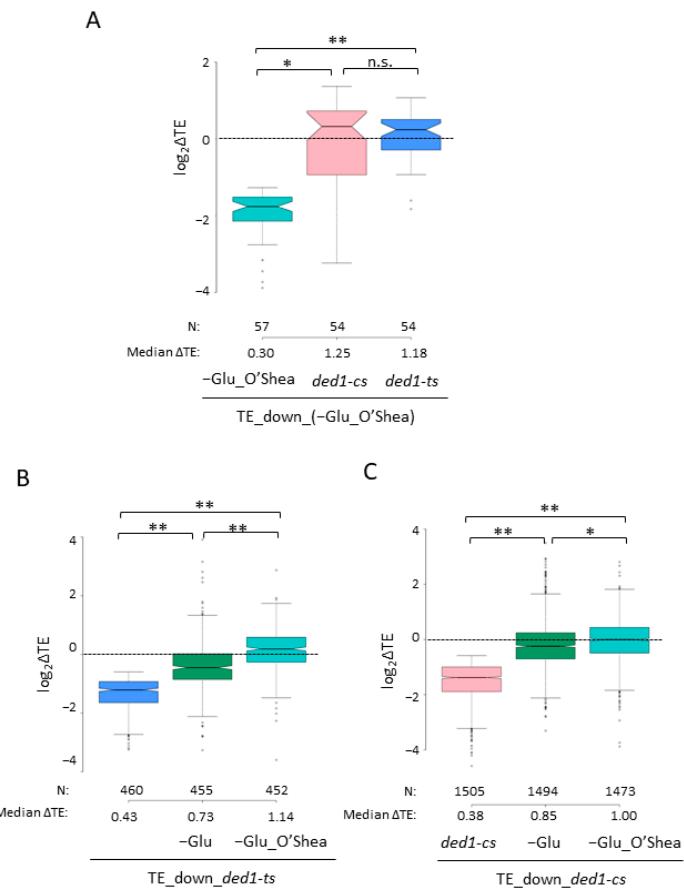


**SUPPLEMENTARY MATERIAL FOR:**

**Down-Regulation of Yeast Helicase Ded1 by Glucose  
Starvation or Heat-Shock Differentially Impairs Translation of Ded1-  
Dependent mRNAs**

