

Figure S1

Saci_1416	MADVNDFLRNWGRQEPTISEKIKNLFKSQQPLRYRLVMANYRLRTTISRLDVYISKLQE	60
Saci_0451	MTAIYILTMISKEFQKIWEGNQKVKIPKSKDPLKYRLVQAQYRVRSMLDVYIGRMQE	60
Nmar_0061	---MPNFDKTWARQETQSVTGKLEAVKPKGALKPRIQTAVNKLQVQISKMDSMLGKLHE	57
Nmar_0029	---MANLSNKWTKPPTTSITEKIGDTVKPKGALKPRVQEGVKRLRLQIQKLDKMLSGLKE	57
Nmar_0816	-----MLSNSWNNTGGESISQKVMGKVKPDEPLKNKIDFAQKKLQFQITKLEGINEKLRV	55
Saci_1373	-----MFDKLSIIFNSDR-----KRKVHLSKAITEISLKLKEQQDRLEAIRRLRE	46
Saci_1601	-----MKKRTIAELLTDIRMAKYKIDMWISKAEN	29
	: : :	
Saci_1416	RDRSLFEKVVESQISKDSARAAMYANEIAEIRKITKQLLTTEIALEQVQLRLETITEIGD	120
Saci_0451	RDKVLFERVVESQMSKDQSRAAMYANELAEIRKITKQLLTQIALEQVSLRLETVTTELGD	120
Nmar_0061	RDAQLFQRVVTAMQQHDTSTSRVLSNELAEIRKVTKMLGNARMSLEQVQLRLTTIHDLDG	117
Nmar_0029	RDEQLFARIVEATQKHDTQTSKVLGNELAEIRKVIKIMSSARVALEQIELRLTTFSDLGD	117
Nmar_0816	KHDQIFEKIVSAHKSNNKAYAQAYANELAQVRKMKNMMSGAKLSMEQVKLRDLTVSELGD	115
Saci_1373	RDKDLFEKVIRSQIEGDIARATIYAQEISDIRKMIKIIYTAYLAIEKVRLKLDTVQELQG	106
Saci_1601	RNK-ALERLSLSNIGRFPLLSKEYIKETELTRKYIVTLVQLKILLEILEIRLETIILGN	88
	:. : : : : * * : : * : : * . : .	
Saci_1416	IFTSLVPVIGVIRELRNVMKGVMPELSIELADLEEGLQEVVLEA-GEFTGARVDFATSSP	179
Saci_0451	IFANLIPVMGVINELKTSKGVMPELSIELGELGEGLQEIIVIEA-GEFSGVSGISATYSP	179
Nmar_0061	AMVAIGPAMSTMKGLKSSLGRFMPEADSELNTMTQTLNGLMMDS-LAGDSFNMESDVSSE	176
Nmar_0029	TVVAIMPTMGLMKNLKSSLGKVMPGAEEAIGQMAEMLGGFMTE-FSGDAAFGMDETTNA	176
Nmar_0816	VVVTLSPLMSIIKGLAPSLNGIMPEANASMQDLSSVLGDVMSSVDLDGDSMSGVPETNA	175
Saci_1373	VSLVLPVPMRILGELKEQVRGIAPEVALALDSITSSVNSIAIET-GALSEKTFVPTVADE	165
Saci_1601	VVTYLSPLVEALNELKGQLG-ASIEFSPIIDEIITETIRTVYIAP---NTVQQSPQINVKE	144
	: * : : * : : : . : .	
Saci_1416	EARKILDEASAVAEQRMKEKFPSLPSFATSVDQKTNANQK-----	219
Saci_0451	EARQILEEASVVAEQRMKEKFPSLPAAGITQQQS-----	214
Nmar_0061	ETEKILQEASAVAEQQIGDKFPSVPSSSTGLSSGTSTSTFE-----	216
Nmar_0029	ESDAILKEAAVAESSAGQMFPSVPTESAAST-ESTSKFY-----	215
Nmar_0816	DTLAILEEAQGVIAQT KASIPDVPDSL KQQIVEKKTDIFI-----	216
Saci_1373	QAKQIMEEAQKMAEVKV RELLPELPHPP SELPKRVAKQVQSSNKK LS EDMILNYIKTTG	225
Saci_1601	EARQLLKEAEDVAKKELKENYKIEI-----	169
	:: :. ** :	
Saci_1416	-----	
Saci_0451	-----	
Nmar_0061	-----	
Nmar_0029	-----	
Nmar_0816	-----	
Saci_1373	GFIDVDYIAKNFDVSKDEVFNVLRRLEEKGLIVLEG	261
Saci_1601	-----	

Figure S1: Multiple sequence alignment of the CdvB genes from *N. maritimus* and *S. acidocaldarius*.

