SUPPLEMENTAL INFORMATION

Nuclear mRNA metabolism drives selective basket assembly on a subset of nuclear pore complexes in budding yeast

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Inventory of Supplemental Information

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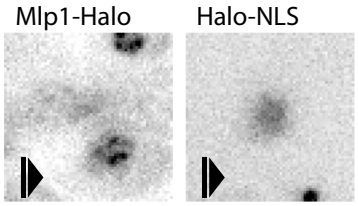

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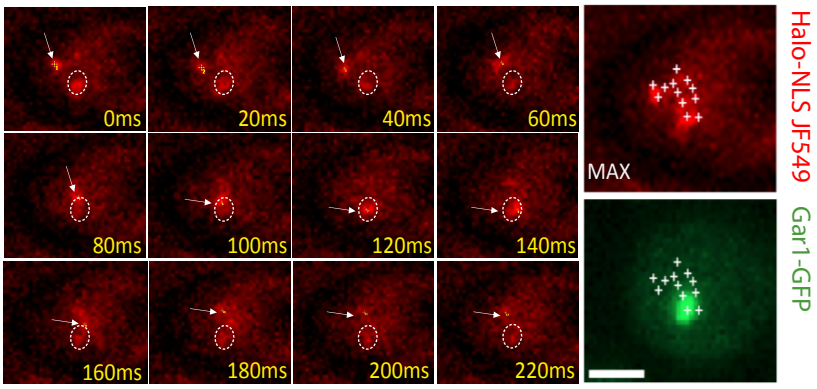

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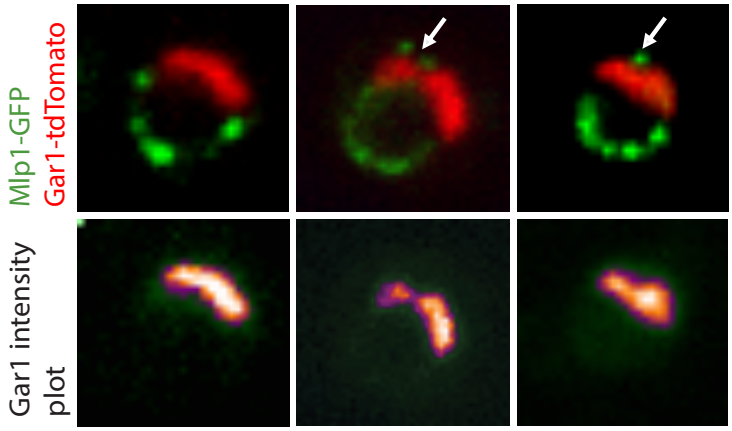
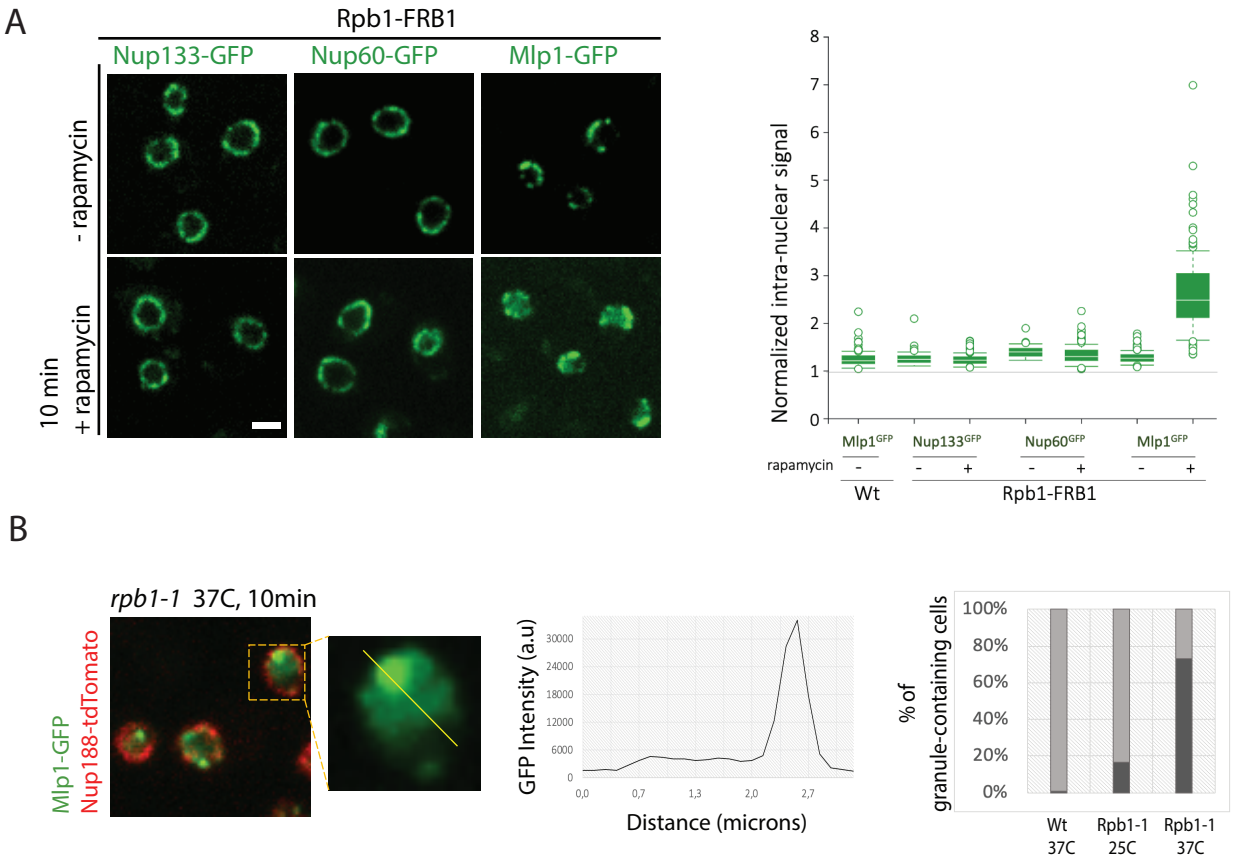


Bensidoun et al. Figure S1

Supplemental Figure S1. Single-protein tracking data for Mlp1-Halo and Halo-NLS, Related to Figure 1.