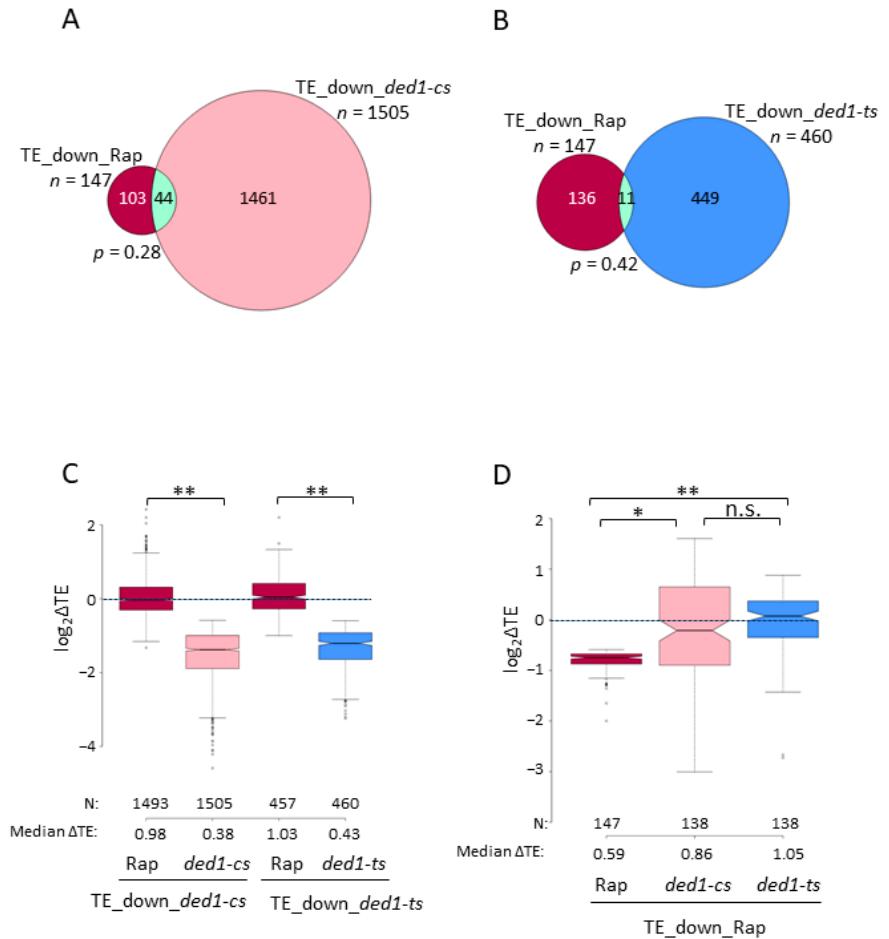
## SUPPLEMENTARY FIGURE LEGENDS

**Fig. S1**



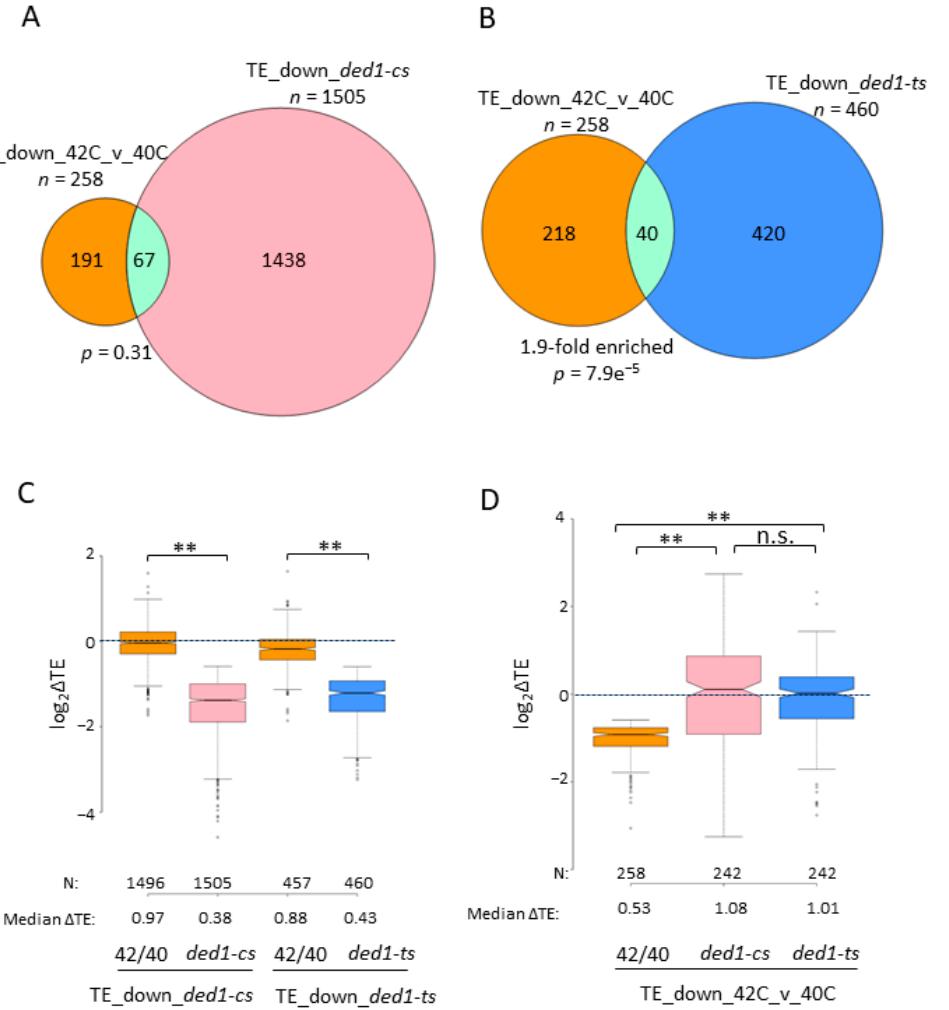
**Figure S1. Ded1-hyperdependent mRNAs generally do not exhibit TE changes as an immediate response to glucose starvation.** (A-C) Notched box plots showing  $\log_2$  fold-changes in TE ( $\log_2\Delta TE$ ) after 15 min of glucose starvation, or in response to the *ded1-CS* or *ded1-ts* mutations, for (A) 57 mRNAs showing significant TE changes after 15 min of glucose starvation (TE\_down\_(*-Glu\_O'Shea*)), (B) the 460 mRNAs showing  $\geq 1.5$ -fold reductions in TE in *ded1-ts* cells at FDR  $< 0.05$ , TE\_down\_ded1-ts mRNAs, and (C) the 1505 mRNAs showing  $\geq 1.5$ -fold reductions in TE in *ded1-ts* cells at FDR  $< 0.05$ , TE\_down\_ded1-CS mRNAs. P-values computed from Mann-Whitney U-test are given (\*,  $P < 10^{-12}$ ; \*\*,  $P < 10^{-15}$ ; n.s., not significant).