Highly conserved and partially conserved residues are highlighted as asterisks and dots, respectively. CdvA binding site and MIM2 motif in Saci_1373 [7] are highlighted in red and purple, respectively. Putative MIM2 motif in Nmar_0816 is highlighted in blue (Figure S5). Cysteine residue in Nmar_0816 is highlighted in green. The multiple sequence alignment was performed using ClustalW2 program.

Figure S2

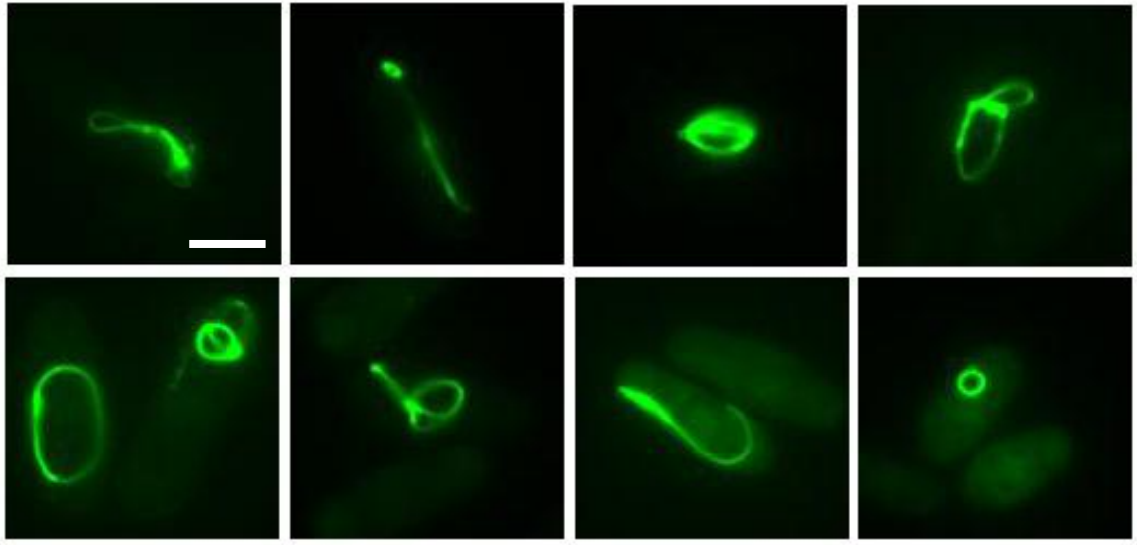
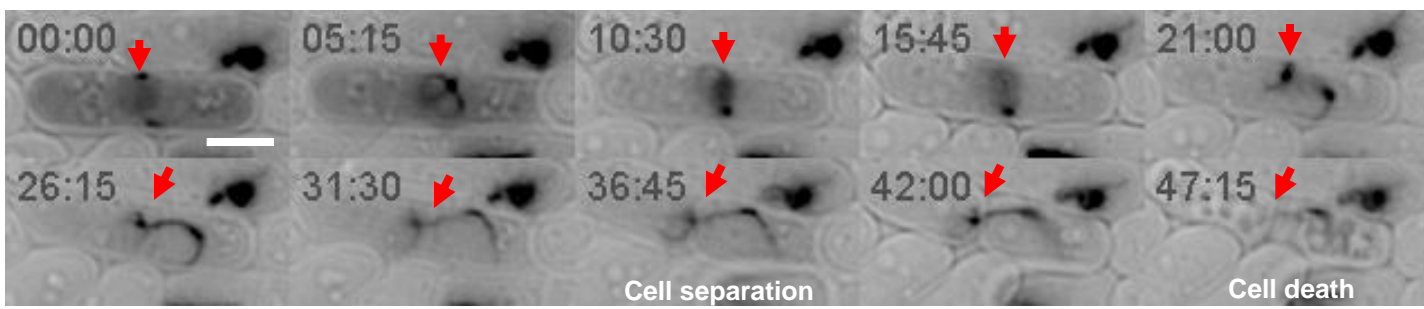


Figure S2: Nmar_0816 forms diverse polymeric structures in yeast

Images of yeast cells expressing Nmar_0816-GFP. Scale bar: 5 μm .

