



I MECCANISMI DI RESISTENZA ALLE TARGET THERAPIES

Lydia Scarfò

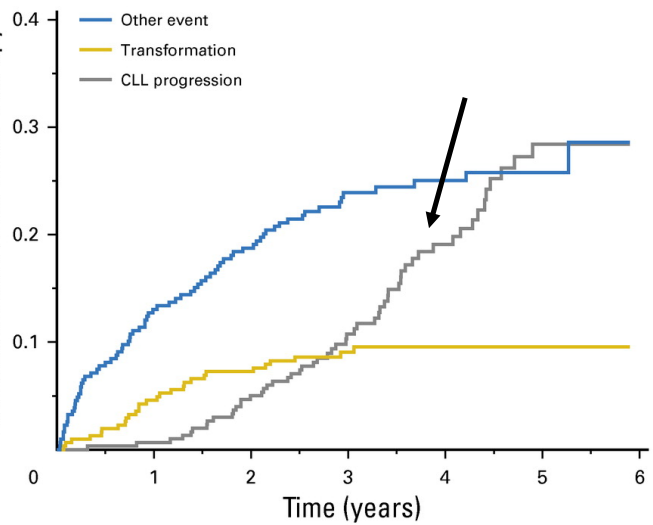
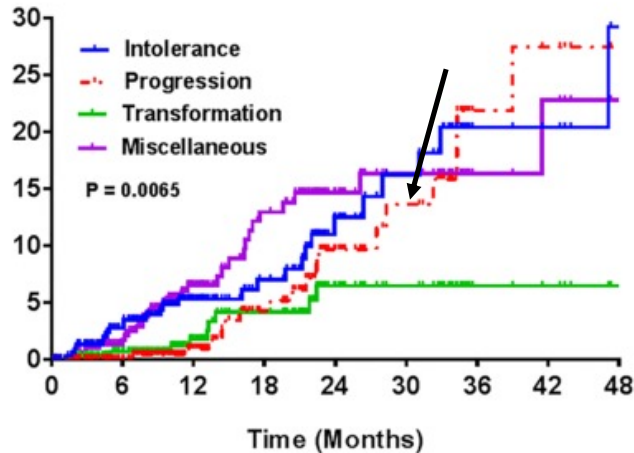
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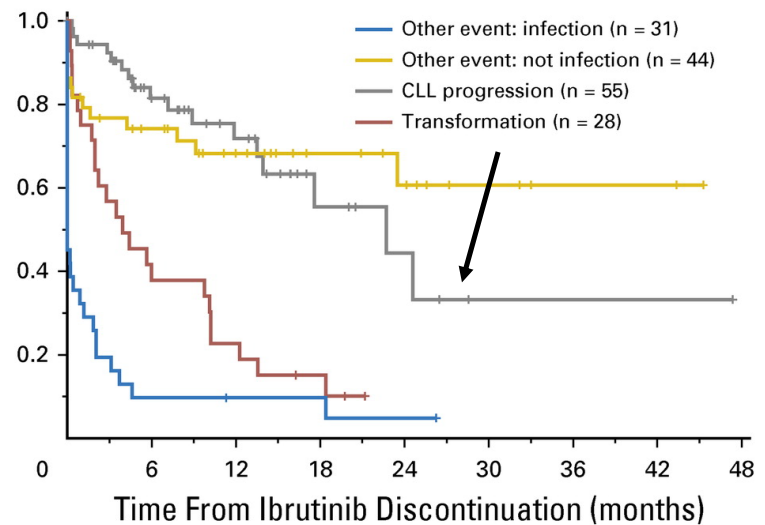
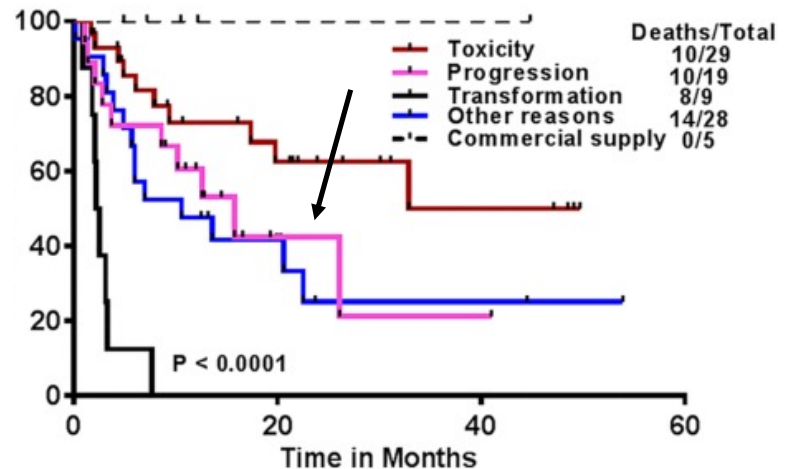


Ibrutinib discontinuation and outcome

Cumulative incidence of discontinuation of ibrutinib therapy



Survival Probability

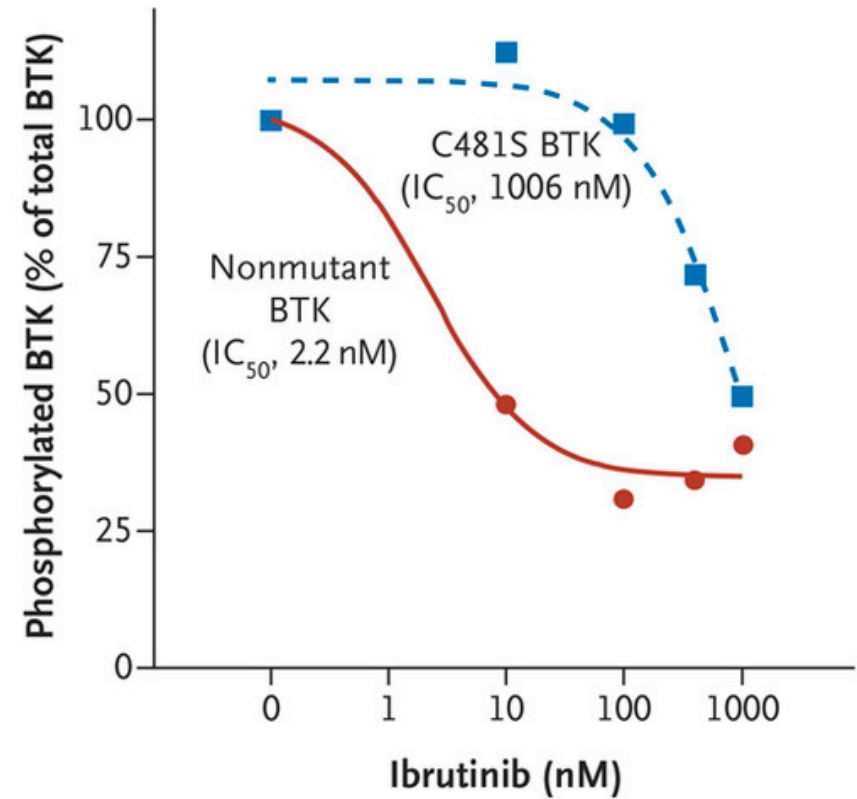
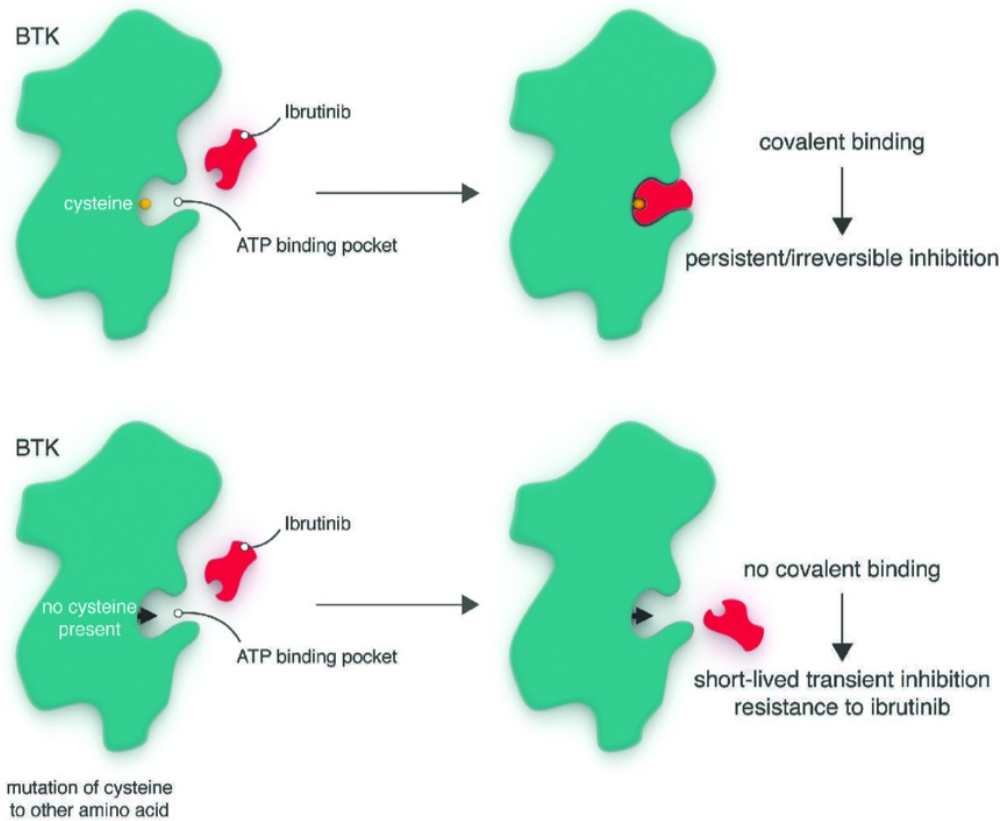


