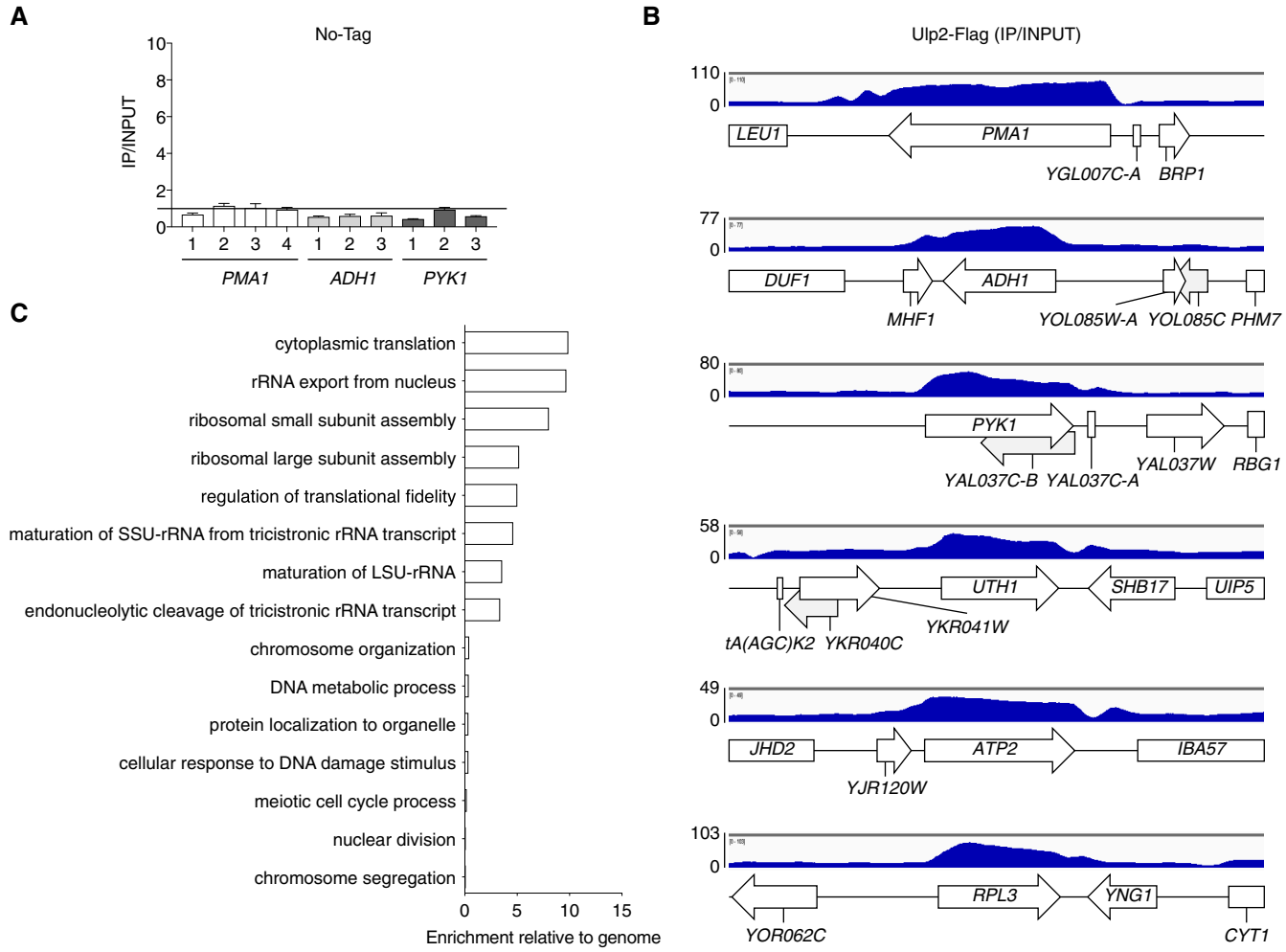
Expanded View Figures



Gene	FPKM	Gene	FPKM	Gene	FPKM	Gene	FPKM	Gene	FPKM
LEU1	134.981	*ADH1*	3386.5	*YAL037C-A*	0	*UTH1*	3621.55	*IBA57*	53.9455
PMA1	450.206	*YOL085W-A*	19.853	*YAL037W*	8.94438	*SHB17*	59.9151	*YOR062C*	94.7822
YGL007C-A	28.8223	*YOL085C*	12.0716	*RBG1*	40.4743	*UIP5*	32.9899	*RPL3*	528.933
BRP1	15.9843	*PHM7*	139.56	*tA(AGC)K2*	0	*JHD2*	10.7548	*YNG1*	161.483
DUF1	50.9489	*PYK1*	526.85	*YKR040C*	0.354616	*YJR120W*	2.64939	*CYT1*	1286.74
MHF1	108.302	*YAL037C-B*	2690.05	*YKR041W*	5.80801	*ATP2*	2680.92		

Figure EV1. Genome-wide analysis of Ulp2-Flag binding sites in chromatin.

A ChIP analysis using anti-Flag agarose in an untagged strain (MHY500), as described in Fig 1E. Black bar indicates