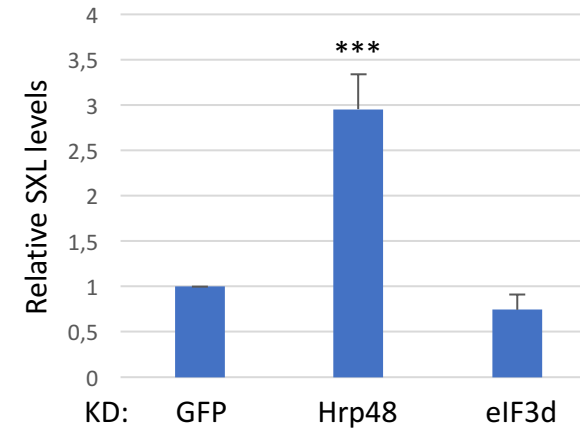
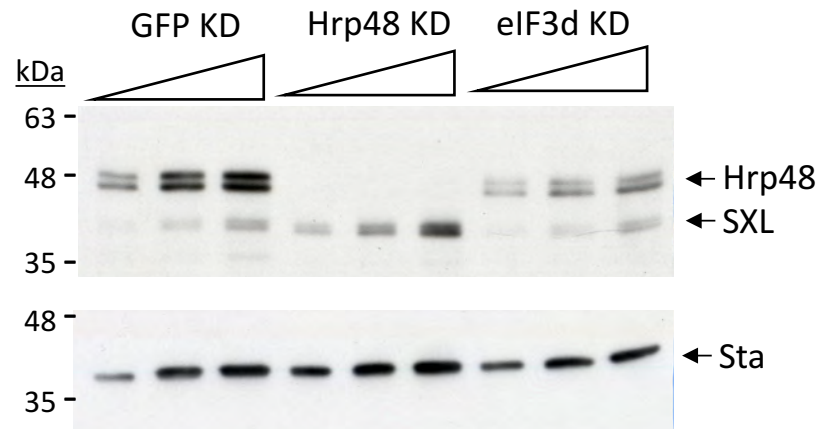
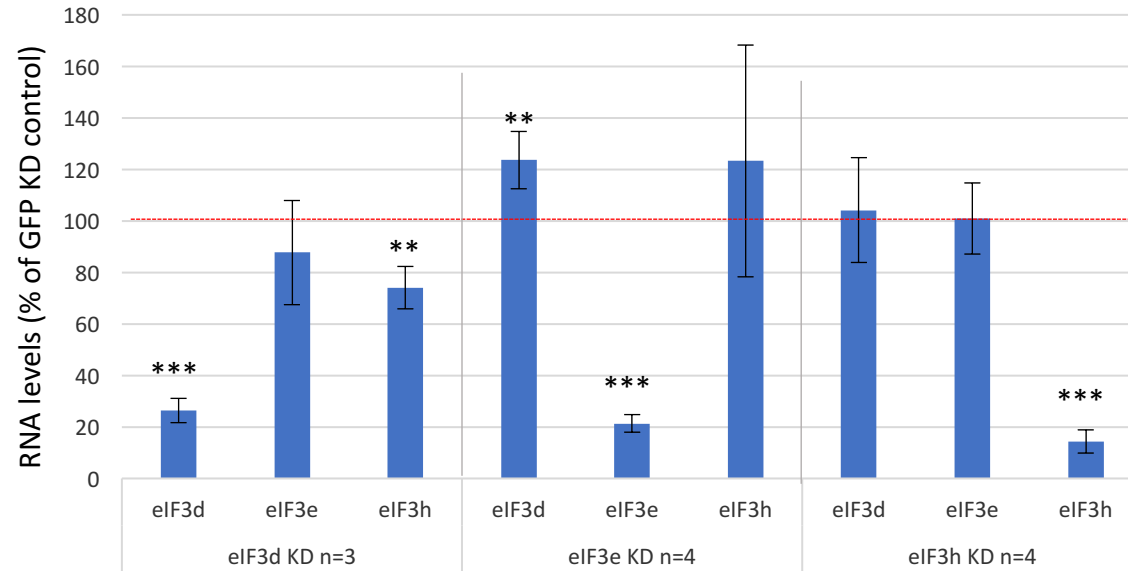


Supplementary Figure 1. Hrp48 represses translation in concert with SXL. Comparison of the translation efficiencies of WT and 5m Firefly msl-2 reporters in the absence or presence of SXL (SXL/RNA molar ratio of 40). Translation was performed in embryo extracts, and Renilla mRNA was co-translated as an internal control. Firefly luciferase was corrected for Renilla expression and plotted relative to WT mRNA in each condition. The error bars represent standard deviation of 3-9 datapoints.



Supplementary Figure 2. Hrp48, but not eIF3d, inhibits *sxl* expression.

Hrp48 and eIF3d were depleted from Kc cells, and the levels of SXL monitored by Western blot and compared to a control depletion (GFP). Increasing amounts of extract (5, 10 and 20 μ g) were loaded to provide a quantitative assessment of SXL levels. The ribosomal protein Stubarista (Sta) is shown as loading control. Quantification of the amount of SXL normalized to Sta and relative to GFP is shown on the right. Error bars represent the standard deviation of quantifications at the three extract amounts loaded.



Supplementary Figure 3. eIF3 subunit RNA levels upon depletion of eIF3d, e or h . Depletion was performed for 4 days, carrying GFP knock-down as negative control. RNA levels were measured by RT-qPCR, normalized for actin and plotted relative to the negative control, which was set to 100% (red line). Error bars represent the standard deviation of 3-4 independent experiments (n).