Jain et al. Cancer 2017; Woyach et al. JCO 2017

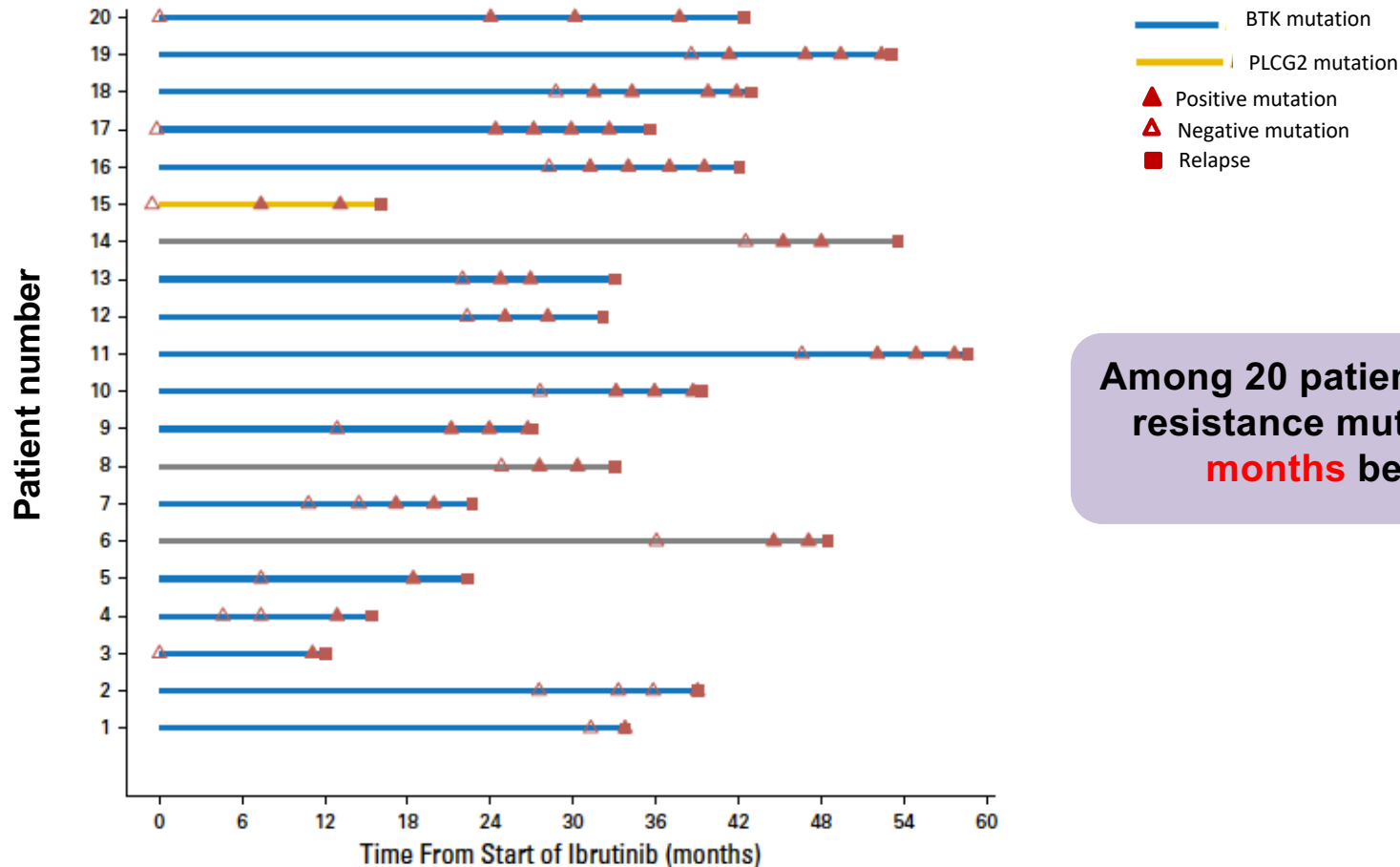
***BTK* and *PLCG2* mutations in CLL patients relapsed on ibrutinib**

Ref.	Pts with mut/total	Analytical Method	<i>BTK</i> mutations	VAF %	<i>PLCG2</i> mutations	VAF %
Woyach, 2014	6/6	WES	C481S	17-60	R665W; L845F S707Y	8-38
Ahn, 2017	8/10	High sensitivity NGS; ddPCR	C481S C481R	1.6-78.2 15.8	6nt del; R665W P664S; S707Y; L845F	0.1-18.3
Woyach, 2017	40/46 (retrospective); 8/8 (prospective)	Targeted Deep Sequencing	C481S C481R C481F C481A	0.2-94.8 18.1 1.1-100 45.3	R665W; S707P; S707F; S707Y; L845F; D993Y; L845/846del	3.6-44
Burger, 2016	2/4	WES; ddPCR	C481S	NR	M1141R; S707F; M1141K; D993H	12.0-35.0 (CCF)
Landau, 2017	5/7	Targeted Deep Sequencing	C481S	2.2-78.2	R665W; S707Y; L845F	0.2-4.7
Kadri, 2017	1/3	Targeted Deep Sequencing	C481S C481R	8.5-90.0 2.5	NR	NR
Kanagal-Shamanna, 2019	16/23	Targeted Deep Sequencing	C481S; C481F C481R; C481Y V537I	11(1-91)	None	NA

Functional characterization of *BTK* mutations



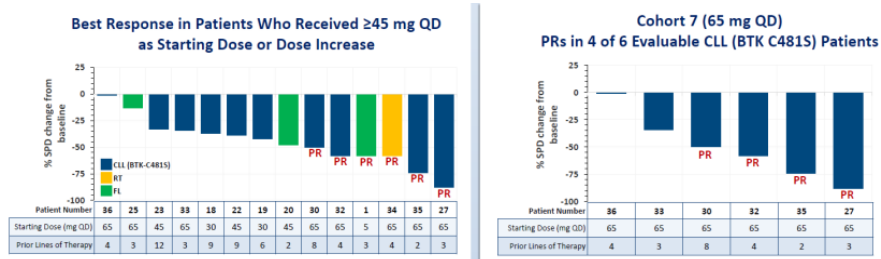
Duration of ibrutinib treatment in relapsed cases



Among 20 patients with CLL progression BTKi resistance mutations could be detected **9.3 months** before clinical progression

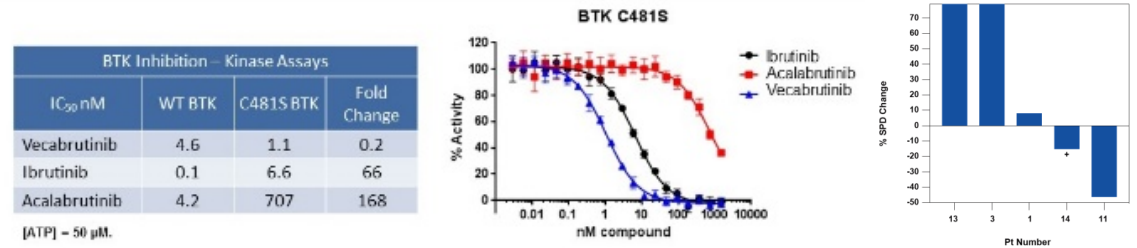
Novel BTK inhibitors inhibit C481S BTK mutants

