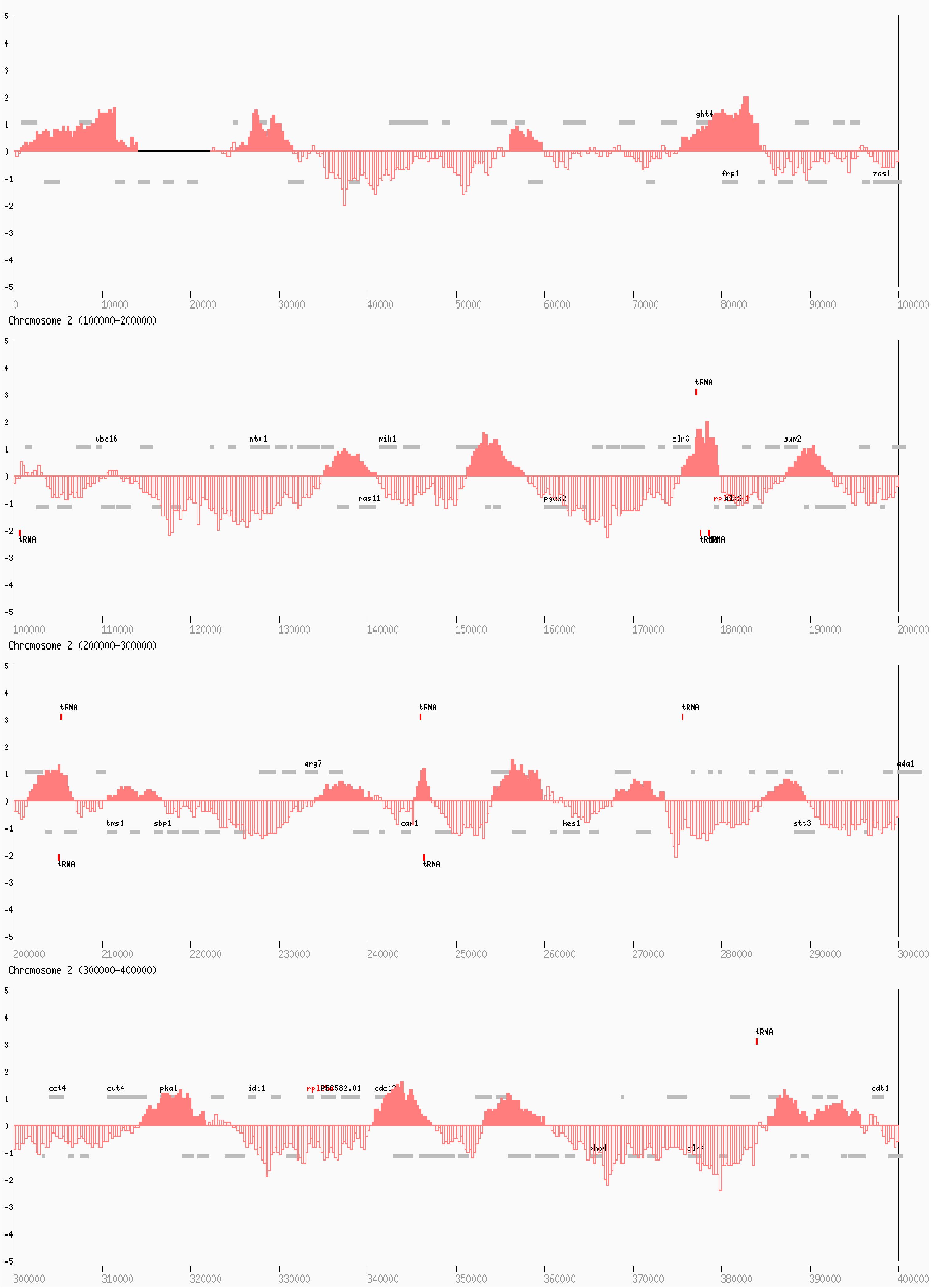
Figure S1

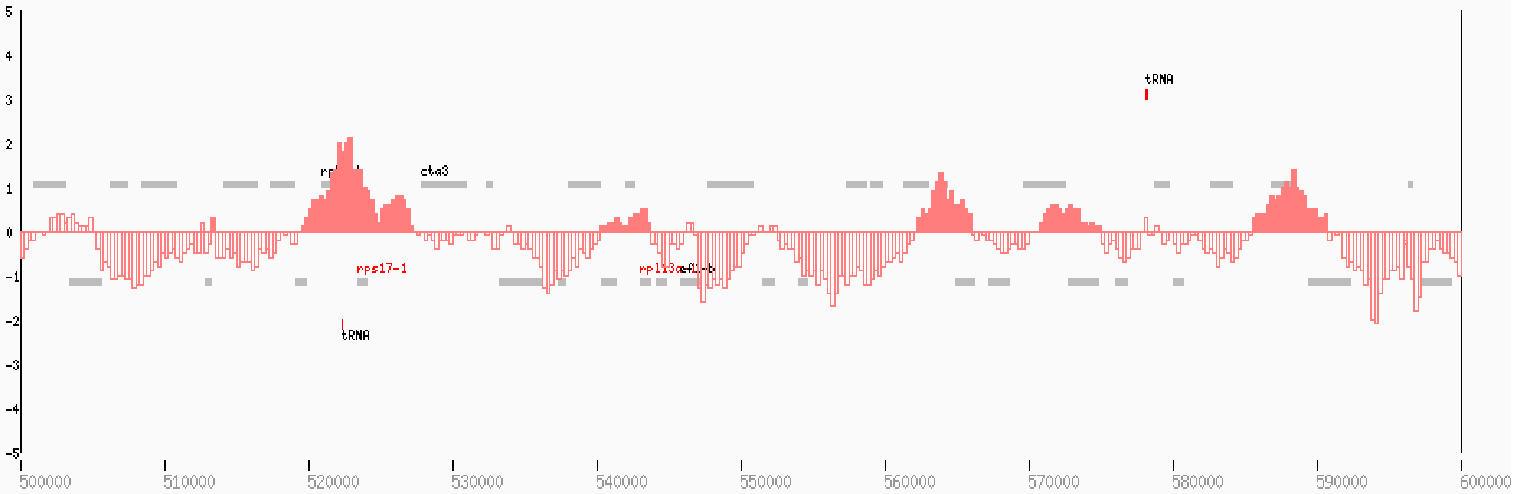
Cohesin association along fission yeast chromosome 2. (**a**) Association profile of cohesin along chromosome 2. *cdc25-22* cells were arrested in G2 by shifting to the restrictive temperature of 36.5° C for six hours in minimal EMM2 medium and processed for ChIP against the epitope-tagged cohesin subunit Rad21-Pk_9. The binding profile of Rad21-Pk_9 along fission yeast chromosome 2, relative to a whole genome DNA sample, is shown. The y-axis scale is $\log_2$. Every bar represents the average of 11 oligonucleotide probes within 250 bp windows. Peaks in solid red were assigned according to the following criteria: Signal intensities were smoothed using a sliding 2.25 kb window. Local maxima were identified, and those with a raw signal intensity above 0.3 were chosen as a peak. Peaks extend from their maximum to both sides until the raw signal $\log_2$ ratio reaches a value below 0. The peak position was defined as the midpoint within the peak. Using these criteria 228 peaks were identified along chromosome 2. The illustrated cohesin binding map shows all open reading frames (ORFs) as grey bars above and below the midline, transcribed from left to right and right to left, respectively. tRNA genes, and genes encoding protein components of the large (*rpl*) and small (*rps*) ribosomal subunit are highlighted in red. The coordinates are of the NCBI fission yeast genome release NC003423.1 (25 Jan 2005). (**b**) List of the cohesin peaks identified in (a). The position, average height and width of each of the 228 peaks is indicated.

(a)

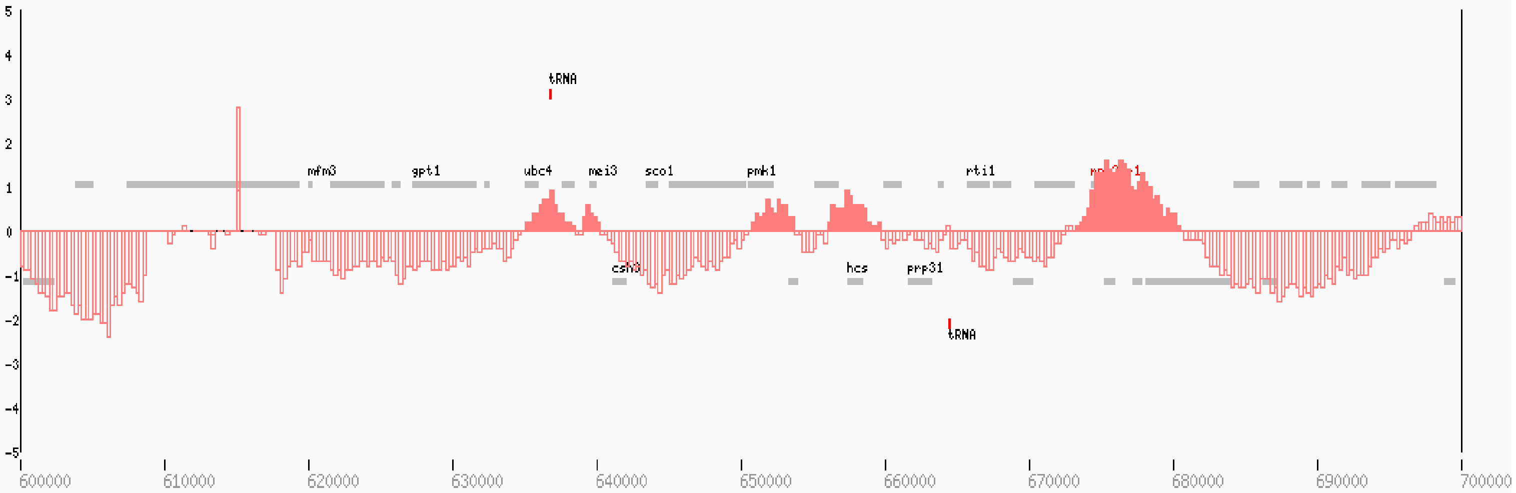

Chromosome 2 (0-100000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
ght4
frp1
zas1
0
10000
20000
30000
40000
50000
60000
70000
80000
90000
100000
Chromosome 2 (100000-200000)
tRNA
ubc16
ntp1
mik1
clr3
sum2
ras11
pguk2
rpl
tRNA
tRNA
100000
110000
120000
130000
140000
150000
160000
170000
180000
190000
200000
Chromosome 2 (200000-300000)
tRNA
tRNA
tRNA
arg7
ada1
tms1
sbp1
car1
kes1
stt3
tRNA
tRNA
200000
210000
220000
230000
240000
250000
260000
270000
280000
290000
300000
Chromosome 2 (300000-400000)
tRNA
cct4
cut4
pka1
idi1
rpl
PBC582.01
cdc1
cdt1
pho4
glr4
300000
310000
320000
330000
340000
350000
360000
370000
380000
390000
400000

Chromosome 2 (400000-500000)

Chromosome 2 (500000-600000)

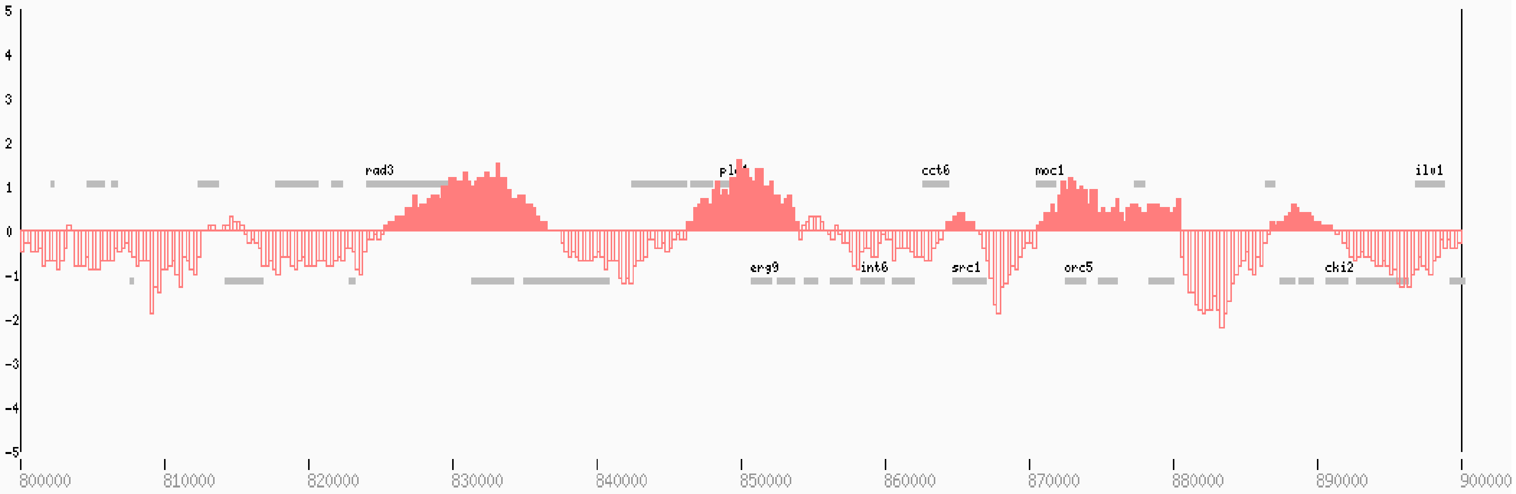


Chromosome 2 (600000-700000)

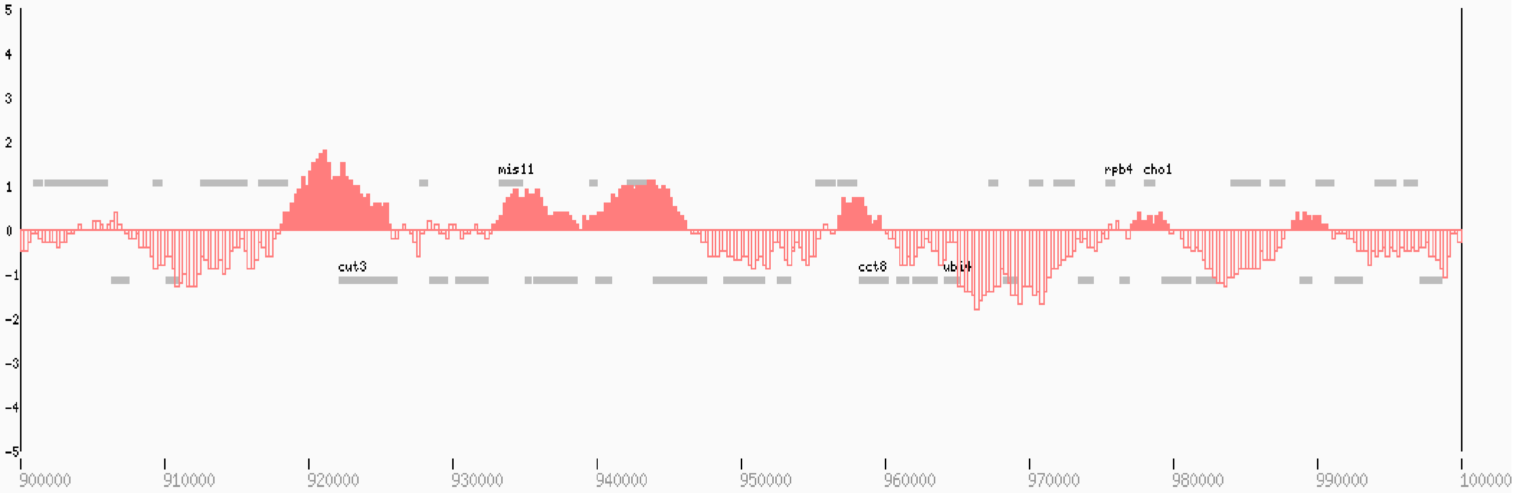


Chromosome 2 (700000-800000)

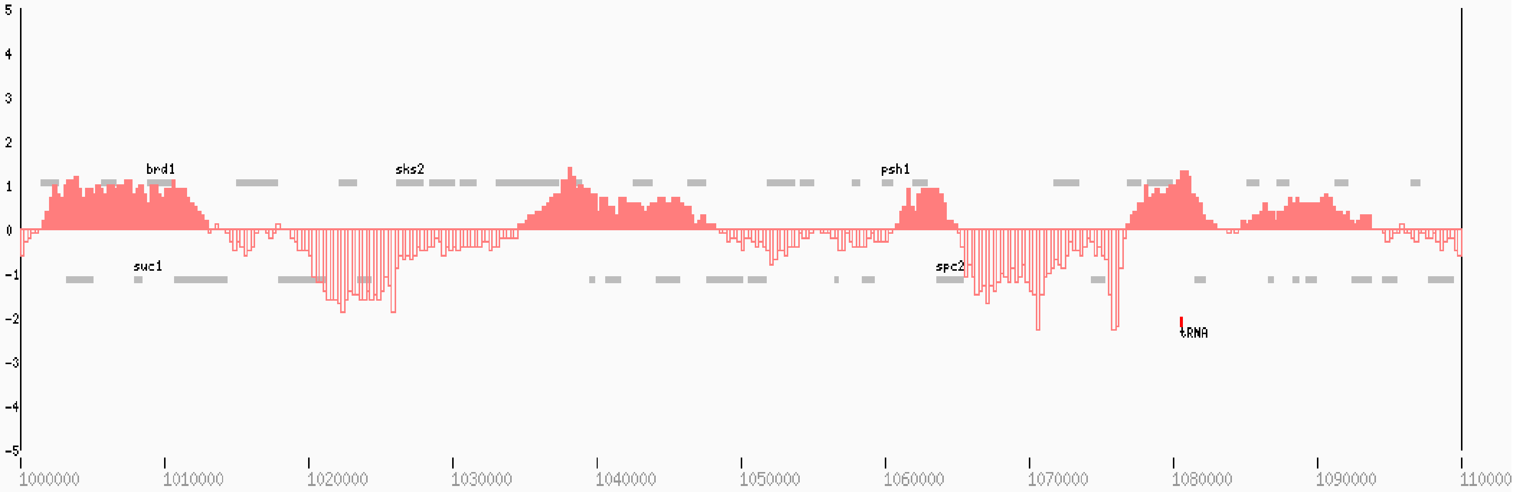
Chromosome 2 (800000-900000)



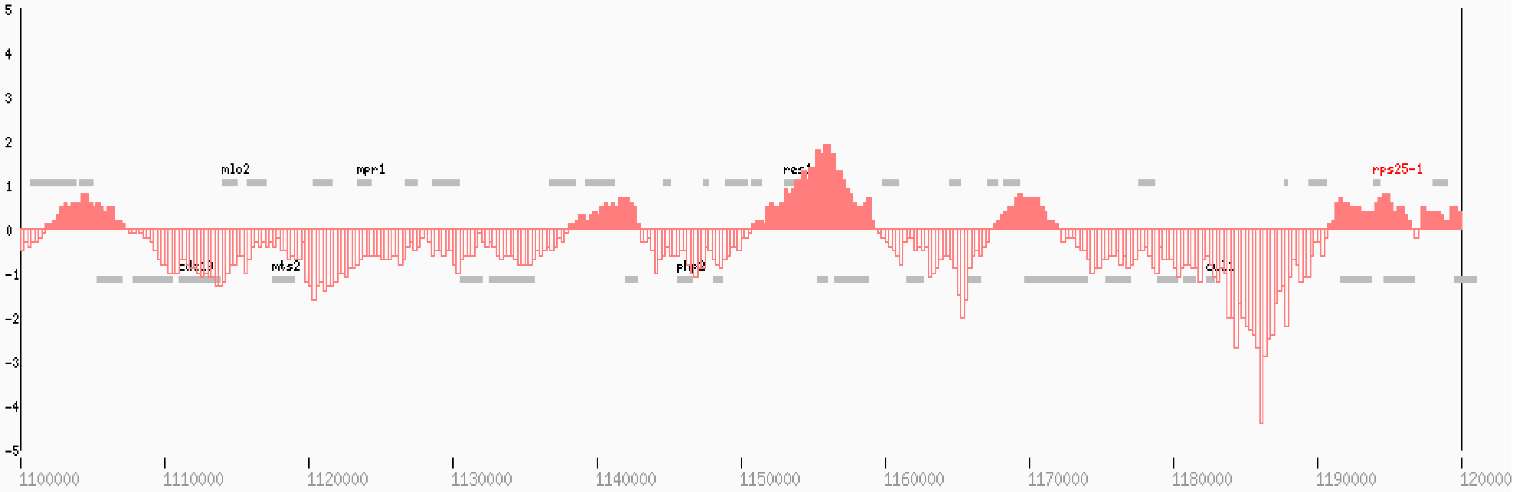
Chromosome 2 (900000-1000000)

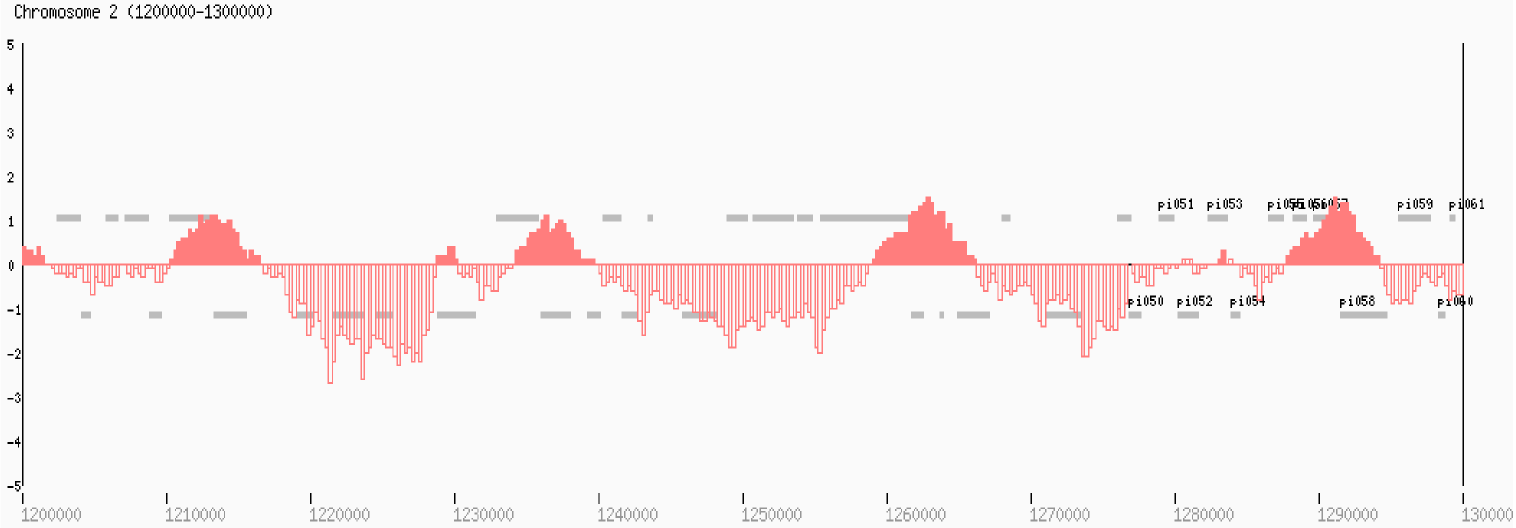


Chromosome 2 (1000000-1100000)



Chromosome 2 (1100000-1200000)




Chromosome 2 (1200000-1300000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
1200000
1210000
1220000
1230000
1240000
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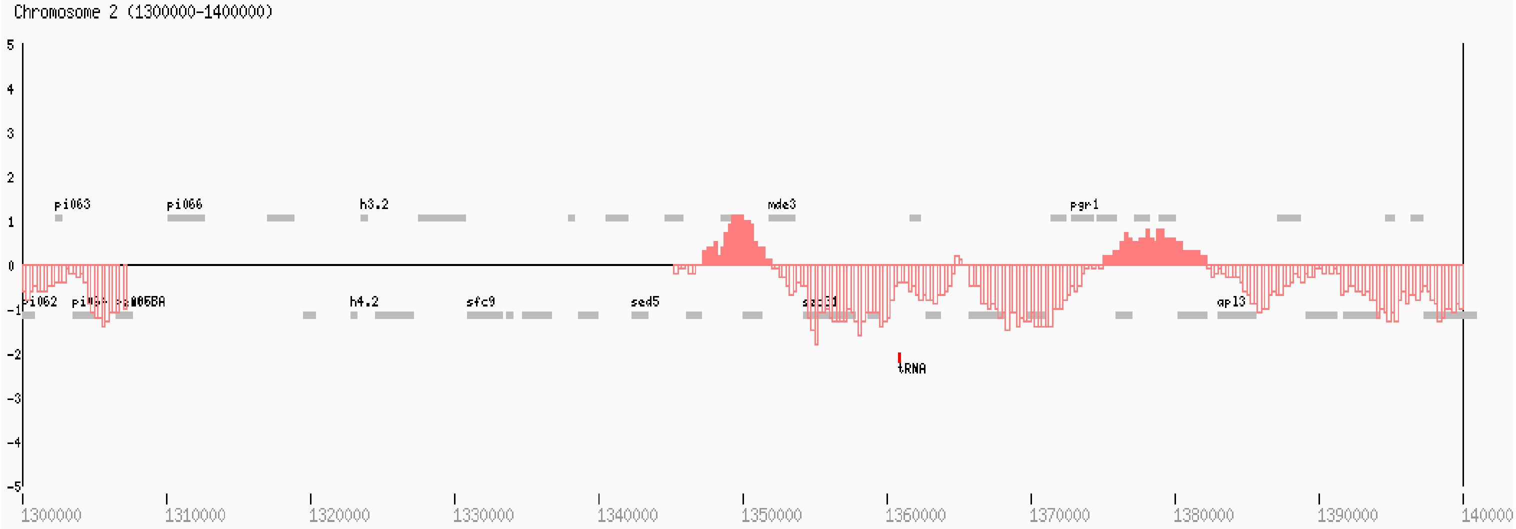
1270000
1280000
1290000
130000
pi051
pi053
pi059
pi061
pi050
pi052
pi054
pi058


Chromosome 2 (1300000-1400000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
1300000
1310000
1320000
1330000
1340000
1350000
1360000
1370000
1380000
1390000
140000
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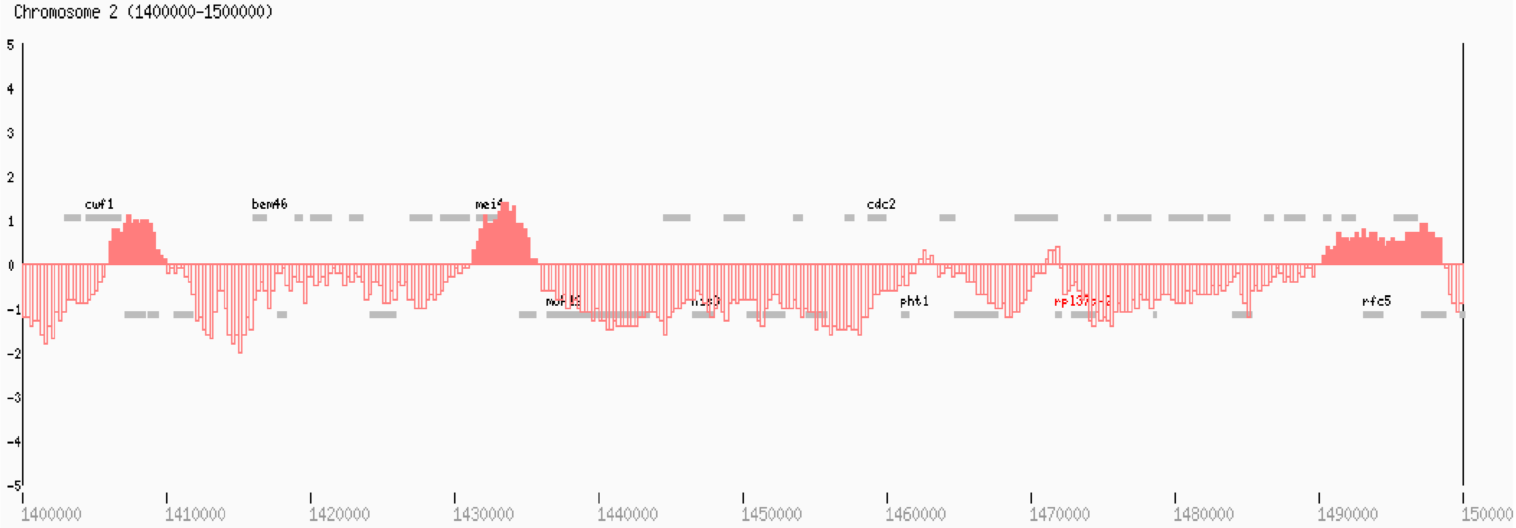
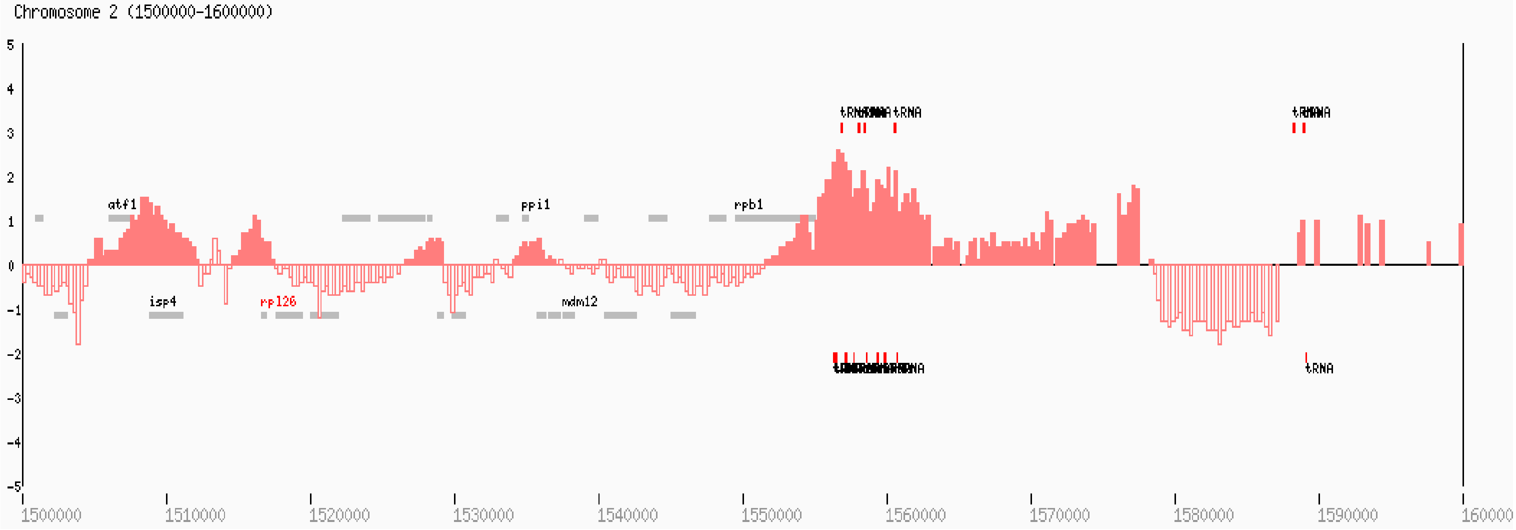
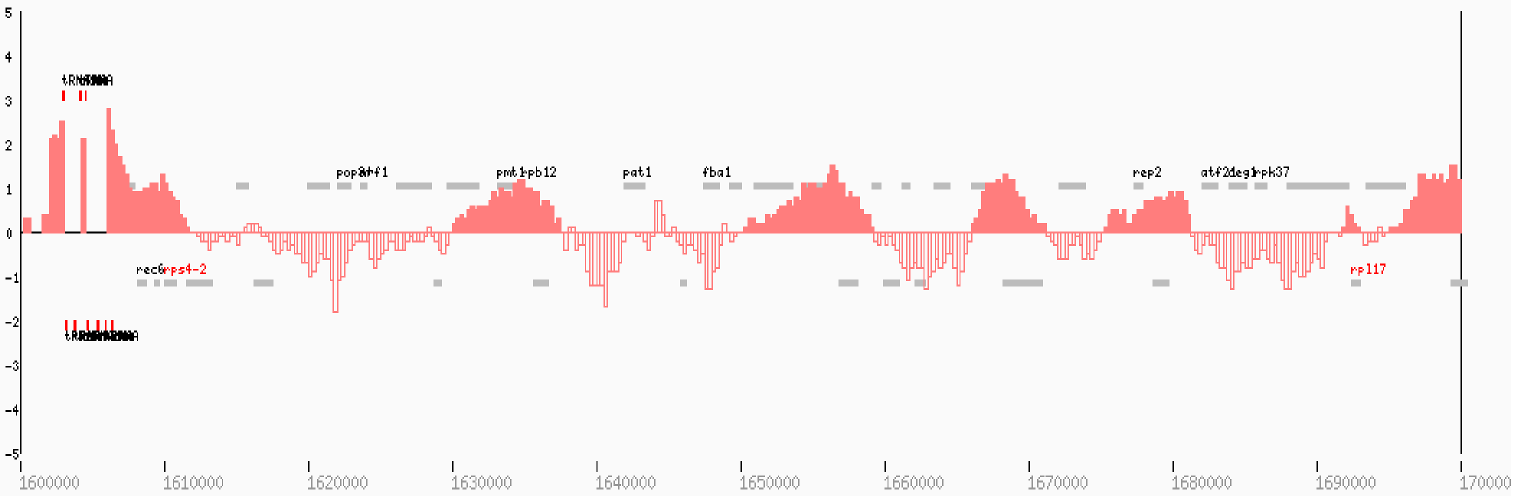
pi066
h3.2
mde3
pgr1
pi062
h4.2
sfc9
sed5
apl3
tRNA

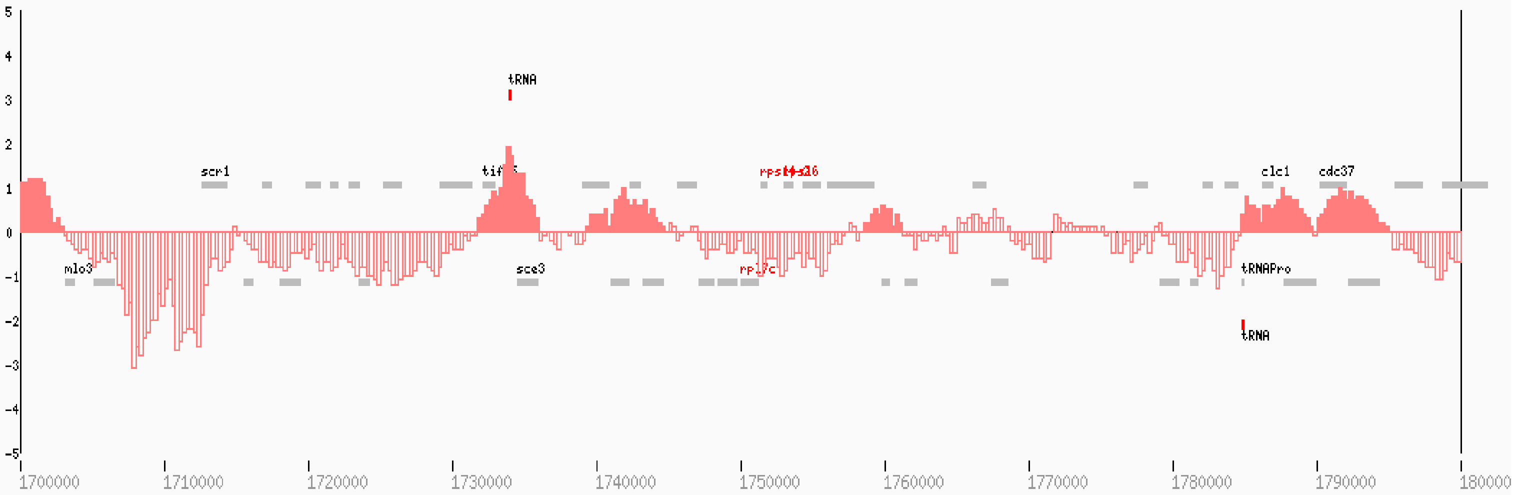

Chromosome 2 (1400000-1500000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
1400000
1410000
1420000
1430000
1440000
1450000
1460000
1470000
1480000
1490000
150000
cuf1
bem46
mei4
cdc2
pht1
rfc5


Chromosome 2 (1500000-1600000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
1500000
1510000
1520000
1530000
1540000
1550000
1560000
1570000
1580000
1590000
160000
tRNA
atf1
ppi1
rpb1
isp4
rpl26
mdm12
tRNA

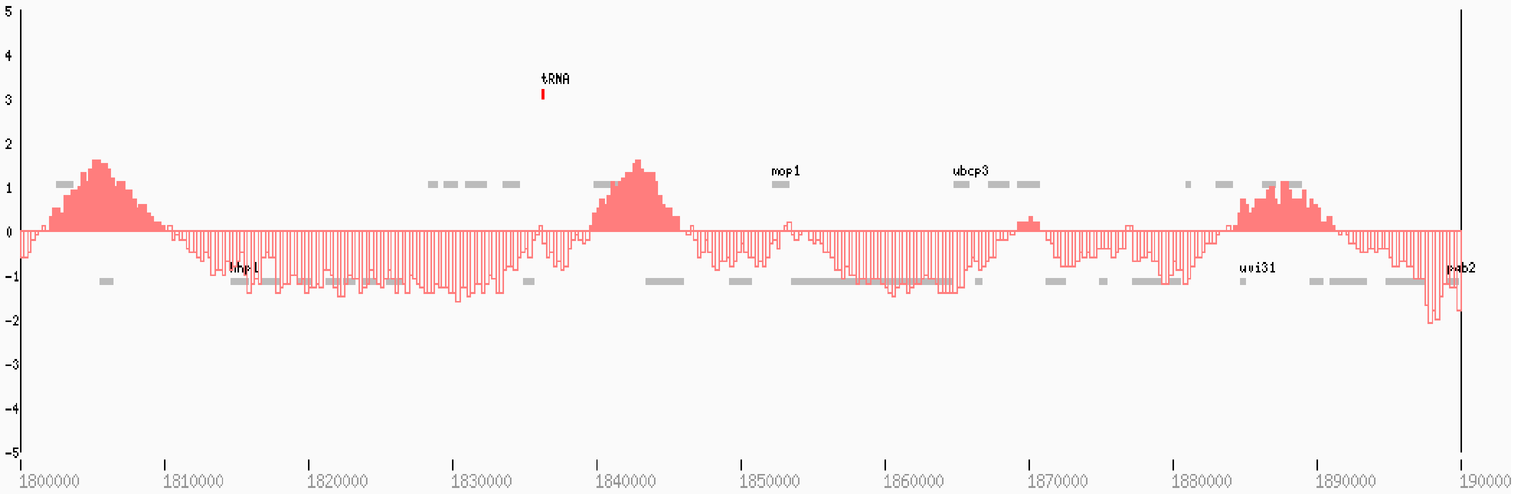
Chromosome 2 (1600000-1700000)



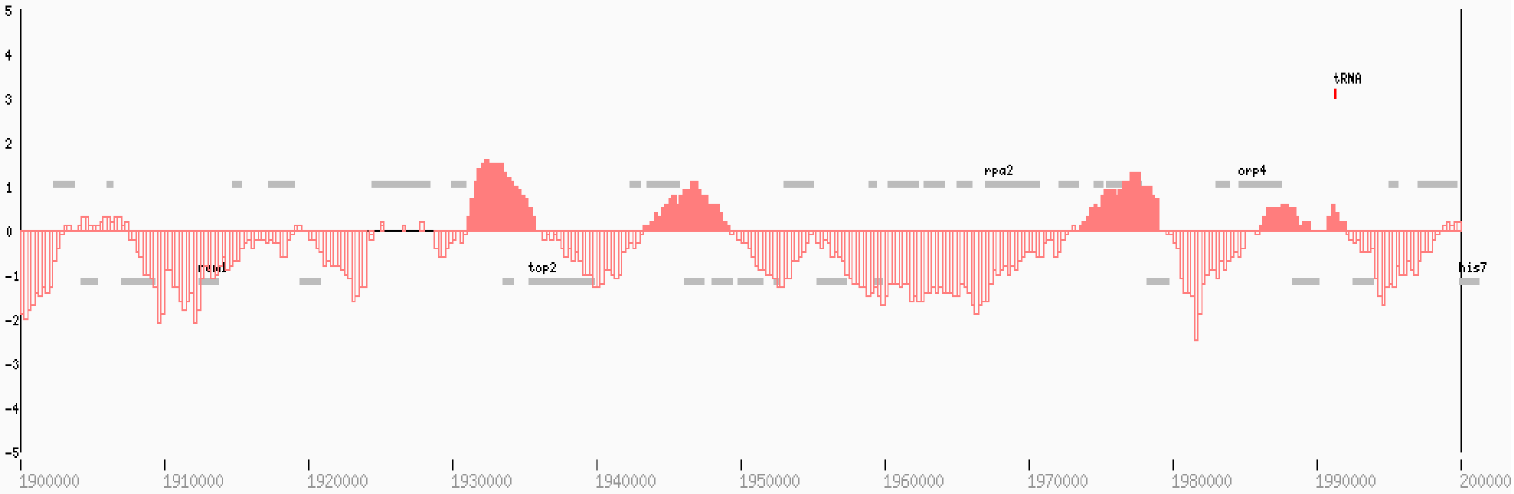
Chromosome 2 (1700000-1800000)

