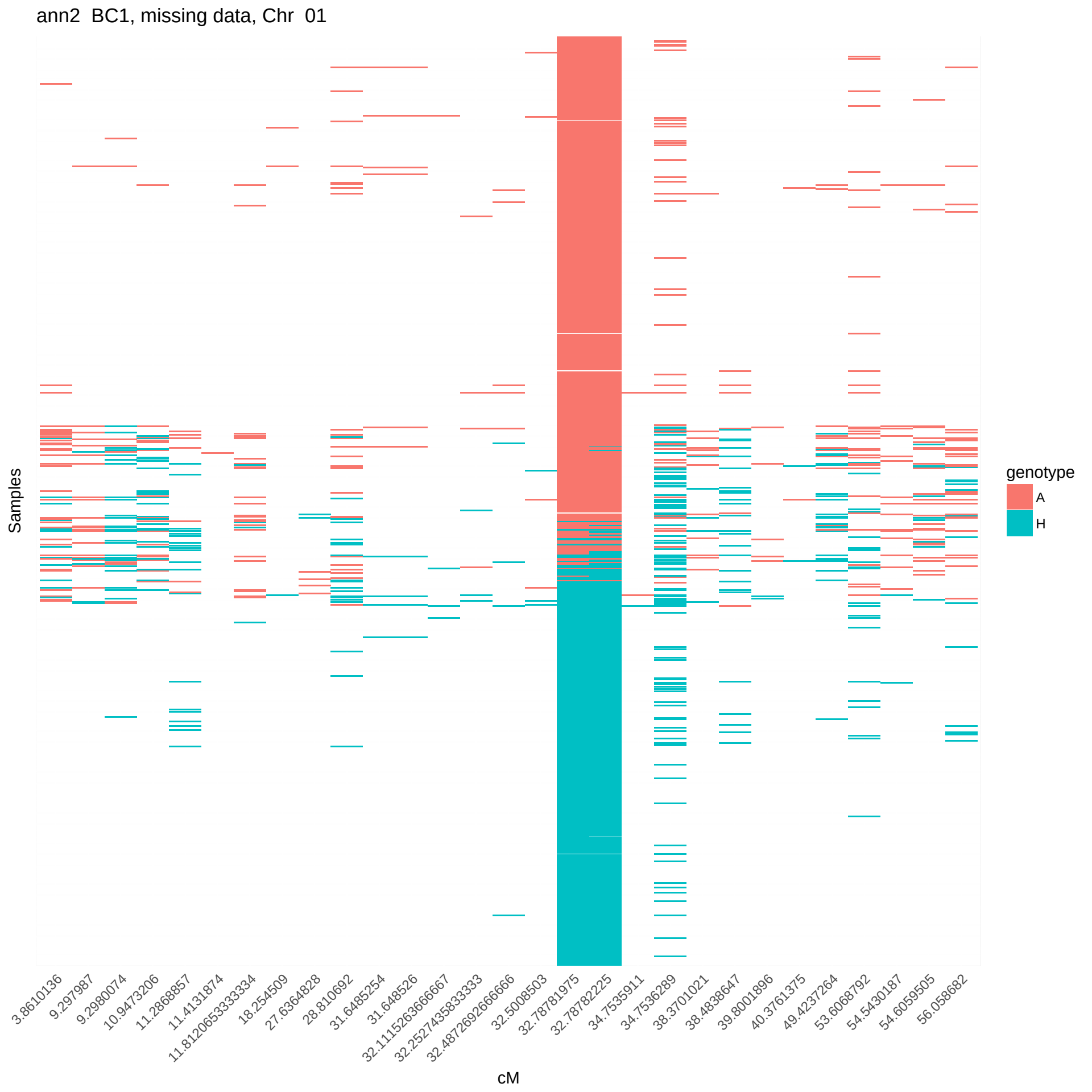
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Samples
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32.4872692666666
32.5008503
32.78781975
32.78782225
34.7535911
34.7536289
38.3701021
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39.8001896
40.3761375
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53.6068792
54.5430187
54.6059505
56.058682
cM


ann2 BC1, missing data, Chr 02
Samples
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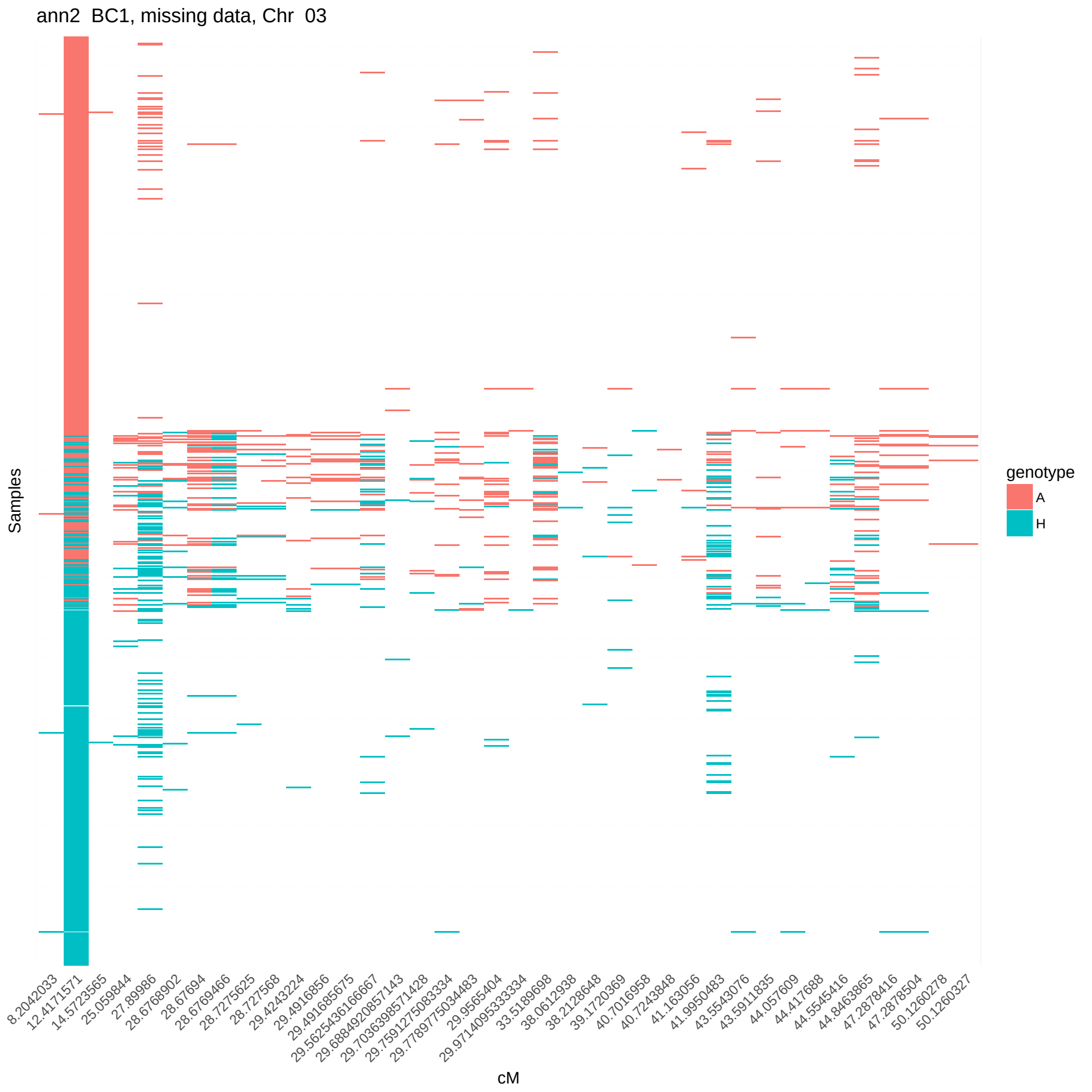
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28.727568
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40.7243848