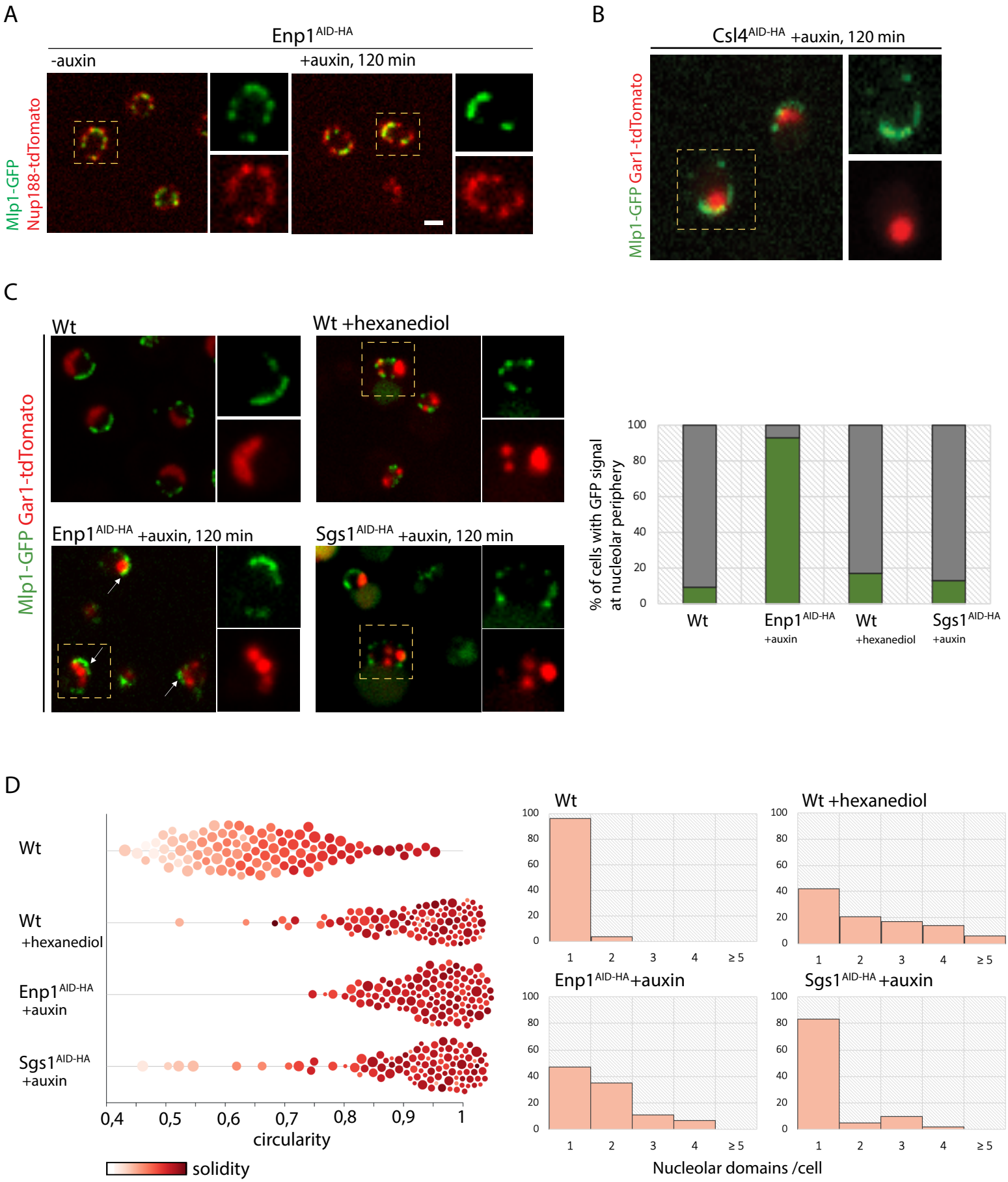
A. Movies of Mlp1-Halo and Halo-NLS diffusion acquired at 20-ms intervals. For Mlp1, early timepoints of the movie show proteins with steady state localization at the nuclear periphery that bleach progressively during image acquisition. **B.** Individual still frames from movie tracking Halo-NLS JF549 (red). White arrows show Halo-NLS JF549 in each frame; dashed circle presents nucleolar area also represented by Gar1-GFP in green. MAX = the maximum intensity projection of all frames with the path highlighted with white crosses. Scale bar=2μm. **C.** Fluorescent microscopy of Mlp1-GFP and Gar1-tdTomato distribution; arrows denoting ectopic baskets. Scan intensity plots measuring Gar1-tdTomato signal as nucleolar marker (lower panels).



Bensidoun et al. Figure S2

Supplemental Figure S2. Mlp1 granule formation in *rpb1-1* cells at non-permissive temperature, Related to Figure 2.

A. Fluorescent microscopy of Nup133-GFP, Nup60-GFP and Mlp1-GFP localization in Rpb1-FRB1 Anchor-Away cells pre- and post-addition of rapamycin (1µg/mL 500 µM, 40 mins) (Jeronimo and Robert, 2014). Bar graph shows quantification of average Mlp1-GFP intranuclear signal intensities in the center of cell nuclei normalized over background signals in all conditions (n=100; Data are represented as mean ± SEM). **B.** Mlp1-GFP granule formation in *rpb1-1* cells at 37^{o}C; line scan intensity plot shows Mlp1-GFP distribution. Nup188-tdTomato signal is shown in red. Histogram quantification of % cells with Mlp1-GFP granules in Wt and *rpb1-1* cells at 25^{o}C and 37^{o}C.

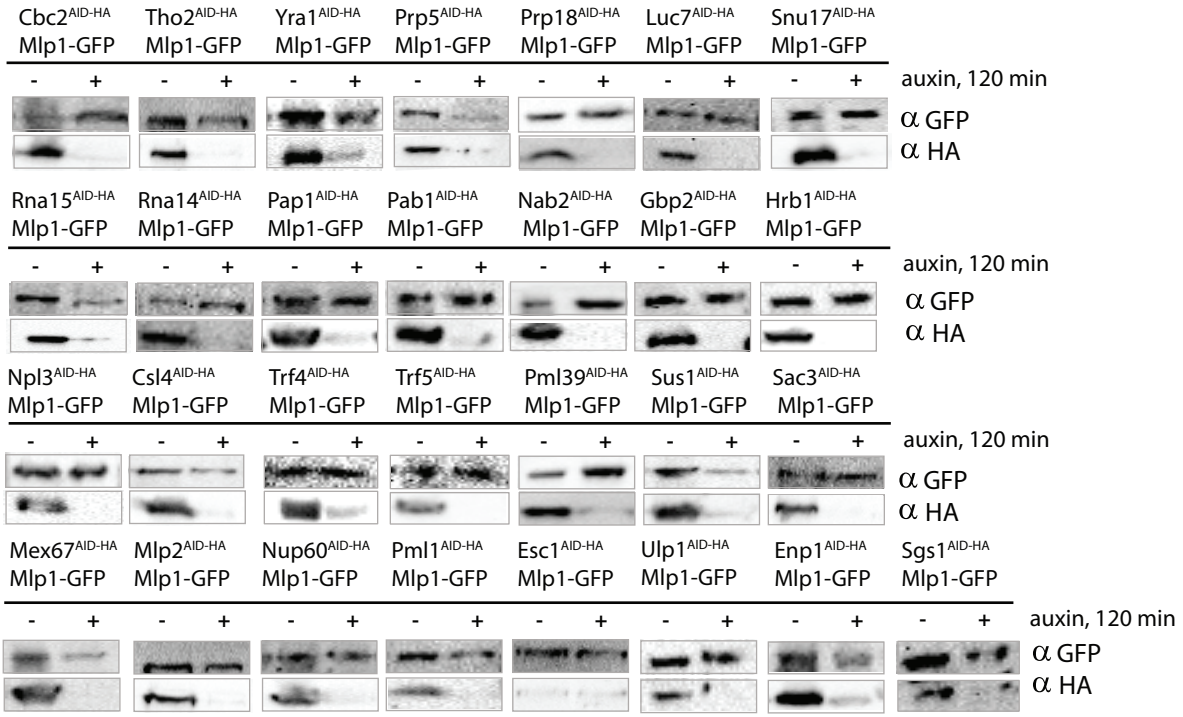


Bensidoun et al. Figure S3

Supplemental Figure S3. Distribution of Mlp1-GFP under different conditions of nucleolar fragmentation, Related to Figure 3.

A. Distribution of Mlp1-GFP along the nuclear and nucleolar peripheries in Enp1^{AID-HA} cells pre- and post-auxin treatment. Nuclear periphery labeled by Nup188-tdTomato. **B** Distribution of Mlp1-GFP along the nucleolar periphery in Csl4^{AID-HA} cells post-auxin treatment. Nucleolus labeled by Gar1-tdTomato. Scale bar =2μm. **C.** Enp1^{AID-HA} cells display fragmented and internalized spherical nucleoli upon Mlp1-GFP relocalization to the nucleolar periphery upon auxin treatment for 120 min. **C.** Structure and fragmentation of nucleolar domains (Gar1-tdTomato, red) in Wt, 1-6 hexanediol (10%, 15 min) treated, Enp1^{AID-HA} and Sgs1^{AID-HA} cells post-auxin treatment. Mlp1-GFP signal along nucleolar region indicated by white arrows. Histogram quantification of % cells with Mlp1-GFP signal along nucleolar periphery (n=100). **D.** Left: Analysis of nucleolar structure based on circularity (x axis) and solidity (color scale) of the nucleolar domains in each strain. The area of the nucleoli/nucleolar domains (ranging from 0.146 to 2.613μm^2) is represented by circle size in the graph (n=100 nucleolar domains for each condition). Right: Bar graphs displaying the number of nucleolar domains in each condition or strain (n=100 cells for each). Scale bar =2μm.