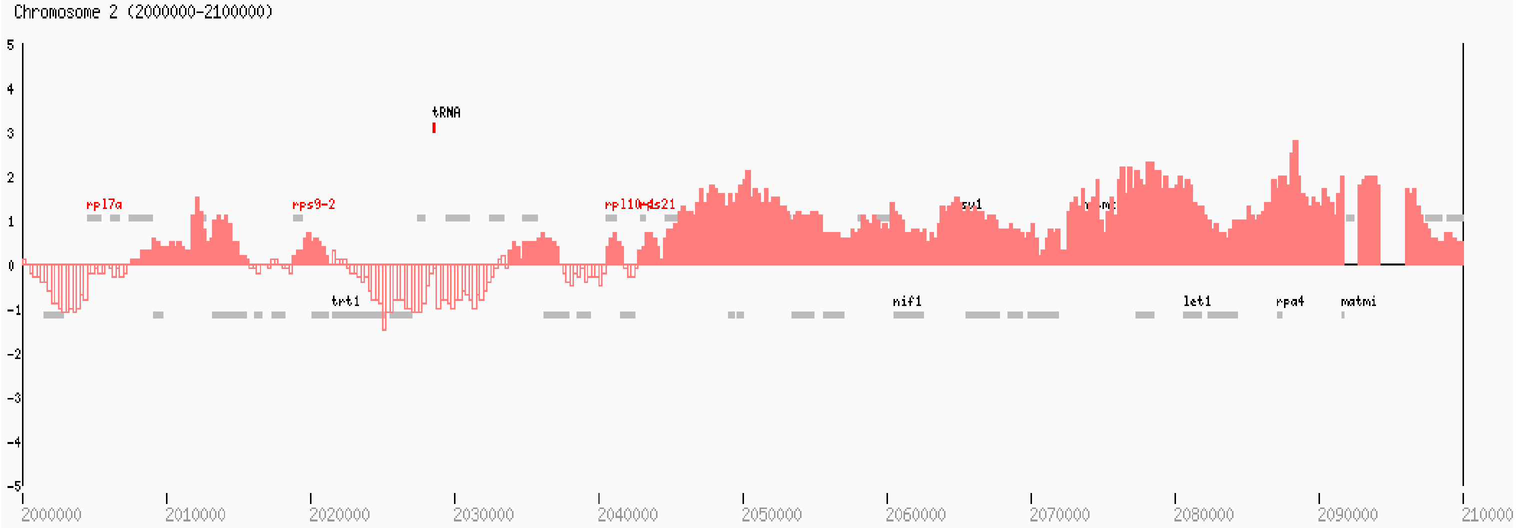


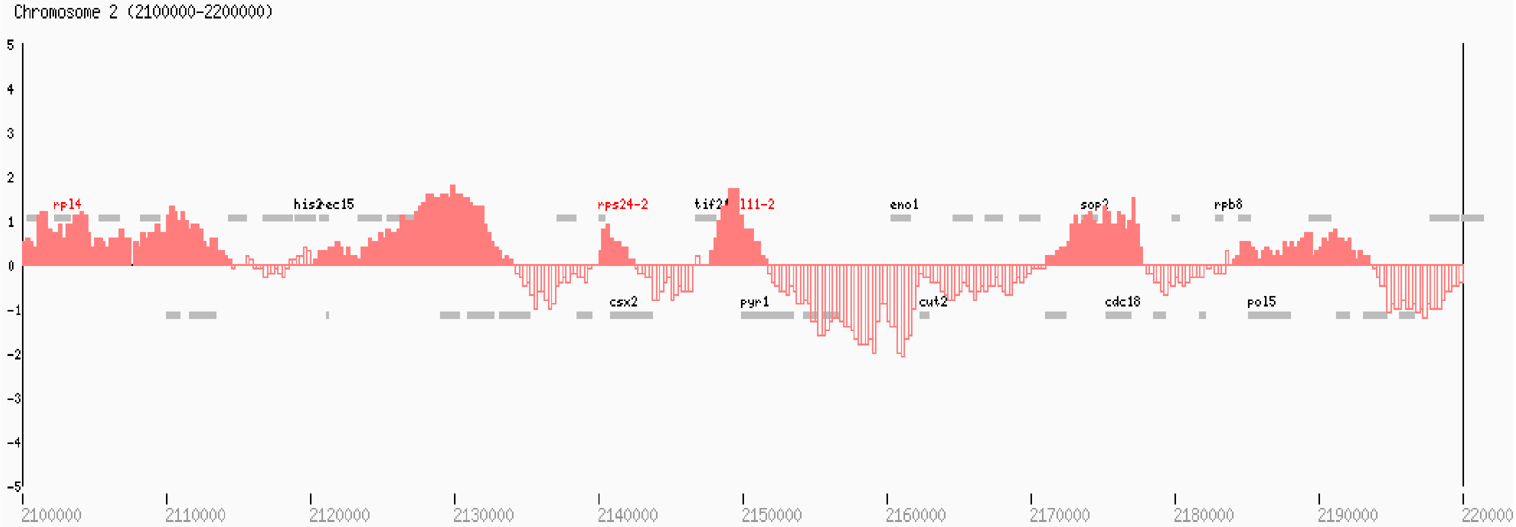
Chromosome 2 (1800000-1900000)

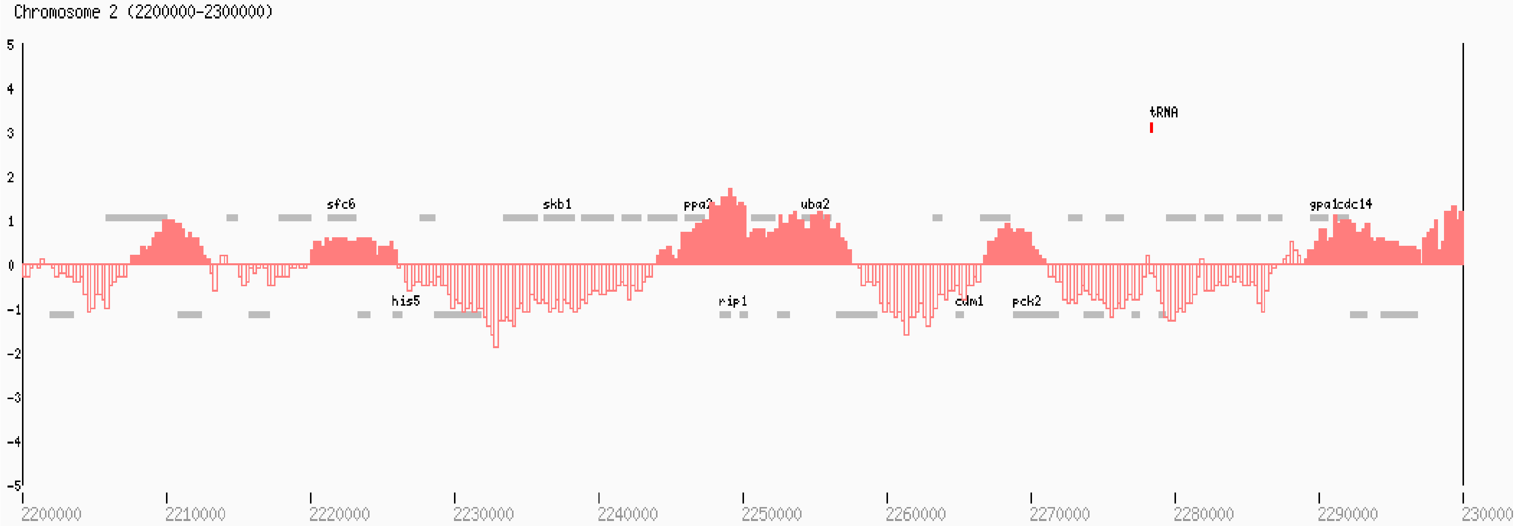


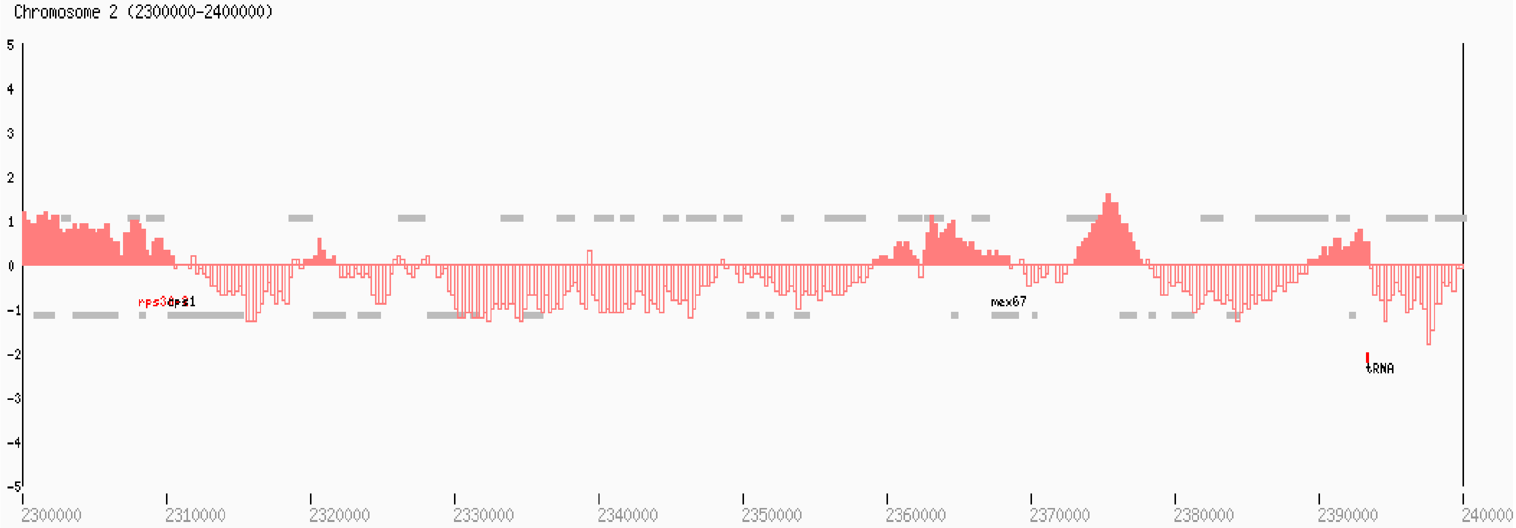
Chromosome 2 (1900000-2000000)



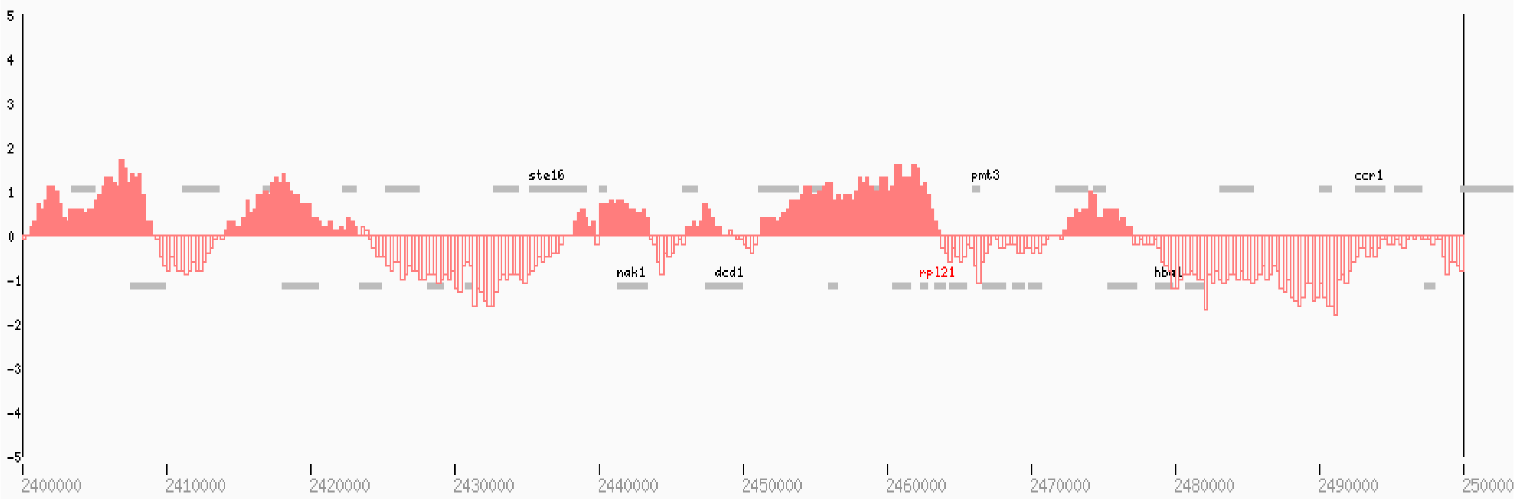

Chromosome 2 (2000000-2100000)


Chromosome 2 (2100000-2200000)

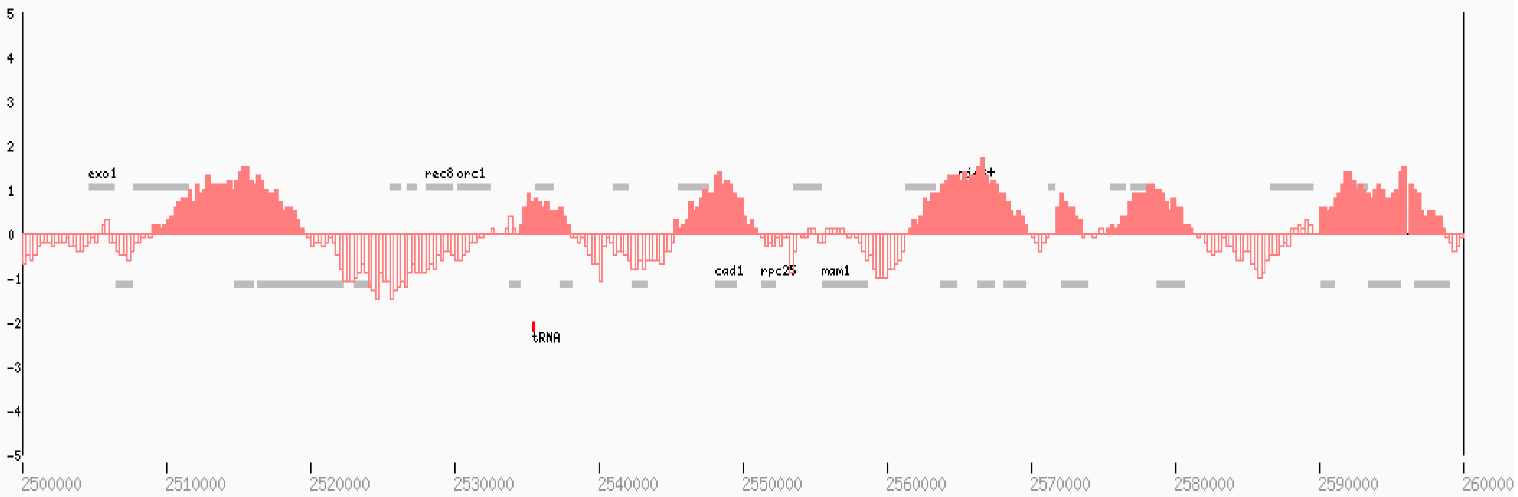

Chromosome 2 (2200000-2300000)


Chromosome 2 (2300000-2400000)

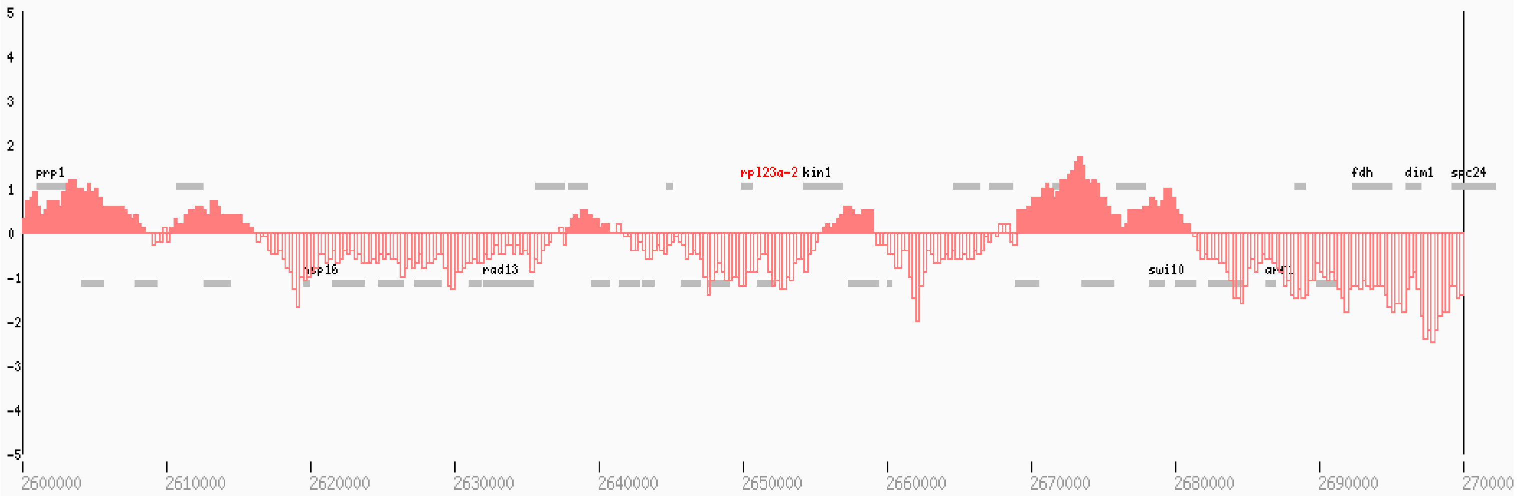
Chromosome 2 (2400000-2500000)



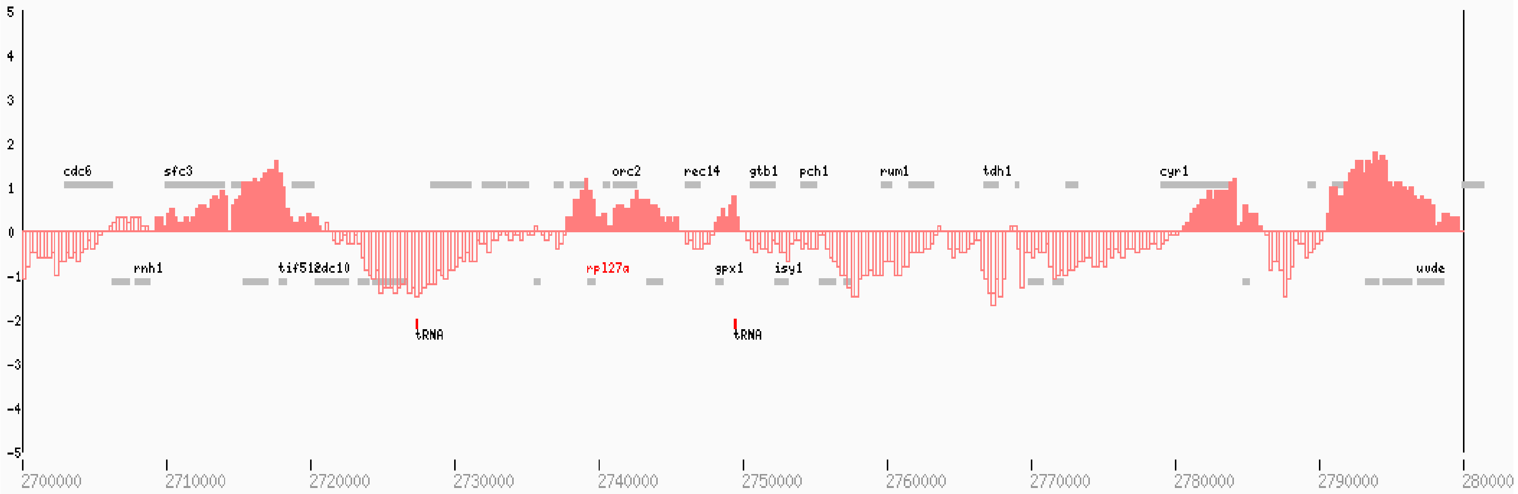
Chromosome 2 (2500000-2600000)



Chromosome 2 (2600000-2700000)

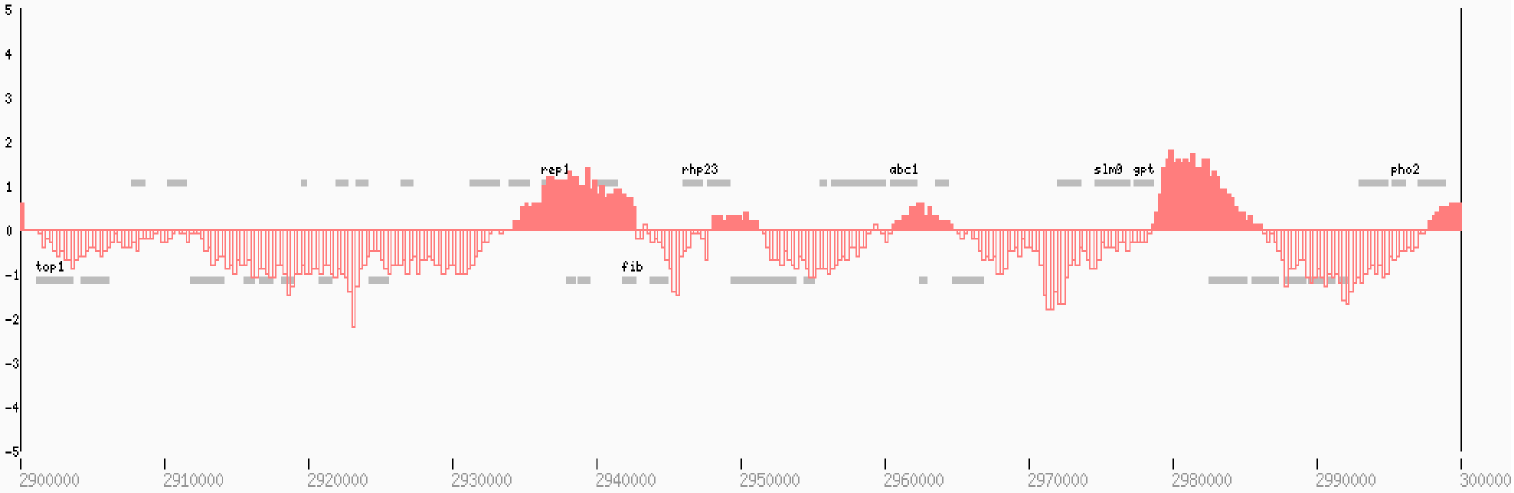


Chromosome 2 (2700000-2800000)

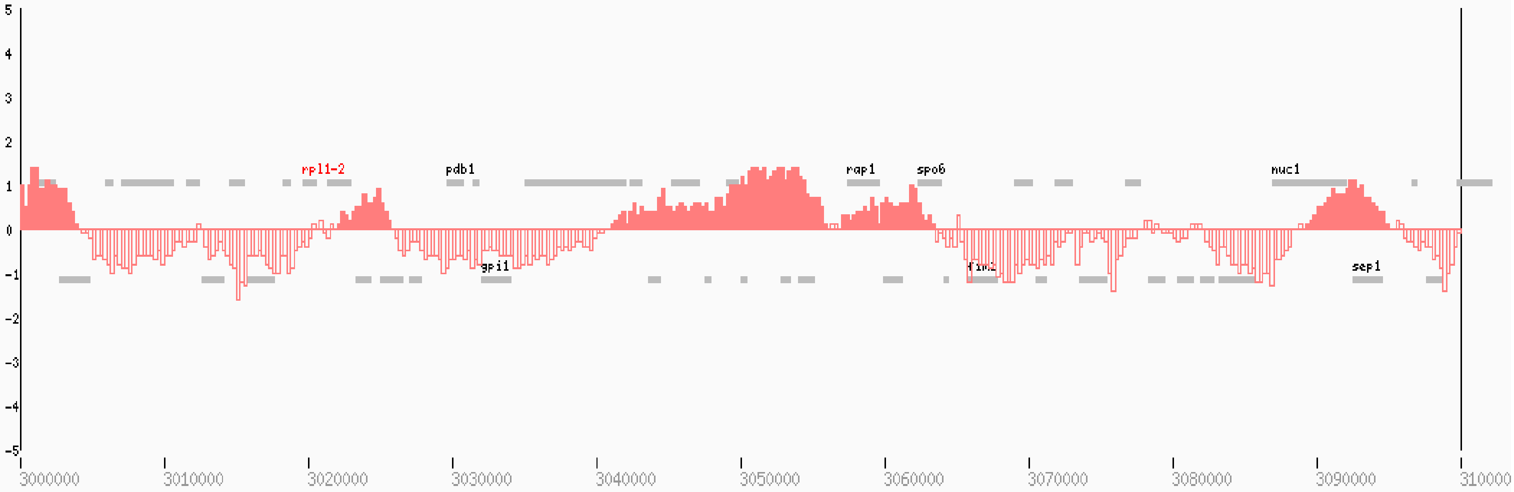


Chromosome 2 (2800000-2900000)

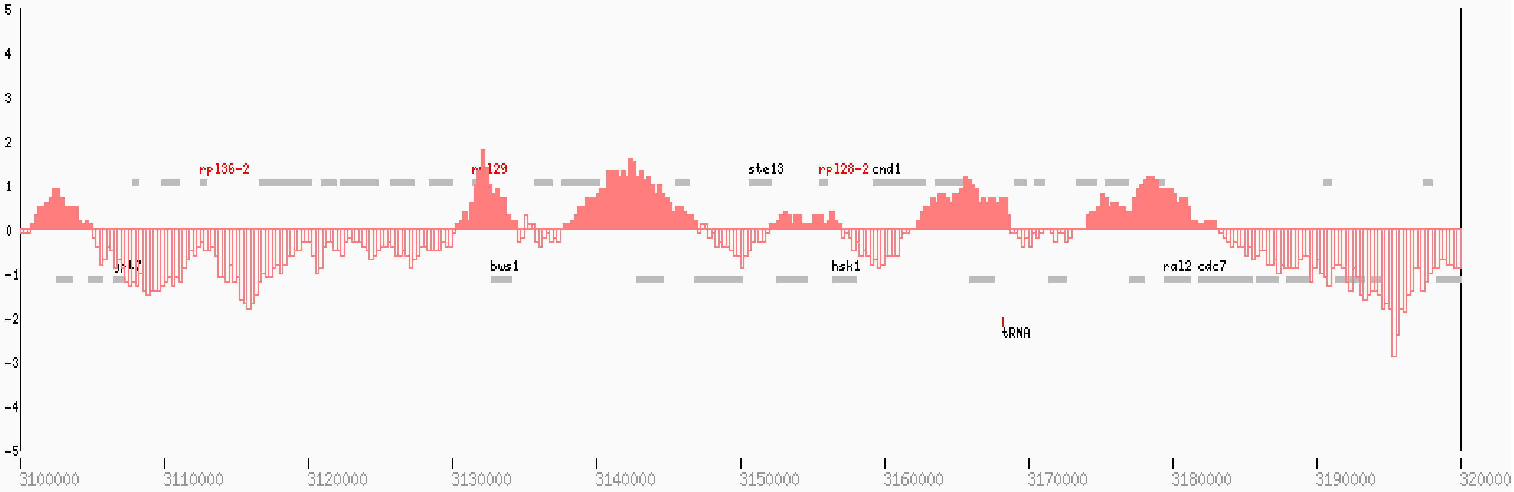
Chromosome 2 (2900000-3000000)

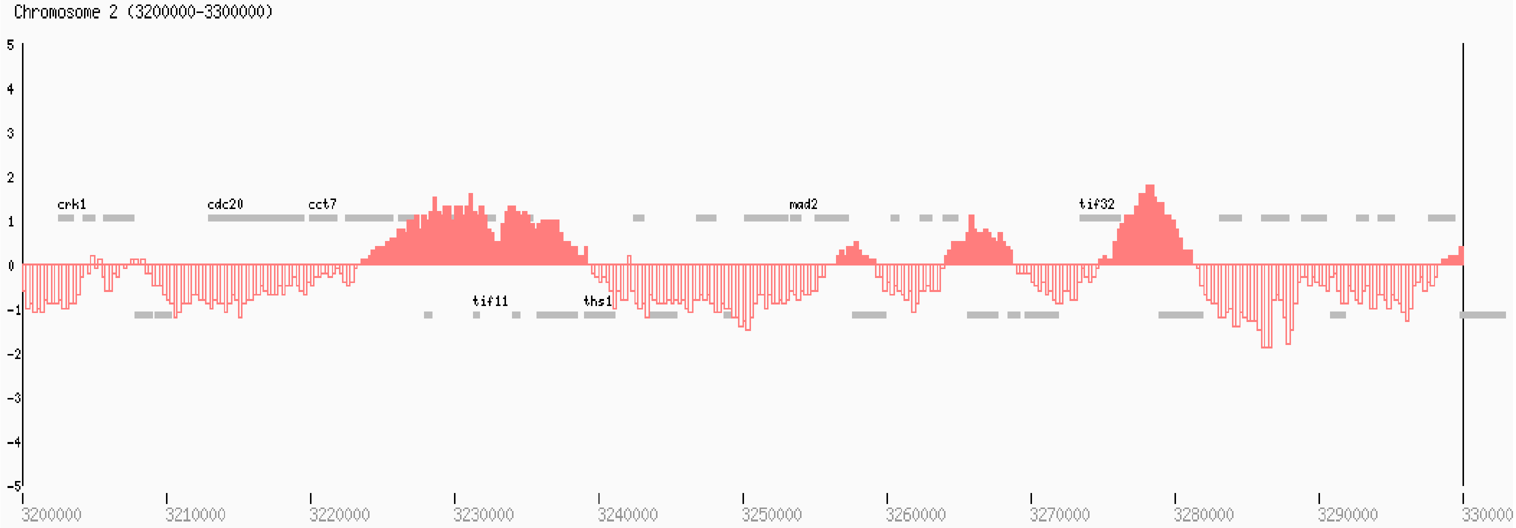


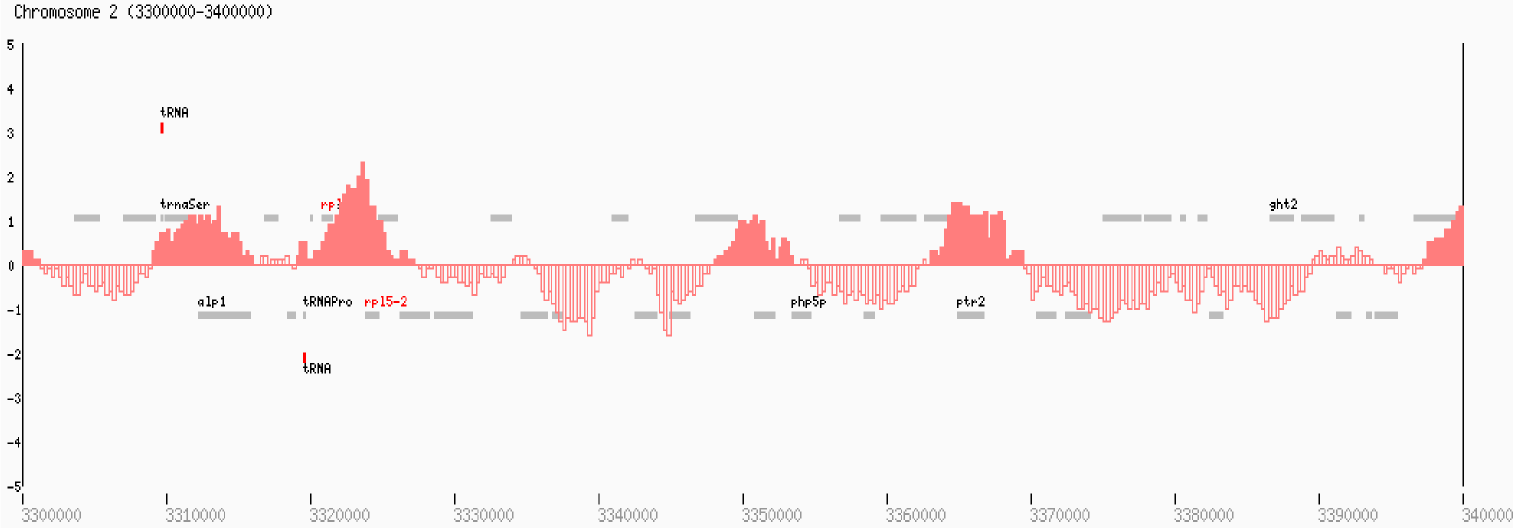
Chromosome 2 (3000000-3100000)

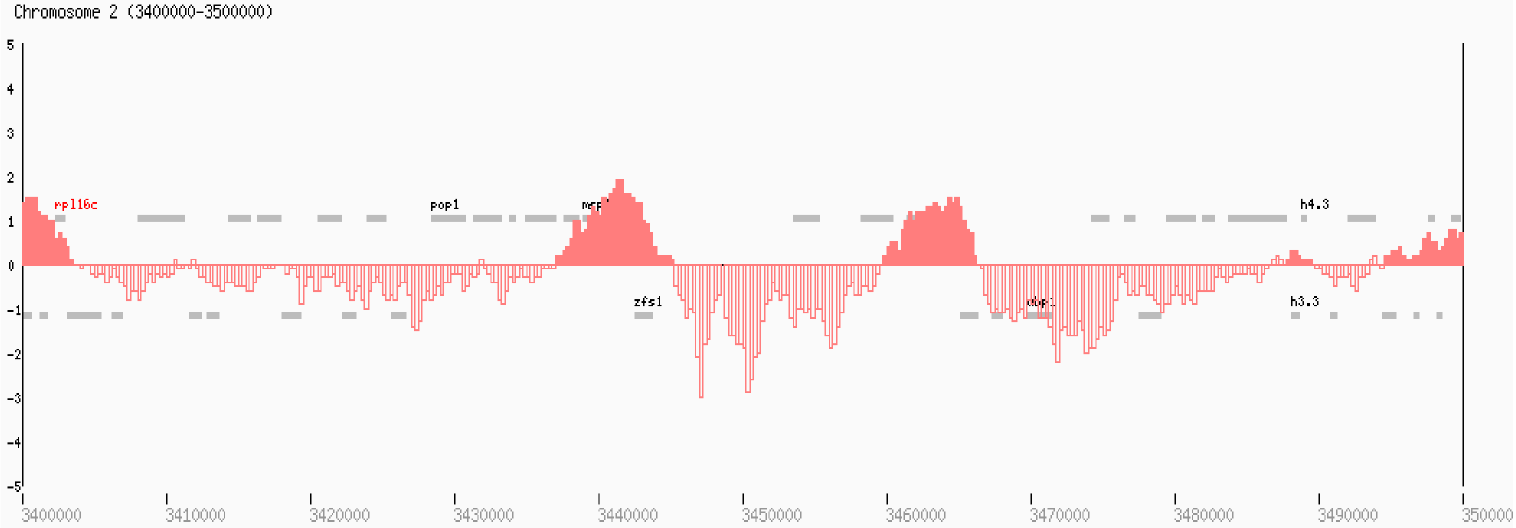


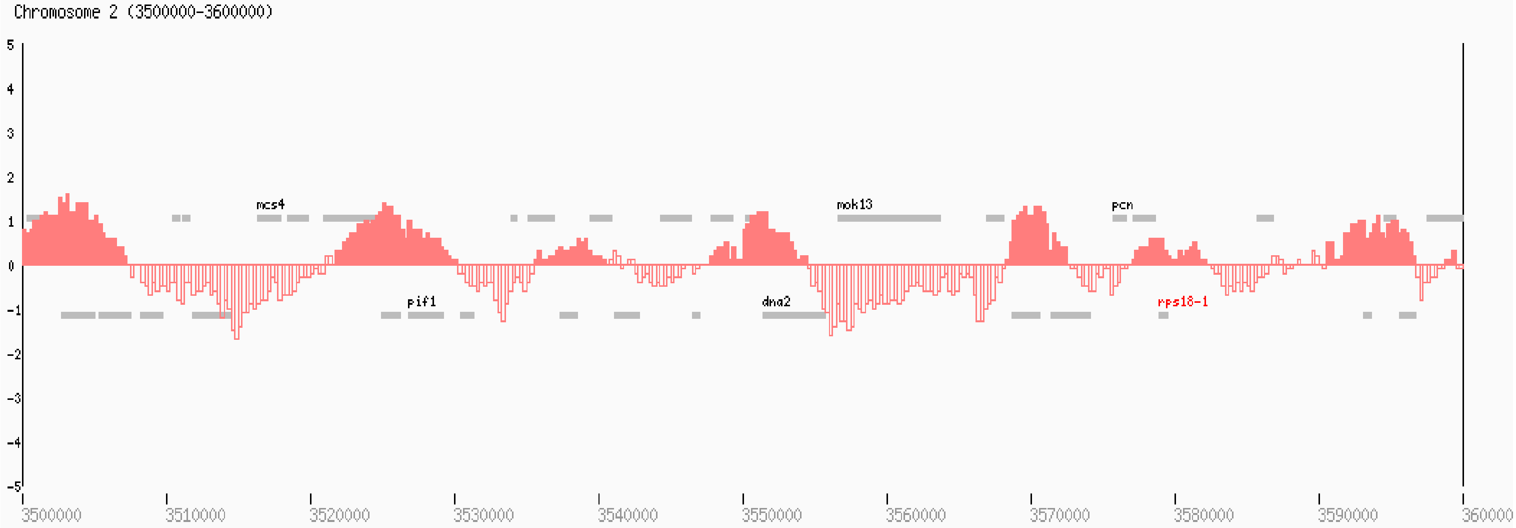
Chromosome 2 (3100000-3200000)



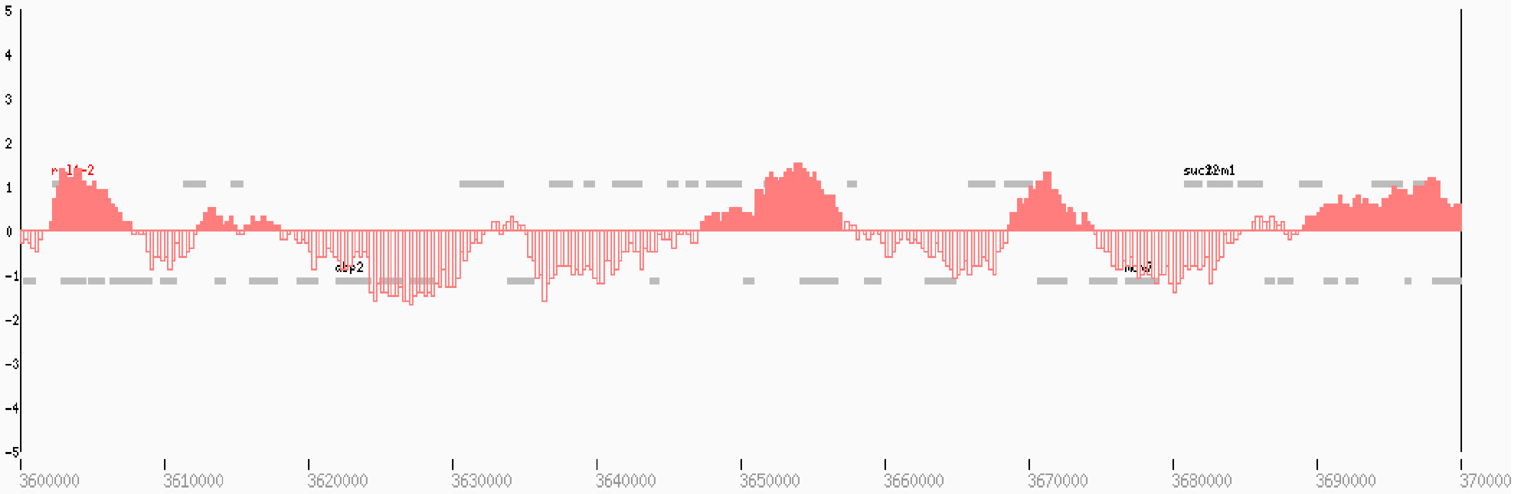

Chromosome 2 (3200000-3300000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
crk1
cdc20
cct7
mad2
tif32
tif11
ths1
3200000
3210000
3220000
3230000
3240000
3250000
3260000
3270000
3280000
3290000
330000


Chromosome 2 (3300000-3400000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
tRNA
trnaSer
ght2
alp1
tRNAPro
rpl15-2
php5p
ptr2
tRNA
3300000
3310000
3320000
3330000
3340000
3350000
3360000
3370000
3380000
3390000
340000

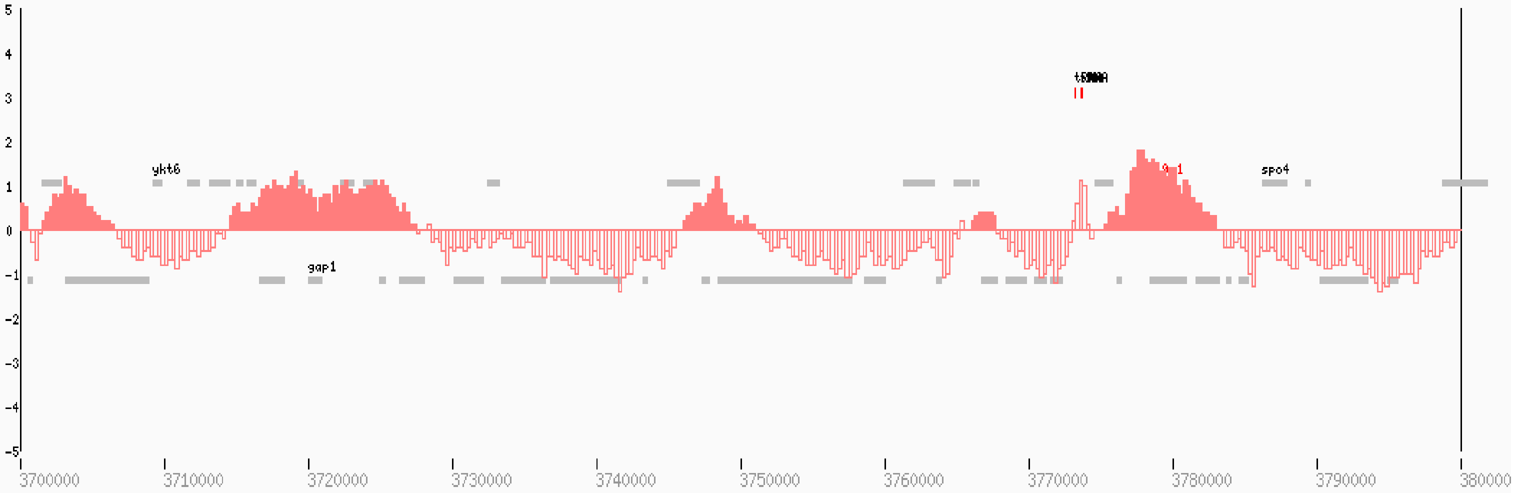

Chromosome 2 (3400000-3500000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
rpl16c
pop1
h4.3
zfs1
h3.3
3400000
3410000
3420000
3430000
3440000
3450000
3460000
3470000
3480000
3490000
350000


Chromosome 2 (3500000-3600000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
mcs4
mok13
pcn
pif1
dna2
rps18-1
3500000
3510000
3520000
3530000
3540000
3550000
3560000
3570000
3580000
3590000
360000

