Table 1:

Library	Description	Location of tag	Mating Type	Genotype	Reference	Coverege
Deletion	A collection where each gene is precisely deleted and replaced with a kanMX4 (encoding G418 Resistance) selection marker. This deletion strategy combines molecular barcodes (UPTAG and DNTAG) flanking the marker, enabling high-throughput identification and quantification of each strain even in pooled cultures. The collection includes haploid (both mating types) and diploid versions, allowing for the assessment of both essential (as heterozygous diploids) and non-essential genes.	NA	MATa MATα Diploid	(a) *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***Δxxx::UPTAG-G418R-DNTAG*** (α) *his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0* ***Δxxx::UPTAG-G418R-DNTAG*** (a/α) *his3Δ1/his3Δ1 leu2Δ0/leu2Δ0 met15Δ0/MET15 LYS2/lys2Δ0 ura3Δ0/ura3Δ0* ***Δxxx::UPTAG-G418R-DNTAG/XXX***	Winzeler et al. 1999 Giaever et al. 2002	Full genome (5120 genes)
C' GFP	Each gene is altered such that the protein it encodes is fused at the C-terminus with a green fluorescent protein (GFP).	C'	MATa	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***XXX-GFP-HIS3***	Huh et al. 2003	Full genome (5206 genes)
C' TAP-Tag	Each gene is altered such that the protein it encodes is fused at the C-terminus with a Tandem Affinity Purification (TAP) tag. This tag allows immunodetection using a single antibody, while purification and interactome analyses are typically performed by sequential binding to IgG and calmodulin beads.	C'	MATa	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***XXX-TAP-HIS3***	Ghaemmaghami et al. 2003	Full genome (4715 genes)

Table 2:

Library	Description	Location of tag	Mating Type	Genotype	Reference	Coverege
mini ORFs	Deletions of small open reading frames (sORFs, <100 amino acids), completing the deletion collection. Including molecular barcodes like those in the yeast deletion library. Built with the same selection markers and the same genotype as the yeast deletion library, so that they can be combined.	NA	MATa MATα Diploid	(a) *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***Δxxx::G418R*** (α) *his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0* ***Δxxx::G418R*** (a/α) *his3Δ1/his3Δ1 leu2Δ0/leu2Δ0 met15Δ0/MET15 LYS2/lys2Δ0 ura3Δ0/ura3Δ0* ***Δxxx::G418R/XXX***	Kastenmayer et al. 2006	247 small genes

TETOff-Promoter	The promoter of each essential gene is replaced with the tetracycline-repressible promoter (TetO7). This design allows for conditional repression of essential genes by the addition of doxycycline.	NA	MATa	*ura3Δ0::URA3-CMV-tTA his3Δ1 leu2Δ0 met15Δ0* ***G418R-TetO7pr-XXX***	Mnaimneh et al. 2004	Essentials (892 genes)
YETI	The promoter of each gene is replaced with the β-estradiol-inducible Z3EV promoter. This system enables titratable gene induction/ repression. The collection covers essential genes in diploid form (YETI-E) and non-essential genes in haploid form (YETI-NE). Each strain is also barcoded.	NA	MATa Diploid	(a) ***barcode-URA3-Z3EVpr-XXX*** *hap1Δ::NATR-ACT1pr-Z3EVTF-ENO2term ura3Δ0 can1Δ::STE2pr-spHIS5 his3Δ1 lyp1Δ* (a/α) ***barcode-URA3-Z3EVpr-XXX*** *hap1Δ::NATR-ACT1pr-Z3EVTF-ENO2term/ HAP1 ura3Δ0/ura3Δ0 can1Δ::STE2pr-spHIS5/CAN1 his3Δ1/his3Δ1 lyp1Δ/LYP1*	Arita et al. 2021	Genome-wide
Temperature-sensitive (ts) 2008	Essential Genes are represented by a temperature-sensitive (ts) allele. These ts alleles allow normal protein function at a permissive temperature (25°C) and impair function at a non-permissive temperature (32-37°C), enabling conditional analysis of essential genes. Each allele is flanked by UPTAG and DNTAG barcodes, enabling high-throughput identification and quantification of each strain even in pooled cultures.	NA	MATa	*ura3Δ0 leu2Δ0 his3Δ1 lys2Δ0 (or LYS2) met15Δ0 (or MET15) can1Δ::LEU2-MFA1pr-His3* ***UPTAG-XXX^ts-URA3-DNTAG***	Ben-Aroya et al. 2008 Stirling et al. 2011	Essentials (362 genes)
Temperature-sensitive (ts) 2011	This collection complements the 2008 ts library by adding strains carrying at least one conditional ts allele.	NA	MATa	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***XXX^ts-G418R***	Li et al. 2011	Essentials (497 genes)
DAmP Hypomorphic Alleles	The 3' untranslated region (UTR) of each essential gene is deleted, altering mRNA stability, causing reduced abundance (two to ten-fold). Built with the same selection markers and genotype as the yeast deletion library, they can be combined.	NA	MATa Diploid	(a) *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***XXX-DAmP-G418R*** (a/α) *his3Δ1/his3Δ1 leu2Δ0/leu2Δ0 met15Δ0/met15Δ0 ura3Δ0/ura3Δ0* ***XXX-DAmP-G418R/XXX***	Breslow et al. 2008	Essentials (842 genes)
C' AID-eGFP	Based on the C'-SWAT parental collection (see section on Modular innovation), each gene is altered such that the	C'	MATα	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI-STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2,* ***NATR-TEF2pr-OsTIR1(F74G), XXX-AID*-eGFP-G418R***	Valenti et al. 2024	Genome-wide