Figure S3

A



B

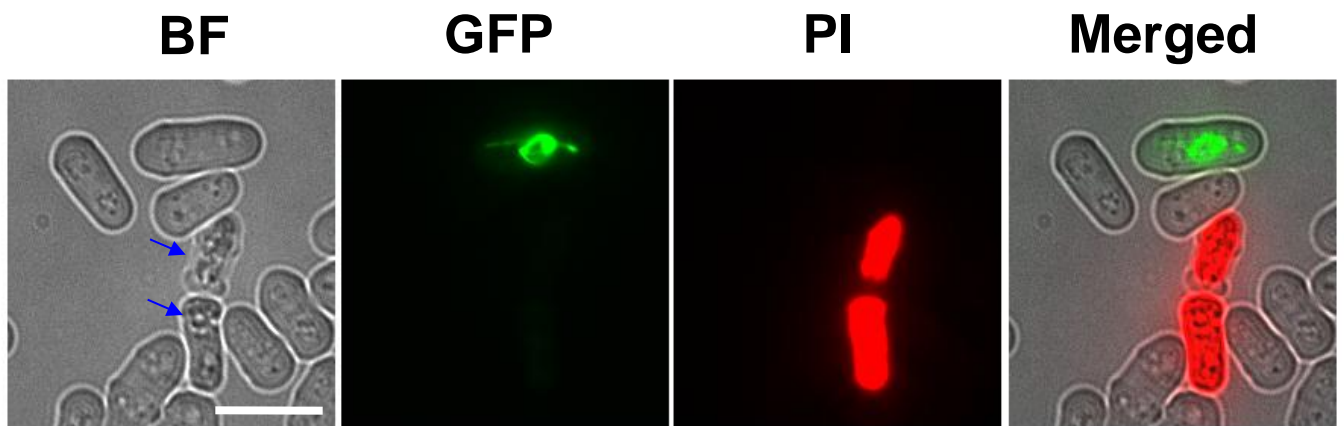


Figure S3: Failure to dissolve Nmar_0816 polymers during yeast cell division causes cell death.

(A) Time-lapse images of yeast cells expressing Nmar_0816-GFP polymers during cell division. Red arrows indicate mid-cell regions. Extensive cytosolic vacuolization of cells at the end of the cell division indicates cell death. Video S2. Scale bar: 5 μm . (B) Images of yeast cells expressing Nmar_0816-GFP and stained with 10 $\mu\text{g/mL}$ propidium iodide to reveal cell death. Blue arrows point to extensively vacuolated cells. BF: bright field; GFP: Nmar_0816-GFP; PI: propidium iodide staining. Scale bar: 10 μm .

Figure S4

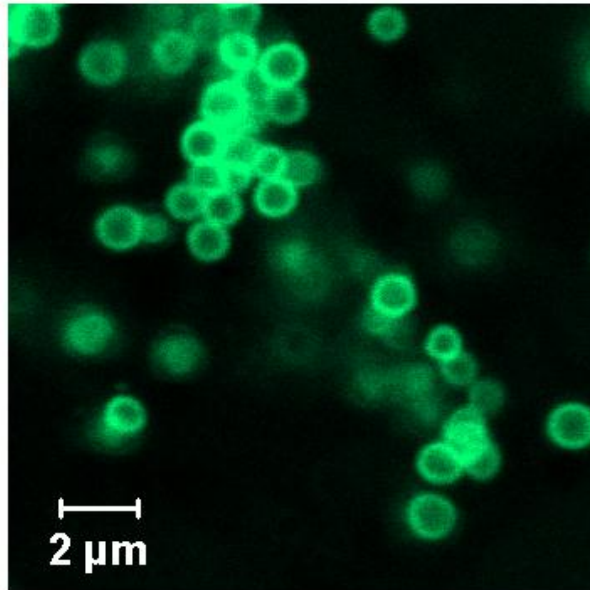


Figure S4: Nmar_0816 localizes to the rim of endosomes in NRK cells.

