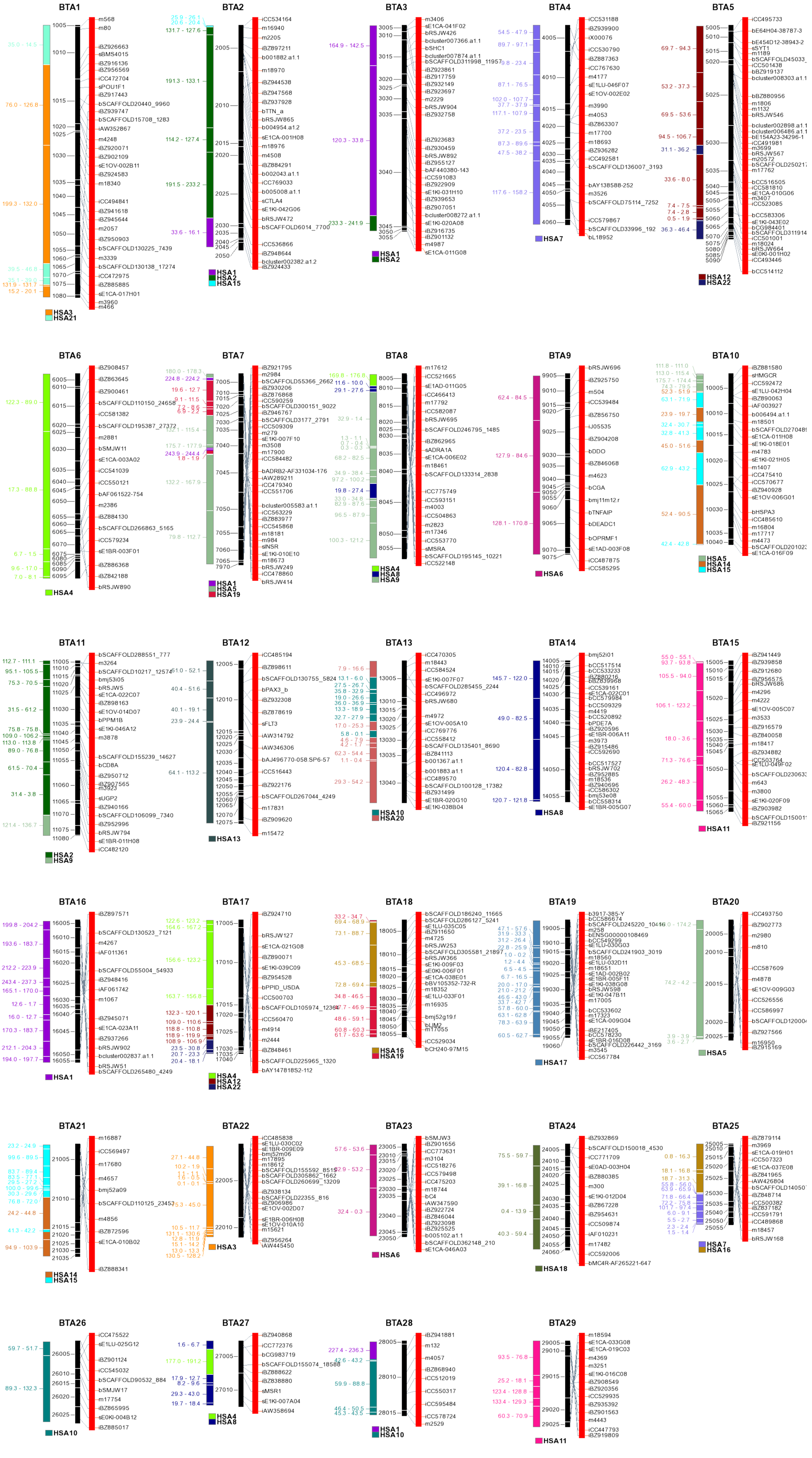
Legend. Coverage of the bovine autosomes by fingerprint contigs and comparative mapping to the human genome (UCSC hg18 assembly). Fingerprint contigs are represented by black boxes in the middle of each chromosome panel. The first one or two digits of contig names represent the bovine chromosome number (1 to 29). The following digit indicates confidence in contig placement (0=confident; 9=uncertain). The last 2 digits indicate the relative position of the contig on the chromosome (numbered in increments of 5 to allow for future assignment of currently unanchored contigs) arranged according to BAC end sequence alignments with the UCSC hg17 assembly and the ILTX-2004 comparative map (van der Wind et al., 2004). The red bars represent the bovine composite linkage-radiation hybrid map, with marker positions indicated by red ticks. A subset of markers is displayed for reference. Grey lines represent links between BAC clones and mapped markers. Colored boxes to the left of contigs represent syntenic human genomic segments assigned to bovine chromosomes. Syntenic segments are assigned based on bovine BAC end