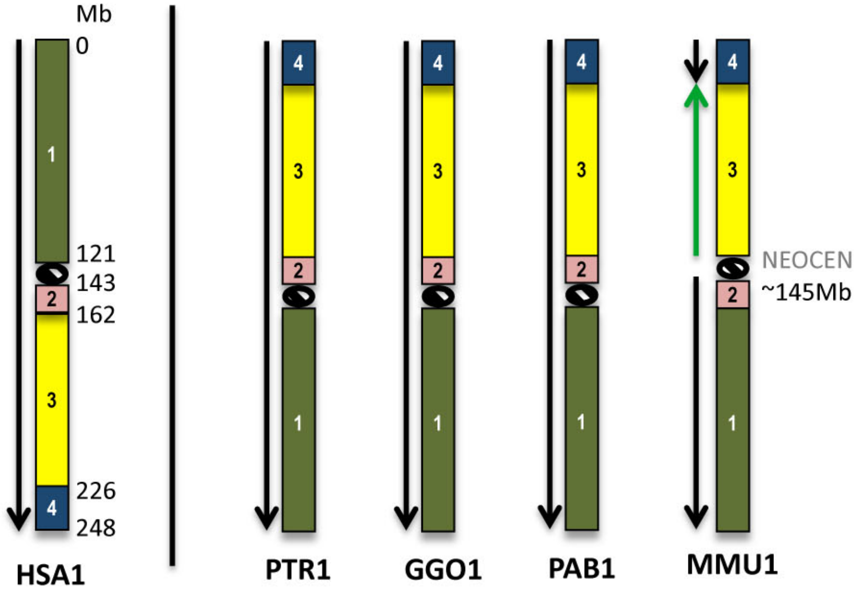
Mb
0
121
143
162
226
248
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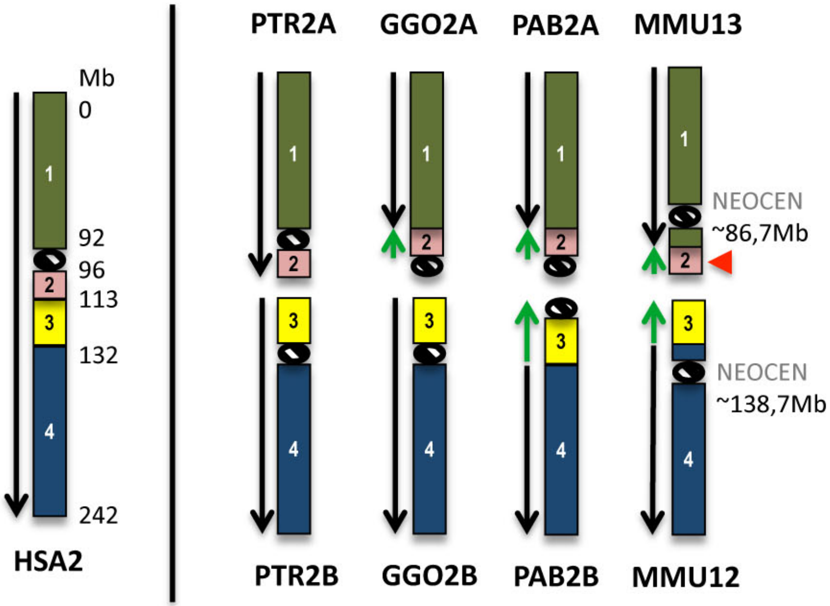
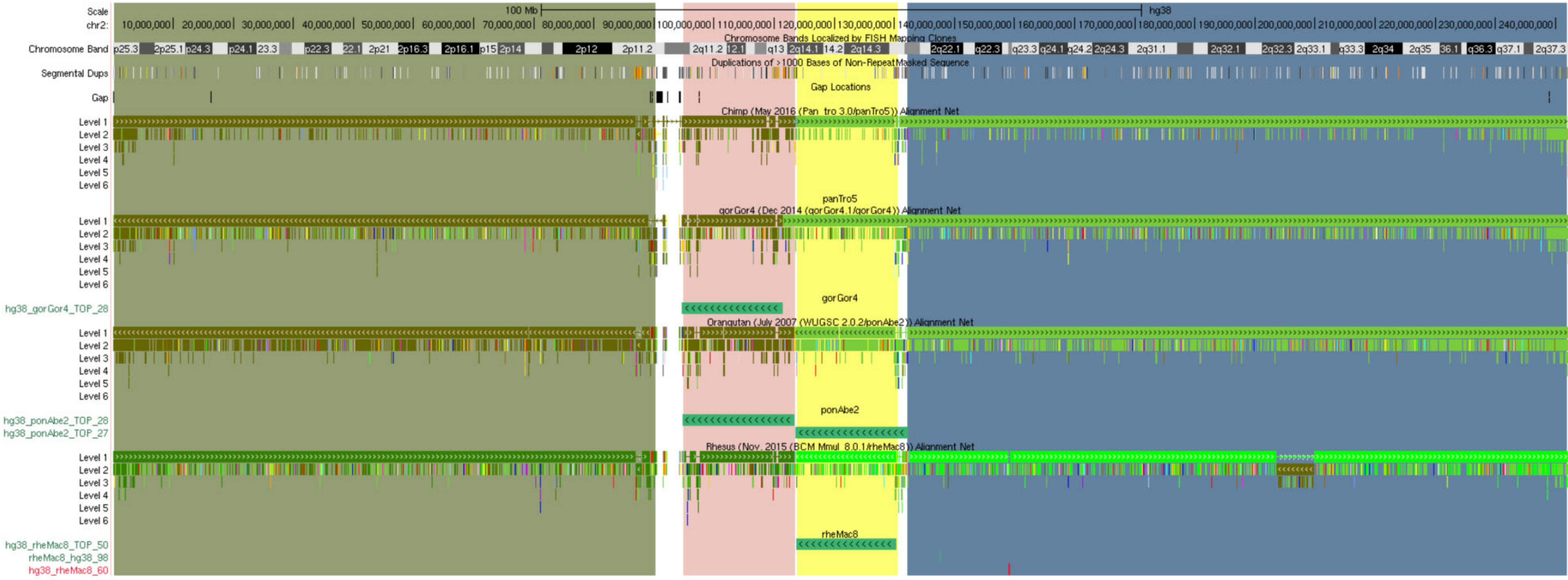
2
3
4
HSA1
PTR1
GGO1
PAB1
MMU1
NEOCEN
~145Mb


Scale
chr1:
100 Mb
hg38
10,000,000 20,000,000 30,000,000 40,000,000 50,000,000 60,000,000 70,000,000 80,000,000 90,000,000 100,000,000 110,000,000 120,000,000 130,000,000 140,000,000 150,000,000 160,000,000 170,000,000 180,000,000 190,000,000 200,000,000 210,000,000 220,000,000 230,000,000 240,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
Gap Locations
Gap
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
hg38_panTro5_2
hg38_panTro5_22
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
gorGor4
hg38_gorGor4_25
hg38_gorGor4_37
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
ponAbe2
hg38_ponAbe2_22
hg38_ponAbe2_55
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
rheMac8
hg38_rheMac8_125
hg38_rheMac8_TOP_51_46
hg38_rheMac8_94


PTR2A
GGO2A
PAB2A
MMU13
Mb
0
92
96
113
132
242
HSA2
1
2
3
4
NEOCEN
~86,7Mb
NEOCEN
~138,7Mb
PTR2B
GGO2B
PAB2B
MMU12


Scale
chr2:
100 Mb
hg38
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20,000,000
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40,000,000
50,000,000
60,000,000
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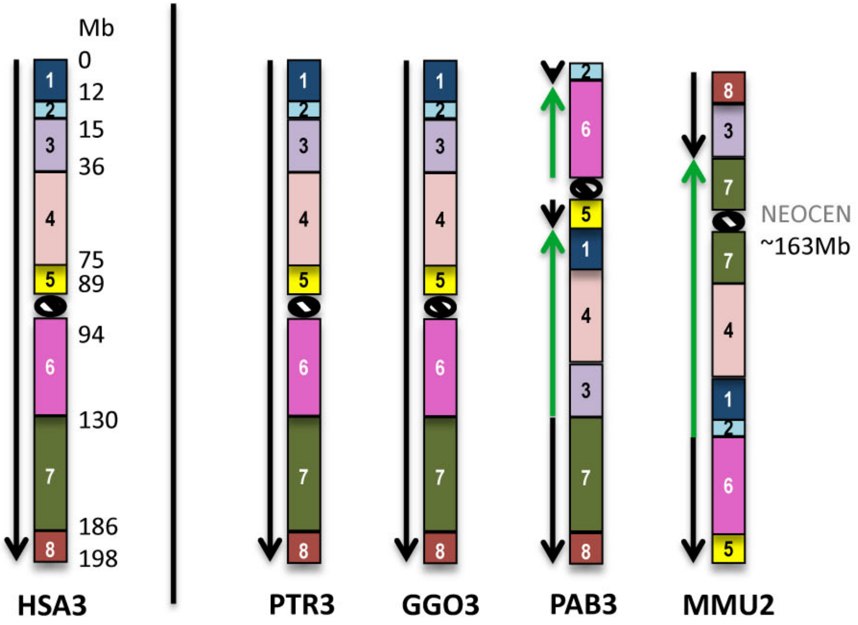
110,000,000
120,000,000
130,000,000
140,000,000
150,000,000
160,000,000
170,000,000
180,000,000
190,000,000
200,000,000
210,000,000
220,000,000
230,000,000
240,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
p25.3
2p25.1
p24.3
p24.1
23.3
p22.3
22.1
2p21
2p16.3
2p16.1
p15
2p14
2p12
2p11.2
2q11.2
12.1
q13
2q14.1
14.2
2q14.3
2q22.1
q22.3
q23.3
q24.1
q24.2
2q24.3
2q31.1
2q32.1
2q32.3
2q33.1
q33.3
2q34
2q35
36.1
q36.3
q37.1
2q37.3
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
Gap Locations
Gap
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
gorGor4
hg38_gorGor4_TOP_28
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
ponAbe2
hg38_ponAbe2_TOP_28
hg38_ponAbe2_TOP_27
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
rheMac8
hg38_rheMac8_TOP_50
rheMac8_hg38_98
hg38_rheMac8_60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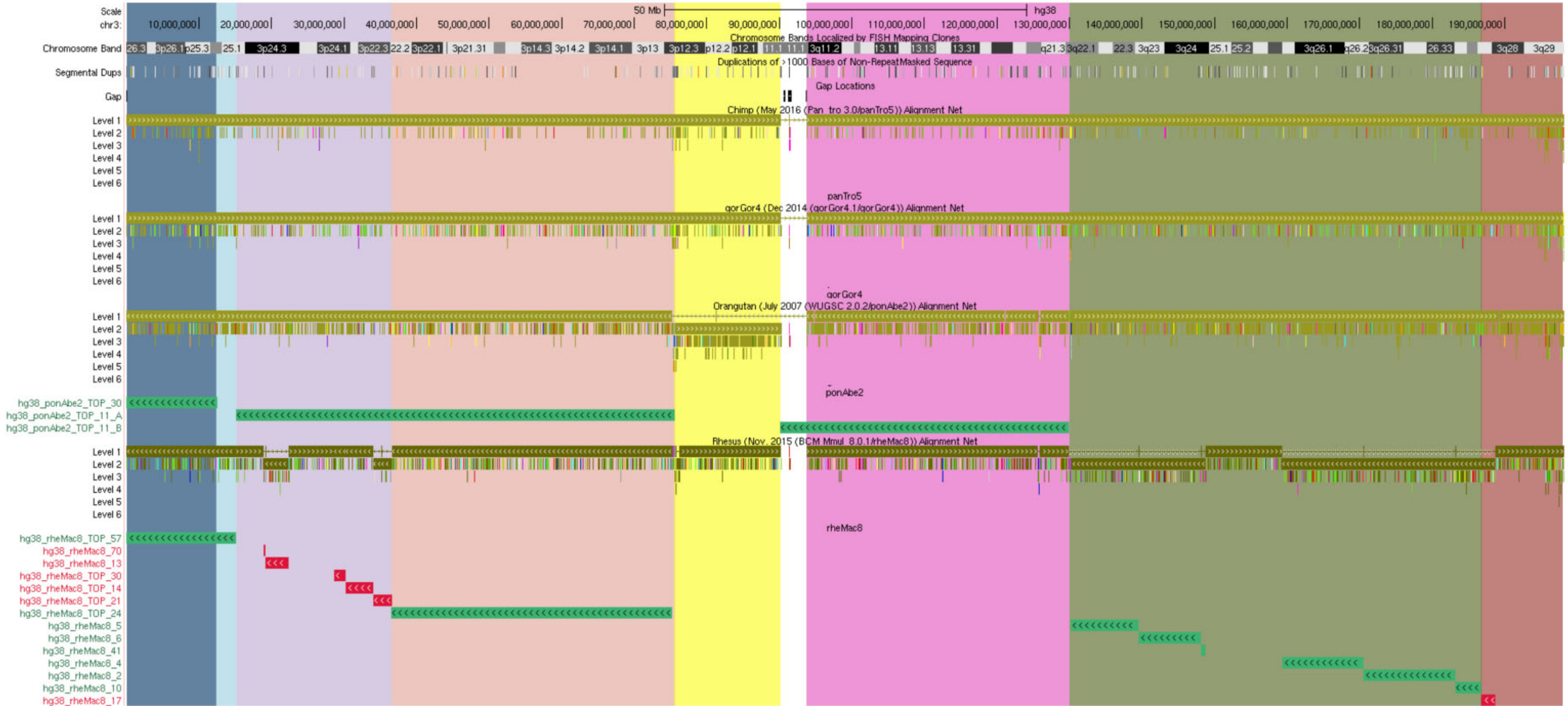
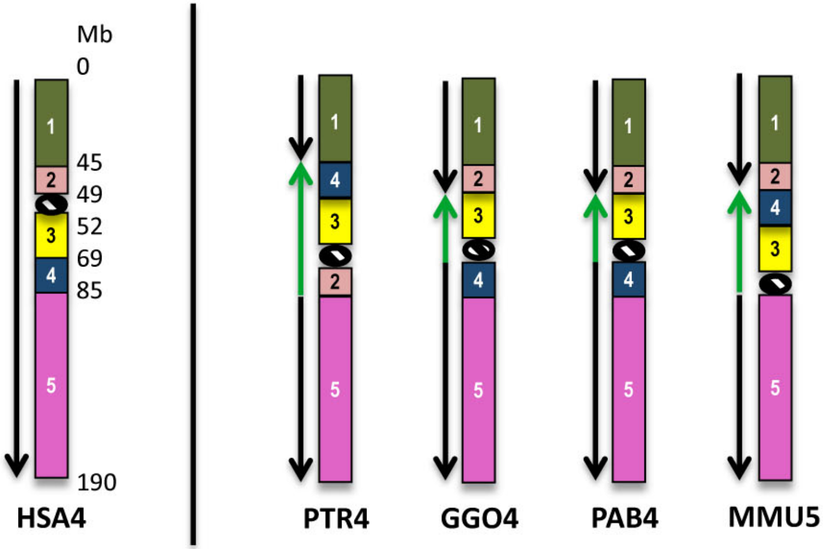
15
36
75
89
94
130
186
198
NEOCEN
~163Mb
HSA3
PTR3
GGO3
PAB3
MMU2


Scale
chr3:
50 Mb
hg38
Chromosome Band
Segmental Dups
Gap
Chromosome Bands Localized by FISH Mapping Clones
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Gap Locations
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
panTro5
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
gorGor4
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
ponAbe2
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
rheMac8
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
hg38_ponAbe2_TOP_30
hg38_ponAbe2_TOP_11_A
hg38_ponAbe2_TOP_11_B
hg38_rheMac8_TOP_57
hg38_rheMac8_70
hg38_rheMac8_13
hg38_rheMac8_TOP_30
hg38_rheMac8_TOP_14
hg38_rheMac8_TOP_21
hg38_rheMac8_TOP_24
hg38_rheMac8_5
hg38_rheMac8_6
hg38_rheMac8_41
hg38_rheMac8_4
hg38_rheMac8_2
hg38_rheMac8_10
hg38_rheMac8_17


Mb
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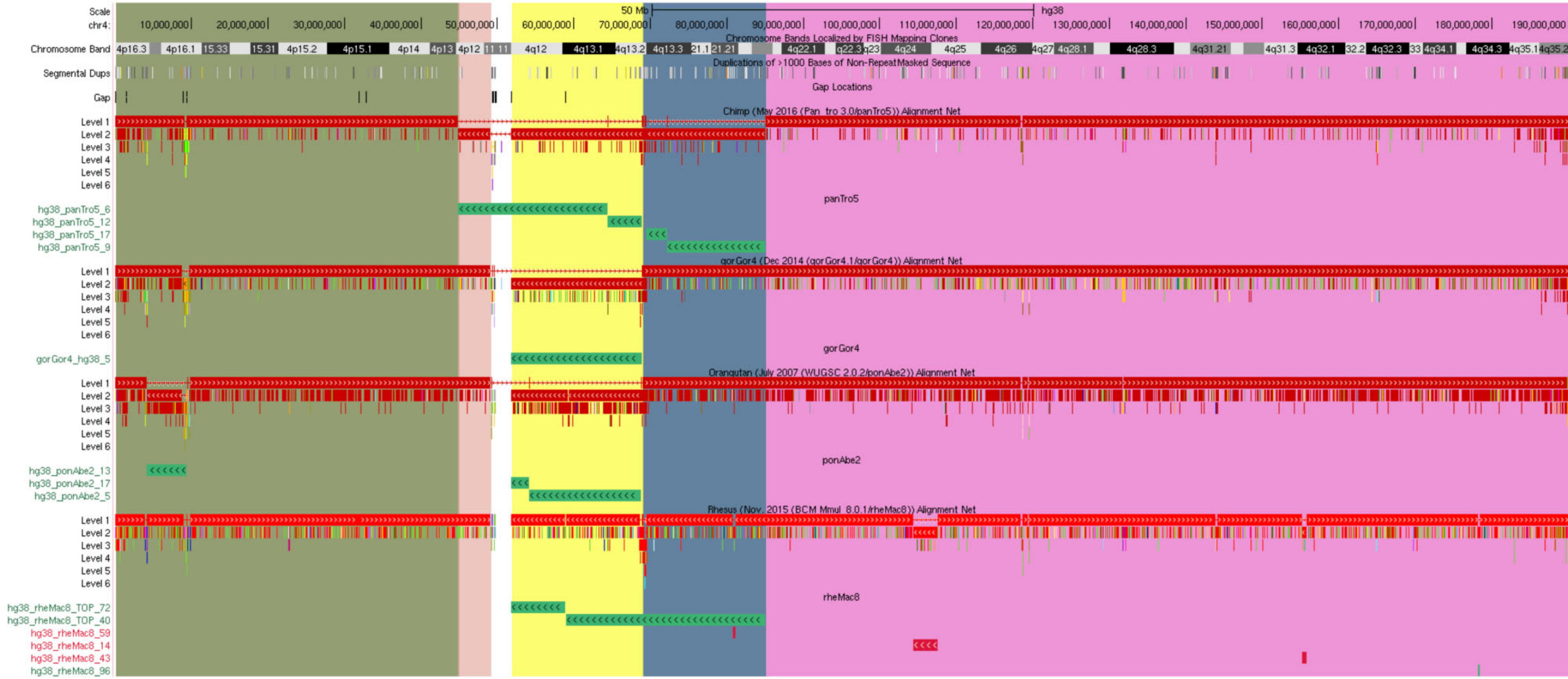
1
45
2
49
52
3
69
4
85
5
190
HSA4
PTR4
GGO4
PAB4
MMU5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chr4:
50 Mb
hg38
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20,000,000
30,000,000
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50,000,000
60,000,000
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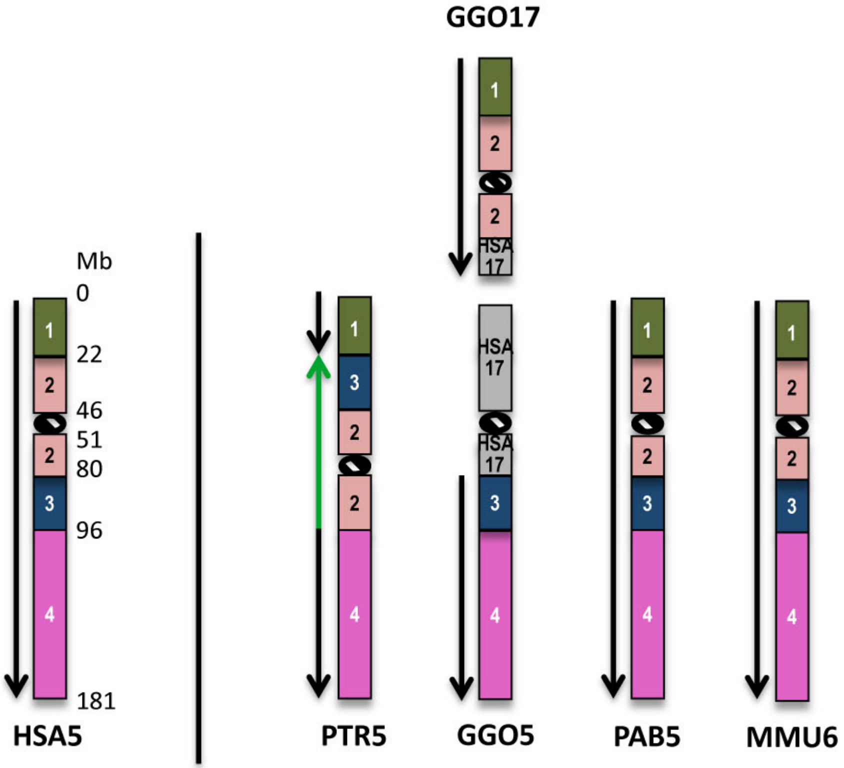
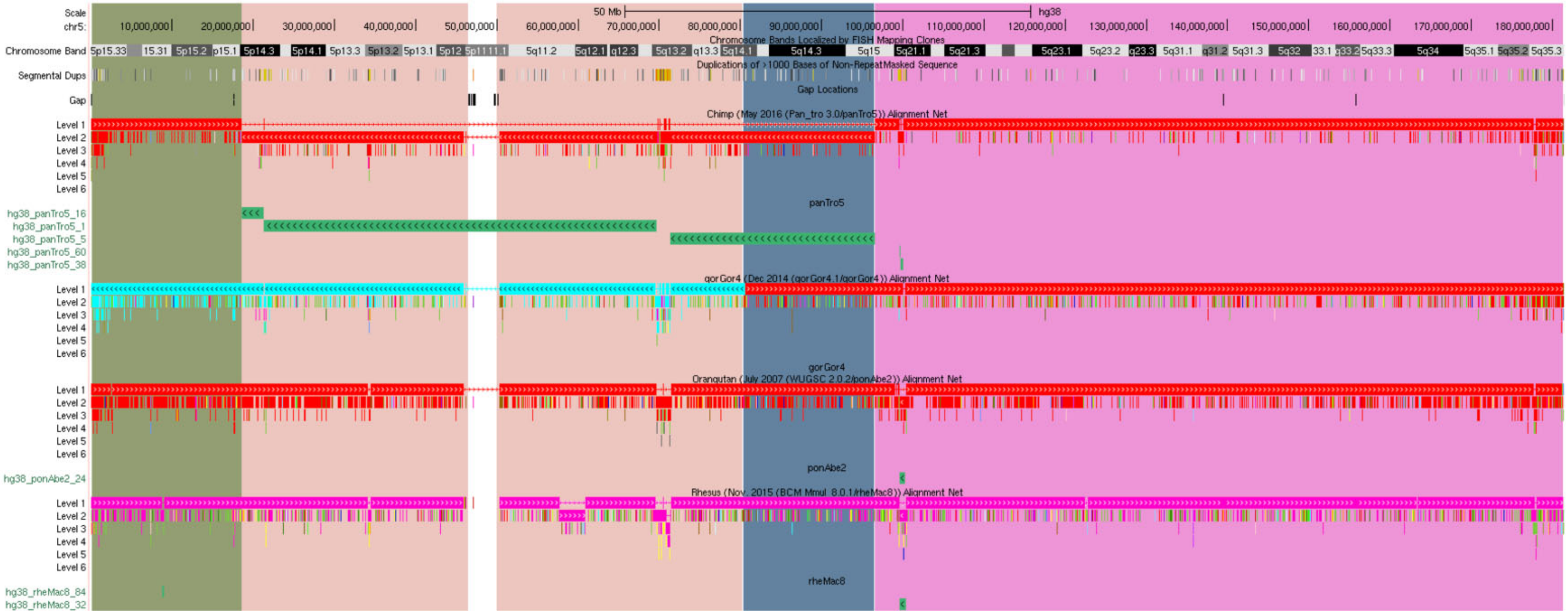
90,000,000
100,000,000
110,000,000
120,000,000
130,000,000
140,000,000
150,000,000
160,000,000
170,000,000
180,000,000
190,000,000
Chromosome Band
Chromosome Bands Localized by FISH Mapping Clones
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Gap
Gap Locations
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
hg38_panTro5_6
hg38_panTro5_12
hg38_panTro5_17
hg38_panTro5_9
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
gorGor4
gorGor4_hg38_5
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
ponAbe2
hg38_ponAbe2_13
hg38_ponAbe2_17
hg38_ponAbe2_5
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
rheMac8
hg38_rheMac8_TOP_72
hg38_rheMac8_TOP_40
hg38_rheMac8_59
hg38_rheMac8_14
hg38_rheMac8_43
hg38_rheMac8_96


GGO17
1
2
2
HSA 17
Mb
0
22
46
51
80
96
181
1
2
2
3
4
HSA5
1
3
2
2
4
PTR5
HSA 17
HSA 17
3
4
GGO5
1
2
2
3
4
PAB5
1
2
2
3
4
MMU6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50 Mb
hg38
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40,000,000
50,000,000
60,000,000
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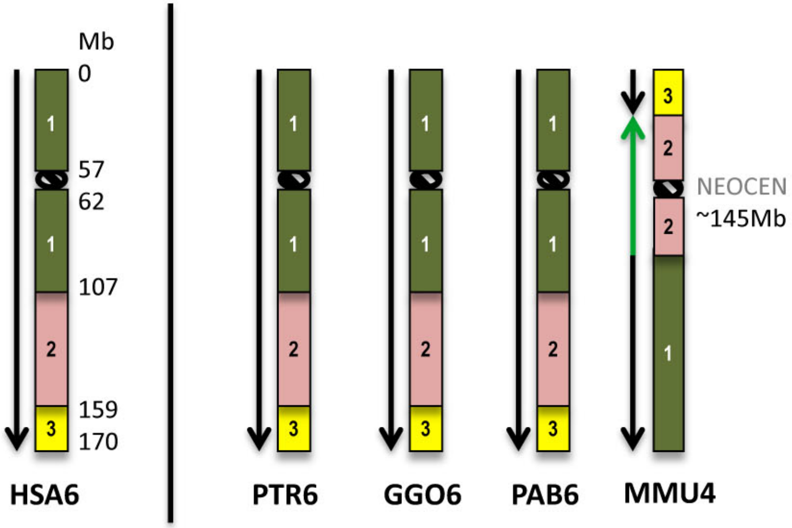
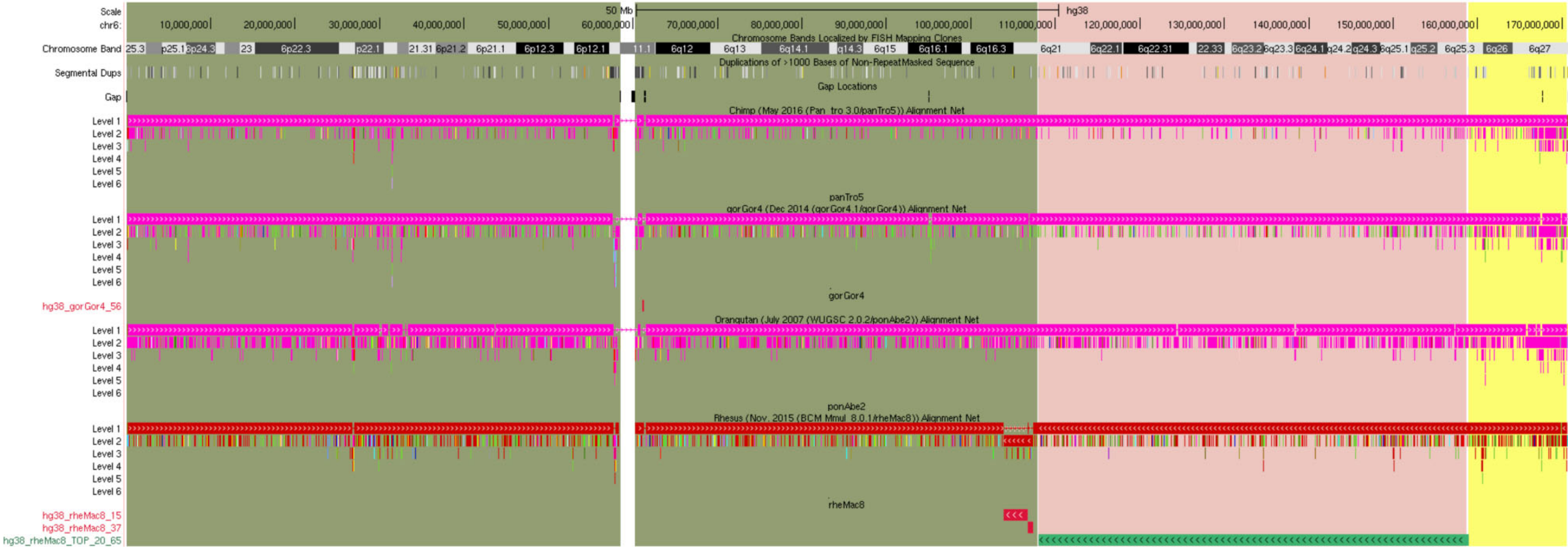
90,000,000
100,000,000
110,000,000
120,000,000
130,000,000
140,000,000
150,000,000
160,000,000
170,000,000
180,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
5p15.33
15.31
5p15.2
p15.1
5p14.3
5p14.1
5p13.3
5p13.2
5p13.1
5p12
5p11
11.1
5q11.2
5q12.1
q12.3
5q13.2
q13.3
5q14.1
5q14.3
5q15
5q21.1
5q21.3
5q23.1
5q23.2
q23.3
5q31.1
q31.2
5q31.3
5q32
33.1
q33.2
5q33.3
5q34
5q35.1
5q35.2
5q35.3
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
Gap Locations
Gap
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
hg38_panTro5_16
hg38_panTro5_1
hg38_panTro5_5
hg38_panTro5_60
hg38_panTro5_38
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
gorGor4
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
ponAbe2
hg38_ponAbe2_24
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
rheMac8
hg38_rheMac8_84
hg38_rheMac8_32


Mb
0
57
62
107
159
170
1
1
2
3
HSA6
PTR6
GGO6
PAB6
MMU4
NEOCEN
~145Mb


Scale
chr6:
50 Mb
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50,000,000
60,000,000
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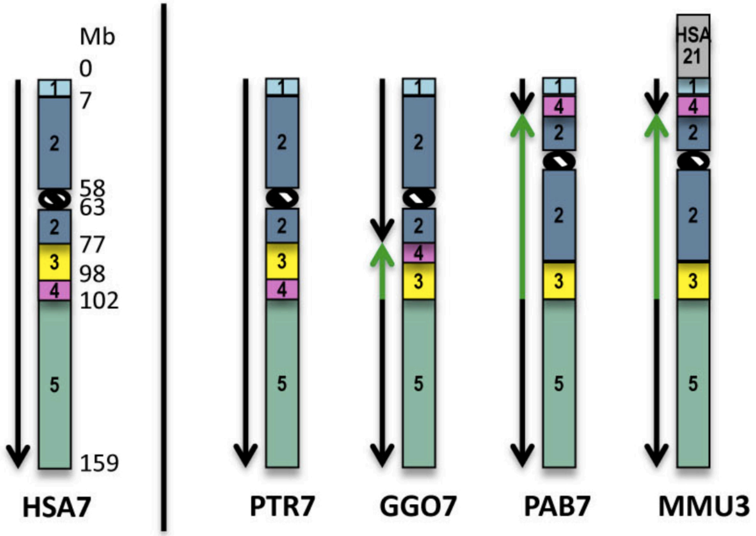
100,000,000
110,000,000
120,000,000
130,000,000
140,000,000
150,000,000
160,000,000
170,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
Gap Locations
Gap
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
gorGor4
hg38_gorGor4_56
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
ponAbe2
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
rheMac8
hg38_rheMac8_15
hg38_rheMac8_37
hg38_rheMac8_TOP_20_65


Mb
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58
63
77
98
102
159
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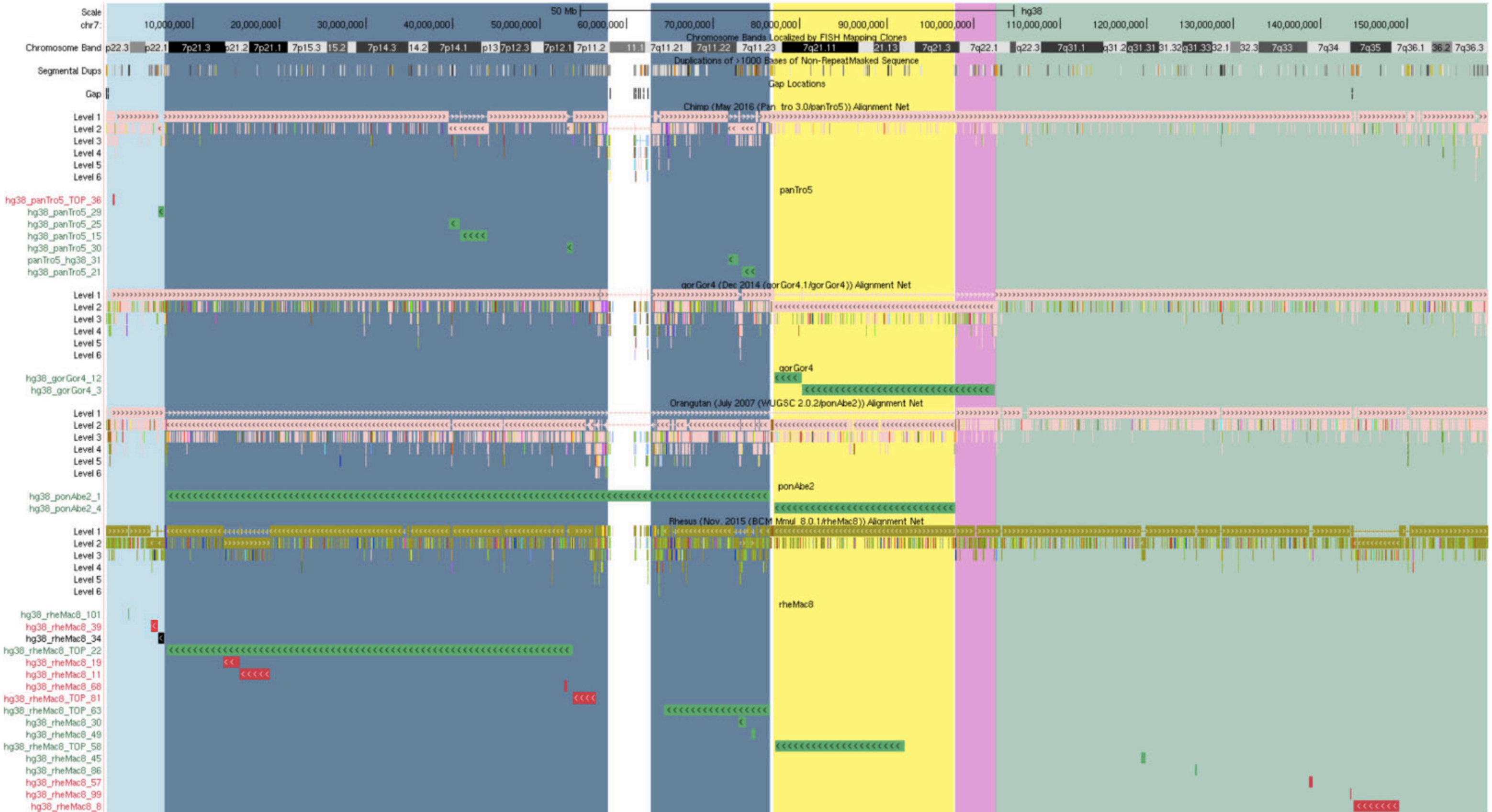
PTR7
GGO7
PAB7
MMU3
HSA 21
1
2
3
4
5


Scale
50 Mb
hg38
chr7:
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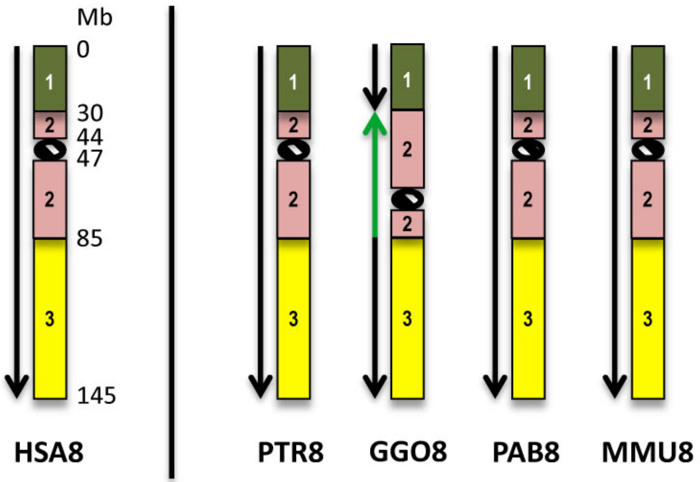
90,000,000
100,000,000
110,000,000
120,000,000
130,000,000
140,000,000
150,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
Gap Locations
Gap
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
hg38_panTro5_TOP_36
hg38_panTro5_29
hg38_panTro5_25
hg38_panTro5_15
hg38_panTro5_30
panTro5_hg38_31
hg38_panTro5_21
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
gorGor4
hg38_gorGor4_12
hg38_gorGor4_3
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
ponAbe2
hg38_ponAbe2_1
hg38_ponAbe2_4
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
rheMac8
hg38_rheMac8_101
hg38_rheMac8_39
hg38_rheMac8_34
hg38_rheMac8_TOP_22
hg38_rheMac8_19
hg38_rheMac8_11
hg38_rheMac8_68
hg38_rheMac8_TOP_81
hg38_rheMac8_TOP_63
hg38_rheMac8_30
hg38_rheMac8_49
hg38_rheMac8_TOP_58
hg38_rheMac8_45
hg38_rheMac8_86
hg38_rheMac8_57
hg38_rheMac8_99
hg38_rheMac8_8


