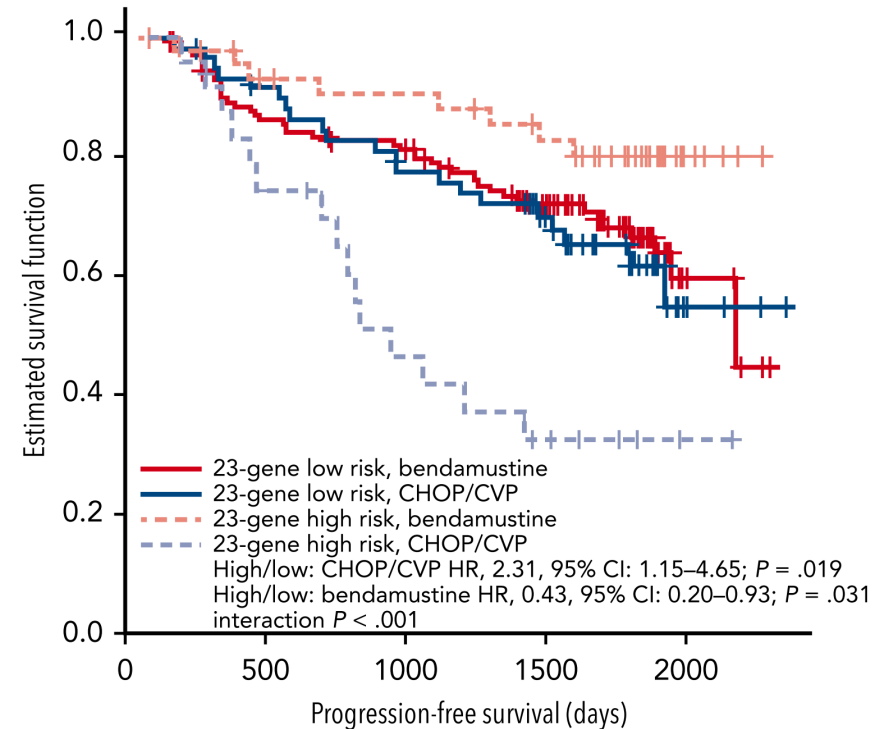
Treatment dependence of 23 gene score

GALLIUM trial

274 samples with RNAseq

High expression of 23 gene predictor:

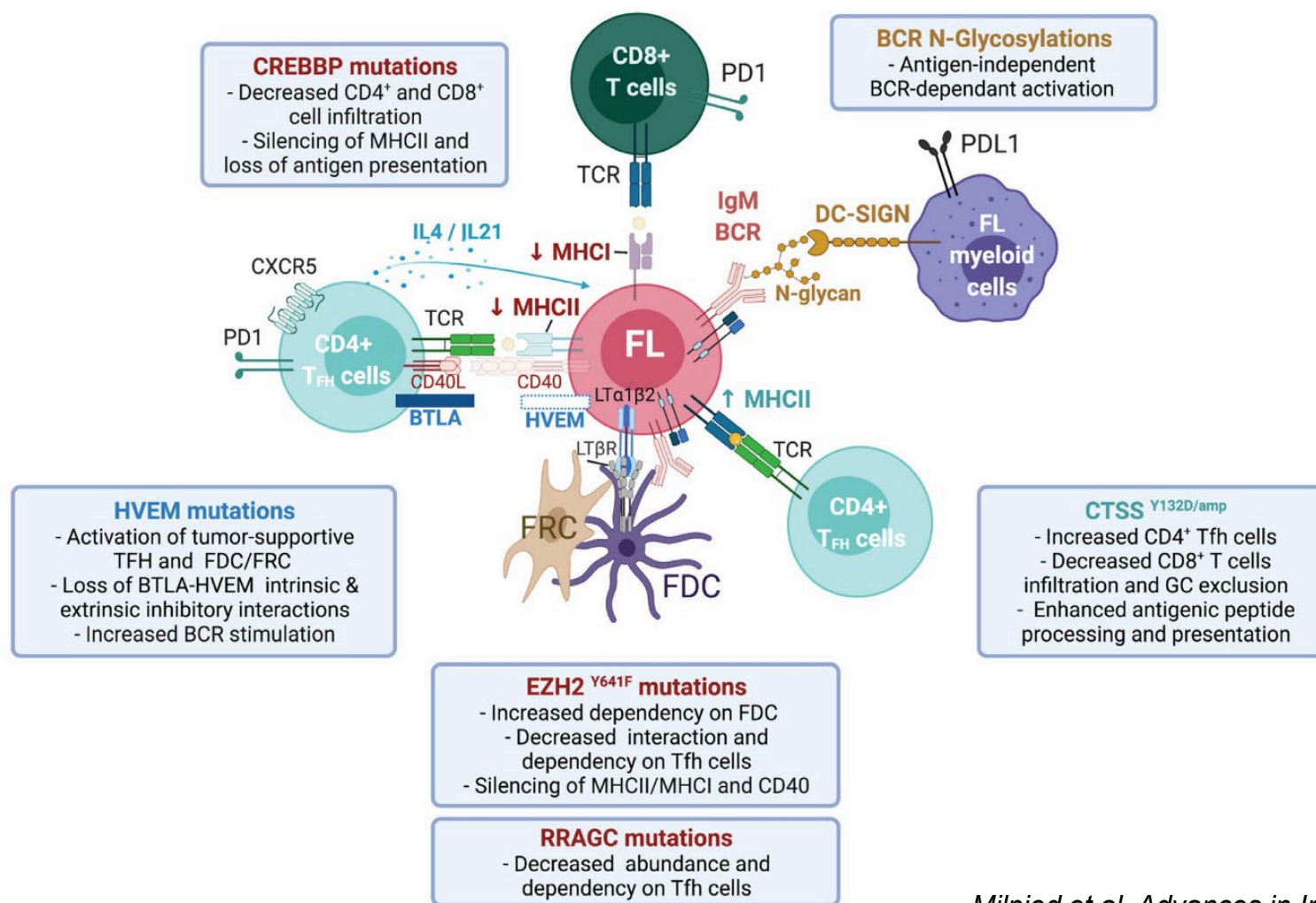
- Worse EFS with CHOP/CVP backbone
- Better EFS with bendamustine backbone



