Supplemental Materials

Molecular Biology of the Cell

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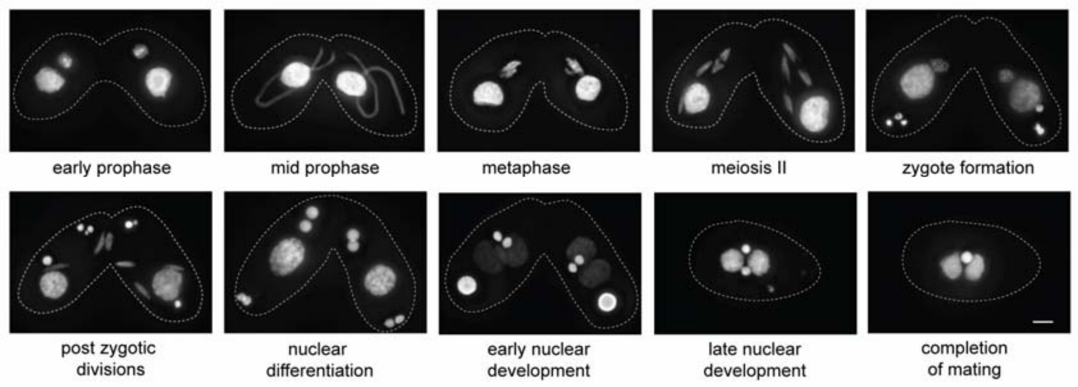

Figure S1. Cytology of mating *Tetrahymena* cells. Sexually reproducing cells undergo a synchronized meiosis and after zygote formation, the new progeny cells initiate the developmental program in two new SN. Prior to re-feeding, cells arrest with two SN and one GN. Scale bar, 5 µm.

