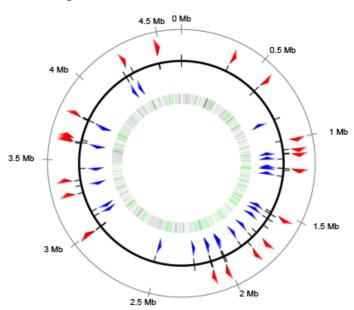
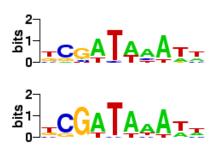
## 1. Analysis of E. coli K12 chromatin immunoprecipitation peaks (back)

# **Predicted binding sites**





Resulting motif

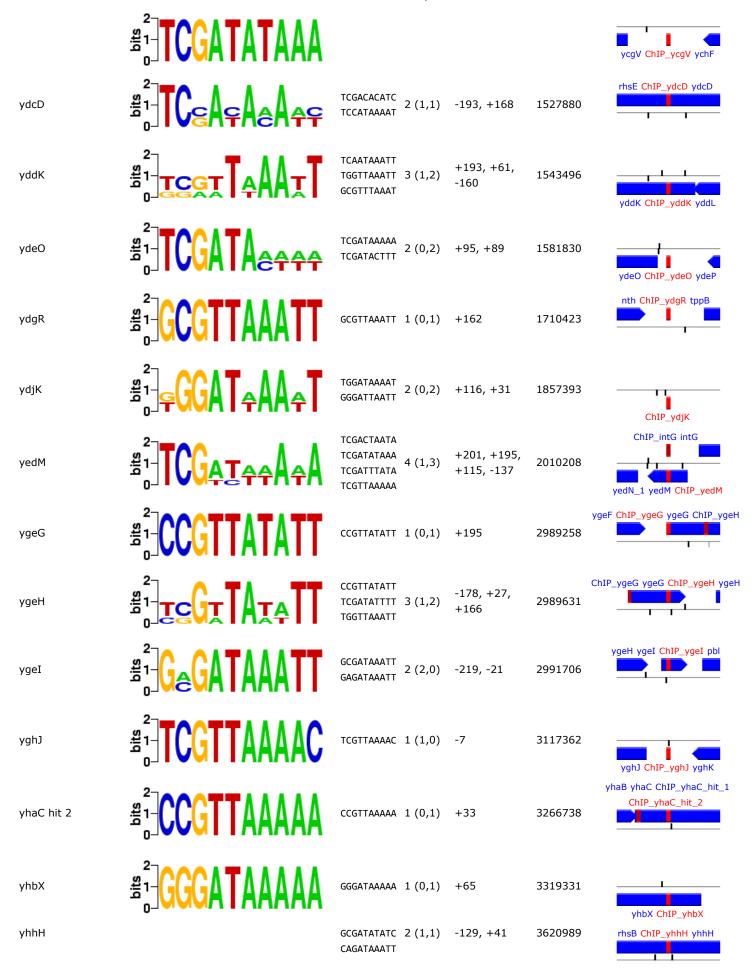


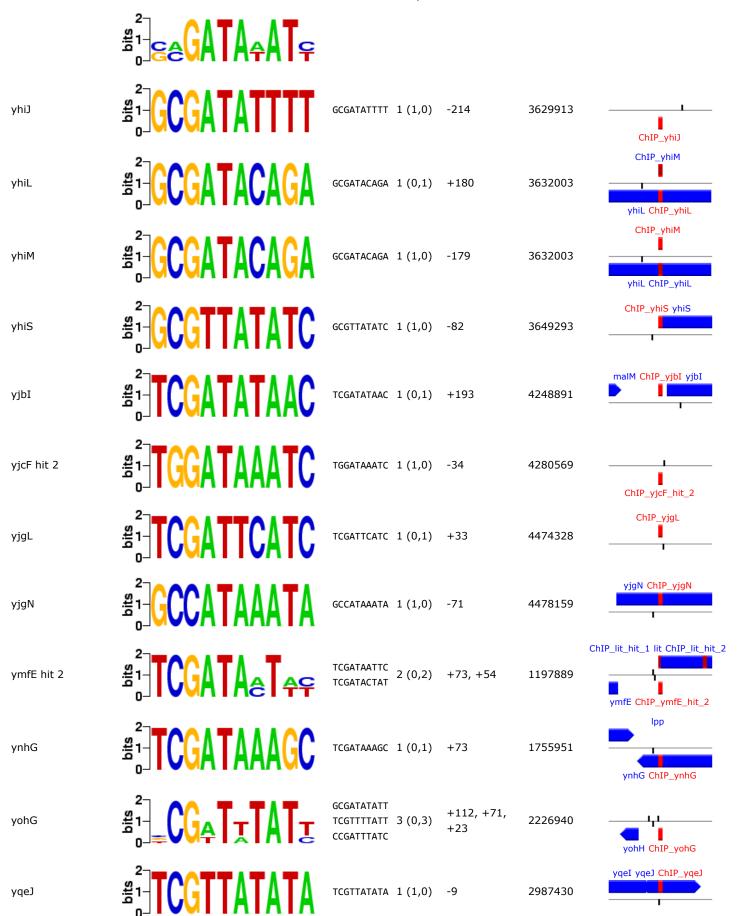
## Chromatin immunoprecipitation peaks with a nearby predicted H-NS binding site (back)

Nearest gene	Binding site logo	Motif bs (u,d) Rel. bs pos	Signal s. Gene locus center
аррҮ		GCGACAAAAT TCGATAAAAAA 2 (2,0) -98, -17	583103 appY ChIP_appY
arpA		TCGATACATT GCGATACAGC TCGATAAAAA GCGTTAAAAAA GCGTTAAAAAA	' 4218504 arpA ChIP_arpA
arpB	E TGGTTAAATT	TGGTTAAATT 1 (0,1) +206	ChIP_arpB 1802220
between icd and ymfD	ECGGATACATT	CGGATACATT 1 (0,1) +137	ChIP_between_icd_and_ymfD  1196104  ymfD
between yedN 2 and yedN 1	EGCGATA ATA	GCGATATATA 2 (1,1) 0, +148	yedL ChIP_between_yedN_2_and_yedN_1 2009441  yedN_2 yedN_1
cmtB	#1-TGGATAAAAA	TGGATAAAAA 1 (1,0) -31	3077215  cmtA cmtB ChIP_cmtB tktA
cspI	ECAGATAAATT	CAGATAAATT 1 (1,0) -10	1636804 cspI ChIP_cspI ydfP

