SUPPLEMENTARY FIGURE AND TABLE LEGENDS

Figure S1. Transcriptional regulation in alternative loci, Related to Figure 2. (A-C) CR regulation of a *LEU2*-integrated reporter is similar to regulation at the *URA3* locus. The GFP reporter with upstream ZF binding sites was integrated into the *LEU2* locus. The full library of 223 CRs was recruited to the reporter, and fold change GFP of induced to uninduced cells was measured by flow cytometry. (A) Fold change GFP measurements for *URA3*-integrated reporter plotted against those obtained from the *LEU2*-integrated reporter. Spearman's rank correlation coefficient indicates strong correlation of reporter regulation by CRs between the two loci. CRs grouped by complex (B) and function (C) and plotted according to the percentage of activators and repressors in each group. Dot colors correspond to the general activities of each complex. (D) The GFP reporter was integrated into the *HIS3* locus. A representative subset of CRs were fused to non-targeting (left) and targeting ZFs (right). ZF-CRs displayed in the same order and coloring (repressors in blue and activators in red) as they appear in Figure 2B. Error bars are standard deviations of three isogenic strains.

Figure S2. Transcriptional regulation of a synthetic reporter by targeted CRs, Related to Figure 2. (A) CRs grouped by gene ontology function terms and plotted according to the percentage of activators and repressors in each group. Dot colors correspond to the general activities of each complex. The reporter was integrated into the *URA3* locus. (B) ChIP-QPCR measurements of the *URA3*-integrated target locus shows a range of CRs modify chromatin according to their expected activities. CRs chosen for analysis are those with known histone-modifying catalytic domains or activities. Pulldown epitopes indicated above each bar. Relative levels of histone modifications are for induced cells normalized to uninduced cells. Error bars are ±SEM with the number of biological replicates indicated on the bottom of each bar. (C)

Quantification of protein levels for 35 CRs (in *URA3*-integrated reporter strains) evenly distributed with repressors, neutral factors, and activators. There is no negative linear correlation with reporter repression or positive linear correlation with activation strength. Protein levels obtained by quantifying western blots of induced and uninduced cultures plotted against fold change GFP fluorescence.

Figure S3. Transcriptional logic in alternative loci, Related to Figure 3. Representative ZF-CRs from Figure 3B show the same six classes of transcriptional logic when the reporter is integrated into the (A) *LEU2* locus and (B) *HIS3* locus. Vertical axes correspond to "Fold Change GFP." (C) The same ZF-CRs from Figure 3C were clustered by complex and show similar trends in synergy when the reporter is integrated into the *LEU2* locus. (D) All 223 CRs were targeted to the *LEU2*-integrated reporter. Activators were clustered by gene ontology function terms and plotted as the percentage of CRs in each term group with "strong synergy" (greater than the average synergy of 0.1). The trend is similar to that observed in Figure 3D. Error bars are standard deviations of three isogenic strains.

Figure S4. Engineering spatial regulation by targeting CRs upstream and downstream of a gene, Related to Figure 4. Fold change in GFP expression for the library of 223 ZF-CR fusions, targeted either upstream (grey bars) or downstream (blue, gold, red bars) of the reporter gene. When targeted to the downstream position, CRs function either as repressors (blue bars, < 0.7 fold change) or neutral elements (gold bars, 0.7 < fold change < 2). None function as activators. Error bars are standard deviations of three isogenic strains.

Figure S5. Simultaneous, differential regulation of two genes, Related to Figure 5. (A-D, left) Schematics of the engineered, dual-gene reporter loci integrated into the *URA3* locus (ZF43-8 operator, grey boxes; ZF97-4 operator, blue boxes). (A-D, top) The combination of non-

targeting and targeting CRs expressed (ZF 43-8, grey; ZF 97-4, blue; truncated non-binding ZF, white). (E and F) Individual CRs show similar simultaneous regulation of two genes integrated into the *LEU2* locus. Non-targeted (left) and targeted (right) ZF-CR fusions. (A-F) Fold change in fluorescence (GFP, green bars; mCherry, red bars). Error bars are standard deviations of three isogenic strains.

Figure S6. Long-range regulation by non-targeting and targeting CRs, Related to Figure 6. (A) Expression of GFP (green bars), mCherry (red bars), and BFP (blue bars) was driven by tandem minimal *CYC1*, *BIO2,* and *CHO1* promoters, respectively, all integrated into the *URA3* locus. Fold change in fluorescence induced by the 27 strongest repressors, 48 strongest activators, and all CRs with histone-modifying catalytic domains when fused to a truncated, non-targeting ZF control (B) or a targeting ZF (43-8) (C). Error bars are standard deviations of three isogenic strains.

Figure S7. Multi-gene regulation and memory by targeted CRs, Related to Figure 7. (A) Heat map of fold change in fluorescence from the triple reporter integrated into the *LEU2* locus for targeting (left) and non-targeting (right) ZF-CRs from Figure 6B. (B and C) FACS measurements of GFP (top), ChIP-QPCR measurements of 3xFLAG-ZF-Sir2 operator occupancy (middle), and H4K16ac promoter enrichment (bottom) normalized to uninduced cells harvested at hour 12 (dotted brown line). (B) Low time resolution experiment revealing a period between 24 and 30 hours where ZF-Sir2 is no longer present at the reporter while H4K16ac remains low. (C) Higher time resolution experiment showed H4K16 remains hypoacetylated for two cell divisions, between 26 and 30 hours, while ZF-Sir2 is no longer bound to the reporter. Error bars are standard deviations of three separate strains. (D) Fold change in fluorescence of *LEU2*-integrated triple reporters with $((CCGNN)_{32})$ or without (random) the $(CCGNN)_{32}$ sequence inserted between GFP and mCherry. Change in multi-gene expression when

expressing targeting (top) or non-targeting (bottom) multi-gene repressors (Sir2, Rph1, Sum1 ZF fusions). The $(CCGNN)_{32}$ sequence robustly insulates only the middle gene (mCherry) from repression by the CRs. Error bars are standard deviations of three isogenic strains.

