Spt16 Spo	Spt16 Spo	Spt16 Spo	Spt16 Spo	Spt16 Spo	Spt16 Spo	Spt16 Spo	Spt16 Spo	Spt16 Spo	Sptte Spo
Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Sptte Sce
Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Sptte Dro
Spt16 Ma	Spt16 Ma	Spt16 Ma	Spt16 Ma	Spt16 Ma	Spt16 Ma	Spt16 Ma	Spt16 Ma	Spt16 Ma	Sptte Ma
Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Sptte Hsa
342 RAKRPDLEPMFVRNLGAGIBIEFRESSLUNAKNP-RVR 380 350 EMTKPLVMPFTKNLGSLIGLEFRESSLUNKKOPKOP-RVR 380 256 KKEKPLVMPFTKNLGSLIGLEFRENSNLLNKKOPKOP-RL 370 357 EKTKPLUNKITKTLGFANDIEFRESSLUN NKKOP-VKLK 373 358 KKOKPDLINKITKTLGFANDIEFRESSLUN NKKOP-VKLK 373 354 KKOKPELLNKITKTLGFANDIEFRESSLUN NKKOPVKLK 373	303 DEEQQKMYSFLYALQKELFEYCR-DGAYDGBIYTKILLL[341 370 BEEMANNYDFLITLQKEIYTNILMPORTKLEVESU EVI 257 TREAMGENYTKISVQEEILKLLVPORTKLEOVYEKTLDFY 258 TREAMGENYTKISVQEELLKELKEHA-HGAKOSVANAUMDVY 259 BOEVGENYNKLLQLGEELLKELKEHA-HGAKOSVANAUMDVY 259 BOEVGENYNKLLQLGEELLKELA-HGAKOSVANAUMDVY 250 ENGENY FLL LGEELLK L.K.G.K.COVY	264 KPSRITDDRNLHG-DVVLCSLGFRVKSVCSNVGRTVLFDP 302 270 RVSRRSTNDQLVGNGCILAGEGIRVKSVCSNVGRTVLFDP 309 218 KFSRVADKNPLHF-GVIVCSLGRVKSVCSNLSRTFLVND 256 257 KFSVVSDKNNHHF-GRIFGELGIRVKSVCSNLVRTLNVDP 256 258 KFSVVSDKNNHHF-GRIFGELGIRVKSVCSNLVRTLNVDP 259 258 KFSRVSDKNNHHF-GRIFGELGIRVKSVCSNLVRTLNVDP 259	237 FF0TKSLK_GDIDLDQLEWCVTPII0S66SVDL 263 2367 FLKQSPDD <u>SALCPPNV</u> KFNFDLLDWTVSPII0S6KKPDL 269 192 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Spt16 Sce	Spt16 Sce	Spti6 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Sptic Sce
Spt16 Dro	Spt16 Dro	Spti6 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Sptic Dro
Spt16 Xla	Spt16 Ma	Spti6 Ma	Spt16 Ma	Spt16 Ma	Spt16 Ma	Spt16 Ma	Spt16 Ma	Spt16 Ma	Sptic Ma
Spt16 Hsa	Spt16 Hsa	Spti6 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Sptic Hsa
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Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Spt16 Sce	Sptt6 Sce
Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Spt16 Dro	Sptt6 Dro
Spt16 Ma	Spt16 Ma	Spt16 Xla	Spt16 Ma	Spt16 Ma	Spt16 Ma	Spt16 Xla	Spt16 XIa	Spt16 Ma	Sptt6 Ma
Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Spt16 Hsa	Sptt6 Hsa
1078 HR 1075 1065 KR <u>SRDDSRDNGHKSKNARH</u> 1085 1055 KK 1057 KK 1005RDNGHKSKNARH 1087 KRSRDDSRDNGHKSKNARH	1015 <u>KKH</u> 1017 1026 1027 SKHG SBS \$P <u>SKSSK KG</u> R HSS \$ <u>0KKISS</u> KD <u>KD</u> 1064 1018 <u>BKBK B</u> <u>CBD</u> <u>S</u> N <u>B</u> <u>C</u> <u>S</u> <u>B</u> <u>C</u> <u>S</u> <u>S</u> <u>S</u> <u>C</u> <u>KKK</u> 1064 1018 <u>BKBK</u> B <u><u>S</u></u> <u>S</u> <u>KSK</u> KG <u>B</u> <u>S</u> <u>S</u> <u>S</u> <u>S</u> <u>C</u> <u>KKK</u> <u>R</u> 1064 1019 <u>BKB</u> <u>K</u> <u>S</u>	997 ESGEDINDELERKENREDAKHDAFEERPS 1014 1012 