

Supplemental Material to:

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A CRISPR-based approach for proteomic analysis of a single genomic locus

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article/29919/](http://www.landesbioscience.com/journals/epigenetics/article/29919/)**

Table S1. Proteins enriched with CRISPR-ChAP-MS analysis of GAL1 promoter chromatin in galactose-containing media enriched >2-fold (with at least 5 spectral counts) with Cas9-PrA/gRNA vs the no gRNA control are listed (86 proteins are categorized as those involved in transcription (11 proteins) and those that are common contaminants)

Identified Proteins (transcription)

REB1_YEAST DNA-binding protein REB1 OS=*Saccharomyces cerevisiae* GN=REB1 PE=1 SV=2
SPT5_YEAST Transcription elongation factor SPT5 OS=*Saccharomyces cerevisiae* GN=SPT5 PE=1 SV=1
TOA2_YEAST Transcription initiation factor IIA small subunit OS=*Saccharomyces cerevisiae* GN=TOA2 PE=1 SV=1
BAF1_YEAST Transcription factor BAF1 OS=*Saccharomyces cerevisiae* GN=BAF1 PE=1 SV=3
SIN3_YEAST Transcriptional regulatory protein SIN3 OS=*Saccharomyces cerevisiae* GN=SIN3 PE=1 SV=2
H2B2_YEAST Histone H2B.2 OS=*Saccharomyces cerevisiae* GN=H2B2 PE=1 SV=2
UME1_YEAST Transcriptional regulatory protein UME1 OS=*Saccharomyces cerevisiae* GN=UME1 PE=1 SV=1
POB3_YEAST FACT complex subunit POB3 OS=*Saccharomyces cerevisiae* GN=POB3 PE=1 SV=1
RSC6_YEAST Chromatin structure-remodeling complex protein RSC6 OS=*Saccharomyces cerevisiae* GN=RSC6 PE=1
RPA14_YEAST DNA-directed RNA polymerase I subunit RPA14 OS=*Saccharomyces cerevisiae* GN=RPA14 PE=1 SV=1
RSC7_YEAST Chromatin structure-remodeling complex subunit RSC7 OS=*Saccharomyces cerevisiae* GN=NPL6 PE=1

Identified Proteins (metabolic, ribosomal, common contaminants)