Mb
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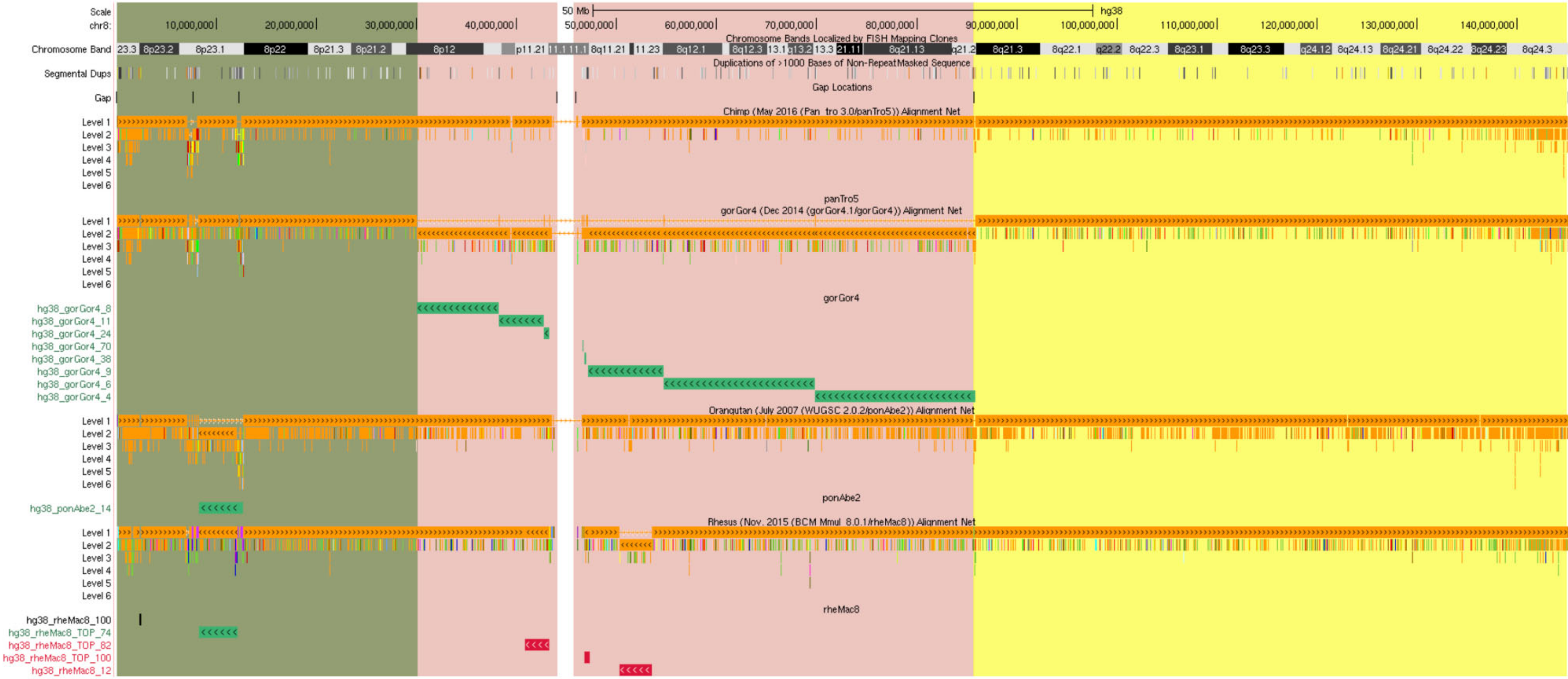
44
47
85
145
1
2
2
3
HSA8
PTR8
GGO8
PAB8
MMU8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hg38
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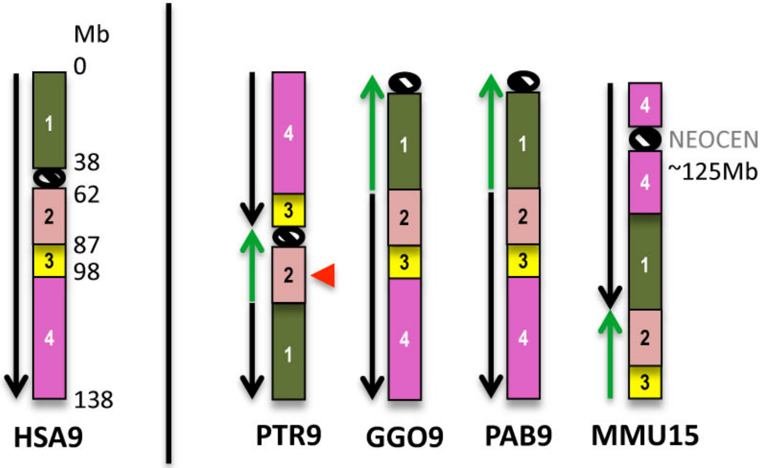
70,000,000
80,000,000
90,000,000
100,000,000
110,000,000
120,000,000
130,000,000
140,000,000
Chromosome Band
Chromosome Bands Localized by FISH Mapping Clones
23.3
8p23.2
8p23.1
8p22
8p21.3
8p21.2
8p12
p11.21
8q11.21
11.23
8q12.1
8q12.3
13.1
q13.2
13.3
21.11
8q21.13
q21.2
8q21.3
8q22.1
q22.2
8q22.3
8q23.1
8q23.3
q24.12
8q24.13
8q24.21
8q24.22
8q24.23
8q24.3
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Gap
Gap Locations
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
gorGor4
hg38_gorGor4_8
hg38_gorGor4_11
hg38_gorGor4_24
hg38_gorGor4_70
hg38_gorGor4_38
hg38_gorGor4_9
hg38_gorGor4_6
hg38_gorGor4_4
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
ponAbe2
hg38_ponAbe2_14
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
rheMac8
hg38_rheMac8_100
hg38_rheMac8_TOP_74
hg38_rheMac8_TOP_82
hg38_rheMac8_TOP_100
hg38_rheMac8_12


Mb
0
38
62
87
98
138
1
2
3
4
HSA9
PTR9
GGO9
PAB9
MMU15
NEOCEN
~125Mb


Scale
chr9:
50 Mb
hg38
10,000,000
20,000,000
30,000,000
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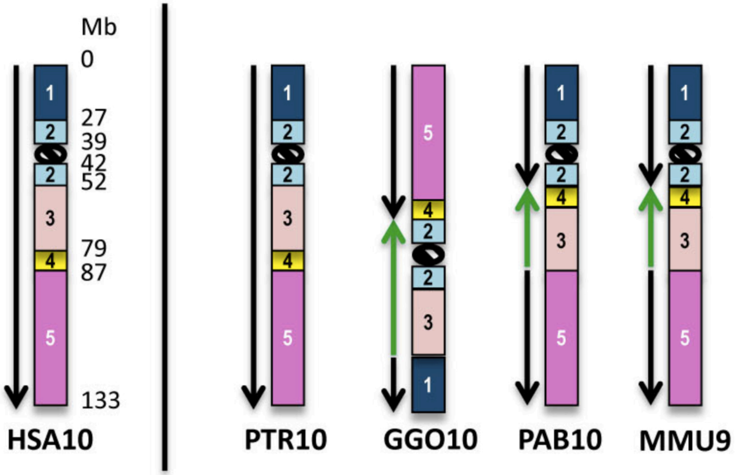
50,000,000
60,000,000
70,000,000
80,000,000
90,000,000
100,000,000
110,000,000
120,000,000
130,000,000
Chromosome Band
Chromosome Bands Localized by FISH Mapping Clones
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Gap
Gap Locations
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
gorGor4
hg38_gorGor4_TOP_21
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
ponAbe2
hg38_ponAbe2_TOP_21
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
rheMac8
hg38_rheMac8_107
hg38_rheMac8_38
hg38_rheMac8_TOP_27_28


Mb
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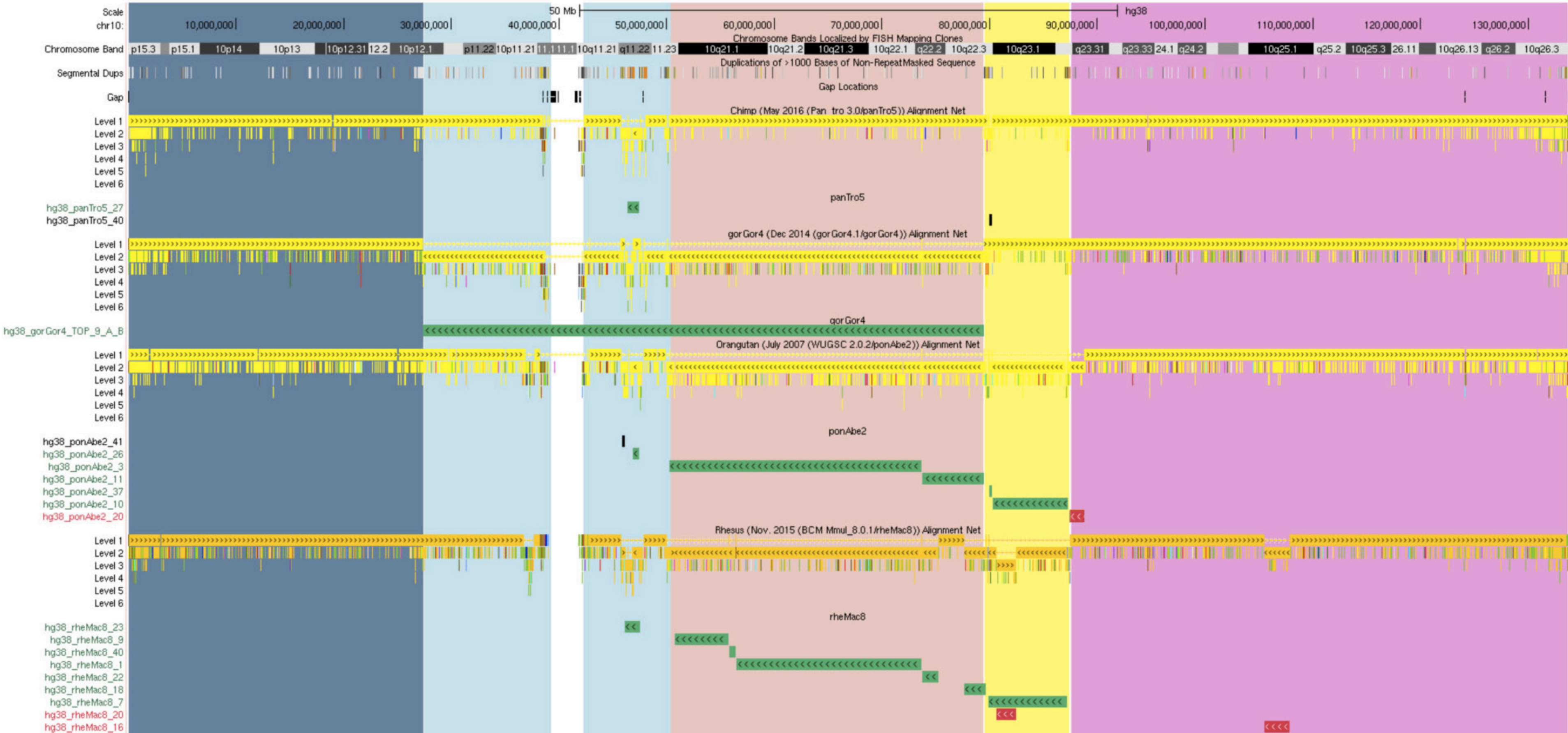
39
42
52
79
87
133
1
2
2
3
4
5
HSA10
PTR10
GGO10
PAB10
MMU9


Scale
chr10:
50 Mb
hg38
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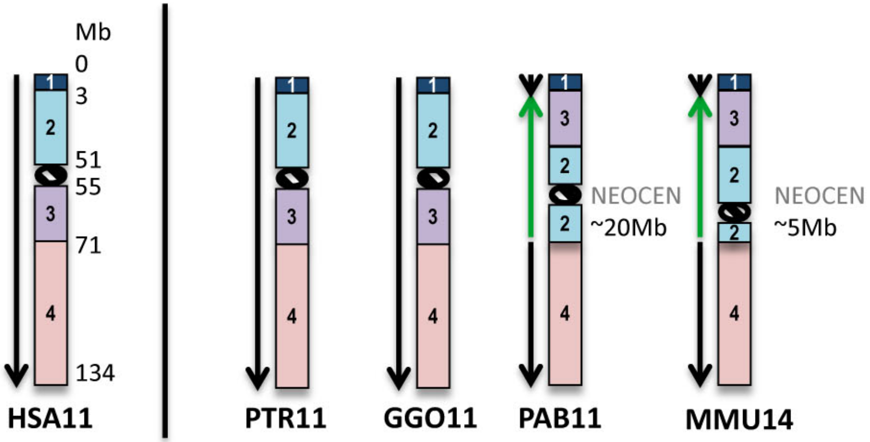
50,000,000
60,000,000
70,000,000
80,000,000
90,000,000
100,000,000
110,000,000
120,000,000
130,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
p15.3 p15.1 10p14 10p13 10p12.31 12.2 10p12.1 p11.22 10p11.21 11.1 11.1 10q11.21 q11.22 11.23 10q21.1 10q21.2 10q21.3 10q22.1 q22.2 10q22.3 10q23.1 q23.31 q23.33 24.1 q24.2 10q25.1 q25.2 10q25.3 26.11 10q26.13 q26.2 10q26.3
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
Gap Locations
Gap
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
hg38_panTro5_27
hg38_panTro5_40
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
gorGor4
hg38_gorGor4_TOP_9_A_B
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
ponAbe2
hg38_ponAbe2_41
hg38_ponAbe2_26
hg38_ponAbe2_3
hg38_ponAbe2_11
hg38_ponAbe2_37
hg38_ponAbe2_10
hg38_ponAbe2_20
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
rheMac8
hg38_rheMac8_23
hg38_rheMac8_9
hg38_rheMac8_40
hg38_rheMac8_1
hg38_rheMac8_22
hg38_rheMac8_18
hg38_rheMac8_7
hg38_rheMac8_20
hg38_rheMac8_16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71
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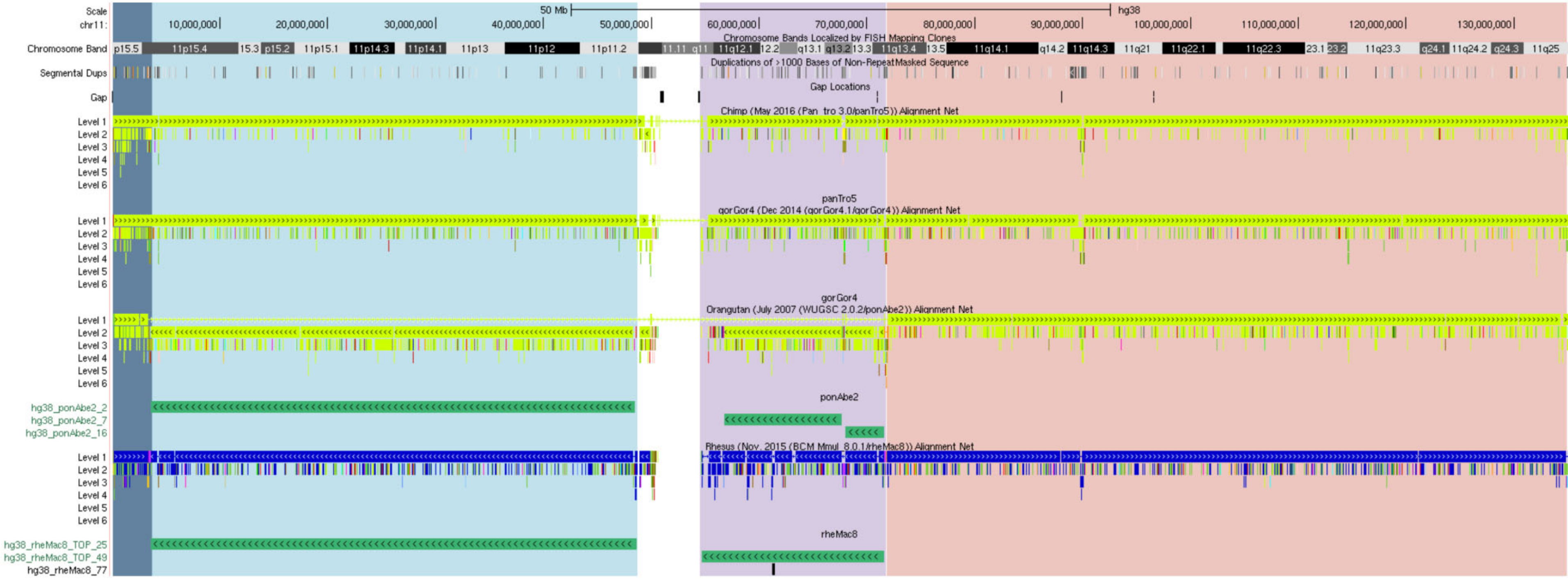
~5Mb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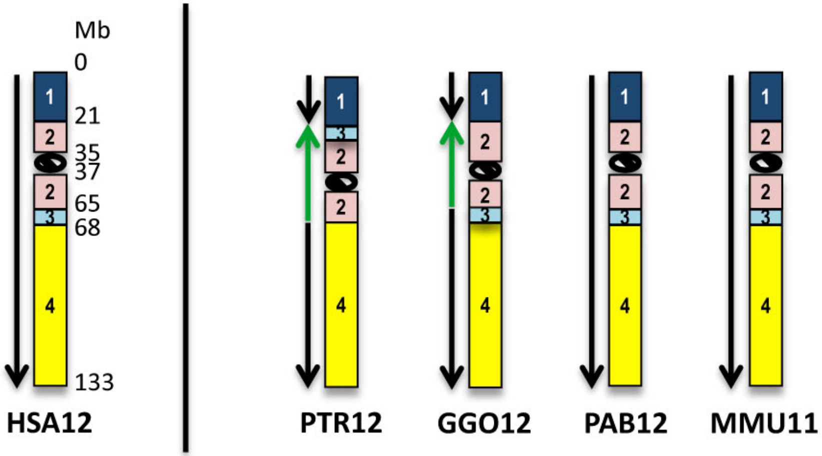
80,000,000
90,000,000
100,000,000
110,000,000
120,000,000
130,000,000
Chromosome Band
Chromosome Bands Localized by FISH Mapping Clones
p15.5 11p15.4 15.3 p15.2 11p15.1 11p14.3 11p14.1 11p13 11p12 11p11.2 11.11 q11 11q12.1 12.2 q13.1 q13.2 13.3 11q13.4 13.5 11q14.1 q14.2 11q14.3 11q21 11q22.1 11q22.3 23.1 23.2 11q23.3 q24.1 11q24.2 q24.3 11q25
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Gap
Gap Locations
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
gorGor4
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
ponAbe2
hg38_ponAbe2_2
hg38_ponAbe2_7
hg38_ponAbe2_16
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
rheMac8
hg38_rheMac8_TOP_25
hg38_rheMac8_TOP_49
hg38_rheMac8_77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PTR12
GGO12
PAB12
MMU11


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hg38
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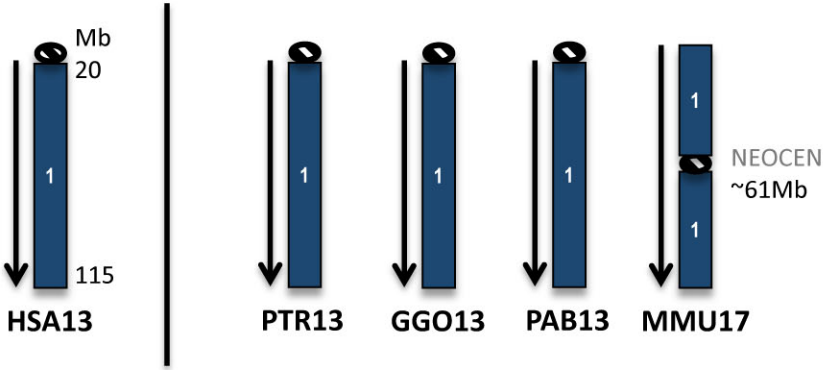
40,000,000
50,000,000
60,000,000
70,000,000
80,000,000
90,000,000
100,000,000
110,000,000
120,000,000
130,000,000
Chromosome Band
Chromosome Bands Localized by FISH Mapping Clones
p13.33
12p13.31
p13.2
13.1
12p12.3
12p12.1
p11.22
p11.21
11.1
q11
12q12
13.11
13.12
q13.13
12q14.1
14.2
q14.3
12q15
12q21.1
12q21.2
12q21.31
21.32
q21.33
12q22
12q23.1
q23.2
12q23.3
q24.11
24.21
24.23
12q24.31
q24.32
12q24.33
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Gap
Gap Locations
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
hg38_panTro5_67
hg38_panTro5_8
hg38_panTro5_50
hg38_panTro5_4
hg38_panTro5_13
hg38_panTro5_53
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
gorGor4
hg38_gorGor4_18
hg38_gorGor4_7
hg38_gorGor4_65
hg38_gorGor4_53
hg38_gorGor4_1
hg38_gorGor4_17
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
ponAbe2
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
rheMac8
hg38_rheMac8_58
hg38_rheMac8_78
hg38_rheMac8_TOP_102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PAB13
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NEOCEN
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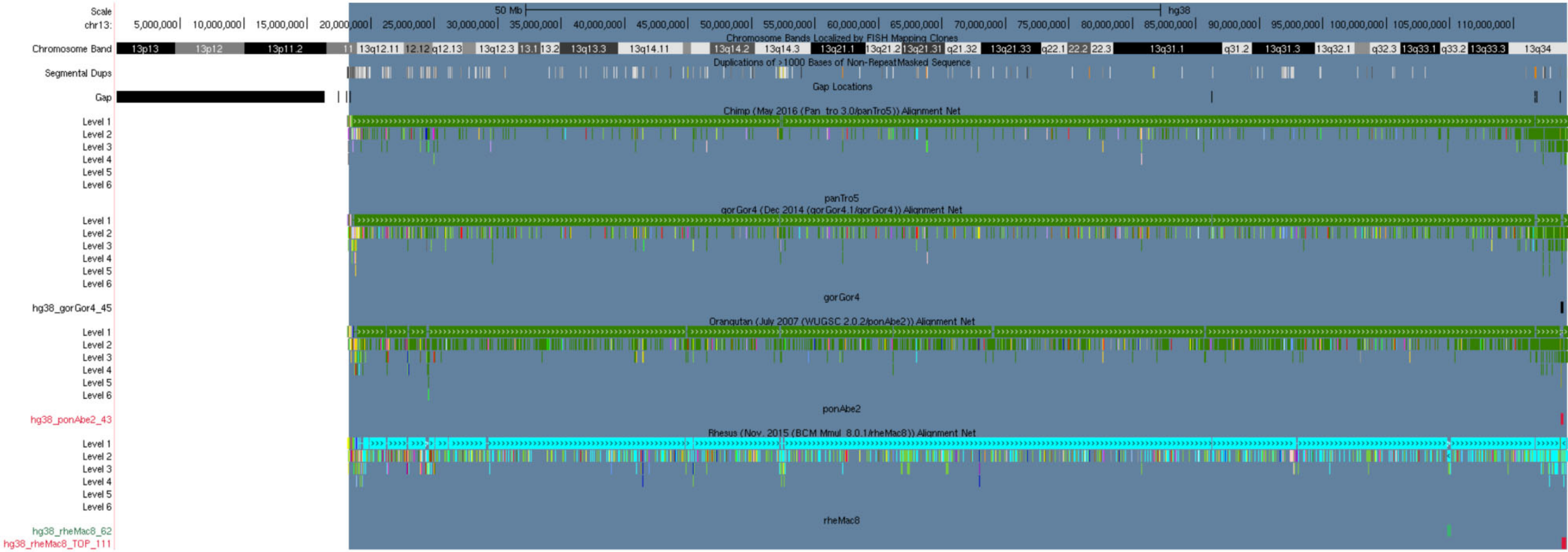
MMU17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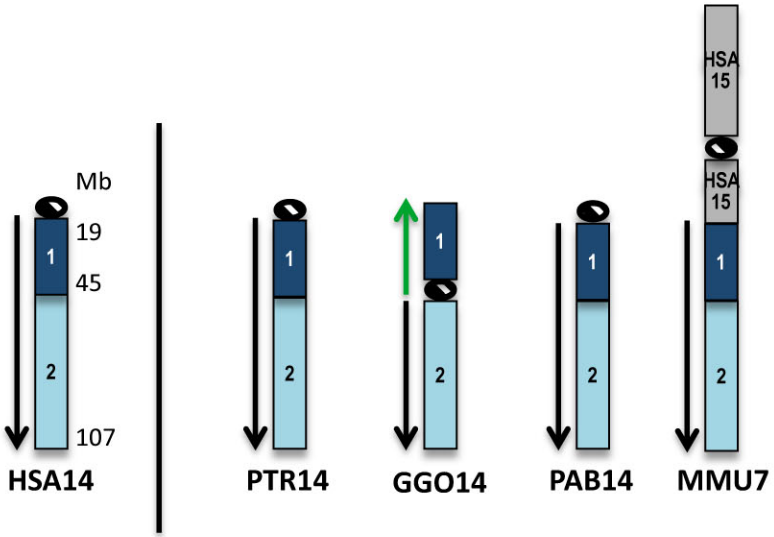
75,000,000
80,000,000
85,000,000
90,000,000
95,000,000
100,000,000
105,000,000
110,000,000
Chromosome Band
Chromosome Bands Localized by FISH Mapping Clones
13p13
13p12
13p11.2
11
13q12.11
12.12
q12.13
13q12.3
13.1
13.2
13q13.3
13q14.11
13q14.2
13q14.3
13q21.1
13q21.2
13q21.31
q21.32
13q21.33
q22.1
22.2
22.3
13q31.1
q31.2
13q31.3
13q32.1
q32.3
13q33.1
q33.2
13q33.3
13q34
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Gap
Gap Locations
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
gorGor4
hg38_gorGor4_45
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
ponAbe2
hg38_ponAbe2_43
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
rheMac8
hg38_rheMac8_62
hg38_rheMac8_TOP_111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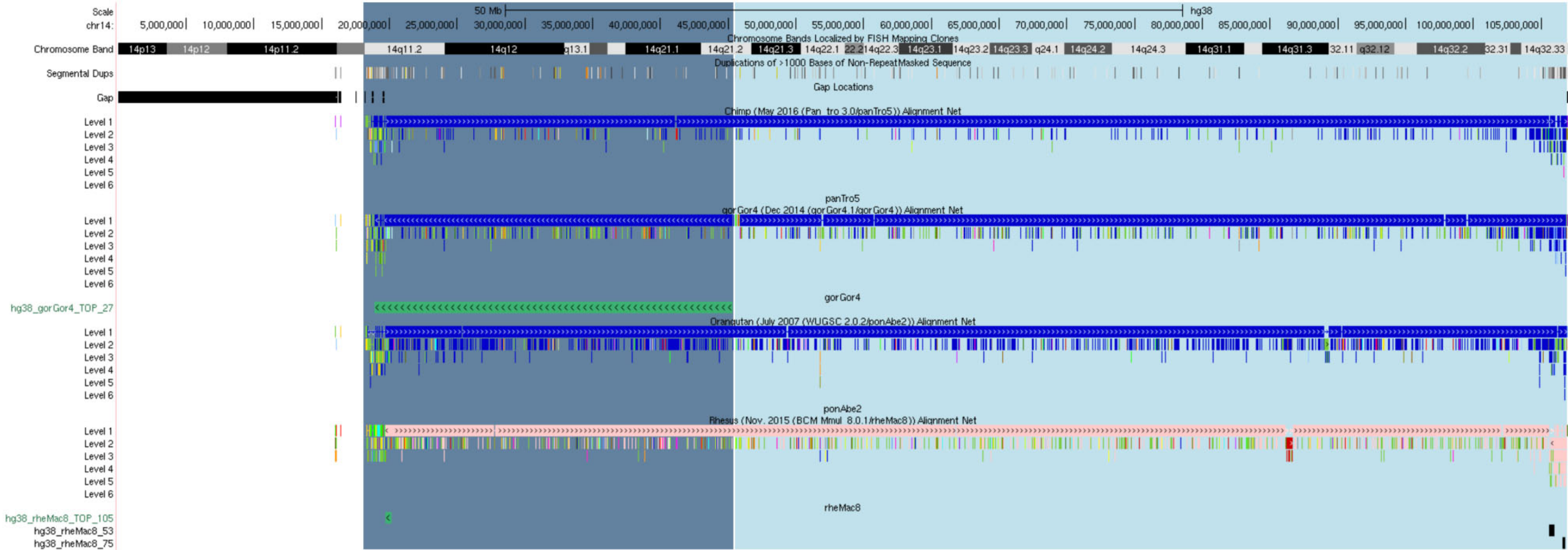
PTR14
GGO14
PAB14
HSA 15
HSA 15
MMU7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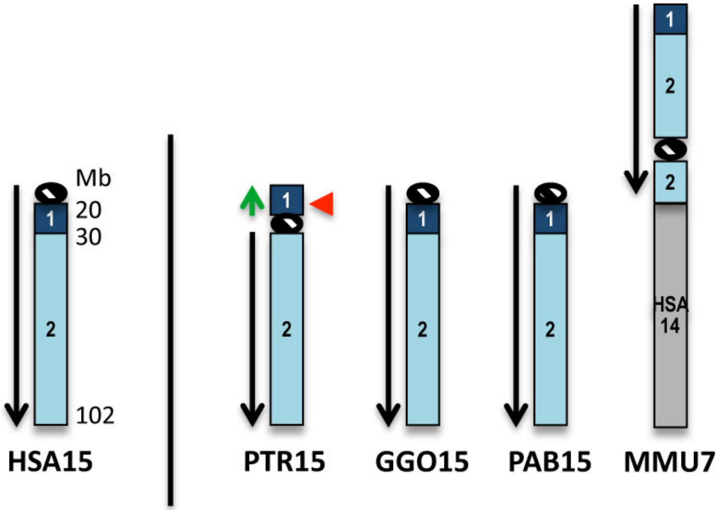
70,000,000
75,000,000
80,000,000
85,000,000
90,000,000
95,000,000
100,000,000
105,000,000
Chromosome Band
Chromosome Bands Localized by FISH Mapping Clones
14p13
14p12
14p11.2
14q11.2
14q12
q13.1
14q21.1
14q21.2
14q21.3
14q22.1
22.2
14q22.3
14q23.1
14q23.2
14q23.3
q24.1
14q24.2
14q24.3
14q31.1
14q31.3
32.11
q32.12
14q32.2
32.31
14q32.33
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Gap
Gap Locations
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
gorGor4
hg38_gorGor4_TOP_27
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
ponAbe2
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
rheMac8
hg38_rheMac8_TOP_105
hg38_rheMac8_53
hg38_rheMac8_75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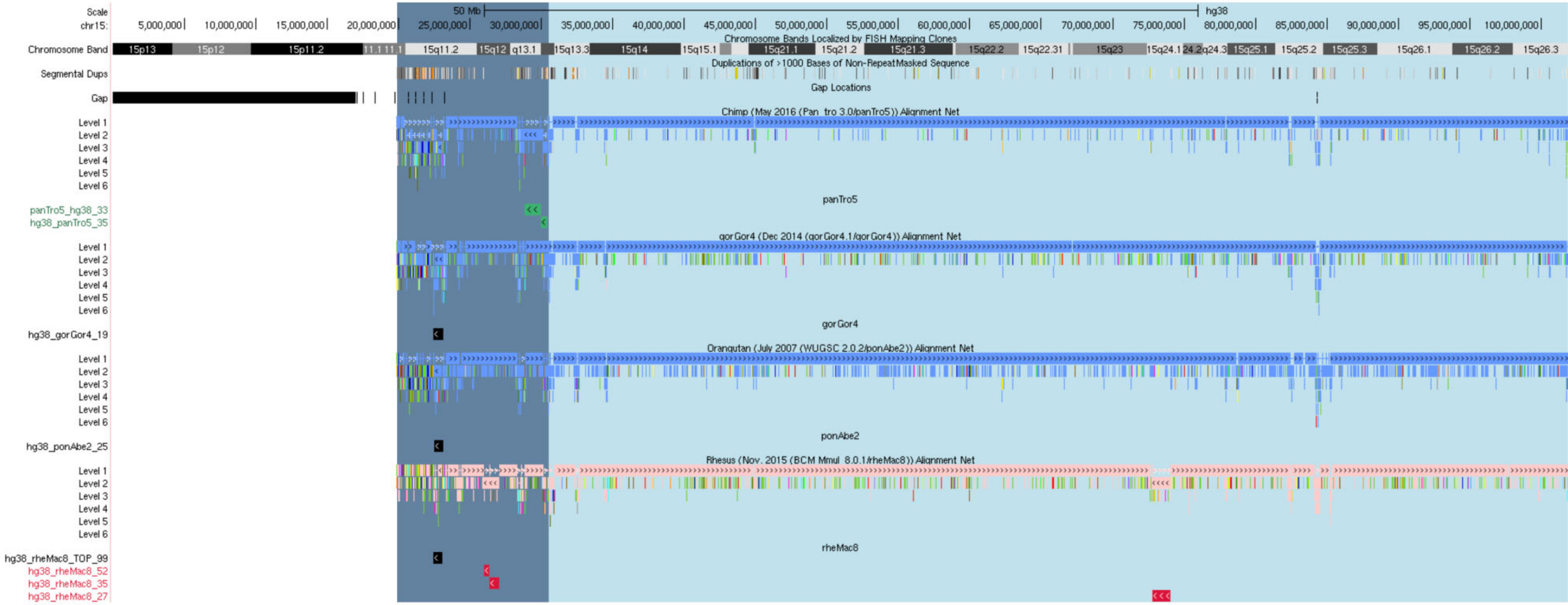
PTR15
GGO15
PAB15
MMU7
HSA 14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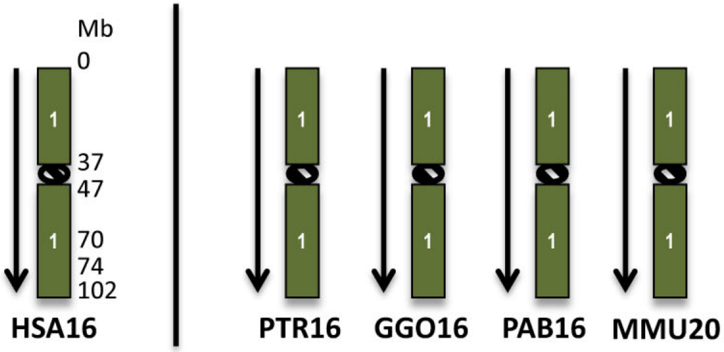
70,000,000
75,000,000
80,000,000
85,000,000
90,000,000
95,000,000
100,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
15p13
15p12
15p11.2
15q11.2
15q12
q13.1
15q13.3
15q14
15q15.1
15q21.1
15q21.2
15q21.3
15q22.2
15q22.31
15q23
15q24.1
24.2
q24.3
15q25.1
15q25.2
15q25.3
15q26.1
15q26.2
15q26.3
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
Gap Locations
Gap
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
panTro5_hg38_33
hg38_panTro5_35
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
gorGor4
hg38_gorGor4_19
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
ponAbe2
hg38_ponAbe2_25
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
rheMac8
hg38_rheMac8_TOP_99
hg38_rheMac8_52
hg38_rheMac8_35
hg38_rheMac8_27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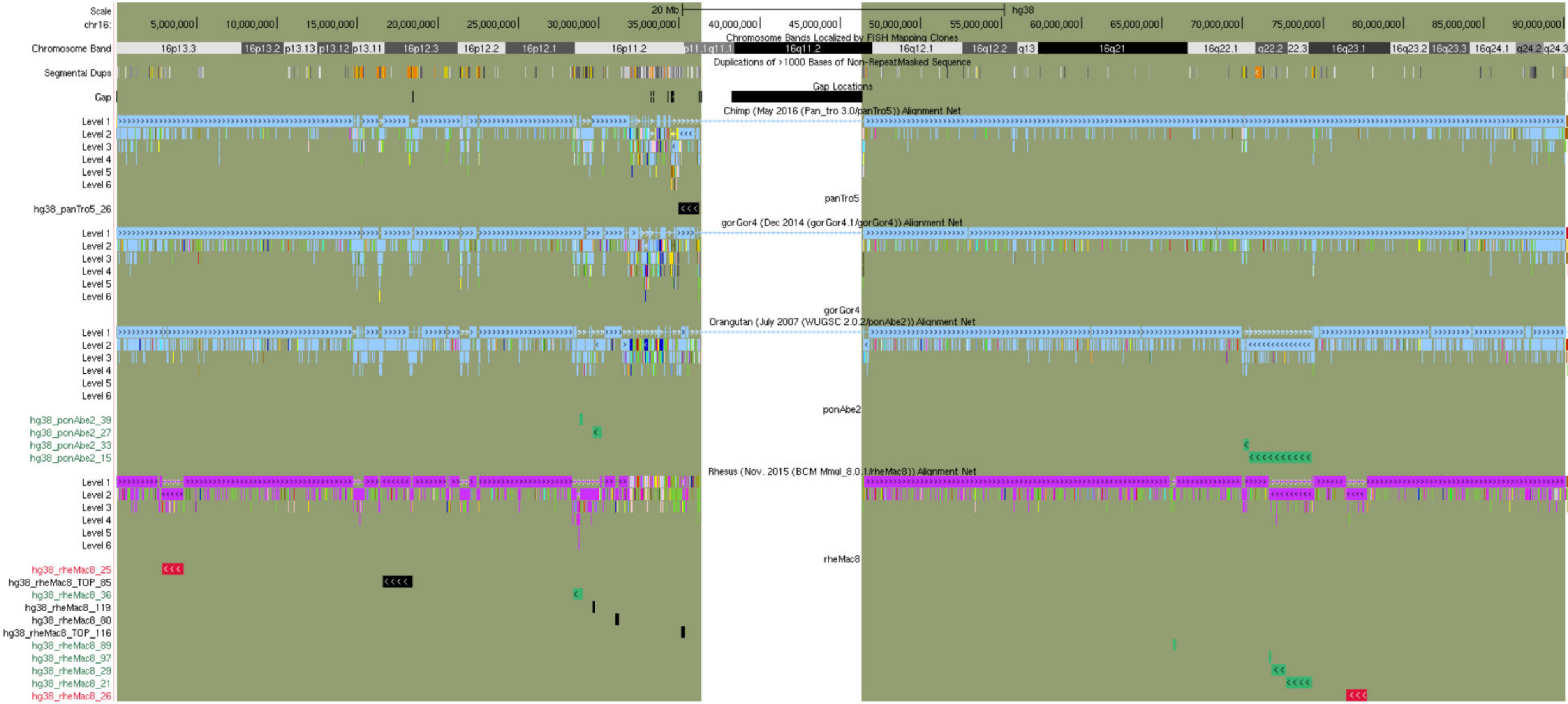
PAB16
MMU20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55,000,000
60,000,000
65,000,000
70,000,000
75,000,000
80,000,000
85,000,000
90,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
16p13.3
16p13.2
p13.13
p13.12
p13.11
16p12.3
16p12.2
16p12.1
16p11.2
p11.1
q11.1
16q11.2
16q12.1
16q12.2
q13
16q21
16q22.1
q22.2
22.3
16q23.1
16q23.2
16q23.3
16q24.1
q24.2
q24.3
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
Gap Locations
Gap
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
hg38_panTro5_26
panTro5
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
gorGor4
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
ponAbe2
hg38_ponAbe2_39
hg38_ponAbe2_27
hg38_ponAbe2_33
hg38_ponAbe2_15
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
rheMac8
hg38_rheMac8_25
hg38_rheMac8_TOP_85
hg38_rheMac8_36
hg38_rheMac8_119
hg38_rheMac8_80
hg38_rheMac8_TOP_116
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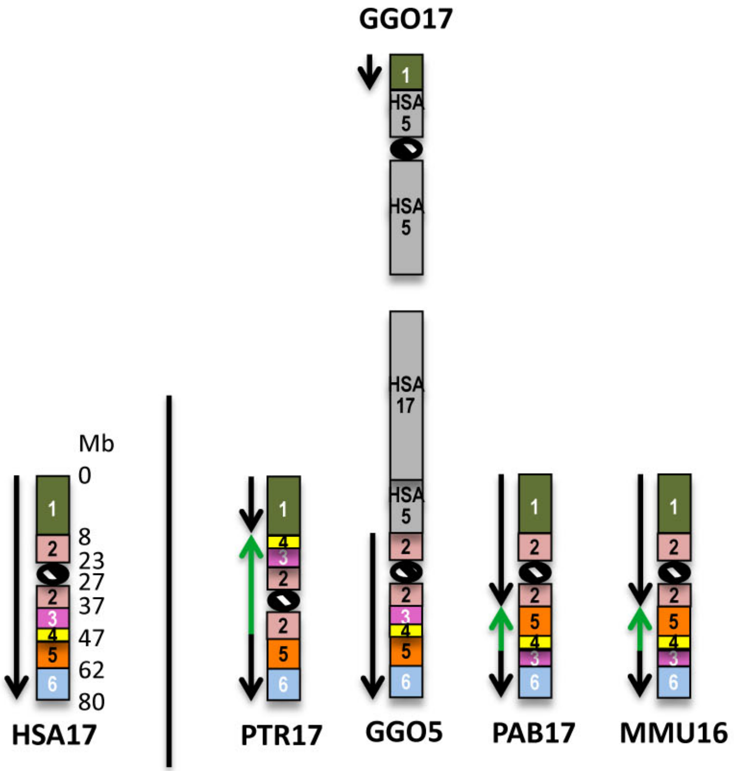
hg38_rheMac8_26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HSA 5
HSA 17
HSA 5
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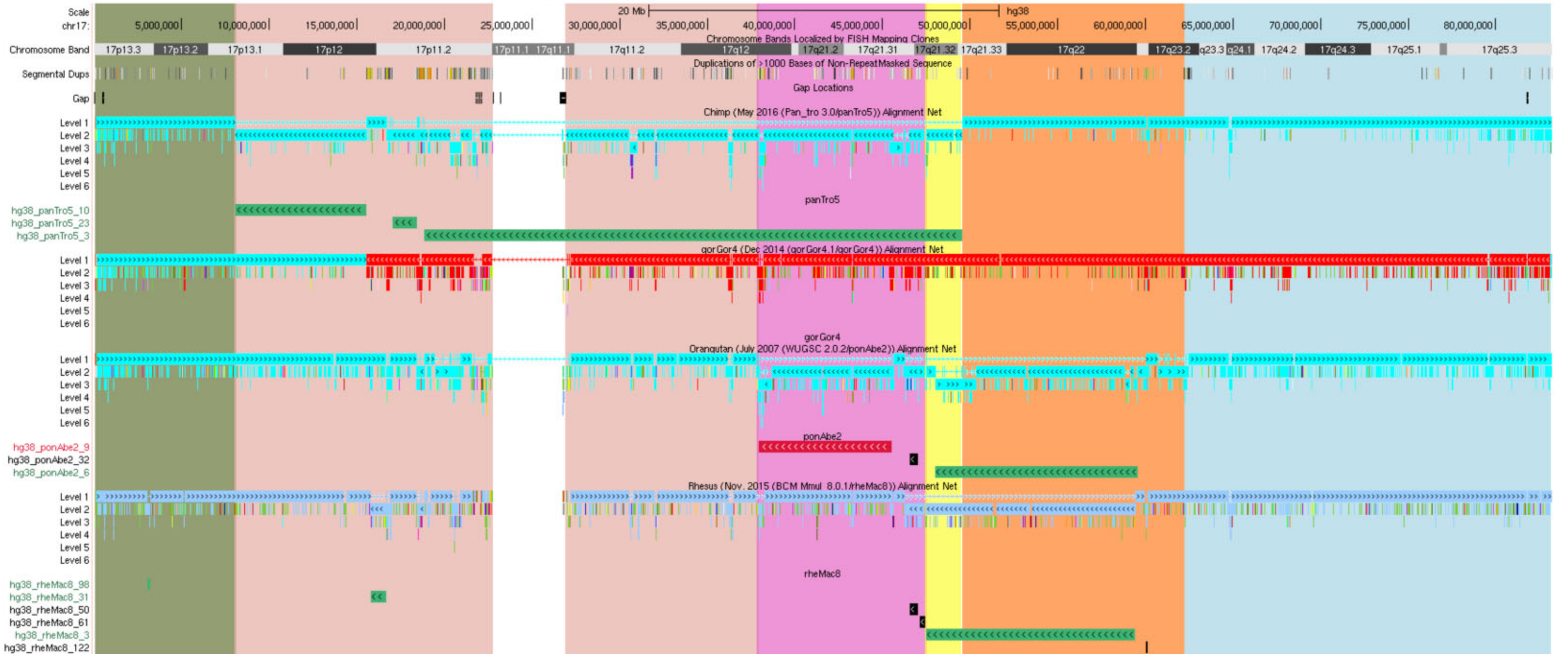
GGO5
PAB17
MMU16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Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
17p13.3
17p13.2
17p13.1
17p12
17p11.2
17p11.1
17q11.1
17q11.2
17q12
17q21.2
17q21.31
17q21.32
17q21.33
17q22
17q23.2
q23.3
q24.1
17q24.2
17q24.3
17q25.1
17q25.3
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
Gap Locations
Gap
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
hg38_panTro5_10
hg38_panTro5_23
hg38_panTro5_3
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
gorGor4
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
ponAbe2
hg38_ponAbe2_9
hg38_ponAbe2_32
hg38_ponAbe2_6
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
rheMac8
hg38_rheMac8_98
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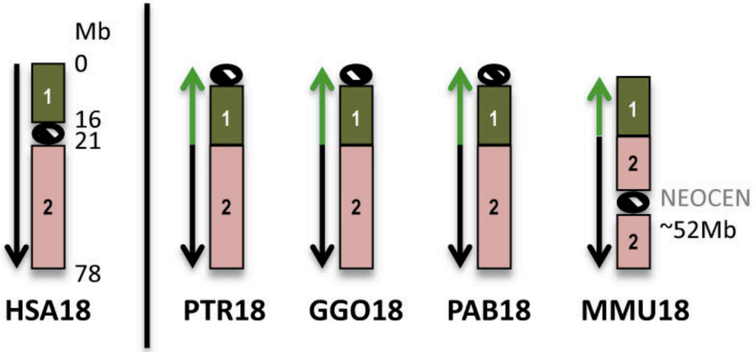
hg38_rheMac8_50
hg38_rheMac8_61
hg38_rheMac8_3
hg38_rheMac8_122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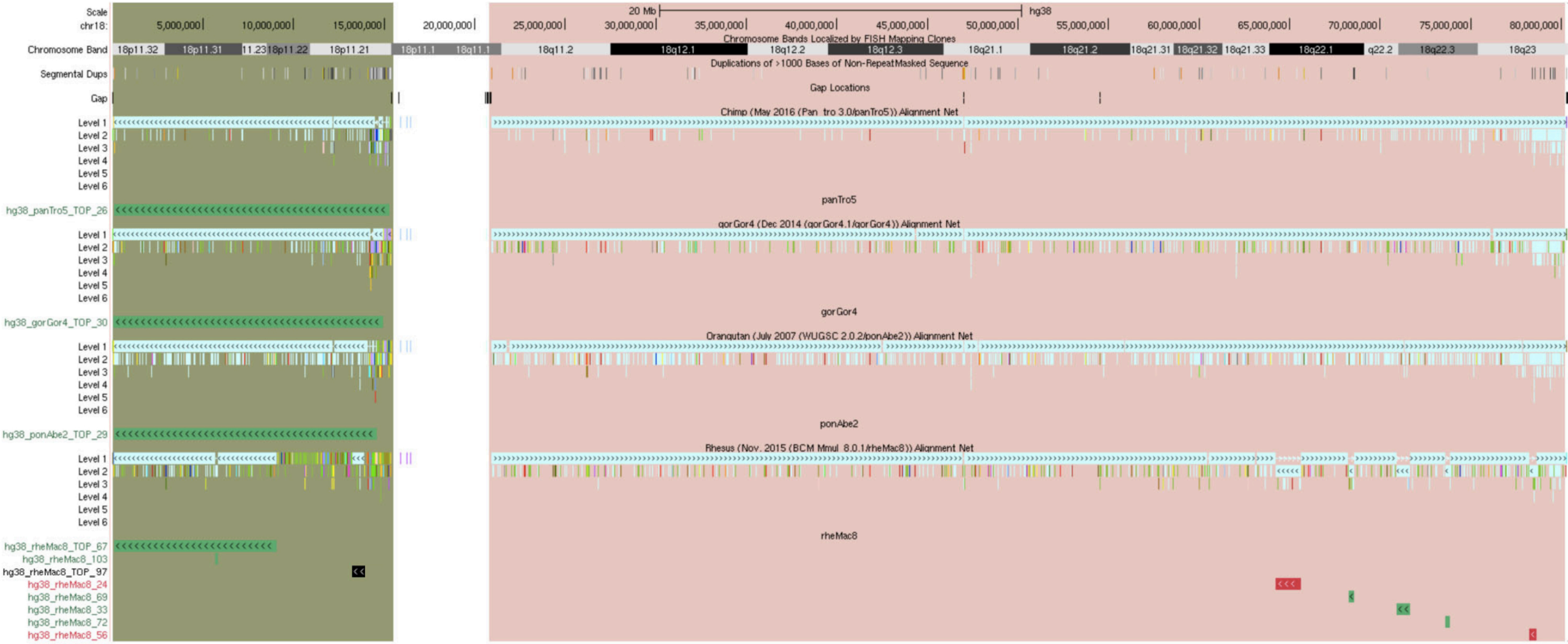
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50,000,000
55,000,000
60,000,000
65,000,000
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75,000,000
80,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
18p11.32
18p11.31
11.23
18p11.22
18p11.21
18p11.1
18q11.1
18q11.2
18q12.1
18q12.2
18q12.3
18q21.1
18q21.2
18q21.31
18q21.32
18q21.33
18q22.1
q22.2
18q22.3
18q23
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
Gap Locations
Gap
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
hg38_panTro5_TOP_26
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
gorGor4
hg38_gorGor4_TOP_30
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
ponAbe2
hg38_ponAbe2_TOP_29
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
rheMac8
hg38_rheMac8_TOP_67
hg38_rheMac8_103
hg38_rheMac8_TOP_97
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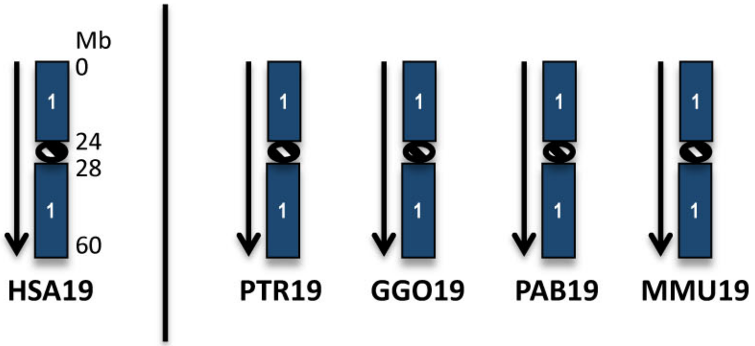
hg38_rheMac8_69
hg38_rheMac8_33
hg38_rheMac8_72
hg38_rheMac8_56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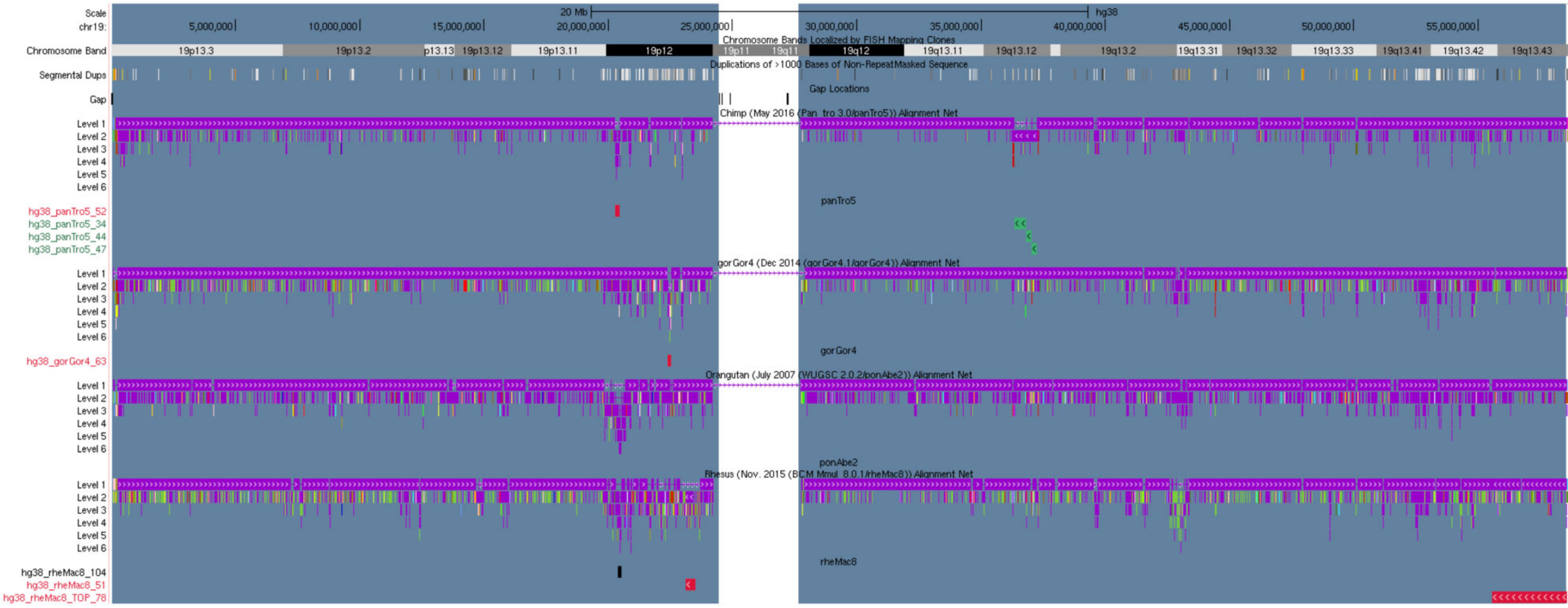
PAB19
MMU19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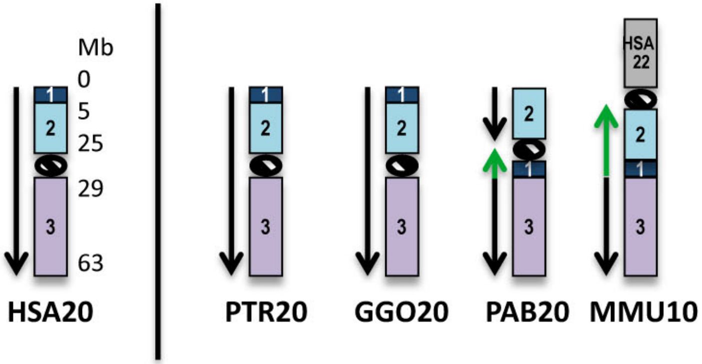
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
19p13.3
19p13.2
p13.13
19p13.12
19p13.11
19p12
19p11
19q11
19q12
19q13.11
19q13.12
19q13.2
19q13.31
19q13.32
19q13.33
19q13.41
19q13.42
19q13.43
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Gap
Gap Locations
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
hg38_panTro5_52
hg38_panTro5_34
hg38_panTro5_44
hg38_panTro5_47
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
gorGor4
hg38_gorGor4_63
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
ponAbe2
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
rheMac8
hg38_rheMac8_104
hg38_rheMac8_51
hg38_rheMac8_TOP_78


