

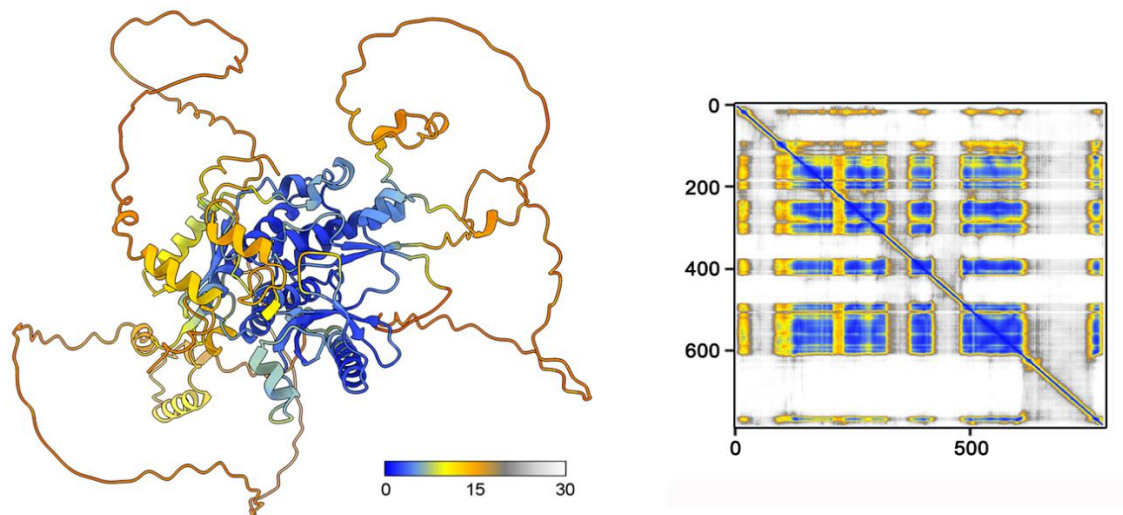
A type II phosphatidylinositol-4-kinase coordinates sorting of cargo polarizing by endocytic recycling

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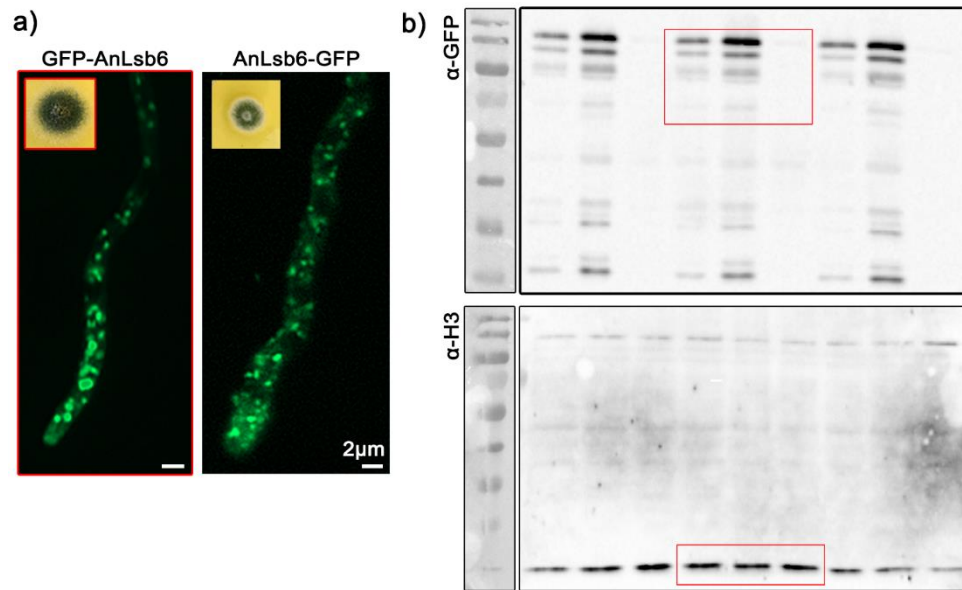
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Supplementary Material



