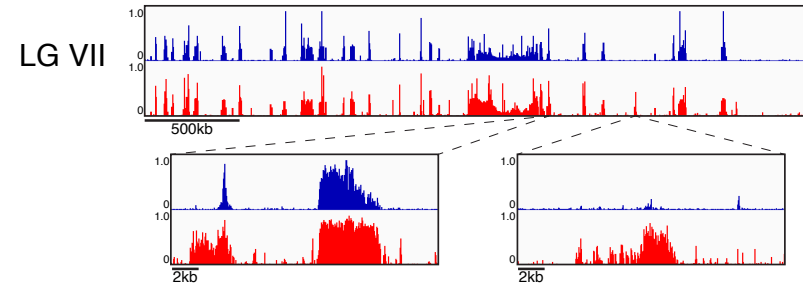
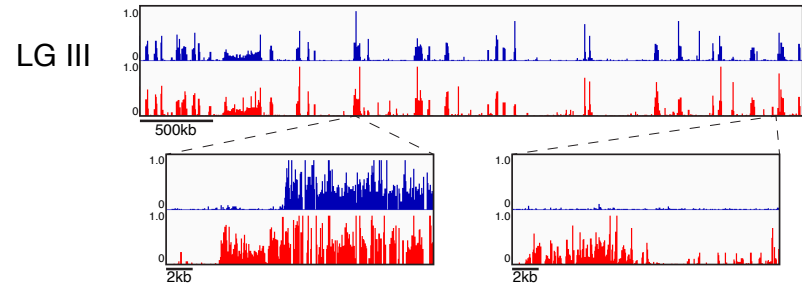
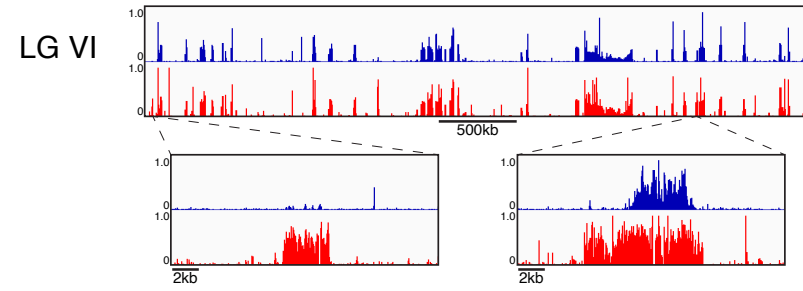
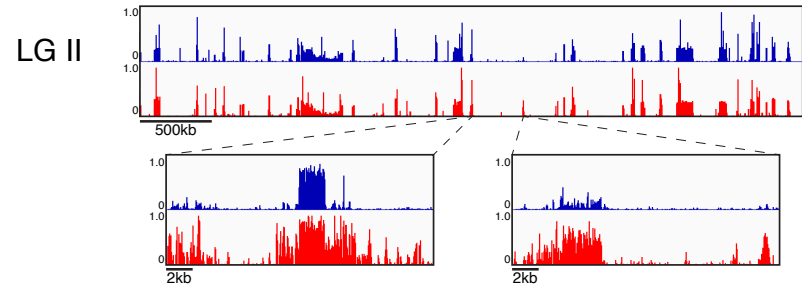
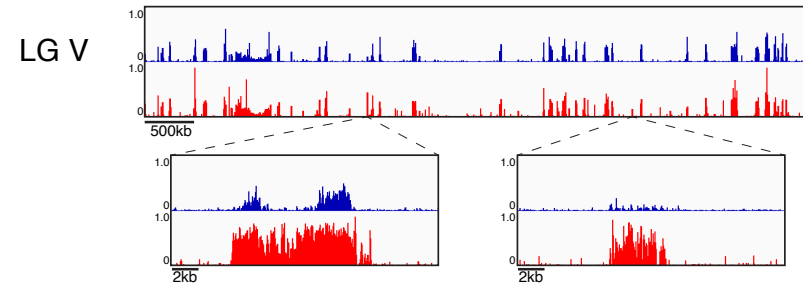
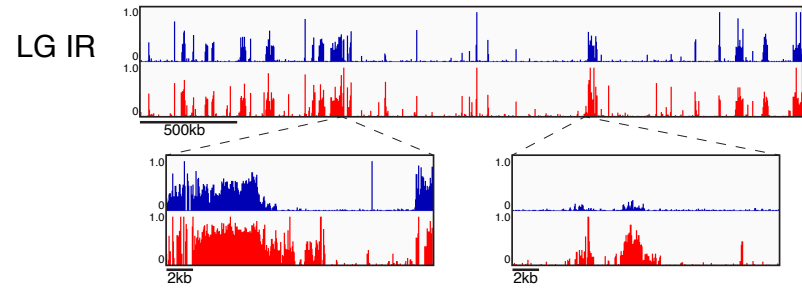
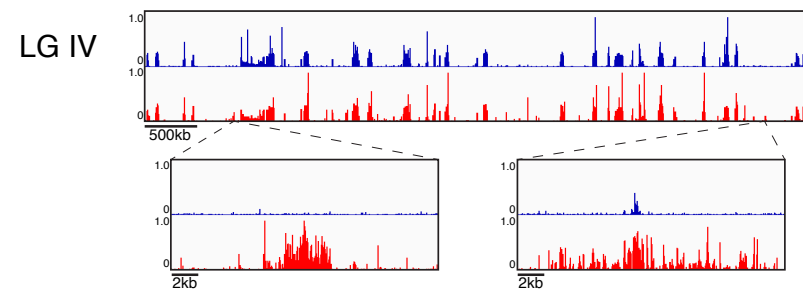
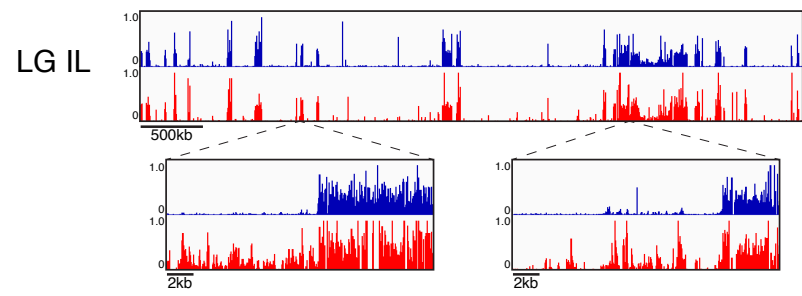
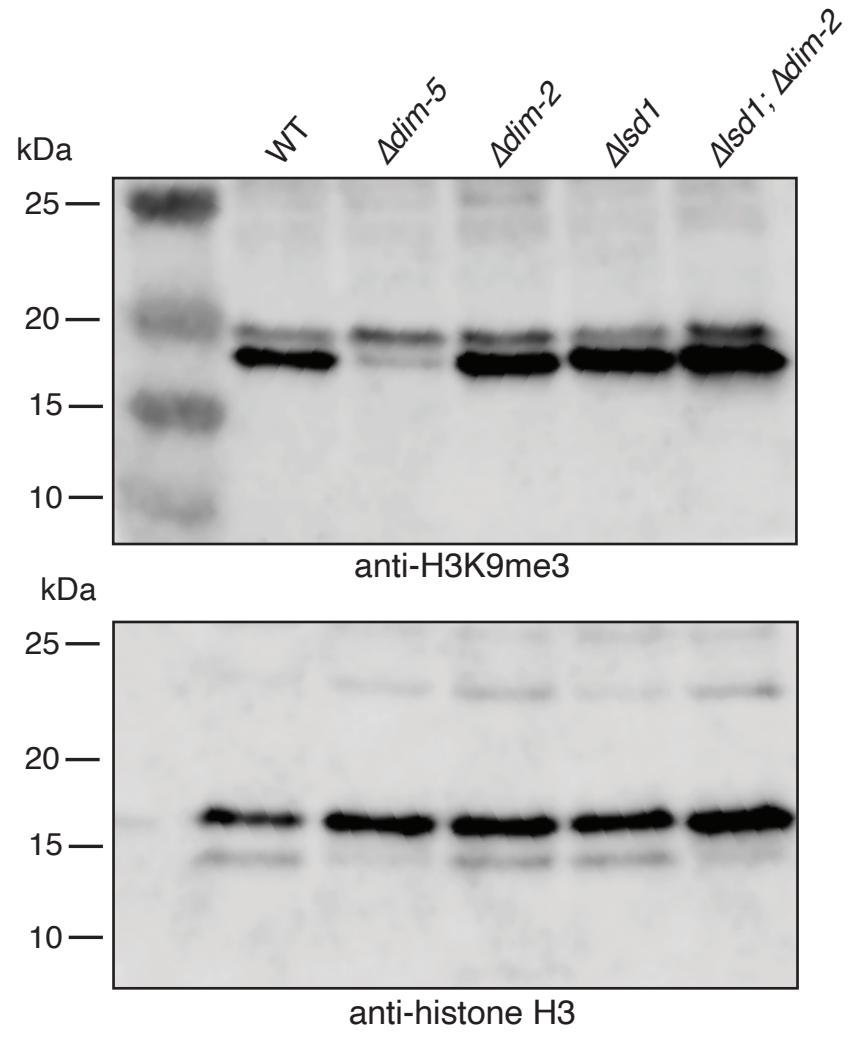
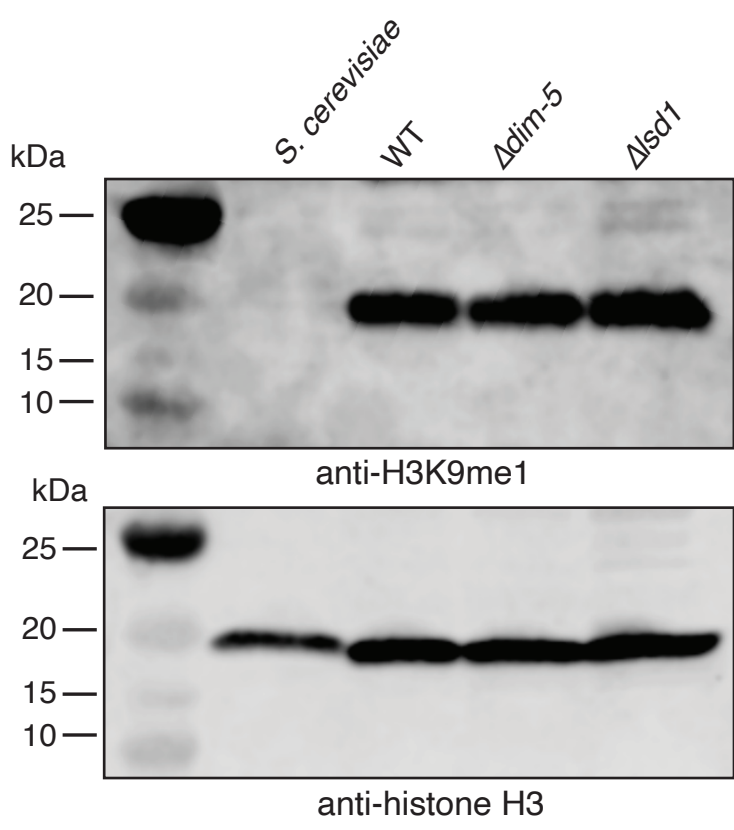