Mb
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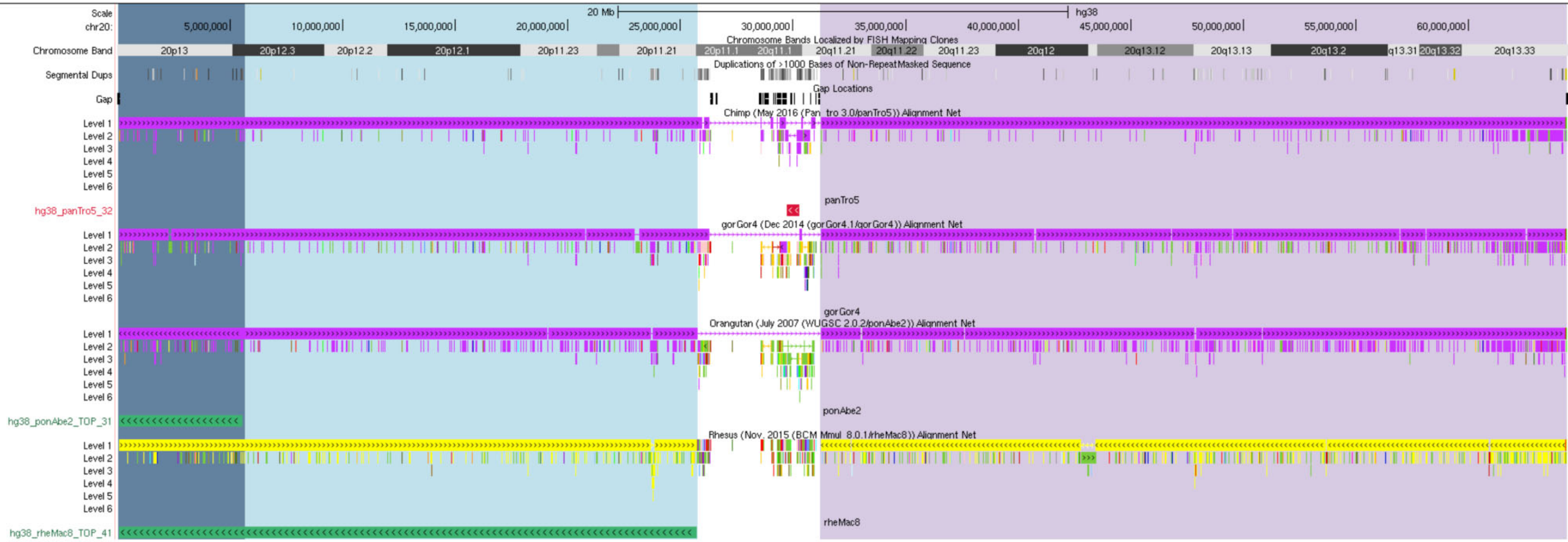
5
25
29
63
1
2
3
HSA22
HSA20
PTR20
GGO20
PAB20
MMU10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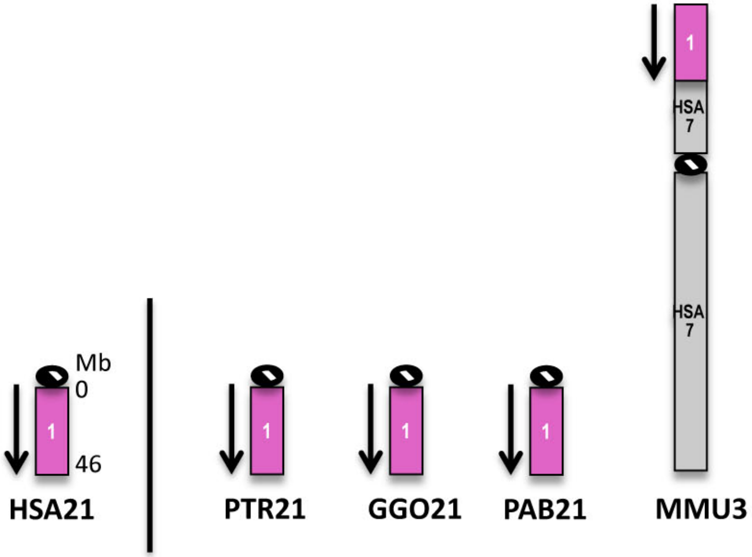
55,000,000
60,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
20p13
20p12.3
20p12.2
20p12.1
20p11.23
20p11.21
20p11.1
20q11.1
20q11.21
20q11.22
20q11.23
20q12
20q13.12
20q13.13
20q13.2
q13.31
20q13.32
20q13.33
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Gap
Gap Locations
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
hg38_panTro5_32
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
gorGor4
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
ponAbe2
hg38_ponAbe2_TOP_31
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
rheMac8
hg38_rheMac8_TOP_41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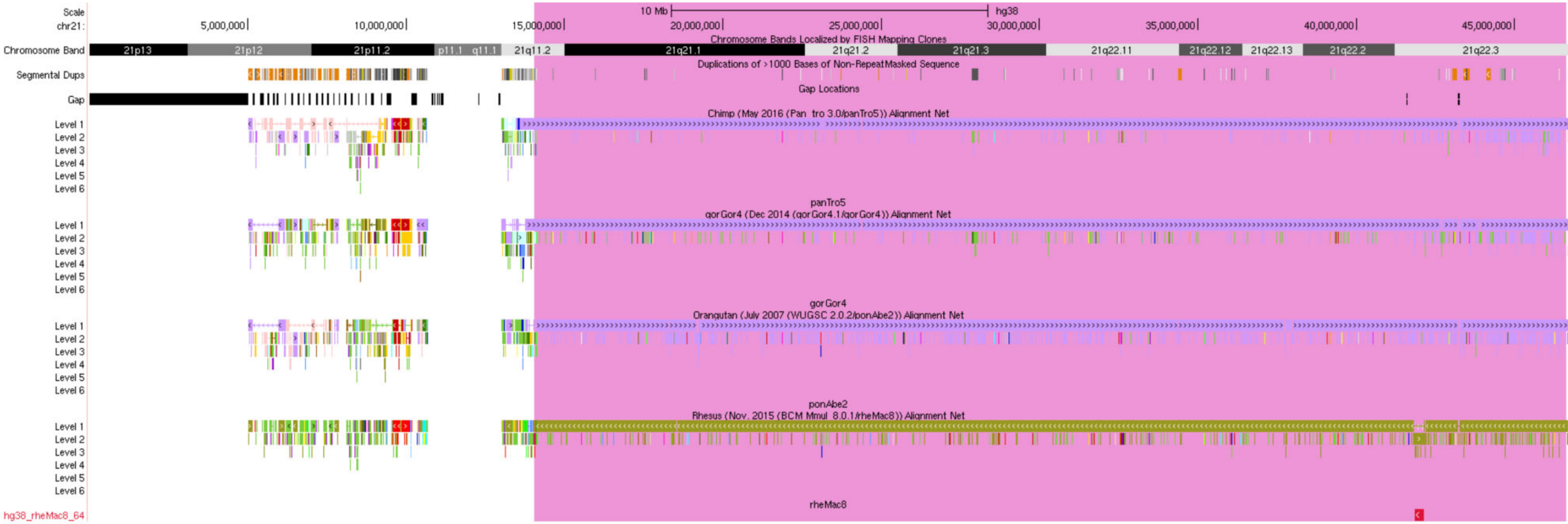
HSA21
PTR21
GGO21
PAB21
MMU3
HSA 7
HSA 7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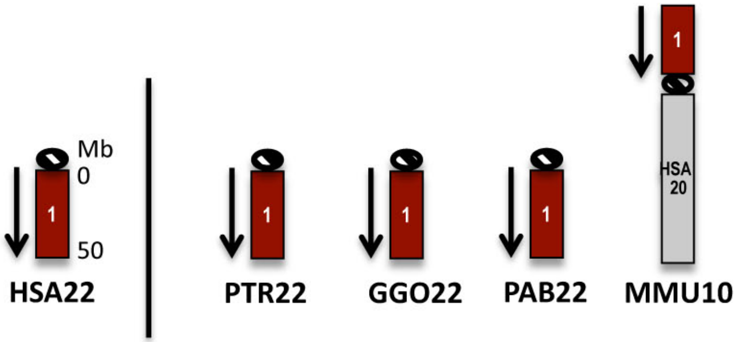
40,000,000
45,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
21p13
21p12
21p11.2
p11.1
q11.1
21q11.2
21q21.1
21q21.2
21q21.3
21q22.11
21q22.12
21q22.13
21q22.2
21q22.3
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
Gap Locations
Gap
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
gorGor4
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
ponAbe2
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
rheMac8
hg38_rheMac8_64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HSA22
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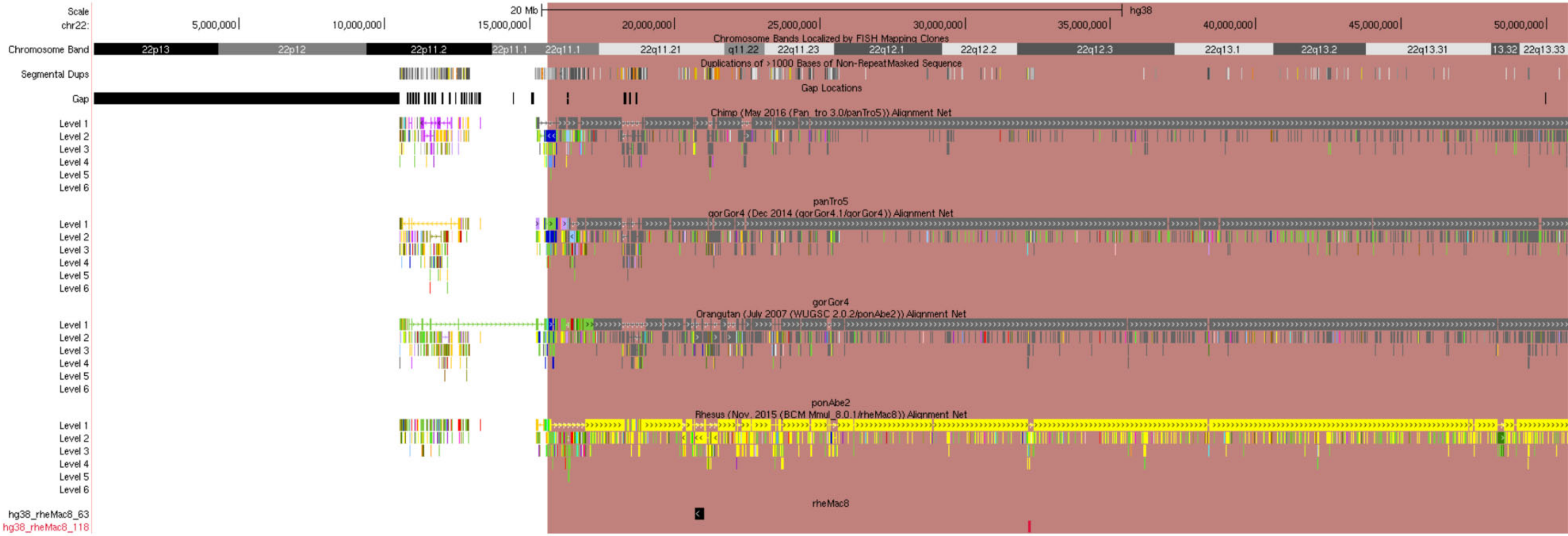
PAB22
HSA 20
MMU10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40,000,000
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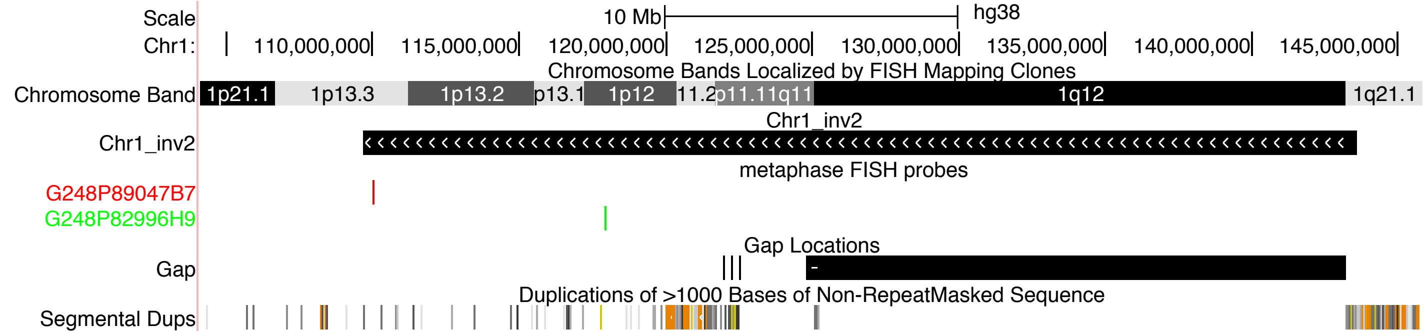
50,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
22p13
22p12
22p11.2
22p11.1
22q11.1
22q11.21
q11.22
22q11.23
22q12.1
22q12.2
22q12.3
22q13.1
22q13.2
22q13.31
13.32
22q13.33
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Gap
Gap Locations
Chimp (May 2016 (Pan_tro 3.0/panTro5)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
panTro5
gorGor4 (Dec 2014 (gorGor4.1/gorGor4)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
gorGor4
Orangutan (July 2007 (WUGSC 2.0.2/ponAbe2)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
ponAbe2
Rhesus (Nov. 2015 (BCM Mmul_8.0.1/rheMac8)) Alignment Net
Level 1
Level 2
Level 3
Level 4
Level 5
Level 6
rheMac8
hg38_rheMac8_63
hg38_rheMac8_118

Supplemental Fig. S1. Map of new and previously described genomic inversions.

