



Weill Cornell Medicine

Mutations in BCL10 as a Biomarker for Precision Therapy in DLBCL

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Background & Unmet Need

- Diffuse large B-Cell Lymphoma (DLBCL) is the most common hematological malignancy
- DLBCL is classified into three subgroups, of which Activated B Cell-like (ABC) DLBCL is the most aggressive and has the poorest outcomes
- Constitutive activation of NF- κ B signaling is a hallmark of ABC-DLBCL, which is largely mediated by B Cell Receptor (BCR) signaling
- BTK inhibitors have had a large impact on treatment of other lymphomas and act downstream of BCR, but show only modest effects in DLBCL
- There are several targets along the BCR signaling pathway, including within the CARD11—BCL10—MALT1 (CBM) complex which can be mutated and may mediate BTK resistance
- **Unmet Need:** Better understanding of somatic mutations in ABC DLBCL to guide precision treatment selection

Technology Overview

- **The Technology:** Use of BCL-10 as a biomarker to guide precision therapy for ABC DLBCL
- **The Discovery:** Genome sequencing revealed that mutations in BCL10 are most common in ABC-DLBCLs
- BCL10 is a part of the CBM complex, which activates NF- κ B signaling downstream of BCR
- Biochemical, structural, and functional analysis demonstrated that BCL10 mutations fall into two distinct classes:
 - Missense mutations in the CARD domain
 - Truncating mutations in the C-terminal
- **PoC Data:** Both BCL10 mutants with truncating and with missense mutations demonstrate resistance to BTK inhibitors
- Mutants with BCL10 truncating mutations are hypersensitive to MALT1 inhibitors, whereas missense BCL10 mutants are not

Inventors:

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Liron David
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Min Xia

Patents:

US Application Filed

Publications:

[Xia et al.](#) *Cancer Discov.* 2022.

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Technology Applications

- Biomarker to guide precision therapy for use of BTK and MALT1 inhibitors for ABC DLBCL
- Biomarker for patient selection in MALT1 inhibitor clinical trials

Technology Advantages

- Determines which patients may benefit from alternatives to BTK inhibitors
- Identifies patients which would be most likely to respond to MALT1 inhibitor therapy

Supporting Data / Figures

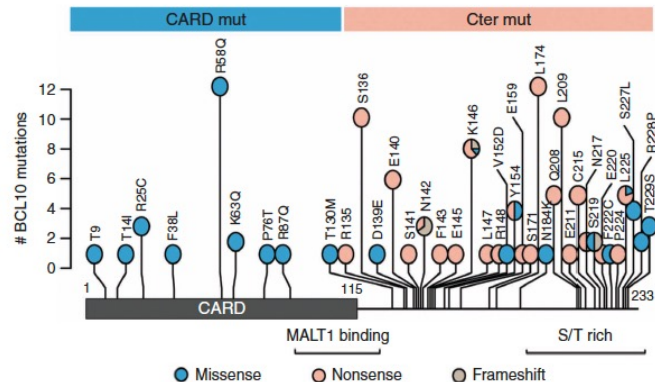


Figure 1: Two categories of BCL10 mutations in DLBCL were identified: Missense mutations in the CARD domain and truncating mutations in the C-terminal.