PYRF_YEAST Orotidine 5'-phosphate decarboxylase OS=*Saccharomyces cerevisiae* GN=URA3 PE=1 SV=2
SCW4_YEAST Probable family 17 glucosidase SCW4 OS=*Saccharomyces cerevisiae* GN=SCW4 PE=1 SV=1
RAS2_YEAST Ras-like protein 2 OS=*Saccharomyces cerevisiae* GN=RAS2 PE=1 SV=4
PWP1_YEAST Periodic tryptophan protein 1 OS=*Saccharomyces cerevisiae* GN=PWP1 PE=1 SV=1
ERG19_YEAST Diphosphomevalonate decarboxylase OS=*Saccharomyces cerevisiae* GN=ERG19 PE=1 SV=2
KEL1_YEAST Kelch repeat-containing protein 1 OS=*Saccharomyces cerevisiae* GN=KEL1 PE=1 SV=1
BGL2_YEAST Glucan 1,3-beta-glucosidase OS=*Saccharomyces cerevisiae* GN=BGL2 PE=1 SV=1
SCW10_YEAST Probable family 17 glucosidase SCW10 OS=*Saccharomyces cerevisiae* GN=SCW10 PE=1 SV=1
FKBP2_YEAST FK506-binding protein 2 OS=*Saccharomyces cerevisiae* GN=FKB2 PE=1 SV=1
YKH7_YEAST Uncharacterized protein YKL077W OS=*Saccharomyces cerevisiae* GN=YKL077W PE=1 SV=1
BRX1_YEAST Ribosome biogenesis protein BRX1 OS=*Saccharomyces cerevisiae* GN=BRX1 PE=1 SV=1
PAL1_YEAST Uncharacterized protein YDR348C OS=*Saccharomyces cerevisiae* GN=YDR348C PE=1 SV=1
KPR1_YEAST Ribose-phosphate pyrophosphokinase 1 OS=*Saccharomyces cerevisiae* GN=PRS1 PE=1 SV=1
YM11_YEAST Uncharacterized protein YMR124W OS=*Saccharomyces cerevisiae* GN=YMR124W PE=1 SV=2
PRS7_YEAST 26S protease regulatory subunit 7 homolog OS=*Saccharomyces cerevisiae* GN=RPT1 PE=1 SV=1
RRP9_YEAST Ribosomal RNA-processing protein 9 OS=*Saccharomyces cerevisiae* GN=RRP9 PE=1 SV=1
CIC1_YEAST Proteasome-interacting protein CIC1 OS=*Saccharomyces cerevisiae* GN=CIC1 PE=1 SV=1
MPM1_YEAST Mitochondrial peculiar membrane protein 1 OS=*Saccharomyces cerevisiae* GN=MPM1 PE=1 SV=1
IDI1_YEAST Isopentenyl-diphosphate Delta-isomerase OS=*Saccharomyces cerevisiae* GN=IDI1 PE=1 SV=2
PEX14_YEAST Peroxisomal membrane protein PEX14 OS=*Saccharomyces cerevisiae* GN=PEX14 PE=1 SV=1
YER0_YEAST Uncharacterized protein YER080W OS=*Saccharomyces cerevisiae* GN=YER080W PE=1 SV=1
RT23_YEAST 37S ribosomal protein S23, mitochondrial OS=*Saccharomyces cerevisiae* GN=RSM23 PE=1 SV=2
BUD21_YEAST Bud site selection protein 21 OS=*Saccharomyces cerevisiae* GN=BUD21 PE=1 SV=1
ELOC_YEAST Elongin-C OS=*Saccharomyces cerevisiae* GN=ELC1 PE=1 SV=1
CDC11_YEAST Cell division control protein 11 OS=*Saccharomyces cerevisiae* GN=CDC11 PE=1 SV=1
RFC2_YEAST Replication factor C subunit 2 OS=*Saccharomyces cerevisiae* GN=RFC2 PE=1 SV=1
EFTU_YEAST Elongation factor Tu, mitochondrial OS=*Saccharomyces cerevisiae* GN=TUF1 PE=1 SV=1
PPN1_YEAST Endopolyphosphatase OS=*Saccharomyces cerevisiae* GN=PPN1 PE=1 SV=1
ETFA_YEAST Probable electron transfer flavoprotein subunit alpha, mitochondrial OS=*Saccharomyces cerevisiae* GN=ETFA PE=1 SV=1

