

Table S1 related to Figure 1 and Figure S1  
Top 105 genes required for proper inclusion formation

ORF	GENE	TTest(P-value manual)	Molecular function	Biological process	Component
1 YOR238W	YOR238W	0.02089	molecular_function	biological_process	cytoplasm
2 YOR154W	YOR154W	0.000107	molecular_function	biological_process	cellular_component
3 YOLO13W-A	YOLO13W-A	2.02E-05	molecular_function	biological_process	cellular_component
4 YNR073C	YNR073C	0.000176	mannitol dehydrogenase activity	biological_process	cellular_component
5 YNL058C	YNL058C	0.000331	molecular_function	biological_process	vacuole, cell cycle-correlated morphology
6 YMR247C	YMR247C	0.002598	ubiquitin-protein ligase activity	chromatin silencing at telomere*	nucleus*
7 YIR110W	YMR1	0.01017	phosphoric monoester hydrolase activity*	vesicle-mediated transport*	cytoplasm
8 YBR104W	YMC2	0.001048	organic acid transmembrane transporter activity	mitochondrial transport	mitochondrion
9 YLR422W	YLR422W	0.00015	molecular_function	biological_process	cytoplasm
10 YGR125W	YGR125W	4.42E-05	molecular_function	biological_process	vacuole, cell cycle-correlated morphology
11 YGR016W	YGR016W	0.004382	molecular_function	biological_process	cellular_component
12 YGL231C	YGL231C	0.000376	molecular_function	biological_process	endoplasmic reticulum
13 YGL159W	YGL159W	0.004296	molecular_function	biological_process	cellular_component
14 YEL023C	YEL023C	4.03E-06	molecular_function	biological_process	cellular_component
15 YDR333C	YDR333C	0.000125	molecular_function	biological_process	cytoplasm
16 YDR326C	YDR326C	0.001427	molecular_function	apoptosis	mitochondrion
17 YDR128W	YDR128W	9.11E-05	molecular_function	biological_process	membrane of vacuole with cell cycle-correlated morphology
18 YDR026C	YDR026C	0.006171	DNA binding	biological_process	nucleus*
19 YCR061W	YCR061W	7.48E-07	molecular_function	regulation of cell size	cytoplasm
20 YCL045C	YCL045C	0.023522	molecular_function	biological_process	endoplasmic reticulum
21 YBR216C	YBP1	0.000281	molecular_function	response to oxidative stress	cytoplasm
22 YAL002W	VP58	0.000656	molecular_function	late endosome to vacuole transport	membrane fraction*
23 YLO29C	VP553	0.046744	protein binding	Golgi to vacuole transport*	cytoplasm*
24 YDR080W	VP541	1.93E-08	Rab guanyl-nucleotide exchange factor activity	vacuole fusion, non-autophagic*	vacuole, cell cycle-correlated morphology*
25 YLR396C	VP533	2.7E-05	ATP binding	vacuole fusion, non-autophagic*	cytosol*
26 YDR089C	VP521	0.001097	GTPase activity*	endocytosis*	mitochondrion*
27 YPL045W	VP516	1.2E-05	molecular_function	protein targeting to vacuole*	membrane of vacuole with cell cycle-correlated morphology*
28 YHL035C	VMR1	0.002721	ATPase activity, coupled to transmembrane movement of substances	transport	mitochondrion*
29 YLR410W	VIP1	0.001919	inositol pyrophosphate synthase activity*	actin cytoskeleton organization and biogenesis*	cytoplasm
30 YLO077C	VAM6	0.000467	Rab guanyl-nucleotide exchange factor activity	telomere maintenance*	vacuole, cell cycle-correlated morphology*
31 VAC17	VAC17	0.0019	protein anchor	vacuole inheritance	vacuolar membrane
32 YLR386W	VAC14	0.000127	enzyme activator activity	vacuole inheritance*	membrane of vacuole with cell cycle-correlated morphology*
33 YFR010W	UBP6	0.001077	ubiquitin-specific protease activity	protein deubiquitination	proteasome regulatory particle (sensu Eukaryota)
34 YLD122W	UBP1	0.00518	ubiquitin-specific protease activity	protein deubiquitination	cytoplasm*