Number at risk

142	117	105	76	5
63	50	43	28	3
45	37	36	31	5
24	17	10	5	1

Immune microenvironment

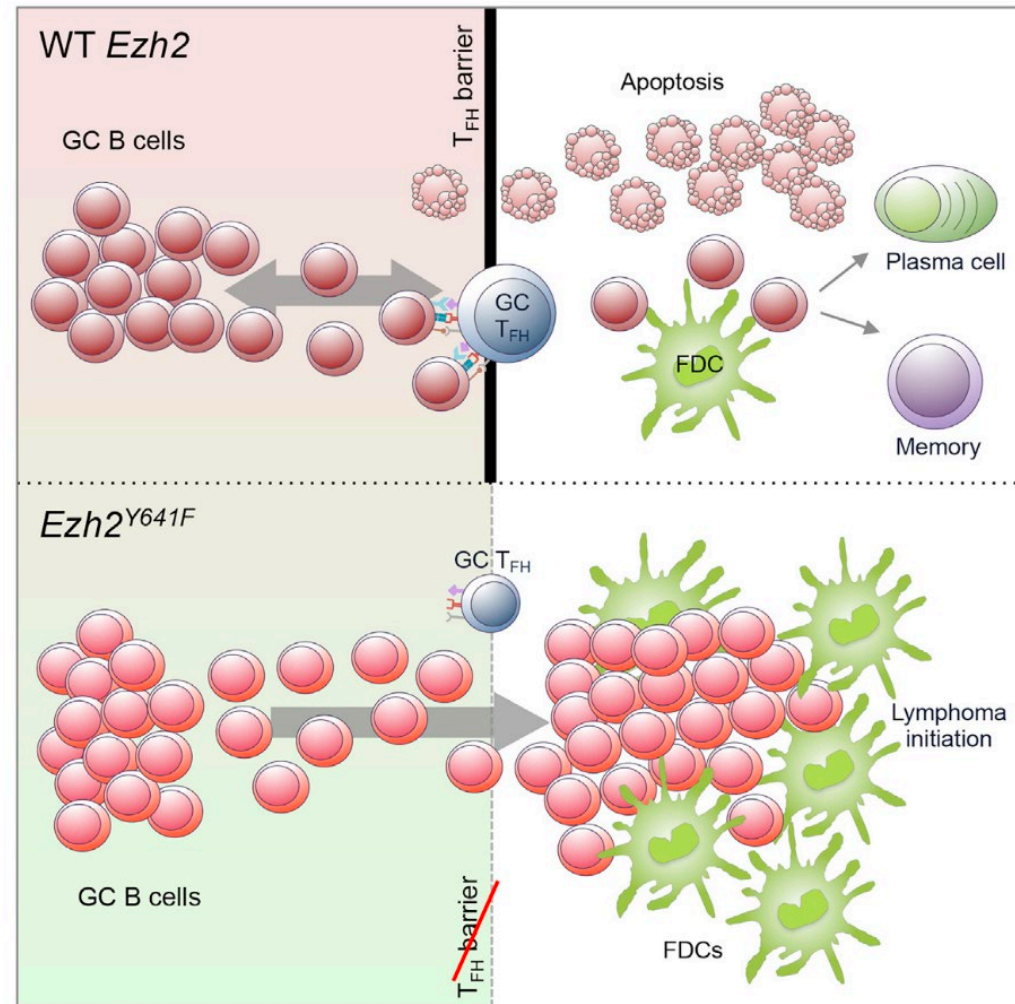


Mutant EZH2 reprograms the immune response