ARQ 531 - ArQule



Woyach et al. EHA 2019

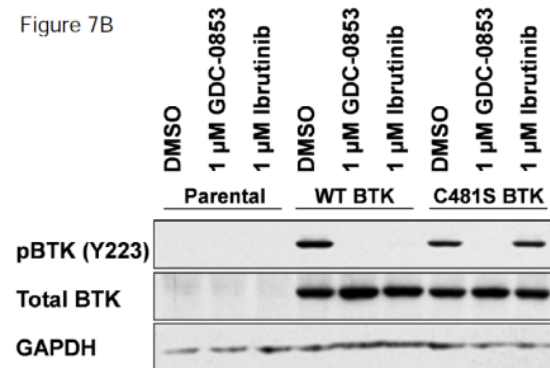
Vecabrutinib - Sunesis



Allan et al. EHA 2019

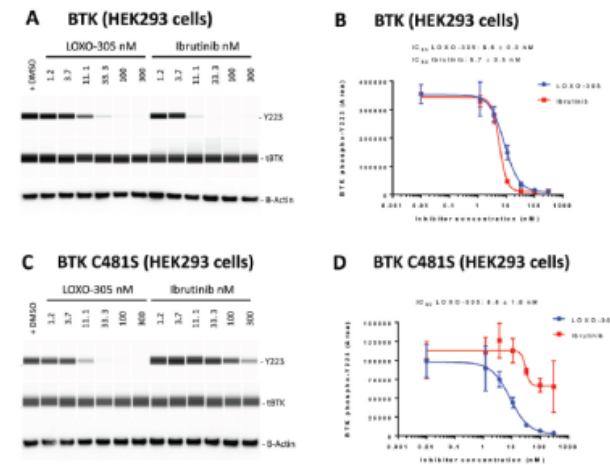
GDC583 - Genentech

Figure 7B



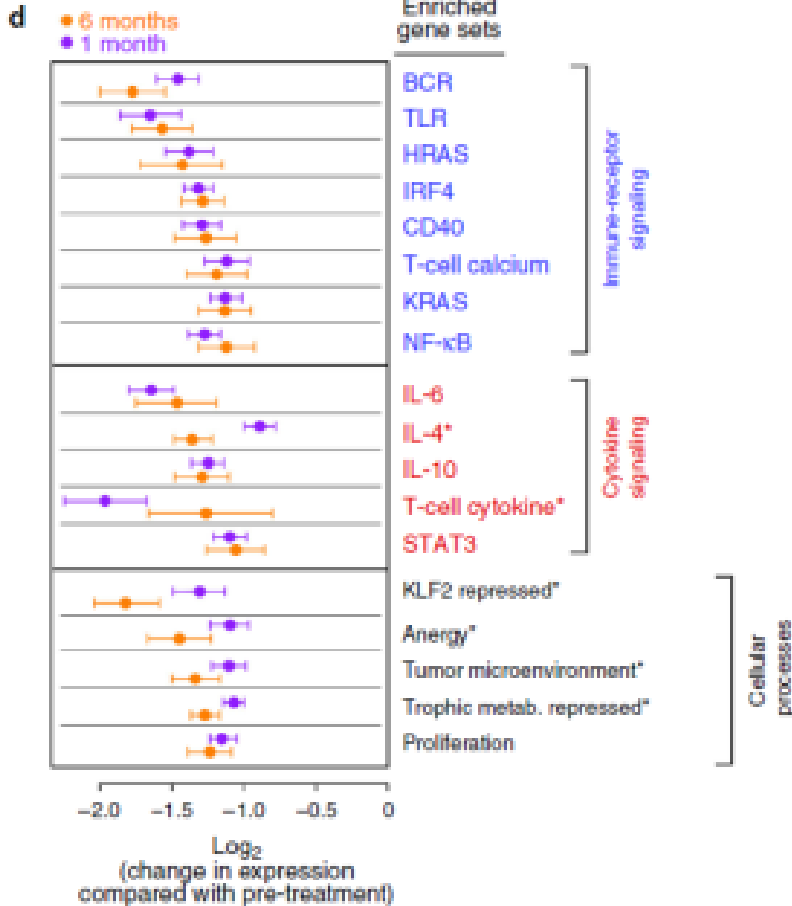
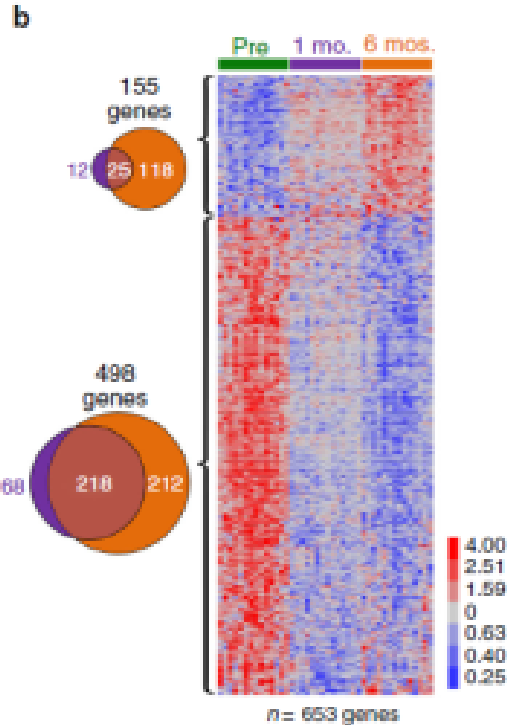
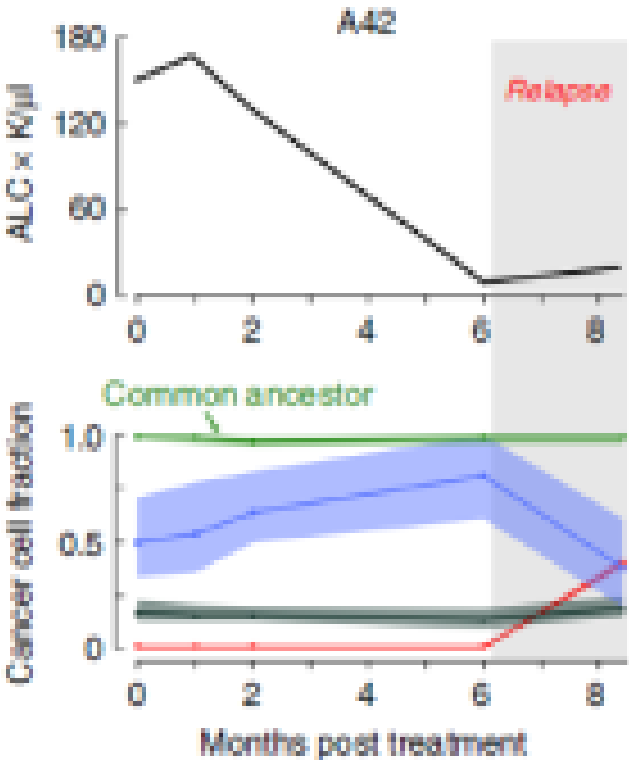
Reiff et al. Blood 2018