GBG_YEAST Guanine nucleotide-binding protein subunit gamma OS=Saccharomyces cerevisiae GN=STE18 PE=1 SV
PUR4_YEAST Phosphoribosylformylglycinamide synthase OS=Saccharomyces cerevisiae GN=ADE6 PE=1 SV=2
SUCB_YEAST Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Saccharomyces cerevisiae GN=LSC
UTP15_YEAST U3 small nucleolar RNA-associated protein 15 OS=Saccharomyces cerevisiae GN=UTP15 PE=1 SV=1
SEC3_YEAST Exocyst complex component SEC3 OS=Saccharomyces cerevisiae GN=SEC3 PE=1 SV=1
AML1_YEAST N(6)-adenine-specific DNA methyltransferase-like 1 OS=Saccharomyces cerevisiae GN=AML1 PE=1 SV
RM10_YEAST 54S ribosomal protein L10, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL10 PE=1 SV=2
UCRI_YEAST Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Saccharomyces cerevisiae GN=RIP1 PE=1
KHSE_YEAST Homoserine kinase OS=Saccharomyces cerevisiae GN=THR1 PE=1 SV=4
SMD1_YEAST Small nuclear ribonucleoprotein Sm D1 OS=Saccharomyces cerevisiae GN=SMD1 PE=1 SV=1
CYC1_YEAST Cytochrome c iso-1 OS=Saccharomyces cerevisiae GN=CYC1 PE=1 SV=2
PET10_YEAST Protein PET10 OS=Saccharomyces cerevisiae GN=PET10 PE=1 SV=3
RT35_YEAST 37S ribosomal protein S35, mitochondrial OS=Saccharomyces cerevisiae GN=MRPS35 PE=1 SV=1
PROF_YEAST Profilin OS=Saccharomyces cerevisiae GN=PFY1 PE=1 SV=2
NOP13_YEAST Nucleolar protein 13 OS=Saccharomyces cerevisiae GN=NOP13 PE=1 SV=1
RM27_YEAST 54S ribosomal protein L27, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL27 PE=1 SV=2
YHA8_YEAST Uncharacterized transporter YHL008C OS=Saccharomyces cerevisiae GN=YHL008C PE=1 SV=1
DYL1_YEAST Dynein light chain 1, cytoplasmic OS=Saccharomyces cerevisiae GN=DYN2 PE=1 SV=1
CDC73_YEAST Cell division control protein 73 OS=Saccharomyces cerevisiae GN=CDC73 PE=1 SV=1
HRB1_YEAST Protein HRB1 OS=Saccharomyces cerevisiae GN=HRB1 PE=1 SV=2
SNZ1_YEAST Pyridoxine biosynthesis protein SNZ1 OS=Saccharomyces cerevisiae GN=SNZ1 PE=1 SV=1
RS9A_YEAST 40S ribosomal protein S9-A OS=Saccharomyces cerevisiae GN=RPS9A PE=1 SV=3
ARPC2_YEAST Actin-related protein 2/3 complex subunit 2 OS=Saccharomyces cerevisiae GN=ARC35 PE=1 SV=1
TRS31_YEAST Transport protein particle 31 kDa subunit OS=Saccharomyces cerevisiae GN=TRS31 PE=1 SV=1
PUT2_YEAST Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae GN=PU
RM51_YEAST 54S ribosomal protein L51, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL51 PE=1 SV=1
LGUL_YEAST Lactoylglutathione lyase OS=Saccharomyces cerevisiae GN=GLO1 PE=1 SV=1
HIS8_YEAST Histidinol-phosphate aminotransferase OS=Saccharomyces cerevisiae GN=HIS5 PE=1 SV=2
NPT1_YEAST Nicotinate phosphoribosyltransferase OS=Saccharomyces cerevisiae GN=NPT1 PE=1 SV=3
METK2_YEAST S-adenosylmethionine synthase 2 OS=Saccharomyces cerevisiae GN=SAM2 PE=1 SV=3
FMP10_YEAST Uncharacterized mitochondrial membrane protein FMP10 OS=Saccharomyces cerevisiae GN=FMP1
YPT31_YEAST GTP-binding protein YPT31/YPT8 OS=Saccharomyces cerevisiae GN=YPT31 PE=1 SV=3
YMX6_YEAST Uncharacterized protein YMR086W OS=Saccharomyces cerevisiae GN=YMR086W PE=1 SV=1
ACPM_YEAST Acyl carrier protein, mitochondrial OS=Saccharomyces cerevisiae GN=ACP1 PE=1 SV=1
RM33_YEAST 54S ribosomal protein L33, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL33 PE=1 SV=4
RL14A_YEAST 60S ribosomal protein L14-A OS=Saccharomyces cerevisiae GN=RPL14A PE=1 SV=1
PBP1_YEAST PAB1-binding protein 1 OS=Saccharomyces cerevisiae GN=PBP1 PE=1 SV=1
GPDM_YEAST Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae GN=GUT2 PE=1
RIB1_YEAST GTP cyclohydrolase-2 OS=Saccharomyces cerevisiae GN=RIB1 PE=1 SV=2
OTC_YEAST Ornithine carbamoyltransferase OS=Saccharomyces cerevisiae GN=ARG3 PE=1 SV=1
UBP6_YEAST Ubiquitin carboxyl-terminal hydrolase 6 OS=Saccharomyces cerevisiae GN=UBP6 PE=1 SV=1
SUR7_YEAST Protein SUR7 OS=Saccharomyces cerevisiae GN=SUR7 PE=1 SV=1
TWF1_YEAST Twinfilin-1 OS=Saccharomyces cerevisiae GN=TWF1 PE=1 SV=1
RN49_YEAST 54S ribosomal protein L49, mitochondrial OS=Saccharomyces cerevisiae GN=MRPL49 PE=1 SV=2
RSM28_YEAST 37S ribosomal protein RSM28, mitochondrial OS=Saccharomyces cerevisiae GN=RSM28 PE=1 SV=2