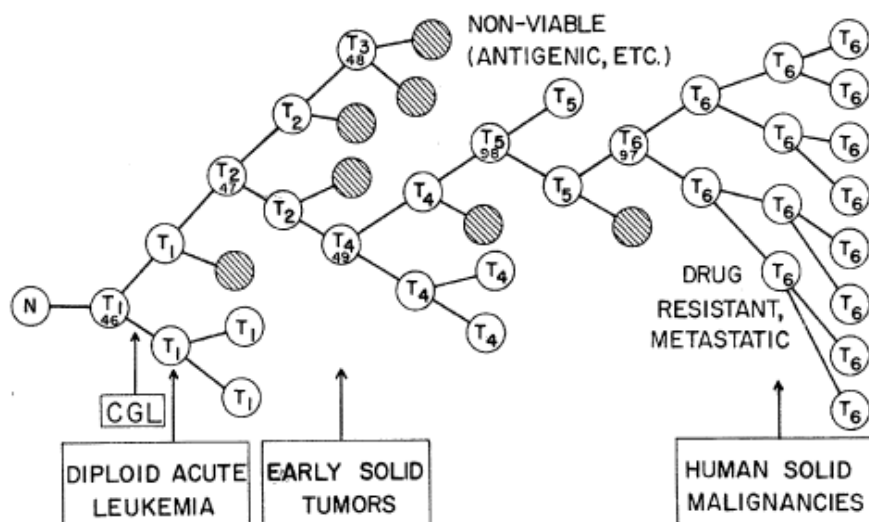
Mutant EZH2 impairs T-cell help

Drives slow expansion of centrocytes

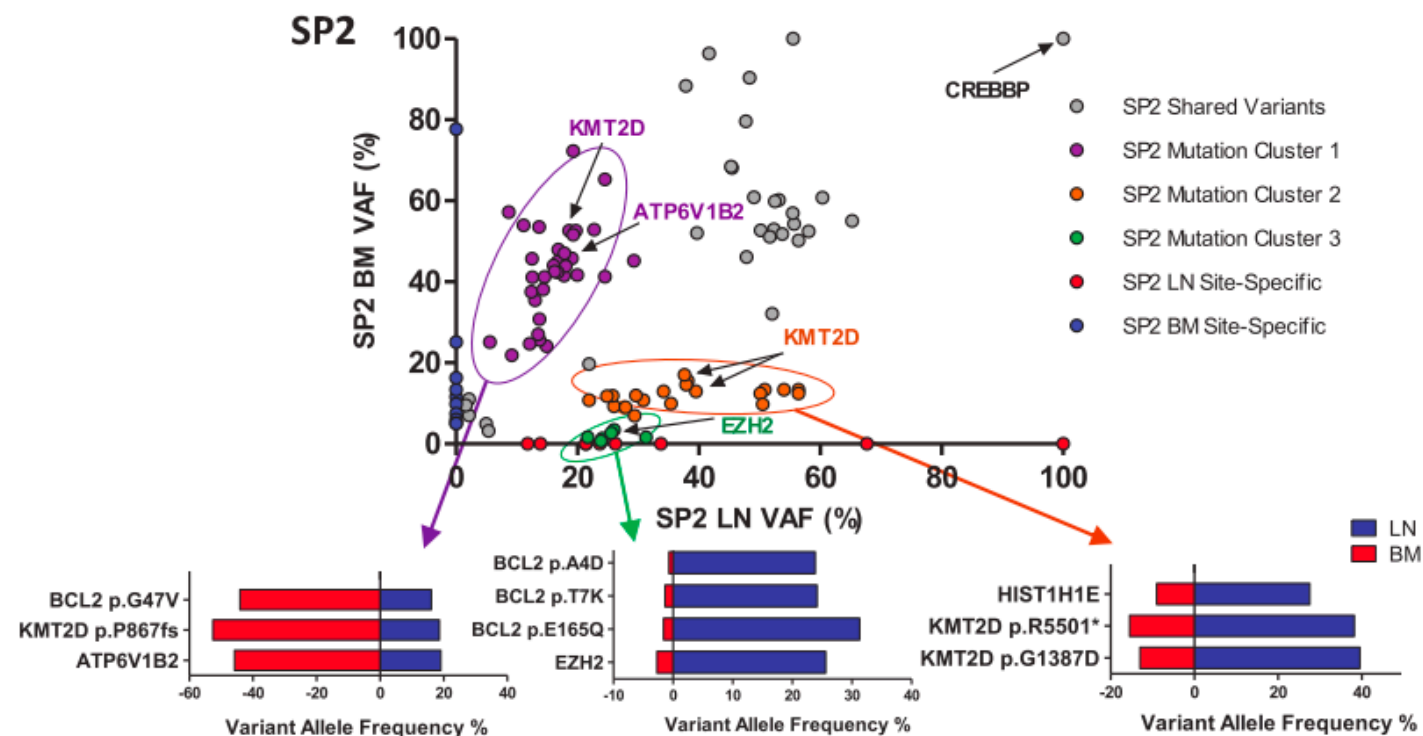
Switch from T-cell to follicular dendritic cell dependency