EEGEDINDELEKKARARADRGHORGANERD 1035 995 STARVOSTMARADRARADRESRVEST 1035 995 STARVOSTMARADREKADRESRVEST 1035 995 STARVOSTMARADREKADRESRVEST 1035 995 STARVOSTMARADRESRVEST 1037 995 STARVOSTMARADRESRVEST 1037 995 STARVOSTMARADRESRVEST 1037 995 STARVOSTARADRESRVEST 1037 995 STARVOSTARADRESRVEST 1037 995 STARVOSTARADRESRVEST 1037 995 STARVOSTARADRESRVEST 1037 996 STARVOSTARADRESRVEST 1037 997 STARVOSTARADRESRVEST 1037 998 STARVOSTARADRESRVEST 1037 998	962 EVEDE- 966 1006 VTGDES 1011 975 ALMA <mark>NLARIGPIWSARLLRKTATIMPONTNNATANSIE</mark> 964 979 SADSEE 966 979 SLGSEE 966 • NLARIGPIWSARLLRKTATIMPONTNAATANSIE	946 EVSEVERSDADPSDEEEEESEEVSEDASEEDGVSES 961 968 EVSEVERSEDDVSDESAFSEDEFOSEVDDD18GDESED 1005 967 SEEETAPTPAPTPARTASATKIPSTORUCULARKART. 964 944 SELEDETFNPSEDDVSDEUDESAFSEDEFOSEVDD18GE 960 944 SELIBDETFNPSEDDVEEEEEDSDEDVSDEUGVSDEESAFSE 960 944 SELIBDETFNPSEDDVEEEEEDSDEDVSSEEAESSDVSKE 970 944 -SELIBDETFNPSEDDVEEEEEDSDEDVSSEFAESSDVSKE 970 947 -SELIBDETFNPSEDDVEEEEEDSDEDVSSEFAESSDVSKE 970 947 -SELIBDETFNPSEDDVEEEEESSDEDVSSEFAESSDVSKE 970 947 -SELIBDETFNPSEDDVEEEEESSDEDVSSEFAESSDVSKE 970	908 NMTTTTKKTVNEDPIGFFEGGANGFLGAPS-DDEG-DDSVE 945 929 NMATTNKSLQDDPVOFFLDGANNFLATGS-DDEASDESEE 967 968 NMGKINKTITDDPEGFFEGGANFLDPES-GSEGENETAE 906 904 NMTKINKTIVDDPEGFFEGGANSLEPEGEGSBAEEGOSE 943 907 NMTKINKTI DDPEGFFEGGANSLEPEGEGSBAEEGOSE 940 NMTKINKTI DDPEGFFEGGANSLEPEGEGSBAEEGOSE 940	468 FQDFRAPPIHINTEREQLDNVKEHLDSCDICFVEGPLN, 907 889 VKDFNKDVTHINTVPLESLDFLKQMLTDMDIPVTVSTIN, 928 828 FKEVNKKVAMVNA IPMNMLDHVKEHLNSCDIAVSEGVQSL 867 864 VKEVGKKVTMINAIPMASLDPIKEHLNSCDIAVEGVQSL 903 861 VKEVSKVTMINAIPMASLDPIKEHLNSCDIAVTEGVQSL 902 961 VKDV KKVTMINAIPM SLD .KEHLNSCDIAVTEGVQSL 903	\$28 TD CLVOLTDTPFFVITLNEIEIAMLERVOFGLKNFDLVFI \$67 \$49 TD CLVOLTBFFLV NLEEVEIGTLERVOFGLKNFDNFV \$67 \$760 SIGSLVNTTEMPFFVITLDEVELVHFERVOFHLKNFDNFV \$67 \$24 SIGSLVNTTEMPFFVITLDEVELUHFERVOFHLKNFDNVIN \$67 \$25 SIGSLVNTTEMPFFVITLDEVELUHFERVOFHLKNFDNVIN \$63 \$25 SIGLVNTTEMPFFVITLDEVELUHFERVOFHLKNFDNVIN \$63 \$25 SIGLVNTTEMPFFVITLDEVELUHFERVOFHLKNFDNVIN \$65 \$26 SIGLVNTTEMPFFVITLDEVELUHFERVOFHLKNFDNVIN \$65 \$27 SIGLVNTTEMPFFVITLDEVELUHFERVOFHLKNFDNVIN \$65 \$28 NUNTEMPFFVITLDEVELUHFERVOFHLKNFDNVIN \$65	788 KSFAEKIAEASEGALELDIFFRENARVPFASNVLLOPT 827 809 KVFADAIAEASNGLLTVENTFROLGFOGVPNASAVFCMPT 848 748 KSFCEVVETHTKSVVEFOTPFREGGFDGAPFASTVLLOPT 847 784 KNFIEXVESLTKEDLEFEIPFROLGFNGAPVASTCLLOPT 823 784 KNFIEXVEALTKEELEFEVPFROLGFNGAPVASTCLLOPT 823 787 KNFIEXVEALTKEELEFEVPFROLGFNGAPVASTCLLOPT 823	752 FOETGNKKRRVHVGOEGELEGEGERARRAAD.DREF 787 769 VDETGGORAGSREARVAGGEDELEGEGERARRAAD.DREF 787 716 TOLGKHGHTHDGRODUARGARRAAD.RKHAAD.KTAF 747 752 TOLGKHGHTHBRODUVAEGLERENARKKKTAF 783 749 TOLGKHGHTHBRODUVAEGLERENARKKKTAF 783 710 LGKHGHTH

