Supplementary legends

Figure S1: DNA copy number changes in a checkpoint mutant subjected to HU. DNA copy number increase is restricted to origin proximal regions. The plots show the ratio between uniquely mapped sequencing reads from a G1 and S-phase sample, normalized to a baseline of 1. Regions lacking data are non-unique sequences where reads were not mapped. Black dots are the raw data points in 1 kb windows. Fourier transformation was applied to generate the smoothed profiles, shown in solid grey. Open circles represent known replication origin locations; arrows represent peak calls.

Figure S2: Mcm4 ChIP-seq data. Profile showing the enrichment of Mcm4 bound sequences in alpha factor arrested cells.

Figure S3: Scatter plots for comparisons between HU peak height and origin replication time. For each origin identified as a peak in the HU dataset the origin replication time is plotted against the HU peak height. (left) The median replication time (Trep in min, from time course analysis) is used as a measure of origin replication time. (right) The inferred mean origin activation time (Yang et al., 2010) is used as a measure of origin activation time. In each case correlation coefficients are given.

Figure S4: Time course analysis of genome replication. *S. cerevisiae* genome replication dynamics from seven time points through a synchronous S-phase (each normalized to the alpha factor arrest): 25 min (light blue), 30 min (red), 35 min (blue), 40 min (gold), 45 min (green), 50 min (violet) and 90 min (grey). Open circles represent known replication origin locations.

Figure S5: Median replication time from time course data. Open circles represent known replication origin locations.

Figure S6: Scatter plots for pairwise comparisons between the copy number approaches to measuring genome replication and two published studies (16,17). Correlation coefficients are given for each comparison.

Figure S7: Distance to nearest confirmed replication origin for peak calls from Trep data.

Figure S8: Comparions of sort-seq biological replicates. Relative copy number replication profiles for diploid *S. cerevisiae*. Replicate 1 (SOLiD sequencing) data points are shown in black, replicate 2 (Illumina sequencing) in red. Dots are raw data points in 1 kb windows.

Figure S9: Sort-seq analysis reveals identical replication dynamics in haploids and diploids. Relative copy number replication profiles from sort-seq for the *S. cerevisiae* genome. Dots are raw data points in 1 kb windows and lines show smoothed profiles (black for diploid, grey for haploid). Bars above the profile indicate 1 kb windows that are significantly different (black for $p < 0.001$; grey for $p < 0.01$).

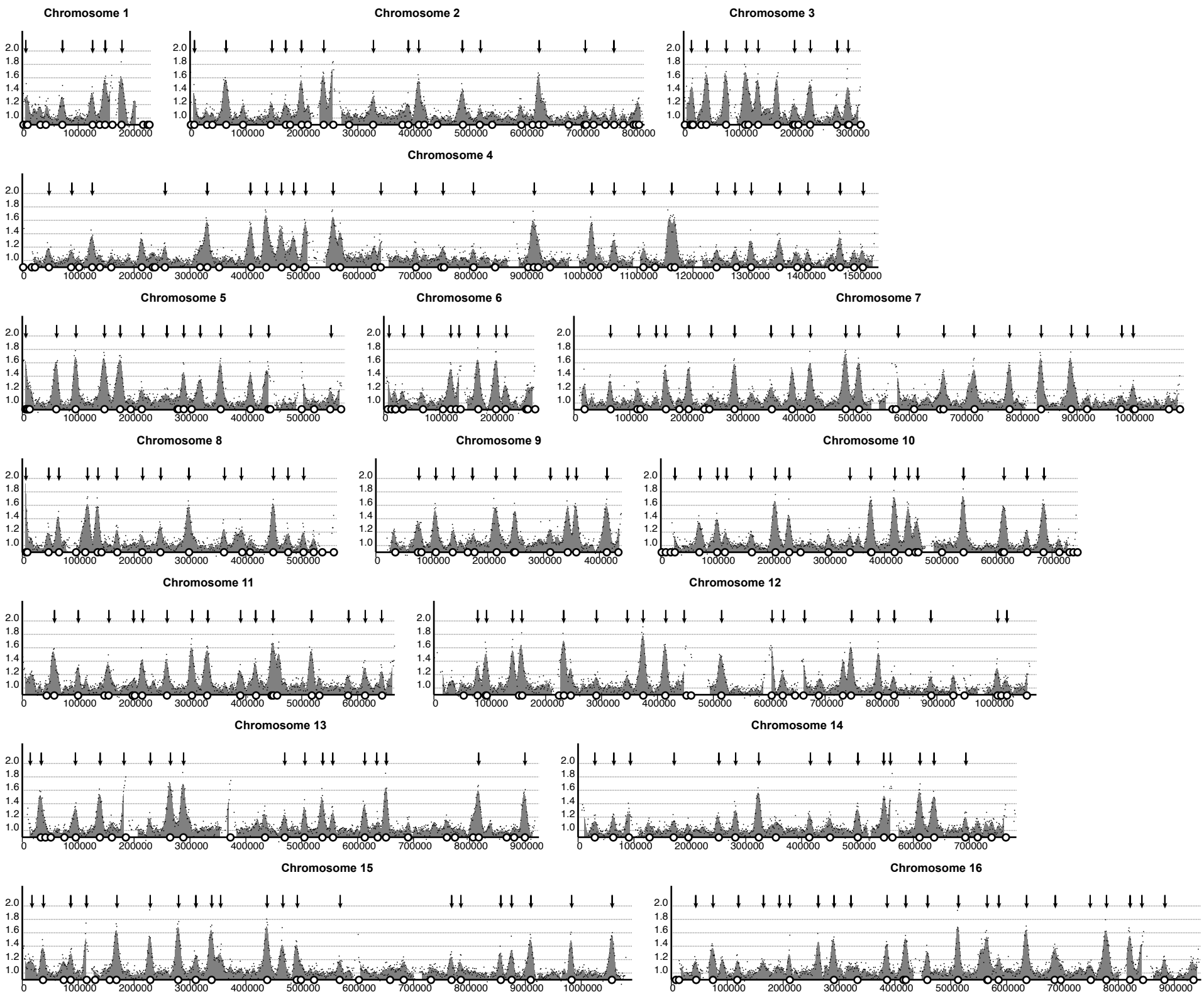
Figure S10: Direct measurement of genome replication in exponentially growing cells. Marker frequency analysis as a proxy for replication time. Grey dots are the raw data points (in 1 kb windows) and the line shows the smoothed profile (left y-axis scale). Black dots show relative copy number from the (Illumina) sort-seq experiment (right y-axis scale). Open circles represent known replication origin locations; blue bars indicate centromere locations.

Table S1: Summary of deep sequencing experiments. Six different experiments are presented with the strain name and pertinent information from each genotype shown. For each experiment the following summary information is presented: the sequencing technology; the strain name; library construction method; a sample description; the mean DNA copy number as measured by flow cytometry (N/A – not applicable); total reads generated; and the total number of reads that mapped uniquely within the nuclear genome. In each case 50 bp sequencing reads were obtained.

Table S2: Genotypes of strains used in this study.

Table S3: Details of confirmed essential sequence elements at 102 replication origins.

Müller, Hawkins, et al. Figure S1



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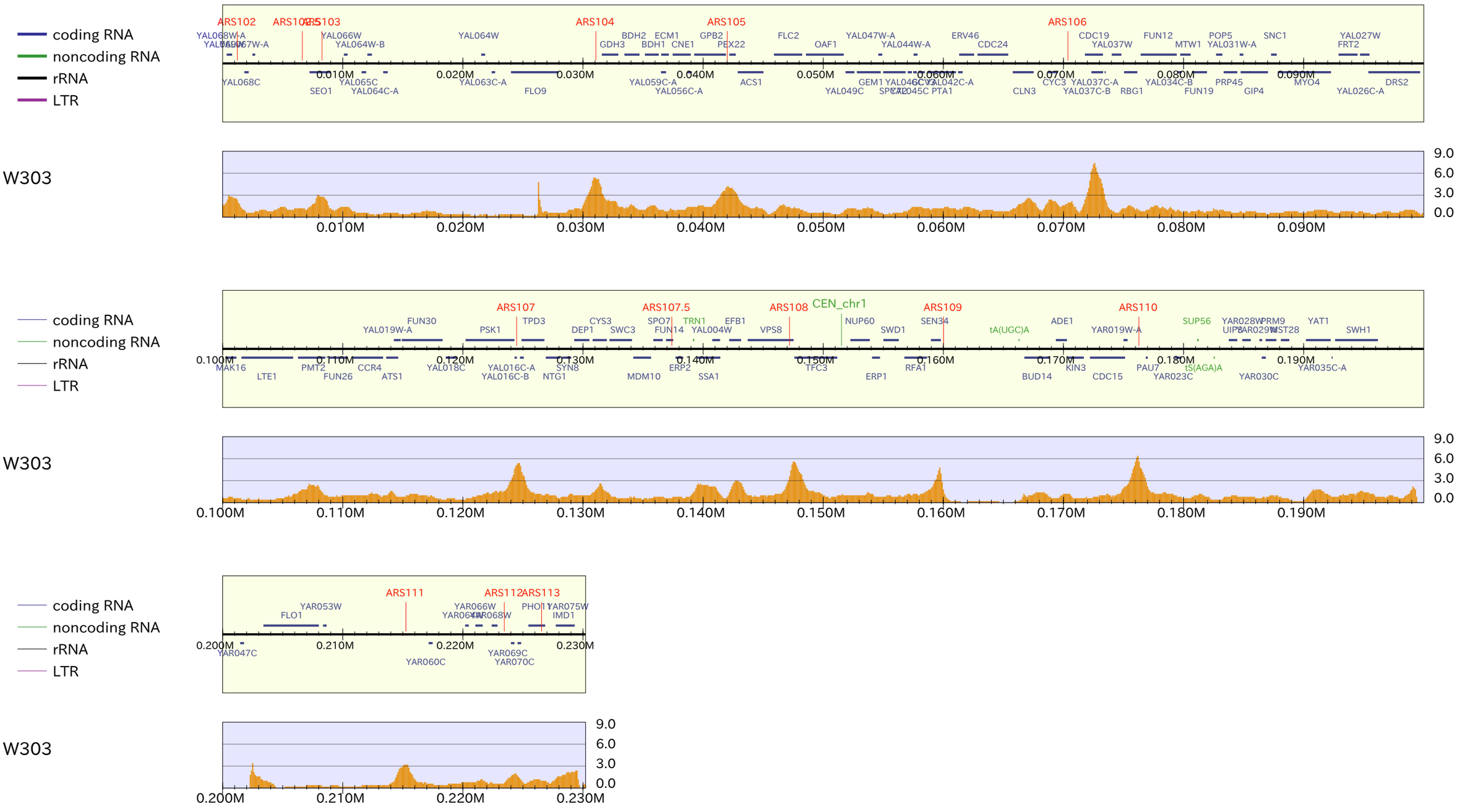
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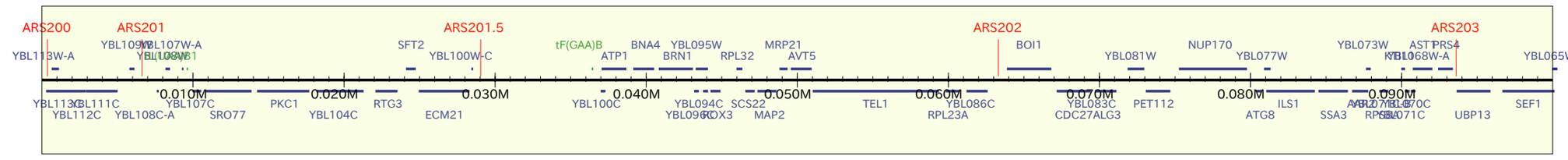

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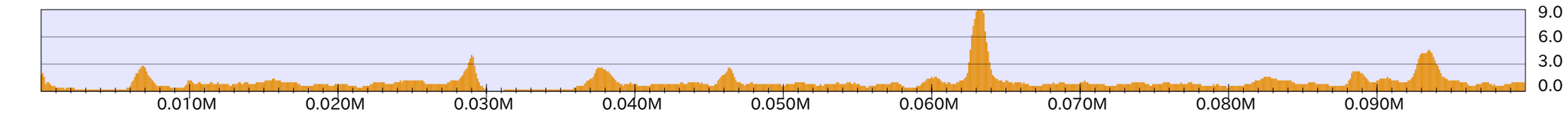

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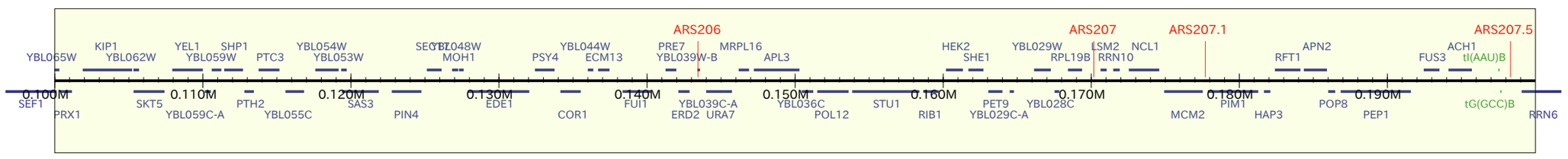

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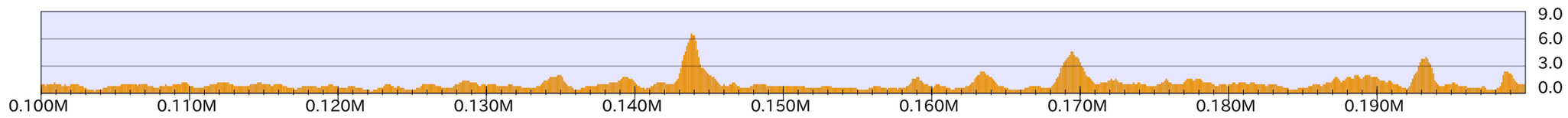

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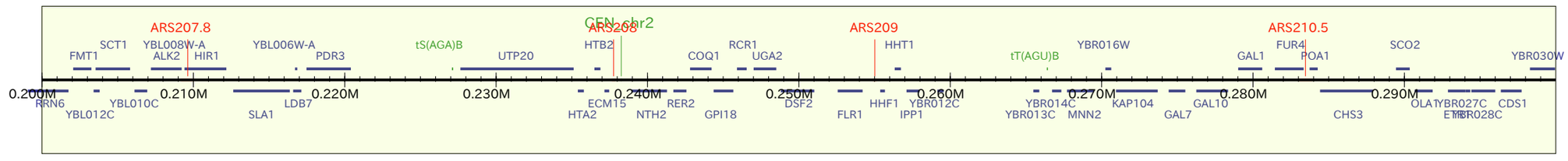

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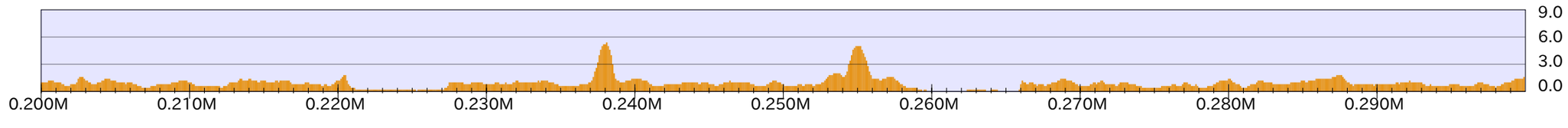

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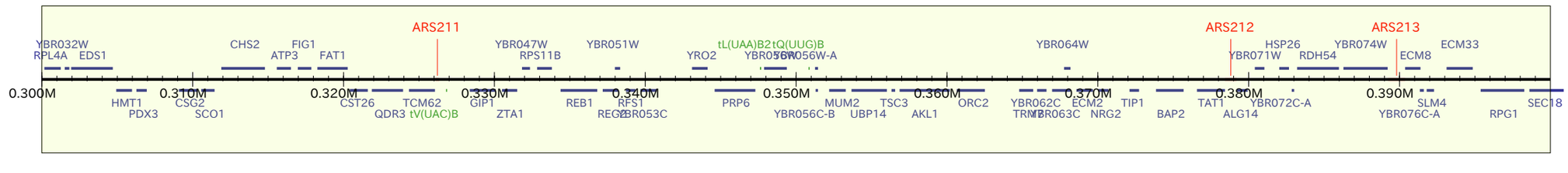

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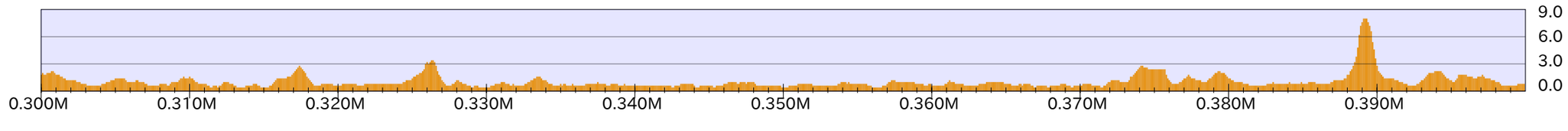

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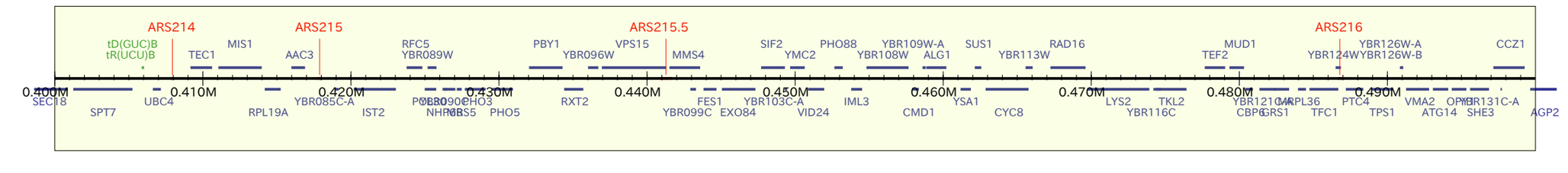

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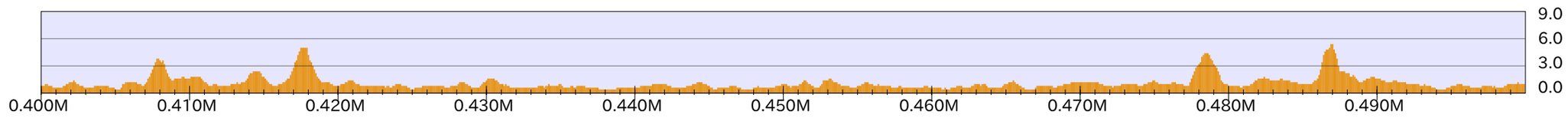

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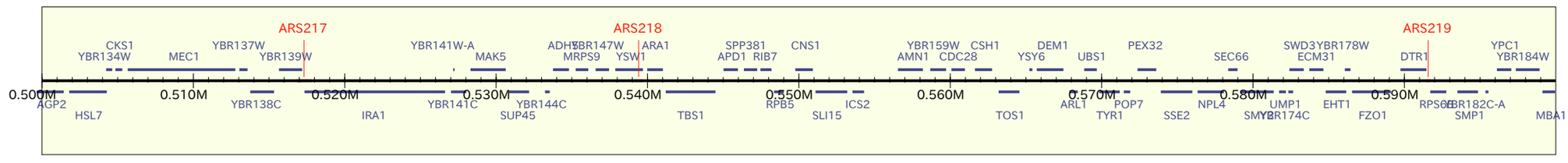

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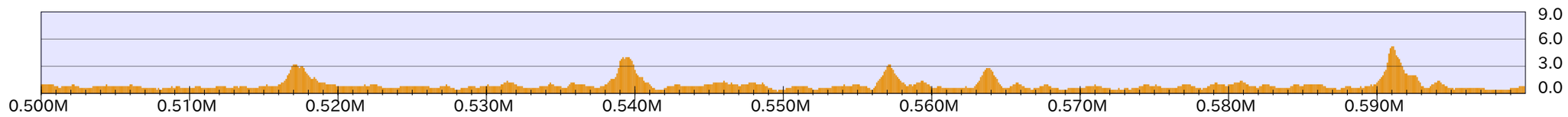

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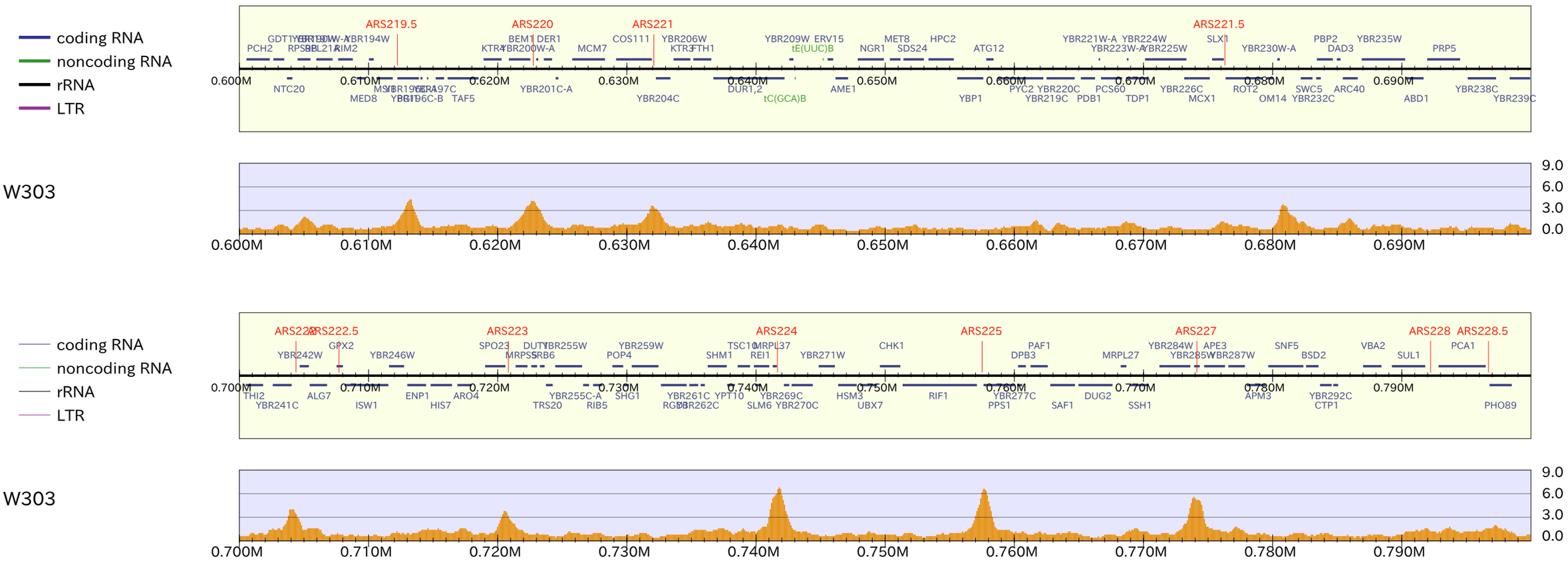
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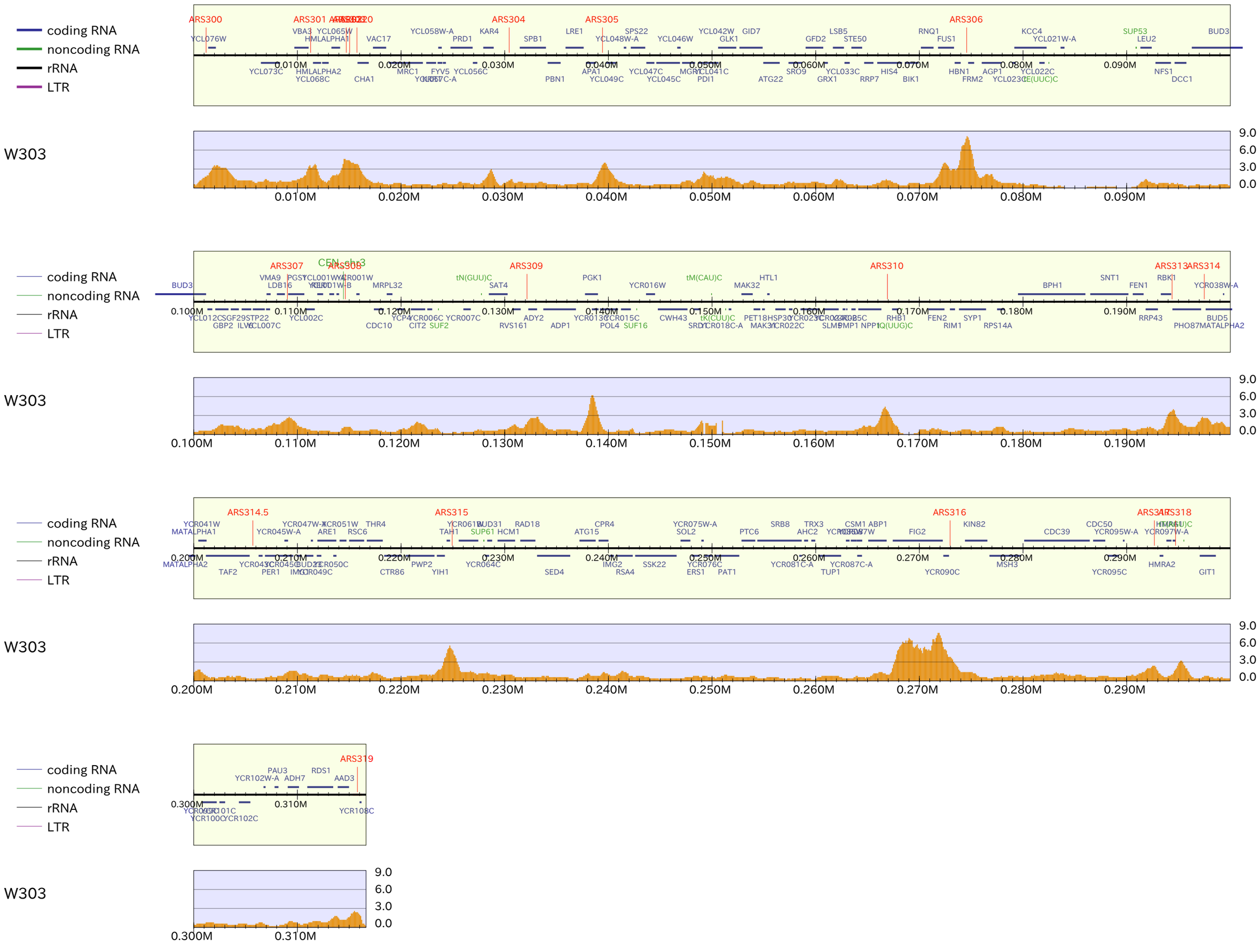
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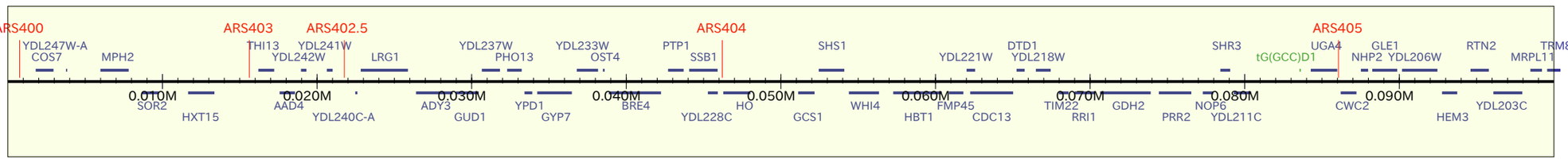