35 YBR082C	UBC4	0.000115	ubiquitin-protein ligase activity	sporulation (sensu Fungi)*	proteasome complex (sensu Eukaryota)
36 YDR074W	TPS2	9.19E-08	trehalose-phosphatase activity	response to stress*	mitochondrion*
37 YNL079C	TPM1	0.000475	actin lateral binding	pseudohyphal growth*	cellular bud neck contractile ring*
38 YDR320C	SWA2	0.012868	protein binding	telomere maintenance*	endoplasmic reticulum membrane
39 YPL106C	SSE1	1.8E-05	ATP binding*	telomere maintenance*	cytoplasm
40 YDL229W	SSB1	0.000655	ATPase activity*	translation*	soluble fraction*
41 YLO124C	SSA2	0.000883	ATPase activity*	response to stress*	cytoplasm*
42 YLD036W	SNK4	2.5E-06	phosphatidylinositol 3-phosphate binding*	protein targeting to vacuole	cytoplasm*
43 YHL025W	SNF5	0.000573	general RNA polymerase II transcription factor activity	chromatin remodeling	SWI/SNF complex*
44 YOR076C	SK07	0.000106	protein binding	mRNA catabolic process*	cytoplasm*
45 YPR189W	SKI3	3.77E-06	translation repressor activity	mRNA catabolic process*	cytoplasm*
46 YLR398C	SKI2	0.003328	RNA helicase activity*	mRNA catabolic process*	cytoplasm*
47 YOR035C	SHE4	0.001134	myosin binding	actin cytoskeleton organization and biogenesis*	cytoplasm
48 YIL076W	SEC28	1.15E-05	molecular_function	ER to Golgi vesicle-mediated transport*	endosome*
49 YBL011W	SC11	0.00017	glycerol-3-phosphate O-acyltransferase activity*	phospholipid biosynthetic process	endoplasmic reticulum
50 YOL067C	RTG1	0.002692	transcription coactivator activity	transcription initiation from RNA polymerase II promoter*	cytoplasm*
51 YLO020C	RPW4	0.000159	transcription factor activity*	telomere maintenance*	proteasome regulatory particle (sensu Eukaryota)
52 YHL023C	RM011	8.08E-06	molecular_function	biological_process	cellular_component
53 YLR039C	RIC1	0.01809	guanyl-nucleotide exchange factor activity	retrograde transport, endosome to Golgi*	nucleus*
54 YNL180C	RHO5	3.1E-06	GTPase activity	Rho protein signal transduction	cytoplasm*
55 YFL047W	RGD2	0.000566	Rho GTPase activator activity	small GTPase mediated signal transduction	cytoplasm*
56 YOL011W	PLB3	0.02531	lysophospholipase activity	phosphatidylserine catabolic process*	plasma membrane*
57 YMR123W	PKR1	2.59E-05	molecular_function	protein complex assembly	endoplasmic reticulum membrane
58 YBL051C	PRN4	0.004882	molecular_function	G2/M transition of mitotic cell cycle*	cytoplasm
59 YCR044C	PER1	0.014096	molecular_function	GPI anchor biosynthetic process*	endoplasmic reticulum*
60 YNL231C	PD816	0.000765	phosphatidylinositol transporter activity	response to drug*	cytoplasm*
61 YAL051W	OAF1	0.001472	DNA binding*	peroxisome organization and biogenesis*	nucleus
62 YNL297C	MON2	0.001237	guanyl-nucleotide exchange factor activity	endocytosis*	cytosol*
63 YLR320W	MMS22	0.009402	molecular_function	response to drug*	nucleus
64 YOR033W	MGA2	0.000244	transcription activator activity	positive regulation of transcription from RNA polymerase II promoter*	endoplasmic reticulum membrane
65 YKL168C	KKQ8	0.048241	protein kinase activity	biological_process	cytoplasm
66 YNL272C	JJJ1	0.000178	ATPase activator activity*	endocytosis*	cytoplasm*
67 YOL081W	IRA2	0.000372	Ras GTPase activator activity	response to stress*	cytoplasm*
68 YLR309C	IMH1	0.002189	molecular_function	vesicle-mediated transport*	cytosol*
69 YPL250C	ICY2	0.044959	molecular_function	biological_process	cellular_component
70 YNR072W	HXT17	3.56E-06	glucose transmembrane transporter activity*	hexose transport	plasma membrane
71 YFL027C	GYP8	0.002878	Rab GTPase activator activity	vesicle-mediated transport	intracellular