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43.5911835
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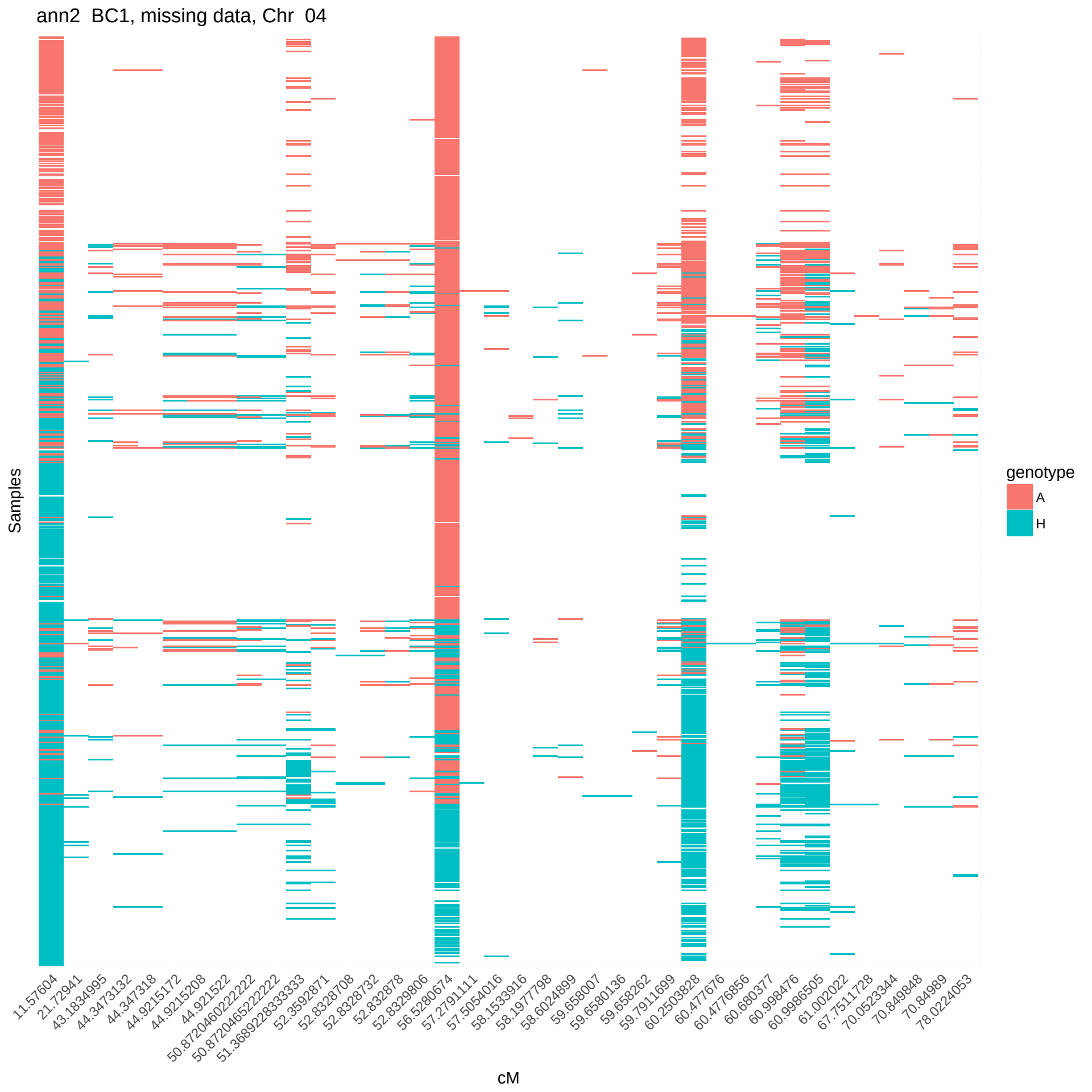
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44.9215208
44.921522
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52.832878
52.8329806
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78.0224053
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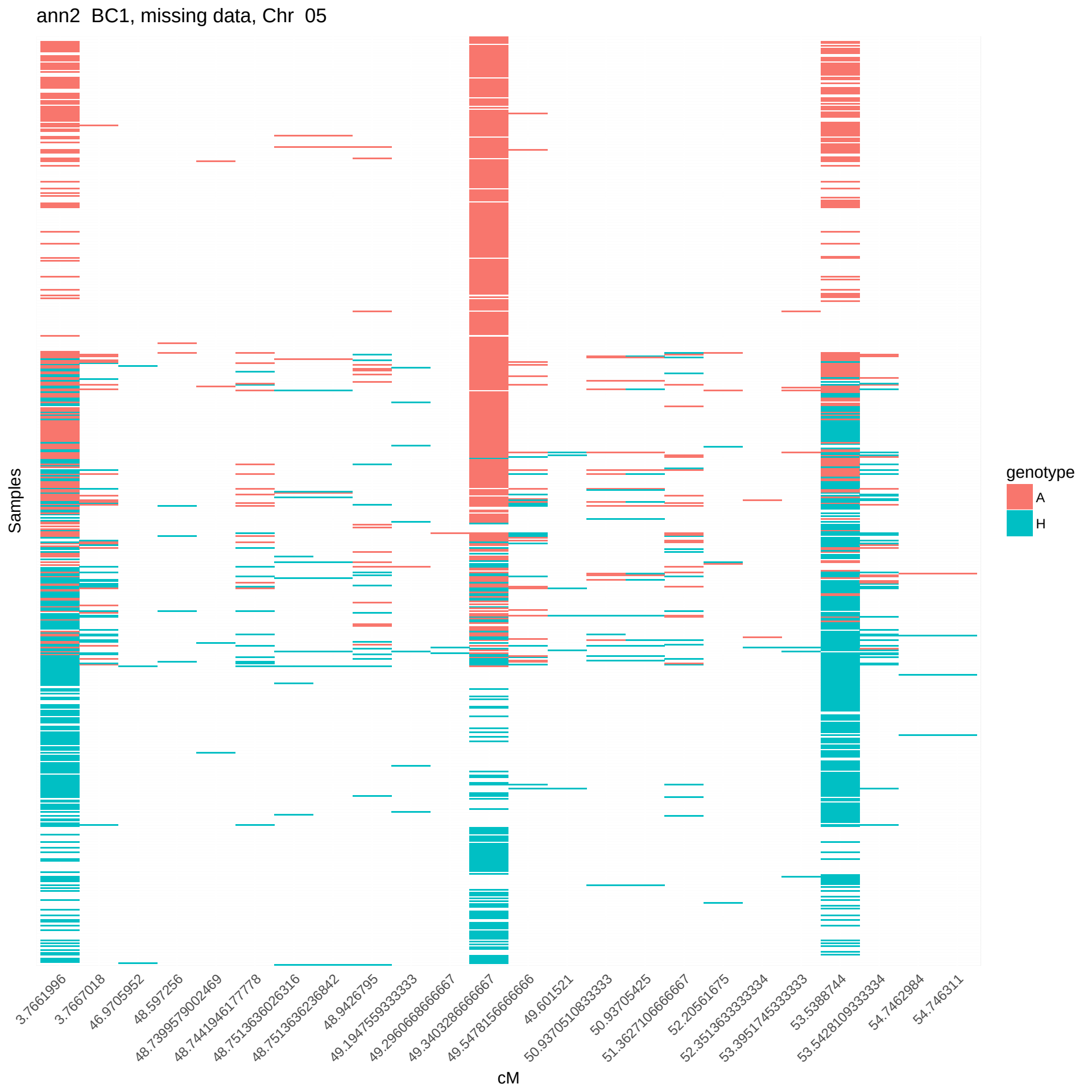
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48.7513636236842
48.9426795
49.1947559333333
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49.3403286666667
49.5478156666666
49.601521
50.9370510833333