Loxo-305 - Loxo Oncology

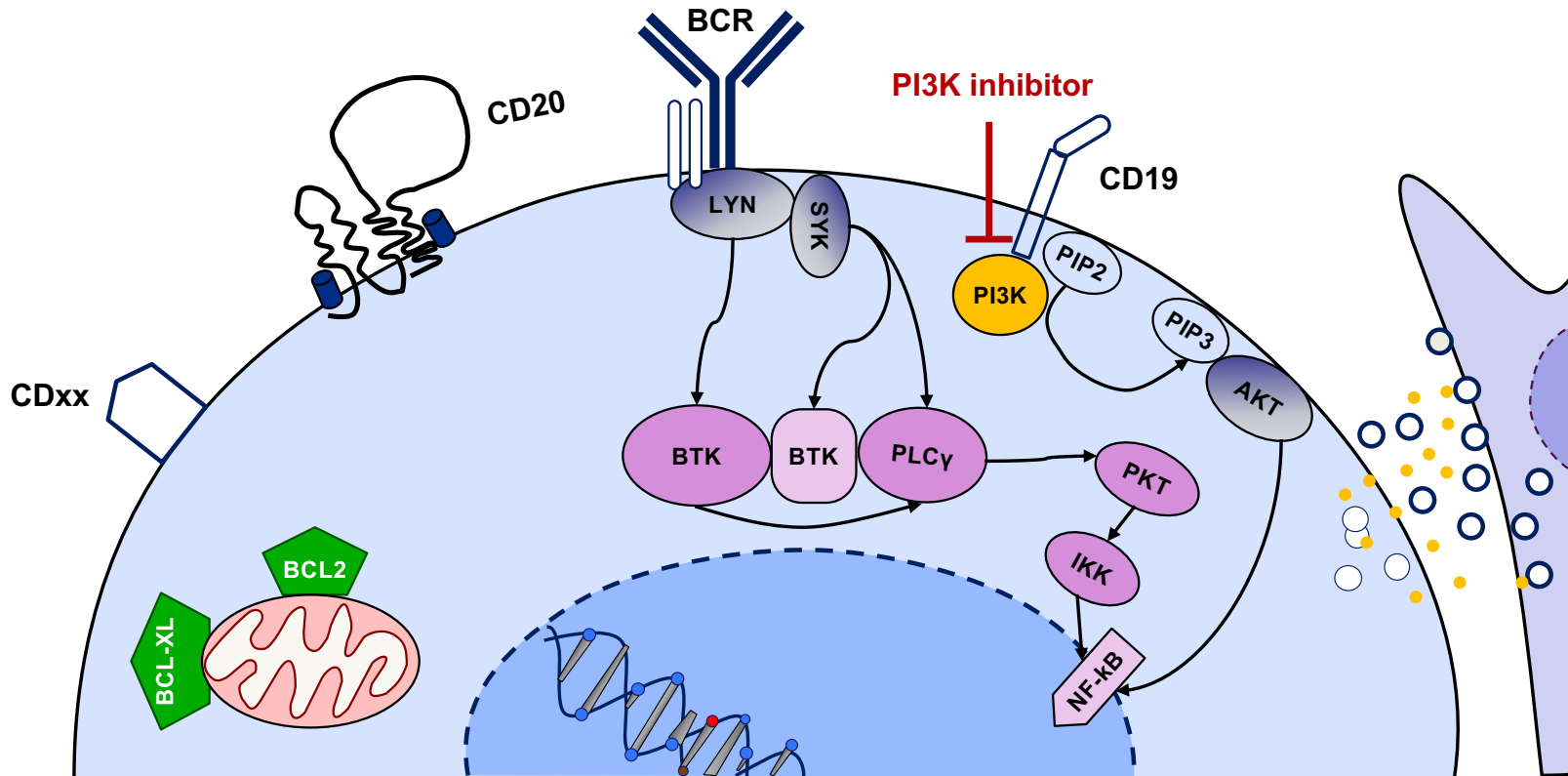


Brandhuber et al. SOHO 2018

Disease progression without BTK or PLCG2 mut

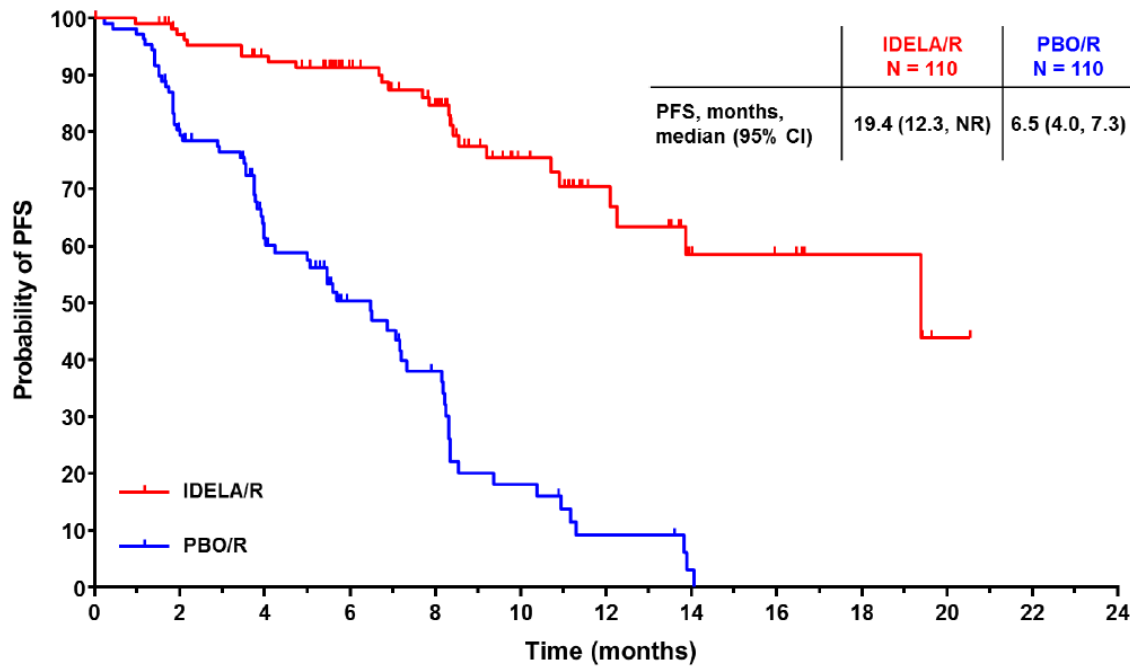


Idelalisib Resistance

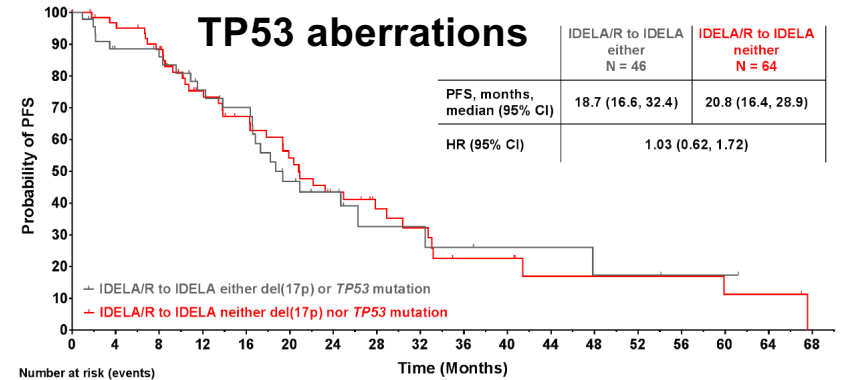


Adapted from Byrd J, et al. *J Clin Oncol* 2014

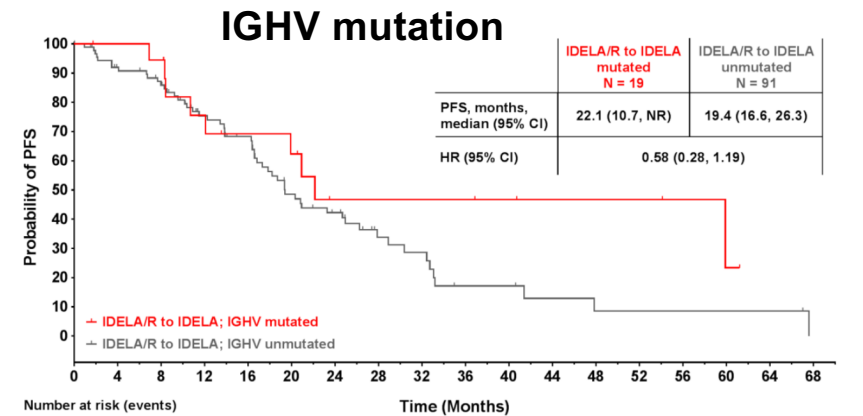
Idelalisib in Relapsed/Refractory patients with CLL



