

Figure S1 Construction of *caf5 Δ* , *obr1 Δ* , *SPCC663.08c Δ* single, double or triple mutants. (A) Schematic illustration of gene replacement by homologous recombination. DNA flanking *caf5⁺*, *obr1⁺* or *SPCC663.08c* shown as hatched boxes (upstream of ATG and downstream of TAA) were PCR amplified from genomic DNA and linked respectively to selectable marker *ura4⁺*, *kanMX6* or *hphMX6* by overlapping PCR, resulting in linear cassettes for homologous recombination in wild type cells. The *caf5 Δ* , *obr1 Δ* or *SPCC663.08c Δ* mutants were selected respectively on EMM medium with leucine but without uracil, YES medium with 50 μ g/ml G418 or YES medium with 75 μ g/ml hygromycin B. Similarly, *caf5 Δ obr1 Δ* was derived from *caf5 Δ* and the triple mutant from *caf5 Δ obr1 Δ* . Mutants were genotyped by genomic PCR with primers outside of the integration cassettes using primers P1/P2, P3/P4 or P5/P6 and confirmed by sequencing the PCR products. (B) Transcript levels of *caf5⁺*, *obr1⁺* or *SPCC663.08c* mRNA determined by qRT-PCR from indicated strains.

Figure S2

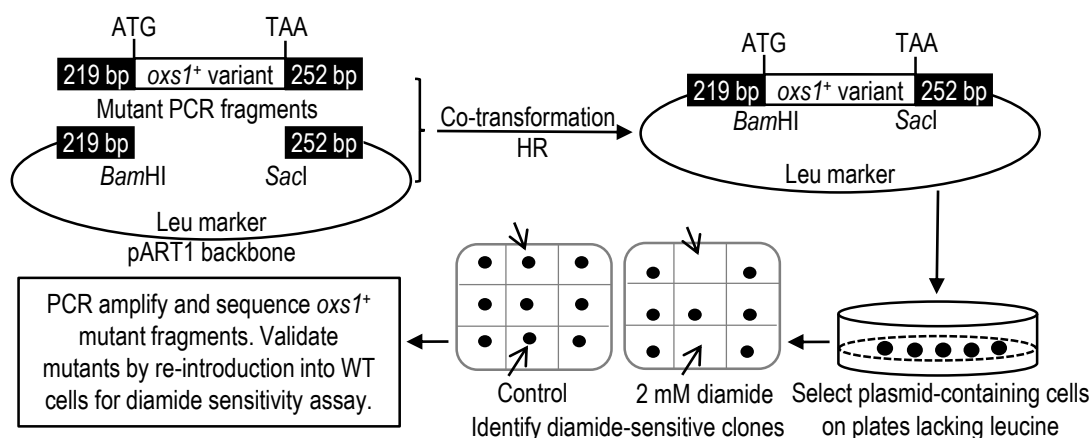


Figure S2 Schematic representation of the screen for base change mutations in *oxs1*⁺. Mutagenized *oxs1*⁺ fragments were generated by error-prone PCR, mixed with *Bam*HI and *Sac*I linearized pART1 vector, transformed into WT cells and plated on media lacking leucine. Circularized plasmids were formed *in vivo* by homologous recombination between the PCR product and gapped vector. Diamide sensitive clones were identified by a spot assay. Mutant *oxs1*⁺ fragments were PCR amplified and sequenced to determine the nucleotide alteration(s).