50.93705425
51.3627106666667
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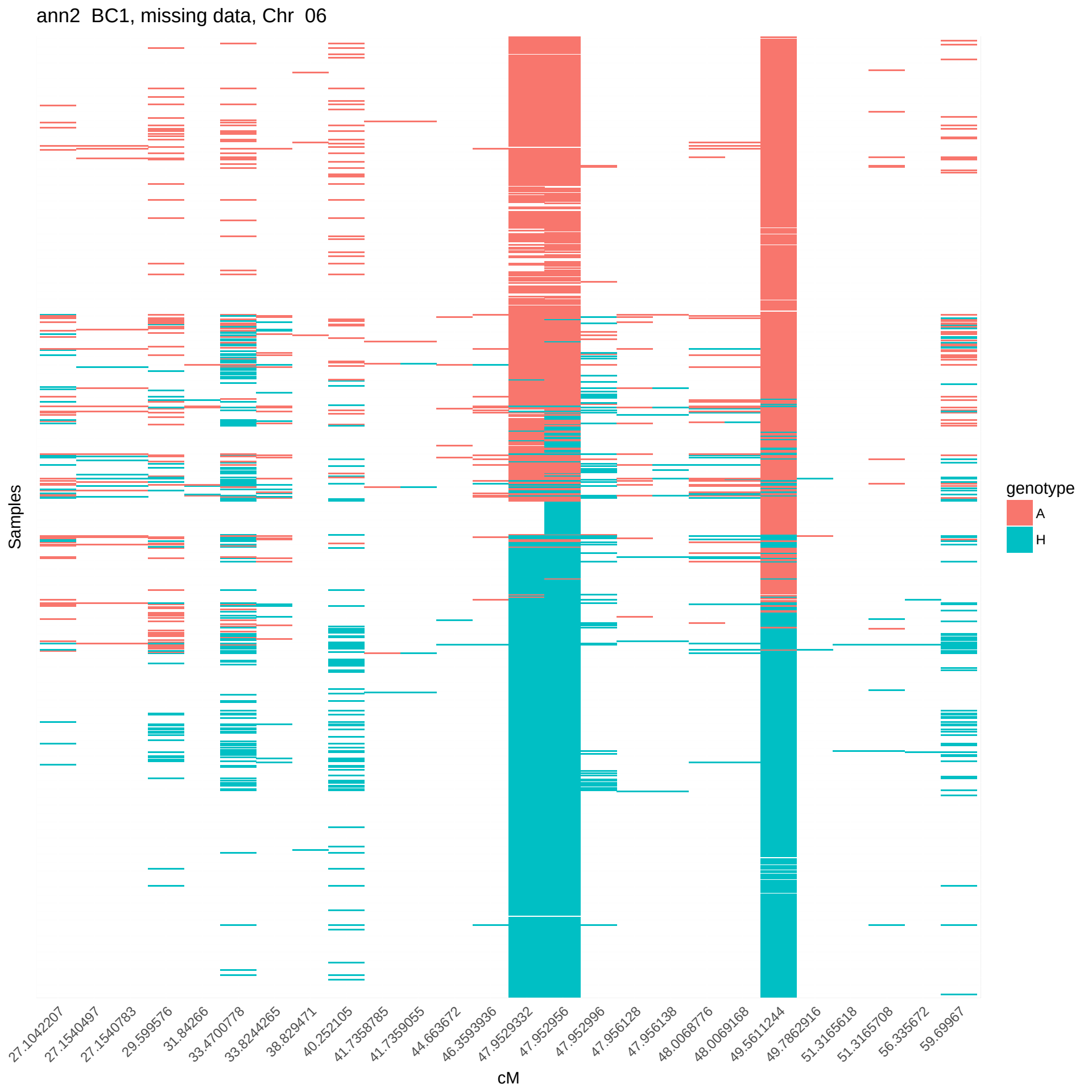
54.7462984
54.746311
cM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41.7359055
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46.3593936
47.9529332
47.952956
47.952996
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47.956138
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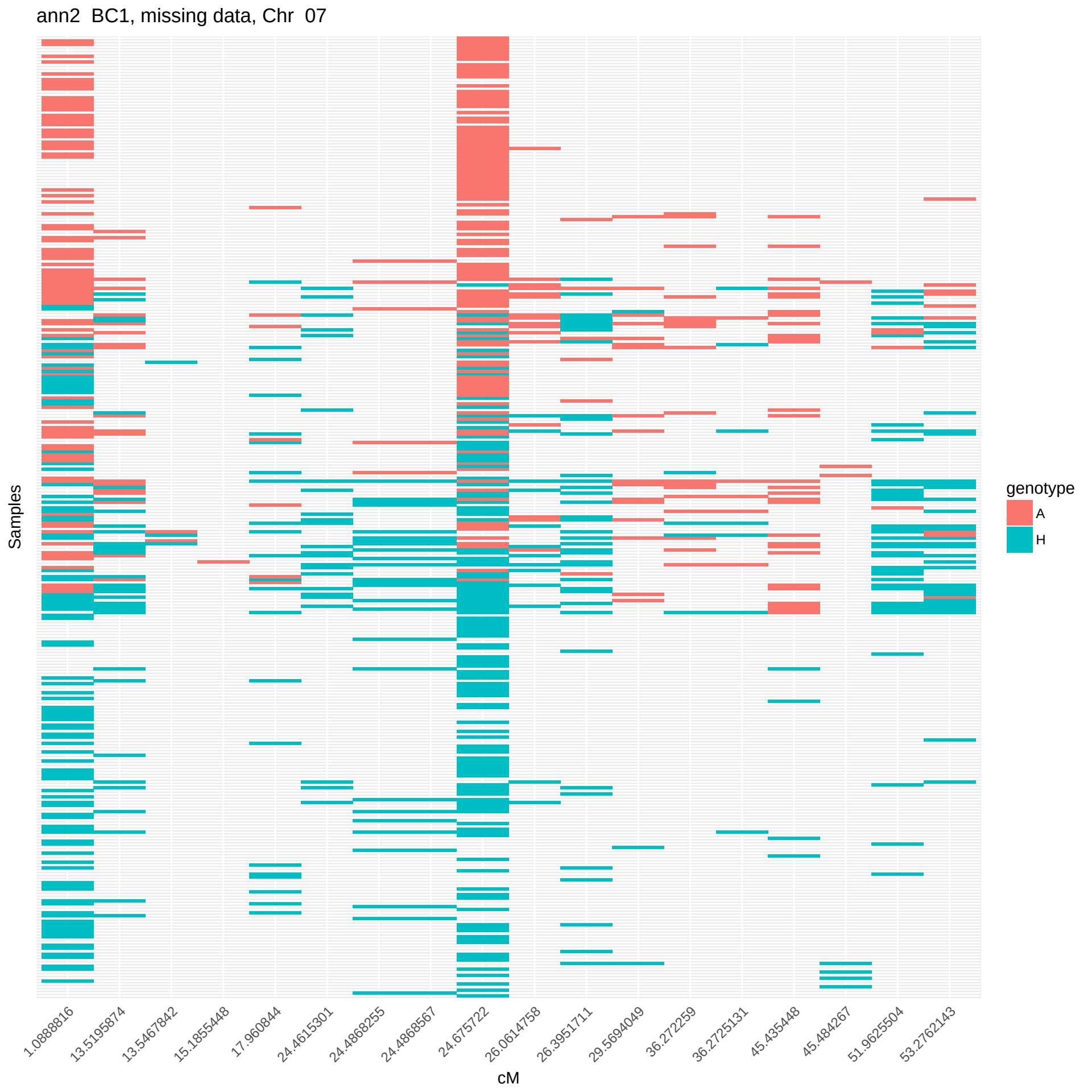
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Samples
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24.4868567
24.675722
26.0614758
26.3951711
29.5694049
36.272259
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45.435448