Table S1. CR-based transcriptional regulation is similar at the *LEU2* locus, Related to Figure 2. Mean GFP values for the CR library targeted to the single GFP reporter (with upstream ZF-CR binding site) integrated into the *LEU2* locus. Values are compared to those obtained with the reporter integrated into the *URA3* locus. Spearman's Ranked Correlation Coefficient indicates strong correlation between activation and repression of the reporter in the two loci.

Table S2. Gene ontology clustering of 223 CRs, Related to Figure 2. (Blue background) Clustering by GO slim macromolecular complex terms. (Green background) Clustering by GO function terms.

Table S3. Co-recruitment of VP16 with CRs, Related to Figure 3. Mean fold change GFP for three biological replicates when targeting ZF fusions with CR only, VP16 only, or both CR and VP16 to the reporter integrated into the *URA3* (blue background) and *LEU2* (green background) loci.

Table S4. Gene ontology clustering of activators by GO function with calculated synergies, Related to Figure 3. Reporter integrated into the *URA3* (yellow background) or *LEU2* (blue background) loci.

Table S5. Clustering and GO function analysis of CRs by upstream and downstream spatial recruitment profiles, Related to Figure 4. CRs clustered by their upstream and

downstream spatial recruitment profiles. Gene ontology function terms associated with each spatial recruitment profile cluster.

Table S6. Primer sequences used to amplify CR ORFs, Related to Experimental Procedures.

Extended Experimental Procedures

Western Blots

Two mL yeast cultures were grown in triplicate to mid log phase in SD-complete media in the presence and absence of inducers. Protein extract samples were prepared from harvested cultures by two methods: 1) by direct lysis in boiling SDS-PAGE sample buffer (200µL), and 2) by TCA precipiation, in which cells were lysed in 200 µL of 0.2M NaOH, 5% beta-mercaptoethanol, followed by precipitation in 20% TCA and resuspension in SDS-PAGE sample buffer. CRs were detected using mouse anti-FLAG (Sigma, F3165) as primary and Alexa Fluor 488 anti-mouse as the secondary antibody (Cell Signaling, #4408). For hexokinase loading controls, rabbit anti-hexokinase (US Biological Life Sciences, H2035-02) and anti-rabbit Alexa Fluor 647 (Cell Signalling, #4414) were used as primary and secondary antibodies, respectively. Blot fluorescence was visualized using a Typhoon FLA 9000 (GE Healthcare). ImageJ was used to quantitate band intensity, with FLAG integrated intensity normalized to hexokinase integrated intensity.

Chromatin Immunoprecipitation – Quantitative PCR

Chromatin immunoprecipitation followed a modified version of a protocol kindly shared by the Moazed Lab (Harvard Medical School). Briefly, 50 mL cultures were inoculated with overnight cultures to an OD600 of 0.05-0.1 in SDC, with or without inducers. At OD600 of 0.9-1.0, cells

were crosslinked with 1% formaldehyde (from a 37% stock, Sigma 47608) for 15 min at room temperature with gentle agitation. Fixation was quenched with a final concentration of 125 mM glycine (EMD 4840 OmniPur) for 5 min at room temperature with gentle agitation. Cells were pelleted for 2 min at 2000 g, washed twice with ice-cold PBS, transferred to bead-beater tubes, and frozen at -80°C. Cell pellets were resuspended in 400 µL ice cold lysis buffer (50 mM HEPES/KOH pH 7.5, 140 mM NaCl, 1 mM ethylenediaminetetraacetic acid, 1% Triton X-100, 0.1% Na-Deoxycholate, 1 mM phenylmethylsulfonyl fluoride, 200 µL Roche cOmplete protease inhibitors). 0.5 mm diameter glass beads were added to 1 mm below the meniscus. Cells were lysed by bead beating on a MagnaLyser (Roche) three times for 45 seconds each at 4500 rpm with 2 min rests at 4°C. Lysate was collected by puncturing the tube with a 21G needle and centrifugation at 2000 g for 2 min into a 2 mL microtube. The pellet was resuspended then sonicated three times using an EpiShear Probe Sonicator (ActiveMotif, Siggers Lab, Boston University) for 20 seconds at 25% amplitude with 2 min. intervening rests on ice, achieving a range of 200-1000 bp DNA fragments. Cell debris was pelleted by centrifugation at max speed for 10 min at 4°C. The supernatant was transferred to a new low retention tube. For the input samples, 40 µL was transferred to another tube with 210 µL TE/1% SDS and stored at -20ºC. Antibodies were added to the pulldown samples and incubated overnight at 4°C on a rotisserie. Equivalent masses of IgG control antibodies were added to parallel samples and were confirmed to yield less than 1% QPCR signal compared to the pulldown of all histone modifications and 3xFLAG tag (data not shown). 30 µL Dynabeads Protein G (10004D, Life Technologies) per culture was added to a low retention tube and washed 3 times with 1 mL ice cold lysis buffer. Dynabeads were resuspended in 100 µL lysis buffer per culture. 100 µL of Dynabead solution was added to each antibody-pulldown sample and incubated at 4°C for 1 hour on the rotisserie. Dynabeads were washed at room temperature on a magnet (twice with 1 mL lysis buffer with transfer to a new tube after the first wash, twice with 1 mL lysis buffer/500 mM NaCl, twice with 10 mM TrisHCl-pH8/250 mM LiCl/0.5% NP-40/0.5% sodium