edia. 1832 protiens were identified and those

is). Enrichment was calculated by normalized NSAF as detailed in Byrum et al., 2013.

(74 proteins) in affinity purifications (Byrum et al., 2013).

| Gene symbol | Accession Numb | MW | gRNA/No gRNA (Fold Change) |
|-------------|----------------|---------|-------------------------------|
| REB1 | P21538 | 92 kDa | 8.1 |
| SPT5 | P27692 | 116 kDa | 5.4 |
| TOA2 | P32774 | 13 kDa | 5.1 |
| BAF1 | P14164 | 82 kDa | 4.7 |
| SIN3 | P22579 | 175 kDa | 4.2 |
| H2B2 | P02294 | 14 kDa | 4.1 |
| UME1 | Q03010 | 51 kDa | 3.2 |
| POB3 | Q04636 | 63 kDa | 3 |
| RSC6 | P25632 | 54 kDa | 2.8 |
| RPA14 | P50106 | 15 kDa | 2.4 |
| RSC7 | P32832 | 50 kDa | 2.1 |
| | | | |
| PYRF | P03962 | 29 kDa | 15 |
| SCW4 | P53334 | 40 kDa | 15 |
| RAS2 | P01120 | 35 kDa | 12 |
| PWP1 | P21304 | 64 kDa | 11 |
| ERG19 | P32377 | 44 kDa | 9.6 |
| KEL1 | P38853 | 131 kDa | 9.6 |
| BGL2 | P15703 | 34 kDa | 9.3 |
| SCW10 | Q04951 | 40 kDa | 7.2 |
| FKBP2 | P32472 | 14 kDa | 6 |
| YKH7 | P36081 | 46 kDa | 6 |
| BRX1 | Q08235 | 34 kDa | 5.8 |
| PAL1 | Q05518 | 55 kDa | 5.8 |
| KPR1 | P32895 | 47 kDa | 5 |
| YM11 | P39523 | 106 kDa | 5 |
| PRS7 | P33299 | 52 kDa | 5 |
| RRP9 | Q06506 | 65 kDa | 5 |
| CIC1 | P38779 | 43 kDa | 4.7 |
| MPM1 | P40364 | 28 kDa | 4 |
| IDI1 | P15496 | 33 kDa | 3.9 |
| PEX14 | P53112 | 38 kDa | 3.6 |
| YER0 | P40053 | 72 kDa | 3.5 |
| RT23 | Q01163 | 56 kDa | 3.3 |
| BUD21 | Q08492 | 24 kDa | 3.2 |
| ELOC | Q03071 | 11 kDa | 3.2 |
| CDC11 | P32458 | 48 kDa | 3.1 |
| RFC2 | P40348 | 40 kDa | 3.1 |
| EFTU | P02992 | 48 kDa | 3 |
| PPN1 | Q04119 | 78 kDa | 3 |
| ETFA | Q12480 | 37 kDa | 3 |

