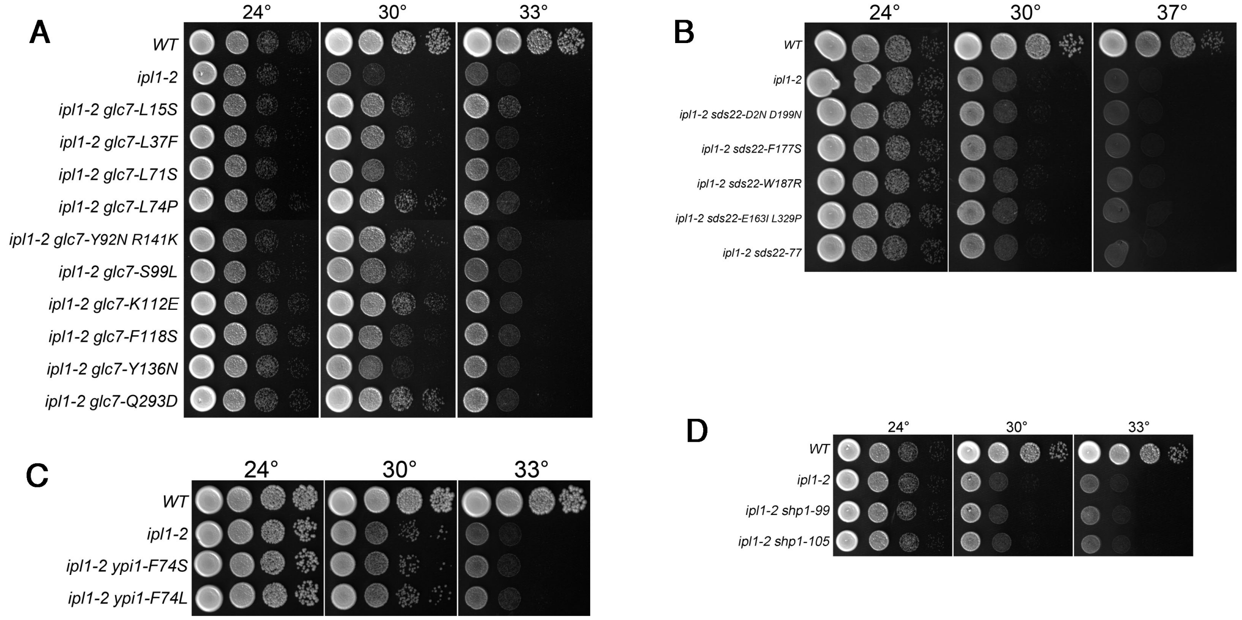

Figure S1 Dominance of *ipl1* suppressors. Cultures of diploid strains homozygous for *ipl1-2* and heterozygous for the designated *ipl1-2* suppressor mutation were serially diluted onto YPD medium and imaged after 40 hr at the designated temperatures. The WT strain is heterozygous for *ipl1-2* (KT1112 X KT1829). Suppressor mutations in *GLC7*, *SDS22*, *YPI1* and *SHP1* are presented in panels (A), (B), (C), and (D), respectively. Note that only the *GLC7* mutant alleles display semi-dominance.

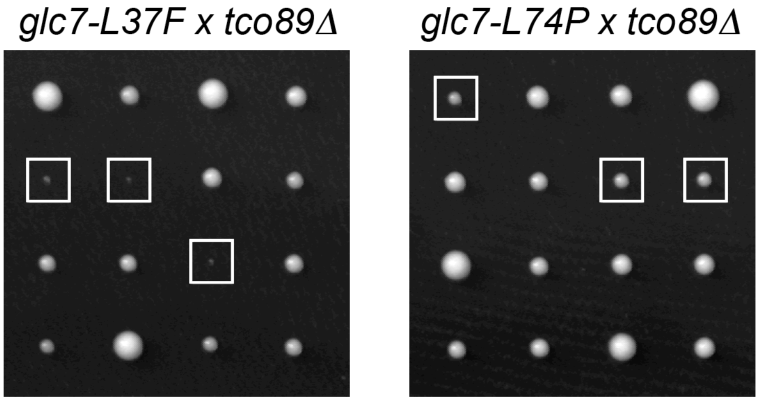

Figure S2 Genetic interactions between *GLC7* mutant alleles and *TCO89*. Images of four tetrads from a cross between *glc7-L37F* (left panel) and *glc7-L74P* (right panel) and a *tco89Δ::kanMX* strain. The boxes identify the *glc7 tco89Δ* double mutants. Each column represents the four spore clones of a tetrad. Note that the rapamycin-sensitive *GLC7* mutant (*glc7-L37F*) exhibits the strongest genetic interaction with *tco89Δ.*

