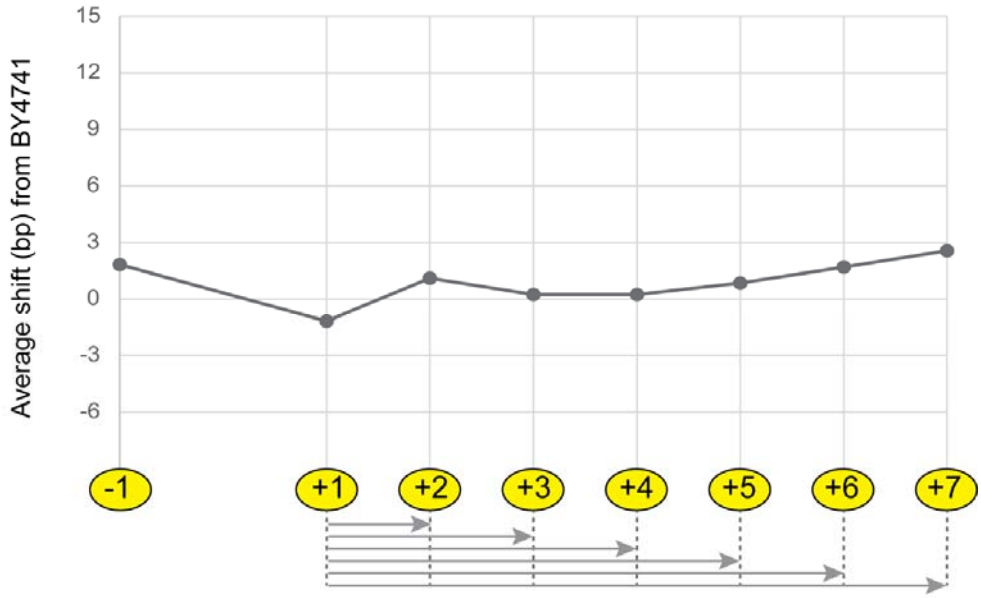
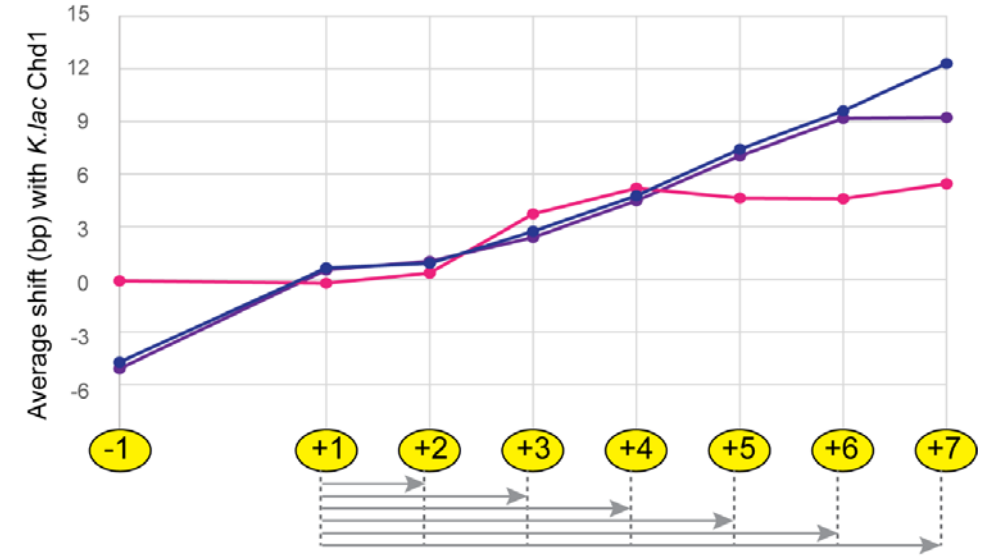
Figure S2

A



BY4741	168	334	495	655	815	971
S.cer Chd1 (integrated)	168 (0.25)	333 (0.96)	495 (0.52)	656 (0.26)	816 (0.31)	972 (0.89)

B



S.cer Chd1 (integrated)2	169	332	495	658	819	975
K.lac Chd1 (integrated)2	170 (0.069)	336 (8.8E-7)	502 (1.8E-12)	665 (5.8E-11)	825 (2.3E-8)	983 (1.9E-7)
S.cer Chd1 (plasmid)	170	336	501	666	828	991
K.lac Chd1 (plasmid)	175 (2.2E-7)	344 (6.3E-12)	512 (2.8E-15)	679 (1.2E-17)	843 (2.7E-19)	1007 (8.9E-15)
S.cer Chd1 (plasmid)2	172	338	505	669	833	999
K.lac Chd1 (plasmid)2	177 (1.1E-7)	345 (8.5E-14)	514 (3.8E-16)	682 (5.3E-23)	849 (9.0E-29)	1019 (4.0E-30)

Figure S2 The *K. lactis CHD1* orthologue can direct wider spacing of *S. cerevisiae* nucleosomes from both plasmid and endogenous expression. Plot of shifts in -1 to +7 nucleosome positions between *S. cerevisiae* and *K. lactis CHD1* swap strains, as in **Figure 2B-C**. In each case, top panel shows distances between equivalent nucleosomes for the pair of strains indicated, while bottom panel shows the average distance of genic nucleosomes from the +1 nucleosome, along with corresponding p-values for the swap strains. (**A**) shows that this metric is specific, as no significant changes are found between wild-type yeast and a "pseudo wild-type" with a genomic *chd1Δ* deletion covered by a plasmid-borne *CHD1* gene. (**B**) shows that effects of *K. lactis CHD1* on nucleosome spacing are reproducible both for genomically-integrated swap strains as well as plasmid-borne *CHD1* swaps.