Number at risk (events)	0	2	4	6	8	10	12	14	16	18	20	24
IDELA/R	110 (0)	101 (3)	93 (7)	73 (9)	59 (14)	31 (19)	20 (21)	9 (24)	7 (24)	4 (24)	1 (25)	0 (25)
PBO/R	110 (0)	84 (21)	48 (38)	29 (46)	20 (53)	9 (63)	4 (67)	1 (69)	0 (70)	0 (70)	0 (70)	0 (70)



Number at risk (events)	0	4	8	12	16	20	24	28	32	36	40	44	48	52	56	60	64	68
IDELA/R to IDELA either	46 (0)	36 (5)	34 (6)	28 (10)	25 (12)	15 (20)	11 (21)	5 (23)	5 (23)	4 (24)	3 (24)	3 (24)	2 (25)	2 (25)	1 (25)	1 (25)	0 (25)	0 (25)
IDELA/R to IDELA neither	64 (0)	59 (2)	53 (7)	37 (14)	31 (18)	25 (24)	19 (29)	13 (31)	10 (33)	6 (36)	6 (36)	3 (37)	3 (37)	3 (37)	3 (37)	2 (38)	2 (38)	0 (39)



Number at risk (events)	0	4	8	12	16	20	24	28	32	36	40	44	48	52	56	60	64	68
IDELA/R to IDELA mutated	19 (0)	18 (0)	17 (1)	12 (4)	10 (5)	9 (6)	5 (8)	5 (8)	5 (8)	5 (8)	4 (8)	3 (8)	3 (8)	3 (8)	2 (8)	1 (9)	0 (9)	0 (9)
IDELA/R to IDELA unmutated	91 (0)	77 (7)	70 (12)	53 (20)	46 (25)	31 (38)	25 (42)	13 (48)	10 (48)	5 (52)	5 (52)	3 (53)	2 (54)	2 (54)	2 (54)	2 (54)	2 (54)	0 (55)

Idelalisib: the quest for resistance mechanisms

Study number	Patient	%CD19+/ CD5 ^a	%CD19+/ CD5 ^b	IGHV status	TP53 status	del17p status
NCT01659021 (IDELA + ofatumumab)	1	93	NA	UM	mutation	deletion
	2	94	90	UM	mutation	deletion
	3	98	NA	UM	mutation	deletion
	4	70	NA	UM	mutation	normal
	5	78	NA	UM	normal	normal
	6	83	NA	M	mutation	normal
	7	93	NA	UM	mutation	deletion
	8	97	NA	UM	normal	normal
	9	92	88	UM	normal	normal
NCT01539512 + NCT01539291 (IDELA + rituximab)	10	76	83*	UM	N/A	deletion
	11	46.2	NA	UM	normal	normal
NCT01539512 (IDELA + rituximab)	12	94	92	UM	mutation	normal
	13	83	19	UM	normal	normal

Sample selection criteria included:

- treatment period of ≥ 180 days
- at least a partial nodal response followed by progression
- progression did not occur within a drug interruption window
- progression was not associated with RT

WES identified no mutations in:

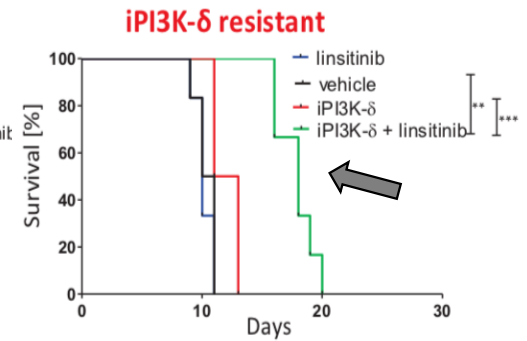
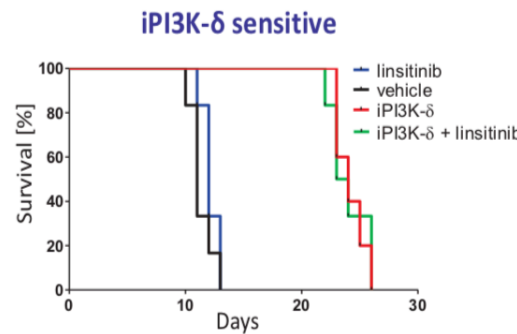
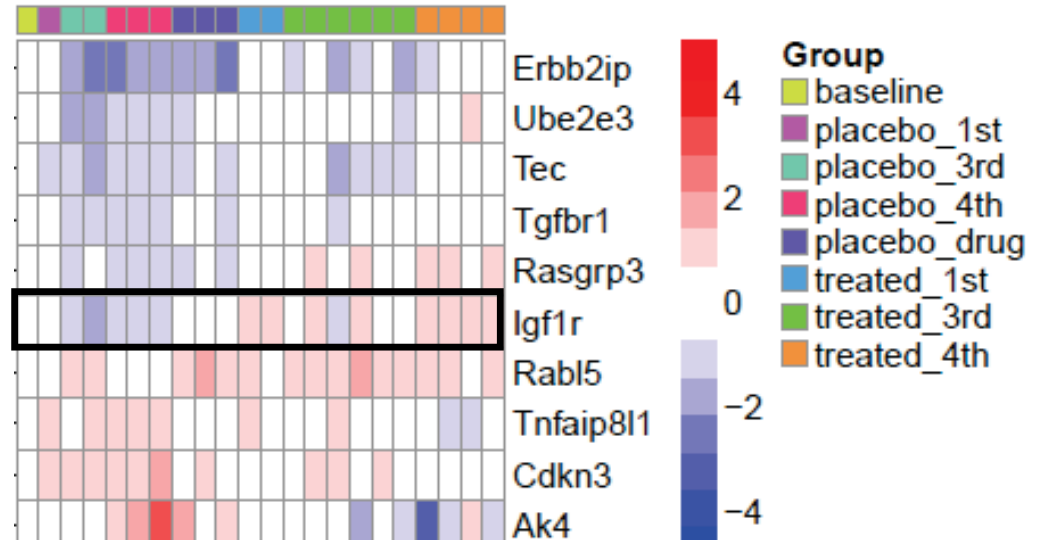
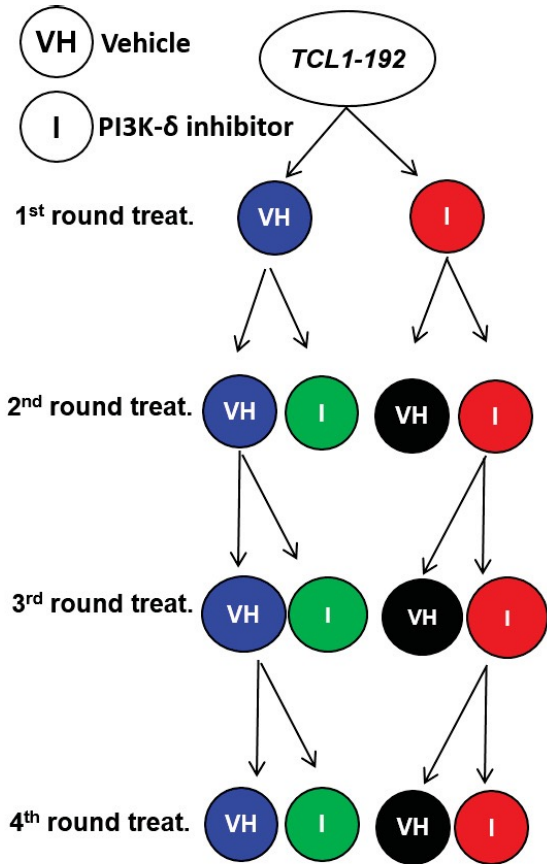
- PI3K signaling or related pathways
- PI3K δ in any sample at any time point

