

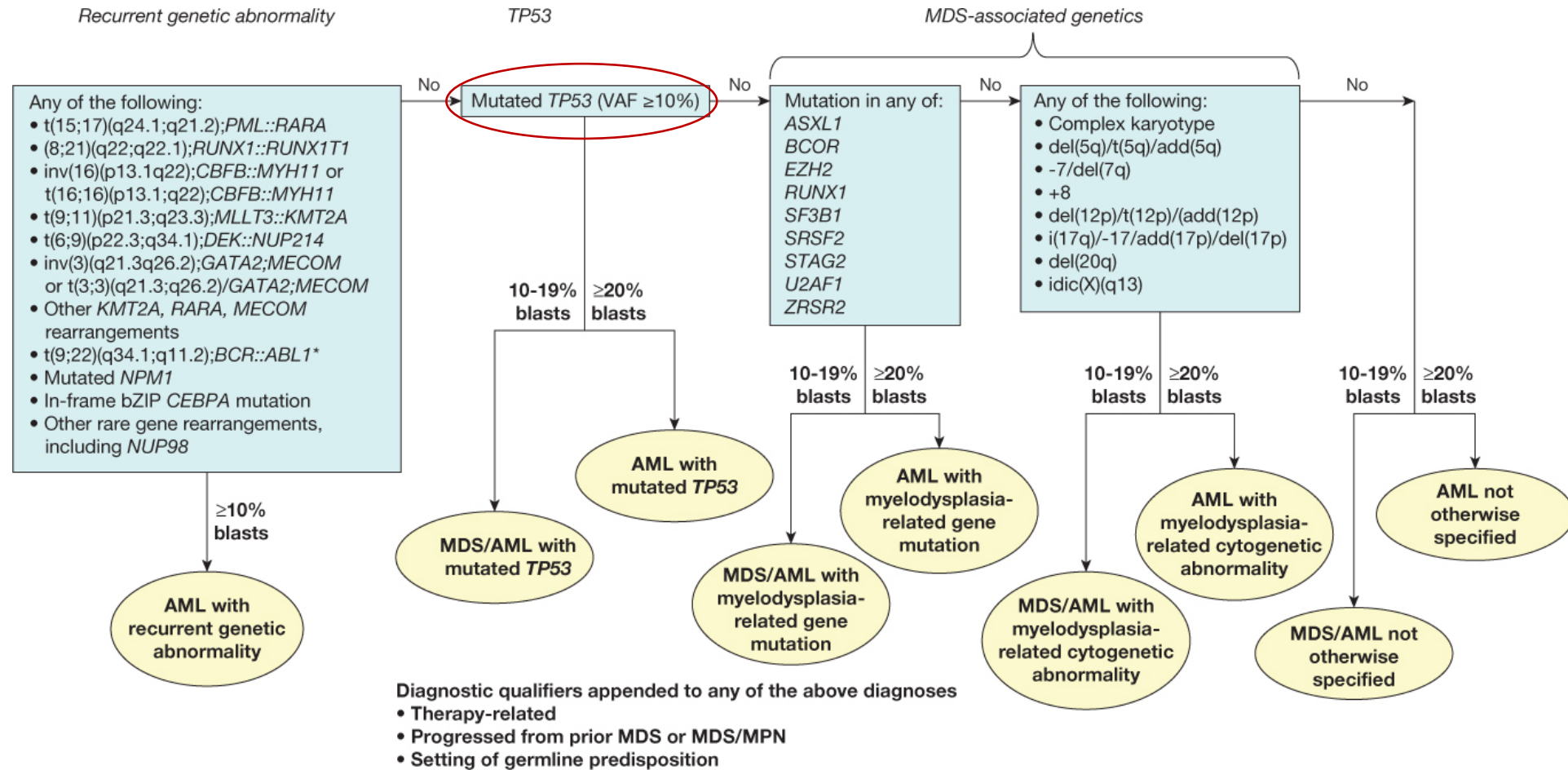
# *TP53* and other classifier mutations

Andrew Wei

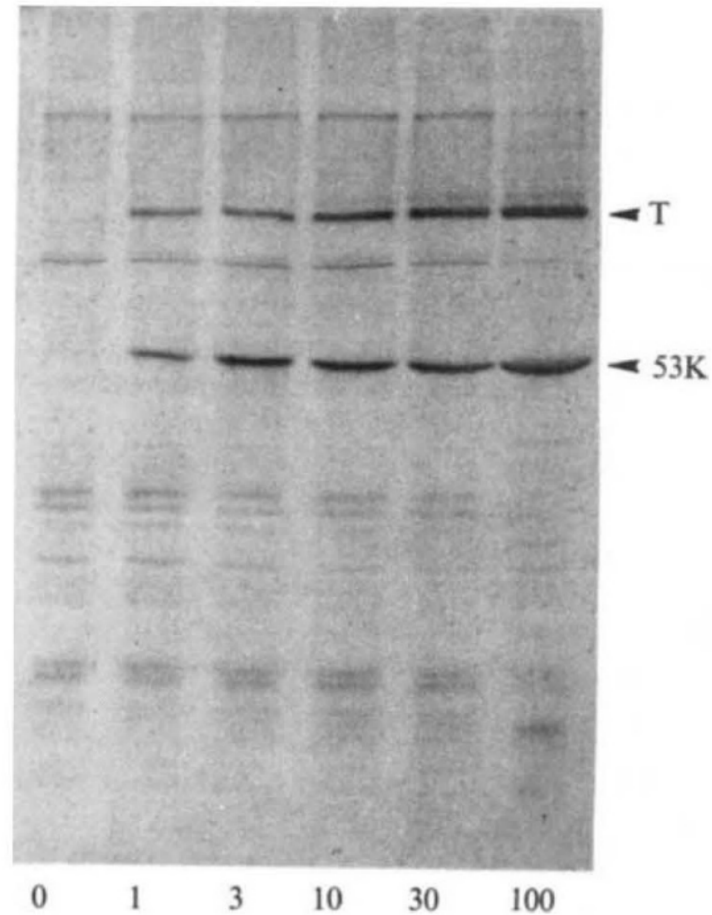
Peter MacCallum Cancer Centre and Royal Melbourne Hospital

Walter and Eliza Hall Institute of Medical Research

# TP53 mutation and ICC 2022 classification



## A novel protein co-immunoprecipitated by anti-SV40 T serum



## Similar protein found in uninfected embryonal carcinoma cells

Linzer DI, Levine AJ. Characterization of a 54K dalton cellular SV40 tumor antigen present in SV40-transformed cells and uninfected embryonal carcinoma cells. *Cell*. **1979**;17:43–52.

Kress M, May E, Cassingena R, May P. Simian virus 40-transformed cells express new species of proteins precipitable by anti-simian virus 40 tumor serum. *J Virol*. **1979**;31:472–83.

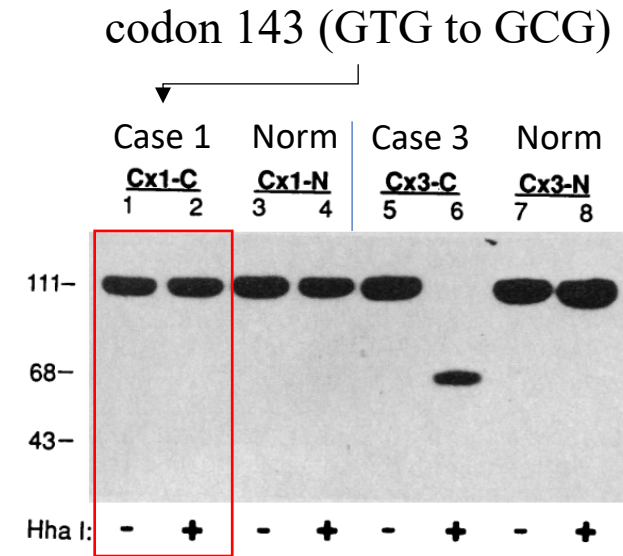
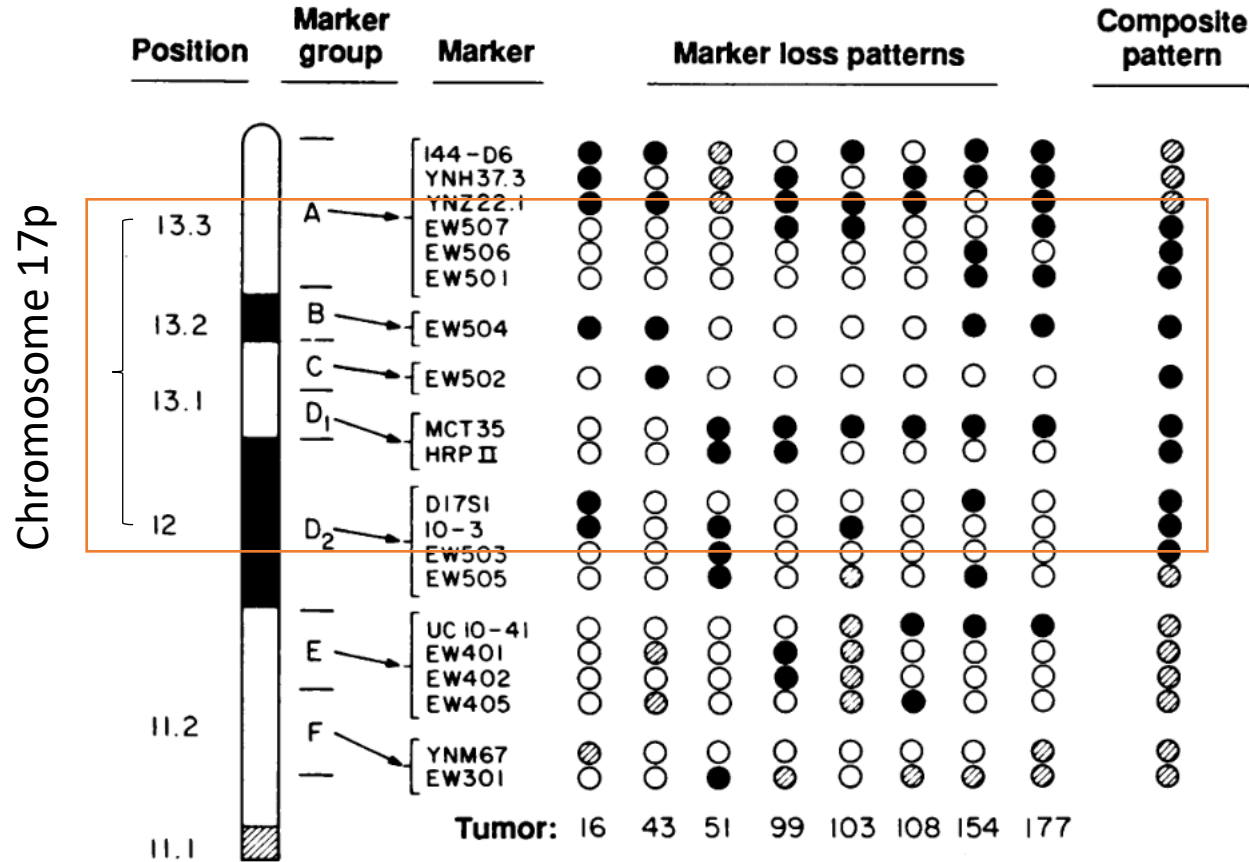
Melero JA, Stitt DT, Mangel WF, Carroll RB. Identification of new polypeptide species (48-55K) immunoprecipitable by antiserum to purified large T antigen and present in SV40-infected and -transformed cells. *Virology*. **1979**;93:466–80.

