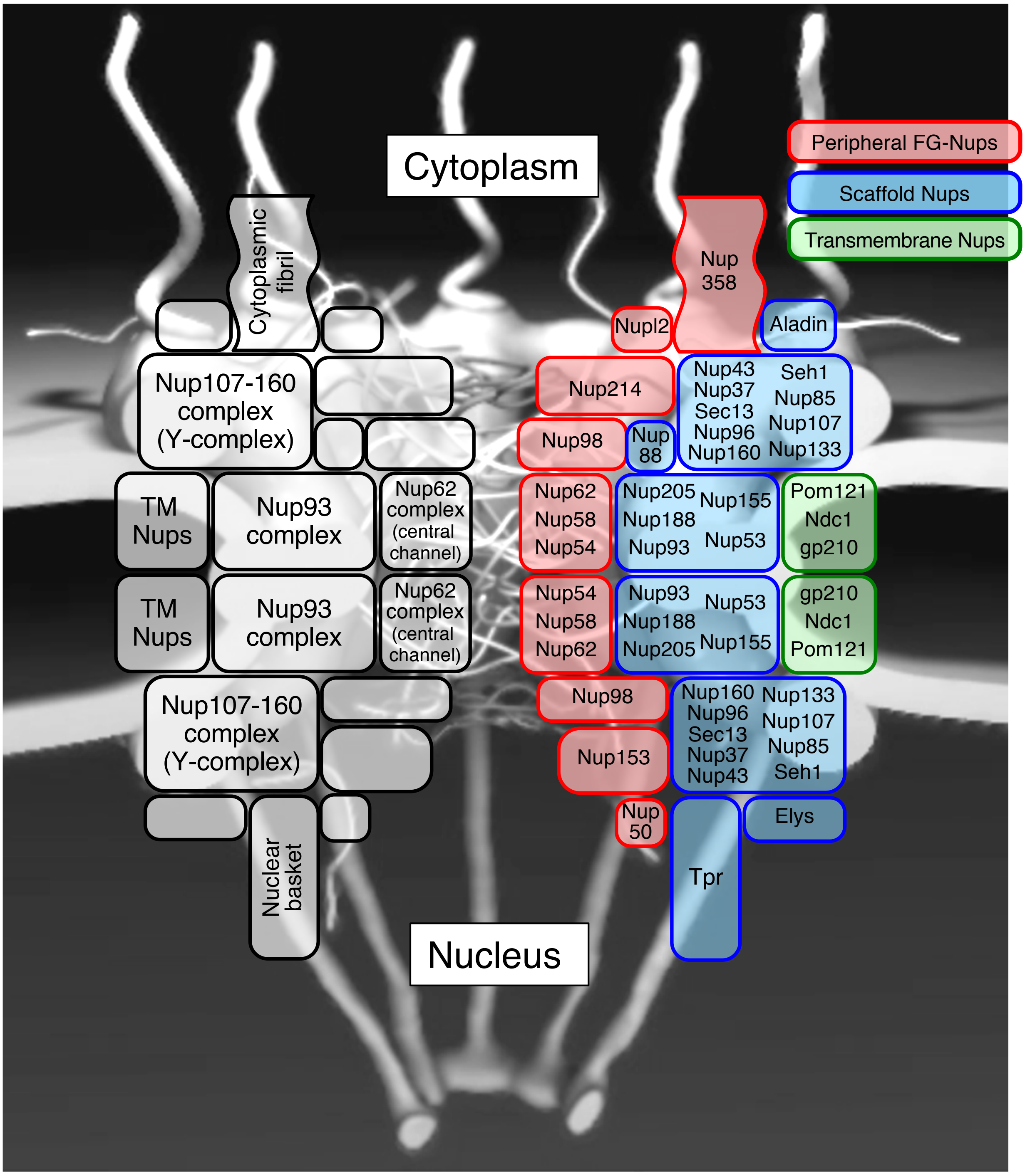

Fig. S1. A general model of the position and components of the major Nup subcomplex in human cells. The left half represents the position of the major subcomplex, and the right part represents the components contained in each subcomplex. Each box represents a subcomplex. Red, blue, and green boxes represent subcomplexes containing peripheral FG-, scaffold, and transmembrane Nups, respectively.