Supplementary Table 1: Proteins identified in the eluates of Hrp48 oligo pull-downs (related to Fig 5B)

Protein Name	Fold change I	p value
Q9V3D2 Coproporphyrinogen-III oxidase OS=Drosophila melanogaster GN=Coprox PE=1 SV=1 - [HEM6_DROME]	5,383527853	1,21E-06
P35500 Sodium channel protein para OS=Drosophila melanogaster GN=para PE=2 SV=3 - [SCNA_DROME]	6,266584697	5,10E-06
P48810 Heterogeneous nuclear ribonucleoprotein 87F OS=Drosophila melanogaster GN=Hrb87F PE=2 SV=2 - [RB87F_DROME]	4,770193564	1,32E-05
P07909 Heterogeneous nuclear ribonucleoprotein A1 OS=Drosophila melanogaster GN=Hrb98DE PE=2 SV=1 - [ROA1_DROME]	4,033534477	5,06E-05
O18404 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Drosophila melanogaster GN=scu PE=1 SV=1 - [HCD2_DROME]	4,901511495	8,93E-05
P25007 Peptidyl-prolyl cis-trans isomerase OS=Drosophila melanogaster GN=Cyp1 PE=1 SV=2 - [PPIA_DROME]	3,751697056	8,09E-05
P13469 DNA-binding protein modulo OS=Drosophila melanogaster GN=mod PE=1 SV=2 - [MODU_DROME]	4,394107337	0,000160652
P40796 La protein homolog OS=Drosophila melanogaster GN=La PE=1 SV=2 - [LA_DROME]	3,086085448	0,000432356
O01367 Protein held out wings OS=Drosophila melanogaster GN=how PE=1 SV=1 - [HOW_DROME]	3,822524003	0,000581246
Q8T8R1 CCHC-type zinc finger protein CG3800 OS=Drosophila melanogaster GN=CG3800 PE=1 SV=1 - [Y3800_DROME]	2,534374453	0,000705428
P07182 Chorion protein S36 OS=Drosophila melanogaster GN=Cp36 PE=3 SV=2 - [CH36_DROME]	2,370073375	0,000914899
Q9VCK0 Eukaryotic translation initiation factor 3 subunit D-1 OS=Drosophila melanogaster GN=eIF-3p66 PE=1 SV=1 - [EI3D1_DROME]	4,472891153	0,001004302
P11420 Protein daughterless OS=Drosophila melanogaster GN=da PE=1 SV=1 - [DA_DROME]	2,998015053	0,001483671
P19109 ATP-dependent RNA helicase p62 OS=Drosophila melanogaster GN=Rm62 PE=1 SV=3 - [DDX17_DROME]	2,033762346	0,001698695
P48809 Heterogeneous nuclear ribonucleoprotein 27C OS=Drosophila melanogaster GN=Hrb27C PE=1 SV=2 - [RB27C_DROME]	6,50342964	0,001835391
P54397 39 kDa FK506-binding nuclear protein OS=Drosophila melanogaster GN=FK506-bp1 PE=1 SV=2 - [FKB39_DROME]	2,31124762	0,00392438
Q9XZF0 Protein yippee OS=Drosophila melanogaster GN=Yippee PE=1 SV=1 - [YIPP_DROME]	0,859191833	0,006356368
Q08473 RNA-binding protein squid OS=Drosophila melanogaster GN=sqd PE=1 SV=3 - [SQD_DROME]	3,594942837	0,010208335
Q9VEW2 Putative SERF-like protein OS=Drosophila melanogaster GN=CG17931 PE=3 SV=1 - [SERFL_DROME]	3,111798522	0,010038663
Q9I7T7 La-related protein CG11505 OS=Drosophila melanogaster GN=CG11505 PE=1 SV=2 - [Y1505_DROME]	3,320522285	0,011167861
Q9VHP0 ATP-dependent RNA helicase bel OS=Drosophila melanogaster GN=bel PE=1 SV=1 - [DDX3_DROME]	0,638819393	0,013590465
Q9VAY7 Protein FAM50 homolog OS=Drosophila melanogaster GN=CG12259 PE=2 SV=1 - [FAM50_DROME]	4,09448207	0,015513207
P02844 Vitellogenin-2 OS=Drosophila melanogaster GN=Yp2 PE=1 SV=2 - [VIT2_DROME]	1,95145009	0,016877668
Q9XZS3 Translation machinery-associated protein 7 homolog OS=Drosophila melanogaster GN=CG13364 PE=4 SV=1 - [TMA7_DROME]	1,028687038	0,019026733
Q05783 High mobility group protein D OS=Drosophila melanogaster GN=HmgD PE=1 SV=1 - [HMGD_DROME]	2,340416268	0,032327205
P02283 Histone H2B OS=Drosophila melanogaster GN=His2B PE=1 SV=2 - [H2B_DROME]	0,572492012	0,034003908
P84029 Cytochrome c-2 OS=Drosophila melanogaster GN=Cyt-c-p PE=1 SV=2 - [CYC2_DROME]	1,201296106	0,033541811
Q9VI75 Phosphatidylinositol-binding clathrin assembly protein LAP OS=Drosophila melanogaster GN=lap PE=1 SV=3 - [PICA_DROME]	1,480253485	0,043675199
P84051 Histone H2A OS=Drosophila melanogaster GN=His2A PE=1 SV=2 - [H2A_DROME]	0,404588327	0,046996776