| | | | |
|-------|-------------|---------|-----|
| GBG | P18852 | 13 kDa | 3 |
| PUR4 | P38972 | 149 kDa | 3 |
| SUCB | P53312 | 47 kDa | 2.9 |
| UTP15 | Q04305 | 58 kDa | 2.9 |
| SEC3 | P33332 | 155 kDa | 2.9 |
| AML1 | P53200 | 29 kDa | 2.9 |
| RM10 | P36520 | 36 kDa | 2.9 |
| UCRI | P08067 | 23 kDa | 2.8 |
| KHSE | P17423 | 39 kDa | 2.8 |
| SMD1 | Q02260 | 16 kDa | 2.8 |
| CYC1 | P00044 | 12 kDa | 2.6 |
| PET10 | P36139 | 31 kDa | 2.6 |
| RT35 | P53292 | 40 kDa | 2.6 |
| PROF | P07274 | 14 kDa | 2.6 |
| NOP13 | P53883 | 46 kDa | 2.6 |
| RM27 | P36526 | 16 kDa | 2.6 |
| YHA8 | P38750 | 70 kDa | 2.6 |
| DYL1 | Q02647 | 10 kDa | 2.5 |
| CDC73 | Q06697 | 44 kDa | 2.5 |
| HRB1 | P38922 | 52 kDa | 2.5 |
| SNZ1 | Q03148 | 32 kDa | 2.5 |
| RS9A | O13516 | 22 kDa | 2.4 |
| ARPC2 | P53731 | 40 kDa | 2.4 |
| TRS31 | Q03337 | 32 kDa | 2.4 |
| PUT2 | P07275 | 64 kDa | 2.4 |
| RM51 | Q06090 | 16 kDa | 2.4 |
| LGUL | P50107 | 37 kDa | 2.4 |
| HIS8 | P07172 | 43 kDa | 2.3 |
| NPT1 | P39683 | 49 kDa | 2.3 |
| METK2 | P19358 | 42 kDa | 2.2 |
| FMP10 | P40098 | 28 kDa | 2.2 |
| YPT31 | P38555 (+1) | 24 kDa | 2.2 |
| YMX6 | Q04279 | 106 kDa | 2.2 |
| ACPM | P32463 | 14 kDa | 2.2 |
| RM33 | P20084 | 10 kDa | 2.2 |
| RL14A | P36105 | 15 kDa | 2.1 |
| PBP1 | P53297 | 79 kDa | 2.1 |
| GPDM | P32191 | 72 kDa | 2.1 |
| RIB1 | P38066 | 38 kDa | 2.1 |
| OTC | P05150 | 38 kDa | 2.1 |
| UBP6 | P43593 | 57 kDa | 2.1 |
| SUR7 | P54003 | 34 kDa | 2.1 |
| TWF1 | P53250 | 37 kDa | 2.1 |
| RN49 | P40858 | 18 kDa | 2.1 |
| RSM28 | Q03430 | 41 kDa | 2.1 |