45.484267
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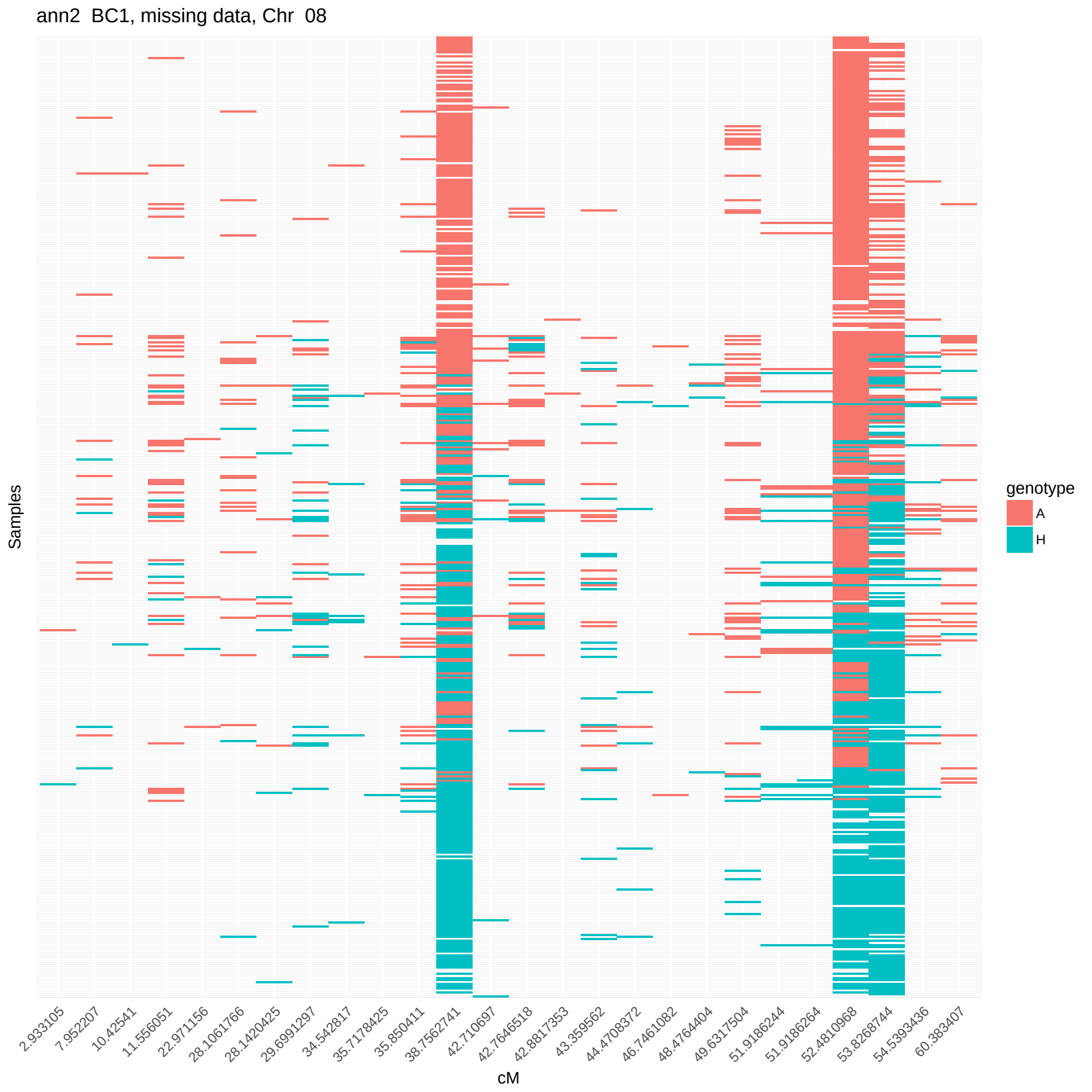
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Samples
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35.7178425
35.850411
38.7562741
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42.7646518
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43.359562
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54.5393436
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cM


ann2 BC1, missing data, Chr 09
Samples
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26.5404081731707
27.324594
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59.8601022
