Supplemental figure legends

Figure S1. Distribution of WGAC pairwise alignments with identity <99%

Figure S2. Distribution of unplaced scaffolds against the proportion of duplicated bases

Figure S3. SD contents of different chromosomes for pig reference genome

Figure S4. A composite map of CNVs, CNVRs, CNV hotspots and SDs based on the *Sus scrofa* 10.2 genome assembly

A1, wild boar; C3, Landrace; D4, Duroc; DN1 and DN5, Diannan small-ear pig; M2, Min pig; MS7 and MS8, Meishan pig; R2, Rongchang pig; W1, Daweizi pig; Y2, Yorkshire; Z2 and Z5, Tibetan pig.

Figure S5. Read depth map around *KIT*

For each individual, the horizontal line indicates the averaged read depth of whole-genome 2-copy copy windows. Read depth of copy windows was painted in different colors according to their values: green for average-2×STDEV<RD<average+2×STDEV, red for RD≥average+3×STDEV, blue for RD≤average-3×STDEV, and grey for other RD values. Tracks on the bottom of the figure include human Ensembl proteins, genes, contigs and %GC (showed from top to bottom), sourcing from Ensembl. Ref, the Duroc sow 2-14; A1, wild boar; C3, Landrace; D4, Duroc; DN1 and DN5, Diannan small-ear pig; M2, Min pig; MS7 and MS8, Meishan pig; R2, Rongchang pig; W1, Daweizi pig; Y2, Yorkshire; Z2 and Z5, Tibetan pig.

Figure S6. Dendrogram of 13 individual pigs from 10 distinct breeds using high density SNP data

The values at the nodes are the percentages of bootstrap results from 1,000 replications of re-samplings, which indicate the reliability of bootstrap test. A1, wild boar; C3, Landrace; D4, Duroc; DN1 and DN5, Diannan small-ear pig; M2, Min pig; MS7 and MS8, Meishan pig; R2, Rongchang pig; W1, Daweizi pig; Y2, Yorkshire; Z2 and Z5, Tibetan pig.

Figure S1

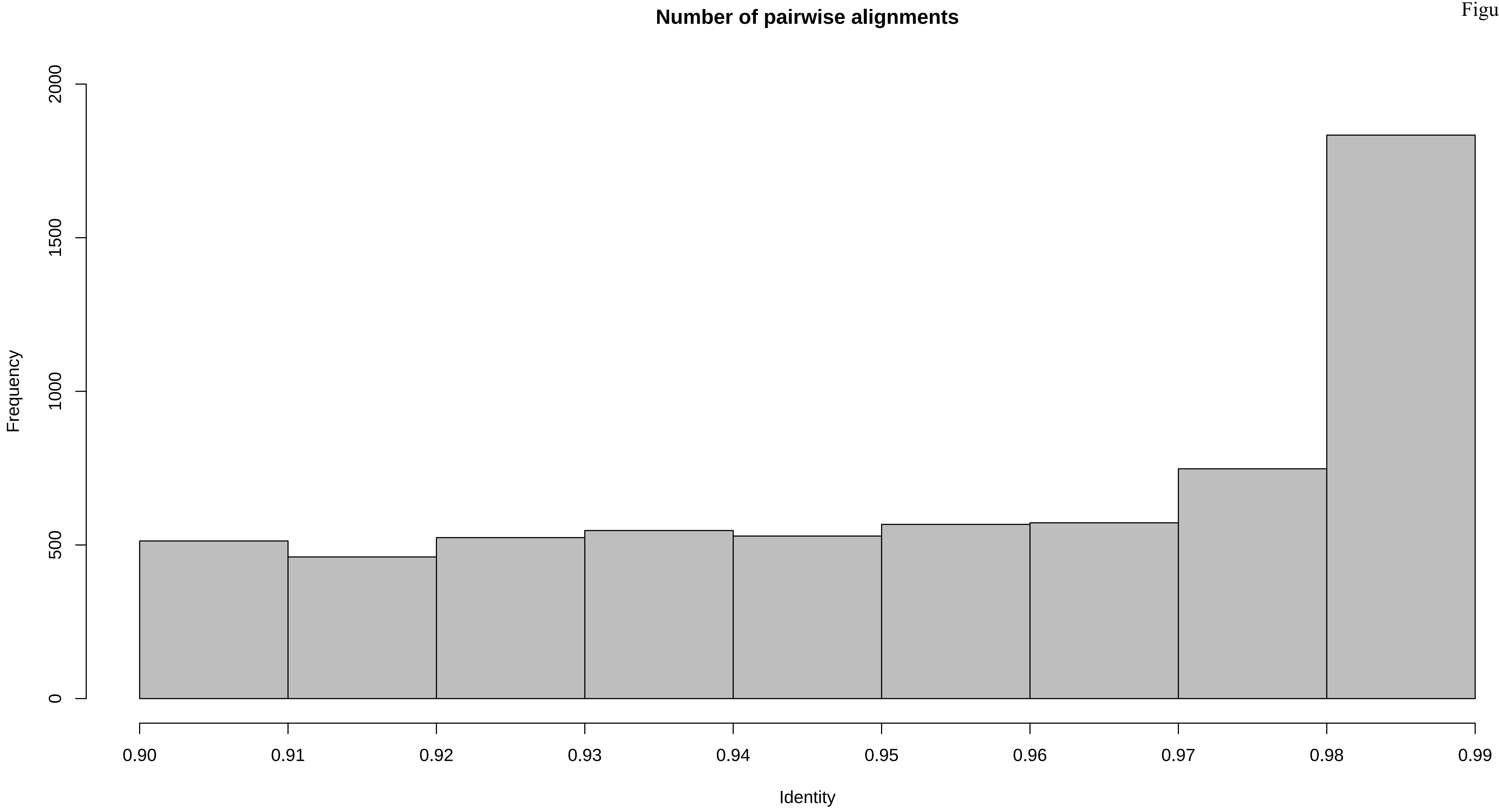

Number of pairwise alignments
Frequency
0
500
1000
1500
2000
0.90
0.91
0.92
0.93
0.94
0.95
0.96
0.97
0.98
0.99
Identity