A



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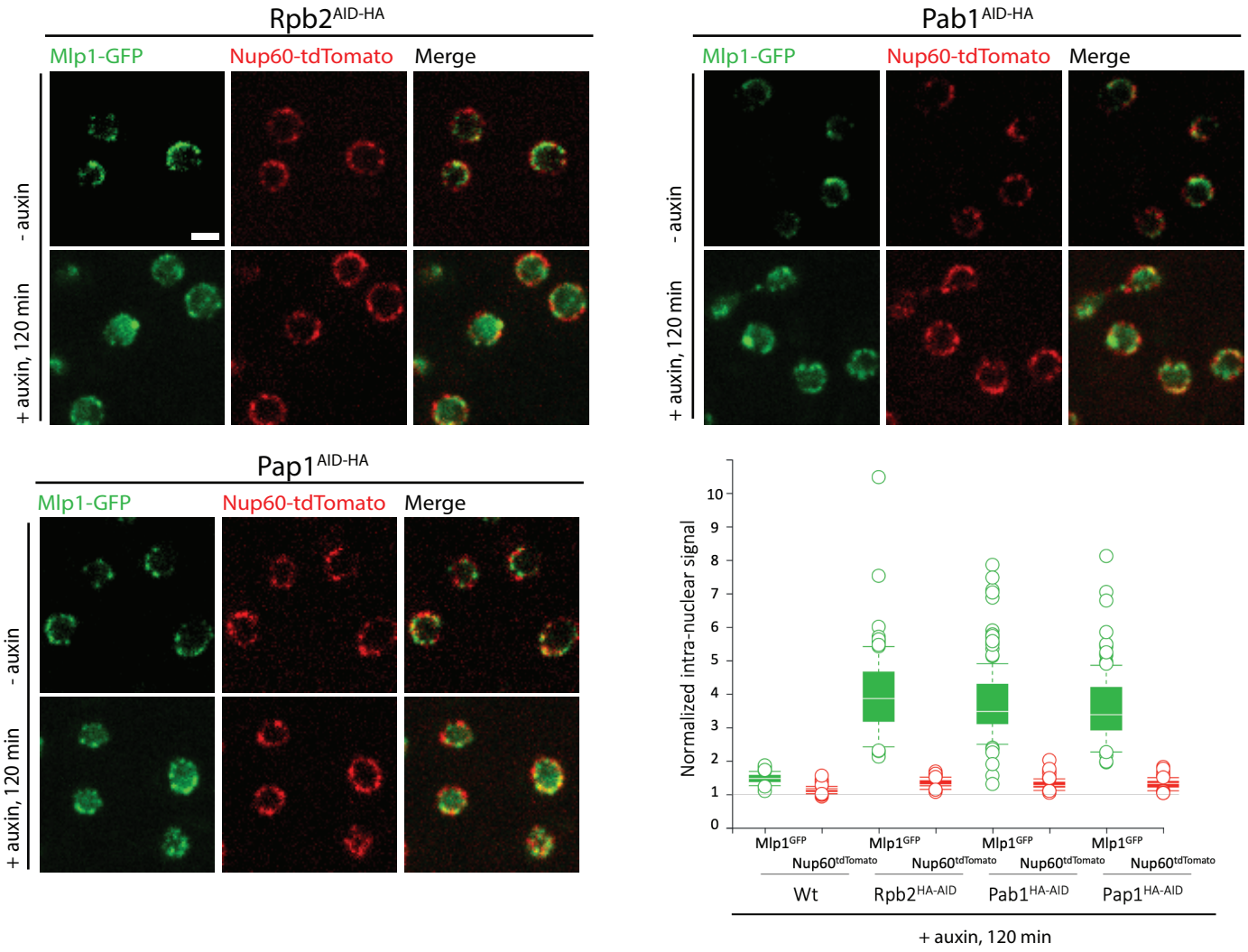
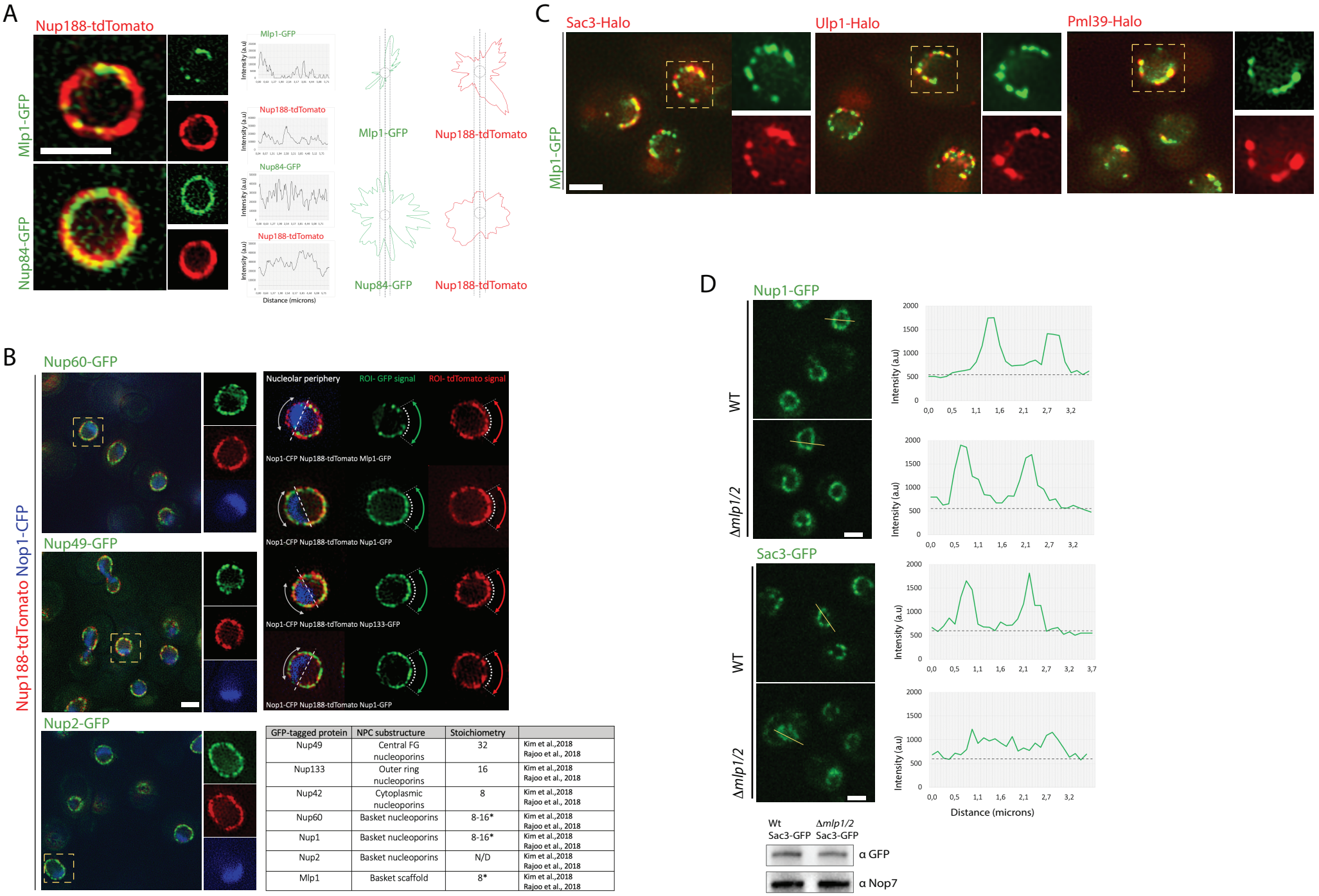


Bensidoun et al. Figure S4

Supplemental Figure S4. Expression and distribution of Mlp1-GFP upon depletion of select nuclear mRNA metabolism factors, Related to Figure 4.

A. Western blot of total cell lysates from Mlp1-GFP/AID-HA-tagged strains pre- and 120 min post-auxin treatment. AID-HA tagged proteins and Mlp1-GFP were detected using anti-HA and anti-GFP antibodies, respectively. **B.** Mlp1-GFP distribution was monitored with respect to the nucleolus in cells where baskets were destabilized upon the addition of auxin and upon heat shock. Graphs represent the overlaps of Mlp1-GFP and Gar1-tdTomato signals (green and red curve respectively). White arrows show Mlp1-GFP signals remaining at the periphery, including in the nucleolar area after basket destabilization. Distribution of Mlp1-GFP and Nup60-tdTomato in $Rpb2^{AID\text{-}HA}$, $Pab1^{AID\text{-}HA}$, and $Pap1^{AID\text{-}HA}$ cells pre- and 120 min post-auxin treatment. Bar graph shows quantification of average Mlp1-GFP and Nup60-tdTomato intranuclear signal intensities in the center of cell nuclei normalized over background signals in all strains 120 min post-auxin treatment (n=100 cells for each strain; Data are represented as mean ± SEM). Scale bar =2µm.