**Fig. S2**



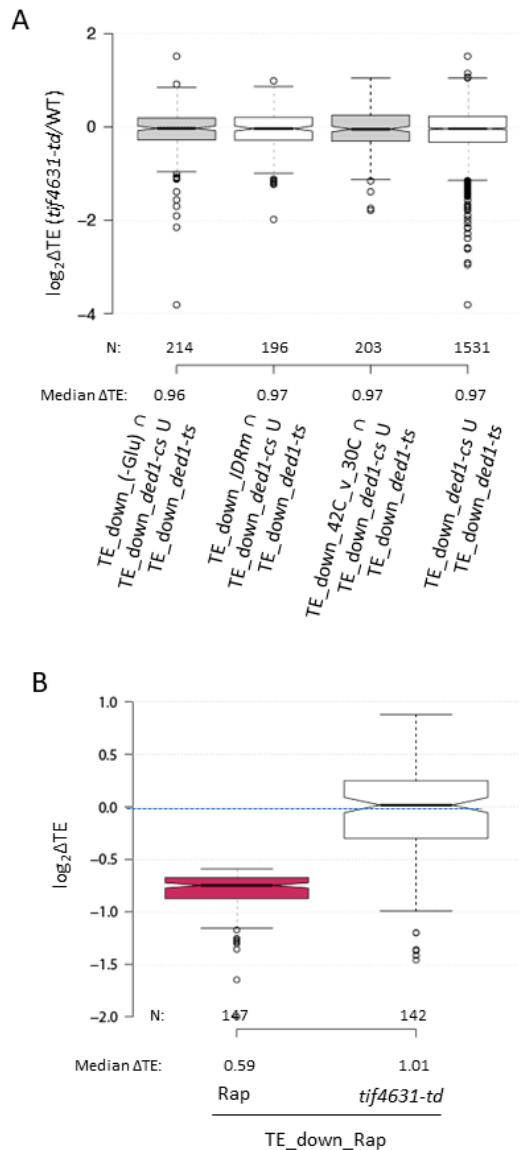
**Figure S2. Rapamycin treatment elicits translational changes largely distinct from those conferred by *ded1-ts* and *ded1-cs* mutations.** (A-B) Overlap between 147 mRNAs exhibiting  $\geq 1.5$ -fold reductions in TE at FDR  $< 0.05$  on rapamycin treatment (TE<sub>down</sub>\_Rap) and either the TE<sub>down</sub>\_ded1-cs group (A) or the TE<sub>down</sub>\_ded1-ts group of mRNAs (B). (C-D) Notched box plots showing  $\log_2$  fold-changes in TE in response to Rap, *ded1-cs*, or *ded1-ts* for the 1505 TE<sub>down</sub>\_ded1-cs mRNAs (cols. 1-2) or the 460 TE<sub>down</sub>\_ded1-ts mRNAs (cols. 3-4). (D) Log<sub>2</sub> fold-changes in TE in response to Rap, *ded1-cs*, or *ded1-ts* for the 147 TE<sub>down</sub>\_Rap mRNAs. *P*-values computed from Mann-Whitney *U*-test are given (\*,  $P < 10^{-9}$ ; \*\*,  $P < 10^{-15}$ ; n.s., not significant).

**Fig. S3**



**Figure S3. A significant fraction of Ded1-hyperdependent mRNAs identified in *ded1-ts* cells is translationally down-regulated by heat-shock of WT cells at 42 °C versus 40 °C.** (A-B) Overlap between TE\_down\_42C\_v\_40C mRNAs and either TE\_down\_ded1-*cs* (A) or TE\_down\_ded1-*ts* (B) mRNAs. One outlier was omitted from the plot to expand the y-axis scale. (C) Log<sub>2</sub>fold changes in TE in response to heat-shock of WT cells at 42°C versus 40 °C (42C/40C), *ded1-*cs**, or *ded1-*ts** for the 1505 TE\_down\_ded1-*cs* mRNAs (cols. 1-2) or 460 TE\_down\_ded1-*ts* mRNAs (cols. 3-4). (D) Log<sub>2</sub>fold-changes in TE in response to heat-shock at 42 °C vs. 40 °C, *ded1-*cs**, or *ded1-*ts** for the 258 TE\_down\_42C\_v\_40C mRNAs. P-values computed from Mann-Whitney U-test are given (\*\*, P < 10<sup>-15</sup>; n.s., not significant).