deoxycholate/1 mM EDTA, and once with 1 mL TE with transfer to a new tube). Bound material was eluted by adding 100 µL of 50 mM Tris-HCl pH 8.0/10 mM EDTA/1% SDS and incubating at 65 °C for 15 min. A second elution (150 µL TE/0.67% SDS, 65°C, 5 min.) was combined with the first. Both input and pulldown samples were then incubated overnight at 65°C to reverse crosslinks. 240 µL TE and 50 µg RNAse A was added to each sample and incubated for 30 min at 37°C. 100 µg Proteinase K and 60 µg blue glycogen was added to each sample and incubated for 2 hours at 37°C. 42 µL 3M NaCl and 550 µL phenol/chloroform/isoamyl alcohol was added, shook vigorously, and spun at max speed for 10 min at 4°C. 475 µL of the aqueous layer was transferred to a new tube and 475 µL chloroform/isoamyl alcohol was added, shook vigorously, and spun at max speed for 10 min at 4°C. 400 µL of the aqueous layer was transferred to a new tube, precipitated with 1 mL ethanol at -20°C temperature overnight, and spun at max speed for 15 min at 4°C. Pellets were washed with 1 mL ice cold 70% ethanol and spun at max speed for 3 min at 4°C. All liquid was removed and the pellet was dried for 5 min at room temperature. Input and pulldown samples were resuspended in 100 and 50 µL, respectively, of 1 mM TrisHCl-pH 8/0.1 mM EDTA. QPCR was performed on a LightCycler 480 using LightCycler 480 Sybr Green Mix (Roche). 5 µL of 1/50 dilution of input and 1/20 dilution of pulldown sample were run in 20 µL QPCR reactions using the following primer pairs: cacatgatcatatggcatgcatgtgct / gggacaacaccagtgaataattcttcacctt for histone marks and cctcgaggtcgacggtatc / tacacgcctggcggatct for 3xFLAG-tagged ZF-Sir2 fusion protein. Both FLAG and H4K16ac pulldowns were selectively enriched and depleted, respectively, at the ZF binding site compared to locations at least 1kb away in cells expressing ZF-Sir2 (data not shown). Furthermore, in triple tandem-reporter strains, in general, expression of non-targeted CRs did not affect gene expression (Figure S6B); and in targeted recruitment of CRs, only GFP and not downstream gene expression was altered (Figure S6C). Thus it is likely histone modifications by targeted CRs are largely locus specific. Primary antibodies were Rb polyclonal anti-H3K9ac (5 µL, ab4441), Rb polyclonal anti-H3K4me3 (3 µL, ab8580), Rb polyclonal anti-

H3K79me2 (5 µL, ab3594), Rb polyclonal anti-H3K36me2 (5 µL, ab9049), and Rb polyclonal IgG isotype control (equivalent mass, ab37415) from Abcam, and Rb polyclonal anti-H4ac (15 µL, 06-866) and Rb polyclonal anti-H4K16ac (5 µL, 07-329) from Millipore. Mouse anti-FLAG (1 µL, F3165) was from Sigma.

ChIP-QPCR Timecourse Experiments

Expression of 3xFLAG-ZF-Sir2 was induced at the beginning of the timecourse by ATc addition. ATc was washed out after 12 hours. A parallel uninduced culture was fixed after 12 hours of culture and cell lysate harvested for ChIP-QPCR analysis. Cells were diluted to the appropriate density to achieve mid-log growth at the specified time points. Yeast culture densities doubled every 2 hours. FACS measurements of GFP (top), pulldowns with anti-FLAG antibody followed by QPCR of the ZF binding region (middle), and pulldowns with anti-H4K16ac antibody followed by QPCR of the promoter region (bottom) were made at each time point. All values were normalized to uninduced cells harvested after 12 hours of culture.

Plasmid Construction

In the host strain, the strong constitutive *TEF1*, *ADH1*, and *TDH3* promoters direct the expression of yeast codon-optimized versions of TetR (Tn10.B tetracycline repressor), the *Escherichia coli Lac* inhibitor (LacI), and the estradiol-responsive hybrid transactivator GAL4-ER-VP16 (GEV: yeast GAL4 DNA binding domain (1-93) fused to the hormone binding domain of human estrogen receptor (282-576) fused to VP16 transactivator domain (Louvion et al., 1993)), respectively.

ZF43-8 binding sequences were cloned directly upstream of the minimal *CYC1* promoter TATA or downstream of the *CYC1* terminator. The *CYC1* promoter drives the expression of yeast enhanced green fluorescent protein (yEGFP) (Cormack et al., 1997) or yeast codon-optimized

mCherry protein, which is preceded by a Kozak consensus sequence. The *BIO2* and *CHO1* promoters drive yeast mCherry and blue fluorescent protein (BFP), respectively.

For experiments where the reporters were integrated into additional loci (LEU2 and HIS3), all reporters were cloned out of the URA3 integration cassette by PCR and inserted into pNH603 and pNH605. The ZF 97-4 - VP16 fusion protein construct was moved by PCR to pSV606 (URA3 single integrating vector, gift from the Lim Lab). For strains where the reporters were integrated into the HIS3 locus, the cassette containing the TetR-regulated GAL1 promoter driving the ZF 43-8 - CRs was moved by PCR to pNH603 (LEU2). A subset of ZF-CRs were cloned into this vector by SbfI and NotI ligation of CR PCR products, as described for the original library construction.

Synergy calculation

(Figure 3C, x-axis): To partition CRs by their synergy with VP16, we calculated synergy as the fraction of GFP signal for cells co-recruiting VP16 and CR that is not accounted for by the sum of GFP signal for cells recruiting VP16 only and a CR only. A simple additive relationship would result in a synergy of 0. We conservatively analyzed only CRs that activated GFP by 2 fold or more on their own (Figure 2B, red bars). The average synergy of all activators was 0.2, above which we defined as CRs with “strong synergy” (Figure 3C, red shading and Figure 3D, y-axis). Activators were clustered by chromatin complex (Figure 3C) and GO Function (Figure 3D, Table S4).