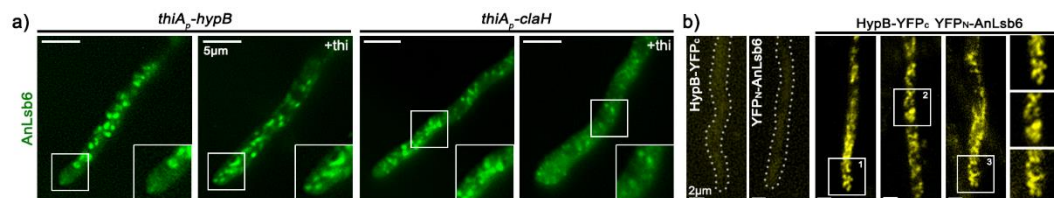
Supplementary Figure 1

Model of AnLsb6 generated with AlphaFold2 (left panel), colored based on Predicted Aligned Error (PAE). The plot of pairwise PAE values per residue is shown on the right panel. Notice the very high model confidence in the area predicted as the PI3/4 kinase domain (see also Figure 1a).



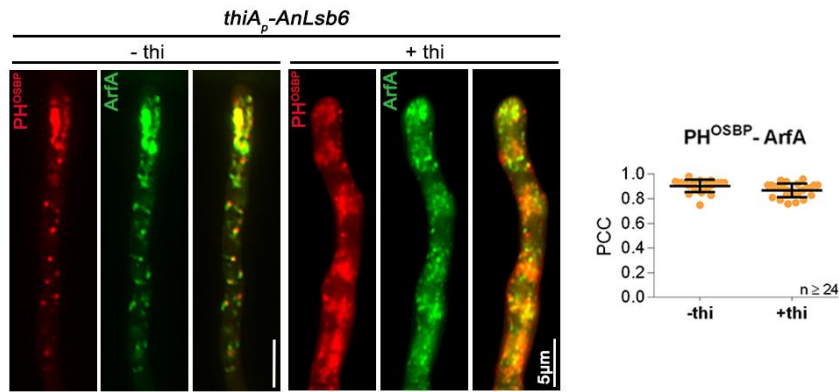
Supplementary Figure 2

a Comparison of N- and C-terminal GFP-tagged versions of ANLsb6. The image of GFP-AnLsb6 and the embedded growth test (highlighted with a red stroke) were also used in Figure 1B and 1C. **b** Uncropped images of the western blots. The cropped areas shown in Figure 1B are highlighted with a red stroke. The protein ladder PageRuler™ Plus (Thermo Fischer Scientific) is also shown for orientation.



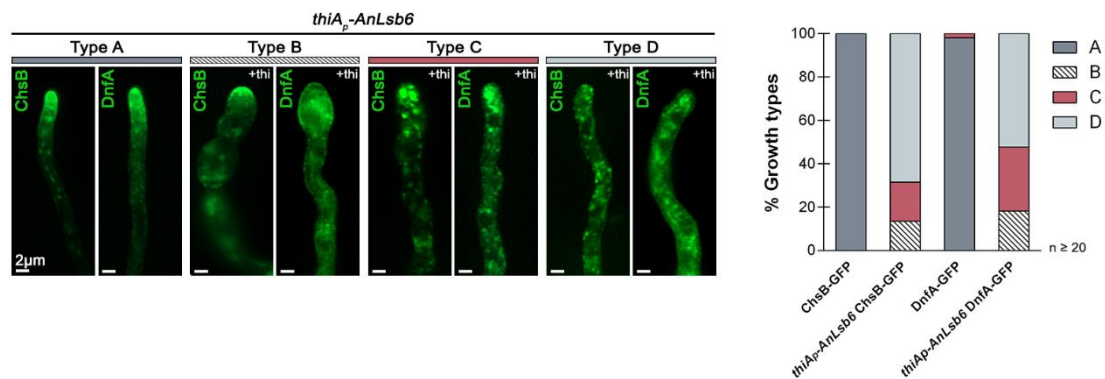
Supplementary Figure 3: AnLsb6 associates with other essential post-Golgi partners.

a Distribution of AnLsb6 at conditions of HypB^{SEC7} and ClaH repression (+thi) in isogenic strains carrying in locus thiamine-repressible alleles of *thiA_p-hypB* and *thiA_p-claH* compared to wt conditions (-thi). Notice the shift of AnLsb6 towards the hyphal apex under *hypB*-repressed conditions and the dis-organization of fluorescent polarized structures to scattered spots and cytoplasmic haze when clathrin ClaH is depleted, suggesting that a significant part of AnLsb6 is operating downstream of ClaH. **b** Bimolecular fluorescence (BiFC) analysis in strains carrying AnLsb6 and HypB^{SEC7} tagged with N-terminal YFP_N and YFP_C, driven under the thiamine promoter *thiA* and the native *hypB* promoter, respectively. Fluorescence signals from single strains expressing either the YFP_N-AnLsb6, or HypB-YFP_C are shown as controls.