Figure S3

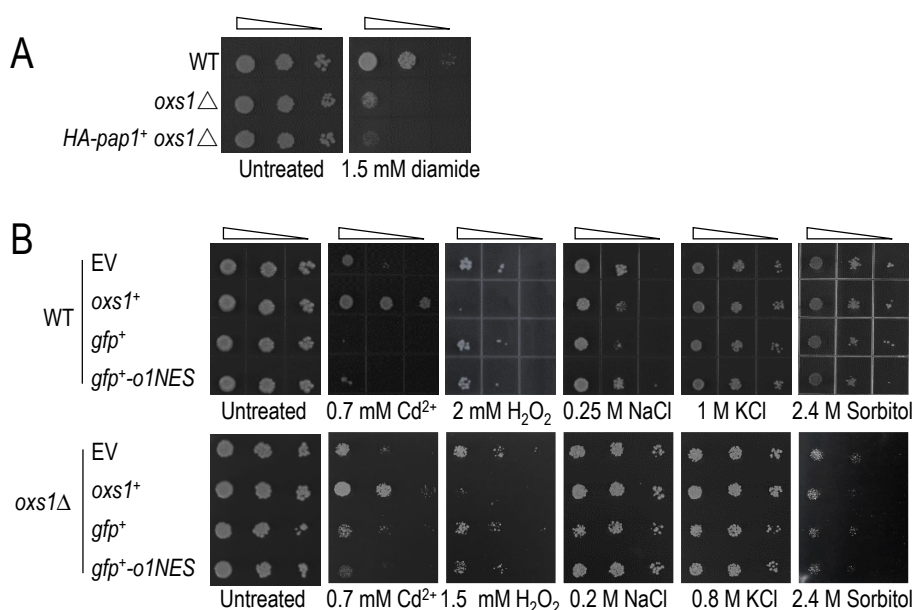


Figure S3 Phenotyping of indicated strains to different stresses. Tolerance of WT, *oxs1*Δ or *HA-pap1*⁺ *oxs1*Δ cells to diamide (A); of WT or *oxs1*Δ cells overproducing Oxs1, GFP or GFP-o1NES to other stresses (B). Serial dilutions of indicated strains spotted onto EMM+Ura plates containing the indicated compounds.

Figure S4

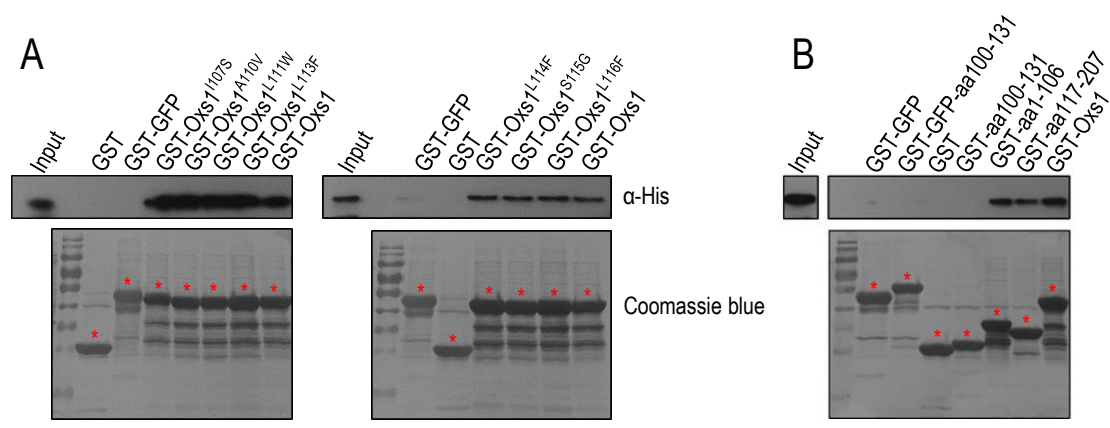


Figure S4 Oxs1 or Oxs1 variants interact with Pap1 *in vitro*. (A) *In vitro* binding of Pap1 to GST-fused to Oxs1 or Oxs1 variants with single amino acid substitution in the NES motif. His-Pap1 was incubated with GST beads bound to the GST-Oxs1 or GST-Oxs1 with indicated mutations (in NES). GST-GFP and GST alone serve as controls. Proteins bound to the beads analyzed by SDS-PAGE and subjected to western blotting with α -His antibody and Coomassie Brilliant Blue staining. Input represents 2% of the total amount of His-Pap1 used in each binding reaction. (B) Binding of GST-Oxs1 amino terminus (aa1-106), carboxyl terminus (aa117-207) or the NES-containing peptide (aa100-131) with Pap1 *in vitro*. In all lanes, asterisk denotes expected band.

Figure S5

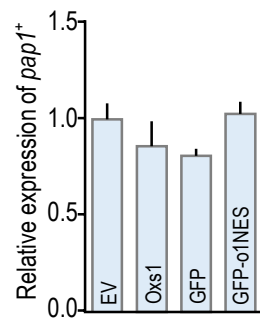


Figure S5 qRT-PCR analysis show that overexpression of the o1NES-conjugate does not alter the mRNA level of *pap1*⁺. Mitotically growing WT cells overproducing Oxs1, GFP or GFP-o1NES were compared to the empty vector (EV) control set as 1.