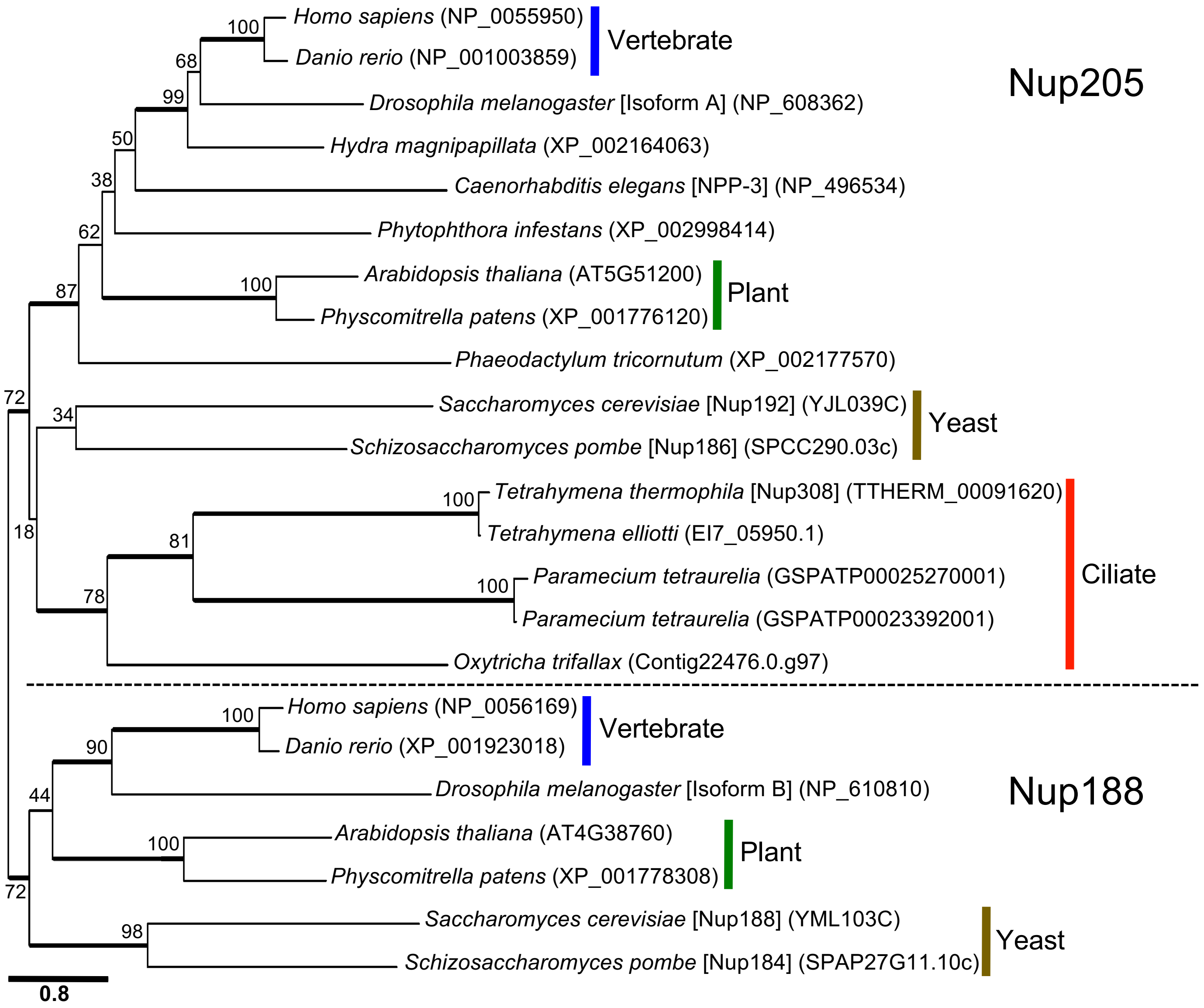

Fig. S2. Molecular phylogenetic tree of ciliate Nup308 with Nup205 and Nup188 family proteins. The amino acid sequences of the assumed orthologs of Nup205 and Nup188 were obtained from Genbank or the databases for each species. Accession numbers of the proteins are shown in parentheses. The sequences were aligned using Muscle in the MEGA 5.0.5 suite (Tamura, K. et al., *Mol. Biol. Evol.* 28, 2731-2739, 2011). All gap regions in the alignments were eliminated for phylogenetic tree reconstruction. The best substitution model and optional parameters were evaluated with Aminosan (Tanabe, A. S., *Mol. Ecol. Resour.* 11, 914-921, 2011) equipped with Treefinder (Jobb, G. et al., *BMC Evol. Biol.* 4, 18, 2004). The maximum likelihood phylogenetic relationships were reconstructed with RAxML (Ver. 7.3.0) (Stamakakis, *Bioinformatics*, 22, 2688-2690, 2006). To evaluate the bootstrap values, 1,000 replicated trees were reconstructed with the same model as performed in the original analyses. The bootstrap values are presented on every node. Bar represents expected amino acid residue substitutions per site.