Figure S2

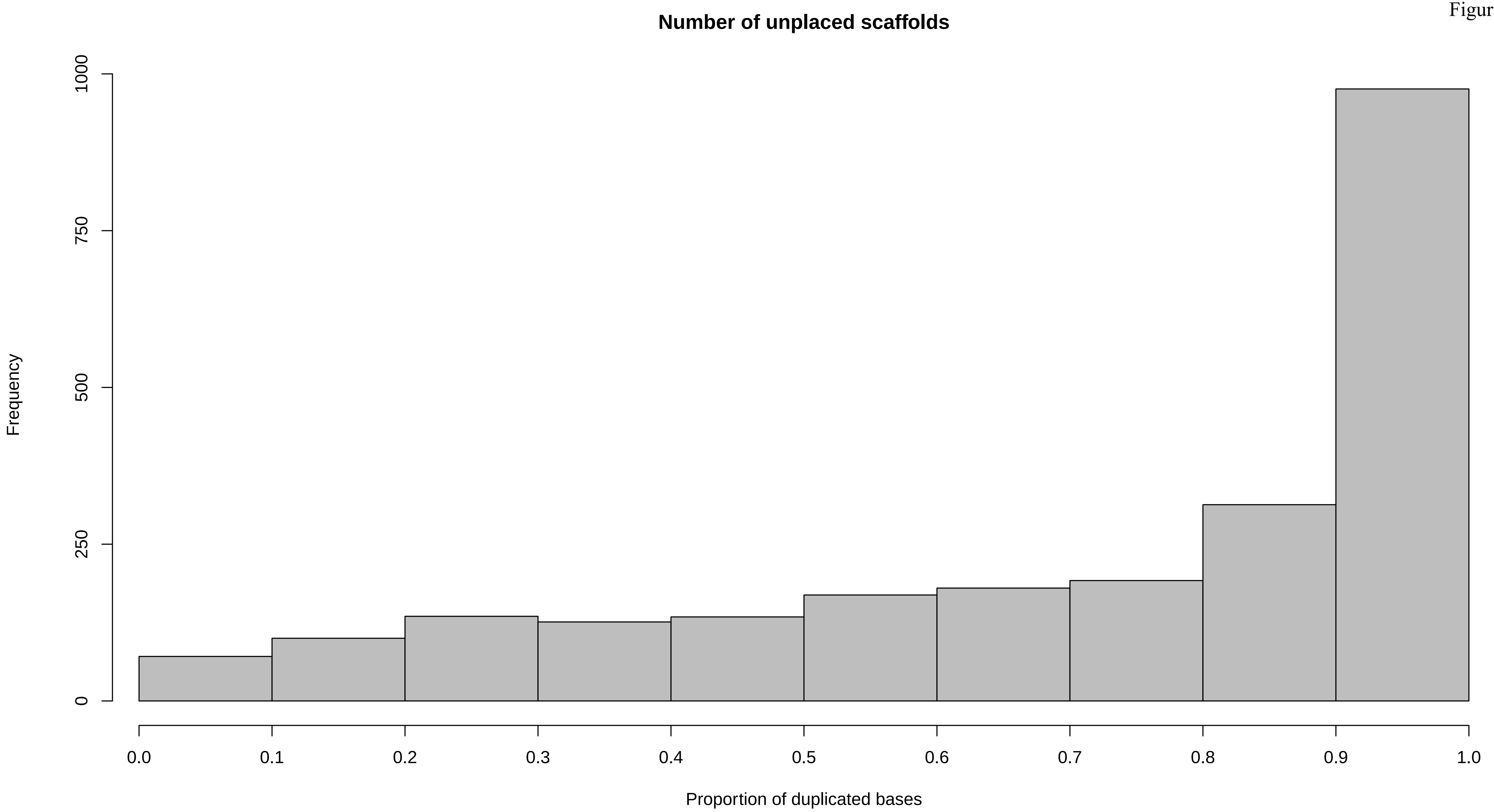
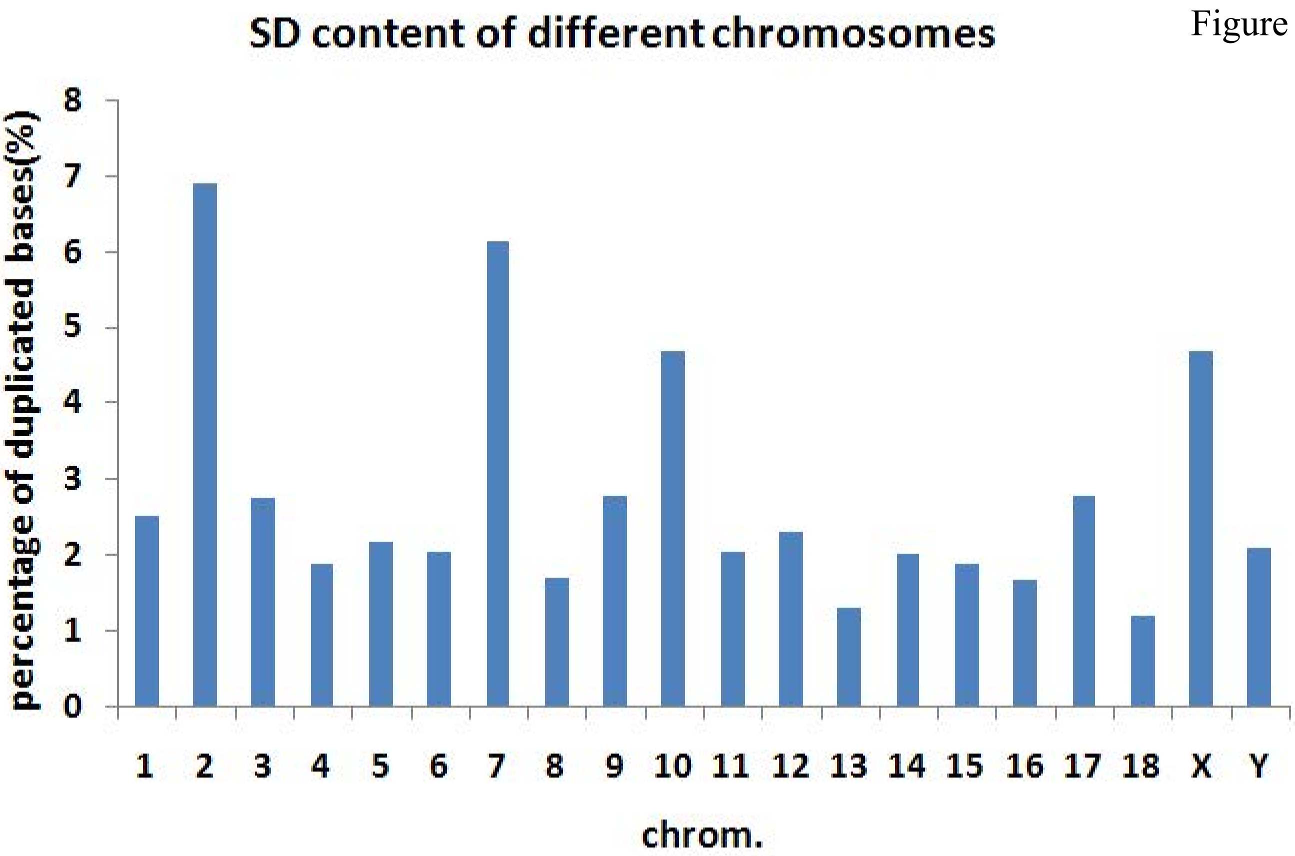

Number of unplaced scaffolds
Frequency
0
250
500
750
1000
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Proportion of duplicated bases

Figure S3


SD content of different chromosomes
percentage of duplicated bases(%)
0
1
2
3
4
5
6
7
8
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
X
Y
chrom.