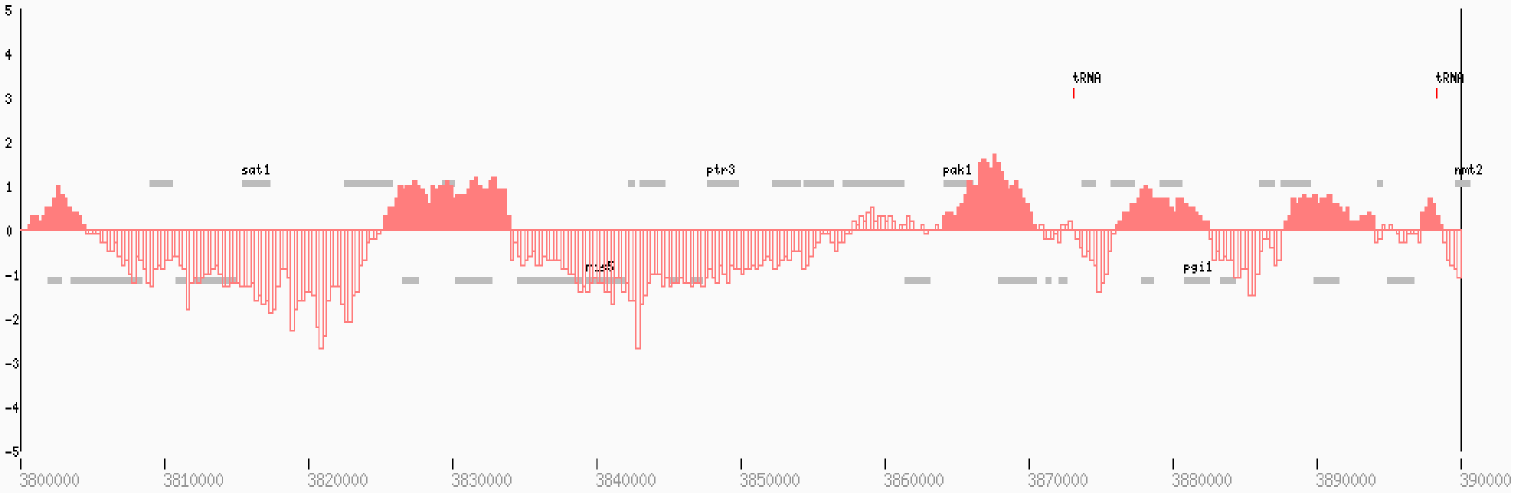
Chromosome 2 (3600000-3700000)



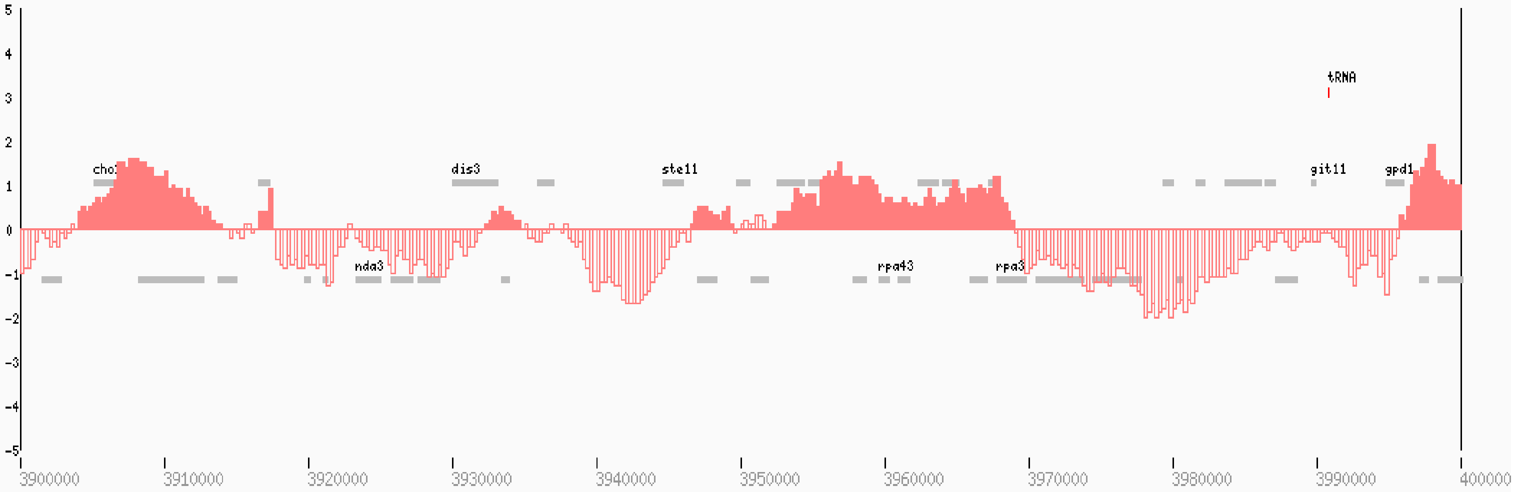
Chromosome 2 (3700000-3800000)



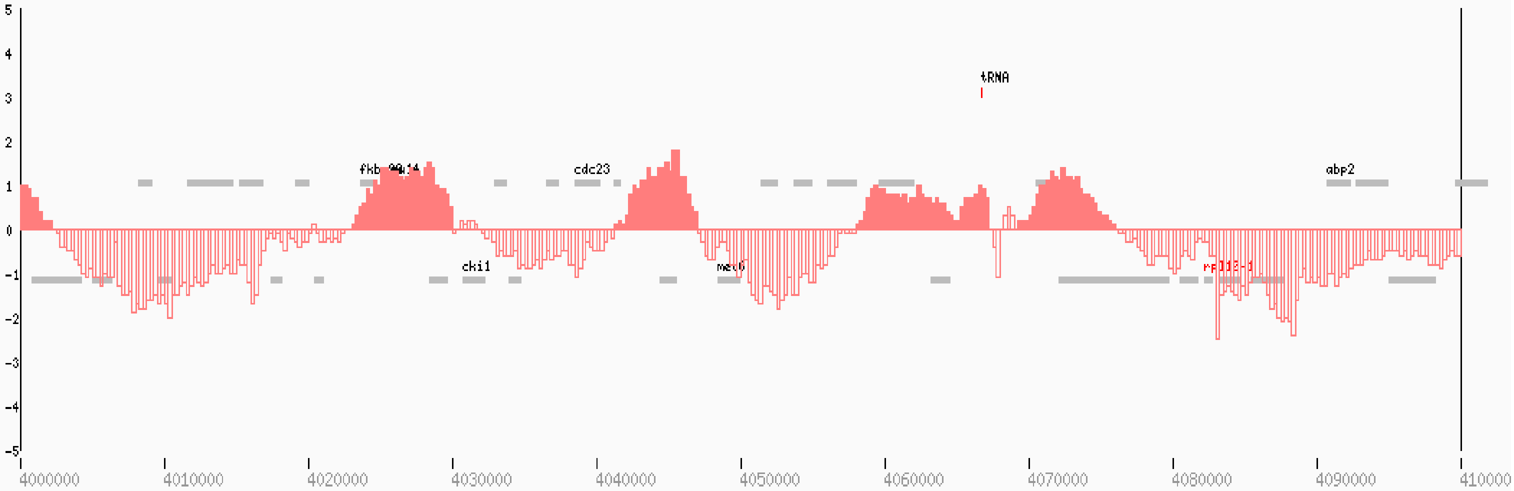
Chromosome 2 (3800000-3900000)



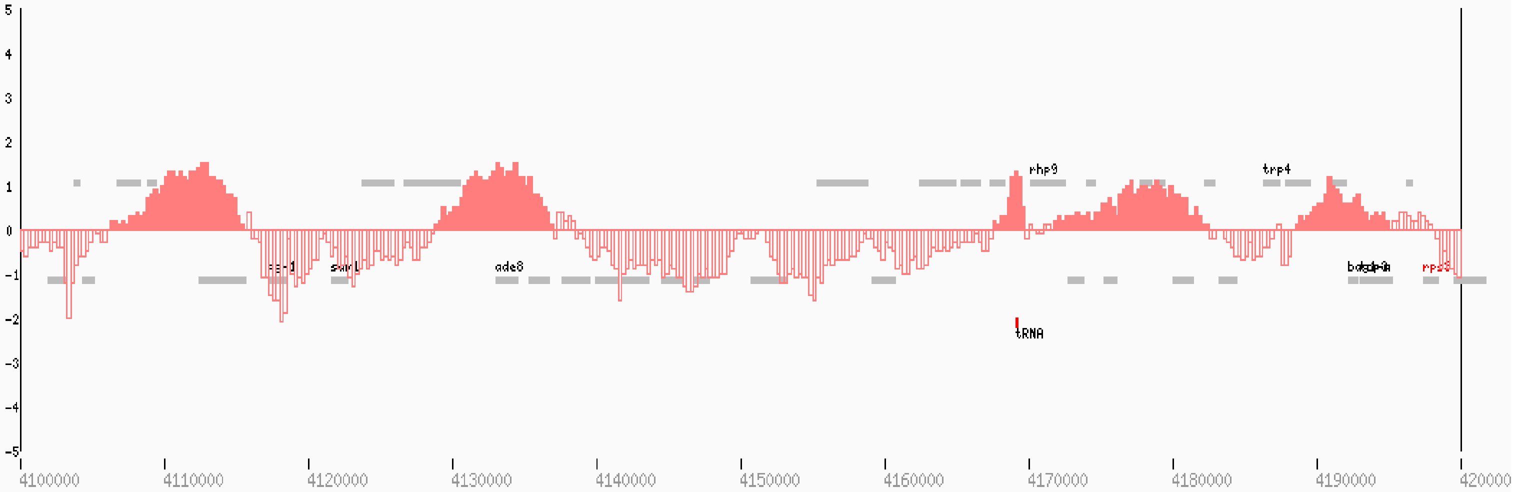
Chromosome 2 (3900000-4000000)



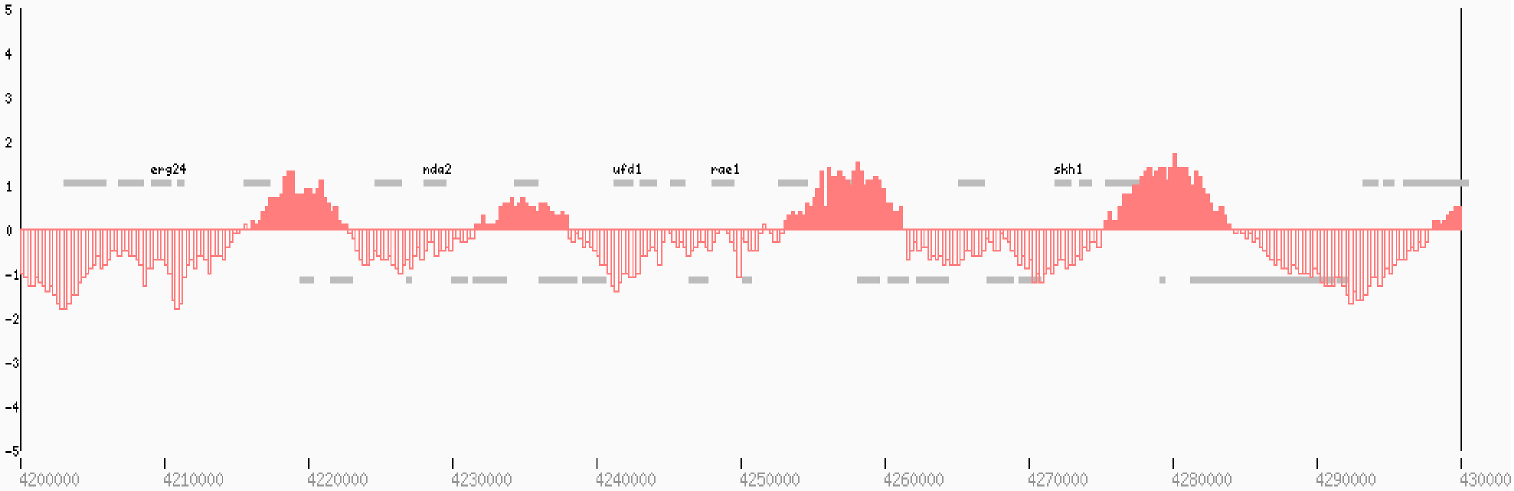
Chromosome 2 (4000000-4100000)



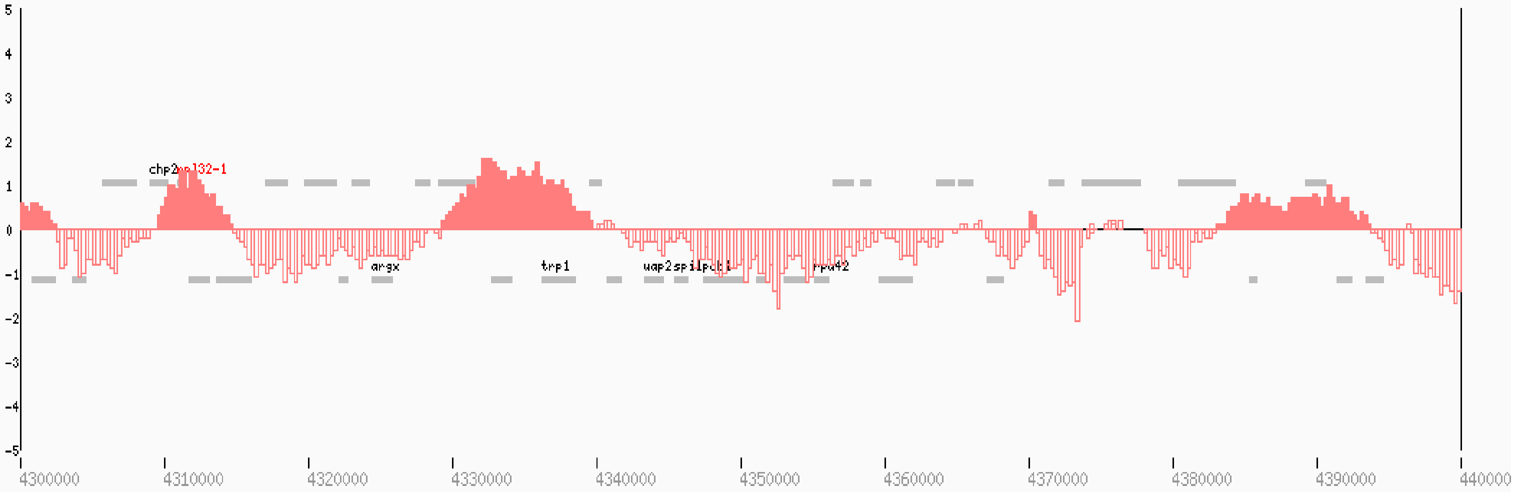
Chromosome 2 (4100000-4200000)

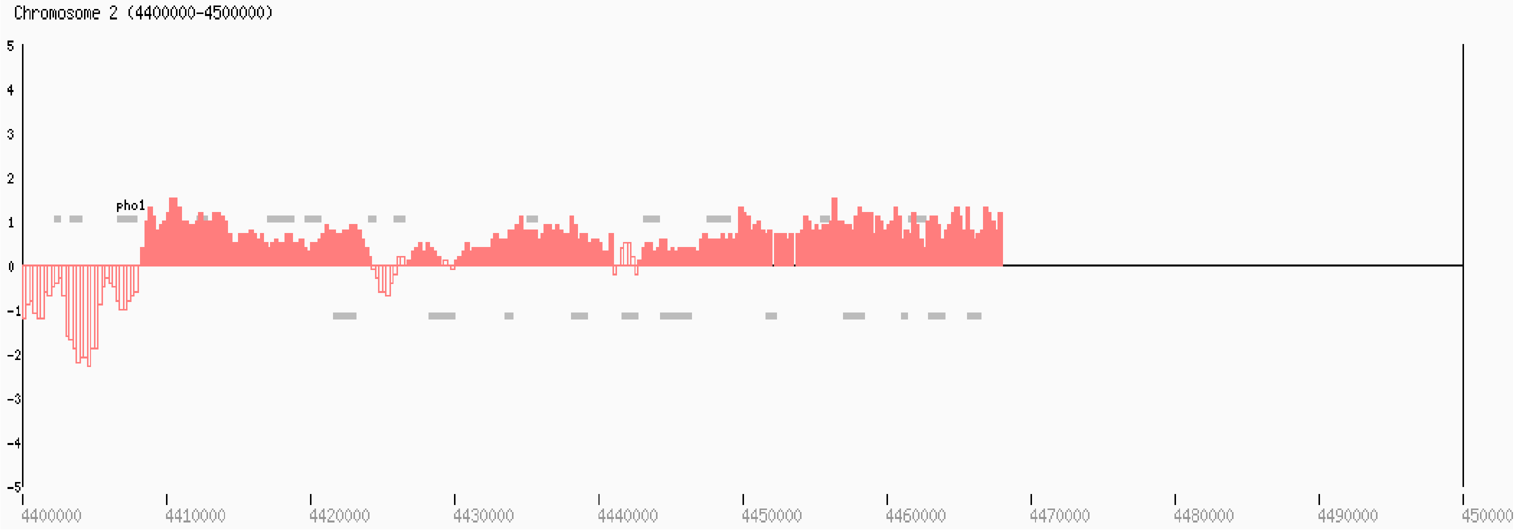


Chromosome 2 (4200000-4300000)



Chromosome 2 (4300000-4400000)




Chromosome 2 (4400000-4500000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
pho1
4400000
4410000
4420000
4430000
4440000
4450000
4460000
4470000
4480000
4490000
450000

(b)

Peak No	Midpoint/bp	Avg height	Width/bp
1	7251	0,74	13000
2	28251	0,76	6000
3	57751	0,62	3500
4	79751	1,11	9000
5	137876	0,57	5750
6	154376	0,85	6250
7	177501	1,19	4000
8	189751	0,63	5000
9	204001	0,84	5000
10	213501	0,30	6000
11	237126	0,42	6250
12	246126	0,78	1750
13	256751	0,95	5500
14	270501	0,46	5500
15	286876	0,51	4750
16	317876	0,80	7250
17	343751	0,93	6500
18	356376	0,66	6750
19	390376	0,63	10250
20	428626	0,53	4250
21	438626	0,78	4250
22	450501	0,57	5500
23	466876	0,70	11750
24	494376	0,30	750
25	523251	0,96	7500
26	541876	0,28	3250
27	564001	0,75	3500
28	572751	0,39	4000
29	588001	0,71	5000
30	636626	0,48	3250
31	639501	0,43	1000
32	652126	0,49	2750
33	657751	0,50	3500
34	676751	0,97	7000
35	719876	0,68	6250
36	729501	1,06	6000
37	784876	0,98	8250
38	793501	0,32	3500
39	830751	0,81	11000
40	850001	0,93	7500
41	865126	0,28	1750
42	875376	0,61	9750
43	888751	0,29	4000
115	2320501	0,21	2000
116	2363626	0,41	9250
117	2375251	0,91	4500
118	2391251	0,41	4000
119	2404626	0,89	8250
120	2418501	0,61	9000
121	2440751	0,55	5000
122	2447126	0,36	2250
123	2457376	0,98	12250
124	2474501	0,54	4500
125	2514126	0,88	10250
126	2536126	0,63	3250
127	2548001	0,74	5500
128	2565501	0,96	8000
129	2572501	0,64	1500
130	2578126	0,65	5750
131	2594251	0,89	8500
132	2604126	0,72	8250
133	2613001	0,43	5500
134	2639126	0,33	2750
135	2657126	0,39	3250
136	2674876	0,80	11750
137	2714876	0,65	11250
138	2741501	0,54	7500
139	2748751	0,50	1500
140	2783126	0,63	5250
141	2795001	1,00	9000
142	2805376	0,59	9250
143	2834251	0,91	7000
144	2850876	0,55	4250
145	2856751	0,40	500
146	2865626	0,64	5250
147	2896751	1,20	6500
148	2938376	0,89	8250
149	2949501	0,27	3000
150	2962501	0,35	4000
151	2982251	1,05	7500
152	3000751	0,78	6000
153	3023751	0,53	3500
154	3048376	0,78	14750
155	3060126	0,49	6250
156	3092001	0,69	5500
157	3102751	0,51	4000

44	921751	1,00	7500
45	935626	0,55	5750
46	942501	0,74	7000
47	958126	0,51	2750
48	978251	0,26	2500
49	989376	0,28	2250
50	1007126	0,86	11250
51	1041251	0,59	13500
52	1062751	0,65	4000
53	1079751	0,76	6000
54	1089126	0,44	8750
55	1104376	0,48	5250
56	1140376	0,44	4750
57	1154876	0,95	8250
58	1169626	0,51	4250
59	1193501	0,52	5500
60	1199251	0,35	4000
61	1213251	0,70	6000
62	1229376	0,30	1250
63	1236876	0,61	5250
64	1262501	0,81	7000
65	1283126		250
66	1290876	0,81	6250
67	1349501	0,65	4500
68	1378501	0,48	7000
69	1407876	0,80	3750
70	1433376	0,94	4250
71	1494251	0,61	8000
72	1508251	0,76	7500
73	1515876	0,64	2750
74	1527751	0,38	2500
75	1535376	0,37	2750
76	1558126	1,24	13250
77	1571876	0,71	12750
78	1600001	1,17	23000
79	1633626	0,73	7250
80	1654626	0,74	8750
81	1668501	0,79	5000
82	1678126	0,61	5750
83	1692251	0,40	1000
84	1698876	0,94	7750
85	1733751	1,03	4000
86	1741876	0,52	5250
87	1759751	0,40	2500
88	1787126	0,61	4750
89	1792376	0,64	4750
158	3132251	0,77	4000
159	3142251	0,83	9000
160	3154376	0,23	4750
161	3165376	0,73	6250
162	3178376	0,63	8750
163	3231251	0,89	15500
164	3257751	0,29	2500
165	3266251	0,62	4500
166	3277876	0,98	6250
167	3299751	0,23	2500
168	3312376	0,79	6750
169	3323001	0,87	8000
170	3350626	0,62	5250
171	3366126	0,88	6250
172	3400251	0,93	6000
173	3441001	1,00	8000
174	3462876	1,05	6250
175	3488501	0,20	1500
176	3500751	0,76	12500
177	3525876	0,78	8250
178	3537876	0,31	4750
179	3551001	0,61	6500
180	3570251	0,93	4000
181	3579501	0,35	5000
182	3593501	0,71	6000
183	3599001	0,10	500
184	3604751	0,91	5500
185	3613501	0,31	2500
186	3616626	0,20	2250
187	3652001	0,84	9500
188	3671376	0,67	5750
189	3694626	0,71	11250
190	3703876	0,61	4750
191	3720876	0,80	12750
192	3748376	0,49	4750
193	3766751	0,38	1500
194	3773376	0,85	750
195	3779001	0,99	7500
196	3802376	0,49	3750
197	3829501	0,91	8500
198	3867126	0,97	6250
199	3879126	0,58	6250
200	3890751	0,53	6000
201	3897876	0,53	1250
202	3908876	0,93	9750
203	3916876	0,40	750

90	1805876	0,90	7750	204	3933376	0,34	2250
91	1842501	0,97	6000	205	3947876	0,40	2750
92	1869876	0,23	1250	206	3960501	0,83	16500
93	1887626	0,65	6750	207	3998876	0,99	6250
94	1933251	1,16	4500	208	4026376	1,10	6750
95	1946126	0,63	5750	209	4044001	1,06	5500
96	1976126	0,86	5250	210	4062501	0,68	9000
97	1987626	0,43	3250	211	4072501	0,79	6500
98	1991251	0,40	1000	212	4110751	0,87	9000
99	2011501	0,58	8000	213	4132751	0,95	8000
100	2019876	0,49	2250	214	4168501	0,73	2000
101	2035376	0,50	3250	215	4177001	0,61	10500
102	2041001	0,60	1000	216	4191626	0,56	6250
103	2078501	1,13	71500	217	4219251	0,70	6500
104	2127001	0,86	13500	218	4234626	0,43	6250
105	2141126	0,53	2250	219	4257001	0,87	8000
106	2149626	1,00	3750	220	4279501	0,97	8500
107	2174251	0,87	6500	221	4300126	0,40	4250
108	2188626	0,42	9250	222	4312001	0,85	5000
109	2210126	0,61	5250	223	4334376	1,01	10250
110	2222876	0,51	5750	224	4388251	0,57	10500
111	2250626	0,90	13250	225	4416126	0,80	15750
112	2268751	0,63	4000	226	4427751	0,39	2000
113	2292876	0,64	7750	227	4435376	0,63	10750
114	2303751	0,80	13000	228	4455251	0,81	25000

Figure S2

Maximal distance analysis between neighboring cohesin peaks. 10,000 random cohesin patterns, distributed among the convergent sites along fission yeast chromosome 2, were created using a bootstrapping approach. The number and widths of the distributed cohesin peaks were those from the observed binding pattern, as assigned in Figure S1. The maximal distance between neighboring cohesin peaks in each of the random distributions was determined and is shown in the histogram below. The red line indicates the maximal distance between two neighboring cohesin-bound convergent sites in the actual observed cohesin pattern.

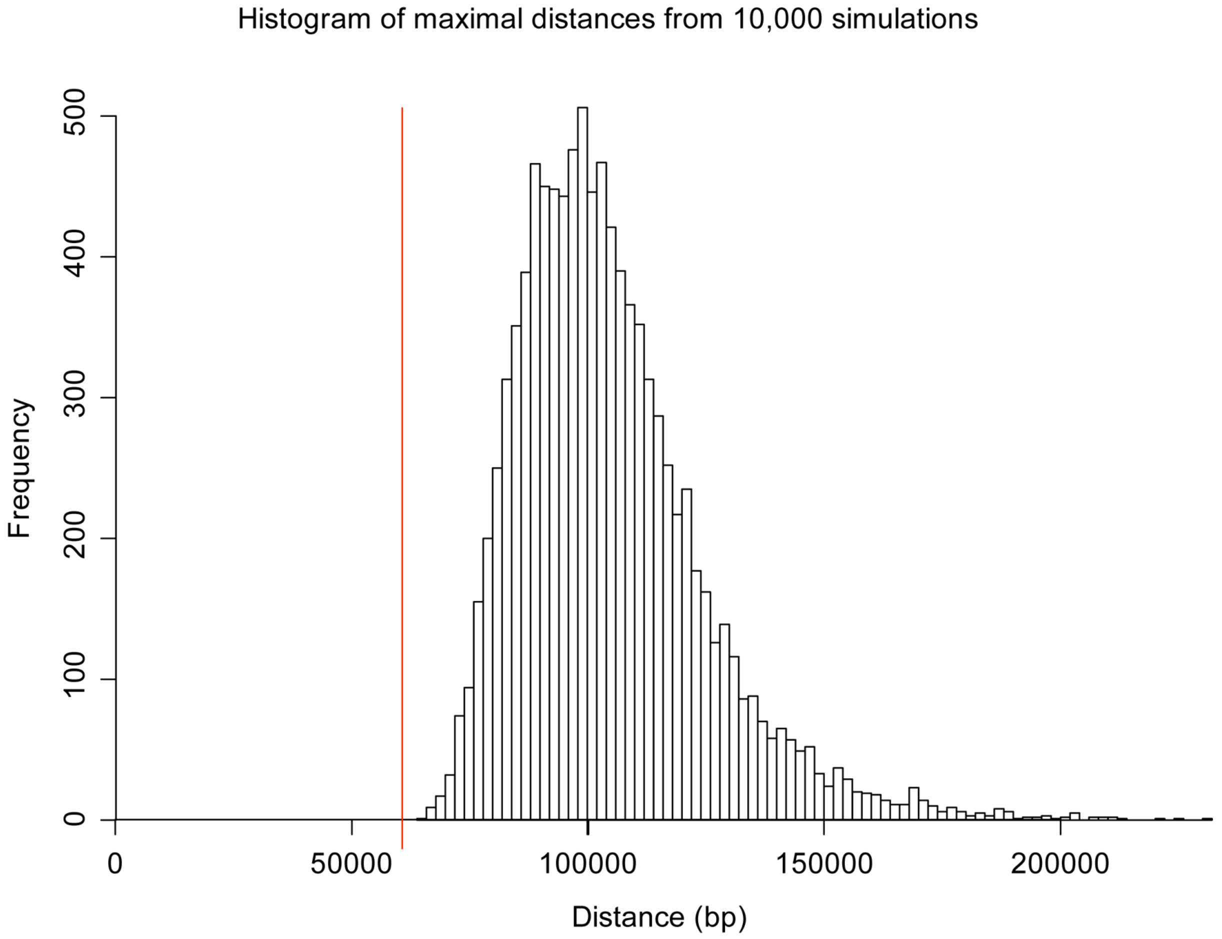


Figure S3

Higher expression levels of convergent gene pairs flanking cohesin binding sites. The distribution of relative mRNA levels from genes flanking cohesin-bound and cohesin-free convergent sites along chromosome 2 is shown. Boxes indicate boundaries of the 25th to the 75th percentile. The median is shown as a bold black line, whiskers extend to 1.5 times the interquartile range, outliers are marked as circles. A Wilcoxon signed ranks test suggests that genes flanking cohesin-bound convergent sites are more strongly expressed than genes flanking cohesin-free convergent sites (p=0.011).

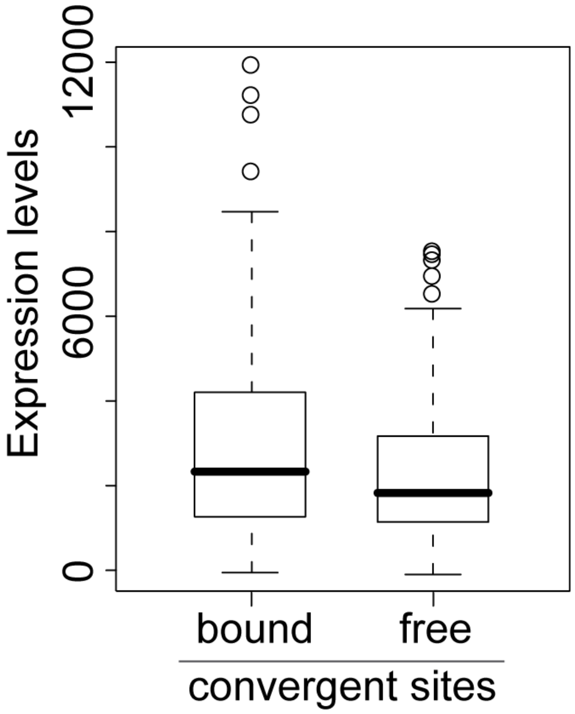
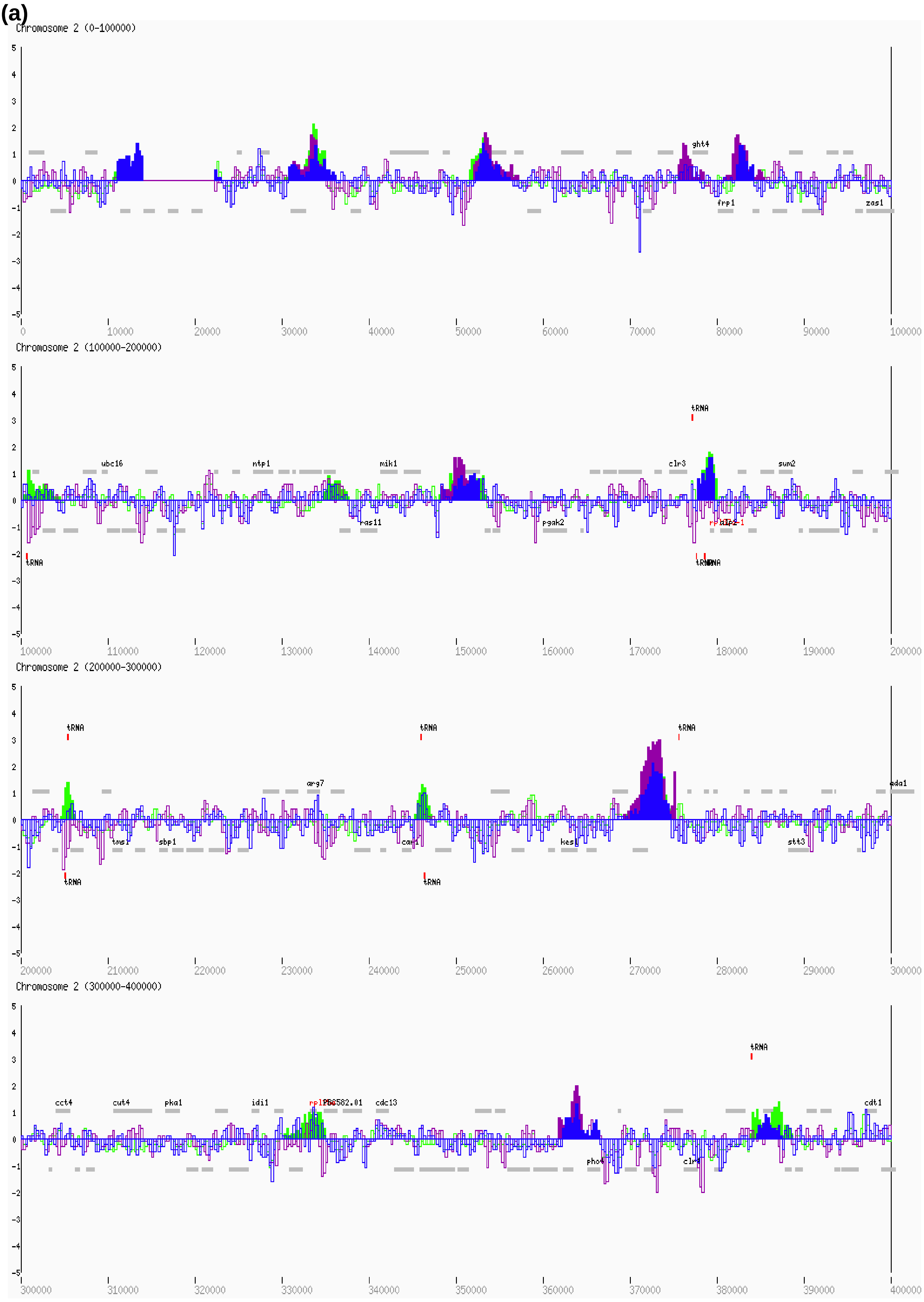
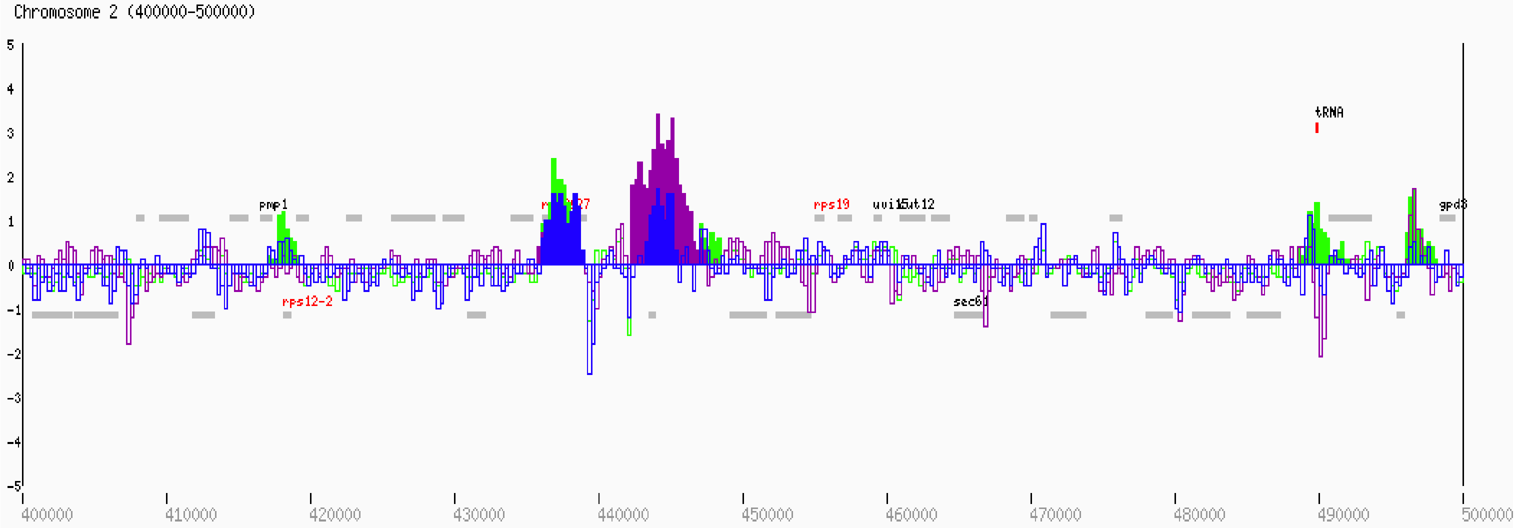
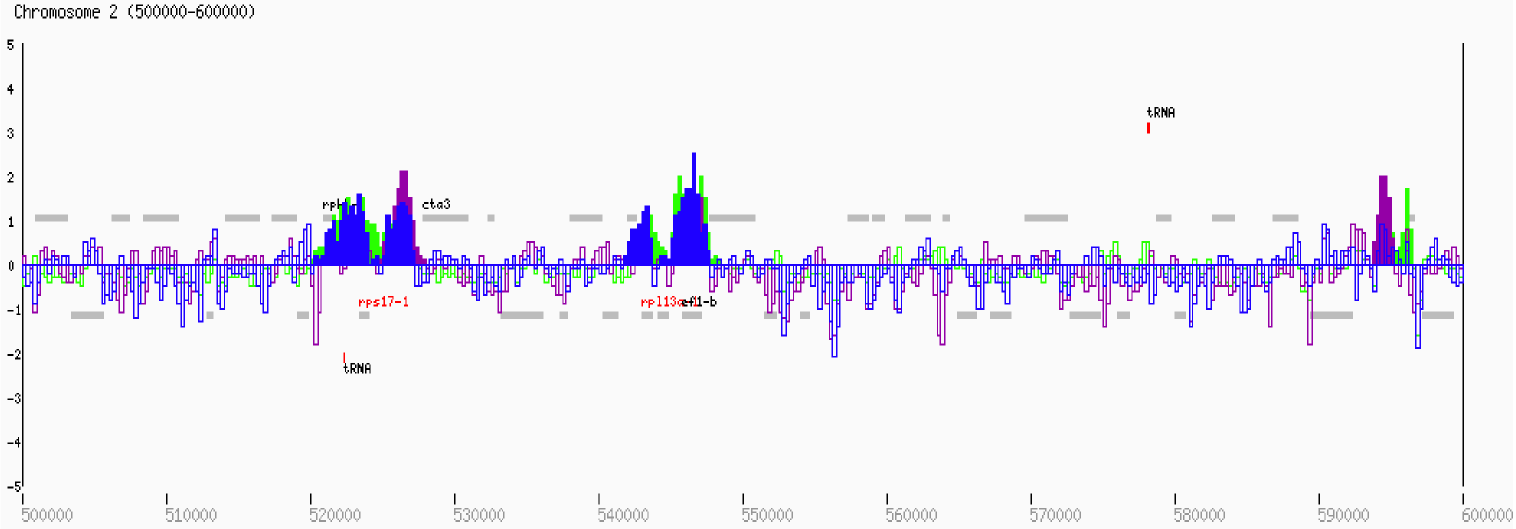


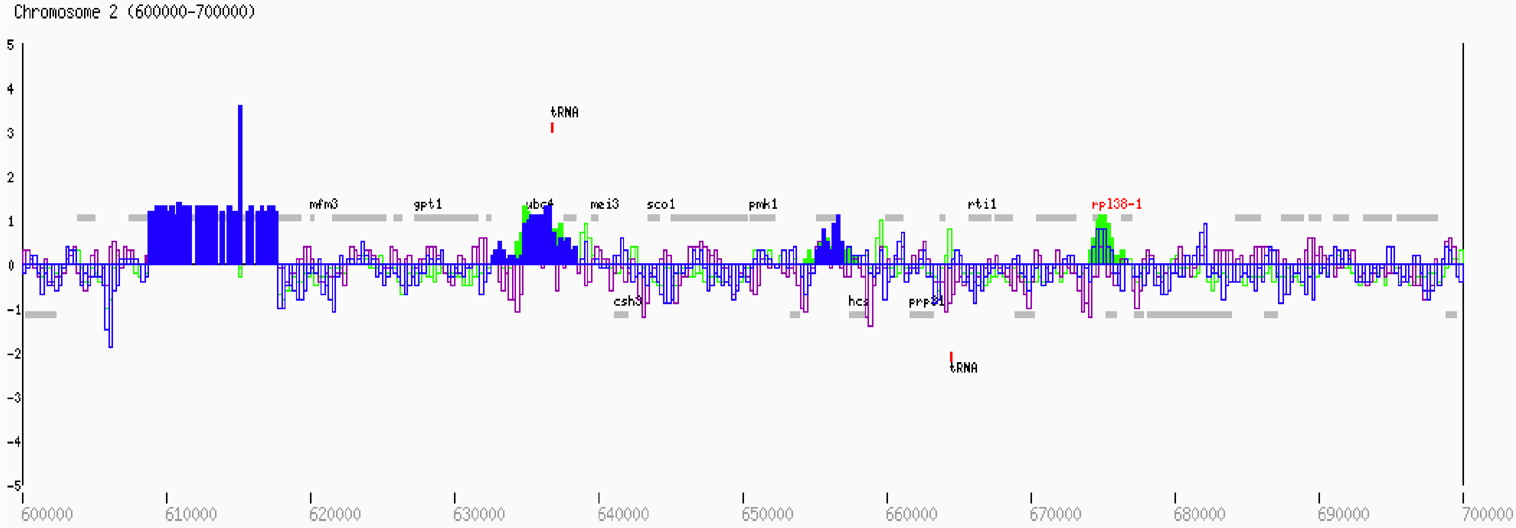
Figure S4

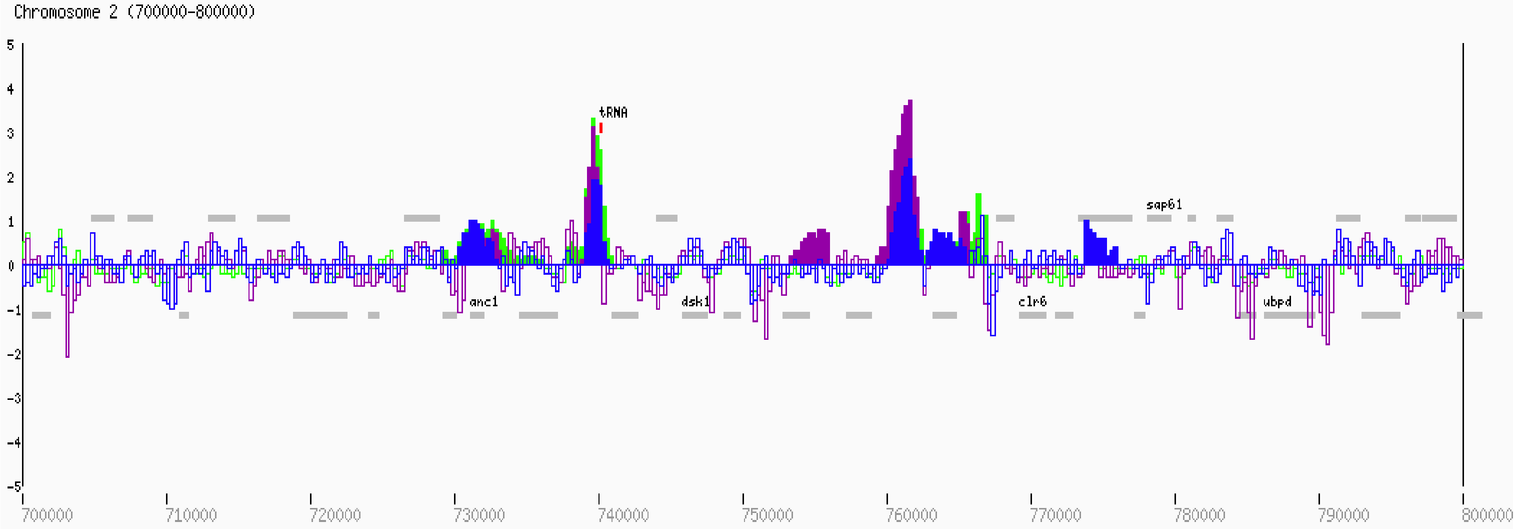
The cohesin loader Mis4/Ssl3 overlaps with tRNA and ribosomal protein genes. (**a**) Binding profile of Mis4 and Ssl3 along fission yeast chromosome 2. Chromatin immunoprecipitation was performed against epitope-tagged Mis4-Pk_9 and Ssl3-Pk_9 from exponentially proliferating cells. As a control, cells without epitope-tagged protein were grown under identical conditions and processed in parallel for chromatin immunoprecipitation with an α-Pk antibody. The map shows an overlay of Mis4 (green), Ssl3 (blue) and the untagged control (purple), as described in Figure S1. Peaks were assigned as detailed in Figure S1, but the threshold for local maxima was a signal intensity of 0.5. The untagged control sample yielded trace amounts of immunoprecipitated DNA, which after amplification led to several strong peaks often in intergenic low complexity regions. Several of these peaks overlapped with Mis4/Ssl3 peaks, which were excluded from the analysis. Peaks in low complexity regions were not observed in chromatin immunoprecipitates of cohesin subunits (compare Figure S1). (**b**) Table of the 72 specific Mis4 peaks assigned as described in (a) along chromosome 2. The position, average height and width of each of the peaks is indicated. The actual number of Mis4 bindings sites might be higher, as some peaks in low complexity regions that have been removed from the analysis may be significant, while others may have remained below recognition by our peak picking parameters. (**c**) The distances of the 72 Mis4 binding sites to the nearest tRNA gene (blue) is shown. 16 lie within 5 kb. The distances of the remaining 56 peaks to the nearest ribosomal protein gene (red) are also shown, of which 18 lie again within 5 kb.