sequence alignment against human genome sequence. Individual human chromosomes are differentially coloured. Coordinates (Mbp start and end) of each segment are indicated. White lines indicate the boundaries of syntenic segments. Boundaries are imposed where there is a change in human chromosome number, a change in orientation within the same human chromosome, or a gap greater than 10% of the last coordinate of the previous syntenic segment. This PDF document contains an oversize page with diagrams for all autosomes, and a page for each autosome.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BTA16
BTA17
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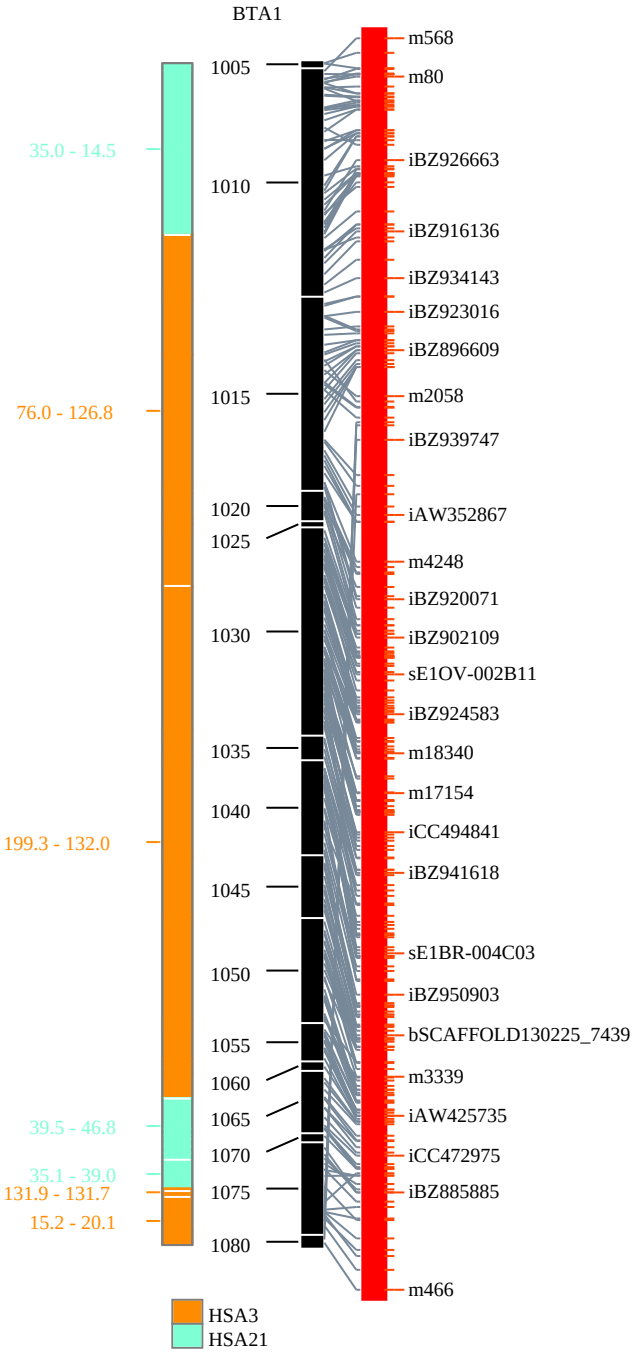
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1080
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76.0 - 126.8
199.3 - 132.0
39.5 - 46.8
35.1 - 39.0
131.9 - 131.7
15.2 - 20.1
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m80
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iBZ923016
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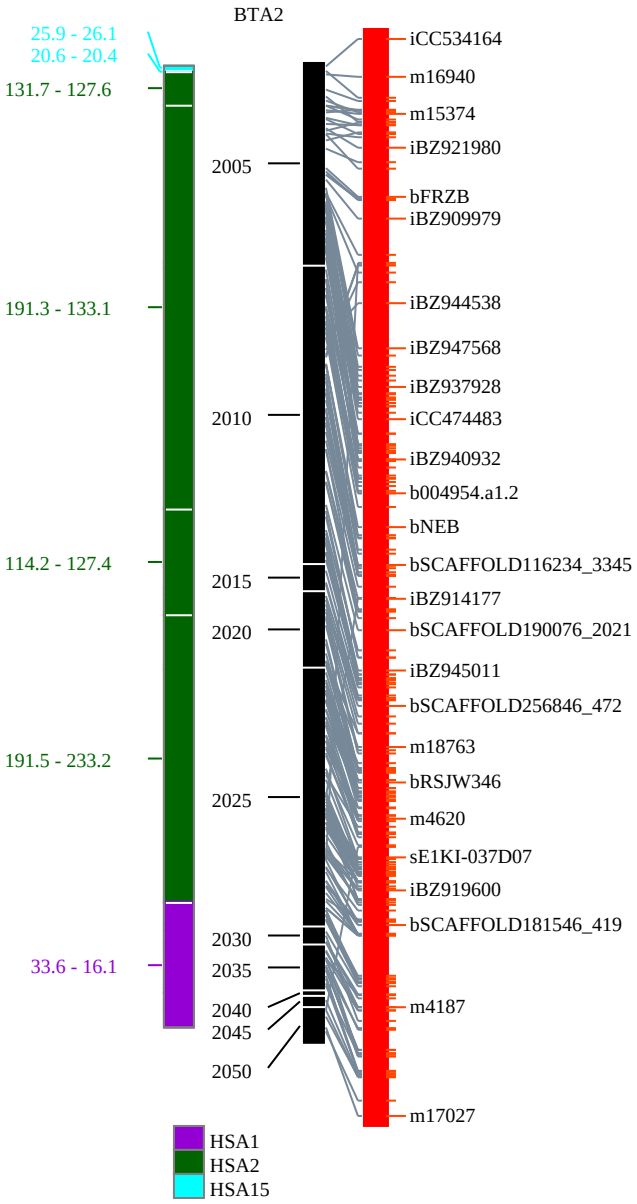
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33.6 - 16.1
