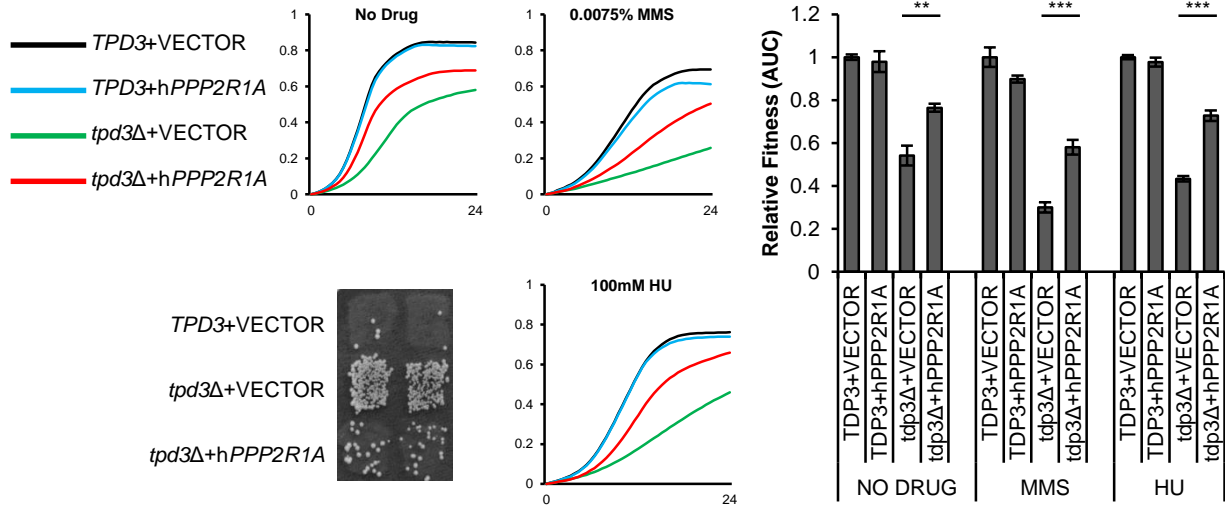
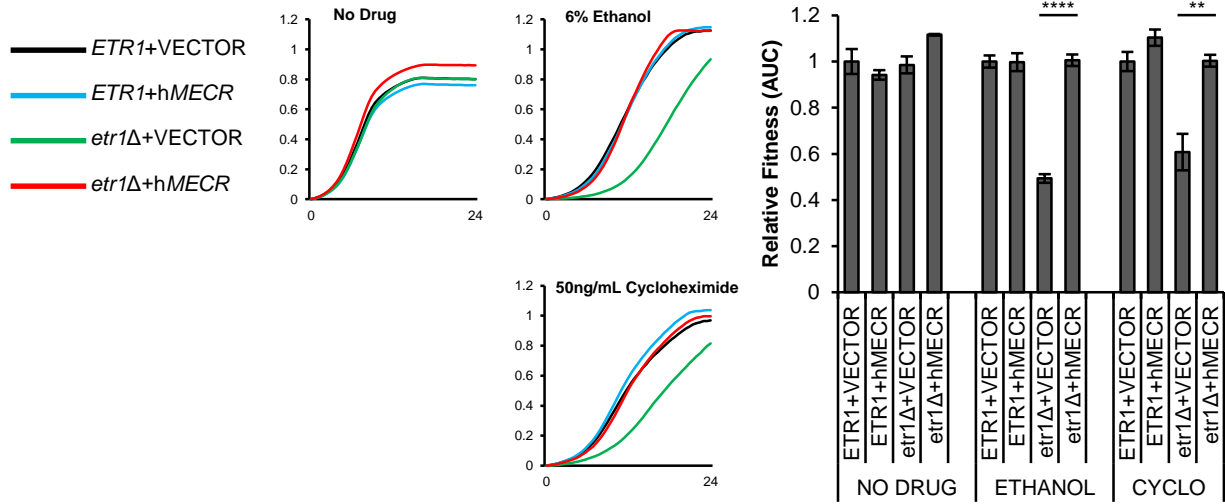
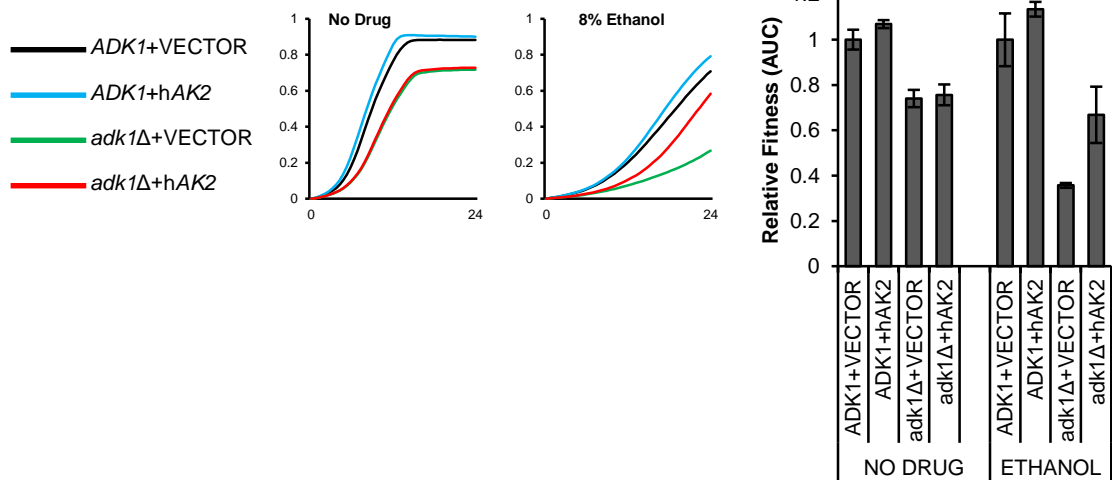
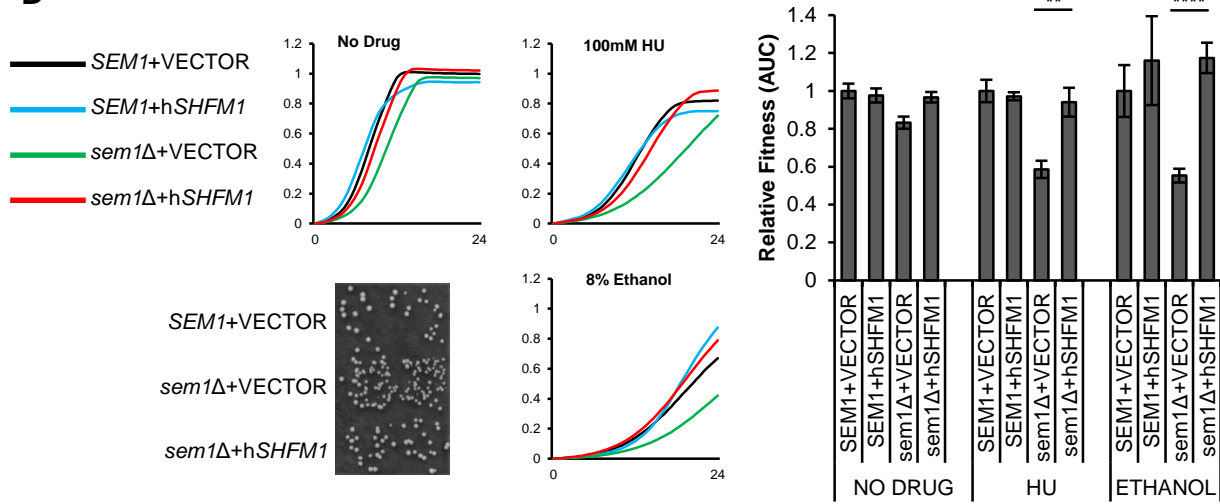
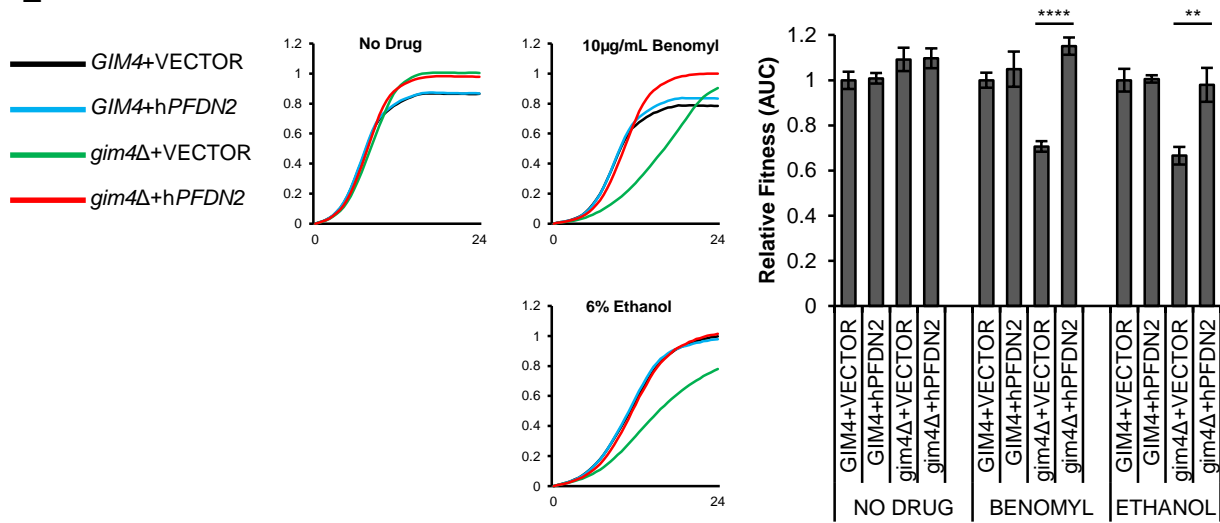


**A****B****C**

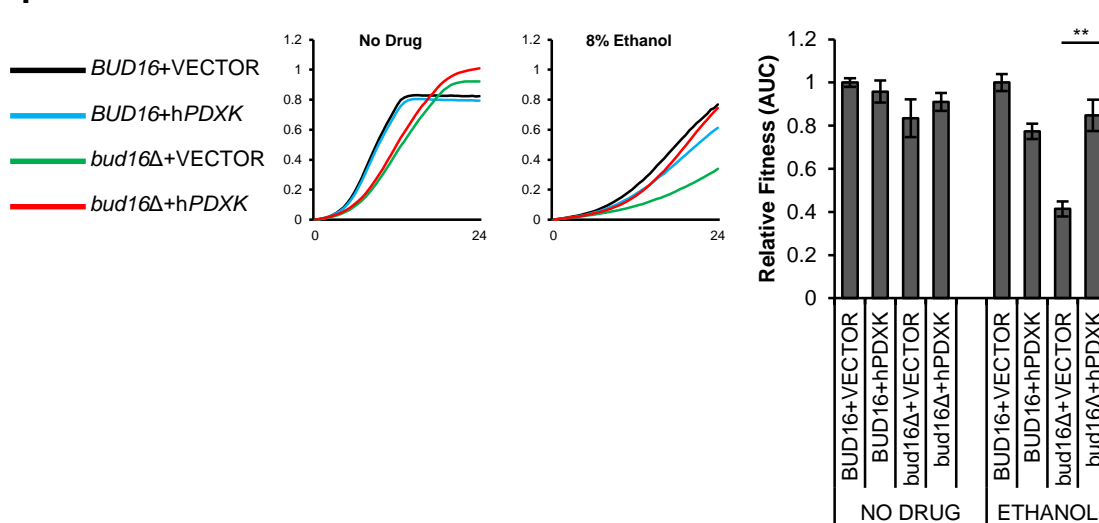
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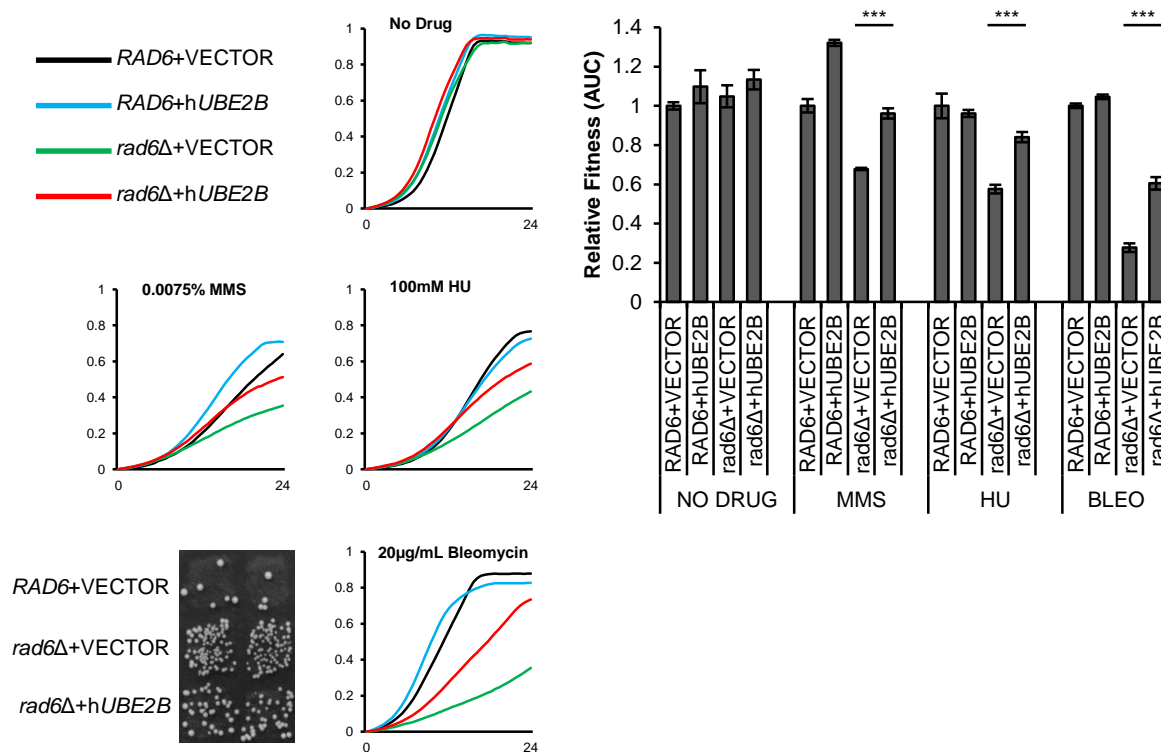