(a)
Chromosome 2 (0-100000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
ght4
frp1
zas1
0
10000
20000
30000
40000
50000
60000
70000
80000
90000
100000
Chromosome 2 (100000-200000)
tRNA
ubc16
ntp1
mik1
clr3
sum2
ras11
pgak2
tRNA
100000
110000
120000
130000
140000
150000
160000
170000
180000
190000
200000
Chromosome 2 (200000-300000)
tRNA
tRNA
tRNA
arg7
ada1
tms1
sbp1
cam1
kes1
stt3
tRNA
tRNA
200000
210000
220000
230000
240000
250000
260000
270000
280000
290000
300000
Chromosome 2 (300000-400000)
tRNA
cct4
cut4
pka1
idi1
cdc13
cdt1
pho4
clr4
300000
310000
320000
330000
340000
350000
360000
370000
380000
390000
400000

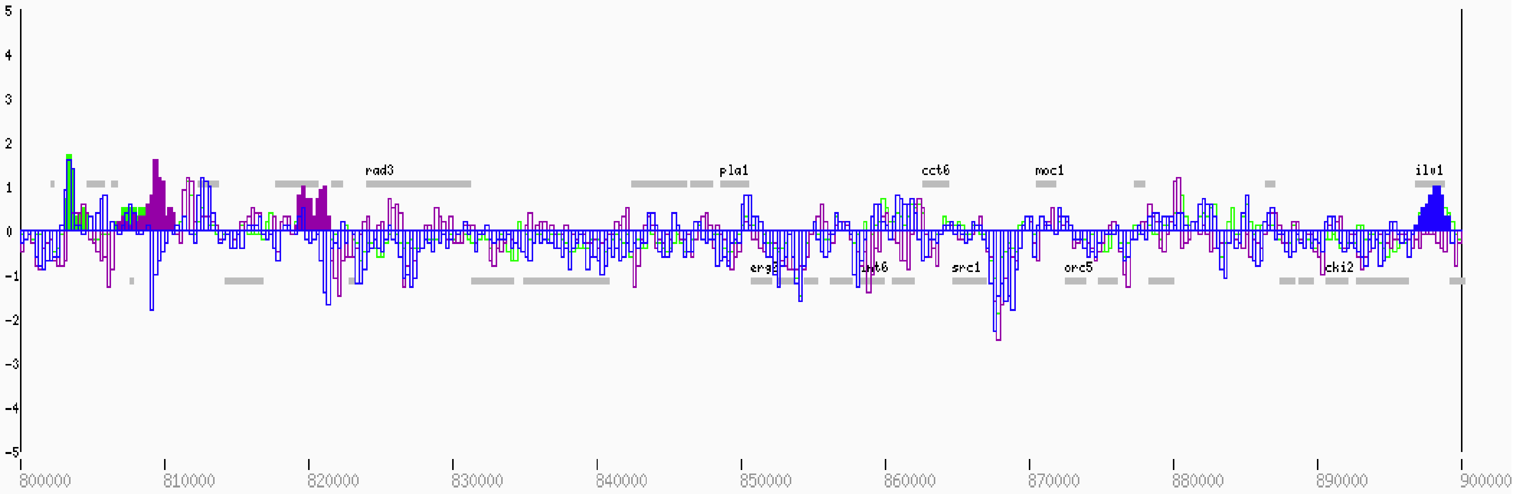

Chromosome 2 (400000-500000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
tRNA
pmp1
rps27
rps19
uvi15ut12
gpd3
rps12-2
sec61
400000
410000
420000
430000
440000
450000
460000
470000
480000
490000
500000


Chromosome 2 (500000-600000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
tRNA
rph1
cta3
rps17-1
rpl13a-1
ef1-b
tRNA
500000
510000
520000
530000
540000
550000
560000
570000
580000
590000
600000

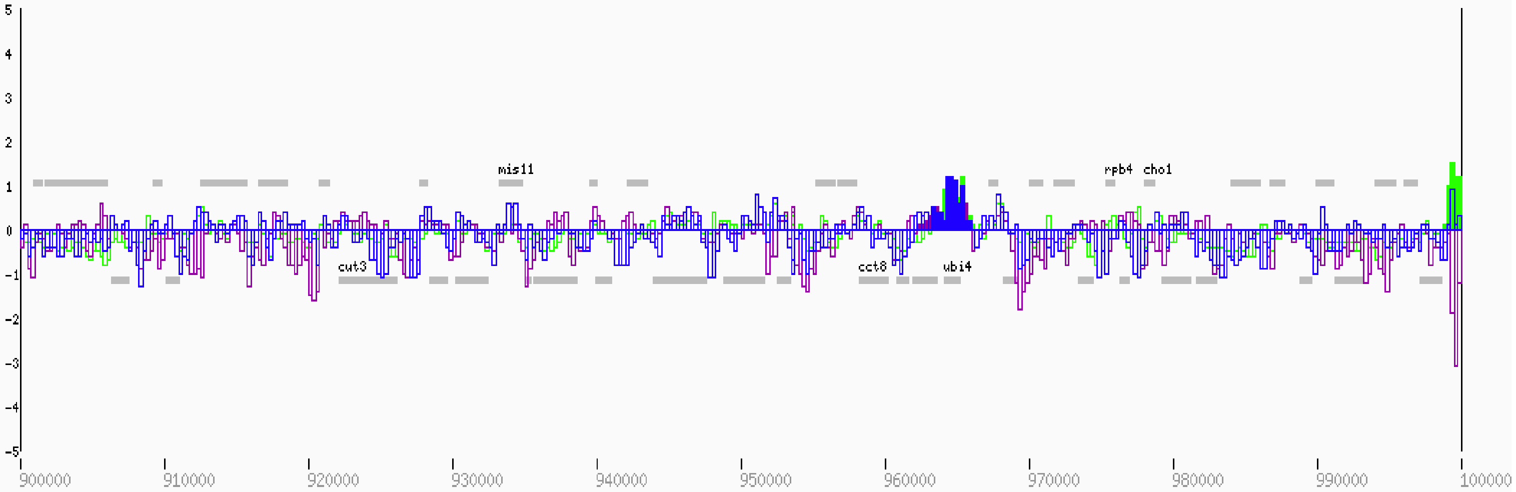

Chromosome 2 (600000-700000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
tRNA
mfm3
gpt1
ubc4
mei3
sco1
pmk1
rti1
rpl38-1
csh3
hcs
prp31
tRNA
600000
610000
620000
630000
640000
650000
660000
670000
680000
690000
700000


Chromosome 2 (700000-800000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
tRNA
sap61
anc1
dsk1
clr6
ubpd
700000
710000
720000
730000
740000
750000
760000
770000
780000
790000
800000

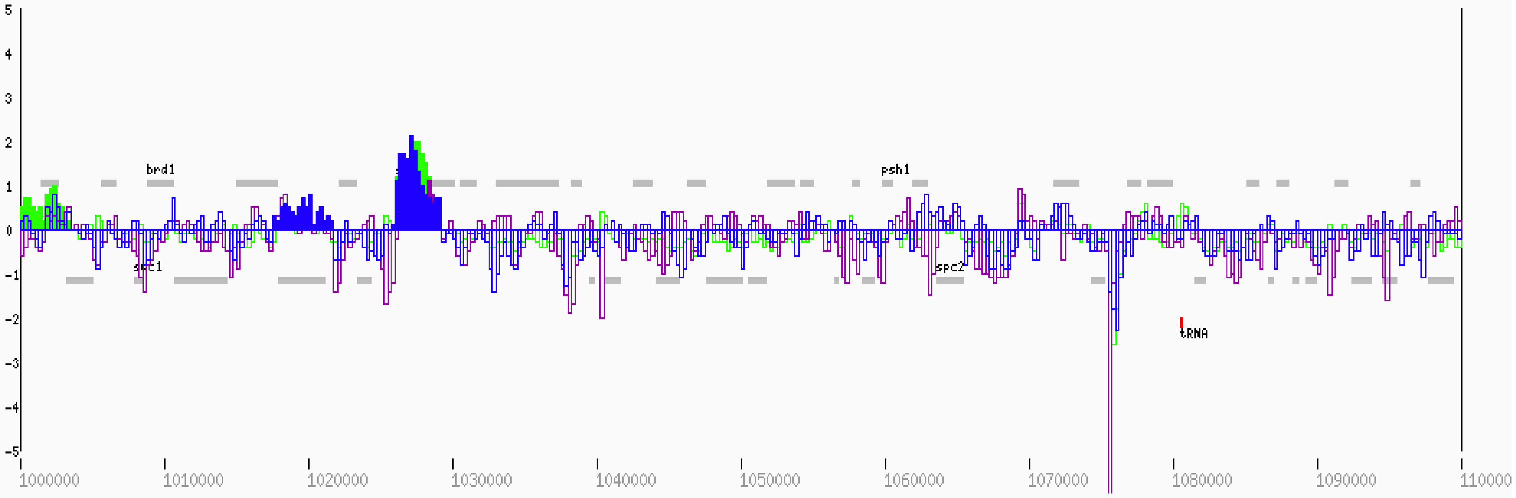
Chromosome 2 (800000-900000)



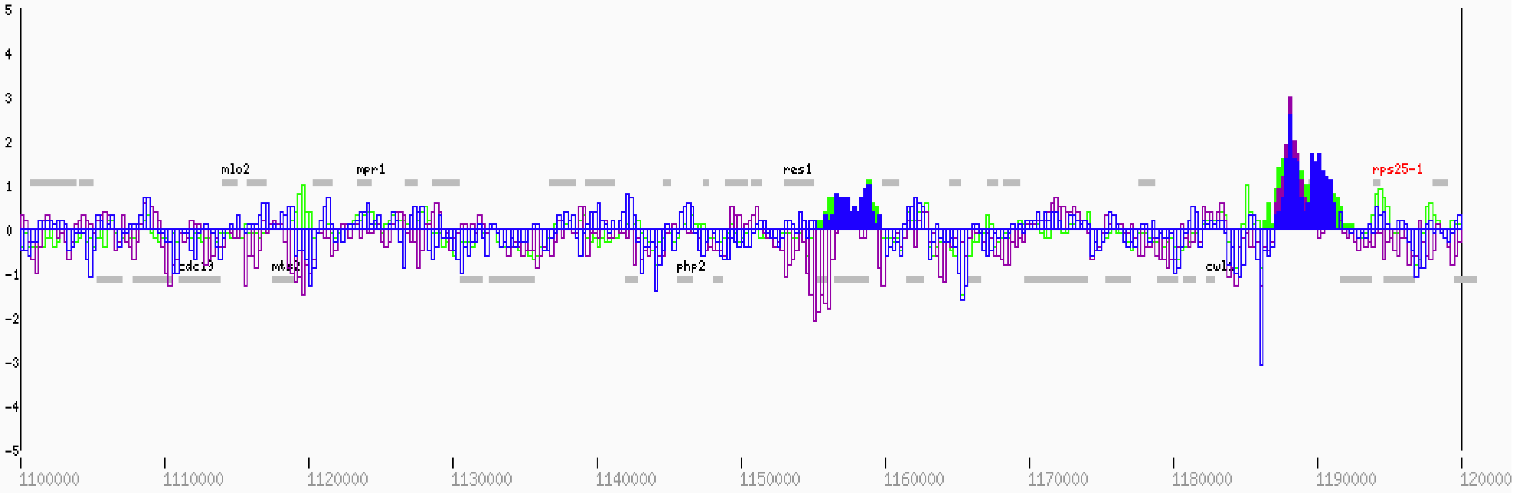
Chromosome 2 (900000-1000000)



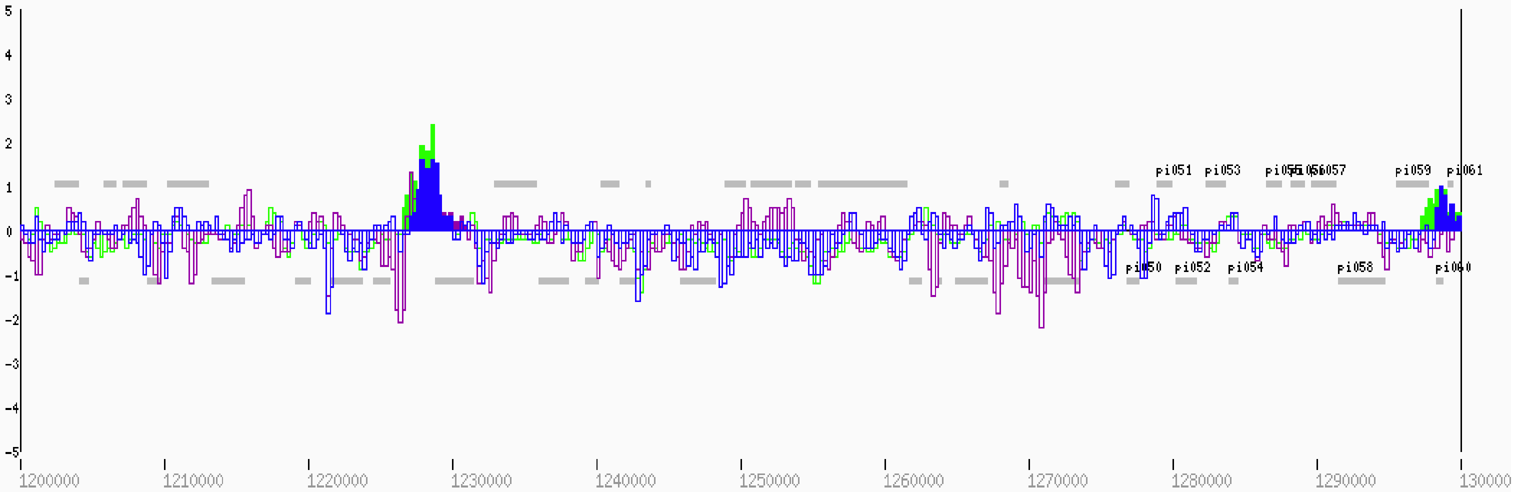
Chromosome 2 (1000000-1100000)



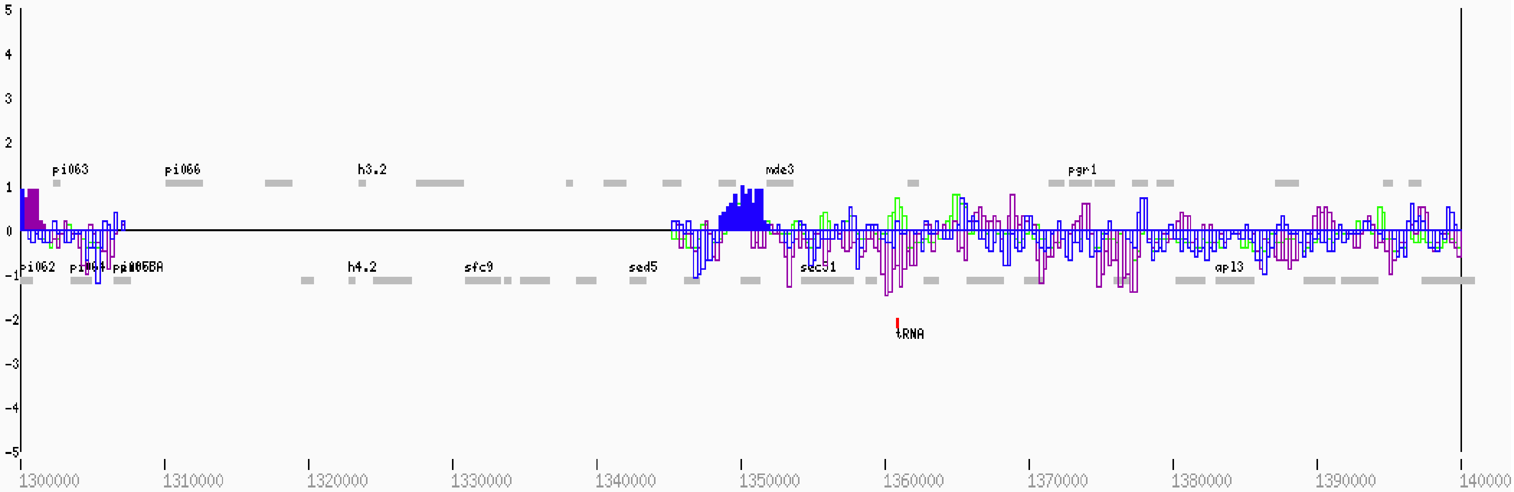
Chromosome 2 (1100000-1200000)



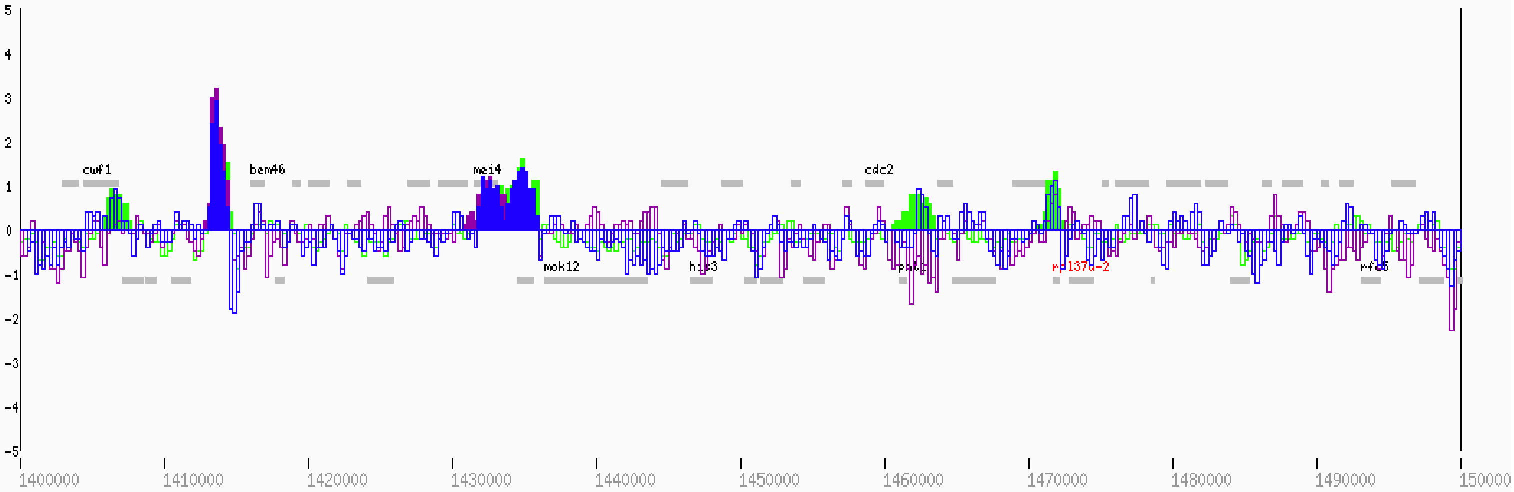
Chromosome 2 (1200000-1300000)



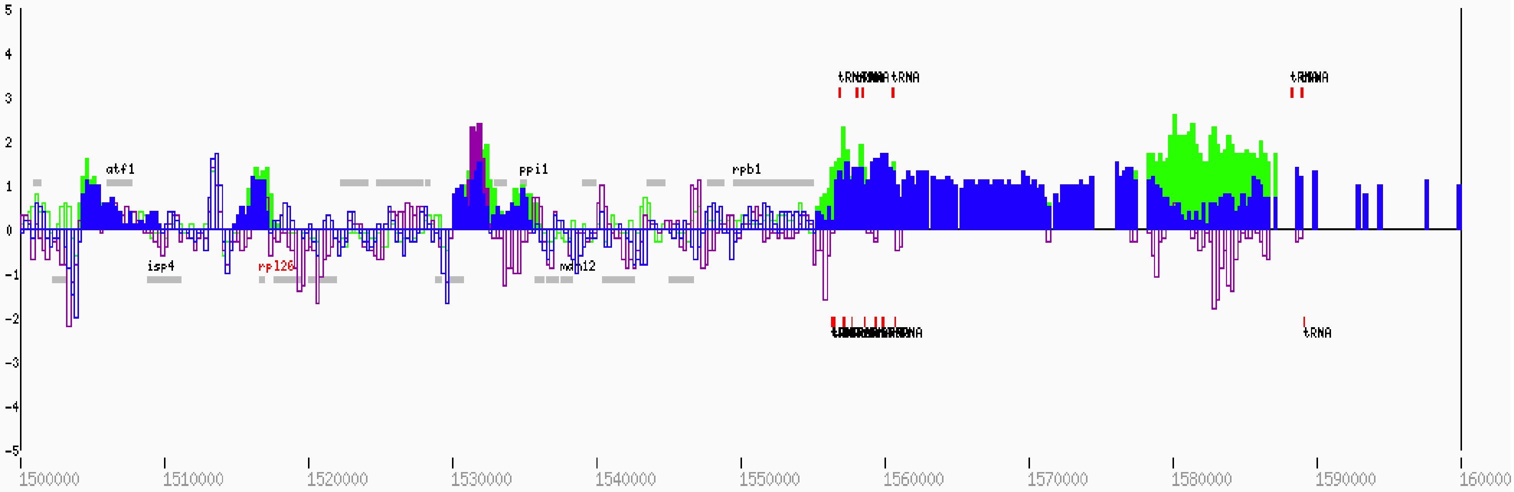
Chromosome 2 (1300000-1400000)



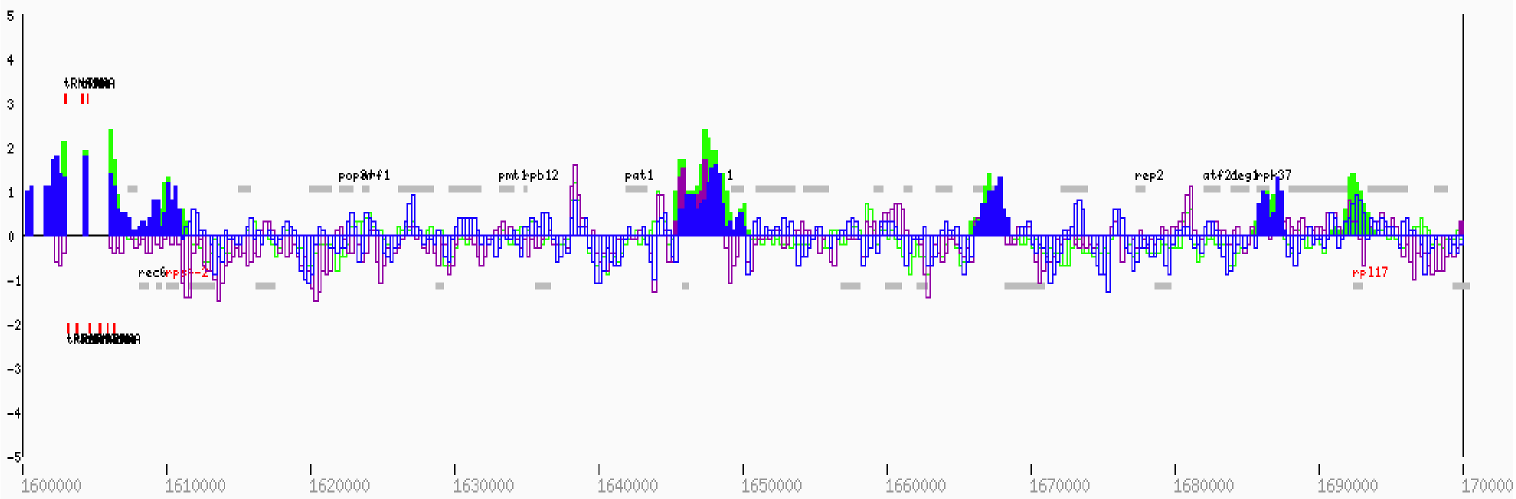
Chromosome 2 (1400000-1500000)



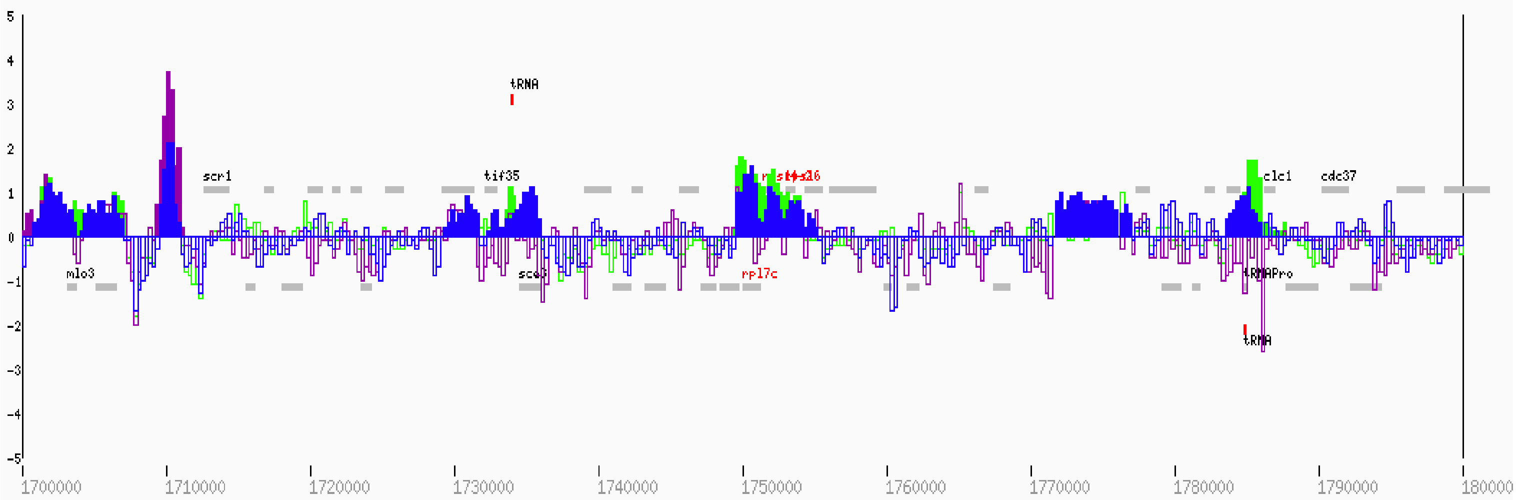
Chromosome 2 (1500000-1600000)



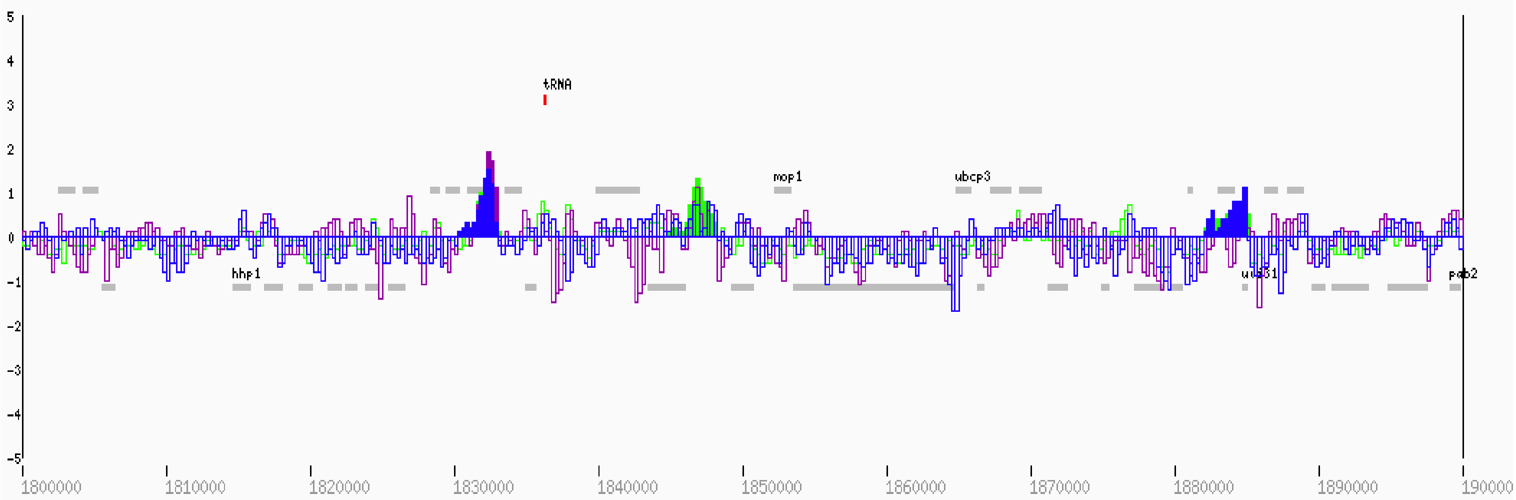
Chromosome 2 (1600000-1700000)



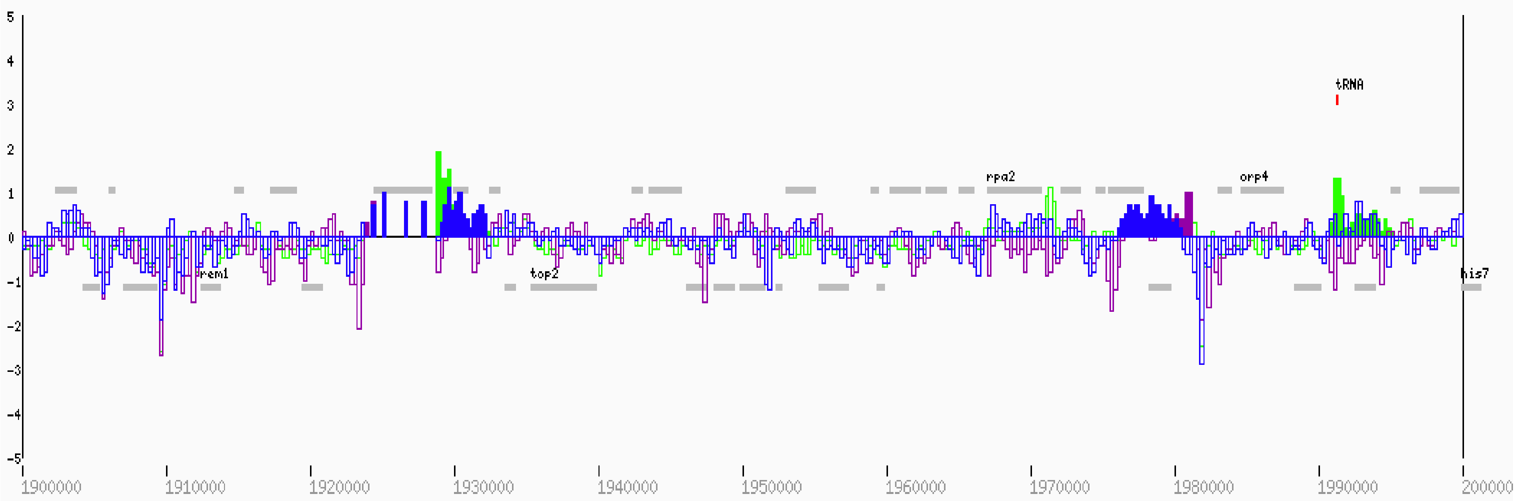
Chromosome 2 (1700000-1800000)



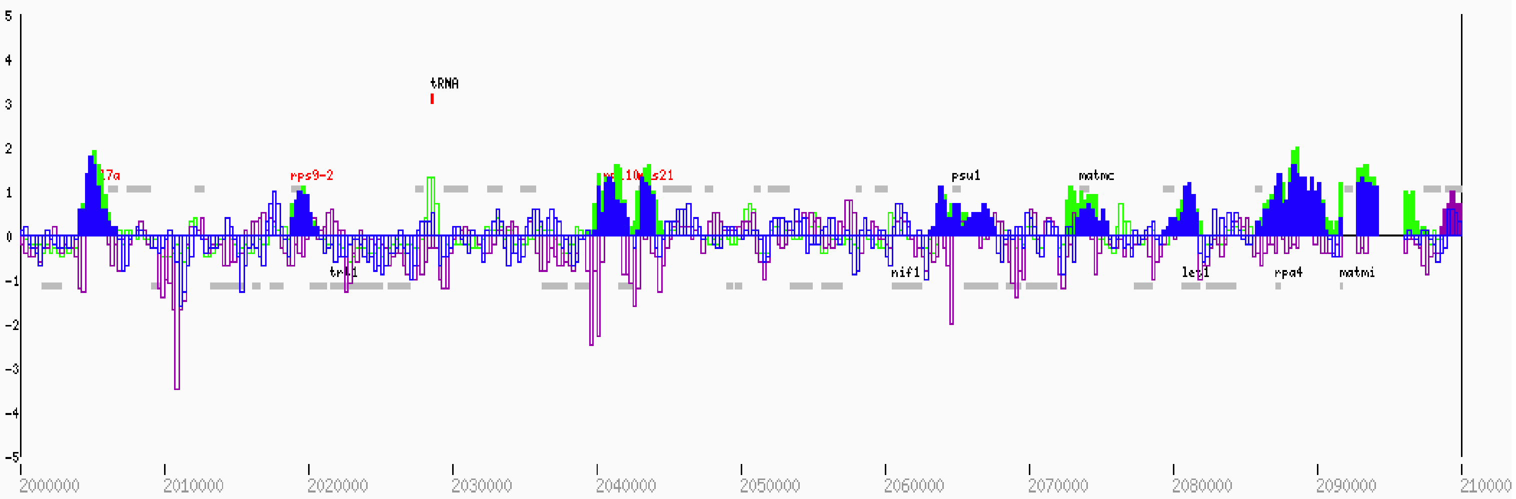
Chromosome 2 (1800000-1900000)



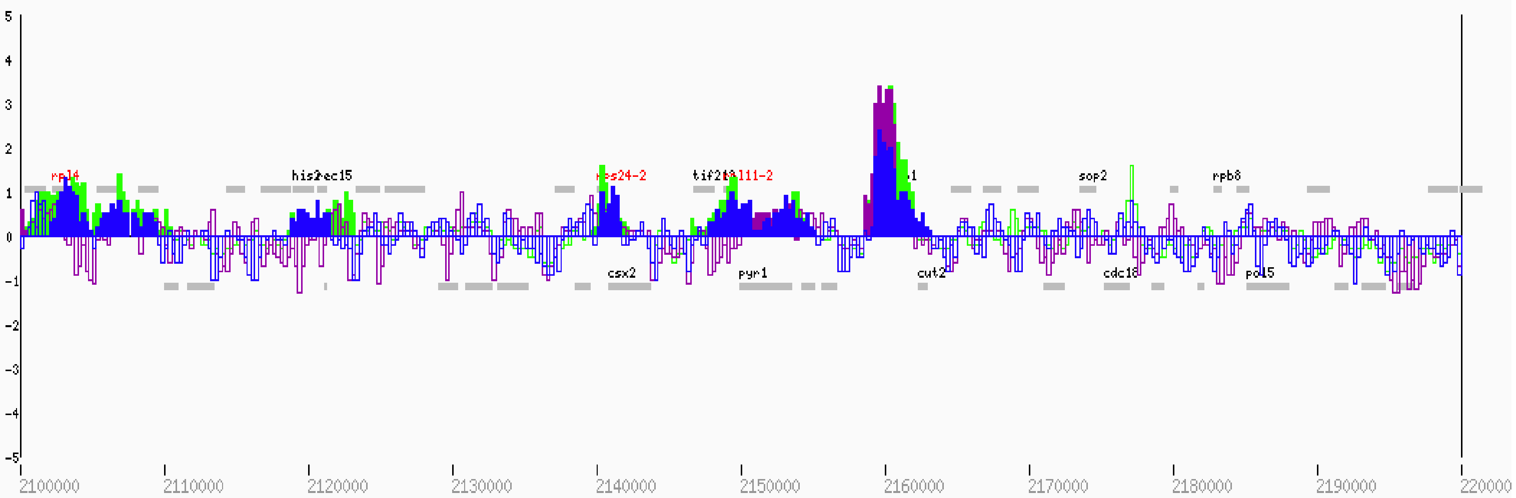
Chromosome 2 (1900000-2000000)



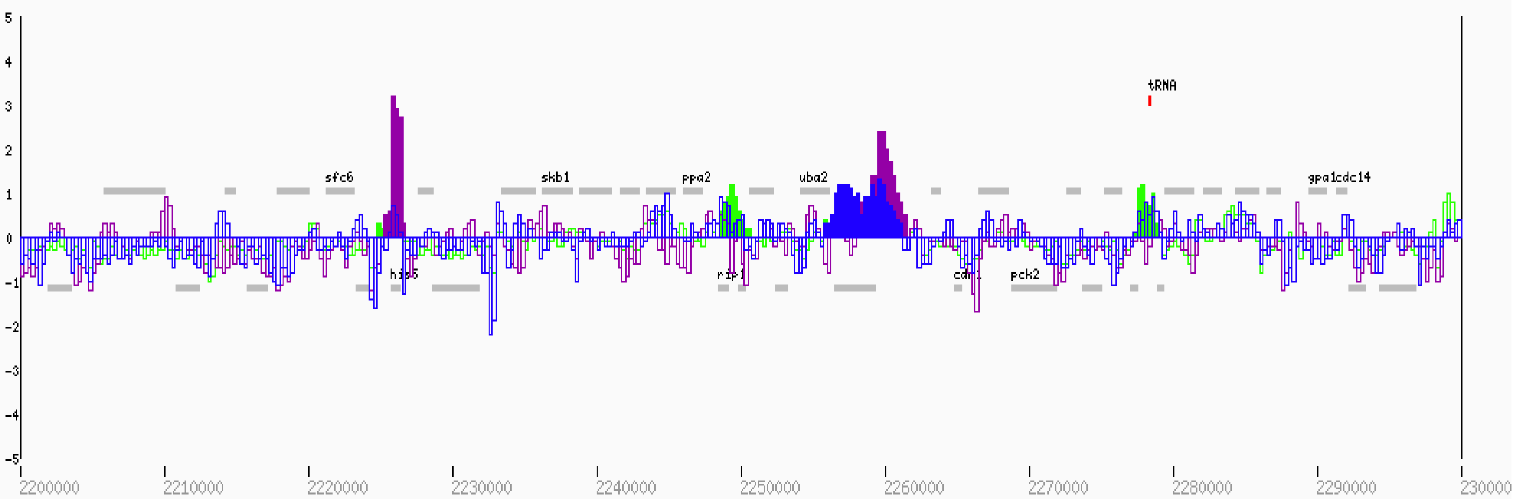
Chromosome 2 (2000000-2100000)



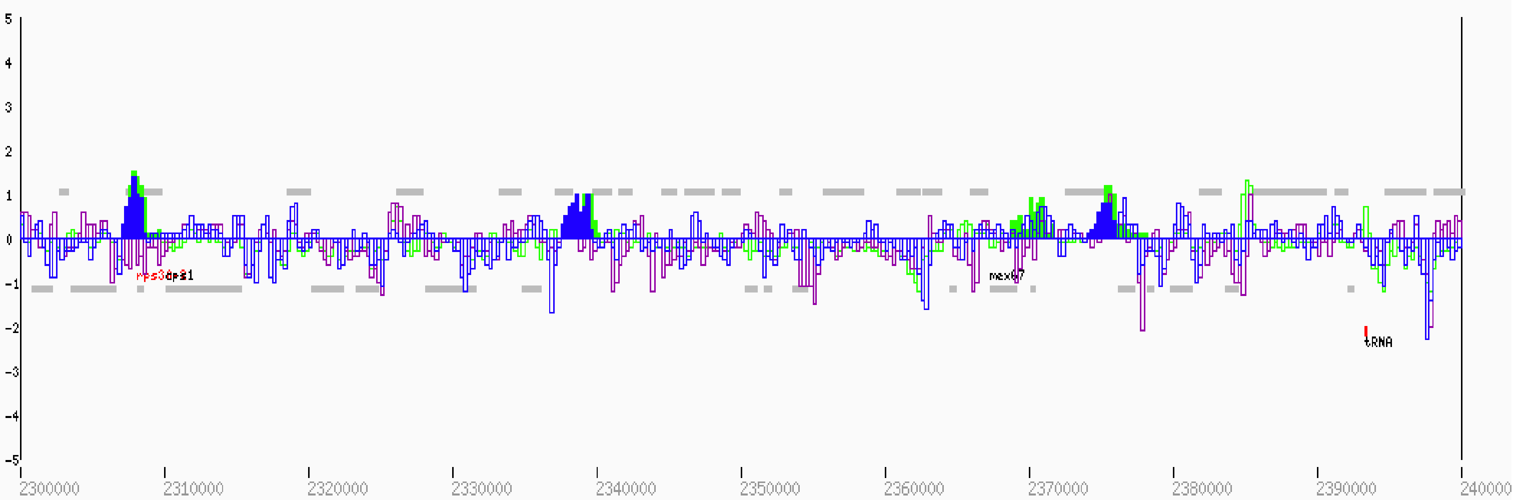
Chromosome 2 (2100000-2200000)