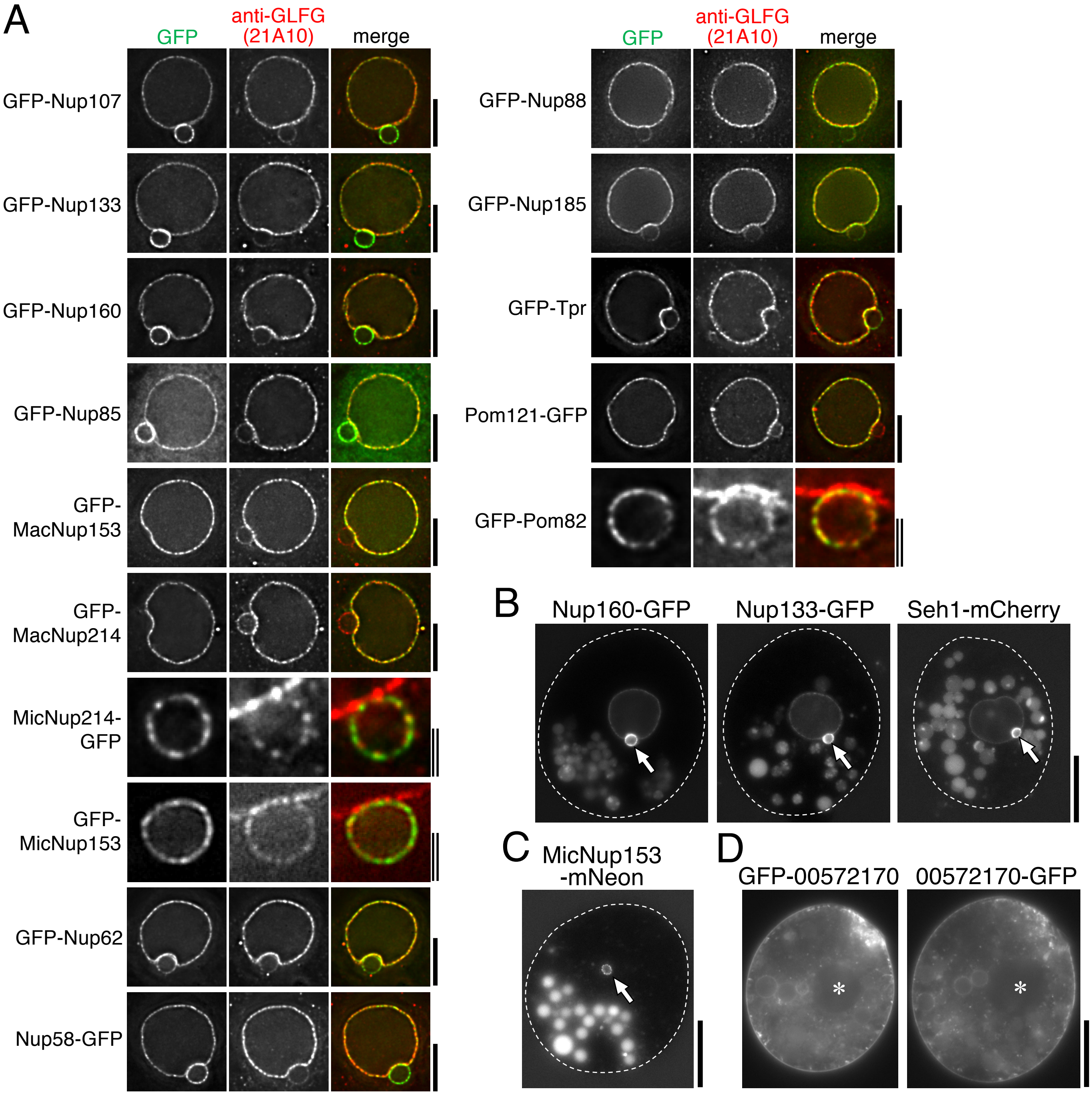

Fig. S3. Localization of *Tetrahymena* Nups tagged with fluorescent proteins. (A) Co-localization of fluorescent protein-tagged Nups with known GLFG-repeat-bearing Nups. The cells expressing GFP-tagged Nups were subjected to immunofluorescence staining using anti-GLFG antibody 21A10 that recognizes mainly MacNup98A localized to the MAC and secondarily some other components localized to the MIC NPC (Iwamoto et al., 2013). The images show GFP-tagged Nups (left panels), known Nups stained with anti-GLFG antibody (middle panels), and merged (right panels; GFP in green and anti-GLFG in red). The MAC and MIC regions are indicated for each Nup except for MicNup214-GFP, GFP-MicNup153, and GFP-Pom82, in which only MICs were indicated as enlarged images. Single lined bars, 5 µm; double lined bars, 2 µm. (B) Images show localization of endogenously GFP-tagged Nups at the C-termini expressed under the control of their native promoters (see Materials and Methods).

White broken lines represent the borders of cells. Arrows indicate the position of the MIC. Bar, 20 µm. (C) The image shows the localization of MicNup153, tagged with mNeon at its C-terminus, expressed under the control of its native promoter. An arrow indicates the position of the MIC. (D) The Ndc1-like protein TTHERM_00572170 tagged with GFP at the N- (GFP-00572170) or C-termini (00572170-GFP) was expressed under over expression condition. Asterisks show the position of the MAC. Bar, 20 µm.