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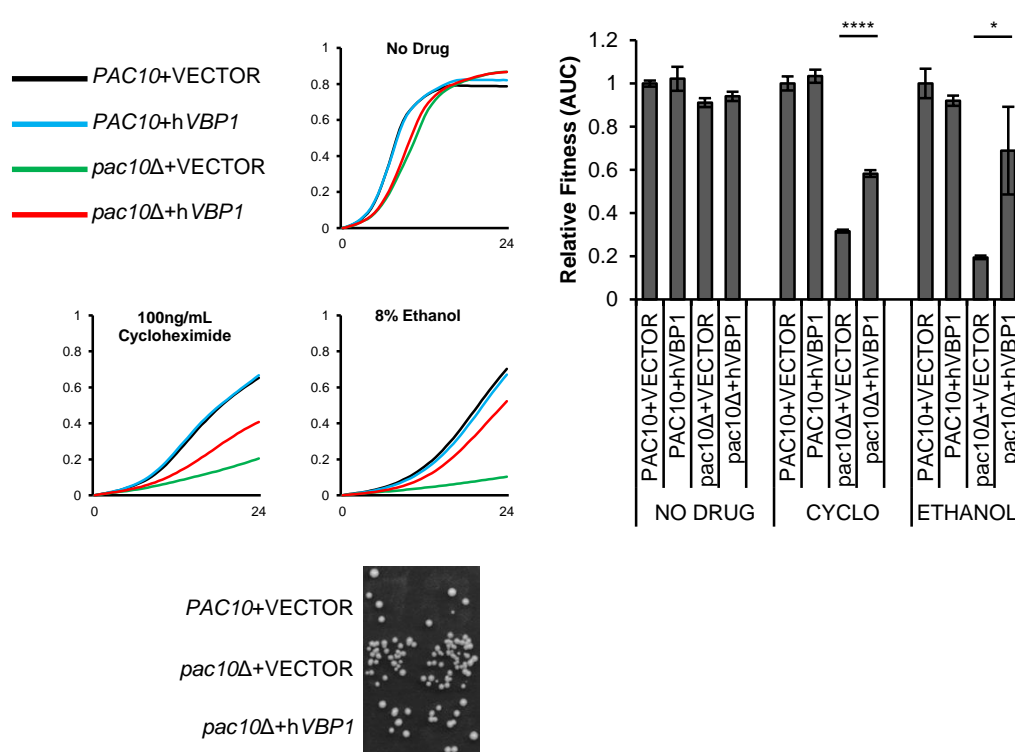
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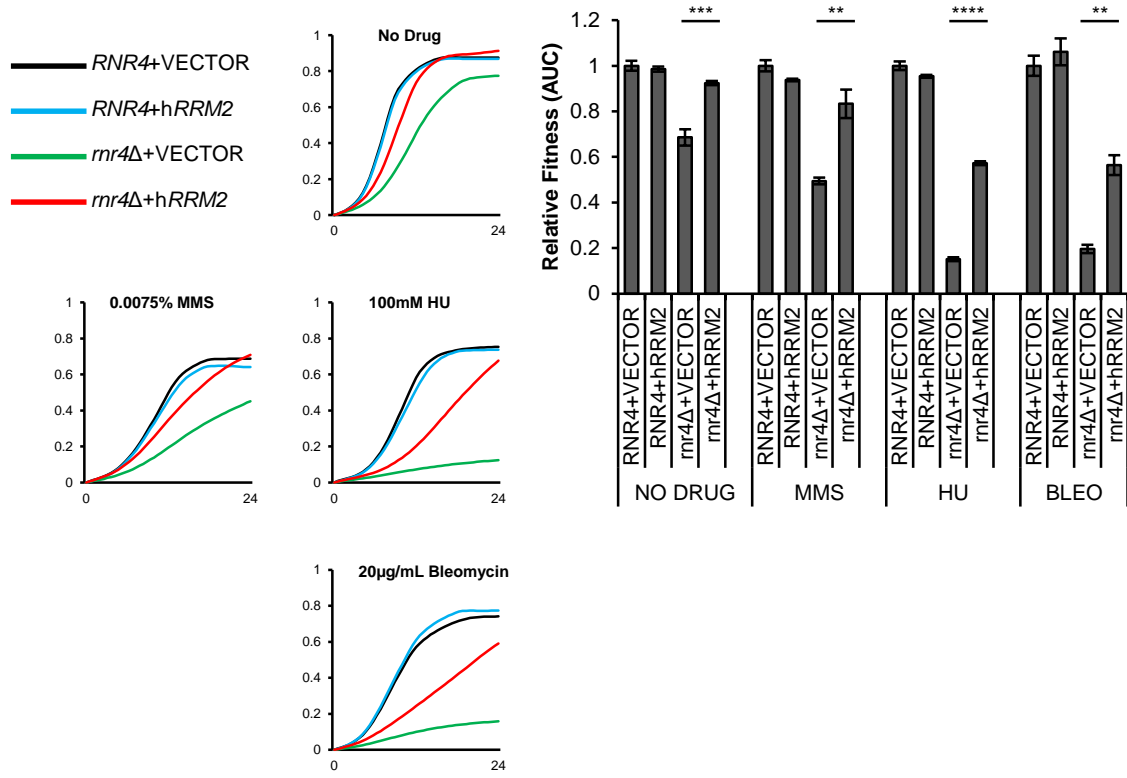
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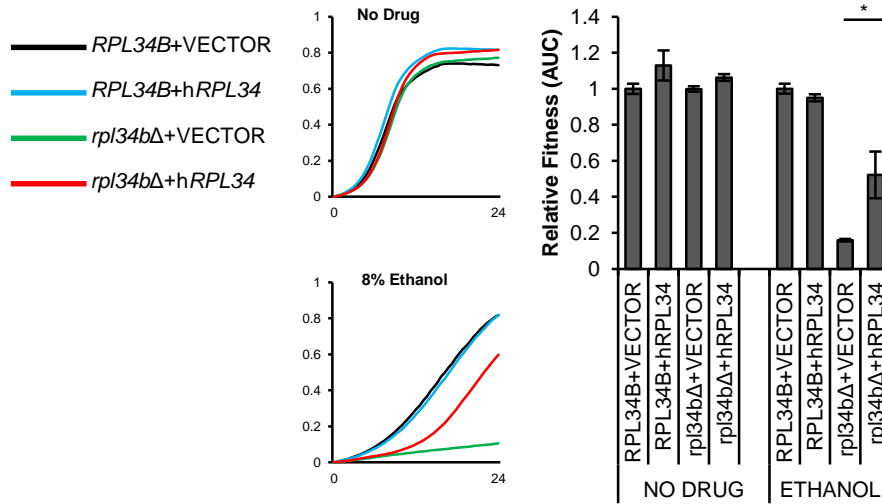
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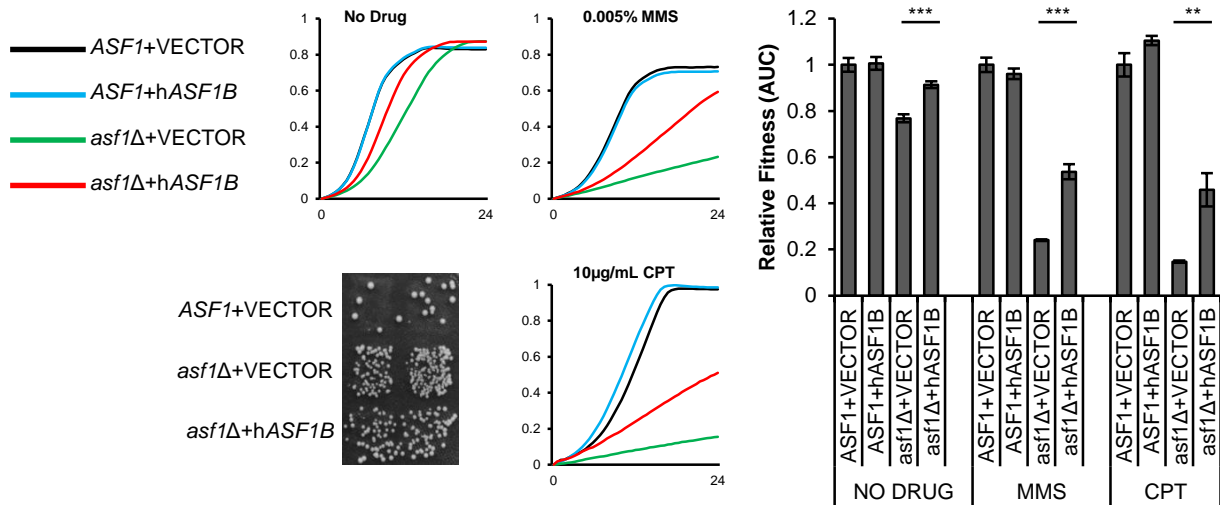