Figure S1. (A) Primary sequence alignments between S. pombe Spt16 and select eukaryotic orthologues

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SSRP1 Spo SSRP1 Sce SSRP1 Dme SSRP1 XIa SSRP1 XIa	SSRP1 Spo SSRP1 Sce SSRP1 Dme SSRP1 Xa SSRP1 Hsa	SSRP1 Spo SSRP1 Sce SSRP1 Dme SSRP1 Ma SSRP1 Hsa	SSRP1 Spo SSRP1 Sce SSRP1 Dme SSRP1 Ma SSRP1 Hsa	SSRP1 Spo SSRP1 Sce SSRP1 Dme SSRP1 XIa SSRP1 Hsa	SSRP1 Spo SSRP1 Sce SSRP1 Dme SSRP1 XIa SSRP1 Hsa	SSRP1 Spo SSRP1 Sce SSRP1 Dme SSRP1 Ma SSRP1 Hsa
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Figure S1. (B) Primary sequence alignments between S. pombe Pob3 (SSRP1) and select eukaryotic orthologues

spt16-GFP



Figure S2. Tagged isoforms of the S. pombe Pob3 and Spt16 proteins are functional.

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- (A) Tagged FPH-Pob3, Spt16-GFP and double tagged strains are functional in the ADE-colorimetric centromere silencing assay.
- (B) Pob3-GFP and Spt16-GFP fusion proteins do not affect centromeric silencing. Serial dilutions of wild-type (WT), $clr4\Delta$, $pob3\Delta$, pob3-GFP and spt16-GFP strains.



Figure S3. *spt16*+ is an essential gene.

Tetrads dissected from the diploid *spt16::kanMX6/spt16+* were grown on YE5S media at 32 degrees Celsius for 2 days. All growing spore clones were G418 sensitive.



Strain EL44 = *pob3+::KanMX6* construction & verification

(a) Primers to amplify the KanR deletion cassette for *pob3*+::KanMX6 strain 200674 Delta FACTsmall::KanR FWD AATGTGTTAATGTGTGAAATTTGAGAATAACCTGGTATAGCTGTTTTCTGACCA

200675 Delta FACTsmall::KanR REV

AATTTGTAATAGCAAAAGACAAGGCTGAAAAGTTGATCCAAATAGACTTCCA ATTTAACATTGCTCAATTTTATAGATCATTAGAATTCGAGCTCGTTTAAAC (includes the pob3's TAA) anneals on the Kanamycin-containing plasmid

(b) Primers to check *pob3*+::KanMX6 deletion by PCR on the <u>5' end</u> and <u>3' end</u> 200676 Delta FACTsmall GCI FWD GCT GAA CCT CGT TCC TCA G