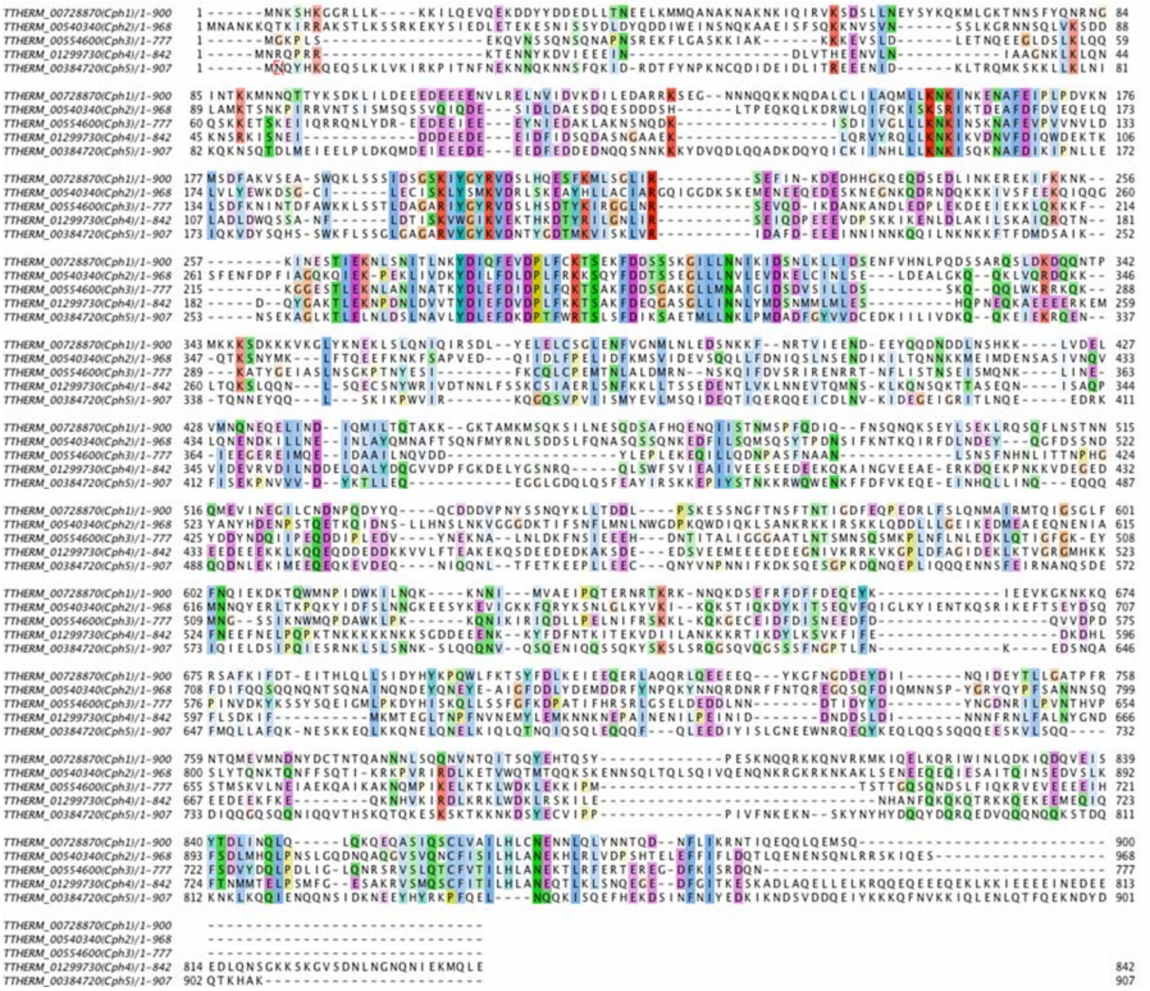

Figure S2. Multiple sequence alignment of *Tetrahymena* Cph proteins.Alignment was produced using the MUSCLE tool from EMBL-EBI (Edgar, 2004). The first 907 aa of Cph5 is shown aligned with the full length proteins of Cph1-4.

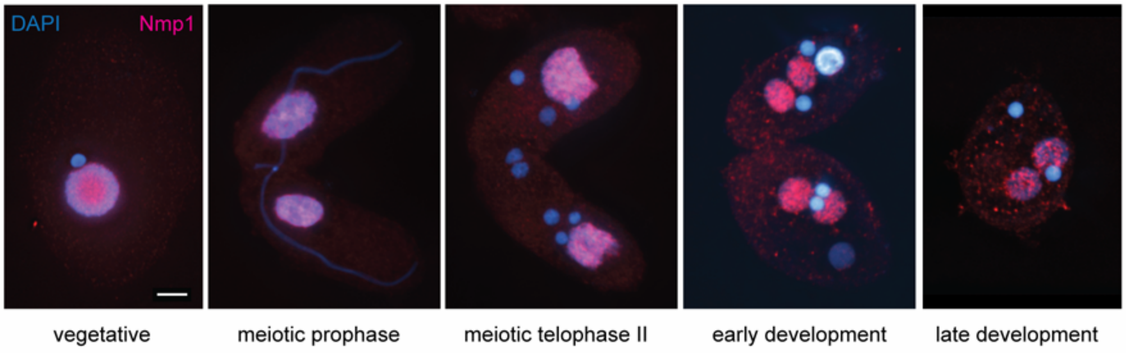

Figure S3. Nmp1 localizes to SN at all stages. Nmp1-HA (red) was visualized by immunostaining throughout development. Scale bar, 5 µm.

Table S1. Proteins associated with Nmp1[1].

Protein ID	Name/function	# peptides
TTHERM_00222270	Nmp1	505
TTHERM_00239400	SET domain protein	389
TTHERM_00310340	PHD zinc finger protein	301
TTHERM_00145290	Aap6, SAGA complex member	177
TTHERM_00384720	**Cph5**	108
TTHERM_00790730	Ada2, SAGA complex member	72
TTHERM_00668050	transmembrane protein, putative	49
TTHERM_00248390	Hat2, histoneacetyltransferase GCN5	29
TTHERM_00392760	**Cpd2**	25
TTHERM_00812950	**Smc2**	19
TTHERM_00242010	TRAF-type zinc finger protein	13
TTHERM_00049310	Chd3, SNF2 family amine-terminal protein	13
TTHERM_00475080	peptidase M1 family aminopeptidase	12
TTHERM_01146030	catalaseheme-binding enzyme	12
TTHERM_00257000	hypothetical protein	10
TTHERM_01093510	Scd6-like-Sm domain protein	10

[1] Condensin proteins are designated in bold text.