Smith AE, Smith R, Paucha E. Characterization of different tumor antigens present in cells transformed by simian virus 40. *Cell*. **1979**;18:335–46.

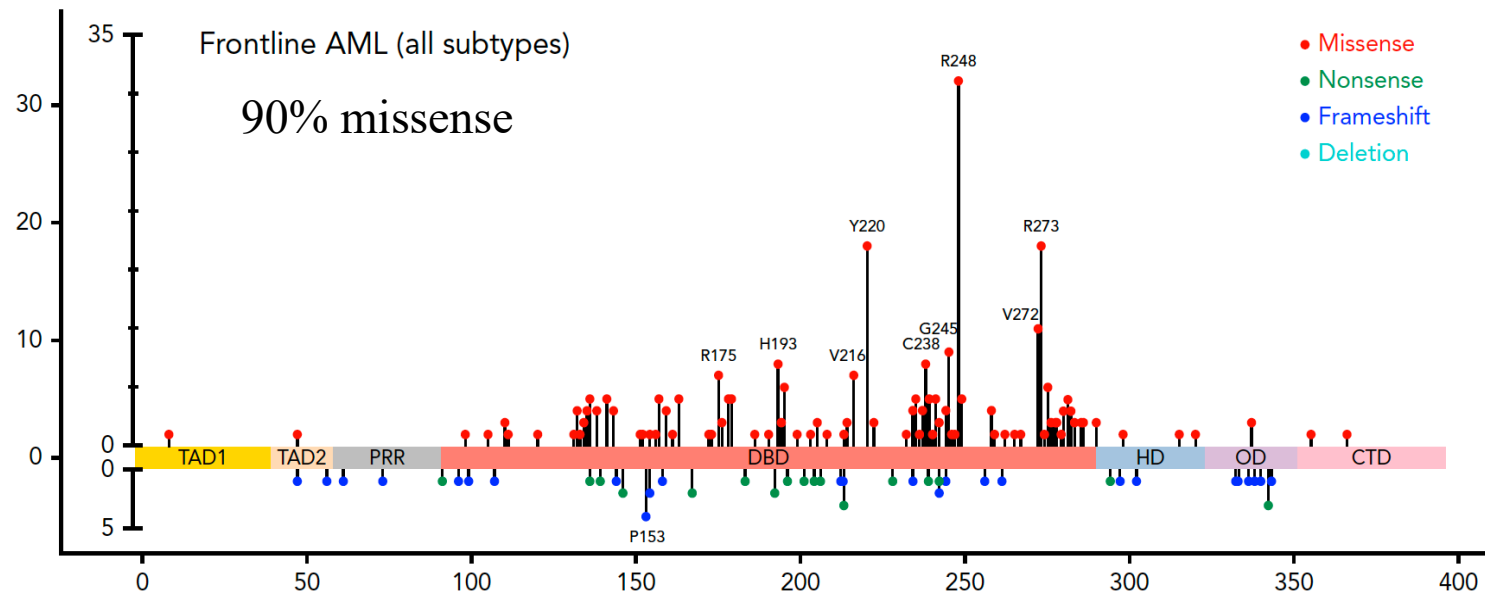
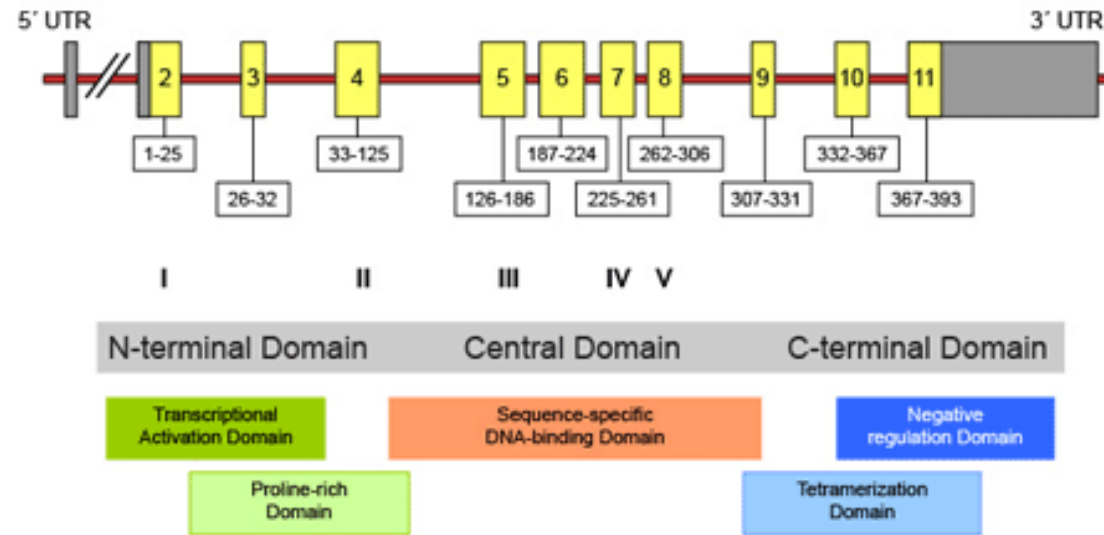
## Transduction of mutant *TP53* cDNA transforms targeted cells

1. Eliyahu D, Raz A, Gruss P, Givol D, **Oren M**. Participation of p53 cellular tumour antigen in transformation of normal embryonic cells. *Nature*. **1984**;312:646–9
2. Jenkins JR, Rudge K, Currie GA. Cellular immortalization by a cDNA clone encoding the transformation-associated phosphoprotein p53. *Nature*. **1984**;312:651–4
3. Parada LF, Land H, Weinberg RA, Wolf D, Rotter V. Cooperation between gene encoding p53 tumour antigen and ras in cellular transformation. *Nature*. **1984**;312:649–51

# TP53 is a tumor suppressor gene



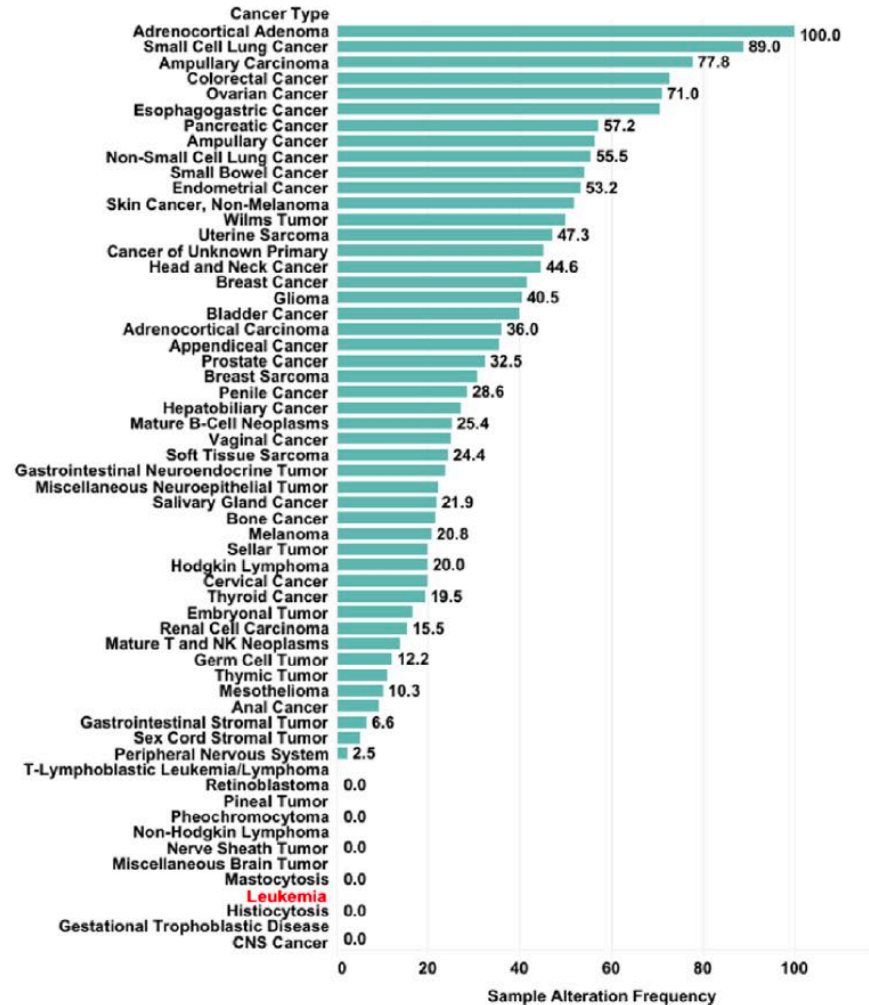
# In AML *TP53* mutations concentrated in the core domain



