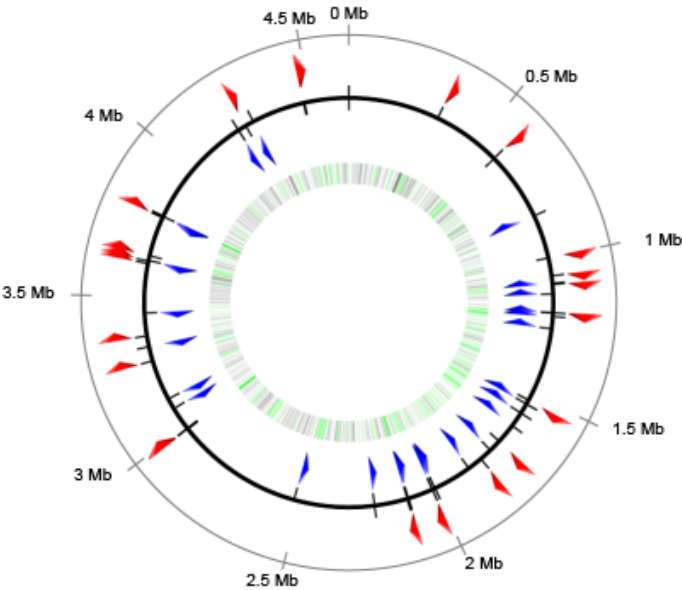


1. Analysis of *E. coli* K12 chromatin immunoprecipitation peaks [\(back\)](#)

Predicted binding sites



Input
motif



Resulting
motif



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

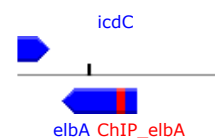
Nearest gene	Binding site logo	Motif alignment	bs (u,d)	Rel. bs pos.	Signal center	Gene locus
appY		GCGACAAAAT TCGATAAAAA	2 (2,0)	-98, -17	583103	
arpA		TCGATACATT GCGATACAGC TCGATAAAAA GCGTTAAAAA	4 (3,1)	+120, -113, -181, -220	4218504	
arpB		TGGTTAAATT	1 (0,1)	+206	1802220	
between icd and ymfD		CGGATACATT	1 (0,1)	+137	1196104	
between yedN 2 and yedN 1		GCGATATATA GCGATAAATA	2 (1,1)	0, +148	2009441	
cmtB		TGGATAAATA	1 (1,0)	-31	3077215	
cspI		CAGATAAATT	1 (1,0)	-10	1636804	