Figure S6

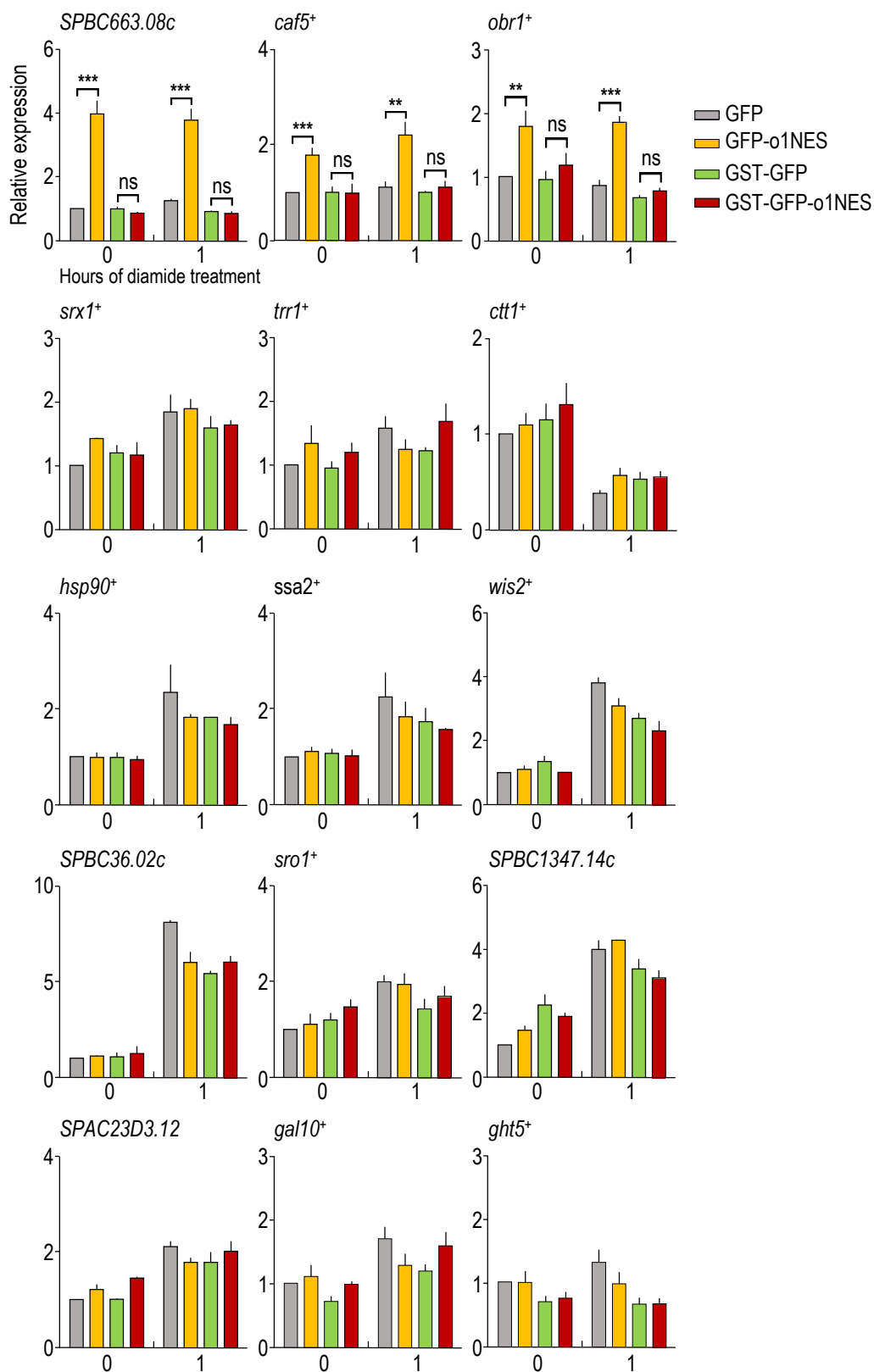


Figure S6 GST-GFP-o1NES fails to activate *SPCC663.08c*, *caf5⁺* or *obr1⁺* before or after 1 hour of diamide treatment. *HA-pap1⁺ oxs1 Δ* cells overproducing GFP, GFP-o1NES, GST-GFP or GST-GFP-o1NES. Data normalized to *act1⁺* mRNA of the strain overproducing GFP. Data represent mean +SEM from ≥ 3 independent experiments. Significant differences from unpaired Student's t-test (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; **** $P < 0.0001$; ns, not significant).

