

Genomic landscape of patients in a phase II study of zanubrutinib in ibrutinib- and/or acalabrutinib-intolerant patients with B-cell malignancies

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SUPPLEMENTAL MATERIAL

Supplemental Table 1. Patient demographics and baseline information.

Characteristics	Cohort 1 (Intolerant to ibrutinib) (n=56)	Cohort 2 (Intolerant to ibrutinib and/or acalabrutinib) (n=15)	Total (N=71)
Indication, n (%)			
CLL	37 (66.1)	9 (60.0)	46 (64.8)
WM	9 (16.1)	2 (13.3)	11 (15.5)
SLL	6 (10.7)	2 (13.3)	8 (11.3)
MCL	2 (3.6)	1 (6.7)	3 (10.3)
MZL	2 (3.6)	1 (6.7)	3 (4.2)
Age, median (range), year	71 (49-91)	73 (51-87)	71 (49-91)
Male, n (%)	30 (53.6)	9 (60.0)	39 (54.9)
ECOG PS 0, n (%)	33 (58.9)	8 (53.3)	41 (57.7)
No. of prior therapy regimens, median (range)	1 (1-12)	2 (1-6)	1.0 (1-12)
Prior BTKi, n (%)	56 (100)	15 (100)	71 (100)
Ibrutinib monotherapy	48 (85.7) ^b	7 (46.7) ^a	54 (76.1)
Ibrutinib combination therapy	9 (16.1) ^b	0	9 (12.7)
Acalabrutinib monotherapy	0	8 (53.3)	7 (9.9)
Time on prior BTKi^c, median (range), months	10.61 (1.1-73.7)	3.33 (0.5-26.9)	NA
Zanubrutinib exposure, median (range), months	17.0 (0.6-28.5)	14.5 (0.5-19.6)	17.0 (0.5- 28.5)
Follow-up, median (range), months	21.2 (1.0-31.7)	10.4 (1.1-20.9)	19.4 (1.0- 31.7)

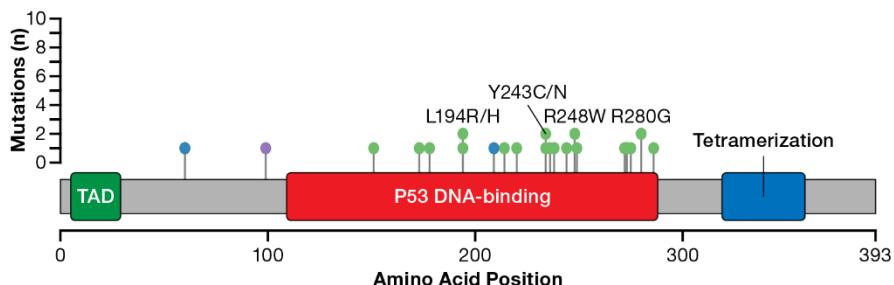
^a Seven patients in cohort 2 had both prior ibrutinib and acalabrutinib therapies. ^b One patient received ibrutinib combination therapy followed by ibrutinib monotherapy. ^c Cumulative ibrutinib exposure for cohort 1 and acalabrutinib for cohort 2. Data cutoff: 6 June 2022.

BTKi, Bruton tyrosine kinase inhibitor; CLL, chronic lymphocytic leukemia; ECOG PS, Eastern Cooperative Oncology Group performance status; MCL, mantle cell lymphoma; MZL, marginal zone lymphoma; NA, not applicable; PD, progressive disease; SLL, small lymphocytic lymphoma; WM, Waldenström macroglobulinemia.

Figure S1. Somatic mutation spectra throughout the whole protein sequences of the four most frequently mutated genes. Lollipop plots depicting common mutations in *TP53* (A), *ATM* (B), *SF3B1* (C), *NOTCH1* (D), and *CHK2* (E). Protein domains and mutation type are color-coded and described in figure legends. Del, deletion; Ins, insertion.