Intratatumoral heterogeneity

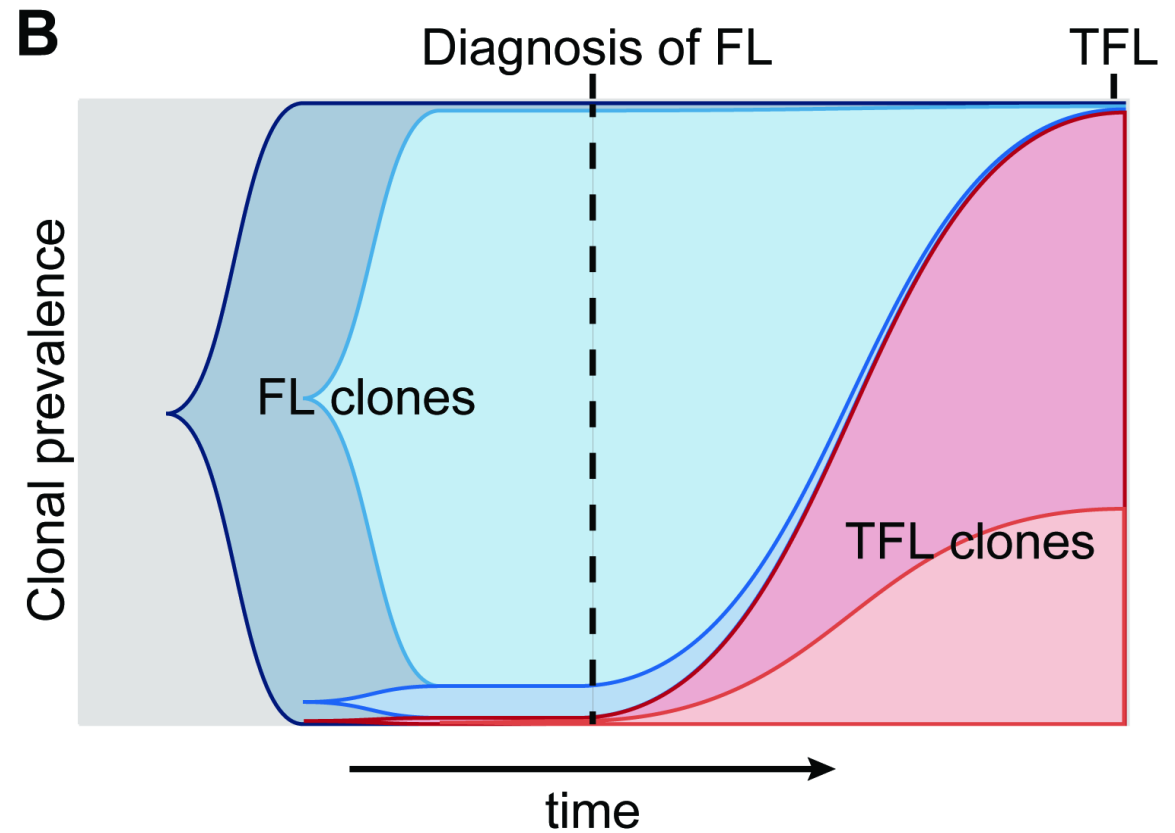
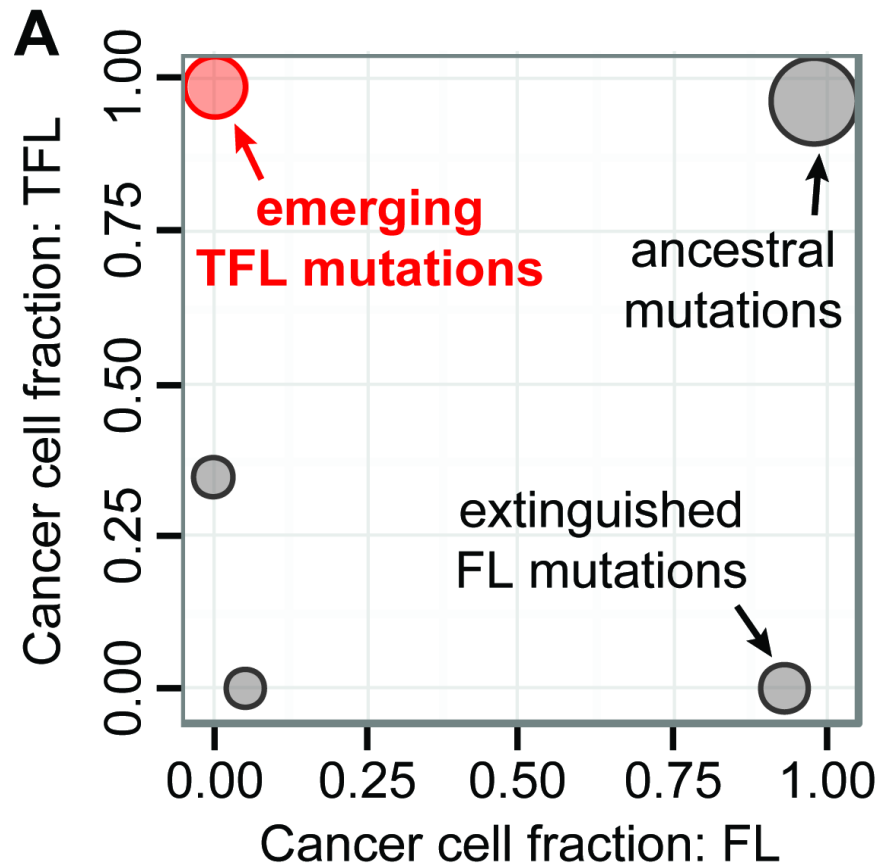