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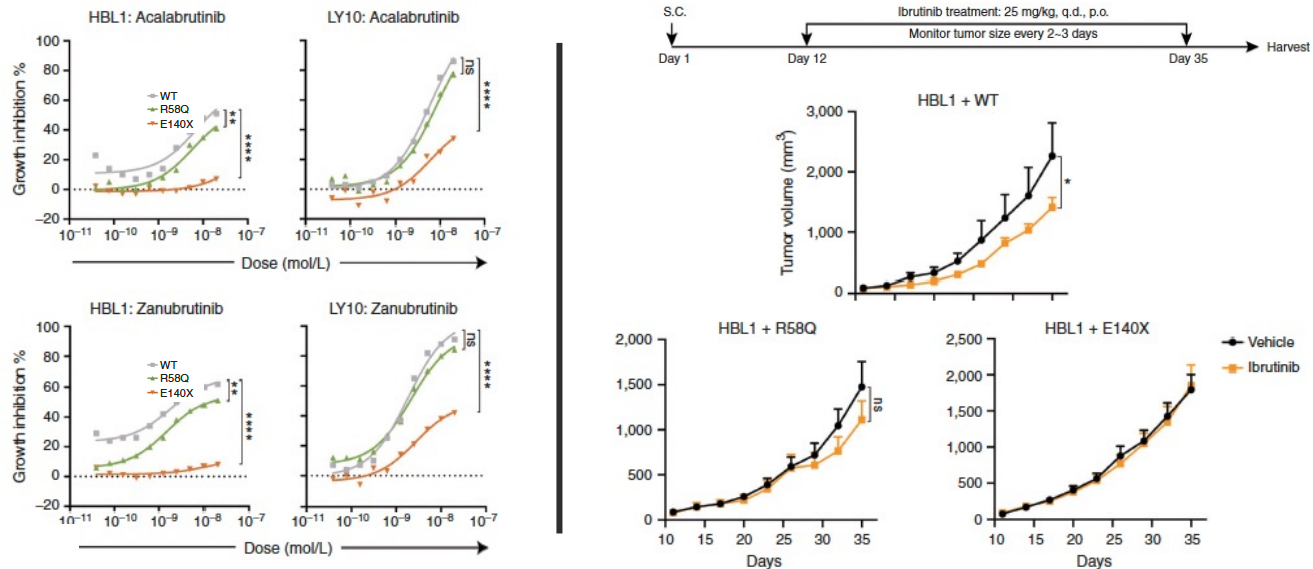


Figure 2: Both missense BCL10 mutants (R58Q) and truncated BCL10 mutants (E140X) demonstrated resistance to BTK inhibitor therapy in *in vitro* (Left) and *in vivo* PDX (Right) models.

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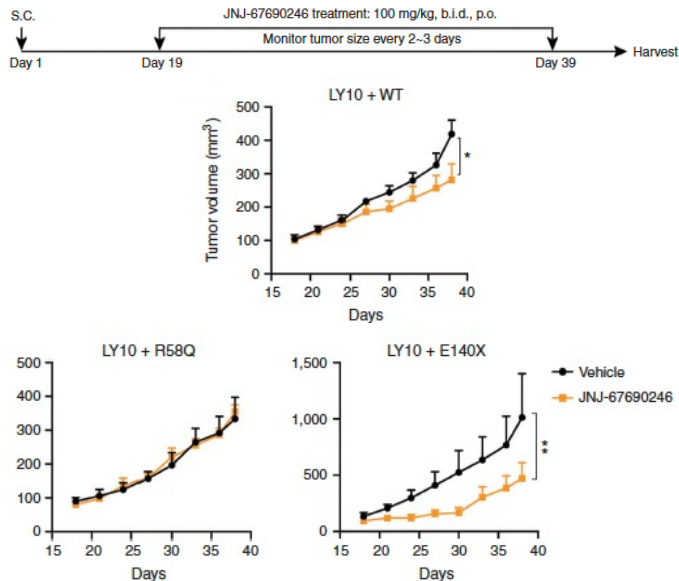
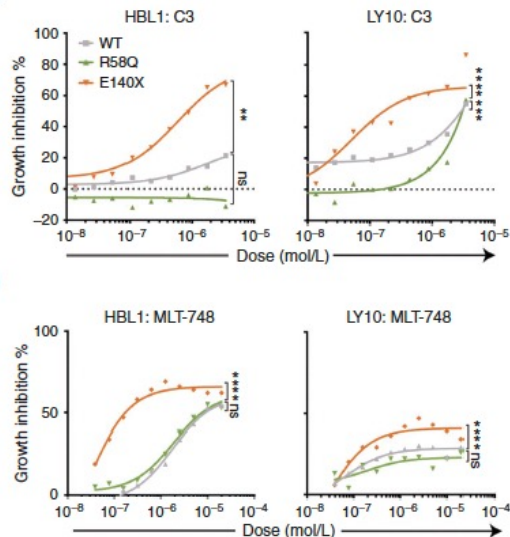


Figure 3: The truncated BCL10 mutants (E140X) demonstrated hypersensitivity to MALT1 inhibitors, whereas the missense mutants (R58Q) did not in both *in vitro* (Left) and *in vivo* PDX (Right) models.

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