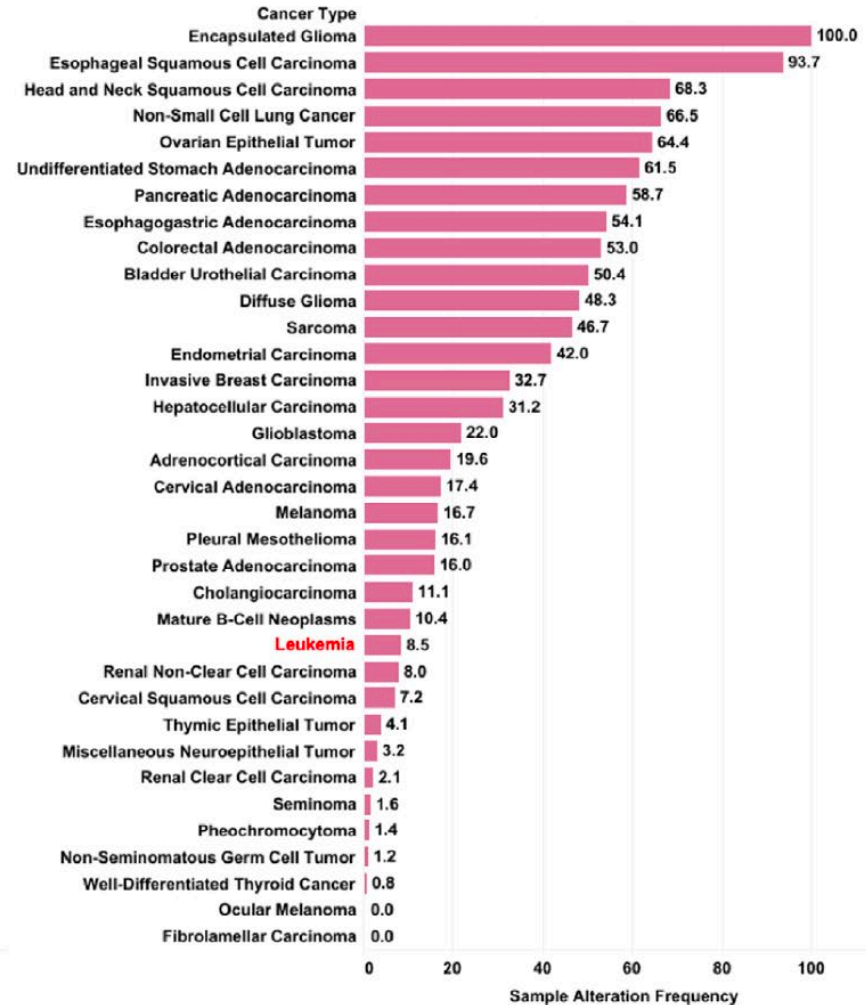


# Frequency of *TP53* mut across human cancers

MSK-IMPACT



TCGA





## Mutated *TP53* more common in older AML

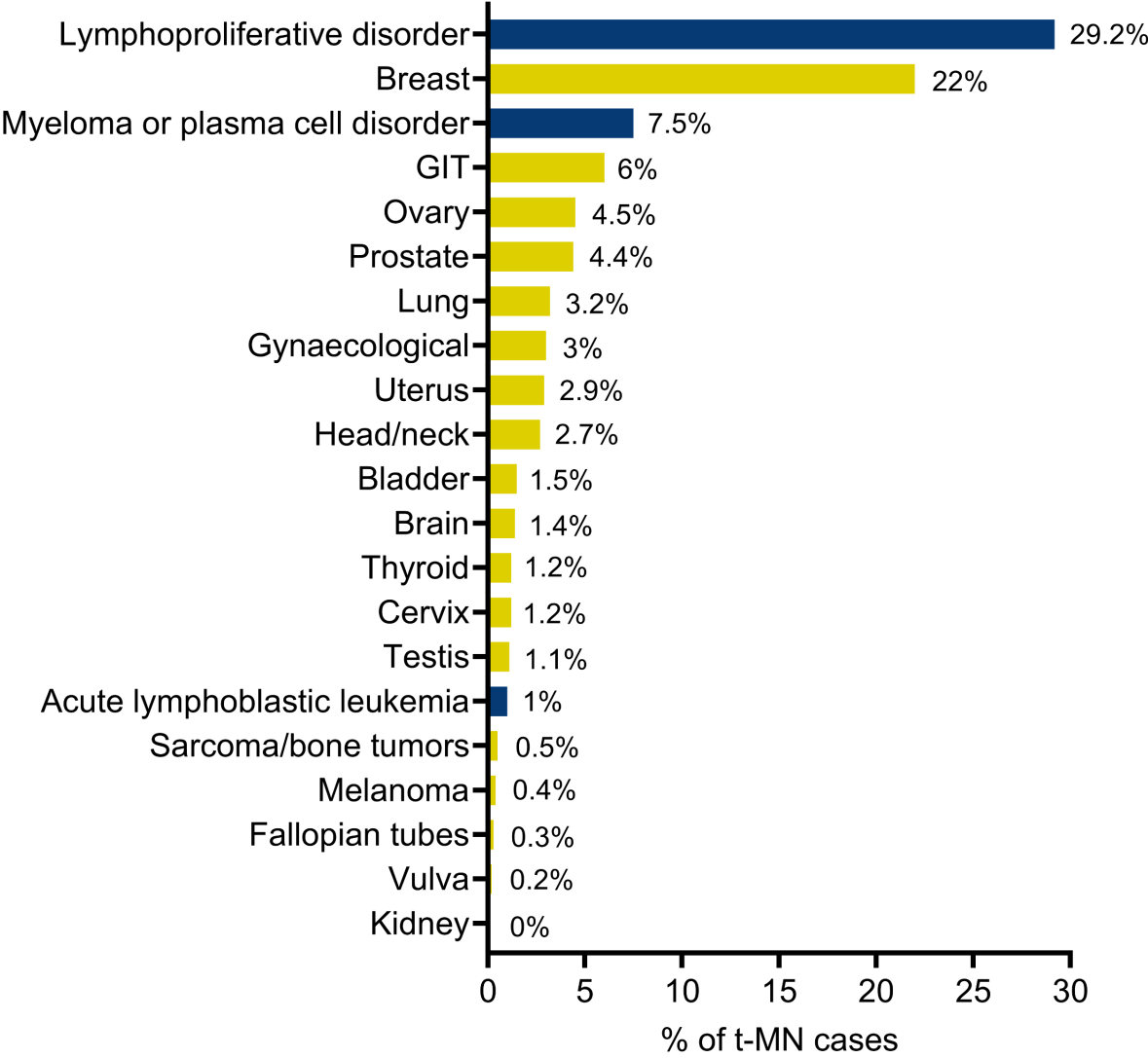
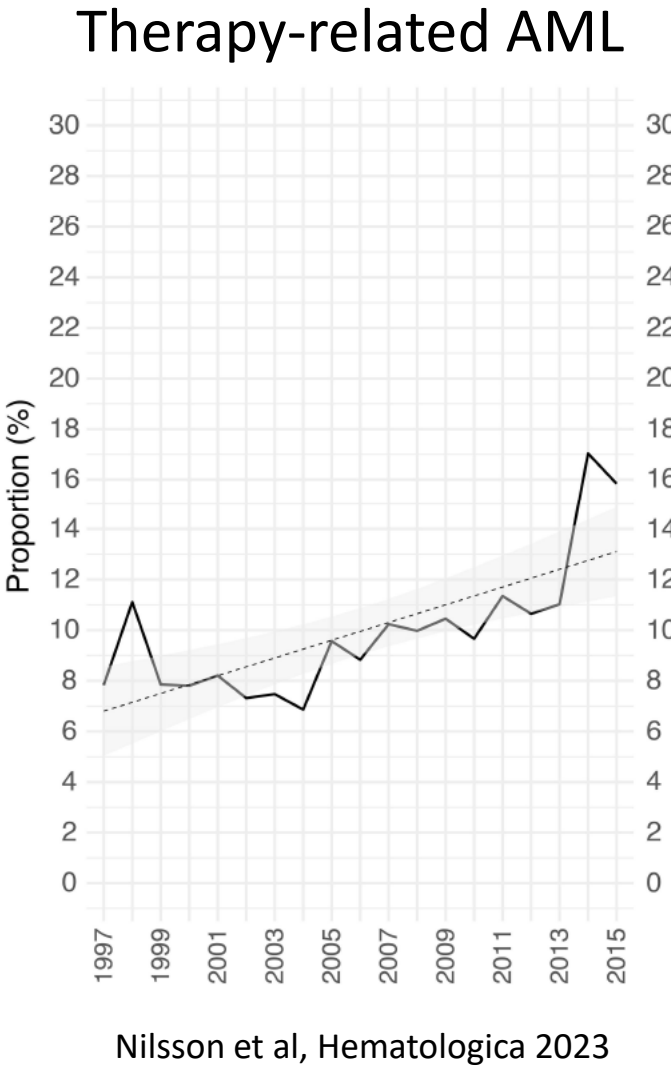
Reference	Age (years)	N	TP53 mutant
Tsai, ASH 2015	15-59	285	4%
Metzeler, Blood 2016	18-59	376	4%
Dohner, Leukemia 2018	≥65	156	21%
DiNardo, NEJM 2020	≥65	52	19%
Metzeler, Blood 2016	≥60	288	18%
Kadia, Lancet Hematol 2018	≥60	196	18%
Welch, NEJM 2016	≥60	54	17%
Prassek, Haematologica 2018	≥75	151	14%
Renaud, Am J Hematol 2018	≥80	88	17%
Tsai, ASH 2015	≥60	177	13%

## ***TP53* mut prevalent in t-MN**

Gene mutation	t-MN(%)
<i>ASXL1</i>	3–17
<i>CEBPA</i>	0–5
<i>DNMT3A</i>	8–27
<i>EZH2</i>	3–4
<i>FLT3</i>	8–16
<i>IDH1</i>	3–5
<i>IDH2</i>	0–5
<i>KMT2A</i>	3
<i>KRAS</i>	11
<i>NPM1</i>	4–16
<i>NRAS</i>	10–13
<i>PTPN11</i>	3–9
<i>RUNX1</i>	11–16
<i>SF3B1</i>	0–3
<i>SRSF2</i>	8–11
<i>TET2</i>	6–14
<b><i>TP53</i></b>	<b>23–37</b>
<i>U2AF1</i>	5–8

Lindsley, Blood 2015  
 Christiansen, Leuk 2005  
 Shih, Haematologica 2013  
 Wong, Nature 2015  
 Bacher, Haematologica 2007  
 Voso, Leuk 2013