value of 1, which is the background signal. Error bars indicate SDs calculated from three independent experiments. See Dataset EV2 for qPCR raw data.

B Representative data from ChIP-seq analysis of Ulp2-Flag. The *y*-axis shows fold enrichment normalized to the input DNA. Arrows and boxes with gene names indicate locations of ORFs. FPKMs of each gene in WT are shown in the bottom graph.

C Gene Ontology (GO) enrichment analysis of the genes displayed in Fig 1G. Bar diagrams indicate the fold enrichment of categories of biological process to the genome using GO data from PANTHER. The genes used in GO biological process are listed in the file Dataset EV1.

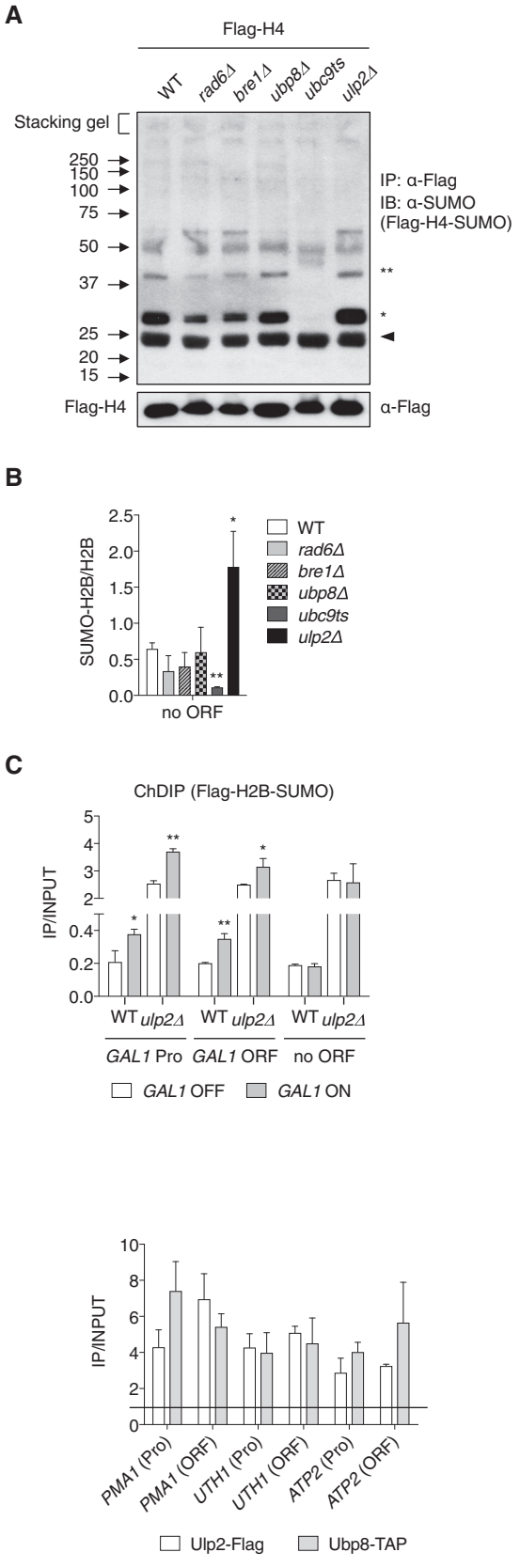


Figure EV2. The analysis of histone sumoylation in mutants.