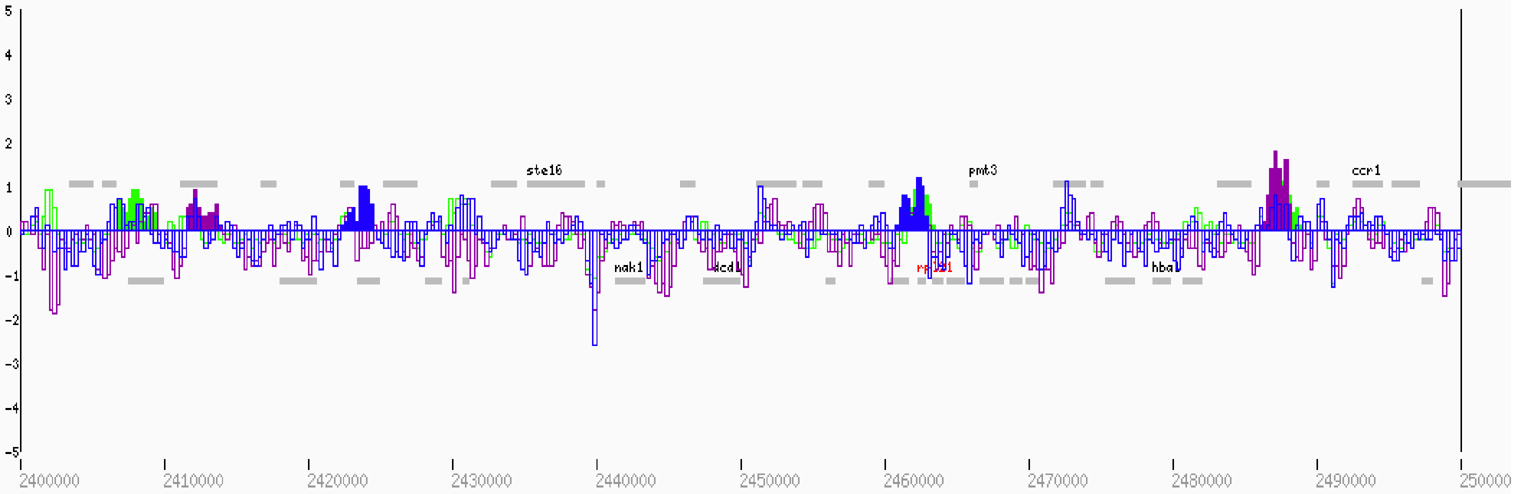
Chromosome 2 (2200000-2300000)



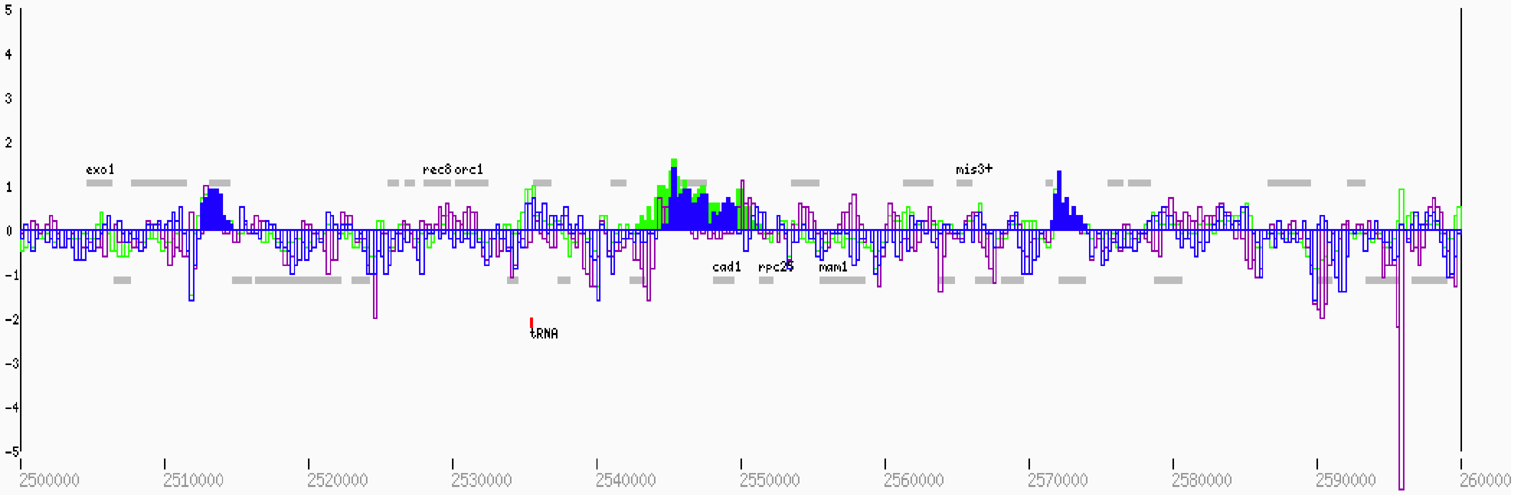
Chromosome 2 (2300000-2400000)



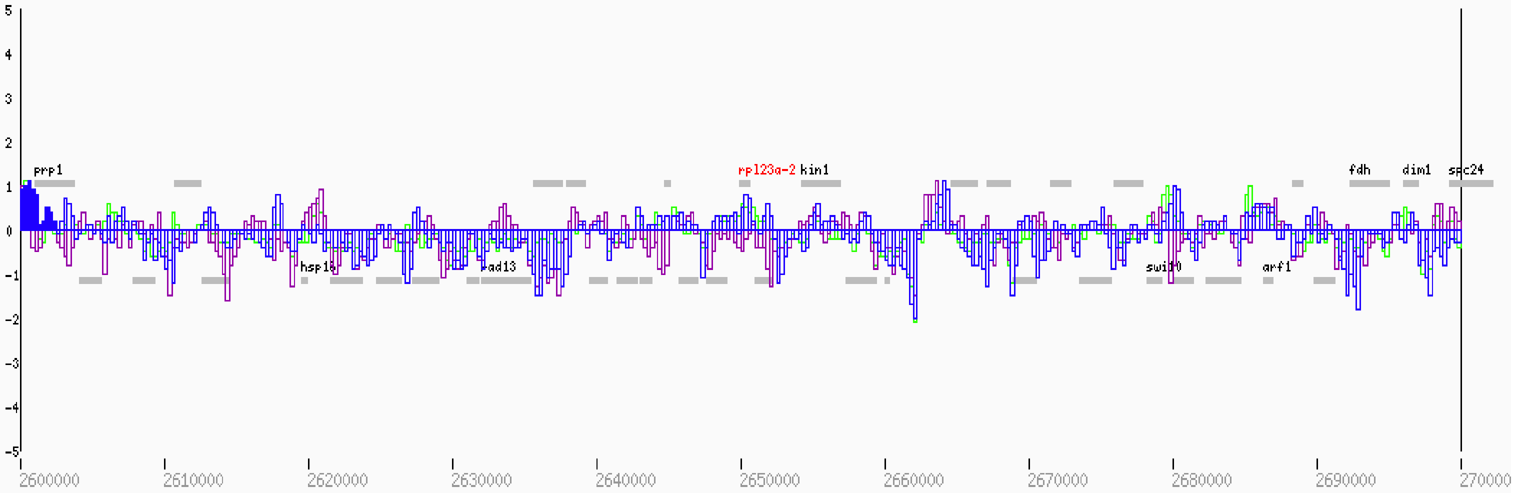
Chromosome 2 (2400000-2500000)



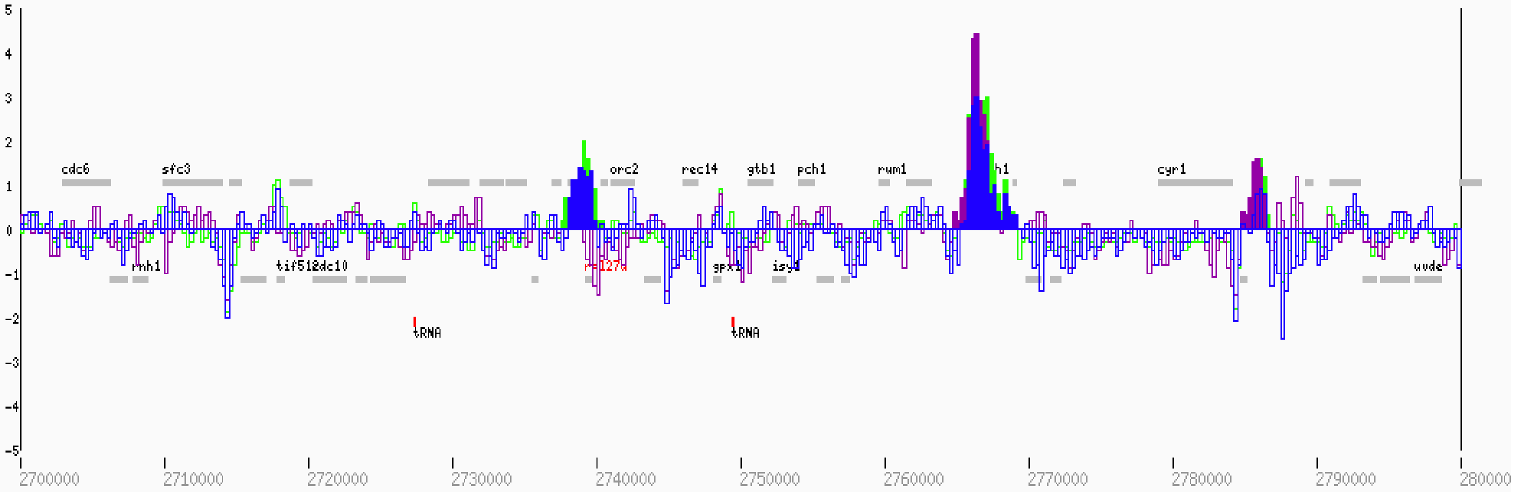
Chromosome 2 (2500000-2600000)



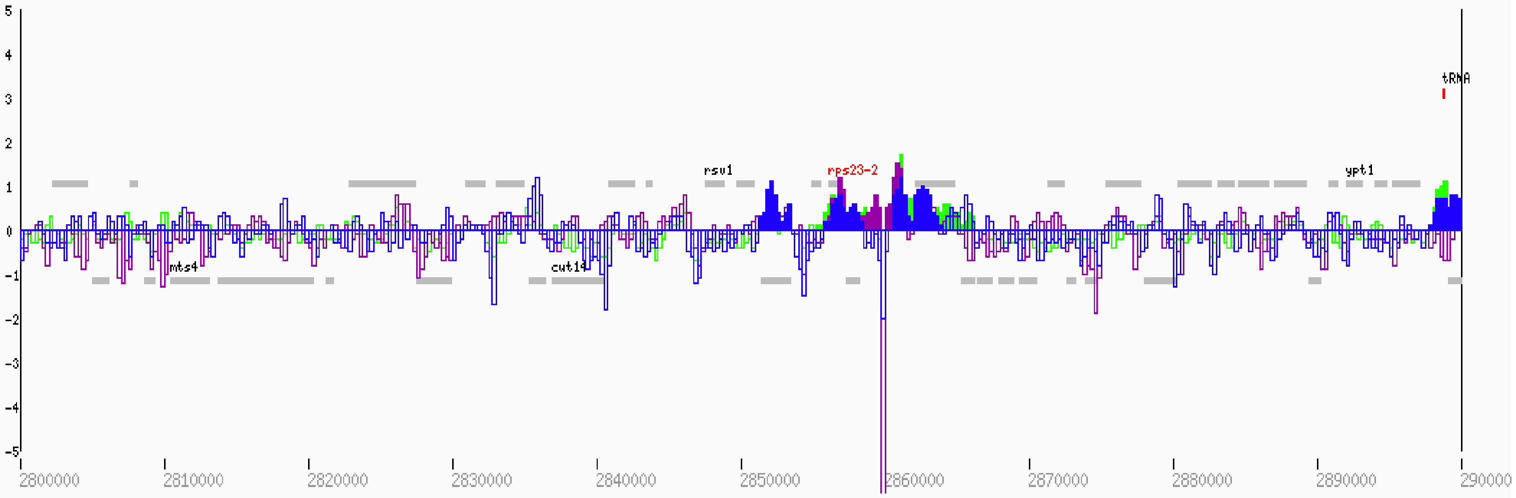
Chromosome 2 (2600000-2700000)



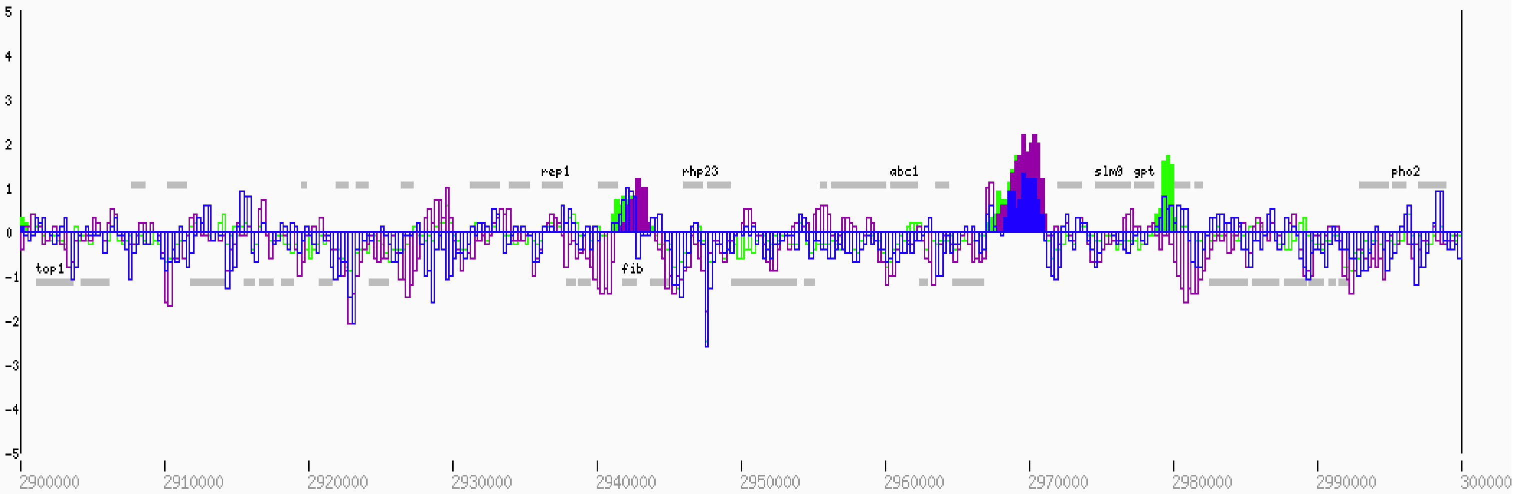
Chromosome 2 (2700000-2800000)



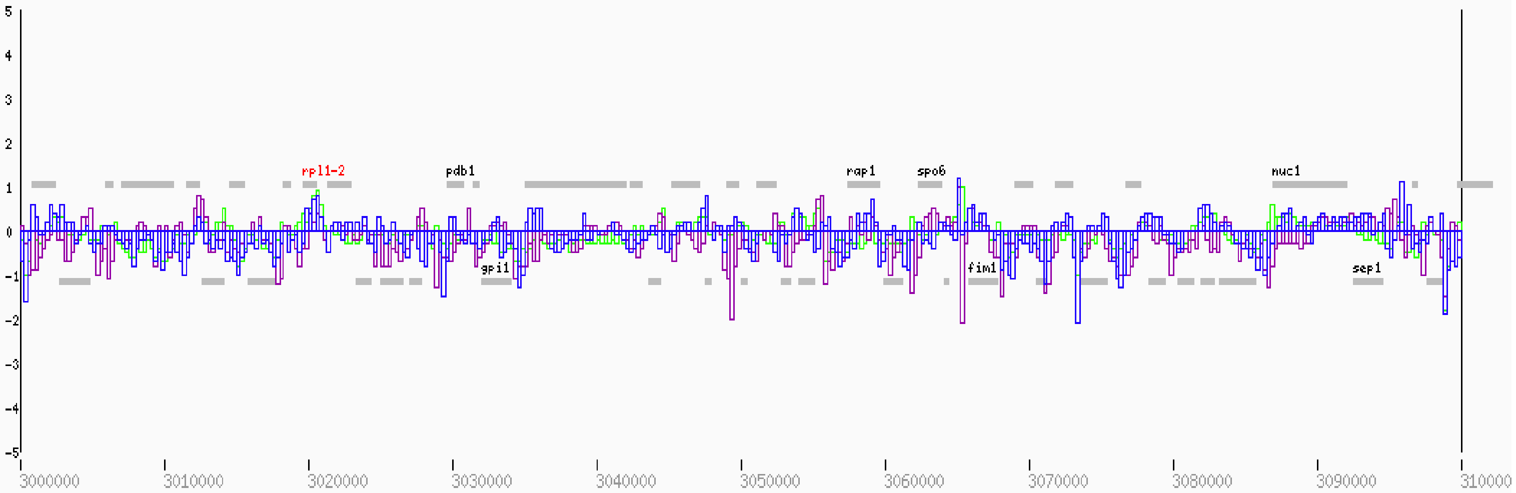
Chromosome 2 (2800000-2900000)



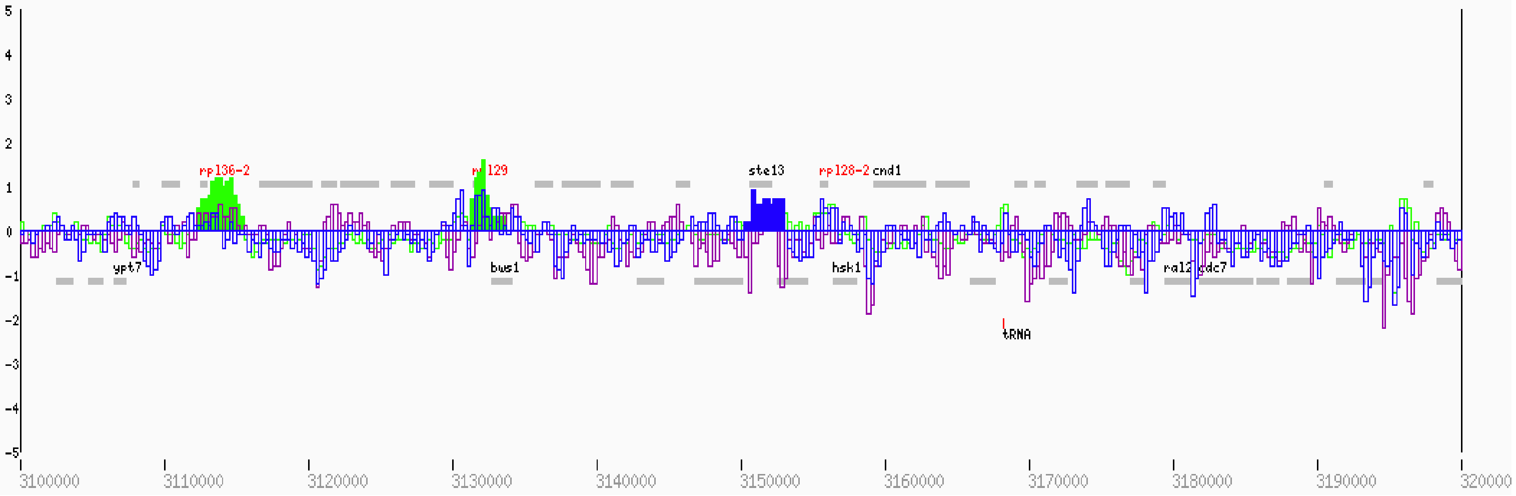
Chromosome 2 (2900000-3000000)



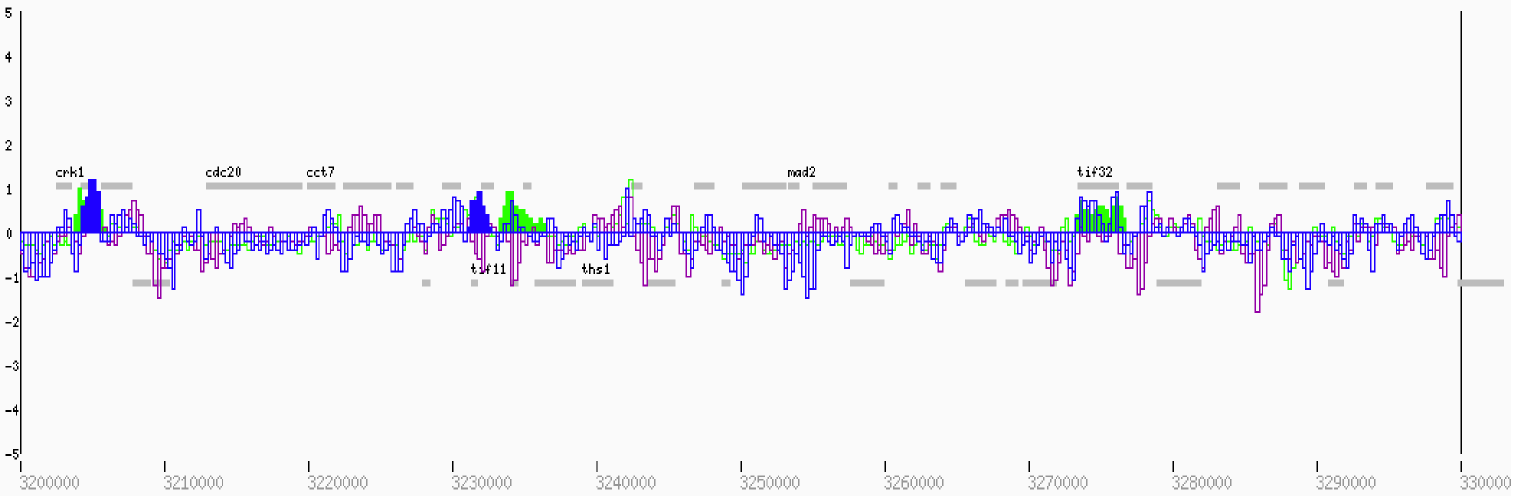
Chromosome 2 (3000000-3100000)



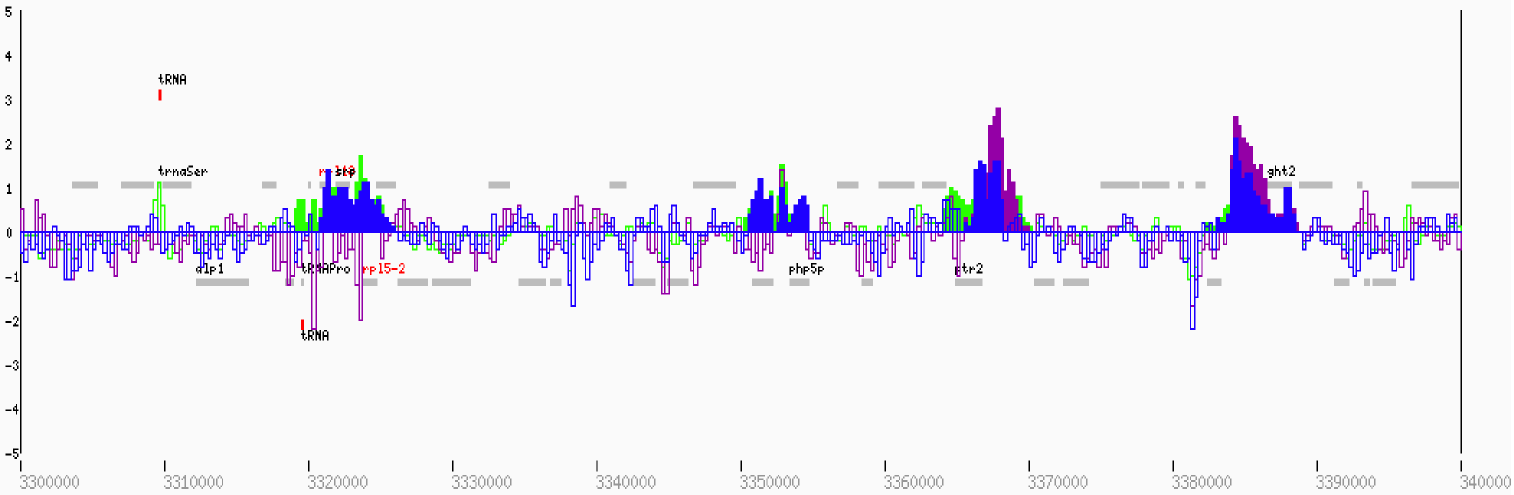
Chromosome 2 (3100000-3200000)



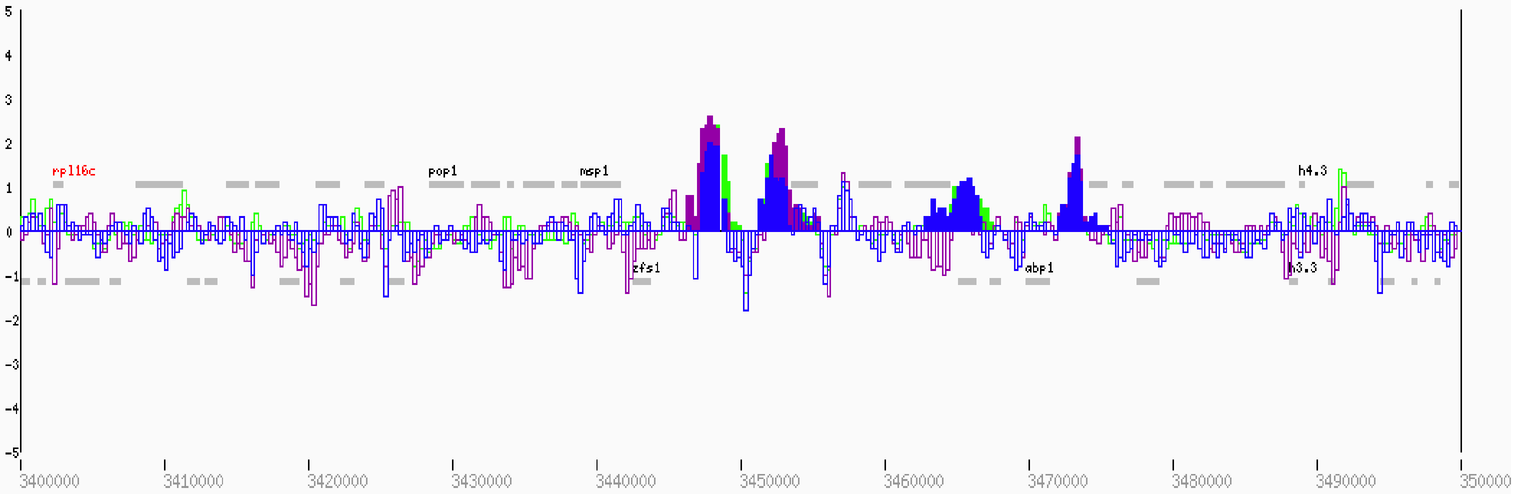
Chromosome 2 (3200000-3300000)



Chromosome 2 (3300000-3400000)



Chromosome 2 (3400000-3500000)



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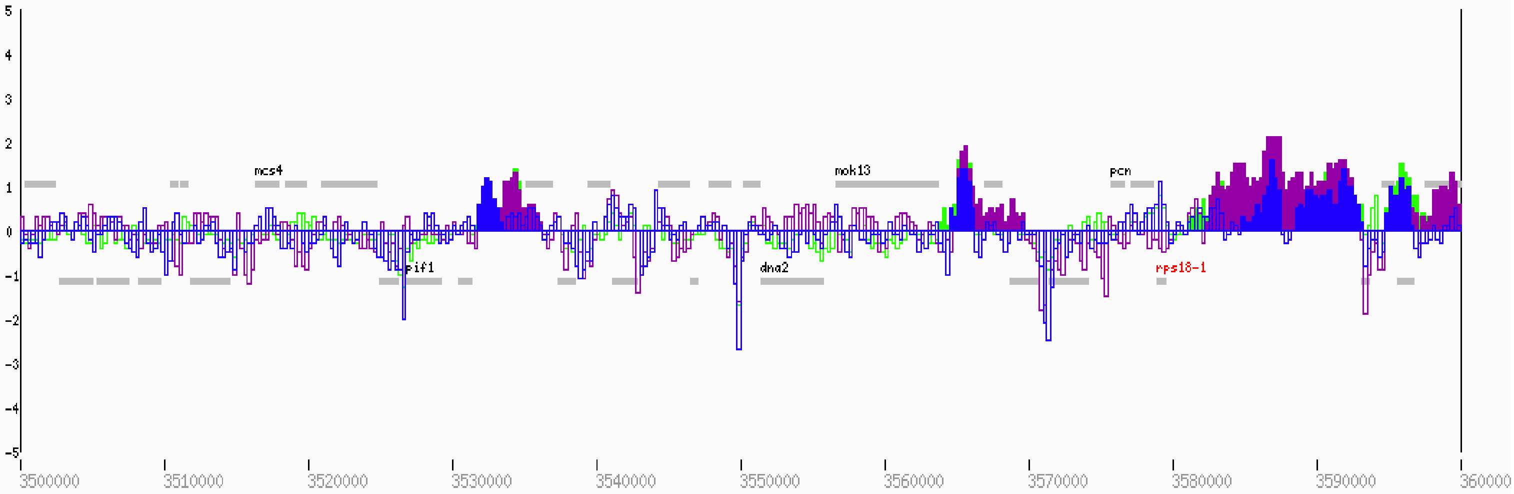

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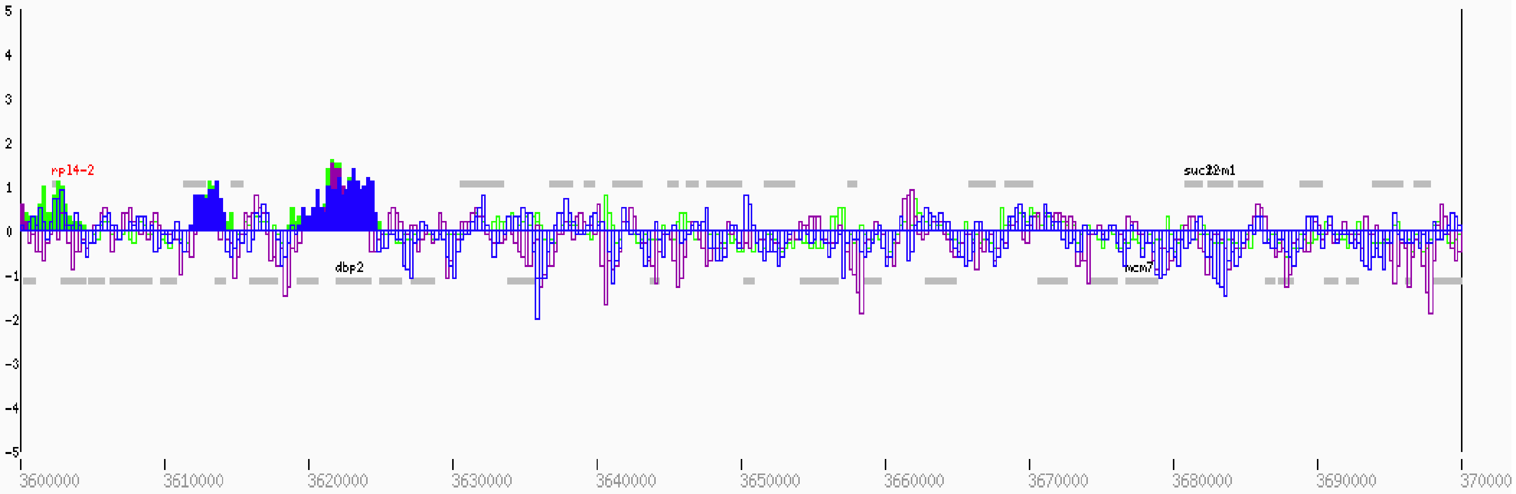
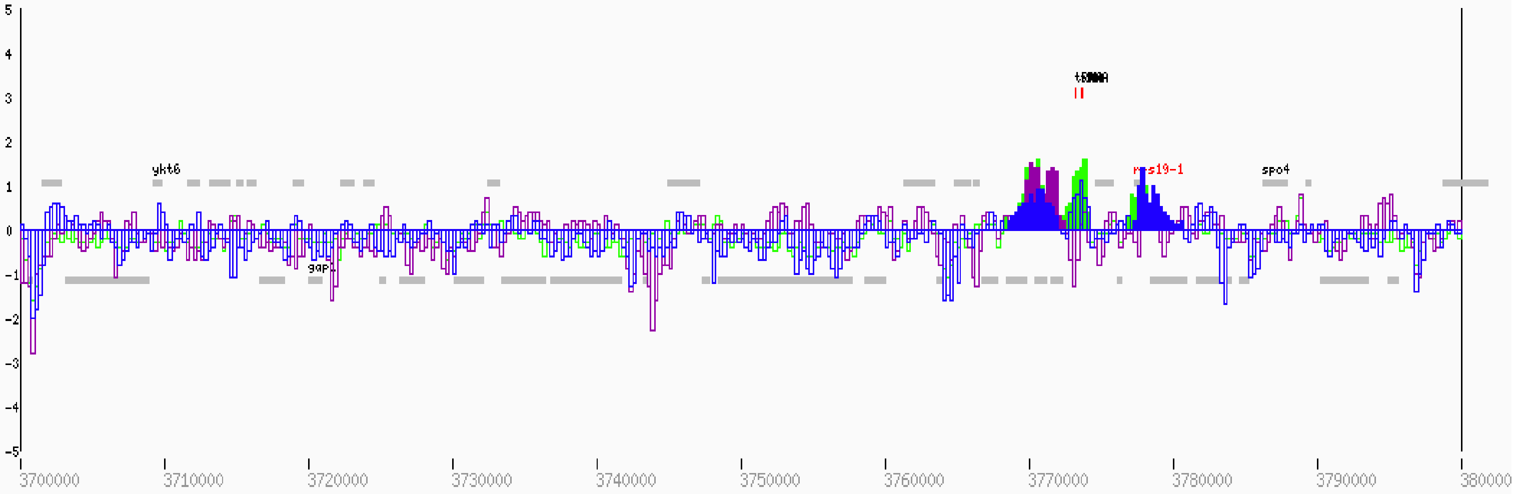
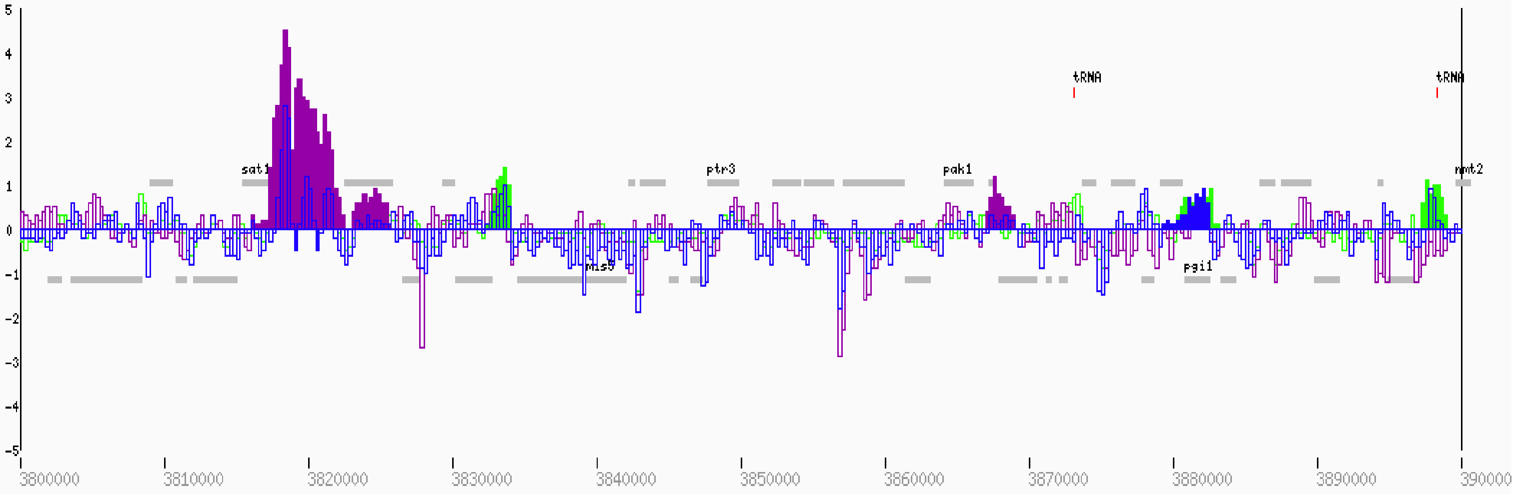


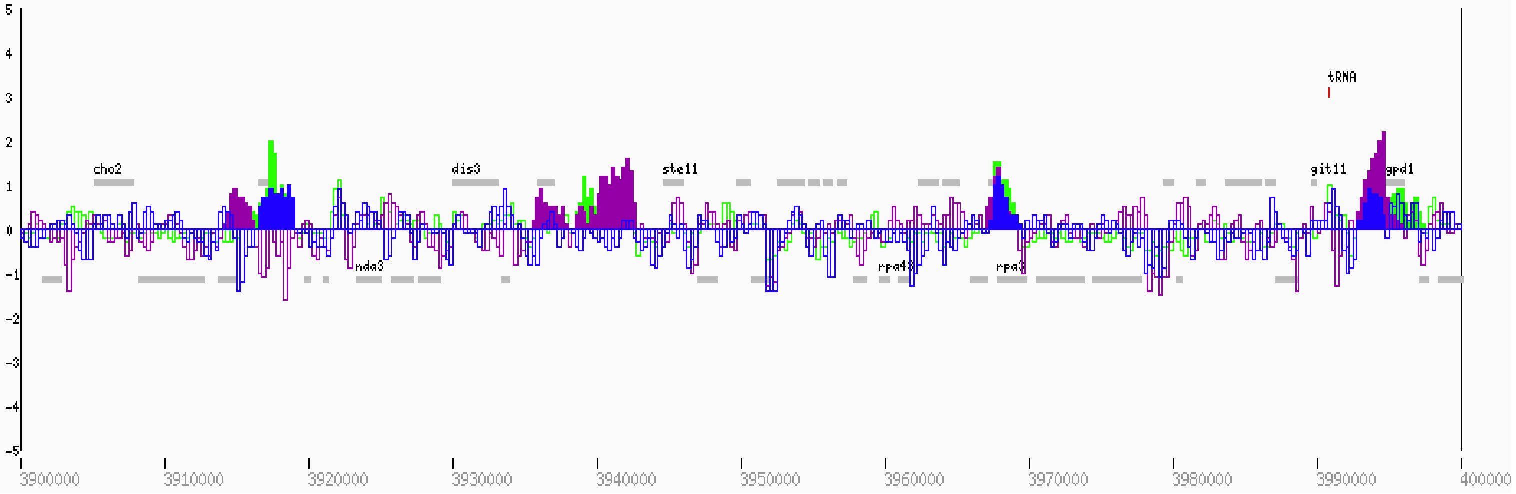
Chromosome 2 (3700000-3800000)



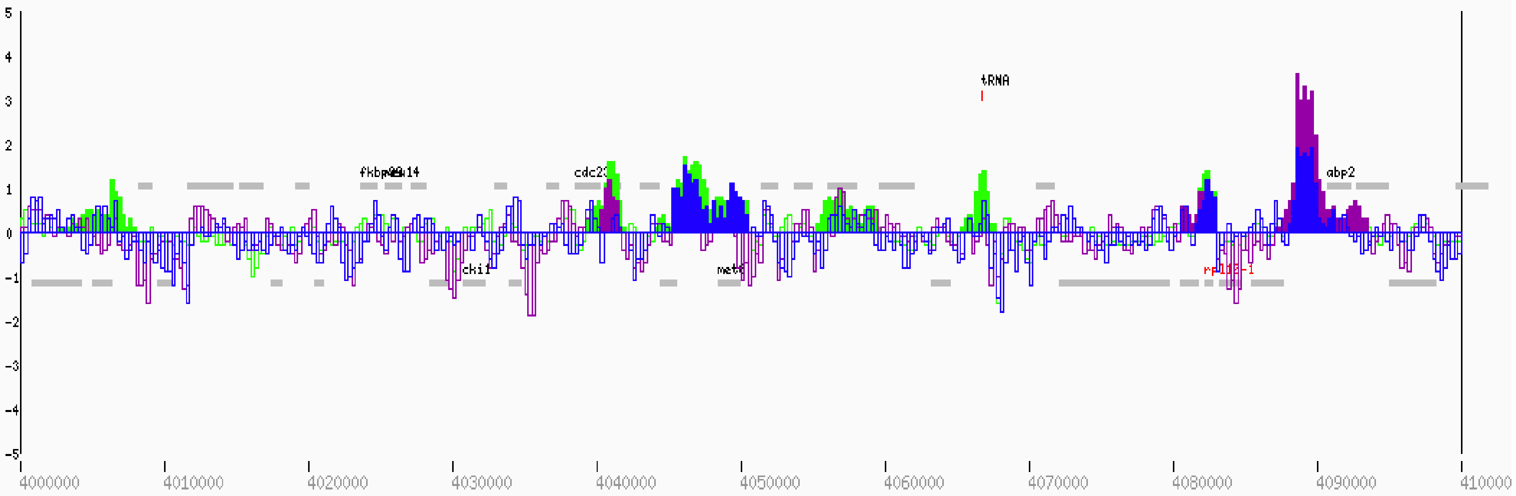
Chromosome 2 (3800000-3900000)



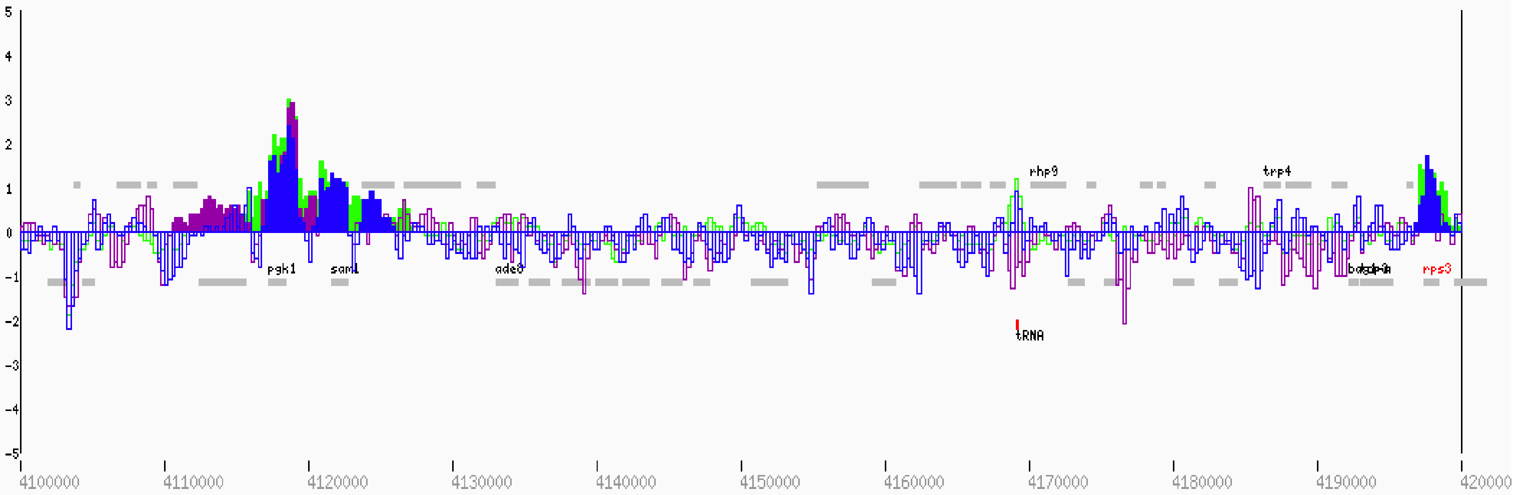
Chromosome 2 (3900000-4000000)