Integration loci

The integration vectors, genomic loci coordinates (S. cerevisiae S288C reference genome), and homology sequences used were as follows:

pNH603, single integrating in the *HIS3* (YOR202W) locus on chromosome XV

Homology arm targeting 721482-721945:

gctgcacggtcctgttccctagcatgtacgtgagcgtatttccttttaaaccacgacgctttgtcttcattcaacgtttcccattgtttttttctact

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cattatataaagtaatgtgatttcttcgaagaatatactaaaaaatgagcaggcaagataaacgaaggcaaag

Homology arm targeting 722826-723144:

Gagatggaggaacgggaaaaagttagttgtggtgataggtggcaagtggtattccgtaagaacaacaagaaaagcatttcatattat

ggctgaactgagcgaacaagtgcaaaatttaagcatcaacgacaacaacgagaatggttatgttcctcctcacttaagaggaaaac

caagaagtgccagaaataacagtagcaactacaataacaacaacggcggctacaacggtggccgtggcggtggcagcttctttag

caacaaccgtcgtggtggttacggcaacggtggtttcttcggtggaaacaacggtggcagc

pNH605, single integrating in the *LEU2* (YCL018W) locus on chromosome III

Homology arm targeting 90677-91388:

ccatttaaatgtttaaacggccacgctggccgaggagaacttctagtatatctacatacctaatattattgccttattaaaaatggaatccc

aacaattacatcaaaatccacattctcttcaaaatcaattgtcctgtacttccttgttcatgtgtgttcaaaaacgttatatttataggataatta

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atatatttcaaggatataccattctaatgtctgcccctaag

Homology arm targeting 92366-92891:

Ccaccgaagtcggtgatgctgtcgccgaagaagttaagaaaatccttgcttaaaaagattctctttttttatgatatttgtacataaactttat

aaatgaaattcataatagaaacgacacgaaattacaaaatggaatatgttcatagggtagacgaaactatatacgcaatctacatac

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aattgcactttaacattaatattgacaaggaggagggcaccacacaaaaagttaggtgtaacagaaaatcatgaaactatgattccta
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pNH607, single-integrating in the *HO* (YLD227C) locus on chromosome IV

Homology arm targeting 47782-48582:

tacctttttgtgcgtgtattgaaatattatgacatattacagaaagggttcgcaagtcctgtttctatgcctttctcttagtaattcacgaaataa
acctatggtttacgaaatgatccacgaaaatcatgttattatttacatcaacatatcgcgaaaattcatgtcatgtccacattaacatcattg
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tggtaggttagatcccaggcgtagaacagtttatcagcgtcttgcattacaatgtactgcag

Homology arm targeting 44543-45042:

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cgttgatgatacgcaaaacgttcaaaccagaaatggcaccggcatccttgg

pSV606, single integrating in the *URA3* (YEL021W) locus on chromosome V

Homology arm targeting 115730-116581:

Ctactgcgccaattgatgacaatacagacgatgataacaaaccgaagttatctgatgtagaaaaggattaaagatgctaagagata
gtgatgatatttcataaataatgtaattctatatatgttaattacctttttgcgaggcatatttatggtgaaggataagttttgaccatcaaaga
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Homology arm targeting 117045-117387:

acccgggaatctcggtcgtaatgatttctataatgacgaaaaaaaaaaaattggaaagaaaaagcttcatggcctttataaaaagga
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pRS406, integrating in the *URA3* (YEL021W) locus on chromosome V

Homology arm targeting 116011-116600:

Tcaattcatcatttttttttattctttttttgatttcggtttctttgaaatttttttgattcggtaatctccgaacagaaggaagaacgaaggaagg
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gcagaatgggcagacattacgaatgcacacggtgtggtgggcccaggtattgttagcggtttgaagcaggcggcagaagaagtaac
aaaggaacctag

Homology arm targeting 116601-116970:

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Supplemental References

Cormack, B.P., Bertram, G., Egerton, M., Gow, N.A., Falkow, S., and Brown, A.J. (1997). Yeast-enhanced green fluorescent protein (yEGFP): a reporter of gene expression in Candida albicans. Microbiology *143 (Pt 2)*, 303-311.

Louvion, J.F., Havaux-Copf, B., and Picard, D. (1993). Fusion of GAL4-VP16 to a steroid-binding domain provides a tool for gratuitous induction of galactose-responsive genes in yeast. Gene *131*, 129-134.

Figure S1

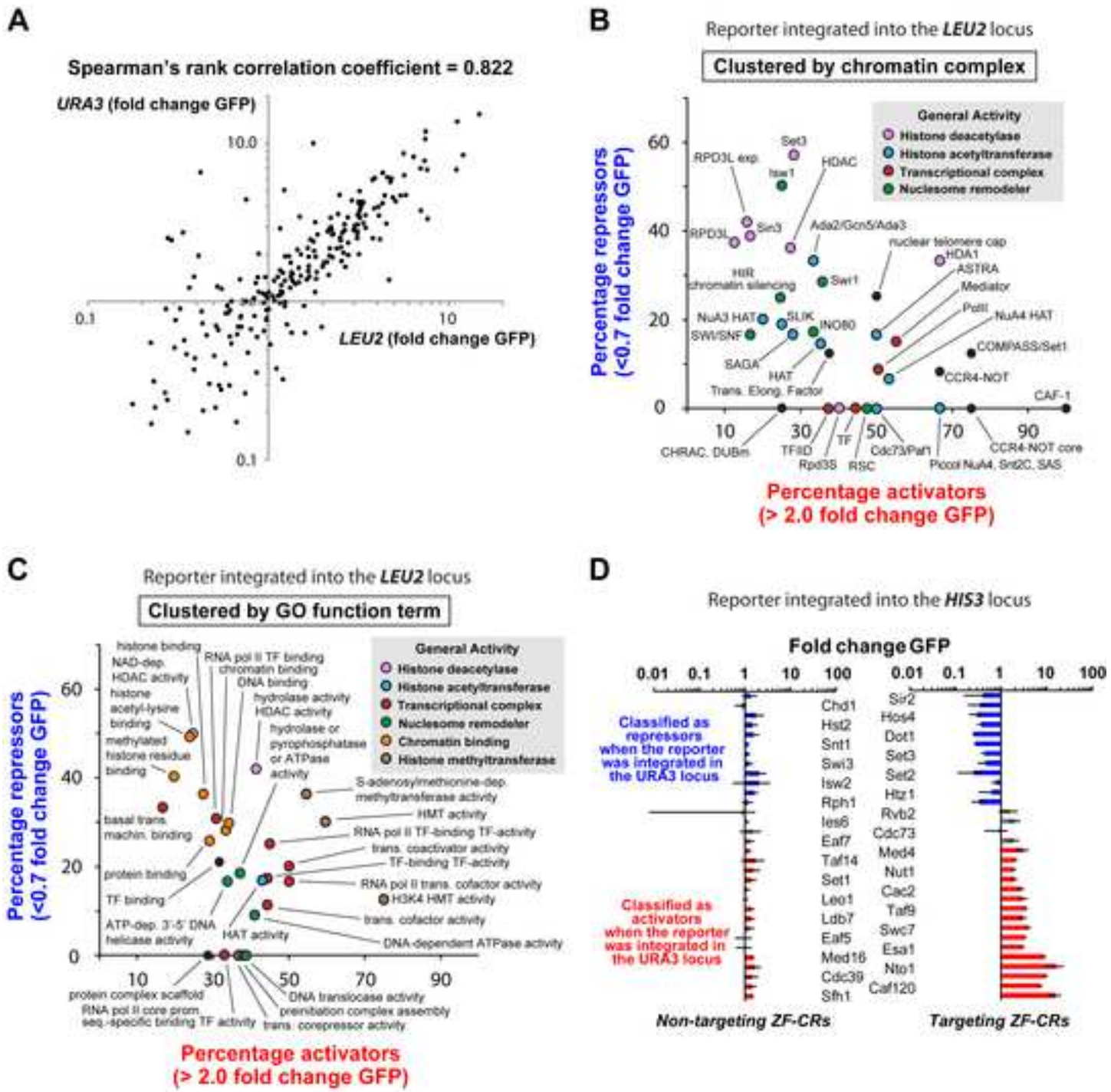
A
Spearman's rank correlation coefficient = 0.822
URA3 (fold change GFP)
LEU2 (fold change GFP)
10.0
0.1
10
0.1
B
Reporter integrated into the LEU2 locus
Clustered by chromatin complex
General Activity
Histone deacetylase
Histone acetyltransferase
Transcriptional complex
Nucleosome remodeler
Percentage repressors (<0.7 fold change GFP)
Percentage activators (> 2.0 fold change GFP)
C
Reporter integrated into the LEU2 locus
Clustered by GO function term
General Activity
Histone deacetylase
Histone acetyltransferase
Transcriptional complex
Nucleosome remodeler
Chromatin binding
Histone methyltransferase
Percentage repressors (<0.7 fold change GFP)
Percentage activators (> 2.0 fold change GFP)
D
Reporter integrated into the HIS3 locus
Fold change GFP
Classified as repressors when the reporter was integrated in the URA3 locus
Classified as activators when the reporter was integrated in the URA3 locus
Non-targeting ZF-CRs
Targeting ZF-CRs