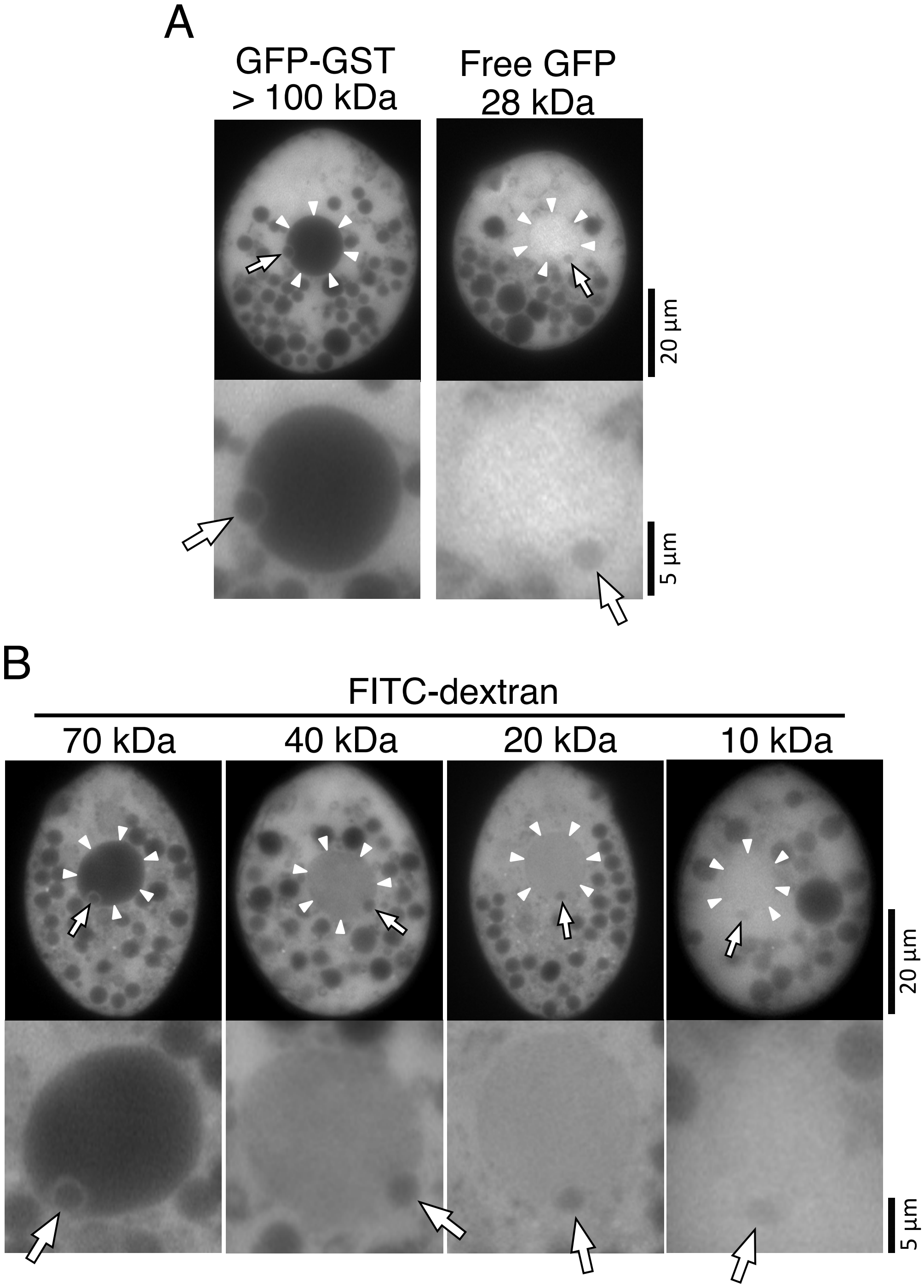

Fig. S4. MAC and MIC exhibit different exclusion sizes regarding nuclear pore permeability. (A) A living *T. thermophila* cell expressing GFP-GST or free GFP is shown in each upper panel. Nuclear regions are enlarged in the lower panels. White triangles indicate the edge of the MAC, and arrows indicate the position of the MIC. (B) Living *T. thermophila* cells into which FITC-dextran of various molecular weights was introduced. The cells were suspended in FITC-dextran (70, 40, 20, or 10 kDa) dissolved at 10 mg/ml in 10 mM Tris-HCl (pH 7.5). Then, the cell suspension was subjected to electroporation at a voltage of 0.1 kV with a capacitance of 0.05 mF. After electroporation, cells were incubated for 30 min at room temperature, and washed with 10 mM Tris-HCl (pH 7.5) three times. The cells were observed by a DeltaVision fluorescence microscopy system as described in Materials and methods. Similar results were obtained in all of three replicated experiments. Typical cells were presented from several hundred cells exhibiting similar nuclear/cytoplasmic fluorescence distribution.

Table S1. Nuclear pore complex proteins of *T. thermophila* and other species

Tetrahymena thermophila	*Trypanosoma brucei*	*S. cerevisiae*	*S. pombe*	*H. sapiens*	*A. thaliana*
--	--	--	--	Nup358/RanBP2	--
MacNup214 (TTHERM_00755929) **MicNup214 (TTHERM_00992810)**	TbNup149, TbNup140	Nup159	Nup146	Nup214/CAN	Nup214
Nup88 (TTHERM_00455610)	TbNup76	Nup82	Nup82	Nup88	Nup88
--	--	Gle1	Gle1	GLE1	GLE1
--	--	Nup42/Rip1	Amo1	hCG1	CG1
MacNup98A (TTHERM_00071070) MacNup98B (TTHERM_000293459) MicNup98A (TTHERM_01080600) MicNup98B (TTHERM_00530720N)	TbNup158	Nup145N, Nup116, Nup100	Nup189N	Nup98	Nup98a, Nup98b
--	--	Gle2	Rae1	RAE1	RAE1
Nup160 (TTHERM_00445990)	TbNup152	Nup120	Nup120	Nup160	Nup160
Nup133 (TTHERM_00486439)	TbNup132, TbNup109	Nup133	Nup132, Nup133	Nup133	Nup133
Nup107 (TTHERM_00037020)	TbNup89	Nup84	Nup107	Nup107	Nup107
Nup96 (TTHERM_00530720C)	TbNup158	Nup145C	Nup189C	Nup96	Nup96
Nup85 (TTHERM_01028760)	TbNup82	Nup85	Nup85	Nup85	Nup75
Seh1 (TTHERM_00954180)	--	Seh1	Seh1	Seh1	Seh1
Sec13 (TTHERM_00194320)	TbSec13	Sec13	(Sec13)	Sec13	Sec13
--	--	--	Nup37	Nup37	--
--	TbNup41	--	--	Nup43	Nup43
Nup308 (TTHERM_00091620)	TbNup225, TbNup181	Nup192	Nup186	Nup205	Nup205
		Nup188	Nup184	Nup188	--
Nup155 (TTHERM_00760460)	TbNup144, TbNup119	Nup170, Nup157	Nup155	Nup155	Nup155
Nup185 (TTHERM_00755920)					
Nup93 (TTHERM_00622800)	TbNup96	Nic96	Nup97, Npp106	Nup93	Nup93a, Nup93b
--	TbNup65	Nup53, Nup59	Nup40	Nup53/MP-44	Nup35
Nup62 (TTHERM_01122680)	TbNup62, TbNup53a, TbNup53b	Nsp1	Nsp1	Nup62	Nup62
Nup58 (TTHERM_00194800)		Nup49	Nup45	Nup58	Nup58
Nup54 (TTHERM_00189060)		Nup57	Nup44	Nup54	Nup54
MacNup153 (TTHERM_00379010) **MicNup153 (TTHERM_00647510)**	TbNup98(?)	Nup1	Nup124	Nup153	Nup136
Nup50 (TTHERM_00260700)	TbNup64(?), TbNup75(?)	Nup2	Nup61	Nup50	Nup50a, Nup50b
--	--	Nup60	Nup60	--	--
Tpr (TTHERM_00268040)	TbNup110, TbNup92	Mlp1, Mlp2	Nup211	TPR	Tpr/NUA
(Ndc1 (TTHERM_00572170))	--	Ndc1	Cut11	NDC1	--
Pom121 (TTHERM_00312730)	--	--	--	POM121	--
Pom82 (TTHERM_00375160)	--	--	--	--	--
gp210 (TTHERM_00101160)	--	Pom152	Pom152	GP210/Nup210	gp210
--	--	Pom34	Pom34/Mug31	--	--
--	--	--	Ely5	ELYS	(Elys/HOS1)
--	TbNup48	--	--	Aladin	ALADIN