Idelalisib resistance: No common mutational mechanism

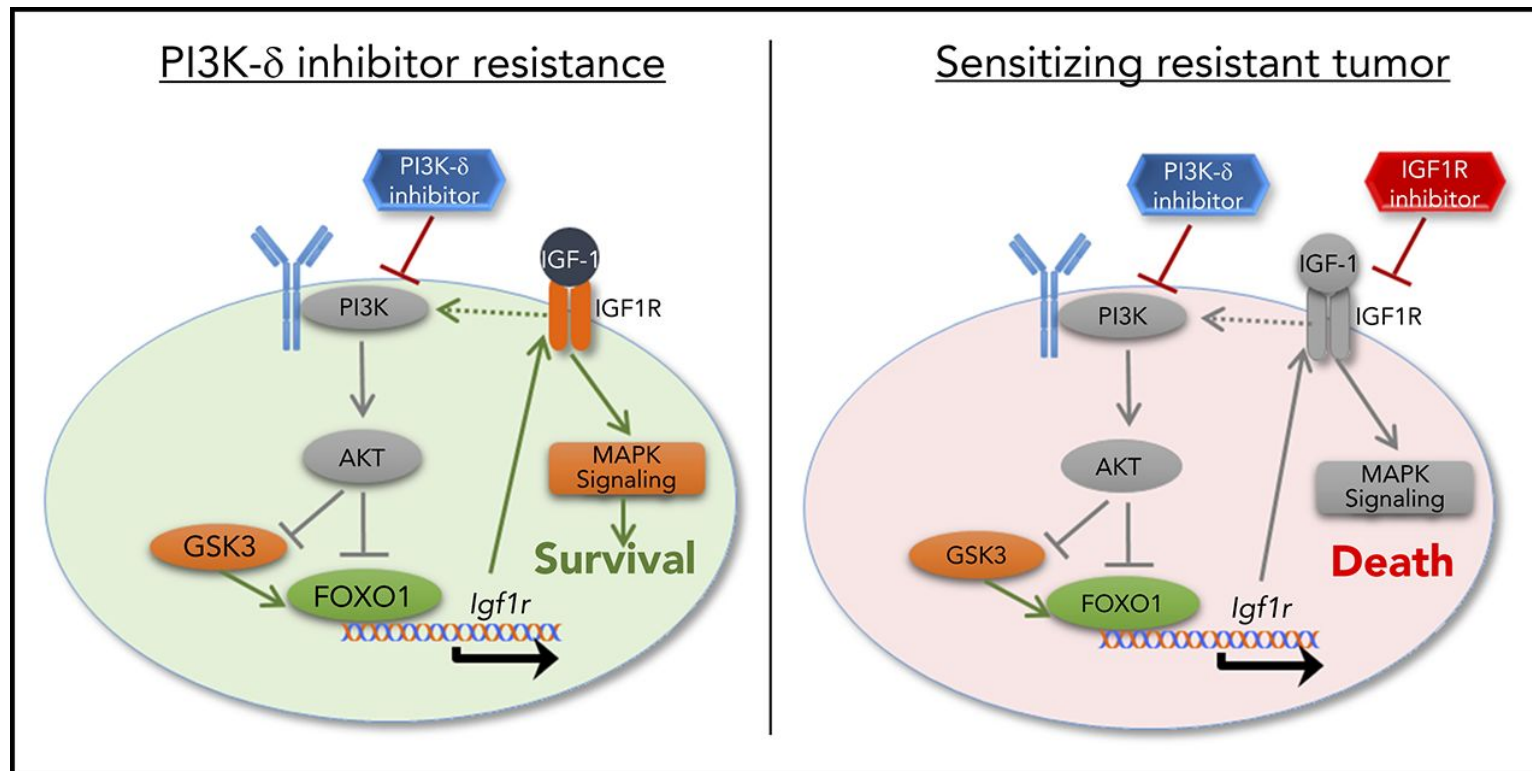
WES of Idelalisib relapsed CLL patients (n=13)

Ghia et al. ASH 2016

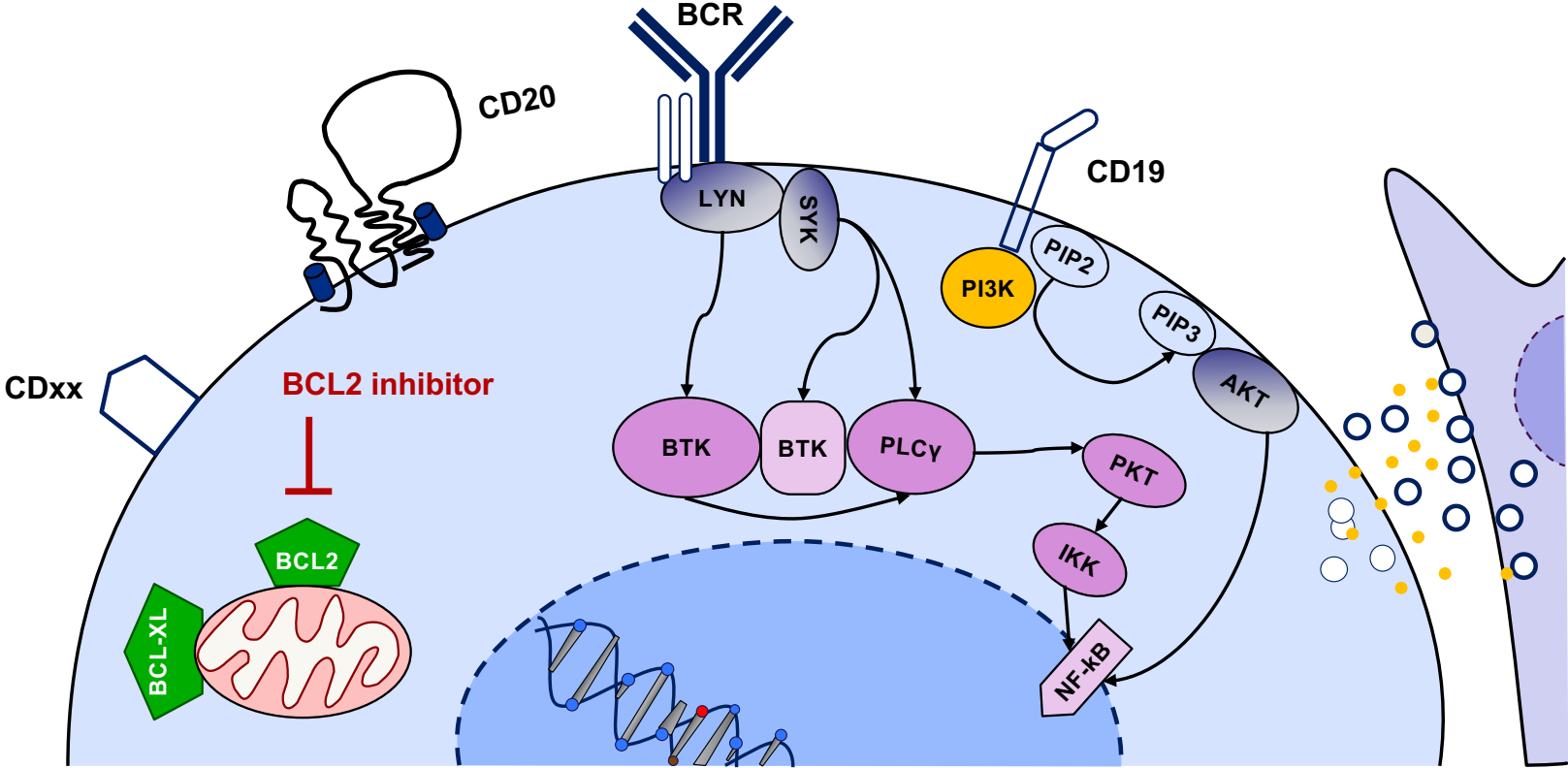
In vivo modeling of resistance to Idelalisib