2005
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2015
2020
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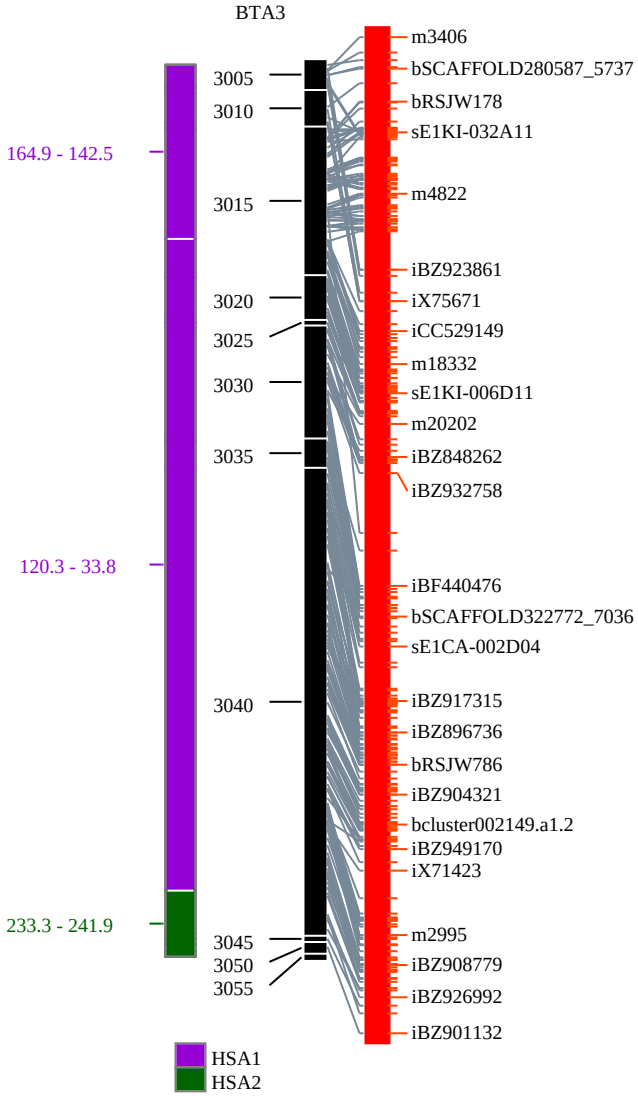
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3005
3010
3015
3020
3025
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164.9 - 142.5
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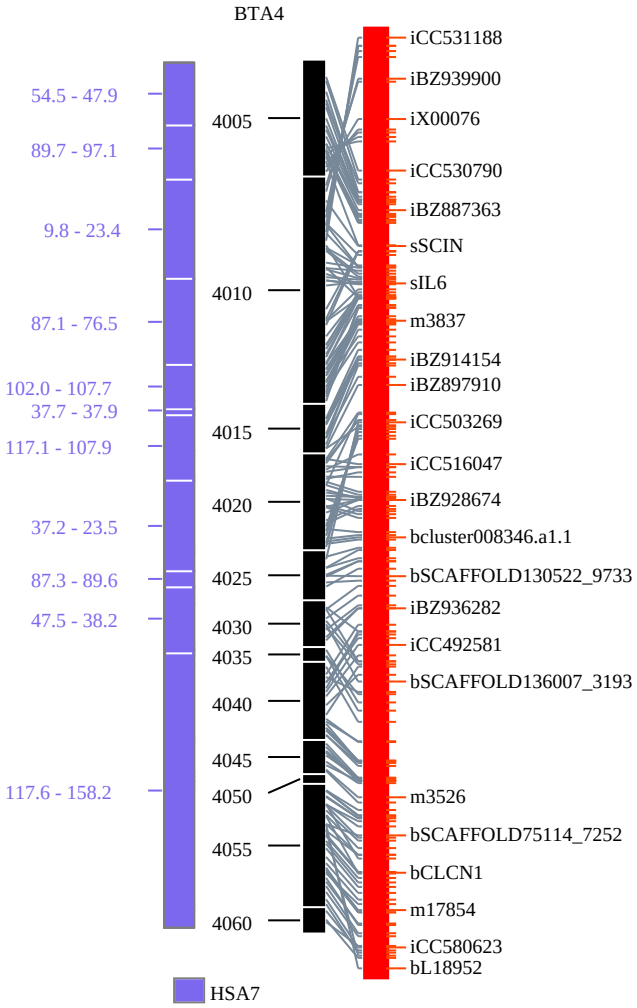
233.3 - 241.9
HSA1
HSA2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117.1 - 107.9
37.2 - 23.5
87.3 - 89.6
47.5 - 38.2
117.6 - 158.2
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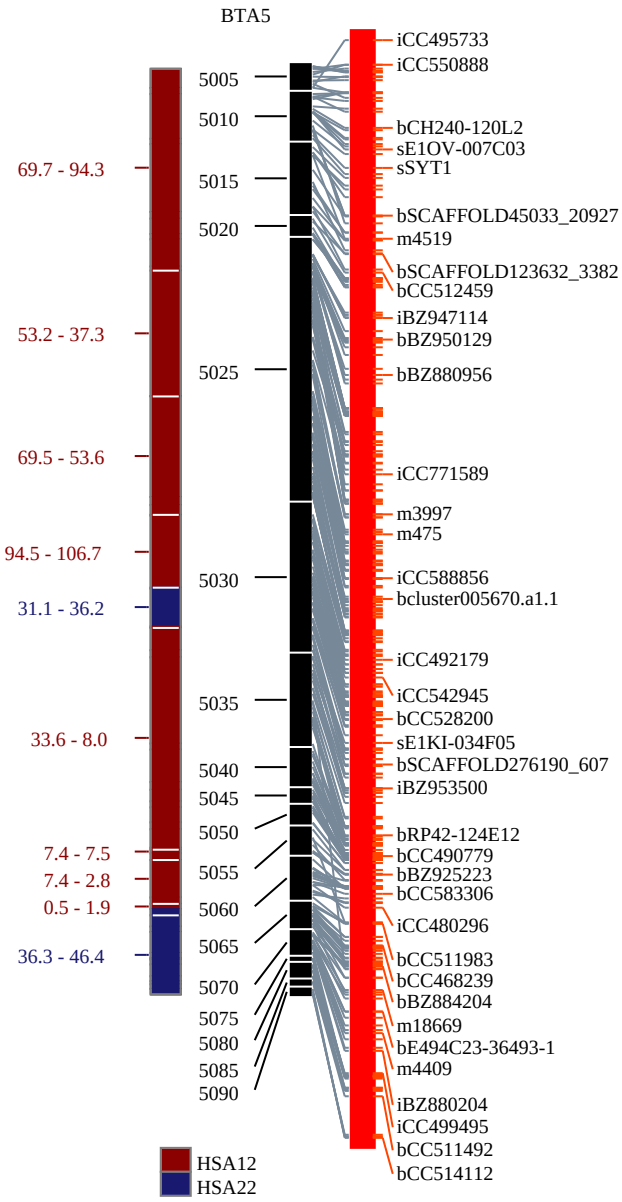
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7.4 - 7.5
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0.5 - 1.9
36.3 - 46.4
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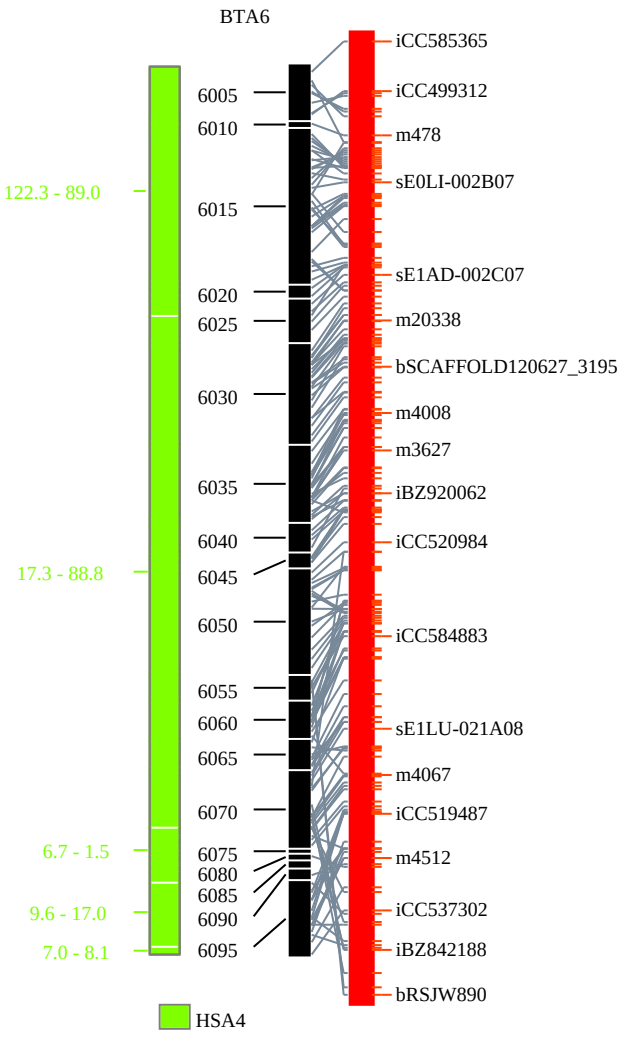
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6095
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9.6 - 17.0
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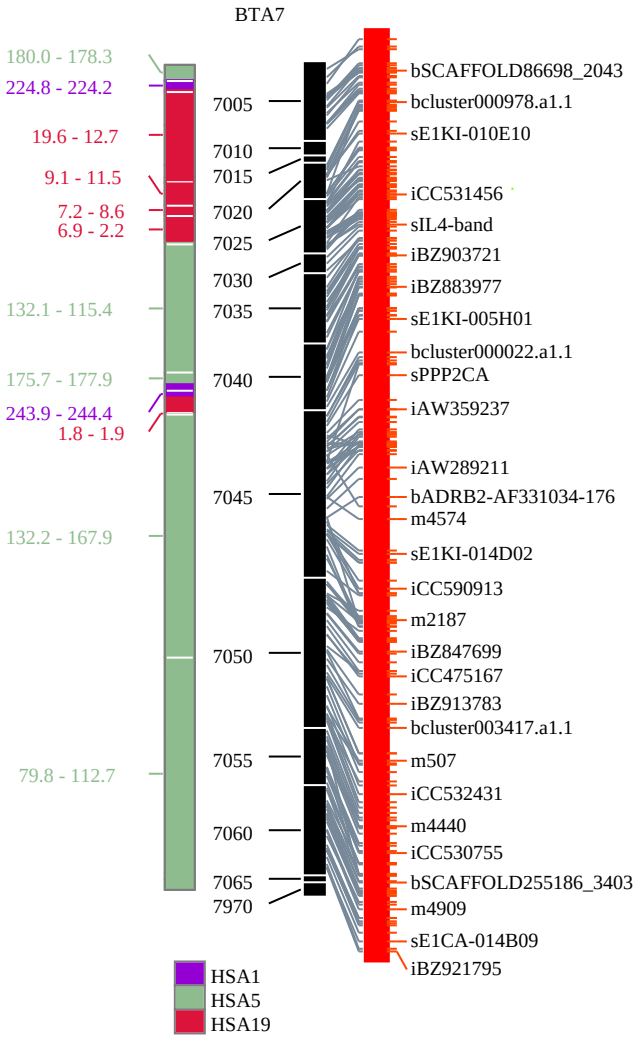
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243.9 - 244.4