72 YDR108W	GS61	0.027575	molecular_function	ER to Golgi vesicle-mediated transport*	TRAPP complex
73 YDL035C	GPR1	0.000732	G-protein coupled receptor activity	pseudohyphal growth*	plasma membrane
74 YER020W	GPA2	0.025873	GTPase activity	sporulation (sensu Fungi)*	mitochondrion*
75 YNL252C	FGE4	0.041414	polyphosphoinositide phosphatase activity	cellular morphogenesis during conjugation with cellular fusion	membrane of vacuole with cell cycle-correlated morphology*
76 YFR019W	FAB1	0.029894	phosphatidylinositol 3-phosphate binding*	Golgi to vacuole transport*	mitochondrion*
77 YDR284C	DPP1	0.008009	phosphatidate phosphatase activity*	signal transduction*	membrane of vacuole with cell cycle-correlated morphology
78 YKL213C	DOA1	0.006477	ubiquitin binding	ubiquitin-dependent protein catabolic process*	cytoplasm*
79 YKR035W-A	DID2	0.000281	molecular_function	protein targeting to vacuole*	cytoplasm*
80 YGR092W	DBF2	0.01203	protein serine/threonine kinase activity	protein amino acid phosphorylation*	cellular bud neck*
81 YIL172W	CP51	0.000501	Gly-X carboxypeptidase activity	proteolysis*	vacuole, cell cycle-correlated morphology
82 YJR032W	CPR7	2.37E-06	unfolded protein binding*	response to stress	cytosol
83 YNL071C	COG8	0.002962	molecular_function	intra-Golgi vesicle-mediated transport	Golgi transport complex
84 YGL005C	COG7	0.000458	molecular_function	intra-Golgi vesicle-mediated transport	mitochondrion*
85 YNL041C	COG6	5.44E-06	molecular_function	intra-Golgi vesicle-mediated transport	Golgi transport complex
86 YNL051W	COG5	0.014216	molecular_function	intra-Golgi vesicle-mediated transport	Golgi transport complex
87 YAL058W	CNE1	0.003926	unfolded protein binding	protein folding*	integral to endoplasmic reticulum membrane
88 YFR014C	CMK1	0.004603	calmodulin-dependent protein kinase activity	protein amino acid phosphorylation*	cytoplasm
89 YIL034C	CAP2	0.002798	actin filament binding	filamentous growth*	actin cortical patch*
90 YKL007W	CAP1	0.000287	actin filament binding	barbed-end actin filament capping	actin cortical patch*
91 YBR048C	CAJ1	1.68E-06	chaperone regulator activity	biological_process	nucleus
92 YOL074C	BRE1	0.000402	ubiquitin-protein ligase activity	telomere maintenance*	nucleus
93 YLO115W	BPT1	0.002503	bilirubin transmembrane transporter activity*	cadmium ion transport*	membrane of vacuole with cell cycle-correlated morphology
94 YIL159W	BNR1	0.009039	cytoskeletal protein binding	actin filament organization*	cellular bud neck contractile ring
95 YPL161C	BEM4	0.00296	molecular_function	telomere maintenance*	cytoplasm*
96 YPL115C	BEM3	0.022488	phosphatidylinositol 3-phosphate binding*	pseudohyphal growth*	intracellular
97 YER155C	BEM2	0.006731	Rho GTPase activator activity	cell wall organization and biogenesis*	mitochondrion*
98 YBL069W	AST1	0.000744	molecular_function	protein targeting to membrane	extrinsic to membrane
99 YBR164C	AKL1	0.001586	GTPase activity	protein targeting to vacuole*	Golgi apparatus*
100 YLR370C	ARC18	0.006132	structural constituent of cytoskeleton	actin filament organization*	Arp2/3 protein complex
101 YOL062C	APM4	0.001185	molecular_function	vesicle-mediated transport*	AP-2 adaptor complex
102 YBR288C	APM3	3.94E-05	molecular_function	vesicle-mediated transport*	AP-3 adaptor complex
103 YPL259C	APM1	0.000123	clathrin binding	vesicle-mediated transport*	AP-1 adaptor complex
104 YBR059C	AKL1	9.14E-05	protein kinase activity	actin cytoskeleton organization and biogenesis*	cytoplasm*
105 YMR092C	AUP1	8.05E-05	actin binding	response to osmotic stress*	cytoplasm*