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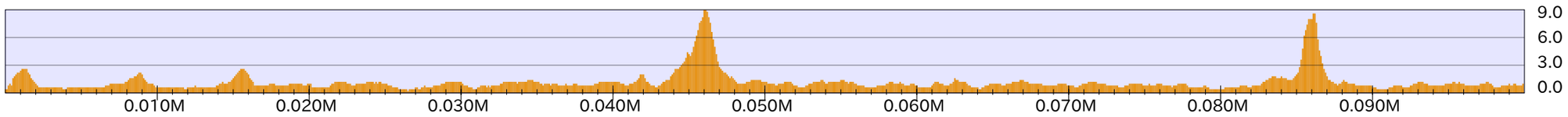

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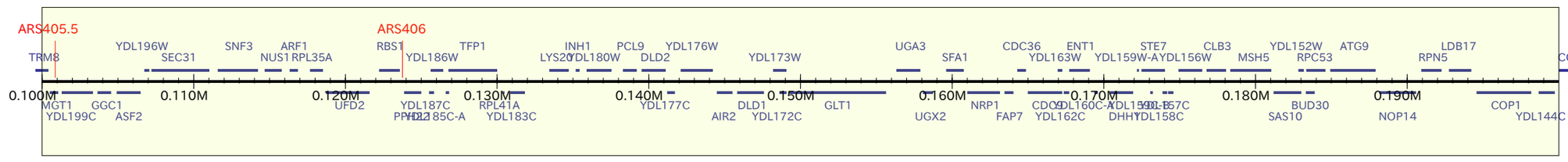

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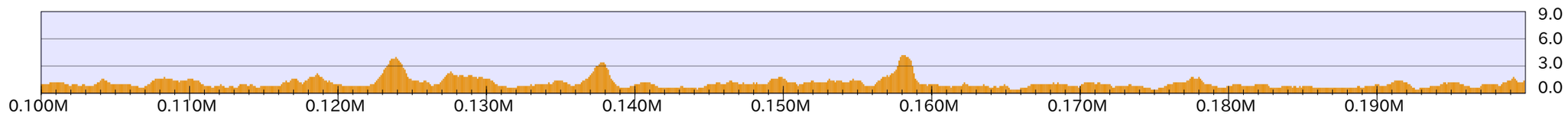

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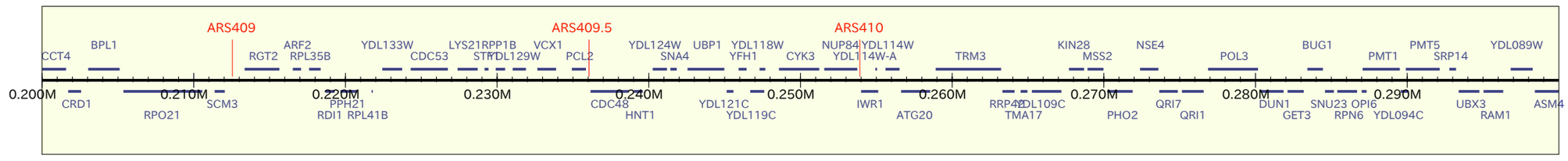

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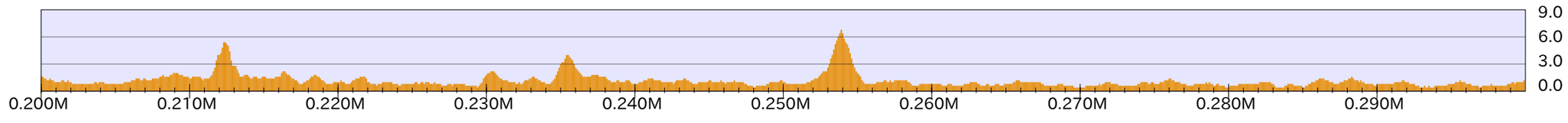

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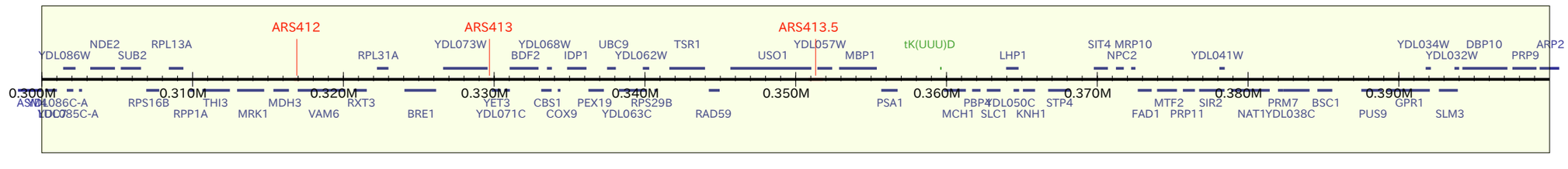

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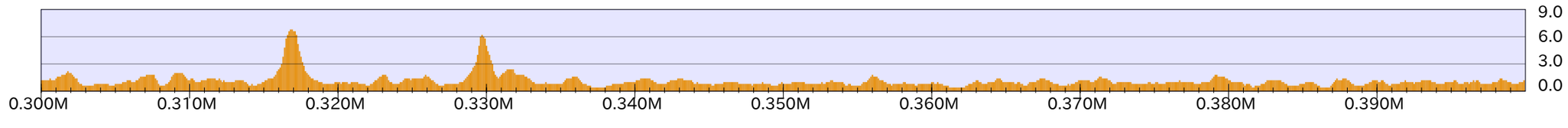

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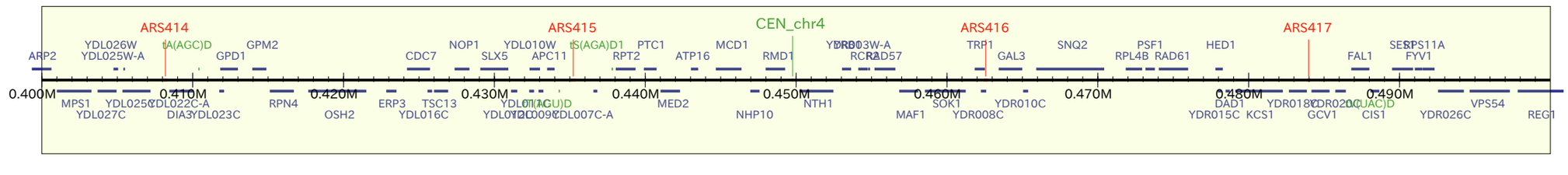

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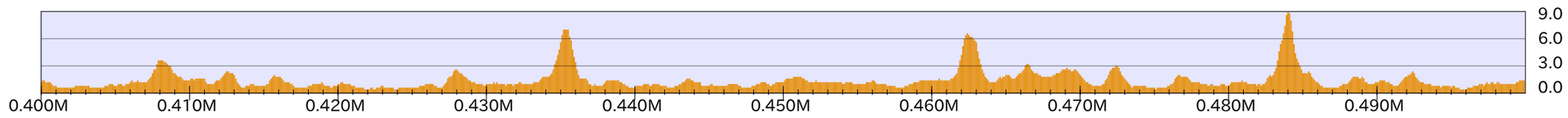

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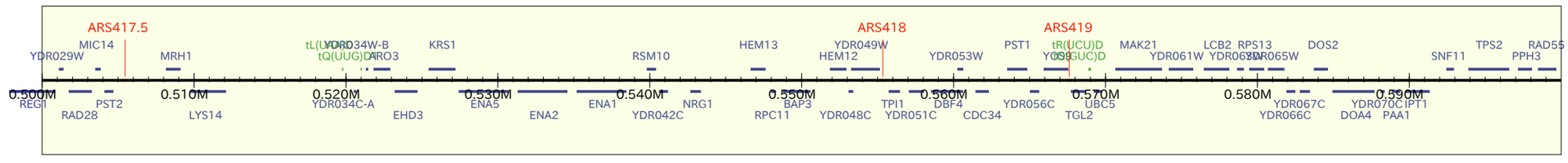

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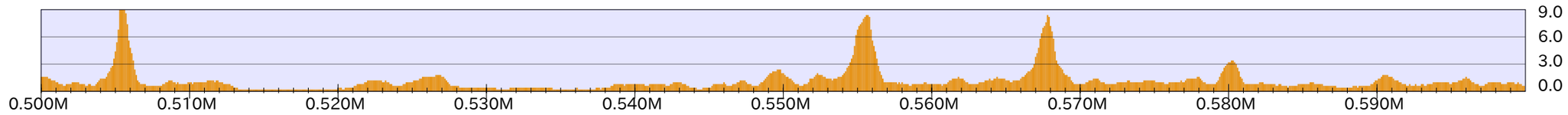

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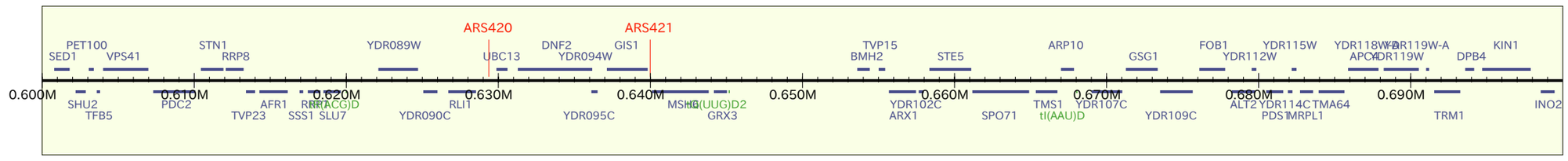

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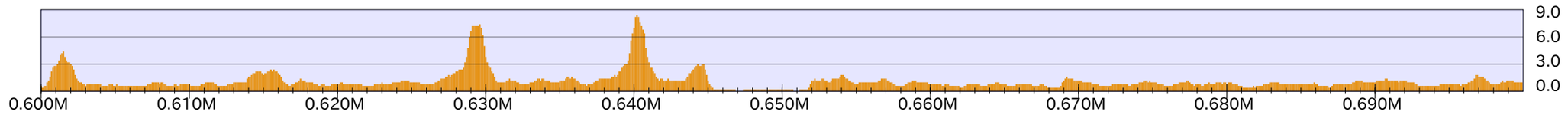

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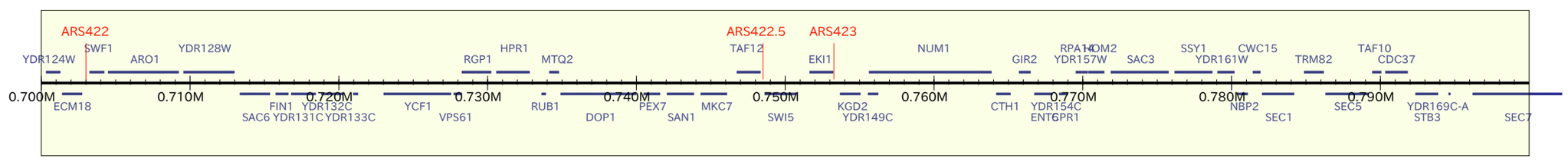

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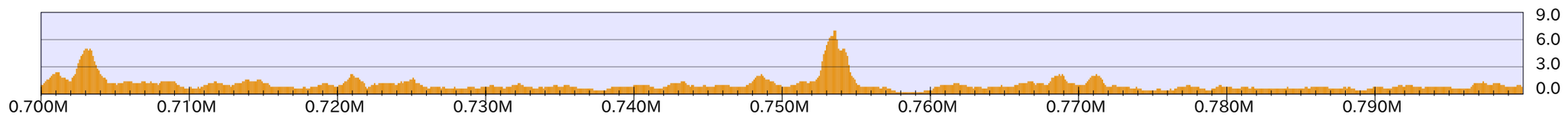

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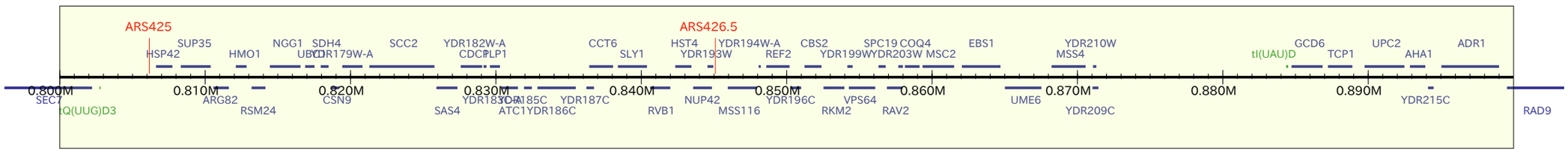

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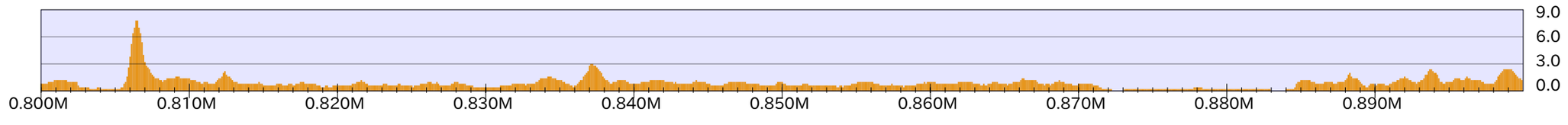

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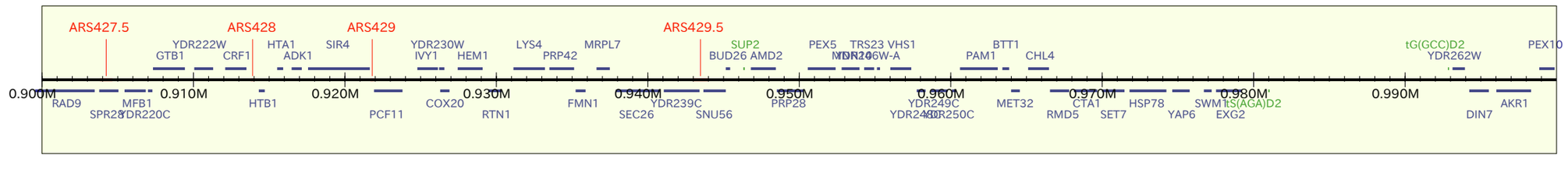

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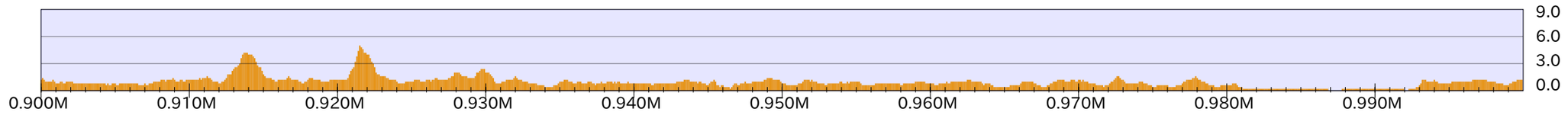

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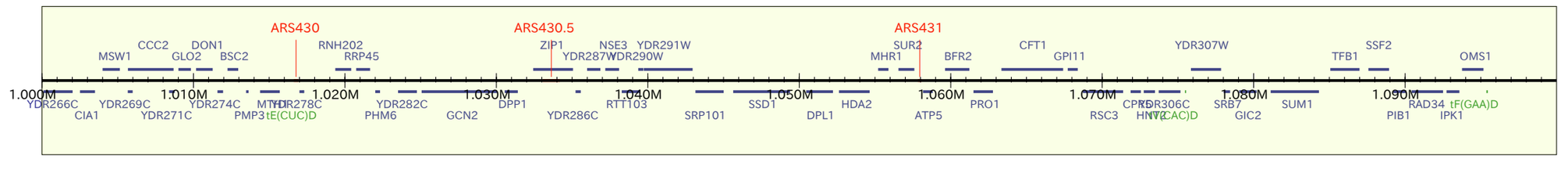

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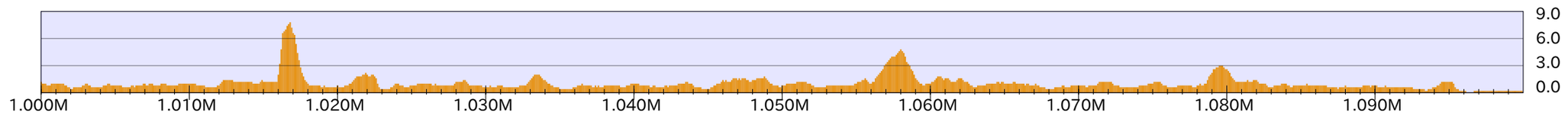

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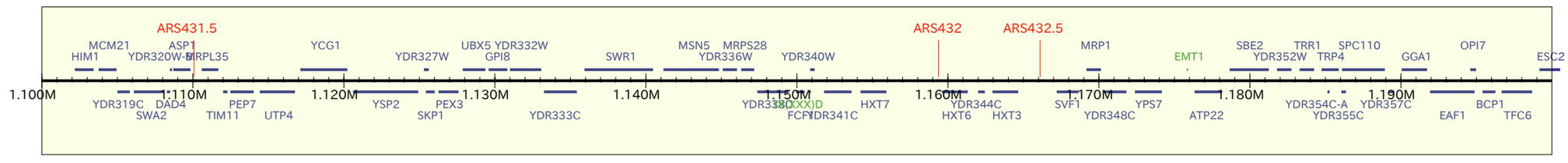

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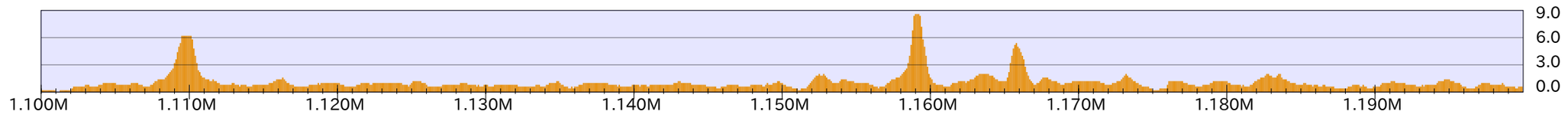

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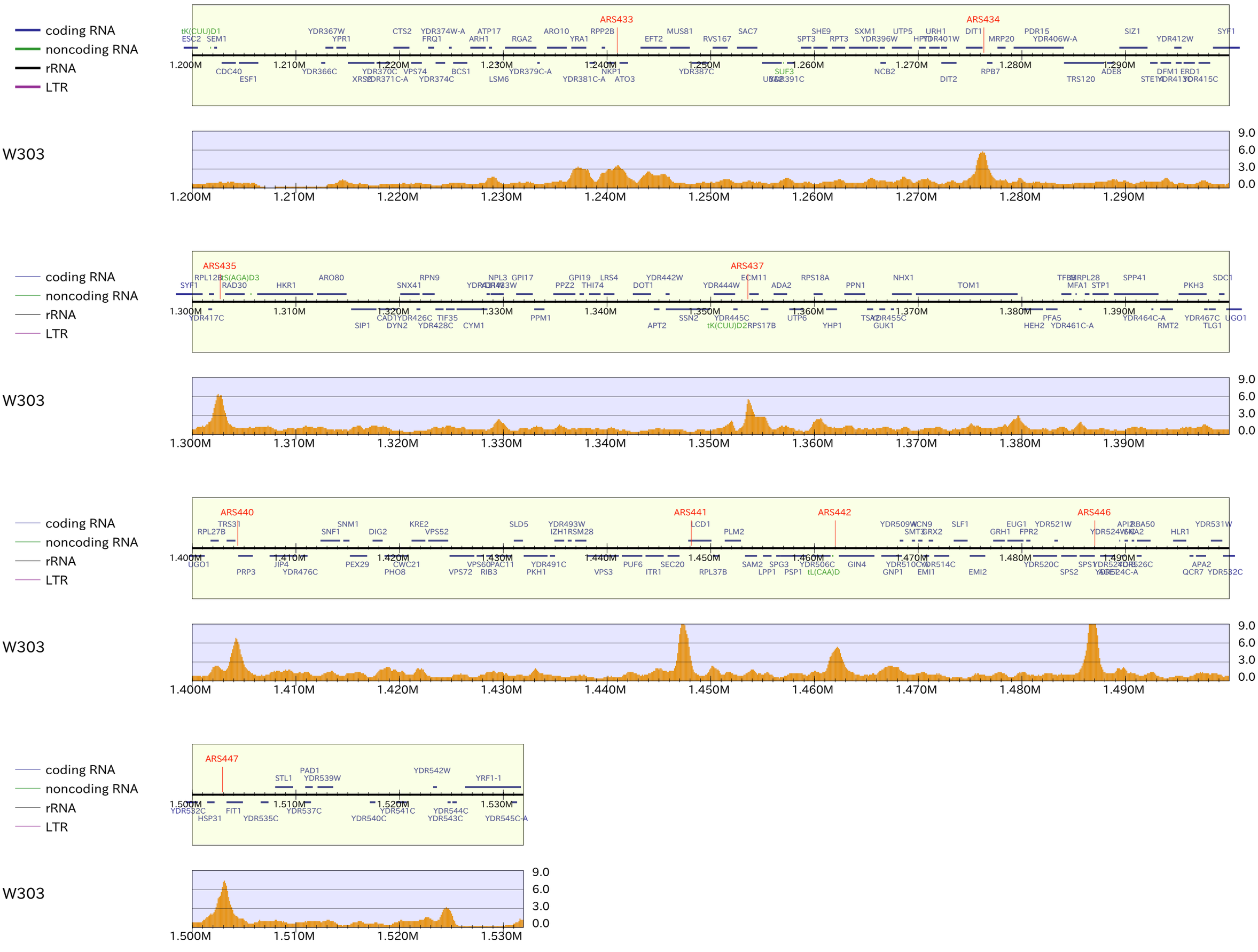
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W303
ARS433
ARS434
ARS435
ARS437
ARS440
ARS441
ARS442
ARS446
ARS447
1.200M
1.210M
1.220M
1.230M
1.240M
1.250M
1.260M
1.270M
1.280M
1.290M
1.300M
1.310M
1.320M
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1.380M
1.390M
1.400M
1.410M
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1.450M
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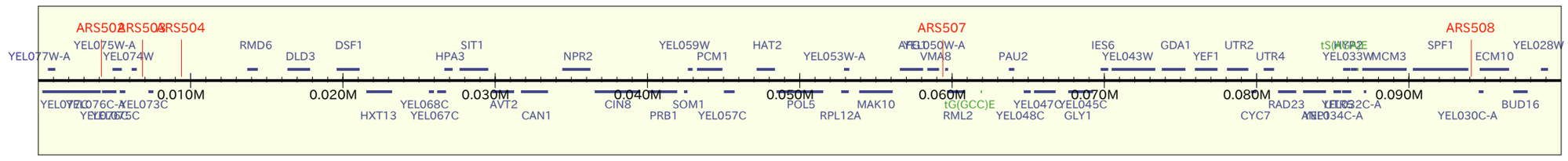
chrV

coding RNA
noncoding RNA
rRNA
LTR



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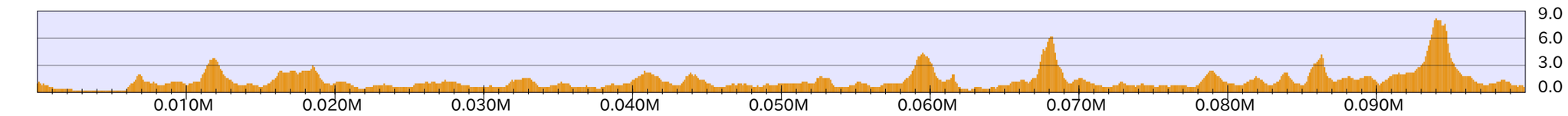
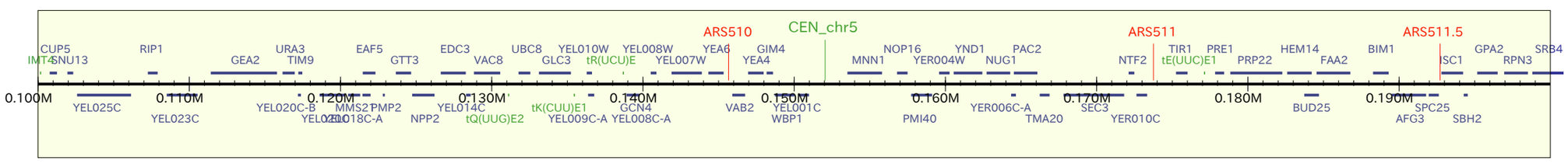