1.8 - 1.9
132.2 - 167.9
79.8 - 112.7
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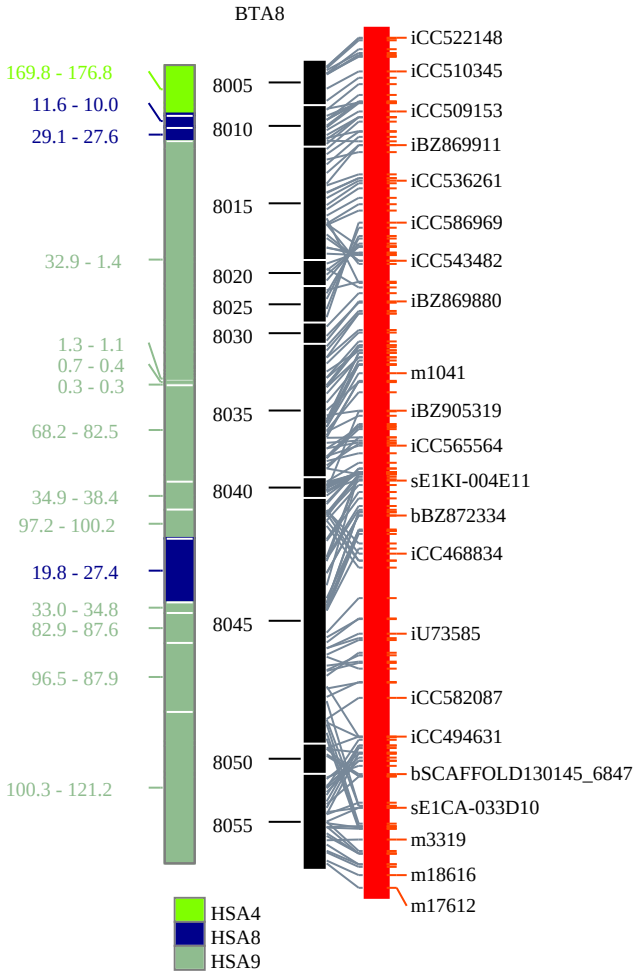
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19.8 - 27.4
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82.9 - 87.6
96.5 - 87.9
100.3 - 121.2
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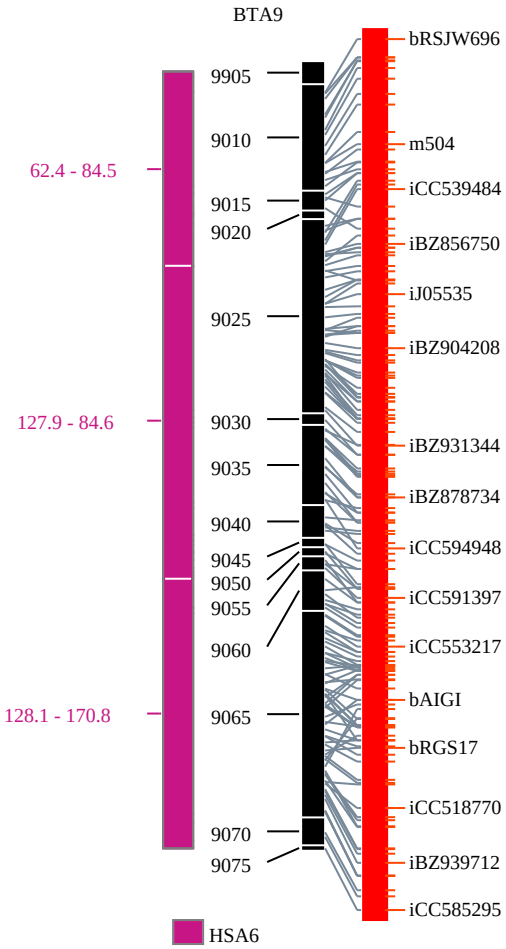
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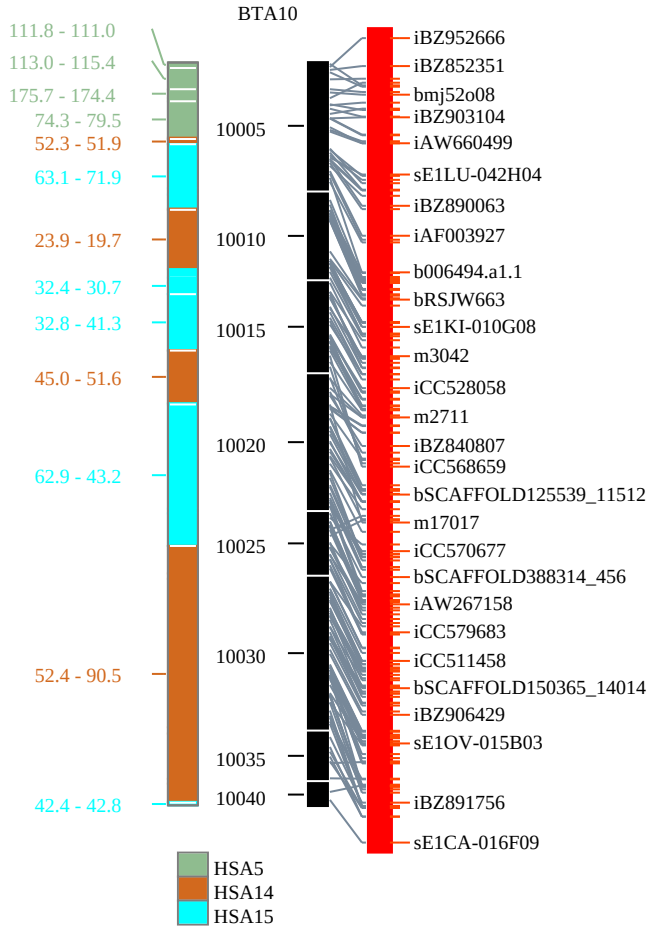
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32.4 - 30.7
32.8 - 41.3
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62.9 - 43.2
52.4 - 90.5
42.4 - 42.8
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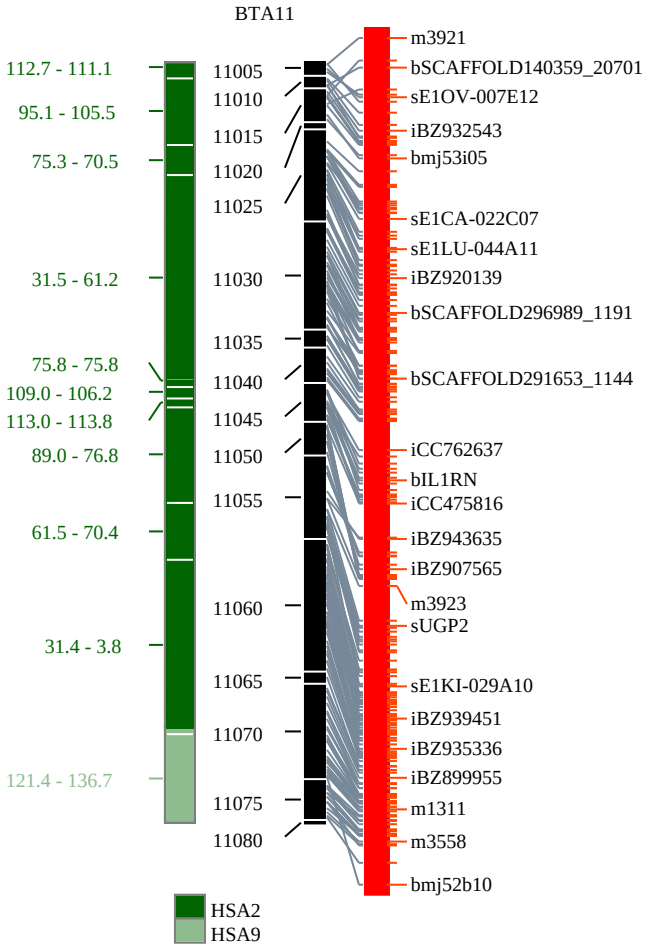
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89.0 - 76.8
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31.4 - 3.8
121.4 - 136.7
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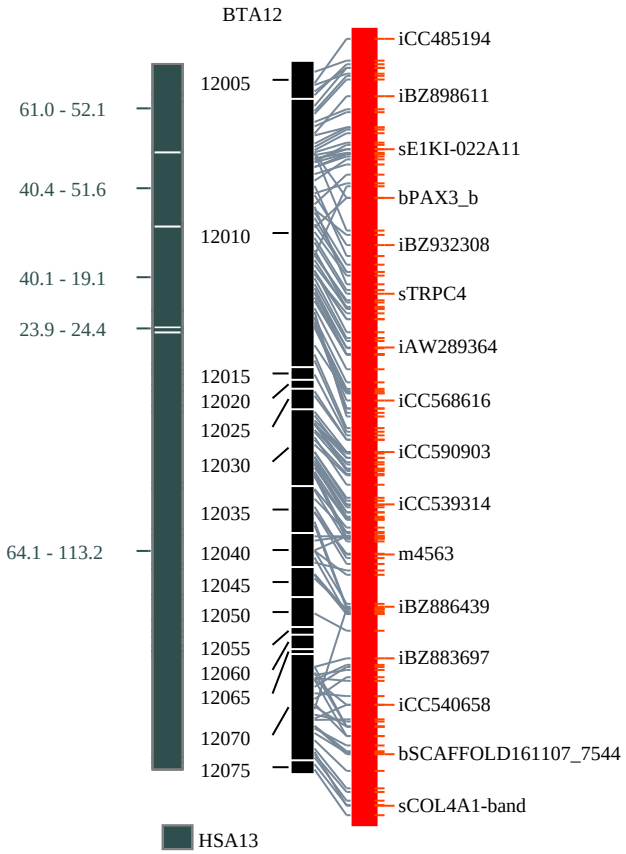
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64.1 - 113.2
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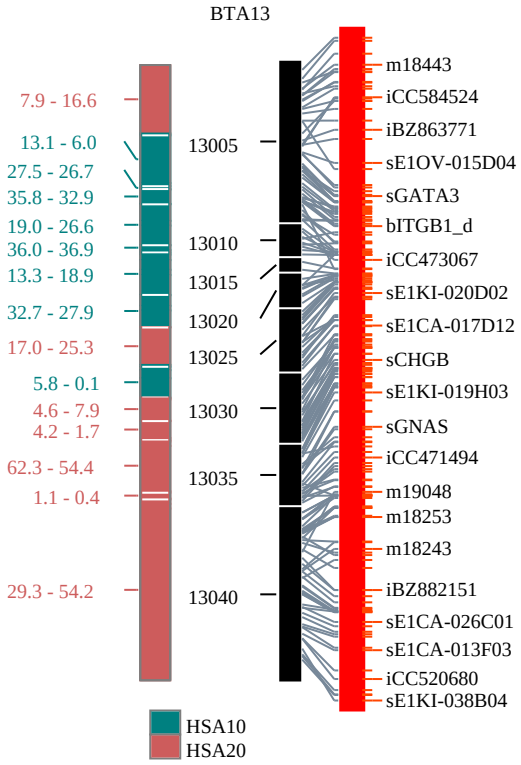