Supplemental Figure 1

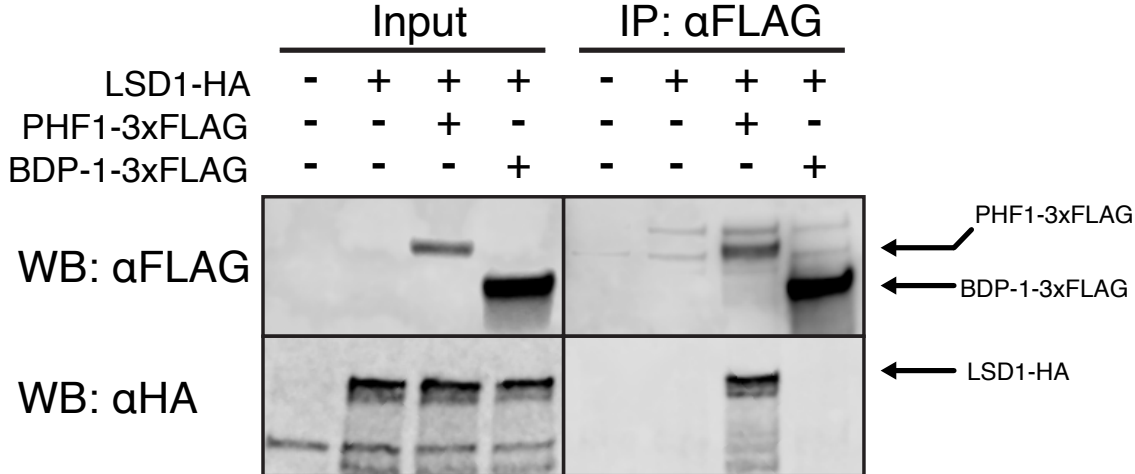


Supplemental Figure 2

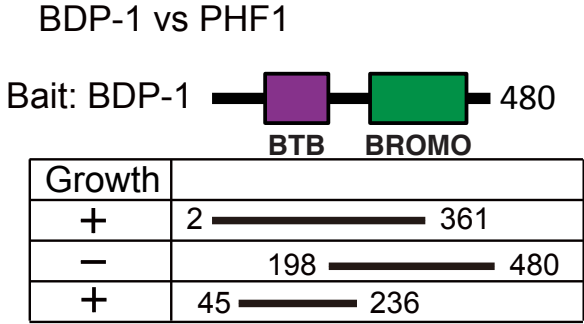
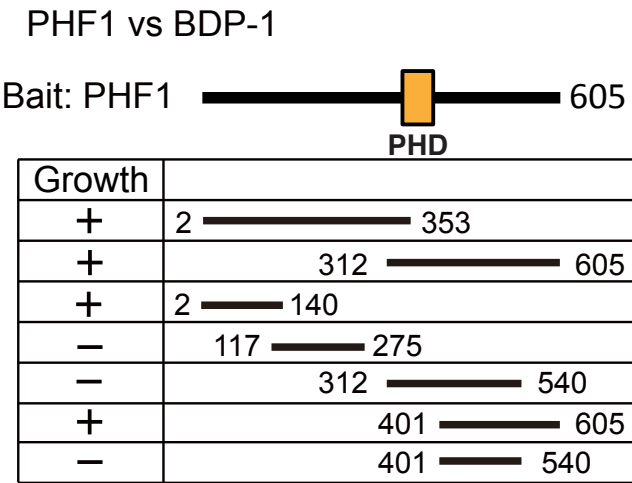


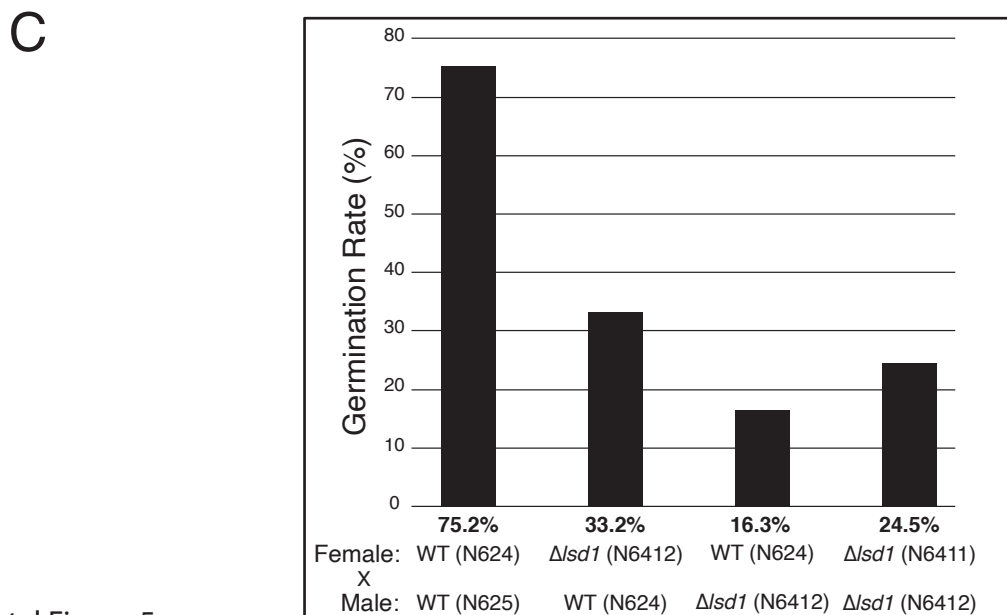
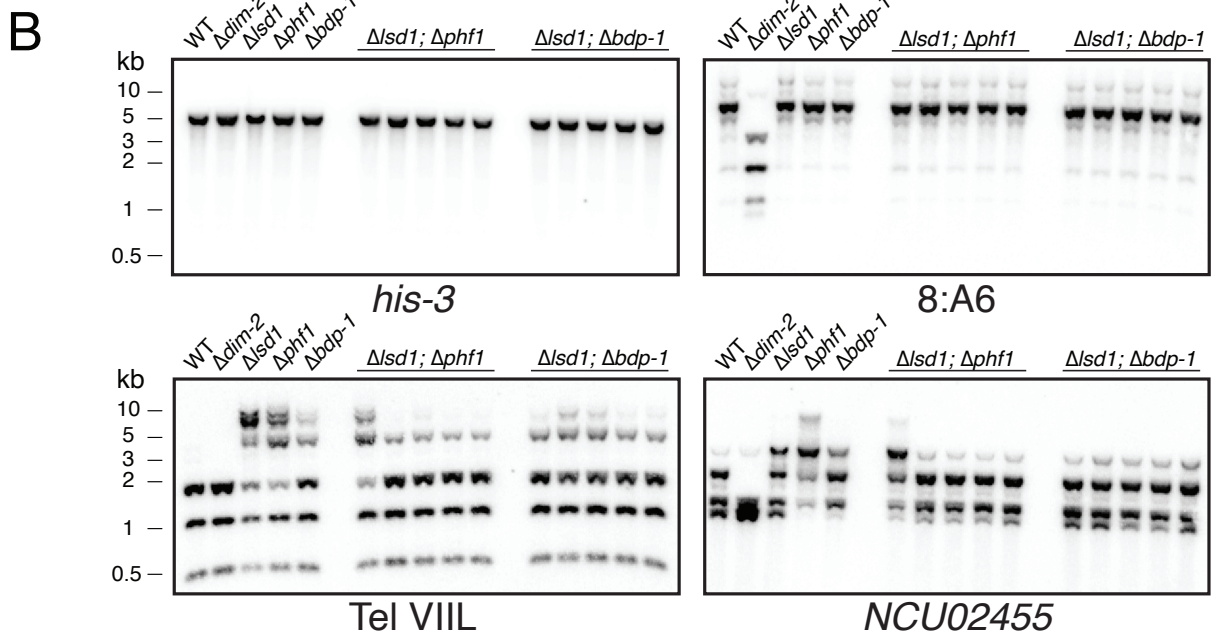
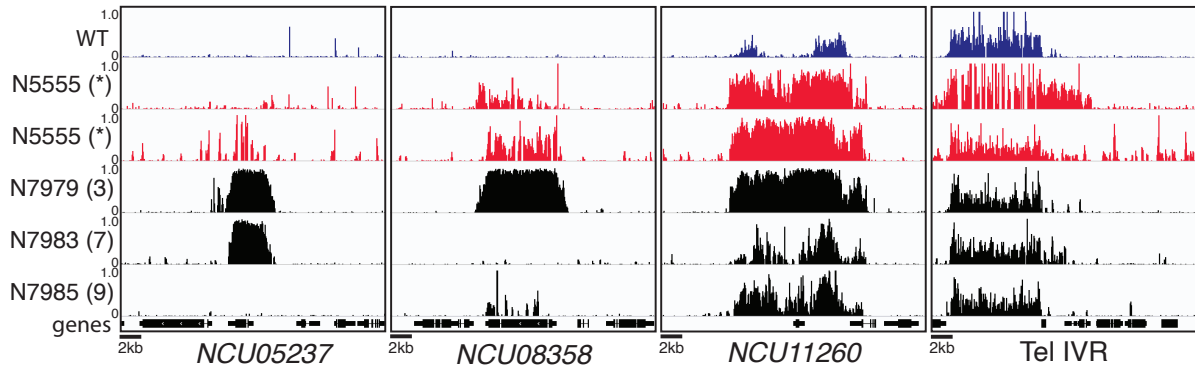
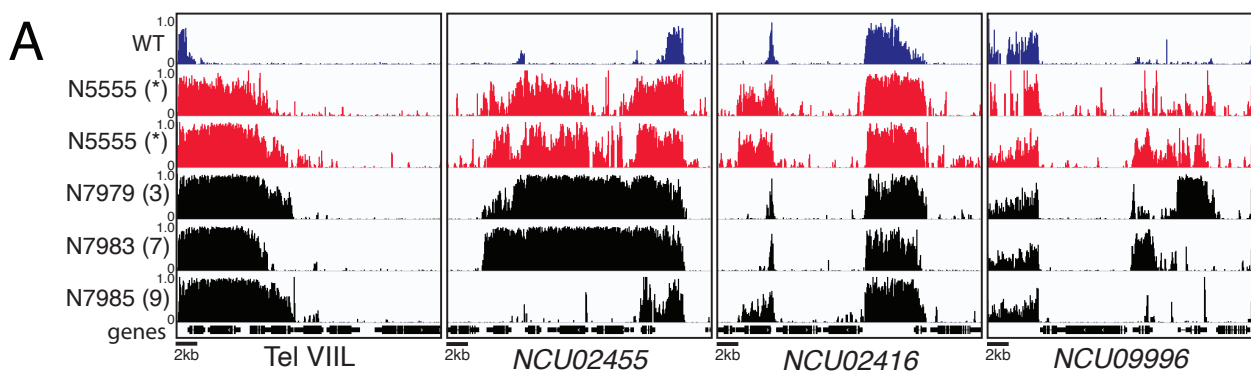
Supplemental Figure 3