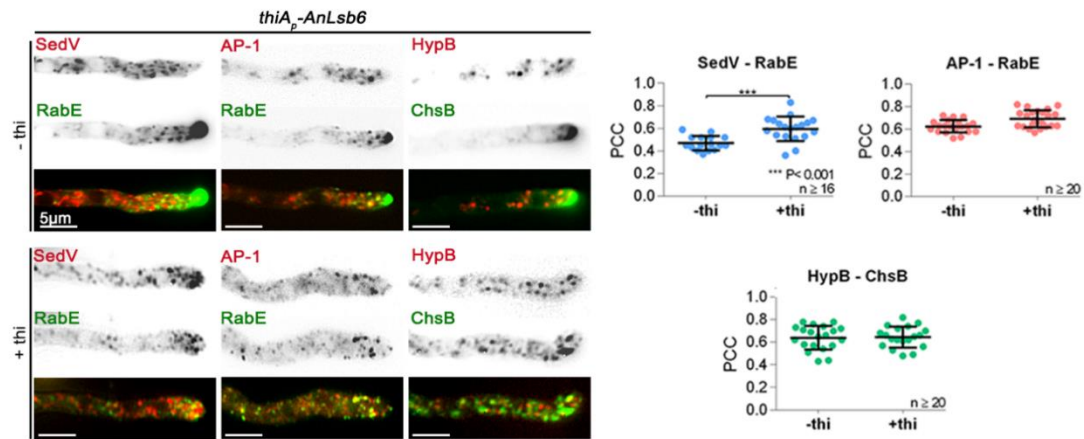
Supplementary Figure 4

Colocalization of PH^{OSBP} with ArfA^{ARF1} at conditions where AnLsb6 is expressed (-thi) or repressed by thiamine (+thi) (left panel), and quantification of PCC (right panel; PCC -thi = 0.91±0.05, P<0.0001, n=24; PCC +thi = 0.87±0.05, P<0.0001, n=27). Raw data on the quantification of co-localization by calculating Pearson's Correlation Coefficient (PCC) are given in Supplementary Data 4. Error bars represent SD.



Supplementary Figure 5

Types of hyphal morphology and subcellular localization of the chitin synthase ChsB and the phospholipid flippase DnfA, observed and quantified under conditions where AnLsb6 is expressed or repressed by thiamine (+thi) (Type A, Dark gray; Type B, Diagonal line pattern; Type C, Dark pink; Type D: Light gray). Raw data on the quantification of growth are given in Supplementary Data 6 (ChsB-GFP, n=20; thiA_p-AnLsb6-GFP n=111; DnfA-GFP n=42; thiA_p-AnLsb6-GFP n=88).



Supplementary Figure 6

Colocalization and relative quantification of GFP- or mRFP/mCherry-tagged protein cargos under conditions where AnLsb6 is expressed (-thi) or repressed by thiamine (+thi). Quantification of colocalization was performed in subapical areas only, for the condition -thi. Notice that, with the exception of the early Golgi marker SedV^{SED5} and the GEF HypB^{SEC7}, the fluorescence signal of all other proteins appears to overlap significantly at regions closer to the hyphal apex. Raw data on the quantification of co-localization by calculating Pearson's Correlation Coefficient (PCC) are given in Supplementary Data 7 (SedV-RabE: -thi n=16, +thi n=18; AP-1-RabE: -thi n=20, +thi n=23; HypB-ChsB: -thi n=20, +thi n=20). Error bars represent SD. See Methods for statistical analysis and statistical tests used.

Supplementary Table 1. Strains used in this study. All *A. nidulans* strains carry the *veA1* mutation affecting sporulation. *pabaA1*, *pyroA4*, *riboB2*, *argB2*, *pyrG89*, *pantoB100*, *biA1*, *nicA2* and *inoB2* are auxotrophic mutations for p-aminobenzoic acid, pyridoxine, riboflavin, arginine, uracil/uridine, D-pantothenic acid, nicotinic acid, biotin and inositol respectively. *yA2* and *wA4* are mutations resulting in yellow and white conidiospore colors respectively. *niiA4* is a loss of function mutant of the nitrite reductase. The *bar* gene encodes glufosinate resistance. *nkuAΔ* reduces the frequency of nonhomologous integration of transforming DNA fragments, improving gene targeting. 5xGA stands for a 5x Gly-Ala linker fused between ORF and the relevant tag. *ura3Δ0 leu2Δ0 his3Δ1 met15Δ0* are *S. cerevisiae* auxotrophic mutations for uracil, leucine, histidine and methionine, respectively.