elbA



TCCATAAATC 1 (0,1) +156

1211166

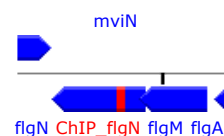


flgN



GCGTTAAAAC 1 (1,0) -201

1128949

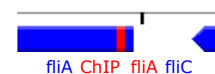


fliA



CCGATTAAAA 1 (1,0) -106

1999764

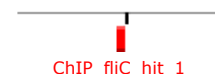


fliC hit 1



CCGATACATA 1 (1,0) -26

2000652

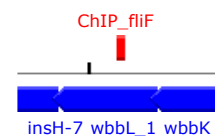


fliF



TCGACATATT 1 (1,0) -157

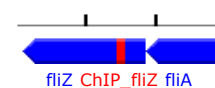
2101252



fliZ

CCGATAATAT
CCGTTAATA 2 (1,1) +171, -173

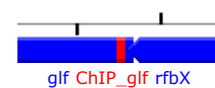
1998948



glf

GCGATTATA
GCGATTAAAA 2 (1,1) +216, -198

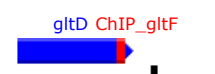
2106311



gltF

GGGATAATTT
TCAATAAATT 2 (0,2) +159, +169

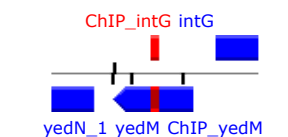
3358590



intG

TCGACTAATA
TCGATATAAA
TCGATTATA
TCGTTAAAAA 4 (3,1) -200, -194,
-114, +138

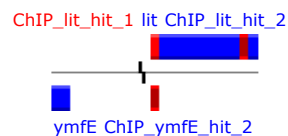
2010208



lit hit 1

TCGATAATTC
TCGATACTAT 2 (2,0) -72, -53

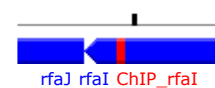