Figure S2

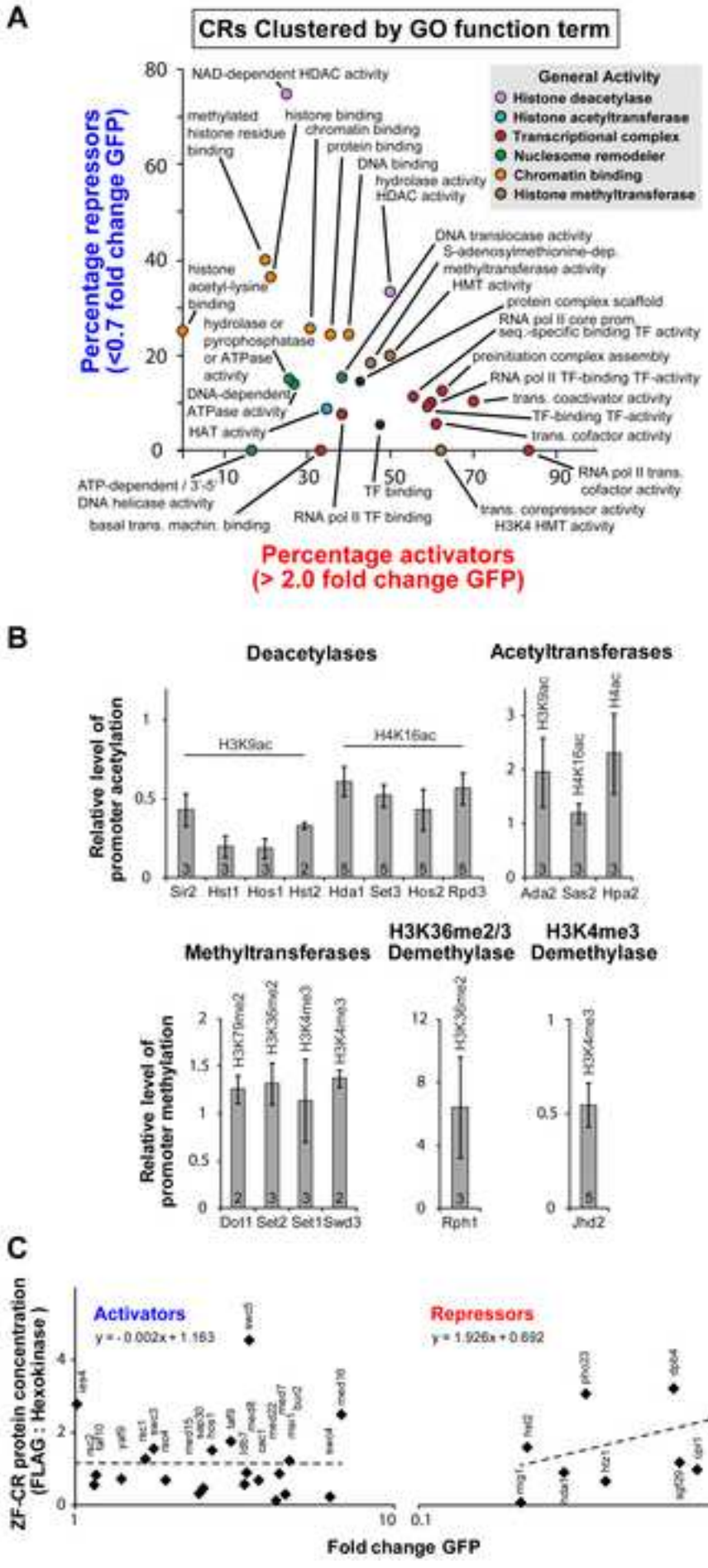
A
CRs Clustered by GO function term
General Activity
Histone deacetylase
Histone acetyltransferase
Transcriptional complex
Nucleosome remodeler
Chromatin binding
Histone methyltransferase
Percentage repressors (<0.7 fold change GFP)
Percentage activators (> 2.0 fold change GFP)
NAD-dependent HDAC activity
methylated histone residue binding
histone binding
chromatin binding
protein binding
DNA binding
hydrolase activity
HDAC activity
DNA translocase activity
S-adenosylmethionine-dep. methyltransferase activity
HMT activity
protein complex scaffold
RNA pol II core prom. seq.-specific binding TF activity
preinitiation complex assembly
RNA pol II TF-binding TF-activity
trans. coactivator activity
TF-binding TF-activity
trans. cofactor activity
RNA pol II trans. cofactor activity
trans. corepressor activity
H3K4 HMT activity
histone acetyl-lysine binding
hydrolase or pyrophosphatase or ATPase activity
DNA-dependent ATPase activity
HAT activity
ATP-dependent DNA helicase activity
basal trans. machin. binding
RNA pol II TF binding
TF binding
B
Deacetylases
Acetyltransferases
Relative level of promoter acetylation
H3K9ac
H4K16ac
Sir2 Hst1 Hos1 Hst2 Hda1 Set3 Hos2 Rpd3
Ada2 Sas2 Hpa2
Methyltransferases
H3K36me2/3 Demethylase
H3K4me3 Demethylase
Relative level of promoter methylation
H3K79me2
H3K36me2
H3K4me3
Dot1 Set2 Set1 Swd3
Rph1
Jhd2
C
ZF-CR protein concentration (FLAG : Hexokinase)
Activators
y = - 0.002x + 1.163
Repressors
y = 1.926x + 0.692
Fold change GFP