Peter Nowell, *Science*, 1976



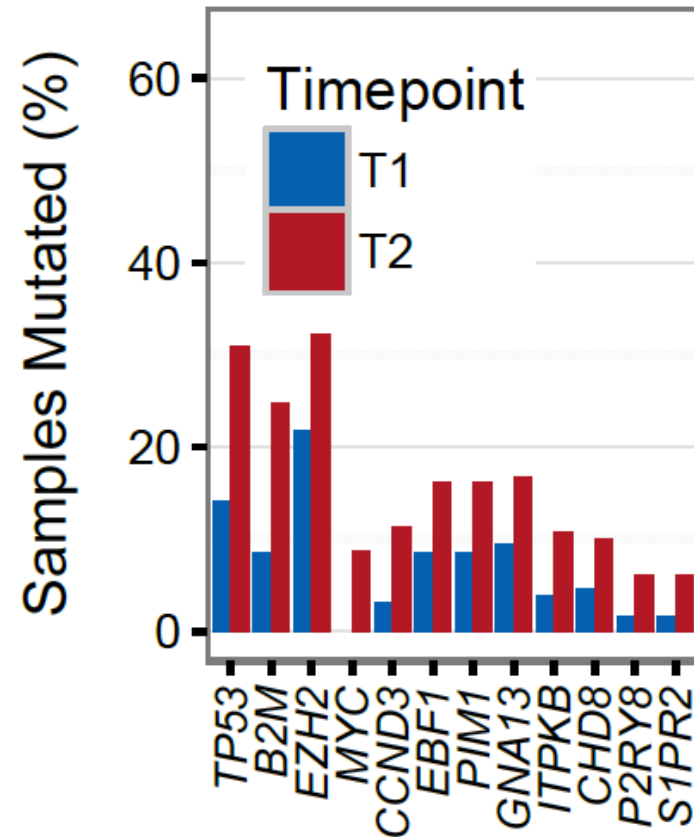
Araf et al, *Leukemia*, 2018

Clonal dynamics of transformation



Kridel and Chan et al. PLOS Medicine 2016

Gene mutations enriched in transformed FL



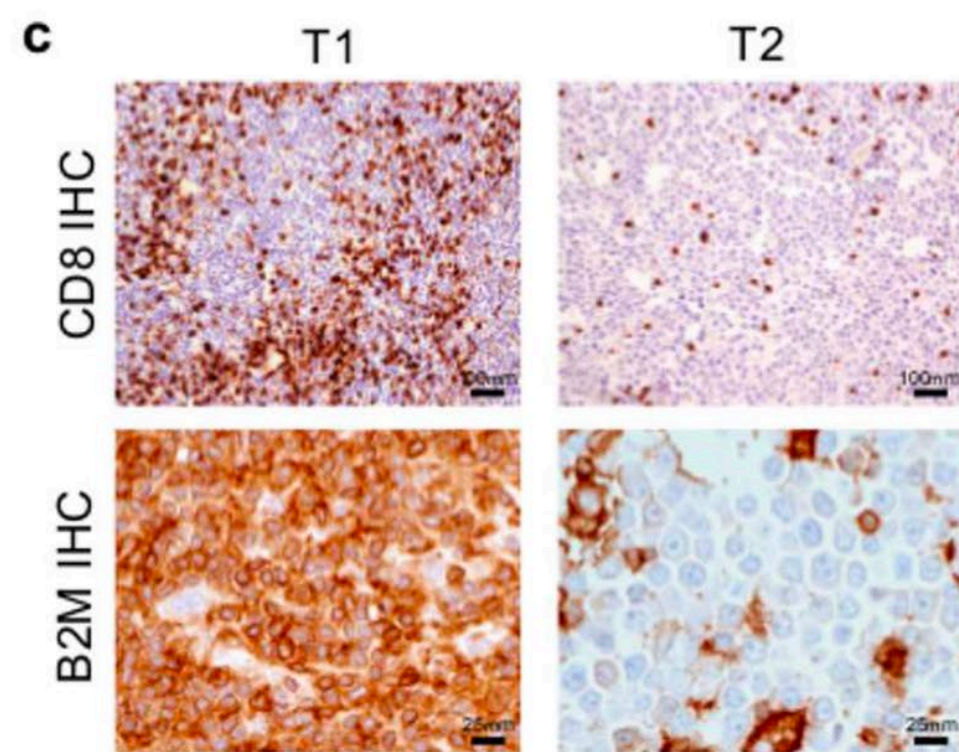