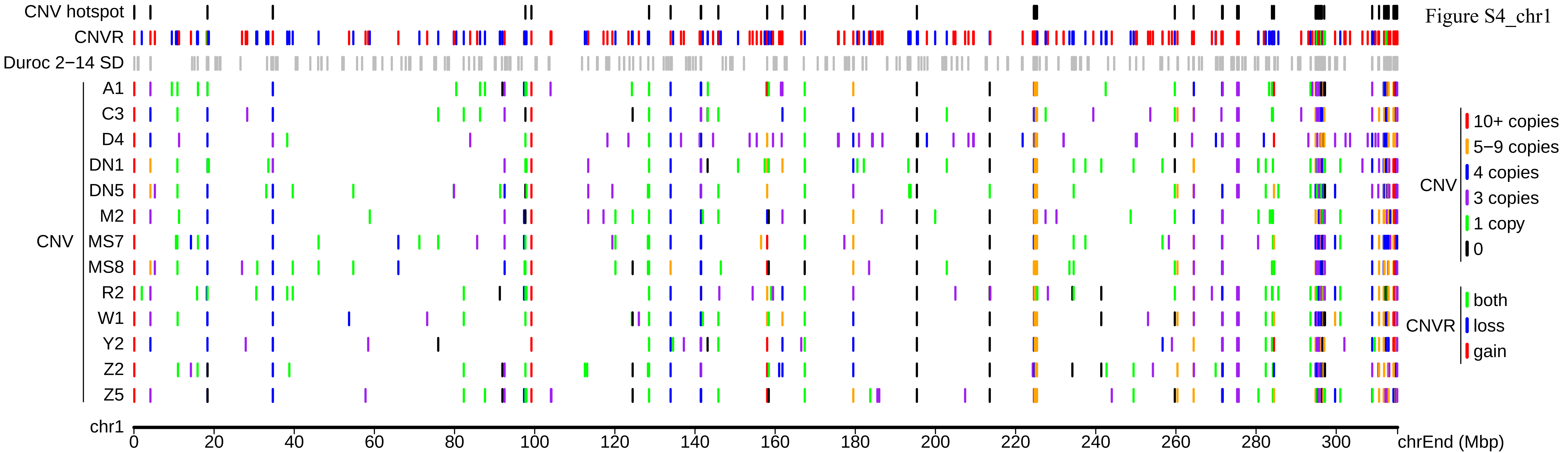


Figure S4_chr1

Figure S4_chr2

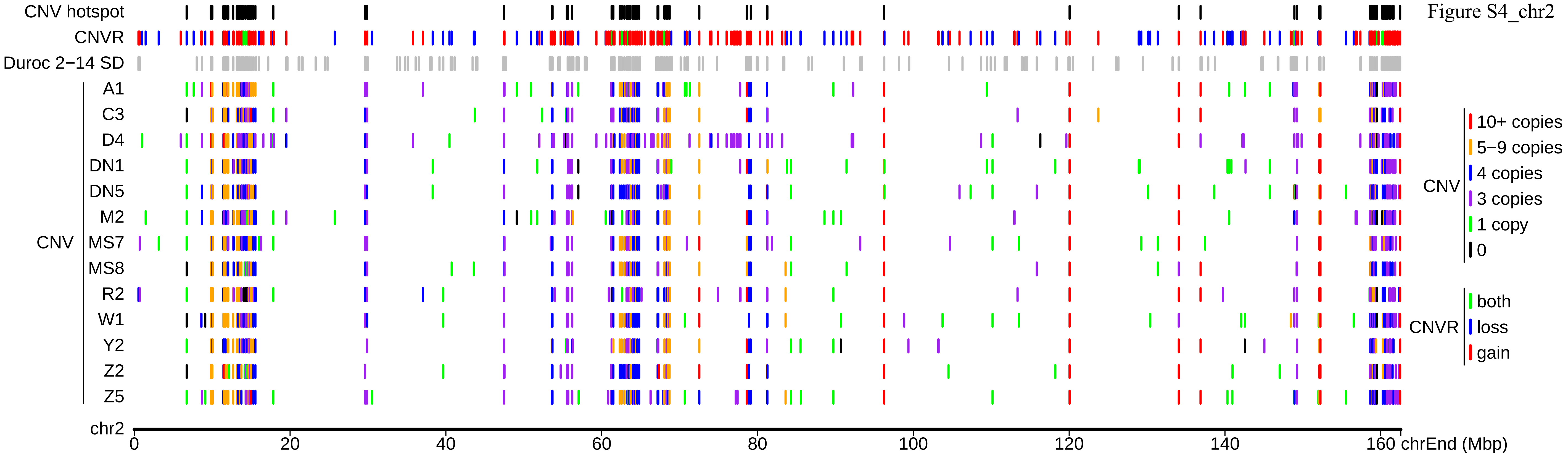


Figure S4_chr3

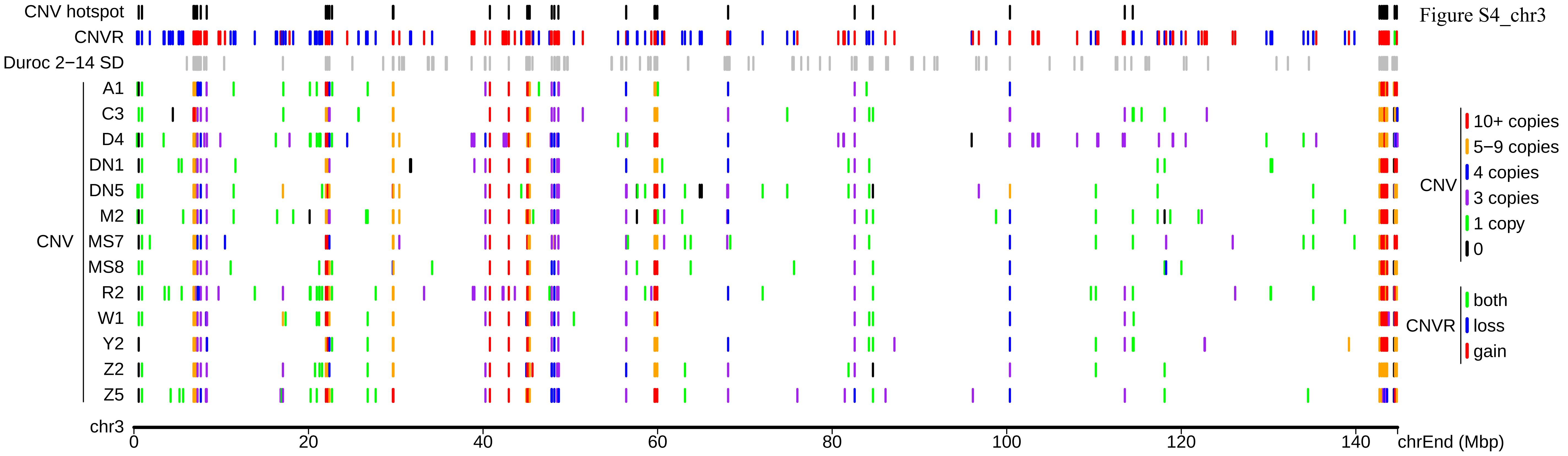
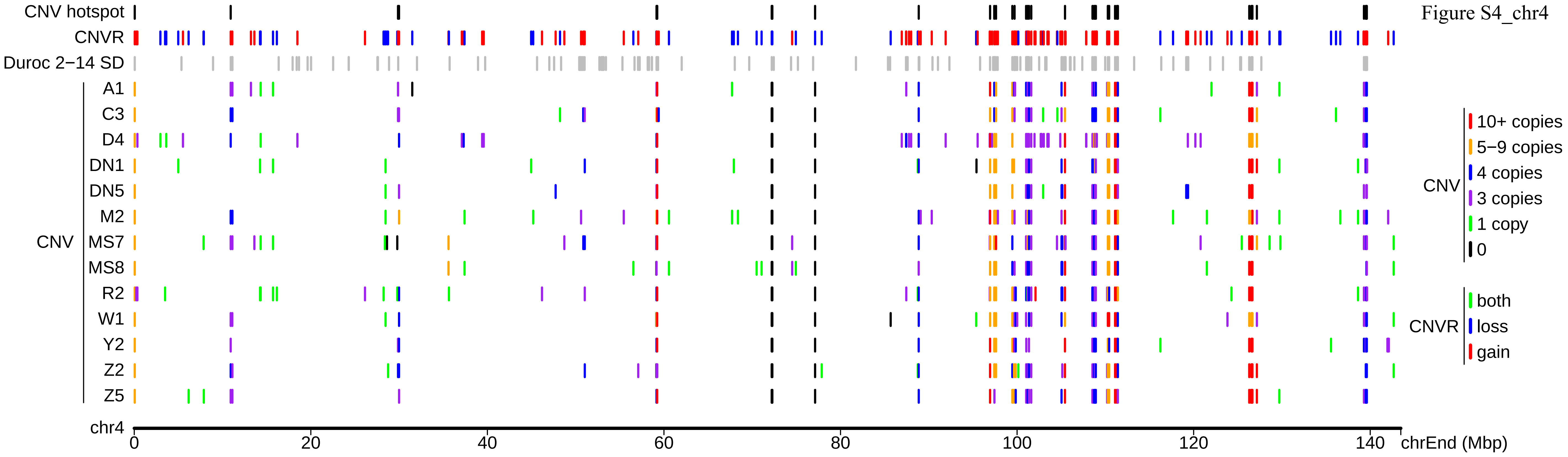


Figure S4_chr4



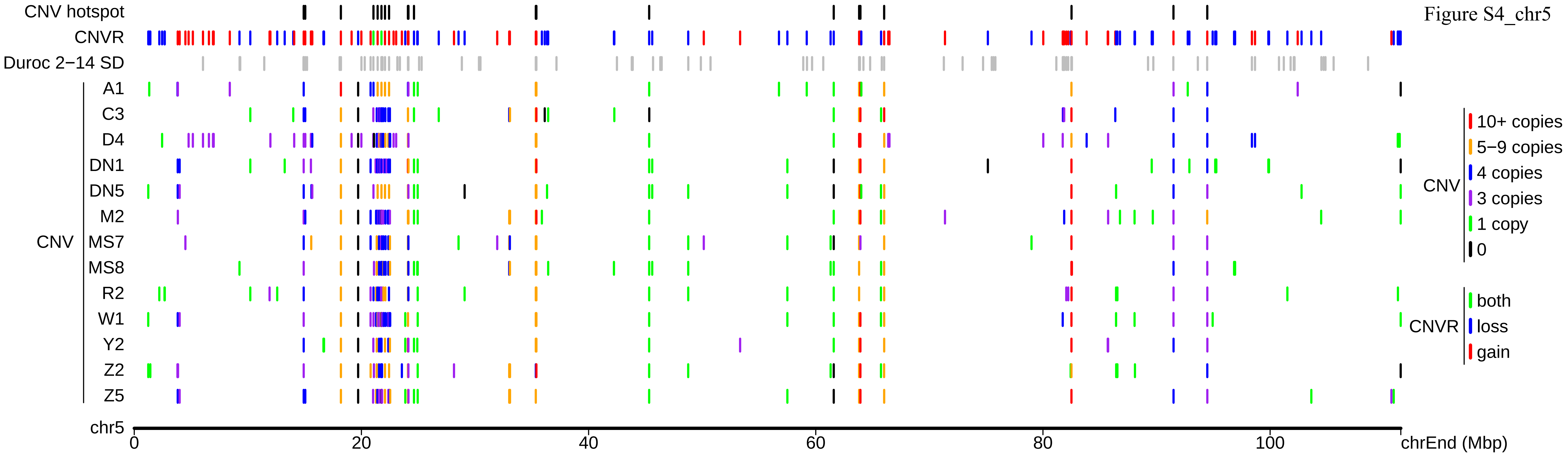

CNV hotspot
CNVR
Duroc 2−14 SD
A1
C3
D4
DN1
DN5
M2
CNV
MS7
MS8
R2
W1
Y2
Z2
Z5
chr5
0
20
40
60
80
100
chrEnd (Mbp)
Figure S4_chr5
10+ copies
5−9 copies
4 copies
CNV
3 copies
1 copy
0
both
CNVR
loss
gain