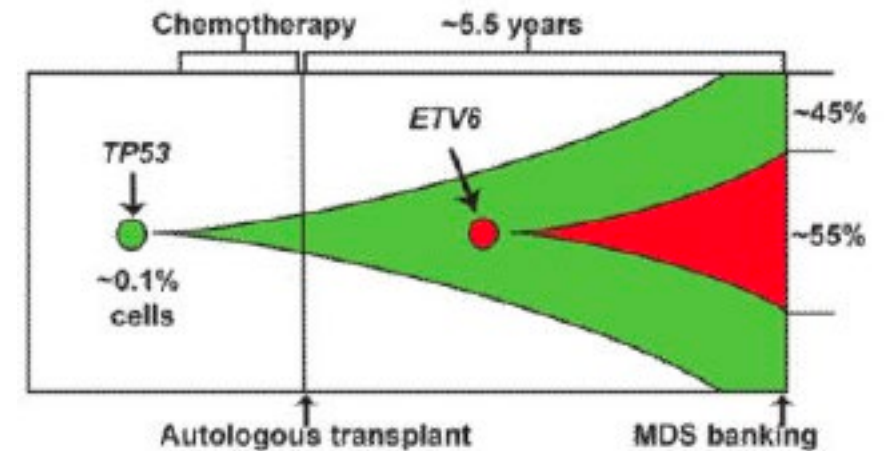
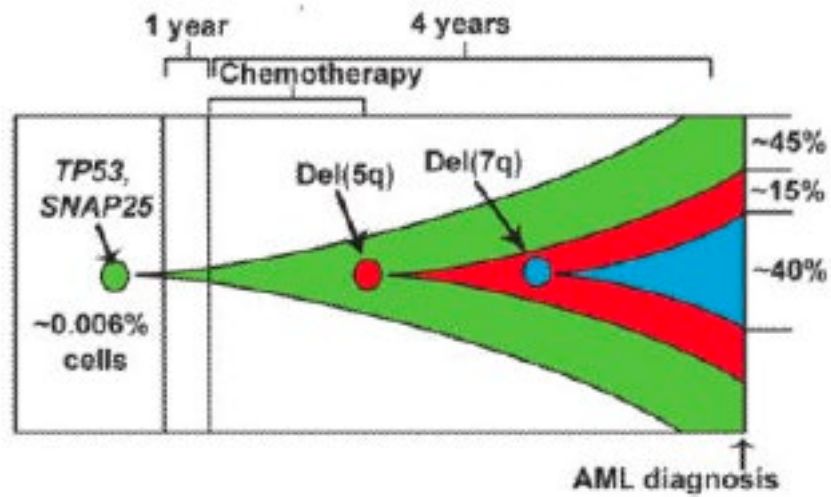
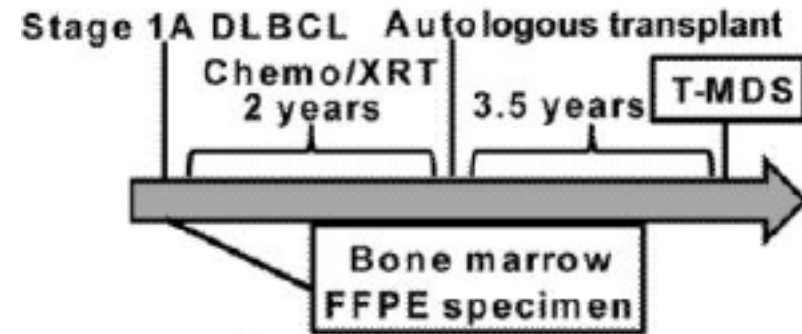
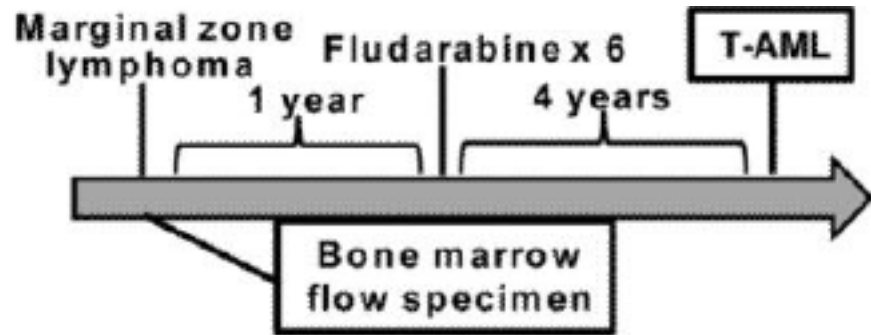
# TP53 mutated AML is increasing in frequency



## Therapy-related MN after prior hematological malignancy

Scenario	Occurrence of t-MDS/AML
FCR/FC for CLL	1.9 % (Laribi et al Hemasphere 2022)
BEACOPP for HL	~1 % (Eichenauer et al, Blood 2014)
CAR-T for R/R NHL	11 % at 2 years (Alkhateeb et al, BCJ 2022)
CAR-T for R/R MM	9 % at 2 years (Martin et al, JCO 2023)
CAR-T for R/R NHL	~9 % at 3 years (Gurney et al, JAMA 2024)
CAR-T for R/R MM	~9 % at 3 years (Gurney et al, JAMA 2024)
CAR-T for R/R NHL	11 % at 3 years (Yeoh et al, ASH 2024)
CAR-T for R/R NHL	If CH at time of CAR-T, 19% tMN at 2 years (Saini et al, Blood Canc Disc 2022)
CAR-T for R/R NHL	If CH at time of CAR-T, 17% tMN at 3 years If TP53 or PPM1D mut at time of CAR-T, 22% tMN at 3 years (Yeoh et al, ASH 2024)

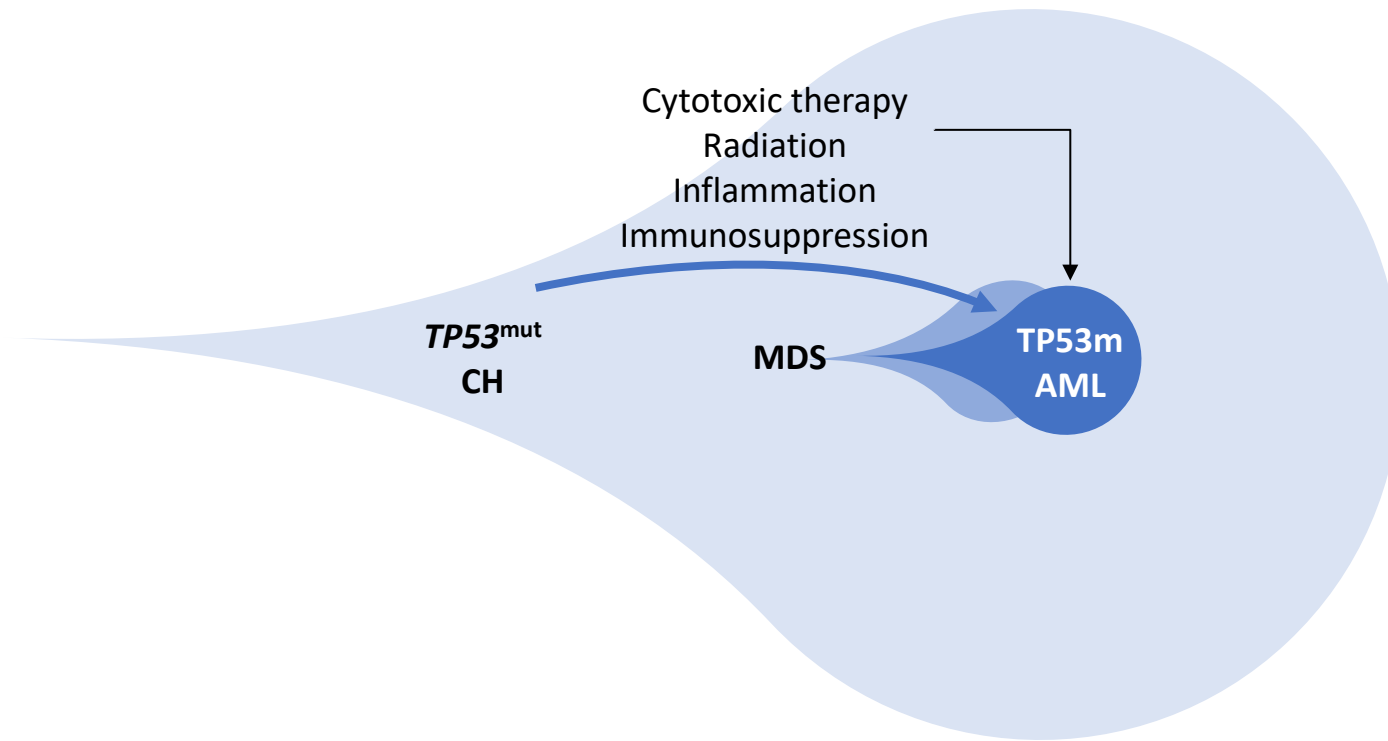
# Mutated *TP53* precedes clinical presentation of t-MN



## Pathogenic *TP53* variants in 9/19 WBC donors 68-89 yo

Sample	Chr	Exon	Start	Stop	Ref	Var	Amino acid	COSMIC ID	Var count	Total read family count	VAF (read-family)	VAF (ddPCR)
34	17	7	7518230	7518230	T	G	D259A	none	13	33085	0.039%	N.D.
99	17	7	7518273	7518273	C	T	G245S	COSM6932	18	41836	0.043%	N.D.
99	17	8	7517849	7517849	C	T	V272M	COSM10891	26	81015	0.032%	N.D.
269	17	8	7517845	7517845	C	T	R273H	COSM10660	489	420026	0.12%	N.D.
271	17	5	7519138	7519138	C	T	V173M	COSM11084	177	182809	0.097%	0.081%
271	17	5	7519174	7519174	C	T	A161T	COSM10739	25	164591	0.015%	N.D.
271	17	NA	7520035	7520035	A	T	SPLICING	COSM152274	23	165672	0.014%	N.D.
271	17	NA	7517934	7517934	C	T	INTRONIC	none	36	333996	0.011%	N.D.
273	17	6	7518990	7518990	A	G	I195T	COSM11089	57	15540	0.37%	0.28%
300	17	6	7518915	7518915	T	C	Y220C	COSM10758	91	316765	0.029%	0.029%
324	17	8	7517819	7517819	G	A	R282W	COSM10704	51	86090	0.059%	N.D.
335	17	7	7518264	7518264	G	C	R248G	COSM11564	245	218077	0.11%	N.D.
338	17	7	7518264	7518264	G	A	R248W	COSM10656	188	51001	0.37%	N.D.