Tetrahymena Nups shown in bold letters are those newly found in this study. Red and blue indicate MAC- and MIC-specific Nups, respectively. A question mark in parentheses indicates an unclear classification. Nup names in parentheses indicate that their NPC localization has not been experimentally confirmed. Two names shown with a slash represent synonyms. Nups of *T. brucei*, *S. cerevisiae*, *S. pombe*, *H. sapiens*, and *A. thaliana* are from the work of Obado et al. (PLOS Biol. 14, e1002365, 2016), Rout et al. (J. Cell Biol. 148, 635-651, 2000), Asakawa et al. (Nucleus 5, 149-162, 2014), Cronshaw et al. (J. Cell Biol. 158, 915-927, 2002), and Tamura et al. (Plant Cell 22, 4084-4097, 2010), respectively. .

Table S2. Proteins identified in co-precipitates with GFP-Nup93

#	Identified Proteins	Gene Model Identifier	Molecular Weight	Number of assigned spectra	
				GFP control	GFP-Nup93
1	Nup308	TTHERM_00091620	308 kDa	0	54
2	Nup93 (bait)	TTHERM_00622800	113 kDa	0	14
3	hypothetical protein	TTHERM_00471040	126 kDa	1	9
4	tubulin/FtsZ family, GTPase domain protein	TTHERM_00558620	50 kDa	0	8
5	Nup58	TTHERM_00194800	45 kDa	0	8
6	tRNA pseudouridine synthase	TTHERM_00095540	48 kDa	0	6
7	hypothetical protein	TTHERM_00148720	17 kDa	0	6
8	translation elongation factor EF-1alpha	TTHERM_00655820	48 kDa	0	4
9	hypothetical protein	TTHERM_00473020	48 kDa	0	4
10	ATP synthase F1, beta subunit	TTHERM_00585260	53 kDa	0	4
11	catalase heme-binding enzyme	TTHERM_01146030	56 kDa	0	3
12	Sm protein	TTHERM_00549650	86 kDa	0	2
13	hypothetical protein	TTHERM_00558350	35 kDa	0	2
14	carboxy-terminal crystallin fold protein 7p, putative	TTHERM_00516380	42 kDa	0	2