Figure S4_chr6

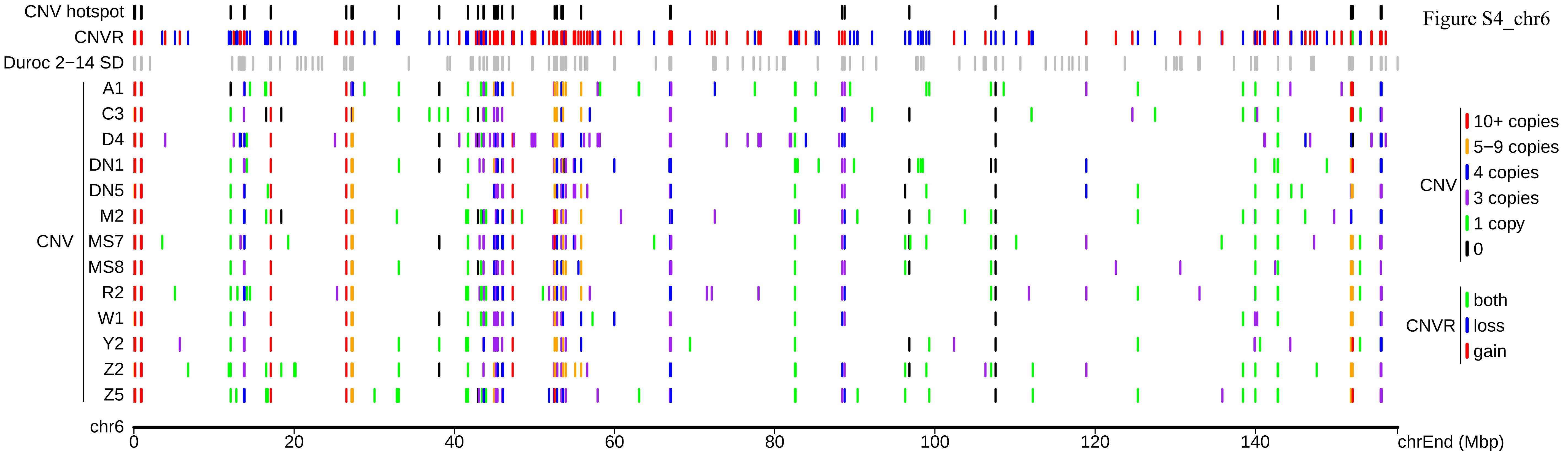


Figure S4_chr7

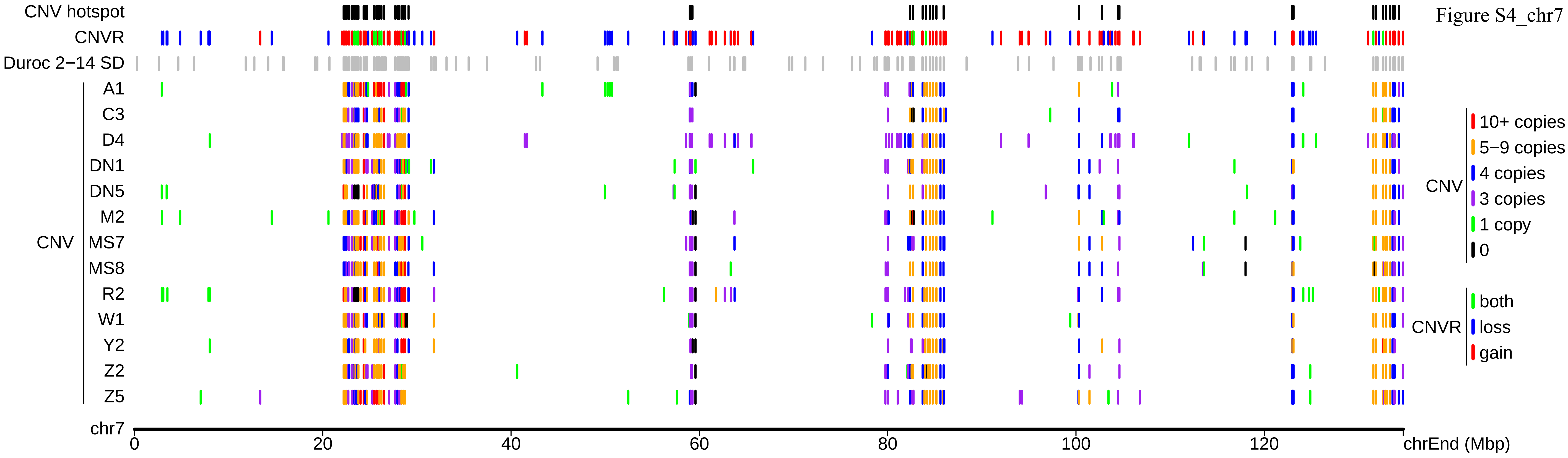


Figure S4_chr8

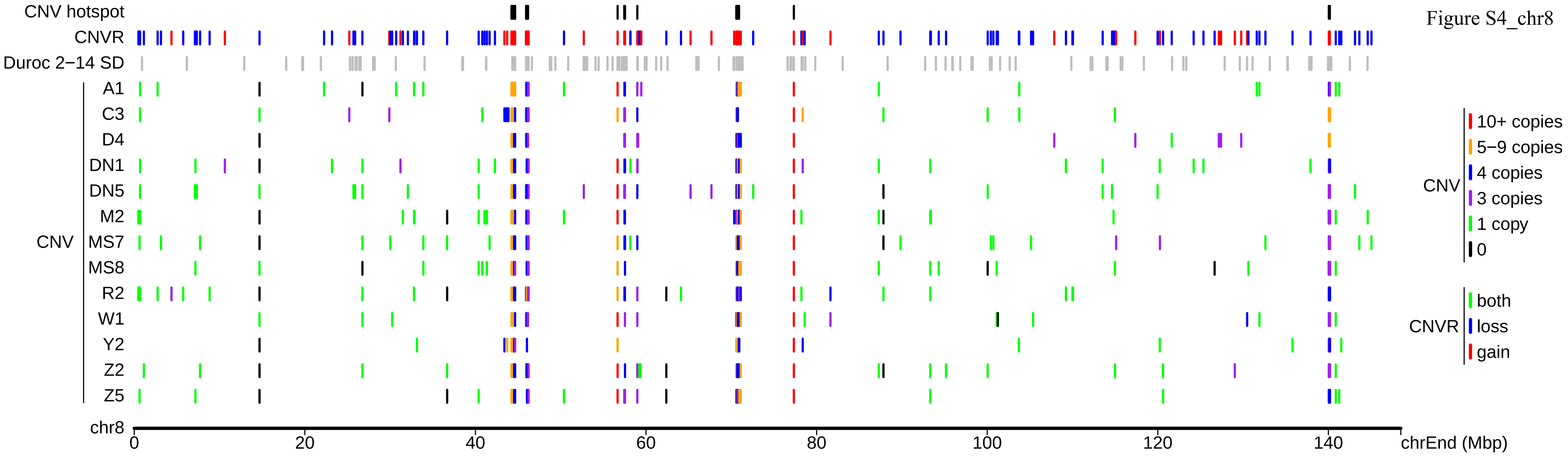


Figure S4_chr9