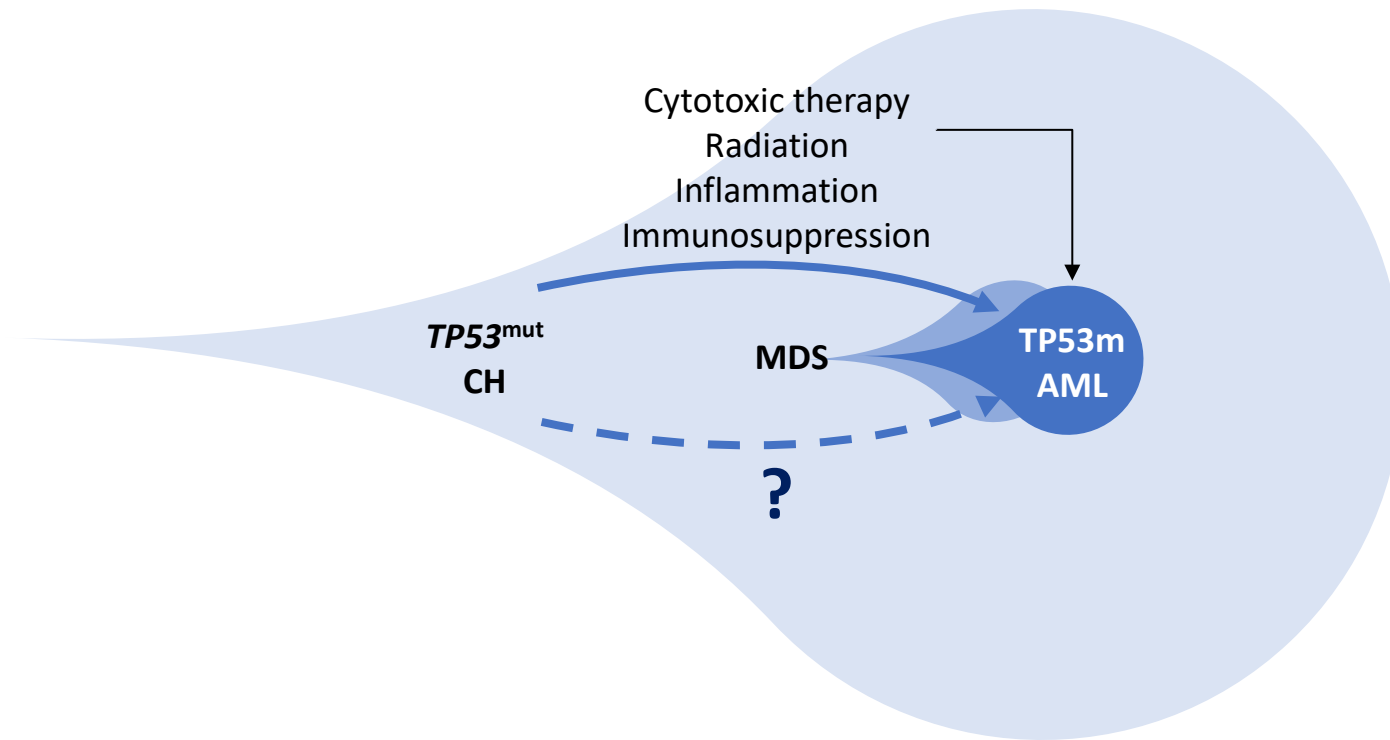
# ***TP53*<sup>mut</sup> feature of older populations**



Age	1-10	11-20	21-30	31-40	41-50	51-60	61-70	71-80
<i>TP53</i> <sup>mut</sup> AML	0	0	0	5%	5%	6%	16%	19%
<i>TP53</i> <sup>mut</sup> MDS	0	0	0	0	0	6%	8%	7%

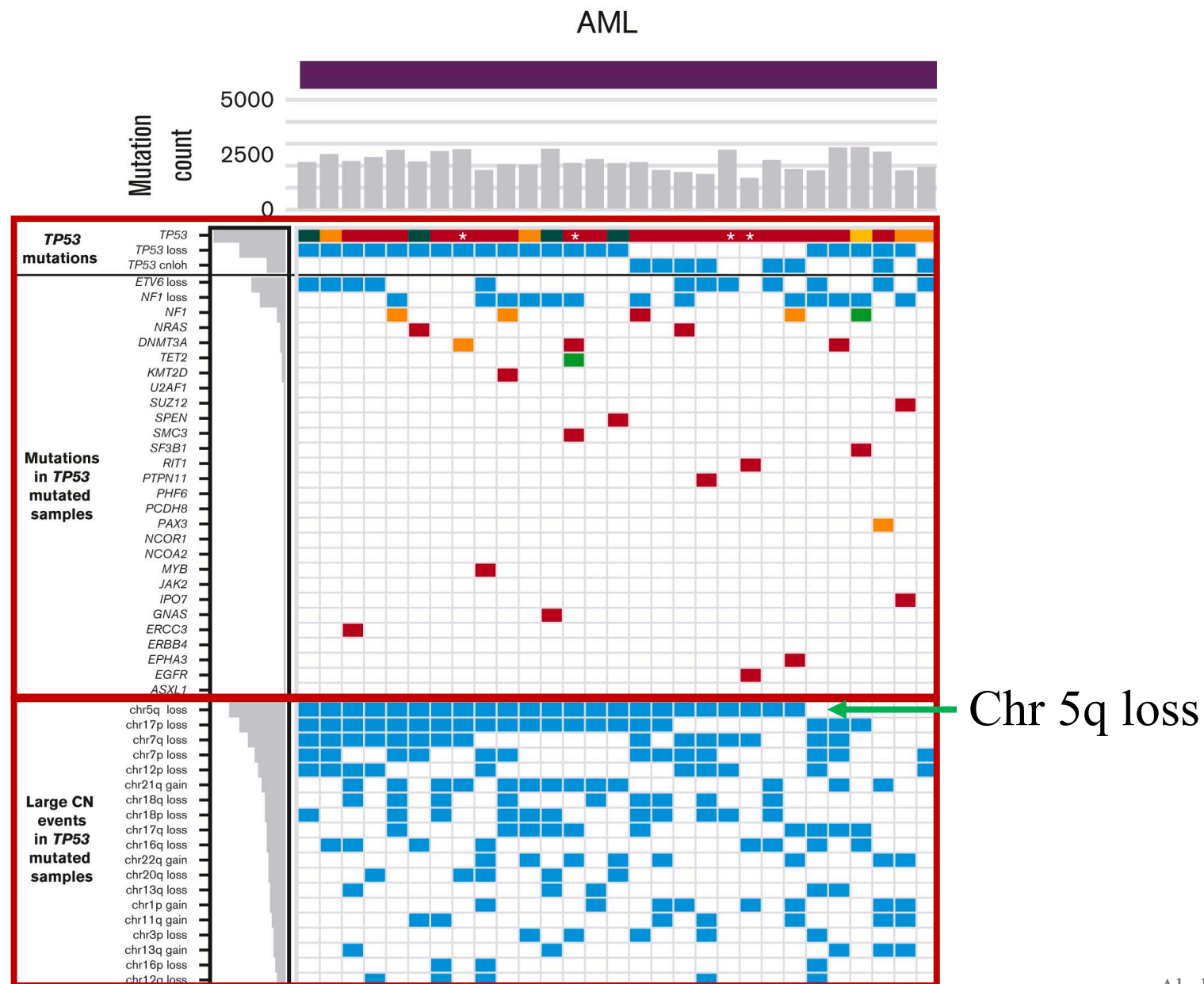


# What are the genomic events leading to $TP53^{\text{mut}}$ AML?



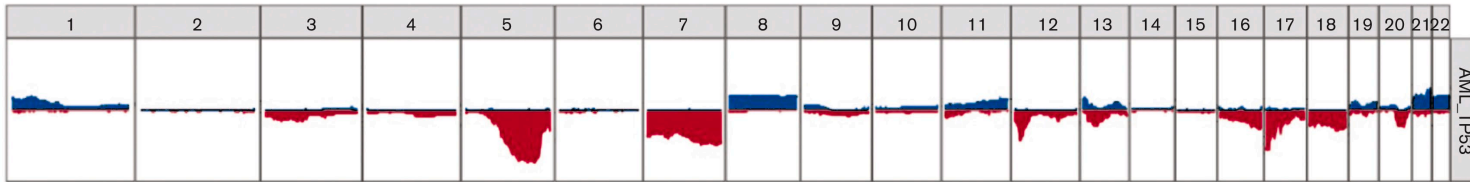
Age	1-10	11-20	21-30	31-40	41-50	51-60	61-70	71-80
$TP53^{\text{mut}}$ AML	0	0	0	5%	5%	6%	16%	19%
$TP53^{\text{mut}}$ MDS	0	0	0	0	0	6%	8%	7%

