Table S1- Single particle and tomographic data collection, processing and modeling of the yeast NPC
Related to Figures 1-6.

Data collection	Single particle		Cryo-ET		
Microscope	Titan-Krios-GIF		Titan-Krios-GIF		
Detector/Energy Filter Slit	K2 Summit		K2 Summit 20 keV		
Image mode	Super-resolution counting		Counting Dose-symmetric & bi-directional		
Frames	40	Frames per tilt image	12		
Total electron dose (e^-/Å^2)	40.0		~100-180		
Nominal pixel size (Å)	2.66		3.43		
Defocus range (µm)	-1.5 to -3.8		-3 to -5		
Movies (after triage)	4015 (3218)		293		
NPCs after cleaning	26049		518		
3D reconstruction	**Spoke**	**Double outer ring**	**Per-spoke**		
Symmetry imposed	C1	C1	C1		
Software	RELION 2.1, 3.0	RELION 2.1, 3.0	EMAN2		
Initial subunits/final particles	208393/145000	208393/45000	3656/3290		
Pixel size (Å)	--	3.99	3.37 (bin2- 6.74)		
Map resolution (Å)-masked FSC threshold 0.143	7.6	11.3	37 (spoke) 40 (C8 protomer)		
Local resolution range (Å)	6.6-11.0	11-17	30-60		
B-factor for sharpening (Å^2)	-423	-800 (ad hoc)	--		
Modeling					
Software-	Chimera, Coot, Phenix, MDFF	Chimera, Coot, MDFF	Chimera, Coot, MDFF		
NPC component	Full spoke	N-ring	Spoke	N-ring	C-ring + Nup82c-Dyn2
Ordered mass (MDa) /protomer	1.69	0.98	1.69	0.49	0.75
Number of proteins	28	14	28	7	19
Chimera map cross-correlation	0.915	0.952	0.9237	0.8750	0.8824