Table S3. Proteins identified in co-precipitates with GFP-Seh1

#	Identified Proteins	Gene Model Identifier	Molecular Weight	Number of assigned spectra	
				GFP control	GFP-Seh1
1	splicing factor 3B subunit 3	TTHERM_00530350	135 kDa	0	4
2	Sm protein	TTHERM_00549650	86 kDa	0	3
3	Pre-mRNA-splicing factor prp46	TTHERM_00684450	63 kDa	0	3
4	Nup85	TTHERM_01028760	86 kDa	0	3
5	small nuclear ribonucleoprotein	TTHERM_01403810	12 kDa	0	3
6	WD domain, G-beta repeat protein	TTHERM_00494570	70 kDa	0	3
7	patatin family phospholipase	TTHERM_00227880	41 kDa	0	2
8	Seh1 (bait)	TTHERM_00954180	42 kDa	0	2
9	peptidyl-prolyl cis-trans isomerase	TTHERM_00051740	20 kDa	0	2
10	hypothetical protein	TTHERM_00558350	35 kDa	0	2
11	G-quartet DNA-binding protein, putative	TTHERM_00499440	41 kDa	0	2
12	U2 snRNP auxilliary splicing factor	TTHERM_00525150	56 kDa	0	2
13	small nuclear ribonucleoprotein	TTHERM_00467959	11 kDa	0	2
14	squalene-tetrahymanol cyclase	TTHERM_01008630	76 kDa	0	2
15	hypothetical protein	TTHERM_00148720	17 kDa	0	2
16	surp module family protein	TTHERM_00013750	69 kDa	0	2
17	high mobility group (HMG) box protein	TTHERM_00660180	16 kDa	0	2
18	histone H4	TTHERM_00189170	11 kDa	0	1
19	tubulin/FtsZ family, GTPase domain protein	TTHERM_00558620	50 kDa	0	1
20	histone H2A	TTHERM_00790790	15 kDa	0	1
21	zinc knuckle protein	TTHERM_00444570	77 kDa	0	1
22	CC1 family splicing factor	TTHERM_00101150	61 kDa	0	1
23	hypothetical protein	TTHERM_00777260	35 kDa	0	1
24	SKIP/SNW domain protein	TTHERM_00942990	50 kDa	0	1
25	ISY1-like splicing family protein	TTHERM_00588910	38 kDa	0	1
26	amylo-alpha-1,6-glucosidase family protein	TTHERM_00128330	183 kDa	0	1
27	C2 domain protein	TTHERM_00225860	33 kDa	0	1
28	gp210	TTHERM_00101160	219 kDa	0	1
29	transmembrane protein, putative	TTHERM_00171720	85 kDa	0	1
30	granule lattice protein	TTHERM_00624730	41 kDa	0	1
31	transmembrane protein, putative	TTHERM_00242460	102 kDa	0	1
32	DnaJ carboxy-terminal domain protein	TTHERM_00101330	42 kDa	0	1

Table S4. Proteins identified in co-precipitates with GFP-Nup85

#	Identified Proteins	Gene Model Identifier	Molecular Weight	Number of assigned spectra	
				GFP control	GFP-Nup85
1	Nup85 (bait)	TTHERM_01028760	86 kDa	0	240
2	hypothetical protein	TTHERM_00530680	220 kDa	0	145
3	hypothetical protein	TTHERM_00565630	258 kDa	0	78
4	Seh1	TTHERM_00954180	42 kDa	0	35
5	Nup160	TTHERM_00445990	177 kDa	0	16
6	40S ribosomal protein S5	TTHERM_01386050	22 kDa	0	11
7	MicNup98B-Nup96	TTHERM_00530720	233 kDa	0	10
8	6-phosphofructokinase	TTHERM_00170320	60 kDa	0	10
9	transmembrane protein, putative	TTHERM_00532090	35 kDa	0	9
10	phosphate carrier protein	TTHERM_00535740	33 kDa	0	8
11	polyubiquitin	TTHERM_00346530	62 kDa	0	7
12	eukaryotic porin protein	TTHERM_00312720	41 kDa	0	7
13	Nup133	TTHERM_00486439	125 kDa	0	6
14	phosphoribosylaminoimidazole synthetase protein	TTHERM_00548120	37 kDa	0	6
15	6-phosphofructokinase	TTHERM_00338460	61 kDa	0	6
16	40S ribosomal protein S11, putative	TTHERM_01109770	18 kDa	0	5
17	40S ribosomal protein S2, putative	TTHERM_00193740	34 kDa	0	5
18	acetyl-CoA acyltransferase	TTHERM_00926980	56 kDa	0	4
19	ADP/ATP transporter on adenylate translocase	TTHERM_00052310	34 kDa	0	4
20	40S ribosomal protein S20	TTHERM_00992760	20 kDa	0	4
21	macronuclear actin	TTHERM_00190950	42 kDa	0	4
22	oxidoreductase, short chain dehydrogenase/reductase family protein	TTHERM_00024130	35 kDa	0	4
23	ribosomal protein S9	TTHERM_00706300	26 kDa	0	3
24	40S ribosomal protein S14	TTHERM_00765300	16 kDa	0	3
25	hypothetical protein	TTHERM_00991610	99 kDa	0	3
26	hypothetical protein	TTHERM_00571650	36 kDa	0	3
27	acyltransferase	TTHERM_00285610	41 kDa	0	3
28	transmembrane protein, putative	TTHERM_00885740	123 kDa	0	3
29	6-phosphofructokinase	TTHERM_00338470	74 kDa	0	3
30	eukaryotic porin protein	TTHERM_00117590	35 kDa	0	3
31	Sec13	TTHERM_00194320	39 kDa	0	2
32	40S ribosomal protein S24	TTHERM_00467660	17 kDa	0	2
33	hypothetical protein	TTHERM_00115400	131 kDa	0	2
34	40S ribosomal protein S18, putative	TTHERM_00131110	18 kDa	0	2
35	transmembrane protein, putative	TTHERM_00713350	11 kDa	0	2
36	Na,H/K antiporter P-type ATPase, alpha subunit family protein	TTHERM_00049030	136 kDa	0	2
37	60S ribosomal protein L28	TTHERM_00487140	21 kDa	0	2
38	3-hydroxyacyl-CoA dehydrogenase	TTHERM_00666640	33 kDa	0	2
39	catalase heme-binding enzyme	TTHERM_01146030	56 kDa	0	2
40	peptidase family S49 protein	TTHERM_00406670	32 kDa	0	2
41	transmembrane protein, putative	TTHERM_00127260	44 kDa	0	2

Table S5. Proteins identified in co-precipitates with GFP-Nup96.