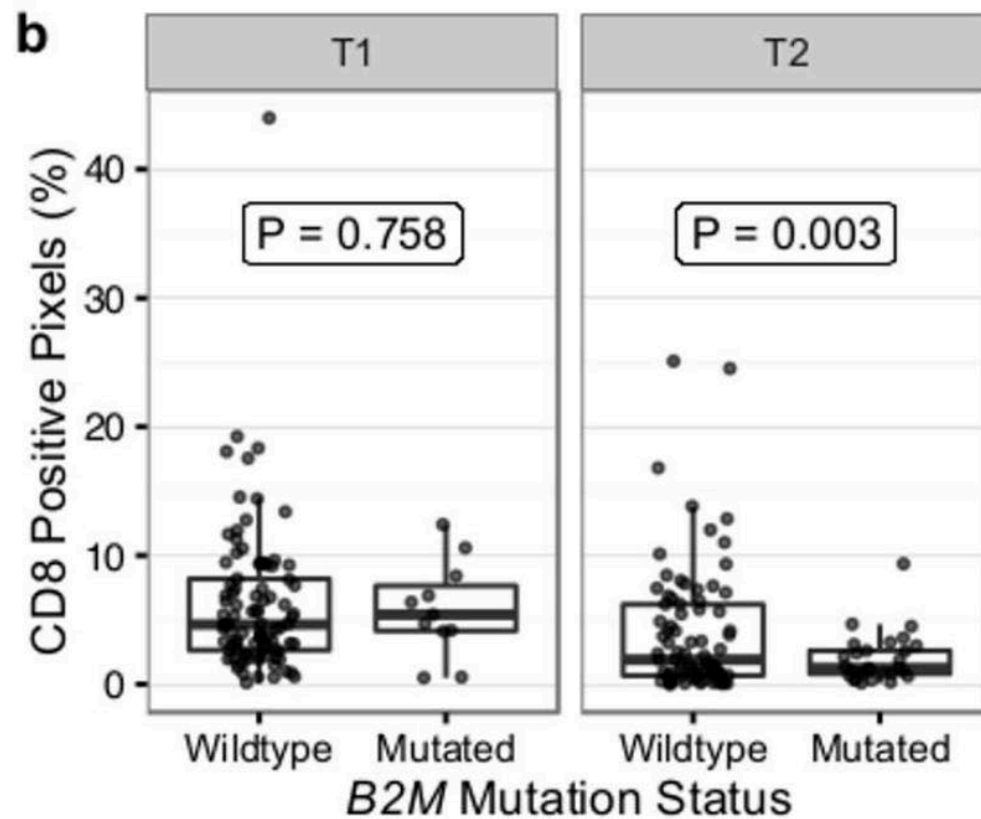
Kridel and Chan et al. PLOS Medicine 2016

- Defective DNA damage response (*TP53*)
- Increased proliferation (*MYC* translocations, *CCND3*)
- Escape from immune surveillance (*B2M*)
- Loss of confinement within germinal centre (*GNA13*, *P2RY8*, *S1PR2*)