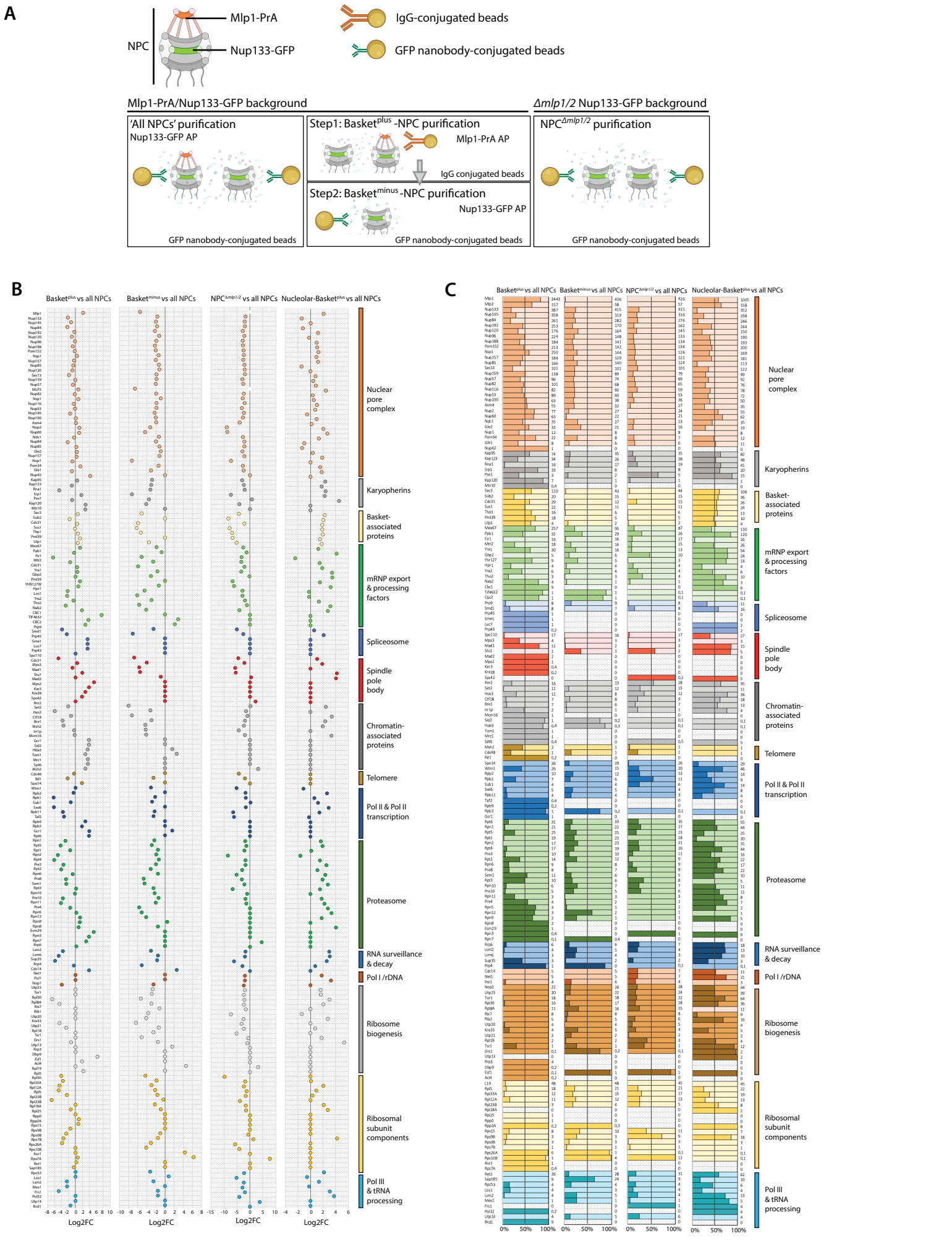


GFP-tagged protein	NPC substructure	Stoichiometry	
Nup49	Central FG nucleoporins	32	Kim et al.,2018 Rajoo et al., 2018
Nup133	Outer ring nucleoporins	16	Kim et al.,2018 Rajoo et al., 2018
Nup42	Cytoplasmic nucleoporins	8	Kim et al.,2018 Rajoo et al., 2018
Nup60	Basket nucleoporins	8-16*	Kim et al.,2018 Rajoo et al., 2018
Nup1	Basket nucleoporins	8-16*	Kim et al.,2018 Rajoo et al., 2018
Nup2	Basket nucleoporins	N/D	Kim et al.,2018 Rajoo et al., 2018
Mlp1	Basket scaffold	8*	Kim et al.,2018 Rajoo et al., 2018

Bensidoun et al. Figure S5

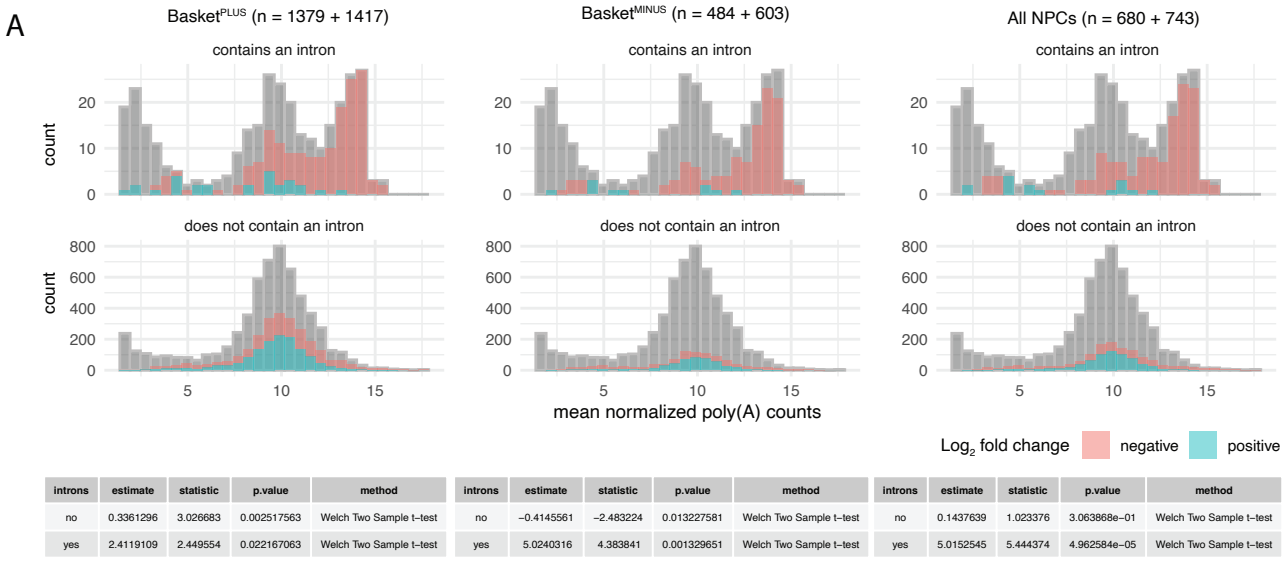
Supplemental Figure S5. Localization of Mlp1, NPC and mRNP components by Structured illumination microscopy, Related to Figure 5.

A. Structured illumination microscopy (SIM) of either Nup84-GFP or Mlp1-GFP (green) and Nup188-tdTomato (red); respective signal intensity distribution shown in line plots and circular diagrams where red dashes delimit nucleolar region; average background signal shown as grey circles and GFP distribution in green. **B.** SIM co-localization analysis of Nop1-CFP (, Nup188-tdTomato, and either Nup60-, Nup49-, or Nup2-GFP. Table indicates stoichiometries of selected Nups measured by either MS and/or different imaging approaches in yeast (*numbers indicated represent an estimation and can vary depending on the study and on the approach chosen). **C.** SIM co-localization analysis of Mlp1-GFP and Sac3-, Ulp1-, and Pml39-Halo. **D.** Top: Distribution of Nup1- or Sac3-GFP in Wt and *Δ mlp1/2* cells; line scan intensity plot shows GFP distribution in a single cell. Bottom: western blot of total cell lysates from Sac3-GFP/ Wt and *Δ mlp1/2* cells. Nucleolar protein Nop7 was used as loading control and proteins detected using either anti-GFP and anti-Nop7 antibodies. Scale bar =2µm.