A



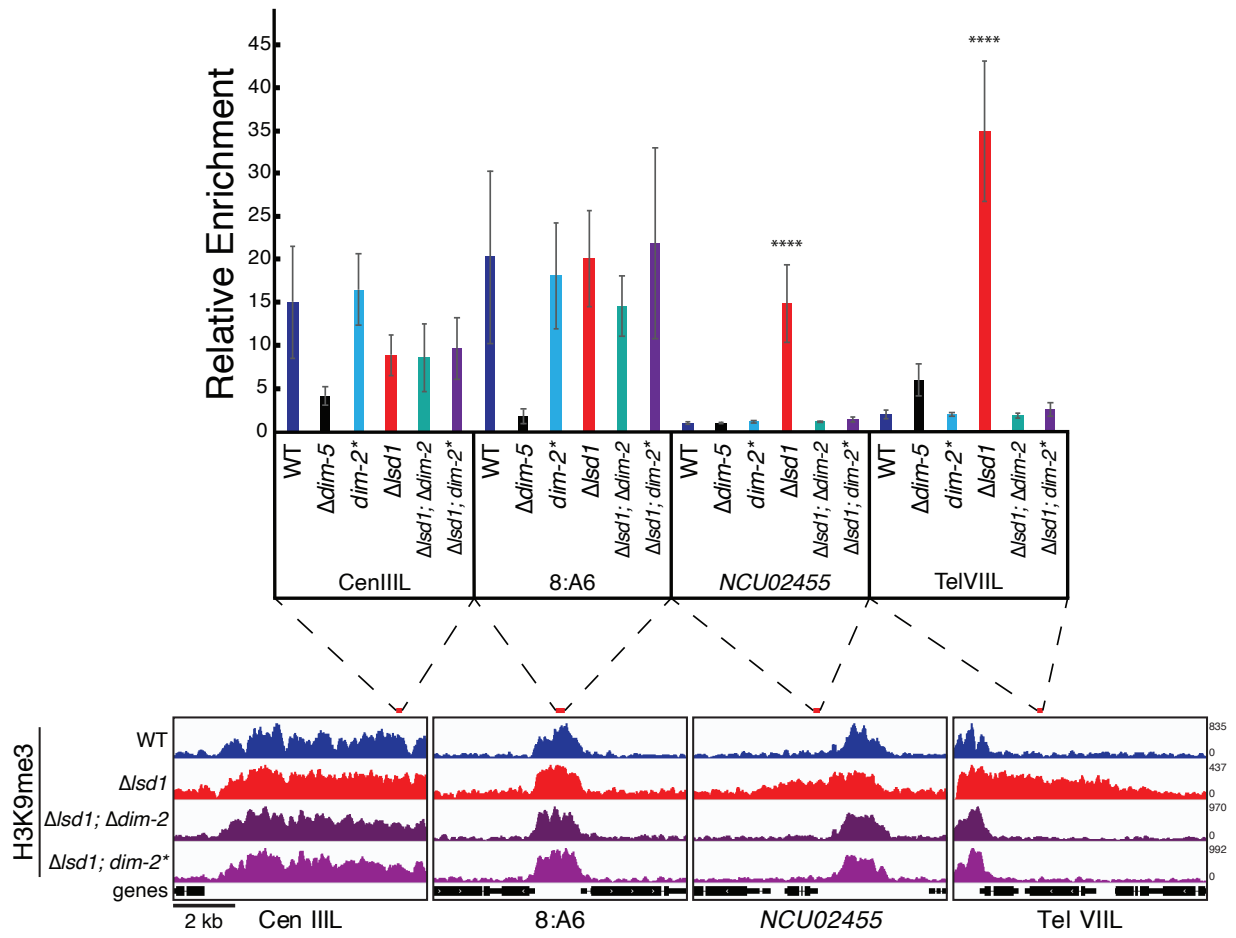
B



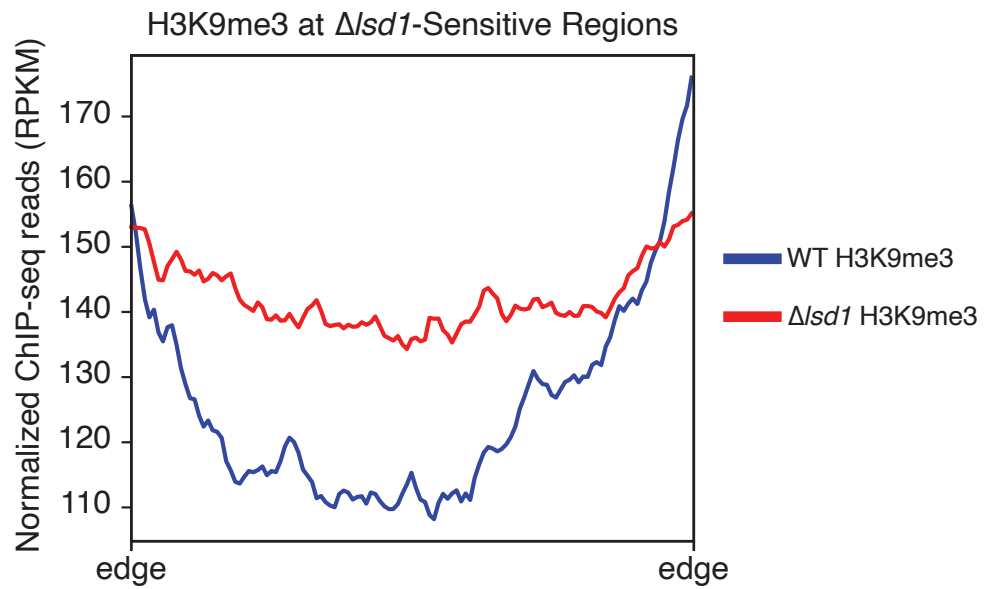


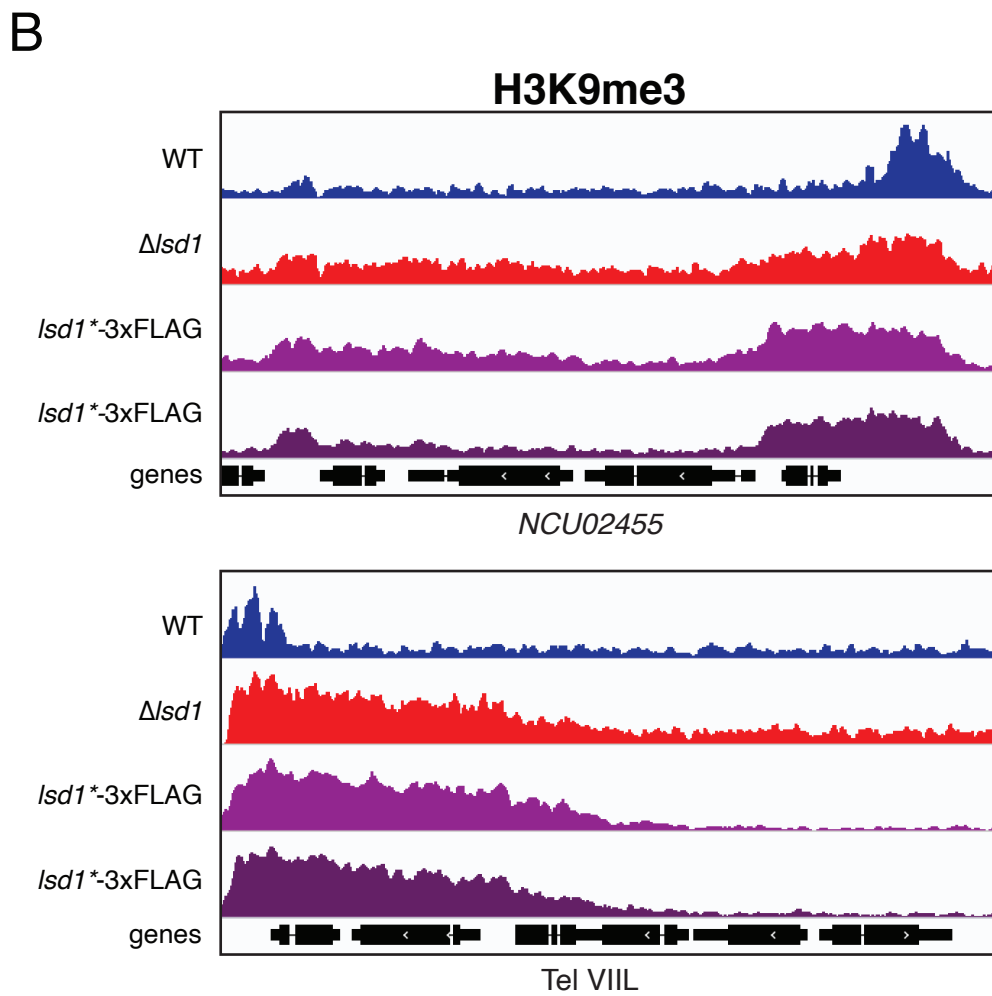
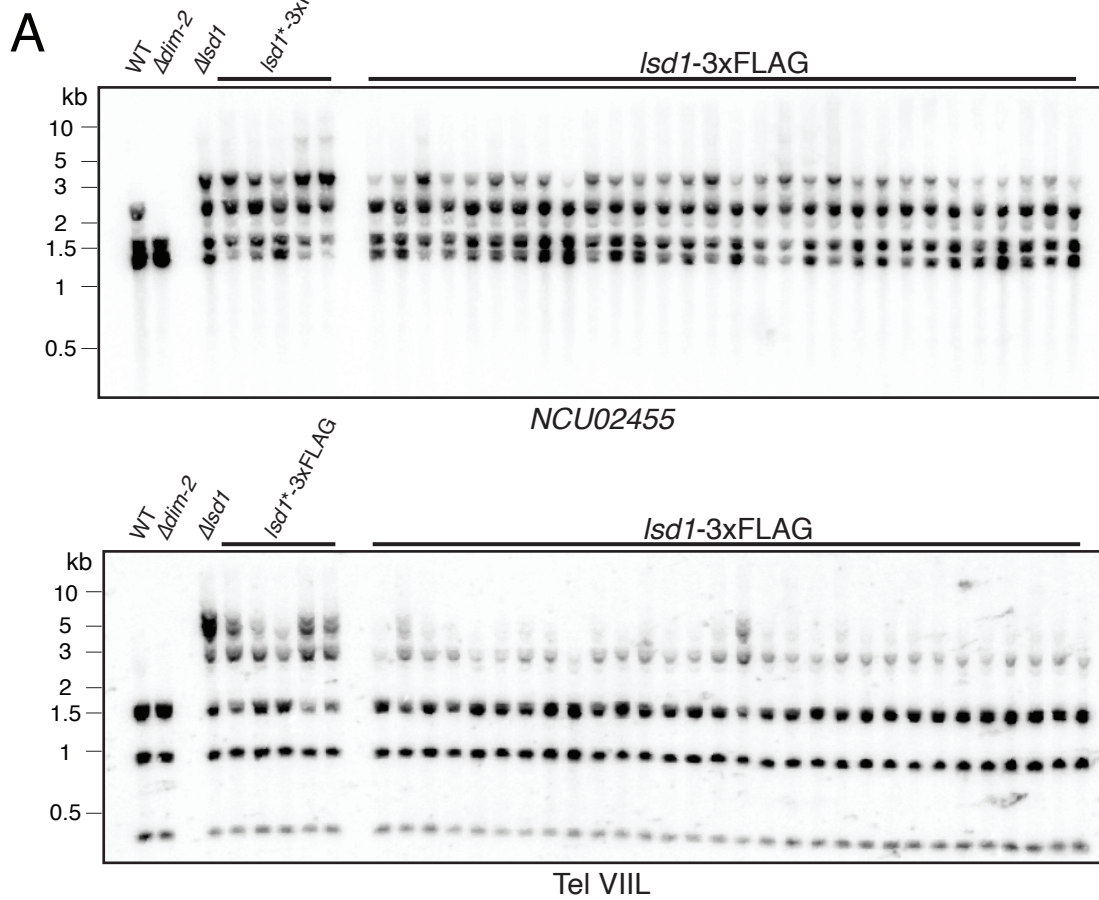
A