coding RNA
noncoding RNA
rRNA
LTR



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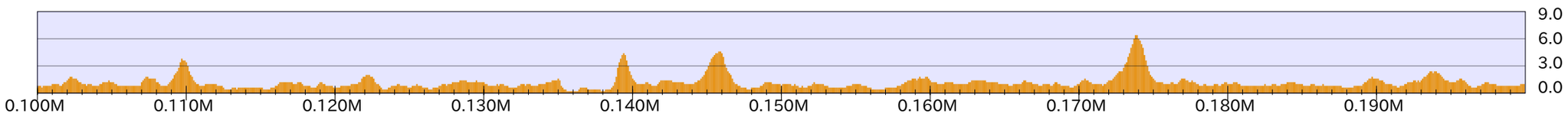
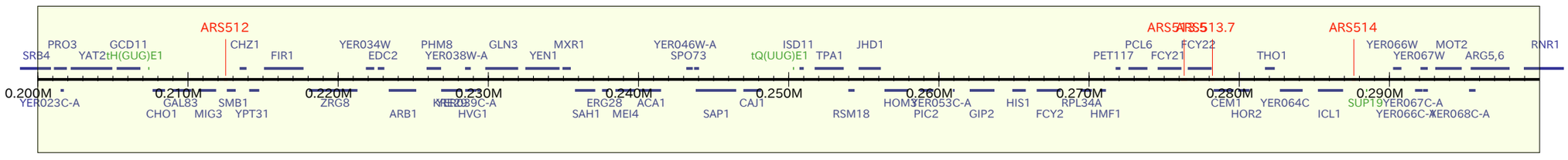


coding RNA
noncoding RNA
rRNA
LTR



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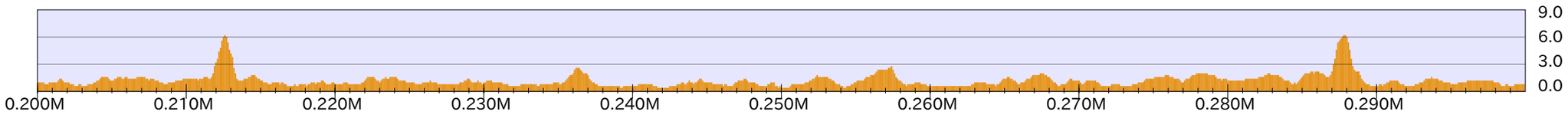
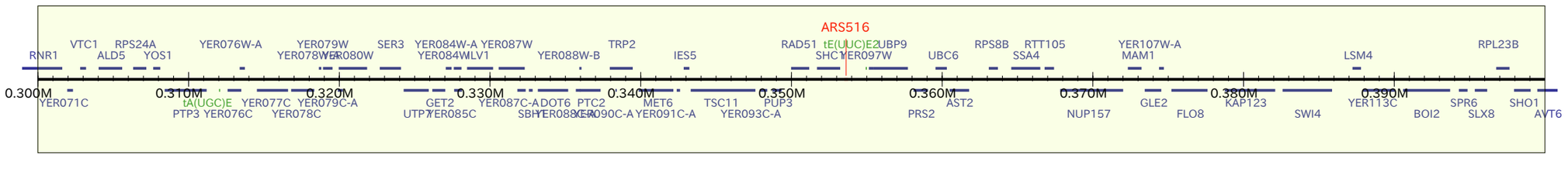


coding RNA
noncoding RNA
rRNA
LTR



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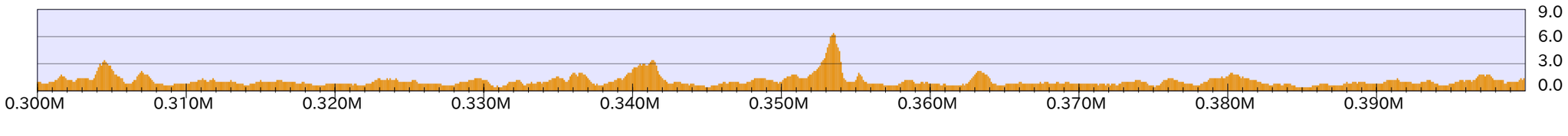

coding RNA
noncoding RNA
rRNA
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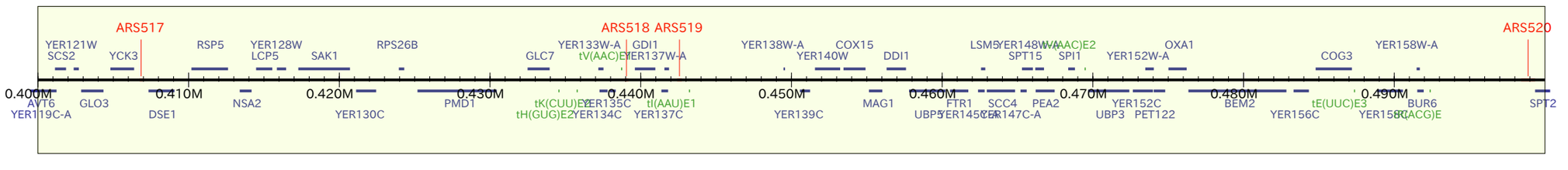

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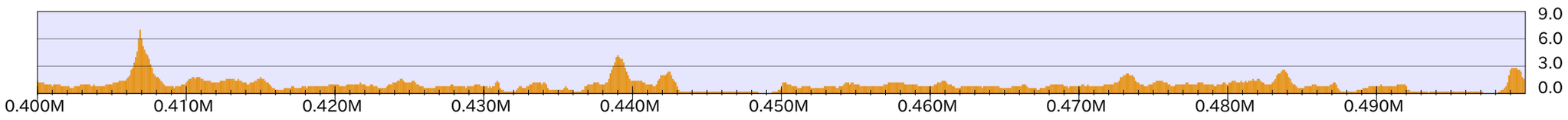
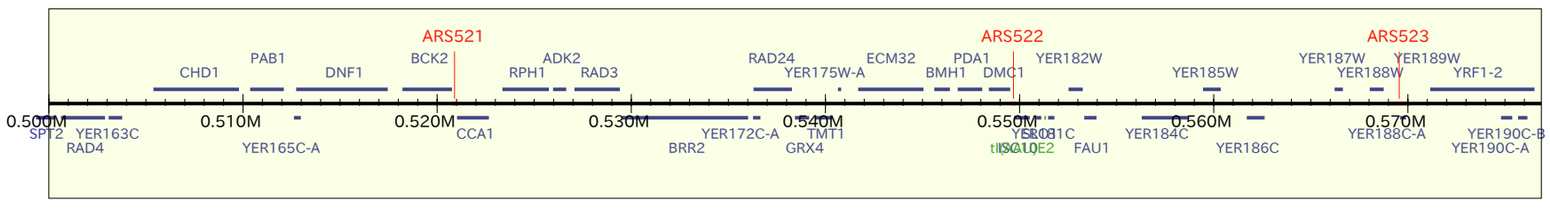


coding RNA
noncoding RNA
rRNA
LTR



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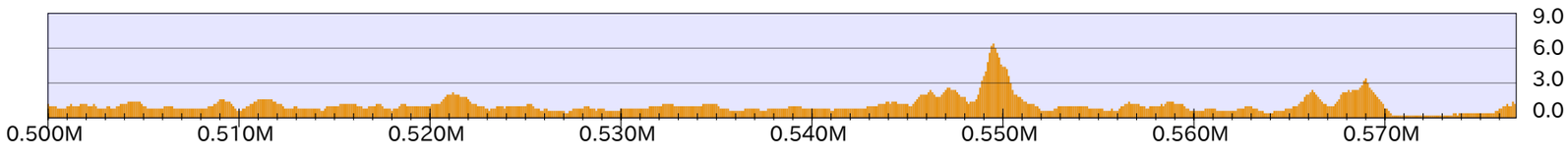
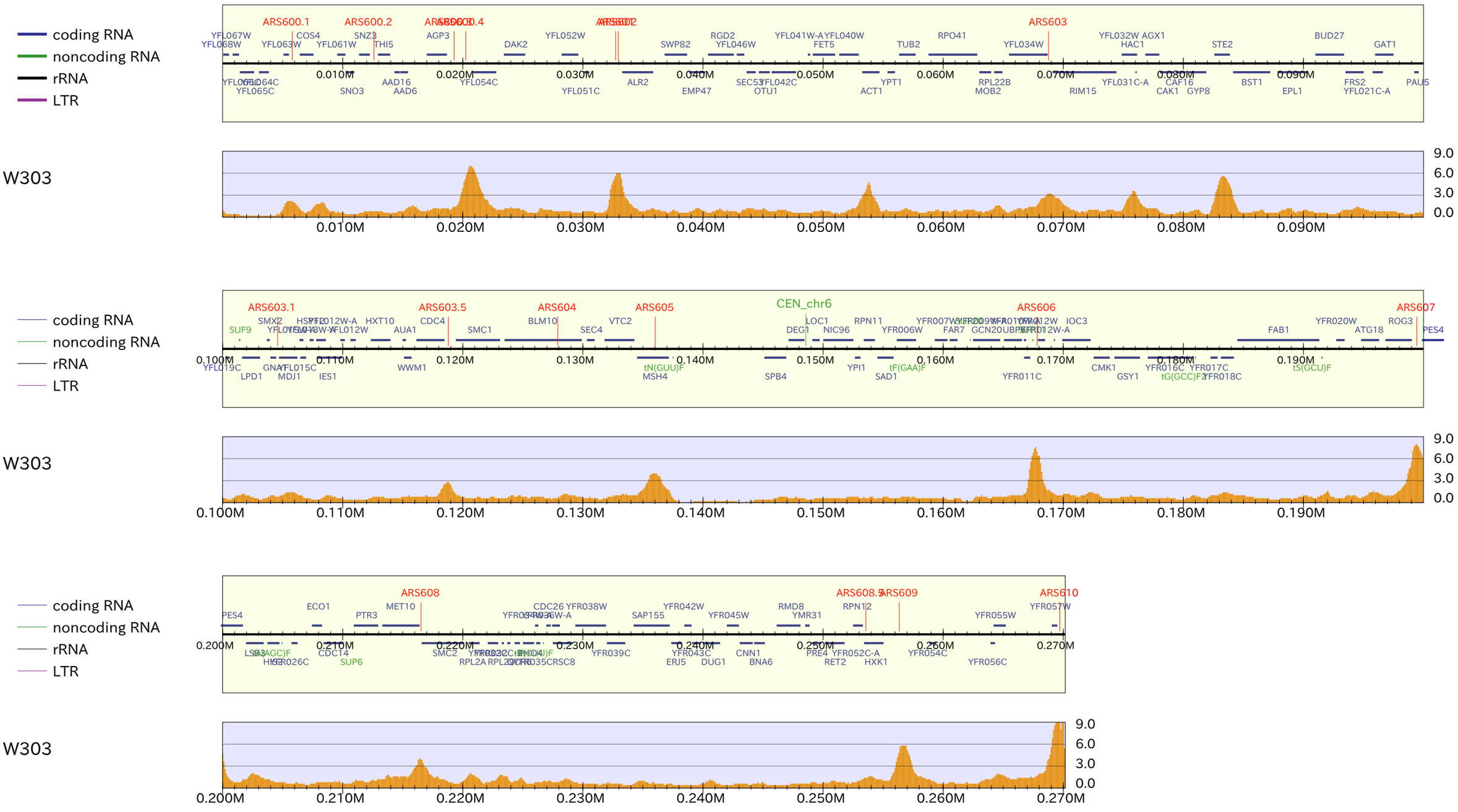


chrVI


coding RNA
noncoding RNA
rRNA
LTR
W303
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ARS600.2
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YFL068W
YFL063W
COS4
YFL061W
SNZ3
THI5
AGP3
DAK2
YFL052W
RGD2
SWP82
YFL046W
YFL041W-A
YFL040W
FET5
TUB2
RPO41
YFL034W
YFL032W
AGX1
HAC1
STE2
BUD27
GAT1
YFL065C
SNO3
AAD16
AAD6
YFL054C
YFL051C
ALR2
EMP47
SEC53
YFL042C
OTU1
YPT1
ACT1
RPL22B
MOB2
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ARS603.5
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ARS605
CEN_chr6
ARS606
ARS607
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SMX2
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HXT10
CDC4
SMC1
BLM10
SEC4
VTC2
LOC1
RPN11
NIC96
YFR006W
FAR7
GCN20
IOC3
FAB1
YFR020W
ATG18
ROG3
PES4
YFL019C
LPD1
GNA1
MDJ1
YFL015C
IES1
AUA1
WWM1
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MSH4
SPB4
DEG1
YPI1
tF(GAA)F
SAD1
YFR011C
CMK1
GSY1
YFR016C
tG(GCC)F2
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tS(GCU)F
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0.140M
0.150M
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coding RNA
noncoding RNA
rRNA
LTR
W303
ARS608
ARS608.5
ARS609
ARS610
PES4
ECO1
PTR3
MET10
CDC26
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YFR034W-A
SAP155
YFR042W
YFR045W
RMD8
YMR31
RPN12
YFR055W
YFR057W
SMC2
YFR039C
YFR043C
ERJ5
DUG1
CNN1
BNA6
PRE4
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RET2
HXK1
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YFR056C
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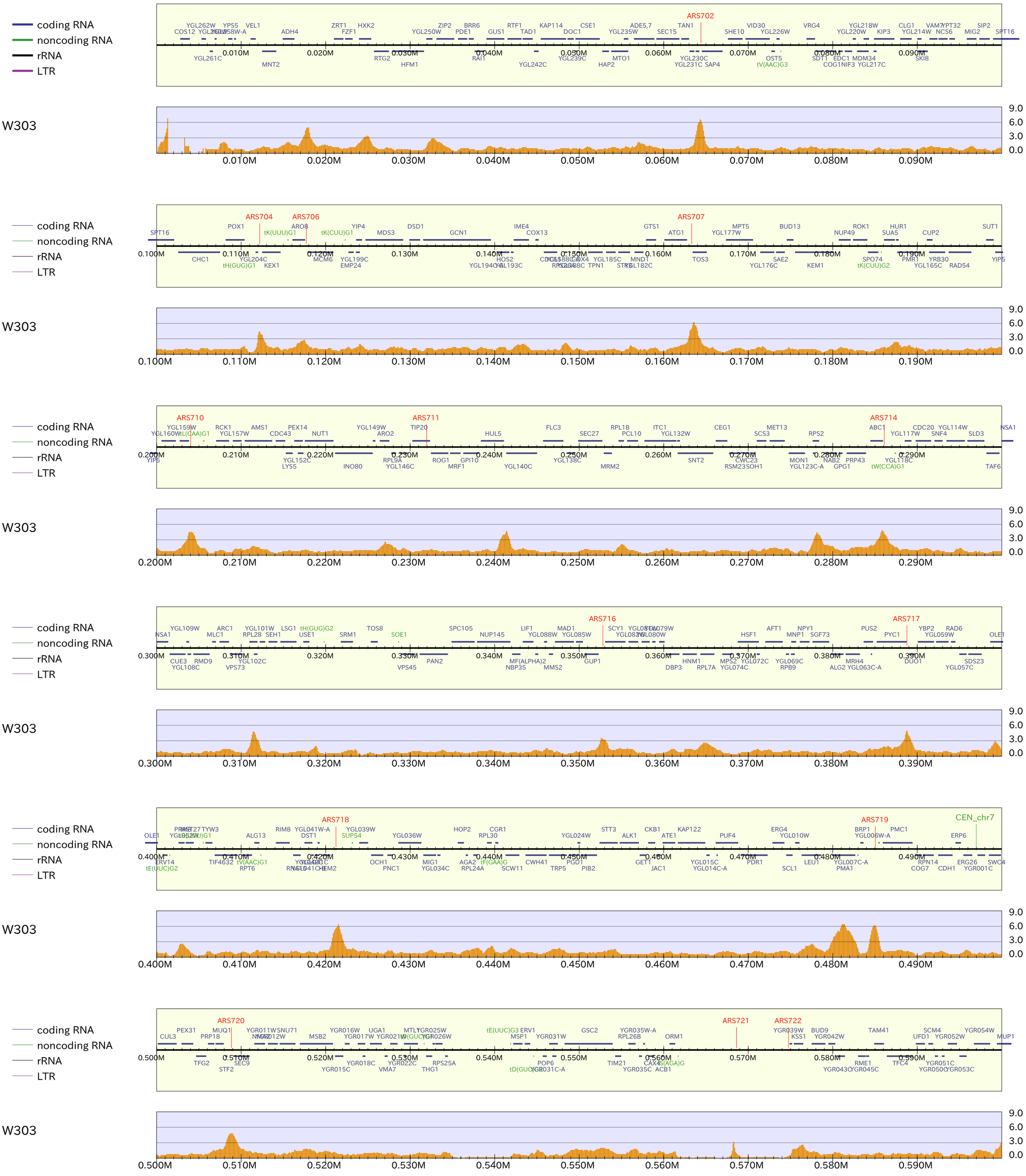
chrVII_1


coding RNA
noncoding RNA
rRNA
LTR
W303
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ARS704
ARS706
ARS707
ARS710
ARS711
ARS714
ARS716
ARS717
ARS718
ARS719
ARS720
ARS721
ARS722
CEN_chr7
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0.020M
0.030M
0.040M
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0.060M
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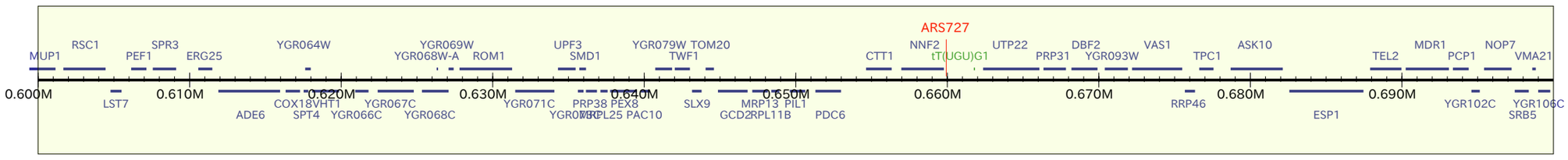
chrVII_2

coding RNA
noncoding RNA
rRNA
LTR



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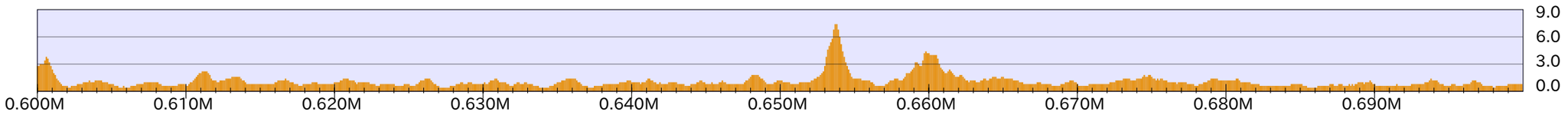
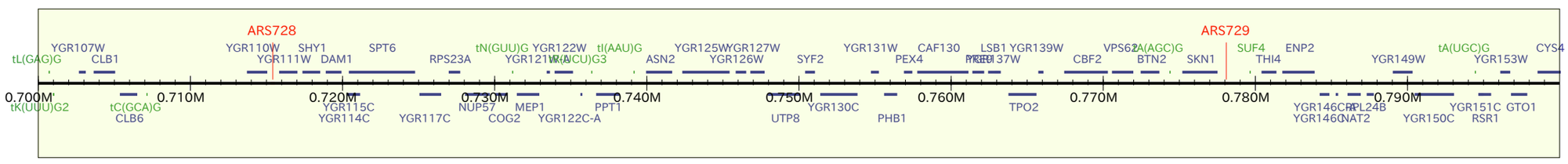


coding RNA
noncoding RNA
rRNA
LTR



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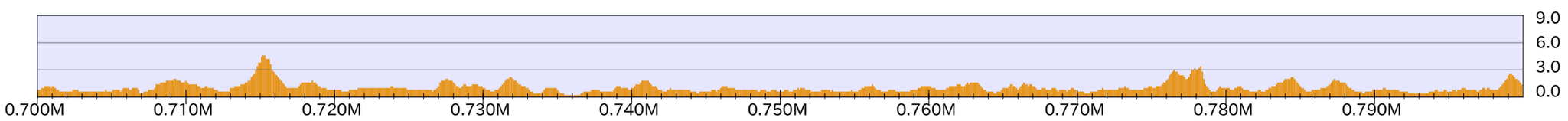
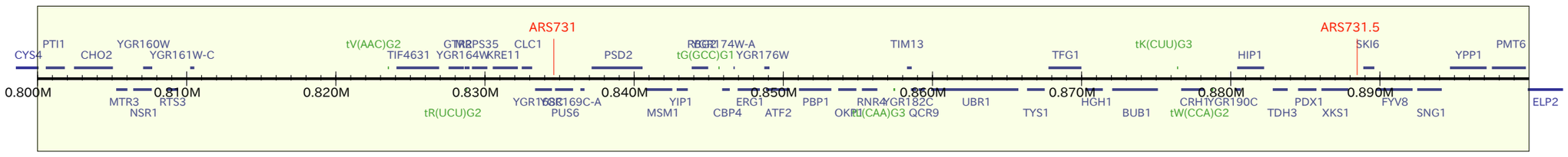


coding RNA
noncoding RNA
rRNA
LTR



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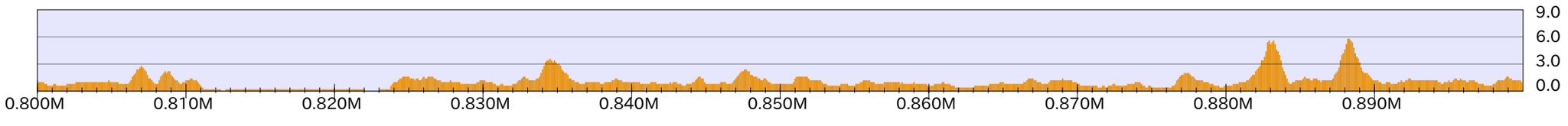
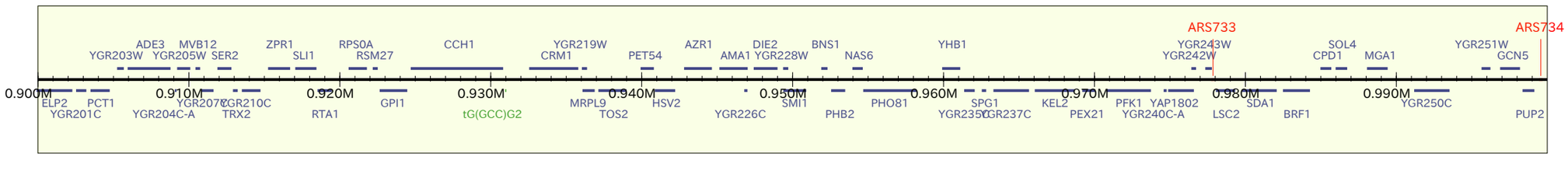


coding RNA
noncoding RNA
rRNA
LTR



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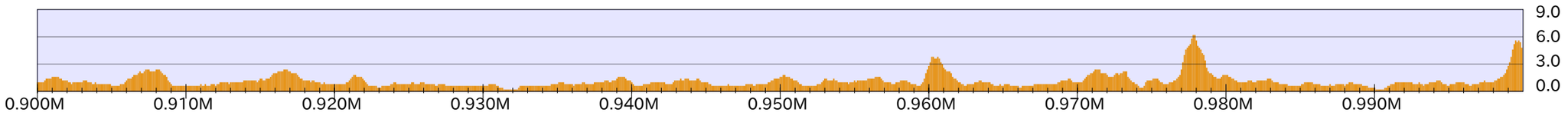
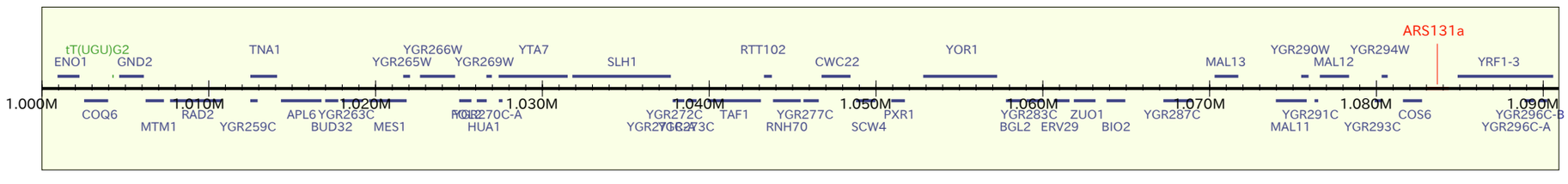


coding RNA
noncoding RNA
rRNA
LTR



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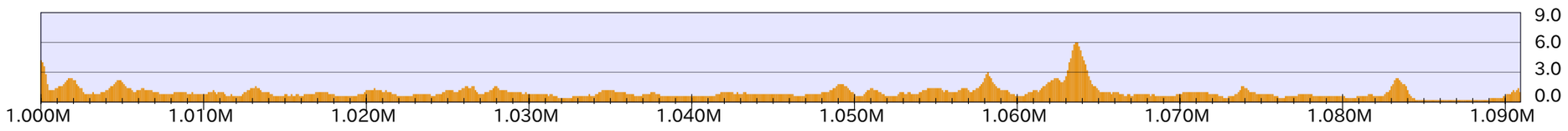
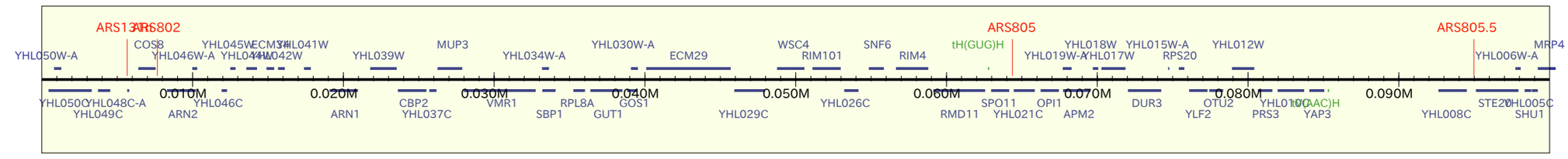