In vivo modeling of resistance to Idelalisib

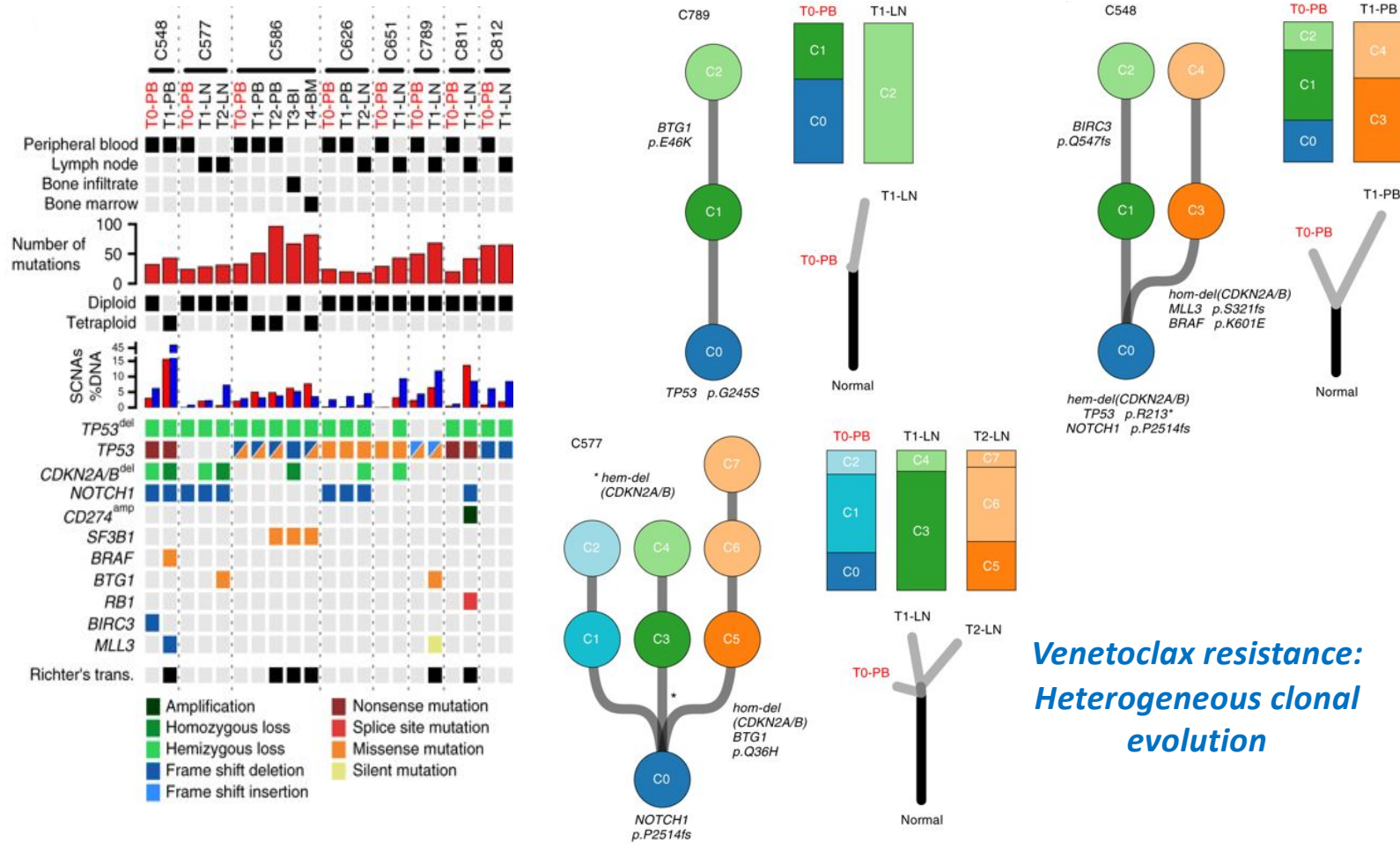


Venetoclax Resistance



Adapted from Byrd J, et al. J Clin Oncol 2014

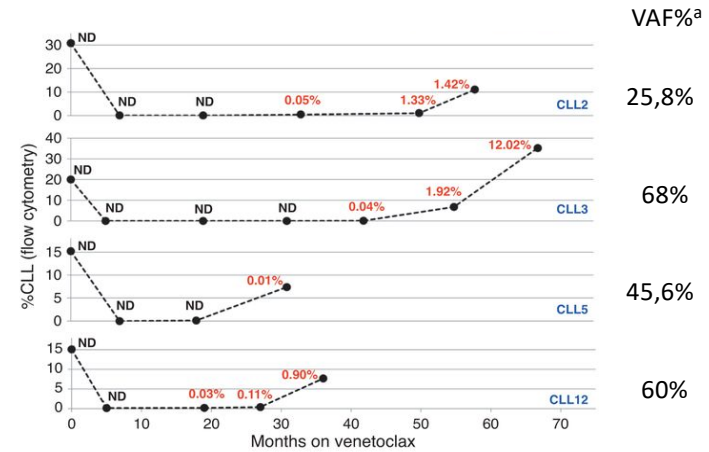
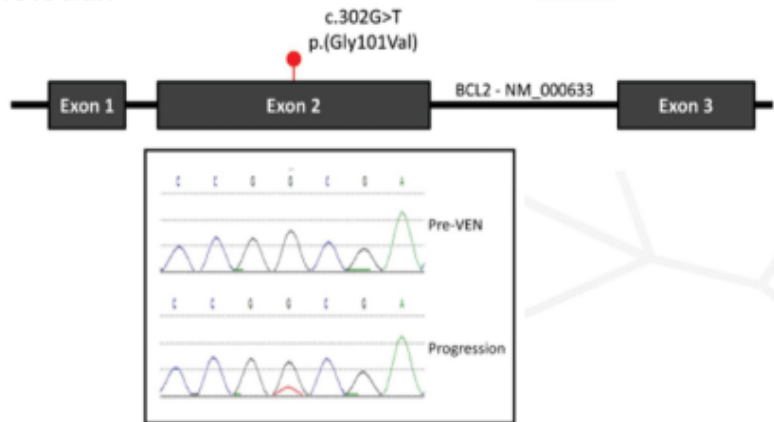
Venetoclax: insights into the clonal dynamics involved in resistance



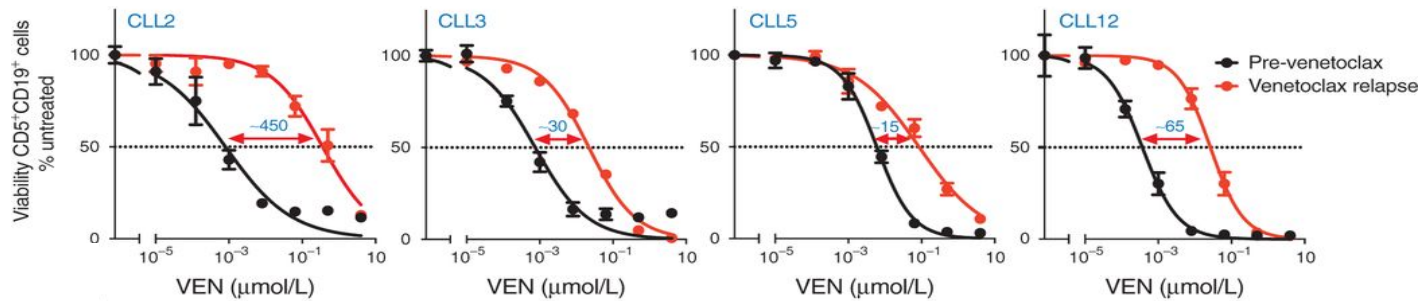
**Venetoclax resistance:
Heterogeneous clonal
evolution**

Venetoclax: mechanisms of resistance

***BCL2* c.302G>T, p.(G101V)** detected in samples from 7/15 (48.7%) patients at CLL-type progression on Venetoclax

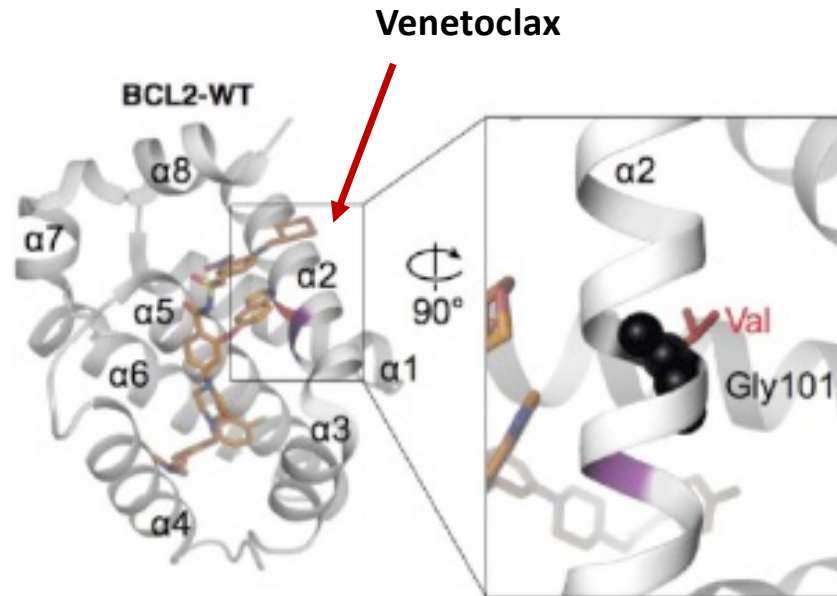


^aCLL cells harboring G101V at progression; calculated by adjusting the measured VAF by the % of CLL cells in the bone marrow determined by flow cytometry.