H3K9me3 ChIP-qPCR



B





qRT-PCR

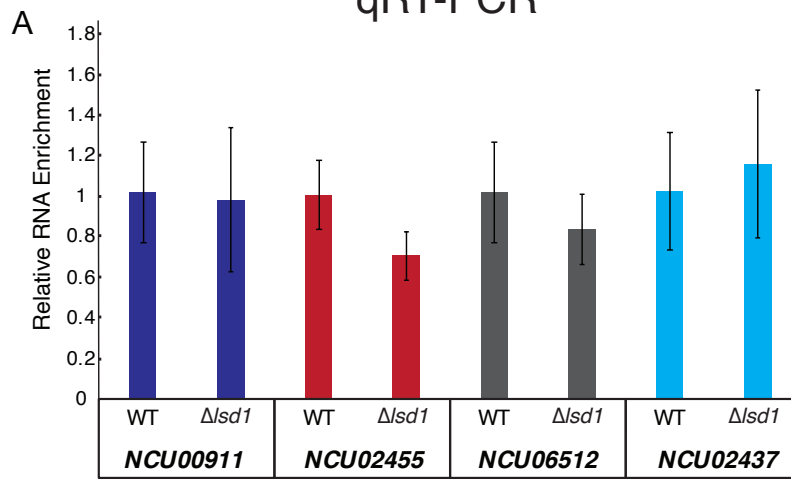
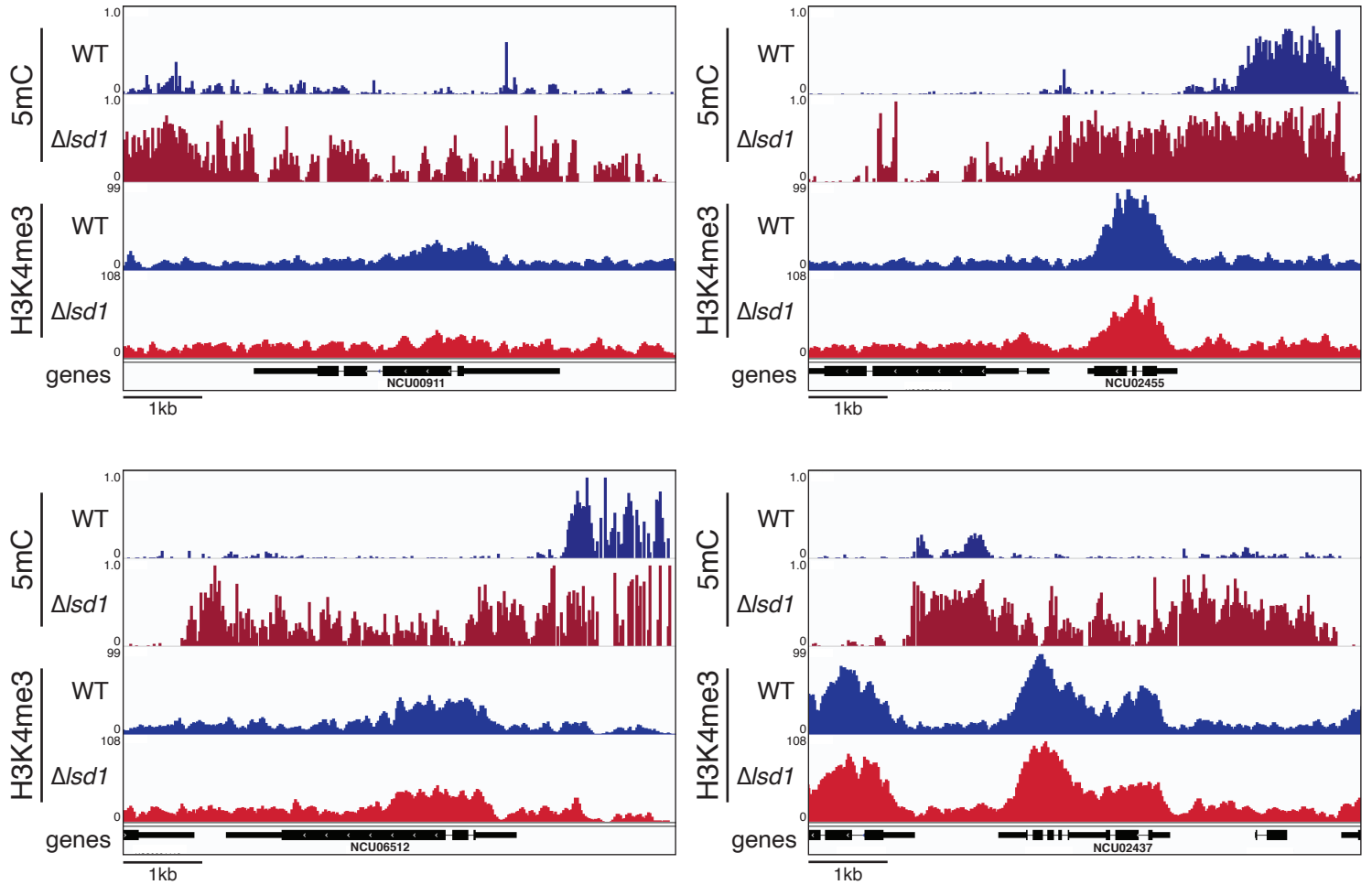
**B**

Table S1. LSD1-associated proteins

| Gene # | Predicted Protein | MW (kDa) | # Unique Peptides | Protein Coverage (%) |
|-----------------|--|----------------|-------------------|----------------------|
| NCU01728 | 6-phosphofructo-2-kinase | 90.463 | 412 | 64.3 |
| NCU09602 | Heat shock 70 kDa protein | 70.553 | 37 | 48.3 |
| NCU09120 | Lysine-specific histone demethylase | 150.481 | 175 | 47.4 |
| NCU07830 | 40S ribosomal protein S14 | 16.019 | 6 | 47.3 |
| NCU07297 | PHD Finger 1 | 63.895 | 76 | 46.8 |
| NCU06047 | 40S ribosomal protein S2 | 28.756 | 18 | 42.6 |
| NCU08693 | Hsp70-like protein | 72.731 | 32 | 40.4 |
| NCU03757 | 60S ribosomal protein L4-A | 38.813 | 17 | 38.8 |
| NCU02075 | Heat shock protein 70 | 63.508 | 28 | 38.3 |
| NCU02707 | 60S ribosomal protein L6 | 22.475 | 9 | 37.1 |
| NCU07829 | 60S ribosomal protein L7 | 28.687 | 12 | 36.7 |
| NCU03703 | 60S ribosomal protein L17 | 20.764 | 5 | 35.5 |
| NCU01948 | Ribosomal protein Srp1 | 18.214 | 4 | 34.4 |
| NCU05554 | 60S ribosomal protein L13 | 23.876 | 9 | 33.6 |
| NCU01827 | 60S ribosomal protein L27 | 15.722 | 3 | 32.6 |
| NCU01452 | 40S ribosomal protein S1 | 29.068 | 8 | 32.4 |
| NCU04173 | Actin | 41.607 | 10 | 31.5 |
| NCU00489 | Cytoplasmic ribosomal protein 10 | 28.666 | 8 | 30.5 |
| NCU07014 | 40S ribosomal protein S17 | 16.942 | 4 | 29.5 |
| NCU02295 | Phosphatidylinositol-4-phosphate 5-kinase its3 | 111.877 | 35 | 29.5 |
| NCU08620 | 40S ribosomal protein S16 | 15.723 | 3 | 28.9 |
| NCU08500 | 40S ribosomal protein S8 | 23.011 | 5 | 28.7 |
| NCU08809 | Bromodomain protein-1 | 53.227 | 13 | 27.3 |
| NCU06226 | 60S ribosomal protein L25 | 17.119 | 5 | 26.9 |
| NCU05275 | Ubiquitin-60S ribosomal protein L40 | 14.637 | 3 | 26.6 |
| NCU08045 | Phosphatidylethanolamine N-methyltransferase | 109.551 | 30 | 26.1 |
| NCU03102 | 40S ribosomal protein S11 | 18.428 | 4 | 26.1 |
| NCU08389 | 60S ribosomal protein L20 | 20.343 | 4 | 25.9 |
| NCU02003 | Elongation factor 1-alpha | 49.672 | 16 | 24.6 |
| NCU02509 | 60S ribosomal protein L11 | 20.084 | 5 | 24.1 |
| NCU06431 | 40S ribosomal protein S22 | 14.82 | 2 | 23.1 |
| NCU08964 | 60S ribosomal protein L10 | 25.325 | 7 | 23.1 |
| NCU04552 | 40S ribosomal protein S26E | 13.546 | 2 | 22.7 |

| | | | | |
|----------|--|---------|----|------|
| NCU03982 | Endoplasmic reticulum chaperone BiP | 72.331 | 9 | 21.9 |
| NCU03038 | 40S ribosomal protein S13 | 16.873 | 4 | 21.9 |
| NCU01776 | 60S ribosomal protein L15 | 24.19 | 10 | 21.7 |
| NCU03302 | 60S ribosomal protein L36 | 11.555 | 3 | 21.2 |
| NCU01949 | 40S ribosomal protein S9 | 21.806 | 5 | 21.1 |
| NCU02181 | 40S ribosomal protein S4 | 29.596 | 5 | 21.1 |
| NCU06843 | 60S ribosomal protein L3 | 44.035 | 5 | 20.9 |
| NCU02744 | 60S ribosomal protein L9 | 21.752 | 4 | 20.2 |
| NCU07408 | 60S acidic ribosomal protein P0 | 33.534 | 5 | 20.1 |
| NCU08269 | Pyridoxamine 5'-phosphate oxidase | 33.614 | 4 | 18.1 |
| NCU03150 | 60S ribosomal protein L24 | 17.611 | 3 | 17.9 |
| NCU01221 | 60S ribosomal protein L16 | 22.901 | 4 | 17.3 |
| NCU00413 | 60S ribosomal protein L2 | 27.356 | 4 | 17.3 |
| NCU06210 | Uncharacterized protein | 15.979 | 3 | 17.3 |
| NCU08334 | Uncharacterized protein | 123.589 | 16 | 16.4 |
| NCU08502 | 40S ribosomal protein S6 | 27.331 | 4 | 15.9 |
| NCU09345 | Thiamine biosynthesis protein NMT-1 | 38.198 | 7 | 15.5 |
| NCU00634 | Ribosomal protein L14 | 15.853 | 2 | 14.8 |
| NCU06110 | Thiamine thiazole synthase | 36.864 | 3 | 14.2 |
| NCU09468 | Tubulin alpha-B chain | 49.966 | 8 | 14 |
| NCU00464 | 60S ribosomal protein L32 | 14.965 | 2 | 13.7 |
| NCU06360 | Histidinol-phosphate aminotransferase | 43.583 | 3 | 13.7 |
| NCU00294 | 60S ribosomal protein L10a | 24.126 | 3 | 12.4 |
| NCU04779 | 60S ribosomal protein L8 | 23.863 | 2 | 11.4 |
| NCU05599 | 40S ribosomal protein S5 | 23.68 | 2 | 11.3 |
| NCU04137 | Vacuolar protein sorting-associated protein Vps5 | 64.1 | 6 | 11.2 |
| NCU00475 | 40S ribosomal protein S18 | 17.768 | 2 | 10.9 |
| NCU01589 | Heat shock protein 60 | 60.489 | 4 | 10.1 |