200641 General Check integ KanR REV CAA TTC AAC GCG TCT GTG AGG

200837 GCI KAN 3' FWD TAT GGA ACT GCC TCG GTG AG

200903 BJM GCI REV TTT ACC ACT CGG ATT CAT CG

5' end (200676/200641) expected amplicon: 604bp 3' end (200903/200837) expected amplicon: 552bp





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Spel

pob3+

pob3+ pob3∆∷kan

pob3+ pob3∆∷kan

pob3⁺ pob3∆∷kan

pob3∆∷kan

ω







2 kb —



upstream probe:

kan probe:

2.6 kb + 2.0 kb

probe:

EtBr

ORF

upstream

kan

2.6 kb

0.5 kb —

1 & -

Figure S5. Soutern blot verification of pob3+ gene deletion in S. pombe.

DNA fragments obtained by restriction enzymes Ncol and Spel. (A) Diagram showing the wild-type pob3+ strain and pob3A::kanMX6 knockout strain, including the probes and expected sizes of

(B) Southern blot for pob3+ and pob3A::kanMX6 strains using the indicated radiolabelled ORF, upstream and kan probes.

Lejeune *et al.* Figure S5

Α Hydroxy-Urea (mM) 0 15 an 17 WT 2, sile 130 pob3∆ 藏 10 $clr4\Delta$: 4 ® Camptothecine (mM) Β 0 10 WT 编 频 104 1.10 pob3∆ rad3∆ 33 UV (Joules/m²) С 0 150 WT 10 . 1 :. 12 pob3∆ 34 27 rad3∆ 6-Aza-Uracil (mg/ml) D 0 2 $tfs1\Delta$ WT 潑 $tfs1\Delta pob3\Delta$ pob3∆ -----3

Figure S6. The small subunit of the *S. pombe* chromatin remodeling complex FACT (Pob3) has a role in genome stability.

Sensitivity of wild-type, *pob3*∆ deletion and reference yeast strains to:
(A) Hydroxyurea (HU), which reveals defects in DNA replication.
(B) camptothecine (CPT) and (C) ultra-violet (UV) radiation, both of which reveal defects in controlling induced DNA damage.
(D) 6-aza-uracil (6AU), a small molecule that affects intracellular GTP levels and is commonly used to screen for mutants affecting transcript elongation.



Figure S7. GFP-Swi6 delocalization assay.

GFP-Swi6 is functional and a good marker for centromeres and telomeres (Pidoux *et al.*, 2000).

GFP-Swi6 fluorescence images of wild-type (WT), $clr4\Delta$ and $pob3\Delta$ cells. GFP-Swi6 is delocalized from centromeres and telomeres in $clr4\Delta$ mutants, as opposed to WT and $pob3\Delta$ cells.

Table S1. Gene expression profiling of a *pob3* Δ strain relative to wild-type *S. pombe*.

LOWER expression 15 genes (total)	in <i>pob3</i> Δ versus WT. 2-fold cut-off (3 of 4 data points):
Gene Name	Gene dB Product description
SPCC965.14c	putative cytidine and deoxycytidylate deaminase zinc-binding protein
SPAC644.05c	putative deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23); dUTP pyrophosphatase
rps10-2	40S ribosomal protein S10
sou1	sorbitol utilization protein sou1; short chain dehydrogenase
SPAC926.05c	dnaj protein
SPBC609.05	similar to S. cerevisiae POB3 protein that binds to DNA polymerase
= <i>pob3</i>	I; putative structure specific recognition protein
SPAC1B3.16c	MFS transporter of unknown specificity
SPAC5D6.05	Protein that plays a role in cell separation, mating and differentiation
SPAC694.03	hypothetical protein; similar to S. cerevisiae YCL047C
SPAC29B12.04	putative pyridoxine (vitamin B6) biosynthetic enzyme; by similarity to yeast snz1
SPCC622.19	hypothetical protein; (conserved in fungi- Gaillardin et al)
SPBC146.08c	putative elongation initation factor eIF1a
SPBP23A10.03c	hypothetical protein; similar to S. cerevisiae YDR511W
vtil	putative vesicle transport V-snare protein
SPBC1709.06	conserved hypothetical protein; UPF0034 family
HIGHER expression	n in <i>pob3</i> ∆ <i>versus</i> WT. 2-fold cut-off (3 of 4 data points):
44 genes (total)	
Gene Name	Gene dB Product description
fio1	iron transport multi-copper oxidase precursor
hsp9	heat shock protein hsp9
hsp16	heat shock protein hsp16
SPAC29A4.06c	hypothetical protein; contains Pfam-B_33047; shares conserved region with <i>Drosophila</i> CG15747; <i>Arabidopsis</i> F12K2.14; and C. elegans C16C10.6; predicted coiled-coil
cox1	
lys7	putative alpha-aminoadipate reductase small chain, sixth step in lysine biosynthesis pathway- from ACPS domain
fip1	iron permease
frp1	ferric reductase transmembrane componen
SPAC212.06c	pseudogene; truncated C-terminal of DNA helicase in rearranged telomeric region
SPAC212.08c	hypothetical protein; possibly <i>S. pombe</i> specific; duplicated in telomeric region; contains N-term predicted signal sequence
SPAC212.11	DNA helicase possibly pseudo
SPACIF8.03c	MFS efflux transporter of unknown specificity
SPAC1F8.03c SPAC750.07c	MFS efflux transporter of unknown specificity very hypothetical protein