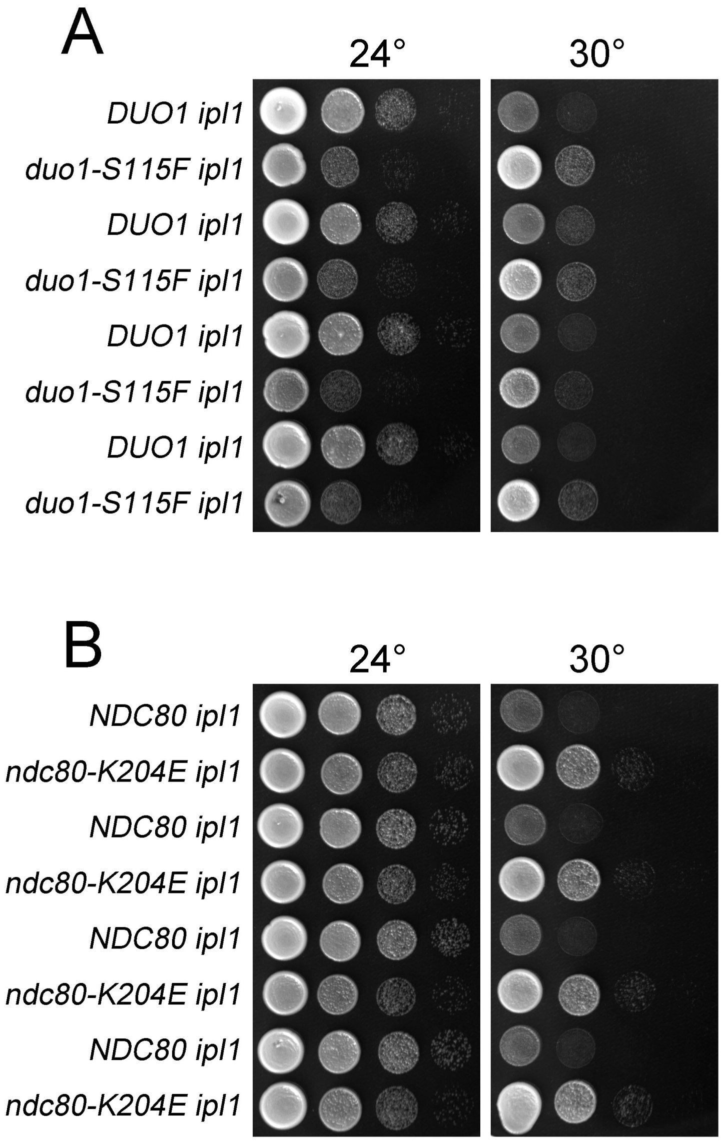

Figure S3 Confirmation of *duo1-S155F* and *ndc80-K204E* alleles. Cultures of ascospore clones were serially diluted onto YPD medium and imaged after 28-30 hr at the designated temperatures. (A) Haploid spore clones from a diploid strain KT3349 (*ipl1-2/IPL1 duo1Δ::kan/DUO1* pRS303:duo1-S115F). All the clones are *ipl1-2* and contain either wild-type *DUO1* or pRS303:*duo1-S115F*. As expected the pRS303-*duo1-S115F* clones are also cold sensitive, arresting as large budded cells at 14°. (B) Haploid spore clones from a diploid strain KT3350 (*ipl1-2/IPL1 ndc80Δ::kan/NDC80* pRS316:*ndc80-K204E*). All the clones are *ipl1-2* and contain either wild-type *NDC80* or pRS316:*ndc80-K204E.*