Figure S3

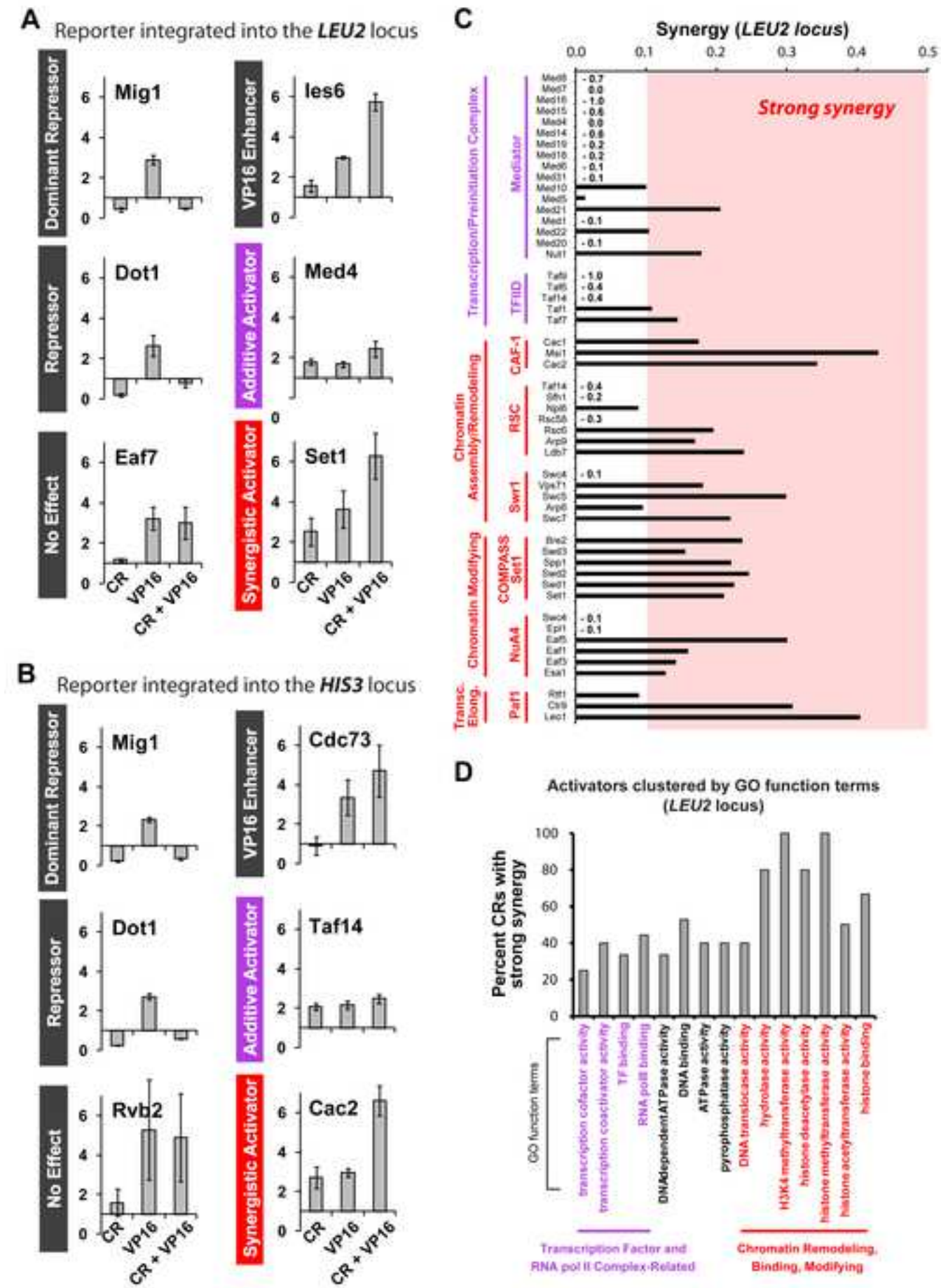
Figure S3
A
Reporter integrated into the LEU2 locus
Dominant Repressor
Mig1
Ies6
VP16 Enhancer
Repressor
Dot1
Med4
Additive Activator
No Effect
Eaf7
Set1
Synergistic Activator
CR
VP16
CR + VP16
B
Reporter integrated into the HIS3 locus
Dominant Repressor
Mig1
Cdc73
VP16 Enhancer
Repressor
Dot1
Taf14
Additive Activator
No Effect
Rvb2
Cac2
Synergistic Activator
CR
VP16
CR + VP16
C
Synergy (LEU2 locus)
0.0
0.1
0.2
0.3
0.4
0.5
Strong synergy
Transcription/Preinitiation Complex
Mediator
TFIID
Chromatin Assembly/Remodeling
CAF-1
RSC
Swr1
Chromatin Modifying
COMPASS Set1
NuA4
Transc. Elong.
Paf1
Med8
Med7
Med16
Med15
Med4
Med14
Med19
Med18
Med6
Med31
Med10
Med5
Med21
Med1
Med22
Med20
Nut1
Taf9
Taf6
Taf14
Taf1
Taf7
Cac1
Msi1
Cac2
Taf14
Sfh1
Nps6
Rsc58
Rsc6
Arp9
Ldb7
Swc4
Vps71
Swc5
Arp6
Swc7
Bre2
Swd3
Spp1
Swd2
Swd1
Set1
Swc4
Epl1
Eaf5
Eaf1
Eaf3
Esa1
Rtf1
Ctr9
Leo1
D
Activators clustered by GO function terms (LEU2 locus)
Percent CRs with strong synergy
100
80
60
40
20
0
GO function terms
transcription cofactor activity
transcription coactivator activity
TF binding
RNA pol II binding
DNA/dependentATPase activity
DNA binding
ATPase activity
pyrophosphatase activity
DNA translocase activity
hydrolase activity
H3K4 methyltransferase activity
histone deacetylase activity
histone methyltransferase activity
histone acetyltransferase activity
histone binding
Transcription Factor and RNA pol II Complex-Related
Chromatin Remodeling, Binding, Modifying