	protein it encodes is tagged at the C-terminus with a minimized auxin-inducible degron (AID*) followed by an enhanced GFP (eGFP). This design allows both visualization of protein localization and abundance (through the GFP tag) and rapid, conditional protein depletion (using the AID system). Each strain also contains the modified OsTIR1(F74G). adaptor for E3 ubiquitin ligases. Upon the addition of the modified auxin analog 5-Ph-IAA, the Tir1 adaptor targets the AID* fused protein for degradation via the ubiquitin-proteasome pathway.					
C' AID-Monomeric Neon Green (mNG)	Two libraries, all Based on the C'-SWAT parental collection (see section on Modular innovation), and on AID*. V1: Each gene is altered such that the protein it encodes is tagged with mNG-AID*-3myc and is represented as either containing or lacking the OsTIR1 for control. V2: Each gene is altered such that the protein it encodes is fused to AID*-3myc, and the OsTIR is regulated by the galactose inducible/glucose inhibited GAL1pr. These libraries offer versatile tools for conditional, proteome-wide protein depletion.	C'	MATα	*V1 (OsTIR1- set): lyp1Δ his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 can1Δ::STE3pr-LEU2-GAL1pr-NLS-I-SCEI* ***XXX-mNG-AID*-3myc-HygroR*** *V1 (OsTIR1+ set): his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 can1Δ::STE3pr-LEU2-GAL1pr-NLS-I-SCEI* ***lyp1Δ::GAL1pr-OsTIR1(F74G)-NATR XXX-mNG-AID*-3myc-HygroR*** *V2 (OsTIR1+ set): his3Δ1 leu2Δ0 ura3Δ0 met15Δ0 can1Δ::STE3pr-LEU2-GAL1pr-NLS-I-SCEI* ***lyp1Δ::GAL1pr-OsTIR1(F74G)-NATR XXX-AID*-3myc-HygroR***	Gameiro et al. 2024	Genome-wide
Sigma collection-Filamentous growth deletion	Gene deletions were introduced into the filamentation-competent Σ1278b yeast strain background. The library includes both haploid and homozygous diploid deletions.	NA	MATa MATα Diploid	(a) *can1Δ::STE2pr-Sp_his5 lyp1Δ::STE3pr-LEU2 his3::his3G leu2Δ ura3Δ* ***Δxxx::G418R*** (α) *can1Δ::STE2pr-Sp_his5 lyp1Δ::STE3pr-LEU2 his3::his3G leu2Δ ura3Δ* ***Δxxx::G418R*** (a/α) *can1Δ::STE2pr-Sp_his5 / CAN1 lyp1Δ::STE3pr-LEU2 / LYP1 his3::his3G / his3::his3G leu2Δ / leu2Δ ura3Δ / ura3Δ* ***Δxxx::G418R / Δxxx::G418R***	Ryan et al. 2012	Full genome (4028 genes in haploids and 3900 genes in homozygous diploid)

Table 3:

Library	Description	Location of tag	Mating Type	Genotype	Reference	Coverege
C' DHFR-PCA	Two collections in which each gene is altered such that the protein it encodes is fused to complementary fragments of the methotrexate (MTX)-resistant dihydrofolate reductase (DHFR), one part in each mating type, and with different selections. Upon mating of strains from the complementing libraries and diploid selection, if proteins interact, their fused DHFR fragments would also reconstitute enzymatic activity. Upon addition of MTX, the endogenous, essential DHFR is inhibited, allowing strains to grow only if the reconstituted DHFR is active.	C'	MATa MATα	(a) *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***XXX-DHFR1,2-NATR*** (α) *his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0* ***XXX-DHFR3-HygroR***	Tarassov et al. 2008	Full genome (4320 genes in MATa and 4470 genes in MATα)
C' Split Venus	Derived from the TAP library by manual replacement of the TAP cassette, each gene is altered such that the protein it encodes is C-terminally tagged with split fragments of the Venus fluorescent protein: VN (N-terminal part) and VC (C-terminal part).	C'	MATa MATα	(a) *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***XXX-VN-URA3*** (α) *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***XXX-VC-LEU2***	Kim et al. 2019 Sung et al. 2013	Full genome (5911 genes in MATa and 5671 genes in MATα)
Tandem Fluorescent Protein Timer (tFT)	Each gene is altered such that the protein it encodes is seamlessly C-terminally tagged with an immature tandem fluorescent timer (mCherry–SceI site-URA3-sfGFP). This form of the cassette allows for genetic crossing of the library with a strain of choice. Upon excision induction by galactose, the tandem fluorescent timer recombines to its mature form (mCherry-sfGFP), suitable for measuring protein age by a simple fluorescent readout.	C'	MATα	Genotype before excision: *his3Δ1 met15Δ0 ura3Δ0 can1Δ::STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2 leu2Δ::GAL1pr-I-SCEI-natNT2* ***ORF-mCherry-SceIsite-SpCYC1term-ScURA3-SceIsite-mCherryΔN-sfGFP*** Genotype after excision: *his3Δ1 met15Δ0 ura3Δ0 can1Δ::STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2 leu2Δ::GAL1pr-I-SCEI-natNT2* ***ORF-mCherry- -sfGFP***	Khmelinskii et al. 2014	Full genome (4044 genes)

Table 4:

Library	Description	Location of tag	Mating Type	Genotype	Reference	Coverege
N'-SWAT parental	Each gene is altered such that the protein it encodes is N-terminally tagged with GFP and expressed under the constitutive NOP1 promoter, flanked by the SWAp-Tag (SWAT) sequences to enable cassette swapping. To ensure proper targeting, proteins containing a Mitochondrial Targeting Signal (MTS) or a Signal Peptide (SP) also have a synthetic MTS/SP before the GFP tag, respectively.	N'	MATa	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***HygroΔN'-URA3-spNOP1pr-sfGFP-XXX***	Weill et al. 2018	Full genome (5457 genes)
C'-SWAT parental	Each gene is capped by a CYC1 terminator flanked by the SWAT sequences to enable high-throughput modification of the 3' of the gene.	NA	MATa	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***XXX-CYC1term-scURA3-HygroRΔN'-ALG9term***	Meurer et al. 2018	Full genome (5661 genes)

Table 5:

Library	Description	Location of tag	Mating Type	Genotype	Reference	Coverege
N' SWAT NATIVEpr-GFP	Derived from the parental N'-SWAT collection, each gene is altered such that the protein it encodes is N-terminally tagged with GFP without altering the native sequence of the promoter and N-terminal targeting signals (MTS or SP).	N'	MATα	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI-STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2* ***XXXpr-sfGFP-XXX***	Weill et al. 2018	Genome-wide
N' SWAT TEF2pr-mCherry	Derived from the parental N'-SWAT collection, each gene is altered such that the protein it encodes is N-terminally tagged with mCherry and expressed under the strong, constitutive TEF2 promoter.	N'	MATα	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI-STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2* ***NATR-TEF2pr-mCherry-XXX***	Weill et al. 2018	Genome-wide
C'-SWAT mNG	Based on the C'-SWAT parental collection, each gene is altered such that the protein it encodes is tagged at the C-terminus with the bright fluorescent protein mNG followed by ADH1 terminator.	C'	MATa	*his3Δ1 met15Δ0 ura3Δ0 leu2Δ0::GAL1pr-NLS-SceI-NATR can1Δ::STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2* ***XXX-mNG-ADH1term-HygroR***	Meurer et al. 2018	Genome-wide

C'-SWAT mNG-NATIVEterm	Based on the C'-SWAT parental collection, each gene is altered such that the protein it encodes is tagged at the C-terminus with the bright fluorescent protein mNG without altering the native sequence of the terminator.	C'	MATa	*his3Δ1 met15Δ0 ura3Δ0 leu2Δ0::GAL1pr-NLS-SceI-NATR can1Δ::STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2* ***XXX-mNG -NATIVEterm***	Meurer et al. 2018	Genome-wide
C'-SWAT mScarlet-I	Based on the C'-SWAT parental collection, each gene is altered such that the protein it encodes is tagged at the C-terminus with the bright fluorescent protein mScarlet-I.	C'	MATa	*his3Δ1 met15Δ0 ura3Δ0 leu2Δ0::GAL1pr-NLS-SceI-NATR can1Δ::STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2* ***XXX-mScarlet-I-ADH1term-HygroR***	Meurer et al. 2018	Genome-wide