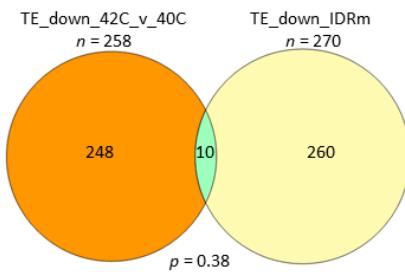
**Fig. S4**



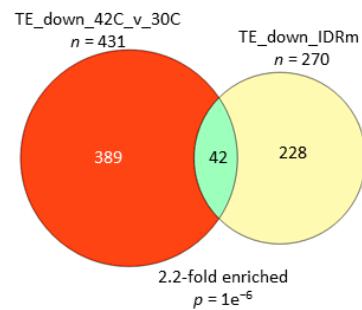
**Figure S4.** Depletion of eIF4G does not preferentially reduce the TEs of subsets of Ded1-hyperdependent mRNAs translationally down-regulated by glucose starvation, the *DED1-IDRm* mutation, or heat-shock at 42°C versus 30°C, nor the mRNAs translationally downregulated by Rap. (A) Log<sub>2</sub> fold- changes in TE conferred by depletion of eIF4G in a *tif4631-td* *tif4632Δ* mutant for the 1566 mRNAs showing 1.5-fold TE reductions in response to either *ded1-cs* or *ded1-ts* mutations (col. 4) or the subsets of these mRNAs that also show TE reductions in response to either glucose starvation (217 mRNAs, col. 1), the *DED1-IDRm* mutation (201 mRNAs, col. 2), or heat shock at 42°C versus 30°C (203 mRNA, col. 3). (B) Log<sub>2</sub> fold changes in TE conferred by Rap (col. 1) or depletion of eIF4G in a *tif4631-td* *tif4632Δ* mutant (col. 2) for the 147 TE\_down\_Rap mRNAs.

**Fig. S5**

A

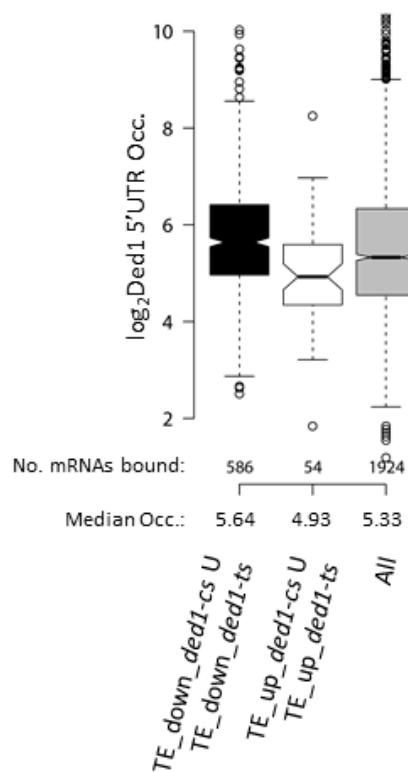


B



**Figure S5.** The mRNAs translationally impaired by the *DED1-IDRm* mutation are enriched for those impaired by heat-shock at 42 °C versus 30 °C but not by heat-shock at 42 °C versus 40 °C. (A–B) Overlap of TE\_down\_IDRm mRNAs with either TE\_down\_42C\_v\_40C (A) or TE\_down\_42C\_v\_30C (B) mRNAs.

**Fig. S6**



**Figure S6. Ded1-hyperdependent mRNAs exhibit greater than average 5'UTR Ded1 occupancies.** UV-crosslinking RNA immunoprecipitation (CRAC) data for Ded1 obtained from control, non-stressed cells (taken from Bresson et al. (2020)) was analyzed for the 1566 Ded1-hyperdependent mRNAs (TE<sub>down</sub>\_ded1-cs U TE<sub>down</sub>\_ded1-ts, described in Fig. 5, cols. 9-12), the 1756 Ded1-hypodependent mRNAs (showing TE increases of >1.5-fold at FDR<0.05 in either ded1-cs or ded1-ts cells), and all 5423 mRNAs analyzed in this study. The log<sub>2</sub> reads per million in the 5'UTR or beginning of the ORF bound to Ded1 are plotted. Note that only 3% of the Ded1-hypodependent mRNAs showed detectable Ded1 binding, compared to 37% and 35% of the Ded1-hyperdependent and all mRNAs, respectively, implying a much lower median Ded1 occupancy than indicated here for the hypodependent group.