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32.7 - 27.9
17.0 - 25.3
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4.6 - 7.9
4.2 - 1.7
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29.3 - 54.2
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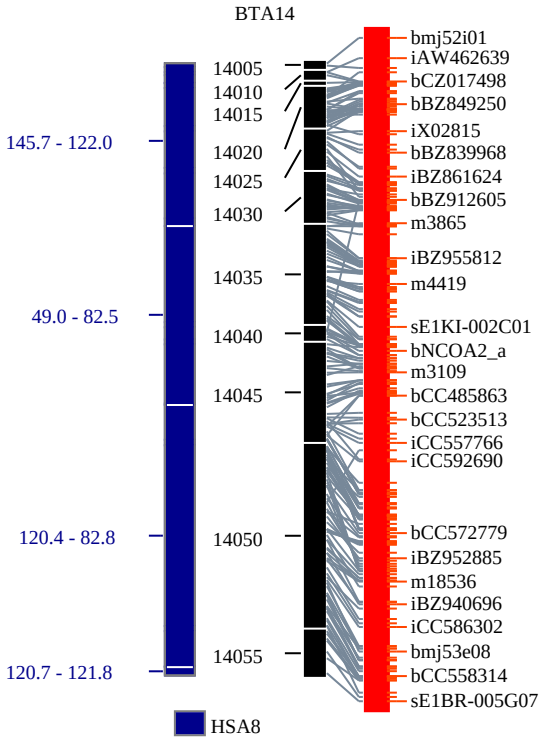
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120.7 - 121.8
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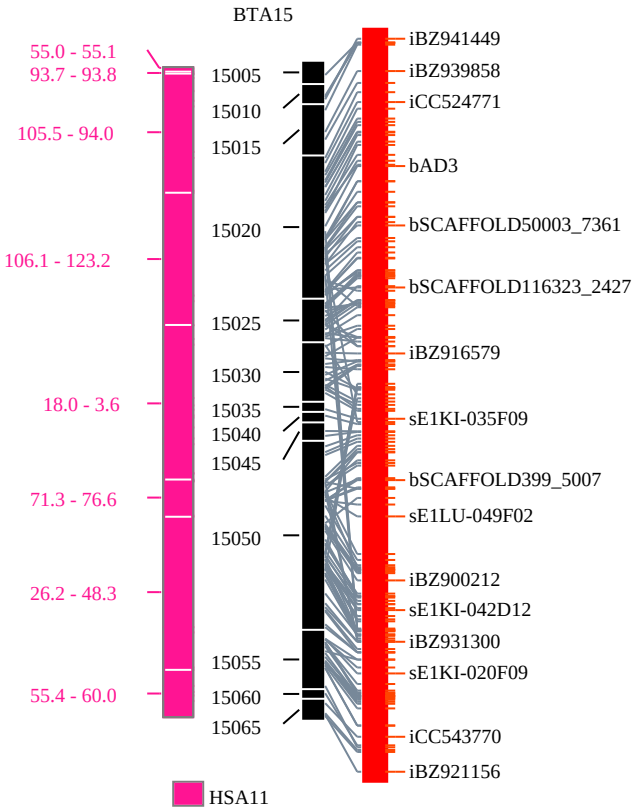
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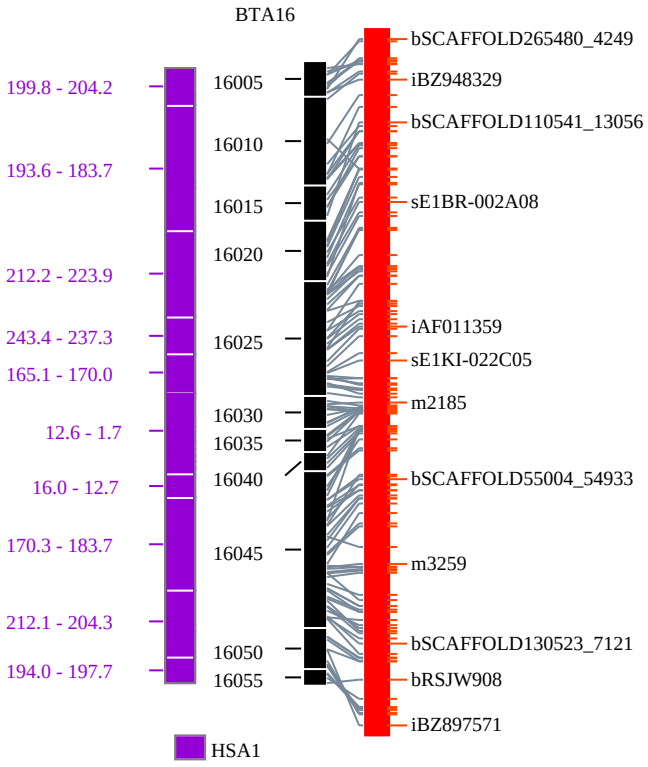
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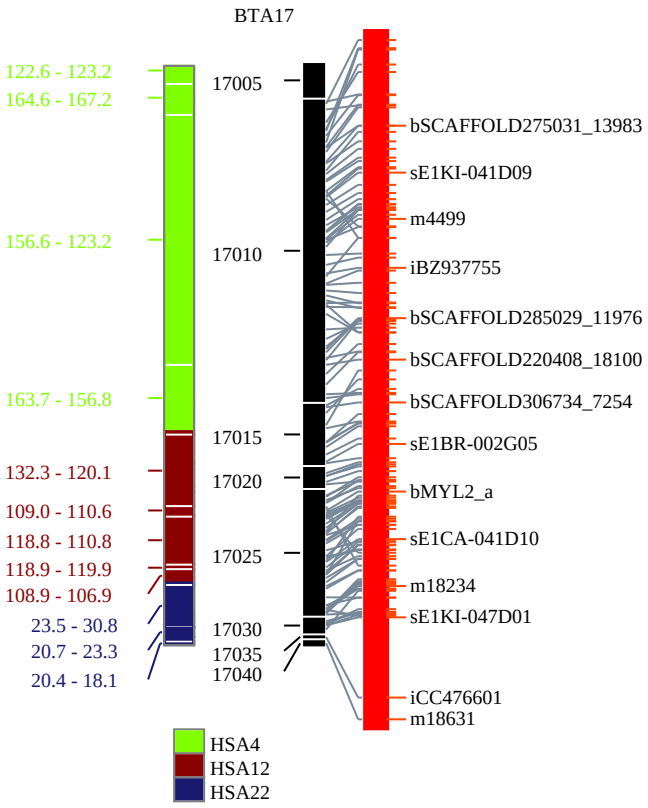
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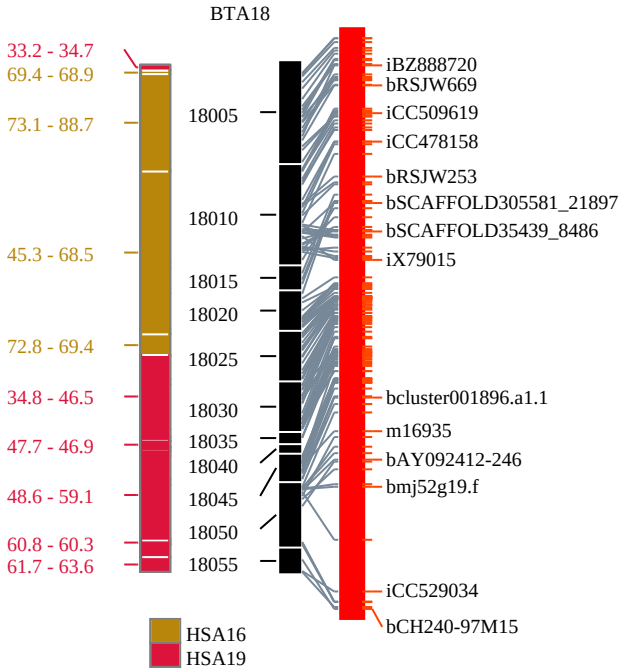
HSA22


BTA18
33.2 - 34.7
69.4 - 68.9
73.1 - 88.7
45.3 - 68.5
72.8 - 69.4
34.8 - 46.5
47.7 - 46.9
48.6 - 59.1
60.8 - 60.3
61.7 - 63.6
18005
18010
18015
18020
18025
18030
18035
18040
18045
18050
18055
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iCC509619
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bRSJW253
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iX79015
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bmj52g19.f