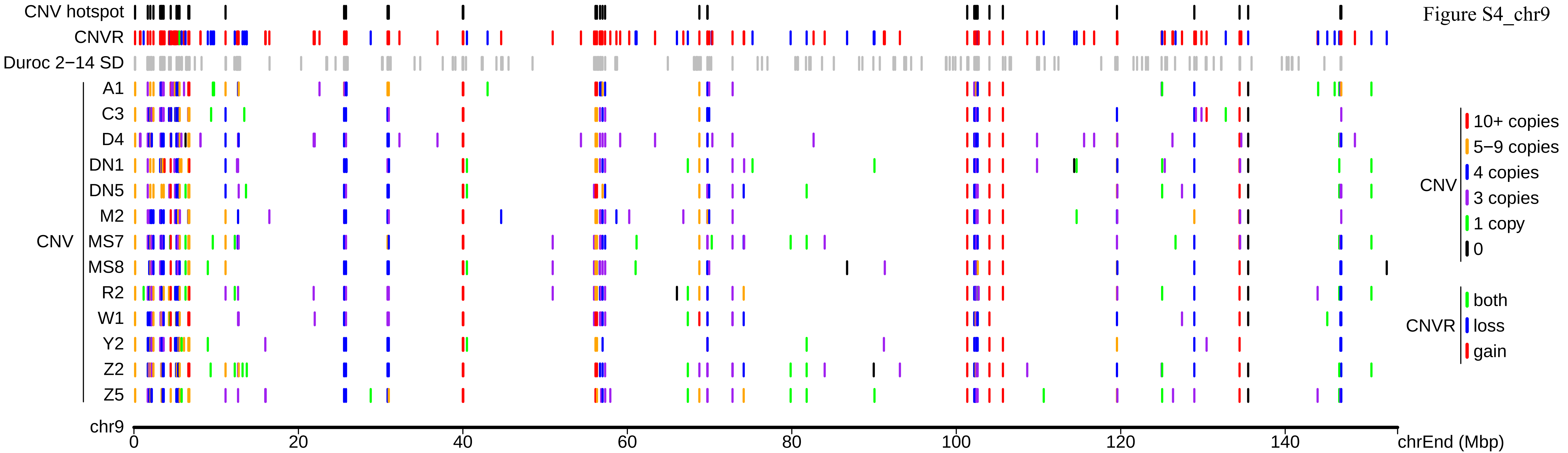


Figure S4_chr10

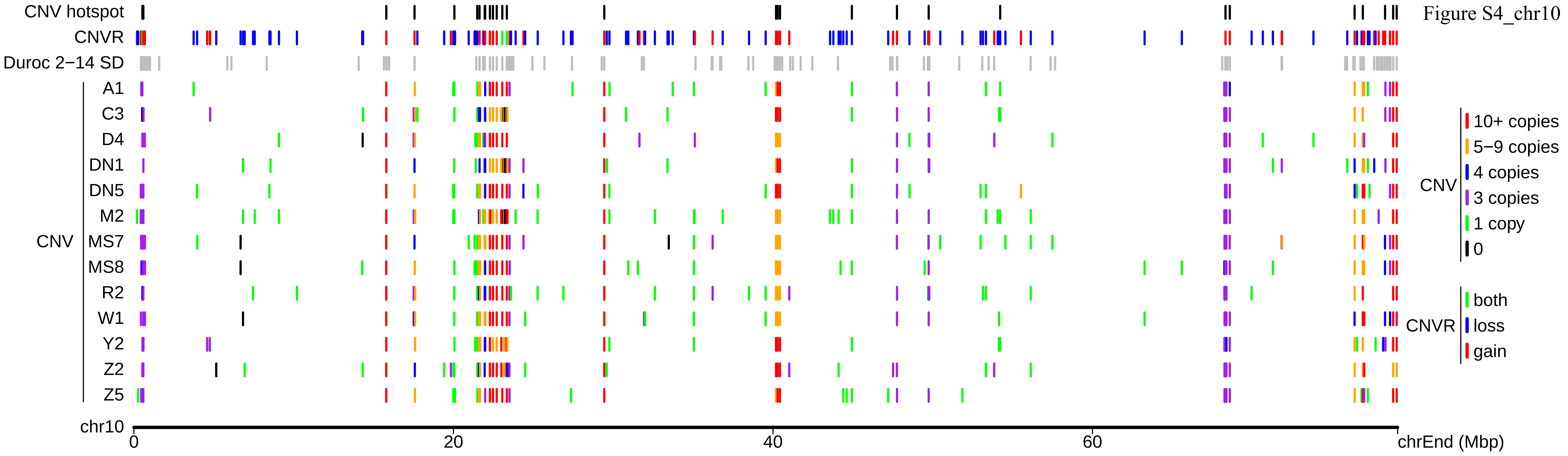


Figure S4_chr11

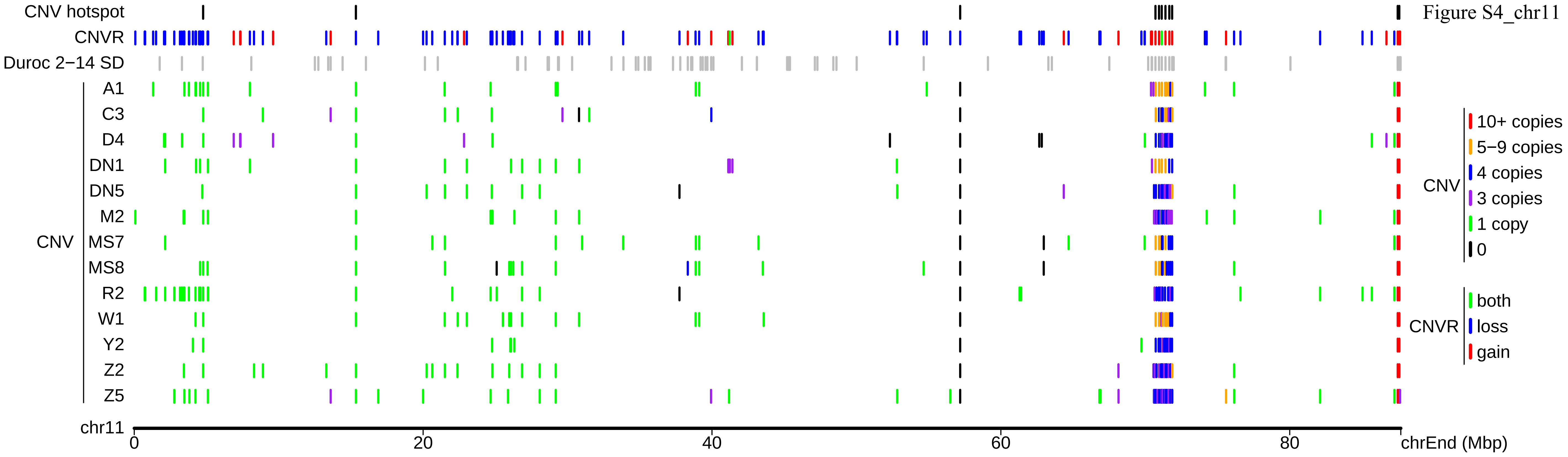


Figure S4_chr12