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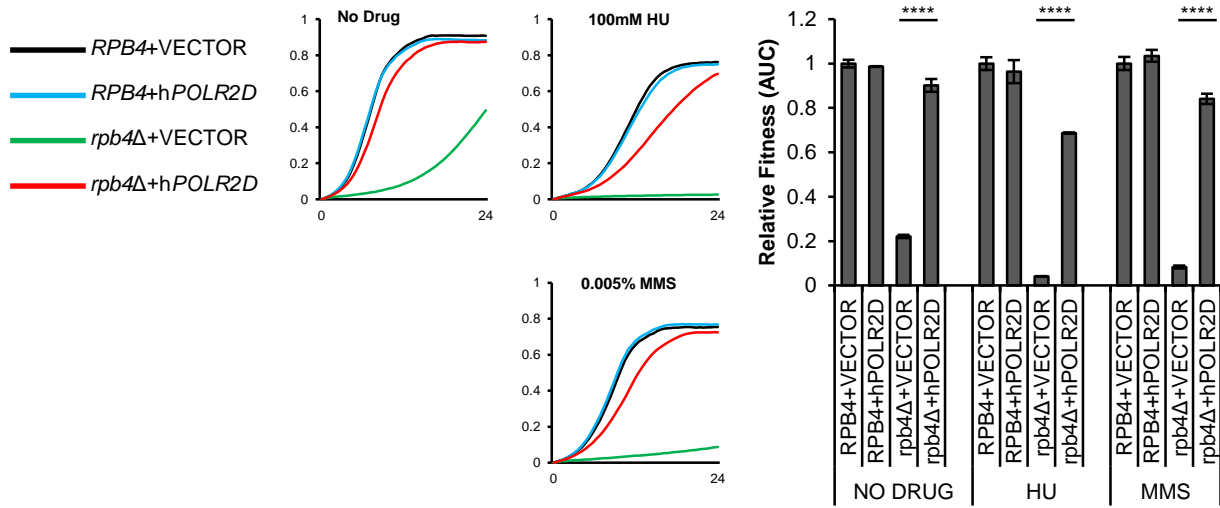
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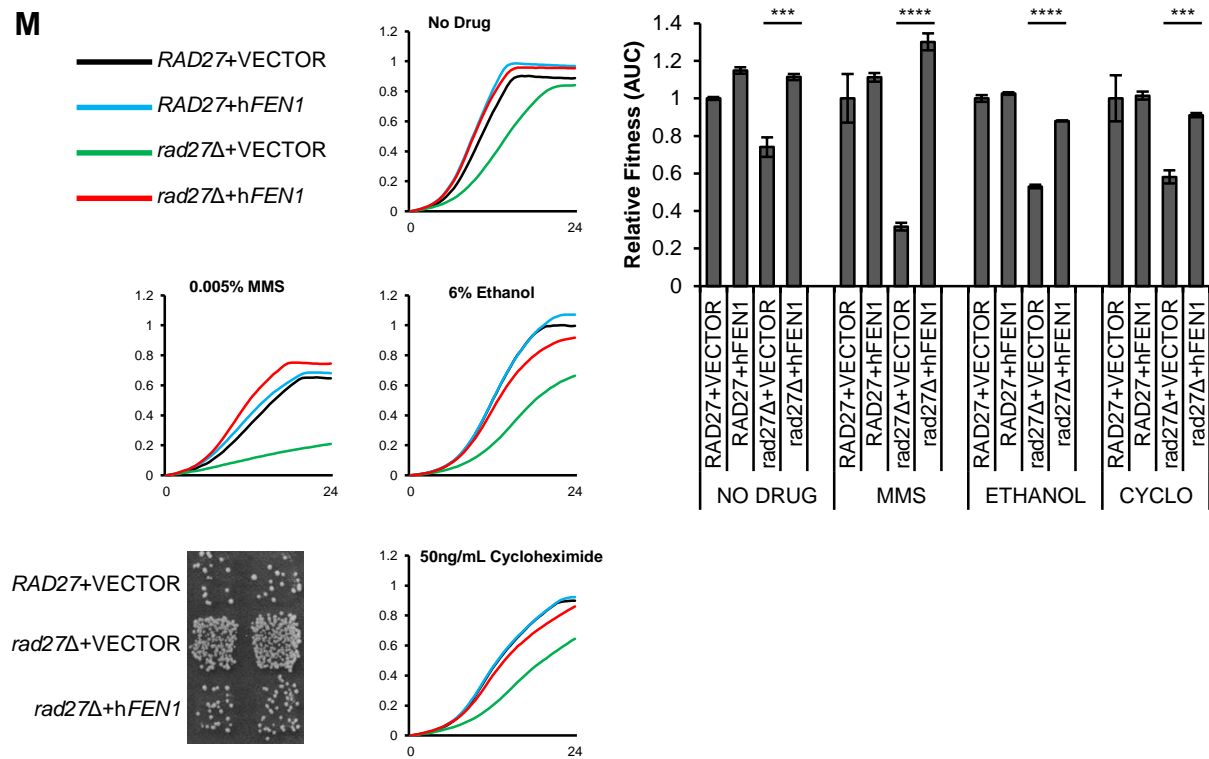
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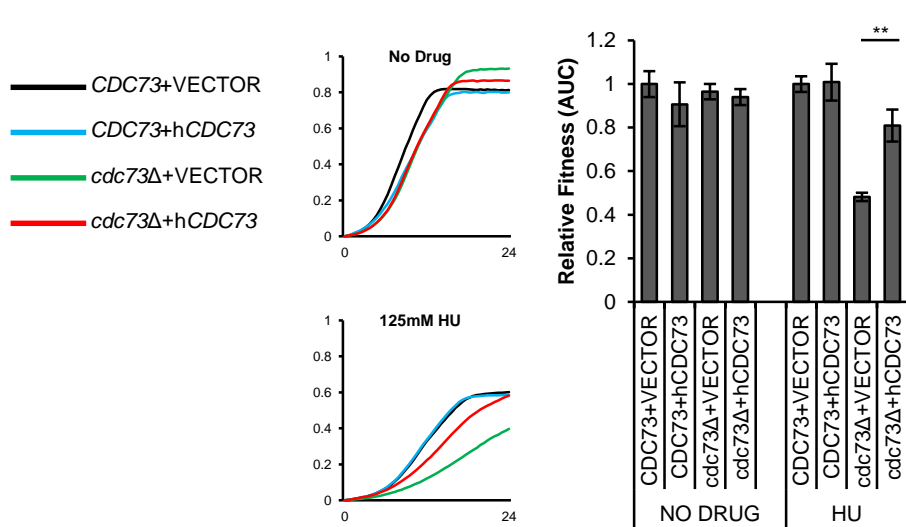