Chromosome ideograms for human, chimpanzee, gorilla, orangutan and macaque together with the UCSC Genome Browser views of the inversions detected in the study. Ideograms only show previously reported inversions larger than 5 Mb. Synteny blocks, distinguished by colors and numbers, represent regions that are inverted in a least one of the species analyzed, but the order of the markers within the block is conserved in all the different species. Green arrows on the left of each ideogram indicate inverted blocks with respect to human orientation. Small red arrows on the right of the ideograms represent inversions known from previous studies but not detected by net alignments. In the bottom panel, UCSC Genome Browser views of the net alignments and inversions predicted in the present study between human and nonhuman primate genomes. Regions called to be inverted in the present study are shown as green, red and black horizontal bars, and represent real, false and not determined (ND) inversions, respectively. Synteny block colors are consistent with upper panel, and allow to compare regions found to be inverted in the present study with previously identified inversions.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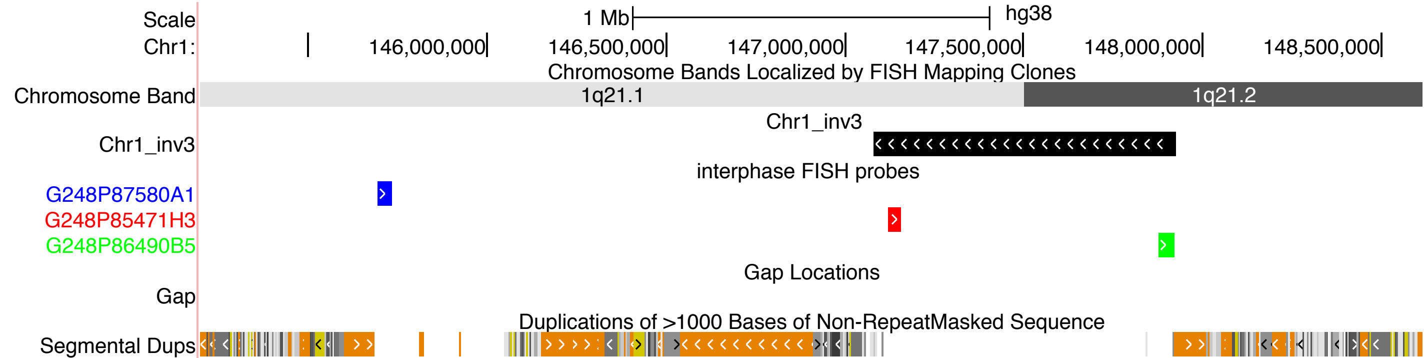
130,000,000
135,000,000
140,000,000
145,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
1p21.1
1p13.3
1p13.2
p13.1
1p12
11.2
p11.1
1q11
1q12
1q21.1
Chr1_inv2
Chr1_inv2
metaphase FISH probes
G248P89047B7
G248P82996H9
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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147,500,000
148,000,000
148,500,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
1q21.1
1q21.2
Chr1_inv3
Chr1_inv3
interphase FISH probes
G248P87580A1
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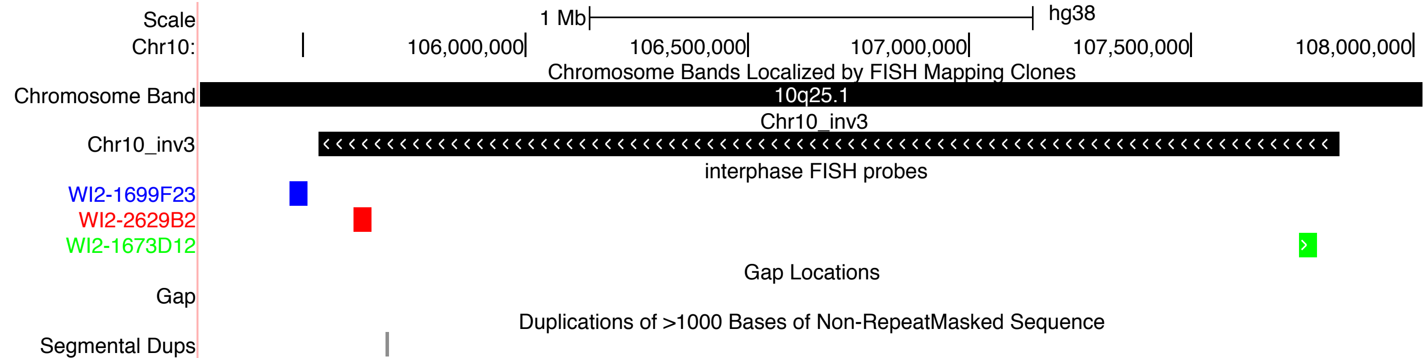
G248P86490B5
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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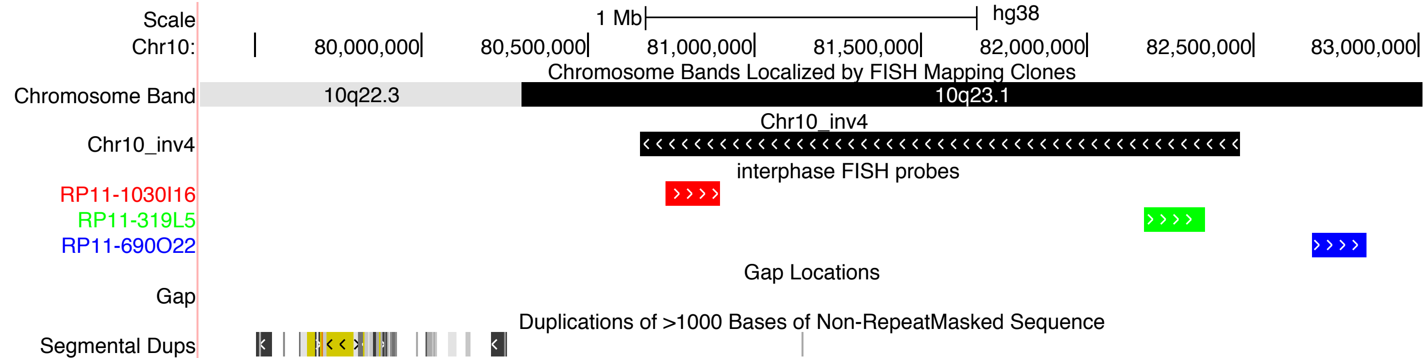
106,500,000
107,000,000
107,500,000
108,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
10q25.1
Chr10_inv3
Chr10_inv3
interphase FISH probes
WI2-1699F23
WI2-2629B2
WI2-1673D12
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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81,500,000
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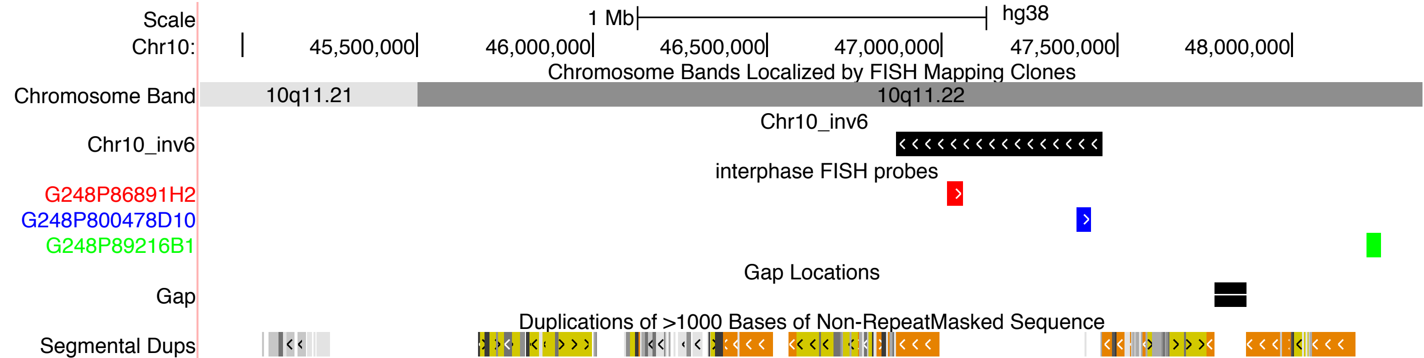
82,500,000
83,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
10q22.3
10q23.1
Chr10_inv4
Chr10_inv4
interphase FISH probes
RP11-1030I16
RP11-319L5
RP11-690O22
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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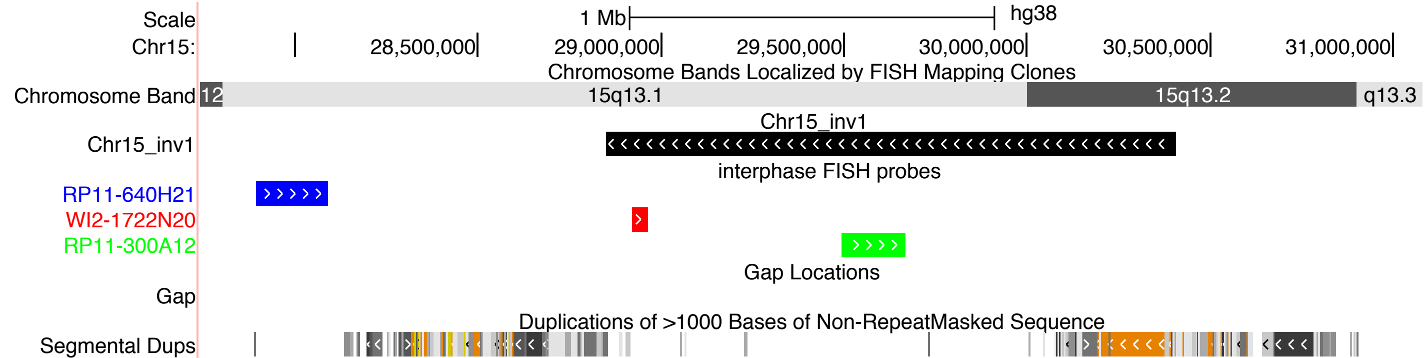
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
10q11.21
10q11.22
Chr10_inv6
Chr10_inv6
interphase FISH probes
G248P86891H2
G248P800478D10
G248P89216B1
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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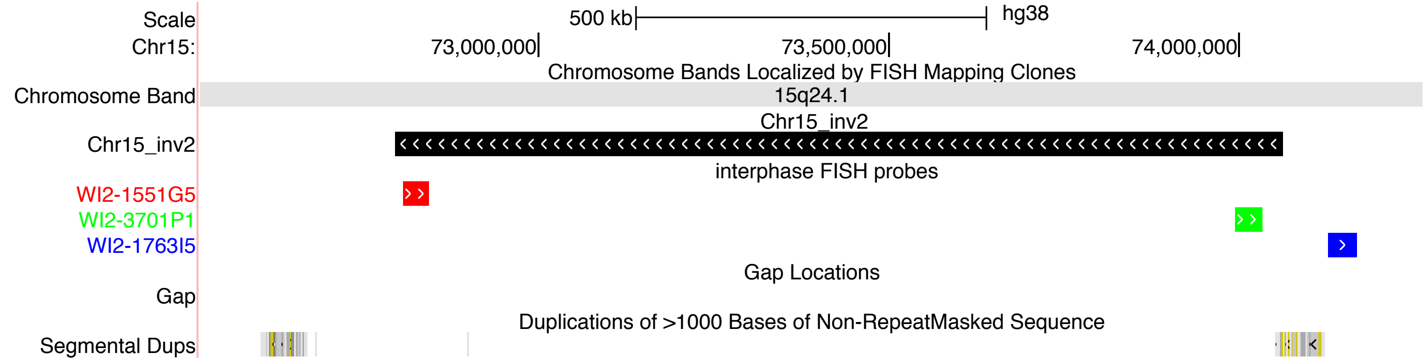
Chromosome Band
12
15q13.1
15q13.2
q13.3
Chr15_inv1
Chr15_inv1
interphase FISH probes
RP11-640H21
WI2-1722N20
RP11-300A12
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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15q24.1
Chr15_inv2
Chr15_inv2
interphase FISH probes
WI2-1551G5
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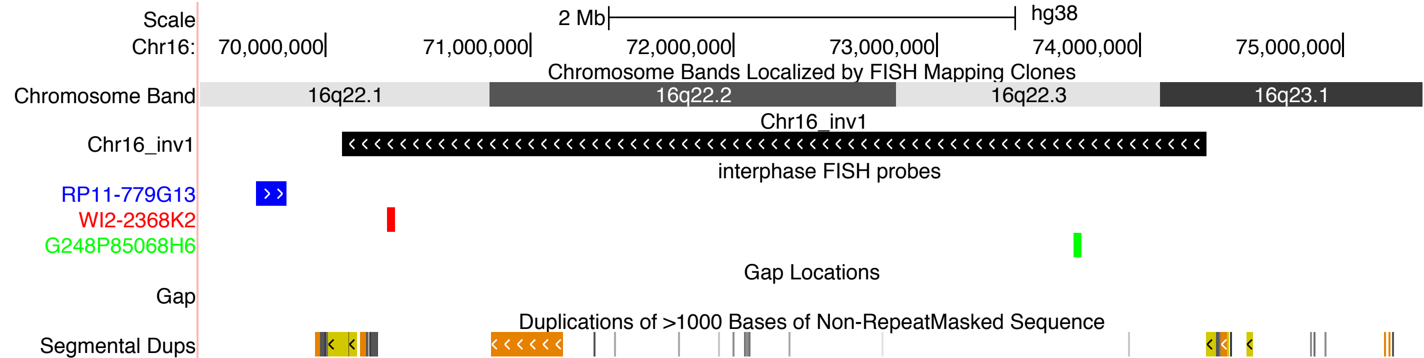
WI2-1763I5
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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72,000,000
73,000,000
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Chromosome Band
16q22.1
16q22.2
16q22.3
16q23.1
Chr16_inv1
Chr16_inv1
interphase FISH probes
RP11-779G13
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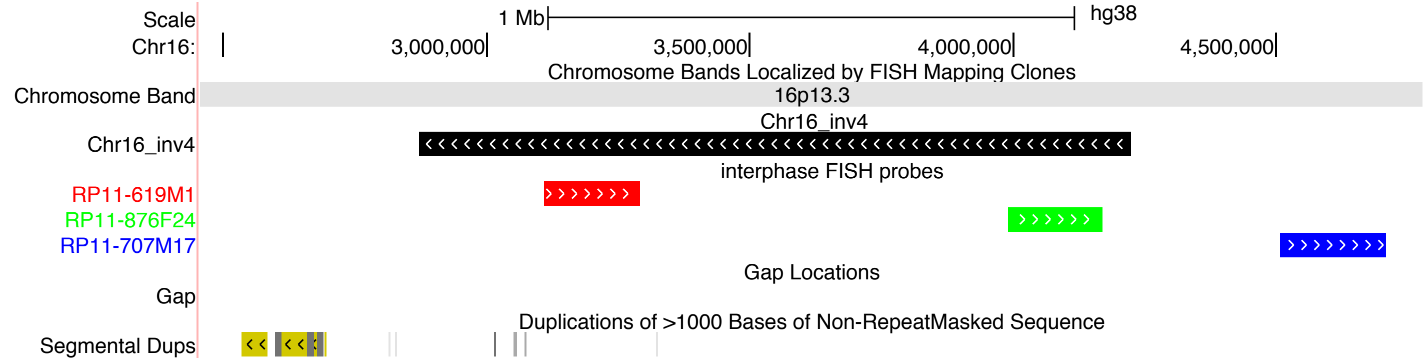
G248P85068H6
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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interphase FISH probes
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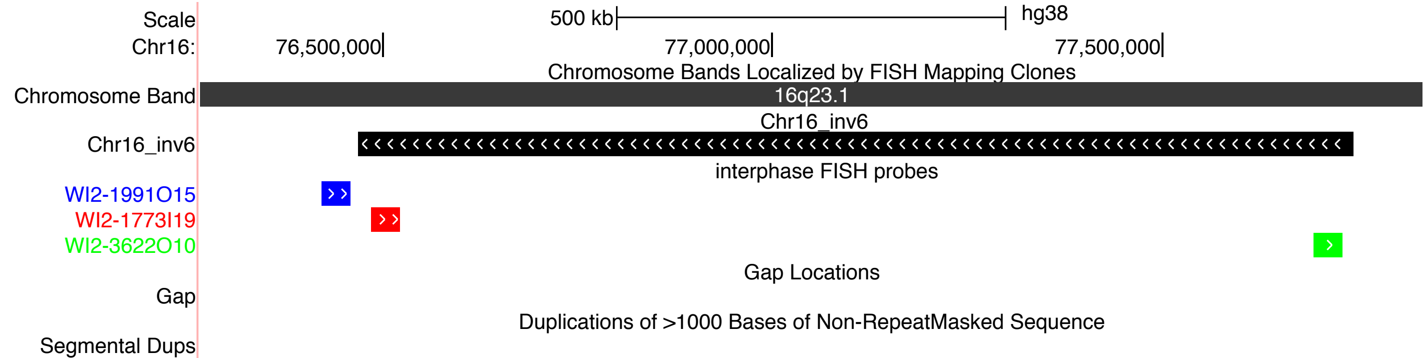
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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interphase FISH probes
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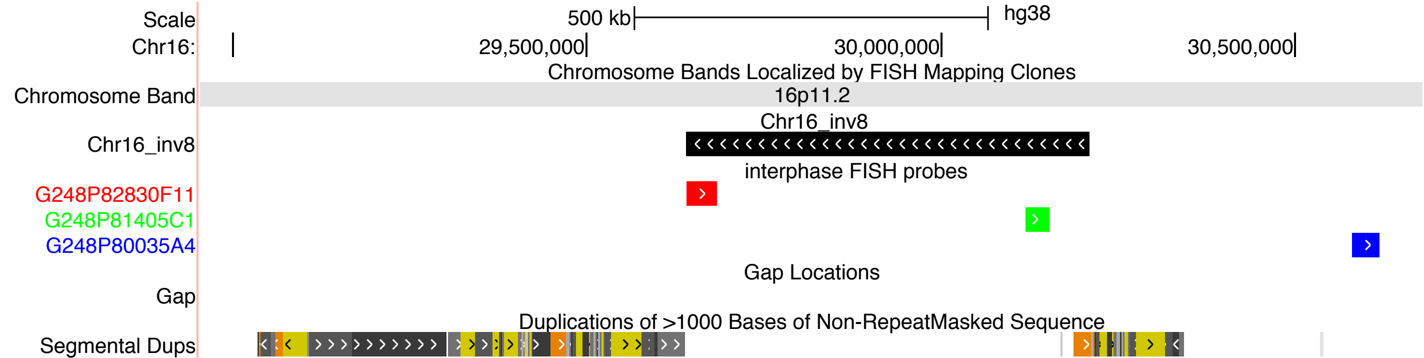
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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interphase FISH probes
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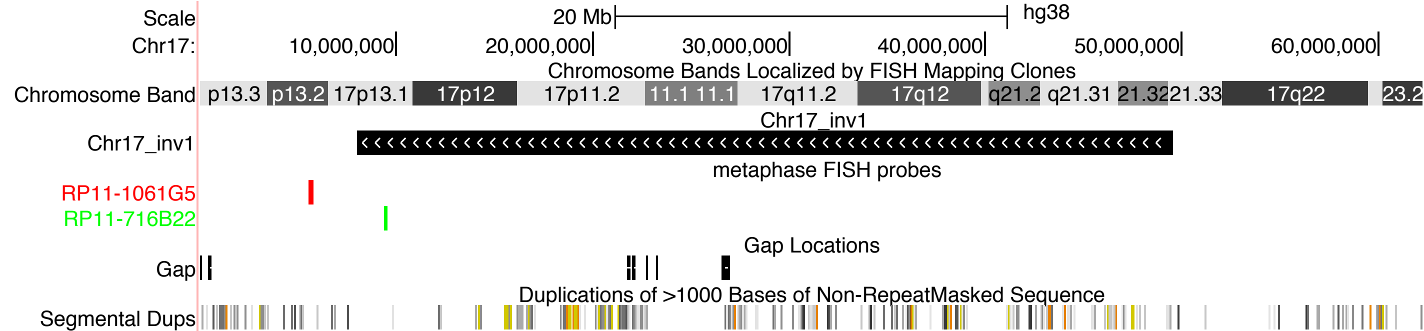
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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Chromosome Band
p13.3
p13.2
17p13.1
17p12
17p11.2
11.1
11.1
17q11.2
17q12
q21.2
q21.31
21.32
21.33
17q22
23.2
Chr17_inv1
Chr17_inv1
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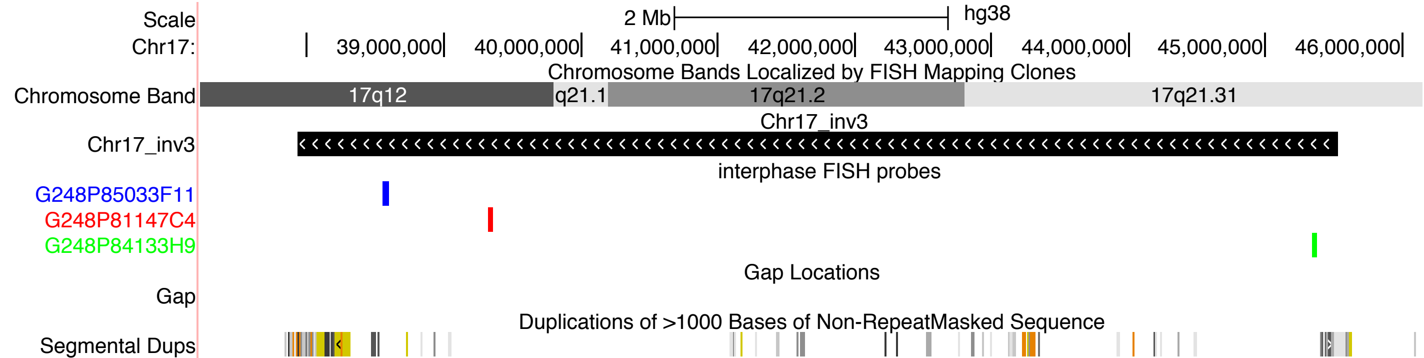
RP11-1061G5
RP11-716B22
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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46,000,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
17q12
q21.1
17q21.2
17q21.31
Chr17_inv3
Chr17_inv3
interphase FISH probes
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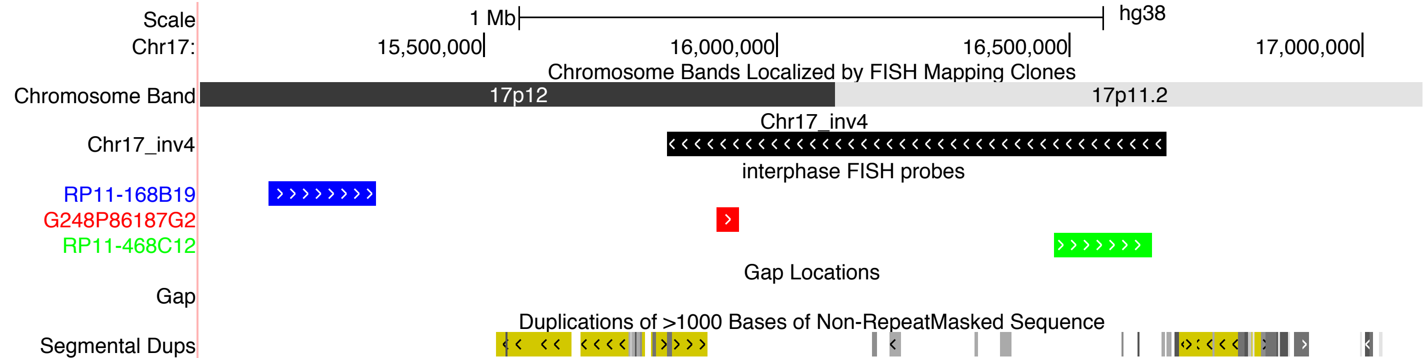
G248P84133H9
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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Chr17_inv4
interphase FISH probes
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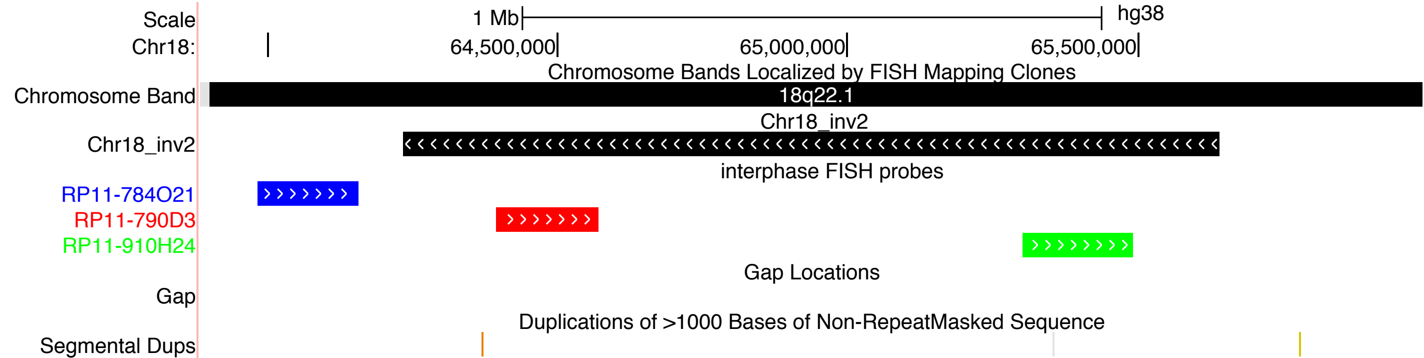
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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Chr18_inv2
interphase FISH probes
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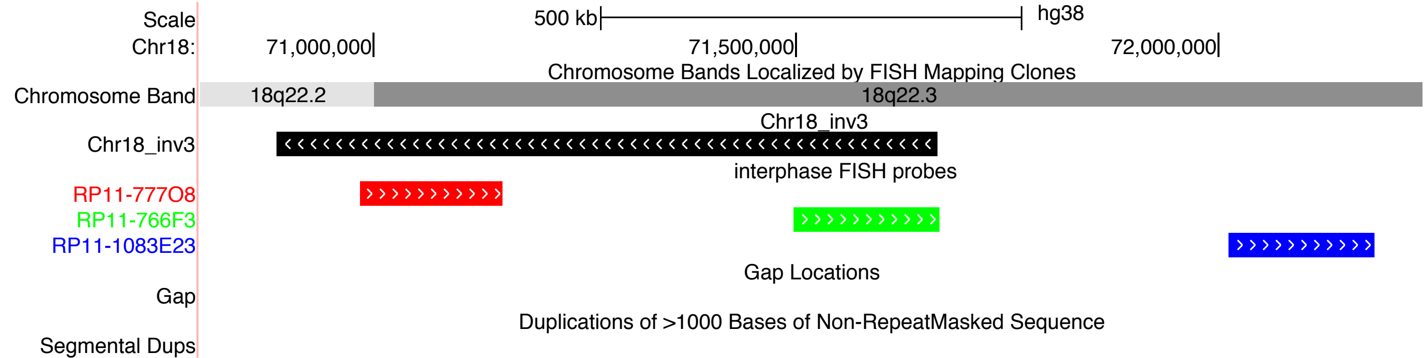
RP11-910H24
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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Chromosome Band
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18q22.3
Chr18_inv3
Chr18_inv3
interphase FISH probes
RP11-777O8
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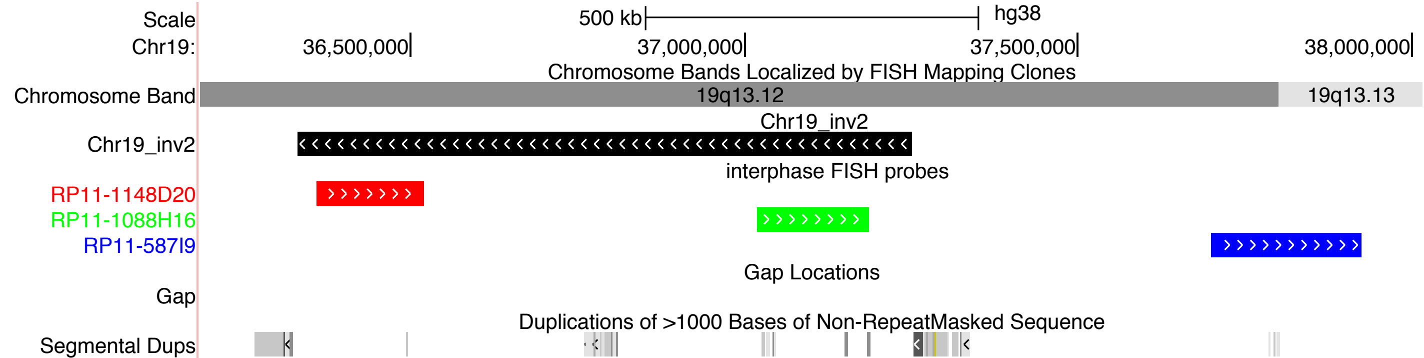
RP11-1083E23
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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19q13.12
19q13.13
Chr19_inv2
Chr19_inv2
interphase FISH probes
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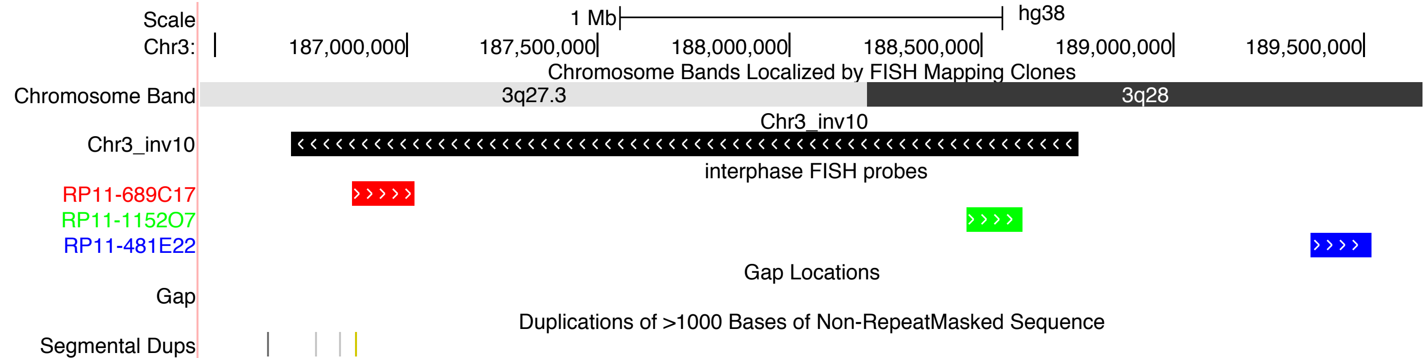
RP11-1088H16
RP11-587I9
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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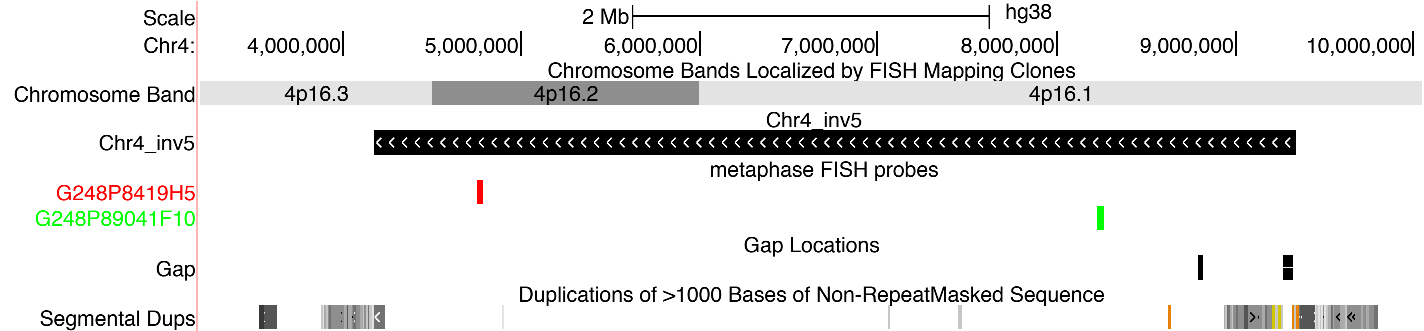
Chromosome Band
3q27.3
3q28
Chr3_inv10
Chr3_inv10
interphase FISH probes
RP11-689C17
RP11-1152O7
RP11-481E22
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
4p16.3
4p16.2
4p16.1
Chr4_inv5
Chr4_inv5
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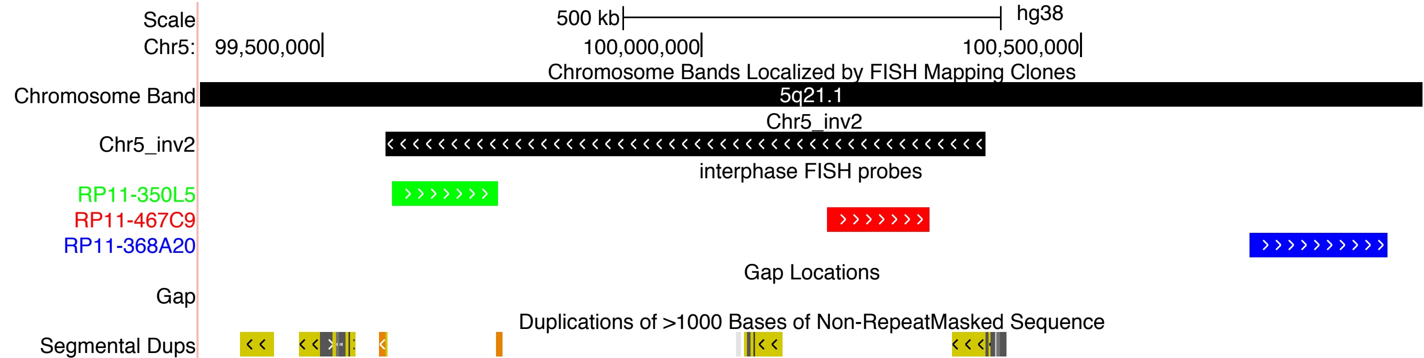
G248P89041F10
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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Chr5_inv2
Chr5_inv2
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Gap Locations
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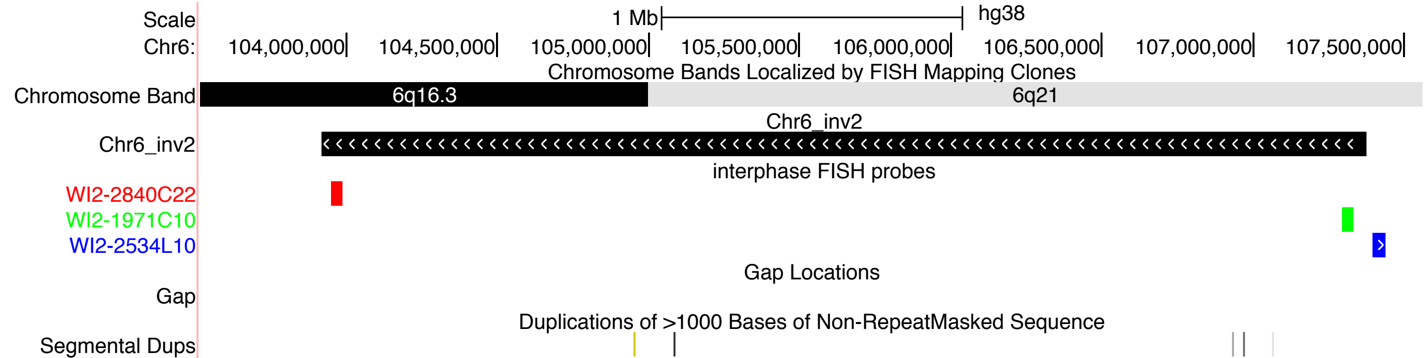
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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6q21
Chr6_inv2
Chr6_inv2
interphase FISH probes
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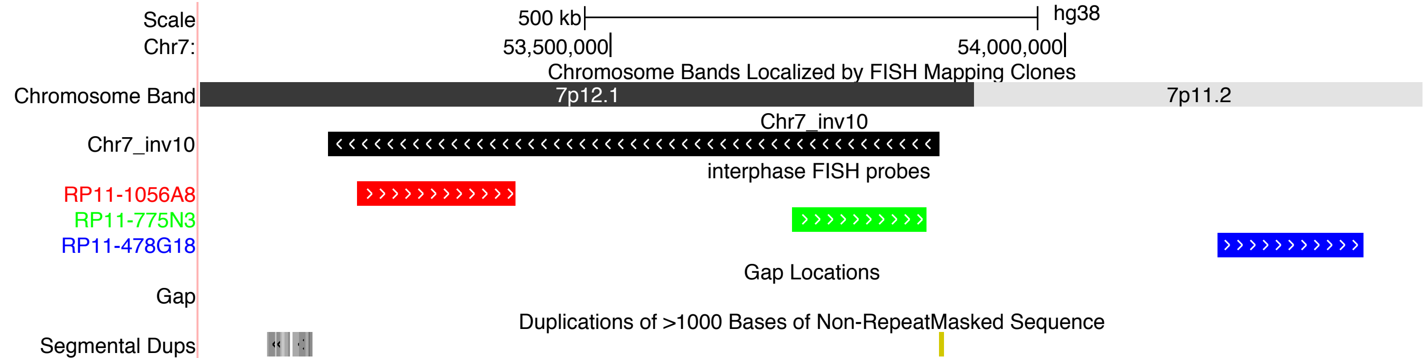
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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7p11.2
Chr7_inv10
Chr7_inv10
interphase FISH probes
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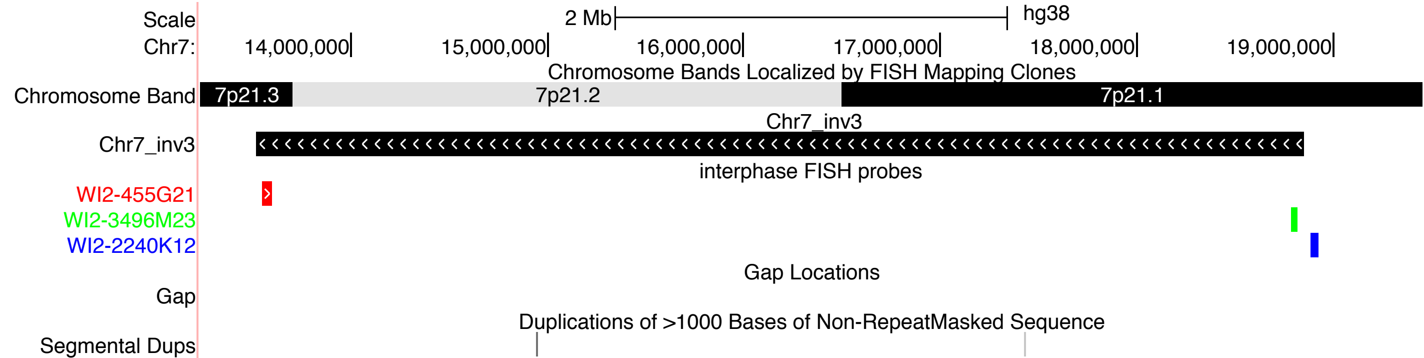
RP11-775N3
RP11-478G18
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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7p21.2
7p21.1
Chr7_inv3
Chr7_inv3
interphase FISH probes
WI2-455G21
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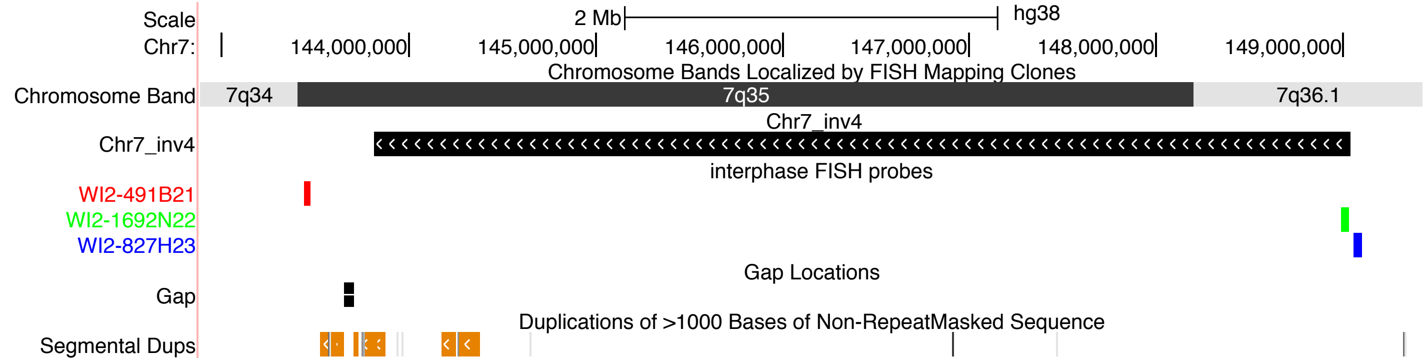
WI2-2240K12
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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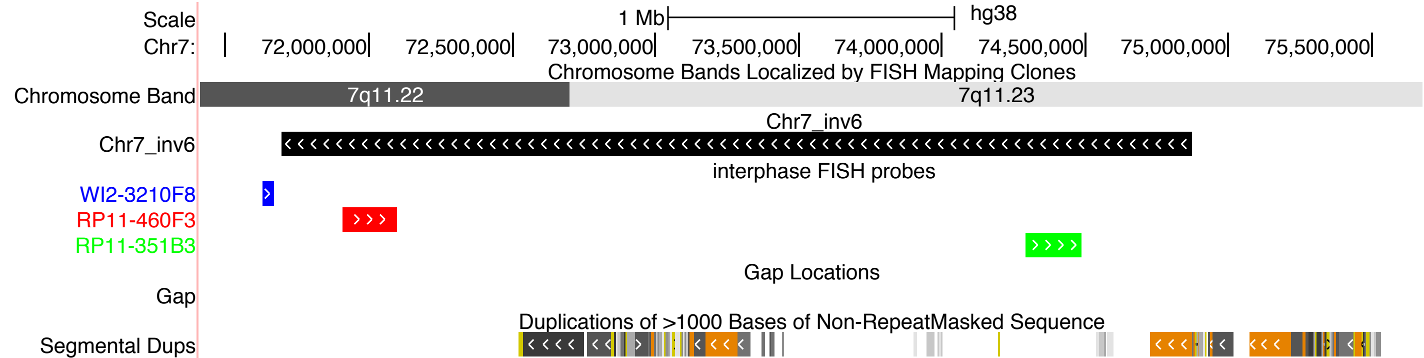
7q35
7q36.1
Chr7_inv4
Chr7_inv4
interphase FISH probes
WI2-491B21
WI2-1692N22
WI2-827H23
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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Chromosome Band
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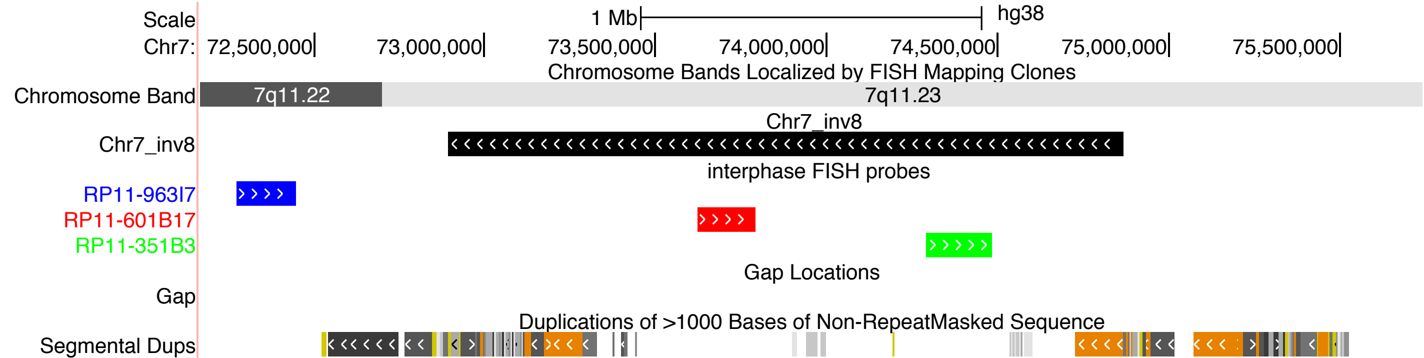
7q11.23
Chr7_inv6
Chr7_inv6
interphase FISH probes
WI2-3210F8
RP11-460F3
RP11-351B3
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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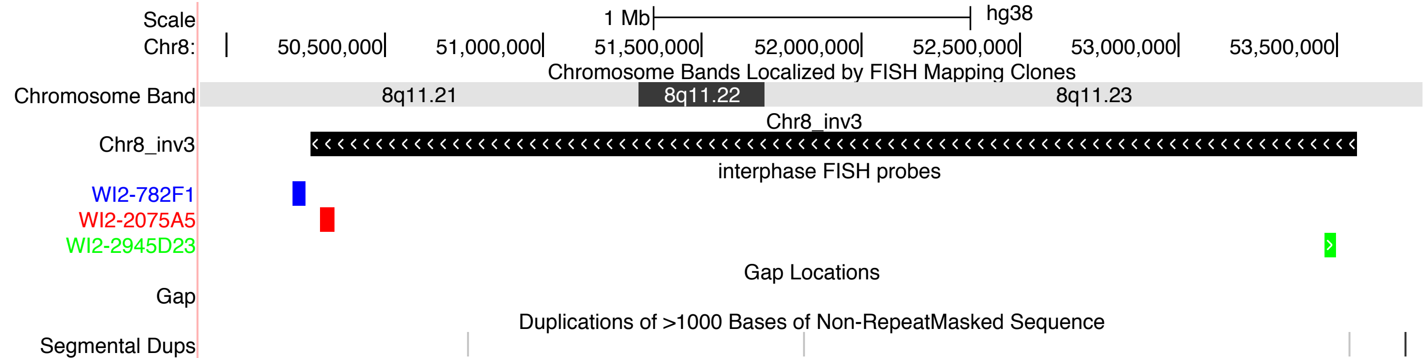
Chromosome Band
7q11.22
7q11.23
Chr7_inv8
Chr7_inv8
interphase FISH probes
RP11-963I7
RP11-601B17
RP11-351B3
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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53,500,000
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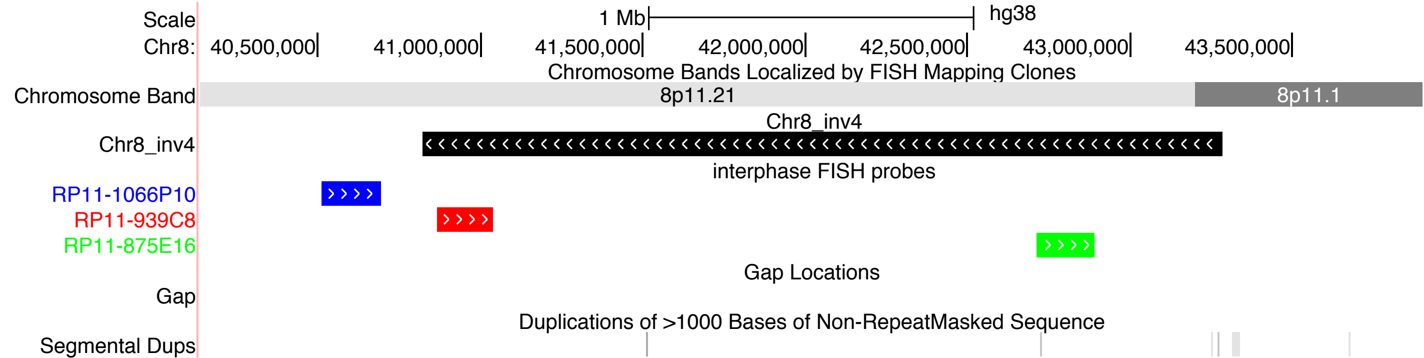
Chromosome Band
8q11.21
8q11.22
8q11.23
Chr8_inv3
Chr8_inv3
interphase FISH probes
WI2-782F1
WI2-2075A5
WI2-2945D23
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups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43,500,000
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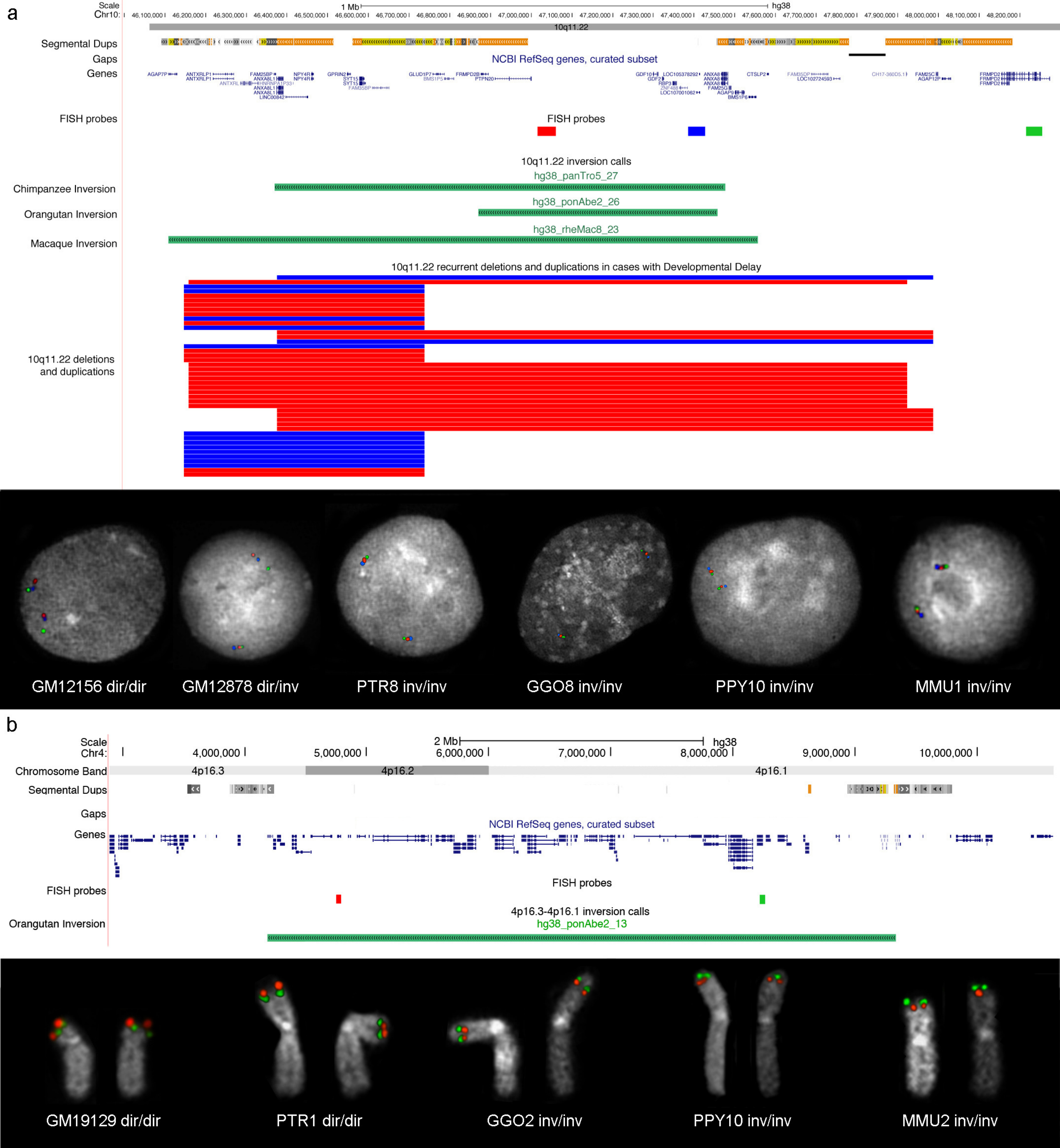
Chromosome Band
8p11.21
8p11.1
Chr8_inv4
Chr8_inv4
interphase FISH probes
RP11-1066P10
RP11-939C8
RP11-875E16
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups

Supplemental Fig. S2. FISH experiments and probe locations.