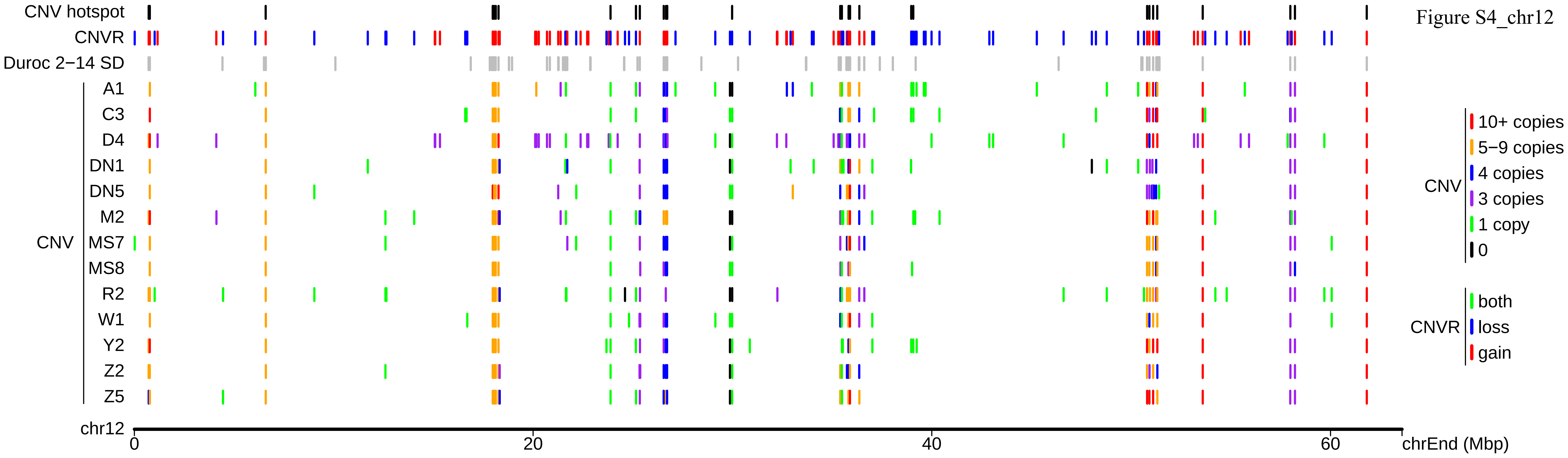


Figure S4_chr13

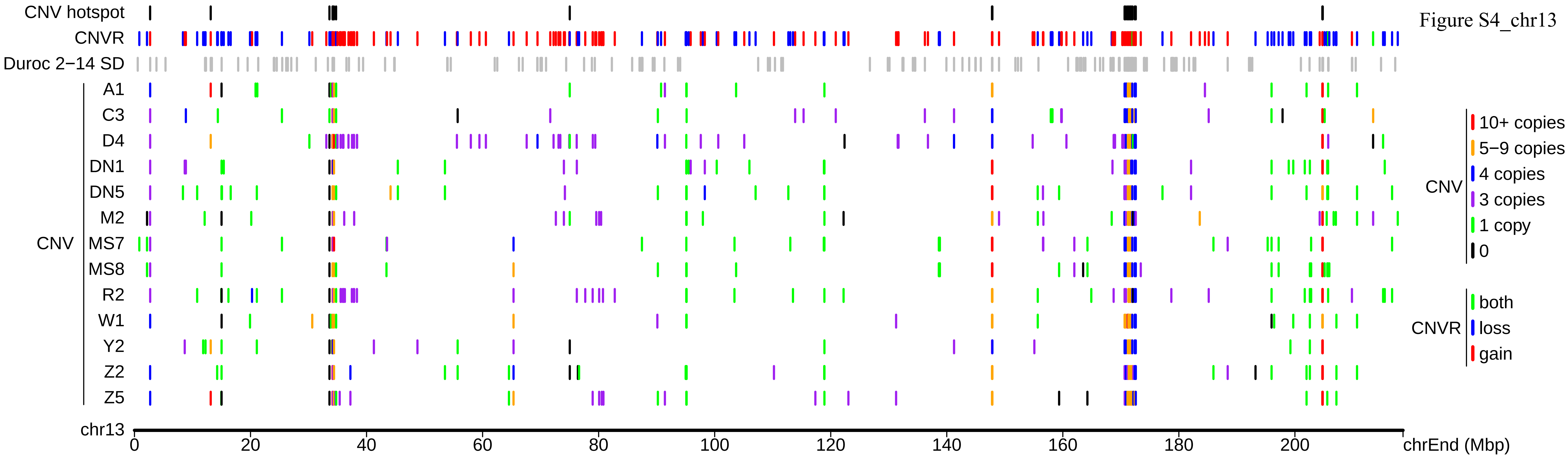


Figure S4_chr14

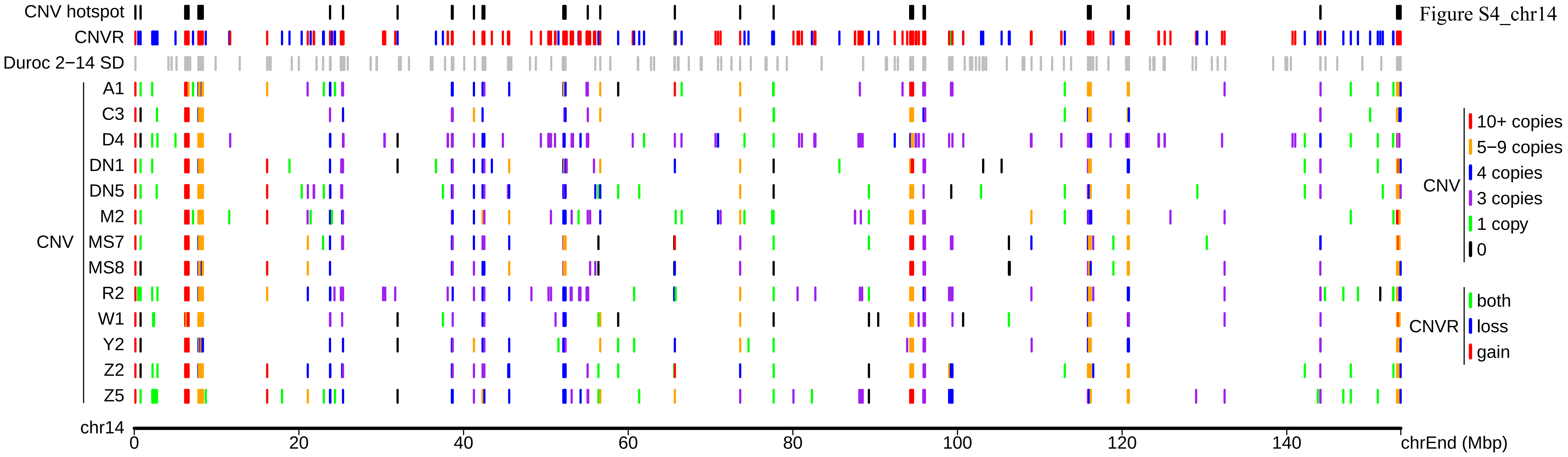
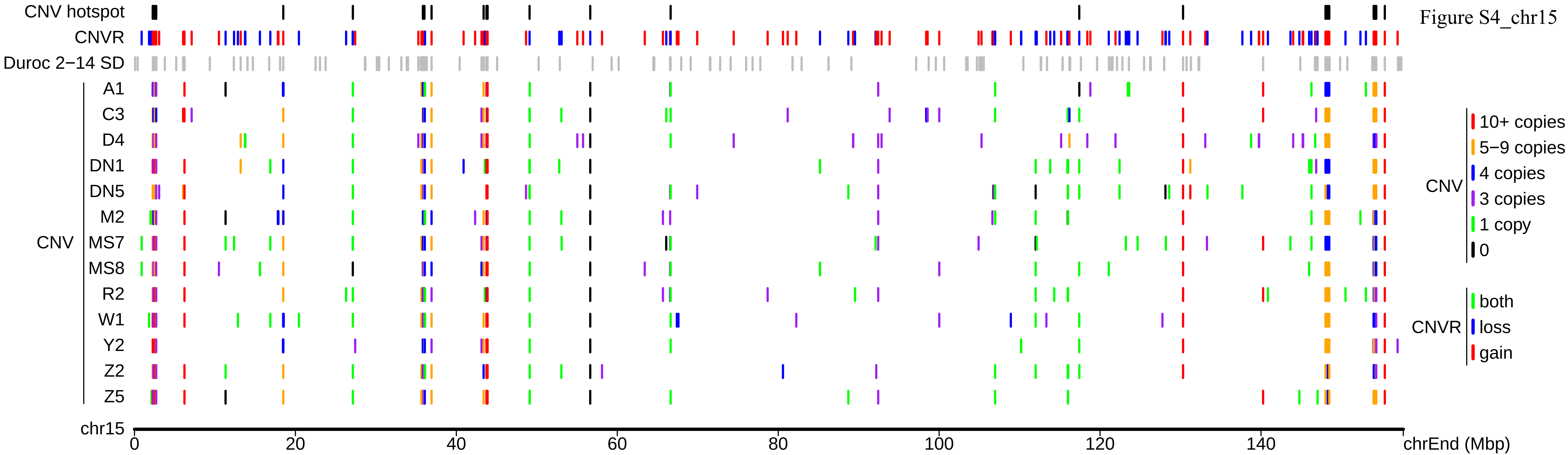