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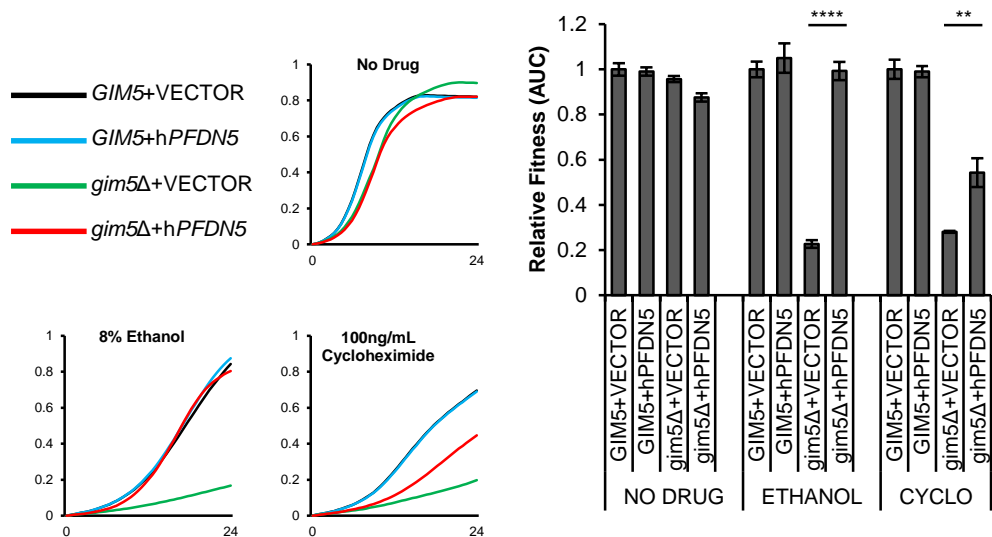
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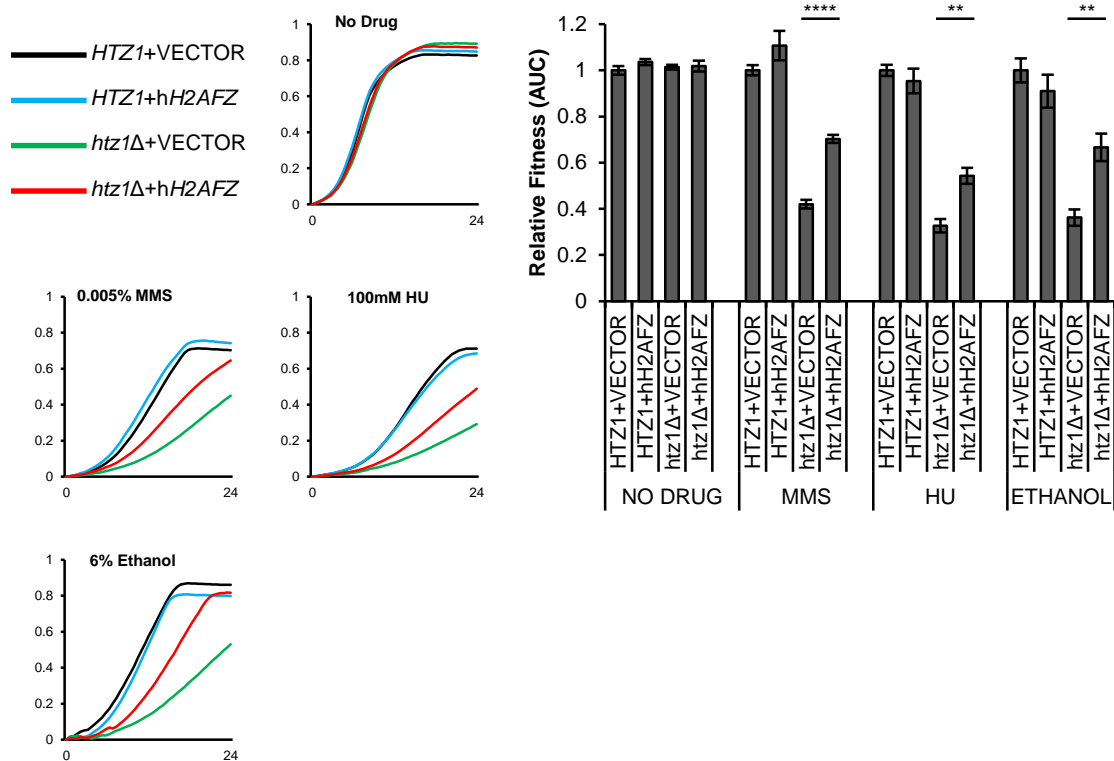
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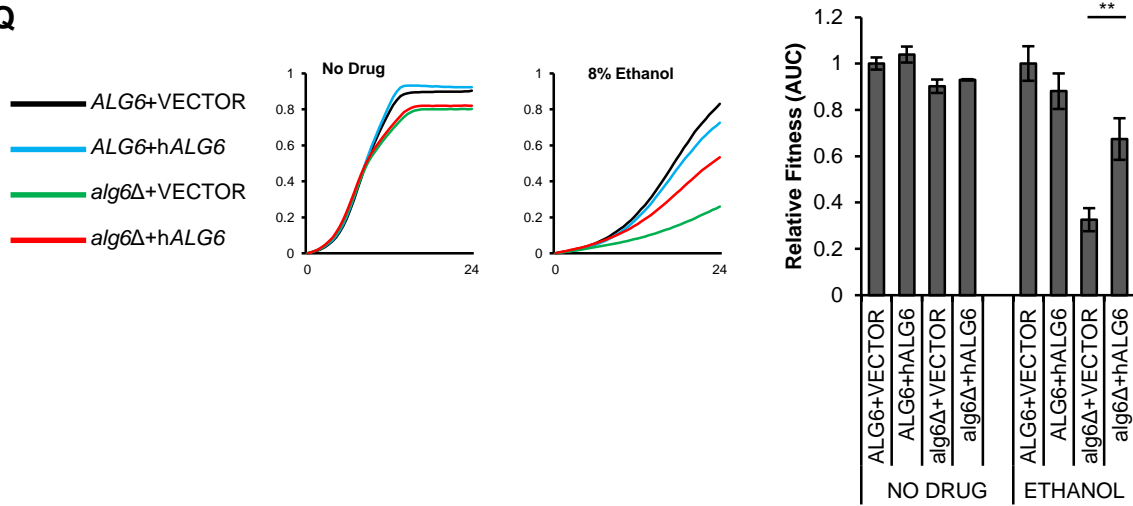
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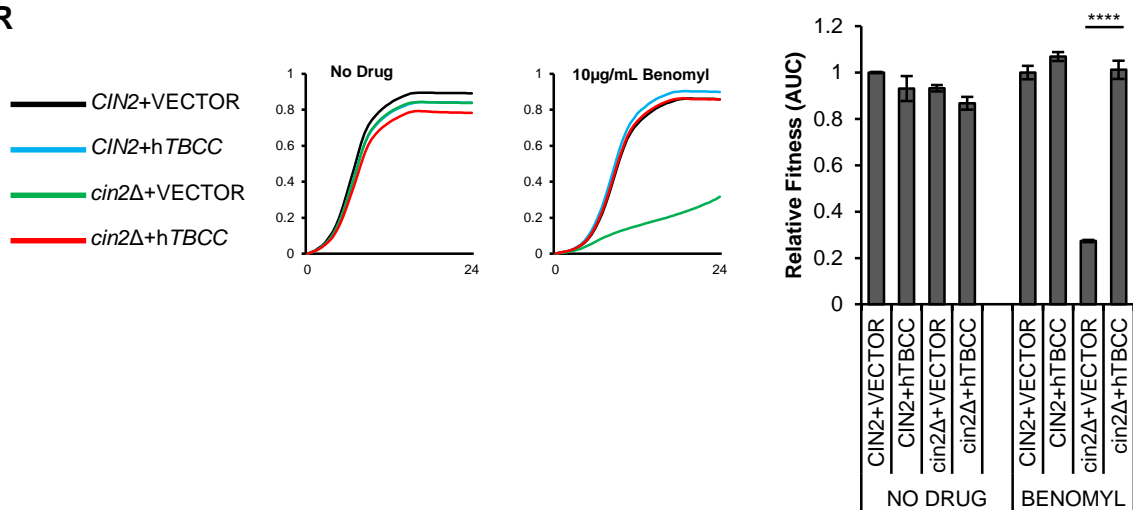
P