SPAC1782.01	similar to S. cerevisiae Ecm29 cell wall stucture/biosynthesis protein
SPAC22F8.12c	hypothetical protein; serine-rich protein; sequence orphan; predicted
	N-terminal signal sequence
pim1	putative peptide transporter
SPAC1002.19	putative GTP cyclohydrolase; riboflavin biosynthesis
SPCC338.12	putative proteinase precursor
SPAC9E9.04	conserved hypothetical protein; putative endoplasmic reticulum
	transmembrane protein; similar to S. cerevisiae YET1; contains
	predicted N-term signal sequence; contains 2 predicted
	transmembrane helices; contains predicted C-term coiled-coil
SPCC965.07c	Glutathione S-transferase
srp14	signal recognition particle 14 kda protein
SPAC11H11.05c	very hypothetical protein
SPAC1002.17c	probable uracil phosphoribosyltransferase
SPBPJ4664.02	hypothetical protein; sequence orphan; low similarity to
	glycoamylases and other cell surface proteins; contains ~250-270
	copies of a 13 AA repeat, NSSTPITSSSIL; contains predicted N-
	terminal signal sequence
SPAC22F8.05	putative alpha, alpha-trehalose-phosphate synthase
SPBC1921.06c	hypothetical protein; sequence orphan; contains predictd N-term
	signal sequence
SPBC2/B12.03c	putative c-5 sterol desaturase
SPCC1/39.08c	short chain dehydrogenase; putative sorbitol utilization
SPAPBIAII.03	putative FMN dependent dehydrogenase; similar to lactate
SDAC10C12.00	aenyarogenase
SPAC19G12.09	
SPBC337.00C	2 iconnonvienalata dahudratasa
1012	3-isopropyinalate denydratase
	In the protein
KIPO	kinesin-like protein
SPAC12B10.10	region
50024	nutative component of the CODII costs involved in endeployment
Sec24	reticulum to Golgi transport
cdc16	cell division control protein 16: spindle assembly checkpoint
cucio	component: GTPase-activating protein (GAP) for Sng1p GTPase:
	essential two-component GEE for the GTPase spg1 (with byr4)
SPBPB2B2.01	putative amino-acid permease
SPAC637.03	hypothetical protein: sequence orphan: contains 8 predicted
	transmembrane segments contains predicted N-term signal sequence
SPBC21D10.10	bromodomain protein
SPBC887.16	very hypothetical protein
SPAC27D7.05c	hypothetical protein: sequence orphan: has transcript from
	microarray
SPAC27D7.06	putative electron transfer flavoprotein alpha-subunit precursor