Bouska et al, Blood, 2014
Okosun, Nature Genetics, 2014
Pasqualucci, Cell Reports, 2014
Bouska et al, Leukemia, 2016

Tumor microenvironment changes in transformed FL

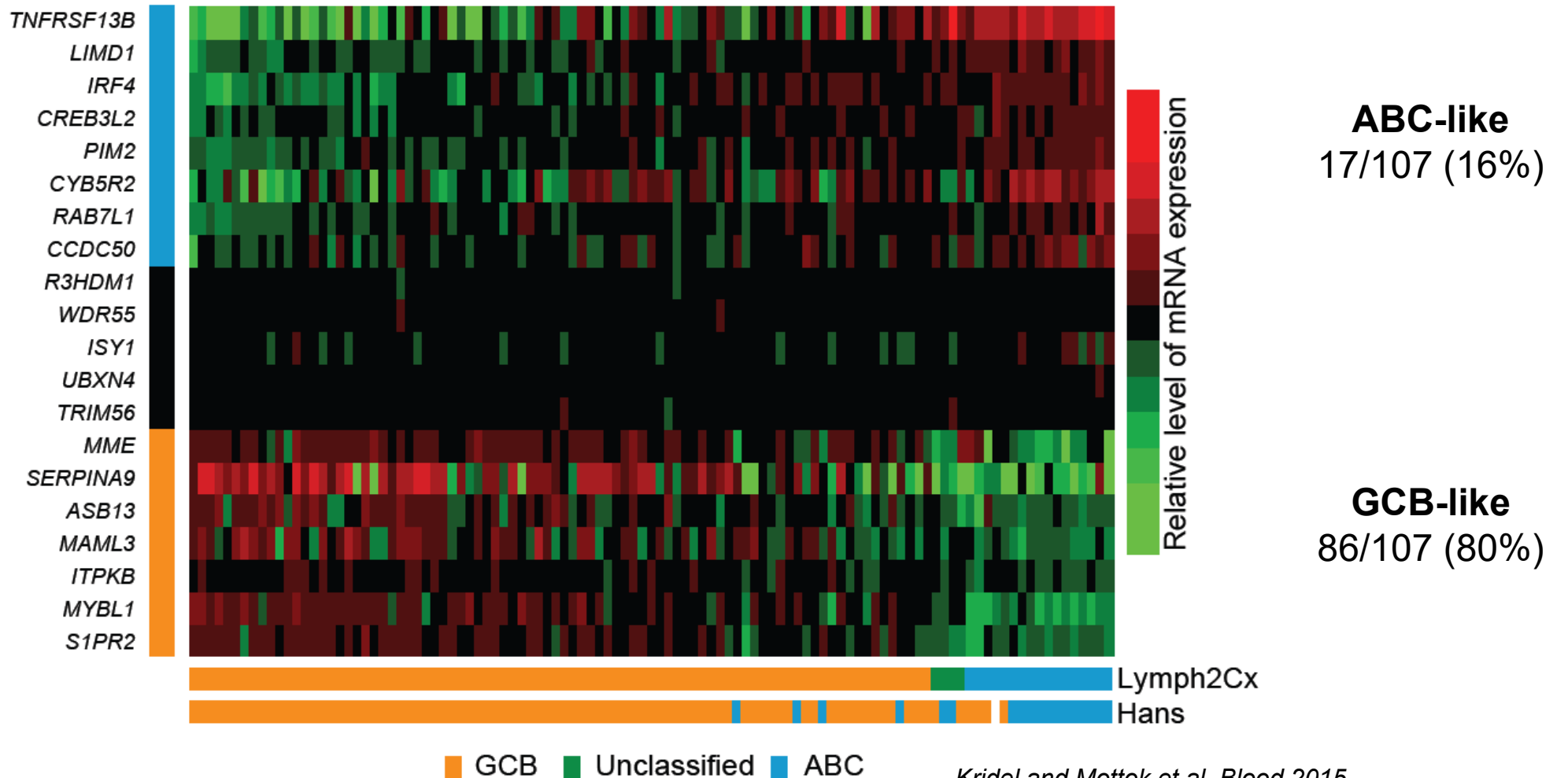
Reduced CD8+ T-cell infiltrate in transformed biopsies with *B2M* mutations