Figure S4_chr15



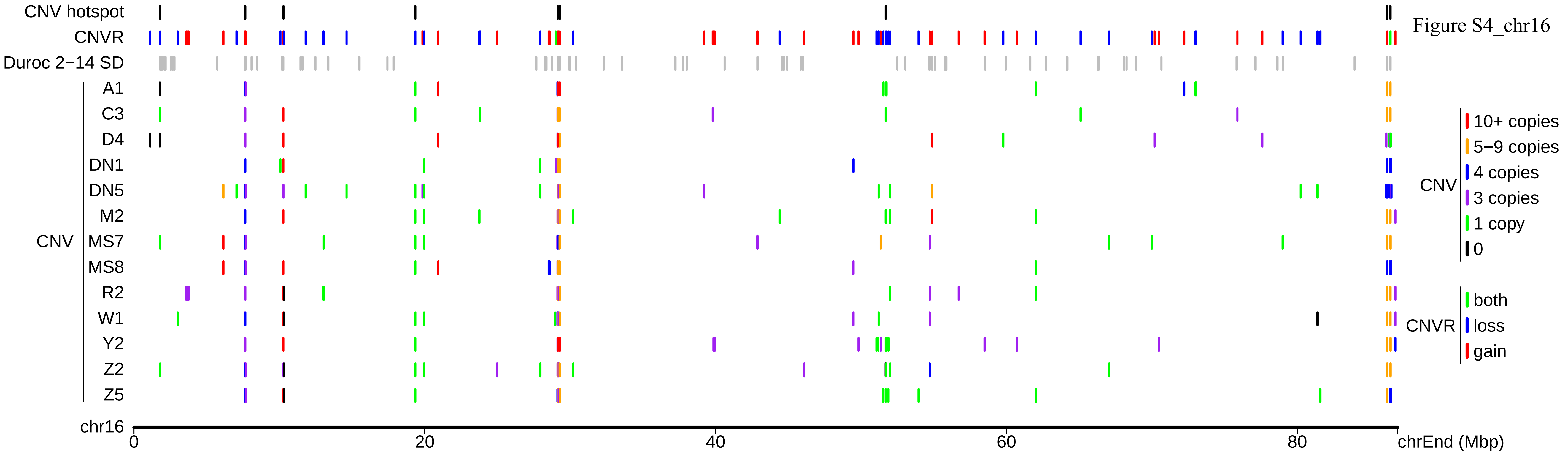


Figure S4_chr16

Figure S4_chr17

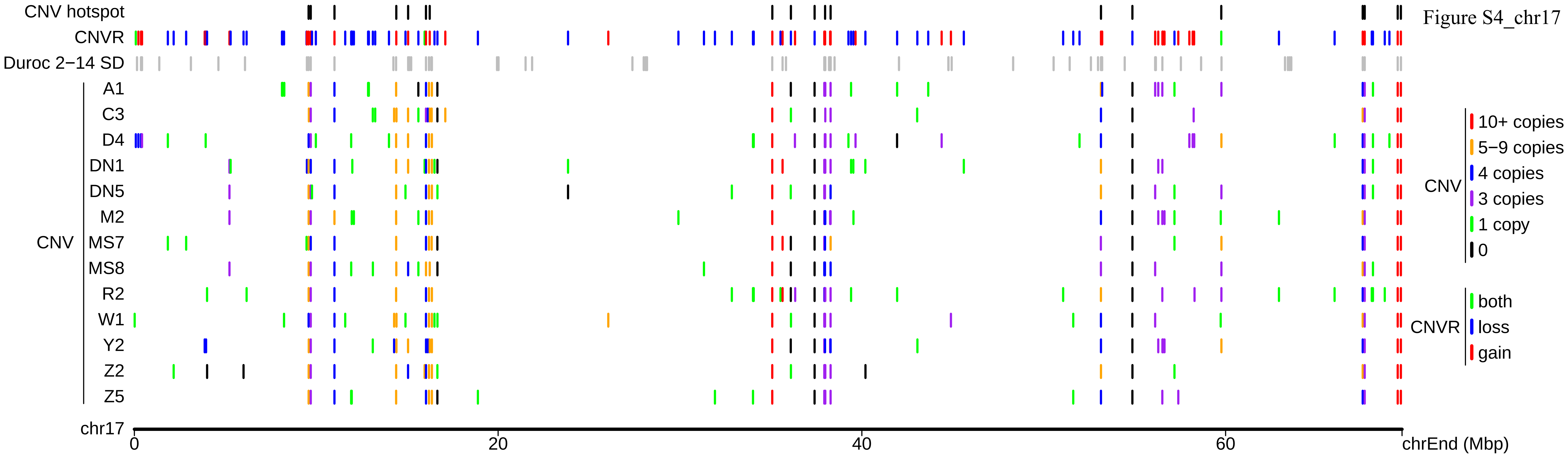


Figure S4_chr18

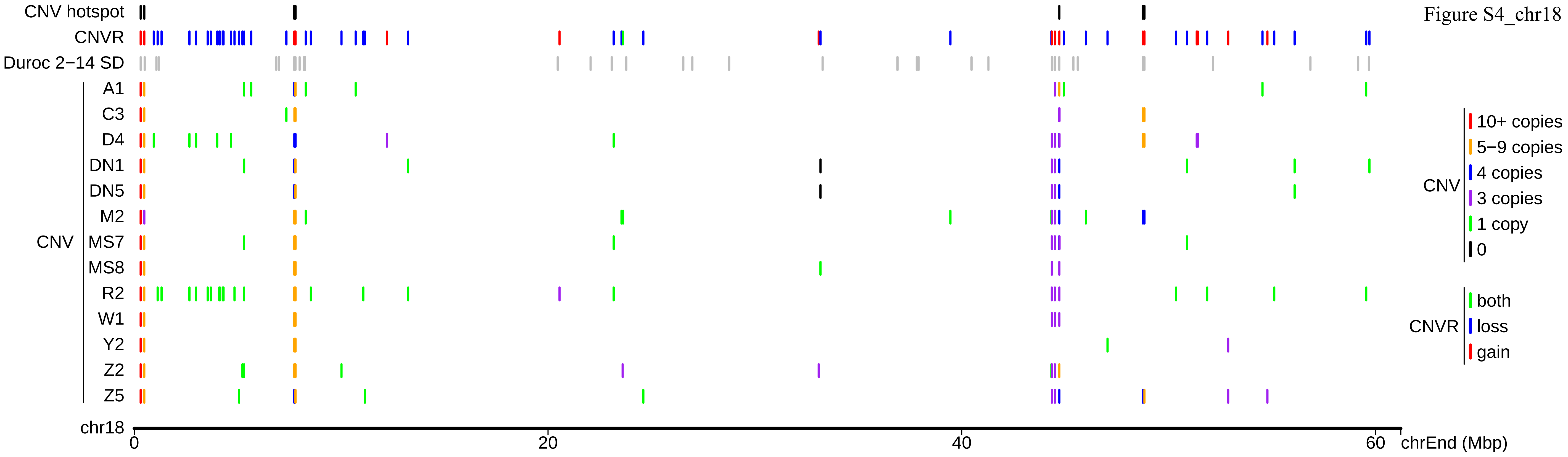


Figure S4_chrX

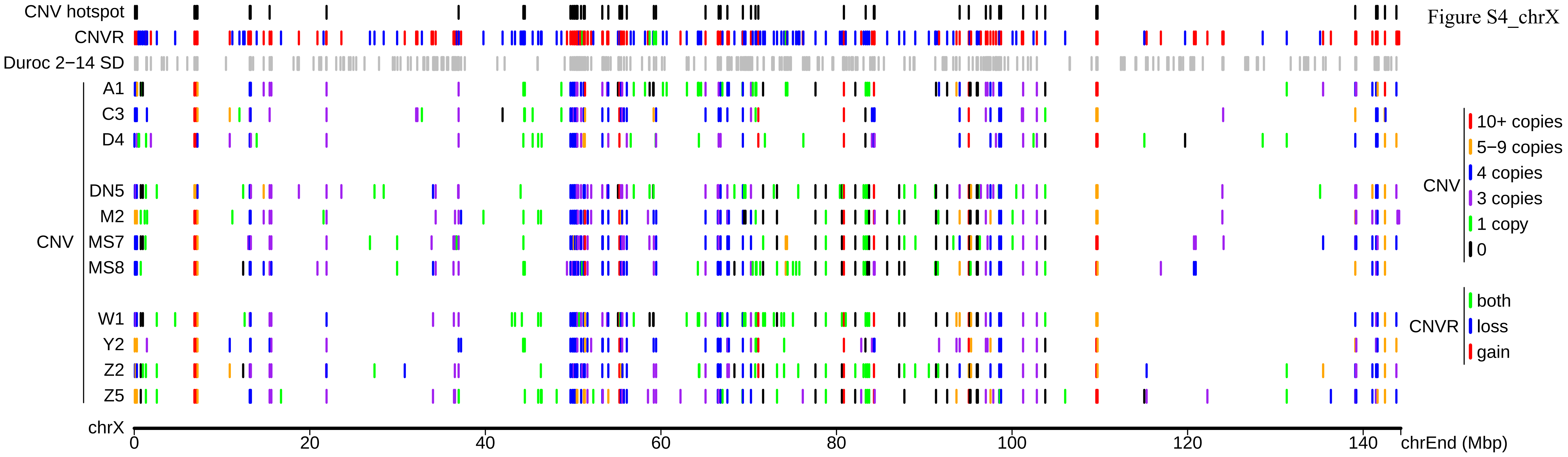


Figure S5

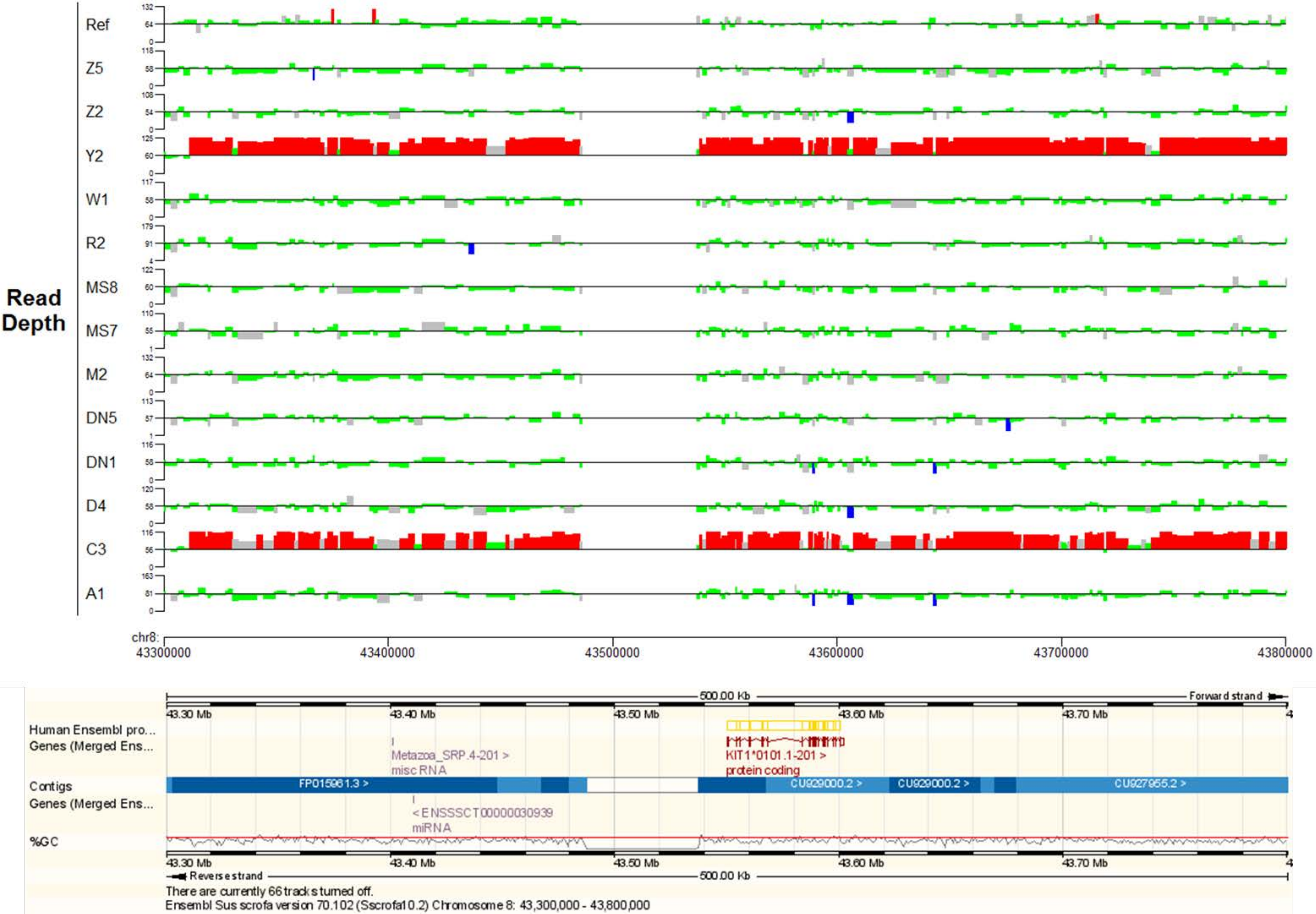
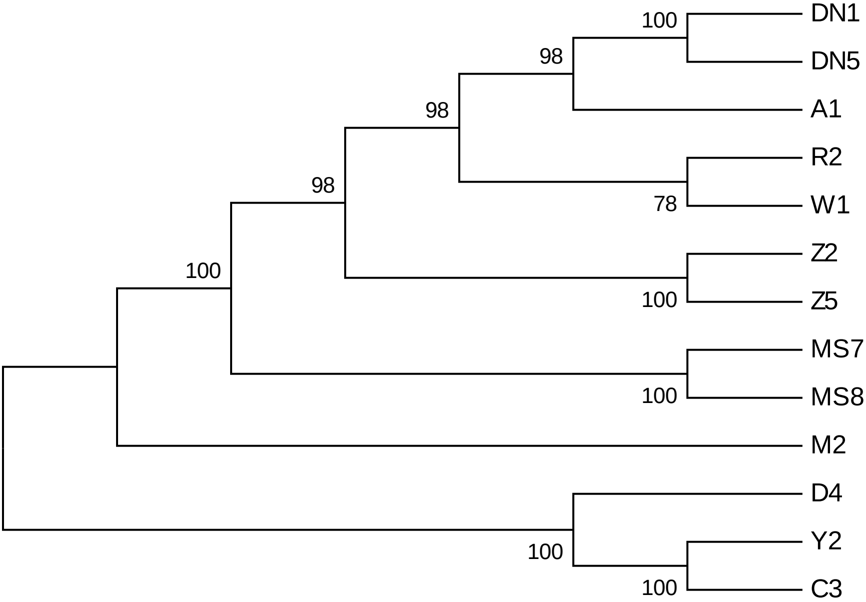

Read Depth
Ref
132
64
0
Z5
118
58
0
Z2
108
54
0
Y2
125
60
0
W1
117
58
0
R2
179
91
4
MS8
122
60
0
MS7
110
55
1
M2
132
64
0
DN5
113
57
1
DN1
116
58
0
D4
120
58
0
C3
116
56
0
A1
163
81
0
chr8:
43300000
43400000
43500000
43600000
43700000
43800000
500.00 Kb
Forward strand
43.30 Mb
43.40 Mb
43.50 Mb
43.60 Mb
43.70 Mb
Human Ensembl pro...
Genes (Merged Ens...
Metazoa_SRP.4-201 >
misc RNA
KIT1*0101.1-201 >
protein coding
Contigs
FP015961.3 >
CU929000.2 >
CU929000.2 >
CU927955.2 >
Genes (Merged Ens...
< ENSSSCT00000030939
miRNA
%GC
43.30 Mb
43.40 Mb
43.50 Mb
43.60 Mb
43.70 Mb
Reverse strand
500.00 Kb
There are currently 66 tracks turned off.
Ensembl Sus scrofa version 70.102 (Sscrofa10.2) Chromosome 8: 43,300,000 - 43,800,000

Figure S6


100
DN1
98
DN5
98
A1
R2
98
78
W1
Z2
100
100
Z5
MS7
100
MS8
M2
D4
Y2
100
100
C3