chrVIII

coding RNA
noncoding RNA
rRNA
LTR



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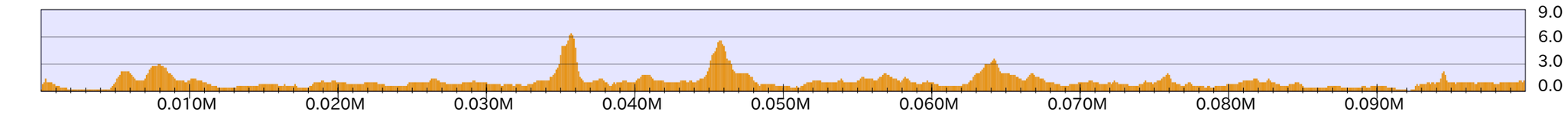
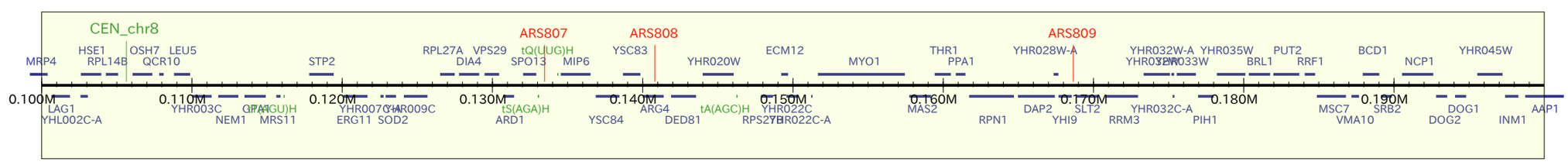


coding RNA
noncoding RNA
rRNA
LTR



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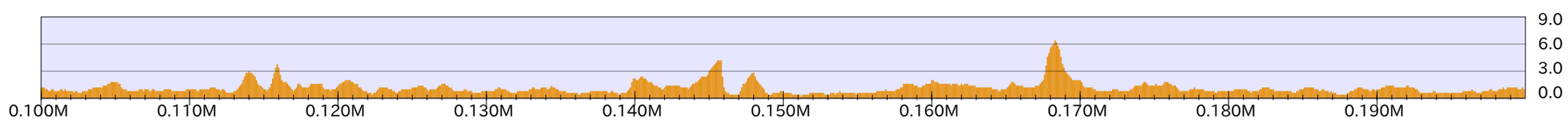
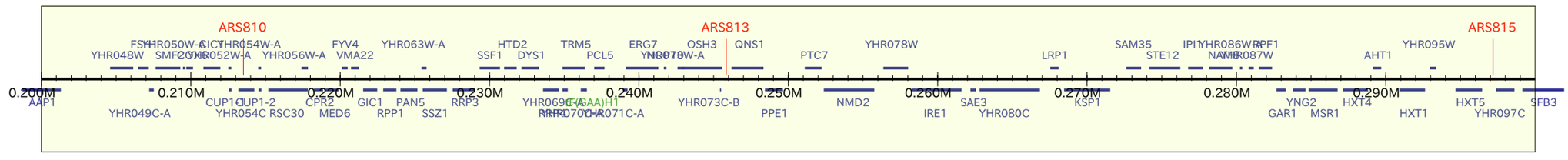


coding RNA
noncoding RNA
rRNA
LTR



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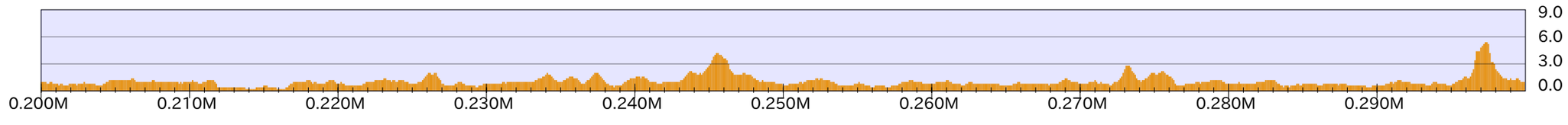
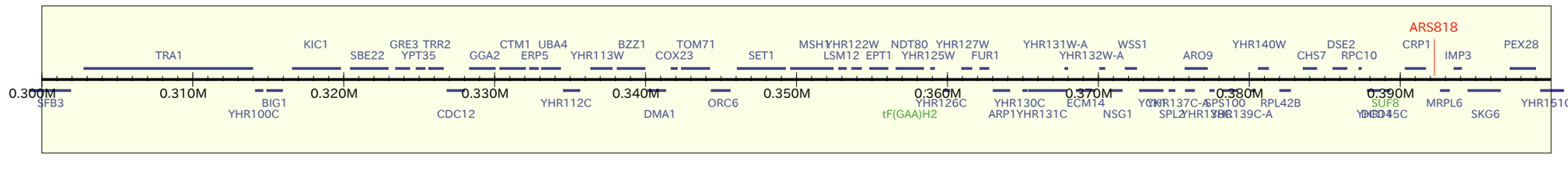


coding RNA
noncoding RNA
rRNA
LTR



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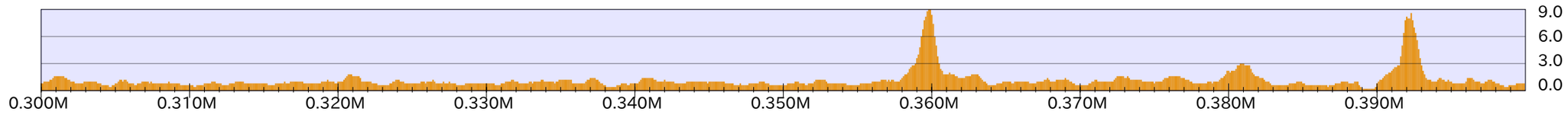
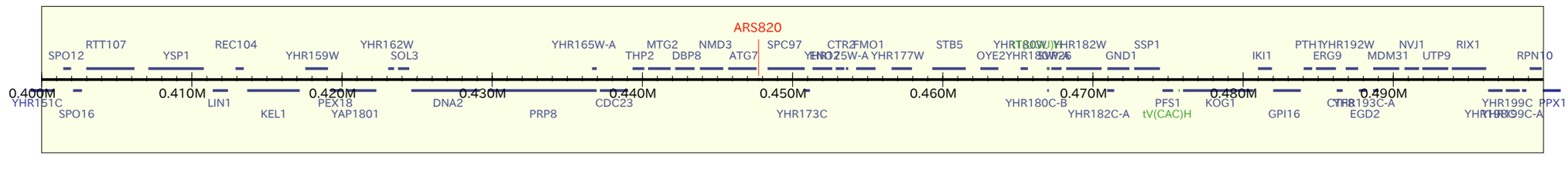


coding RNA
noncoding RNA
rRNA
LTR



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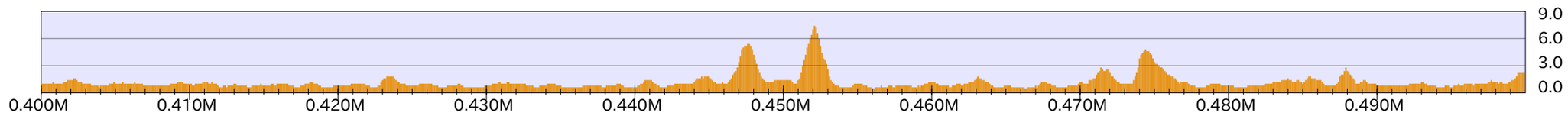
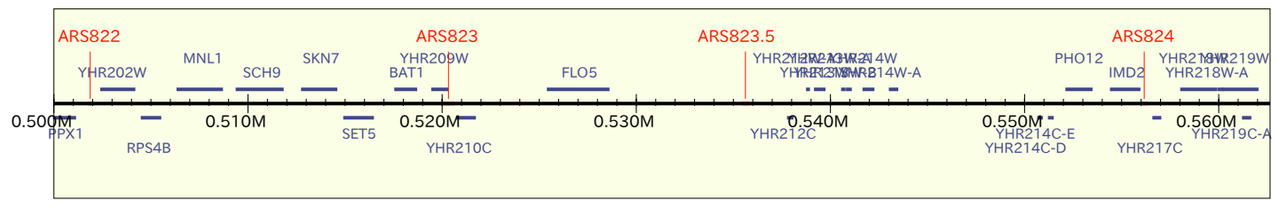


coding RNA
noncoding RNA
rRNA
LTR



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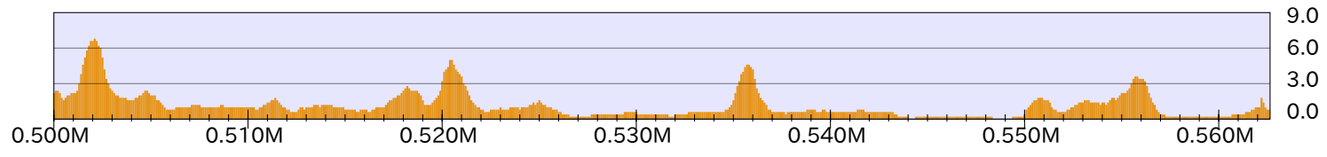
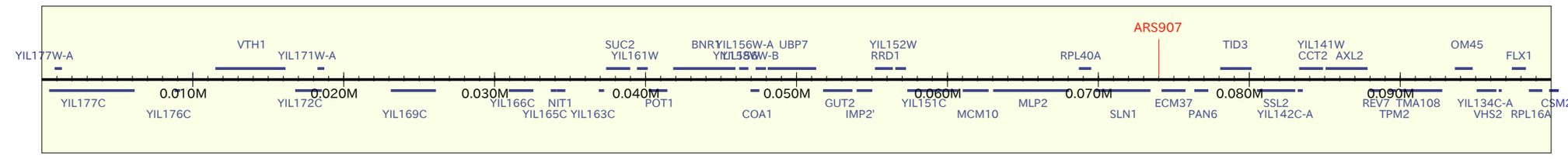


chrIX

coding RNA
noncoding RNA
rRNA
LTR



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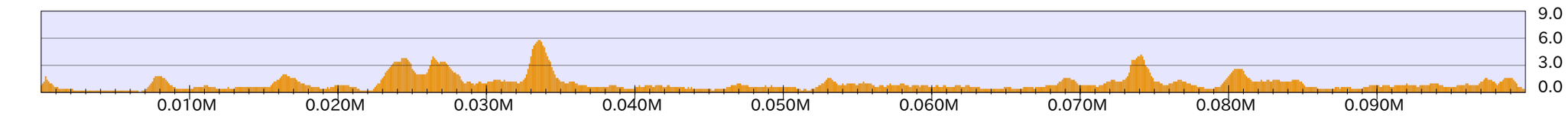
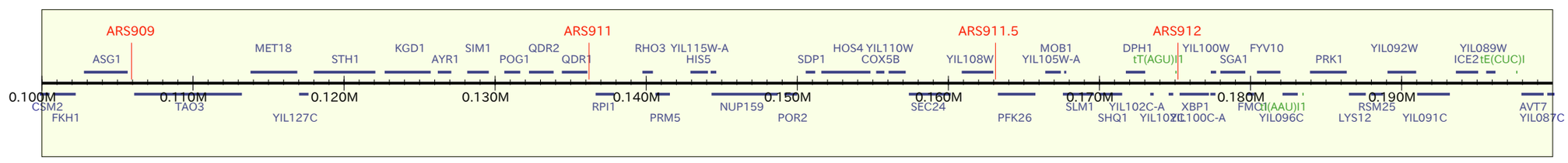


coding RNA
noncoding RNA
rRNA
LTR



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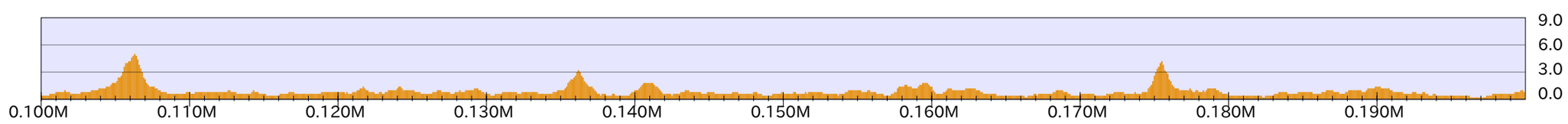
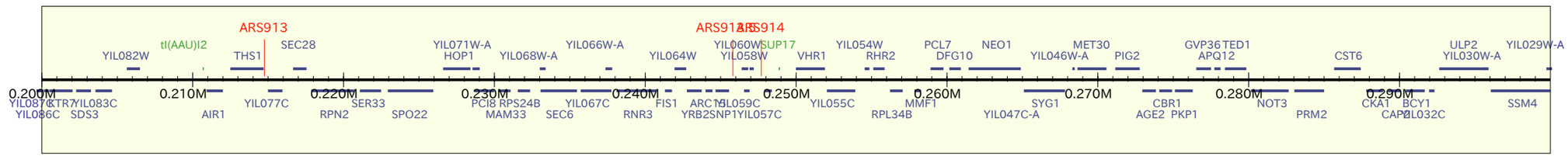


coding RNA
noncoding RNA
rRNA
LTR



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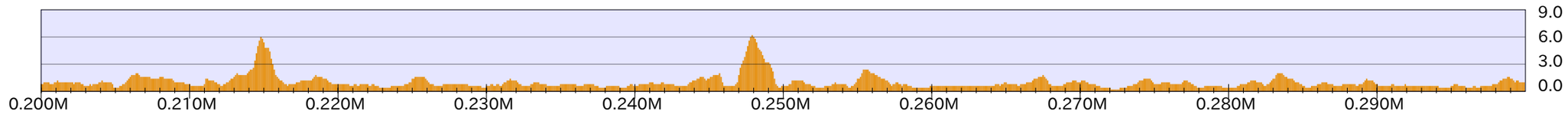
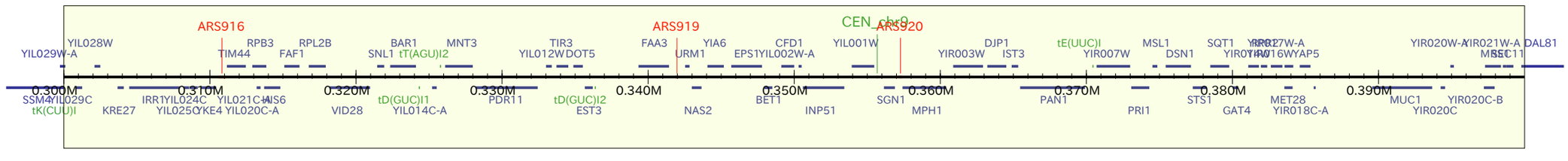


coding RNA
noncoding RNA
rRNA
LTR



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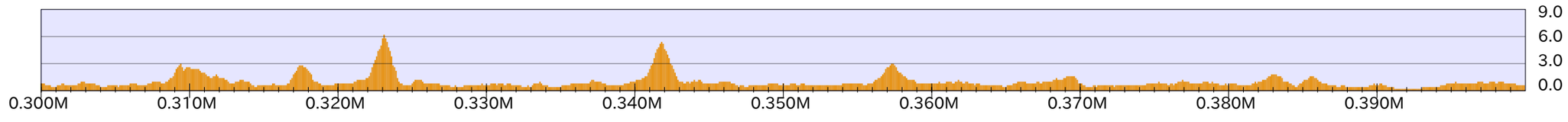
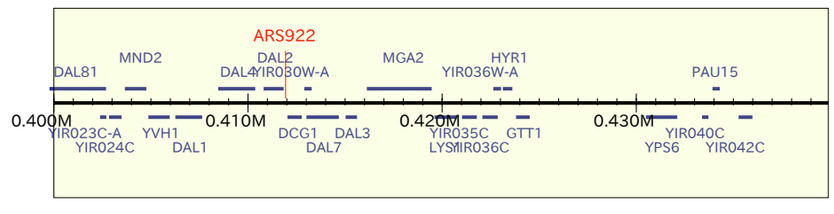


coding RNA
noncoding RNA
rRNA
LTR



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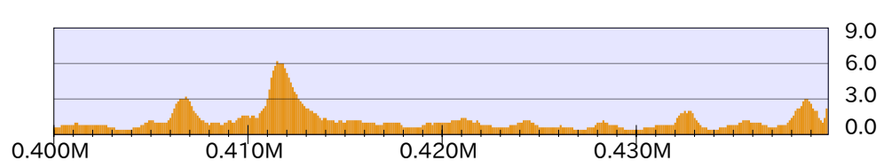
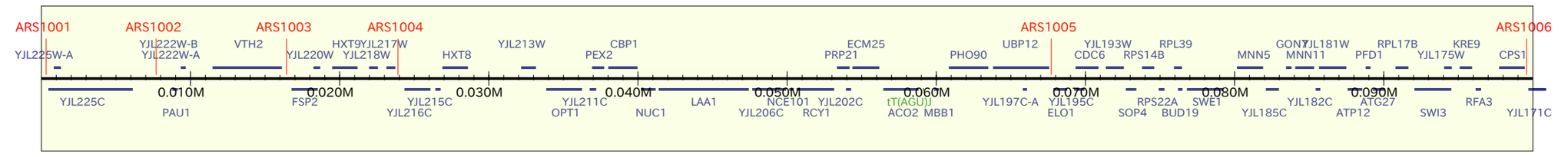


chrX_1

coding RNA
noncoding RNA
rRNA
LTR



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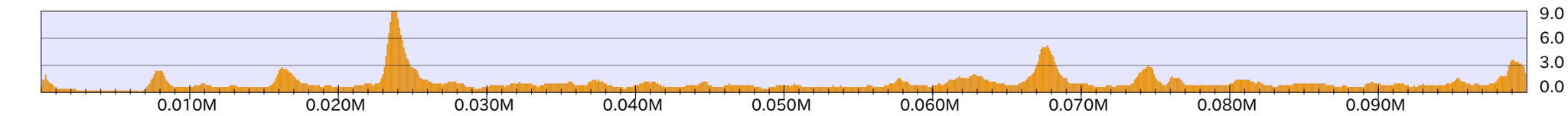
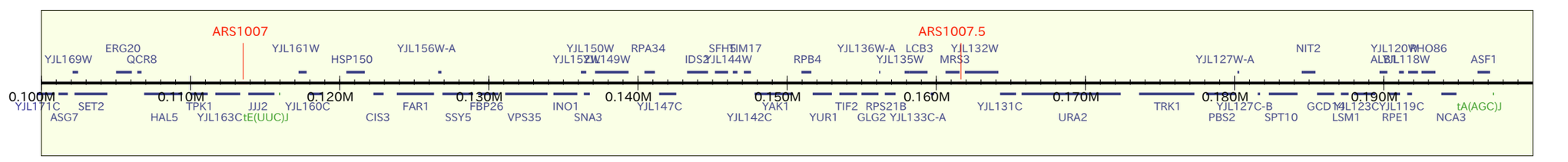


coding RNA
noncoding RNA
rRNA
LTR



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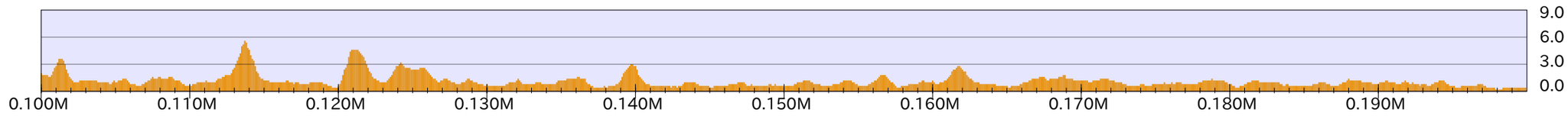

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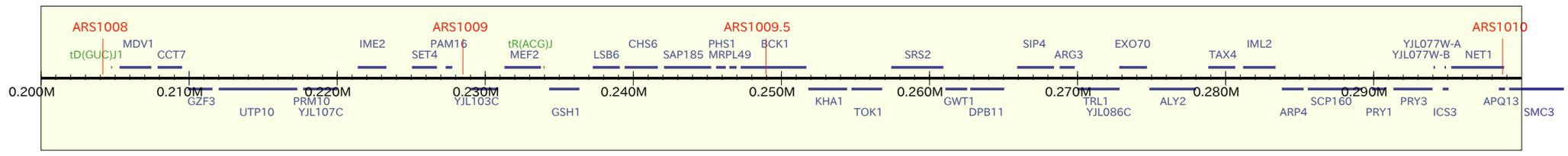
noncoding RNA
rRNA
LTR



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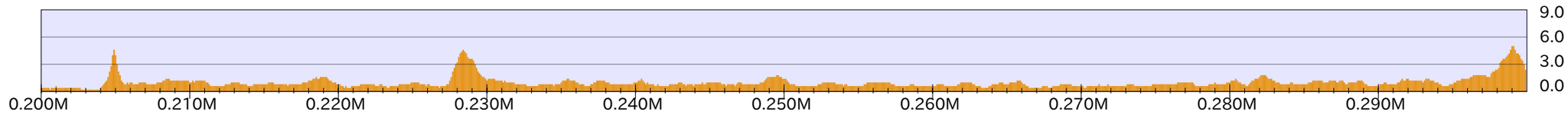
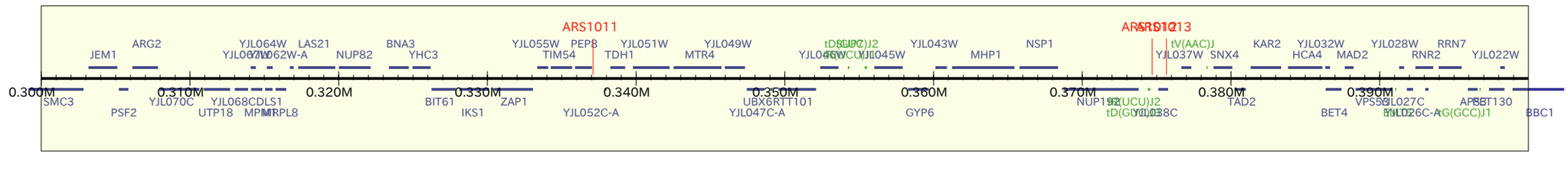


coding RNA
noncoding RNA
rRNA
LTR



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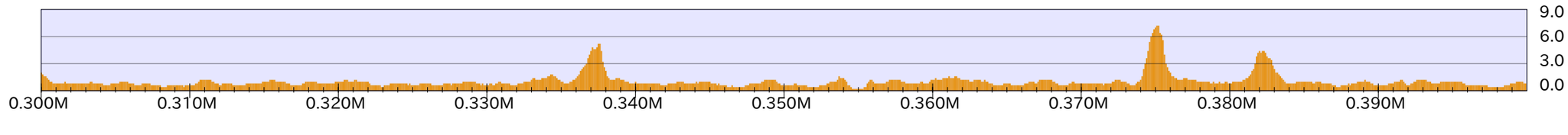
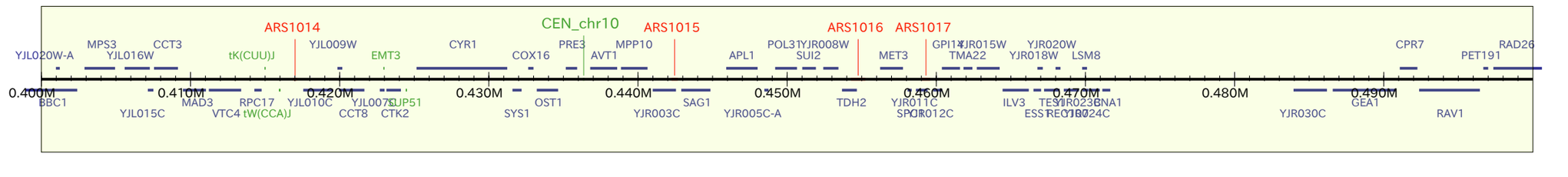


coding RNA
noncoding RNA
rRNA
LTR



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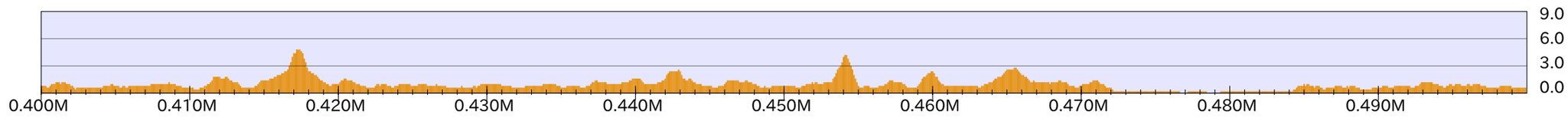
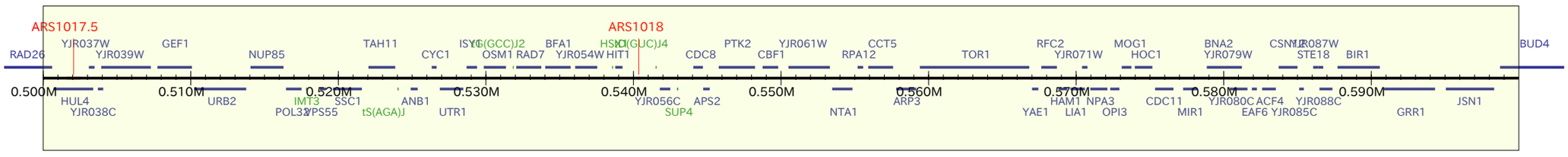
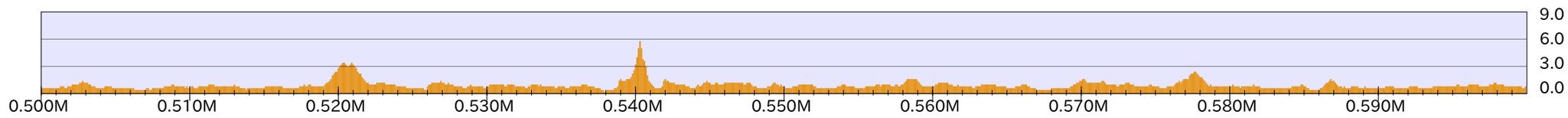