Table 6:

Library	Description	Location of tag	Mating Type	Genotype	Reference	Coverege
N' SWAT split-DHFR	Derived from the parental N'-SWAT collection, two libraries employ the split DHFR approach (See above) by seamless tagging. Mating of strains from opposite mating types is enabled by selection cassettes at a distal, inert locus.	N'	MATa MATα	(a) *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI::STE2pr-SpHIS5 lyp1Δ::STE3pr-LEU2* ***chrV VCAJ1-TPA1::NATR NATIVEpr- DHFR[1,2]-XXX*** (α) *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI::STE2pr-SpHIS5 lyp1Δ::STE3pr-LEU2* ***chrV VCAJ1-TPA1::HygroR NATIVEpr-DHFR[3]-XXX***	Weill et al. 2018	Genome-wide
N' SWAT split-Venus	Derived from the parental N'-SWAT collection, two libraries builds on the split Venus approach (See above).	N'	MATa MATα	(a) *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI::STE2pr-SpHIS5 lyp1Δ::STE3pr-LEU2* ***G418R::CET1pr-VN-XXX*** (α) *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI::STE2pr-SpHIS5 lyp1Δ::STE3pr-LEU2* ***HygroR-TEF2pr-VC-XXX***	Weill et al. 2018	Genome-wide
C'-SWAT split-β-galactosidase	Based on the C'-SWAT parental collection, each gene is altered such that the protein it encodes is fused to the alpha subunit of β-galactosidase at its C-terminus.	C'	MATα	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2* ***XXX-alpha-ADH1ter-HygroR***	Mark et al. 2023	Genome-wide

C'-SWAT 3xGFP11	Based on the C'-SWAT parental collection, each gene is altered such that the protein it encodes is C-terminally tagged with three repeats of the small subunit of a split GFP (3×GFP11). The library also expresses MTS-mCherry as a mitochondrial marker. The library can be mated with a strain harboring the big subunit of the split GFP (GFP1–10) for visualizing reconstitution of the complete GFP signal.	C'	MATα	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI::STE2pr-SpHIS5 lyp1Δ::STE3pr-LEU2 ura3::NATR ho::MTS(Su9)-mCherry-MET15* ***XXX-3xGFP11-NATIVEter***	Bykov et al. 2024	Genome-wide
C'-SWAT SmBiT	Based on the C'-SWAT parental collection, A pair of libraries in which each gene is altered such that the protein it encodes is C-terminally tagged with either SmBiT (Small BiT, MATa) or LgBiT (Large BiT, MATα) fragments of NanoLuc luciferase.	C'	MATa	(a) *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***XXX-SmBiT-NATR*** *fcy1Δ::STE2pr-spHIS5-GAL1pr-NLS-SceI*	Lazarewicz et al. 2024	Genome-wide
C'-SWAT LgBiT			MATα	(α) *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***XXX-LgBiT-10HIS-HygroR*** *can1Δ::STE3pr-LEU2-GAL1pr-NLS-SceI lyp1Δ*	Le Boulch et al., 2020	
C'-SWAT NanoLuc	Based on the C'-SWAT parental collection, each gene is C-terminally tagged with full-length NanoLuc luciferase.	C'	MATα	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***XXX-NanoLuc-HygroR*** *can1Δ::STE3pr-LEU2-GAL1pr-NLS-SceI lyp1Δ*	Lazarewicz et al. 2024	Genome-wide

Table 7:

Library	Description	Location of tag	Mating Type	Genotype	Reference	Coverege
N'-SWAT BioID-HA tag	Derived from the parental N'-SWAT collection, each gene is altered such that the protein it encodes is tagged at the N-terminus with a BioID2-HA tag under the control of the *CYC1* promoter. The BioID2 provides the capacity to biotinylate available lysine residues in proximal proteins.	N'	MATα	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI-STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2* ***HygroR-CYC1pr-BioID-HA-XXX***	Fenech et al. 2023	Genome-wide
N'-SWAT BirA/ ABOLISH	Derived from the parental N'-SWAT collection, each gene is altered such that the protein it encodes is fused to BirA at its N-terminus under its native promoters. BirA has the capacity to specifically biotinylate proteins carrying an AviTag. This library integrates the ABOLISH system, where the endogenous biotin ligase Bpl1 is fused to an AID* tag, allowing for controlled degradation of Bpl1 to reduce background biotinylation.	N'	MATa	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI-STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2* ***BPL1-AID*-9myc-NATR Nativepr-BirA-XXX***	Fenech et al. 2023	Genome-wide