Table S2. PHF1-associated proteins

| Gene # | Predicted Protein | MW (kDa) | # Unique Peptides | Protein Coverage (%) |
|-----------------|--|-----------------|--------------------------|-----------------------------|
| NCU01728 | 6-phosphofructo-2-kinase | 90.463 | 189 | 61.3 |
| NCU09120 | Lysine-specific histone demethylase | 150.481 | 177 | 42.1 |
| NCU07297 | PHD Finger 1 | 63.895 | 74 | 32.1 |
| NCU08693 | Hsp70-like protein | 72.731 | 16 | 31.6 |
| NCU07014 | 40S ribosomal protein S17 | 16.942 | 4 | 29.5 |
| NCU09602 | Heat shock 70 kDa protein | 70.553 | 17 | 28.9 |
| NCU08809 | Bromodomain protein-1 | 53.227 | 15 | 24 |
| NCU01776 | 60S ribosomal protein L15 | 24.19 | 5 | 23.6 |
| NCU07830 | 40S ribosomal protein S14 | 16.019 | 5 | 23.3 |
| NCU03857 | Isocitrate dehydrogenase [NADP] | 51.848 | 8 | 20.6 |
| NCU04173 | Actin | 41.607 | 5 | 19.5 |
| NCU09345 | Thiamine biosynthesis protein NMT-1, variant 2 | 38.198 | 3 | 19 |
| NCU08389 | 60S ribosomal protein L20 | 20.343 | 4 | 19 |
| NCU03150 | 60S ribosomal protein L24 | 17.611 | 3 | 18.6 |
| NCU03757 | 60S ribosomal protein L4-A | 38.813 | 5 | 17.7 |
| NCU03982 | Endoplasmic reticulum chaperone BiP | 72.331 | 10 | 17.2 |
| NCU03038 | 40S ribosomal protein S13 | 16.873 | 2 | 17.2 |
| NCU03806 | 60S ribosomal protein L28 | 16.597 | 3 | 15.4 |
| NCU05275 | Ubiquitin-60S ribosomal protein L40 | 14.637 | 2 | 14.1 |
| NCU07829 | 60S ribosomal protein L7 | 28.687 | 2 | 14.1 |
| NCU02075 | Heat shock protein 70 | 63.508 | 8 | 14 |
| NCU02435 | Histone H2B | 14.841 | 2 | 13.9 |
| NCU08045 | Phosphatidylethanolamine N-methyltransferase | 109.551 | 10 | 13.8 |
| NCU02003 | Elongation factor 1-alpha | 49.672 | 10 | 10.9 |

Table S3. BDP-1-associated proteins

| Gene # | Predicted Protein | MW (kDa) | # Unique Peptides | Protein Coverage (%) |
|-----------------|------------------------------|-----------------|--------------------------|-----------------------------|
| NCU08809 | Bromodomain protein-1 | 53.227 | 173 | 45.4 |
| NCU01728 | 6-phosphofructo-2-kinase | 90.463 | 97 | 41.8 |
| NCU11181 | Small COPII coat GTPase sar1 | 21.583 | 4 | 27.5 |
| NCU01249 | Importin subunit alpha | 59.696 | 25 | 25.7 |
| NCU02003 | Elongation factor 1-alpha | 49.672 | 18 | 22.6 |
| NCU02075 | Heat shock protein 70 | 63.508 | 18 | 16.2 |
| NCU09602 | Heat shock 70 kDa protein | 70.553 | 6 | 11.9 |

Table S4. Lysine methyltransferase KOs screened for loss of H3K9me1 in *Δdim-5* background

| SET Domain Proteins - (Freitag, 2017) | |
|--|----------|
| NCU01206 | set-1 |
| NCU00269 | set-2 |
| NCU01932 | ash1 |
| NCU04389 | set-4 |
| NCU06119 | set-5 |
| NCU09495 | set-6 |
| NCU07496 | set-7 |
| NCU01973 | set-8 |
| NCU08733 | set-9 |
| NCU08551 | hlm-1 |
| NCU10039 | set-11 |
| NCU00970 | |
| NCU02088 | |
| NCU00089 | |
| NCU06658 | set-13 |
| NCU09827 | rkm-3 |
| NCU09581 | set-18 |
| NCU02158 | rkm-2 |
| NCU04381 | rkm-5 |
| NCU02962 | set-14 |
| NCU00870 | set-16 |
| NCU08472 | set-17 |
| | |
| Non-SET Domain KMTs - (Falnes et al., 2016) | |
| NCU06266 | dot-1 |
| NCU07459 | PrmA |
| NCU01669 | |
| NCU07132 | PRKMT2 |
| NCU02608 | VC PKMT |
| NCU07181 | EEF2 KMT |
| NCU03708 | METTL21A |
| NCU04775 | |
| NCU00487 | METTL10 |
| NCU02917 | |
| NCU04602 | Efm6 |
| | |

| WRAD Complex - (Patel et al., 2011) | |
|--|--------|
| NCU02104 | RbBP5 |
| NCU03037 | DPY-30 |

Table S5. List of genes downregulated in Δ *lsd-1* (Methylated genes identified by bisulfite-seq are in yellow)

| Gene# | WT FPKM | Δ <i>lsd1</i> FPKM | Fold Change (log ₂) | P Value | Predicted Protein |
|-----------------|--------------------|---------------------------|---------------------------------|-----------------|---|
| NCU09968 | 1298.609113 | 1.628015575 | -9.639637022 | 4.29E-118 | Hypothetical protein |
| NCU05122 | 623.8966022 | 4.102681214 | -7.248596084 | 1.67E-32 | Hypothetical protein |
| NCU05788 | 754.7072016 | 9.963947109 | -6.243055867 | 9.73E-32 | Hypothetical protein |
| NCU09964 | 169.5522468 | 2.474665639 | -6.098352481 | 7.17E-24 | Hypothetical protein |
| NCU09969 | 87.48231749 | 1.628015575 | -5.747805032 | 1.07E-12 | Transposase of Sly1-1 |
| NCU02919 | 114.8728848 | 3.321315703 | -5.112139624 | 6.04E-11 | cupin domain-containing protein |
| NCU08842 | 1165.895936 | 39.20294291 | -4.894333255 | 1.87E-31 | Hypothetical protein |
| NCU05852 | 81.2099852 | 4.167965767 | -4.284241792 | 8.27E-10 | glucuronan lyase-1 |
| NCU16875 | 807.377254 | 41.67760855 | -4.275898539 | 1.03E-22 | Hypothetical protein |
| NCU00732 | 5847.188501 | 349.8500354 | -4.062934559 | 1.03E-21 | trichothecene C-15 hydroxylase |
| NCU02920 | 39.28880678 | 2.409381086 | -4.027383849 | 9.41E-05 | short-chain dehydrogenase/reductase SDR |
| NCU00607 | 4909.488324 | 311.8834007 | -3.976493996 | 5.17E-67 | Hypothetical protein |
| NCU01958 | 25.17856627 | 1.628015575 | -3.951009728 | 0.003347461 | mating-type protein A-1 |
| NCU02061 | 59.5929699 | 4.037396661 | -3.883644909 | 9.47E-07 | Hypothetical protein |
| NCU09278 | 1080.307022 | 81.27225877 | -3.732534581 | 3.44E-52 | oxidoreductase |
| NCU09424 | 307.546009 | 26.11353375 | -3.557932649 | 7.04E-24 | Hypothetical protein |
| NCU07138 | 304.3823196 | 26.24410286 | -3.535819375 | 1.27E-23 | Hypothetical protein |
| NCU02918 | 46.56120666 | 4.102681214 | -3.504489483 | 6.29E-05 | polyketide synthase 6 |
| NCU02022 | 101.0061937 | 9.182581598 | -3.45940014 | 1.05E-09 | Hypothetical protein |
| NCU04928 | 1154.74088 | 109.0790927 | -3.404122643 | 3.12E-47 | Hypothetical protein |
| NCU10040 | 4303.169207 | 419.1670244 | -3.35980244 | 5.90E-28 | Hypothetical protein |
| NCU09698 | 188.8680239 | 18.95067505 | -3.317057323 | 2.79E-15 | Hypothetical protein |
| NCU01957 | 123.8326353 | 12.95884005 | -3.256383085 | 1.26E-10 | AR2 |
| NCU09639 | 83.66553563 | 9.963947109 | -3.069844187 | 2.68E-07 | Hypothetical protein |
| NCU02296 | 784.8286074 | 95.92234983 | -3.032438723 | 1.06E-17 | Allantoinase |
| NCU09357 | 772.8077392 | 94.75337525 | -3.027860302 | 1.58E-33 | stage V sporulation protein K |
| NCU09356 | 673.2386795 | 82.8349898 | -3.022805865 | 3.09E-31 | Hypothetical protein |
| NCU07767 | 25.26364323 | 3.25603115 | -2.955876296 | 0.014934947 | Hypothetical protein |
| NCU08037 | 38.19198066 | 4.949331278 | -2.947964225 | 0.00131088 | Hypothetical protein |

| | | | | | |
|-----------------|--------------------|--------------------|---------------------|-----------------|---|
| NCU07736 | 964.0395692 | 127.6360113 | -2.917056934 | 2.26E-34 | Pep5 homolog |
| NCU05569 | 388.4156863 | 54.24474128 | -2.840046278 | 9.84E-21 | Hypothetical protein |
| NCU05980 | 34.92486542 | 4.949331278 | -2.818949041 | 0.003377901 | serine protease-13 |
| NCU05948 | 181.5864496 | 27.34984201 | -2.731052145 | 1.92E-11 | Hypothetical protein |
| NCU08545 | 73.74908254 | 11.20025537 | -2.719093476 | 1.33E-05 | Hypothetical protein |
| NCU08535 | 958.0141475 | 146.3908327 | -2.71022175 | 1.02E-09 | acetyl-CoA carboxylase-1 |
| NCU08674 | 1820.530339 | 281.2529381 | -2.694418711 | 2.35E-37 | Pentatricopeptide repeat protein |
| NCU09441 | 32.0164069 | 4.949331278 | -2.693505892 | 0.007623791 | Hypothetical protein |
| NCU07468 | 1446.764531 | 234.823901 | -2.623178972 | 8.60E-34 | NAD-epimerase/dehydratase-1 |
| NCU00866 | 1356.289532 | 222.5790928 | -2.607275199 | 1.12E-32 | DUF1275 domain-containing protein |
| NCU07547 | 73.31703042 | 12.30804364 | -2.574546889 | 3.06E-05 | phosphoprotein P0-2 |
| NCU09638 | 43.33078913 | 7.293427812 | -2.570723585 | 0.002132984 | polyketide synthase 5 |
| NCU09640 | 66.37576398 | 11.39610903 | -2.542115232 | 0.000129153 | MFS toxin efflux pump |
| NCU08223 | 193.979309 | 33.86190431 | -2.51816776 | 1.15E-06 | Hypothetical protein |
| NCU00721 | 359.909944 | 63.03766468 | -2.513349969 | 1.00E-16 | proline-specific permease |
| NCU08191 | 73.54223091 | 12.8935555 | -2.511922789 | 4.33E-05 | Hypothetical protein |
| NCU06043 | 1115.716534 | 197.5712982 | -2.497525251 | 9.59E-09 | GPR/FUN34 family protein |
| NCU06341 | 199.5293136 | 35.49196901 | -2.491036195 | 3.81E-11 | MFS transporter |
| NCU03887 | 2343.042943 | 421.0746203 | -2.476235569 | 1.29E-34 | carbon catabolite regulation-3 |
| NCU05723 | 1946.064513 | 356.7333137 | -2.447641683 | 9.65E-33 | kinetochore protein-11 |
| NCU06468 | 302.8417598 | 55.87480598 | -2.438294335 | 2.65E-14 | midasin |
| NCU06666 | 2462.144605 | 455.7076446 | -2.433735018 | 8.60E-34 | inositol-3-phosphate synthase |
| NCU10610 | 55.73031591 | 10.48417441 | -2.410249073 | 0.000691106 | Hypothetical protein |
| NCU06140 | 60.49211881 | 11.52667813 | -2.391770391 | 0.003469222 | Hypothetical protein |
| NCU04435 | 317.6668066 | 60.56299904 | -2.391005795 | 2.50E-14 | general amino acid permease AGP3 |
| NCU03257 | 3719.436454 | 719.048313 | -2.370923436 | 2.44E-34 | ammonium transporter MEP1 |
| NCU01400 | 719.5671643 | 140.3969485 | -2.357617775 | 1.14E-21 | Hypothetical protein |
| NCU08968 | 29.5700309 | 5.795981342 | -2.351010895 | 0.022199811 | dimethyladenosine transferase |
| NCU03321 | 158.5623307 | 31.12814959 | -2.34875835 | 2.88E-07 | ribosome biogenesis-59 |
| NCU04923 | 1065.752249 | 210.3383828 | -2.341088055 | 1.88E-12 | Gld1 |
| NCU02802 | 377.1772067 | 74.88871646 | -2.332422226 | 3.36E-15 | mitochondrial ornithine carrier protein |