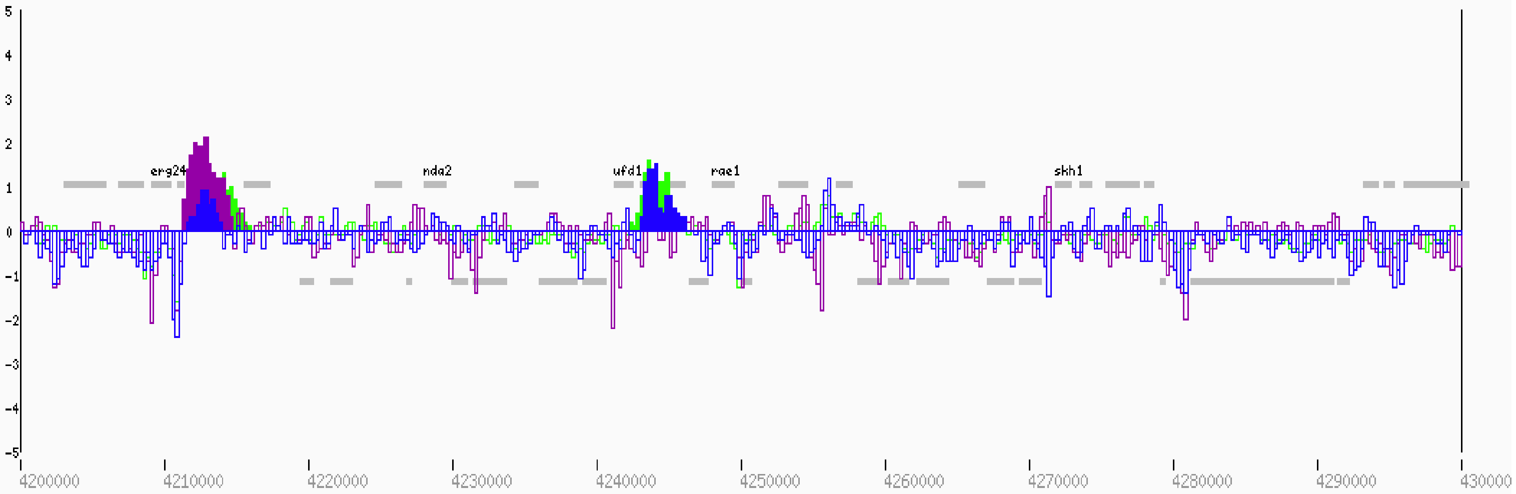
Chromosome 2 (4000000-4100000)



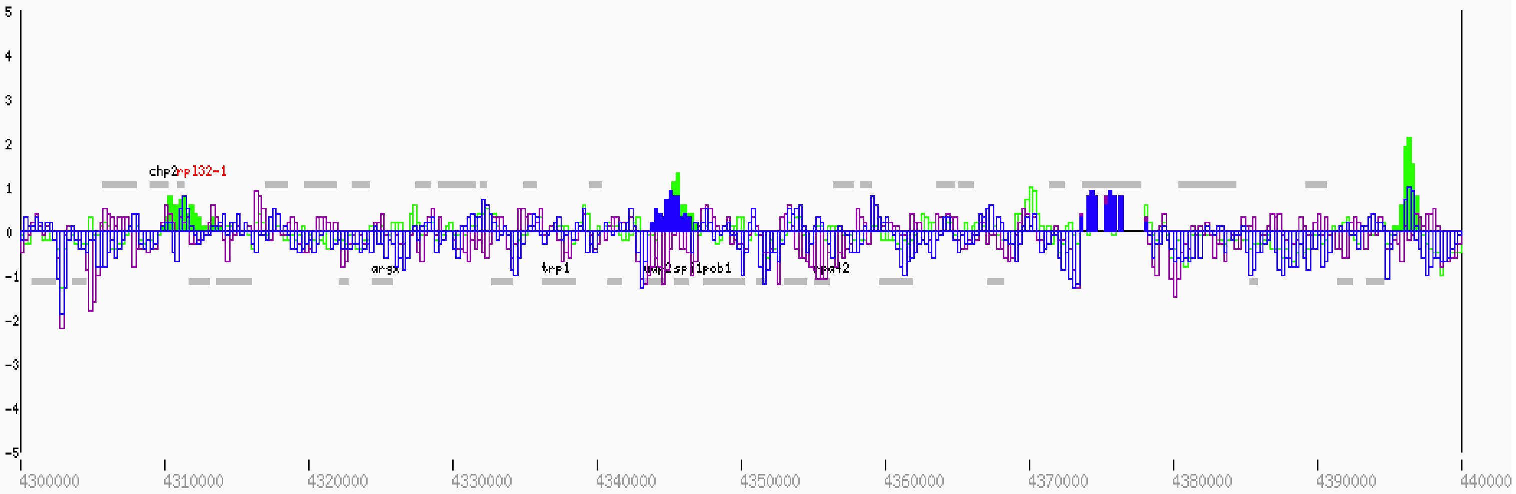
Chromosome 2 (4100000-4200000)

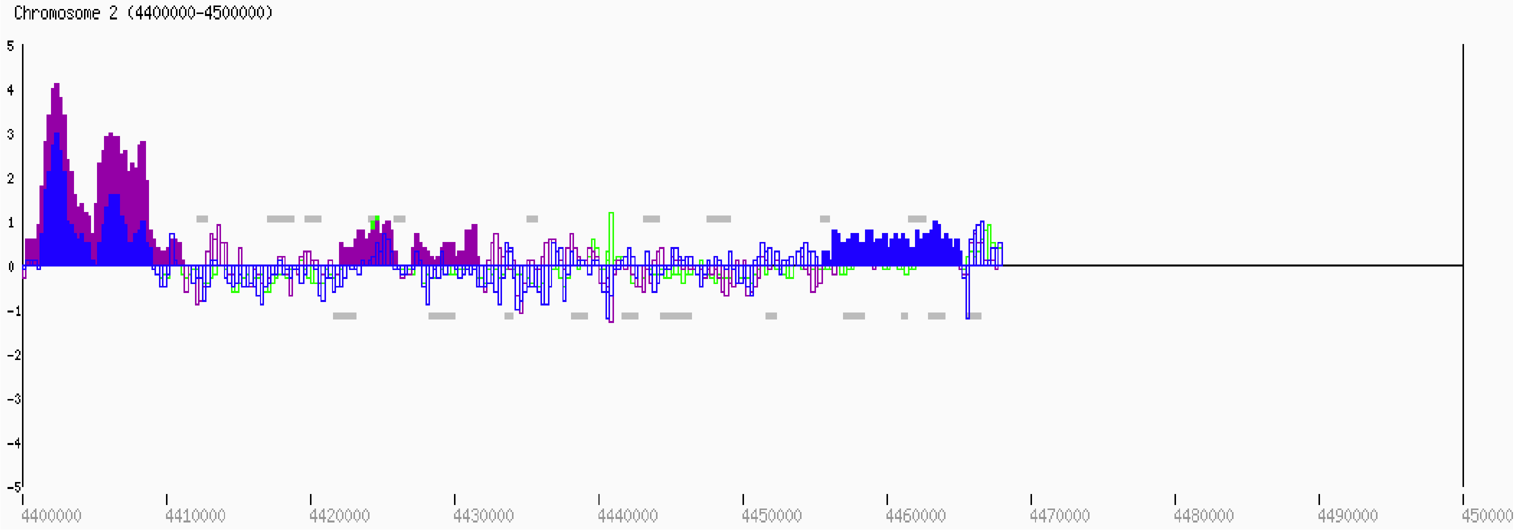


Chromosome 2 (4200000-4300000)



Chromosome 2 (4300000-4400000)




Chromosome 2 (4400000-4500000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
4400000
4410000
4420000
4430000
4440000
4450000
4460000
4470000
4480000
4490000
450000

(b)

Peak No	Midpoint/bp	Avg height	Width/bp
1	12251	0,53	3500
2	101876	0,47	3750
3	136001	0,55	3000
4	178751	1,11	2500
5	205376	0,82	1750
6	246126	0,75	2250
7	332876	0,63	4250
8	385501	0,82	4000
9	490001	0,60	3500
10	496876	0,85	2250
11	636001	0,80	4500
12	656376	0,48	3250
13	675126	0,63	2750
14	803751	0,77	2000
15	1001126	0,71	4750
16	1157376	0,50	4750
17	1298626	0,60	3250
18	1462001	0,53	3000
19	1471626	0,83	1750
20	1505376	0,73	3250
21	1516376	0,88	2750
22	1610001	0,63	3000
23	1667001	0,74	3000
24	1686376	0,66	2250
25	1692626	0,86	2250
26	1734501	0,64	2500
27	1751626	1,16	5250
28	1785376	0,90	2750
29	1847001	0,77	2500
30	2005001	1,18	2500
31	2019626	0,63	2250
32	2042001	0,97	5000
33	2065001	0,51	3000
34	2073501	0,90	2500
35	2080876	0,68	2250
36	2091251	0,96	11500
37	2104126	0,68	10750
38	2121626	0,58	3250
39	2140876	0,61	2750
40	2249501	0,64	2500
41	2278126	0,85	1750
42	2307751	1,03	2000
43	2338751	0,57	2500
44	2375626	0,58	2750
45	2408001	0,56	3000
46	2546876	0,73	8250
47	2738876	0,92	3250
48	2857376	0,53	3750
49	2899126	0,63	2750
50	2979376	1,00	1750
51	3113751	0,86	3500
52	3132376	0,73	2750
53	3204626	0,72	2250
54	3234751	0,45	3500
55	3322126	0,73	6750
56	3351751	0,64	3500
57	3465501	0,59	4000
58	3613251	0,55	3000
59	3777751	0,70	2500
60	3833126	0,98	1750
61	3881376	0,54	2750
62	3898001	0,79	2000
63	3916876	0,79	3750
64	4005251	0,51	4000
65	4047751	0,94	5500
66	4057251	0,58	4500
67	4066501	0,64	2500
68	4197876	1,02	2750
69	4243876	1,11	2750
70	4311126	0,55	2750
71	4345626	0,64	2750
72	4396376	1,13	1750

(c)

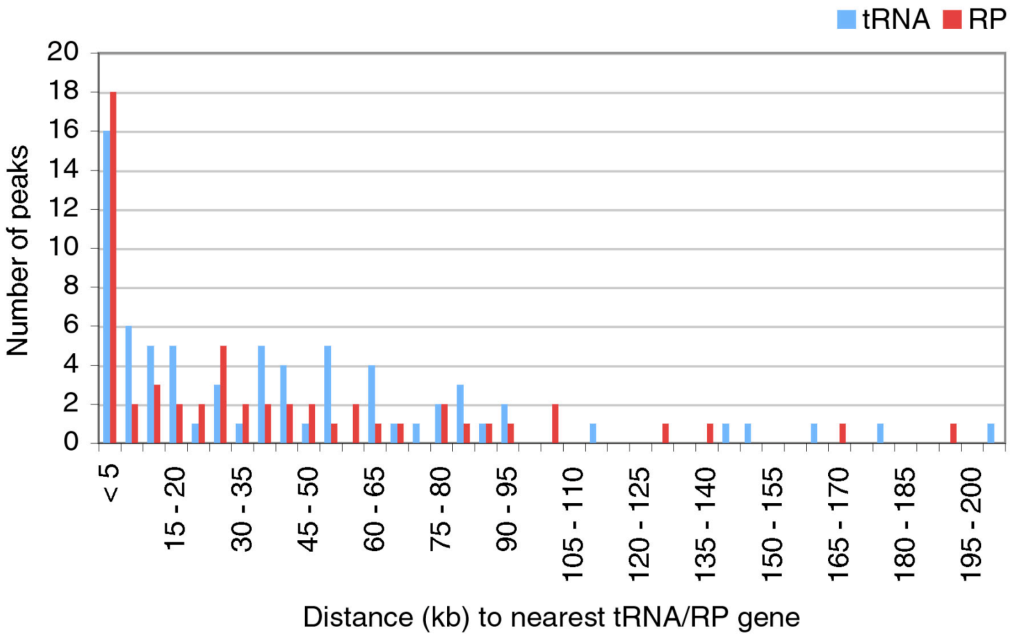
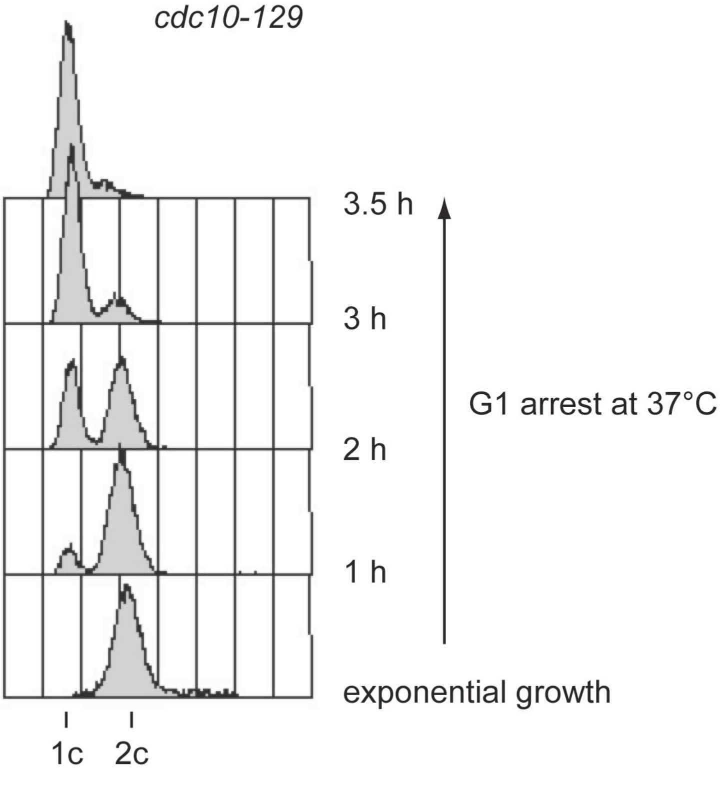

tRNA
RP
Number of peaks
20
18
16
14
12
10
8
6
4
2
0
< 5
15 - 20
30 - 35
45 - 50
60 - 65
75 - 80
90 - 95
105 - 110
120 - 125
135 - 140
150 - 155
165 - 170
180 - 185
195 - 200
Distance (kb) to nearest tRNA/RP gene

Figure S5

Similar Mis4 localization in exponentially growing and in G1 arrested cells. The Mis4 localization pattern along chromosome 2 in exponentially growing cells is compared to the pattern observed in cells arrested in G1 using the *cdc10-129* temperature sensitive mutation. (**a**) Exponentially growing *cdc10-129* cells were shifted to the restrictive temperature of 37°C for 3.5 hours. G1 arrest was confirmed by flow cytometry of DNA content. (**b**) Chromatin immunoprecipitation was performed against epitope-tagged Mis4-Pk_9 from the G1 arrested cells 3.5 hours after temperature shift. The association pattern along chromosome 2 is shown (brown) in comparison to that observed in exponentially growing cells that are predominantly in the G2 phase of the cell cycle (geen, data reproduced from Figure S4).

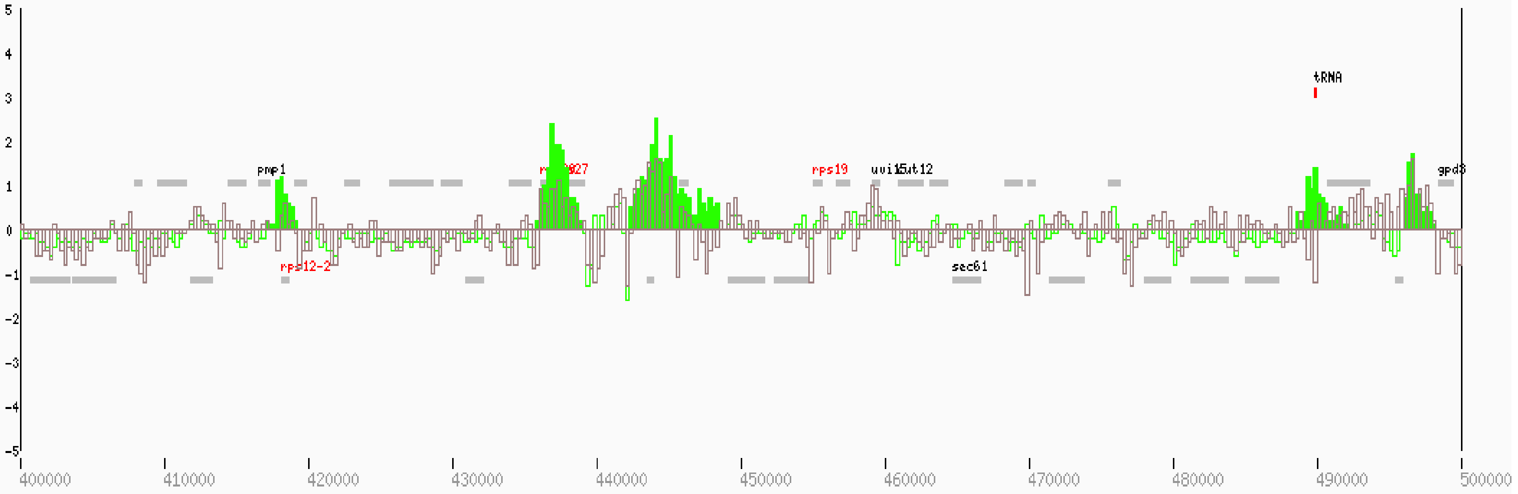
(a)



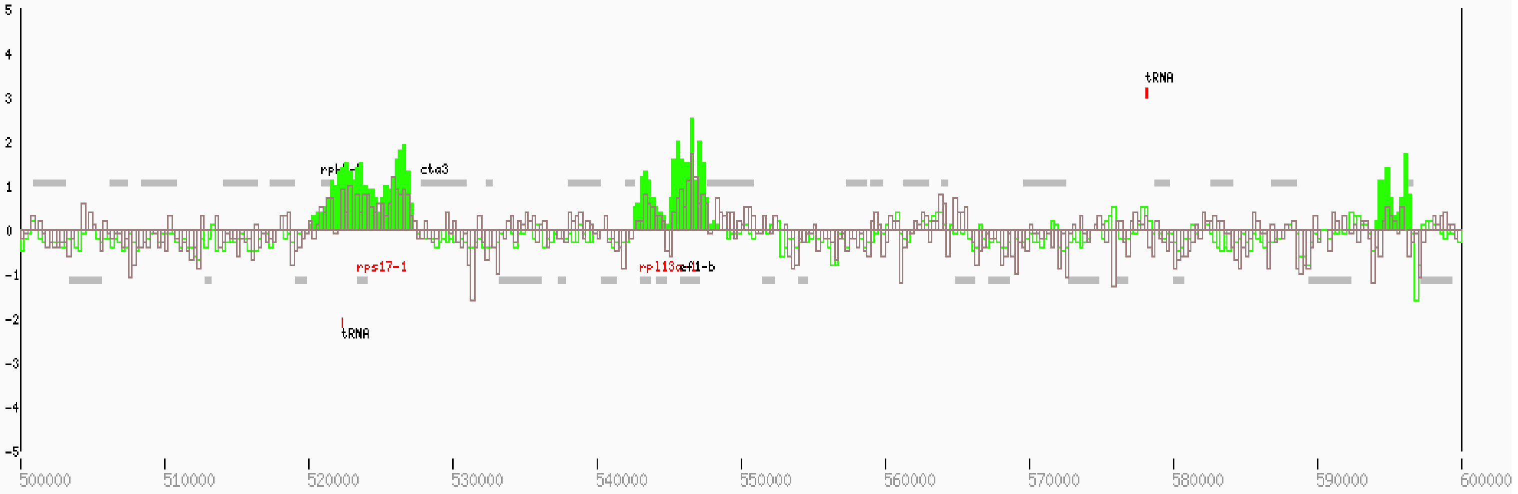
(b)


Chromosome 2 (0-100000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
0
10000
20000
30000
40000
50000
60000
70000
80000
90000
100000
ght4
frp1
zas1
Chromosome 2 (100000-200000)
100000
110000
120000
130000
140000
150000
160000
170000
180000
190000
200000
tRNA
ubc16
ntp1
mik1
clr3
sum2
ras1
pgak2
tRNA
tRNA
Chromosome 2 (200000-300000)
200000
210000
220000
230000
240000
250000
260000
270000
280000
290000
300000
tRNA
tRNA
tRNA
arg7
ada1
tms1
sbp1
car1
kes1
stt3
tRNA
tRNA
Chromosome 2 (300000-400000)
300000
310000
320000
330000
340000
350000
360000
370000
380000
390000
400000
tRNA
cct4
cut4
pka1
idi1
PBC582.01
cdc13
cdt1
pho4
clr4

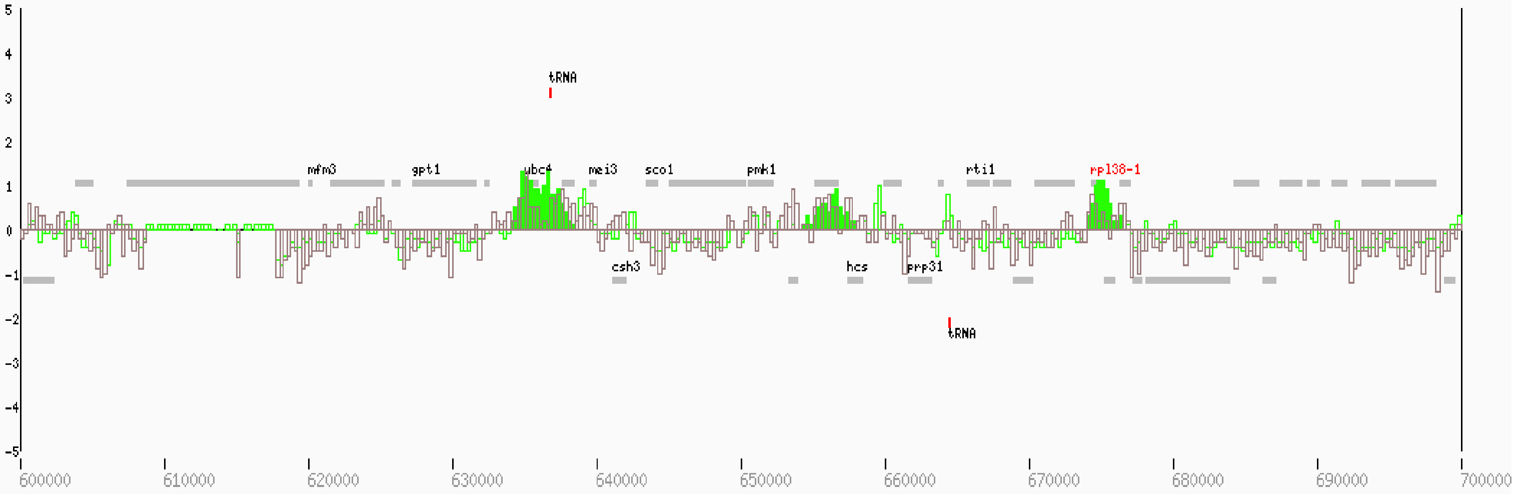
Chromosome 2 (400000-500000)



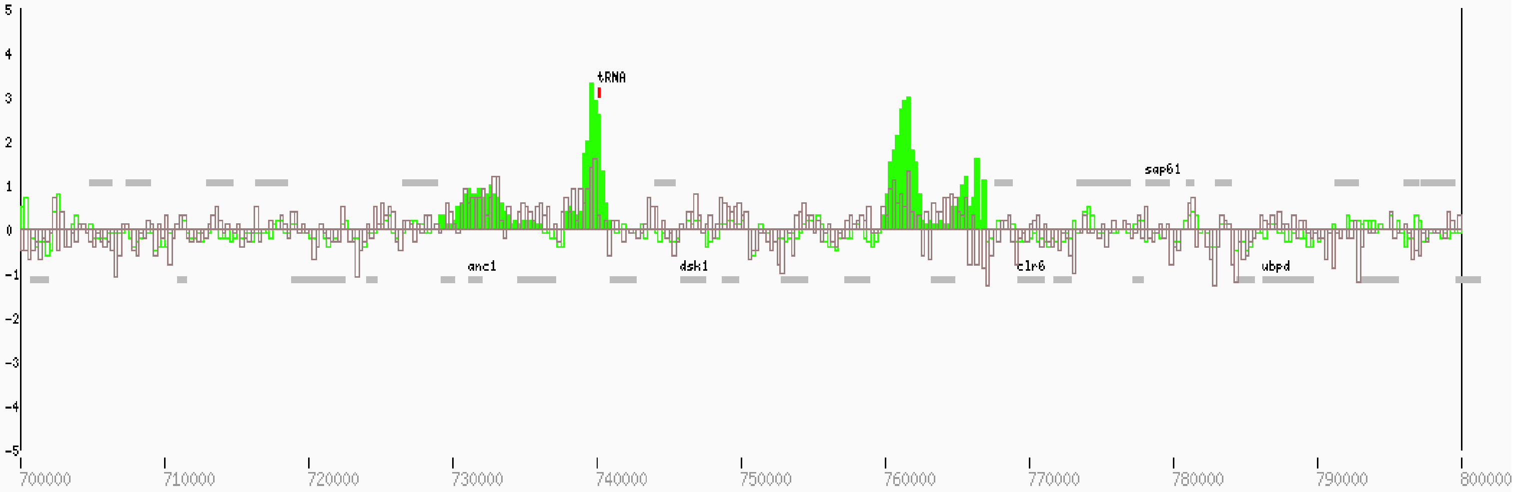
Chromosome 2 (500000-600000)



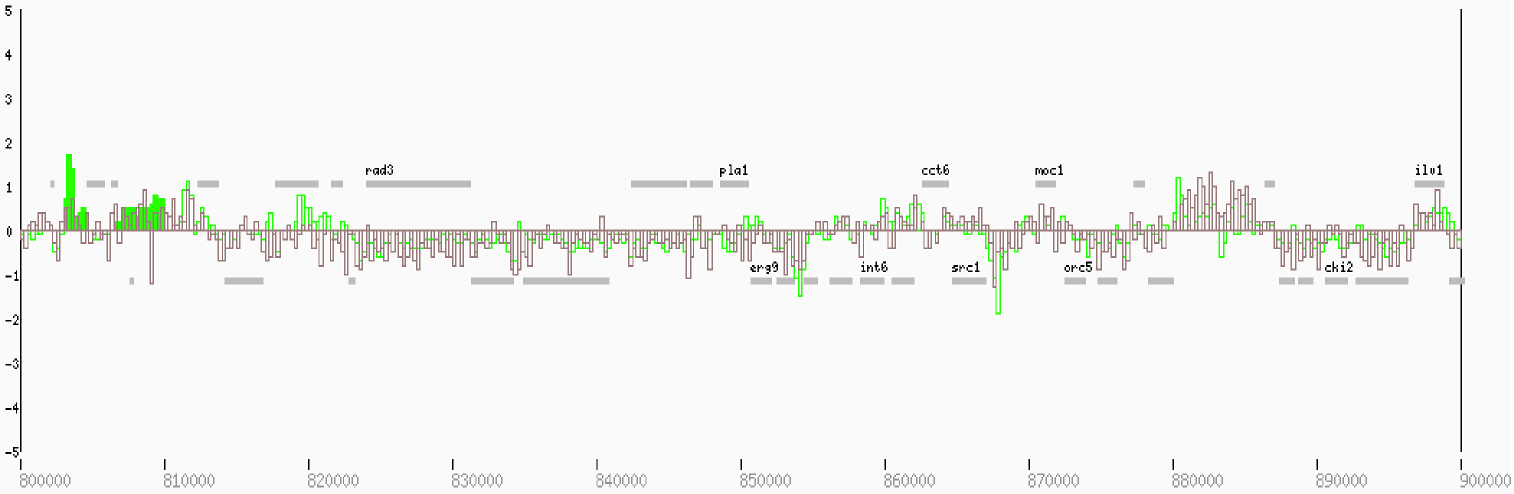
Chromosome 2 (600000-700000)



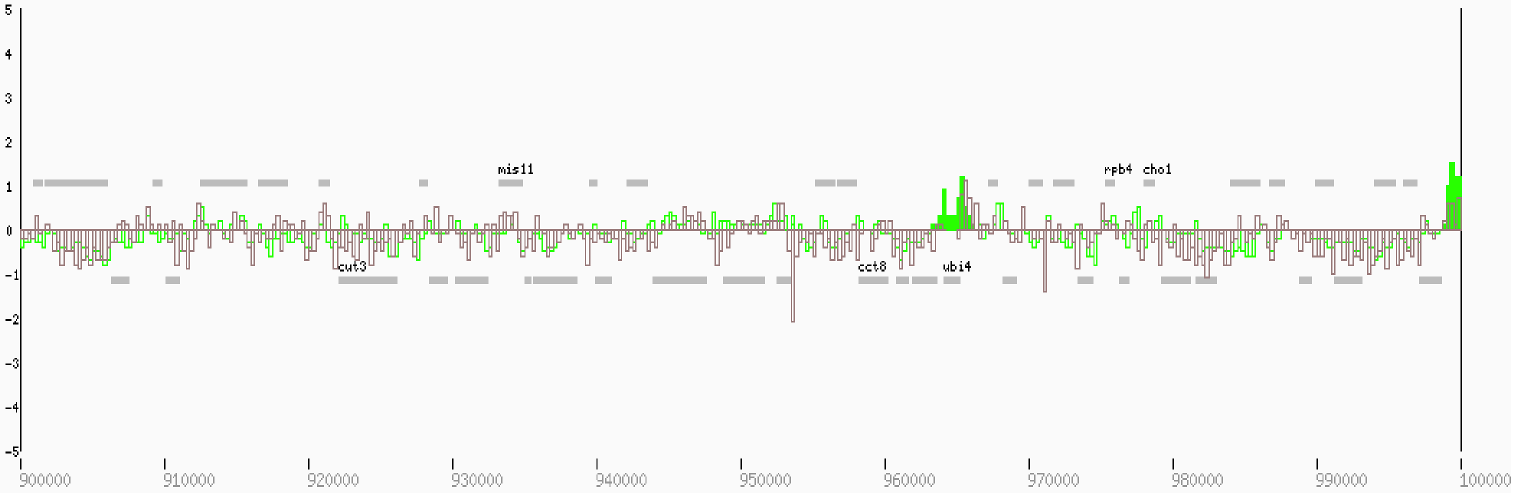
Chromosome 2 (700000-800000)



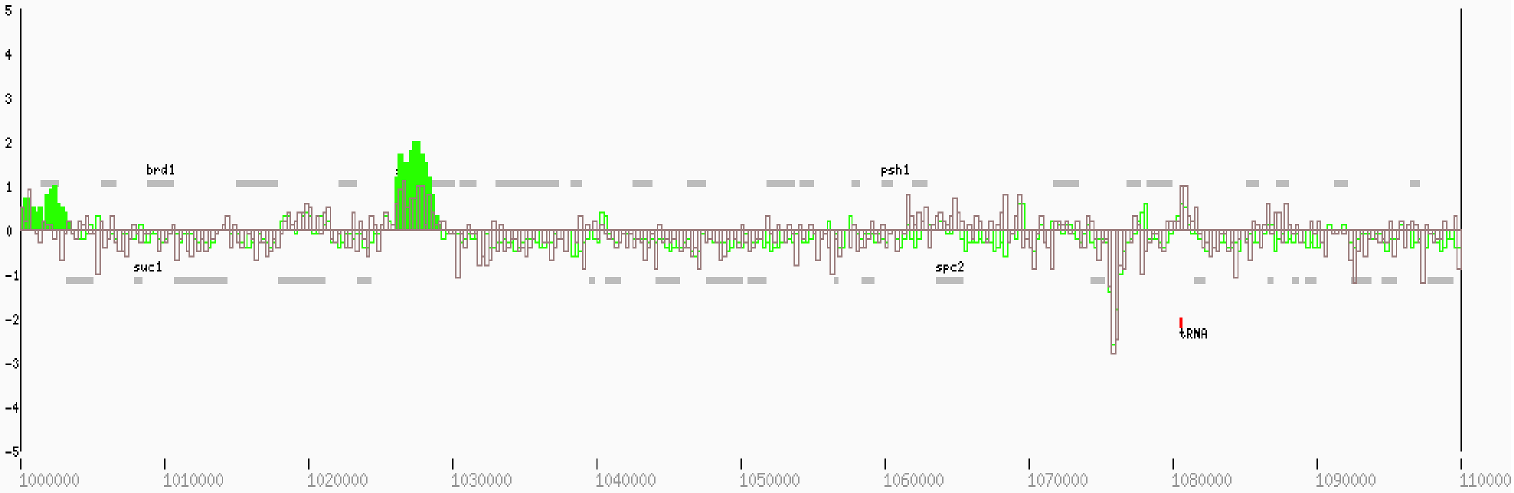
Chromosome 2 (800000-900000)



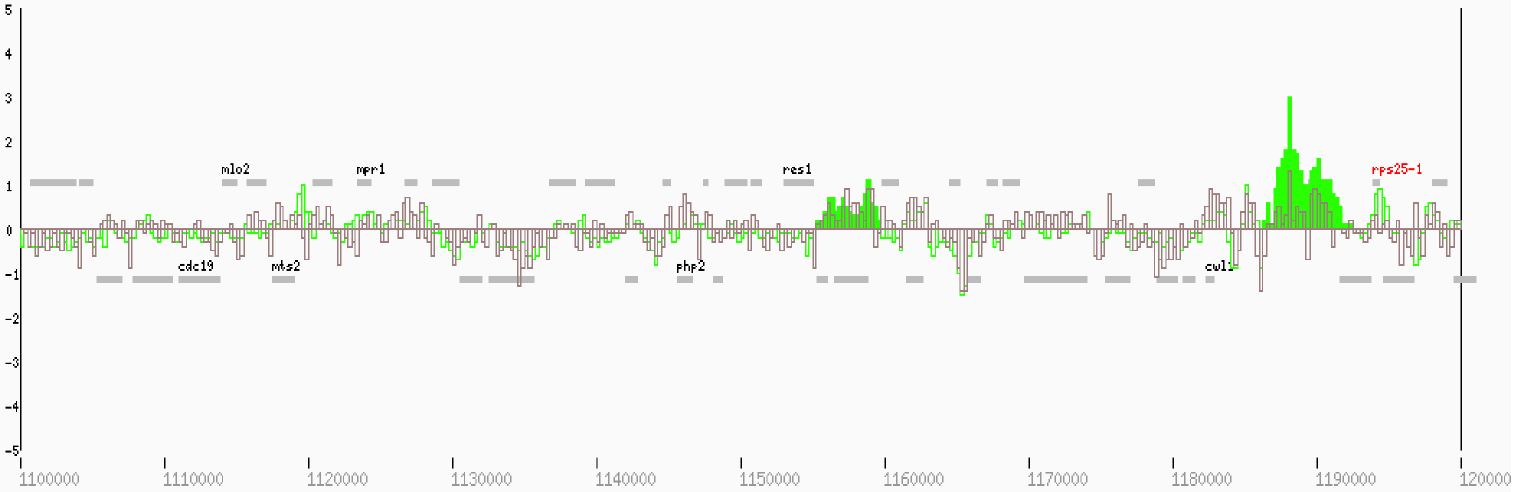
Chromosome 2 (900000-1000000)



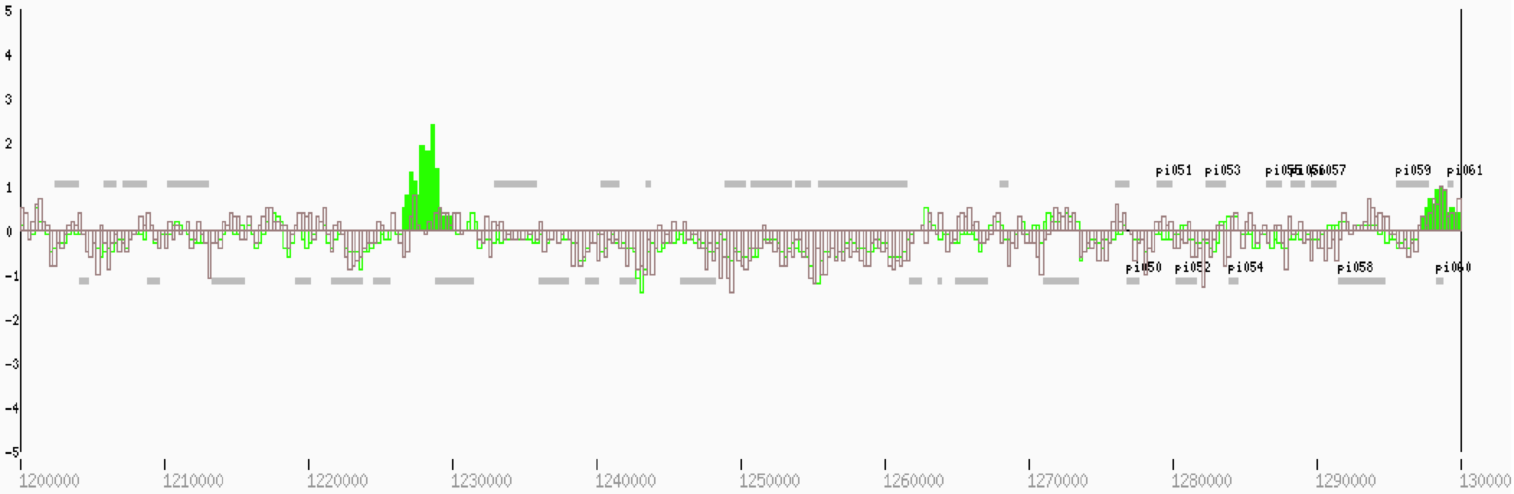
Chromosome 2 (1000000-1100000)



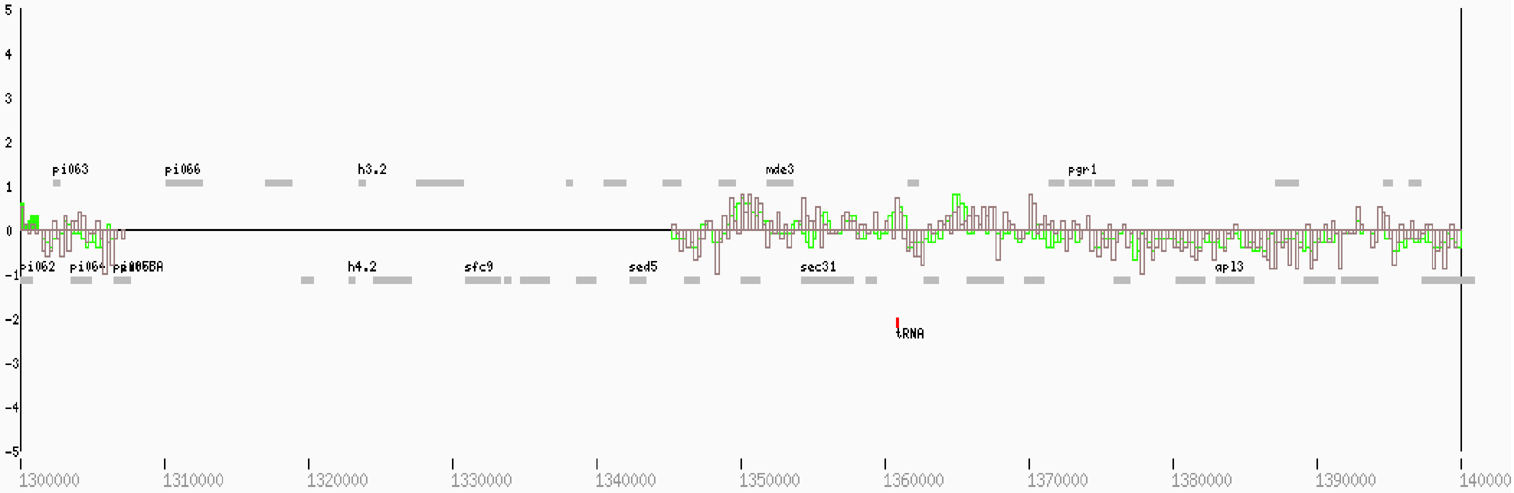
Chromosome 2 (1100000-1200000)



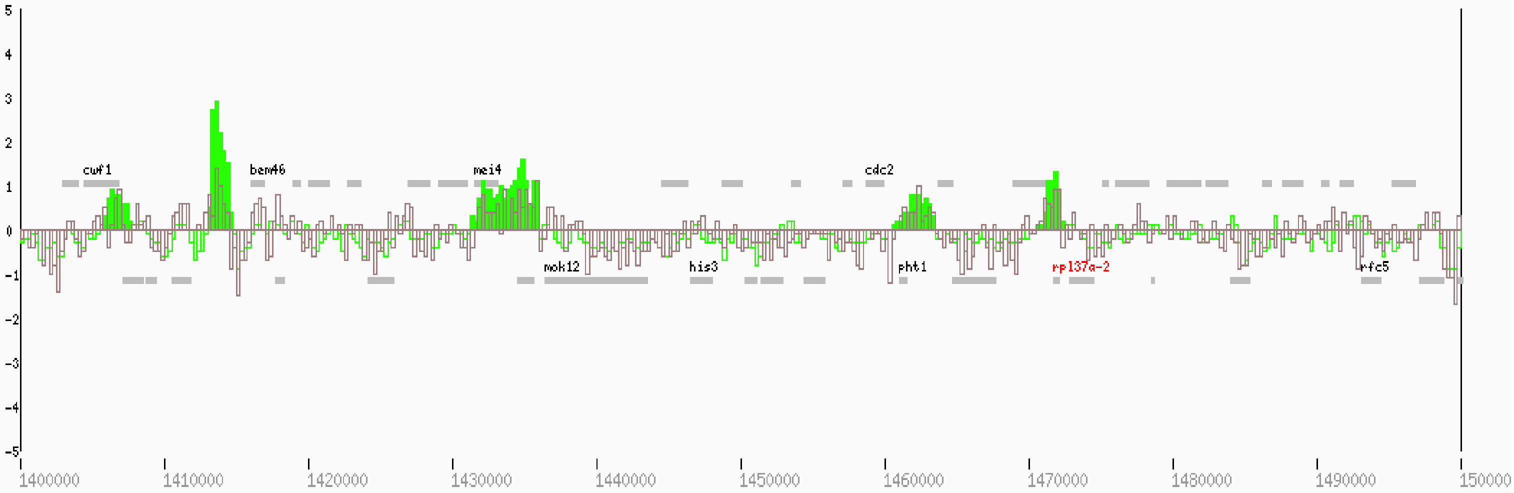
Chromosome 2 (1200000-1300000)