Strain	Genotype	Reference
TNO2A7	<i>nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	6
mRFP-PH ^{OSBP}	<i>pyroA4[pyroA::gpdA^m::mRFP-PH^{OSBP}] inoB2 niiA4 wA4</i>	7
mCherry-sedV	<i>pyroA4[pyroA^{mut}::gpdA^m-mCherry-sedV] nkuAΔ::bar, wA4, niiA4 inoB2</i>	8
abpA-mRFP	<i>abpA-mRFP::AFpyrG yA2 pabaA1 pyrG89</i>	1
claL-GFP	<i>claL^(5xGA)GFP::AFpyrG nkuAΔ::argB pyroA4 riboB2 pyrG89</i>	4
claH-GFP	<i>claH^(5xGA)GFP::AFpyrG nkuAΔ::argB pyroA4 riboB2 pyrG89</i>	4
claH-mRFP	<i>claH^(5xGA)mRFP::AFpyroA nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	2
GFP-chsB	<i>GFP-chsB::AFpyrG nkuAΔ::argB pyroA4 riboB2 pantoB100</i>	2
dnfA-GFP	<i>dnfA-GFP::AFpyrG nkuAΔ::argB pyrG89 pabaA1 pyroA4</i>	10
mCherry-synA	<i>fwA1 pyrG89 pyroA4 nicA2 nkuAΔ::argB AFpyG-mCherry-synA yA::AFpyroA tpmAp-GFP-tpmA fwA1 nicA2</i>	11
GFP-PH ^{PLC6}	<i>[gpdA-GFP-PH^{PLC6}]-argBmut::argB2 pabaA1 yA2</i>	7
uapA-GFP	<i>uapAΔ::uapA-GFP::AFriboB uapCΔ::AFpyrG nkuAΔ::argB pabaA1 pyroA4 riboB</i>	3
GFP-rabE	<i>GFP-RabE::AFpyrG nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	4
ap1σ-GFP	<i>ap1σ^(5xGA)GFP::AFpyrG nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	5
thiA _p -hypB	<i>thiAp-hypB::AFpyrG nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	2
thiA _p -claH	<i>thiAp-claH::AFpyroA nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	4
thiA _p -rabA rabBΔ	<i>thiA_p-rabA::AFpyroA rabBΔ::AFpyrG nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	2
arfA-GFP	<i>arfA-(5xGA)GFP::AFpyrG nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
hypB-mScarlet	<i>hypB^(5xGA)mScarlet::AFriboB nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
gga2-GFP	<i>gga2^(5xGA)GFP::AFpyrG nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
Anlsb6Δ	<i>Anlsb6Δ::AFpyrG nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
thiA _p -Anlsb6	<i>thiAp-Anlsb6::AFpyrG nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
thiA _p -FLAG-Anlsb6	<i>thiApFLAG-Anlsb6::AFpyrG nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
thiA-GFP-Anlsb6	<i>thiAp-GFP-Anlsb6::AFpyrG nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
GFP-Anlsb6	<i>GFP-Anlsb6::AFpyrG nkuAΔ::argB pyroA4 riboB2 pyrG89</i>	this study
Anlsb6-GFP	<i>Anlsb6^(5xGA)GFP::AFpyrG nkuAΔ::argB pyroA4 riboB2 pyrG89</i>	this study
GFP-Anlsb6 mRFP-PH ^{OSBP}	<i>GFP-Anlsb6::AFpyrG [pyroA::gpdAmp-mRFP-PH^{OSBP}]pyroA4 inoB2</i>	this study
GFP-Anlsb6 mCherry-sedV	<i>GFP-Anlsb6::AFpyrG pyroA4::[pyroA::gpdAmp-mCherry-sedV] nkuAΔ::argB inoB2</i>	this study
GFP-Anlsb6 ArfA-mRFP	<i>GFP-Anlsb6::AFriboB arfA^(5xGA)mRFP::AFpyrG nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
GFP-Anlsb6 HypB-mScarlet	<i>GFP-Anlsb6::AFpyrG hypB^(5xGA)mScarlet::AFriboB nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
GFP-Anlsb6 ClaH-mRFP	<i>GFP-Anlsb6::AFpyrG claH^(5xGA)mRFP::AFpyroA nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
GFP-Anlsb6	<i>GFP-Anlsb6::AFriboB thiAp-hypB::AFpyrG nkuAΔ::argB pyrG89 riboB2 pyroA4</i>	this study