Figure S7

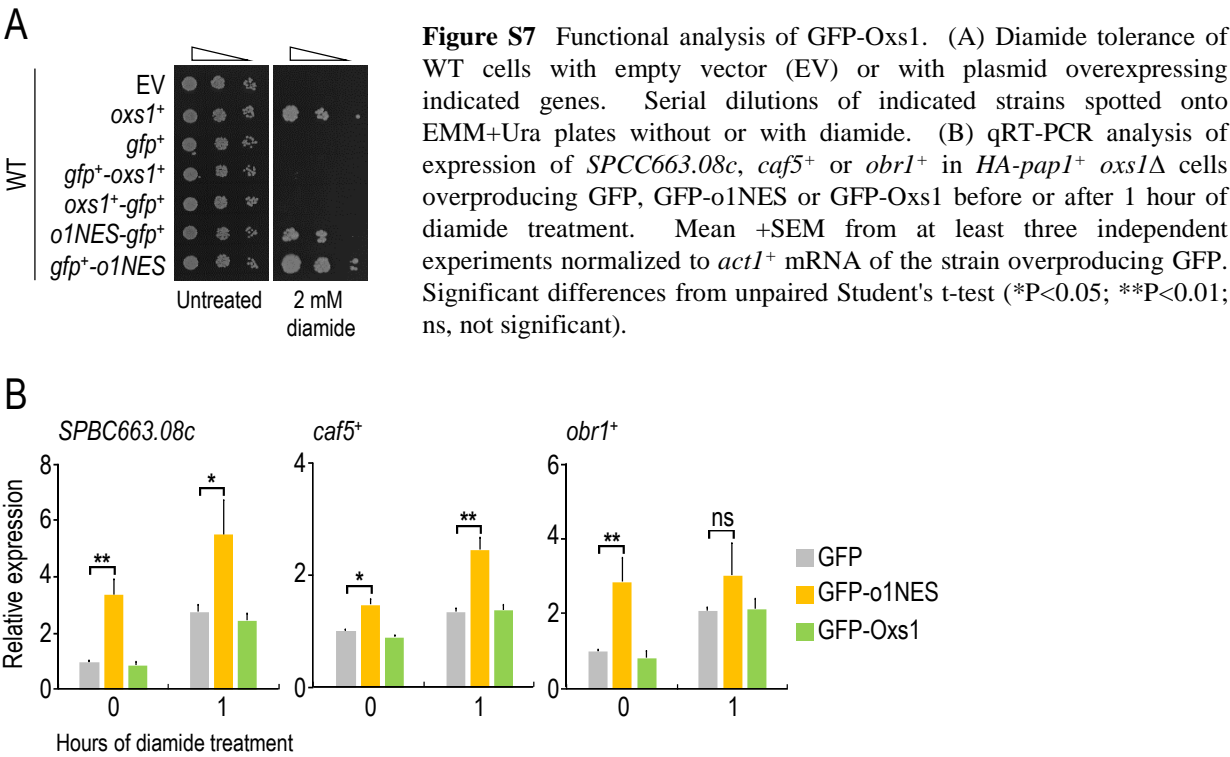


Figure S8

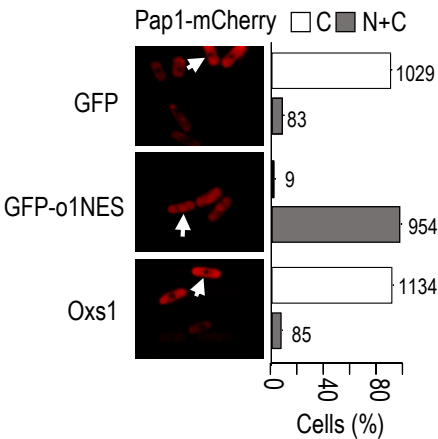


Figure S8 Pap1-mCherry is cytoplasmic-only when co-overproduced with *Oxs1*. Subcellular localization of Pap1-mCherry by fluorescence microscopy on WT cells co-overproducing indicated proteins. Pap1 displays observable nuclear localization in cells overproducing GFP-*o1NES*, but mainly cytoplasmic in strains overproducing *Oxs1* or the control GFP. Arrows point to nuclei. Frequency of cells with Pap1-mCherry signals shown on the right: C = exclusively cytoplasmic; N+C = nuclear and cytoplasmic. Bar graph data represent mean +SEM from 3 independent experiments, with total number of cells scored shown (from Table S4).