N'-SWAT AviTag/ ABOLISH	Derived from the parental N'-SWAT collection, each gene is altered such that the protein it encodes has an N-terminal AviTag fusions seamlessly integrated, allowing native promoter regulation on the background of the OsTir1 adaptor. This library should be used in combination with the BirA library, and they are created in opposite mating types. The library also incorporates the ABOLISH system.	N'	MATα	*leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI-STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2* ***BPL1-AID*-6HA-HygroR his3Δ1::OsTIR1-HIS3 Nativepr-AviTag-XXX***	Fenech et al. 2023	Genome-wide
N'-SWAT TurboID-HA tag	Derived from the parental N'-SWAT collection, each gene is altered such that the protein it encodes is tagged at the N-terminus with TurboID-HA under the control of the *CYC1* promoter. TurboID is a highly active biotin ligase capable of rapidly biotinylating proximal proteins on available lysine residues.	N'	MATα	*hisΔ1 leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI-STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2* ***HygroR-CYC1pr-TurboID-HA-XXX***	Fenech et al. 2023	Genome-wide
N'-SWAT TurboID-HA tag/ ABOLISH	Derived from the parental N'-SWAT collection, this library enhances the TurboID-HA N' library by incorporating the ABOLISH system.	N'	MATα	*leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI-STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2* ***HygroR-CYC1pr-TurboID-HA-XXX, BPL1-AID*-9myc-G418R his3Δ1::OsTIR1-HIS3***	Fenech et al. 2023	Genome-wide
C'-SWAT Myc-HRV-Flag tag	Based on the C'-SWAT parental collection, each gene is altered such that the protein it encodes is tagged with a C-terminal myc epitope followed by a human rhinovirus (HRV) 3C protease cleavage site, and a 3xFLAG tag for efficient protein purification.	C'	MATa	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 can1Δ::GAL1pr-SceI-NLS-STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2* ***XXX-myc-HRV-3xFlag-ADH1term-G418R***	Reinhard et al. 2022	Genome-wide
N'-SWAT HaloTag	Derived from the parental N' and C'-SWAT collections, each gene is altered such that the protein it encodes is fused with the Halo tag, either at its N- or C-terminus (respectively).	N'	MATα	*his3Δ1 ura3Δ0 met15Δ0 lyp1Δ can1Δ::STE3pr-LEU2-GAL1pr-NLS-I-SCEI* ***leu2Δ::NATR-TEF1pr-mNeonGreen-CYC1term pdr5Δ::HygroR NATIVEpr-HaloTag-3myc-XXX***	Gameiro et al. 2024	Genome-wide
C'-SWAT HaloTag		C'	MATα	*his3Δ1 ura3Δ0 met15Δ0 lyp1Δ can1Δ::STE3pr-LEU2-GAL1pr-NLS-I-SCEI* ***leu2Δ::NATR-TEF1pr-mCherry-CYC1term pdr5Δ::HygroR XXX-HaloTag-3myc-NATIVEterm***	Gameiro et al. 2024	

C'-SWAT H2O2 biosensor	Based on the C'-SWAT parental collection, each gene is altered such that the protein it encodes is C-terminally tagged with the hydrogen peroxide (H_2O_2) sensor HyPer7, enabling the detection of local redox changes at the level of individual proteins. A corresponding control library using a redox-insensitive mutant of the sensor (SypHer7) allows to detect and exclude non-specifc sensor responses.	C'	MATa	*his3Δ1 ura3Δ0 leu2Δ0::GAL1pr-NLS-I-SCEI-natNT2can1Δ::STE2pr-SpHIS5 lyp1Δ::STE3pr-LEU2* ***XXX-HyPer7-ADH1term-HygroR or XXX-SypHer7-ADH1term-HygroR***	Kritsiligkou et al. 2023	Genome-wide
N'-SWAT HA tag	Derived from the parental N'-SWAT collection, each gene is altered such that the protein it encodes is N-terminally tagged with a 3xHA epitope under the regulation of the TEF1 promoter.	N'	MATa	*his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* ***TEF1pr-3HA-XXX-NATR*** *can1Δ::GAL1pr-SceI-STE2pr-spHIS5 lyp1Δ::STE3pr-LEU2*	Baruch et al. 2025	Genome-wide