Figure S4

FIGURE S4

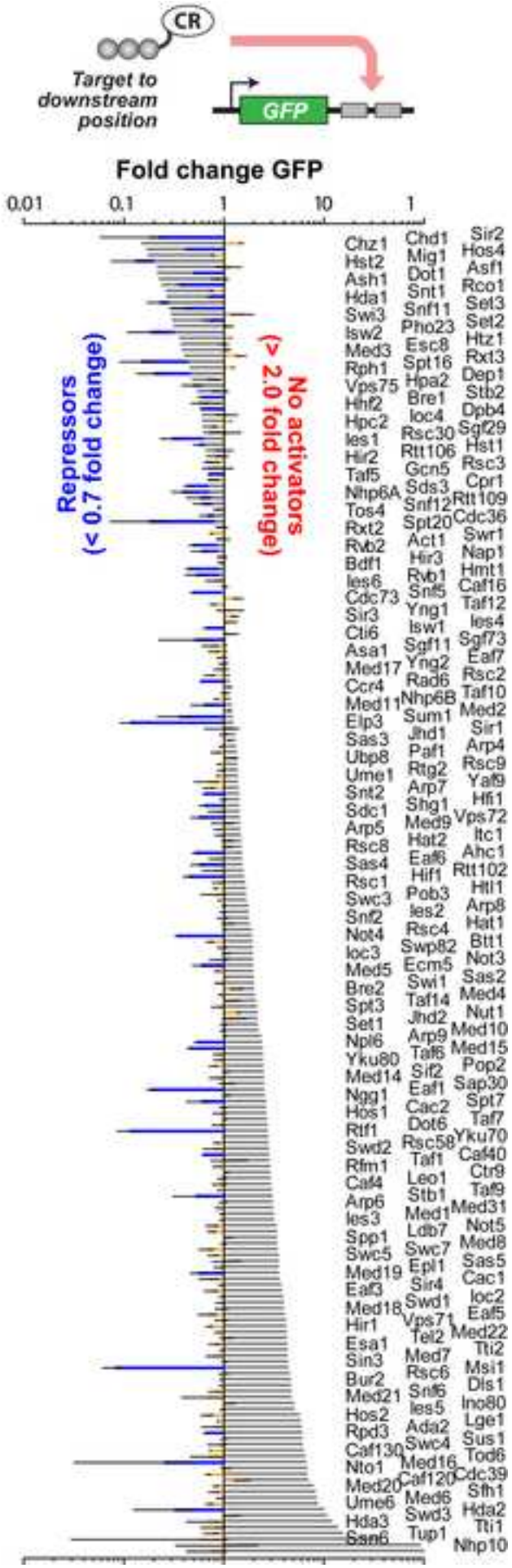

Figure S5

FIGURE S5