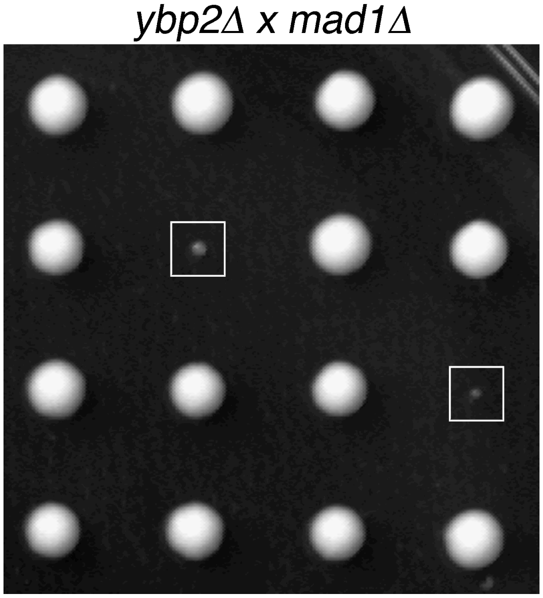

Figure S4 Genetic interactions between *ybp2Δ and mad1Δ* mutant alleles. Images of four tetrads from a cross between *ybp2Δ::kanMX* and a *mad1Δ::HIS3* strain. The boxes identify the *ybp2Δ mad1Δ double mutants.* Each column represents the four spore clones of a tetrad.

Table S1 Strain list

strain	genotype	Source or reference
KT1112	*MAT***a** *leu2 ura3 his3*	(Stuart et al., 1994)[a]
KT1113	*MAT*α *leu2 ura3 his3*	(Frederick and Tatchell, 1996)[b]
KT1687	*MAT*α *mad1::HIS3*	this study
KT1688	*MAT***a** *mad1::HIS3*	this study
KT1829	*MAT*α *ipl1-2 (H352Y)*	(Hsu et al., 2000)[c]
KT1963	*MAT***a** *ipl1-2*	(Bharucha et al., 2008)[d]
KT2856	*MAT***a** *SDS22-mCitrine::SpHis5 POM34-mCherry::SpHis5*	this study
KT2865	*MAT***a** *ipl1-R150K H352Y*	this study
KT2867	*MAT***a** *ipl1-S167L H352Y*	this study
KT2869	*MAT***a** *ipl1-G347E H352Y*	this study
KT2878	*MAT***a** *ipl1-2 ndc80-K204E ura3::GFP-TUB1::URA3*	this study
KT2881	*MAT***a** *YPI1-13Myc:kanMX6*	this study
KT2934	*MAT*α *ipl1-2 sds22-D2N D119N*	this study
KT2936	*MAT*α *ipl1-2 sds22-77(Cterm frameshift)*	this study
KT2938	*MAT*α *ipl1-2 glc7-L71S*	this study
KT2939	*MAT*α *ipl1-2 glc7-S99L*	this study
KT2940	*MAT*α *ipl1-2 glc7-L37F*	this study
KT2963	*MAT*α *sds22-D2N D119N*	this study
KT2964	*MAT*α *sds22-77*	this study
KT2961	*MAT*α *duo1-S115F (rev76)*	this study
KT2967	*MAT*α *duo1-S115F (rev81)*	this study
KT2969	*MAT*α *glc7-L71S*	this study
KT2970	*MAT*α *glc7-S99L*	this study
KT2973	*MAT*α *glc7-L37F*	this study
KT3052	*MAT*α *ipl1-2 sds22-E163I L329P*	this study