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70.373499
75.5925752
78.780179
89.1940411
cM


ann2 BC1, missing data, Chr 10
Samples
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A
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50.1840058
50.328551175
51.1590891
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51.9275339
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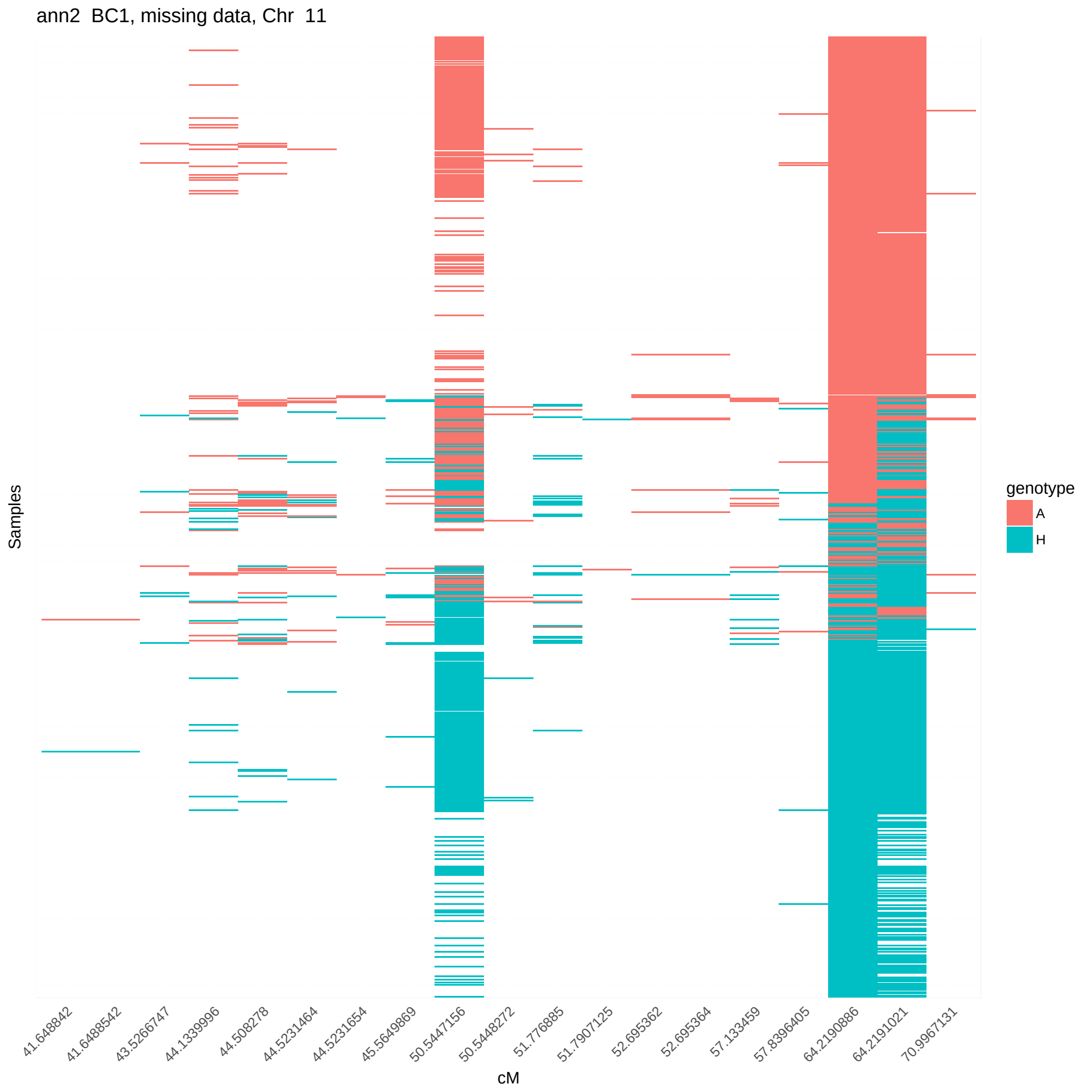
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Samples
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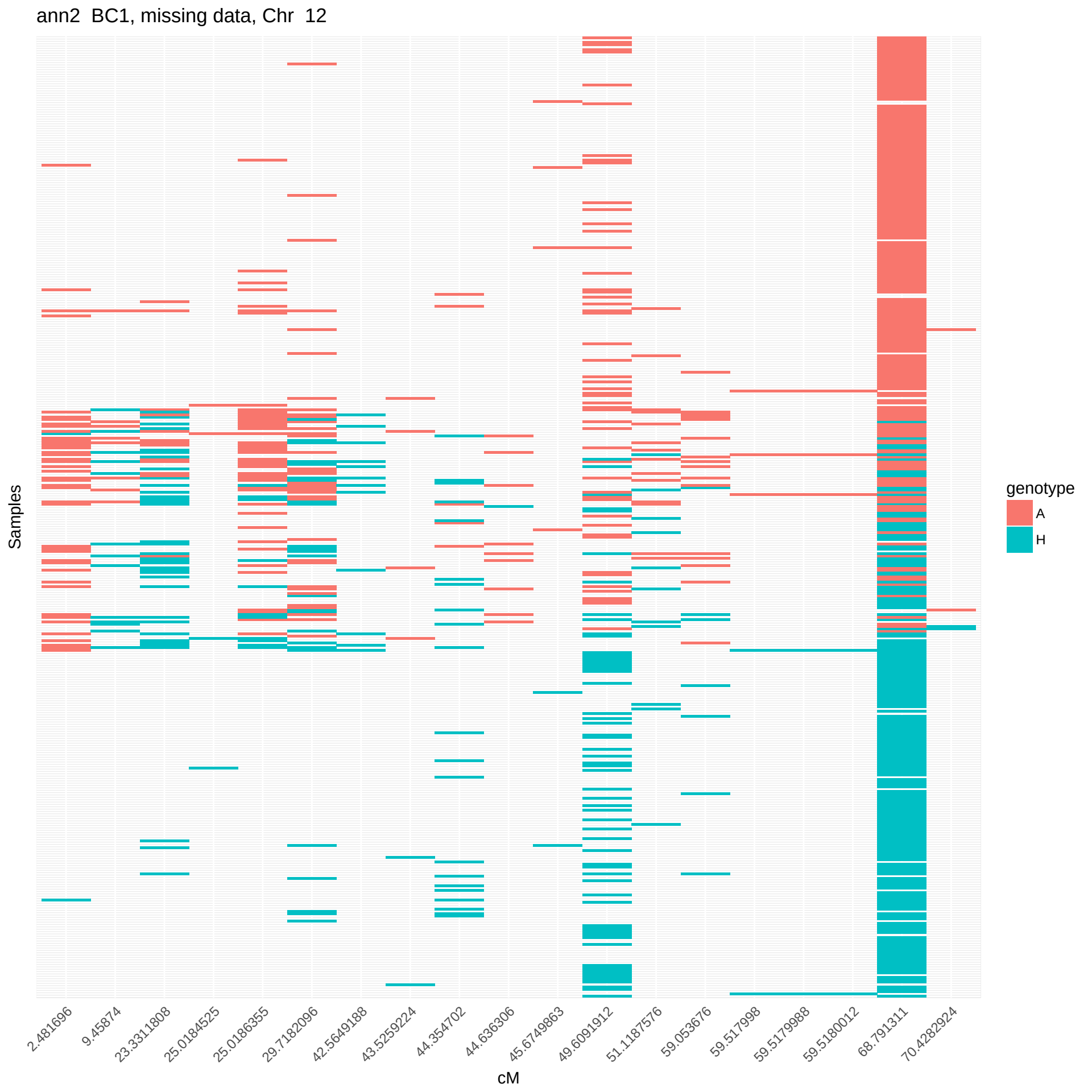
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Samples