A
NPC
Mlp1-PrA
Nup133-GFP
IgG-conjugated beads
GFP nanobody-conjugated beads
Mlp1-PrA/Nup133-GFP background
Δmlp1/2 Nup133-GFP background
'All NPCs' purification
Nup133-GFP AP
GFP nanobody-conjugated beads
Step1: Basket^plus -NPC purification
Mlp1-PrA AP
IgG conjugated beads
Step2: Basket^minus -NPC purification
Nup133-GFP AP
GFP nanobody-conjugated beads
NPC^Δmlp1/2 purification
GFP nanobody-conjugated beads
B
Basket^plus vs all NPCs
Basket^minus vs all NPCs
NPC^Δmlp1/2 vs all NPCs
Nucleolar-Basket^plus vs all NPCs
Log2FC
Nuclear pore complex
Karyopherins
Basket-associated proteins
mRNP export & processing factors
Spliceosome
Spindle pole body
Chromatin-associated proteins
Telomere
Pol II & Pol II transcription
Proteasome
RNA surveillance & decay
Pol I /rDNA
Ribosome biogenesis
Ribosomal subunit components
Pol III & tRNA processing
C
Basket^plus vs all NPCs
Basket^minus vs all NPCs
NPC^Δmlp1/2 vs all NPCs
Nucleolar-Basket^plus vs all NPCs
0%
50%
100%
Nuclear pore complex
Karyopherins
Basket-associated proteins
mRNP export & processing factors
Spliceosome
Spindle pole body
Chromatin-associated proteins
Telomere
Pol II & Pol II transcription
Proteasome
RNA surveillance & decay
Pol I /rDNA
Ribosome biogenesis
Ribosomal subunit components
Pol III & tRNA processing

Supplemental Figure S6. Method and data analysis for complexes co-isolated by differential affinity purification with basket-containing and basket-less NPCs, Related to Figure 6.

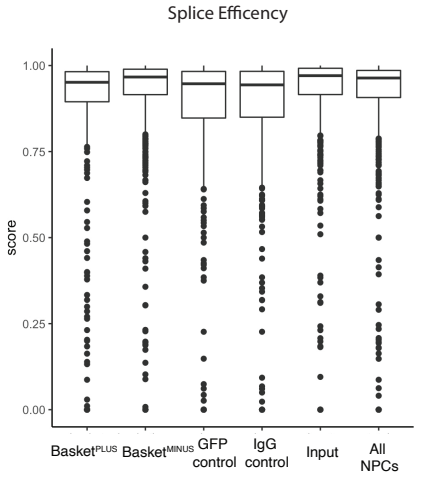
A. Illustration of the NPCs affinity purifications. All NPCs were affinity purified via GFP-nanobodies-conjugated beads using yeast cell extracts from an Mlp1-PrA/Nup133-GFP double-tagged strain. Separation of basket-containing and basket-less NPCs was achieved from an Mlp1-PrA/Nup133-GFP double-tagged strain using a differential affinity purification approach, whereby Mlp1-PrA associated complexed ($Basket^{plus}$) were isolated via IgG-conjugated beads, followed by the isolation of Nup133-GFP associated complexed ($Basket^{minus}$) via GFP-nanobodies from the flow-through. Nup133-GFP associated complexed ($Basket^{minus}$) were also isolated from *Δ mlp1/2/* Nup133-GFP cells. n=3 for each condition. **B.** All NPCs, Mlp1-PrA ($Basket^{plus}$), and Nup133-GFP ($Basket^{minus}$) associated complexes were isolated from Mlp1-PrA/Nup133-GFP, *Δ mlp1/2*/Nup133-GFP cells and Mlp1-PrA/Nup133-GFP/$Enp1^{AID-HA}$ cells 120 min post-auxin treatment. Proteins were included if identified as a high confidence interaction (i.e., at least five exclusive spectrum counts (ESC) in two biological replicates) and grouped according to their cellular functions. Each protein is presented as log2(FC) over proteins identified in 'All NPCs'. **C.** Histograms showing normalized exclusive spectral counts of all proteins co-purified with the different pore APs relative to proteins identified in "All NPCs". Bars represent percentage of peptide levels over 'All NPCs'; only median ESC ≥ 10 were considered for quantitative analysis. Proteins were grouped according to their cellular functions.

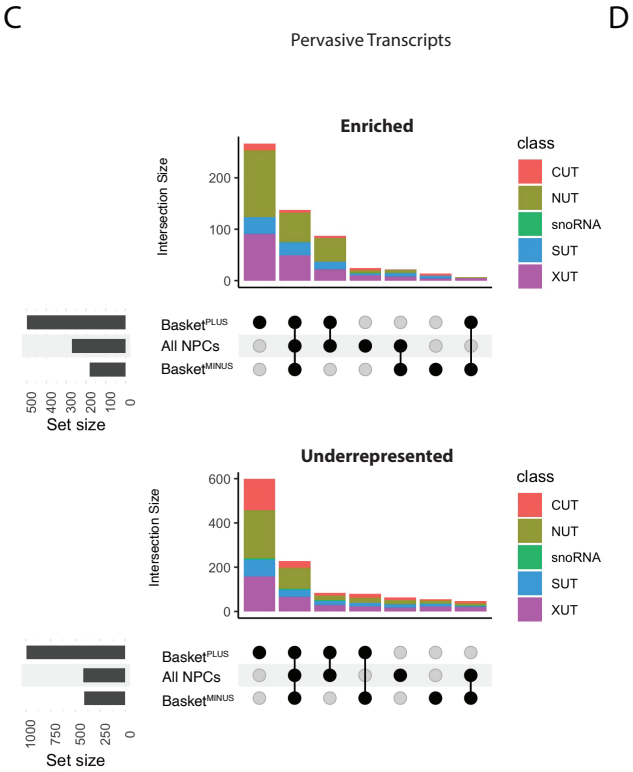


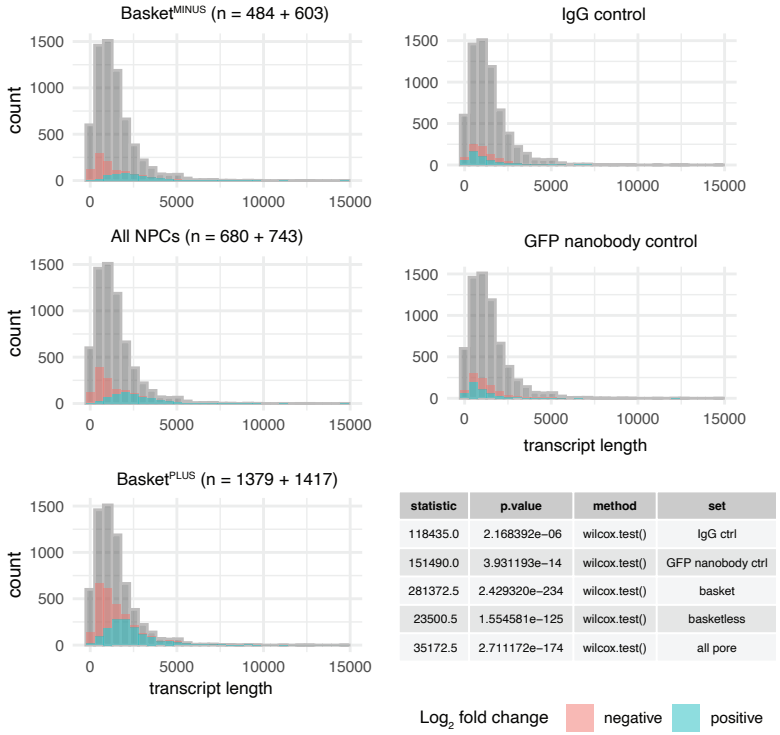
introns	estimate	statistic	p.value	method
no	0.3361296	3.026683	0.002517563	Welch Two Sample t–test
yes	2.4119109	2.449554	0.022167063	Welch Two Sample t–test

introns	estimate	statistic	p.value	method
no	−0.4145561	−2.483224	0.013227581	Welch Two Sample t–test
yes	5.0240316	4.383841	0.001329651	Welch Two Sample t–test

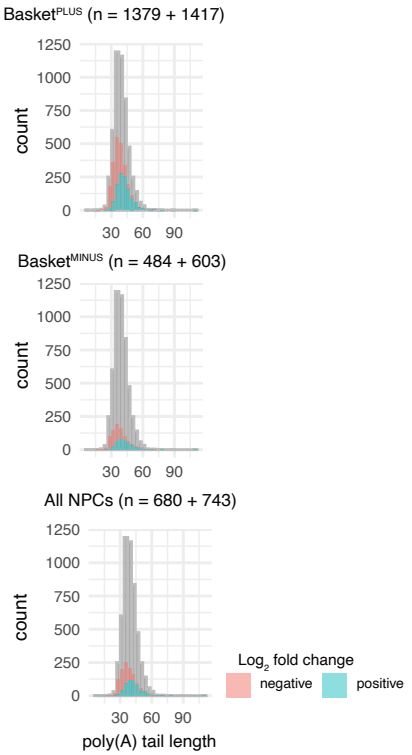
introns	estimate	statistic	p.value	method
no	0.1437639	1.023376	3.063868e–01	Welch Two Sample t–test
yes	5.0152545	5.444374	4.962584e–05	Welch Two Sample t–test







statistic	p.value	method	set
118435.0	2.168392e–06	wilcox.test()	IgG ctrl
151490.0	3.931193e–14	wilcox.test()	GFP nanobody ctrl
281372.5	2.429320e–234	wilcox.test()	basket
23500.5	1.554581e–125	wilcox.test()	basketless
35172.5	2.711172e–174	wilcox.test()	all pore



Bensidoun et al. Figure S7

Figure S7. Analysis of transcript features of co-isolated RNAs across affinity-purified basket-containing and basket-less NPC samples, Related to Figure 7.