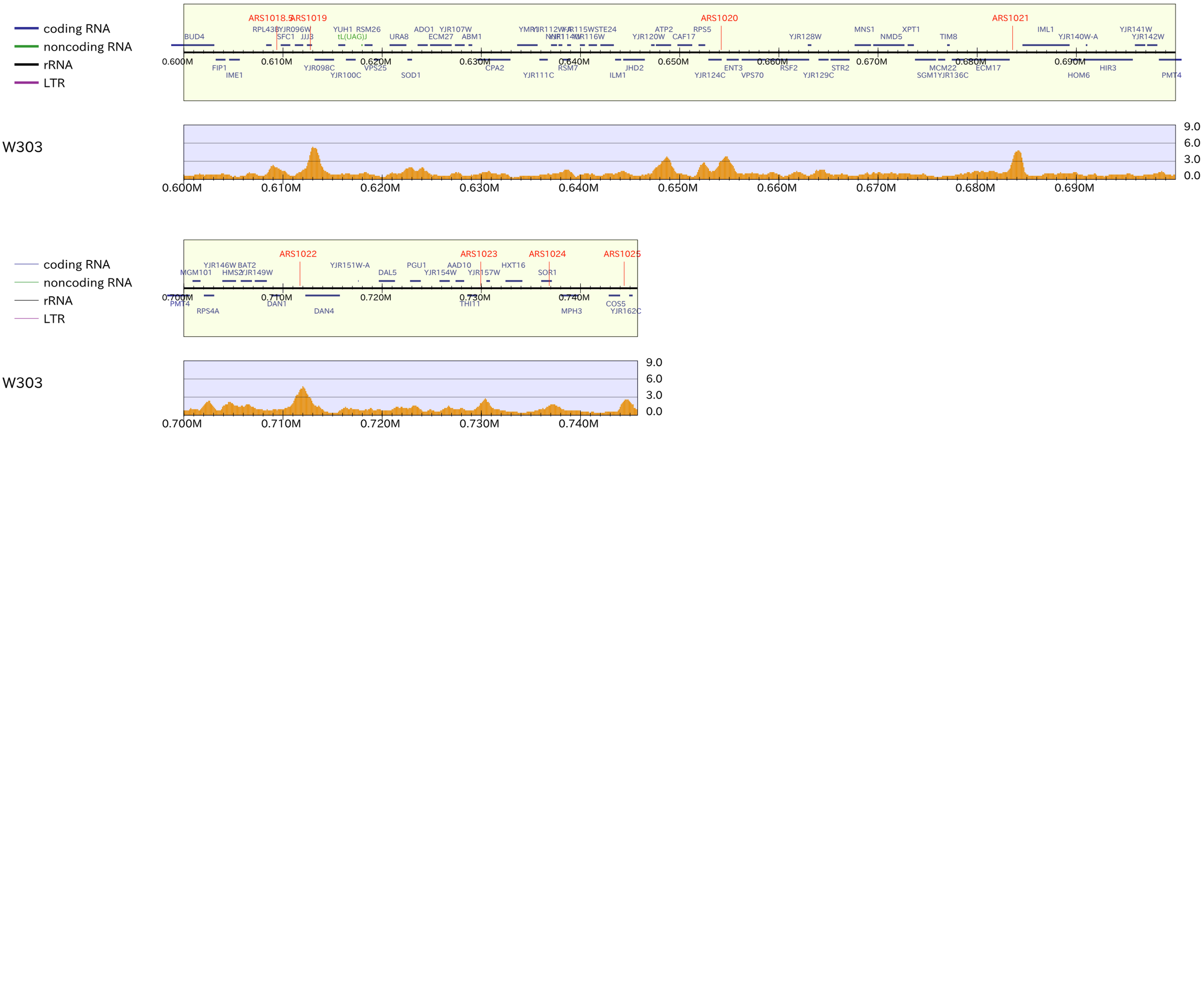
coding RNA
noncoding RNA
rRNA
LTR



W303



chrX_2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noncoding RNA
rRNA
LTR
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ARS1019
ARS1020
ARS1021
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RPL43B
YJR096W
SFC1
JJJ3
YUH1
RSM26
tL(UAG)J
URA8
ADO1
YJR107W
ECM27
ABM1
YJR120W
ATP2
CAF17
RPS5
YJR128W
MNS1
NMD5
XPT1
TIM8
IML1
YJR140W-A
YJR141W
YJR142W
FIP1
IME1
YJR098C
YJR100C
VPS25
SOD1
CPA2
YJR111C
RSM7
JHD2
ILM1
ENT3
YJR124C
VPS70
RSF2
YJR129C
STR2
MCM22
SGM1
YJR136C
ECM17
HOM6
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ARS1023
ARS1024
ARS1025
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BAT2
MGM101
HMS2
YJR149W
YJR151W-A
DAL5
PGU1
YJR154W
AAD10
YJR157W
HXT16
SOR1
PMT4
RPS4A
DAN1
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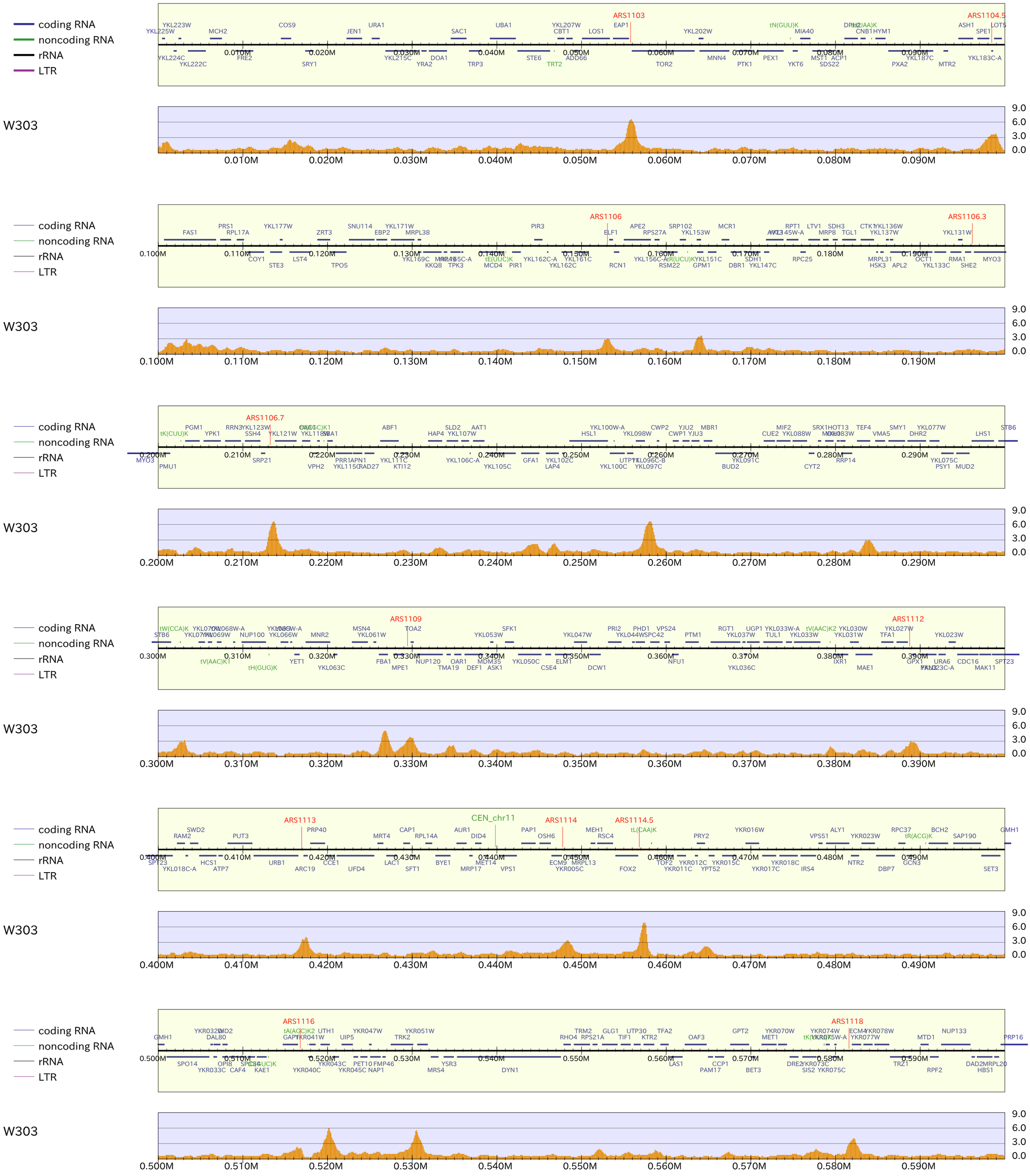
chrXI_1


coding RNA
noncoding RNA
rRNA
LTR
W303
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ARS1104.5
ARS1106
ARS1106.3
ARS1106.7
ARS1109
ARS1112
ARS1113
CEN_chr11
ARS1114
ARS1114.5
ARS1116
ARS1118
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0.030M
0.040M
0.050M
0.060M
0.070M
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0.100M
0.110M
0.120M
0.130M
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0.190M
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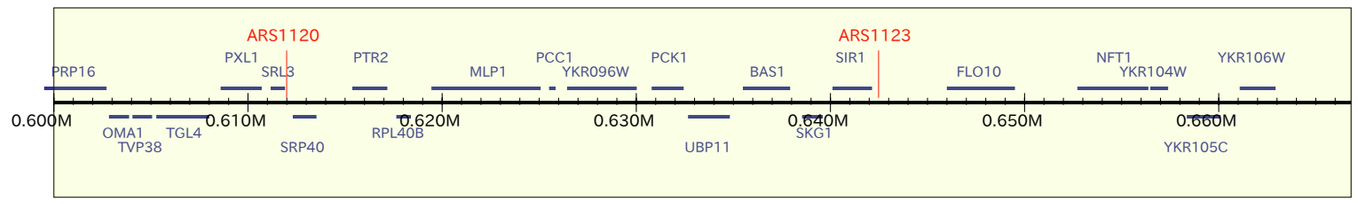
chrXI_2

coding RNA
noncoding RNA
rRNA
LTR



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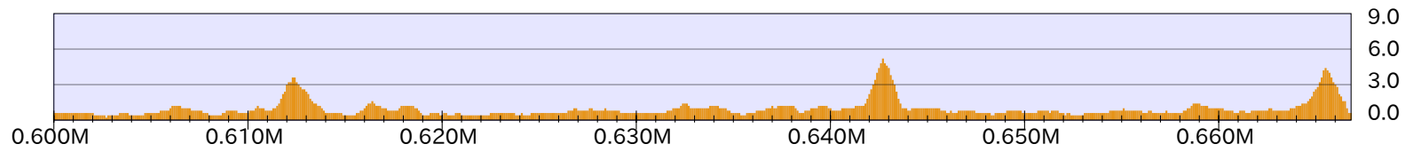
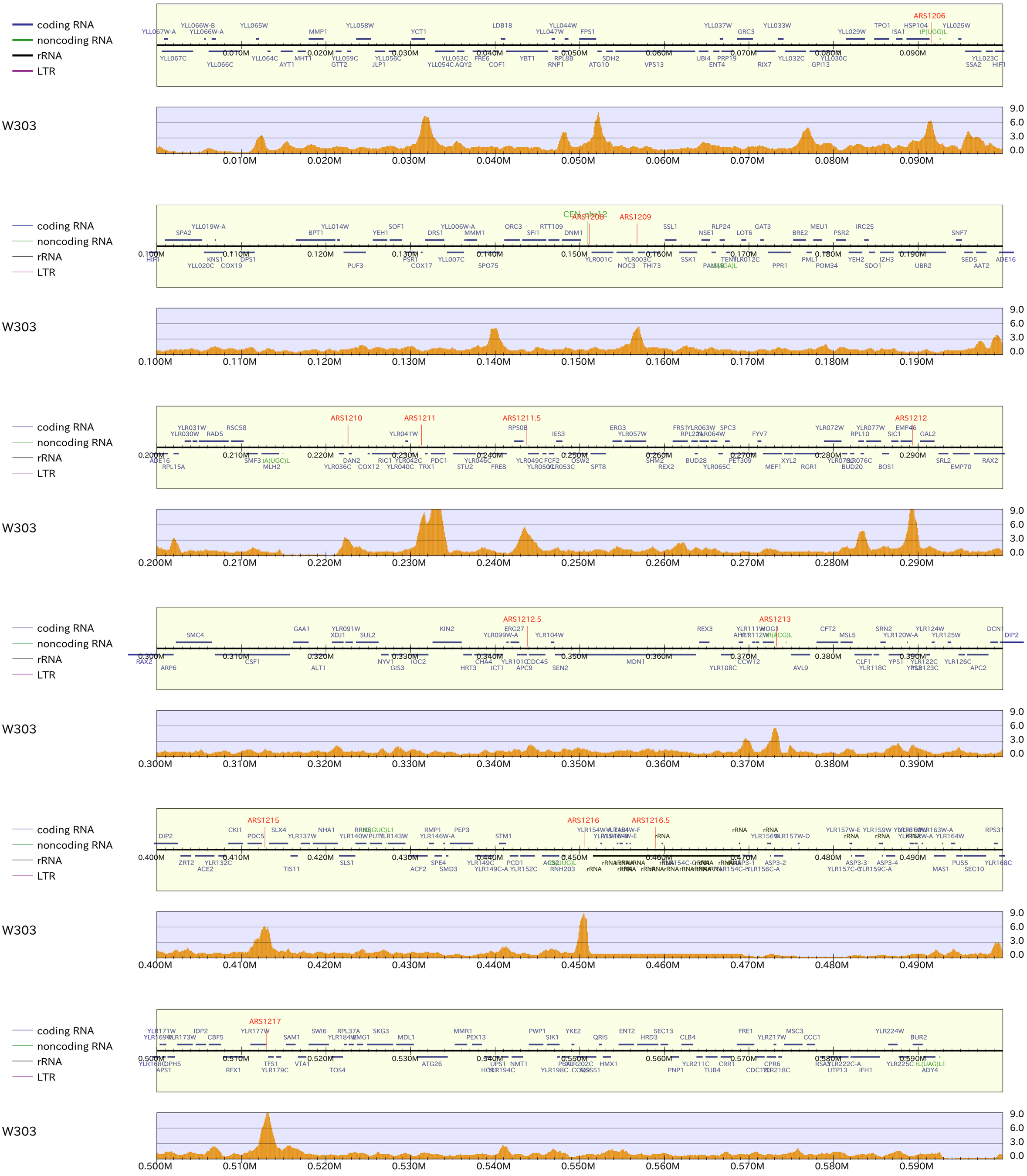


chrXII_1


coding RNA
noncoding RNA
rRNA
LTR
W303
ARS1206
ARS1210
ARS1211
ARS1211.5
ARS1212
ARS1212.5
ARS1213
ARS1215
ARS1216
ARS1216.5
ARS1217
CEN_chr12
ARS1208
ARS1209
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0.050M
0.060M
0.070M
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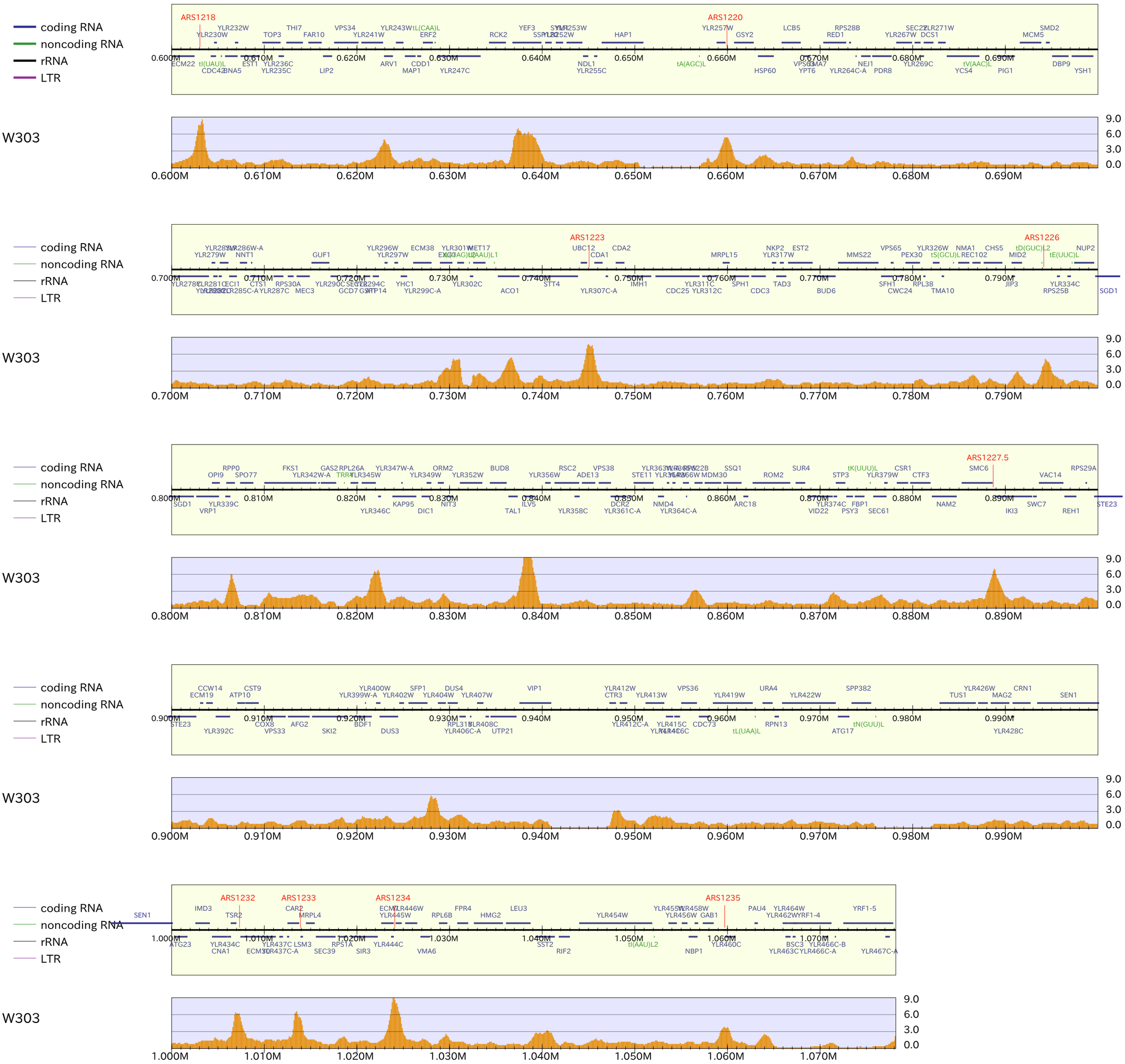
chrXII_2


coding RNA
noncoding RNA
rRNA
LTR
W303
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ARS1223
ARS1226
ARS1227.5
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ARS1233
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ARS1235
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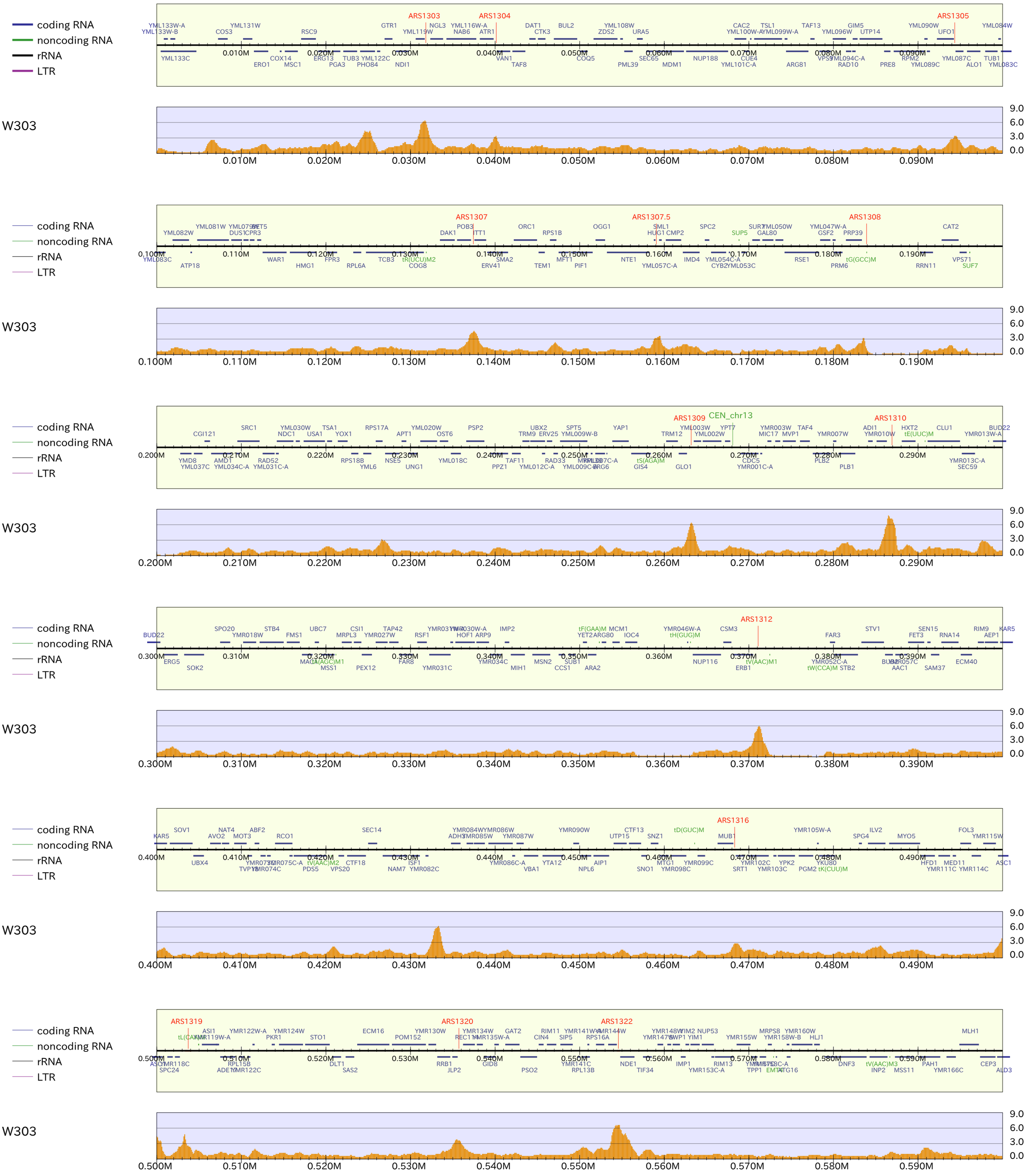
chrXIII_1


coding RNA
noncoding RNA
rRNA
LTR
W303
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ARS1304
ARS1305
ARS1307
ARS1307.5
ARS1308
ARS1309
CEN_chr13
ARS1310
ARS1312
ARS1316
ARS1319
ARS1320
ARS1322
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0.020M
0.030M
0.040M
0.050M
0.060M
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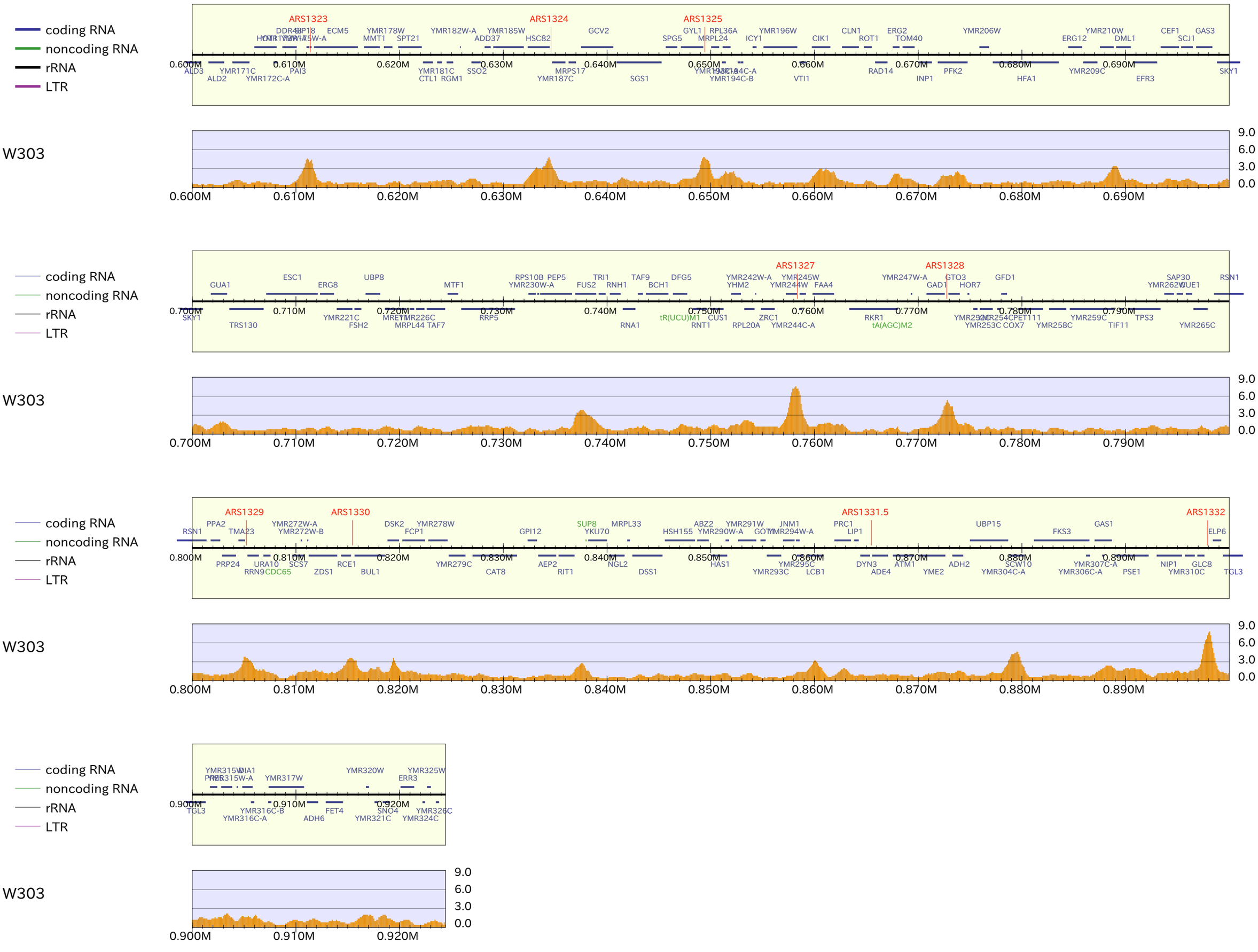
chrXIII_2