| | | | | | |
|----------|-------------|-------------|--------------|-------------|--|
| NCU08595 | 131.7280972 | 26.17881831 | -2.33109122 | 1.98E-07 | ribosome biogenesis-49 |
| NCU04656 | 6063.223324 | 1211.708776 | -2.32304196 | 2.02E-35 | MFS transporter |
| NCU10732 | 1056.940942 | 211.9623002 | -2.318015173 | 2.05E-24 | mitochondrial dicarboxylate transporter |
| NCU07307 | 3385.377427 | 681.9529179 | -2.311572641 | 1.70E-12 | fatty acid synthase beta subunit dehydratase |
| NCU16445 | 1169.802809 | 236.3377405 | -2.307343424 | 3.58E-07 | Hypothetical protein |
| NCU08793 | 1489.572378 | 304.8979535 | -2.288499853 | 3.46E-27 | Hypothetical protein |
| NCU05277 | 266.4130323 | 55.02815591 | -2.27542277 | 5.81E-12 | Hypothetical protein |
| NCU04058 | 316.0136466 | 65.31647666 | -2.274467985 | 2.90E-13 | bZip transcription factor, putative |
| NCU01209 | 46.7105046 | 9.702808898 | -2.267272667 | 0.003351954 | Hypothetical protein |
| NCU04880 | 66.44915938 | 13.80549011 | -2.267008842 | 0.00033323 | Hypothetical protein |
| NCU08137 | 5388.870434 | 1122.479999 | -2.263293162 | 2.96E-33 | Hypothetical protein |
| NCU02051 | 621.3293056 | 129.9801078 | -2.257067252 | 6.09E-19 | Hypothetical protein |
| NCU02850 | 50.63988671 | 10.68002807 | -2.245358739 | 0.002181528 | alcohol dehydrogenase-4 |
| NCU03396 | 415.5301668 | 87.65375197 | -2.245065467 | 2.78E-15 | nucleolar protein nop-58 |
| NCU07607 | 551.3903376 | 116.7601295 | -2.23952627 | 1.70E-16 | sugar transporter-16 |
| NCU00821 | 194.8550948 | 41.35118578 | -2.236401048 | 3.14E-09 | sugar transporter-15 |
| NCU03154 | 1124.758 | 238.922484 | -2.235000098 | 1.45E-23 | Pantothenate kinase |
| NCU04307 | 221.6109186 | 47.08188257 | -2.234785051 | 4.25E-10 | phenylalanine-7 |
| NCU02369 | 12094.58684 | 2581.25601 | -2.228216346 | 2.30E-06 | Polygalacturonase |
| NCU00337 | 38.41051385 | 8.205362428 | -2.226862301 | 0.010800571 | nuclear export protein Noc3 |
| NCU03646 | 3893.578696 | 839.8215372 | -2.212942095 | 3.19E-23 | Hypothetical protein |
| NCU08287 | 1465.328005 | 316.6266327 | -2.210369123 | 8.65E-13 | pyrABCN |
| NCU10895 | 403.1256258 | 87.39261376 | -2.205646239 | 1.12E-14 | mutS ortholog 4 protein |
| NCU09990 | 33.53611071 | 7.293427812 | -2.201046459 | 0.019902591 | Hypothetical protein |
| NCU07308 | 2147.106919 | 467.1792838 | -2.200345827 | 5.02E-11 | fatty acid synthase alpha subunit reductase |
| NCU07034 | 298.4177576 | 65.31852579 | -2.191769252 | 8.65E-12 | Hypothetical protein |
| NCU01595 | 37.35289257 | 8.205362428 | -2.186581005 | 0.014009037 | rRNA maturation-11 |
| NCU04205 | 1214.158682 | 267.3944581 | -2.182915514 | 9.67E-10 | aspartyl protease-17 |
| NCU01066 | 43.8112205 | 9.702808898 | -2.174826043 | 0.0064656 | L-amino acid oxidase |
| NCU05045 | 59.06415926 | 13.08940915 | -2.173882977 | 0.001144557 | MFS monocarboxylate transporter |
| NCU04931 | 2107.870596 | 468.8664365 | -2.168537388 | 7.65E-27 | Hypothetical protein |
| NCU07656 | 36.51129735 | 8.140077876 | -2.165228431 | 0.015486455 | Hypothetical protein |
| NCU08397 | 1219.390089 | 272.1397393 | -2.163740178 | 2.87E-23 | Hypothetical protein |

| | | | | | |
|----------|-------------|-------------|--------------|-------------|--------------------------------------|
| NCU03963 | 141.1065653 | 31.84423054 | -2.147681196 | 5.30E-07 | 5'-methylthioadenosine phosphorylase |
| NCU05089 | 256.2321739 | 58.0883334 | -2.141131296 | 1.27E-10 | MFS monocarboxylate transporter |
| NCU08358 | 521.3123521 | 118.3269588 | -2.139369239 | 3.03E-07 | Hypothetical protein |
| NCU06720 | 469.3179012 | 106.8655652 | -2.134768435 | 2.59E-13 | serine protease-11 |
| NCU10009 | 703.2591114 | 161.432631 | -2.123124113 | 4.52E-18 | ATP-binding cassette transporter |
| NCU09267 | 2023.443583 | 466.3408302 | -2.11735597 | 2.51E-12 | copper radical oxidase |
| NCU06409 | 50.49976319 | 11.65724724 | -2.115049474 | 0.018446542 | ribosome biogenesis-51 |
| NCU01070 | 187.5434901 | 43.49942866 | -2.108156829 | 3.04E-08 | Hypothetical protein |
| NCU12050 | 71.86154759 | 16.7350985 | -2.102342963 | 0.000574717 | Hypothetical protein |
| NCU02188 | 97.04928829 | 22.7269335 | -2.094314596 | 4.50E-05 | arabinose-proton symporter |
| NCU01195 | 3242.903706 | 762.0927989 | -2.089247597 | 7.63E-27 | Glu/Leu/Phe/Val dehydrogenase |
| NCU08976 | 2072.168412 | 490.1082183 | -2.079969017 | 2.69E-12 | fatty acid metabolism-1 |
| NCU09045 | 279.1828973 | 66.03255762 | -2.079961133 | 1.13E-10 | heterokaryon incompatibility-16 |
| NCU04583 | 148.8986014 | 35.2308308 | -2.079419801 | 5.50E-07 | acetyltransferase |
| NCU05235 | 143.932454 | 34.12304252 | -2.076573735 | 1.11E-06 | ribosome biogenesis protein RLP24 |
| NCU07449 | 37.80580067 | 9.052012493 | -2.062297128 | 0.017756085 | Hypothetical protein |
| NCU05153 | 395.3702874 | 95.01451346 | -2.056984648 | 4.40E-08 | carbohydrate O-acetyltransferase |
| NCU00777 | 64.37312166 | 15.49879024 | -2.054302821 | 0.001321596 | Methyltransferase |
| NCU02653 | 40.55327969 | 9.833378004 | -2.044059588 | 0.013287485 | allantoate permease |
| NCU05629 | 54.86119741 | 13.35054737 | -2.038887218 | 0.002660797 | Hypothetical protein |
| NCU02729 | 86.84090661 | 21.29477158 | -2.027875533 | 0.00017198 | transducin family protein |
| NCU09465 | 59.03663598 | 14.58685562 | -2.01694159 | 0.002660797 | diphthamide biosynthesis protein 3 |
| NCU09841 | 154.6512974 | 38.35629284 | -2.011483742 | 8.75E-07 | phosphotyrosine protein phosphatase |
| NCU01083 | 135.9585824 | 33.79866888 | -2.00812889 | 2.52E-06 | S-adenosylmethionine decarboxylase |
| NCU01611 | 977.4291351 | 243.0884006 | -2.007511055 | 1.36E-18 | carnitine-1 |

Table S6. List of genes upregulated in *Δlsd-1*

| Gene# | WT FPKM | <i>Δlsd1</i> FPKM | Fold Change (log2) | P Value | Predicted Protein |
|--------------|----------------|--------------------------|---------------------------|----------------|--|
| NCU08570 | 2.020991173 | 26.89489927 | 3.73419766 | 0.000472711 | Hypothetical protein |
| NCU07822 | 15.45061596 | 190.932765 | 3.627328438 | 9.84E-21 | Hypothetical protein |
| NCU09685 | 8.603600908 | 86.34806091 | 3.32715127 | 1.92E-07 | Hypothetical protein |
| NCU08271 | 56.29582425 | 458.4454975 | 3.025650409 | 2.01E-27 | guanine triphosphate binding-15 |
| NCU04697 | 9.585319651 | 72.6731399 | 2.922523792 | 1.95E-06 | cyanide hydratase |
| NCU04407 | 54.69104348 | 338.0437769 | 2.627833595 | 3.96E-12 | RNA methyltransferase-5 |
| NCU07497 | 104.7078682 | 608.5493532 | 2.539004414 | 7.52E-24 | Hypothetical protein |
| NCU07938 | 117.2199952 | 678.3786605 | 2.532872105 | 0.022071512 | MFS transporter |
| NCU04823 | 528.4854863 | 2818.412899 | 2.414947226 | 0.000877967 | alcohol dehydrogenase-12 |
| NCU07111 | 166.2067219 | 840.9556766 | 2.339051034 | 3.01E-13 | metallo-beta-lactamase-2 |
| NCU00578 | 29.22054861 | 138.8995021 | 2.248986257 | 6.17E-06 | peptidyl-prolyl cis-trans isomerase-like 1 |
| NCU04237 | 565.7933057 | 2599.938824 | 2.200130665 | 5.93E-27 | phosphopantothenoylcysteine decarboxylase |
| NCU03109 | 14.6574 | 65.57761488 | 2.161574216 | 0.002772376 | Hypothetical protein |
| NCU06513 | 81.33175987 | 362.5925305 | 2.156458469 | 1.30E-13 | Hypothetical protein |
| NCU06974 | 508.5207769 | 2236.773077 | 2.137040275 | 2.74E-17 | histidinol-phosphatase |
| NCU01058 | 12.99506554 | 56.32974872 | 2.115933126 | 0.000997833 | Hypothetical protein |
| NCU07995 | 8.074790268 | 33.79661976 | 2.065382266 | 0.014600114 | Hypothetical protein |