# Typical AML driver mutations lacking in *TP53* mutated AML



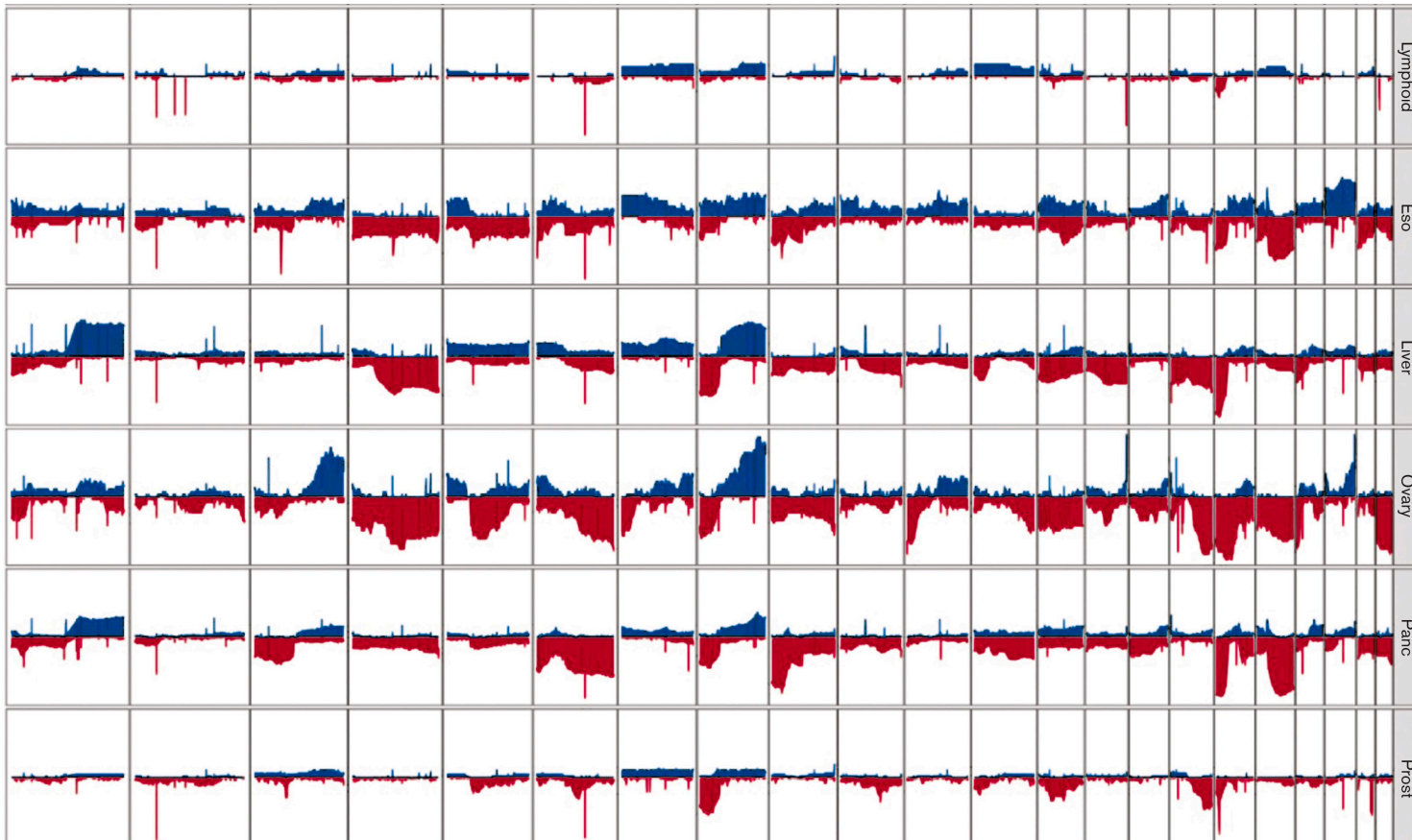
# Copy number landscape of TP53 mut cancer is tissue specific