thiA _p -hypB		
GFP-Anlsb6 thiA _p -claH	<i>GFP-Anlsb6::AFpyrG thiAp-claH::AFpyroA nkuAΔ::argB pyrG89 riboB2 pyroA4</i>	this study
YFPn-Anlsb6	<i>thiAp-(5xGA)YFPn-Anlsb6::AFpyrG nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
hypB-YFPc	<i>hypB-(5xGA)YFPc::AFriboB nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
YFPn-Anlsb6 hypB-YFPc	<i>thiAp-(5xGA)YFPn- Anlsb6::AFpyrG hypB-(5xGA)YFPc::AFriboB nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
thiA _p -Anlsb6 mRFP-PH ^{OSBP}	<i>thiAp-Anlsb6::AFpyrG pyroA4::[pyroA-gpdApm-mRFP-PH^{OSBP}] riboB2</i>	this study
thiA _p -Anlsb6 GFP-chsB	<i>thiAp-Anlsb6::AFpyrG GFP-chsB::AFpyrG nkuAΔ::argB pyroA4 riboB2 pantoB100</i>	this study
thiA _p -Anlsb6 dnfA-GFP	<i>thiAp-Anlsb6::AFpyrG dnfA-GFP::AFpyrG nkuAΔ::argB pyroA4</i>	this study
thiA _p -Anlsb6 mCherry-synA	<i>thiAp-Anlsb6::AFpyrG AFpyrG-mCherry-synA nkuAΔ::argB pyroA4</i>	this study
thiA _p -Anlsb6 uapA-GFP	<i>uapAΔ::uapA-GFP thiAp-Anlsb6::AFpyrG nkuAΔ::argB pyrG89 pyroA4</i>	this study
thiA _p -Anlsb6 GFP-PH ^{PLCδ}	<i>thiAp-Anlsb6::AFpyrG [gpdA::GFP::PH^{PLCδ}]-argBmut::argB2 pyroA4</i>	this study
thiA _p -Anlsb6 hypB-mScarlet	<i>thiAp-Anlsb6::AFpyrG hypB^(5xGA)mScarlet::AFriboB nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
thiA _p -Anlsb6 gga2-GFP	<i>thiAp-Anlsb6::AFriboB gga2^(5xGA)GFP::AFpyrG nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
thiA _p -Anlsb6 arfA-GFP	<i>thiAp-Anlsb6::AFriboB arfA^(5xGA)GFP::AFpyrG nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
thiA _p -Anlsb6 GFP-rabE	<i>thiAp-Anlsb6::AFriboB GFP-RabE::AFpyrG nkuAΔ:argB pyrG89 pyroA4 riboB2</i>	this study
thiA _p -Anlsb6 ap1σ-GFP	<i>thiAp-Anlsb6::AFriboB ap1σ-(5xGA)GFP::AFpyrG nkuAΔ::argB pyrG89 riboB2 pyroA4</i>	this study
thiA _p -Anlsb6 GFP-rabE mCherry-sedV	<i>thiAp-Anlsb6::AFriboB GFP-RabE::AFpyrG pyroA4::[pyroA::gpdApm-mCherry-sedV] nkuAΔ:argB inoB2</i>	this study
thiA _p -Anlsb6 GFP-rabE ap1σ-mRFP	<i>thiAp-Anlsb6::AFpyroA ap1σ^(5xGA)mRFP::AFpyrG GFP-RabE::AFpyrG pyroA4</i>	this study
thiA _p -Anlsb6 mRFP-PH ^{OSBP} arfA-GFP	<i>thiAp-Anlsb6::AFriboB arfA^(5xGA)GFP::AFpyrG [pyroA-gpdApm-mRFP-PH^{OSBP}]pyroA4 nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
thiA _p -Anlsb6 hypB- mScarlet GFP-chsB	<i>GFP-chsB::AFpyrG thiAp-Anlsb6::AFpyrG hypB^(5xGA)mScarlet::AFriboB nkuAΔ::argB pyroA4 riboB2 pantoB100</i>	this study
GFP-chsB thiA _p -rabC	<i>GFP-chsB::AFpyrG thiAp-RabC::AFriboB nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
GFP-chsB thiA _p -rabA	<i>GFP-chsB::AFpyrG thiAp-RabA::AFriboB nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
GFP-chsB rabBΔ	<i>GFP-chsB::AFpyrG rabBΔ::AFpyroA nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
GFP-chsB thiA _p -rabE	<i>GFP-chsB::AFpyrG thiAp-RabE::AFriboB nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
thiA _p -Anlsb6 mRFP-rabA GFP-chsB	<i>GFP-chsB::AFpyrG thiAp-Anlsb6::AFpyrG gpdApm-mRFP-rabA::AFriboB nkuAΔ::argB pyrG89 pyroA4 riboB2 pantoB100</i>	this study
thiA _p -Anlsb6 mRFP-rabB GFP-chsB	<i>GFP-chsB::AFpyrG thiAp-Anlsb6::AFpyrG gpdApm-mRFP-rabB-panB nkuAΔ::argB pyrG89 pyroA4 riboB2 pantoB100</i>	this study