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A
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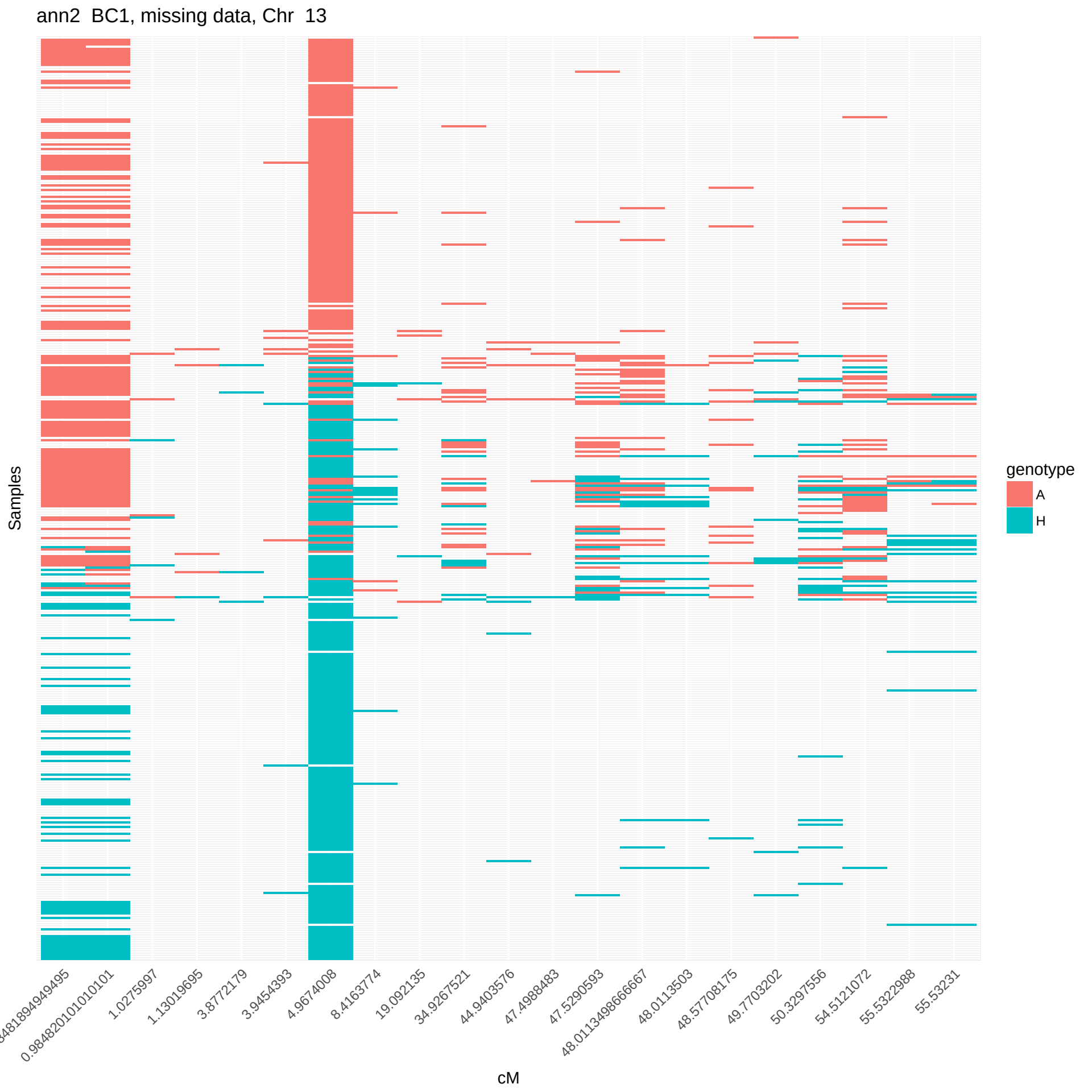
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Samples
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44.9403576
47.4988483
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55.53231
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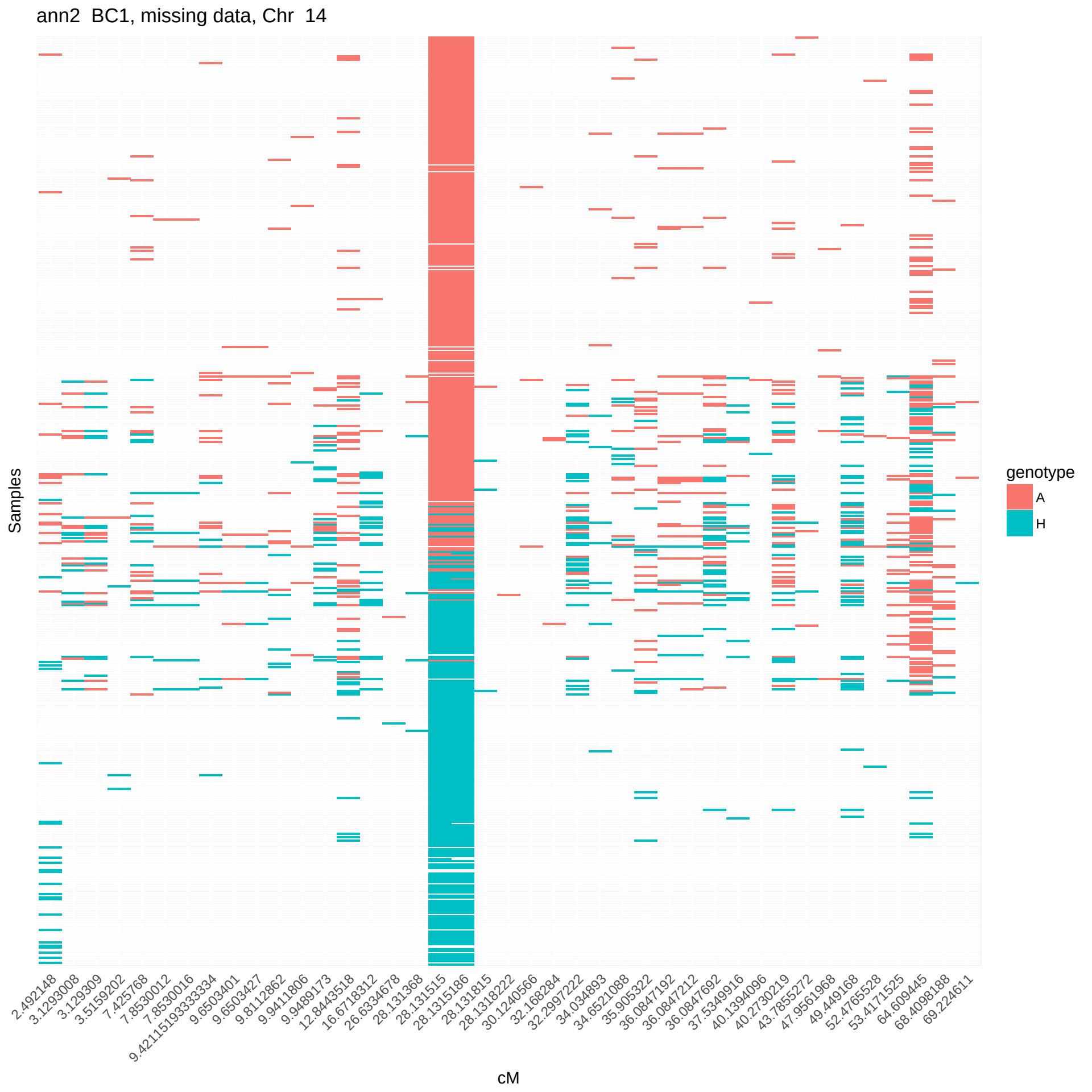
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Samples
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7.8530016
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9.6503427
9.8112862
9.9411806
9.9489173