#	Identified Proteins	Gene Medel Identifier	Molecular Weight	Number of assigned spectra	
				GFP control	GFP-Nup96
1	MicNup98B-Nup96 (bait)	TTHERM_00530720	233 kDa	0	129
2	Nup133	TTHERM_00486439	125 kDa	0	13
3	Nup160	TTHERM_00445990	177 kDa	0	12
4	Nup107	TTHERM_00037020	109 kDa	0	10
5	Serine/Threonine kinase	TTHERM_00992980	98 kDa	0	8
6	Sec13	TTHERM_00194320	39 kDa	0	7
7	D-hydantoinase family protein	TTHERM_00400750	112 kDa	0	6
8	gp210	TTHERM_00101160	219 kDa	0	5
9	Nup85	TTHERM_01028760	86 kDa	0	4
10	phosphoribosylaminoimidazole synthetase protein	TTHERM_00548120	37 kDa	0	4
11	40S ribosomal protein S11, putative	TTHERM_01109770	18 kDa	0	3
12	40S ribosomal protein S2, putative	TTHERM_00193740	34 kDa	0	2
13	ADP/ATP transporter on adenylate translocase	TTHERM_00052310	34 kDa	0	2
14	AAA family ATPase	TTHERM_00295050	127 kDa	0	2
15	hypothetical protein	TTHERM_00613630	67 kDa	0	2
16	60S ribosomal protein L5	TTHERM_00736480	34 kDa	0	2

Table S6. Proteins identified in co-precipitates with GFP-Nup185

#	Identified Proteins	Gene Model Identifier	Molecular Weight	Number of assigned spectra	
				GFP control	GFP-Nup185
1	Nup185 (bait)	TTHERM_00755920	185 kDa	0	380
2	Tpr	TTHERM_00268040	165 kDa	0	83
3	gp210	TTHERM_00101160	219 kDa	0	18
4	Serine/Threonine kinase	TTHERM_00992980	98 kDa	0	8
5	cyclic nucleotide-binding domain protein	TTHERM_00941370	148 kDa	0	5
6	hypothetical protein	TTHERM_00579030	117 kDa	0	4
7	acetyl-CoA acyltransferase	TTHERM_00926980	56 kDa	0	3
8	polyubiquitin	TTHERM_00346530	62 kDa	0	3
9	40S ribosomal protein S5	TTHERM_01386050	22 kDa	0	2
10	40S ribosomal protein S2, putative	TTHERM_00193740	34 kDa	0	2
11	D-hydantoinase family protein	TTHERM_00400750	112 kDa	0	2
12	hypothetical protein	TTHERM_00661740	34 kDa	0	2
13	papain family cysteine protease	TTHERM_00079610	37 kDa	0	2
14	peroxisomal 3-ketoacyl-CoA thiolase B	TTHERM_00899460	44 kDa	0	2
15	hypothetical protein	TTHERM_01014740	16 kDa	0	2
16	hypothetical protein	TTHERM_00048950	120 kDa	0	2
17	thioredoxin-dependent peroxide reductase	TTHERM_00295170	30 kDa	0	2
18	SURF1 family protein	TTHERM_00338280	47 kDa	0	2
19	50S ribosomal protein L4	TTHERM_00564280	42 kDa	0	2
20	hypothetical protein	TTHERM_00323030	66 kDa	0	2
21	cGMP-dependent kinase 5-1	TTHERM_00046530	90 kDa	0	2