coding RNA
noncoding RNA
rRNA
LTR
W303
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ARS1325
ARS1327
ARS1328
ARS1329
ARS1330
ARS1331.5
ARS1332
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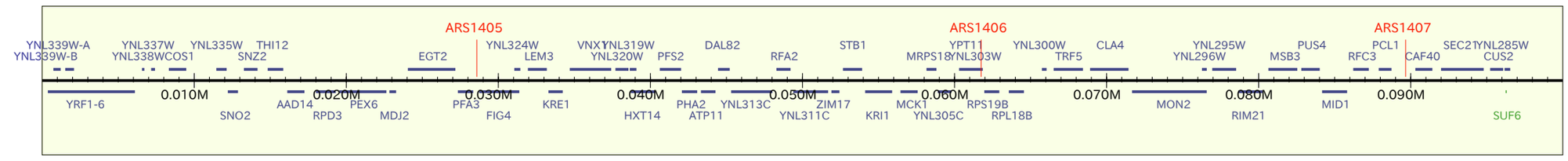
chrXIV_1

coding RNA
noncoding RNA
rRNA
LTR



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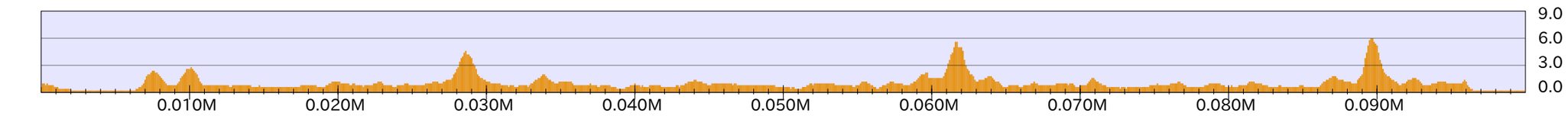
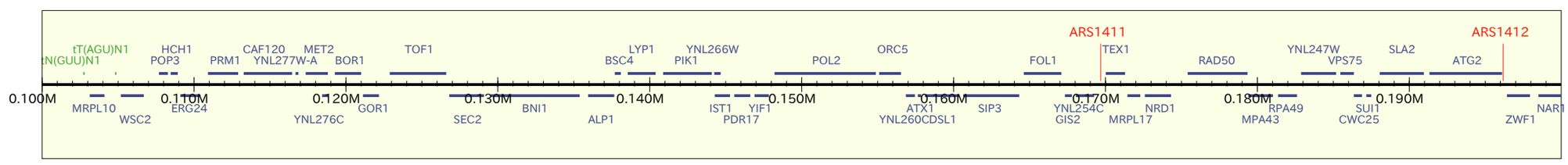


coding RNA
noncoding RNA
rRNA
LTR



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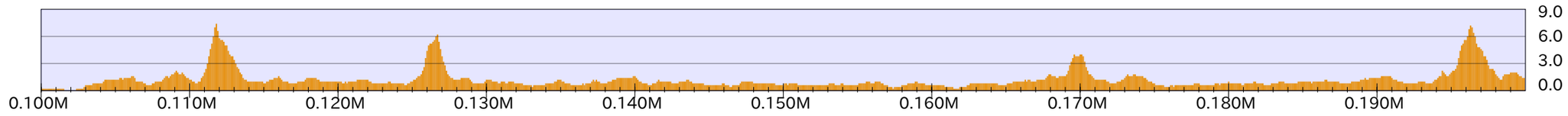
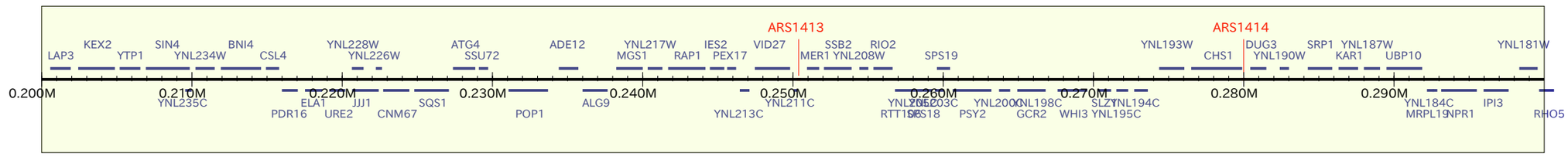


coding RNA
noncoding RNA
rRNA
LTR



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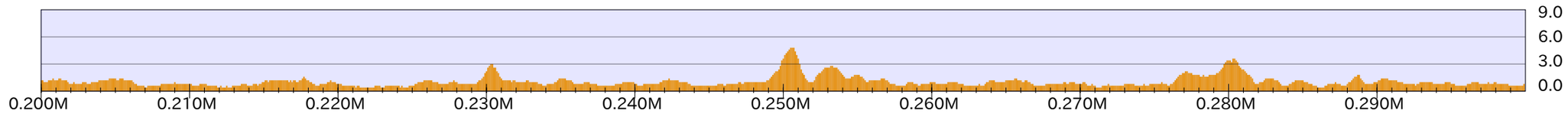
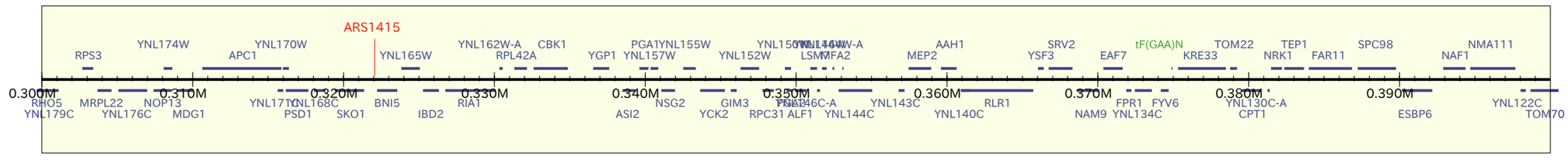


coding RNA
noncoding RNA
rRNA
LTR



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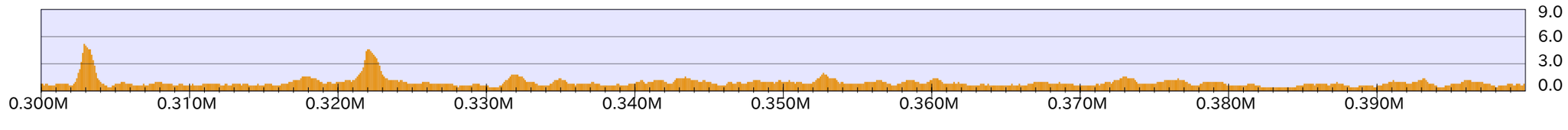
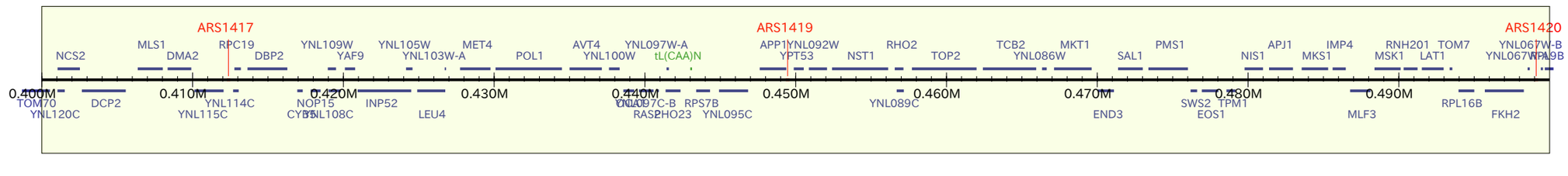


coding RNA
noncoding RNA
rRNA
LTR



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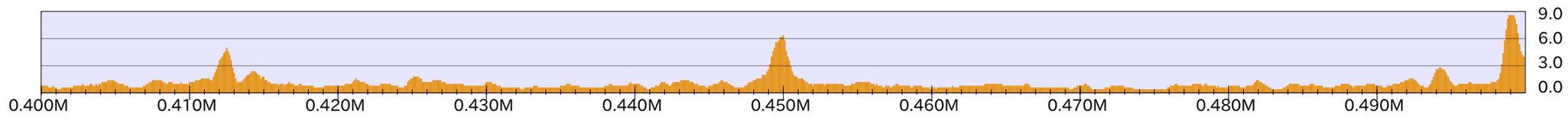
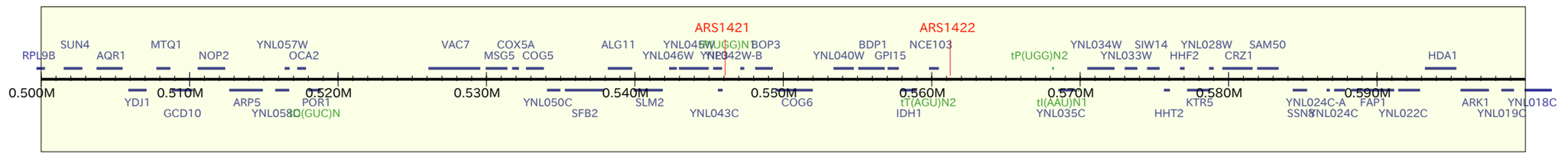
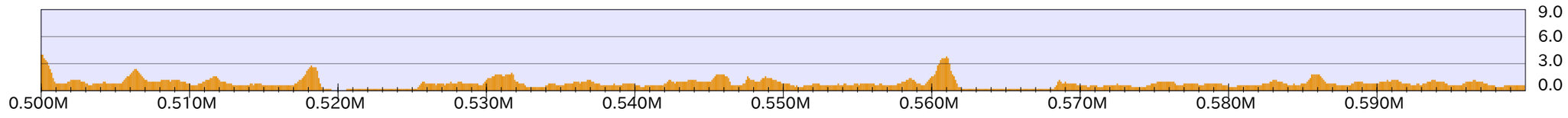


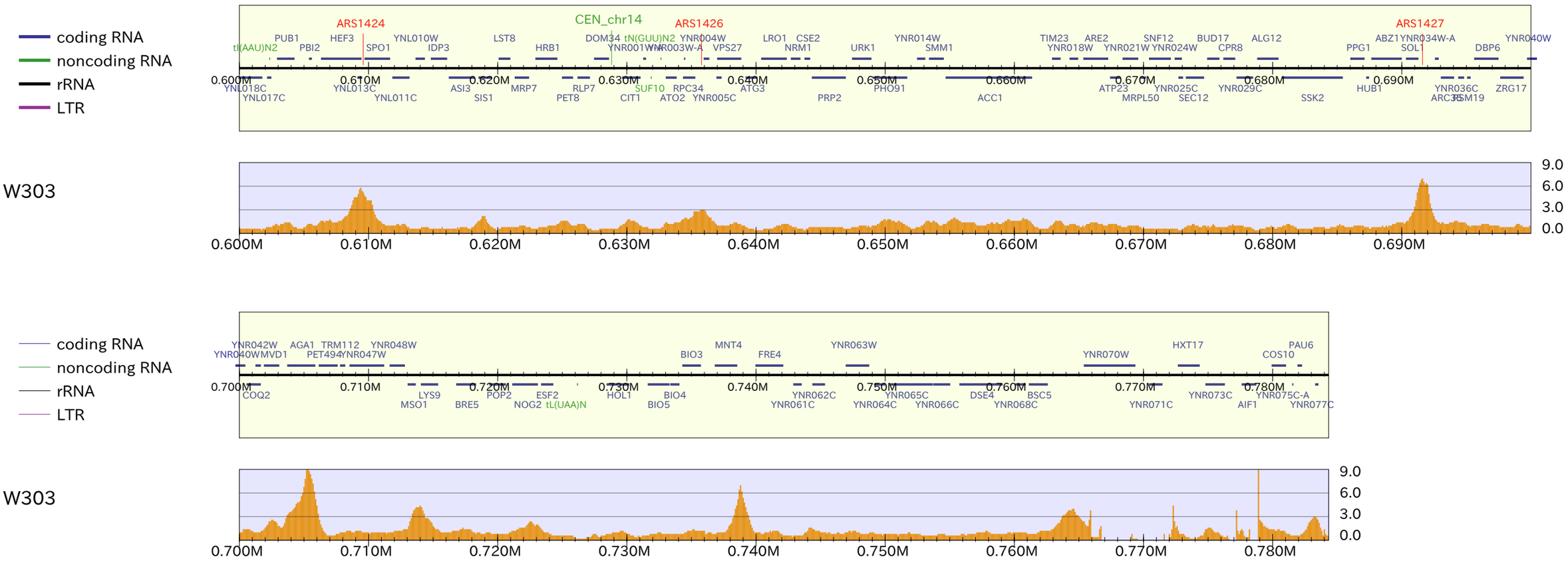
coding RNA
noncoding RNA
rRNA
LTR



W303



chrXIV_2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noncoding RNA
rRNA
LTR
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CEN_chr14
ARS1426
ARS1427
W303
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0.660M
0.670M
0.680M
0.690M
9.0
6.0
3.0
0.0
coding RNA
noncoding RNA
rRNA
LTR
W303
0.700M
0.710M
0.720M
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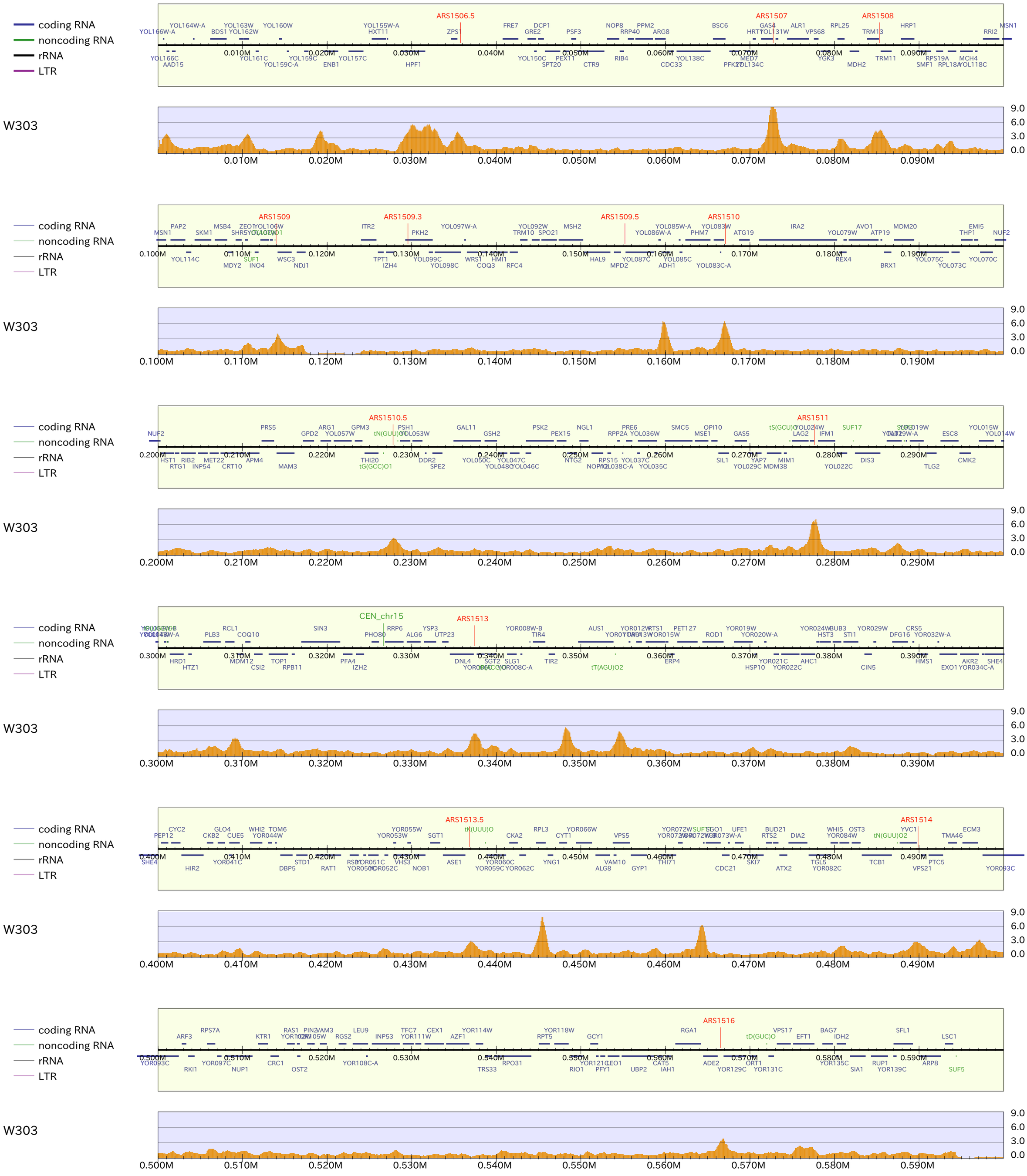
chrXV_1


coding RNA
noncoding RNA
rRNA
LTR
W303
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ARS1509
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ARS1510
ARS1510.5
ARS1511
CEN_chr15
ARS1513
ARS1513.5
ARS1514
ARS1516
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0.020M
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0.040M
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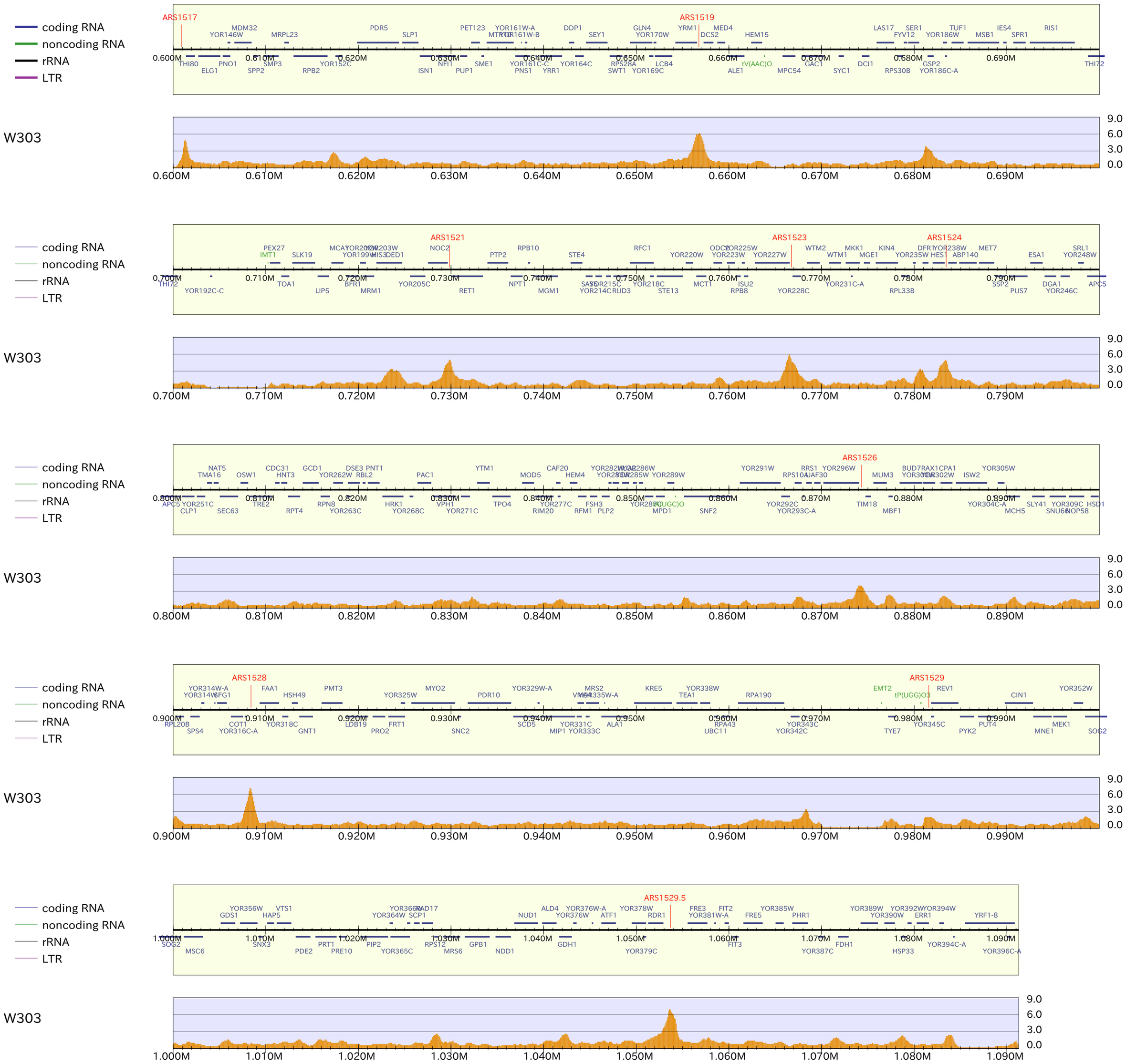
chrXV_2



W303

W303

W303

W303

chrXVI_1

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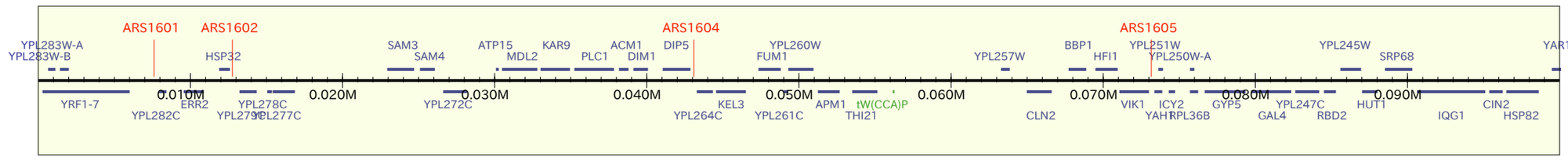
rRNA
LTR



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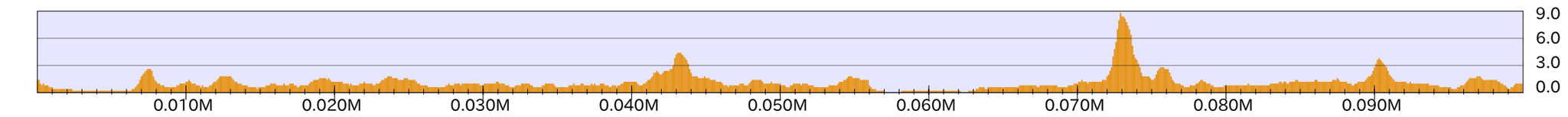

coding RNA
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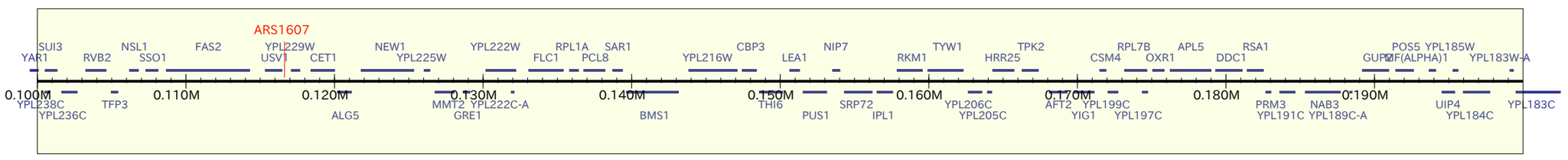
rRNA
LTR



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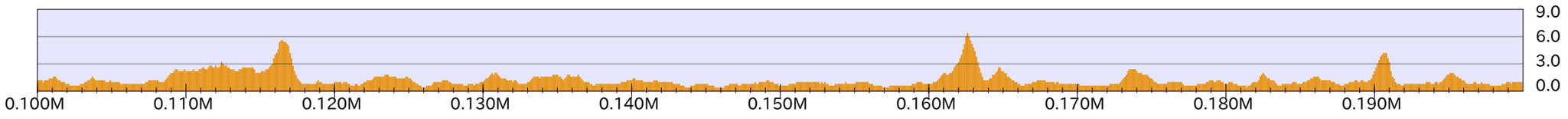
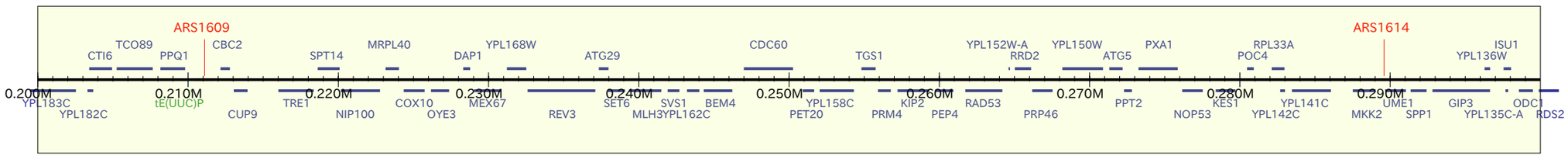


coding RNA
noncoding RNA
rRNA
LTR



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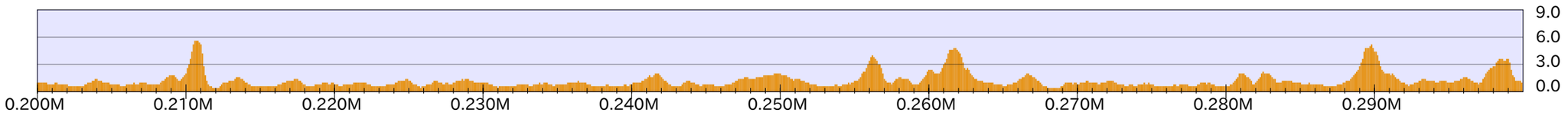