Table S2. Sequences of primers.

Epitope tagging

CAPD2stopRV-GFP	aagttcttcacccttagaaaccatggatccaaactcctcatcaaagtcatc
CAPD2-3'FW	atgggcccgagaagcctaaacccaaac
CAPD2-3'UTR-RV	tactcgaggccttttctcatattttgaacg
CAPD2-3'UTR-FW	cccgggggatctgaattcgatatcaagctttatatgtgtgaatgtctaaacaac
Brn5ctermFW	ctcgagtttttcagcaagatcttgagaagtattccatacc
Brn5stopRV	gaacatcataaggataggatccatctttaaagatataaaaattttatccttc
Brn5_3FW	ggatctgaattcgatatcaagcttggaaacatctcatgtttaaataaatt
Brn5_3RV	ggagatcttctagaaagatgaagcatattggcaaatatttac
Nmp1ctermFW	ctcgagtttttcagcaagatgcaagtttaaaatgtttaatcagaag
Nmp1stopRV	GAACATCATAAGGATAGGATCCttggttgttgttagaactgc
Nmp1_3FW	ggatctgaattcgatatcaagcttcgtgttagaaaagtattaattagcattg
Nmp1_3RV	ggagatcttctagaaagatcaaatttcctgaattcagagc

RNAi

CAPD2FWapa	atgggcccgtgaagctgatcctaaccg
CAPD2RVxho	tactcgagcatcaacagcaccaccttc
CAPD2FWpme	cgtttaaacgtgaagctgatcctaaccg
CAPD2RVxma	tacccgggcatcaacagcaccaccttc
Brn5ifwApa	atgggcccgatagatgaaggtgaaattgg
Brn5ifwPme	cgtttaaacgatagatgaaggtgaaattgg
Brn5irvXho	tactcgagcttttggaccagattcttgag
Brn5irvXma	tacccgggcttttggaccagattcttgag

CRISPR construct

CapD2Cas9T3s	agttgaagctcatcaaaataagaa
CapD2Cas9T3as	aaacttcttattttgatgagcttc
CapD2del11FW	gacgaagcagaaaggtaag
CapD2crisprSeqRV	ccacctgtattctttttgcc

IES PCR

Scc3 5'flankFW	gaaagaagattcttttggtg
Scc3 5'flankRV	caccaaaagaatcttctttc
Scc3 ies FW	gcttttaagtagttatccaac
M002	agcttaaacaaatgccatattgag
M1194	gtggggagggagaaggattcaac
55122451_FW	agcttttaagaaatagagaatgaataa
55122451_RV	tccatcgctttcataacttt
CapD2 3'UTR-FW	cccgggggatctgaattcgatatcaagctttatatgtgtgaatgtctaaacaac
CapD2 3'UTR-RV	tactcgaggccttttctcatattttgaacg
CapD2 ies RV2	cagggtttgagaaaacatgg
IES 7 MDSL-112	ggattgattggcataaatgga

IES 7 MDSR-158	aagcccagaataccgcagttc
IES 11 MDSL-42	gggcacaatatactaaggcaattt
IES 11 MDSR	gggcacgttgataccagttt

Supplemental data. Mass spectrometry data sets for immunoprecipitations of Cpd1-HA, Nmp1-HA, and Cpd2-HA. Sheet 1 includes data sets for samples prepared from vegetative WT cells and vegetative and 14 h mating cells expressing Cpd2-HA. Sheet 2 contains data from vegetative Cpd1-HA cells and 14 h Nmp1-HA, compared with vegetative or 14 h mating WT cells. Sheet 3 contains data from IPs of HA-Cph4 at 8 h of mating, compared with 8 h mating WT cells.