Supporting Information

Small et al. 10.1073/pnas.1400517111

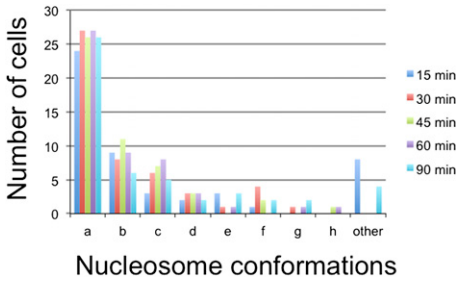

Fig. S1. Additional GpC protection patterns are observed when cells are incubating for shorter or longer times with GpC methyltransferase. Cells were permeabilized and incubated for 15 through 90 min with M.CviPI DNA methyltransferase as indicated. DNA was extracted, digested, and bisulfite-converted. After PCR amplification, 50 clones for each time point were sequenced. Only at 15 and 90 min were GpC protection patterns observed other than the conformations a through h.

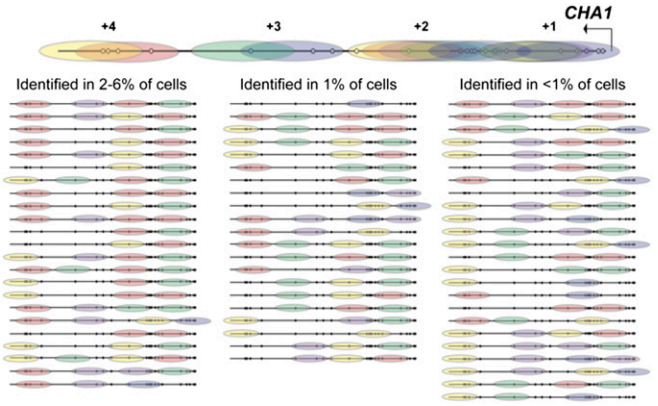

Fig. S2. Nucleosome architectures for *CHA1*. Nucleosome architecture of 481 cells from two bulk experiments revealed 68 conformations of nucleosomes in the 5′ region of *CHA1*. An overlay of all possible nucleosome positions is depicted.

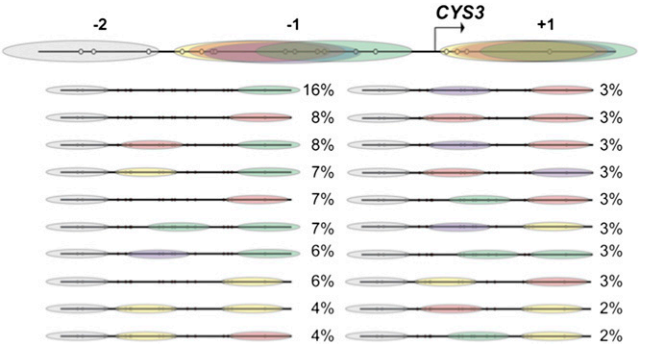

Fig. S3. Nucleosome architectures for *CYS3*. Nucleosome architecture of 550 cells from two bulk experiments revealed 20 conformations of nucleosomes in the *CYS3* promoter. An overlay of all possible nucleosome positions is depicted.

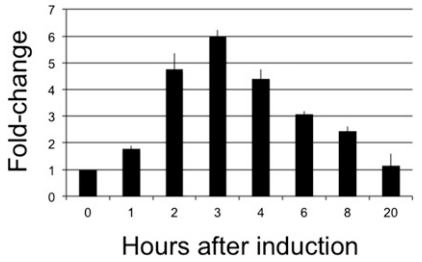

Fig. S4. The acid phosphatase *PHO5* expression is induced upon phosphate starvation. Cells were grown in rich media overnight and shifted to phosphate starvation media. Cells were collected at the indicated time points and RNA-extracted. The fold change is based on using TaqMan probes for *PHO5* and *UBC*6 as a control.