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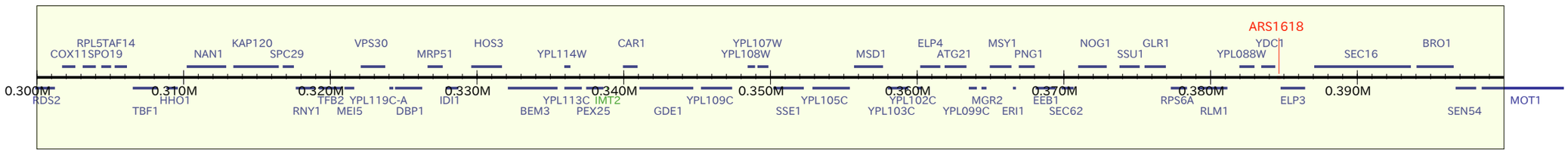

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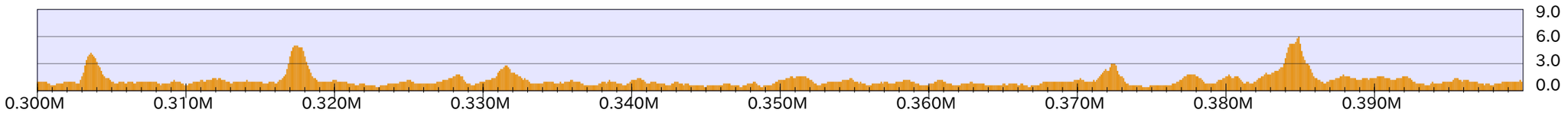

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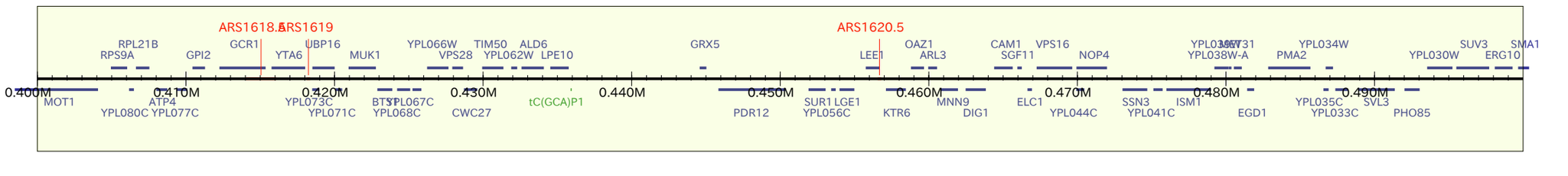

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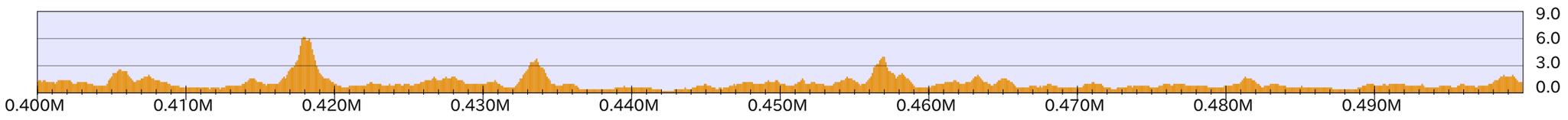

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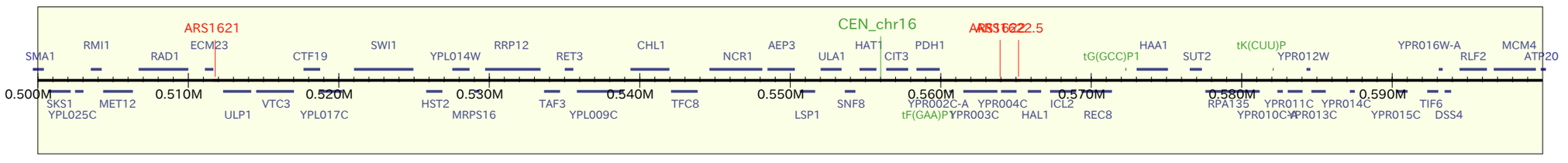

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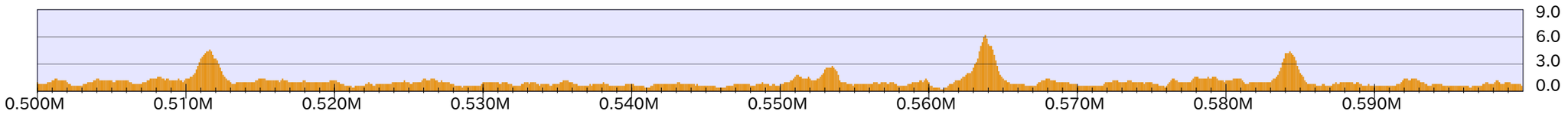
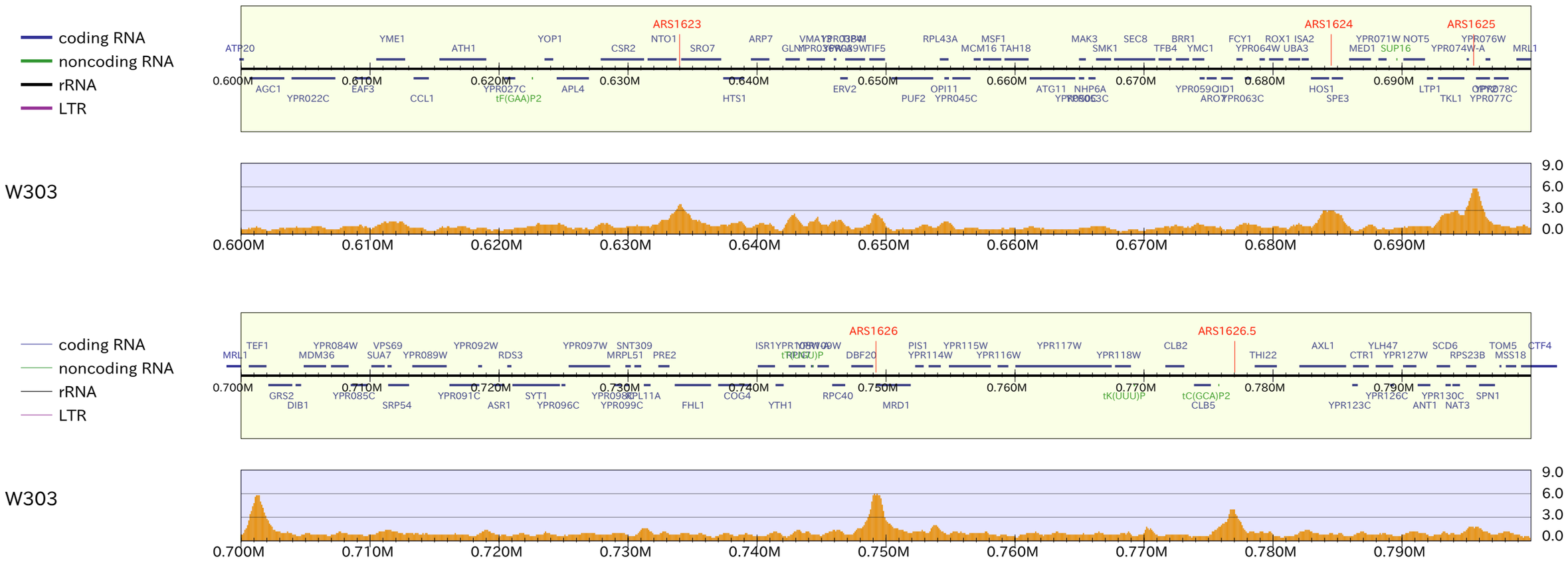


chrXVI_2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ARR3
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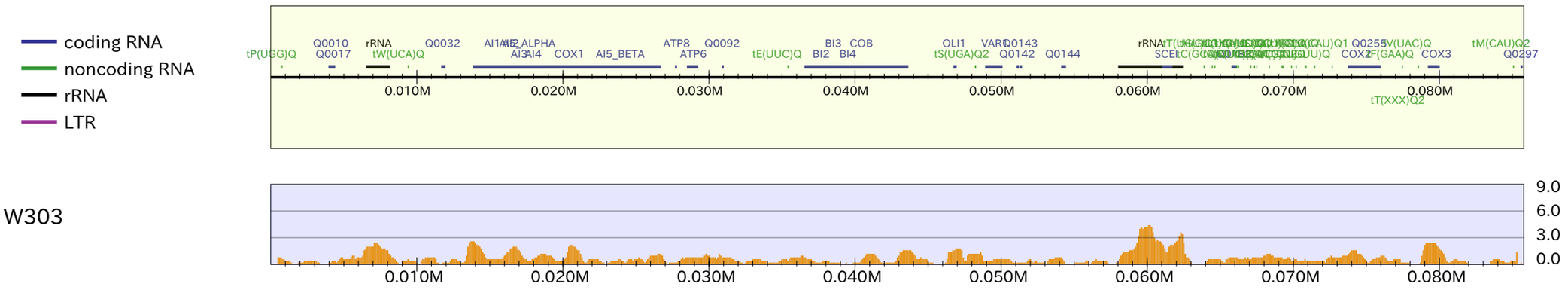
chrM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ALPHA
AI3
AI4
COX1
AI5_BETA
ATP8
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ATP6
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BI4
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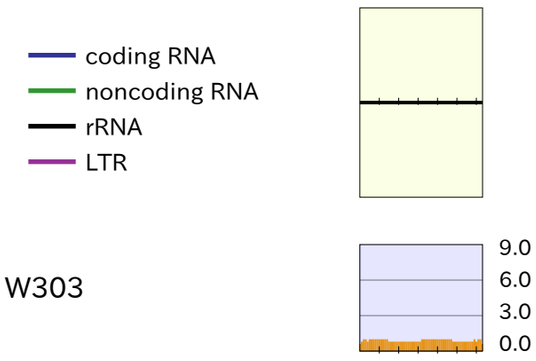
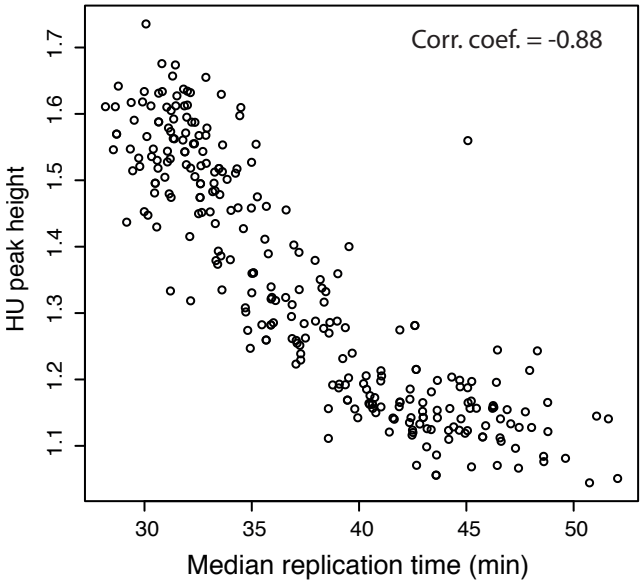
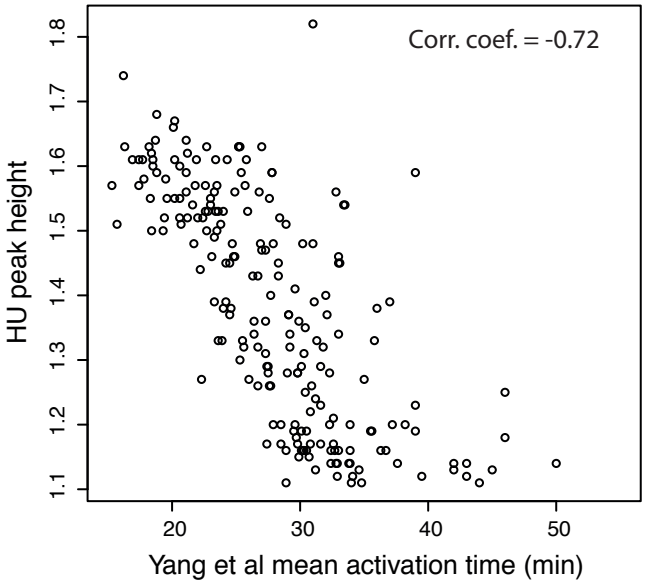
chr2micron