Image of NRK cells expressing GFP-Nmar_0816.

Figure S5

hvps20	---MGNLFGRKKQSRVTEQDKAILQLKQQRDKLRQYQKRIAQQQLERERALARQLLRDGRK	57
SpVps20	---MG-----VNSSKINDKDRSILSIKEQRDKLLRYSKRLEKIEQLEIDIARKCLRDSDK	52
hSnf7-1	MSGLGRLFGKGKKEKGPTPEEAIQKLKETEKILIKKQEFLQKIQQELQTAKKYGTK-NK	59
SpSnf7	MSGFLRWFG-GNRSKD-TTKDTIVRFQEMLALYDKKEEVLERQIAEQTEIARKNATT-NK	57
Nmar_0061	-----MPNFDKTWARQETQSVTGKLR EAVKPPQGALKPRIQTAVNKLQVQISKMDS	50
Nmar_0029	-----MANLSNKWTKPPTTSITEKIGDTVKPKGALKPRVQEGVKRLRLQIQKLDK	50
Nmar_0816	-----MLSNSWNNTGGESISQKVMGKVKPDEPLKNKIDFAQKKLQFQITKLEG	48
hvps24	---MGLFGKTQEKPPKELVNEWSLKIRKEMRVVDRQIRDIQREEEKVKRSVKDAAKKGQK	57
SpVps24	--MQTVRSYFFGPTPQEQRNKWQSIIRKEQRQLDRQVYHLKAGRKKADEVQLKLAKQSDI	58
	. : :	
hvps20	ERAKLLLLKKKRYQEQLLDRTENQISSLEAMVQSIEFTQIEMKVM EGLQFGNECLNMH QV	117
SpVps20	RGALRALKAKKLYSGLITQTYGQLGNIEQLLSTIEFTLIQKDV MFGLQEGTNLIRQLQAD	112
hSnf7-1	RAALQALRRKKRFEQQLAQTDGTLSTLEFQREAIENATTNAEVLRTMELAAQSMKKAYQD	119
SpSnf7	RLALTALKRKKMHENELVKIEGSRNNIEQQLFSIQANLN FETLQAMRQGAEAMKSIQRG	117
Nmar_0061	MLGKLHERDAQLFQRVVTAMQQH-DTSTSRVLSNELAEIRKVTKMLGNARMSLEQVQLRL	109
Nmar_0029	MLSGLKERDEQLFARIVEATQKH-DTQTSKVLGNELAEIRKVIKIMSSARVALEQIELRL	109
Nmar_0816	INEKLRVKHDQIFEKIVSAHKS-NKAYAQAYANELAQVRKMKNMVSGAKLSMEQVKLRL	107
hvps24	DVCIVLAKEMIRSRKAVSKLYASKAHMNSVLMGMKNQLAVLRVAGSLQKSTEVMKAMQSL	117
SpVps24	TNMRILAKEIARANRHGKRLAESKALLGSLSLQLNDQMAM LKIQGTMQSSTKIMQDVSSL	118
	: :	
hvps20	MSIEEVERILDETQEAVEYQRQIDELLAGSFTQ---EDED AILEELSAITQE Q-----	167
SpVps20	MPLERVGRICNDRDEAMS YVDEVNDMLQGRMSR---DQEDEIQEELDSLIREQEDEKVKD	169
hSnf7-1	MDIDKVDELMTDITEQQEVAQQISDAISRPMGFGDDVDEDELLEEELEEQEE-----	172
SpSnf7	MDADKVDQIMDKIRDQQTISEEISTMISTPVG LNAEIDEDELANELDELQQME-----	170
Nmar_0061	TTIHDLGDAMVAIGPAMSTMKGLKSSLGRFMPEAD-SELNTMTQT LNLGMMS-----	161
Nmar_0029	TTFSDLGDTVVAIMPTMGLMKNLKLSSLGKVMPGA E-AEIGQMAEMLGGFMTE-----	161
Nmar_0816	DTVSELGDVVVTLSPCMSIIKGLAPSLNGIMPEAN-ASMQD LSSVLGDVMSGSS-----	160
hvps24	VKIPEIQATMREL SKEMMKAGIIEEMLEDTFESMD--DQEEMEEEAEMEIDR-----	167
SpVps24	IRLPQLSETMRNLSMELTKAGVLEEMRDEMFLPVE--DDEELMDL ADEDEEVQEILT KYN	176
	: : . : .	
hvps20	IELP-----EVPSEPLPEKIP---ENVPVKARPRQAE LVAAS-----	201
SpVps20	LEKPGFTPSTGVDVLP SVPLKNAIPSLDESFPKAASVSNTSSAVVIDEELRKDPVLG	226
hSnf7-1	--LAQELLNVGDKEE EPSVKLPSPS--THLPAGPAP-KVDEDEEALKQLAEWS--	222
SpSnf7	--LDSKMLGA-EKPPVHTPAVPAVPSQVKDLPSISK PQELDEEEELRKLQAEFSL--	222
Nmar_0061	LAGDSFNMESDVSSEETEKILQEASAVAEQQIGDKFPSVPSSTGLSSGTSTSTFE--	216
Nmar_0029	FSGDAAFGMDETTNAESDAILKEAAVAESSAGQMFP SVPTESAAST-ESTSKFY--	215
Nmar_0816	VDLGDSMSVGPETNADTLAILEEAQGVIA GQTKASIPDVPDSLKQQIVEKKTDFI-	216
hvps24	ILFEITAGALGKAPSKVTDALPEPEPPGAMAASEDEEEEEEEALEAMQSRLATLRS--	222
SpVps24	VIPAPSEKAADAATHREOSLKOALPSLNGIAKDS TEIDEEQLLDIRDKLDALKS--	231