## Myeloid malignancies



TP53 mut AML/MDS

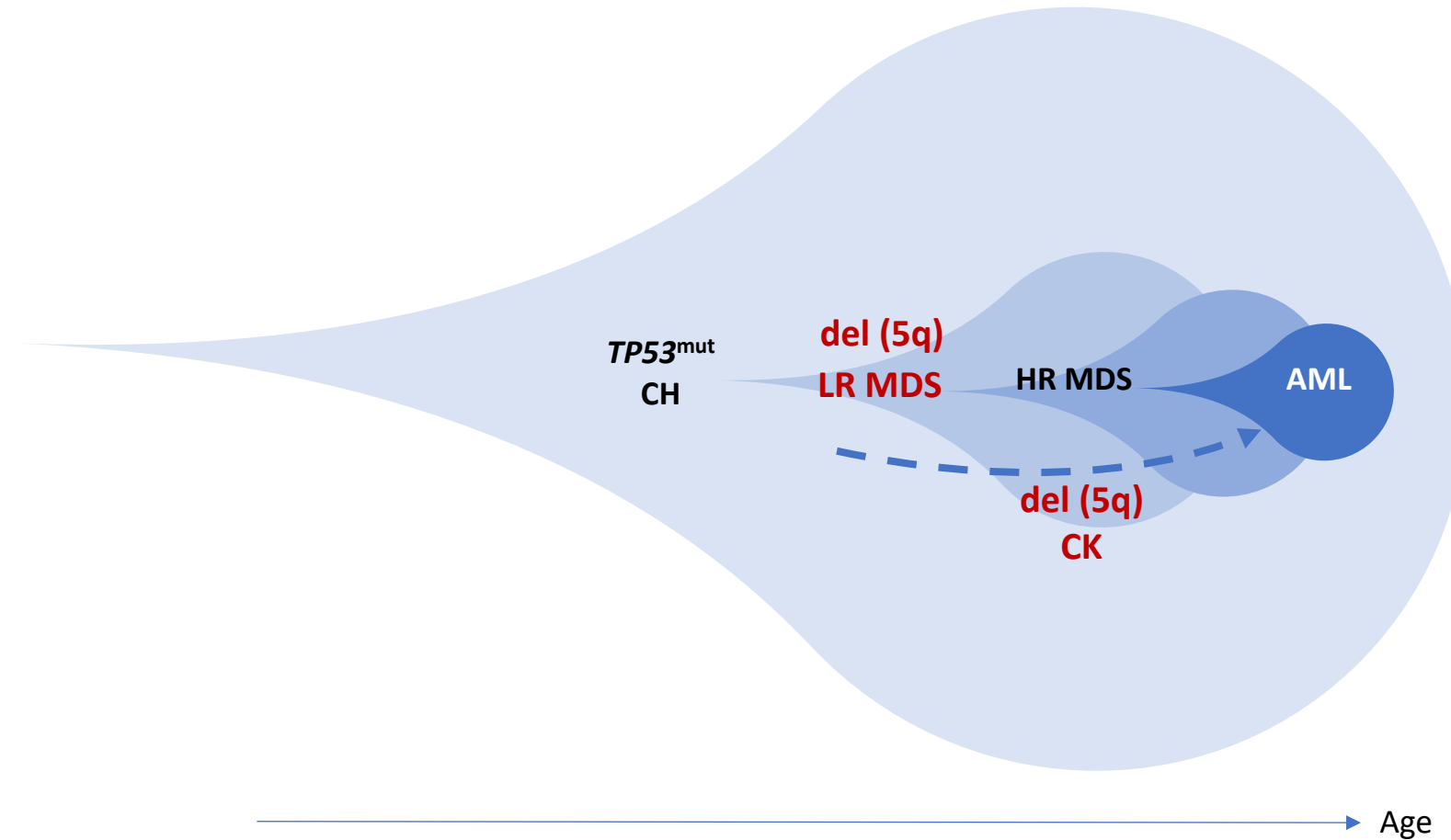
## Other cancers



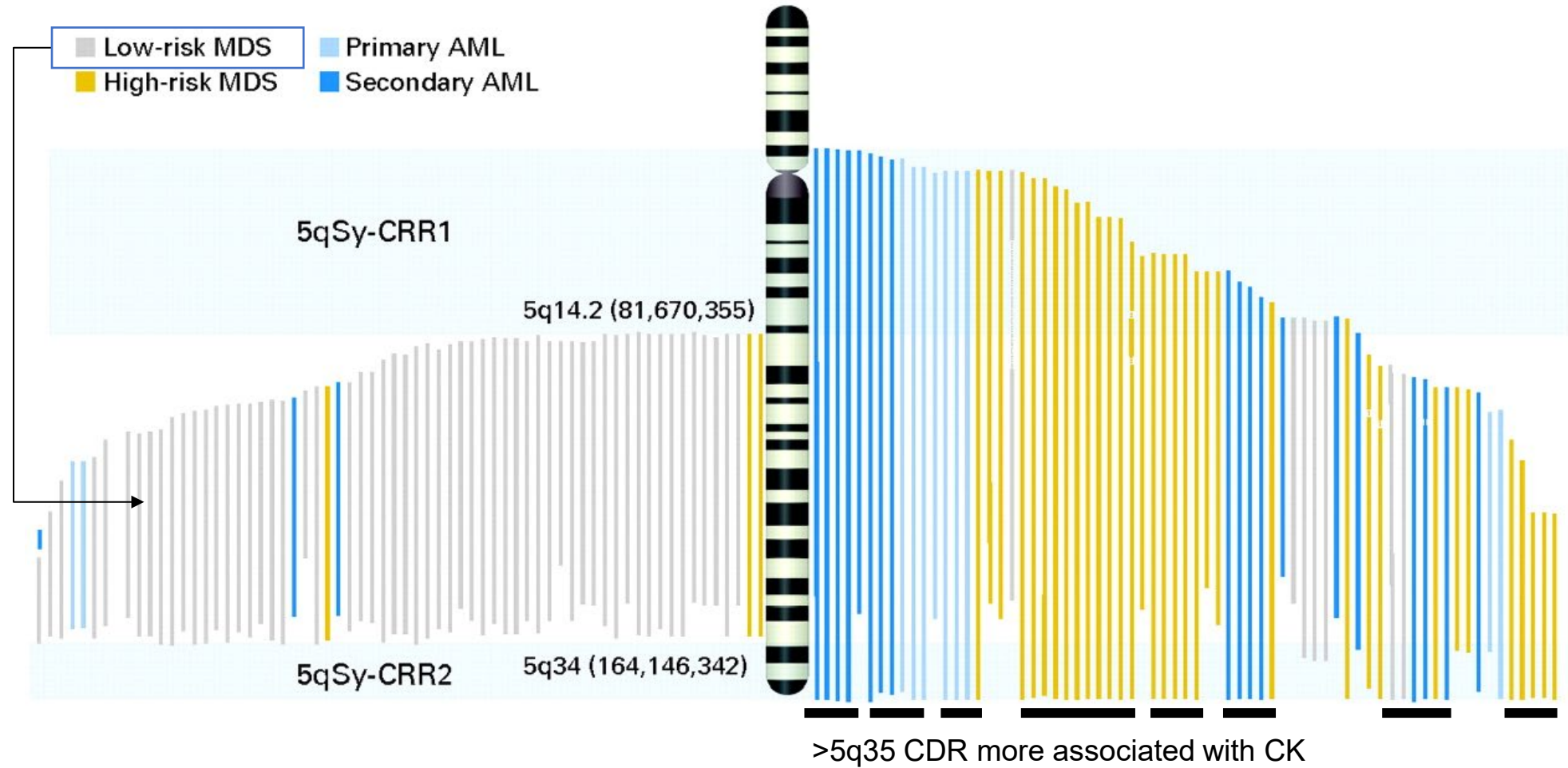
Lymphoid malignancies

Solid cancers

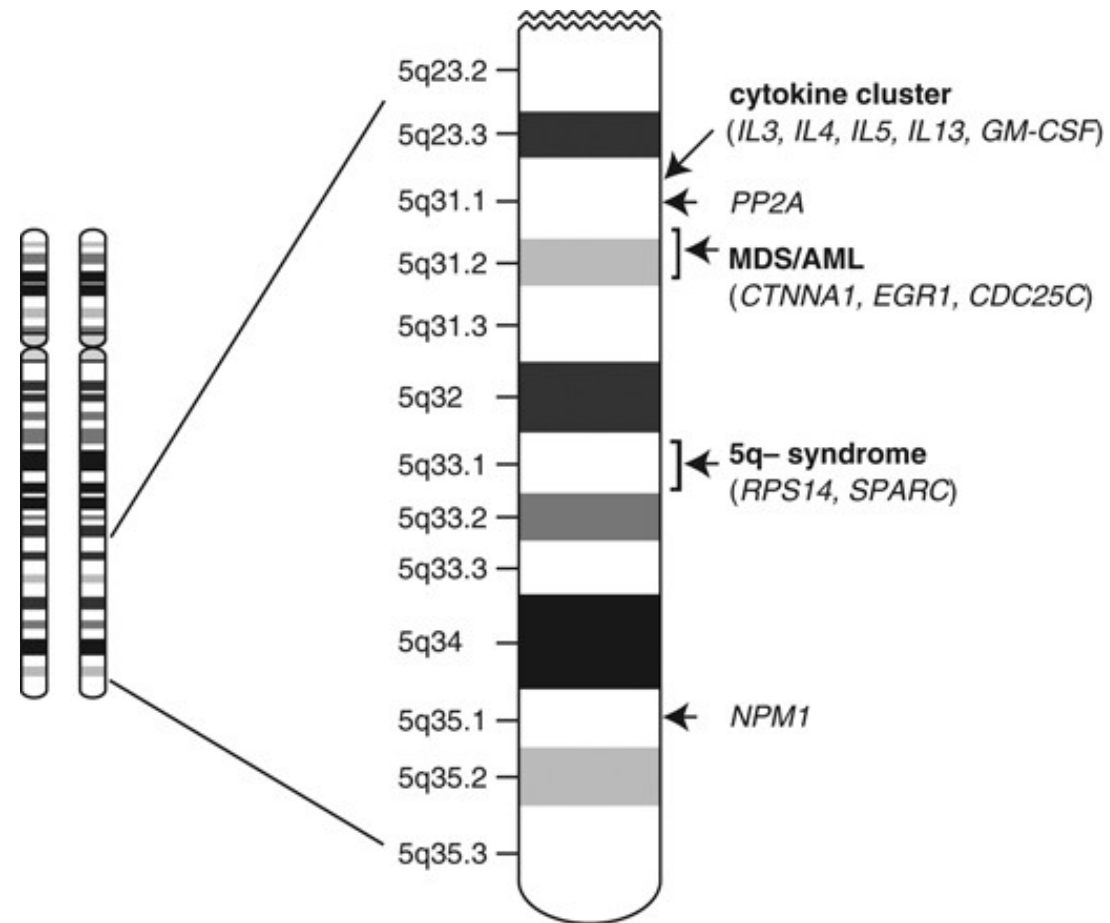
## Two faces of del(5q)