KT3059	*MATα ipl1-2 glc7-F118S*	this study
KT3062	*MATα ipl1-2 glc7-L15S*	this study
KT3064	*MATα ipl1-2 glc7-K112E*	this study
KT3066	*MATα ipl1-2 glc7-Q293D*	this study
KT3242	*MAT***a** *GLC7-mCitrine:SpHis5 POM34-mCherry:SpHis5*	(Tatchell et al., 2011)[e]
KT3255	*MAT***a** *ndc80-K204E*	this study
KT3257	*MAT***a** *ipl1-2 ndc80-K204E*	this study
KT3292	*MATα sds22-E163I L329P*	this study
KT3302	*MATα glc7-F118S*	this study
KT3304	*MATα glc7-L15S*	this study
KT3308	*MATα glc7-K112E*	this study
KT3310	*MATα glc7-Q293D*	this study
KT3317	*MAT***a** *PDS1-13Myc:kanMX6 SPC42-3XGFP:TRP1 bar1-1 ndc80-K204E*	this study
KT3319	*MAT***a** *PDS1-13Myc:kanMX6 SPC42-3XGFP:TRP1 bar1-1*	this study
KT3320	*MAT***a** *PDS1-13Myc:kanMX6 SPC42-3XGFP:TRP1 bar1-1 ndc80-K204E ipl1-2*	this study
KT3351	*MATα sds22-F177S*	this study
KT3353	*MATα ipl1-2 sds22-F177S*	this study
KT3355	*MATα glc7-Y136N*	this study
KT3358	*MATα ipl1-2 glc7-Y136N*	this study
KT3359	*MATα glc7-L74P*	this study
KT3361	*MATα ipl1-2 glc7-L74P*	this study
KT3363	*MATα glc7-Y92N R141K*	this study
KT3365	*MATα ipl1-2 glc7-Y92N R141K*	this study
KT3368	*MATα ipl1-2 ypi1-F74S*	this study
KT3370	*MATα ipl1-2 ypi1-F74L*	this study
KT3381	*MATα ipl1-2 sds22-W187R*	this study
KT3383	*MAT***a** *IPL1-13Myc:kanMX6*	this study

KT3385	*MATα duo1-S115F*	this study
KT3386	*MATα ipl1-2 duo1-S115F*	this study
KT3389	*MAT***a** *IPL1-13Myc:kanMX6 tco89-71*	this study
KT3391	*MAT***a** *IPL1-13Myc:kanMX6 glc7-L74P*	this study
KT3392	*MAT***a** *IPL1-13Myc:kanMX6 glc7-Y92N R141K*	this study
KT3395	*MAT***a** *IPL1-13Myc:kanMX6 shp1-105*	this study
KT3396	*MAT***a** *IPL1-13Myc:kanMX6 shp1-99*	this study
KT3400	*MAT***a** *ipl1-2 ybp2Δ::kanMX6*	this study
KT3401	*MATα ipl1-2 ybp2Δ::kanMX6*	this study
KT3403	*MATα ybp2Δ::kanMX6*	this study
KT3409	*MATα ipl1-2 duo1-S115F ybp2Δ::kanMX6*	this study
KT3410	*MATα duo1-S115F ybp2Δ::kanMX6*	this study
KT3412	*MATα shp1-99*	this study
KT3413	*MATα shp1-99 ipl1-2*	this study
KT3415	*MAT***a** *shp1-99 ipl1-2*	this study
KT3416	*MATα shp1-105*	this study
KT3417	*MAT***a** *shp1-105 ipl1-2*	this study
KT3419	*MATα shp1-105 ipl1-2*	this study
KT3424	*MAT***a** *GLC7-mCitrine:SpHis5 POM34-mCitrine:SpHis5 ipl1-2 shp1-105*	this study
KT3247	*MAT***a** *YPI1-13Myc:kanMX6 ipl1-2 shp1-105*	this study
KT3428	*MAT***a** *SDS22-mCitrine:SpHis5 POM34-mCherry:SpHis5 ipl1-2 shp1-105*	this study
KT3449	*MAT***a***/MATα ipl1-2/IPL1 duo1Δ::kanMX6 pRS306:duo1-S115F*	this study
KT3450	*MAT***a***/MATα ipl1-2/IPL1 ndc80Δ::kanMX6 pRS313:ndc80-K204E*	this study

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[a] Stuart, J.S., Frederick, D.L., Varner, C.M., and Tatchell, K. (1994). The mutant type 1 protein phosphatase encoded by *glc7-1* from *Saccharomyces cerevisiae* fails to interact productively with the *GAC1*-encoded regulatory subunit. Mol Cell Biol *14*, 896-905.

[b] Frederick, D.L., and Tatchell, K. (1996). The *REG2* gene of *Saccharomyces cerevisiae* encodes a type1 protein phosphatase-binding protein that functions with Reg1p and the Snf1p protein kinase to regulate growth. Mol Cell Biol *16*, 2922-2931.