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28.131815
28.1318222
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32.2997222
34.034893
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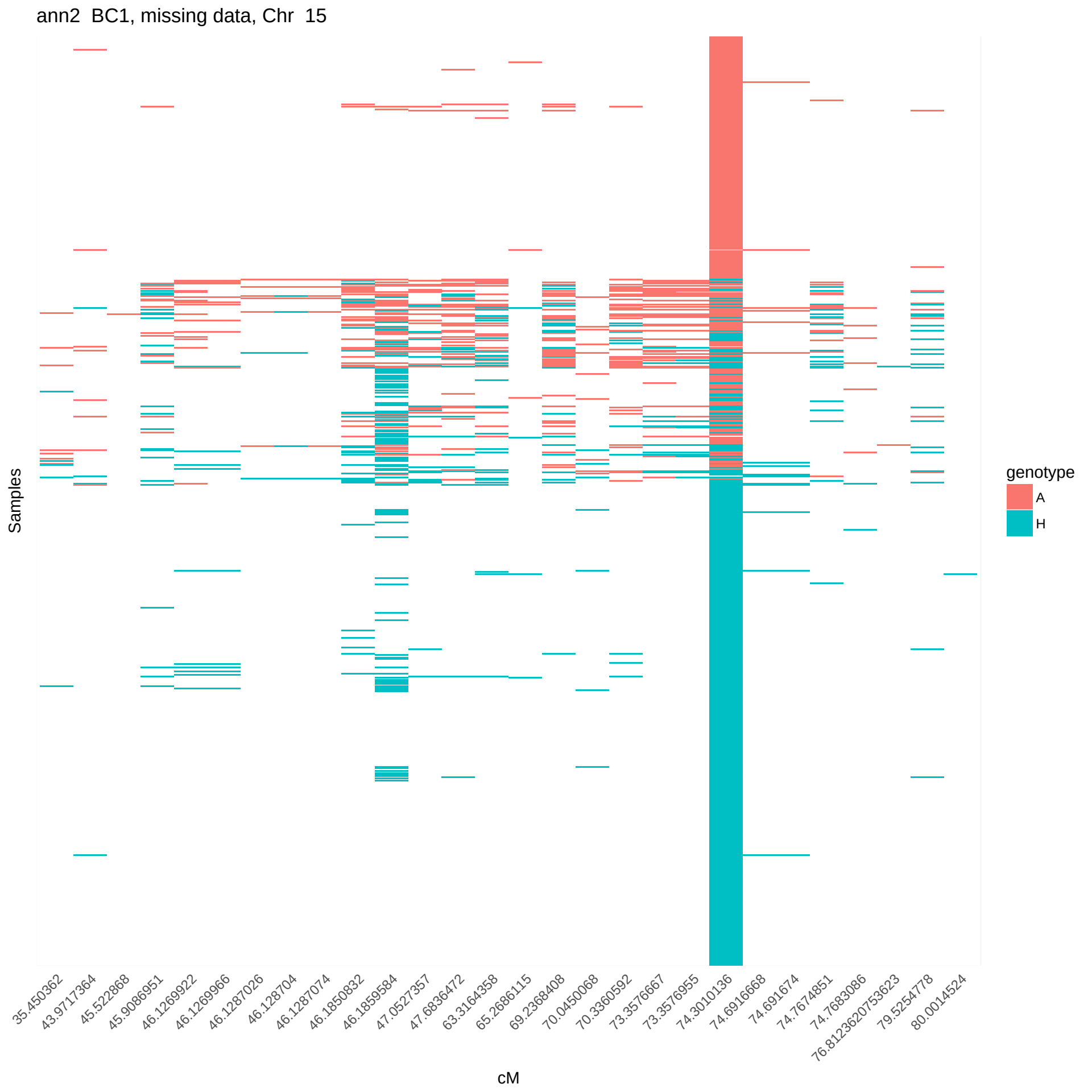
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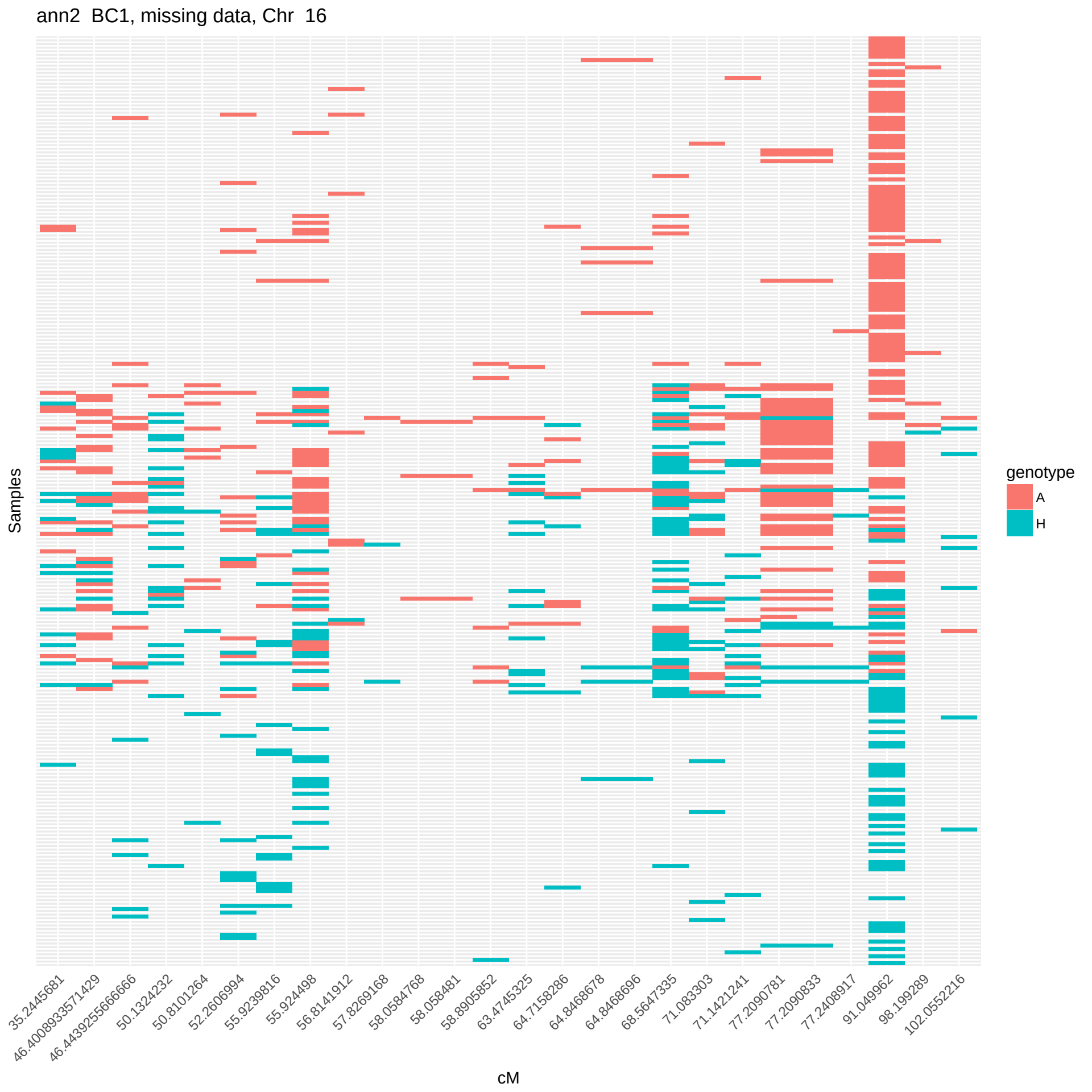
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ann2 BC1, missing data, Chr 17
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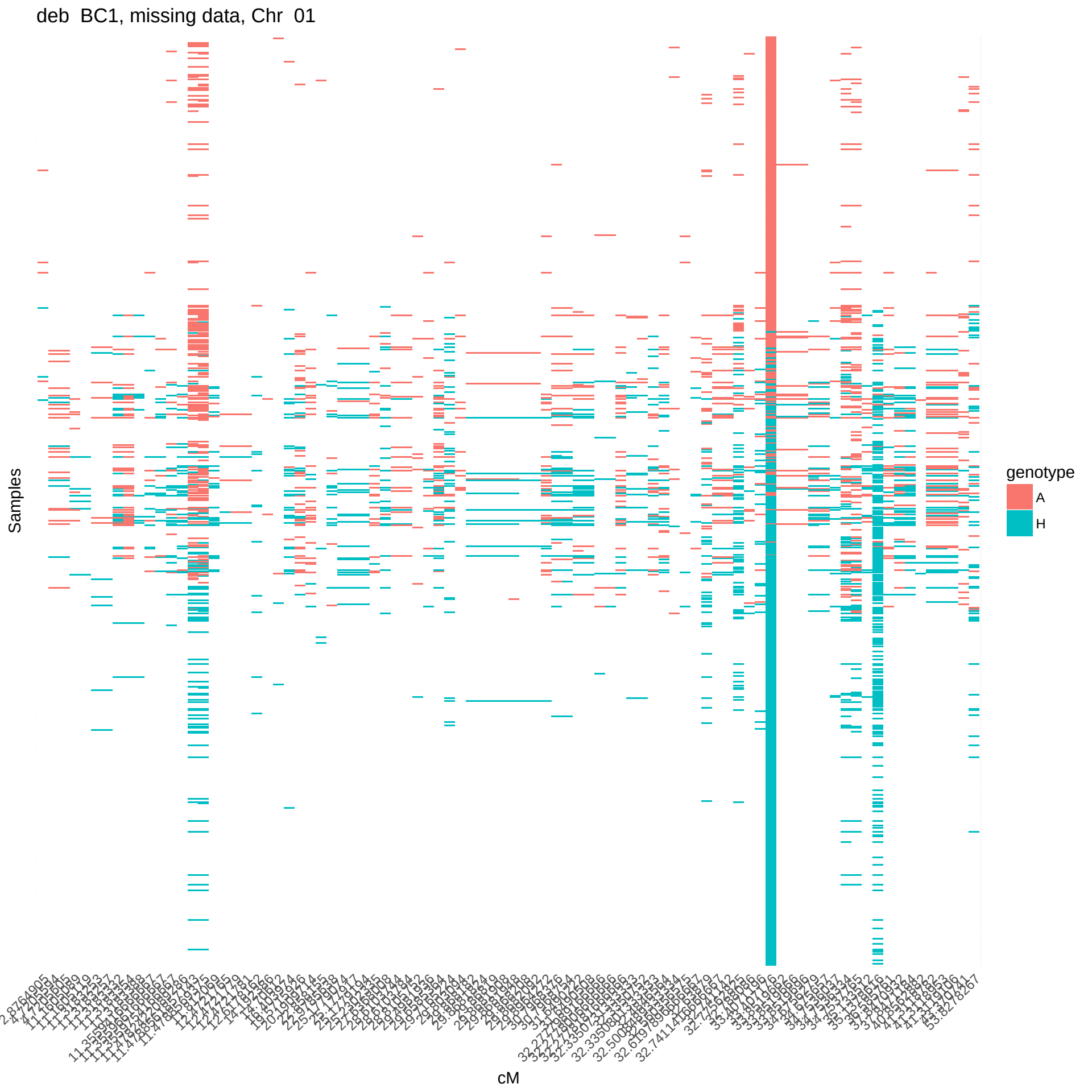
deb BC1, missing data, Chr 01
Samples
cM
genotype
A
H


deb BC1, missing data, Chr 02
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cM
