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The yeast ERAD-C ubiquitin ligase Doa10 recognizes an intramembrane degron

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In Figure 4 A, the horizontal black line indicating the transmembrane domains in Sbh sequences was inadvertently misaligned during the production process. Below is the corrected version of the figure.

The HTML and PDF versions of this article have been corrected. The error remains only in the print version.

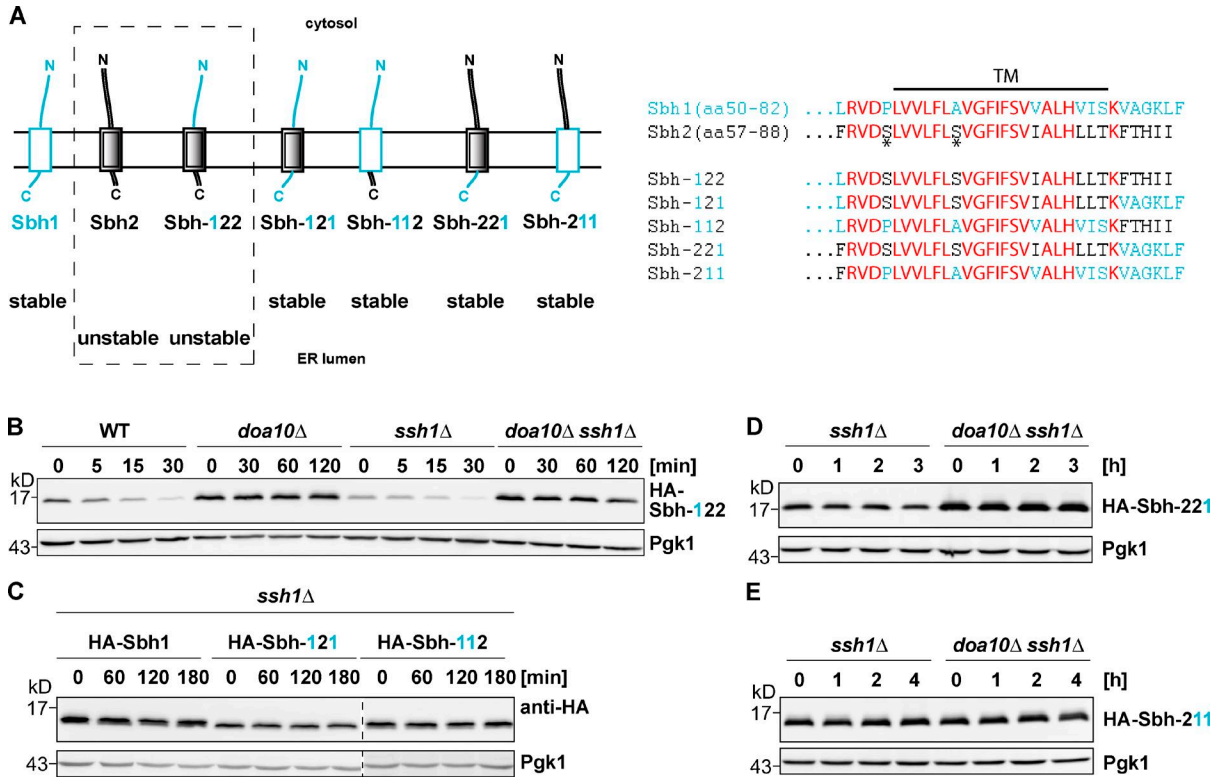

Figure 4. **Investigation of Sbh1/Sbh2 chimeric proteins.** Both Sbh2 TM and ER-luminal regions contribute to the degron. (A) Schematic representation of Sbh1, Sbh2, and Sbh1/Sbh2 chimeric proteins used in this study. Sbh1-derived regions are depicted in light blue, and Sbh2-derived regions are shown in black. The nomenclature for Sbh1/Sbh2 chimeric proteins is as follows: "Sbh-XYZ" designates a chimeric protein in which the number at position X indicates the source of the cytosolic domain ("1": Sbh1; or "2": Sbh2), the number at position Y indicates the source of the TM helix, and the number at position Z indicates the source of the ER-luminal domain, respectively. (right) Comparison of Sbh1, Sbh2, and Sbh1/Sbh2 chimera TA sequences. Residues depicted bold in red represent identical residues shared between Sbh1 and Sbh2; residues depicted in light blue are Sbh1-specific residues, and residues depicted in black indicate residues specific for Sbh2; the black horizontal line indicates the TM helix, and the asterisks indicate Sbh2 residues Ser61 and Ser68, respectively. N, N terminal; C, C terminal. (B) Degradation of HA–Sbh-122. chx chase as in Fig. 1 B. Note: There are different chase times for WT and *ssh1Δ* strains (30-min chase) and *doa10Δ* and *doa10Δ ssh1Δ* strains (120-min chase). (C) Degradation of HA-Sbh1, HA–Sbh-121, and HA–Sbh-112. All blots are from same experiment/gel but were cropped for clarity (dashed line). (D) Degradation of HA-Sbh-221. (E) Degradation of HA–Sbh-211.