The location of the probes and the type of FISH experiment (in metaphase or interphase) is shown with respect to the genomic regions studied.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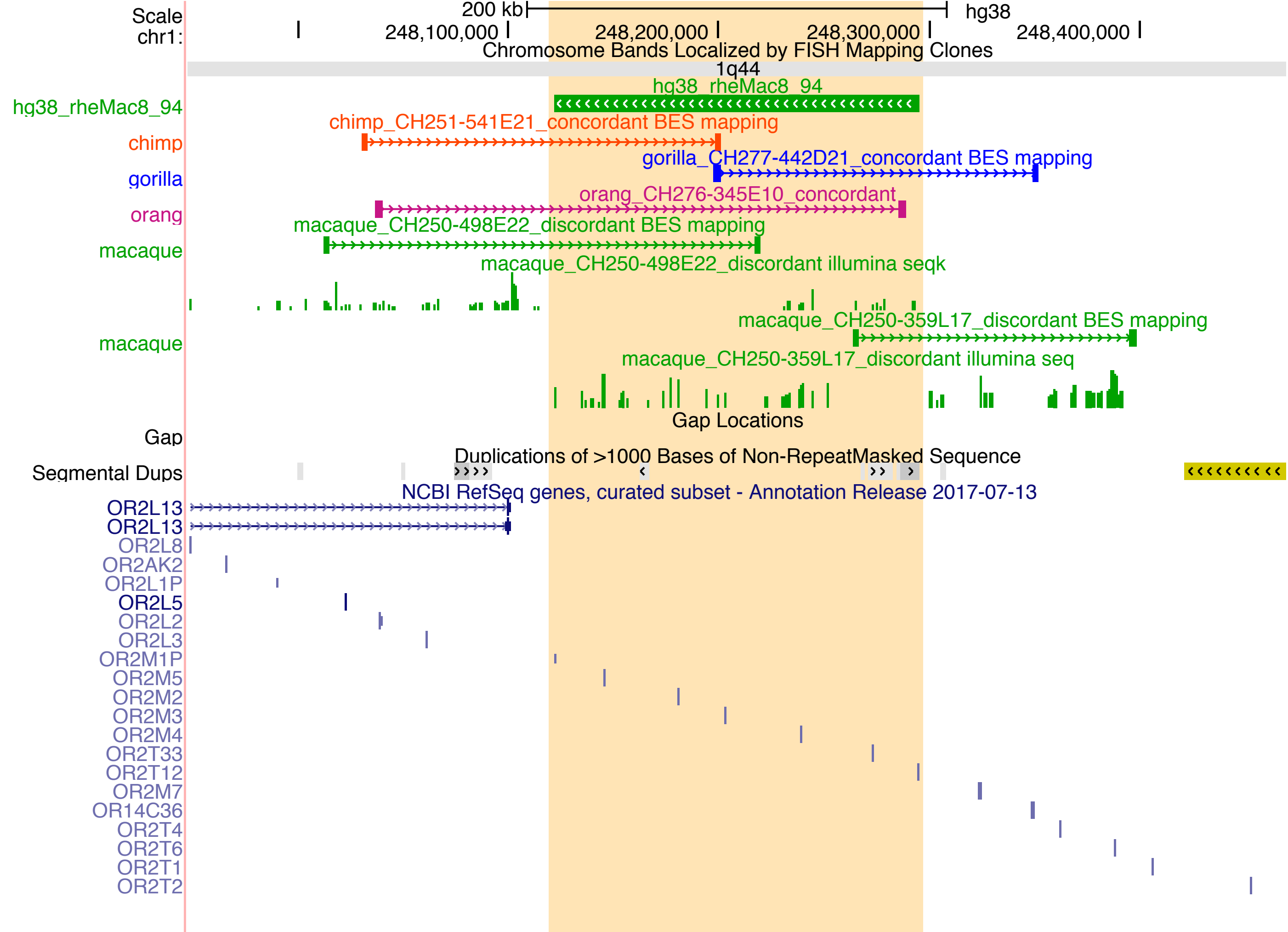
47,900,000
48,000,000
48,100,000
48,200,000
10q11.22
Segmental Dups
Gaps
NCBI RefSeq genes, curated subset
Genes
FISH probes
FISH probes
10q11.22 inversion calls
hg38_panTro5_27
Chimpanzee Inversion
hg38_ponAbe2_26
Orangutan Inversion
hg38_rheMac8_23
Macaque Inversion
10q11.22 recurrent deletions and duplications in cases with Developmental Delay
10q11.22 deletions and duplications
GM12156 dir/dir
GM12878 dir/inv
PTR8 inv/inv
GGO8 inv/inv
PPY10 inv/inv
MMU1 inv/inv
b
Scale
Chr4:
2 Mb
hg38
4,000,000
5,000,000
6,000,000
7,000,000
8,000,000
9,000,000
10,000,000
Chromosome Band
4p16.3
4p16.2
4p16.1
Segmental Dups
Gaps
NCBI RefSeq genes, curated subset
Genes
FISH probes
FISH probes
4p16.3-4p16.1 inversion calls
Orangutan Inversion
hg38_ponAbe2_13
GM19129 dir/dir
PTR1 dir/dir
GGO2 inv/inv
PPY10 inv/inv
MMU2 inv/inv

Supplemental Fig. S3. 10q11.22 and 4p16.3-4p16.1 inversion regions.