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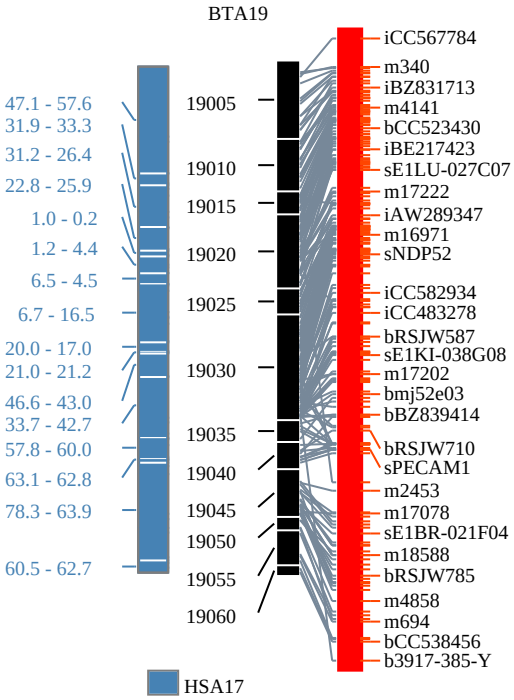
HSA19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47.1 - 57.6
31.9 - 33.3
31.2 - 26.4
22.8 - 25.9
1.0 - 0.2
1.2 - 4.4
6.5 - 4.5
6.7 - 16.5
20.0 - 17.0
21.0 - 21.2
46.6 - 43.0
33.7 - 42.7
57.8 - 60.0
63.1 - 62.8
78.3 - 63.9
60.5 - 62.7
19005
19010
19015
19020
19025
19030
19035
19040
19045
19050
19055
19060
iCC567784
m340
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sNDP52
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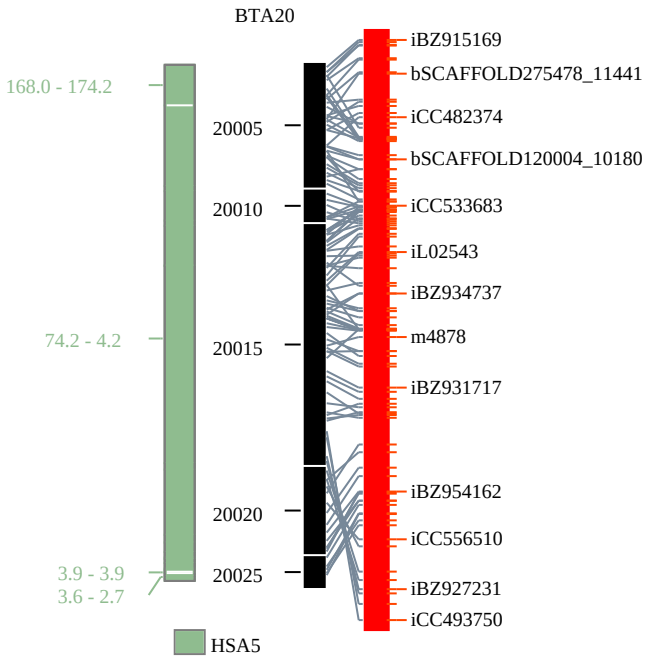
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168.0 - 174.2
74.2 - 4.2
3.9 - 3.9
3.6 - 2.7
HSA5
20005
20010
20015
20020
20025
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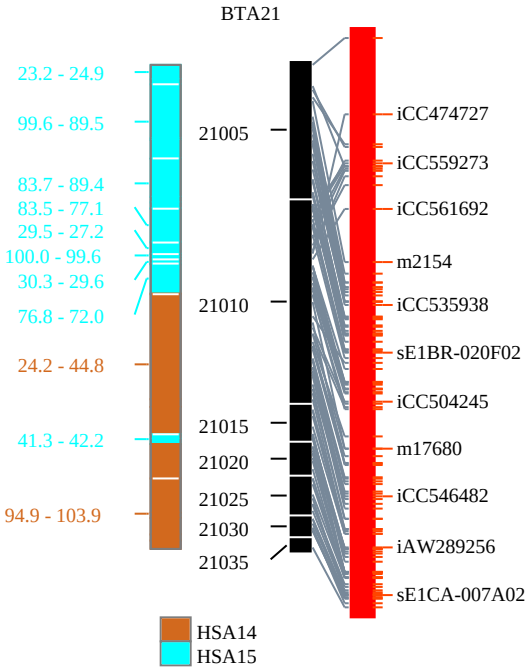
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23.2 - 24.9
99.6 - 89.5
83.7 - 89.4
83.5 - 77.1
29.5 - 27.2
100.0 - 99.6
30.3 - 29.6
76.8 - 72.0
24.2 - 44.8
41.3 - 42.2
94.9 - 103.9
21005
21010
21015
21020
21025
21030
21035
iCC474727
iCC559273
iCC561692
m2154
iCC535938
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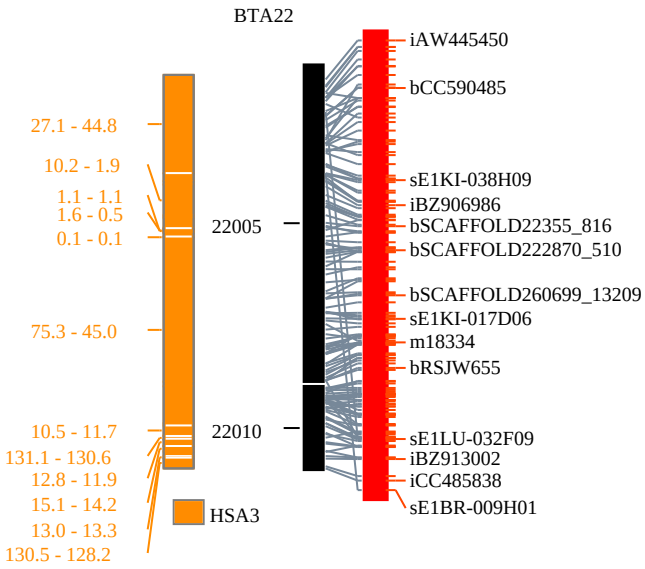