A. Histograms representing transcript enrichment in Basket^{plus}', 'Basket^{minus}' and 'All NPCs' from differential APs over mean transcript expression and intron content in the poly(A) library (grey). **B.** Splicing efficiency for each intron in the *S. cerevisiae* genome was determined across samples using the SPLICE-q library. No significant differences were found for introns associated with basket-containing, basket-less, or all NPCs and the standard RNA-seq library (Input). **C.** Upset plot. Top: Bar graph on the left represents the pervasive transcripts enriched with a log2(FC)< 1 over poly(A) libraries across samples. Bar graph on top represents the pervasive transcripts exclusively enriched while dots in line with bars indicate shared transcript sets. Bottom: Bar graph on the left represents the pervasive transcripts underrepresented with a log2(FC)< 1 over poly(A) libraries across samples. Bar graph on top represents the pervasive transcripts exclusively underrepresented, while dots in line with bars indicate shared transcript sets. **D.** Histograms representing transcript enrichment in Basket^{plus}', 'Basket^{minus}' and 'All NPCs' from differential APs in relation to transcript length observed in poly(A) library (grey). **E.** Histograms representing transcript enrichment in Basket^{plus}', 'Basket^{minus}' and 'All NPCs' from differential APs in relation to poly(A) tail length observed in poly(A) library (grey).

Supplemental Table S2. Plasmids used in this study, Related to STAR Methods

pZUT3 centromeric plasmid carrying GAR1-GFP, URA3	Niepel et al.[112]
centromeric plasmid pEXPGFPNLS_M2NT2 for Nterm2 Mlp1 fragment expression, HIS3	
centromeric plasmid pUG34_GFP-NLS::HIS3	
centromeric plasmid Nop-CFP His3	A Kind gift of P.Chartrand lab
tdTomato tagging: pKAN tdtomato cyc loxP KAN loxP	PDZ264
GFP tagging: yeGFP, klTRP1	PDZ505
GFP tagging: yeGFP, pHyg	PDZ504
Halo tagging: pSJW01 Halo, pHyg	PDZ823, kind gift of Reyes lab
Auxin inducible degron tagging: AID-6HA, pHyg	Morawska et al, 2013
ProteinA tagging: PrA, pHyg	PDZ659

Supplemental Table S3. Primers used in this study, Related to STAR Methods

C-terminal tagging (5'-3')	Sequence
Mlp1-GFP (Fwd)	AAGATGAGGAAGAAAAAGAAACCGATAAGGTGAATGACGAGAACAGTATACGTACGCTGCAGGTCGAC
Mlp1-GFP (Rev)	ACATTGAAAAAGGTTTAGTTTGTATTGATCCCTTGTTTTTACTATCTCCTATCGATGAATTCGAGCTCG
Gar1-tdTomato (Fwd)	GGATCTCGTGGCGGATCTCGTGGTGGTTTCAGAGGAGGTAGAAGAGCTCTAGAACTAGTGGATCC
Gar1-tdTomato (Rev)	CAGATATAGTAAGTTGGAAGAAATGAAGAATTGTGAAAGATAAAGGGCATAGGCCACTAGTGGATCTG
Nup188-tdTomato (Fwd)	CAAGGGTATCAGCAGAGACATTAAAGCATTACAAGATTCACTATTTAAGGACGTTGCTCTAGAACTAGTGGATCC
Nup188-tdTomato (Rev)	GCACTTGCACTGTTCATTATTATATTATGTAGCTTTACATAACCTGCAAAATAAGGCATAGGCCACTAGTGGATCTG
Mlp1-Halo (Fwd)	GAGGAAGAAAAAGAAACCGATAAGGTGAATGACGAGAACAGTATAGGTGACGGTGCTGGTTTA
Mlp1-Halo (Rev)	GCAGAATGAAGCTCCTCCACATTGAAAAAGGTTTAGTTTGTATTGACACAGGAAACAGCTATGACC
Nup188-Halo (Fwd)	CAAGGGTATCAGCAGAGACATTAAAGCATTACAAGATTCACTATTTAAGGACGTTGGTGACGGTGCTGGTTTA
Nup188-Halo (Rev)	GCACTTGCACTGTTCATTATTATATTATGTAGCTTTACATAACCTGCAAAATAAGACACAGGAAACAGCTATGACC
Rpa135-AID-HA (Fwd)	CTATCCGCAATGGGTATAAGATTGCGTTATAATGTAGAGCCCAAACGTACGCTGCAGGTCGAC
Rpa135-AID-HA (Rev)	CCTTCATTTACCATTCTATATCAATTTGGAAAGAAGGGTATTTCTATCGATGAATTCGAGCTCG
Rpb2-AID-HA (Fwd)	ATGAACATTACACCACGTTTATATACCGATCGTTCGAGAGATTTTCGTACGCTGCAGGTCGAC
Rpb2-AID-HA (Rev)	AATGTTTTTTATTATTTTACTTTCTTAGAGTTACAACATTATTTCATCGATGAATTCGAGCTCG
Enp1-AID-HA (Fwd)	CAGGGAGTTTGTTGATCCACAGGAAGCTAATGATGATTTAATGATTGATGTCAATCGTACGCTGCAGGTCGAC
Enp1-AID-HA (Rev)	TGAAAGGGGGAAAGACCGAGCGATATAAAATTGATGAAAAATTGATATTACAGCAATCGATGAATTCGAGCTCG
Csl4-AID-HA (Fwd)	GATGACTTCACCGGTTACAGGCGCTACAGAAAAGCGCAAATGTGCCAAACCTTTTCGTACGCTGCAGGTCGAC
Csl4-AID-HA (Rev)	TACCCTCTTTTAAATATATACGCGTCTATATGCACTGTAGATAAGCTGTTACATAATCGATGAATTCGAGCTCG
Rna14-AID-HA (Fwd)	GAATTTTTTAAATGATCAAGTAGAGATTCCAACAGTTGAGAGCACCAAGTCAGGTCGTACGCTGCAGGTCGAC
Rna14-AID-HA (Rev)	TTATAATAGATGTGTTGGTATAAATATTCATATATACCTATTTATTAACGTAATGATCGATGAATTCGAGCTCG
Rna15-AID-HA (Fwd)	GATGGCTATTTGGGACTTAAAACAAAAAGCATTAAGGGGAGAATTTGGTGCATTTCGTACGCTGCAGGTCGAC
Rna15-AID-HA (Rev)	GTTGCCTCATCATTGCGGAACCGCATTTTTTTTTTGTATTTTTGCCTCCCTAGTTATCGATGAATTCGAGCTCG
Nup60-AID-HA (Fwd)	AAATGGCTTGGTTGATGAAAATAAAGTTGAGGCTTTCAAGTCCCTATATACCTTTCGTACGCTGCAGGTCGAC
Nup60-AID-HA (Rev)	CTTACGTATTGAGTTGGGCTATACGGTAATTATGTCACGGCTAAAATTTTCATTAATCGATGAATTCGAGCTCG
Esc1-AID-HA (Fwd)	TAGGGGGCACGAGCCAAAAAGCCGTGGACAGAATACGCATCCAAGTGTTGACAAACGTACGCTGCAGGTCGAC
Esc1-AID-HA (Rev)	AGAAAAACGCATCGCAATAATTATTACTATCTACATATTCCTGTATACAATTTGAATCGATGAATTCGAGCTCG
Ulp1-AID-HA (Fwd)	TGCGATTAGGATGAGAAGATTTATTGCCCATTTGATTTTAACCGACGCTTTAAAACGTACGCTGCAGGTCGAC
Ulp1-AID-HA (Rev)	CAATGATCTGAATATTTCTACTTATGTATAATAATTGTATATTATAAAAGAATAAATCGATGAATTCGAGCTCG
Mlp2-AID-HA (Fwd)	ACACCAAAAAGGTTAAAGAGAGTCCAGCAAATGATCAAGCTTCCAACGAGCGTACGCTGCAGGTCGAC
Mlp2-AID-HA (Rev)	AAAATATGTAGATGTTTCATATTTATATAATTACATTGTTTAATATTACAATCGATGAATTCGAGCTCG
Yra1-AID-HA (Fwd)	TAAGAAAAGTCTTGAAGATCTGGACAAGGAAATGGCGGACTATTTCGAAAAGAAACGTACGCTGCAGGTCGAC
Yra1-AID-HA (Rev)	GGaaaaattaaatttaataaaaccaaattaaatcaaacaaaaaaTTGACAATTAAATCGATGAATTCGAGCTCG
Tho2-AID-HA (Fwd)	TCAGGCGCTTCCGCAAGGTCCCAAGGGTGGGAATTACGTCAGTAGGTACCAGAGGCGTACGCTGCAGGTCGAC
Tho2-AID-HA (Rev)	GGGAACTATCAAAGTACACGTTAAAATTCAGCTCGGGTATGTTAAGTACTAGTAAATCGATGAATTCGAGCTCG
Sac3-AID-HA (Fwd)	TATATTAGAGCTGAAGATCTTGATCGATTCTGTCAAGAAGAAAGTAAATAATGATCGTACGCTGCAGGTCGAC
Sac3-AID-HA (Rev)	TTCCTAAAGCTATAGAAAAAATGCACATTTCTTTTGTTTATATATTACAAATGCTATCGATGAATTCGAGCTCG
Sus1-AID-HA (Fwd)	GTTTTAAAGCAAATAAGGGAATTTCTTGAAGAGATTGTAGATACACAACGTACGCTGCAGGTCGAC
Sus1-AID-HA (Rev)	TTTCCCGATGAGCATATGTAATAATATTGGGAATTAAGGTGCATTTTCGTATCCTATCGATGAATTCGAGCTCG
Nab2-AID-HA (Fwd)	AAATGCTCCTCCGCAAACCAGTTTTACGCACCAAGAACAAGATACGGAAATGAACCGTACGCTGCAGGTCGAC
Nab2-AID-HA (Rev)	CTTCCATCAAAAGGGTCACAGGAACATGAATTTCGTTCCGTGATTTTAATAGTAAATCGATGAATTCGAGCTCG
Pab1-AID-HA (Fwd)	TTCTGCTGCCTATGAGTCTTTCAAAAAGGAGCAAGAACAACAAACTGAGCAAGCTCGTACGCTGCAGGTCGAC
Pab1-AID-HA (Rev)	AGAAAAAAAAGATGATAAGTTTGTTGAGTAGGGAAGTAGGTGATTACATAGAGCAATCGATGAATTCGAGCTCG