thiA _p -Anlsb6 rabBΔ GFP-chsB	<i>GFP-chsB::AFpyrG thiA_p-Anlsb6::AFpyrG rabBΔ::AFpyroA nkuAΔ::argB pyroA4 riboB2 pantoB100</i>	this study
thiA _p -Anlsb6 thiA _p -rabA GFP-chsB	<i>GFP-chsB::AFpyrG thiA_p-Anlsb6::AFpyrG thiA_p-rabA::AFriboB nkuAΔ::argB pyroA4 riboB2 pantoB100</i>	this study
thiA _p -Anlsb6 rabBΔ mCherry-synA	<i>AFpyG-mcherry-synA thiA_p-Anlsb6::AFpyrG rabBΔ::AFpyroA nkuAΔ::argB pyroA4</i>	this study
GFP-chsB rabBΔ thiA _p -rabA	<i>GFP-chsB::AFpyrG rabBΔ::AFpyroA thiA_p-rabA::AFriboB nkuAΔ::argB pyrG89 pyroA4 riboB2</i>	this study
thiA _p -Anlsb6 GFP-chsB rabBΔ thiA _p -rabA	<i>thiA_p-Anlsb6::AFpyrG GFP-chsB::AFpyrG rabBΔ::AFpyroA thiA_p-rabA::AFriboB nkuAΔ::argB pyroA4 riboB2 pantoB100</i>	this study
thiA _p -Anlsb6 GFP-chsB rabBΔ thiA _p -rabC	<i>thiA_p-Anlsb6::AFpyrG GFP-chsB::AFpyrG rabBΔ::AFpyroA thiA_p-rabC::AFriboB nkuAΔ::argB pyroA4 riboB2 pantoB100</i>	this study
Anlsb6 _p -lsb6	<i>Anlsb6_p-lsb6-panB thiA_p-Anlsb6::AFpyrG GFP-chsB::AFpyrG pyroA4 pabaA1 pantoB100</i>	this study
gpdA _p -lsb6	<i>gpdA_p-lsb6-panB thiA_p-Anlsb6::AFpyrG GFP-chsB::AFpyrG pyroA4 pabaA1 pantoB100</i>	this study
Anlsb6 _p -pik1	<i>Anlsb6_p-pik1-panB thiA_p-Anlsb6::AFpyrG GFP-chsB::AFpyrG pyroA4 pabaA1 pantoB100</i>	this study
gpdA _p -pik1	<i>gpdA_p-pik1-panB thiA_p-Anlsb6::AFpyrG GFP-chsB::AFpyrG pyroA4 pabaA1 pantoB100</i>	this study
S288C	<i>S288C: MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0</i>	Euroscarf
TSA116	<i>Y40675/TSA116: BY4741; MATa ura3Δ0 leu2Δ0 his3Δ1 met15Δ0 pik1-139:kanMX</i>	Euroscarf
pik1Δ	<i>BY4741; MATa ura3Δ0 leu2Δ0 his3Δ1 met15Δ0 pik1-139:kanMX PCJ313 (CEN-ARS LEU2 HIS3 MET25)</i>	this study
pik1Δ-pFL038	<i>BY4741; MATa ura3Δ0 leu2Δ0 his3Δ1 met15Δ0 pik1-139:kanMX PCJ313 (CEN-ARS LEU2 HIS3 MET25) pFL038-ura</i>	this study
pik1Δ-pCG563	<i>BY4741; MATa ura3Δ0 leu2Δ0 his3Δ1 met15Δ0 pik1-139:kanMX PCJ313 (CEN-ARS LEU2 HIS3 MET25) pCG563-ura</i>	this study
pik1 _p -Anlsb6	<i>BY4741; MATa ura3Δ0 leu2Δ0 his3Δ1 met15Δ0 pik1-139:kanMX PCJ313 (CEN-ARS LEU2 HIS3 MET25) pFL038-pik1_p-Anlsb6-ura</i>	this study
gal1 _p -Anlsb6	<i>BY4741; MATa ura3Δ0 leu2Δ0 his3Δ1 met15Δ0 pik1-139:kanMX PCJ313 (CEN-ARS LEU2 HIS3 MET25) pCJ563- gal1_p-Anlsb6-ura</i>	this study