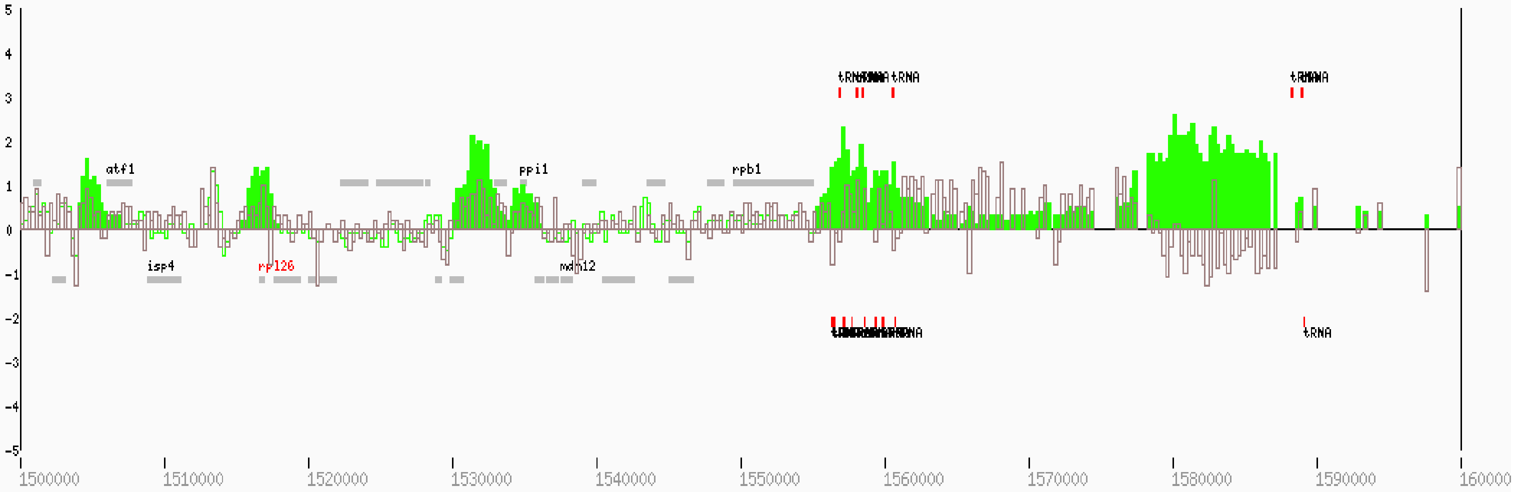
Chromosome 2 (1300000-1400000)



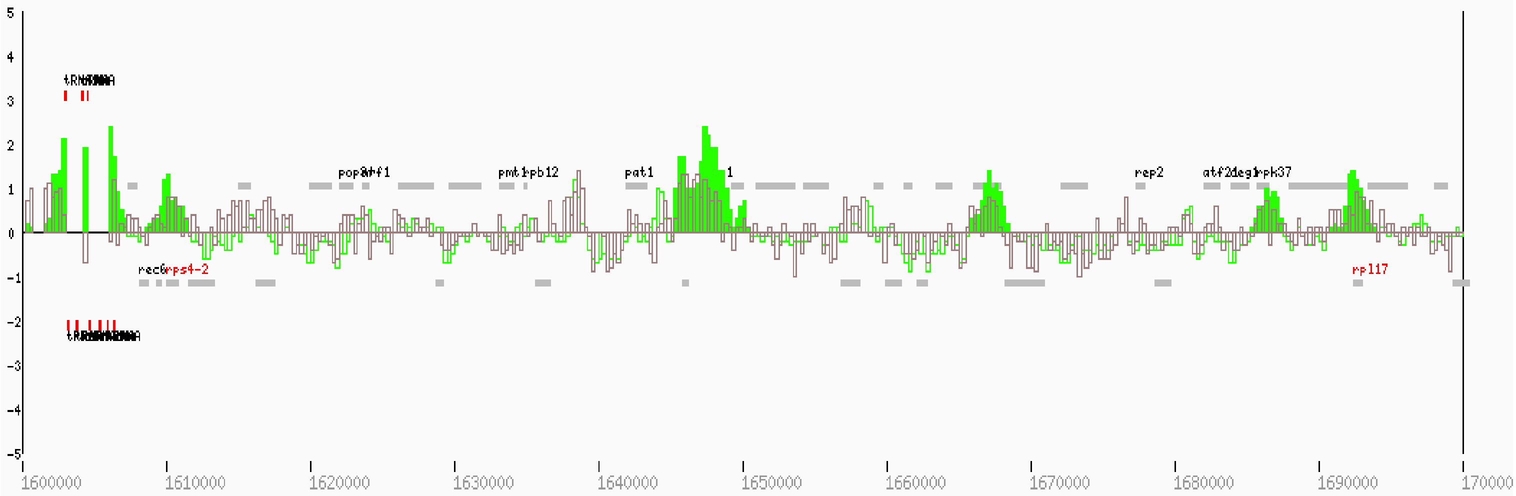
Chromosome 2 (1400000-1500000)



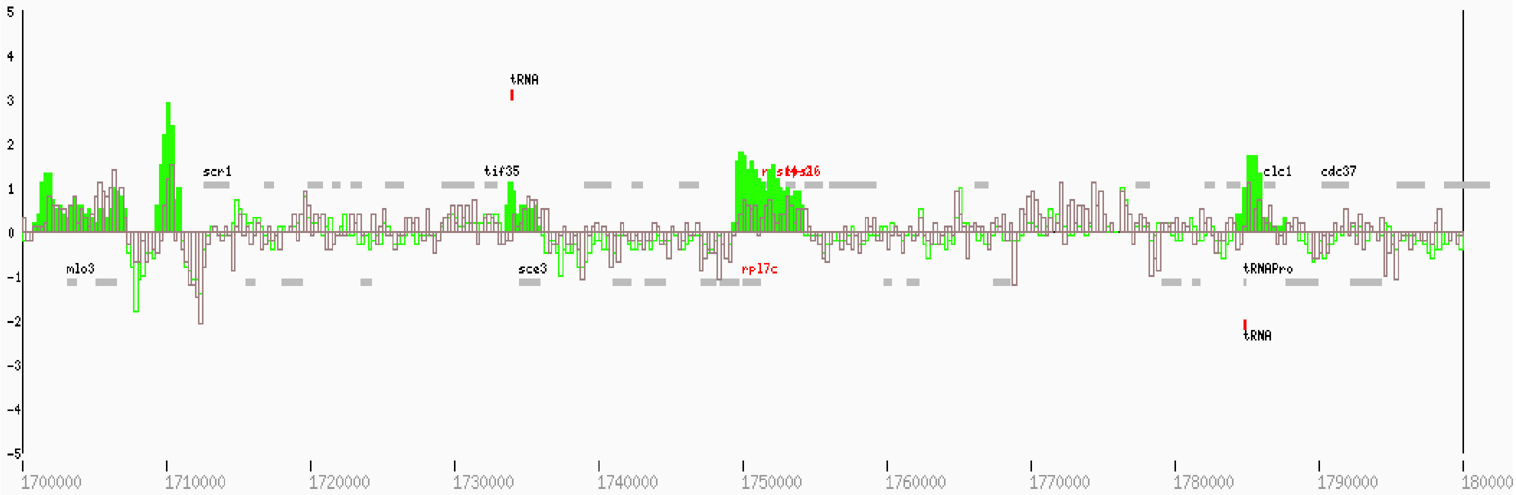
Chromosome 2 (1500000-1600000)



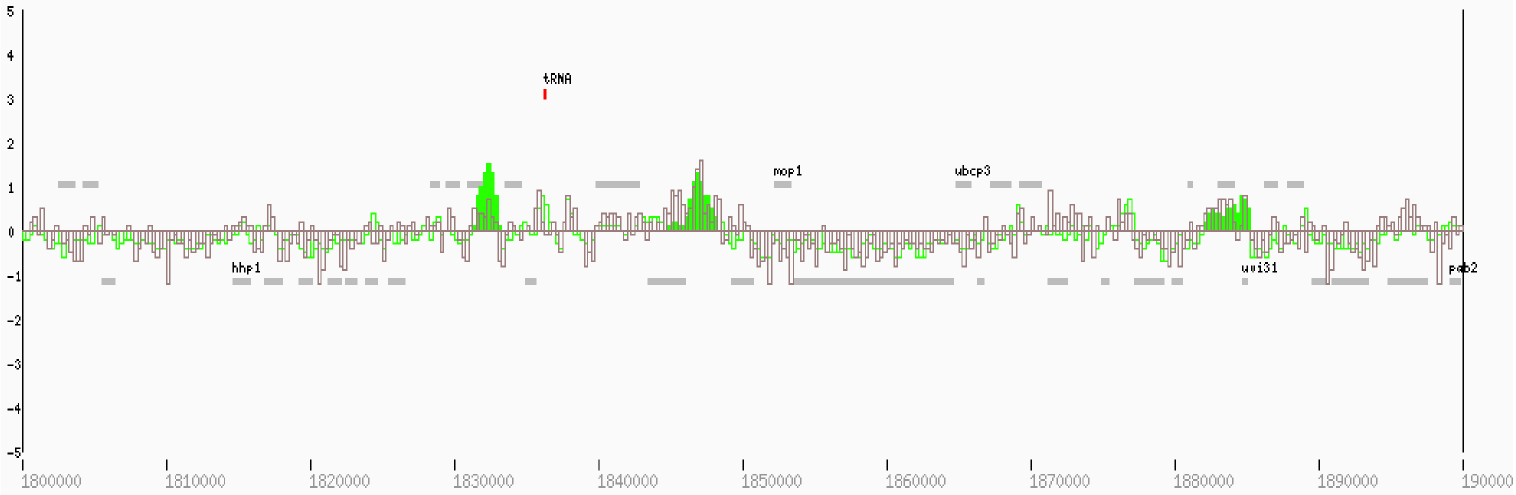
Chromosome 2 (1600000-1700000)



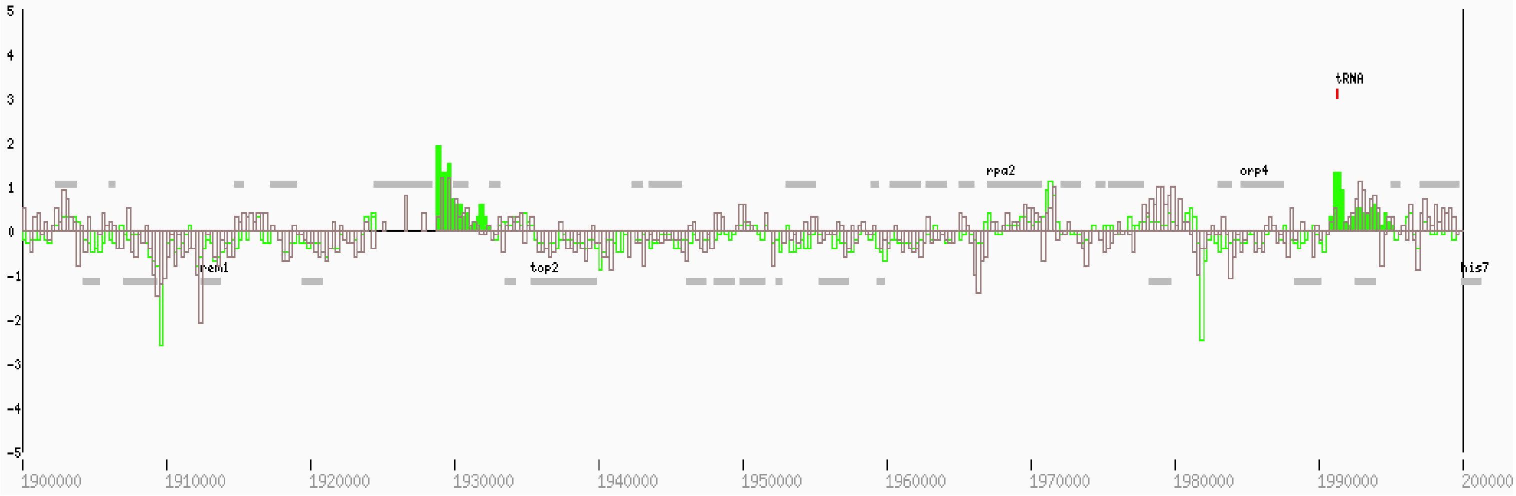
Chromosome 2 (1700000-1800000)



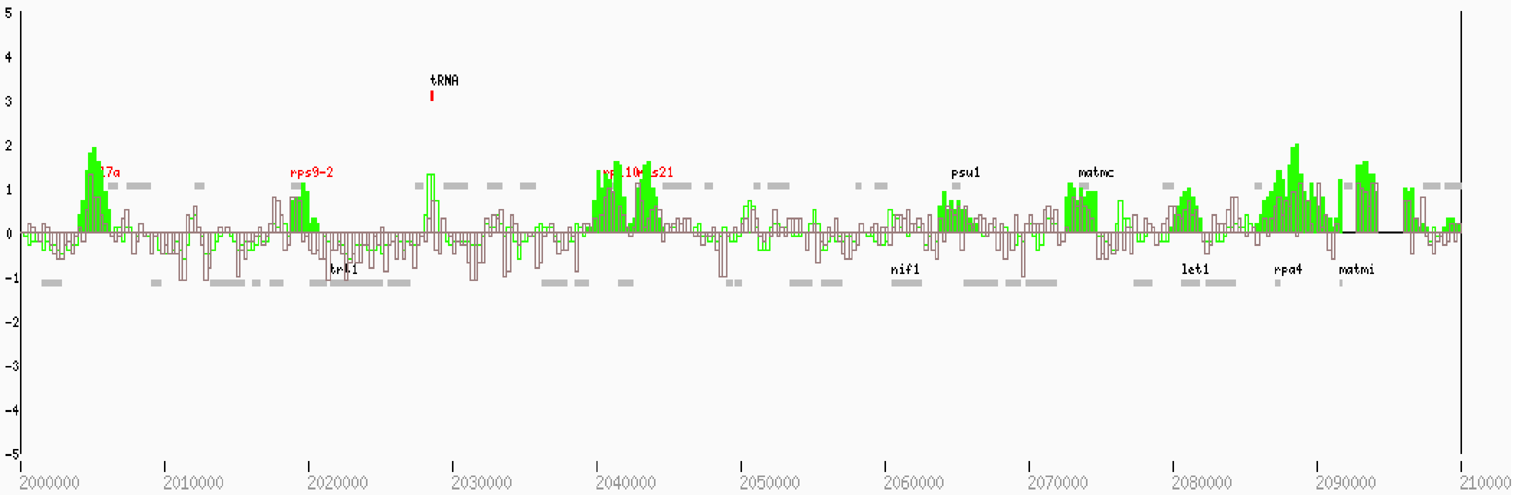
Chromosome 2 (1800000-1900000)



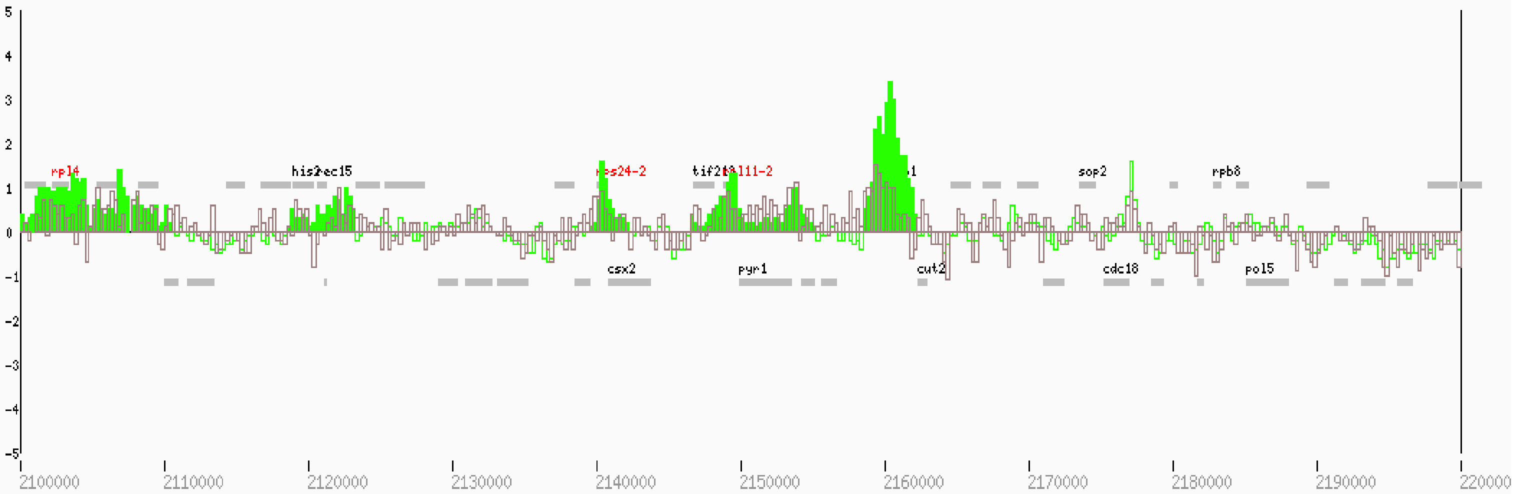
Chromosome 2 (1900000-2000000)



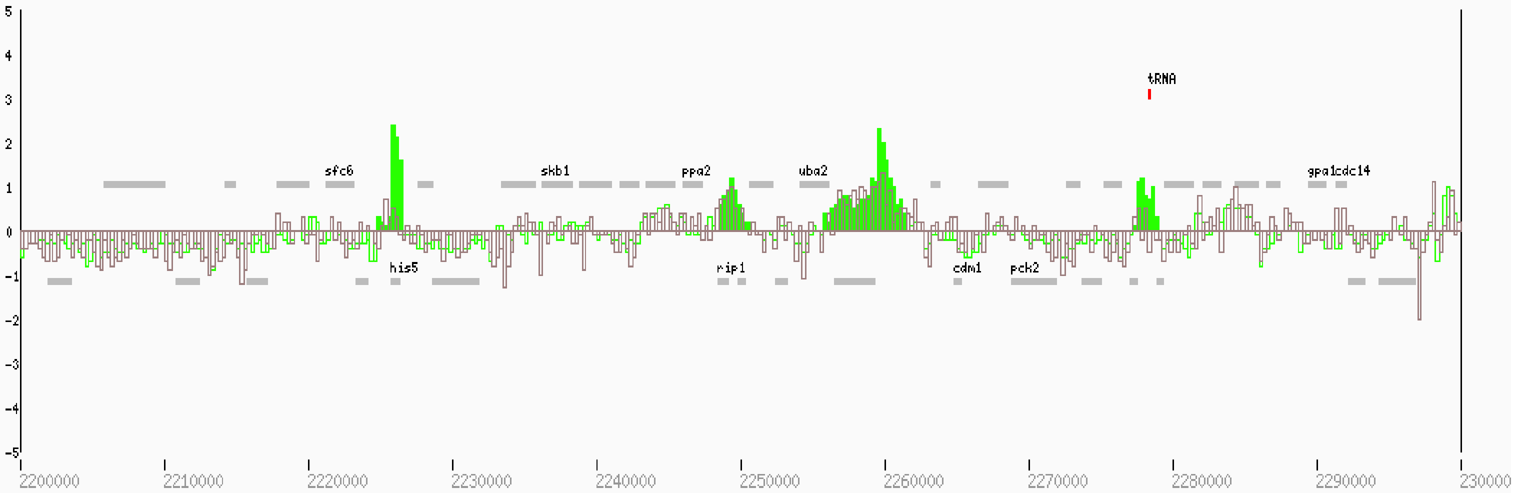
Chromosome 2 (2000000-2100000)



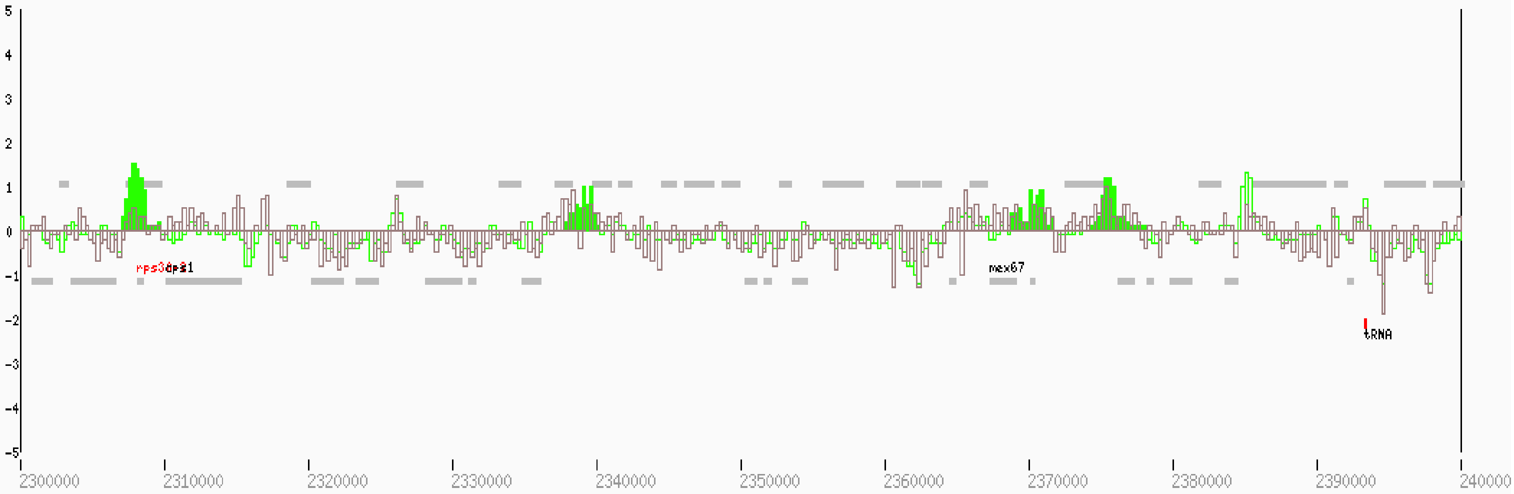
Chromosome 2 (2100000-2200000)

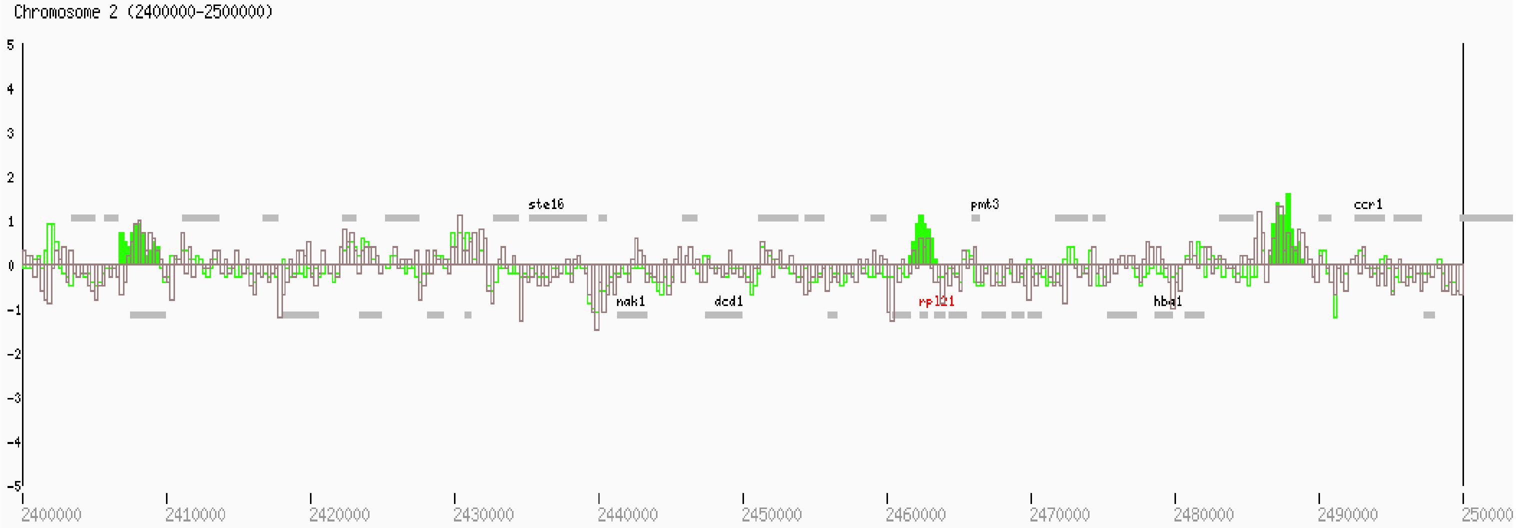


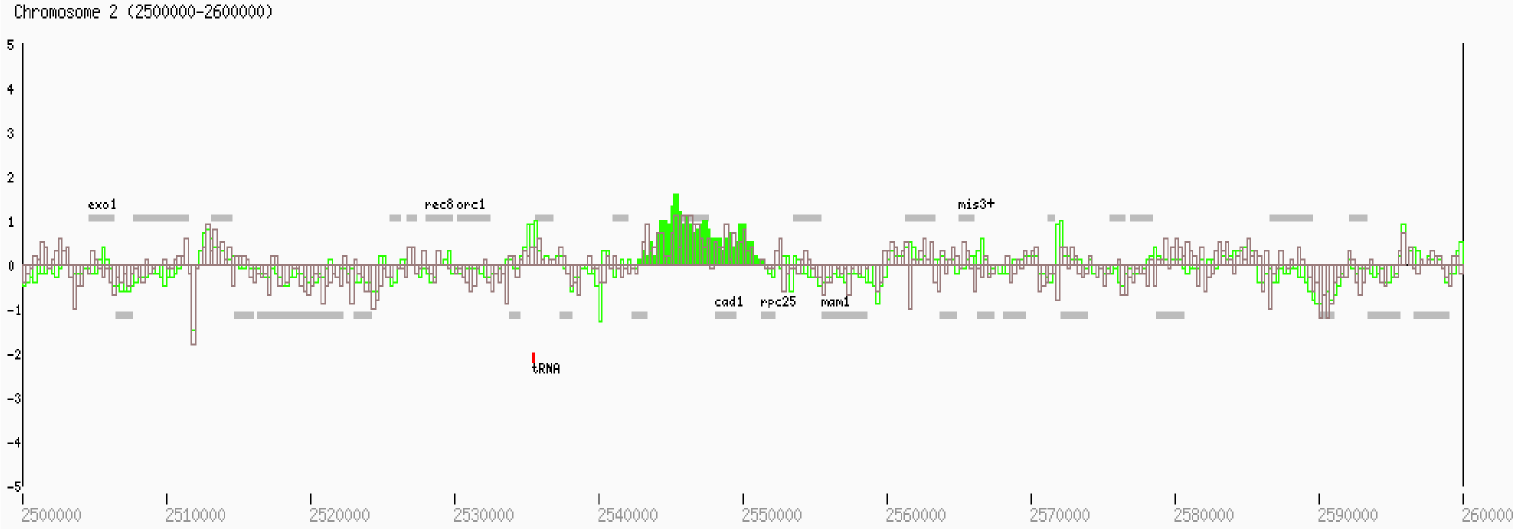
Chromosome 2 (2200000-2300000)

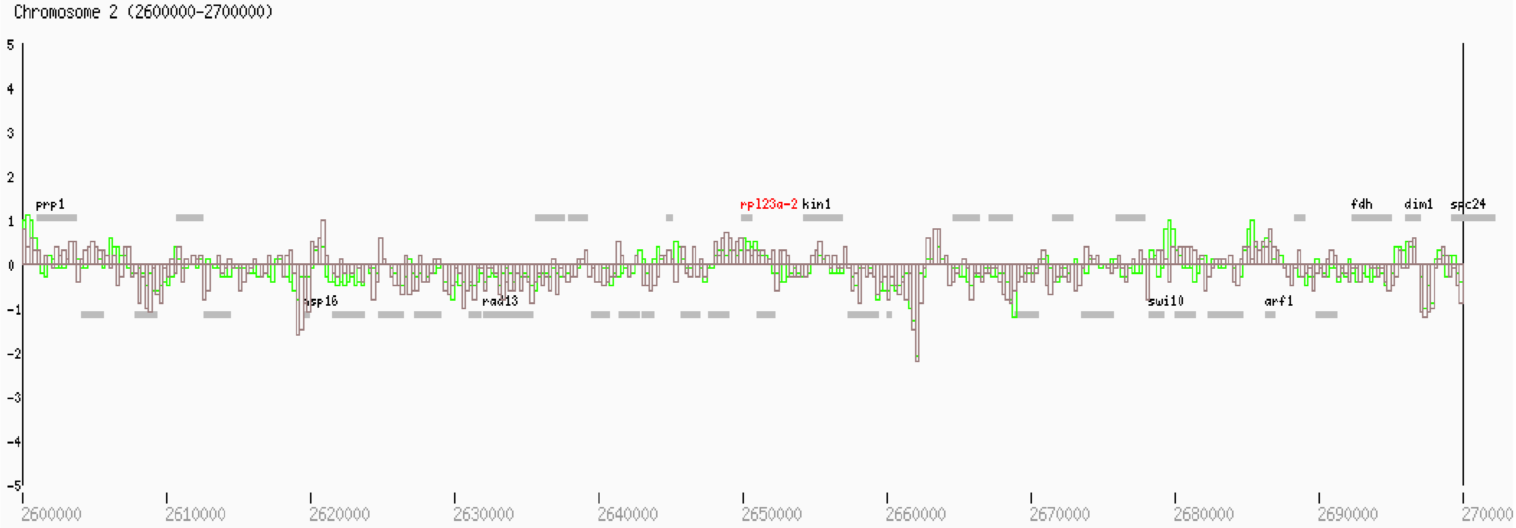


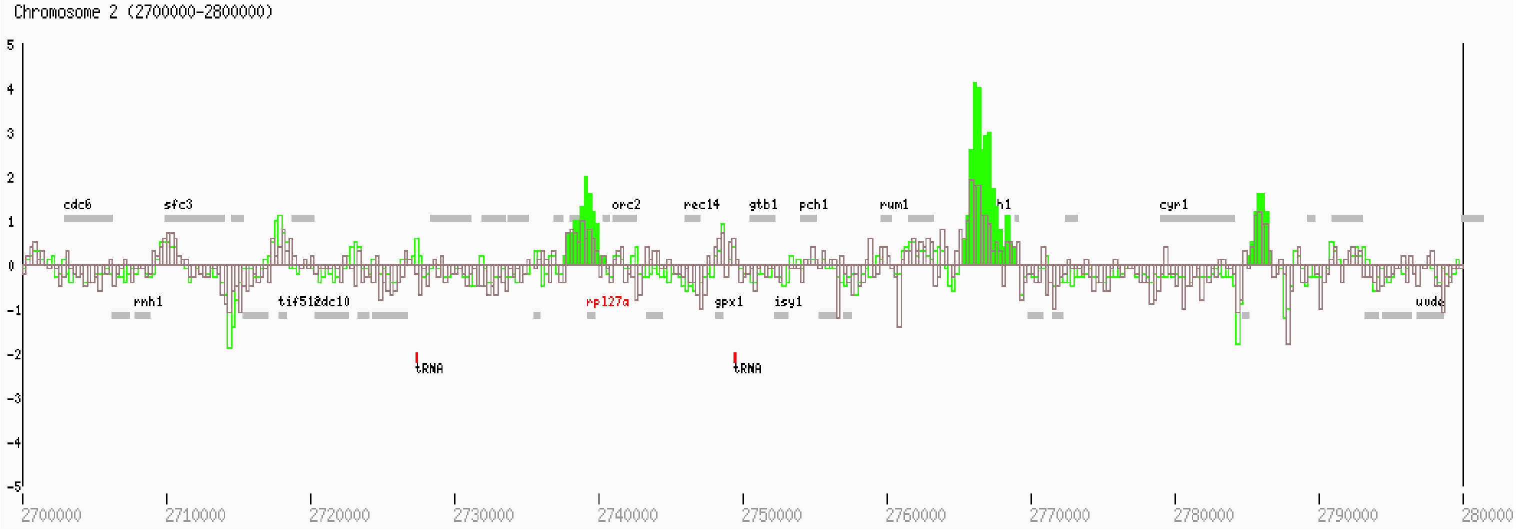
Chromosome 2 (2300000-2400000)



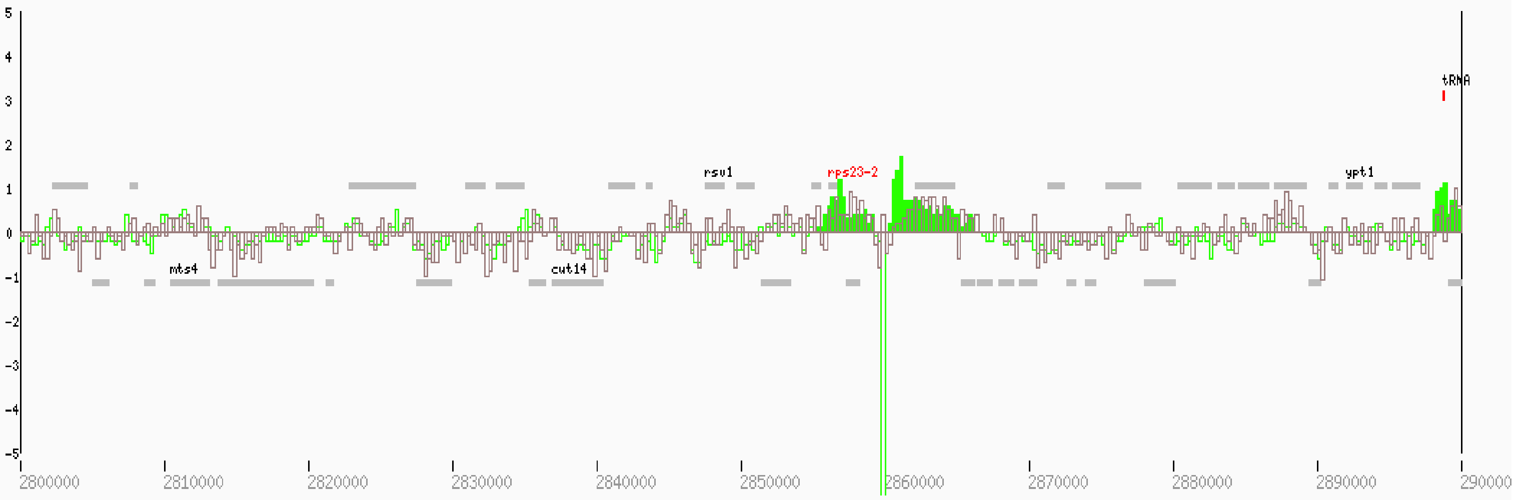

Chromosome 2 (2400000-2500000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
ste16
pmt3
ccr1
nak1
dcd1
rpl21
hba1
2400000
2410000
2420000
2430000
2440000
2450000
2460000
2470000
2480000
2490000
250000


Chromosome 2 (2500000-2600000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
exo1
rec8
orc1
mis3+
cad1
rpc25
mam1
tRNA
2500000
2510000
2520000
2530000
2540000
2550000
2560000
2570000
2580000
2590000
260000

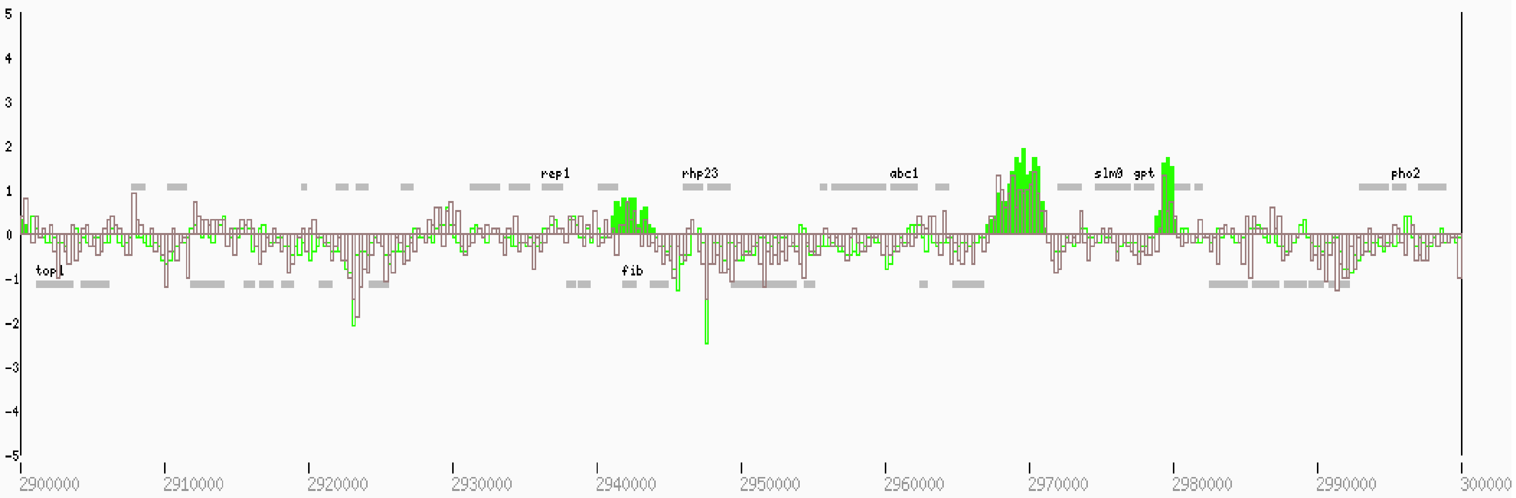

Chromosome 2 (2600000-2700000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
prp1
rpl23a-2
kin1
fdh
dim1
spc24
sp16
rad13
swi10
arf1
2600000
2610000
2620000
2630000
2640000
2650000
2660000
2670000
2680000
2690000
270000


Chromosome 2 (2700000-2800000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
cdc6
sfc3
orc2
rec14
gtb1
pch1
rum1
h1
cyr1
rnh1
tif512dc10
rpl27a
gpx1
isy1
uvde
tRNA
tRNA
2700000
2710000
2720000
2730000
2740000
2750000
2760000
2770000
2780000
2790000
280000

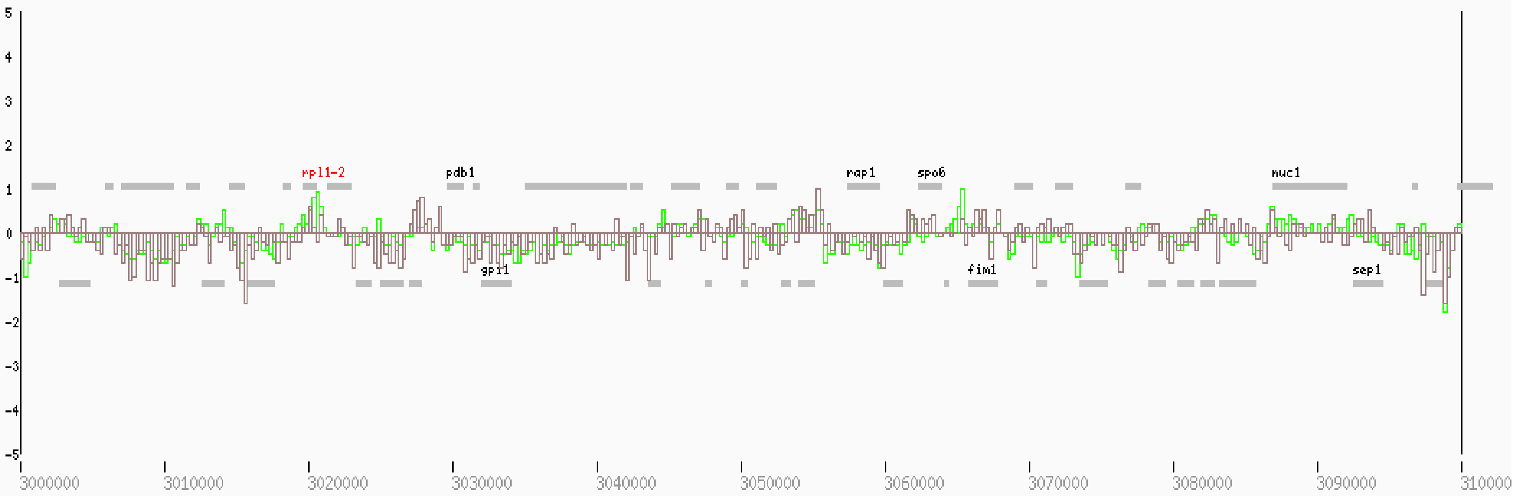
Chromosome 2 (2800000-2900000)



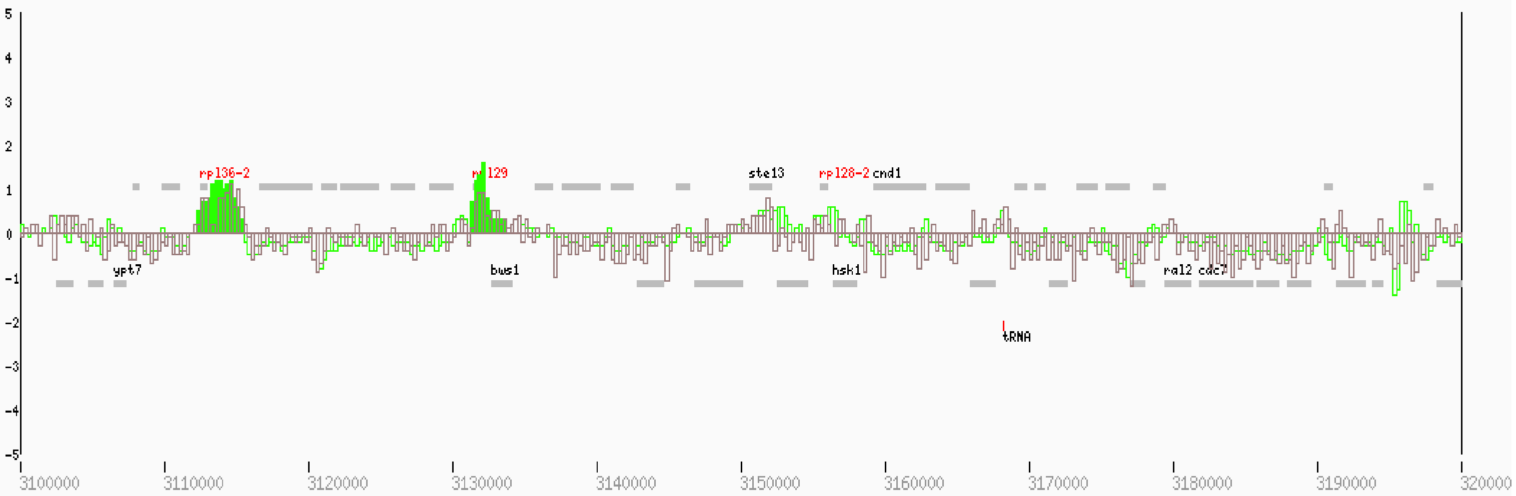
Chromosome 2 (2900000-3000000)