Pap1-AID-HA (Fwd)	AGATGCTGCTTCAGGTGACAACATCAATGGCACAACCGCAGCTGTTGACGTAAACCGTACGCTGCAGGTCGAC
Pap1-AID-HA (Rev)	GTTTATGACTGATTAACCTATATTAATAAACTATTCAACTATAAATAGGAATGTCATCGATGAATTCGAGCTCG
Pml39-AID-HA (Fwd)	GAAATTGGGCGTGGGAGAAAGACTAAATAAATTAGAGGCTGTTCTACAAACTTTACGTACGCTGCAGGTCGAC
Pml39-AID-HA (Rev)	CAGCATGGGGGCATATACAAGCATATGAGAAATTTGGATAATGTATTACATCTAATATCGATGAATTCGAGCTCG
Pml1-AID-HA (Fwd)	TACACTTTCAGAATTTGAAGAAGATACCGATTACGAACTCATCTTCATGAATGTACGTACGCTGCAGGTCGAC
Pml1-AID-HA (Rev)	CAGCATTCAAAGAAGAATAATTAAAACACACTGAAAGTGTGTTTCTTATATATGGATCGATGAATTCGAGCTCG
Prp5-AID-HA (Fwd)	GGGGTCGTAAAGGCTGCAAGCTTGTCTTTGAAGAGTACTAAATACCGTACGCTGCAGGTCGAC
Prp5-AID-HA (Rev)	AACTACGAAAGTATATAGCACCACGAGTGAGTTAAATTCTAAAAAATCGATGAATTCGAGCTCG
Snu17-AID-HA (Fwd)	ATAGCTGATAGACTGTGGAGTCGTAAAGAATTTCGCTTGGGGACCCGTACGCTGCAGGTCGAC
Snu17-AID-HA (Rev)	GAGCGAGCCTTTCCCTTTTGGGACGCGCGCCAAGGCCCTTCTGTTATCGATGAATTCGAGCTCG
Luc7-AID-HA (Fwd)	AACGCCAGCAAGACAGCTACTACACTACCCGGAAGACGCTTTGTGCGTACGCTGCAGGTCGAC
Luc7-AID-HA (Rev)	TCCTTCGAACAAAATTTTTCTAGCATCATTTTTTTATGTATGGCCATCGATGAATTCGAGCTCG
Mex67-AID-HA (Fwd)	AAAGGGTTTTCAGAGTAGCATGAATGGCATCCCTAGAGAAGCATTTGTGCAGTTCCGTACGCTGCAGGTCGAC
Mex67-AID-HA (Rev)	GCTTAAACTGTATATTTTTTGTGATACTGTGCGGCTGAAACAGGGAACAATATCAATCGATGAATTCGAGCTCG
Hrb1-AID-HA (Fwd)	GAATAATTATAACTATGGGGGTTGTGATTTGGATATATCGTACGCTAAACGCCTCCGTACGCTGCAGGTCGAC
Hrb1-AID-HA (Rev)	ATAAATACTTGTCGCAGATCCAATAGGTGAGAAAGTATATAGATCGAGAGTAGTTATCGATGAATTCGAGCTCG
Cbc2-AID-HA (Fwd)	TACTTTCAGACCAGGTTTCGATGAAGAAAGAGAAGATGATAACTACGTACCTCAGCGTACGCTGCAGGTCGAC
Cbc2-AID-HA (Rev)	ATATATATATATATATCTGTGTGTAGAATCTTTCTCAGATATAAATTGATTGATTATCGATGAATTCGAGCTCG
Gbp2-AID-HA (Fwd)	AAATAATTATAATTATGGTGGTTGTAGTTTACAGATCTCTTATGCTAGACGTGATCGTACGCTGCAGGTCGAC
Gbp2-AID-HA (Rev)	TTATTTATACGTTATCATAAAGTACACAGGTCATGGTTCGGTTGGTGCTTAGGAAATCGATGAATTCGAGCTCG
Npl3-AID-HA (Fwd)	TCCAAGAGATGCATACAGAACCAGAGATGCTCCACGTGAAAGATCACCAACCAGGCGTACGCTGCAGGTCGAC
Npl3-AID-HA (Rev)	ACAATTCATATCTTTTGTTAATTTCTCCTTTTTTTTTCTCAACTATATAAATGGCATCGATGAATTCGAGCTCG
Prp18-AID-HA (Fwd)	TAAAAGATTAATAACTTTTGAAGAATGGTATACCAGCAACCACGATAGCTTAGCCCGTACGCTGCAGGTCGAC
Prp18-AID-HA (Rev)	TTATTTTGGCCGCATGATATCGTGCCACGCGATAACGAAAACAATAGTTCAACAAATCGATGAATTCGAGCTCG
Nup84-GFP (Fwd)	TGGAAAGTTAAAAGAGTATCTGGATCTCGTTGCTCGCACAGCAACCCTTTCGAACCGTACGCTGCAGGTCGAC
Nup84-GFP (Rev)	TAAAATTATTGCTGTTTACTTAAAATATAAACTTATTCTGCAATACATTAATTGAATCGATGAATTCGAGCTCG
Nup60-GFP (Fwd)	AAATGGCTTGGTTGATGAAAATAAAGTTGAGGCTTTCAAGTCCCTATATACCTTTCGTACGCTGCAGGTCGAC
Nup60-GFP (Rev)	CTTACGTATTGAGTTGGGCTATACGGTAATTATGTCACGGCTAAAATTTTCATTAATCGATGAATTCGAGCTCG
Nup49-GFP (Fwd)	GCCGTGTTACATCAAAAAACGAAAACACTGGCATCATTGAGCATAGCTCTAGAACTAGTGGATCC
Nup49-GFP (Rev)	TGTACAAGACATTTGTACTTGTTATACGCACTATATAAACTTTCAGCATAGGCCACTAGTGGATCTG
Nup133-GFP (Fwd)	TGTAGCGAAAGAAAAAAACTATACCATCAACTATGAAACCAACACTGTAGAATACCGTACGCTGCAGGTCGAC
Nup133-GFP (Rev)	TATTATCATTCCCCAGTAAAGTTTATTATATATATGTAAAATTGTATTATAGATAATCGATGAATTCGAGCTCG
Ulp1-GFP (Fwd)	TGCGATTAGGATGAGAAGATTTATTGCCCATTTGATTTTAACCGACGCTTTAAAACGTACGCTGCAGGTCGAC
Ulp1-GFP (Rev)	CAATGATCTGAATATTTCTACTTATGTATAATAATTGTATATTATAAAAGAATAAATCGATGAATTCGAGCTCG
Pml39-GFP (Fwd)	AGGAGAAATAAAACATTATTCCCCAGGAATTGAGAGGAAAGTAGGGCAGTTACTACGTACGCTGCAGGTCGAC
Pml39-GFP (Rev)	CAGCATGGGGGCATATACAAGCATATGAGAAATTTGGATAATGTATTACATCTAATATCGATGAATTCGAGCTCG
Mex67-GFP (Fwd)	AAAGGGTTTTCAGAGTAGCATGAATGGCATCCCTAGAGAAGCATTTGTGCAGTTCCGTACGCTGCAGGTCGAC
Mex67-GFP (Rev)	GCTTAAACTGTATATTTTTTGTGATACTGTGCGGCTGAAACAGGGAACAATATCAATCGATGAATTCGAGCTCG
Sac3-GFP (Fwd)	TATATTAGAGCTGAAGATCTTGATCGATTCTGTCAAGAAGAAAGTAAATAATGATCGTACGCTGCAGGTCGAC
Sac3-GFP (Rev)	TTCCTAAAGCTATAGAAAAAATGCACATTTCTTTTGTTTATATATTACAAATGCTATCGATGAATTCGAGCTCG
Mlp2-GFP (Fwd)	ACACCAAAAAGGTTAAAGAGAGTCCAGCAAATGATCAAGCTTCCAACGAGCGTACGCTGCAGGTCGAC
Mlp2-GFP (Rev)	AAAATATGTAGATGTTTCATATTTATATAATTACATTGTTTAATATTACAATCGATGAATTCGAGCTCG
Ulp1-Halo (Fwd)	TGCGATTAGGATGAGAAGATTTATTGCCCATTTGATTTTAACCGACGCTTTAAAAGGTGACGGTGCTGGTTTA
Ulp1-Halo (Rev)	CAATGATCTGAATATTTCTACTTATGTATAATAATTGTATATTATAAAAGAATAAACACAGGAAACAGCTATGACC
Pml39-Halo (Fwd)	GAAATTGGGCGTGGGAGAAAGACTAAATAAATTAGAGGCTGTTCTACAAACTTTAGGTGACGGTGCTGGTTTA