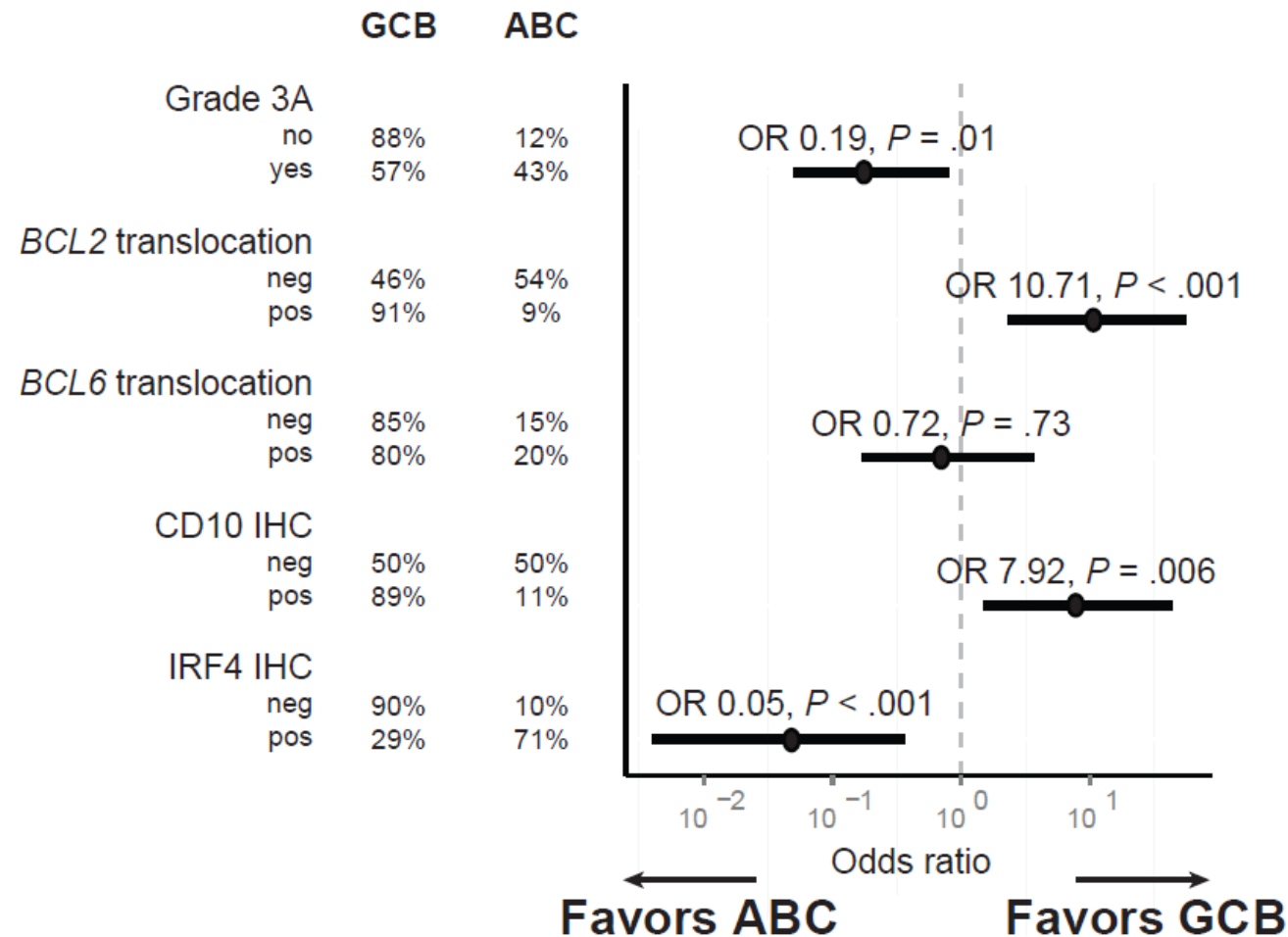
Kridel and Chan et al. PLOS Medicine 2016

Cell of origin of transformed FL

Samples passing QC: 107 out of 110 (97%)



FL → transformation into GCB or ABC



Kridel and Mottok et al. Blood 2015

Conclusions

- Epigenetic reprogramming is a hallmark of FL and has therapeutic implications:
 - Targeting EZH2 with small molecule inhibitors
 - EZH2 mutations may help select choice of frontline chemotherapy?
- Microenvironment remains insufficiently characterized
 - yet its composition is modulated by (epi)genetic alterations
 - predictive of response to immune therapies?
- Progression and transformation occur through branching evolution
- Molecular features of underlying FL are associated with phenotype of transformed FL

Audience response question

What are the prognostic implications of *EZH2* mutations for patients treated with frontline immunochemotherapy?

- *EZH2* mutations predict response to tazemetostat but have no prognostic relevance for immunochemotherapy-treated patients
- *EZH2* mutations are associated with longer PFS in patients treated with R-CHOP/CVP
- *EZH2* mutations are associated with shorter PFS in patients treated with R-CHOP/CVP
- *EZH2* regulates gene expression and has no impact on tumor-immune interactions