iCC504245
m17680
iCC546482
iAW289256
sE1CA-007A02
HSA14
HSA15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27.1 - 44.8
10.2 - 1.9
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1.1 - 1.1
1.6 - 0.5
22005
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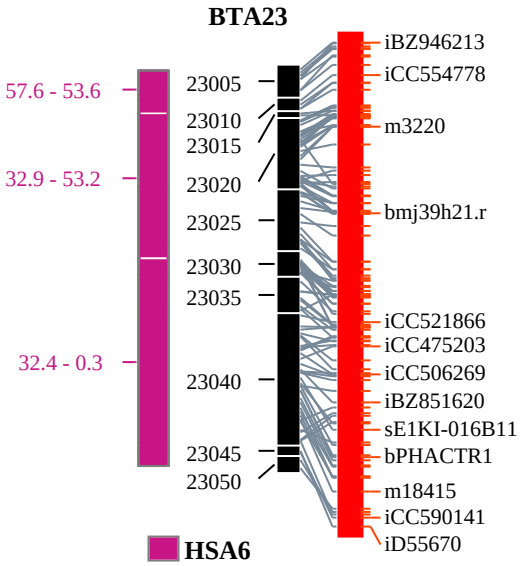
0.1 - 0.1
bSCAFFOLD222870_510
bSCAFFOLD260699_13209
75.3 - 45.0
sE1KI-017D06
m18334
bRSJW655
10.5 - 11.7
22010
sE1LU-032F09
131.1 - 130.6
iBZ913002
12.8 - 11.9
iCC485838
15.1 - 14.2
sE1BR-009H01
HSA3
13.0 - 13.3
130.5 - 128.2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57.6 - 53.6
32.9 - 53.2
32.4 - 0.3
23005
23010
23015
23020
23025
23030
23035
23040
23045
23050
iBZ946213
iCC554778
m3220
bmj39h21.r
iCC521866
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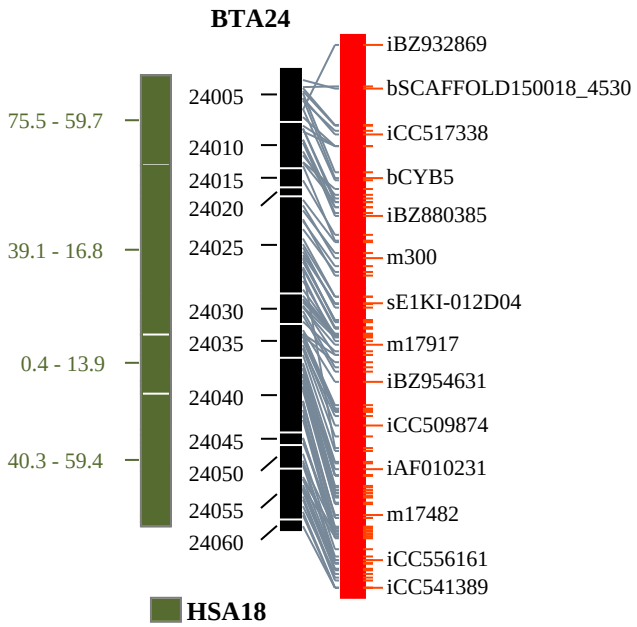
HSA6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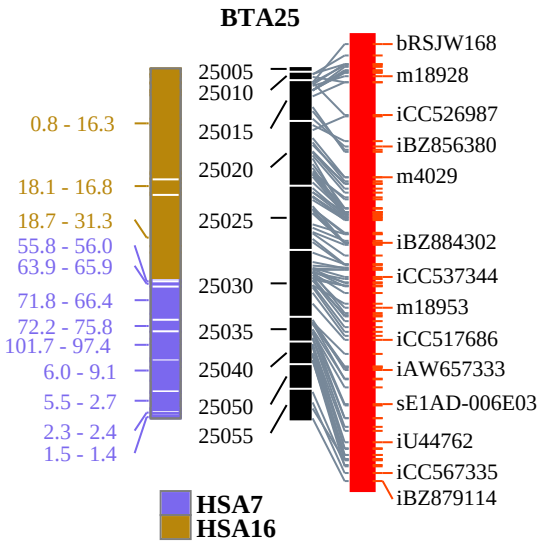
iCC509874
iAF010231
m17482
iCC556161
iCC541389
24005
24010
24015
24020
24025
24030
24035
24040
24045
24050
24055
24060
75.5 - 59.7
39.1 - 16.8
0.4 - 13.9
40.3 - 59.4
HSA18


BTA25
0.8 - 16.3
18.1 - 16.8
18.7 - 31.3