| Identified F | Gene Symb | Accession # | MW | Spectral counts | | Normalized NSAF values | |
|--------------|-----------|-------------|---------|-----------------|---------|------------------------|------------|
| | | | | gRNA | No gRNA | gRNA | No gRNA |
| PYRF_YEAS | PYRF | P03962 | 29 kDa | 657 | 45 | 2.3034 | 0.15574 |
| SCW4_YEA | SCW4 | P53334 | 40 kDa | 43 | 3 | 0.11355 | 0.0076196 |
| RAS2_YEAS | RAS2 | P01120 | 35 kDa | 10 | 1 | 0.030093 | 0.0025358 |
| PWP1_YEA | PWP1 | P21304 | 64 kDa | 10 | 1 | 0.02054 | 0.0019358 |
| ERG19_YEA | ERG19 | P32377 | 44 kDa | 9 | 1 | 0.022174 | 0.0023133 |
| KEL1_YEAS | KEL1 | P38853 | 131 kDa | 6 | 1 | 0.0054931 | 0.00057277 |
| BGL2_YEAS | BGL2 | P15703 | 34 kDa | 78 | 10 | 0.23854 | 0.02567 |
| REB1_YEAS | REB1 | P21538 | 92 kDa | 5 | 1 | 0.0067677 | 0.00083919 |
| SCW10_YEA | SCW10 | Q04951 | 40 kDa | 24 | 3 | 0.067308 | 0.0093606 |
| FKBP2_YEA | FKBP2 | P32472 | 14 kDa | 5 | 1 | 0.028788 | 0.0047652 |
| YKH7_YEAS | YKH7 | P36081 | 46 kDa | 5 | 1 | 0.010224 | 0.0017008 |
| BRX1_YEAS | BRX1 | Q08235 | 34 kDa | 10 | 2 | 0.032329 | 0.0055678 |
| PAL1_YEAS | PAL1 | Q05518 | 55 kDa | 5 | 1 | 0.010082 | 0.0017505 |
| SPT5_YEAS | SPT5 | P27692 | 116 kDa | 5 | 1 | 0.0056711 | 0.001046 |
| TOA2_YEAS | TOA2 | P32774 | 13 kDa | 5 | 1 | 0.026691 | 0.005273 |
| KPR1_YEAS | KPR1 | P32895 | 47 kDa | 8 | 2 | 0.020962 | 0.004191 |
| YM11_YEA | YM11 | P39523 | 106 kDa | 6 | 2 | 0.0070735 | 0.001414 |
| PRS7_YEAS | PRS7 | P33299 | 52 kDa | 5 | 1 | 0.011132 | 0.0022086 |
| RRP9_YEAS | RRP9 | Q06506 | 65 kDa | 5 | 1 | 0.01006 | 0.0020314 |
| CIC1_YEAS | CIC1 | P38779 | 43 kDa | 6 | 1 | 0.014793 | 0.0031713 |
| BAF1_YEAS | BAF1 | P14164 | 82 kDa | 5 | 1 | 0.0072098 | 0.0015254 |
| SIN3_YEAS | SIN3 | P22579 | 175 kDa | 5 | 1 | 0.0037565 | 0.00088897 |
| H2B2_YEAS | H2B2 | P02294 | 14 kDa | 81 | 87 | 0.021748 | 0.0053125 |
| MPM1_YEA | MPM1 | P40364 | 28 kDa | 10 | 3 | 0.03595 | 0.0090786 |
| IDI1_YEAS | IDI1 | P15496 | 33 kDa | 18 | 5 | 0.054499 | 0.014115 |
| PEX14_YEA | PEX14 | P53112 | 38 kDa | 11 | 3 | 0.032705 | 0.0090831 |
| YER0_YEAS | YER0 | P40053 | 72 kDa | 11 | 3 | 0.018477 | 0.0052646 |
| RT23_YEAS | RT23 | Q01163 | 56 kDa | 5 | 2 | 0.010978 | 0.0033269 |
| BUD21_YEA | BUD21 | Q08492 | 24 kDa | 6 | 2 | 0.023279 | 0.0073049 |
| UME1_YEA | UME1 | Q03010 | 51 kDa | 6 | 2 | 0.014875 | 0.0046531 |
| ELOC_YEAS | ELOC | Q03071 | 11 kDa | 5 | 2 | 0.041449 | 0.012996 |
| CDC11_YEA | CDC11 | P32458 | 48 kDa | 12 | 4 | 0.033015 | 0.010509 |
| RFC2_YEAS | RFC2 | P40348 | 40 kDa | 6 | 2 | 0.014126 | 0.0046262 |
| EFTU_YEAS | EFTU | P02992 | 48 kDa | 40 | 14 | 0.095198 | 0.0321 |
| PPN1_YEAS | PPN1 | Q04119 | 78 kDa | 14 | 5 | 0.017319 | 0.0058652 |
| POB3_YEAS | POB3 | Q04636 | 63 kDa | 12 | 4 | 0.024482 | 0.0082034 |
| ETFA_YEAS | ETFA | Q12480 | 37 kDa | 11 | 4 | 0.027632 | 0.009349 |
| GBG_YEAS | GBG | P18852 | 13 kDa | 5 | 2 | 0.035393 | 0.011696 |
| PUR4_YEAS | PUR4 | P38972 | 149 kDa | 5 | 2 | 0.0042212 | 0.0014279 |
| SUCB_YEAS | SUCB | P53312 | 47 kDa | 27 | 10 | 0.059446 | 0.020597 |
| UTP15_YEA | UTP15 | Q04305 | 58 kDa | 8 | 3 | 0.01818 | 0.0063459 |
| SEC3_YEAS | SEC3 | P33332 | 155 kDa | 7 | 3 | 0.0060227 | 0.0020559 |
| AML1_YEA | AML1 | P53200 | 29 kDa | 5 | 2 | 0.017364 | 0.006086 |
| RM10_YEA | RM10 | P36520 | 36 kDa | 5 | 2 | 0.013874 | 0.0047367 |
| UCRI_YEAS | UCRI | P08067 | 23 kDa | 18 | 7 | 0.068993 | 0.024609 |
| KHSE_YEAS | KHSE | P17423 | 39 kDa | 9 | 3 | 0.019995 | 0.0071271 |
| SMD1_YEA | SMD1 | Q02260 | 16 kDa | 8 | 3 | 0.040301 | 0.0143 |