Pml39 Halo (Rev)	CAGCATGGGGGCATATACAAGCATATGAGAATTTGGATAATGTATTACATCTAATACACAGGAAACAGCTATGACC
Sac3-Halo (Fwd)	TATATTAGAGCTGAAGATCTTGATCGATTCTGTCAAGAAGAAAGTAAATAATGATGGTGACGGTGCTGGTTTA
Sac3-Halo (Rev)	TTCCTAAAGCTATAGAAAAAATGCACATTTCTTTTGTTTATATATTACAAATGCTACACAGGAAACAGCTATGACC
Nab2-tdTomato (Fwd)	AAATGCTCCTCCGCAAACCAGTTTTACGCACCAAGAACAAGATACGGAAATGAACGCTCTAGAACTAGTGGATCC
Nab2-tdTomato (Rev)	TTGAATAGGTGTCTTCCATCAAAAGGGTCACAGGAACATGAATTTCGTTCCGTGAGCATAGGCCACTAGTGGATCTG
Sac3-tdTomato (Fwd)	TATATTAGAGCTGAAGATCTTGATCGATTCTGTCAAGAAGAAAGTAAATAATGATGCTCTAGAACTAGTGGATCC
Sac3-tdTomato (Rev)	TTCCTAAAGCTATAGAAAAAATGCACATTTCTTTTGTTTATATATTACAAATGCTGCATAGGCCACTAGTGGATCTG
Pml39-tdTomato (Fwd)	GAAATTGGGCGTGGGAGAAAGACTAAATAAATTAGAGGCTGTTCTACAAACTTTAGCTCTAGAACTAGTGGATCC
Pml39-tdTomato (Rev)	CAGCATGGGGGCATATACAAGCATATGAGAATTTGGATAATGTATTACATCTAATGCATAGGCCACTAGTGGATCTG
Ulp1-tdTomato (Fwd)	TGCGATTAGGATGAGAAGATTTATTGCCCATTTGATTTTAACCGACGCTTTAAAAGCTCTAGAACTAGTGGATCC
Ulp1-tdTomato (Rev)	CAATGATCTGAATATTTCTACTTATGTATAATAATTGTATATTATAAAAGAATAAGCATAGGCCACTAGTGGATCTG
Mlp1-PrA (Fwd)	GACTGAAGATGAGGAAGAAAAAGAAACCGATAAGGTGAATGACGAGAACAGTATAGGTGAAGCTCAAAAACTTAAT
Mlp1-PrA (Rev)	CCTCCACATTGAAAAAGGTTTAGTTTGTATTGATCCCTTGTTTTTACTATCTCCTATCGATGAATTCGAGCTCG
Nup60-tdTomato (Fwd)	AAATGGCTTGGTTGATGAAAATAAAGTTGAGGCTTTCAAGTCCCTATATACCTTTGCTCTAGAACTAGTGGATCC
Nup60-tdTomato (Rev)	CTTACGTATTGAGTTGGGCTATACGGTAATTATGTCACGGCTAAAATTTTCATTAGCATAGGCCACTAGTGGATCTG
Nup2-GFP (Fwd)	CGCTCATTTACGAAAGCTATTGAAGATGCTAAAAAAGAAATGAAACGTACGCTGCAGGTCGAC
Nup2-GFP (Rev)	ATATGAGGGTTCTATTCTATTTAAAATTGTTAACTGTATTTACTC ATCGATGAATTCGAGCTCG
Nup42-GFP (Fwd)	CATCAAGCTATCATTAAATTTCGACCCGAGCAACGACTCAACTGTACGGATCCCCGGGTTAATTAA
Nup42-GFP (Rev)	TAATGCATTTTTCATTAGATATATATATATATTCATATATATTGTGAATTCGAGCTCGTTTAAAC
Nup1-GFP (Fwd)	GGGCGGTGGTGTTATGGCGAACAGAAAGATTGCAAGAATGAGGCACTCTAAAAGGCGTACGCTGCAGGTCGAC
Nup1-GFP (Rev)	TAGGAATATATATCCTTCAGAAAAGCAACACAATACCTAATTACATAACCGATATATCGATGAATTCGAGCTCG
Nup49-GFP (Fwd)	GAATCGCCGTGTTACATCAAAAAACGAAAACACTGGCATCATTGAGCATACGTACGCTGCAGGTCGAC
Nup49-GFP (Rev)	GACATTTGTACTTGTTATACGCACTATATAAACTTTCAGGGCGATTTACATCGATGAATTCGAGCTCG
Trf4-AID-HA (Fwd)	TCTAGCGAAGATGATGATGAAGATGGATATAATCCTTATACCCTTCGTACGCTGCAGGTCGAC
Trf4-AID-HA (Rev)	CAGTGATGTACAGTTCAGTGCATCATTTAAACAAAAAGGCACATAATCGATGAATTCGAGCTCG
Trf5-AID-HA (Fwd)	GCTCAAACGAGAAGGGACTACTGGCTCTCTAAAGGCCAGGCTCTTCGTACGCTGCAGGTCGAC
Trf5-AID-HA (Rev)	TATTCTTGTATAAATAGTAAATAGTCTATAAGAGTCTATATTGTGATCGATGAATTCGAGCTCG
Sgs1-AID-HA (Fwd)	AGGTTTTAGAAATTACCGAGGTCACTACAGAGGAAGAAAGCGTACGCTGCAGGTCGAC
Sgs1-AID-HA (Rev)	ATCGATGAATTCGAGCTCGGAATGGTGTCGTAGTTATAAGTAACACTATTTATTTTTCTACTCT