**Table S1.** Ribosome profiling datasets used in current study.

Strain background	Growth conditions	Source	GEO accession numbers	CHX treatment	values from DESeq2 ( $\log_2\Delta TE$ )
$\Sigma$ 1278b	3h Glu starvation in YP medium	(Vaidyanathan et al. 2014); GSE51532	GSM1247439 GSM1247440 GSM1247441 GSM1247442 GSM1247443 GSM1247444 GSM1247445 GSM1247446 GSM1247447 GSM1247448 GSM1247449 GSM1247450	Yes	-Glu
BY4741	Treatment with 12.5 nM Rap in YPD medium for 30 min	(Nedialkova and Leidel 2015); GSE67387	GSM1646015 GSM1646016 GSM1646017 GSM1646051 GSM1646052 GSM1646053 GSM1646027 GSM1646028 GSM1646029 GSM1646057 GSM1646058 GSM1646059	Yes	Rap
W303	Heat-shock of WT for 10 min at 42°C vs 40°C in YPD medium	(Iserman et al. 2020); GSE131176 (ribo) & GSE141029 (mRNA)	GSM3765213 GSM3765214 GSM3765215 GSM3765216 GSM4192627 GSM4192628 GSM4192629 GSM4192630	No	42C/40C
W303	Heat-shock of WT for 10 min at 42°C vs 30°C in YPD medium	(Iserman et al. 2020); GSE131176 (ribo) & GSE141029 (mRNA)	GSM3765211 GSM3765212 GSM3765215 GSM3765216 GSM4192625 GSM4192626 GSM4192629 GSM4192630	No	42C/30C
W303	<i>DED1-IDRm</i> vs. WT at 42°C in YPD medium	(Iserman et al. 2020);	GSM3765215 GSM3765216	No	<i>IDRm</i> /WT

		GSE131176 (ribo) & GSE141029 (mRNA)	GSM3765221 GSM3765222 GSM4192629 GSM4192630 GSM4192635 GSM4192636		
BY4741	WT shifted to SC medium lacking glucose for 15 min	(Zid and O'Shea 2014); GSE56622	GSM1365918 GSM1387087 GSM1365925 GSM1387091 GSM1365921 GSM1387089 GSM1365928 GSM1387093	Yes	-Glu_O'Shea
S288C	<i>tif4631-td</i> ( <i>tif4632Δ::kanMX6</i> <i>P<sub>CUP1</sub>-UBI-R-DHFRts-HA-tif4631-td</i> vs. WT ( <i>tif4632Δ::kanMX6</i> <i>TIF4631</i> ), in SC+2% raffinose, 2% galactose at 36°C for 2h	Zinshteyn et al. (2017); GSE87614	GSM2335482 GSM2335484 GSM2335486 GSM2335488 GSM2335490 GSM2335492 GSM2335494 GSM2335496	Yes	<i>tif4631-td</i>
BY4741	<i>ded1-cs</i> and WT shifted to SC medium at 15°C for 10 min	(Sen et al. 2019); GSE 111255	GSM3027242 GSM3027243 GSM3027244 GSM3027245 GSM3027248 GSM3027249 GSM3027250 GSM3027251	Yes	<i>ded1-cs</i>
BY4741	<i>ded1-ts</i> and WT shifted to SC medium at 37°C for 2h	(Sen et al. 2019); GSE 111255	GSM3027254 GSM3027255 GSM3027256 GSM3027257 GSM3027260 GSM3027261 GSM3027262 GSM3027263	Yes	<i>ded1-ts</i>
BY4741	<i>tif1-ts</i> and WT shifted to SC medium at 37°C for 1h	(Sen et al. 2015); GSE 66411	GSM1622004 GSM1622005 GSM1622006 GSM1622007 GSM1622008 GSM1622009 GSM1622010 GSM1622011	Yes	<i>tif1-ts</i>

			GSM1622012 GSM1622013 GSM1622014 GSM1622015 GSM1622016 GSM1622017 GSM1622018 GSM1622019		
BY4741	<i>tif3Δ</i> and WT shifted to SC medium at 37°C for 1h	(Sen et al. 2016); GSE 81966	GSM2178815 GSM2178816 GSM2178817 GSM2178818 GSM2178819 GSM2178820 GSM2178821 GSM2178822	Yes	<i>tif3Δ</i>