| | | | | | | | |
|------------|-------|------------|---------|-----|-----|-----------|-----------|
| RSC6_YEAS' | RSC6 | P25632 | 54 kDa | 7 | 3 | 0.015875 | 0.00569 |
| CYC1_YEAS' | CYC1 | P00044 | 12 kDa | 117 | 68 | 0.61144 | 0.2352 |
| PET10_YEA | PET10 | P36139 | 31 kDa | 17 | 7 | 0.048927 | 0.019041 |
| RT35_YEAS' | RT35 | P53292 | 40 kDa | 12 | 5 | 0.031711 | 0.011999 |
| PROF_YEAS | PROF | P07274 | 14 kDa | 11 | 4 | 0.058874 | 0.023044 |
| NOP13_YE/ | NOP13 | P53883 | 46 kDa | 6 | 3 | 0.017094 | 0.0065024 |
| RM27_YEA' | RM27 | P36526 | 16 kDa | 5 | 2 | 0.024505 | 0.0095335 |
| YHA8_YEAS | YHA8 | P38750 | 70 kDa | 5 | 2 | 0.009366 | 0.0036348 |
| DYL1_YEAS' | DYL1 | Q02647 | 10 kDa | 10 | 4 | 0.073508 | 0.029371 |
| CDC73_YEA | CDC73 | Q06697 | 44 kDa | 9 | 4 | 0.018285 | 0.0073158 |
| HRB1_YEAS | HRB1 | P38922 | 52 kDa | 9 | 4 | 0.020922 | 0.0084023 |
| SNZ1_YEAS | SNZ1 | Q03148 | 32 kDa | 5 | 3 | 0.006198 | 0.0025142 |
| RS9A_YEAS | RS9A | O13516 | 22 kDa | 151 | 156 | 0.0091554 | 0.0037905 |
| ARPC2_YEA | ARPC2 | P53731 | 40 kDa | 15 | 7 | 0.044768 | 0.018359 |
| TRS31_YEA' | TRS31 | Q03337 | 32 kDa | 8 | 4 | 0.026095 | 0.010779 |
| RPA14_YEA | RPA14 | P50106 | 15 kDa | 7 | 3 | 0.036547 | 0.01524 |
| PUT2_YEAS | PUT2 | P07275 | 64 kDa | 6 | 3 | 0.012072 | 0.0051256 |
| RM51_YEA' | RM51 | Q06090 | 16 kDa | 6 | 3 | 0.035158 | 0.014913 |
| LGUL_YEAS | LGUL | P50107 | 37 kDa | 5 | 2 | 0.012764 | 0.0053001 |
| HIS8_YEAS' | HIS8 | P07172 | 43 kDa | 9 | 5 | 0.024457 | 0.010784 |
| NPT1_YEAS | NPT1 | P39683 | 49 kDa | 5 | 2 | 0.010476 | 0.0046279 |
| METK2_YE/ | METK2 | P19358 | 42 kDa | 79 | 75 | 0.038801 | 0.017378 |
| FMP10_YE/ | FMP10 | P40098 | 28 kDa | 14 | 8 | 0.055633 | 0.0252 |
| YPT31_YEA | YPT31 | P38555 (+1 | 24 kDa | 9 | 4 | 0.028763 | 0.012951 |
| YMX6_YEA' | YMX6 | Q04279 | 106 kDa | 8 | 5 | 0.0073219 | 0.0033862 |
| ACPM_YEA' | ACPM | P32463 | 14 kDa | 8 | 4 | 0.046487 | 0.021428 |
| RM33_YEA' | RM33 | P20084 | 10 kDa | 7 | 3 | 0.054493 | 0.024282 |
| RL14A_YEA | RL14A | P36105 | 15 kDa | 111 | 121 | 0.010356 | 0.0050431 |
| PBP1_YEAS | PBP1 | P53297 | 79 kDa | 32 | 16 | 0.050084 | 0.024091 |
| GPDM_YEA | GPDM | P32191 | 72 kDa | 17 | 8 | 0.026484 | 0.012419 |
| RIB1_YEAS' | RIB1 | P38066 | 38 kDa | 16 | 9 | 0.043642 | 0.020754 |
| RSC7_YEAS' | RSC7 | P32832 | 50 kDa | 13 | 7 | 0.029347 | 0.014198 |
| OTC_YEAST | OTC | P05150 | 38 kDa | 13 | 6 | 0.031697 | 0.015373 |
| UBP6_YEAS | UBP6 | P43593 | 57 kDa | 9 | 5 | 0.019729 | 0.0094804 |
| SUR7_YEAS | SUR7 | P54003 | 34 kDa | 8 | 4 | 0.021538 | 0.010088 |
| TWF1_YEA' | TWF1 | P53250 | 37 kDa | 8 | 4 | 0.020141 | 0.0093864 |
| RN49_YEAS | RN49 | P40858 | 18 kDa | 6 | 3 | 0.026689 | 0.012968 |
| RSM28_YE/ | RSM28 | Q03430 | 41 kDa | 6 | 3 | 0.014043 | 0.0067459 |