CLL cells harboring p.G101V are less sensitive to Venetoclax

BCL2 Gly101Val occurs near the BH3-binding groove

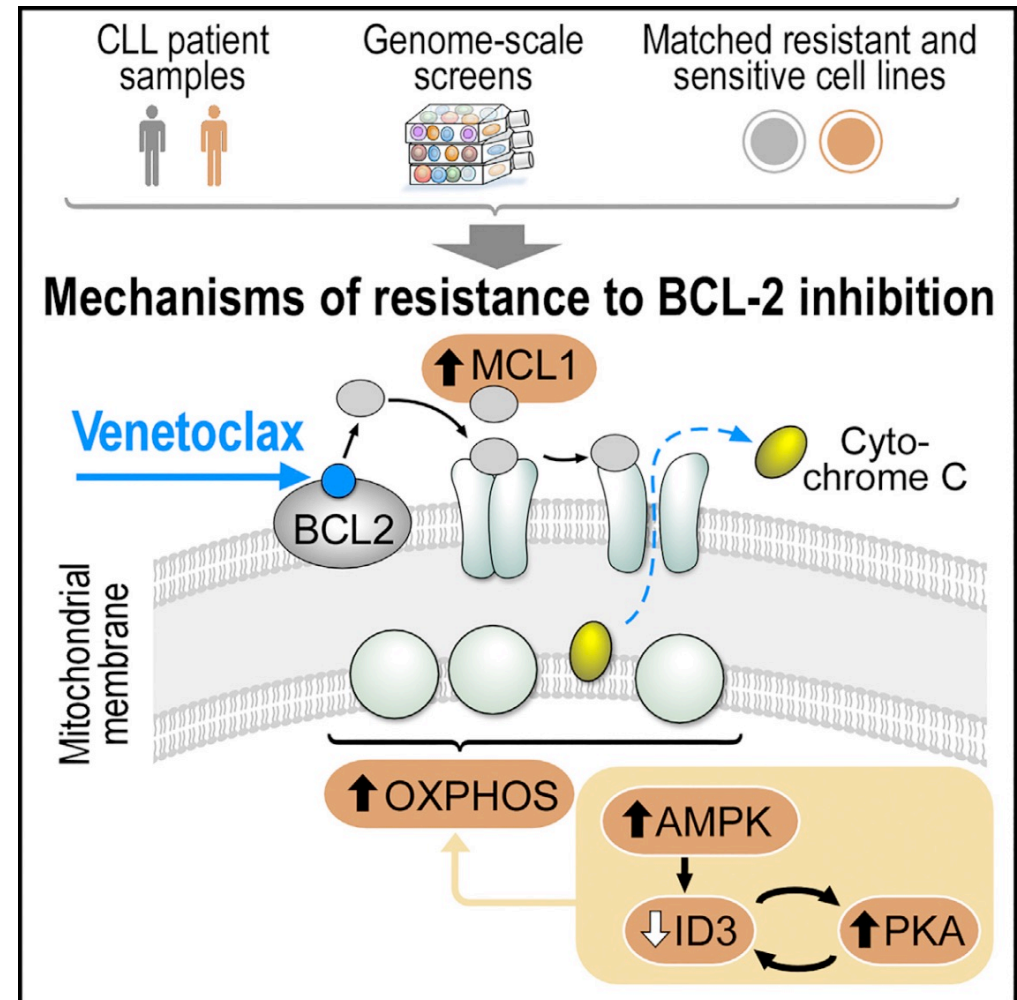
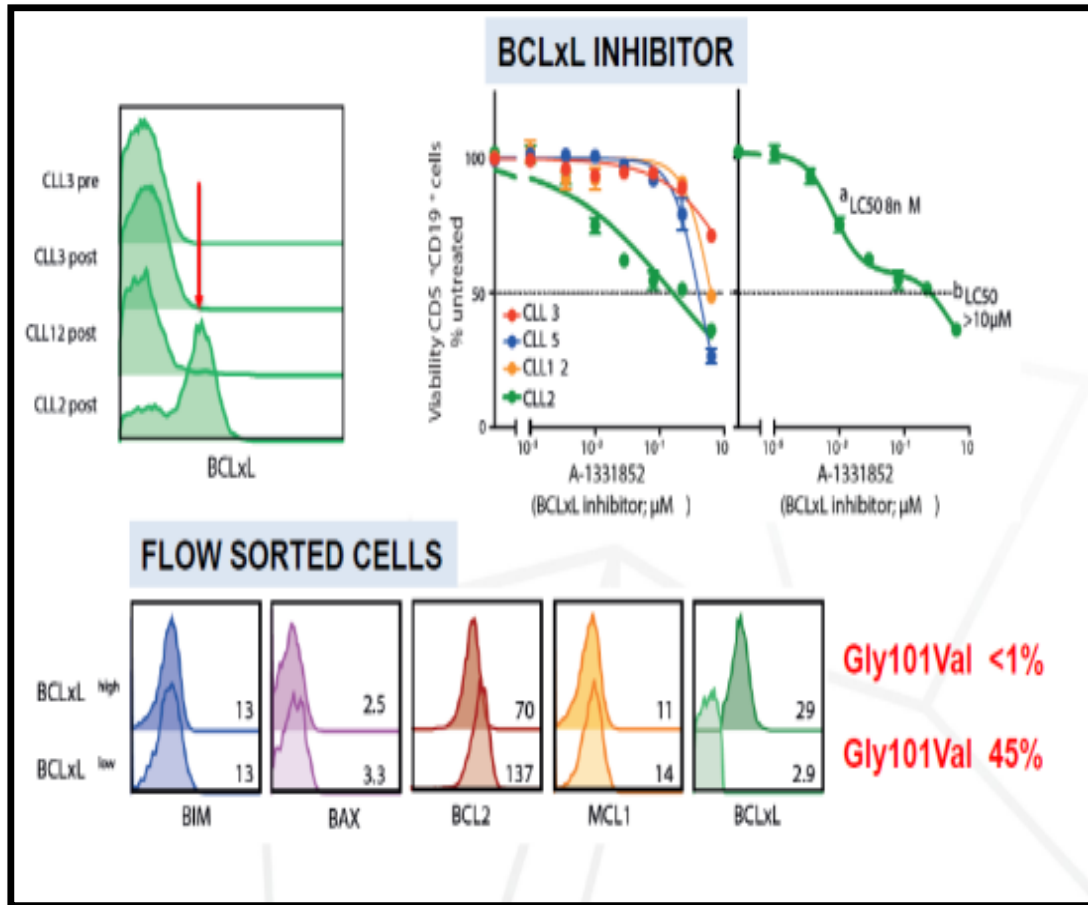


- Highly conserved residue
- Faces away from inside of binding groove
- Proximal to P4 pocket

Population	Number assessed	<i>BCL2</i> Gly101Val detected (%)	<i>BCL2</i> Phe104Leu detected (%)
Venetoclax-naïve CLL	96	0 (0%)	0 (0%)
CLL-type progression on venetoclax	15	7 (46.7%)	0 (0%)
Other B-cell malignancies			
- Follicular lymphoma	28	0 (0%)	0 (0%)
- Mantle cell lymphoma	28	0 (0%)	0 (0%)
- Diffuse large B-cell lymphoma	47	0 (0%)	0 (0%)
- Lymphoplasmacytic lymphoma	95	0 (0%)	0 (0%)
- Multiple myeloma	103	0 (0%)	0 (0%)
Cancer database (COSMIC ^a)	47,628	0 (0%)	2 (0.004%)
Population database (gnomAD ^b)	30,836	0 (0%)	0 (0%)

G101V reduces the affinity of BCL2 for venetoclax by 180 fold

Alternative resistance mechanisms can co-exist



Resistance mechanisms to targeted agents: Outstanding questions

- i. these *mutations are not observed in all relapsing patients*;
- ii. *variant allelic frequencies* at the time of relapse can vary considerably and are *often less than 10%*

- iii. could we use these **mutations to identify patients likely to relapse** and direct therapy toward resistant clones before patients have overt clinical relapses?
- iv. what comes after **resistance has developed toward all novel drugs**?



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