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Supplementary Table 2. Oligonucleotides used in this study.

	Sequence 5' - 3'
pGEM-AnLsb6-(5xGA)GFP::AFpyrG/pGEM-GFP-AnLsb6::AFpyrG/ pGEM-GFP-AnLsb6::AFriboB	
Anlsb6 5 Apal F	CGCGGGGCCCCGTCTCGAAGGGTATCTGTCAGCCTG
Anlsb6 5 SpeI R	CGCGACTAGTGAAGACTGCCAGACTTTCGGCTCC
Anlsb6 ORF SpeI F	CGCGACTAGTATGCCGAAAAACAATCGACCCGC
Anlsb6 ORF NotI R	CGCGGCGGCCGCGCCATGACAGACTGTTGTCAATGG
Anlsb6 ORF SphI F	CGCGCATGCGGGATCGAAGAAAAGCTTGGATGG
Anlsb6 ORFs SpeI R	CGCGACTAGTGCACCAAGTAAAAACAGGATTTTACTC
GAGFP SpeI F	GCGCACTAGTGGAGCTGGTGCAGGCGCTGGAG
AFpyrG SpeI R	CGCGACTAGTCTGTCTGAGAGGAGGCACTGATG
AFriboB SpeI F	CGCGACTAGTAAGCTTGATATCACAATCAGCTTTTC
pGEM-thiAp-Ansb6::AFpyrG/ pGEM-thiAp-Anlsb6::AFriboB/pGEM-thiAp-Anlsb6::AFpyroA/pGEM-thiApFLAG-Anlsb6::AFpyrG	
Anlsb6 5 Apal F	CGCGGGGCCCCGTCTCGAAGGGTATCTGTCAGCCTG
Anlsb6 5 SpeI R	CGCGACTAGTGAAGACTGCCAGACTTTCGGCTCC
Anlsb6 3 SpeI F	CGCGACTAGTCGCTGGGCTTTCCATATCACCGG
Anlsb6 3 NotI R	CGCGGCGGCCGCTCCAAGTTCGCTGTTCCACACAG
thiA SpeI F	CGCGACTAGTCGACCTGGCACCTACAGAAGAATCC
thiA XbaI R	CGCGTCTAGAGTTGACTCAGTTCAATGGTTCGAC
thiA FLAG R	CGCGACTAGTCGCGACTAGTCTTGTCTGTCGCTGCTTGTAGTCCATGTTGACTCAGTTCAATGGTTC
AFpyrG SpeI F	CGCGACTAGTGCCTCAAACAATGCTCTTCACCC
AFpyrG SpeI R	CGCGACTAGTCTGTCTGAGAGGAGGCACTGATG
AFriboB SpeI F	CGCGACTAGTAAGCTTGATATCACAATCAGCTTTTC
AFriboB SpeI R	CGCGTCTAGACCCGGGCTGCAGGAATTCGATAAG
AFpyroA SpeI F	CGCGACTAGTGGACATCAGATGCTGGATTAC
AFpyroA SpeI R	CGCGACTAGTGCAGTGTCTACATAATGAAGG
pGEM-arfA-(5xGA)GFP::AFpyrG	
arfA 5 Apal F	CGCGGGGCCCCGGCGGCTGAATTTCTCGACCTG
arfA ORFs SpeI R	CGCGACTAGTGTGCGGCCAGTCTTCCGCAG
arfA 3 SpeI F	CGCGACTAGTGCGGTAGTTGTGATGAATGGATAG
arfA 3 NotI R	CGCGGCGGCCGCCCCTCATCCACAGCATCCGCAAAGAC
GAGFP SpeI F	GCGCACTAGTGGAGCTGGTGCAGGCGCTGGAG
AFpyrG SpeI R	CGCGACTAGTCTGTCTGAGAGGAGGCACTGATG
pGEM-hypB-(5xGA)mScarlet::AFriboB	
hypB ORF Apal F	CGCGGGGCCCCCTAGGGCCTTGACATACCTTTTCG
hypB ORFs SpeI R	CGCGACTAGTGCGCCGCGACGCTATGCTTGCGAG
hypB 3 SpeI F	CGCGACTAGTCCGCTTTAGACGGCTCCTATATTAG
hypB 3 NotI R	CGCGGCGGCCGCGAGAAGCGGATGCGAGTTGCCTGAG
GAmScar SpeI F	CGCGACTAGTGGAGCAGGTGCTGGTGCTGGTGCTGGAGCAGTGAGCAAGGGCGAGGCAGTG
mScar XbaI R	CGCGTCTAGATTACTTGTACAGCTCGTCCATGCCGCC
AFpyrG SpeI F	CGCGACTAGTGCCTCAAACAATGCTCTTCACCC
AFpyrG SpeI R	CGCGACTAGTCTGTCTGAGAGGAGGCACTGATG
pGEM-gga2-(5xGA)GFP::AFpyrG	
gga2 ORF Apal F	CGCGGGGCCCCGTGAGAACTGTGTTGACCTGGGTTG
gga2 ORF SpeI NS R	CGCGACTAGTTGCAATGCCAGCGGTGGTACC
gga2 3 SpeI F2	CGCGACTAGTCGCCACTACTCGGCCACGATTAG
gga2 3 NotI R2	CGCGGCGGCCGCCCAGAGCGTTCCAATCCACCCAG
GAGFP SpeI F F	GCGCACTAGTGGAGCTGGTGCAGGCGCTGGAG
AFpyrG SpeI F R	CGCGACTAGTCTGTCTGAGAGGAGGCACTGATG
pGEM-Anlsb6p-lsb6-panB/pGEM-gpdAp-lsb6-panB	
Anlsb6 pr Apal F	CGCGGGGCCCCGCGCTTGATCAGTGATGAACCGTTC
Anlsb6 5 SpeI R2	CGCGACTAGTGAAATAATATTGAAAGGGGCGTGAATGAAAGGC
Lsb6 SpeI F	CGCGACTAGTATGAGTAACGAAGCTTACCAGCATGATC
Lsb6 NotI R	CGCGGCGGCCGCTCAACACCAGGTGAATACGGGGGTG