a) UCSC Genome Browser view of the 10q11.22 region illustrating inversion calls between human and chimpanzee, human and orangutan, and human and macaque. FISH probes used to validate the inversion are shown. Recurrent microdeletions/microduplications are described at the 10q11.22 locus. At the bottom, FISH results on interphase nuclei show that the inversion is polymorphic in human while all the other nonhuman primates tested carry the inverted haplotype. b) UCSC Genome Browser view of the 4p16.3-4p16.1 region illustrating the inversion call between human and macaque. FISH probes used to validate the inversion are shown. At the bottom, FISH results on metaphase nuclei show that the region was is in inverted orientation in gorilla, orangutan and macaque.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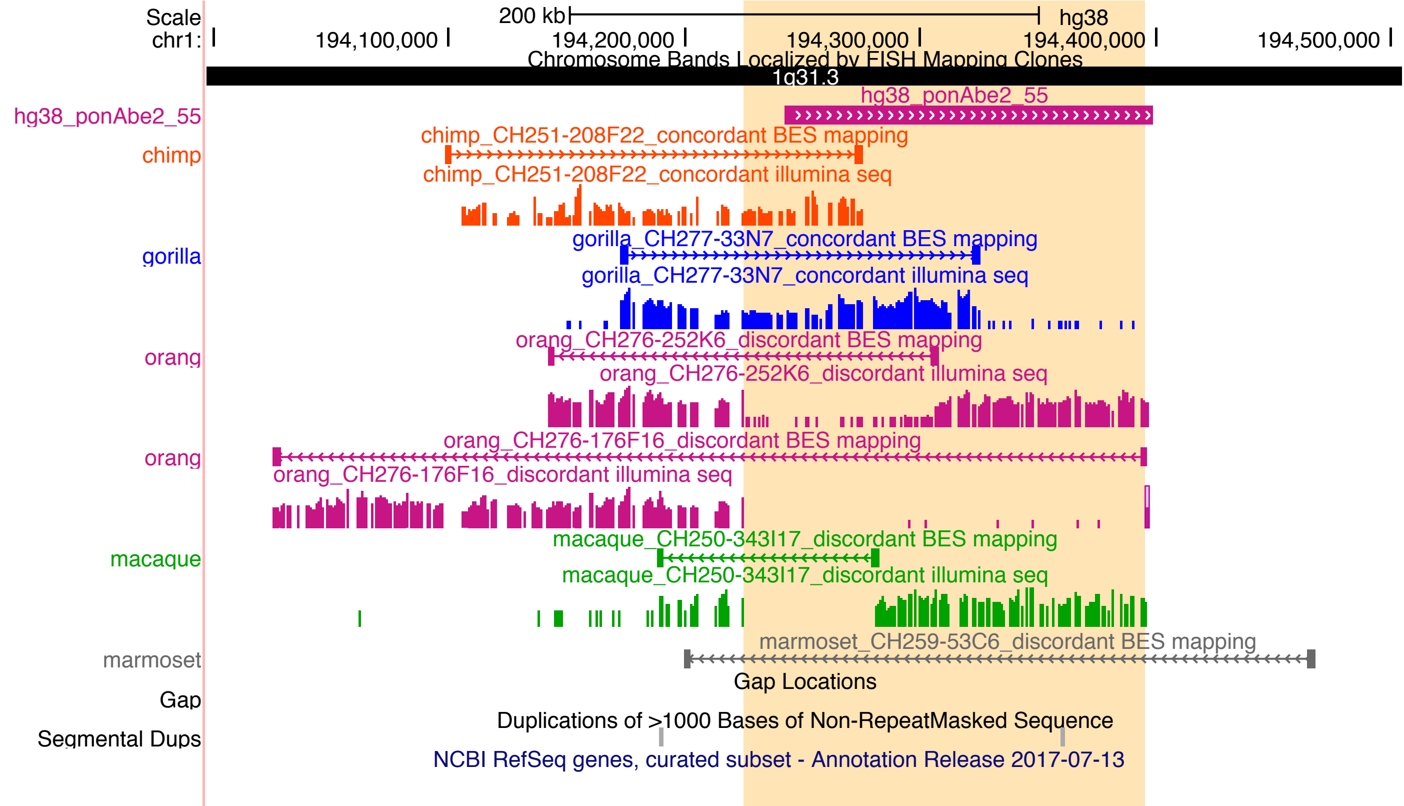
hg38_rheMac8_94
chimp
chimp_CH251-541E21_concordant BES mapping
gorilla
gorilla_CH277-442D21_concordant BES mapping
orang
orang_CH276-345E10_concordant
macaque
macaque_CH250-498E22_discordant BES mapping
macaque_CH250-498E22_discordant illumina seqk
macaque
macaque_CH250-359L17_discordant BES mapping
macaque_CH250-359L17_discordant illumina seq
Gap
Gap Locations
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
OR2L13
OR2L13
OR2L8
OR2AK2
OR2L1P
OR2L5
OR2L2
OR2L3
OR2M1P
OR2M5
OR2M2
OR2M3
OR2M4
OR2T33
OR2T12
OR2M7
OR14C36
OR2T4
OR2T6
OR2T1
OR2T2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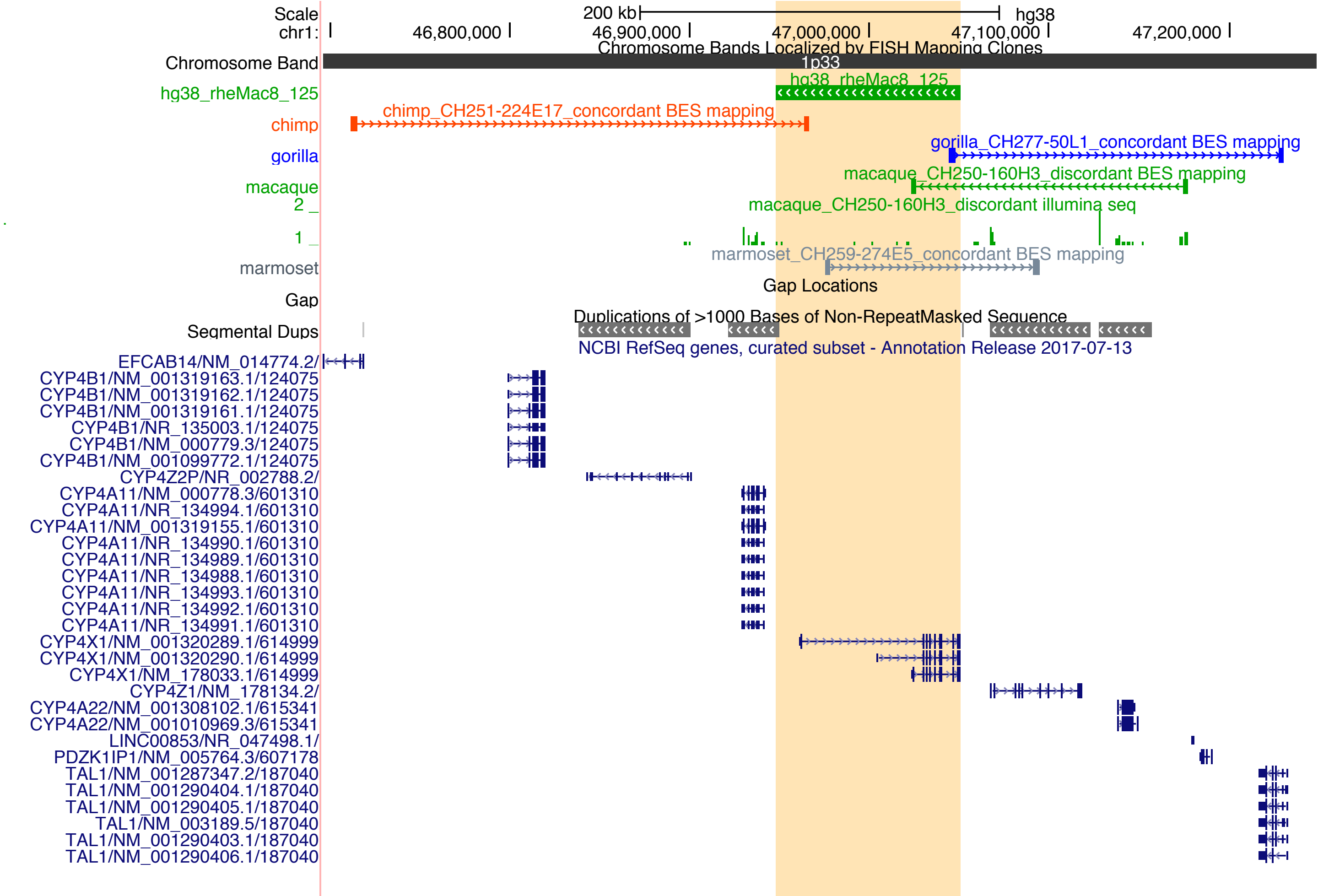
hg38_ponAbe2_55
hg38_ponAbe2_55
chimp
chimp_CH251-208F22_concordant BES mapping
chimp_CH251-208F22_concordant illumina seq
gorilla
gorilla_CH277-33N7_concordant BES mapping
gorilla_CH277-33N7_concordant illumina seq
orang
orang_CH276-252K6_discordant BES mapping
orang_CH276-252K6_discordant illumina seq
orang
orang_CH276-176F16_discordant BES mapping
orang_CH276-176F16_discordant illumina seq
macaque
macaque_CH250-343I17_discordant BES mapping
macaque_CH250-343I17_discordant illumina seq
marmoset
marmoset_CH259-53C6_discordant BES mapping
Gap
Gap Locations
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13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hg38_rheMac8_125
chimp
chimp_CH251-224E17_concordant BES mapping
gorilla
gorilla_CH277-50L1_concordant BES mapping
macaque
macaque_CH250-160H3_discordant BES mapping
2 _
macaque_CH250-160H3_discordant illumina seq
1 _
marmoset
marmoset_CH259-274E5_concordant BES mapping
Gap
Gap Locations
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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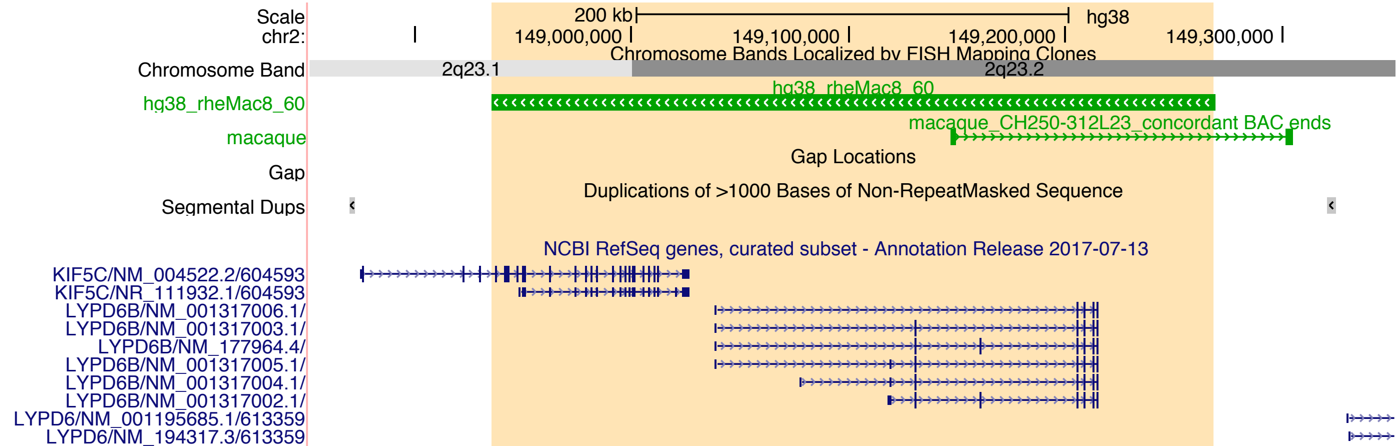
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hg38_rheMac8_60
macaque
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Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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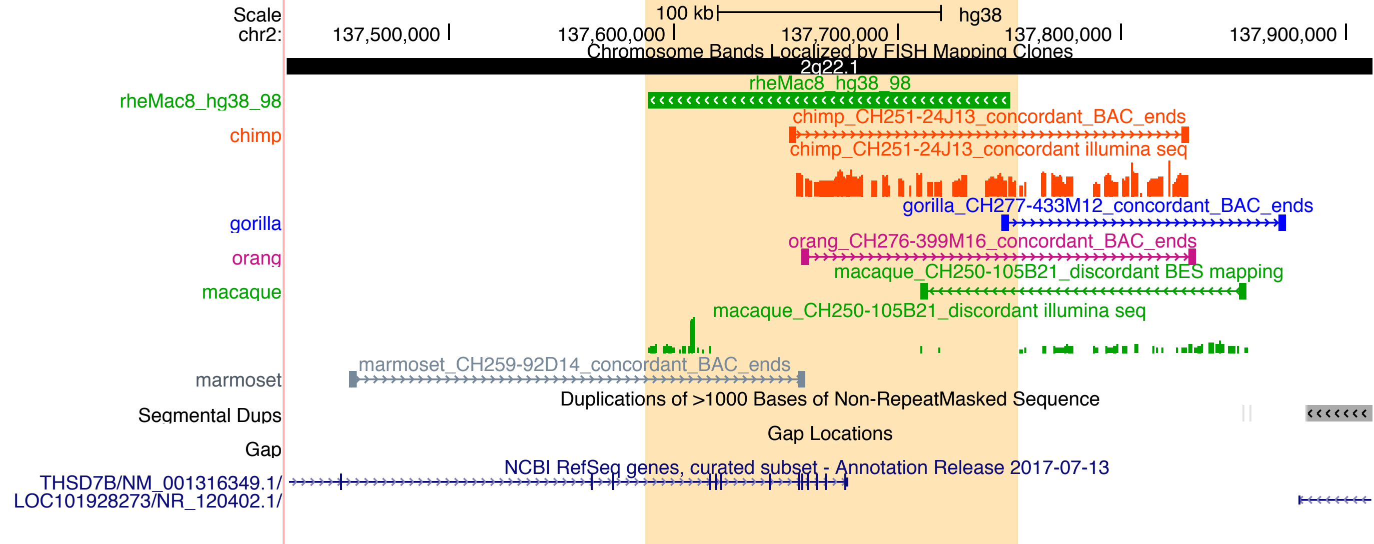
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rheMac8_hg38_98
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gorilla
gorilla_CH277-433M12_concordant_BAC_ends
orang
orang_CH276-399M16_concordant_BAC_ends
macaque
macaque_CH250-105B21_discordant BES mapping
macaque_CH250-105B21_discordant illumina seq
marmoset
marmoset_CH259-92D14_concordant_BAC_ends
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Gap
Gap Locations
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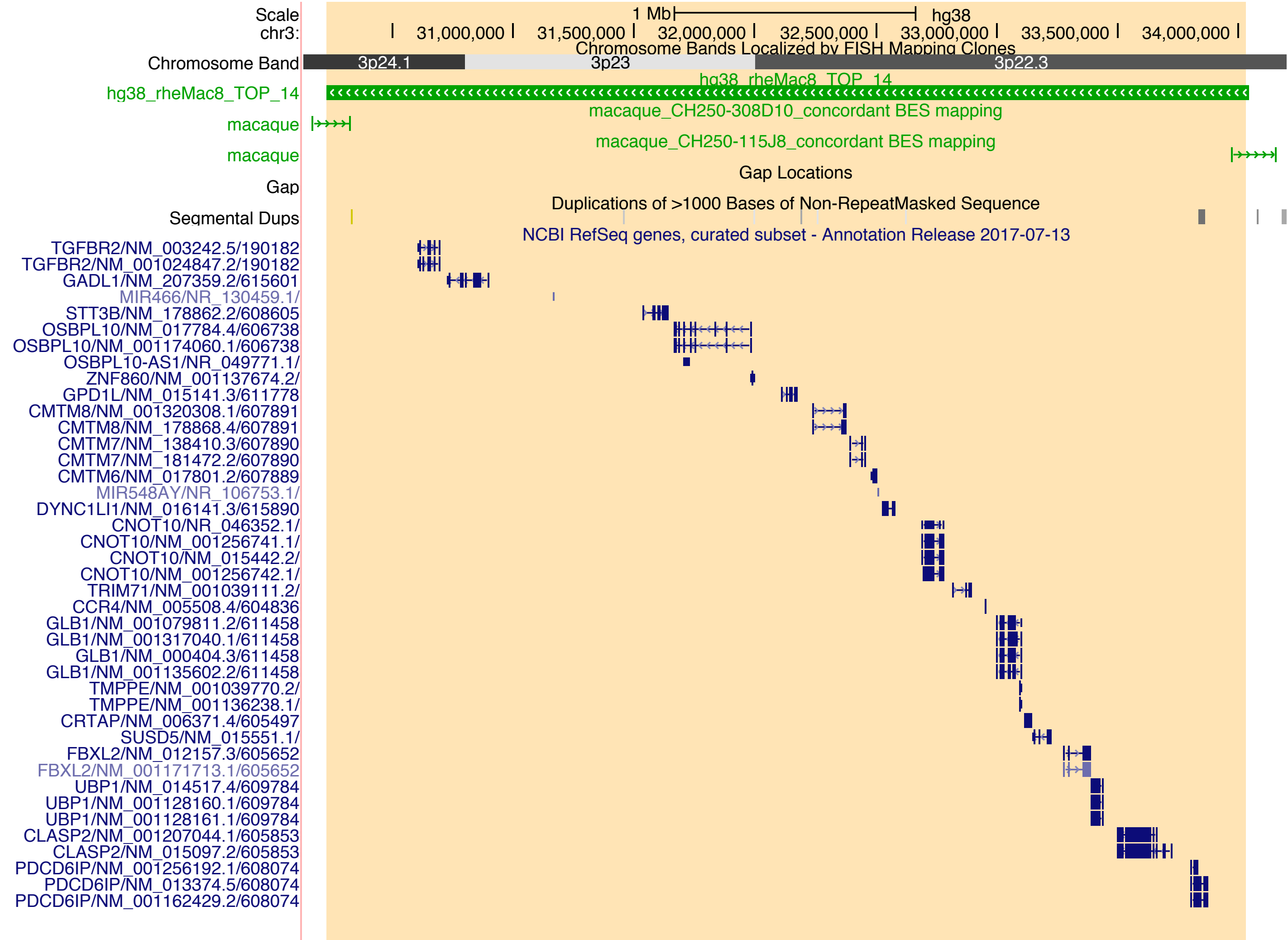
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3p23
3p22.3
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hg38_rheMac8_TOP_14
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macaque
macaque_CH250-115J8_concordant BES mapping
macaque
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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CNOT10/NM_001256742.1/
TRIM71/NM_001039111.2/
CCR4/NM_005508.4/604836
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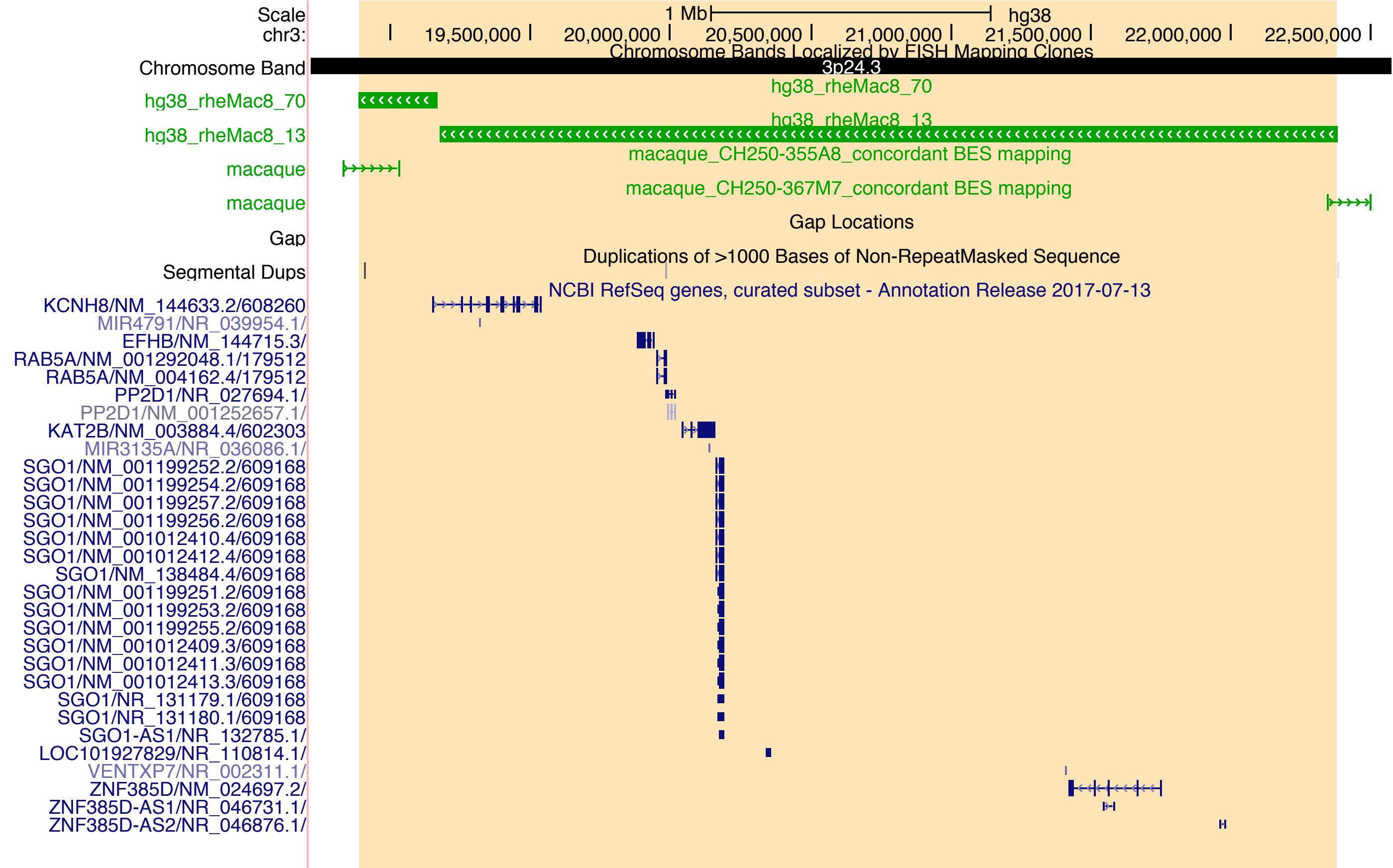
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Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
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hg38_rheMac8_70
hg38_rheMac8_13
hg38_rheMac8_13
macaque
macaque_CH250-355A8_concordant BES mapping
macaque
macaque_CH250-367M7_concordant BES mapping
Gap
Gap Locations
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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SGO1/NM_001012409.3/609168
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SGO1/NR_131180.1/609168
SGO1-AS1/NR_132785.1/
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VENTXP7/NR_002311.1/
ZNF385D/NM_024697.2/
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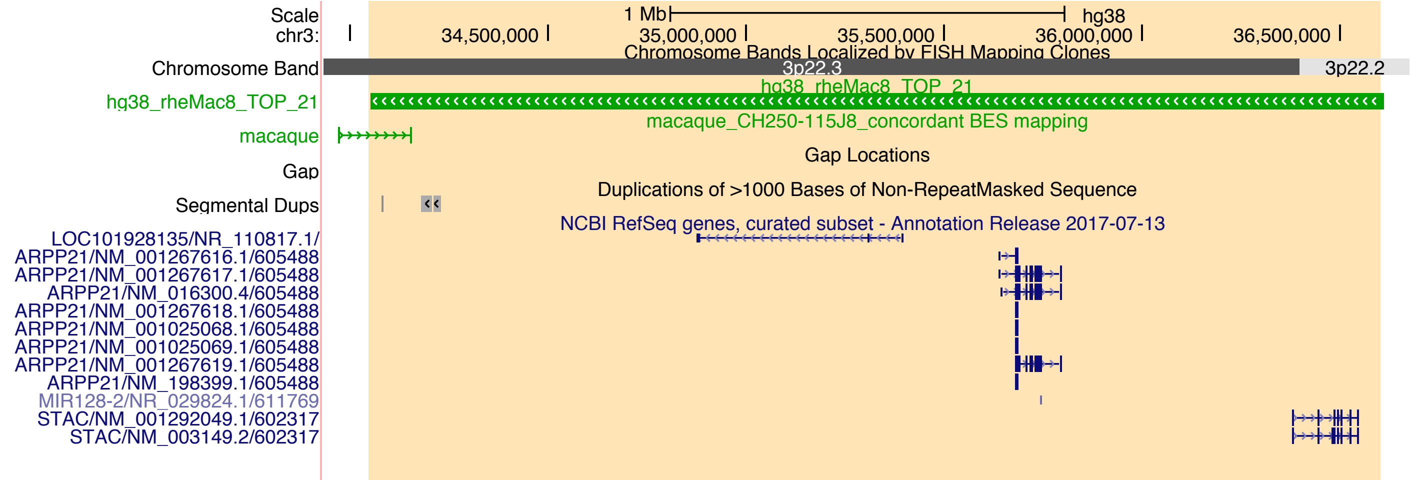
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3p22.2
hg38_rheMac8_TOP_21
hg38_rheMac8_TOP_21
macaque_CH250-115J8_concordant BES mapping
macaque
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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ARPP21/NM_001267617.1/605488
ARPP21/NM_016300.4/605488
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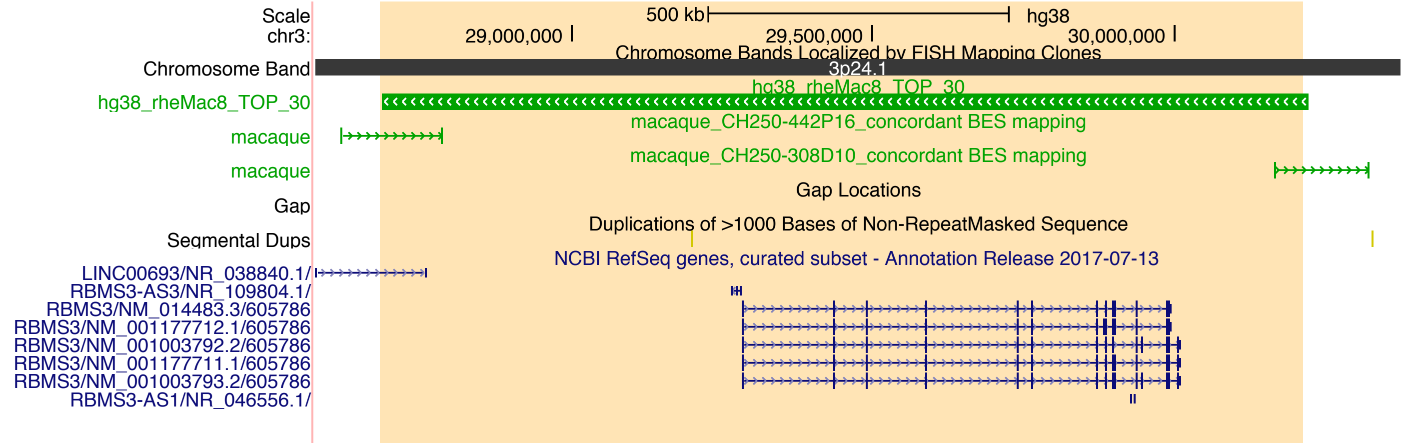
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macaque
macaque_CH250-308D10_concordant BES mapping
macaque
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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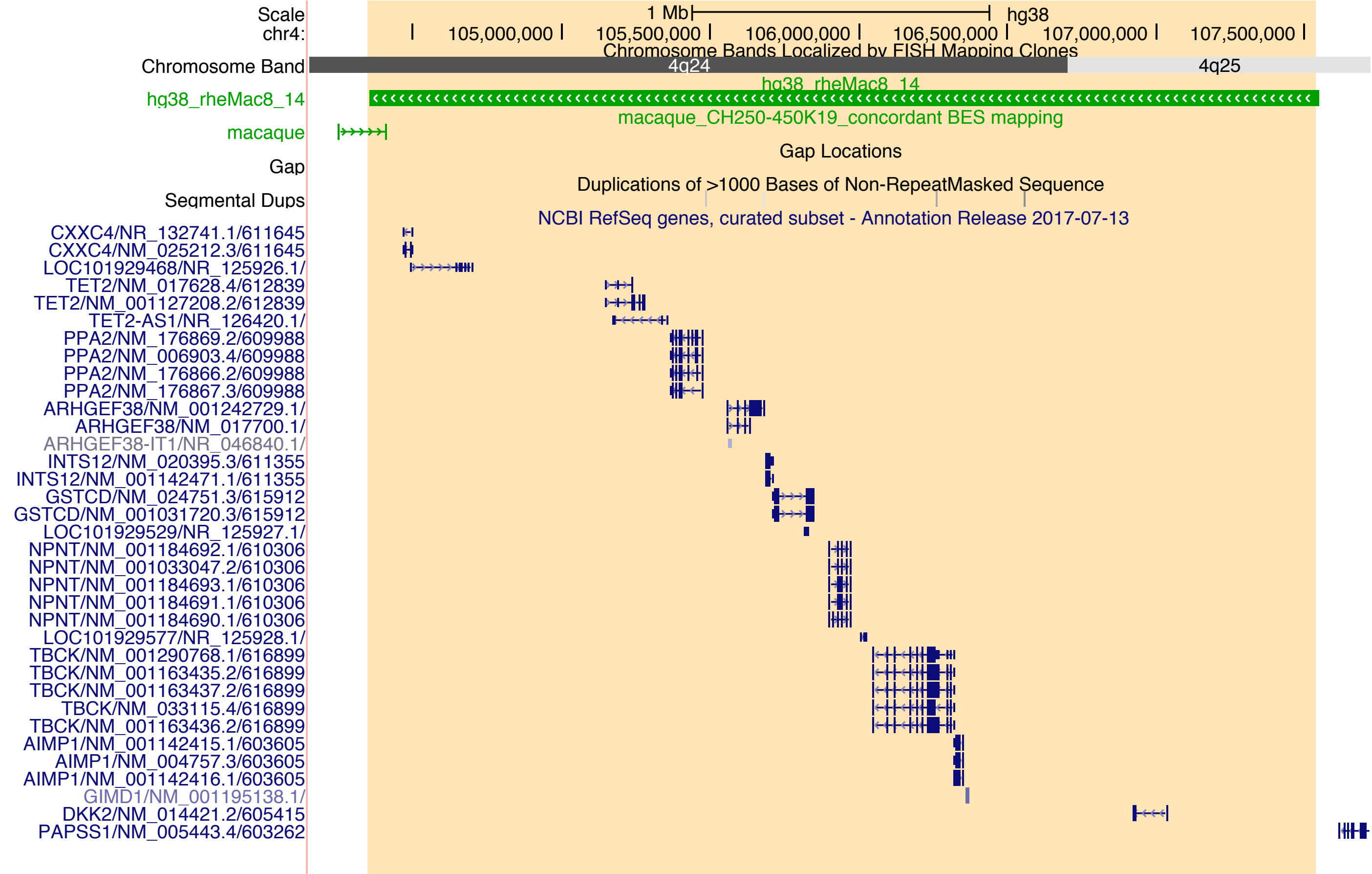
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hg38_rheMac8_14
macaque_CH250-450K19_concordant BES mapping
macaque
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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PPA2/NM_176867.3/609988
ARHGEF38/NM_001242729.1/
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INTS12/NM_020395.3/611355
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GSTCD/NM_024751.3/615912
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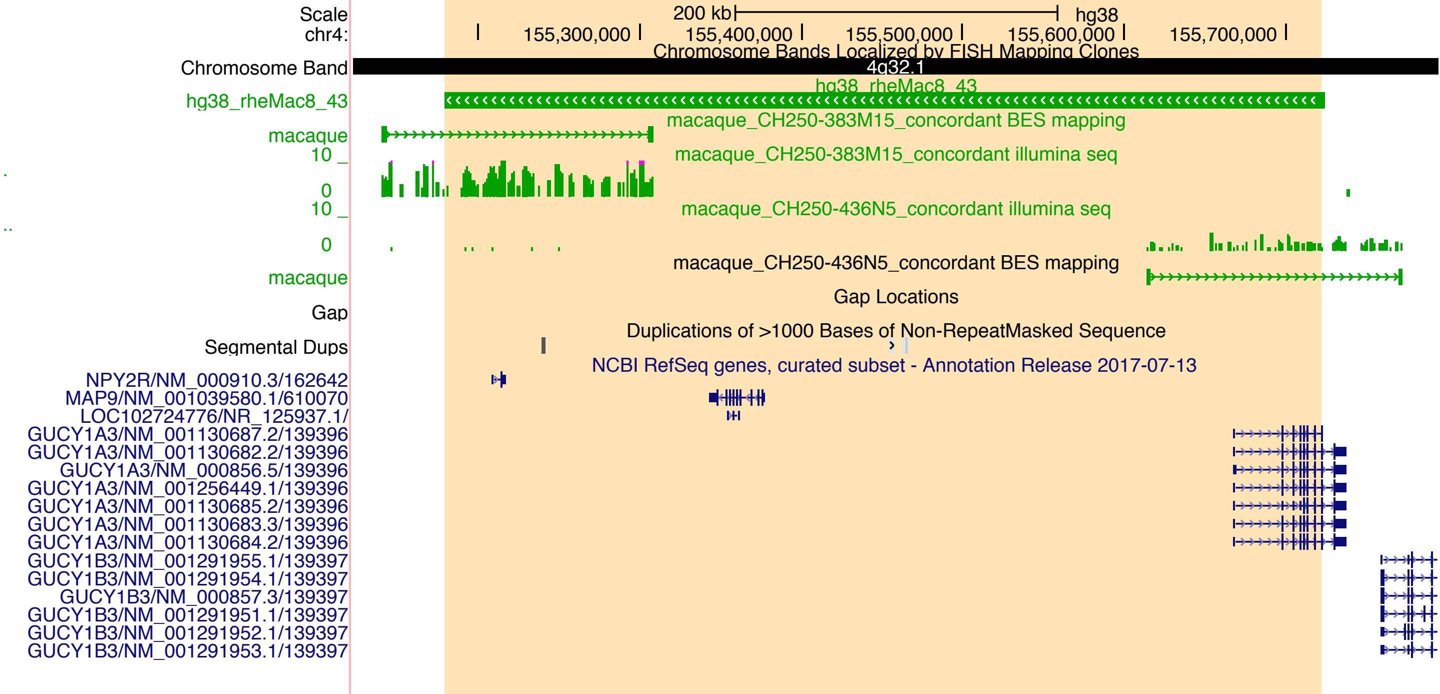
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macaque
10 _
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macaque_CH250-436N5_concordant BES mapping
macaque
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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GUCY1A3/NM_001256449.1/139396
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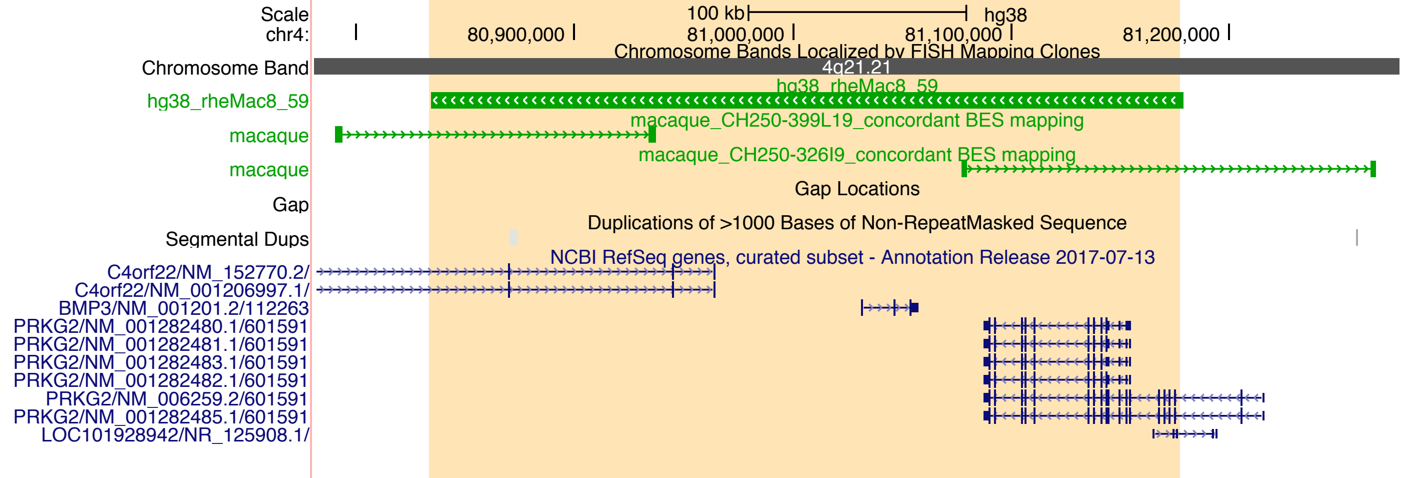
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macaque
macaque_CH250-326I9_concordant BES mapping
macaque
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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PRKG2/NM_001282482.1/601591
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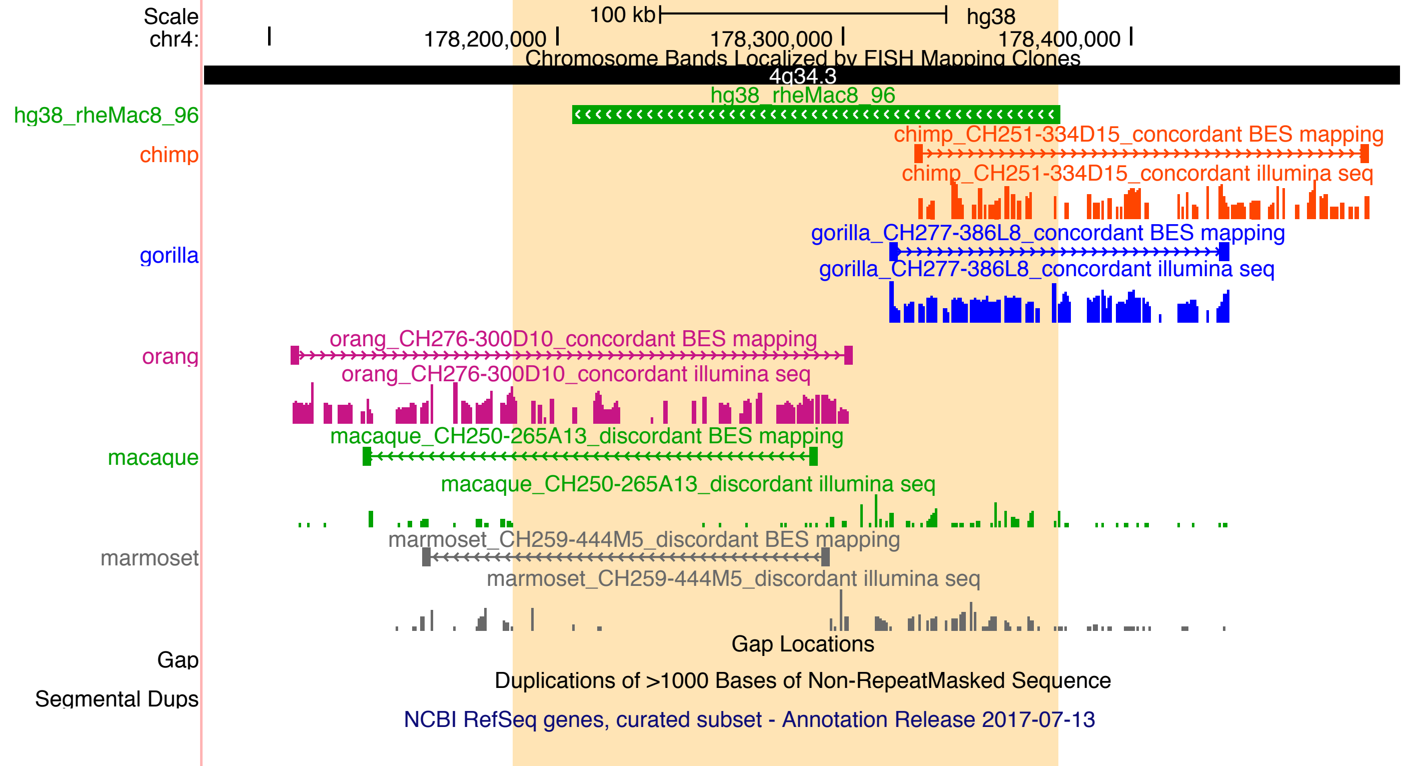
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gorilla
gorilla_CH277-386L8_concordant BES mapping
gorilla_CH277-386L8_concordant illumina seq
orang
orang_CH276-300D10_concordant BES mapping
orang_CH276-300D10_concordant illumina seq
macaque
macaque_CH250-265A13_discordant BES mapping
macaque_CH250-265A13_discordant illumina seq
marmoset
marmoset_CH259-444M5_discordant BES mapping
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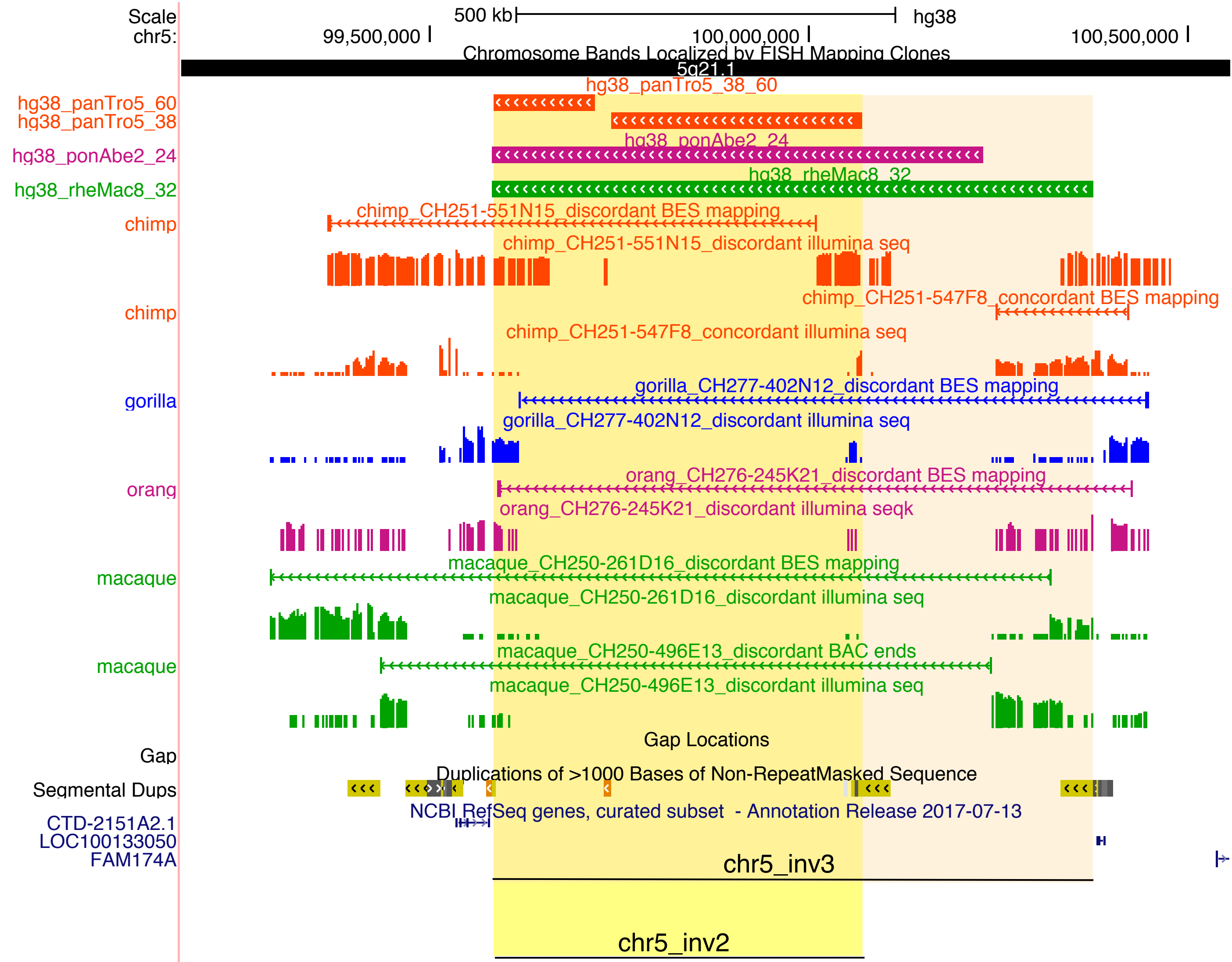
Gap Locations
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13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hg38_rheMac8_32
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chimp_CH251-551N15_discordant BES mapping
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gorilla_CH277-402N12_discordant BES mapping
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macaque_CH250-261D16_discordant BES mapping
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Gap
Gap Locations
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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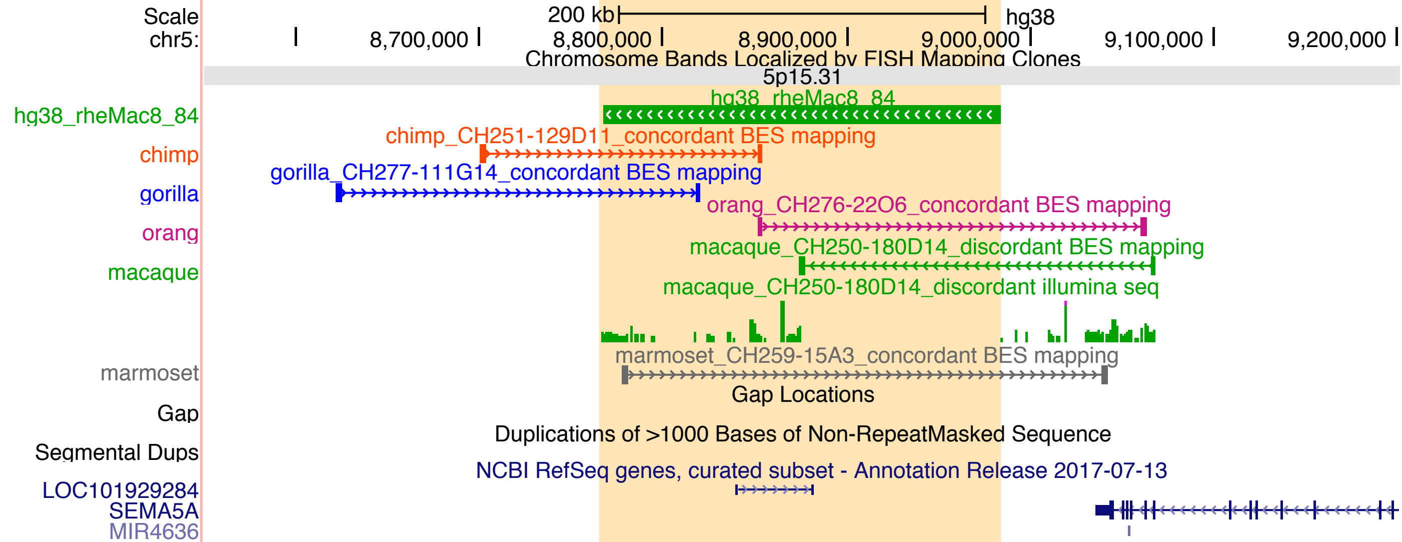
chr5_inv2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chimp
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gorilla
orang_CH276-22O6_concordant BES mapping
orang
macaque_CH250-180D14_discordant BES mapping
macaque
macaque_CH250-180D14_discordant illumina seq
marmoset_CH259-15A3_concordant BES mapping
marmoset
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
LOC101929284
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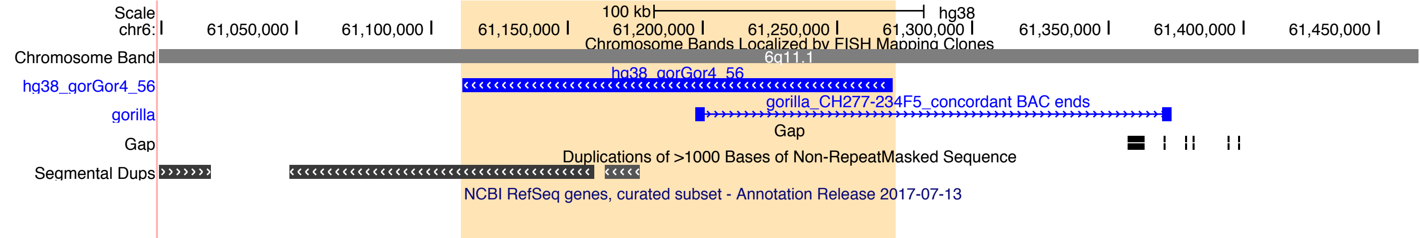
MIR4636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Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
6q11.1
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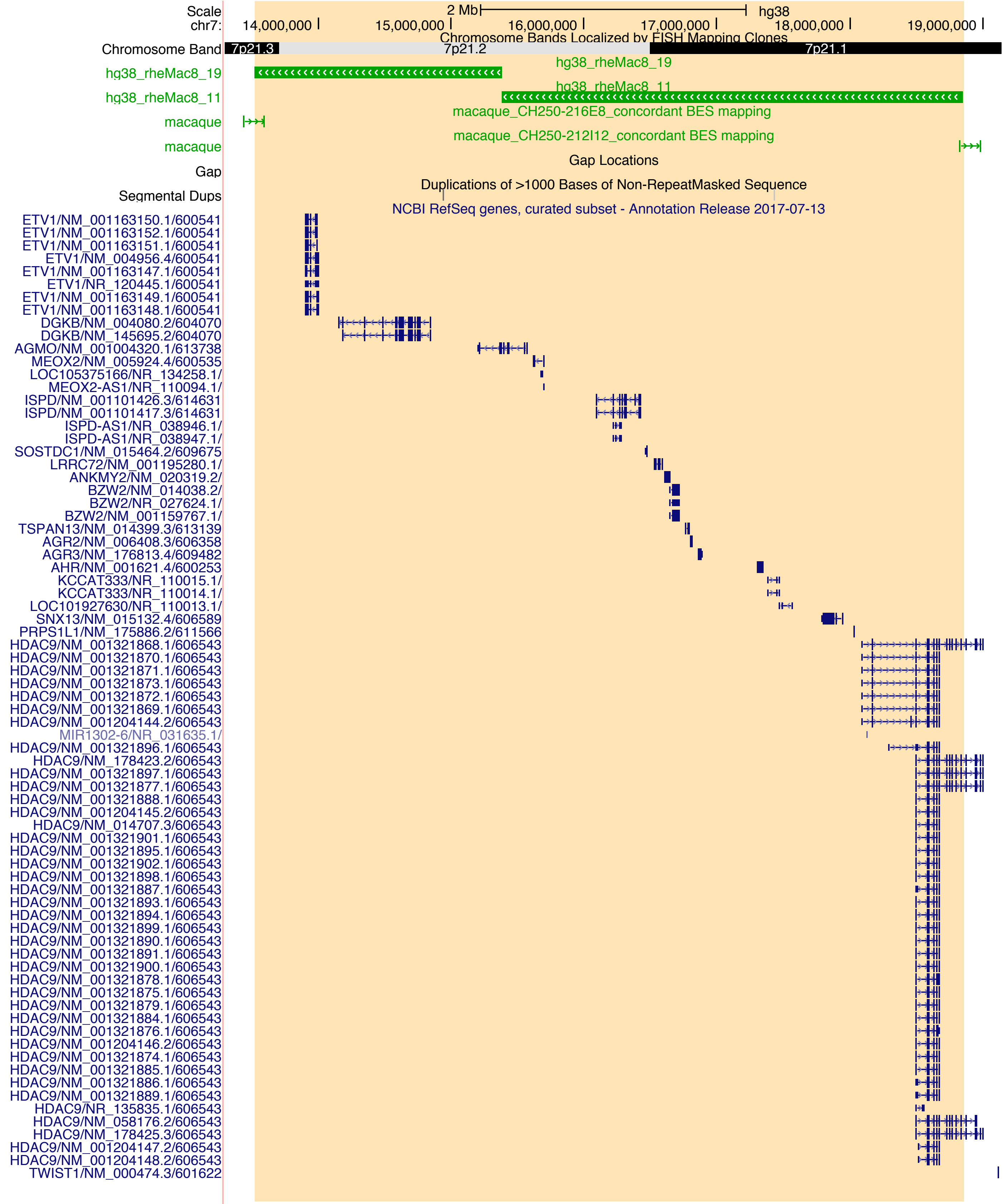
hg38_gorGor4_56
gorilla_CH277-234F5_concordant BAC ends
gorilla
Gap
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13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7p21.3
7p21.2
7p21.1
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macaque
macaque_CH250-212I12_concordant BES mapping
macaque
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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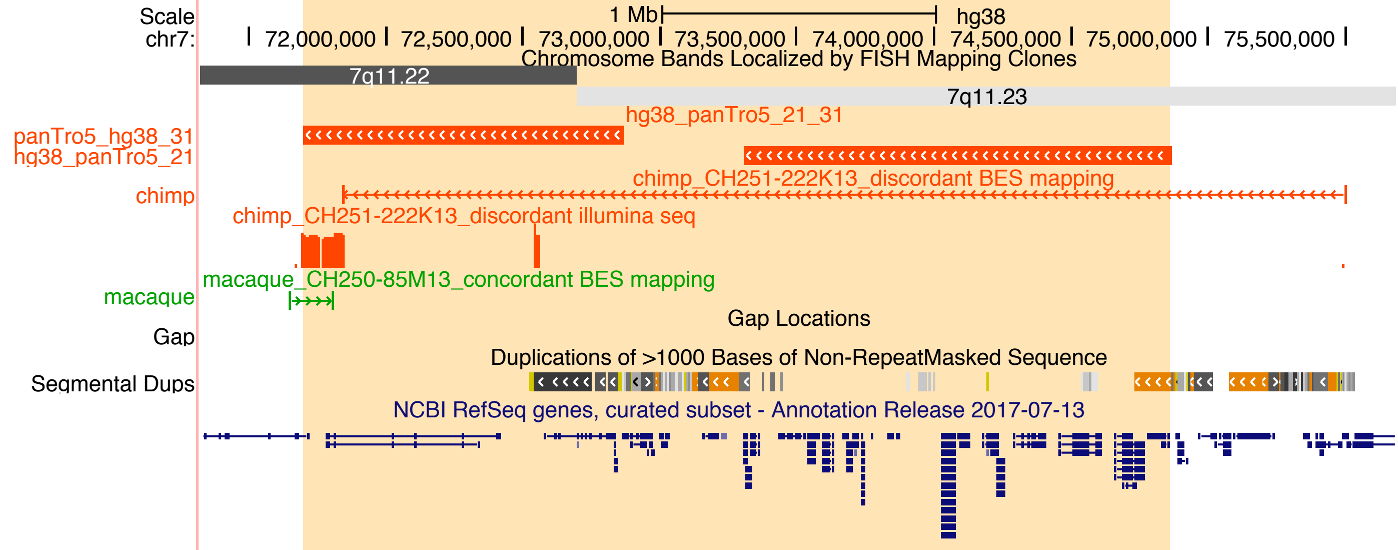
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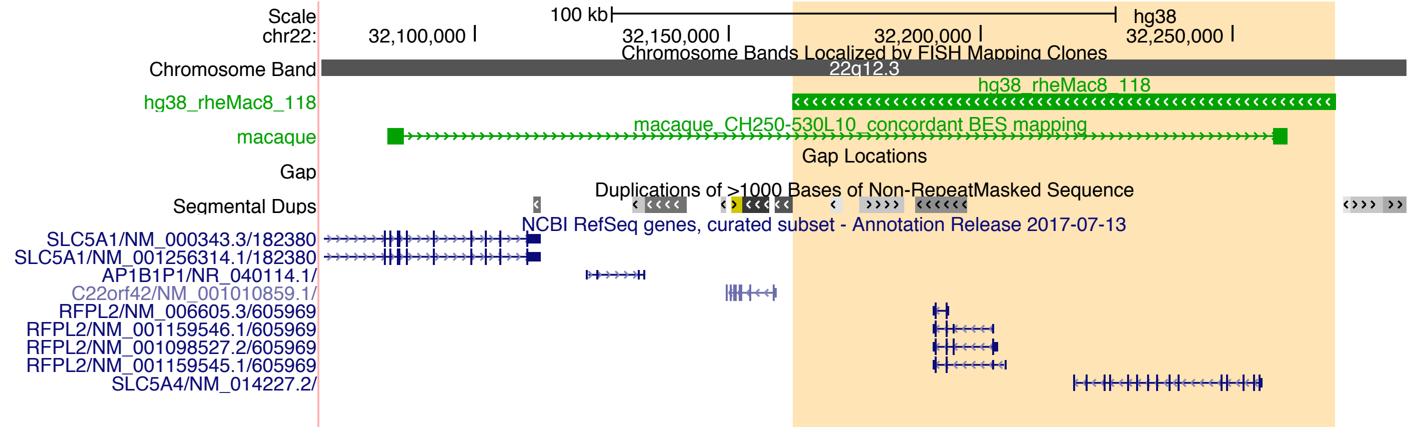
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13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macaque
macaque_CH250-530L10_concordant BES mapping
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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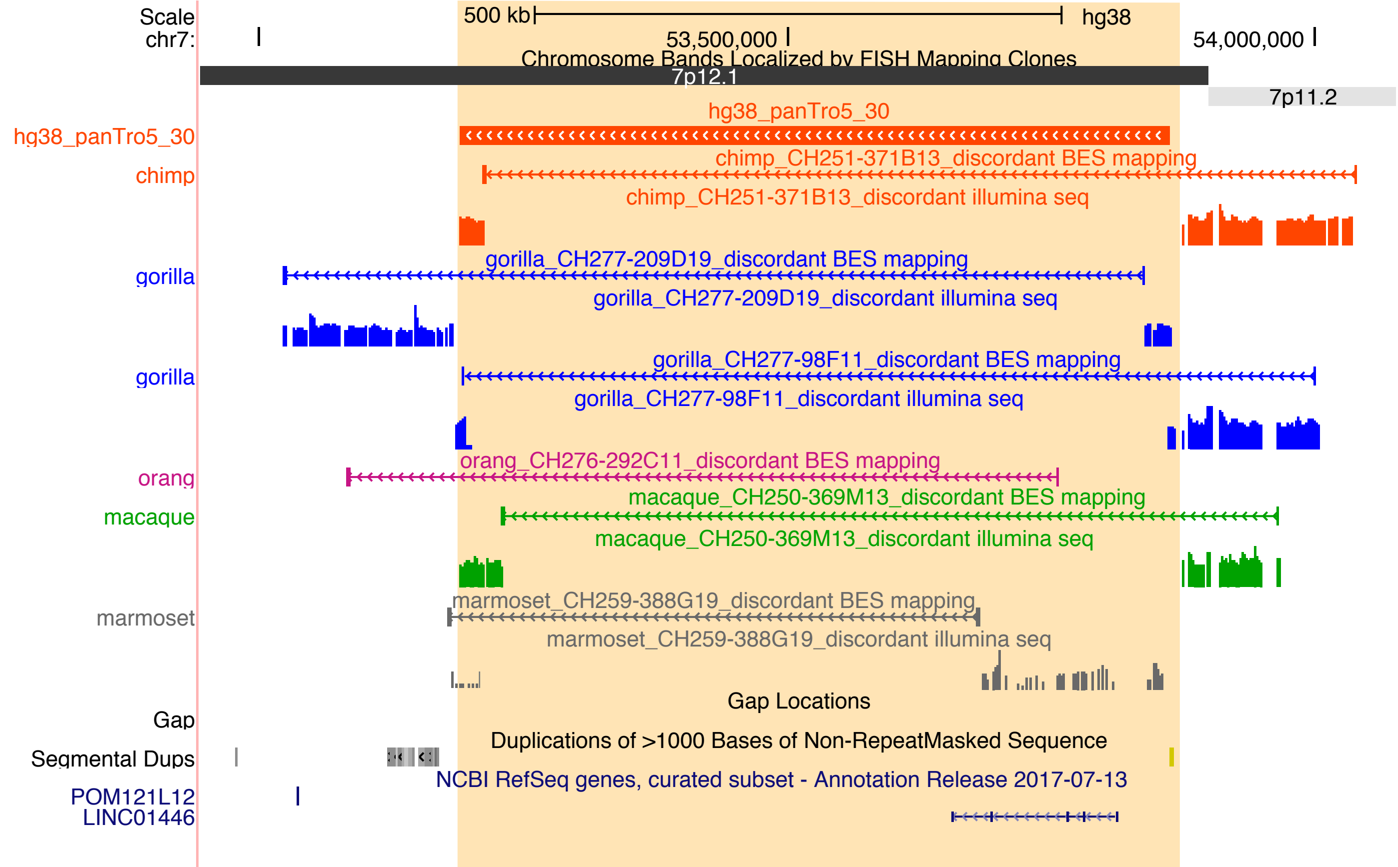
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gorilla_CH277-209D19_discordant BES mapping
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gorilla
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orang_CH276-292C11_discordant BES mapping
macaque
macaque_CH250-369M13_discordant BES mapping
macaque_CH250-369M13_discordant illumina seq
marmoset
marmoset_CH259-388G19_discordant BES mapping
marmoset_CH259-388G19_discordant illumina seq
Gap
Gap Locations
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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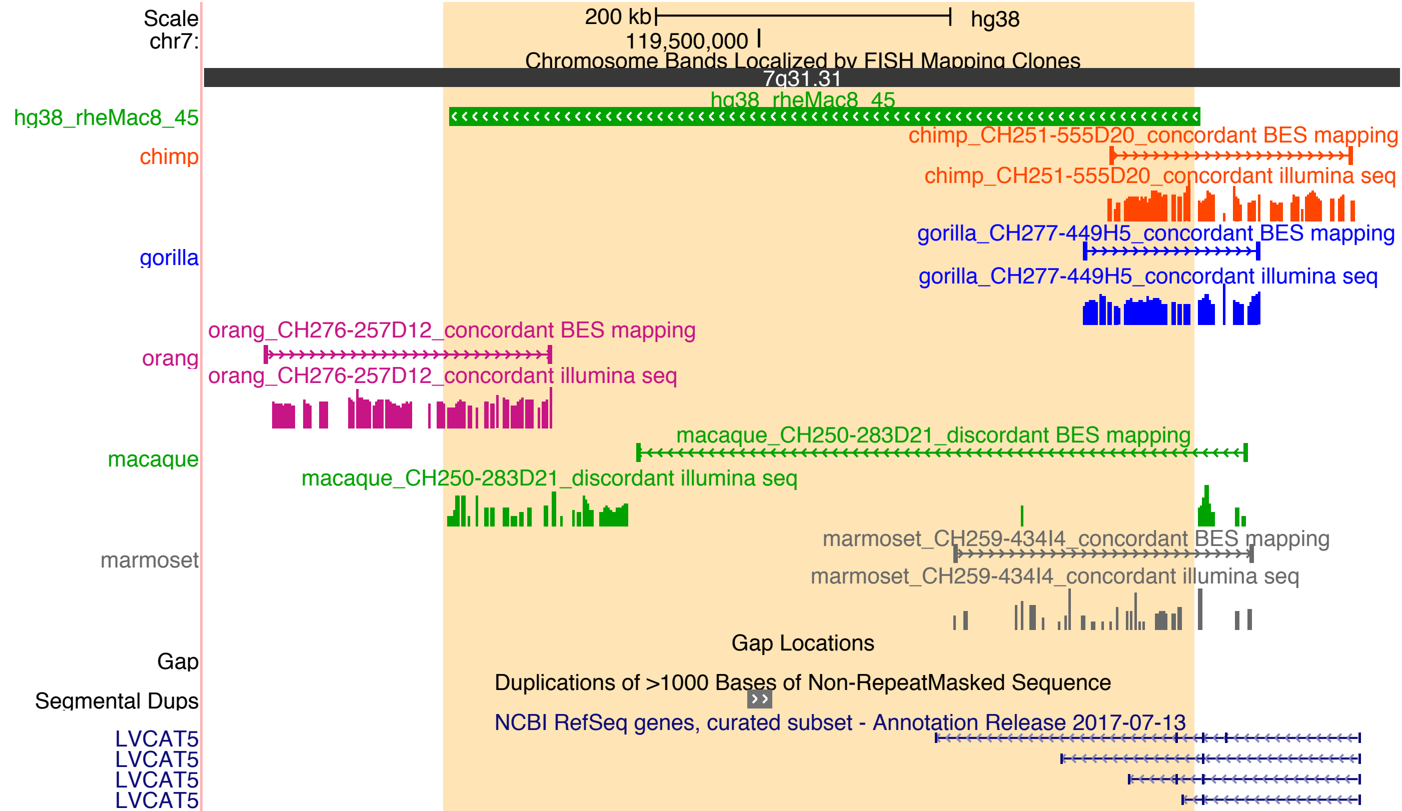
LINC01446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gorilla
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orang
orang_CH276-257D12_concordant BES mapping
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macaque
macaque_CH250-283D21_discordant BES mapping
macaque_CH250-283D21_discordant illumina seq
marmoset
marmoset_CH259-434I4_concordant BES mapping
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Gap
Gap Locations
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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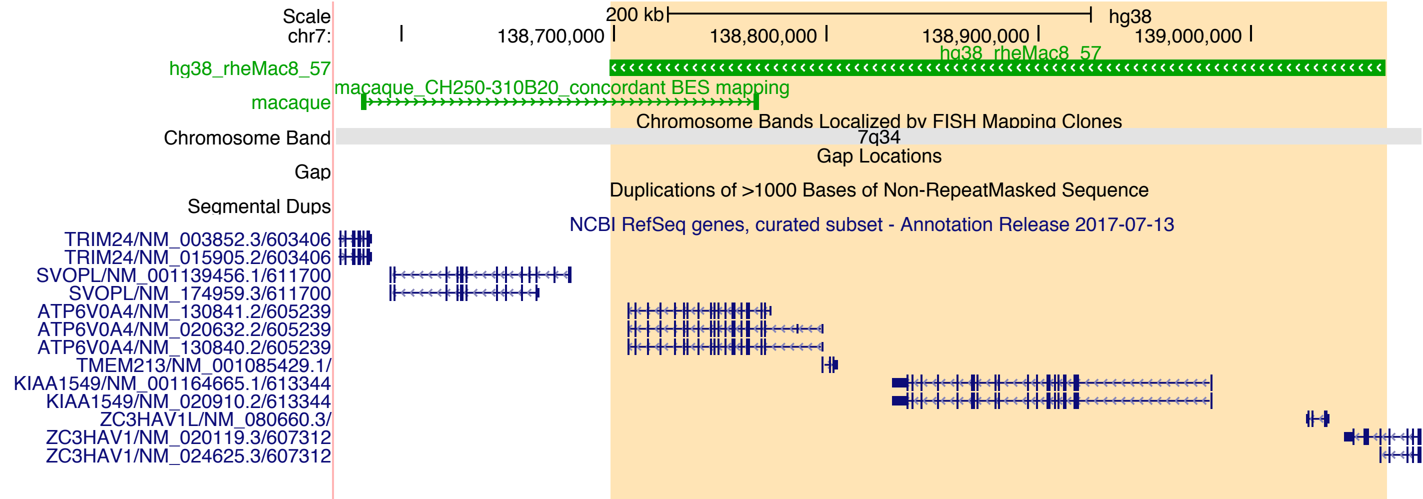
LVCAT5
LVCAT5
LVCAT5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macaque
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
7q34
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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TRIM24/NM_015905.2/603406
SVOPL/NM_001139456.1/611700
SVOPL/NM_174959.3/611700
ATP6V0A4/NM_130841.2/605239
ATP6V0A4/NM_020632.2/605239
ATP6V0A4/NM_130840.2/605239
TMEM213/NM_001085429.1/
KIAA1549/NM_001164665.1/613344
KIAA1549/NM_020910.2/613344
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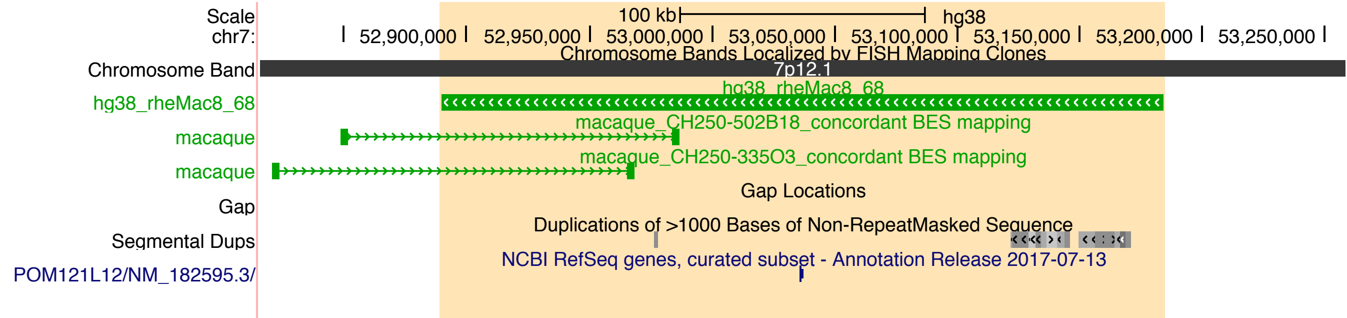
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Chromosome Bands Localized by FISH Mapping Clones
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hg38_rheMac8_68
macaque_CH250-502B18_concordant BES mapping
macaque
macaque_CH250-335O3_concordant BES mapping
macaque
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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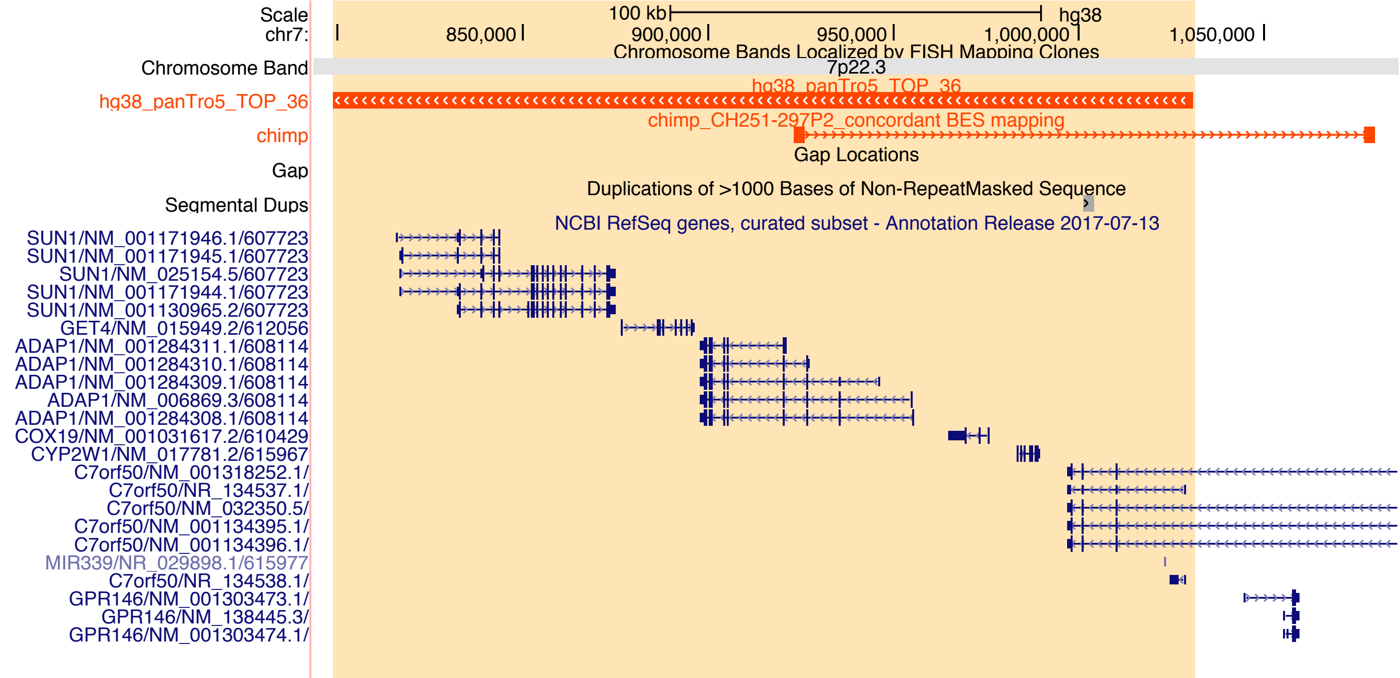
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hg38_panTro5_TOP_36
chimp_CH251-297P2_concordant BES mapping
chimp
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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GET4/NM_015949.2/612056
ADAP1/NM_001284311.1/608114
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MIR339/NR_029898.1/615977
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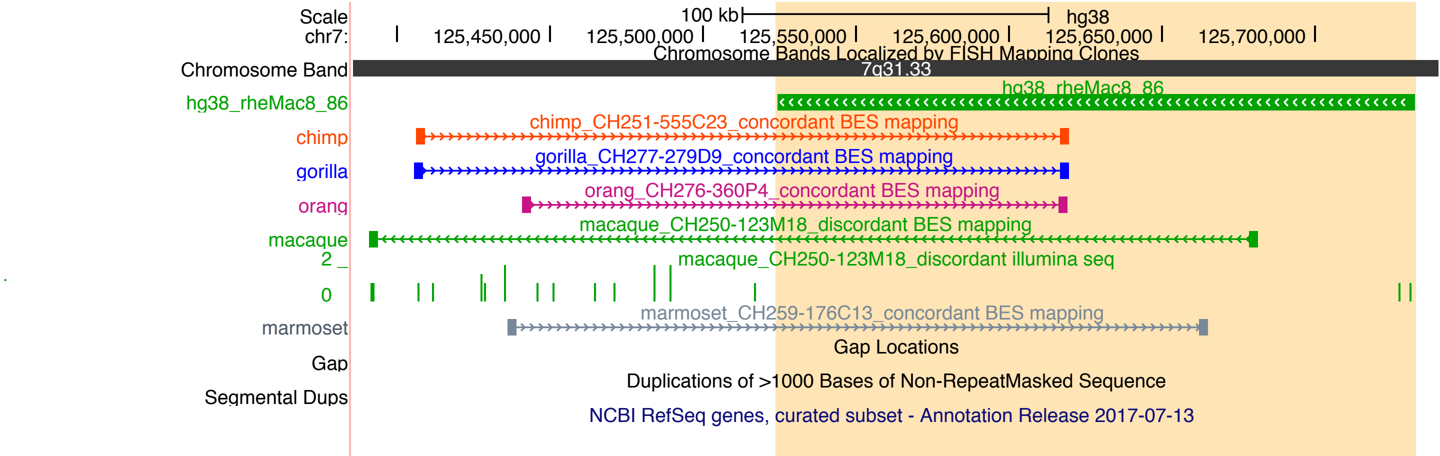
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Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
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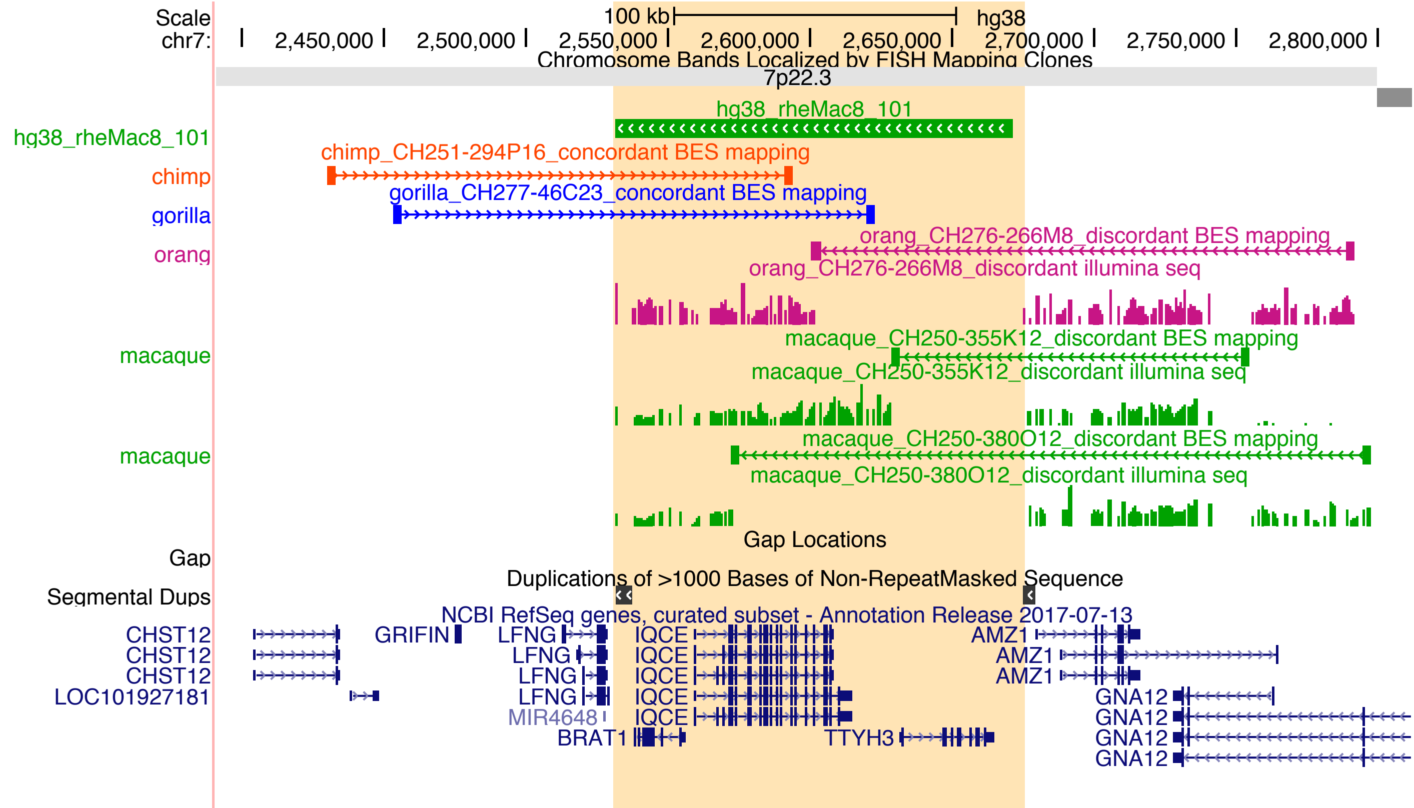