**Q**



**R**



**Figure S1. Complementation assays identify human genes that rescue chemical sensitivity and/or CIN defects of nonessential yeast genes.**

For each human-yeast pair, complementation that was observed in the screen using spot assays was validated with liquid growth assays (shown here). Yeast strains (wild-type or knockout mutants) containing a vector control or indicated human cDNA cloned in a yeast expression vector were grown in media +/- chemical at the indicated concentrations. Each represented curve is the average of 3 replicates per media condition. For each panel, x-axis represents time in hours, while y-axis represents OD600 readings. Fitness of each strain was quantified by calculating area under the curve (AUC) of each replicate independently. Strain fitness was defined as the AUC of each yeast strain relative to the AUC of the wild-type strain containing the vector control and grown in the same media condition (mean +/- SD). Student's t-test. \* $p < 0.05$ ; \*\* $p < 0.01$ ; \*\*\* $p < 0.001$ ; \*\*\*\* $p < 0.0001$ . For ALF assays, 2 independent isolates are shown per strain. (A) hPPP2R1A/yTPD3 (B) hMECR/yETR1 (C) hAK2/yADK1 (D) hSHFM1/ySEM1 (E) hPFDN2/yGIM4 (F) hPDXK/yBUD16 (G) hUBE2B/yRAD6 (H) hVBP1/yPAC10 (I) hRRM2/yRNR4 (J) hRPL34/yRPL34B (K) hASF1B/yASF1 (L) hPOLR2D/yRPB4 (M) hFEN1/yRAD27 (N) hCDC73/yCDC73 (O) hPFDN5/yGIM5 (P) hH2AFZ/yHTZ1 (Q) hALG6/yALG6 (R) hTBCC/yCIN2.