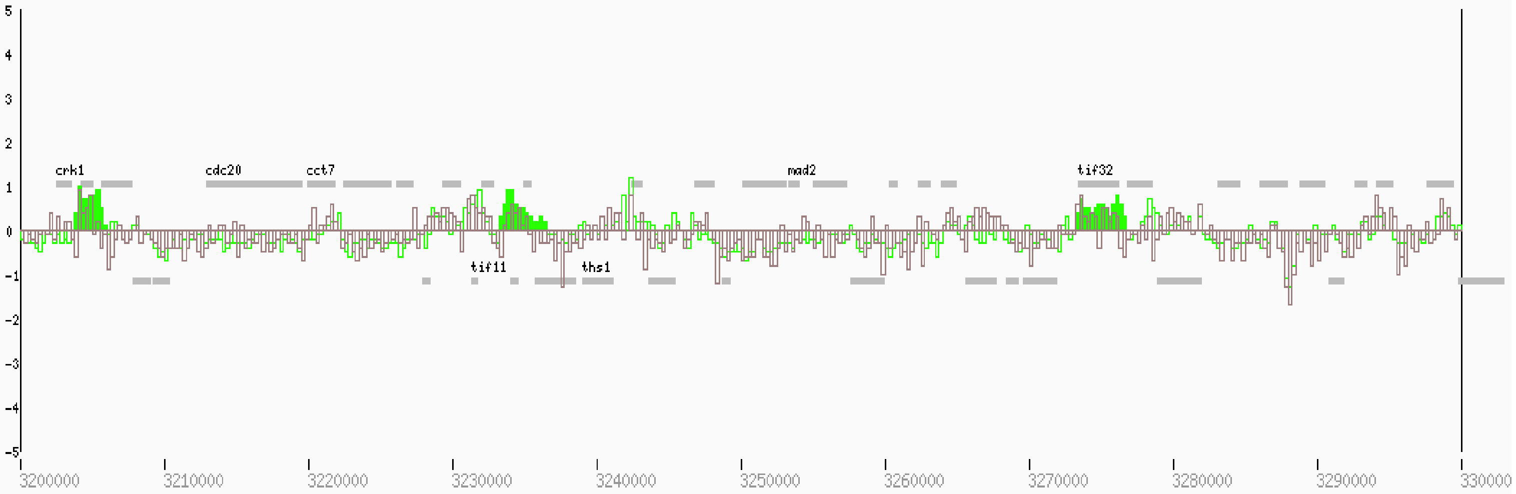
Chromosome 2 (3000000-3100000)



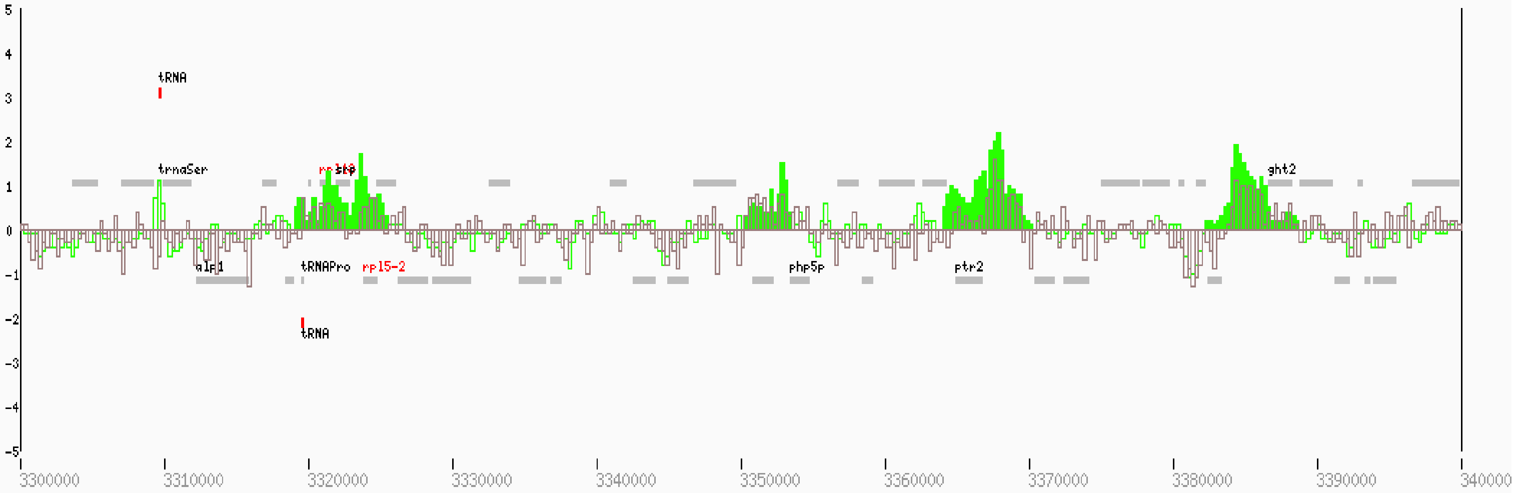
Chromosome 2 (3100000-3200000)



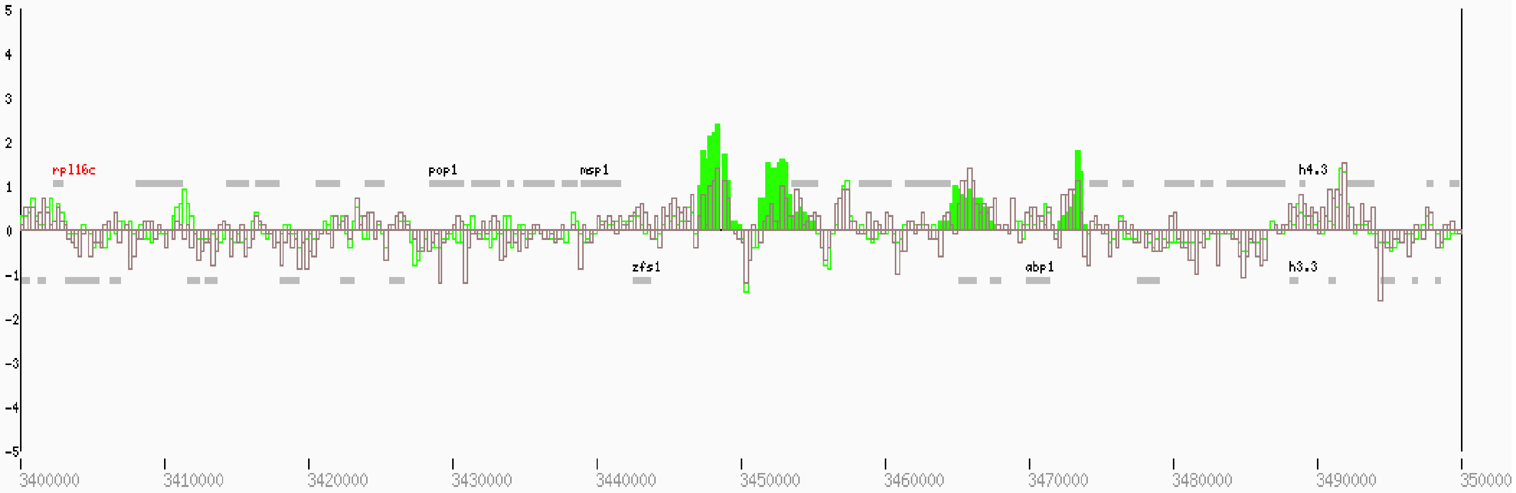
Chromosome 2 (3200000-3300000)



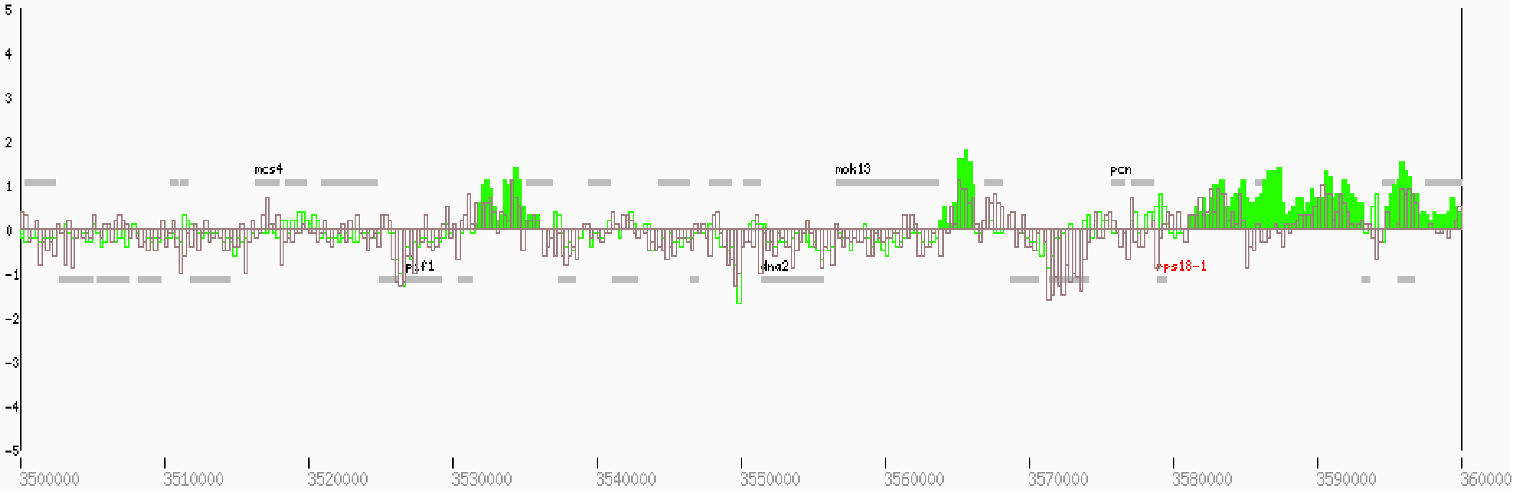
Chromosome 2 (3300000-3400000)

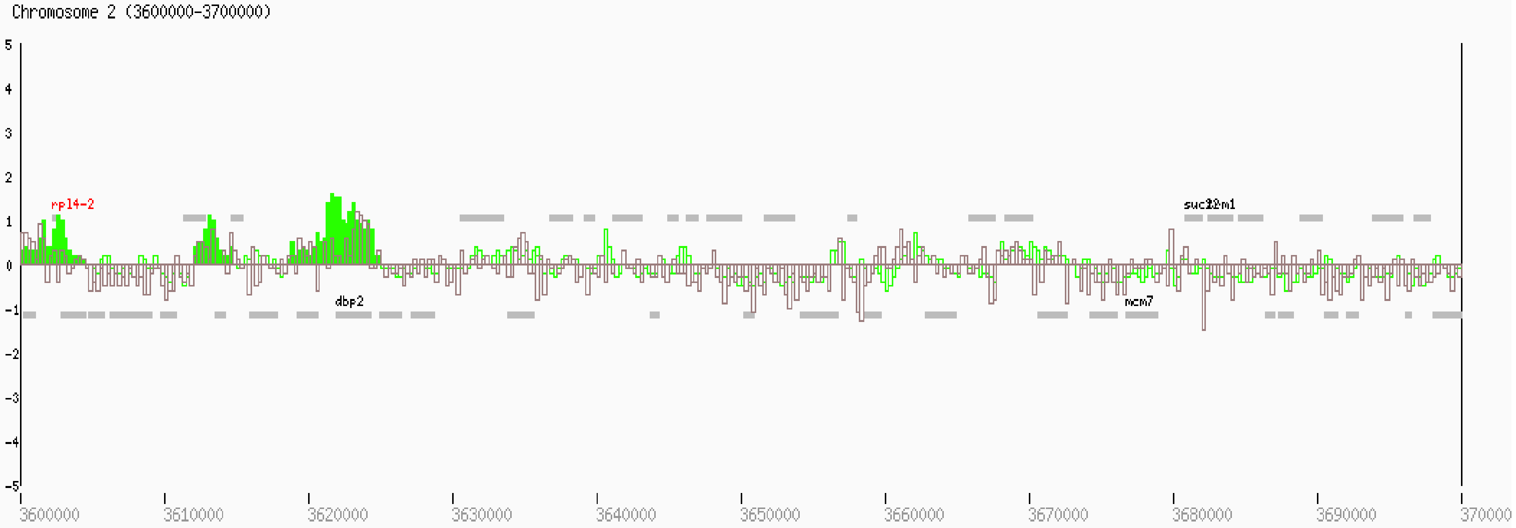


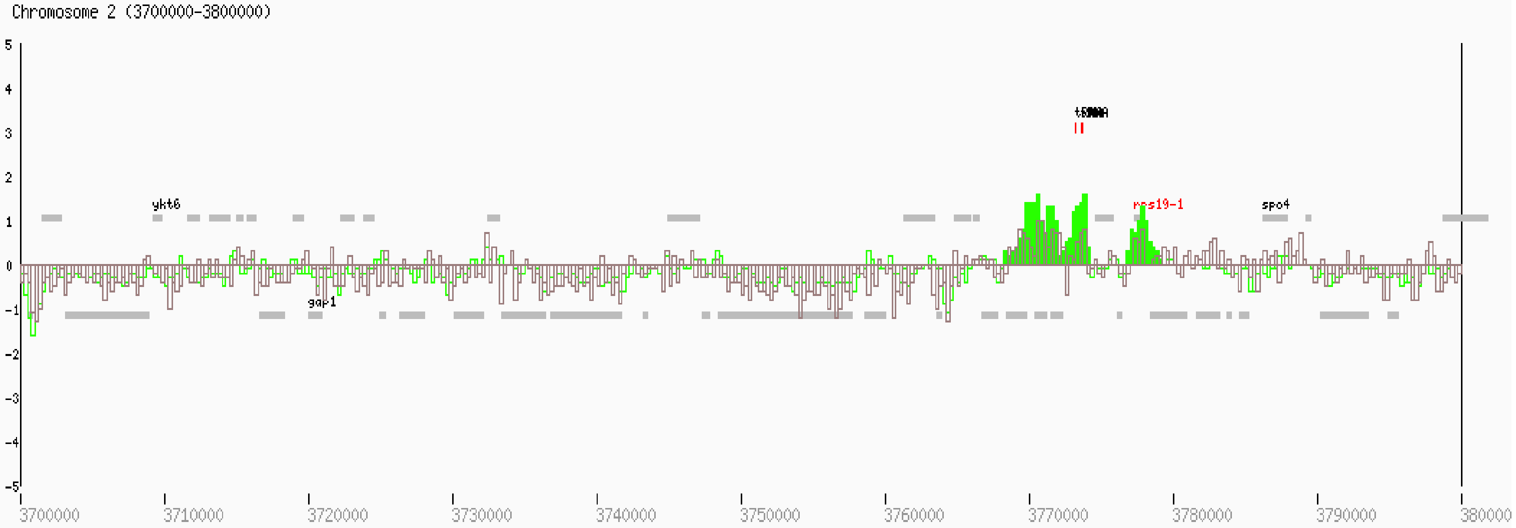
Chromosome 2 (3400000-3500000)

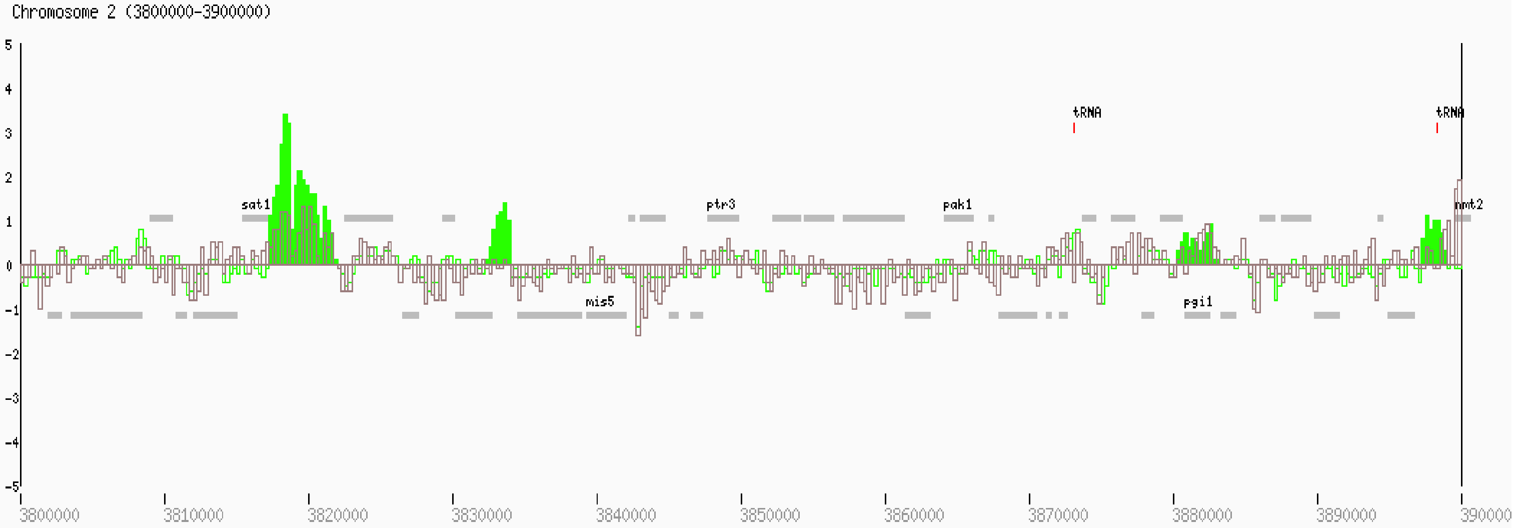


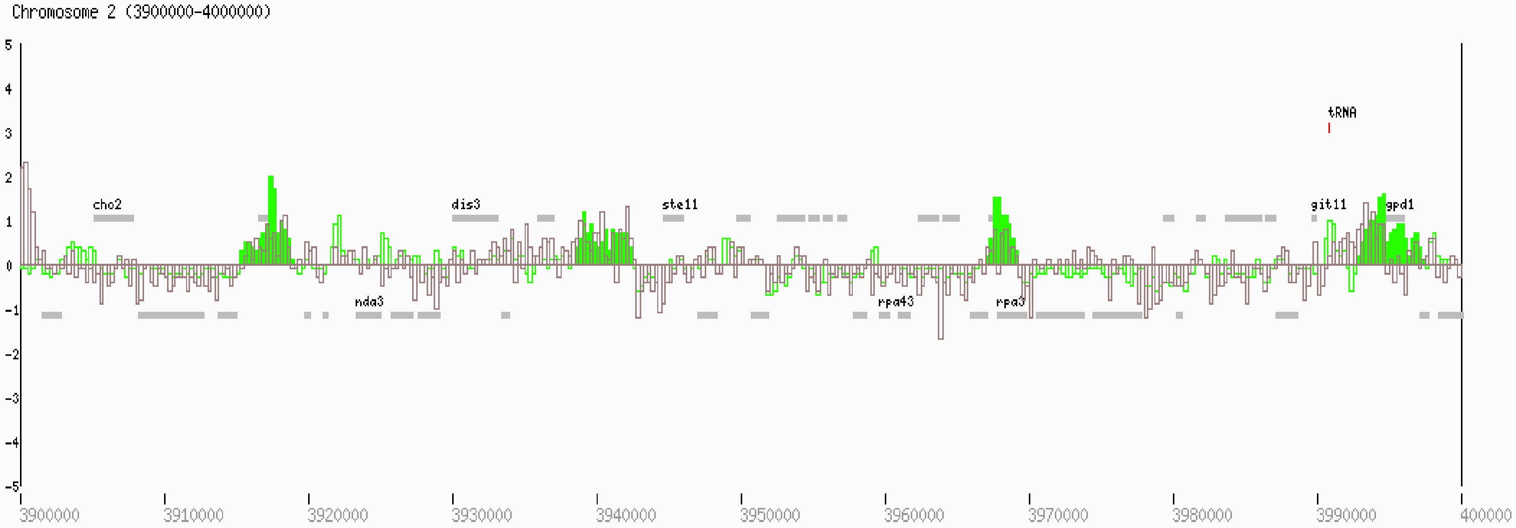
Chromosome 2 (3500000-3600000)



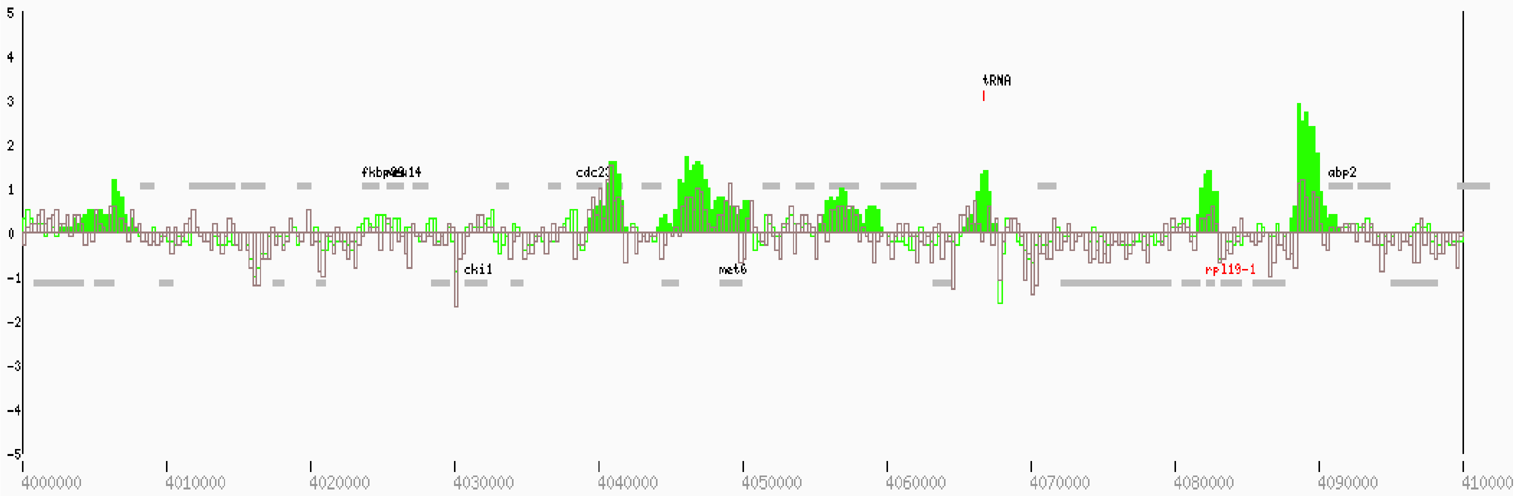

Chromosome 2 (3600000-3700000)


Chromosome 2 (3700000-3800000)

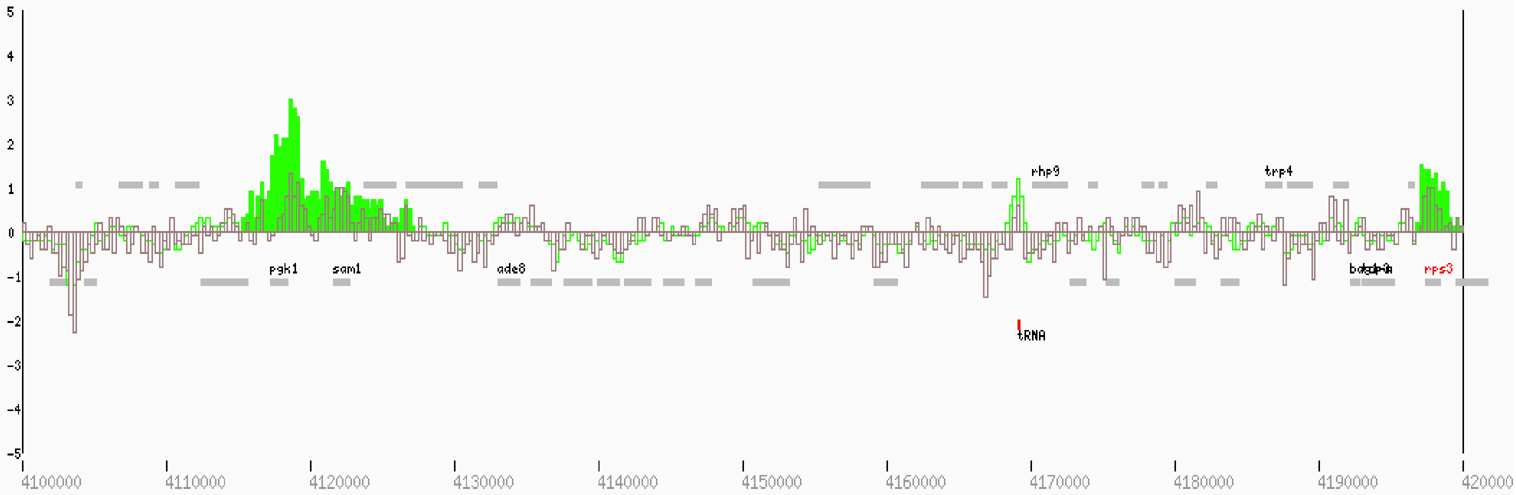

Chromosome 2 (3800000-3900000)


Chromosome 2 (3900000-4000000)

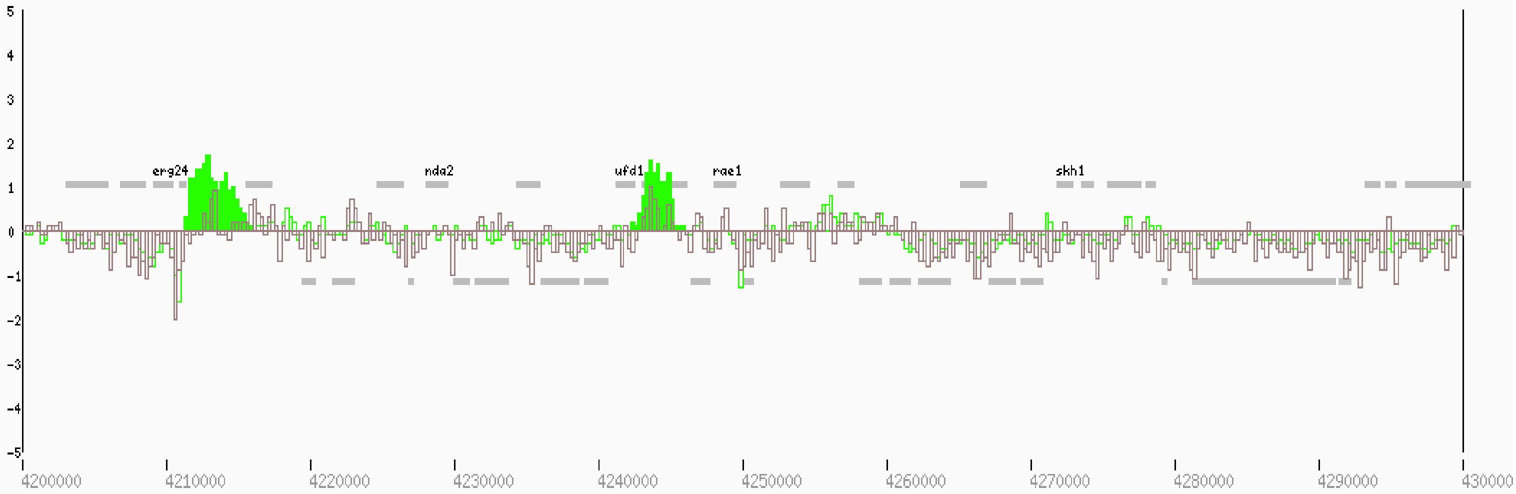
Chromosome 2 (4000000-4100000)



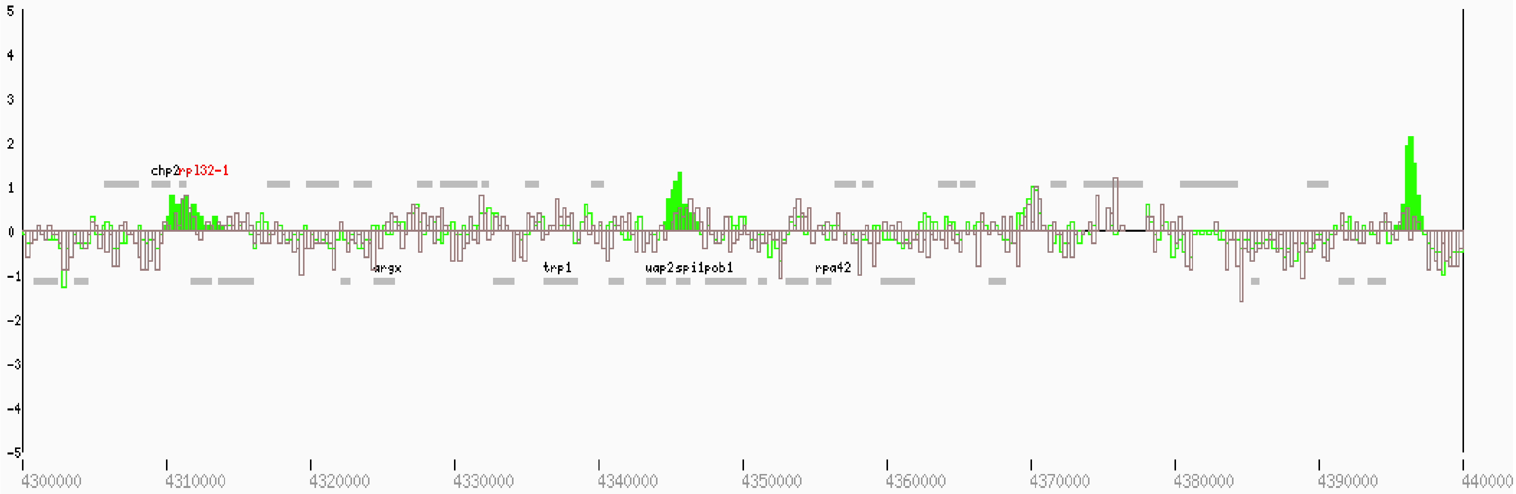
Chromosome 2 (4100000-4200000)



Chromosome 2 (4200000-4300000)



Chromosome 2 (4300000-4400000)



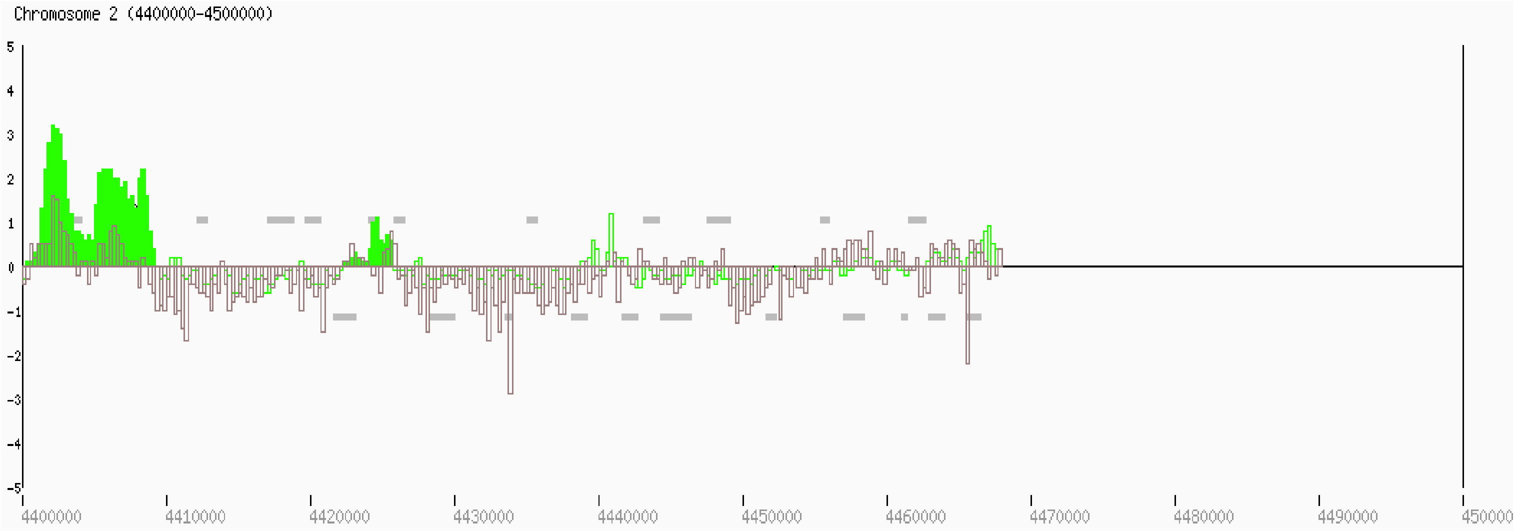

Chromosome 2 (4400000-4500000)
5
4
3
2
1
0
-1
-2
-3
-4
-5
4400000
4410000
4420000
4430000
4440000
4450000
4460000
4470000
4480000
4490000
450000

Figure S6

Mis4/Ssl3 binding sites correlate with strongly expressed genes. This graph compares the relative mRNA levels of ribosomal protein genes, Mis4-bound genes other than ribosomal protein genes, and all remaining genes that are not associated with Mis4 along chromosome 2. tRNA genes were excluded from this analysis. Box boundaries mark the 25th to 75th percentile surrounding the median (bold line). Whiskers extend to 1.5 times the interquartile range. Outliers are indicated as circles. Wilcoxon signed ranks tests suggest that Mis4-bound genes are significantly more strongly expressed than non-bound genes.

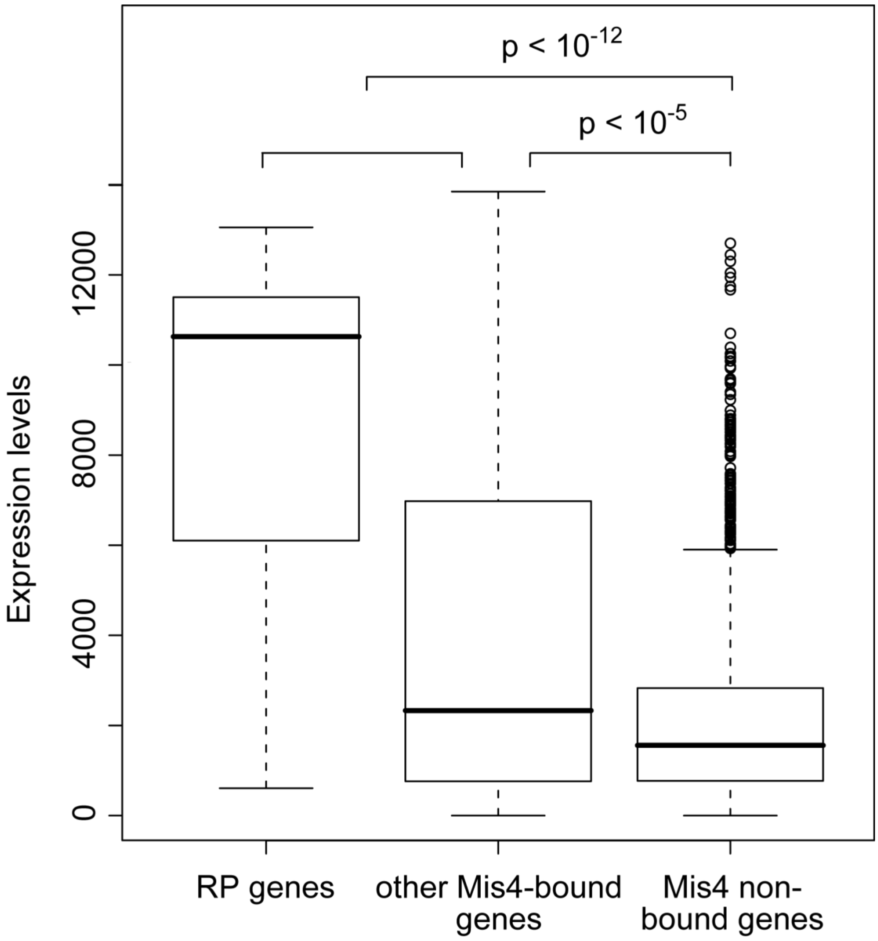


Figure S7

The cohesin pattern along chromosome arms remains qualitatively unchanged during cohesin removal in mitosis. Cells were arrested in G2 and synchronously released into mitotic progression. Chromatin immunoprecipitation was performed against the Rad21-Pk$_9$ cohesin subunit. A 100 kb region on the left arm of chromosome 2 in G2-arrested cells is compared to the patterns at the indicated timepoints after release when the majority of cells were in metaphase and in anaphase, respectively (compare Figure 7).

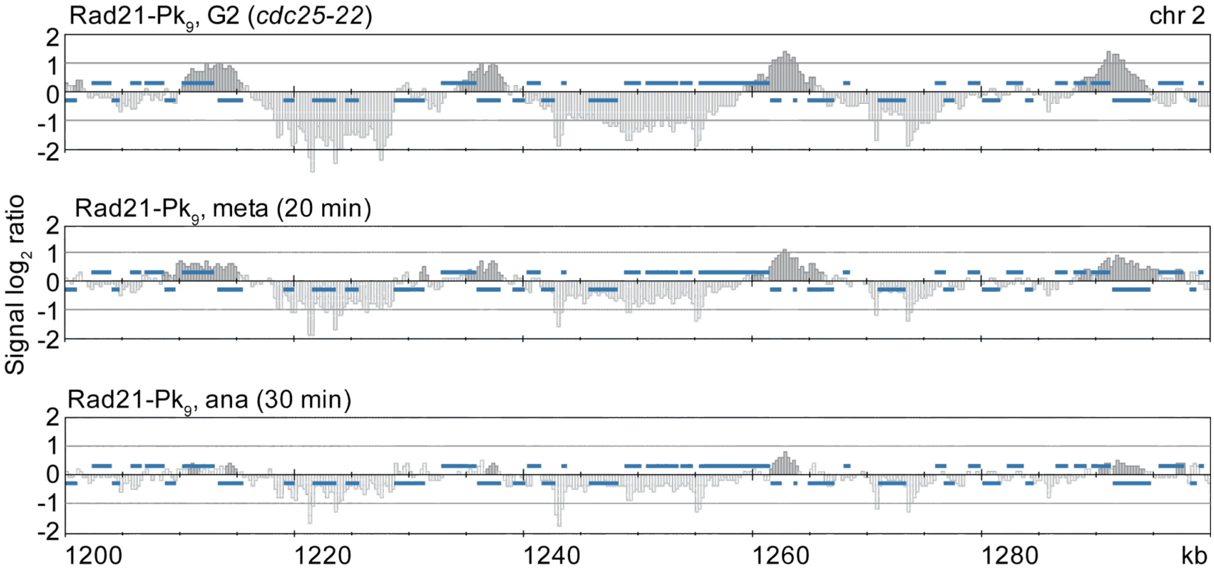


Table S1

Yeast strains used in this study.

Strain	Genotype	Usage
Y252	h^{-} *leu1-32 nda3-KM311 cnd2-Pk*$_{9}$*-kanMX6*	Fig. 3
Y2197	h^{90} *leu1-32 ade6-M216 rad21-HA*$_{3}$*-kanMX6*	Fig. 1, A1
Y2447	h^{90} *leu1-32 psc3-Pk*$_{9}$*-kanMX6*	Fig. 1
Y2460	h^{90} *leu1-32*	Fig. A4
Y2468	h^{90} *leu1-32 mis4-Pk*$_{9}$*-kanMX6*	Fig. 3, 4, 7 A4
Y2699	h^{-} *leu1-32 cdc25-22 rad21-Pk*$_{9}$*-kanMX6 SV40p-GFP-atb2-LEU2*	Fig. 1, 2, 3, 4, 5, 7, A1, A7
Y2703	h^{90} *nda3-KM311 rad21-Pk*$_{9}$*-kanMX6*	Fig. 5
Y2828	h^{-} *pds5-Pk*$_{9}$*-kanMX6*	Fig. 1
Y2863	h^{-} *leu1-32 cdc10-129 rad21-Pk*$_{9}$*-kanMX6*	Fig. 2, 7
Y3071	h^{+} *ssl3-Pk*$_{9}$*-kanMX6*	Fig. 3, A4
Y3127	h^{-} *ura4-D18 rad21-3eGFP-kanMX6 mis4-Pk*$_{9}$*-kanMX6*	Fig. 3
Y3169	h^{+} *leu1-32 cdc25-22 ssl3-Pk*$_{9}$*-kanMX6 SV40p-GFP-atb2-LEU2*	Fig. 6
Y3250	h^{90} *leu1-32 cdc25-22 cnd2-Pk*$_{9}$*-kanMX6 SV40p-GFP-atb2-LEU2*	Fig. 6
Y3272	h^{-} *leu1-32 ura4-D18 cdc25-22 rad21-Pk*$_{9}$*-kanMX6 SV40p-GFP-atb2-LEU2 swi6::ura4*$^{+}$	Fig. 2
Y3298	h^{90} *leu1-32 ura4-D18 his3-D1 lys1 ade6-M210 mis4-Pk*$_{9}$*-kanMX6 mis6-GFP-LEU2*	Fig. 6
Y3300	h^{90} *leu1-32 ura4-D18 rad21-Pk*$_{9}$*-kanMX6 mis6-GFP-LEU2*	Fig. 5
Y3303	h^{90} *leu1-32 his3-D1 cut14-Pk*$_{9}$*-kanMX6 mis6-GFP-LEU2*	Fig. 6
Y3350	h^{90} *leu1-32 mis4-Pk*$_{9}$*-kanMX6 fhl1-GFP-hygMX6*	Fig. 3
Y3351	h^{90} *leu1-32 mis4-Pk*$_{9}$*-kanMX6 sfc3-GFP-hygMX6*	Fig. 3
Y3359	h^{90} *leu1-32 sfc6-Pk*$_{9}$*-kanMX6*	Fig. 3
Y3384	h^{90} *leu1-32 mis4-GFP-hygMX6 cnd2-Pk*$_{9}$*-kanMX6*	Fig. 3
Y3385	h^{-} *leu1-32 mis4-GFP-hygMX6 ssl3-Pk*$_{9}$*-kanMX6*	Fig. 3
Y3403	h^{90} *leu1-32 fhl1-Pk*$_{9}$*-kanMX6*	Fig. 3
Y3586	h^{-} *leu1-32 ark1-as3-hygMX6 cdc25-22 rad21-Pk9-kanMX6 SV40p-GFP-atb2-LEU2*	Fig. 7
Y3650	h^{-} *leu1-32 ura4-D18 ade6-M210 mis4-Pk*$_{9}$*-kanMX6 SPBTRNAGLY.05Δ SPBTRNAARG.04Δ*	Fig. 4
Y3724	h^{90} *leu1-32 ura4-D18 cdc25-22 rad21-Pk*$_{9}$*-kanMX6 SPBTRNAGLY.05Δ SPBTRNAARG.04Δ*	Fig. 4
Y3863	h^{90} *leu1-32 mis4-Pk*$_{9}$*-kanMX6 cdc10-12*	Fig. A5

Generation of these strains was based on previously described strains and constructs: *cdc25-22* [54], *nda3-KM311* [55], *cdc10-129* [56], *SV40p-GFP-atb2-LEU2* [57], and *ark1-as3* [41]. A *mis6-GFP-LEU2* strain was a kind gift from Kazu Tomita.