[c] Hsu, J.-Y., Sun, Z.-W., Li, X., Ruben, M., Tatchell, K., Bishop, D.K., Grushcow, J.M., Brame, C.J., Caldwell, J.A., Hunt, D.F.*, et al.* (2000). Mitotic phosphorylation of histone H3 is goverened by Ipl1/aurora kinase and Glc7p/PP1 phosphatase in budding yeast and nematodes. Cell *102*, 279-291.

[d] Bharucha, J.P., Larson, J.R., Gao, L., Daves, L.K., and Tatchell, K. (2008). Ypi1, a Positive Regulator of Nuclear Protein Phosphatase Type 1 Activity in Saccharomyces cerevisiae. Mol Biol Cell *19*, 1032-1045.

[e] Tatchell, K., Makrantoni, V., Stark, M.J., and Robinson, L.C. (2011). Temperature-sensitive ipl1-2/Aurora B mutation is suppressed by mutations in TOR complex 1 via the Glc7/PP1 phosphatase. Proc Natl Acad Sci U S A *108*, 3994-3999.

Table S2 Primers Used

PRIMER	SEQUENCE, 5’- 3’
pBR-247F	GATGCAATTTCTATGCGCAC
pBR-559R	CAAGGAATGGTGCATGCAAG
DUO1-F	GATGAGAGGTTTTTGGACCTC
DUO1-R	CCTGTTGAAACTAAGGCATG
DUO1-Fa	CCTGCTCGTTGTACATATC
DUO1-Ra	CAACCTGTAGCCGTATTAAG
GLC7-F	CGTAACACAAGTTAACACC
GLC7-R	GAGTGATGATTGCATCTTCC
IPL1-F	GCAATTGCTCAAGTGAATG
IPL1-R	GCAATATACGATGCCGAAAAG
IPL1-SEQ	CGCTAAATCATCCGAATC
NDC80-F	GAATACATTCACAGGAGAGG
NDC80-R	GGTGGAATTGAACAAAATGC
NDC80-1644F	CTGTAGGTGGCTCTAATTG
NDC80-Fa	CTGGATCCCCAGATGGTTATAACTG
NDC80-Ra	CTTCTAGACCACCGTCTTCTTATTC
SDS22-F	CTCTCTCCTCCCTTTTTCTC
SDS22-R	GCGAACTTTAACTAGATGG
SHP1-F	GTGGACAGCTTAGTTAAGAC
SHP1-R	CTGCTCCAAAAGCAGTATTG

SHP1-303F	CAAGGTAGCAACGAGTACTTG
YBP2-F	CGTTTCGCTGTGAAACTAAC
YBP2-R	CGTACTTTCTGGGTTCCAATG
YBP2-571F	GTAACAACCAACGTTCAGG
YPI1-F	CCGTTTCTTAGCTTAAAGGC
YPI1-R	CAATACAGAATGCCAAGGG
IPL1-F2	GATACTAAGAAACAAGCCCTTTTGGGAAAATAAGCGGTTACGGATCCCCGGGTTAATTAA
IPL1-R1	ATTAATAGTGCCCTTCAAACGATTCTGTCATACTTTAATTGAATTCGAGCTCGTTTAAAC
NDC80-F2	GTTACGAAATTTGGAGTTTGAAACTGAACATAACGTAACAAATCGGATCCCCGGGTTAATTAA
NDC80-R1	CTTTGCTGTAGATTGCTCGGGTATTATATATCATTTATTTTAGAATTCGAGCTCGTTTAAAC
PDS1-F2	AGAAGGCCTCGATCCTGAAGAACTAGAGGACTTAGTTACTCGGATCCCCGGGTTAATTAA
PDS1-R1	ACGTGTATATATGTTGTGTGTATGTGAATGAGCAGTGGATGAATTCGAGCTCGTTTAAAC
SHP1-F2	CGCTGATCTGCTGAACTCCGTTGTCGTGCAAAGATGGGCACGGATCCCCGGGTTAATTAA
SHP1-R1	GTTGAAGTCTTTTCCCGTTTCTGTTTTTGTATATTTATGCGAATTCGAGCTCGTTTAAAC