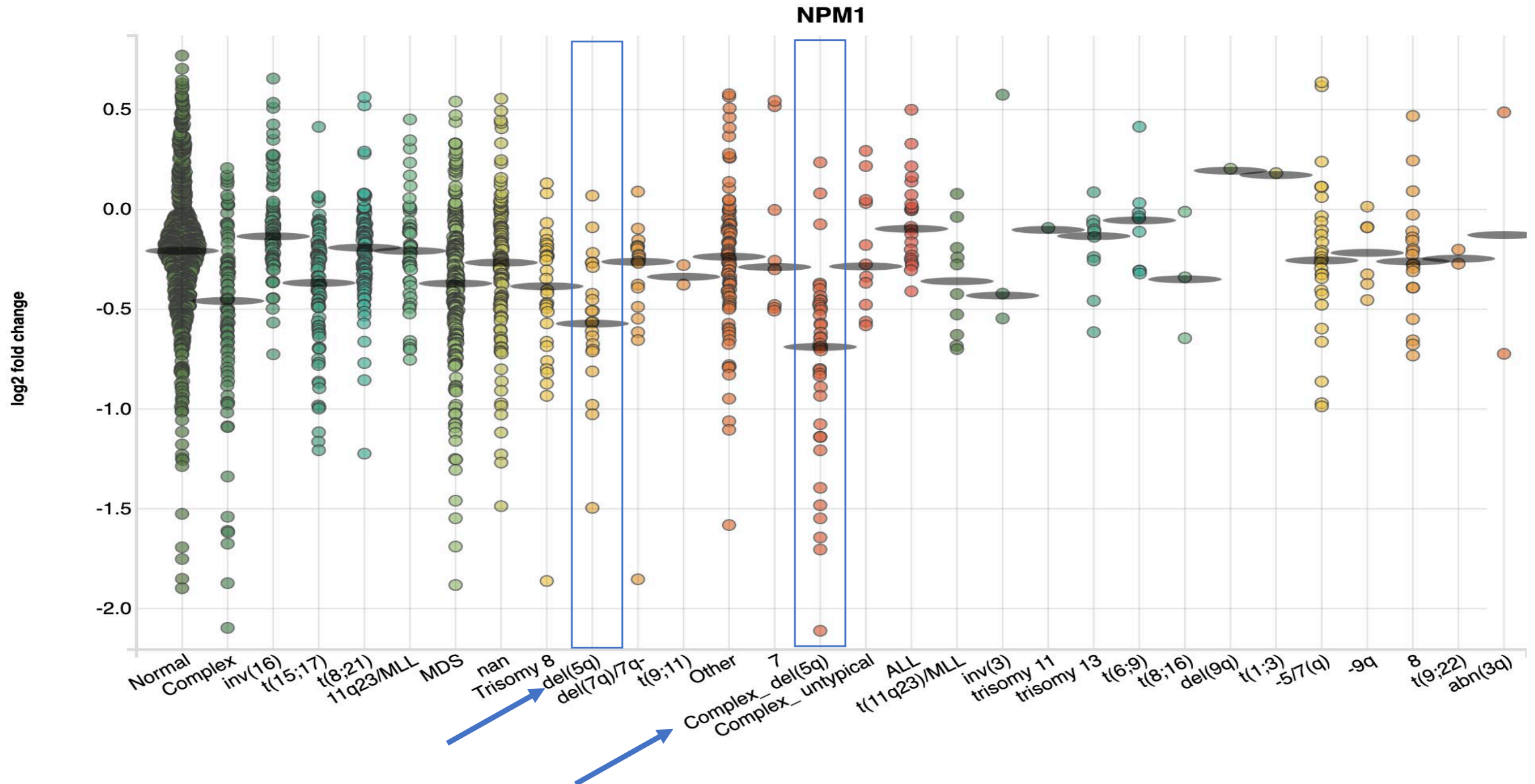
# Patterns of del(5q) loss in MN



# Candidate 5q genes

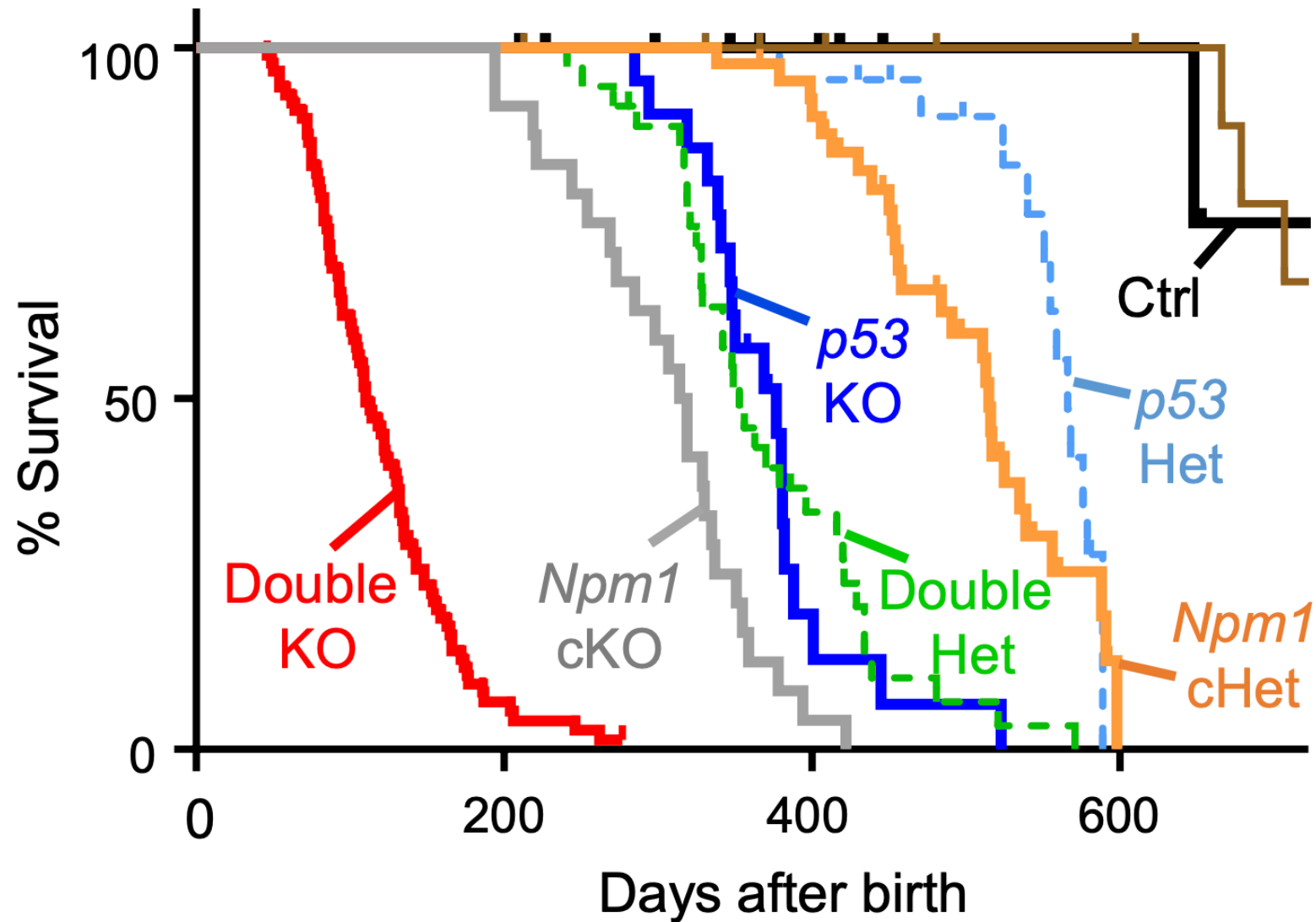


# Reduced NPM1 expression in del(5q) AML



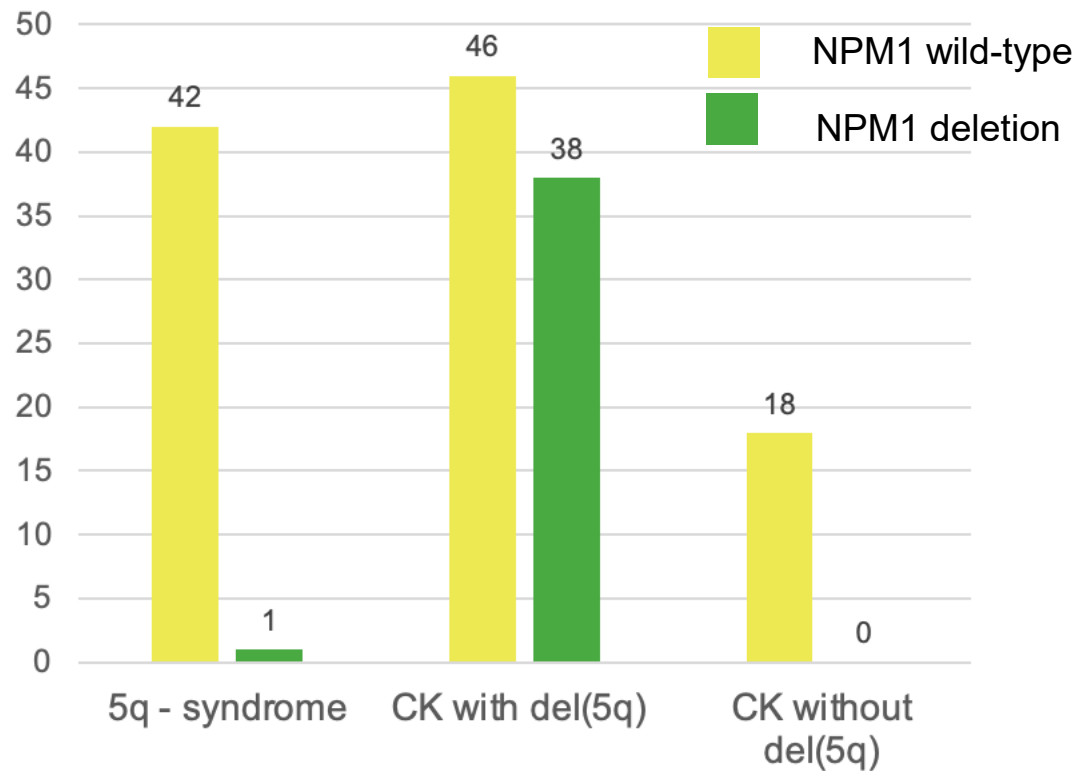


## *Npm1<sup>F/F</sup>p53<sup>-/-</sup> Vav1Cre<sup>+</sup>* DKO mice develop rapid AML



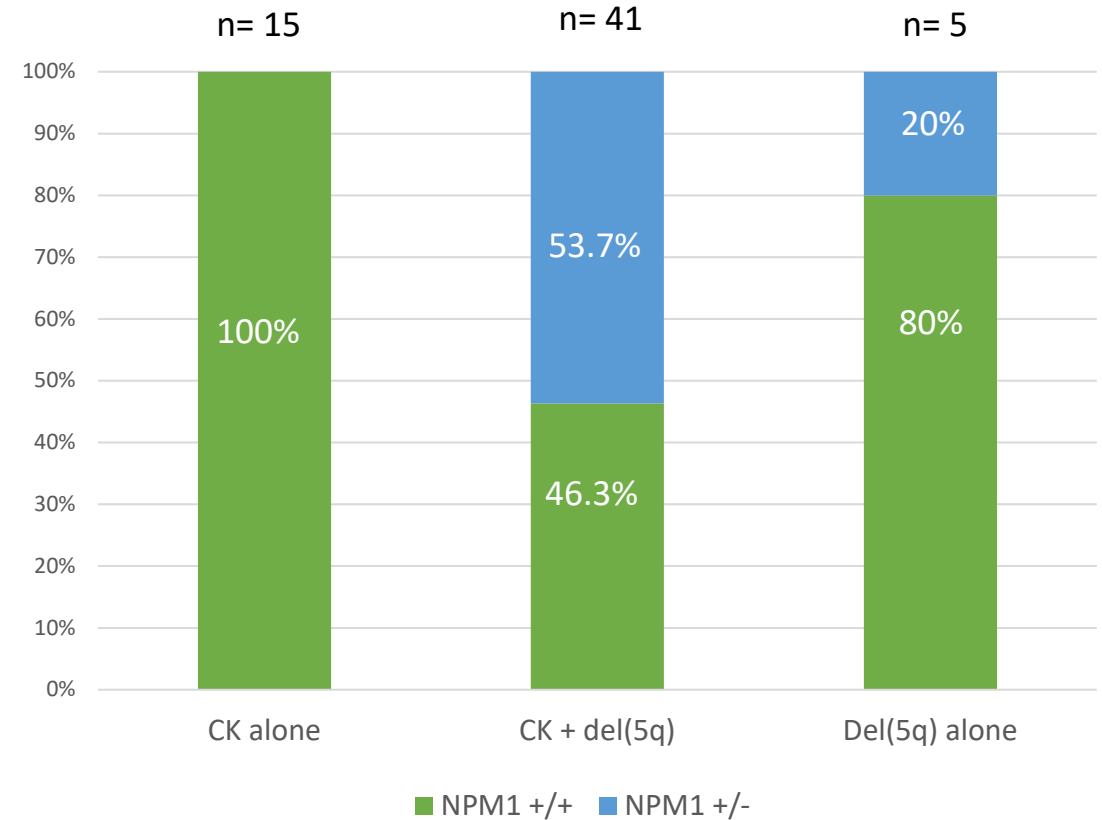
## ***NPM1* loss in CK with del (5q)**

***NPM1* deletion in 45%**



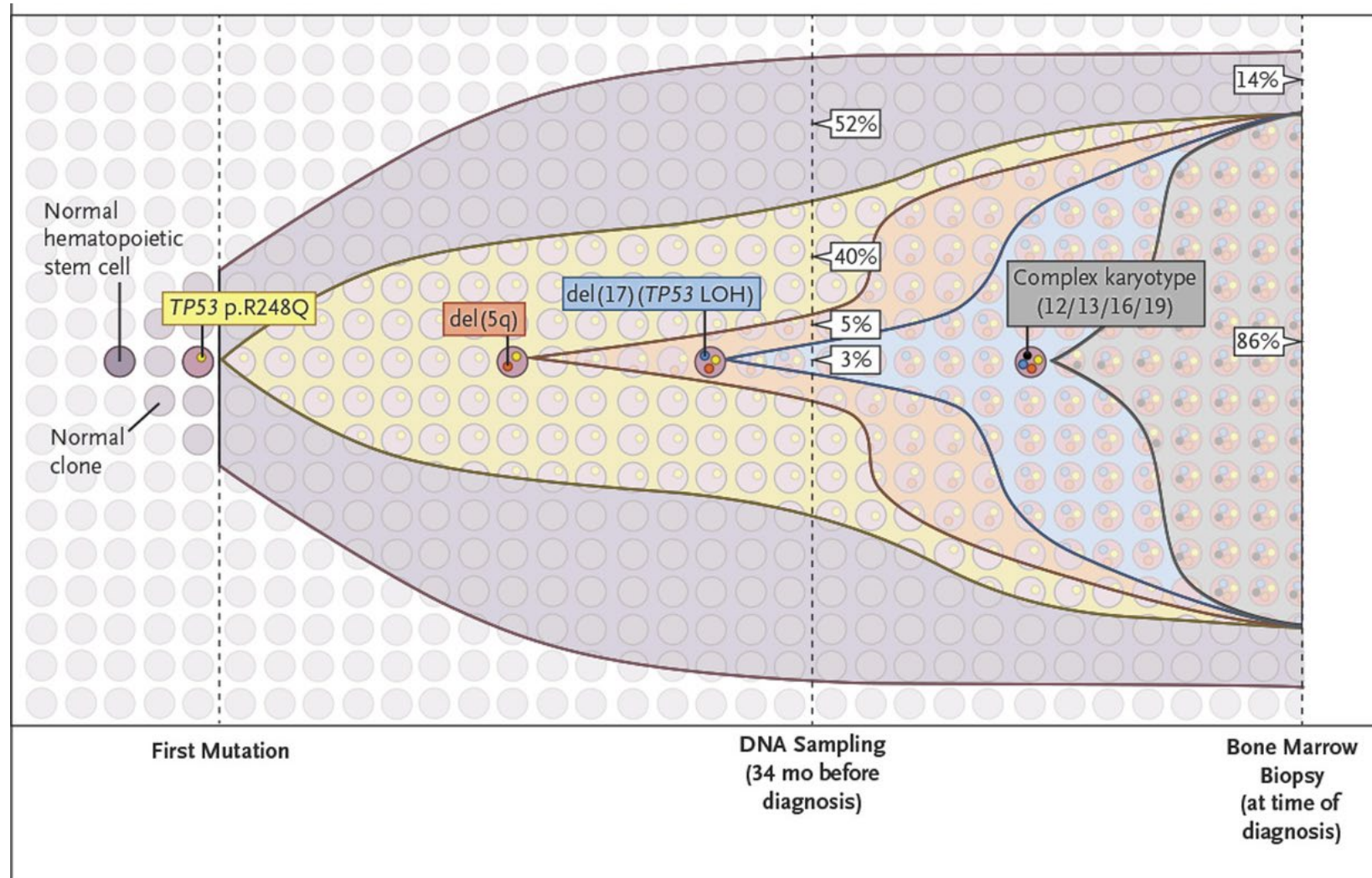
La Starza. *PLoS One*. 2010.

***NPM1* deletion in 54%**



Malalasakera et al, unpublished

# Is there an ordered process to the development of *TP53* mut AML?



## Conclusions

- Frequency of *TP53* mut AML increasing
- Copy number changes associated with leukemic transformation
- Whether events leading to *TP53* mut myeloid transformation stochastic or iterative remains to be determined