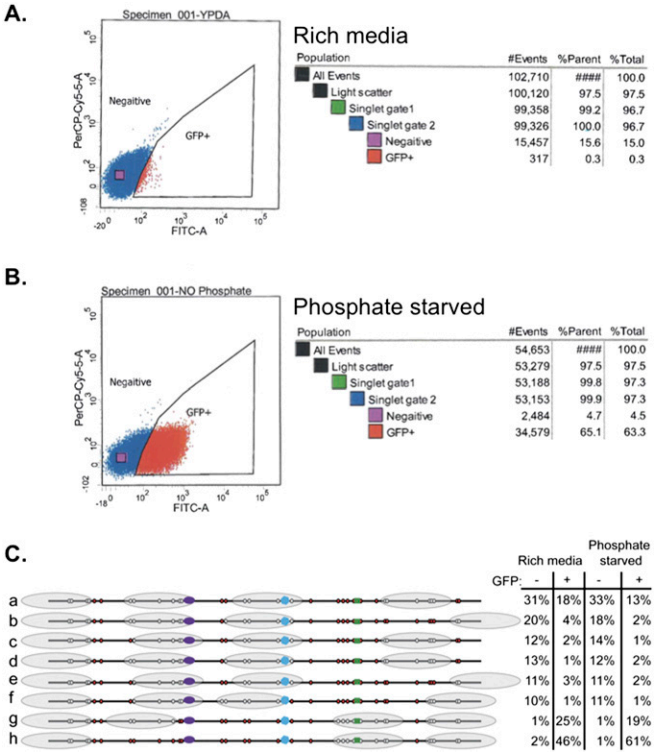

Fig. S5. Nucleosome architecture changes correlate with *PHO5* expression. (*A*) *PHO5* C-terminal GFP-tagged cells grown in rich media were sorted on the FACS Aria for GFP-positive and GFP-negative cells. (*B*) *PHO5* C-terminal GFP-tagged cells grown in rich media and shifted to phosphate starvation media for 3 h were sorted on the FACS Aria for GFP-positive and GFP-negative cells. (*C*) Nucleosome architecture for 86 GFP-negative cells and 92 GFP-positive cells grown in rich media and 94 GFP-negative cells and 89 GFP-positive cells grown in phosphate starvation media.

Table S1. Sequences of primers used in this study

Primer	Sequence
Bisulfite sequencing primers	
Pho5_BiS_F	TATAAGGATTTGAAAGTTGTATTTAATAAGA
Pho5_BiS_R	ATCTTTTTGGGTACCAATCTTGTCGACATC
Cha1_BiS_F	AATATTATTATTATGTTAATTTTTTTTTGGAAAG
Cha1_BiS_R	CCTTAAATAATACCATTATATAAACCACCTCC
Cys3_BiS_F	TTAGAGATTTTGAAATTAATGATGATTTTTATTAGTGG
Cys3_BiS_R	CTTTCCAAATTCTCTCTATTAAAATTTTAAAATC
PHO5 Nucleosome scanning primers	
Pho5_1F	ATGCGCAAATATGTCAACG
Pho5_2F	TCATCTTATGTGCGCTGCT
Pho5_3F	GCGGACGTCGTCTATAAACTT
Pho5_4F	TCAAACGAAGGTAAAAGGTTCA
Pho5_5F	GTTTTCGCATAGAACGCAAC
Pho5_6F	AACGCAACTGCACAATGC
Pho5_7F	CAACTGCACAATGCCAAAA
Pho5_8F	AAATGAATCGATACAACCTTGG
Pho5_9F	CTCACACGTGGGACTAGCA
Pho5_10F	TTTTCGAAGAGATCGCACA
Pho5_11F	TTTTCGAAGAGATCGCACA
Pho5_12F	GGCAAGGCATATACCCATTT
Pho5_13F	TGAATTGTCGAAATGAAACGTA
Pho5_14F	ATAAGCGCTGATGTTTTGCTAAG
Pho5_15F	AGTCGAGGTTAGTATGGCTTCA
Pho5_16F	CAAGCAAATTCGAGATTACCAA
Pho5_1R	AAGCGCTATGAACCTTTTACCT
Pho5_2R	CAGACAAAGAAAAAGCGCTATGA
Pho5_3R	CAGTTGCGTTCTATGCGAAA
Pho5_4R	GCATTGTGCAGTTGCGTTCT
Pho5_5R	CCAAGGTTGTATCGATTCATTT
Pho5_6R	AGTCCCACGTGTGAGTGC
Pho5_7R	AGTCCCACGTGTGAGTGC
Pho5_8R	TAATTTGGCATGTGCGATCT
Pho5_9R	TGCCTTGCCAAGTAAGGTG
Pho5_10R	TCGACAATTCAAAGATGTTTACC
Pho5_11R	CCTCGACTTAGCAAAACATCA
Pho5_12R	TGAAGCCATACTAACCTCGACT
Pho5_13R	AATCTCGAATTTGCTTGCTCT
Pho5_14R	ATTGGTAATCTCGAATTTGCTTG
Pho5_15R	GCCTAAGGGAATGGTACCTG
Pho5_16R	TGTCGACATCGGCTAGTTTG
CHA1 Nucleosome scanning primers	
Cha1_1F	CCGGAAAGGCTTCTGCAC
Cha1_2F	CCGGAAAGGCTTCTGCAC
Cha1_3F	CAACCAAGTGGCTCCTTCA
Cha1_4F	CAACCAAGTGGCTCCTTCA
Cha1_5F	TCATGAAAAGTGCCATTCG
Cha1_6F	CCTCAGGTTTTCGCTAGTTCTG
Cha1_7F	AATGCCGGTTTTGCTGCT
Cha1_8F	TGCTGCAACAGCATGTCA
Cha1_9F	GTACAGTCGTGGTTCCTACAGC
Cha1_10F	ACACCGGTGCCCAGGTTA
Cha1_11F	ACACCGGTGCCCAGGTTA
Cha1_12F	TGCCTACTGGAAAGAAGCAG
Cha1_13F	TGAGCCCATTTATGTTCATCC
Cha1_14F	CCGGATATTTGGGAAGGAC
Cha1_15F	TCGCAACATATTTCCGTGA
Cha1_1R	TGGCACTTTTCATGATGAGATT
Cha1_2R	TTTTGAATTCGAATGGCACT
Cha1_3R	CGCCAGAACTAGCGAAAAC
Cha1_4R	GCAGCAAAACCGGCATTA
Cha1_5R	CAGTCTTTGACATGCTGTTGC

Table S1. Cont.