Table S7. Strains used in this study

| Strains | Genotype | Source |
|---------|--|-----------------------------|
| N150 | <i>mat A</i> | FGSC#2489 |
| N624 | <i>mat A his-3-</i> | This Study |
| N625 | <i>mat a his-3-</i> | FGSC#6524 |
| N1909 | <i>mat a his-3::P_{qa}::dim-2^{C926A}; Δdim-2::hph</i> | Kouzminova and Selker, 2001 |
| N2930 | <i>mat A his-3; Δmus-52::bar⁺</i> | Honda et al., 2008 |
| N3435 | <i>mat A his-3; Δhda-1::hph</i> | Honda et al., 2016 |
| N3752 | <i>mat A</i> | FGSC#2489 |
| N3753 | <i>mat a</i> | FGSC#4200 |
| N3944 | <i>mat A; Δdim-5::bar</i> | Lewis et al., 2010 |
| N3998 | <i>mat A his-3::P_{hda-1}::hda-1^{D263N}-3xFLAG; Δhda-1::hph</i> | Honda et al., 2016 |
| N4711 | <i>mat A his-3; Δdim-2::hph</i> | This Study |
| N5555 | <i>mat a Δlsd1::hph</i> | FGSC#11964 |
| N5637 | <i>mat A his-3; dim-5-Dam::hph</i> | This Study |
| N6220 | <i>mat A; Δbdp-1::hph</i> | FGSC# 11957 |
| N6221 | <i>mat a; Δphf1::hph</i> | FGSC# 14344 |
| N6271 | <i>mat ? Δlsd1::hph; Δbdp-1::hph</i> | This Study |
| N6272 | <i>mat ? Δlsd1::hph; Δphf1::hph</i> | This Study |
| N6300 | <i>mat A his-3- lsd1-3xFLAG::hph</i> | This Study |
| N6301 | <i>mat A his-3- lsd1-HA::hph</i> | This Study |
| N6307 | <i>mat A his-3- lsd1-3xFLAG::hph</i> | This Study |
| N6308 | <i>mat a his-3; phf1-3xFLAG::hph</i> | This Study |
| N6309 | <i>mat A his-3; phf1-3xFLAG::hph</i> | This Study |
| N6310 | <i>mat a his-3; bdp-1-3xFLAG::hph</i> | This Study |
| N6313 | <i>mat A his-3; phf1-3xFLAG::hph</i> | This Study |
| N6314 | <i>mat a his-3; phf1-3xFLAG::hph</i> | This Study |
| N6337 | <i>mat a Δlsd1::hph; Δdim-2::hph</i> | This Study |
| N6395 | <i>mat A his-3; lsd1-HA::hph; phf1-3xFLAG::hph</i> | This Study |
| N6396 | <i>mat A his-3- lsd1-HA::hph; bdp-1-3xFLAG::hph</i> | This Study |
| N6411 | <i>mat A his-3- Δlsd1::nat-1</i> | This Study |
| N6412 | <i>mat a his-3- Δlsd1::nat-1</i> | This Study |
| N6414 | <i>mat a his-3; Δphf1::nat-1</i> | This Study |
| N6416 | <i>mat a his-3; Δbdp-1::nat-1</i> | This Study |
| N6679 | <i>mat a his-3::dim-2^{C926A} Δlsd1::nat-1; Δdim-2::hph</i> | This Study |
| N7899 | <i>his-3- lsd1^{NK972,973AA}-3xFLAG::nat-1</i> | This Study |
| N7943 | <i>his-3- lsd1^{NK972,973AA}-3xFLAG::nat-1</i> | This Study |
| N7944 | <i>his-3- lsd1^{NK972,973AA}-3xFLAG::nat-1</i> | This Study |
| N7945 | <i>his-3- lsd1^{NK972,973AA}-3xFLAG::nat-1</i> | This Study |

| | | |
|-------|---|------------|
| N7946 | <i>his-3- lsd1^{NK972,973AA}-3xFLAG::nat-1</i> | This Study |
| N7977 | <i>mat a Δlsd1::hph</i> | This Study |
| N7978 | <i>mat a Δlsd1::hph</i> | This Study |
| N7979 | <i>mat ? Δlsd1::hph</i> | This Study |
| N7980 | <i>mat a Δlsd1::hph</i> | This Study |
| N7981 | <i>mat a Δlsd1::hph</i> | This Study |
| N7982 | <i>mat a Δlsd1::hph</i> | This Study |
| N7983 | <i>mat ? Δlsd1::hph</i> | This Study |
| N7984 | <i>mat a Δlsd1::hph</i> | This Study |
| N7985 | <i>mat a Δlsd1::hph</i> | This Study |
| N8040 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8041 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8042 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8043 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8044 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8045 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8046 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8047 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8048 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8049 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8050 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8051 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8052 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8053 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8054 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8055 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8056 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8057 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8058 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8059 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8060 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8061 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8062 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8063 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8064 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8065 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8066 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8067 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8068 | <i>his-3-? lsd1-3xFLAG::hph</i> | This Study |
| N8081 | <i>Δlsd1::hph; Δdim-2::hph</i> | This Study |
| N8082 | <i>Δlsd1::hph; Δdim-2::hph</i> | This Study |
| N8083 | <i>his-3::dim-2^{C926A} Δlsd1::nat-1; Δdim-2::hph</i> | This Study |
| N8084 | <i>his-3::dim-2^{C926A} Δlsd1::nat-1; Δdim-2::hph</i> | This Study |
| N8089 | <i>his-3::Phda-1::hda-1D263N-3xFLAG Δlsd1::nat-1; Δhda-1::hph</i> | This Study |

| | | |
|-------|---|------------|
| N8090 | <i>his-3::Phda-1::hda-1D263N-3xFLAG</i> <i>Δlsd1::nat-1; Δhda-1::hph</i> | This Study |
| N8105 | <i>mat ? Δlsd1::hph; Δbdp-1::hph</i> | This Study |
| N8106 | <i>mat ? Δlsd1::hph; Δbdp-1::hph</i> | This Study |
| N8107 | <i>mat ? Δlsd1::hph; Δbdp-1::hph</i> | This Study |
| N8108 | <i>mat ? Δlsd1::hph; Δbdp-1::hph</i> | This Study |
| N8109 | <i>mat ? Δlsd1::hph; Δphf1::hph</i> | This Study |
| N8110 | <i>mat ? Δlsd1::hph; Δphf1::hph</i> | This Study |
| N8111 | <i>mat ? Δlsd1::hph; Δphf1::hph</i> | This Study |
| N8112 | <i>mat ? Δlsd1::hph; Δphf1::hph</i> | This Study |

Table S8. Primers used in this study

| Primer | Sequence |
|---|---|
| For 3xFLAG-tagging LSD1 | |
| <i>LSD1</i> KI FP1 | 5'-TAGCTCTTATGGCTGGCGAC-3' |
| <i>LSD1</i> KI RP2 | 5'-CCGCCTCCGCCTCCGCCGCCTCCGCCCCAGTCATCGCAACATCA-3' |
| <i>LSD1</i> KI FP3 | 5'-TATACGAAGTTATGGATCCGAGCTCGAGGTTAAGACGTTATCAAG-3' |
| <i>LSD1</i> KI RP4 | 5'-TTGTTTGGGGCGCTTGATGG-3' |
| For 3xFLAG-tagging PHF1 | |
| <i>NCU07297(Phf1)</i> KI FP1 | 5'-GTCACAGACGGAAACGCATC-3' |
| <i>NCU07297(Phf1)</i> KI RP2 | 5'-TCCGCCTCCGCCTCCGCCGCCTCCGCCTACCCTCAAGCCATTCTC-3' |
| <i>NCU07297(Phf1)</i> KI FP3 | 5'-CTATACGAAGTTATGGATCCGAGCTCGGAAGACTTTGAGCGTGTC-3' |
| <i>NCU07297(Phf1)</i> KI RP4 | 5'-ACCTAGTACTGGCATTATC-3' |
| For 3xFLAG-tagging BDP-1 | |
| <i>Bdf1(NCU08809)</i> KI FP1 | 5'-CGACTACGAGGTTCTCATCG-3' |
| <i>Bdf1(NCU08809)</i> KI RP2 | 5'-TCCGCCTCCGCCTCCGCCGCCTCCGCCGTTAGATCCCTCTTGCC-3' |
| <i>Bdf1(NCU08809)</i> KI FP3 | 5'-CTATACGAAGTTATGGATCCGAGCTCGCGCTCTGTCCAAATGGAC-3' |
| <i>Bdf1(NCU08809)</i> KI RP4 | 5'-GTTGCAGTGCTATTCCATCG-3' |
| For Δlsd1::nat-1 KO | |
| 6696 | 5'-TGGGGCAACGGGAACGAAGA-3' |
| 6697 | 5'-GCTCCAGCCAAGCCCCAAAAACGTGAGGCGCAGAGAGAGG-3' |
| 6698 | 5'-TGAGCATGCCCTGCCCTGAGCATAGATGCAAACGTCGCC-3' |
| 6699 | 5'-CAAAGAACGCCGCGAGATG-3' |
| For Δphf1::nat-1 KO | |
| 5284 | 5'-GGCCGCGATCGAGAATGGGA-3' |
| 6694 | 5'-GCTCCAGCCAAGCCCCAAAAAGCGACAGCATTGACCACGTG-3' |
| 6695 | 5'-TGAGCATGCCCTGCCCTGAGGCTCCCTCCTCTCTCC-3' |
| 5285 | 5'-CTGGGCTCTCTGCGAGGGTC-3' |
| For Δbdp-1::nat-1 KO | |
| 6700 | 5'-CGGAGTTGTGCGGTGATGGC-3' |
| 6701 | 5'-GCTCCAGCCAAGCCCCAAAAAAGCTCCCGCAGAACCAAGC-3' |
| 6702 | 5'-TGAGCATGCCCTGCCCTGACGTGCGATGCTAAGCCTCCA-3' |
| 5289 | 5'-CGCCGTCCAGCAAACGTTCA-3' |
| 4883 | 5'-AACCCATCCGCCGGTACGCG-3' |

| | |
|---------------------------------------|--|
| 4884 | 5'-TCCTTCACCACCGACACCGTCTTCC-3' |
| For catalytic-null LSD1-3xFLAG | |
| 6716 | 5'-GCCACGCCCAAGTAACAACG-3' |
| 6717 | 5'-TGACGGCCGCGAGAACACCAAAGCCTATACGTTCCG-3' |
| 6718 | 5'-TCTCGCGCCGTCATCCTCGTGTAACAAGGAGGCAT-3' |
| 6720 | 5'-CCTCCGCCTCCGCCTCCGCCGCCTCCGCCCCAGTCATCGCAACATCAA-3' |
| 6721 | 5'-GAGCTCGGTACCAAGCTTGATGCATAGCGGTTAAGACGTTATCAAGTAAGTGAG-3' |
| 6722 | 5'-AAATAAAAGCCGCAGACGGG-3' |
| Southern Hybridization Probes | |
| Tel VIII (2391bp) | |
| 5272 | 5'-GGCATCCGTGGGTGTCCCAG-3' |
| 5273 | 5'-TTCCCGTCCCTACCAGGCAT-3' |
| NCU02455 (910bp) | |
| 5440 | 5'-GCTGCCAGGTGTCCAACACTAC-3' |
| 5442 | 5'-CAGCTCATTGTGCTCCTGGA-3' |
| NCU10040 (1071bp) | |
| 5446 | 5'-TCCGCCTTCAACTCTTCCGC-3' |
| 5448 | 5'-GCCAGCGTGTGACGGTCATC-3' |
| NCU04942 (1056bp) | |
| 5449 | 5'-CCTGTGGCGGTTAGCGACAA-3' |
| 5451 | 5'-TGACACCAGCGCTGTCACCG-3' |
| NCU05569 (1172bp) | |
| 6692 | 5'-ACCAGTGTGTCCTCAACCCAG-3' |
| 6693 | 5'-GGTGGTCTTGGTCGAGGCCT-3' |
| his-3 (2631bp) | |
| 1665 | 5'-GACGGGGTAGCTTGGCCCTAATTAACC-3' |
| 3128 | 5'-CGATTTAGGTGACACTATAG-3' |
| 8:A6 (605bp) | |
| 1877 | 5'-TGGTTGGTCGATTGTGGTGG-3' |
| 1878 | 5'-TTTTGAGGATCCGCCATCCG-3' |
| actin (717bp) | |
| 3211 | 5'-CACGGTGTGCTTACCAACTG-3' |
| 3212 | 5'-GTCGGAGAGACCAGGGTACA-3' |
| pan-1 (1007bp) | |
| 3181 | 5'-CGATAAGCTTGATATCGAATTCAGGTTGTCCGGCCATCTCAGTCTGATCC-3' |
| 3182 | 5'-TCGCATACGCCAACCCATGC-3' |
| qPCR | |
| ChIP-qPCR | |