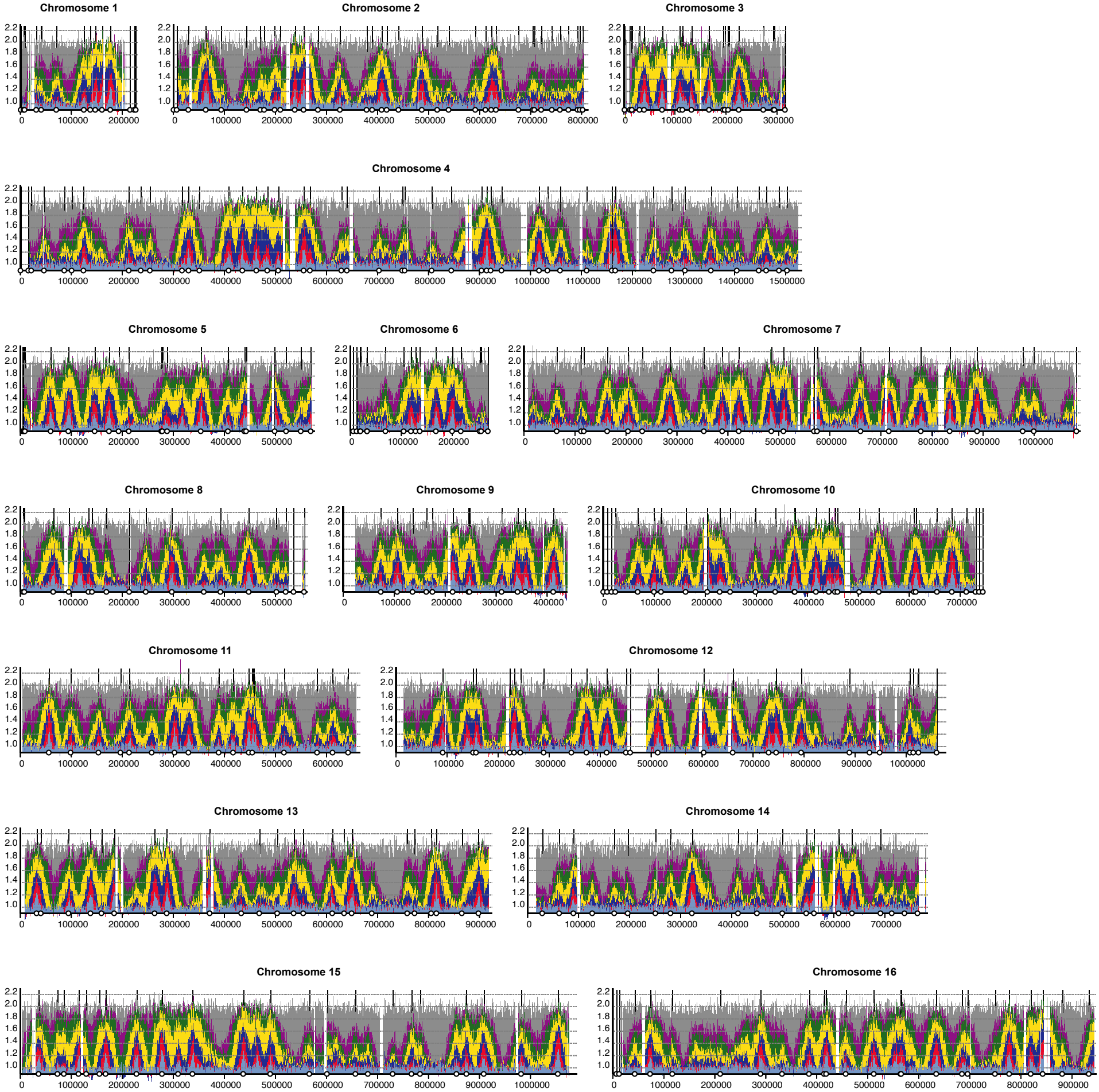
W303

Müller, Hawkins, et al. Figure S3

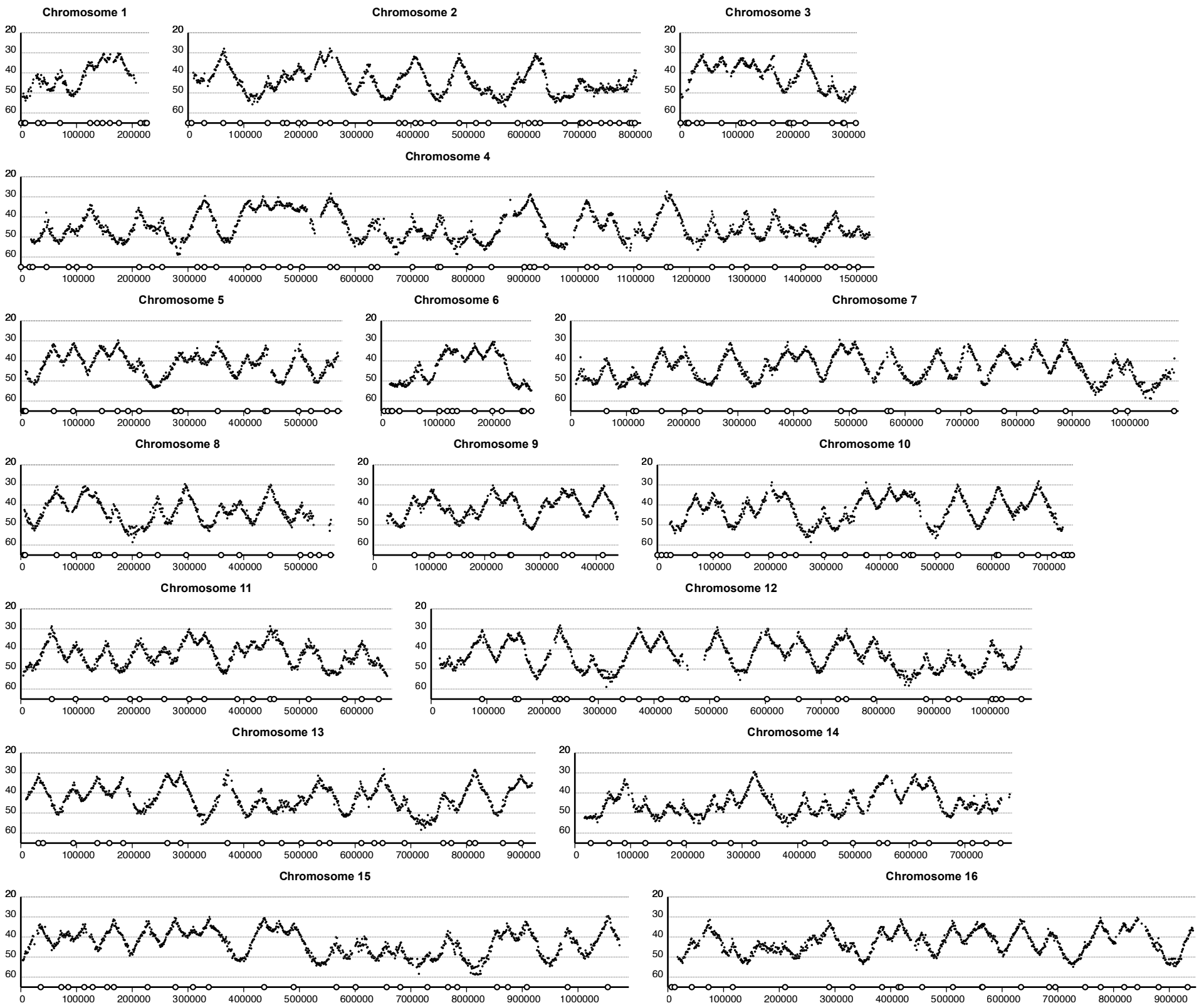




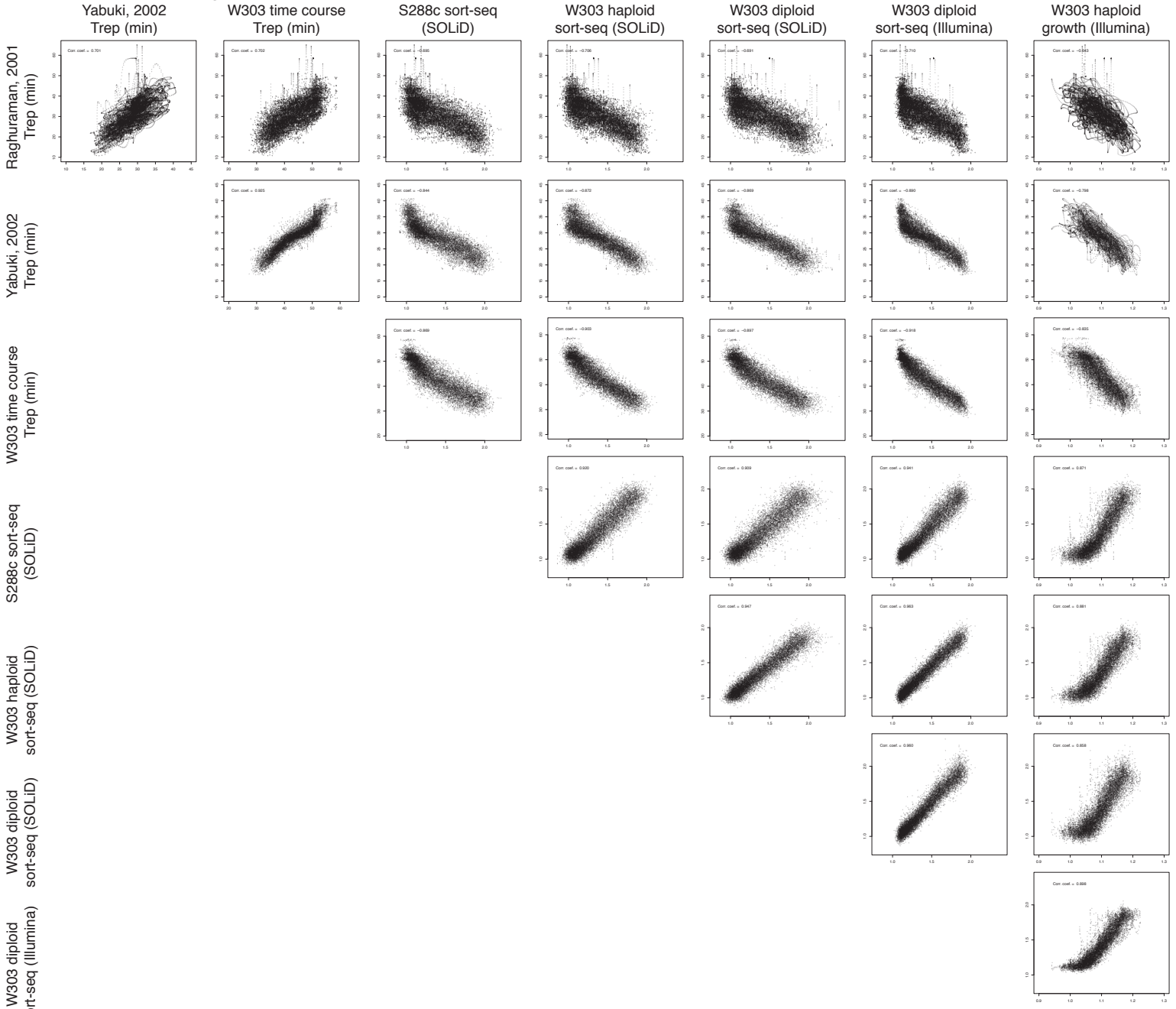
Müller, Hawkins, et al. Figure S4



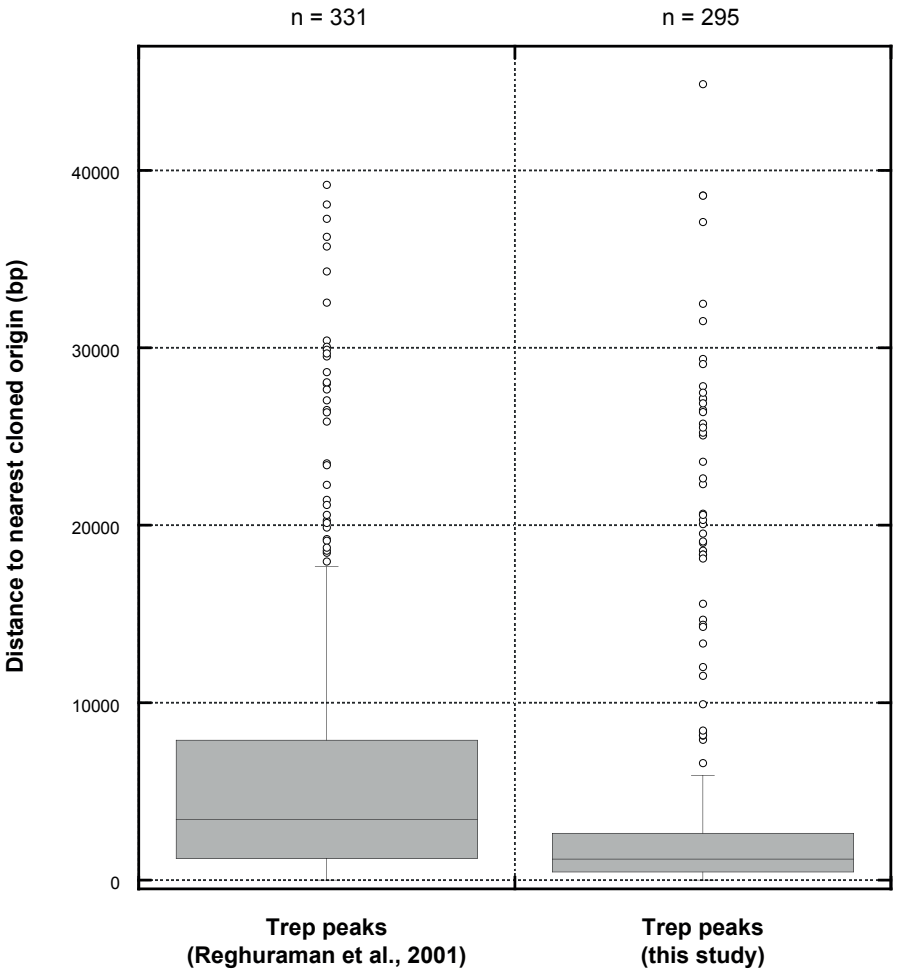
Müller, Hawkins, et al. Figure S5



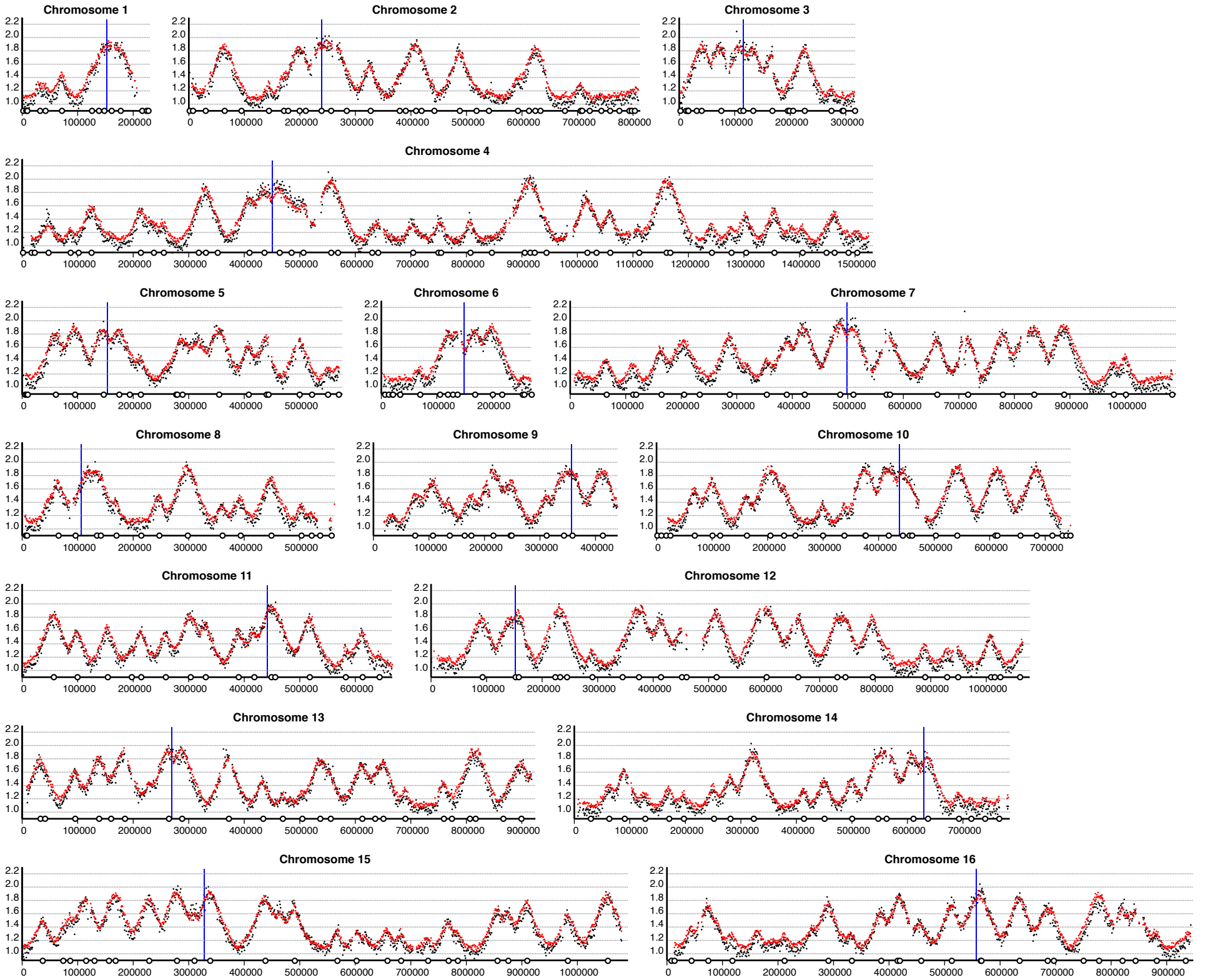
Müller, Hawkins, et al. Figure S6



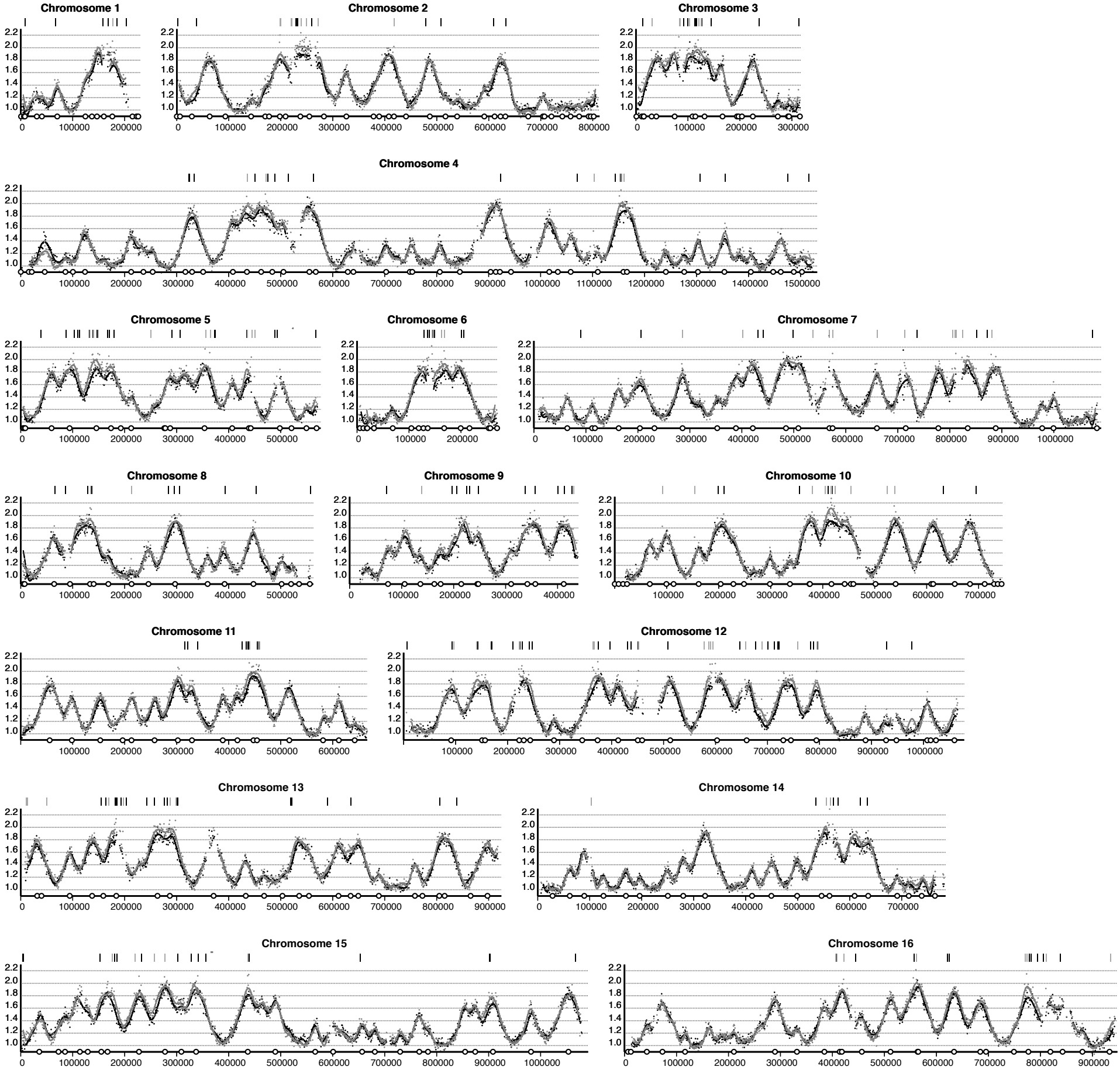
Müller, Hawkins, et al. Figure S7



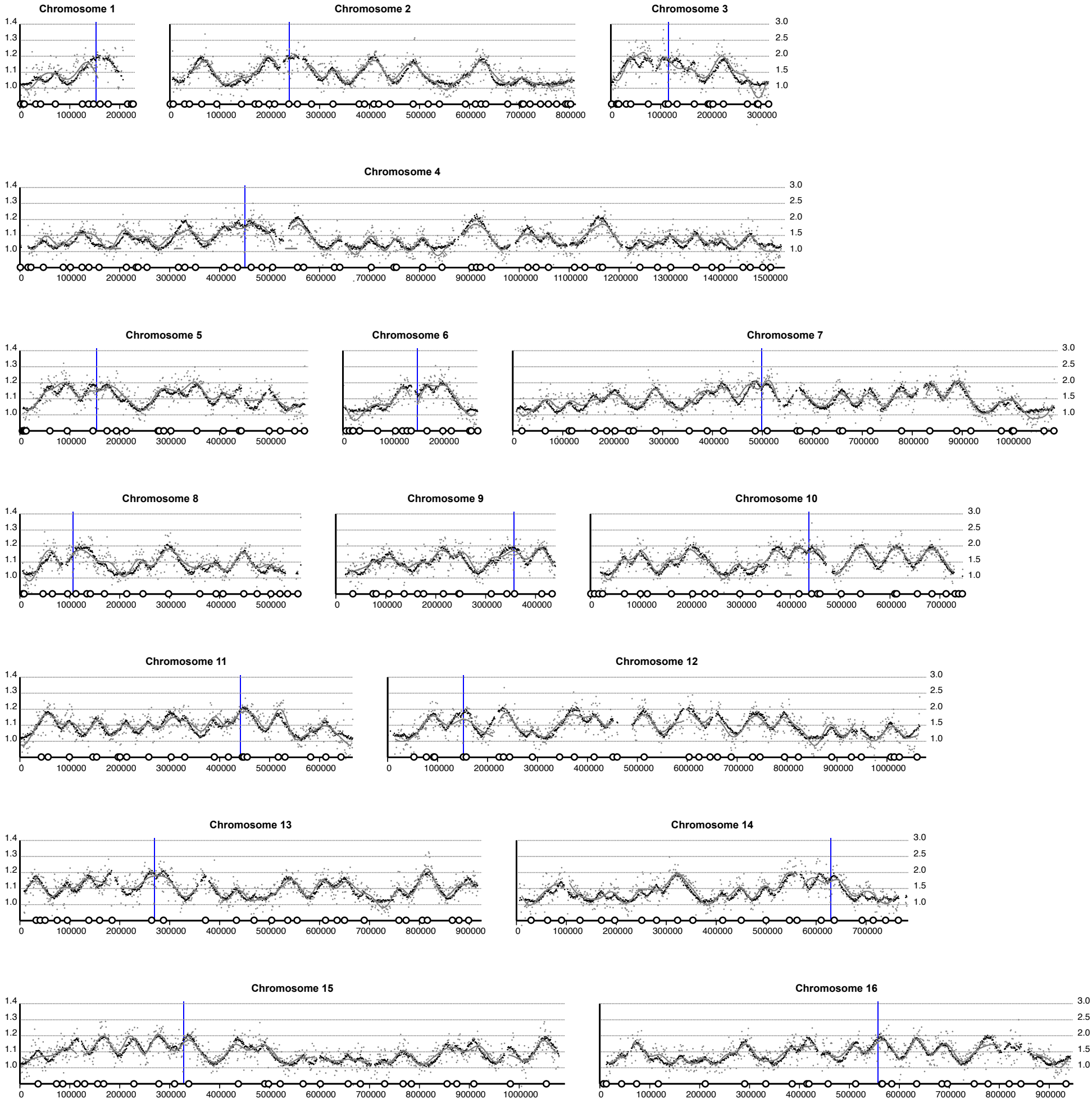
Müller, Hawkins, et al. Figure S8



Müller, Hawkins, et al. Figure S9



Müller, Hawkins, et al. Figure S10



Technology & sequencing platform	Strain & Selected Genotype	Library construction	Sample	Mean Copy Number by Flow Cytometry	Total Reads	Uniquely Mapping Reads
SOLiD 5500 system	AUY077 MATa	5500 SOLiD Fragment library core kit (Applied biosystems, 4464412)	Alpha factor arrest	1.00	17,679,718	16,056,228
			25 min release	1.06	23,564,200	20,997,274
			30 min release	1.09	24,993,881	22,501,754
			35 min release	1.21	26,283,891	23,893,069
			40 min release	1.40	27,809,830	25,386,748
			45 min release	1.56	23,736,925	21,968,165
			50 min release	1.68	22,005,344	20,535,997
			90 min release	1.95	32,053,518	29,619,880
SOLiD 3 plus system	CAY106 *MATa rad53Δ sml1Δ*	SOLiD Fragment Library Construction Kit (Applied biosystems, 4443471	Alpha factor arrest	N/A	19,075,049	18,675,416
			60 min in HU	N/A	13,712,377	13,317,219
SOLiD 4 system	T7107 Haploid	SOLiD Fragment Library Construction Kit (Applied biosystems, 4443471)	G2 phase sorted cells	N/A	21,461,618	20,442,400
			S phase sorted cells	N/A	16,935,636	16,205,005
SOLiD 4 system	T9475 Diploid	SOLiD Fragment Library Construction Kit (Applied biosystems, 4443471)	G2 phase sorted cells	N/A	45,368,930	43,734,400
			S phase sorted cells	N/A	24,346,946	23,183,066
Illumina HiSeq2000	T9475 Diploid	NEBNext DNA Library Prep Master Mix Set for Illumina	G2 phase sorted cells	N/A	164,698,046	131,816,351
			S phase sorted cells	N/A	195,717,543	155,734,122
Illumina HiSeq2000	T7107 Haploid	NEBNext DNA Library Prep Master Mix Set for Illumina	Stationary phase cells	N/A	293,409,051	234,532,691
			Exponential phase cells	N/A	262,092,475	213,008,532

Müller, Hawkins et al. (2013) Supplementary Table S1

Strain name	Genotype	Source
AUY077	ade2-1 trp1-1 can1-100 leu2-3,112 his3-11,15 ura3 GAL+ ssd1,d2 RAD5+	this study
CAY106	MATa; ade2-1; trp1-1; can1-100; leu2,3-112; his3-11,15; ura3; ssd1: bar1::TRP1; sml1::URA3 rad53::LEU2	this study
T7107	MATa, RAD5, BUD4, leu2, ura3, trp1, ade2, his3	Tomoyuki Tanaka
T9475	MatA/MATalpha, RAD5/RAD5, BUD4/BUD4, leu2/leu2, ura3/ura3, trp1/trp1, ade2/ade2, his3/his3	Tomoyuki Tanaka

Origin name	ACS sequence	Reference
ARS202	TTTTAATTTTT	This study
ARS209	TTTTATGTTTT	(Bouton and Smith)
ARS214	ATTTATATTTT	(Hoggard *et al.*)
ARS219.5	TTCTATATTTT	(Hoggard *et al.*)
ARS224	TTTAACGTTTT	This study
ARS301	TTTTATGTTTT	(Sharma *et al.*)
ARS302	TTTTATATTTT	(Sharma *et al.*)
ARS303	ATTTATATTTT	(Vujcic *et al.*)
ARS304	TTATAAATTT	(Bouton and Smith 1986)
ARS305	TTATATGTTTT	(Huang and Kowalski)
ARS306	ATTTATATTTA	(Theis *et al.*)
ARS307	ATTTATGTTTT	(Palzkill and Newlon)
ARS309	GTTTATATCTT	(Theis and Newlon)
ARS310	TTTTACTTTTT	(Theis and Newlon)
ARS313	TTTTACTTTTA	(Chang *et al.*)
ARS315	TTTTATGTTTT	(Crampton *et al.*)
ARS316	TTTCAAATTTA	(Chang *et al.*)
ARS317	TTTTATATTTA	(Chang *et al.*)
ARS318	TATCATGTTTT	(Chang *et al.*)
ARS319	TTTTATGTTTA	(Chang *et al.*)
ARS320	TTTTATGTTAT	(Vujcic *et al.*)
ARS404	TTTAATATTTT	(Kearsey)
ARS416	TTTTATGTTTA	(Celniker *et al.*)
ARS422	ATTAATGTTTT	This study
ARS423	TTTTACATTTT	(Hoggard *et al.*)
ARS428	TTTTATATTTT	(Hoggard *et al.*)
ARS432	TTTTTTTCTTTTCT	(Nieduszynski *et al.*)
ARS432.5	TTATTTACATTTTGT	(Nieduszynski *et al.*)
ARS442	ATTTATGTTTA	(Hoggard *et al.*)
ARS512	AATTATGTTTA	(Hoggard *et al.*)

ARS514	ATTTATGTTTT	(Hoggard *et al.*)
ARS516	ATTTACTTTTT	(Hoggard *et al.*)
ARS601	ATTTCCATTTT	(Shirahige *et al.*)
ARS602	TTATACGTTTA	(Shirahige *et al.*)
ARS603	TTTAAAGTTTT	(Shirahige *et al.*)
ARS603	TTTCATATTTT	(Shirahige *et al.*)
ARS603.5	TTCCATATTTT	(Yamashita *et al.*)
ARS604	TTTTACGTTTT	(Shirahige *et al.*)
ARS605	AATTACGTTTT	(Shirahige *et al.*)
ARS606	ATTTATATTTT	(Shirahige *et al.*)
ARS607	GTTTATATTTA	(Shirahige *et al.*)
ARS608	TTTTACTTTTA	(Shirahige *et al.*)
ARS609	TTTTATGTTTT	(Shirahige *et al.*)
ARS702	TTTTTAATATTTTGT	(Nieduszynski *et al.*)
ARS704	TTTTATACGTTTATG	(Nieduszynski *et al.*)
ARS707	CATTTTATAATTTGT	(Nieduszynski *et al.*)
ARS710	TTTTTTATATTTATT	(Nieduszynski *et al.*)
ARS714	TTATTTACTTTTAGT	(Nieduszynski *et al.*)
ARS716	AATTACGTTTA	(Hoggard *et al.*)
ARS717	TTATTTAACTTTTGT	(Nieduszynski *et al.*)
ARS718	AAATTATTGTTTAGT	(Nieduszynski *et al.*)
ARS719	TTATTTATGTTTTGC	(Nieduszynski *et al.*)
ARS721	GTATTTATATTTAGC	(Nieduszynski *et al.*)
ARS727	TATTTTATGTTTACT	(Nieduszynski *et al.*)
ARS728	TTGTTTATATTTTGT	(Nieduszynski *et al.*)
ARS729	TTTTTTACCTTTTGT	(Nieduszynski *et al.*)
ARS731	TGTATATAGTTTAGT	(Nieduszynski *et al.*)
ARS731.5	ATTTTAATATTTTGT	(Nieduszynski *et al.*)
ARS733	TTTTTTAATTTTTTT	(Nieduszynski *et al.*)
ARS809	TTAGACATTTA	(Hoggard *et al.*)
ARS818	TTTCATGTTTT	(Hoggard *et al.*)
ARS822	TTATACATTTT	(Hoggard *et al.*)
ARS911	GTTTATGTTTT	(Hoggard *et al.*)

ARS920	TTTTATATTTT	(Hoggard *et al.*)
ARS1001	TTTTATGTTTA	(Xu *et al.*)
ARS1002	TTTTATGTTTA	(Xu *et al.*)
ARS1003	TTTTATTTTTA	(Xu *et al.*)
ARS1004	TTTTTAGTTTT	(Xu *et al.*)
ARS1005	TTATATGTTTT	(Xu *et al.*)
ARS1007	ATATATATTTA	(Xu *et al.*)
ARS1007.5	ATCTATGTTTA	(Xu *et al.*)
ARS1009	ATTTATATTTA	(Xu *et al.*)
ARS1011	TTTTATGTTTA	(Xu *et al.*)
ARS1014	TTTTATATTTA	(Xu *et al.*)
ARS1015	ATTTATATTTT	(Xu *et al.*)
ARS1018	TTTTACATTTA	(Xu *et al.*)
ARS1019	TTTTATCTTTA	(Xu *et al.*)
ARS1020	ATTTACATTTT	(Xu *et al.*)
ARS1021	TTGTTTAACATTAGT	(Nieduszynski *et al.*)
ARS105	ATTAACAATTA	(Hoggard *et al.*)
ARS1114	TTTTATGTTTT	(Hoggard *et al.*)
ARS1118	TTTTACATTTA	This study
ARS1123	TTTTATATTTA	(Hoggard *et al.*)
ARS1216.5	GTTTATGTTTT	(Nieduszynski *et al.*)
ARS1307	ATTTATGTTTT	(Hoggard *et al.*)
ARS1320	ATTTATATTTA	(Hoggard *et al.*)
ARS1323	GTTTATGTTTA	(Hoggard *et al.*)
ARS1324	TTTTACTATTT	This study
ARS1325	TTTCATATTTT	(Hoggard *et al.*)
ARS1329	ATTTAGTCTTT	(Hoggard *et al.*)
ARS1332	TTTTATGTTTG	(Hoggard *et al.*)
ARS1405	TTTTATTTTTA	(Hoggard *et al.*)
ARS1413	ATTTGTATTTA	(Friedman *et al.*)
ARS1420	CTTTATGTTTA	(Hoggard *et al.*)
ARS1513	TTTTACCTTTT	(Hoggard *et al.*)
ARS1521	TTTTATATTTT	(Hoggard *et al.*)

ARS1526	ATTTTAATATTTGTT	(Nieduszynski *et al.*)
ARS1528	TTTGTTTATGTTTAGGT	(Breier *et al.*)
ARS1528	GTTTATGTTTA	(Hoggard *et al.*)
ARS1529.5	TTGTTTAAATTTTGT	(Nieduszynski *et al.*)
ARS1529.5	GTTTAAATTTT	(Hoggard *et al.*)
ARS1625	ATTTACGTTTA	(Hoggard *et al.*)
ARS1626.5	TTATTTATATTTTGG	(Nieduszynski *et al.*)
ARS1631	TTTTATATTTG	(Hoggard *et al.*)

Bouton AH, Smith MM. 1986. Fine-structure analysis of the DNA sequence requirements for autonomous replication of Saccharomyces cerevisiae plasmids. *Molecular and cellular biology* **6**(7): 2354-2363.

Breier AM, Chatterji S, Cozzarelli NR. 2004. Prediction of Saccharomyces cerevisiae replication origins. *Genome Biol* **5**(4): R22.

Celniker SE, Sweder K, Srienc F, Bailey JE, Campbell JL. 1984. Deletion mutations affecting autonomously replicating sequence ARS1 of Saccharomyces cerevisiae. *Molecular and cellular biology* **4**(11): 2455-2466.

Chang F, Theis JF, Miller J, Nieduszynski CA, Newlon CS, Weinreich M. 2008. Analysis of chromosome III replicators reveals an unusual structure for the ARS318 silencer origin and a conserved WTW sequence within the origin recognition complex binding site. *Mol Cell Biol* **28**(16): 5071-5081.

Crampton A, Chang F, Pappas DL, Frisch RL, Weinreich M. 2008. An ARS element inhibits DNA replication through a SIR2-dependent mechanism. *Mol Cell* **30**(2): 156-166.

Friedman KL, Diller JD, Ferguson BM, Nyland SV, Brewer BJ, Fangman WL. 1996. Multiple determinants controlling activation of yeast replication origins late in S phase. *Genes Dev* **10**(13): 1595-1607.

Hoggard T, Shor E, Müller CA, Nieduszynski CA, Fox CA. 2013. Linking ORC-Origin Binding Mechanisms to the Regulation of Origin Activation Time. *PLoS Genet, in press.*

Huang RY, Kowalski D. 1996. Multiple DNA elements in ARS305 determine replication origin activity in a yeast chromosome. *Nucleic Acids Res* **24**(5): 816-823.

Kearsey S. 1984. Structural requirements for the function of a yeast chromosomal replicator. *Cell* **37**(1): 299-307.

Nieduszynski CA, Knox Y, Donaldson AD. 2006. Genome-wide identification of replication origins in yeast by comparative genomics. *Genes Dev* **20**(14): 1874-1879.

Palzkill TG, Newlon CS. 1988. A yeast replication origin consists of multiple copies of a small conserved sequence. *Cell* **53**(3): 441-450.

Sharma K, Weinberger M, Huberman JA. 2001. Roles for internal and flanking sequences in regulating the activity of mating-type-silencer-associated replication origins in Saccharomyces cerevisiae. *Genetics* **159**(1): 35-45.

Shirahige K, Iwasaki T, Rashid MB, Ogasawara N, Yoshikawa H. 1993. Location and characterization of autonomously replicating sequences from chromosome VI of Saccharomyces cerevisiae. *Mol Cell Biol* **13**: 5043–5056.

Theis JF, Newlon CS. 1997. The ARS309 chromosomal replicator of Saccharomyces cerevisiae depends on an exceptional ARS consensus sequence. *Proc Natl Acad Sci U S A* **94**(20): 10786-10791.

Theis JF, Newlon CS. 2001. Two compound replication origins in Saccharomyces cerevisiae contain redundant origin recognition complex binding sites. *Mol Cell Biol* **21**(8): 2790-2801.

Theis JF, Yang C, Schaefer CB, Newlon CS. 1999. DNA sequence and functional analysis of homologous ARS elements of Saccharomyces cerevisiae and S. carlsbergensis. *Genetics* **152**(3): 943-952.

Vujcic M, Miller CA, Kowalski D. 1999. Activation of silent replication origins at autonomously replicating sequence elements near the HML locus in budding yeast. *Mol Cell Biol* **19**(9): 6098-6109.

Xu W, Aparicio JG, Aparicio OM, Tavaré S. 2006. Genome-wide mapping of ORC and Mcm2p binding sites on tiling arrays and identification of essential ARS consensus sequences in S. cerevisiae. *BMC Genomics* **7**: 276.

Yamashita M, Hori Y, Shinomiya T, Obuse C, Tsurimoto T, Yoshikawa H, Shirahige K. 1997. The efficiency and timing of initiation of replication of multiple replicons of Saccharomyces cerevisiae chromosome VI. *Genes to Cells* **2**: 655-666.