hg38_rheMac8_86
hg38_rheMac8_86
chimp_CH251-555C23_concordant BES mapping
chimp
gorilla_CH277-279D9_concordant BES mapping
gorilla
orang_CH276-360P4_concordant BES mapping
orang
macaque_CH250-123M18_discordant BES mapping
macaque
2 _
macaque_CH250-123M18_discordant illumina seq
0
marmoset_CH259-176C13_concordant BES mapping
marmoset
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13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7p22.3
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hg38_rheMac8_101
chimp_CH251-294P16_concordant BES mapping
chimp
gorilla_CH277-46C23_concordant BES mapping
gorilla
orang_CH276-266M8_discordant BES mapping
orang
orang_CH276-266M8_discordant illumina seq
macaque_CH250-355K12_discordant BES mapping
macaque
macaque_CH250-355K12_discordant illumina seq
macaque_CH250-380O12_discordant BES mapping
macaque
macaque_CH250-380O12_discordant illumina seq
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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CHST12
CHST12
LOC101927181
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LFNG
LFNG
LFNG
LFNG
MIR4648
BRAT1
IQCE
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IQCE
IQCE
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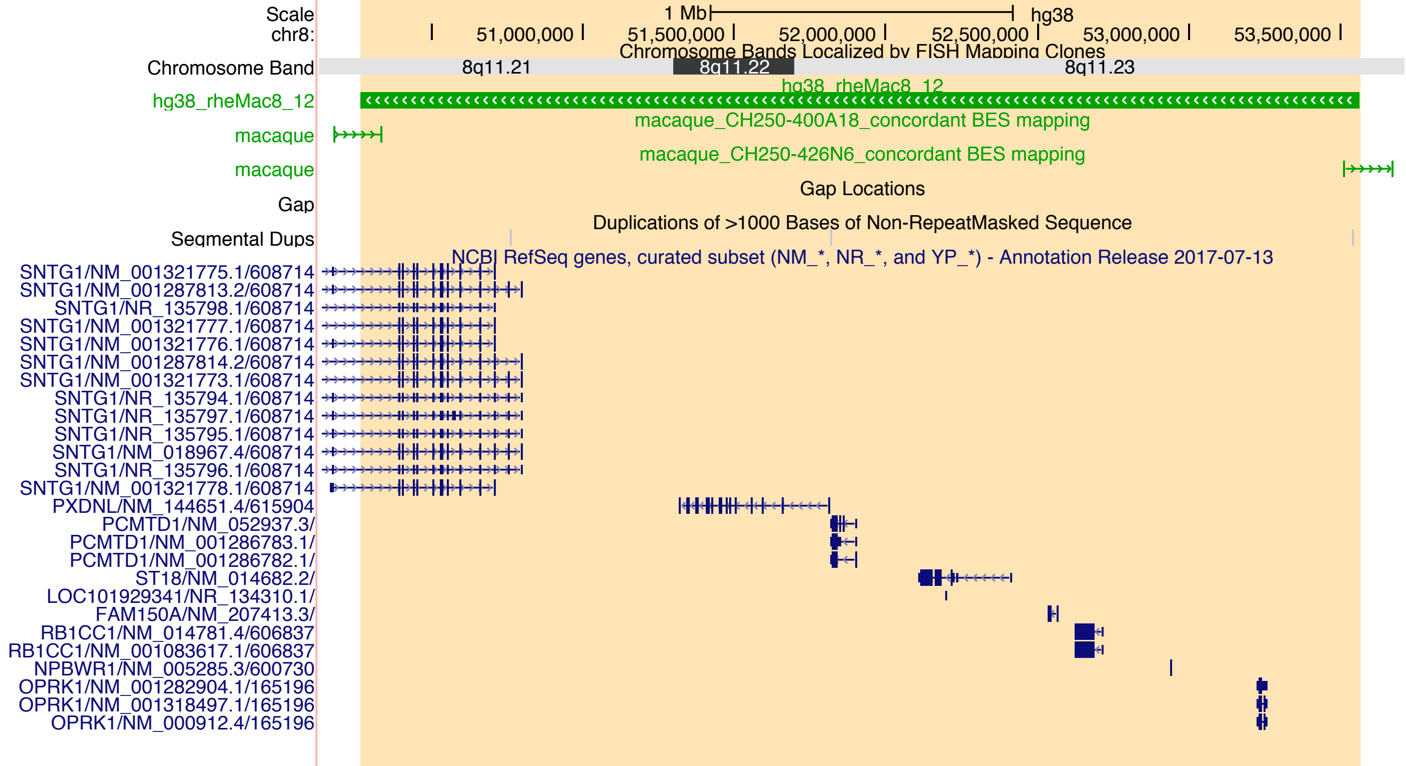
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Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
8q11.21
8q11.22
8q11.23
hg38_rheMac8_12
hg38_rheMac8_12
macaque_CH250-400A18_concordant BES mapping
macaque
macaque_CH250-426N6_concordant BES mapping
macaque
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset (NM_*, NR_*, and YP_*) - Annotation Release 2017-07-13
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SNTG1/NM_018967.4/608714
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PXDNL/NM_144651.4/615904
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ST18/NM_014682.2/
LOC101929341/NR_134310.1/
FAM150A/NM_207413.3/
RB1CC1/NM_014781.4/606837
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NPBWR1/NM_005285.3/600730
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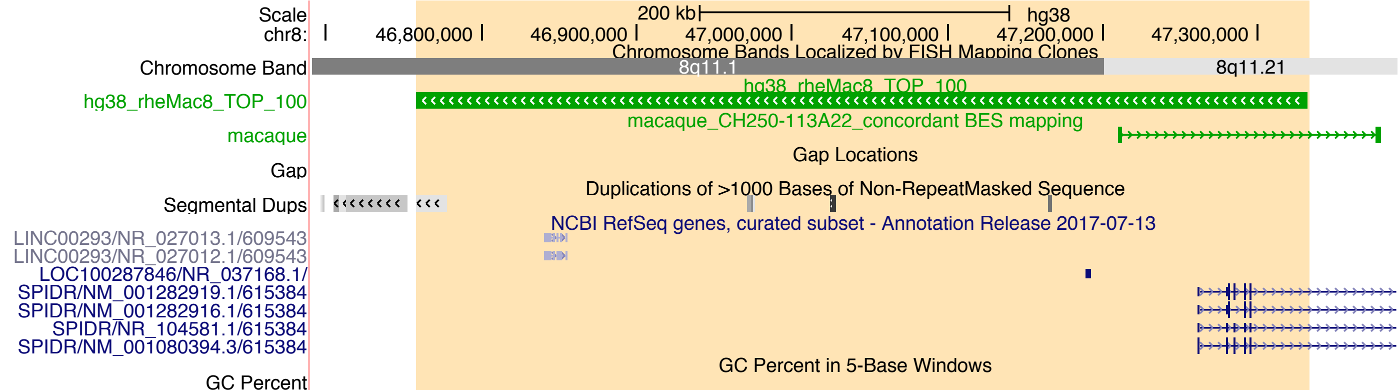
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Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
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8q11.21
hg38_rheMac8_TOP_100
hg38_rheMac8_TOP_100
macaque_CH250-113A22_concordant BES mapping
macaque
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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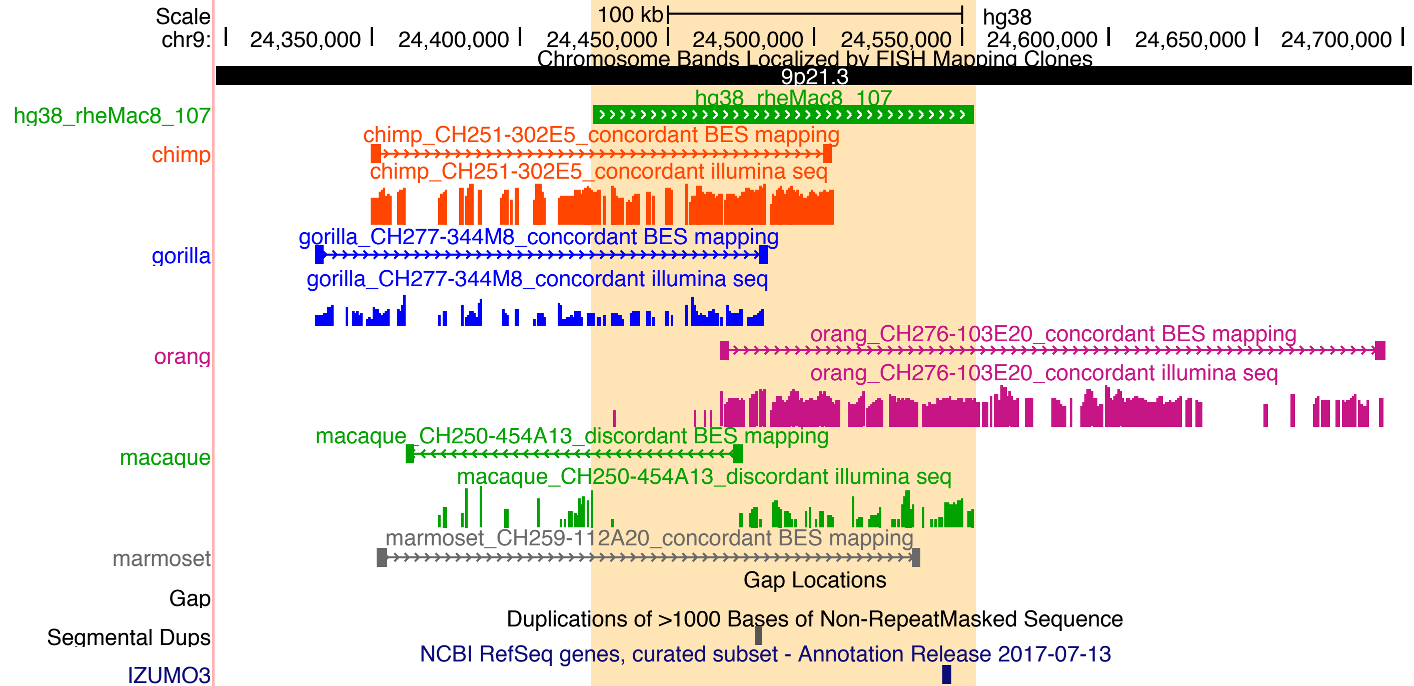
GC Percent in 5-Base Windows
GC Percent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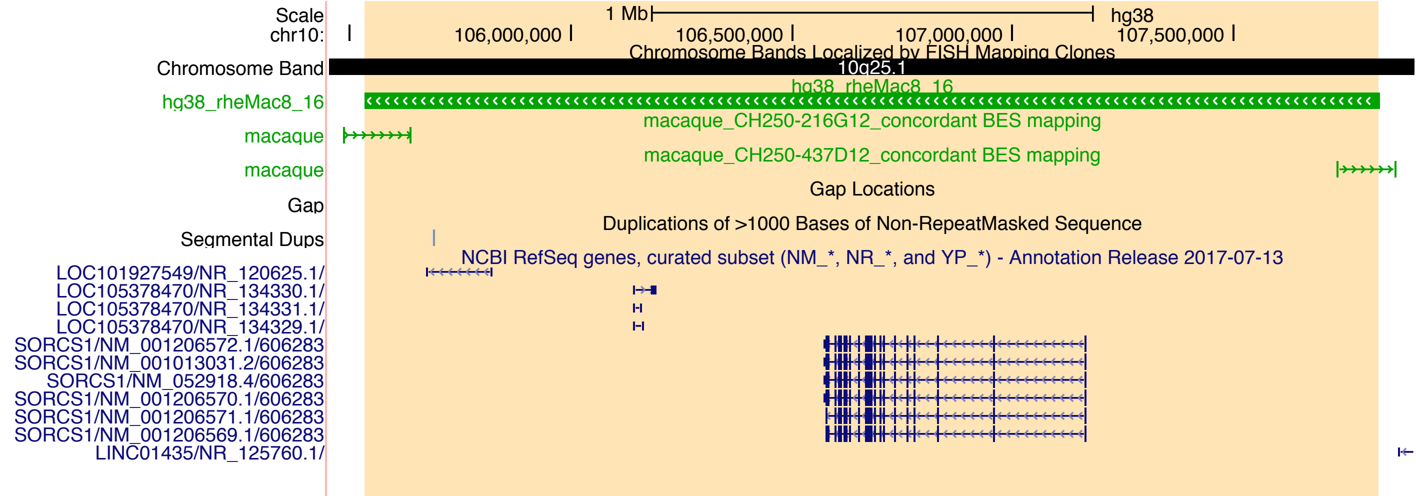
Chromosome Bands Localized by FISH Mapping Clones
9p21.3
hg38_rheMac8_107
hg38_rheMac8_107
chimp
chimp_CH251-302E5_concordant BES mapping
chimp_CH251-302E5_concordant illumina seq
gorilla
gorilla_CH277-344M8_concordant BES mapping
gorilla_CH277-344M8_concordant illumina seq
orang
orang_CH276-103E20_concordant BES mapping
orang_CH276-103E20_concordant illumina seq
macaque
macaque_CH250-454A13_discordant BES mapping
macaque_CH250-454A13_discordant illumina seq
marmoset
marmoset_CH259-112A20_concordant BES mapping
Gap
Gap Locations
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
IZUMO3
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13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Chromosome Bands Localized by FISH Mapping Clones
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hg38_rheMac8_16
macaque_CH250-216G12_concordant BES mapping
macaque
macaque_CH250-437D12_concordant BES mapping
macaque
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset (NM_*, NR_*, and YP_*) - Annotation Release 2017-07-13
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SORCS1/NM_052918.4/606283
SORCS1/NM_001206570.1/606283
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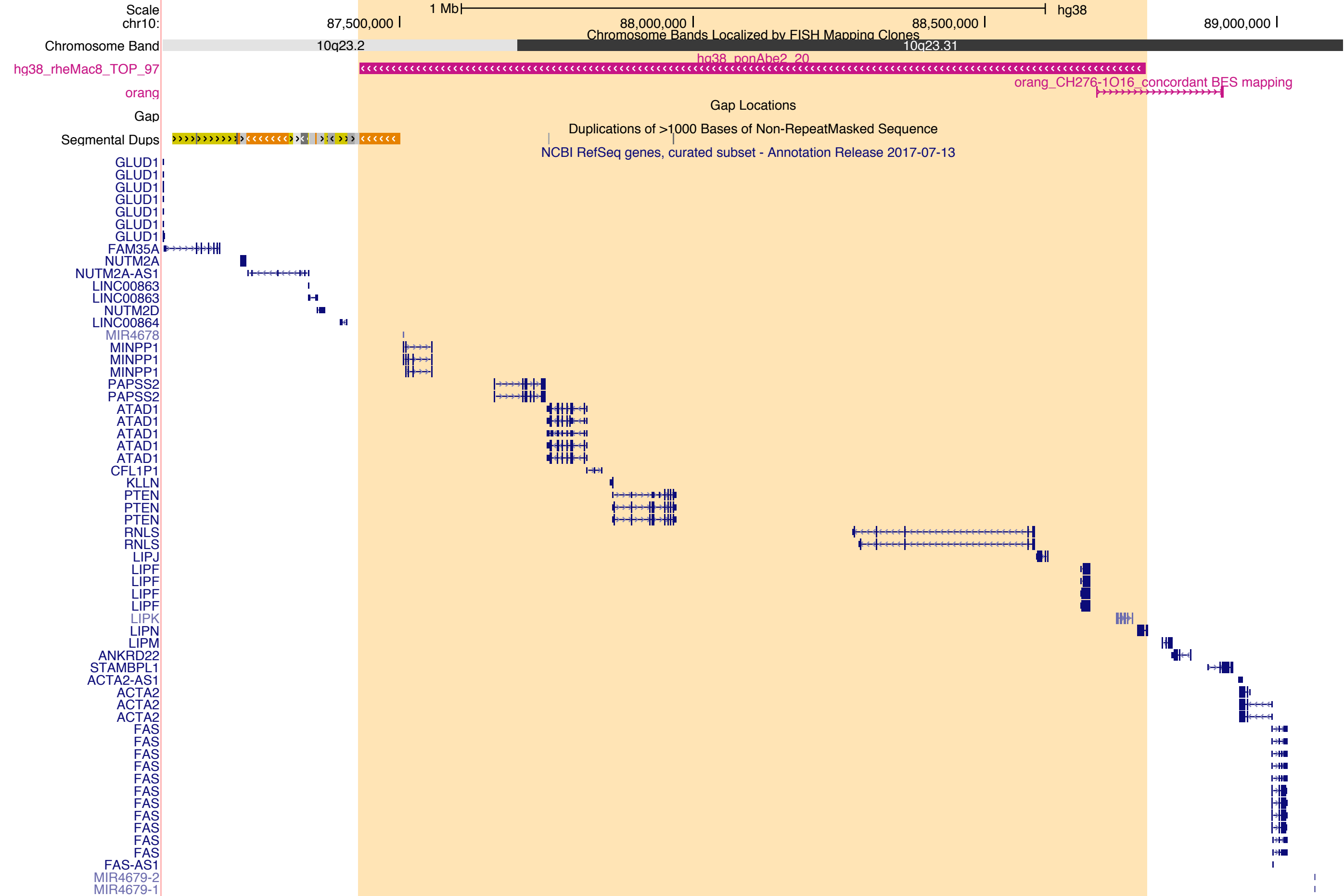
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Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
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10q23.31
hg38_rheMac8_TOP_97
hg38_ponAbe2_20
orang
orang_CH276-1O16_concordant BES mapping
Gap
Gap Locations
Segmental Dups
Duplications of >1000 Bases of Non-RepeatMasked Sequence
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
GLUD1
GLUD1
GLUD1
GLUD1
GLUD1
GLUD1
GLUD1
FAM35A
NUTM2A
NUTM2A-AS1
LINC00863
LINC00863
NUTM2D
LINC00864
MIR4678
MINPP1
MINPP1
MINPP1
PAPSS2
PAPSS2
ATAD1
ATAD1
ATAD1
ATAD1
ATAD1
CFL1P1
KLLN
PTEN
PTEN
PTEN
RNLS
RNLS
LIPJ
LIPF
LIPF
LIPF
LIPF
LIPK
LIPN
LIPM
ANKRD22
STAMBPL1
ACTA2-AS1
ACTA2
ACTA2
ACTA2
FAS
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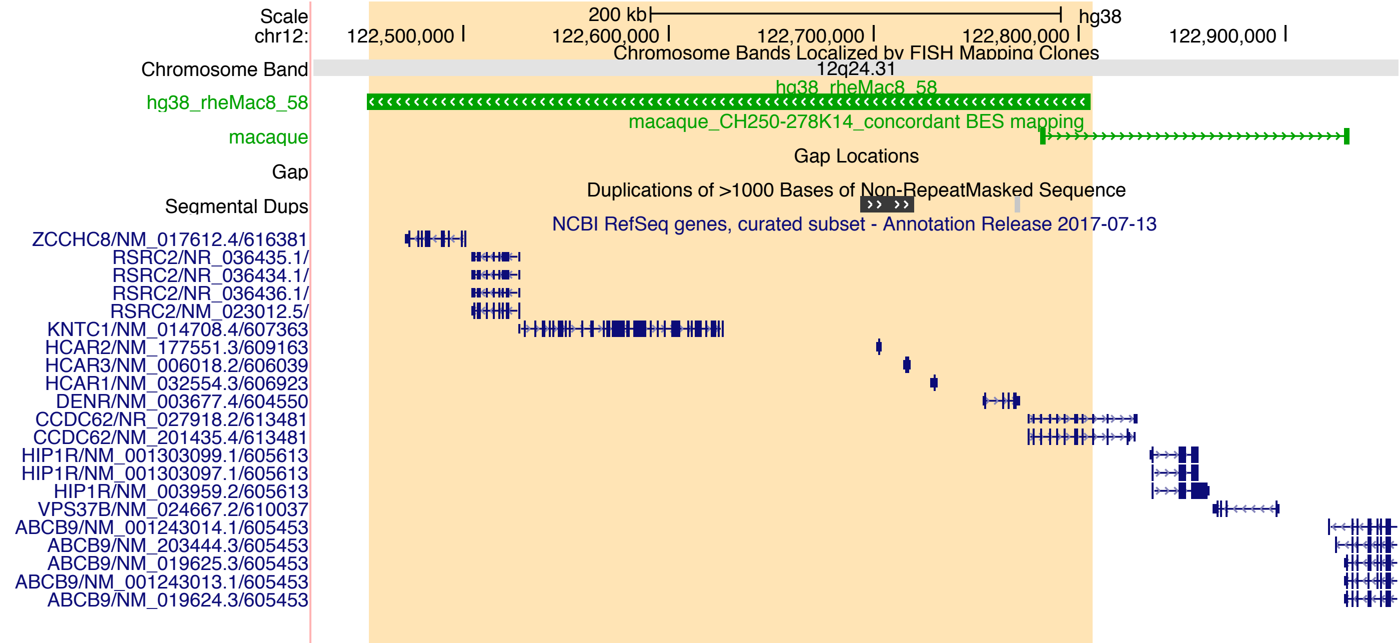
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Chromosome Band
12q24.31
hg38_rheMac8_58
hg38_rheMac8_58
macaque_CH250-278K14_concordant BES mapping
macaque
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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RSRC2/NR_036434.1/
RSRC2/NR_036436.1/
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KNTC1/NM_014708.4/607363
HCAR2/NM_177551.3/609163
HCAR3/NM_006018.2/606039
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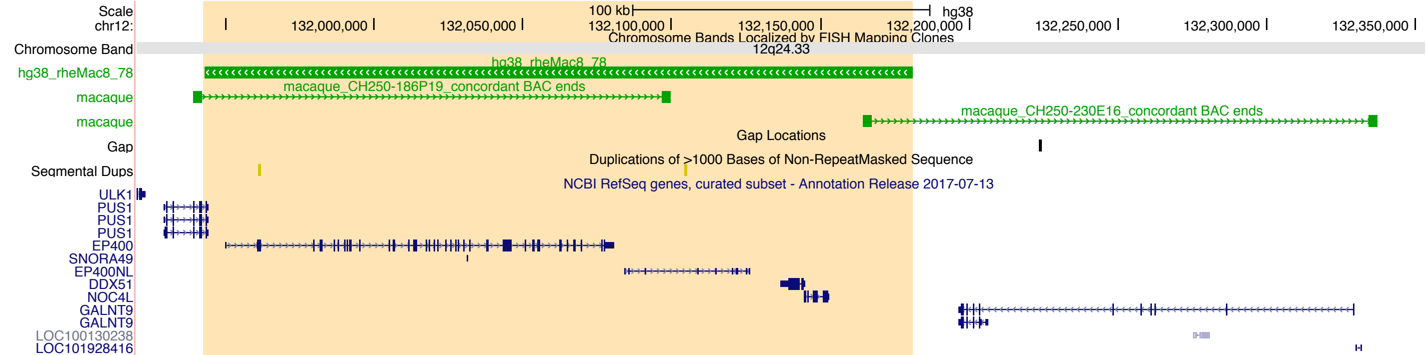
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Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
12q24.33
hg38_rheMac8_78
hg38_rheMac8_78
macaque_CH250-186P19_concordant BAC ends
macaque
macaque
macaque_CH250-230E16_concordant BAC ends
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
ULK1
PUS1
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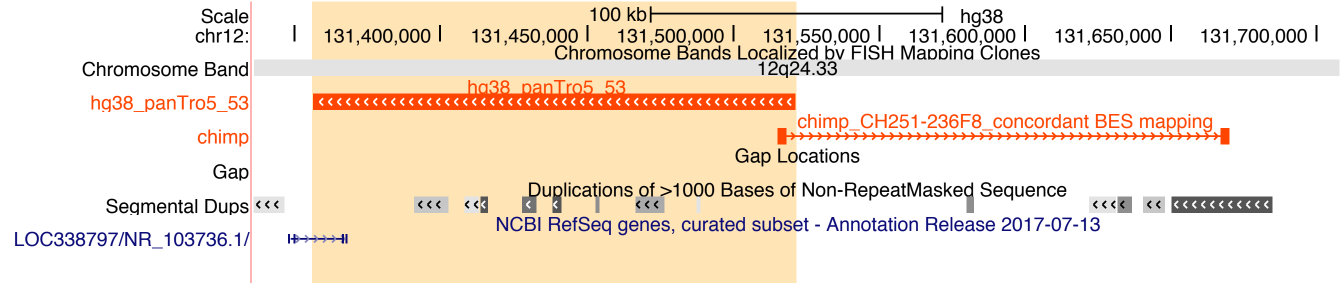
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Chromosome Band
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hg38_panTro5_53
chimp
chimp_CH251-236F8_concordant BES mapping
Gap Locations
Gap
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Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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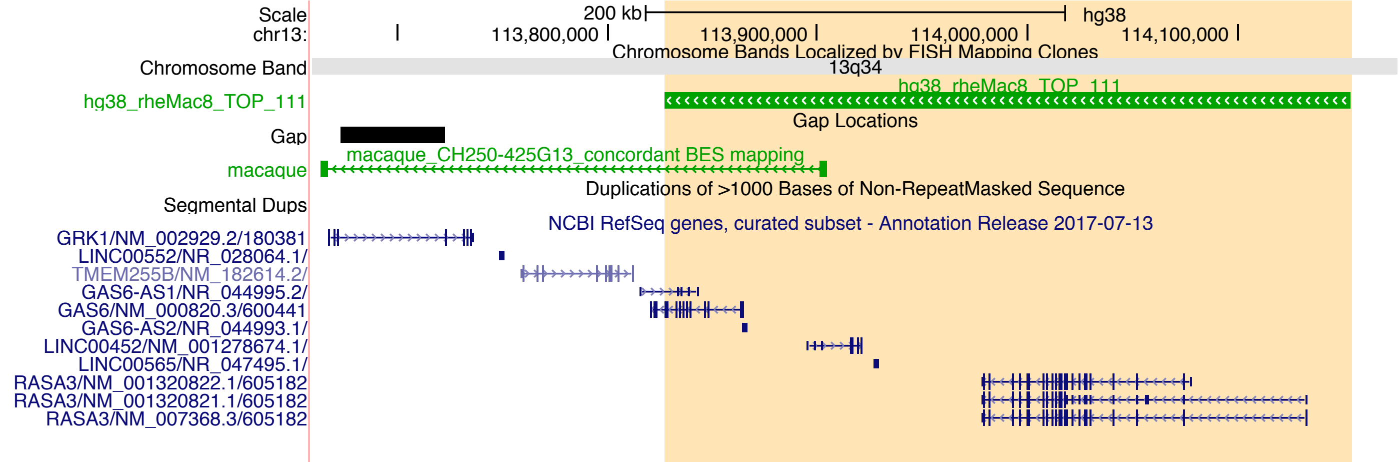
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hg38_rheMac8_TOP_111
Gap Locations
Gap
macaque_CH250-425G13_concordant BES mapping
macaque
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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GAS6-AS2/NR_044993.1/
LINC00452/NM_001278674.1/
LINC00565/NR_047495.1/
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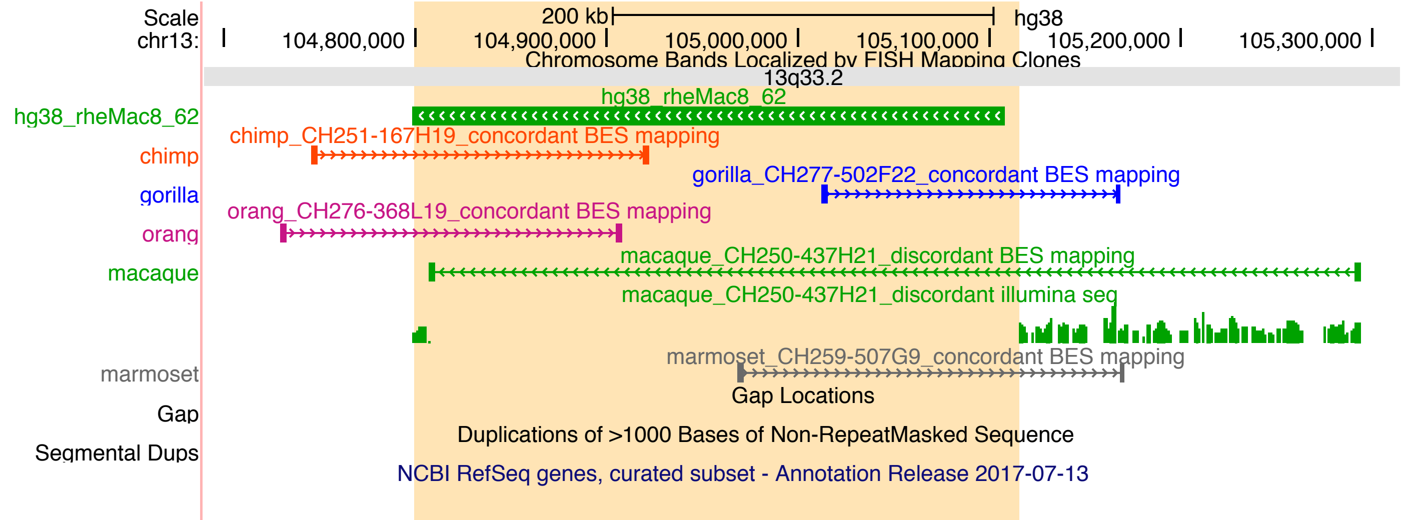
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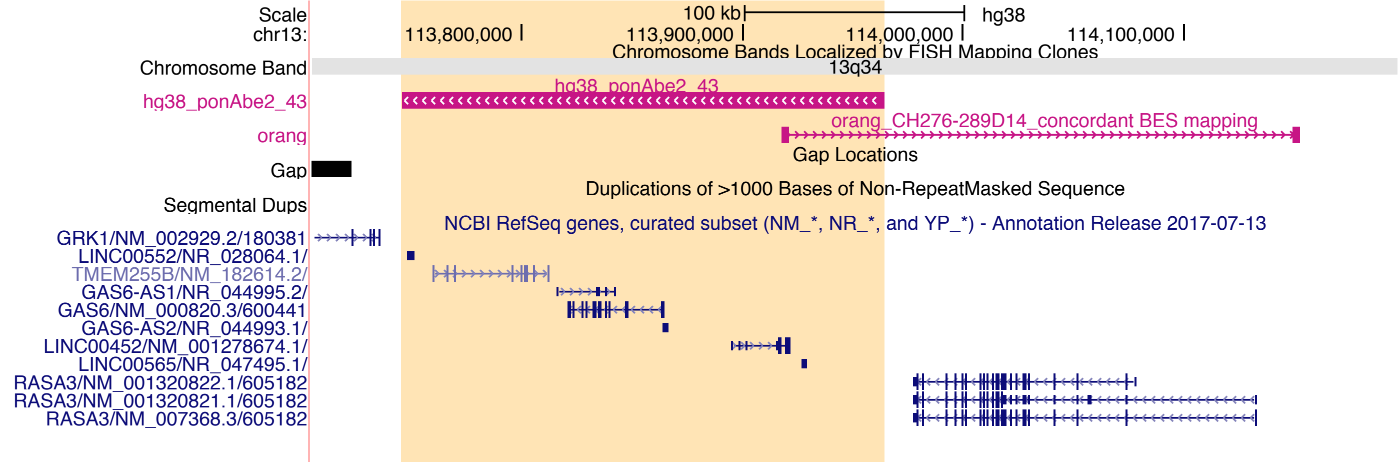
hg38_rheMac8_62
chimp_CH251-167H19_concordant BES mapping
chimp
gorilla_CH277-502F22_concordant BES mapping
gorilla
orang_CH276-368L19_concordant BES mapping
orang
macaque_CH250-437H21_discordant BES mapping
macaque
macaque_CH250-437H21_discordant illumina seq
marmoset_CH259-507G9_concordant BES mapping
marmoset
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13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hg38_ponAbe2_43
orang
orang_CH276-289D14_concordant BES mapping
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset (NM_*, NR_*, and YP_*) - Annotation Release 2017-07-13
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LINC00565/NR_047495.1/
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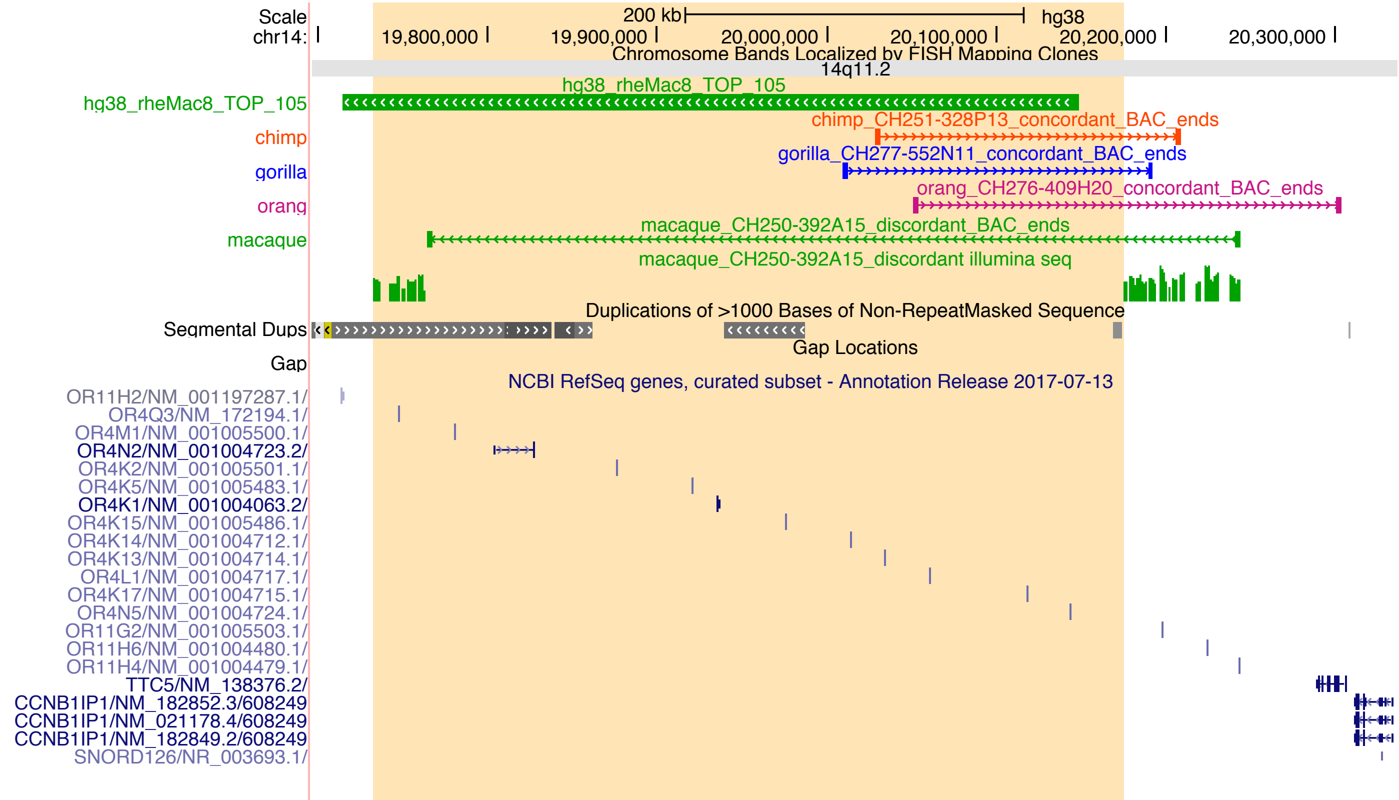
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hg38_rheMac8_TOP_105
chimp
chimp_CH251-328P13_concordant_BAC_ends
gorilla
gorilla_CH277-552N11_concordant_BAC_ends
orang
orang_CH276-409H20_concordant_BAC_ends
macaque
macaque_CH250-392A15_discordant_BAC_ends
macaque_CH250-392A15_discordant illumina seq
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
Gap Locations
Gap
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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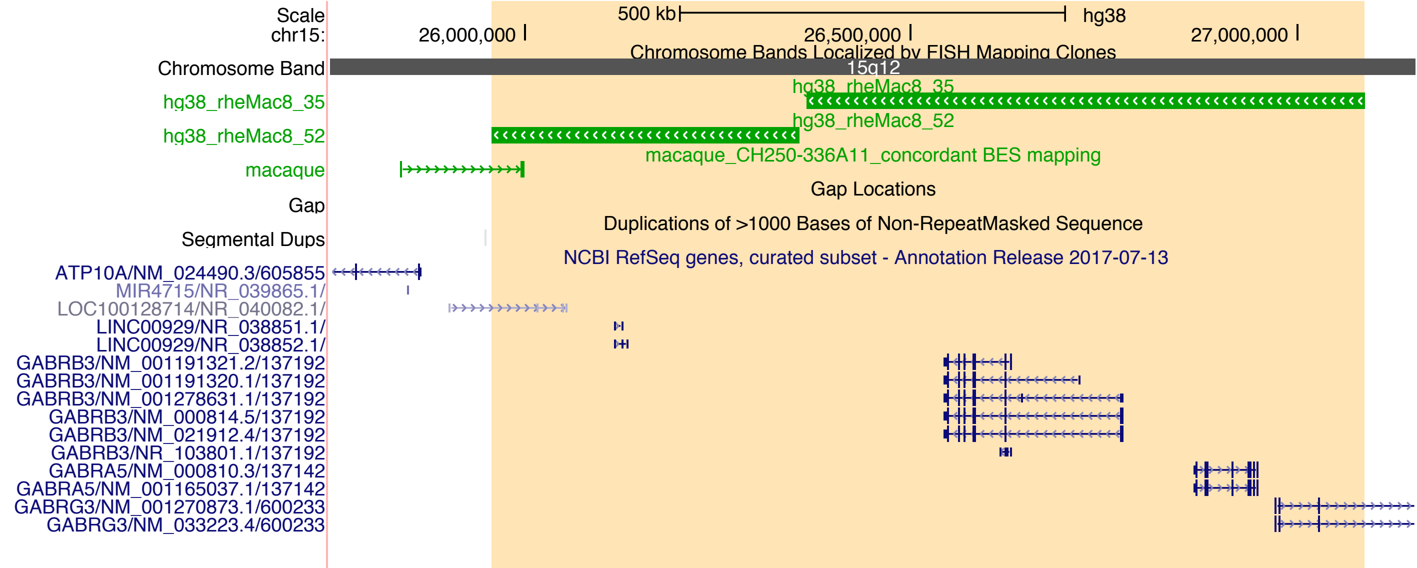
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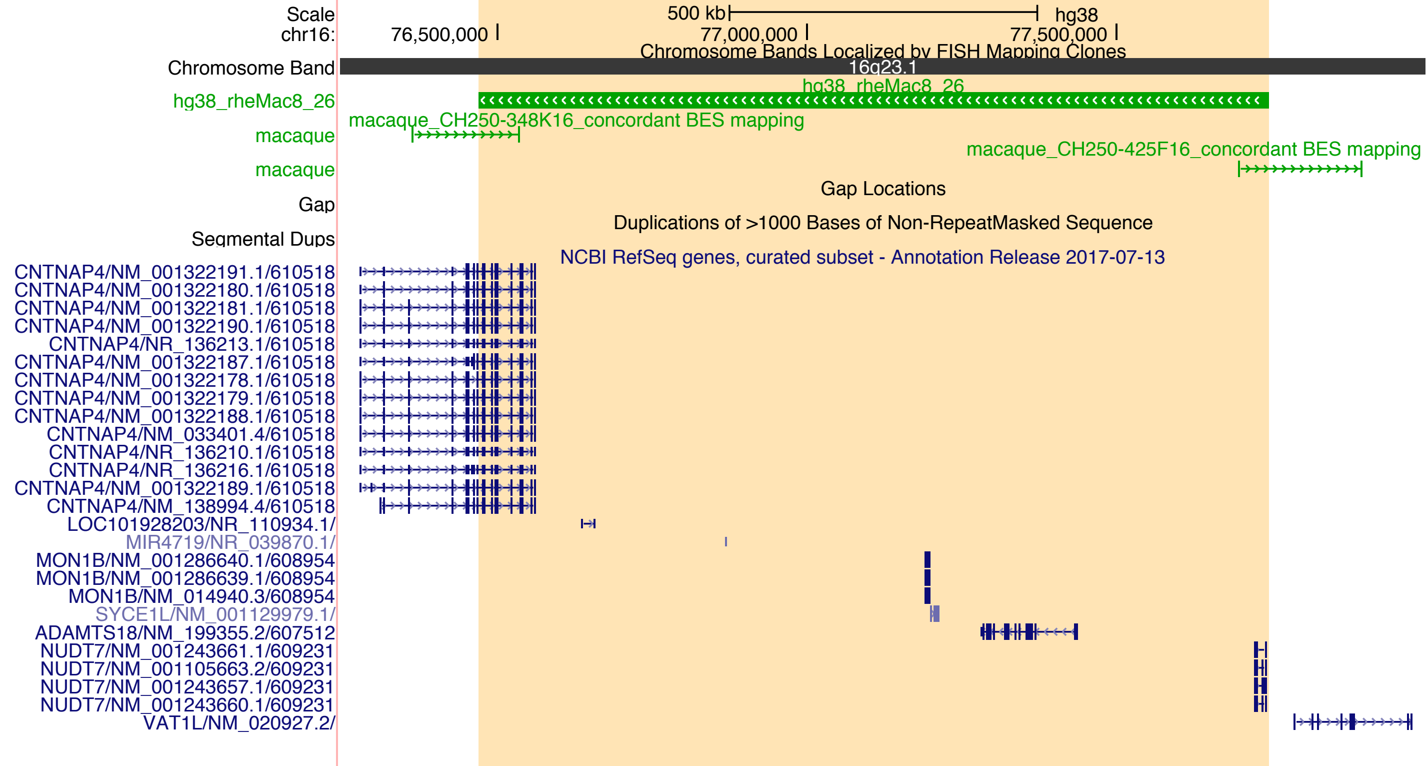
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macaque
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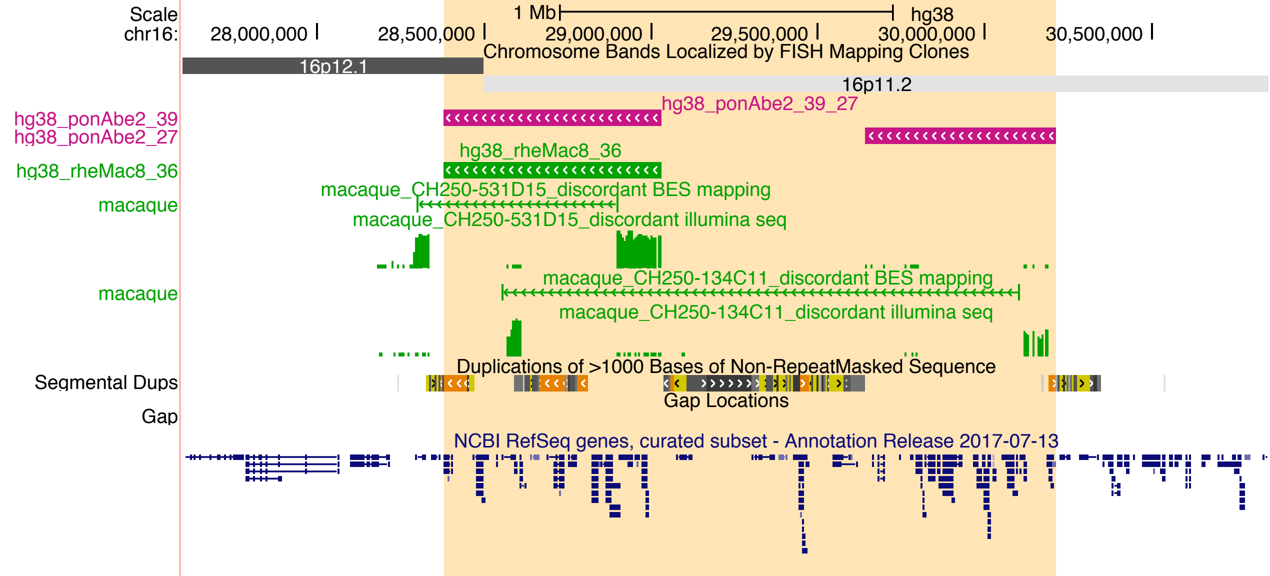
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Segmental Dups
Gap Locations
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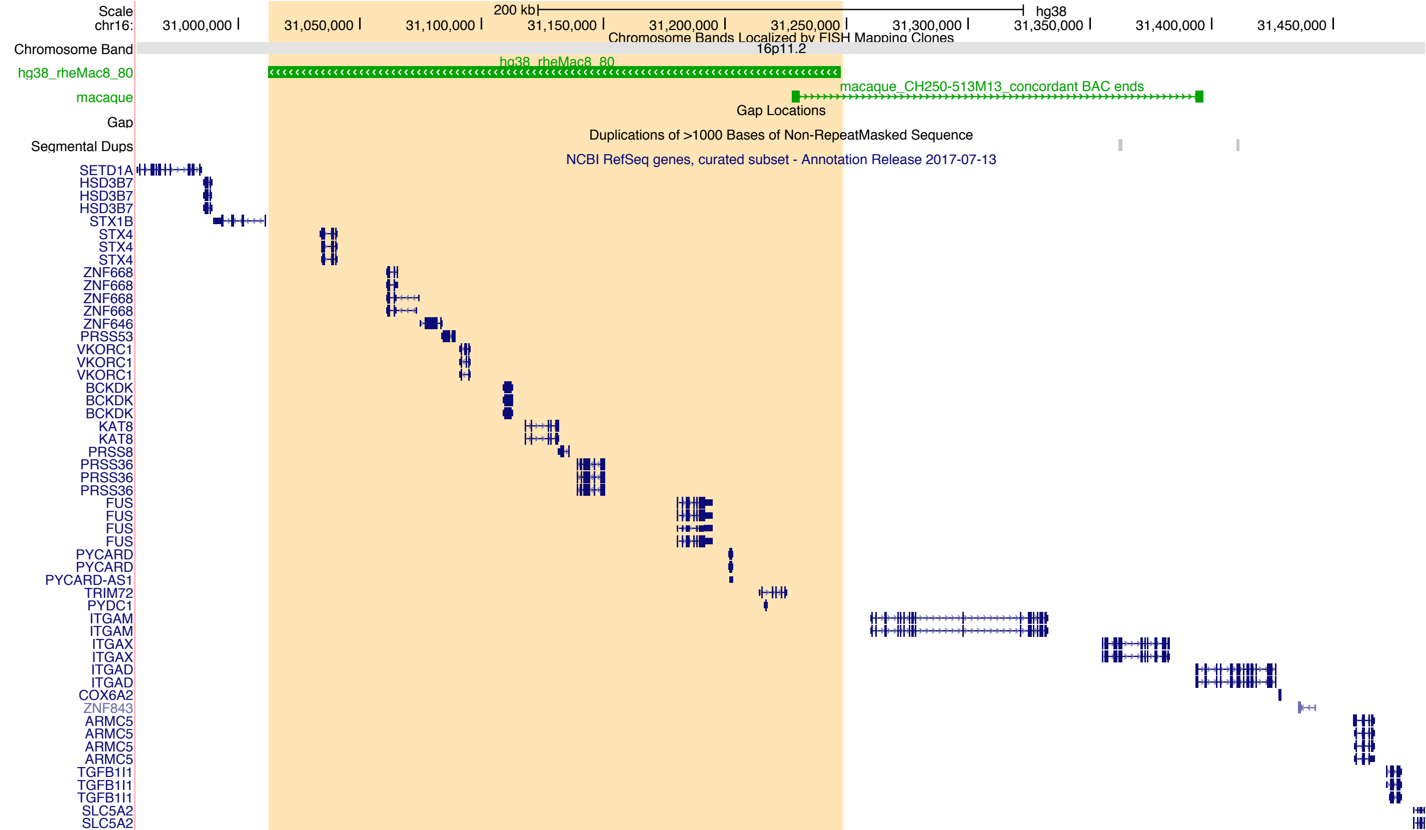
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13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HSD3B7
STX1B
STX4
STX4
STX4
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VKORC1
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BCKDK
BCKDK
KAT8
KAT8
PRSS8
PRSS36
PRSS36
PRSS36
FUS
FUS
FUS
FUS
PYCARD
PYCARD
PYCARD-AS1
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PYDC1
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ITGAX
ITGAX
ITGAD
ITGAD
COX6A2
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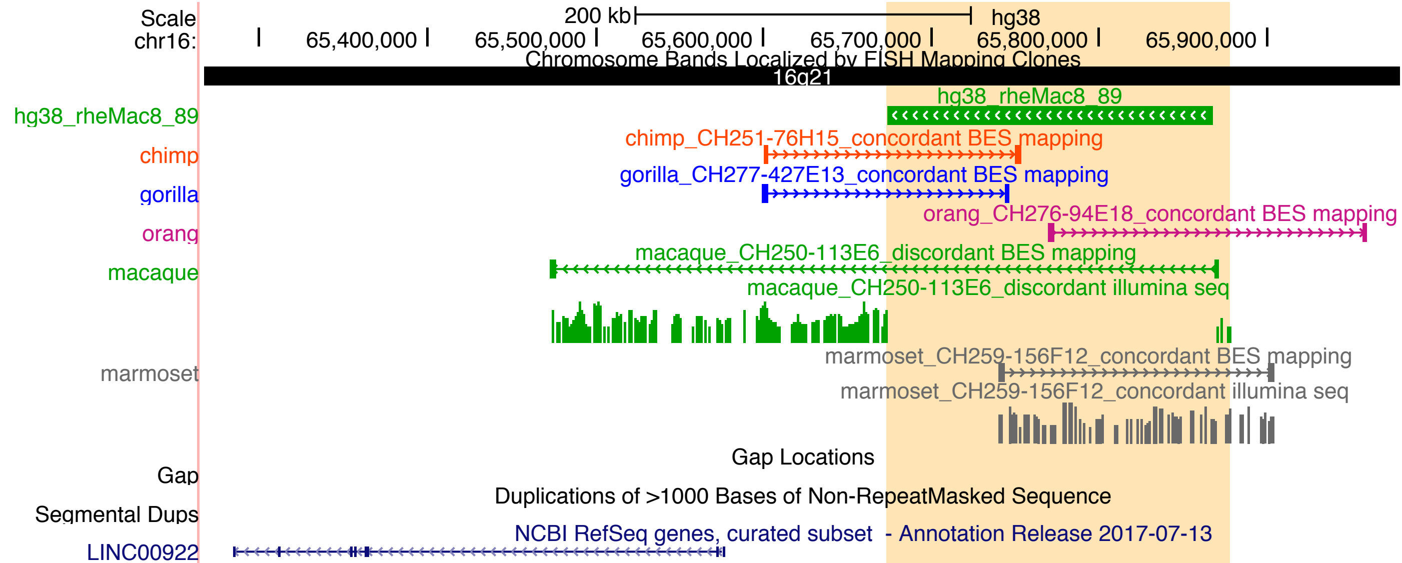
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gorilla
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orang
orang_CH276-94E18_concordant BES mapping
macaque
macaque_CH250-113E6_discordant BES mapping
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marmoset_CH259-156F12_concordant BES mapping
marmoset_CH259-156F12_concordant illumina seq
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Gap Locations
Segmental Dups
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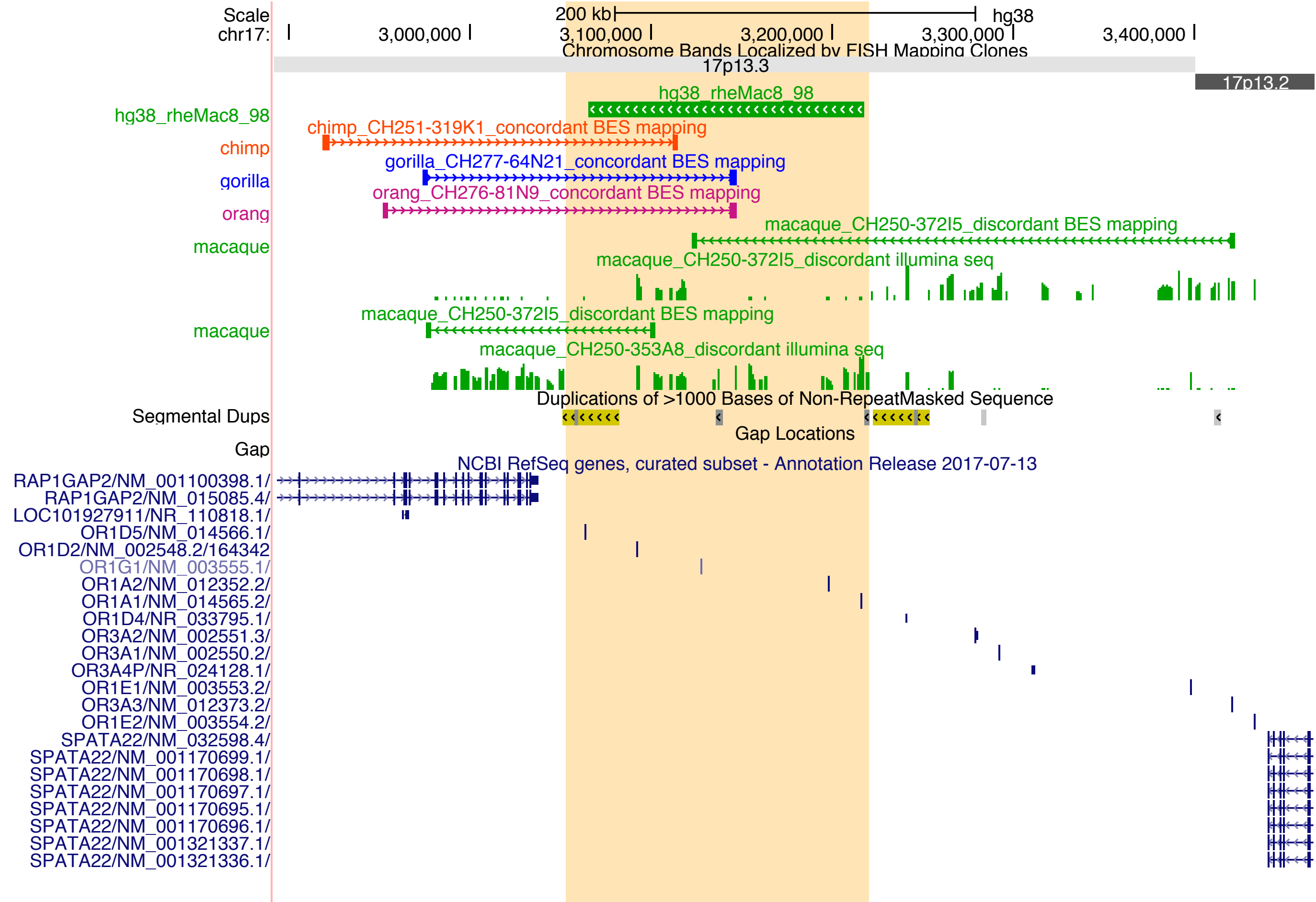
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orang
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macaque
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macaque
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OR1A1/NM_014565.2/
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OR3A1/NM_002550.2/
OR3A4P/NR_024128.1/
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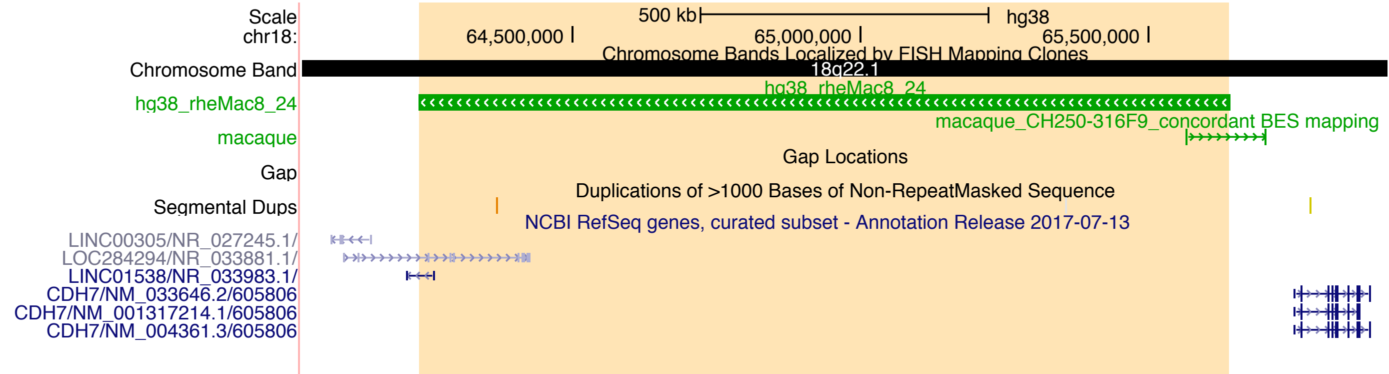
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macaque
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
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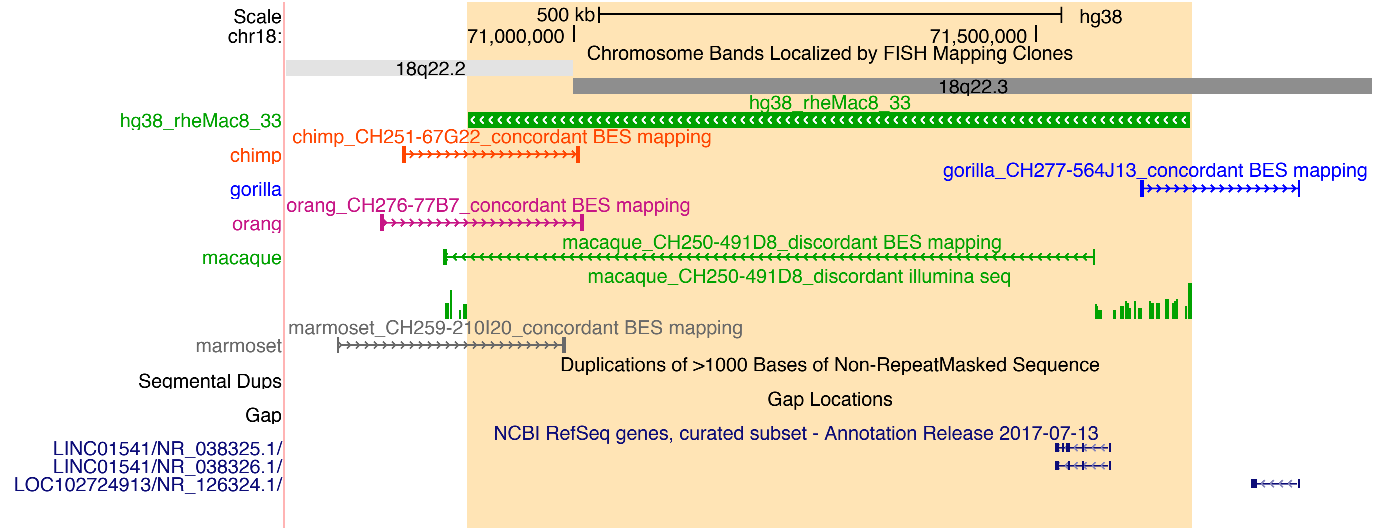
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gorilla
orang_CH276-77B7_concordant BES mapping
orang
macaque_CH250-491D8_discordant BES mapping
macaque
macaque_CH250-491D8_discordant illumina seq
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marmoset
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
Gap Locations
Gap
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
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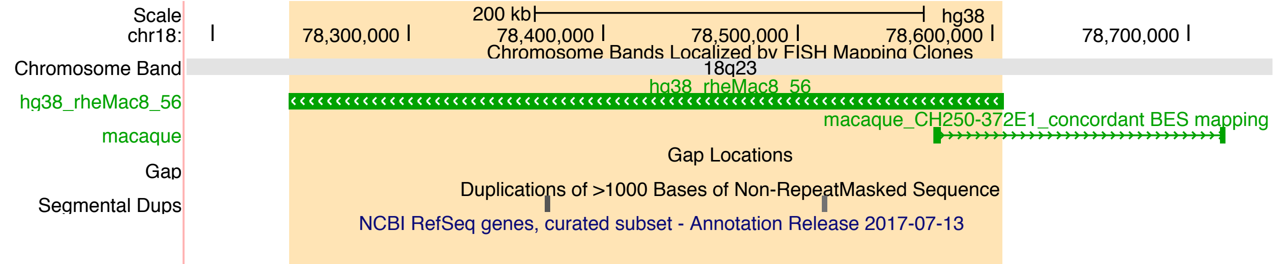
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Gap
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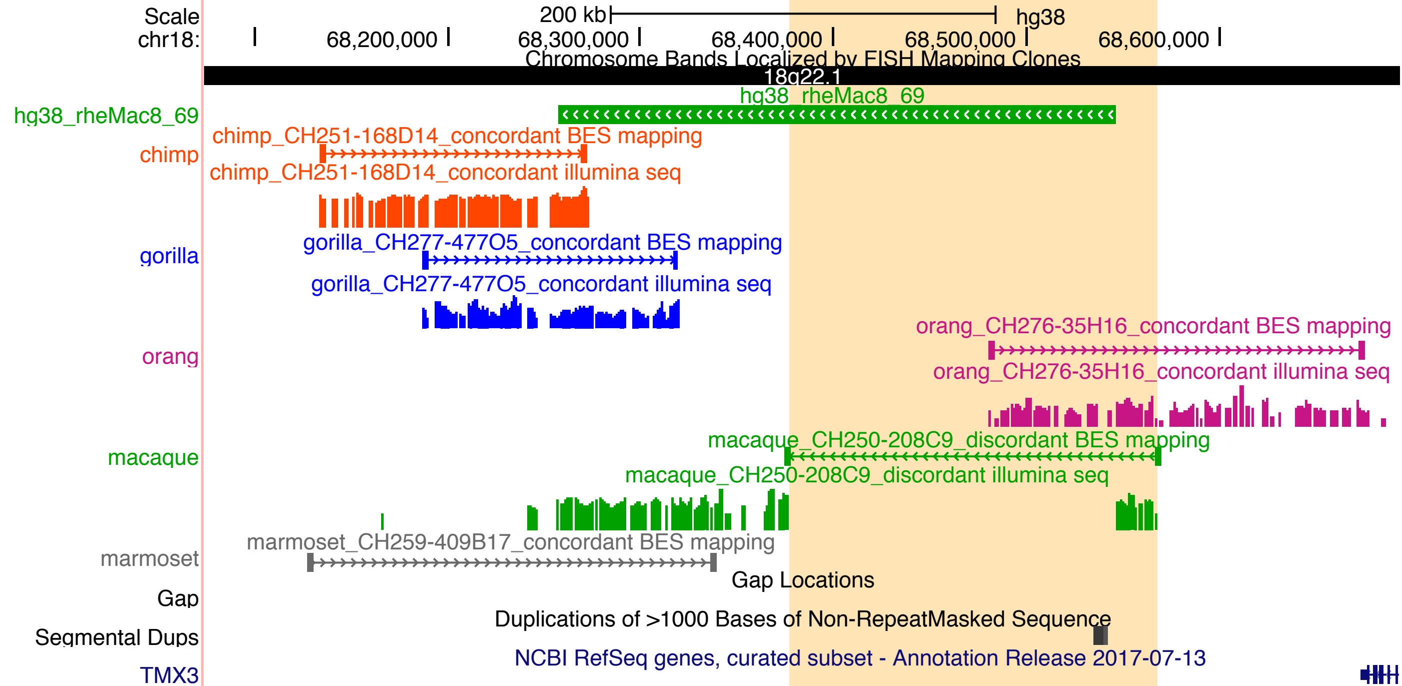
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13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Segmental Dups
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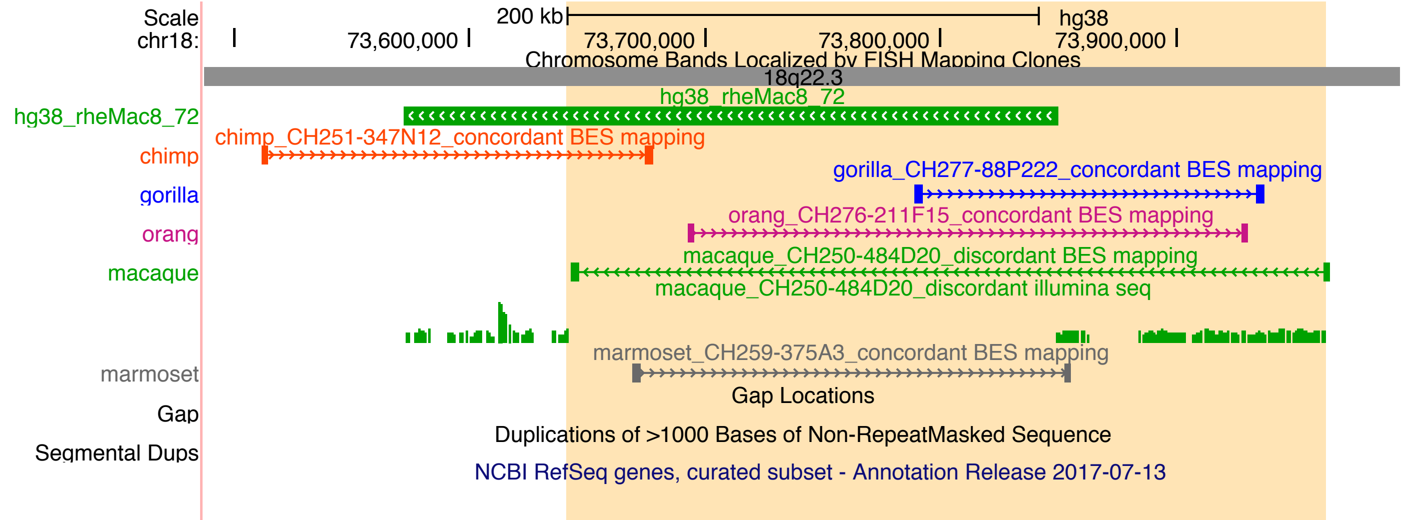
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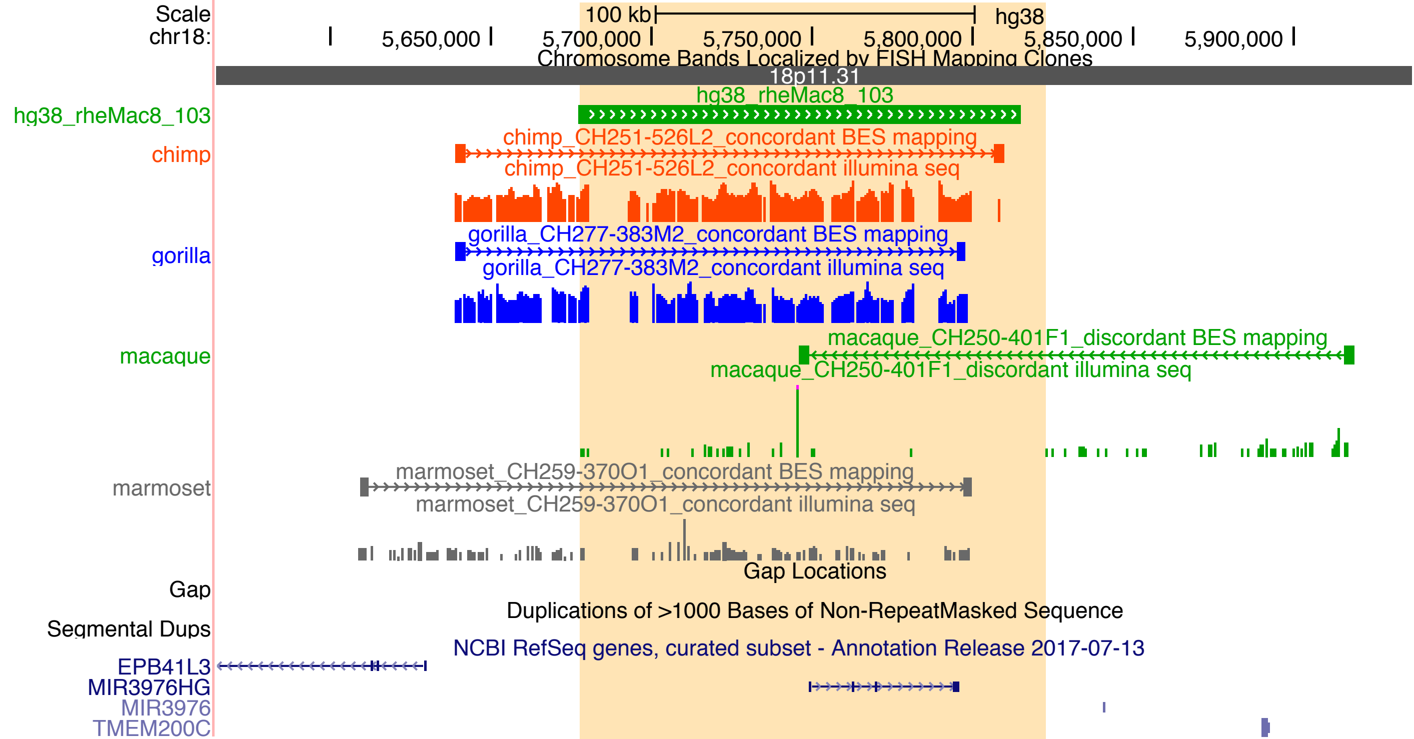
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Gap Locations
Segmental Dups
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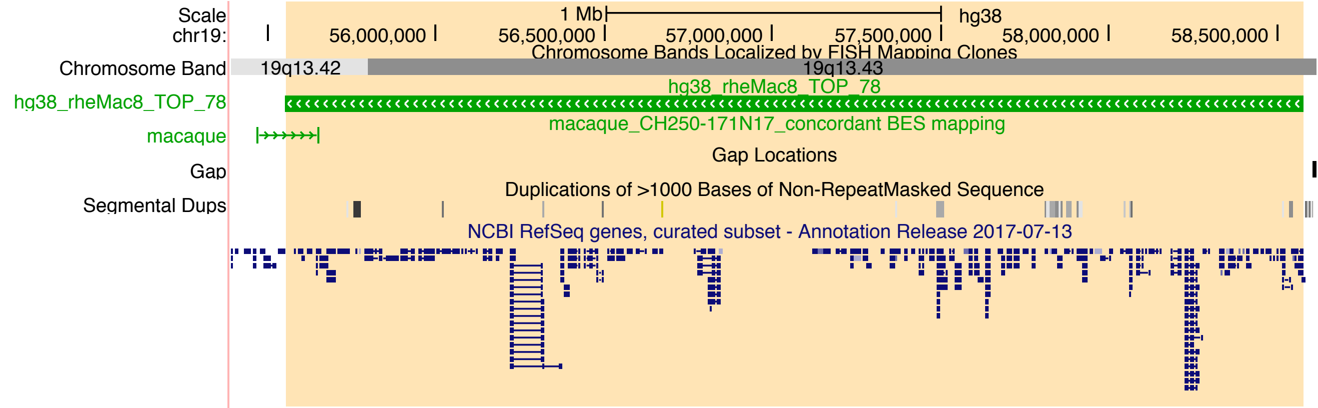
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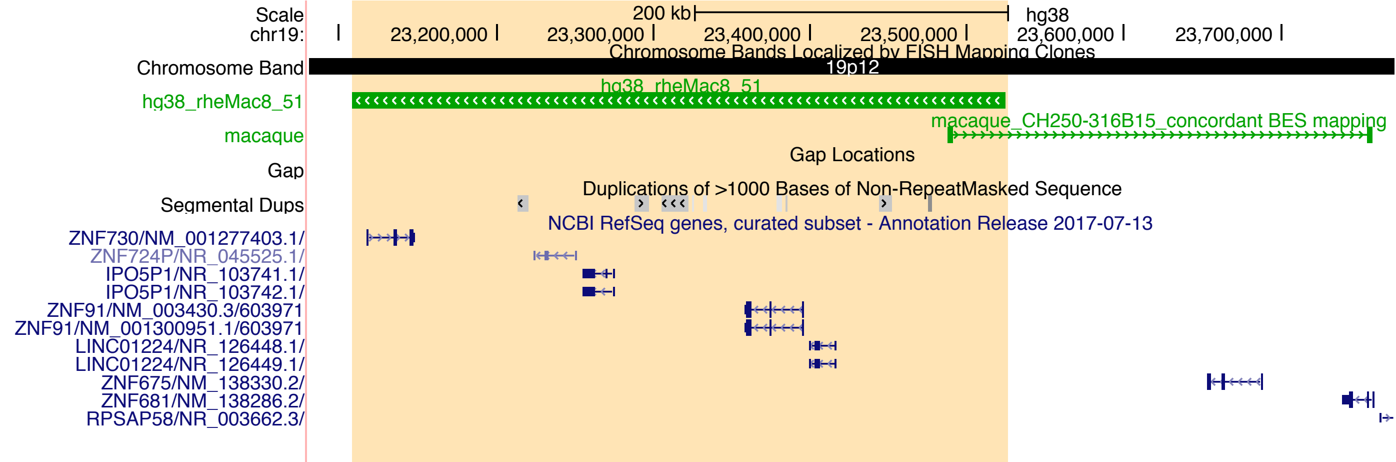
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13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macaque
Gap Locations
Gap
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Segmental Dups
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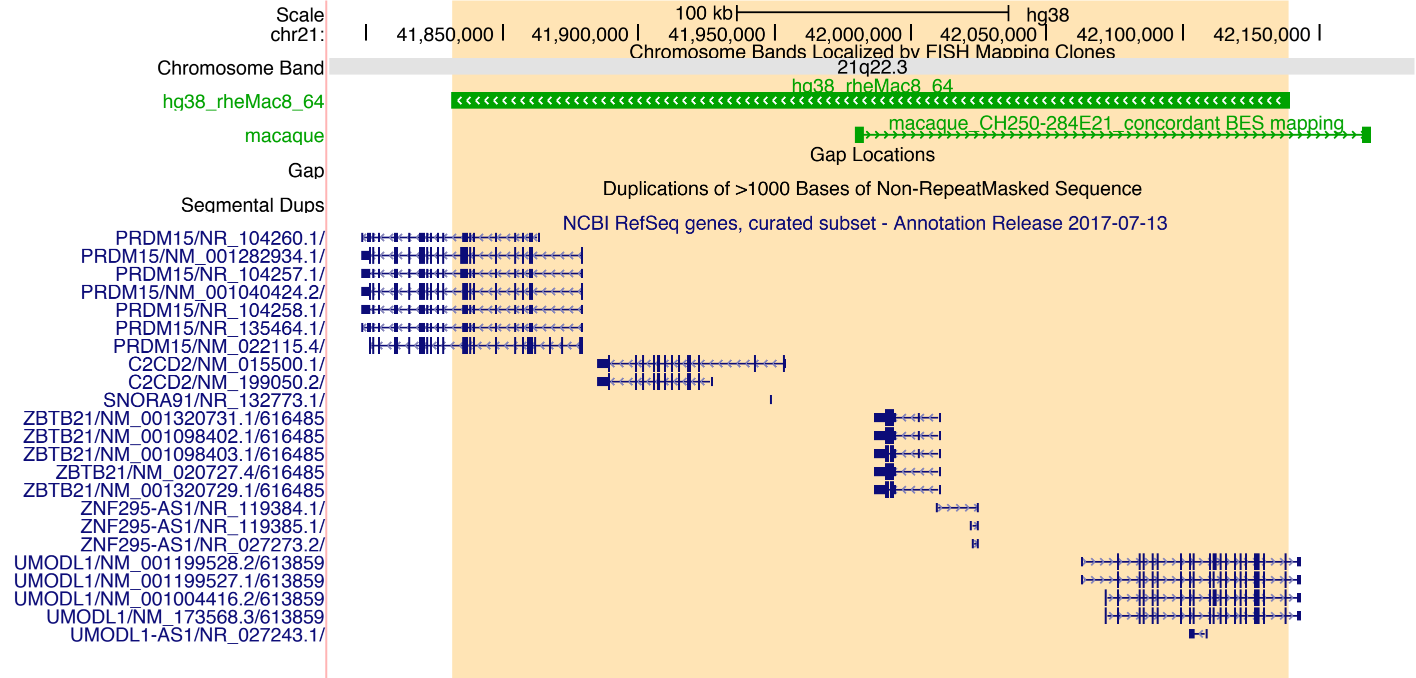
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Gap Locations
Gap
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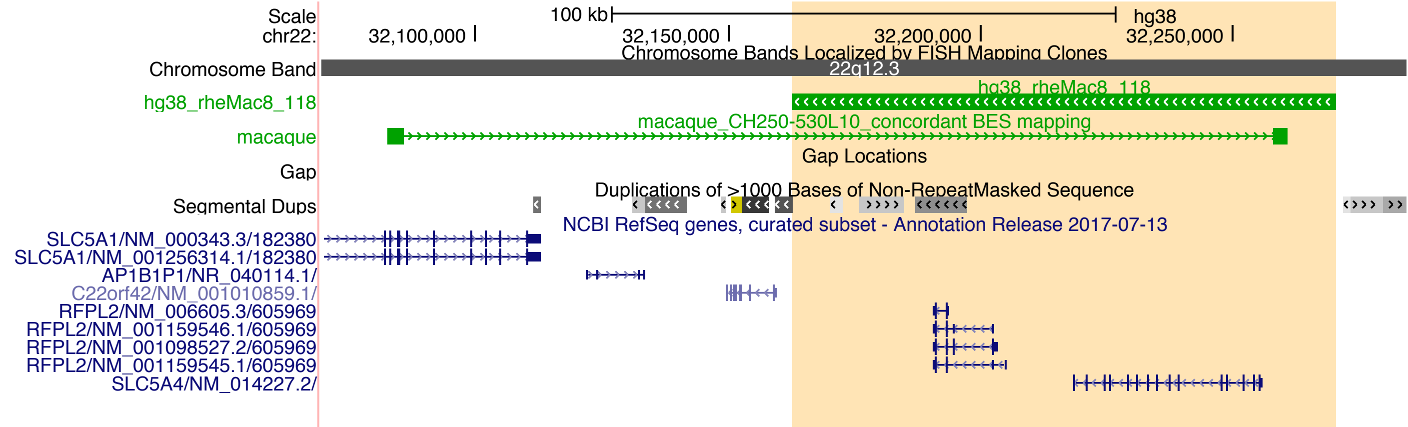
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macaque_CH250-530L10_concordant BES mapping
macaque
Gap Locations
Gap
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Segmental Dups
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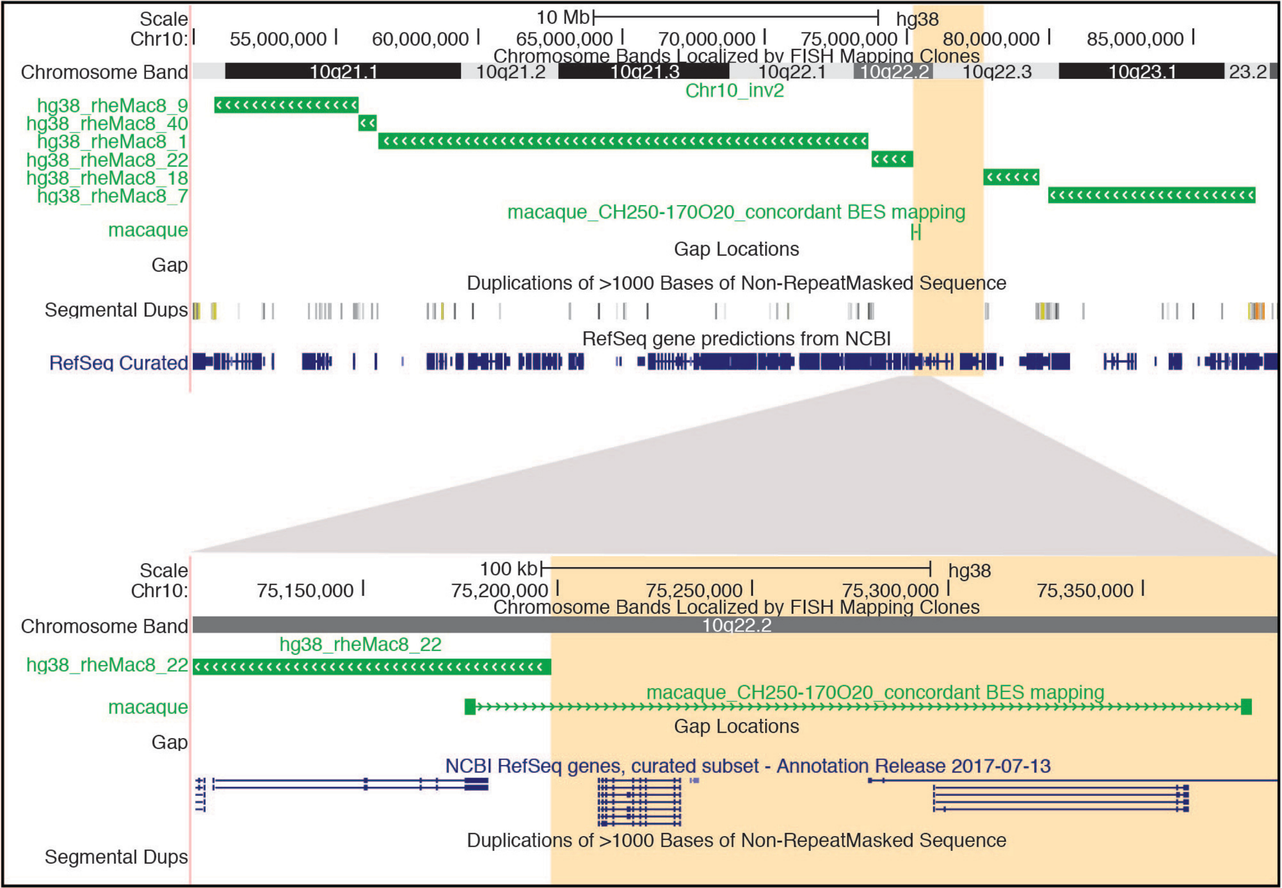
Supplemental Fig. S4. Experimental validation by BES pair mapping and Illumina sequencing of BAC clones.