11/5/2020 k12.chip.html TCCATAAATC 1(0,1)1211166 elbA icdC#1-TCCATAAATC elbA ChIP\_elbA mviN g1-GCGTTAAAAC flgN GCGTTAAAAC 1 (1,0) 1128949 flgN ChIP\_flgN flgM flgA ELCCGATTAAAA CCGATTAAAA 1 (1,0) fliA 1999764 #1-CCGATACATA fliC hit 1 CCGATACATA 1 (1,0) 2000652 ChIP\_fliC\_hit\_1 ChIP fliF #1-TCGACATATT fliF TCGACATATT 1 (1,0) 2101252 insH-7 wbbL\_1 wbbK #1 CCG+ T+A+++ fliZ 2(1,1)+171, -173 1998948 2 (1,1) glf +216, -198 2106311 glf ChIP\_glf rfbX gltD ChIP\_gltF gltF 2(0,2)+159, +169 3358590 TCAATAAATT ChIP\_intG intG **TCGACTAATA** #1-TCGATAAAA -200, -194, TCGATATAAA intG 4 (3,1) 2010208 TCGATTTATA -114, +138 TCGTTAAAAA yedN\_1 yedM ChIP\_yedM ChIP\_lit\_hit\_1 lit ChIP\_lit\_hit\_2 #1-TCGATAeTee TCGATAATTC 2 (2,0) lit hit 1 1197889 TCGATACTAT ymfE ChIP\_ymfE\_hit\_2 2 (2,0) rfaI 3800215 TGGATAAAAA rfaJ rfaI ChIP\_rfaI 2 (1,1) +80, -200 rfaJ 3799266 rfaY rfaJ ChIP\_rfaJ rfaC ChIP\_rfaL rfaL GGGATTAATT 1(0,1)3794786 rfaL +68 rfaS hit 1 3801921 TCGATTAATC 1(0,1)+207