pGEM-Anlsb6p-pik1-panB/ pGEM-gpdAp-pik1-panB	
Anlsb6 pr ApaI F	CGCGGGGCGCGCTTGATCAGTGATGAACCGTTC
Anlsb6 5 SpeI R2	CGCGACTAGTGAAATAATATTGAAAGGGGCGTGAATGAAAGGC
Pik1 XbaI F	CGCGTCTAGAATGCATAAAGCATCCAGTTCAAAGAAAAGC
Pik1 NotI R	CGCGGCGGCCGCTCAGCTATATATACCCTGTGTAATAAGTTGAAATTGG
pFL038-pik1p-Anlsb6-ura/pCJ563- gal1p-Anlsb6-ura	
Pik1 pr F	TCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTCGAGCTCTTGCATAGTCACAGA
Pik1 R	CACACAGGAAACAGCTATGACCATGATTACGCCAAGCTTGCATGCGATAATAATTTATATGTATGGTTAAT
Pik1 ups F	CTCCTTGATTCTTTAGCCG
Pik1 down R	CGAGCTCAAGATTCCGAAAG
Anlsb6 PIK1pr F	TTCATTGCGAGCGTTTCGTTTTCATTAAGCATTGTTCTCTTCACTATGCCGAAAAACAATCGACC
Anlsb6 R	TTGCAAATTGTTTTCCAGTTCTGTACAGCTATTTTCCTTCTCAGCACCAAGTAAAAACAGGAT
Anlsb6 GAL1 F	TGTTAATATACCTCTATACTTTAACGTCAAGGAGAAAAAACTATAATGCCGAAAAACAATCGACC
Anlsb6 R	TTGCAAATTGTTTTCCAGTTCTGTACAGCTATTTTCCTTCTCAGCACCAAGTAAAAACAGGAT