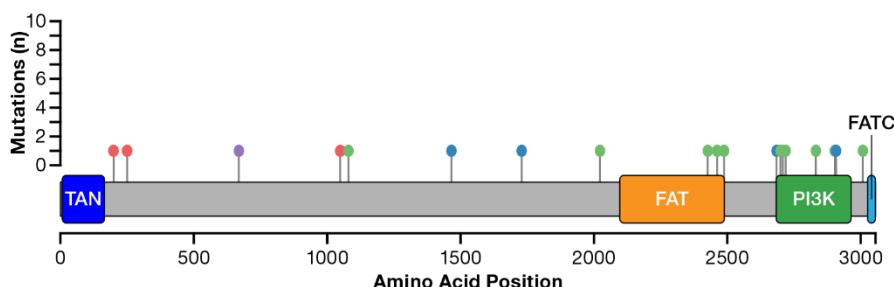
a. *TP53* Mutations

- Missense_Mutation
- Frame_Shift_Ins
- Frame_Shift_Del



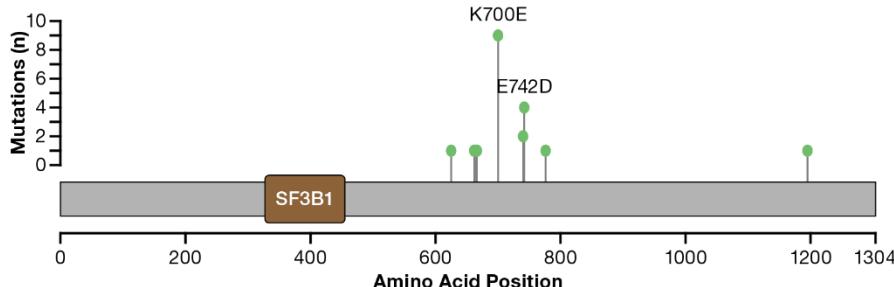
b. *ATM* Mutations

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- Frame_Shift_Ins
- Frame_Shift_Del



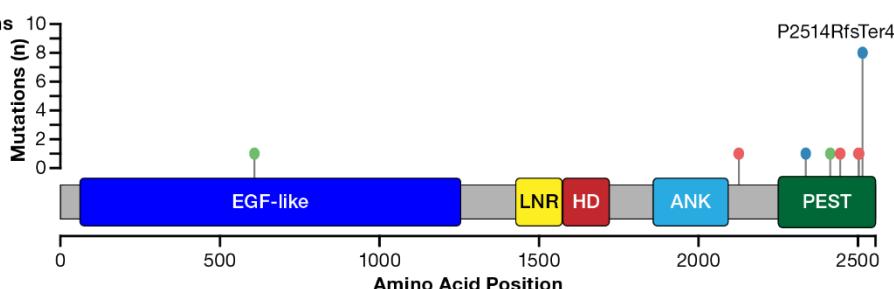
c. *SF3B1* Mutations

- Missense_Mutation



d. *NOTCH1* Mutations

- Missense_Mutation
- Nonsense_Mutation
- Frame_Shift_Del



e. *CHEK2* Mutations

- Missense_Mutation
- Nonsense_Mutation

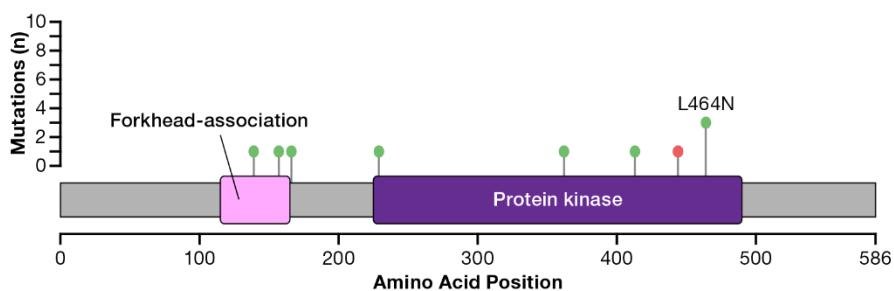


Table S2. Patients with progressive disease who did not have mutations in *BTK* or *PLCG2* had mutations in other known BTK inhibitor resistance genes at baseline.

Patient	Indication	Baseline gene mutations associated with progressive disease
4	CLL	<i>ATM, FBXW7</i>
5	MCL	<i>CCND1-IGH fusion</i>
6	CLL	<i>MCL1, TP53</i>
7	CLL	<i>TP53, SF3B1, FBXW7</i>
8	CLL	<i>TP53, NOTCH1, BRAF, SF3B1, MAPK14</i>

BTK, Bruton tyrosine kinase gene; CLL, chronic lymphocytic leukemia, MCL, mantle cell lymphoma; *PLCG2*, phospholipase C gamma 2 gene.