Primer	Sequence
Cha1_6R	TCGCTGTAGGAACCACGAC
Cha1_7R	GGCACCGGTGTTCCTGAT
Cha1_8R	GGCACCGGTGTTCCTGAT
Cha1_9R	GTATCTGCTTCTTTCCAGTAGGC
Cha1_10R	GGGCTCAATGACCTGAGAG
Cha1_11R	CCGGATTATCGAAGGGATG
Cha1_12R	CCGGATTATCGAAGGGATG
Cha1_13R	CACGGAAATATGTTGCGATT
Cha1_14R	CCTCCACCAACGCTGCAT
Cha1_15R	CAGCTAAACCATACCTTTCCAA
CYS3 Nucleosome scanning primers	
Cys3_1F	CCACGTCCCCATCAAACT
Cys3_2F	GACGCTGAGCTGTATCACG
Cys3_3F	GGCAGAGGACCTCGCTTG
Cys3_4F	CCAACCCGGTGGACAAAC
Cys3_5F	AACGAGATTAGCGACCTCGAA
Cys3_6F	ACTCCTTCCCGGGTGCTC
Cys3_7F	CAACGACGACTTCCACCA
Cys3_8F	CACACTGGACCCCATACCA
Cys3_9F	TCACGTGATCTCAGCCAGTT
Cys3_10F	TGCCAGGTAGATGGAACTTG
Cys3_11F	GTGCCGTGCCAGATTGAA
Cys3_12F	TTGAGGCCTATACACATAGACATTT
Cys3_13F	TGCTACCAAGGCCATTCA
Cys3_14F	CCATTCATGCCGGTGAAC
Cys3_15F	CCCATTTCTTTGTCCACCA
Cys3_16F	CAGAGAGAACTTGGAAAGAGCA
Cys3_1R	GCTTTCGCAAGCGAGGTC
Cys3_2R	CACCGGGTTGGCTCTGTA
Cys3_3R	GGCCTTCGAGGTCGCTAA
Cys3_4R	GAGCACCCGGGAAGGAGT
Cys3_5R	GGCCCACTGGTGGAAGTC
Cys3_6R	GGTATGGGGTCCAGTGTGG
Cys3_7R	AGGGTGGAATTACATAGCGTTAC
Cys3_8R	CGCCACAACTGGCTGAGA
Cys3_9R	ACCTGGCATCTTATGCTTTAAATA
Cys3_10R	CTTGTGTGTATATGTATAAGGTGCAAA
Cys3_11R	TGGTAGCAAATTTATCAGATTCTTG
Cys3_12R	GGCCTTGGTAGCAAATTTATCA
Cys3_13R	GGGTTAGCTGGAGAAGATTGTT
Cys3_14R	ACCGATAGGGTTAGCTGGAG
Cys3_15R	CGGCAACTGCTCTTTCCA
Cys3_16R	GAAGCGATTGCAAGATTGTGG
PHO5 QuikChange primers	
ECS54_F	CGCACATGCCAAATTATAAAATTAATCACCTTACTTGG
ECS54_R	CCAAGTAAGGTGATTAATTTTATAATTTGGCATGTGCG
ECS45_F	GATTAAAAGAATTAATTAAATAGGCAATC
ECS45_R	GATTGCCTATTTAATTAATTCTTTTAATC
ECS62_F	ATGTAAGCGGACGTCGTCTATAAACTTCAAAAAAAAAAAAAAAGGTTCATAGCGCTTTTTCTTTGTCTG
ECS62_R	CAGACAAAGAAAAAGCGCTATGAACCTTTTTTTTTTTTTTTGAAGTTTATAGACGACGTCCGCTTACAT
ECS68_F	CAACGTATTTGGAAGTCATCTTATGTGCGCTGCTTTTTTTTTTTCTCATGTAAGCGGACGTCGTCTATAA
ECS68_R	TTATAGACGACGTCCGCTTACATGAGAAAAAAAAAAAGCAGCGCACATAAGATGACTTCCAAATACGTTG
ECS53_F	GTTTTCTTATGTAAGCTTACGTCGTC
ECS53_R	GACGACGTAAGCTTACATAAGAAAAC
ECS56_F	GCGCAAATATGTCAAAGTATTTGGAAG
ECS56_R	CTTCCAAATACTTTGACATATTTGCGC

F, forward; R, reverse.

Other Supporting Information Files

Dataset S1 (XLSX)