A Immunoblot analysis of immunoprecipitated Flag-tagged histone H4 using anti-SUMO antibodies in the indicated mutants, as described in Fig 4A. The upper and lower panels show Flag-H4-SUMO and Flag-H4 (loading control), respectively. One and two asterisks indicate mono- and di-sumoylated histones (upper panel), respectively, and the arrowhead represents a non-specific band.

B ChDIP of Flag-H2B-SUMO in the indicated strains at a nontranscribed site ("no ORF") as in Fig 6D. Error bars indicate the SD from three independent assays.

C ChDIP of Flag-H2B-SUMO in WT and *ulp2Δ* strains during *GAL1* gene induction, described as in Fig 5D. For *GAL1* induction, cells grown in SD-Trp medium with 2% glucose were shifted to SD-Trp medium containing 2% raffinose. After 2 h, the medium was replaced with SD-Trp medium containing 2% galactose and then incubated for 1 h. *GAL1* OFF and ON indicate uninduced and induced conditions, respectively. The error bars represent the SD from three ChDIP assays.

Data information: Asterisks indicate statistically significant differences compared with WT in (B) and significant differences between uninduced and induced cells in (C) using a two-tailed Student's *t*-test (*$P < 0.05$; **$P < 0.01$). See Dataset EV2 for qPCR raw data.

Source data are available online for this figure.

Figure EV3. Ubp8 (SAGA) is also associated with TFIID-dominated genes.

ChIP analysis using anti-Flag agarose or IgG-Sepharose beads in strains with the indicated tags, analyzed as in Fig 1E. The qPCR signals in the promoter (Pro) or ORF of *PMA1*, *UTH1*, and *ATP2* were quantitated and normalized to an internal background control and input DNA. Horizonal line indicates value of 1, the background signal. Error bars indicate SDs calculated from four ChIP assays. See Dataset EV2 for qPCR raw data.

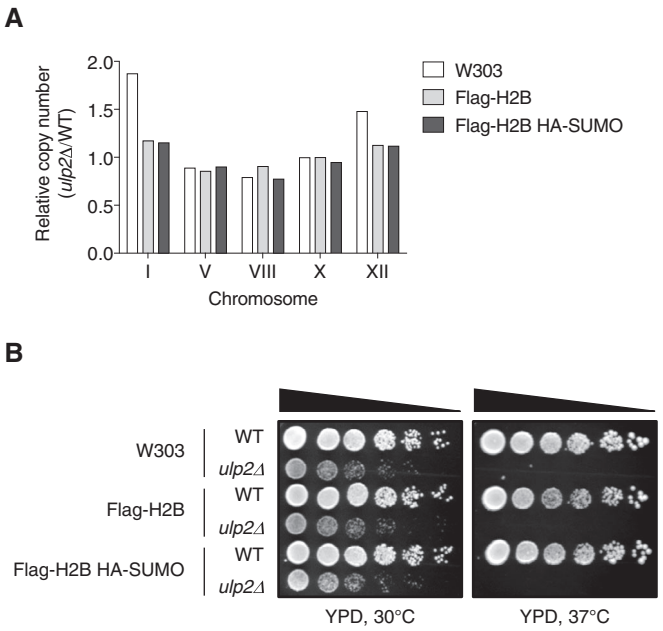


Figure EV4. Test of aneuploidy and cellular growth in *ulp2Δ* derivatives.

A qPCR ploidy assays of *ulp2Δ* strains (W303 background) expressing no tagged protein (MHY5816), Flag-H2B (MHY10249), or Flag-H2B and HA-SUMO (MHY10255). Copy number of the five tested chromosomes was normalized to the euploid WT strains. See Dataset EV2 for qPCR raw data.

B Growth assay of *ulp2Δ* strains shown in (A). After spotting cells in fivefold serial dilutions, the YPD plates were incubated for 2 and 4 days at 30 and 37°C, respectively.