1197889



rfaI

CCGATAAAT
TGGATAAAAA 2 (2,0) -64, -73

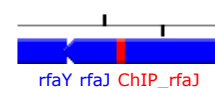
3800215



rfaJ

TGGATAAATT
TCGTTTATTT 2 (1,1) +80, -200

3799266

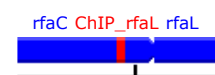


rfaL



GGGATTAATT 1 (0,1) +68

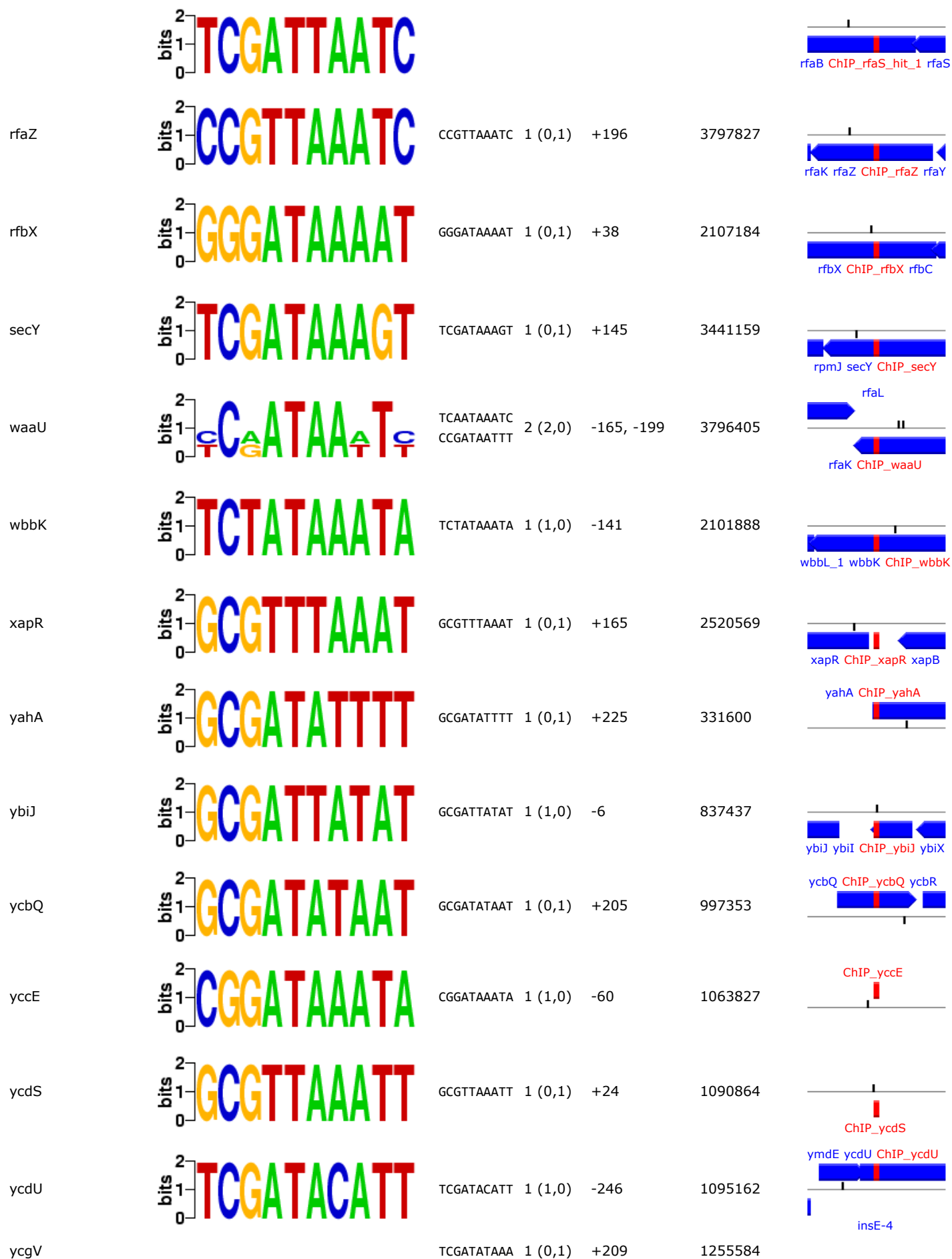
3794786

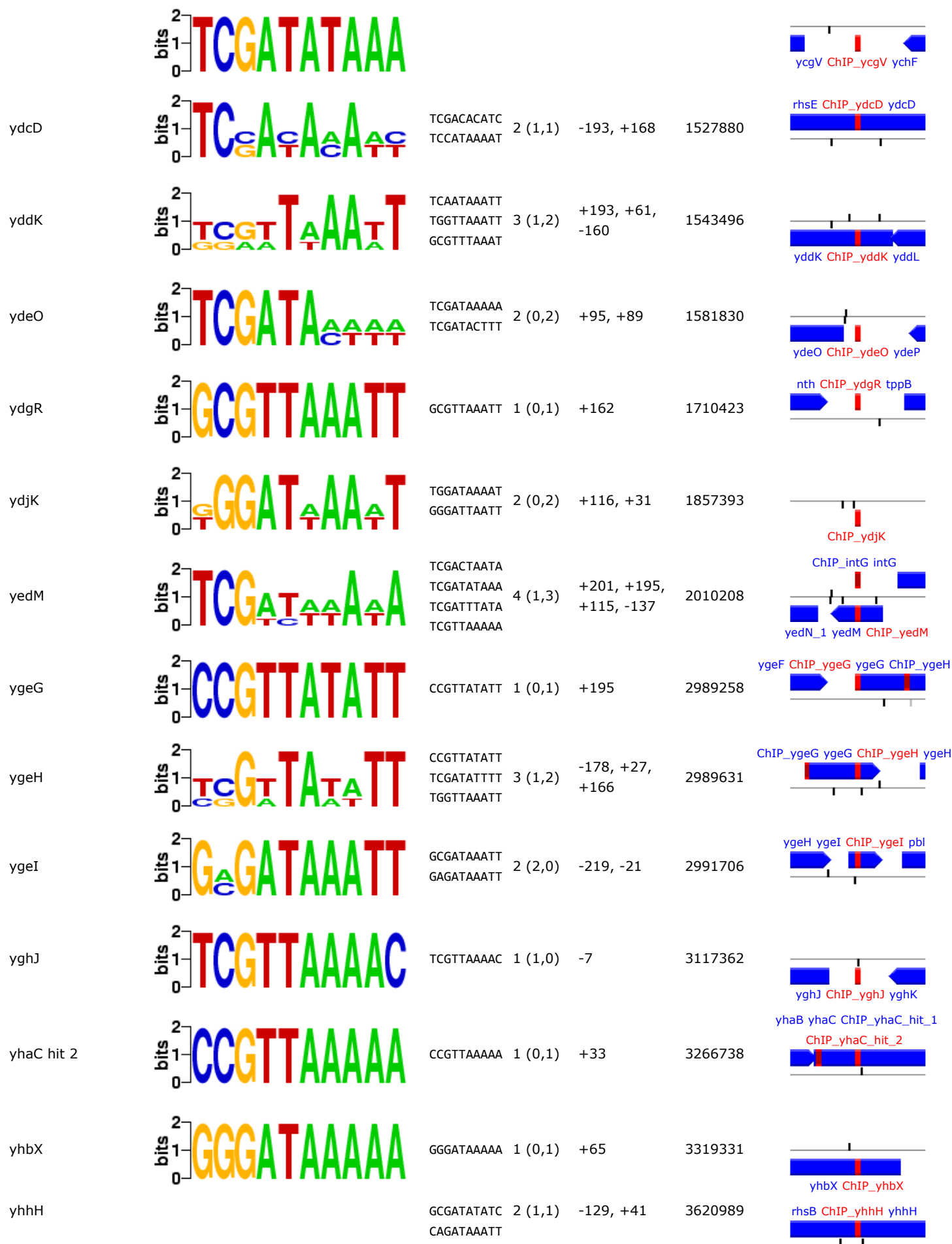


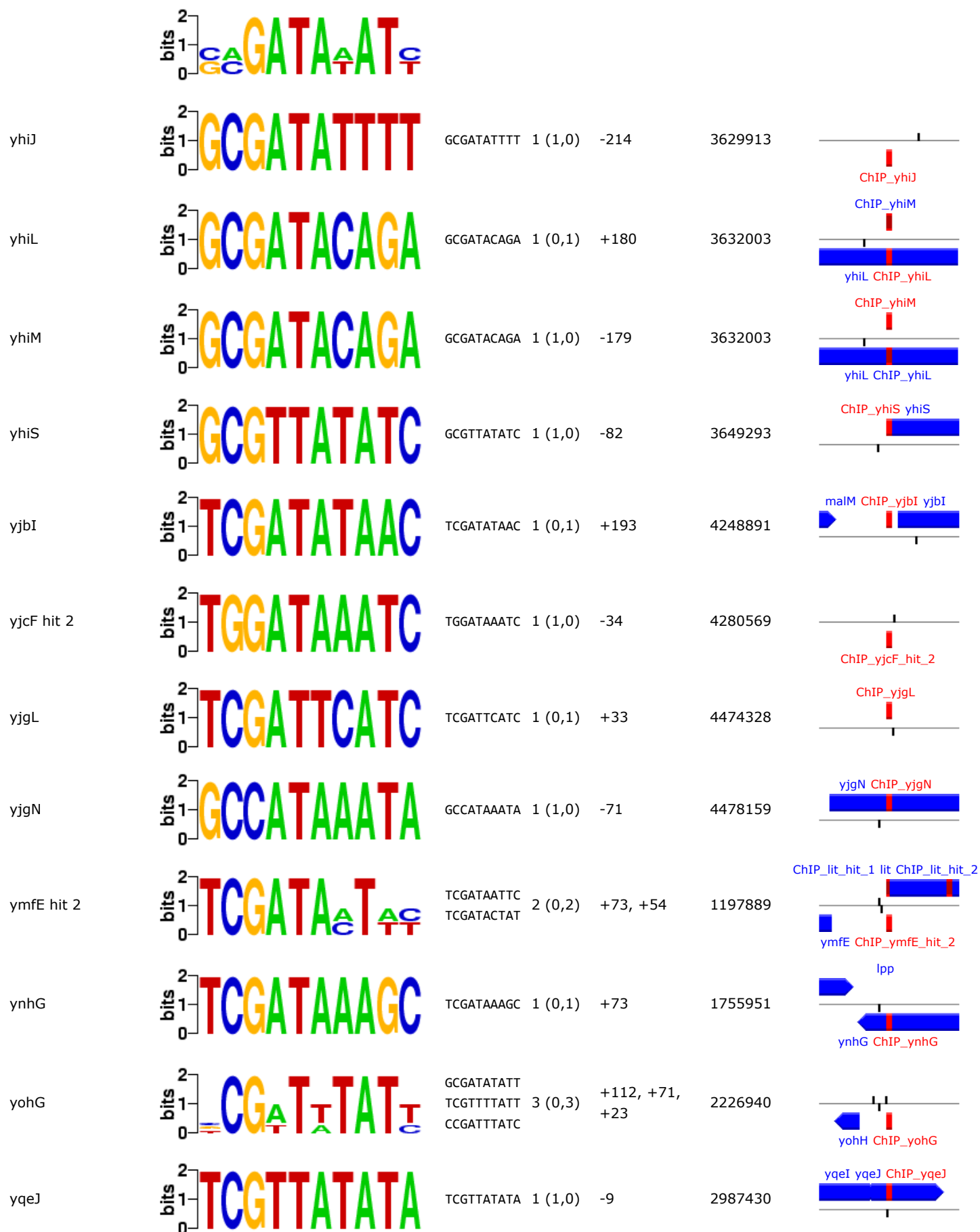
rfaS hit 1

TCGATTAATC 1 (0,1) +207

3801921







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