| | |
|---------------------------------------|--------------------------------------|
| hH4 (102bp) | |
| 4082 | 5'-CATCAAGGGGTCATTCAC-3' |
| 4083 | 5'-TTTGAATCACCTCCAG-3' |
| | |
| Cen III L (169bp) | |
| 5250 | 5'-CGACTATCCGAACCGGAAGGAG-3' |
| 5251 | 5'-CCGAATCCGGCTCAGTACAGC-3' |
| | |
| 8:A6 (302bp) | |
| 1823 | 5'-GGATGGCGGATCCTCAAAAATA-3' |
| 1824 | 5'-TAACCGCCGCTTTTTAAATTAGGA-3' |
| | |
| NCU02455 (158bp) | |
| 5440 | 5'-GCTGCCAGGTGTCCAACACTAC-3' |
| 5441 | 5'-GAGGCTAGTAGCGACAGCGA-3' |
| | |
| Tel VIII (208bp) | |
| 5272 | 5'-TTCCCGTCCCTACCAGGCAT-3' |
| 5273 | 5'-GAGCGGAGGTGGACTTTGCG-3' |
| | |
| RT-qPCR | |
| NCU02840 (104bp) | |
| 6271 | 5'-CCCTCTCAGACGAGGATATTCA-3' |
| 6272 | 5'-GCTCTGCTGCTTCTCCTTTAT-3' |
| | |
| NCU00911 (207bp) | |
| 6636 | 5'-GACAACAAAGGCCAAGGACG-3' |
| 6637 | 5'-ACCTGGATCCAGTATGAGCC-3' |
| | |
| NCU02455 (228bp) | |
| 6638 | 5'-TTGATAACCTGACCACCGCC-3' |
| 6639 | 5'-TTTCCTGTCGCTGTCGCTAC-3' |
| | |
| NCU06512 (219bp) | |
| 6640 | 5'-GAGGGGATGATGTGCGACACC-3' |
| 6641 | 5'-CCCCCTAATCTCCGTTTGT-3' |
| | |
| NCU02437 (196bp) | |
| 6642 | 5'-AGGAGACGATGGACACGACC-3' |
| 6643 | 5'-TACGTCAACCGAAACGACGC-3' |
| | |
| Yeast two-hybrid | |
| PHF1 constructs | |
| 418 MfeI- Phf1(NCU07297) 2aa FP | 5'-ATCCAATTGGCAGACCAGACACCAAACGT-3' |
| 419 Phf1(NCU07297) 605aa BamHI RP | 5'-CGGGATCCTATACCCTCAAGCCATTCT-3' |
| 513 Phf1(NCU07297) 353aa BamHI RP | 5'-CGGGATCCTAGGCTTGCTCGGCTGTGCGCT-3' |

| | |
|--|---------------------------------------|
| 610 <i>MfeI</i> - <i>Phf1</i> (NCU07297) 117aa FP | 5'-ATCCAATTGCCCTGGTCCAGCCGAGCAT-3' |
| 611 <i>Phf1</i> (NCU07297) 275aa <i>Bam</i> HI RP | 5'-CGGGATCCTATTTCGTCCGCGTCTTGTTGTT-3' |
| 612 <i>Eco</i> RI- <i>Phf1</i> (NCU07297) 312aa FP | 5'-CGAATTCACCAAATCCGGCCGTC AAGT-3' |
| 695 <i>Eco</i> RI- <i>Phf1</i> (NCU07297) 401aa FP | 5'-CGAATTCGTATGTTTCGCTGTGTGTGGC-3' |
| 696 <i>Phf1</i> (NCU07932) 540aa <i>Bam</i> HI RP | 5'-CGGGATCCTAGCCTTGGTTCTCTTGGCTCG-3' |
| 710 <i>Phf1</i> 140aa <i>Bam</i> HI RP | 5'-CGGGATCCTACAAAGAAAGGTTCTTCTTGA-3' |
| 711 <i>Eco</i> RI- <i>Phf1</i> 401aa FP | 5'-CGAATTCGTATGTTTCGCTGTGTGTGGC-3' |
| BDP-1 constructs | |
| 420 <i>MfeI</i> - <i>Bdp1</i> (NCU08809) 2aa FP | 5'-ATCCAATTGGACATGAGTGCCTCGCCTAC-3' |
| 421 <i>Bdp1</i> (NCU08809) 478aa <i>Bam</i> HI RP | 5'-CGGGATCCTAGTTAGATCCCTCTTGGC-3' |
| 514 <i>MfeI</i> - <i>Bdp1</i> (NCU08809) 198aa FP | 5'-ATCCAATTGGAGTACCGCCGAATCACAAA-3' |
| 515 <i>Bdp1</i> (NCU08809) 236aa <i>Ban</i> HI RP | 5'-CGGGATCCTAGTAATCGGCCGCCAGGAAA-3' |
| 615 <i>Bdp1</i> (NCU08809) 361aa <i>Bam</i> HI RP | 5'-CGGGATCCTACAGTTTCTTGGAGGTGGTAA-3' |
| 691 <i>Eco</i> RI- <i>Bdp1</i> (NCU08809) 45aa FP | 5'-CGAATTC AACGAGACACACGATGACCA-3' |
| 707 <i>Eco</i> RI- <i>Bdp1</i> 45aa FP | 5'-CGAATTC AACGAGACACACGATGACCA-3' |
| 708 <i>Bdp1</i> 236aa <i>Bam</i> HI RP | 5'-CGGGATCCTAGTAATCGGCCGCCAGGAAA-3' |

1 **Supplemental Figure 1. Schematic representation of human, *S. pombe*, and Neurospora**
2 **LSD1 homologs with predicted domains and amino acid lengths.**

3

4 **Supplemental Figure 2. Δ *lsd1* strains exhibit hyper DNA methylation at select loci genome-**
5 **wide.**

6 WGBS tracks displaying DNA methylation in WT (blue) and Δ *lsd1* (red) strains across all
7 Neurospora linkage groups.

8

9 **Supplemental Figure 3. H3K9me1 and -me3 in Δ *lsd1* strains.**

10 Western blot analysis of H3K9me1 in WT, Δ *dim-5*, and Δ *lsd1* cell extracts (left panel) and
11 H3K9me3 in WT, Δ *dim-5*, Δ *dim-2*, Δ *lsd1*, and Δ *lsd1*; Δ *dim-2* cell extracts (right panel). Cell
12 extract from *S. cerevisiae*, which possesses no methylation on lysine 9 of histone H3, is included
13 as a negative control for H3K9me1. hH3 levels are included as a loading control for both blots.

14

15 **Supplemental Figure 4. Coimmunoprecipitation and yeast two-hybrid analysis of LSDC**
16 **members.**

17 (A) Coimmunoprecipitation analysis of LSDC members. Pull downs were performed with
18 antibodies to epitopes on indicated proteins.

19 (B) Summary of results of yeast two-hybrid analysis of PHF1 and BDP-1. PHF1 fragments were
20 fused to the GAL4 DNA binding domain and co-expressed with full length BDP-1 fused to the
21 GAL4 activation domain (left), or full length PHF1 was fused to the GAL4 DNA binding
22 domain and co-expressed with BDP-1 fragments fused to GAL4-activating domain (right). All
23 constructs were co-transformed into PJ69-4A yeast, and transformants were tested on SD agar
24 plates without Ade, His, Leu, and Ura. Growth results are at the left of each fragment schematic.

25

26 **Supplemental Figure 5. Δ *lsd1* strains exhibit variable extents of hyper DNA methylation.**

27 (A) WGBS tracks showing variable hyper DNA methylation in replicate bisulfite sequencing of
28 the same Δ *lsd1* strain (red) and three different asexually-propagated Δ *lsd1* strains (black). DNA

29 methylation-sensitive Southern hybridization analysis of Tel VIII and NCU02455 and the
30 pedigree of the $\Delta lsd1$ strains are presented in Figure 2B.

31 **(B)** DNA methylation-sensitive Southern hybridization analysis of LSD complex double
32 knockout siblings with the indicated probes. Strains (left to right): N3753, N4711, N5555,
33 N6414, N6416, N6272, N8109, N8110, N8111, N8112, N6271, N8105, N8106, N8107, and
34 N8108.

35 **(C)** Ascospore germination rates of heterozygous and homozygous $\Delta lsd1$ strain crosses.

36

37 **Supplemental Figure 6. $\Delta lsd1$ strains exhibit DNA methylation-dependent hyper H3K9me3.**

38 **(A)** ChIP-qPCR validation of H3K9me3 ChIP-seq from Figure 3A. qPCR amplicons are
39 displayed as red bars above H3K9me3 ChIP-seq tracks from Figure 3A. H3K9me3 enrichment
40 was normalized to antibody-specific background levels at the histone H4 gene, *hH4*. Quadruple
41 asterisks indicate $p < 0.0001$.

42 **(B)** Metaplot displaying the averaged profile of H3K9me3 enrichment in WT and $\Delta lsd1$ strains
43 as determined by ChIP-seq over identified $\Delta lsd1$ -sensitive regions.

44

45 **Supplemental Figure 7. *lsd1-3xFLAG* Neurospora strains exhibit slight hyper DNA
46 methylation, but less so than catalytic-null *lsd-3xFLAG* strains.**

47 **(A)** DNA methylation-sensitive Southern hybridization analysis comparing DNA methylation
48 levels in catalytic null LSD1-3xFLAG strains (indicated by an asterisk) and WT LSD1-3xFLAG
49 siblings at two $\Delta lsd1$ -sensitive regions. Strains (left to right): N3753, N4711, N5555, N7943,
50 N7944, N7945, N7946, N7899, N6300, N8040, N8041, N8042, N8043, N8044, N8045, N8046,
51 N8047, N8048, N8049, N8050, N8051, N8052, N8053, N8054, N8055, N8056, N8057, N8058,
52 N8059, N8060, N8061, N8062, N8063, N8064, N8065, N8066, N8067, and N8068.

53 **(B)** ChIP-seq tracks showing H3K9me3 enrichment in WT, $\Delta lsd1$, and catalytic null (indicated
54 by an asterisk) *lsd1* strains at selected $\Delta lsd1$ -sensitive regions.

55 **Supplemental Figure 8. Modest changes in gene expression in regions hypermethylated in
56 $\Delta lsd1$ strains.**

57 (A) RT-qPCR results showing mRNA levels of indicated genes that become methylated in $\Delta lsd1$
58 methylated strains.

59 (B) WGBS and H3K4me3 ChIP-seq tracks showing DNA methylation and H3K4me3
60 enrichment, respectively, in indicated strains over the selected genes in illustrated in panel A.

61

62 **Table S1. LSD1-associated proteins.**

63

64 **Table S2. PHF1-associated proteins.**

65

66 **Table S3. BDP-1-associated proteins.**

67

68 **Table S4. Putative lysine methyltransferase KOs screened for loss of H3K9me1 in $\Delta dim-5$**
69 **background.**

70

71 **Table S5. List of genes downregulated in $\Delta lsd1$.**

72 Methylated genes identified by bisulfite sequencing are in yellow.

73

74 **Table S6. List of genes upregulated in $\Delta lsd1$.**

75

76 **Table S7. Strains used in this study.**

77

78 **Table S8. Primers used in this study.**

79