	TCGATTAATC				rfaB ChIP_rfaS_hit_1 rfaS
rfaZ	ECCGTTAAATC	CCGTTAAATC 1 (0,1)	+196	3797827	rfaK rfaZ ChIP_rfaZ rfaY
rfbX	GGGATAAAAT	GGGATAAAAT 1 (0,1)	+38	2107184	rfbX ChIP_rfbX rfbC
secY	TCGATAAAGT	TCGATAAAGT 1(0,1)	+145	3441159	rpmJ secY ChIP_secY
waaU		TCAATAAATC CCGATAATTT 2 (2,0)	-165, -199	3796405	rfaL  II  rfaK ChIP_waaU
wbbK	E TOTATAAATA	ТСТАТАААТА 1 (1,0)	-141	2101888	wbbL_1 wbbK ChIP_wbbK
xapR	GCGTTTAAAT	GCGTTTAAAT 1 (0,1)	+165	2520569	xapR ChIP_xapR xapB
yahA	g 1-GCGATATTTT	GCGATATTTT 1 (0,1)	+225	331600	yahA ChIP_yahA
ybiJ	good GCGATTATAT	GCGATTATAT 1 (1,0)	-6	837437	ybiJ ybiI ChIP_ybiJ ybiX
ycbQ	ECGATATAAT	GCGATATAAT 1 (0,1)	+205	997353	ycbQ ChIP_ycbQ ycbR
yccE	E CGGATAAATA	CGGATAAATA 1 (1,0)	-60	1063827	ChIP_yccE
ycdS	E CGTTAAATT	GCGTTAAATT 1 (0,1)	+24	1090864	ChIP_ycdS
ycdU	TCGATACATT	TCGATACATT 1 (1,0)	-246	1095162	ymdE ycdU ChIP_ycdU insE-4
ycgV		TCGATATAAA 1 (0,1)	+209	1255584	





### 59 of 99 regions (or 59.6%) contained a predicted H-NS binding site. These are:

appY, arpA, arpB, between icd and ymfD, between yedN 2 and yedN 1, cmtB, cspI, elbA, flgN, fliA, fliC hit 1, fliF, fliZ, glf, gltF, intG, lit hit 1,

rfaI, rfaJ, rfaL, rfaS hit 1, rfaZ, rfbX, secY, waaU, wbbK, xapR, yahA, ybiJ, ycbQ, yccE, ycdS, ycdU, ycgV, ydcD, yddK, ydeO, ydgR, ydjK, yedM, ygeG, ygeH, ygeI, yghJ, yhaC hit 2, yhbX, yhhH, yhiJ, yhiL, yhiM, yhiS, yjbI, yjcF hit 2, yjgL, yjgN, ymfE hit 2, ynhG, yohG, yqeJ

## No binding sites were predicted near the following signals (40 of 99):

between ydeE and ydeH, between yhdJ and yhdU, between yibG and yibH, elaD, emrY, fliC hit 2, fliD, hemB, kgtP, lit hit 2, oppA, rfaB, rfaS hit 2, rfc, rplL, secG, tap, wbbI, yafF, yaiT, ybcL, ybcM, ybfL, yceD, yceF, yddJ, yehA, yfdH, yfdI, yfgF, yfjW, yhaC hit 1, yibA, yibG, yjcF hit 1, yjhC, yjiT, ymfE hit 1, yqeH, ytfI