Table S7. Primers used in this study

Target	Primer name	Primer direction	Sequence (5’→3’)
Nup85 cDNA	01028760_F(XhoI)	Fwd	CGCTCGAGATGATACCTGAAAACAATAAC
	01028760_R(ApaI)	Rev	CCGGGCCCTCATAATGTATAGCTGTTCATAAC
Nup160 cDNA	00445990_F(XhoI)	Fwd	GGCTCGAGATGGATAAAATGATAGAAGAATAAATATAGG
	00445990_R(ApaI)	Rev	CCGGGCCCTCATTCTACTTAAAATAGAGAAGC
Nup133 cDNA	00486439_F(XhoI)	Fwd	GGCTCGAGATGGATTAAGCATATAAGCAG
	00486439_R(ApaI)	Rev	CCGGGCCCTCAATTTGGAGAAAGTTTTTTTTTAGAAGTTGTC
Nup107 cDNA	00037020_F(XhoI)	Fwd	GGCTCGAGATGTAGAAATTAGACGCTAACAAAGTG
	00037020_R(ApaI)	Rev	CCGGGCCCTCATAAATTTAGTACAGTTCTC
MicNup214 GFP-tagging 5’ flanking sequence	186_5'/F(XbaI)	Fwd	CGTCTAGAACATTTAAAATTAATAACAGCAACC
	186_5'/R(BamHI)	Rev	CCGGATCCTCCTTAATTCATATTACAATTTTTAG
MicNup214 GFP-tagging 3’ flanking sequence	186_3'/F(SalI)	Fwd	GCGTCGACTTAAATATGAAATATTCCATAAGG
	186_3'/R(KpnI)	Rev	CCGGTACCATCGAAGGCATTATAAATCTATGTTCC
MicNup153 mNeon-tagging 5’ flanking sequence	00647510_5FWD_Sac	Fwd	AGGGAACAAAAGCTGGAGCTCGTCTTTAACATCAAAGTAAGCTT
	00647510_5REV3_dSacI	Rev	CGGCCGCCACCGCGGTGGCCTATTCTTTTACTGTTTTAATTATG
MicNup153 mNeon-tagging 3’ flanking sequence	00647510 3 FWD Xho	Fwd	TCGATACCGTCGACCTCGAGCACTATCCAAATTGATCATTTGAT
	00647510 3 REV Xho	Rev	GTACCGGGCCCCCCCTCGAGCAGTAAAAGTAATCTTGAGGATAC
MicNup153 cDNA	93.m00153/F(XhoI)	Fwd	GGCTCGAGATGAACTAGGCATATTAGTATTC
	93.m00153/R(ApaI)	Rev	GCGGGCCCTGACAAATCATATTCTTTTACTG
MacNup214 cDNA	00755920C_F(XhoI)	Fwd	CGCTCGAGATGTTCTCAAGTTAAGTATC
	00755920C_R(ApaI)	Rev	CCGGGCCCTCATTTTCTTGGTCTATAAAAAGC
MacNup153 cDNA	40.m00240/FWD/Xho	Fwd	GGCTCGAGATGGATAAGAATGGCTTTATAAAGCGTGACTTTGC
	40.m00240/REV/Apa	Rev	CCGGGCCCTCAAATTCTTTGCTTGTTATTTGTATTTTTTTTC
Nup62 cDNA	001122680_F(XhoI)	Fwd	GGCTCGAGATGTTCAATTAATAACAAGG
	001122690_R(ApaI)	Rev	GCGGGCCCTCAAATTTAGTCTGCAAC
Nup58 cDNA	00194800_F(XhoI)	Fwd	GGCTCGAGATGTCACTTTTTAATTAGAATTAAGGAG
	00194800_R2(KpnI)	Rev	CCGGTACCTTAGATTCTTTTTTCGTTTGGTTGC
Nup88 cDNA	00455610_F(XhoI)	Fwd	GGCTCGAGATGGAGAATAACCTTTTAGAATCAAG
	00455610_R(ApaI)	Rev	CCGGGCCCTCAATTATCTTGAGGATTGGTTTAAATGATC
Nup185 cDNA	00755920N_F(XhoI)	Fwd	CGCTCGAGATGGAGAATTTAGAGAGTAC
	00755920N_R(ApaI)	Rev	GCGGGCCCTCAAAAGTCTAATTAATAATATATGG
Tpr cDNA	00268040_F(XhoI)	Fwd	CGCTCGAGATGGATAGCAATTAAGCCGCAGAC
	00268040_R(ApaI)	Rev	CCGGGCCCTCAAATAAAAAGTCTAATCAAATCTTCG
Pom121 cDNA	30.m00269/F(XhoI)	Fwd	CGCTCGAGATGGAAAATTAGCAAGTAC
	30.m00269/R(ApaI)	Rev	CCGGGCCCTCATTATGTAGCACTCTCTG
	30.m00269/R2(KpnI)	Rev	GCGGTACCTGATTATGTAGCACTCTCTG
Pom82 cDNA	Pom82_F1(XhoI)	Fwd	ATCTCGAGATGAACGCCTAAAATAACAAC
	Pom82_R1(ApaI)	Rev	ATGGGCCCTCAGAAAAGCAATGAGCGGATT
Pom82ΔTM cDNA	Pom82_R2(ApaI)	Rev	ATGGGCCCTCAAAGCATATTCTTTTCTTTTAATAGATC
TTHERM_00572170 (Ndc1-like)	00572170_F2(XhoI)	Fwd	GGCTCGAGATGTTTGGTTTAAGTTTAAACTAAATAGC
	00572170_R(KpnI)	Rev	CCGGTACCATTATTTTTAGATTCACTTTCAGCC
	00572170_R2(ApaI)	Rev	CCGGGCCCTCAATTATTTTTAGATTCACTTTCAGCC
Nup160 GFP-tagging 5’ flanking sequence	Nup160_5F(SacI)	Fwd	CCGAGCTCTCATGAAGATGATTTAGCAGAGC
	Nup160_5R(BamHI)	Rev	CCGGATCCTTCTACTTAAAATAGAGAAGCAATTTGC
Nup160 GFP-tagging 3’ flanking sequence	Nup160_3F(SalI)	Fwd	CCGTCGACTAGAATGATTGGAAGTCCTCCAC
	Nup160_3R(KpnI)	Rev	CCGGTACCTTCAATTGATTTATGTAGTAACC
Nup133 GFP-tagging 5’ flanking sequence	Nup133_5F(SacI)	Fwd	CCGAGCTCATGTTTTAGAACGATGTGCTTAAATC
	Nup133_5R(BamHI)	Rev	CCGGATCCATTTGGAGAAAGTTTTTTTTTAGAAGTTGTC
Nup133 GFP-tagging 3’ flanking sequence	Nup133_3F(SalI)	Fwd	GCGTCGACAATGTTAATATTTGTTAATCCAAG
	Nup133_3R(KpnI)	Rev	CCGGTACCCTTTCCTATTTAATGGAGATATC
Seh1 mCherry-tagging 5’ flanking sequence	Seh1_5'/F(SacI)	Fwd	GCGAGCTCATACACGATATATCATTTGACTG
	Seh1_5'/R(NheI)	Rev	CCGCTAGCTTATTATTCTGAATCCTAAGTTTC
Seh1 mCherry-tagging 3’ flanking sequence	Seh1_3'/F(SalI)	Fwd	GCGTCGACATTGCATATTGAATGACTAACTG
	Seh1_3'/R(KpnI)	Rev	GCGGTACCTACGTACTTATTTACGTTATGCAG