HIGH ex	pression in <i>pob3A</i> cut 2.0 (3 of 4)	44 genes in li	st	
P-value	Similar List Name	Genes in list	Genes in overlap	Reference for gene list
1,07e-7	HIGH expression in <i>rpb7-G150D</i> cut 1.5 (6 of 8)	62	10	Djupedal et al (2005), Genes Dev, 19, 2301
2,56e-6	HIGH expression in <i>clr3D</i> cut 1.5	61	9	Hansen et al (2005), Mol Cell Biol, 25, 590
0,000136	HIGH expression in pSwi6 cut 1.5 (3 of 4)	254	13	Wiren et al (2005), EMBO J, 17, 2906
0,00162	HIGH expression in <i>clr6-1</i> cut 2.0 (6 of 10)	63	7	Wiren et al (2005), EMBO J, 17, 2906
0,00318	HIGH expression in <i>clr6-1 clr3D</i> cut 1.5	570	17	Hansen et al (2005), Mol Cell Biol, 25, 590
0,00472	HIGH expression in <i>clr1D</i> cut 1.5	47	8	Hansen et al (2005), Mol Cell Biol, 25, 590
0,00518	HIGH expression in <i>clr4-681</i> cut1.5	107	8	Hansen et al (2005), Mol Cell Biol, 25, 590
0,0109	LOW IGR WT H4K16Ac H3 Cter corr cut 1.5	1267	24	Wiren et al (2005), EMBO J, 17, 2906
0,0115	LOW IGR WT H4K5Ac H3 Cter corr cut 1.5	1110	22	Wiren et al (2005), EMBO J, 17, 2906
0,0115	HIGH expression in <i>clr6-1</i> (6 of 10) cut 1.5	253	11	Wiren et al (2005), EMBO J, 17, 2906
0,0309	LOW IGR WT H4K12Ac H3 Cter corr cut 1.5	1083	21	Wiren et al (2005), EMBO J, 17, 2906
0,0356	HIGH expression in <i>clr3-735</i> cut1.5	183	9	Hansen et al (2005), Mol Cell Biol, 25, 590
LOW exp	ression in <i>pob3A</i> cut 2.0 (3 of 4)	15 genes in li	st	
P-value	Similar List Name	Genes in list	Genes in overlap	Ref. for gene list
0,0229	LOW expression in <i>rpb7-G150D</i> cut 1.5 (6 of 8)	47	4	Djupedal et al (2005), Genes Dev, 19, 2301
For methods The hyper-ge randomly san	<i>section</i> : Similar gene lists were identified using the automatic hyper-ge ometric distribution test calculates the probability of overlap correspon pled from a universe of <i>u</i> genes:	cometric distribution to ding to k or more generations.	ests in the gene list inspecto es between a list of <i>n</i> genes	or function of Gene Spring v7.2 software (Silicon Genetics), compared against another gene list of <i>m</i> fragments when
$\frac{1}{m}$	$\sum_{i=k}^{n} {m \choose i} {u-m \choose n-i}$			

Table Co H . • 5 1.1.1.1. .

Table S3

Strain list (main figures)