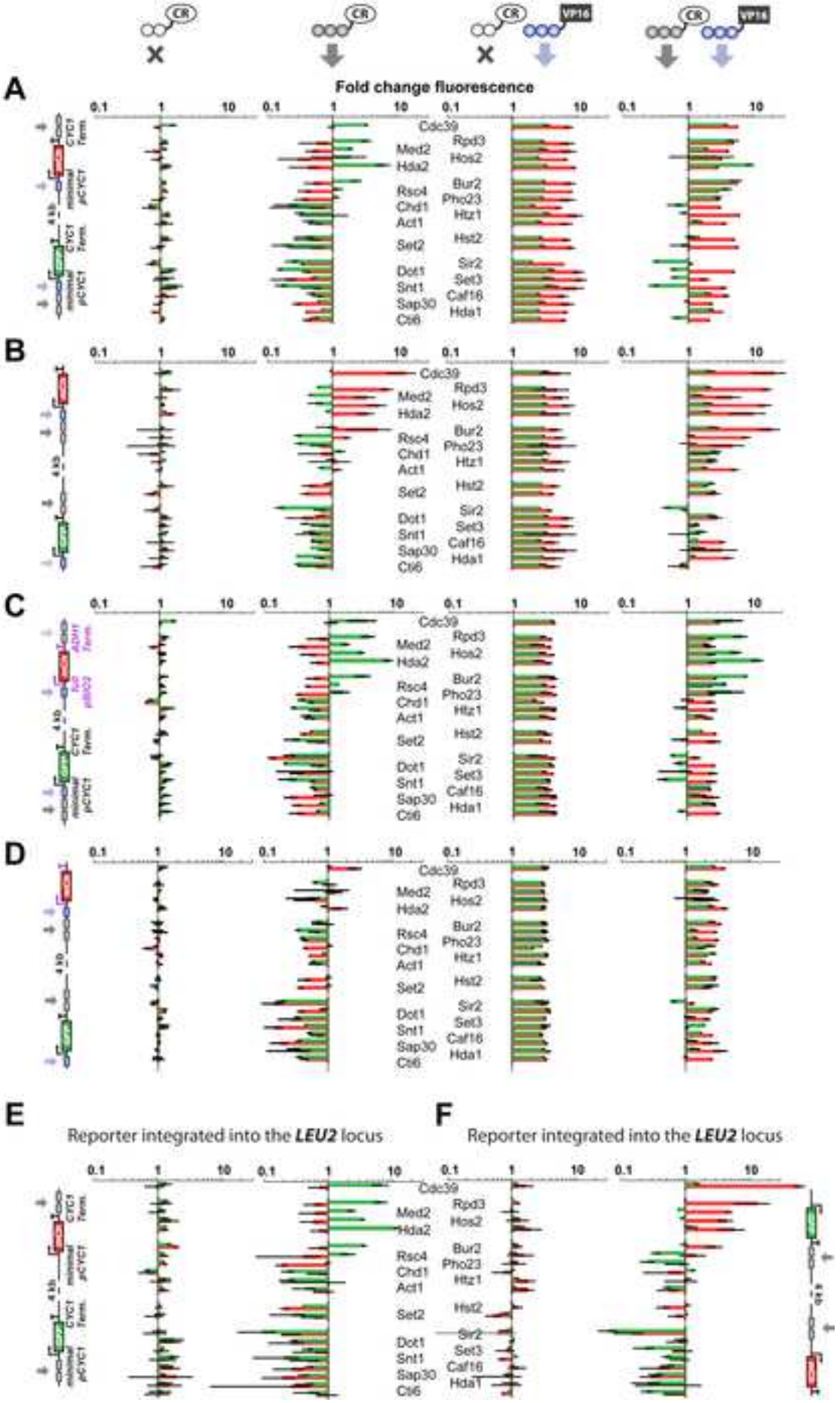

Figure S6

FIGURE S6

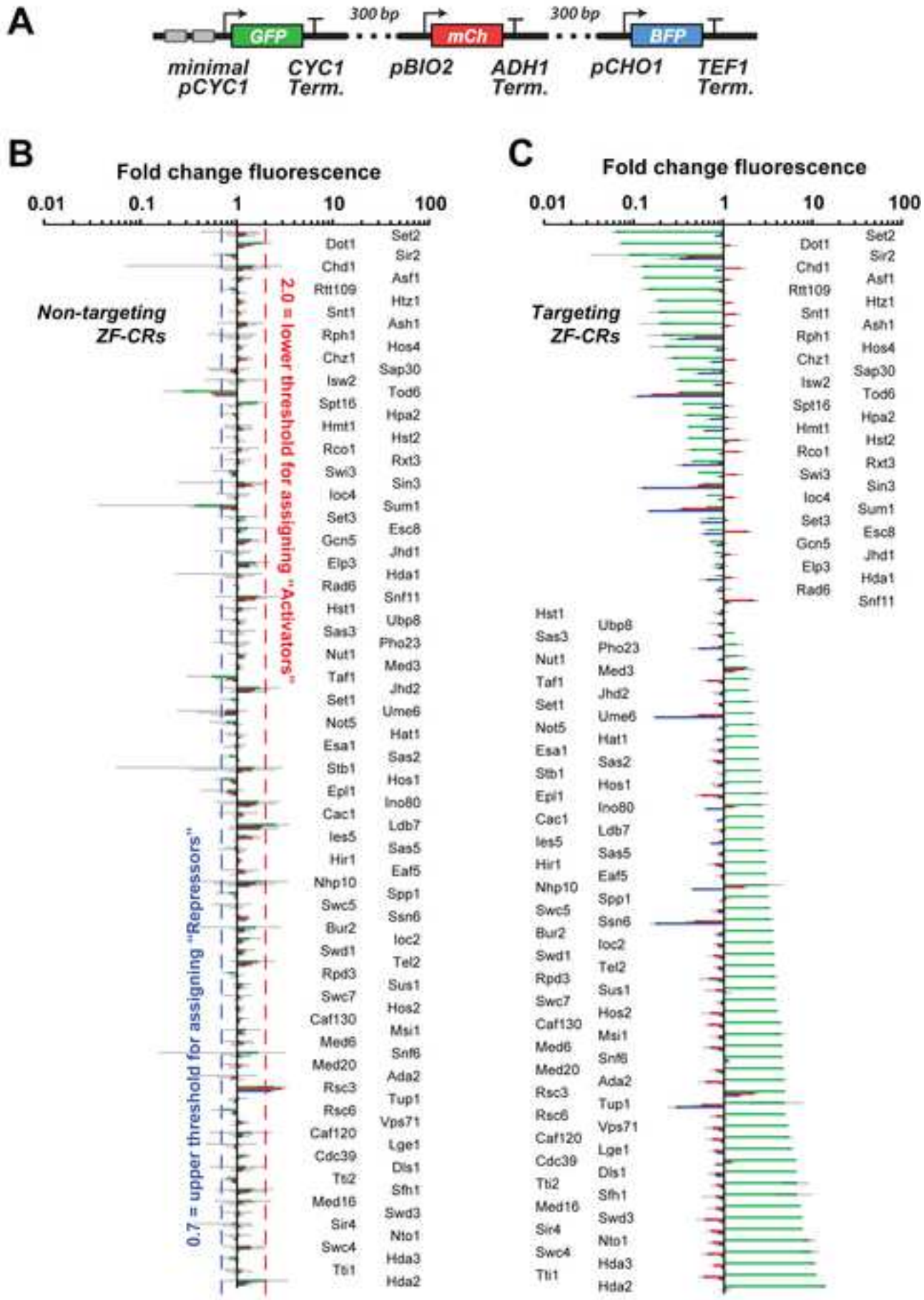

Figure S7

Figure S7