UCSC Genome Browser views of all the inversion calls tested by Illumina sequencing and/or BES pair mapping. All BAC clones spanning the breakpoints of the predicted regions are shown as colored segments. Illumina sequenced discordant clones mapping at the breakpoints of the inversions appear as discontinuous. BES pair mapping of discordant clones supporting the inversion have end pairs that map abnormally far apart and have ends that are incorrectly oriented when mapped to the human reference genome sequence. Segmental duplications, sequence gaps and RefSeq curated genes are also shown for each event.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10q21.3
10q22.1
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23.2
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hg38_rheMac8_40
hg38_rheMac8_1
hg38_rheMac8_22
hg38_rheMac8_18
hg38_rheMac8_7
macaque_CH250-170O20_concordant BES mapping
macaque
Gap Locations
Gap
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups
RefSeq gene predictions from NCBI
RefSeq Curated
Scale
100 kb
hg38
Chr10:
75,150,000
75,200,000
75,250,000
75,300,000
75,350,000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
10q22.2
hg38_rheMac8_22
hg38_rheMac8_22
macaque_CH250-170O20_concordant BES mapping
macaque
Gap Locations
Gap
NCBI RefSeq genes, curated subset - Annotation Release 2017-07-13
Duplications of >1000 Bases of Non-RepeatMasked Sequence
Segmental Dups

Supplemental Fig. S5. Example of a misassembled region in the macaque genome.

The cytogenetic inversion on human Chromosome 10 is 36.5 Mb in size and was detected as six separate smaller inversion calls. Nevertheless, the calls hg38_rheMac8_22 and hg38_rheMac8_18 are interrupted by an interval of 2.5 Mb of sequence in direct orientation. We investigated the orientation of this region by BES pair mapping. Clone CH250-170O20, spanning the proximal breakpoint of this region, demonstrates that it is in the same orientation of its flanking sequences and therefore represents an assembly error.