55.8 - 56.0
63.9 - 65.9
71.8 - 66.4
72.2 - 75.8
101.7 - 97.4
6.0 - 9.1
5.5 - 2.7
2.3 - 2.4
1.5 - 1.4
25005
25010
25015
25020
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25050
25055
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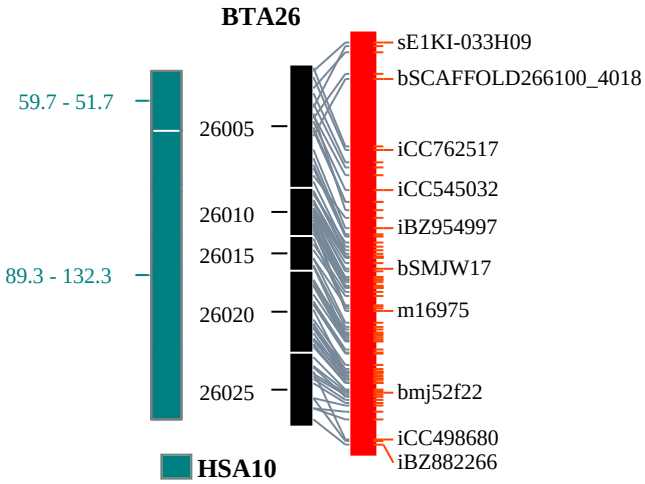
HSA7
HSA16


BTA26
59.7 - 51.7
89.3 - 132.3
26005
26010
26015
26020
26025
sE1KI-033H09
bSCAFFOLD266100_4018
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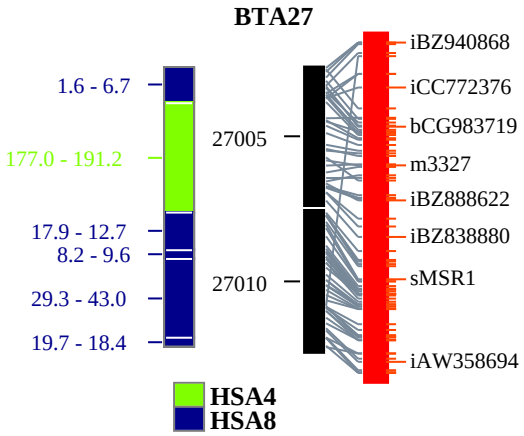
HSA10


BTA27
1.6 - 6.7
177.0 - 191.2
17.9 - 12.7
8.2 - 9.6
29.3 - 43.0
19.7 - 18.4
27005
27010
iBZ940868
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iBZ838880
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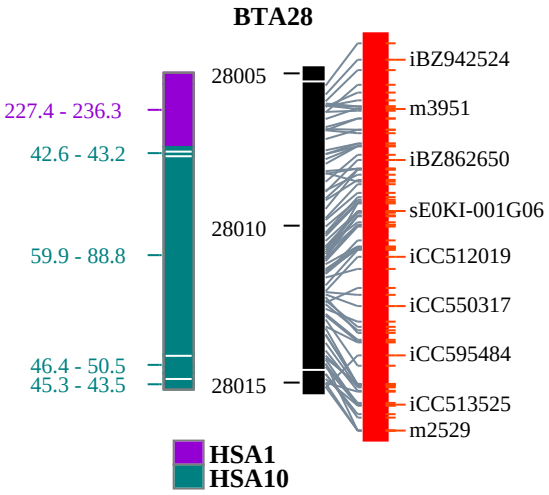
HSA4
HSA8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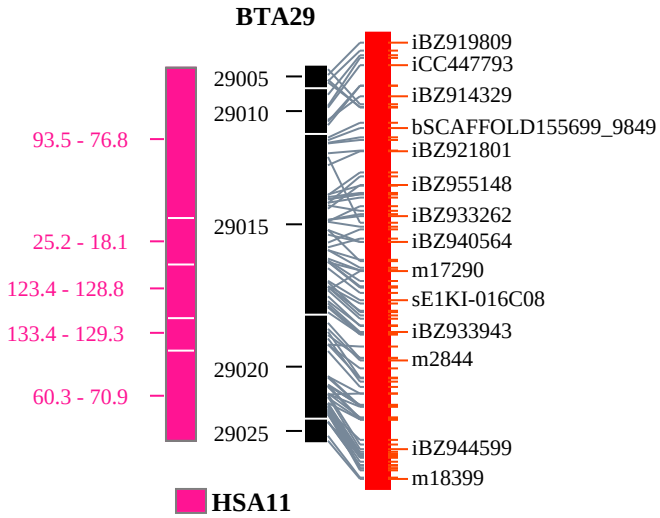
iCC512019
iCC550317
iCC595484
iCC513525
m2529
227.4 - 236.3
42.6 - 43.2
59.9 - 88.8
46.4 - 50.5
45.3 - 43.5
HSA1
HSA10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iBZ933262
iBZ940564
m17290
sE1KI-016C08
iBZ933943
m2844
iBZ944599
m18399
93.5 - 76.8
25.2 - 18.1
123.4 - 128.8
133.4 - 129.3
60.3 - 70.9
HSA11