**gRNA/No gRNA
(Fold Change)**

15
15
12
11
9.6
9.6
9.3
8.1
7.2
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6
5.8
5.8
5.4
5.1
5
5
5
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4.7
4.7
4.2
4.1
4
3.9
3.6
3.5
3.3
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3.1
3.1
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3
3
3
3
2.9
2.9
2.9
2.9
2.9
2.8
2.8
2.8

Table S2. Spectral counts (>2) for PTM-containing histone peptides isolated with GAL1 promoter chromatin

| | Sequence | Modification | No gRNA | Cas9/gRNA |
|------------|-----------------------|---------------------|---------|-----------|
| Histone H4 | (K)GLGkGGAKR(H) | H4K12acK16ac | 7 | 3 |
| Histone H3 | (R)kSTGGkAPR(K) | H3K9acK14ac | 7 | 7 |
| | (R)kQLASKaAR(K) | H3K18acK23ac | 5 | 6 |
| | (R)KSTGGkAPR(K) | H3K14ac | 12 | 17 |
| | (R)KQLASKaAR(K) | H3K23ac | 10 | 13 |
| | (R)KSAPSTGGVK(K) | H3K27ac | 5 | 4 |
| | (R)RFQkSTELLIR(K) | H3K56ac | 11 | 5 |
| | (R)EIAQDFkTDLR(F) | H3K79me | 5 | 4 |
| | (R)EIAQDFkTDLR(F) | H3K79me2 | 7 | 3 |
| H2B | (K)AEkKPASKAPAek(K) | H2BK6acK11ac | 5 | 4 |
| | (K)KPASKAPAekKPAek(K) | H2BK11acK16ac | 9 | 4 |
| | (K)AEkKPASK(A) | H2BK6ac | 7 | 3 |

in using CRISPR-ChAP-MS.

Fold Change =gRNA/No gRNA

0.4285714

1

1.2

1.4166667

1.3

0.8

0.4545455

0.8

0.4285714

0.8

0.4444444

0.4285714