Strain	Genotype
EL18	h+ leu1-32, ade6-216, ura4D18, imr1R(Ncol)::ura4+,
EL32	h+ clr4::kanMX6+, imr1R(Ncol)::ura4+, leu1-32, ade6-216, ura4D18
EL44	h+ pob3::kanMX6+, imr1R(Ncol)::ura4+, ade6-216, leu1-32, ura4D18
EL87	h- pob3::kanMX6, imr1R(Ncol):ura4+, leu1-32, ade6-210, ura4D18
EL93	h+ pob3::kanMX6, otrIR(SphI):ura4, ade6-210, his3D1?, leu1-32, ura4DS/E
EL102	h? pob3::kanMX6, mat3M::ura4, ade6-210, arg3D4, leu1-32, ura4D18
EL105	h? pob3::kanMX6, (rDNA:ura4) Ylp2.4pUCura4.7, ade6-210, leu1-32, his3D1, ura4DS/E,
EL107	h? pob3::kanMX6, otr2:ura4+ ?, TM1:arg3+, TM3:ade6+ ?, tel:his3+, ade6-210, arg3D4, leu1-32, his3D1, ura4D18/DS/E ?
EL127	h- spt16-GFP-kanMX6, otr1R (SphI)::ura4, arg3D4, his3D1, leu1-32, ura4DS/E
EL130	h- pob3-GFP-kanMX6, otr1R (Sphl):ura4, arg3D4, his3D1, leu1-32, ura4DS/E
EL238	h- pob3::natMX6, ade6-210, arg3D4, his3D1, leu1-32, ura4DS/E
EL243	h? pob3::kanMX6, otrIR(SphI):ade6, ade6-210, leu1-32, ura4D18/DS-E?
EL306	h+ FPH-pob3, otrIR(SphI):ade6, ade6-210, leu1-32, ura4-D18
EL319	h? pob3::kanMX6, dcr1::natMX6, otrlR:ura4, ade6-210, his?, leu?, ura4D18/DS-E?
EL332	h? pob3::kanMX6, [CM3112 sup3e], ade6-704, arg3D4?, leu1-32, his3D1, ura4-D18
EL344	h? FPH-pob3, spt16-GFP-kanMX6, otrIR(SphI):ade6, ade6-210, arg3D4?, his3D1?, leu1-32, ura4D18
EL348	h? pob3::natMX6, [Ch16 ade6-216 m23::ura4], ade6-210, arg3D4?, his3D1?, leu1-32, ura4DS/E
FY511	h90 mat3-M::ura4, ade6-216, leu1-32, ura4-D18
FY521	h- [Ch16 ade6-216 m23::ura4], ade6-210, leu1-32, ura4DS/E
FY1034	h? swi6::his1, otr1R (dg-glu BamHI-Spe1 fragment) SphI::ura4, ade6-210, his1-102, leu1-32, ura4-DS/E
FY1180	h+ otr1R(dg-glu)Sphl:ade6, ade6-210, leu1-32, ura4-D18
FY2116	h- [CM3112 sup3e], ade6-704, his3D1, leu1-32, ura4-D18
FY3027	h+ TM1::arg3, TM3::ade6, tel::his3, otr2::ura4, ade6-210, arg3D4, his3D1, leu1-32, ura4-D18/DS-E?
FY3606	h? rik1::leu2,TM1::arg3,TM3::ade6,otr2::ura4, his3::tel, ade6-210, arg3D4, his3D1, leu1-32, ura4D18
FY4134	h- ade6-210, arg3D4, his3D1, leu1-32, ura4DS/E
FY4841	h- otr1R(SphI)::ura4, arg3D4, his3D1, leu1-32, ura4DS/E
FY6084	h- clr4::LEU2+, otr1R(SphI):ura4 ura4D/SE, leu1-32, ade6-210/216?
FY6603	h+ Ylp2.4pUCura4.7, ura4-DS/E, leu1-32, ade6-216
FY6802	h+ tas3::kanMX6, imr1R(Nco1)::ura4+, ade6-216, leu1-32, ura4D18/DS-E?
FY7036	h- dcr1::natMX6, otr1R(dg-glu)Sphl:ade6, ade6-210, his3D1?, leu1-32?, ura4D18/DS-E?

Strain list (Supplementary figures)

Strain	Genotype
EL63	h+ ade6-210 leu1-32
EL90	h+ pob3::kanMX6, ade6-210, arg3D4, his3D1, leu1-32, ura4D18
EL98	h? pob3::kanMX6, ars1(Mlul)::pREP81X-gfp-swi6-LEU2+, ade6-210/216?, leu1-32, ura4-D18
EL111	h+ pob3::kanMX6, ade6-210, leu1-32

- EL115 h? pob3::kanMX6, tfs1::LEU2+, ade6-210, leu1-32, can1-1?
- EL173 h+ tfs1::natMX6, ade6-210, leu1-32
- EL229 h? clr4::LEU2+ otr1R(Sph1):ade6+, ade6-210/216?, leu1-32, ura4D18/DS-E?
- EL345 h? FPH-pob3, spt16-GFP-kanMX6, otrIR(dg-glu)SphI:ade6, ade6-210, arg3D4?, his3D1?, leu1-32, ura4D18
- EL351 h? spt16-GFP-KanMX6, otr1R(dg-glu)Sph1:ade6, ade6-210, arg3D4?, his3D1?, leu1-32, ura4D18/DS-E?
- EL355 h+/h+ spt16::KanMX6/ORF, ade6-M210/ade6-M216, ura4D18/ura4D18, leu1-32/leu1-32
- FY1665 h- rad3::ura4+, ade6-704, leu1-32, ura4-D18
- FY2214 h- ars1(Mlul)::pREP81Xgfpswi6 LEU2+, ade6-210, leu1-32, ura4-D18
- FY3300 h? clr4 :: ura4 ars1(Mlul)::pREP81Xgfpswi6-LEU2+, ade6-210/216?, leu1-32, ura4D18/DS-E?