Figure S5: Multiple sequence alignment of the CdvB genes from *N. maritimus* and ESCRT-III genes from human and fission yeast.

Partially conserved residues are highlighted as dots. hSnf7-1, hVps24, and hVps20 shown here also known as CHMP4a, CHMP3, and CHMP6, respectively. The myristoylation site in Vps20 [8] is highlighted in red. The MIM2 motif in CHMP6 [6] is highlighted in green. The putative MIM2 of Nmar_0816 is highlighted in blue. The multiple sequence alignment was performed using ClustalW2 program.

Figure S6

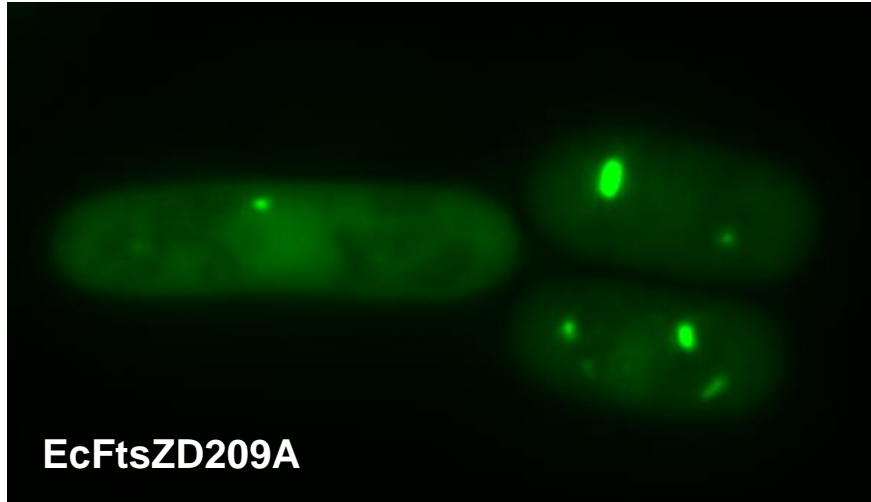


Figure S6: Expression of *E. coli* FtsZ mutant (D209A) in yeast.

Image of yeast cells expressing *E. coli* FtsZ-GFP carrying a mutation at T7 loop (EcFtsZD209A).