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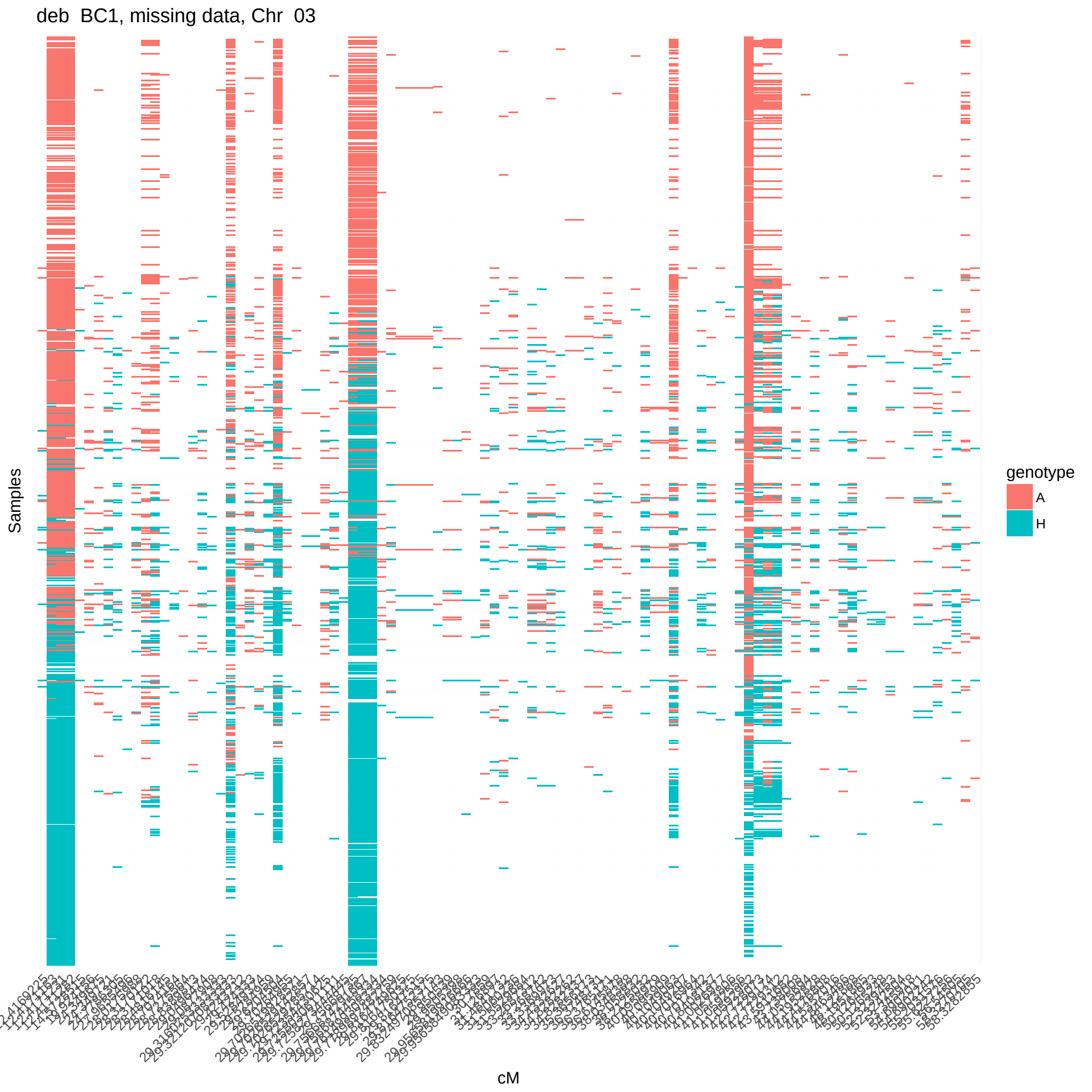
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Samples
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genotype
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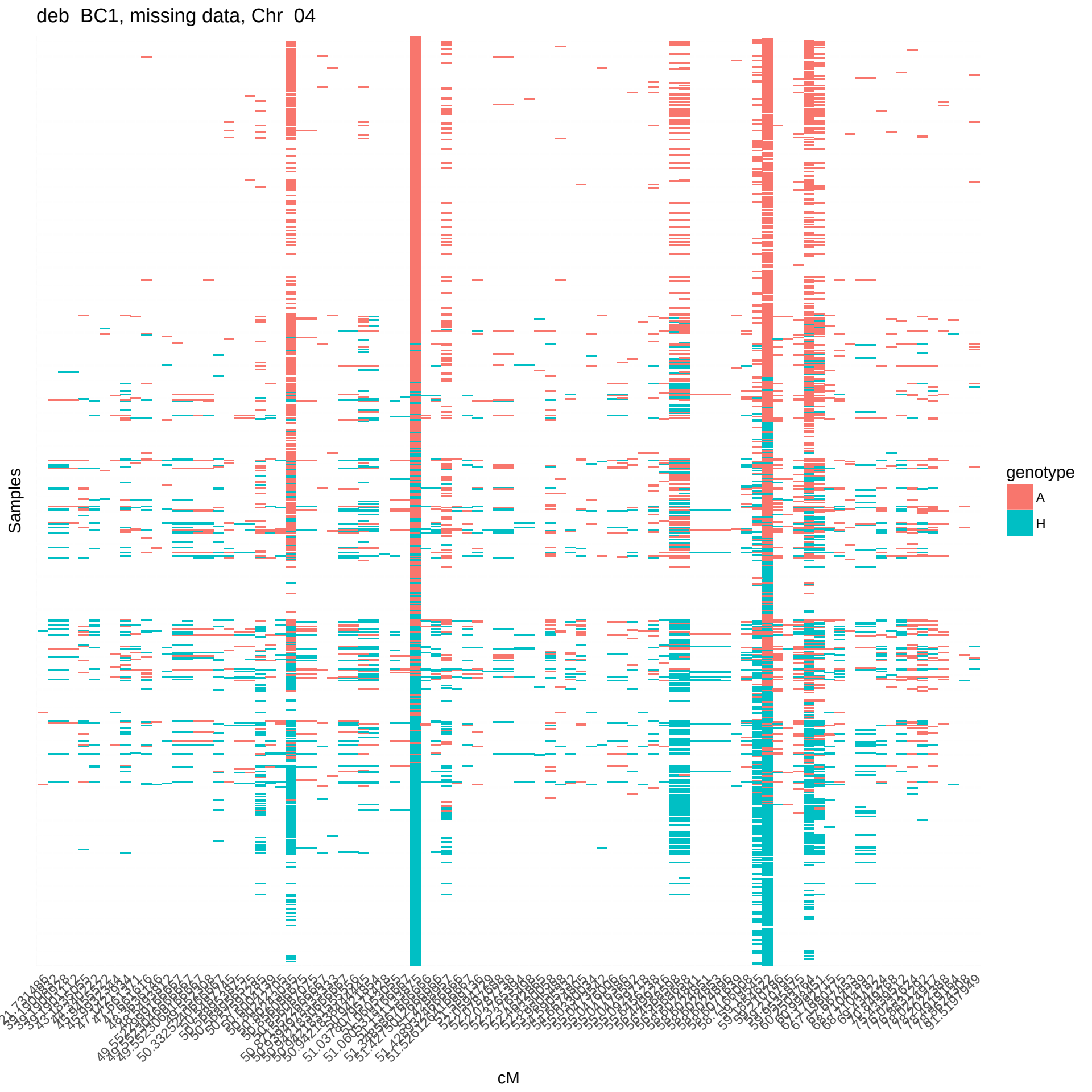
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Samples
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genotype
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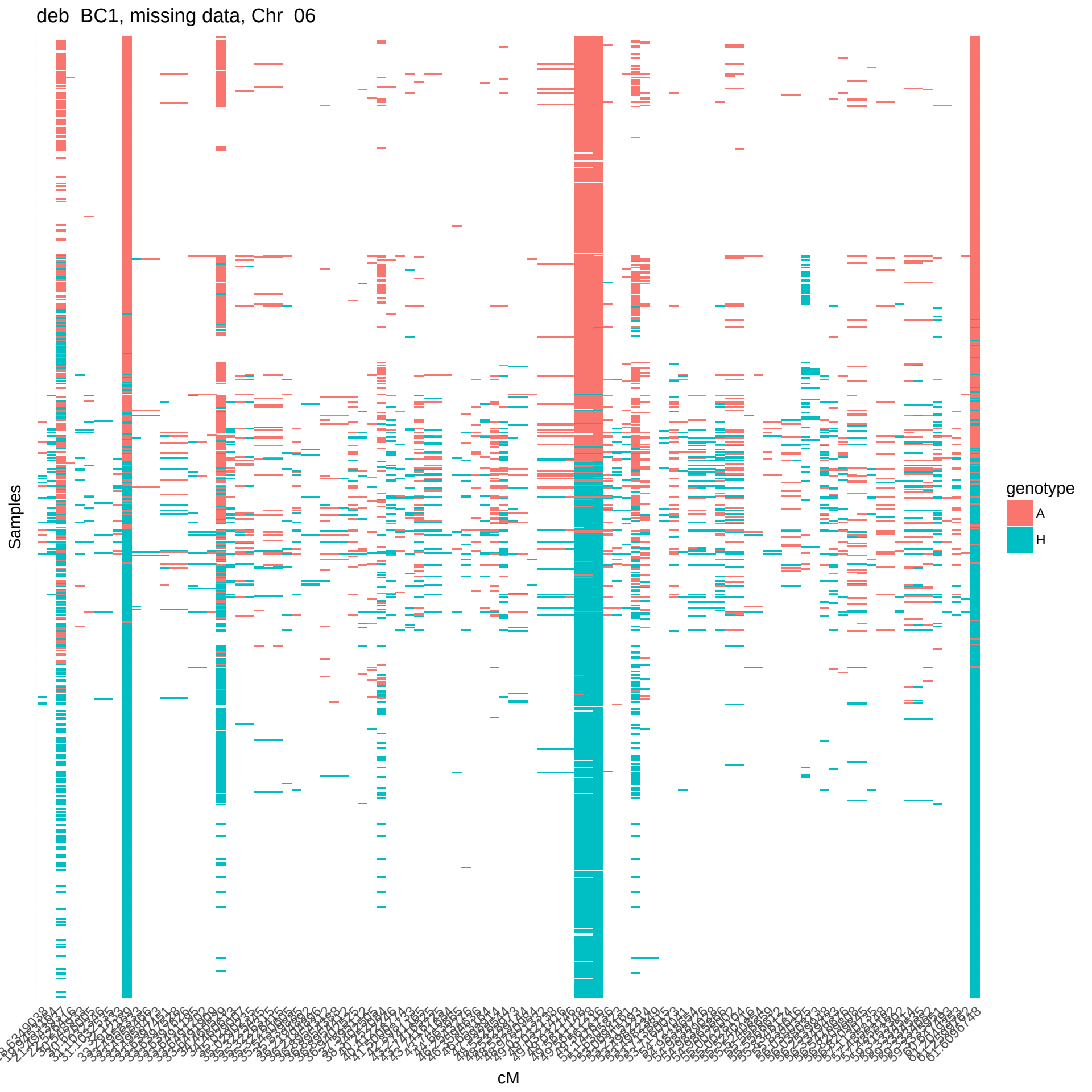
deb BC1, missing data, Chr 05
Samples
cM
genotype
A
H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Samples
cM
genotype
A
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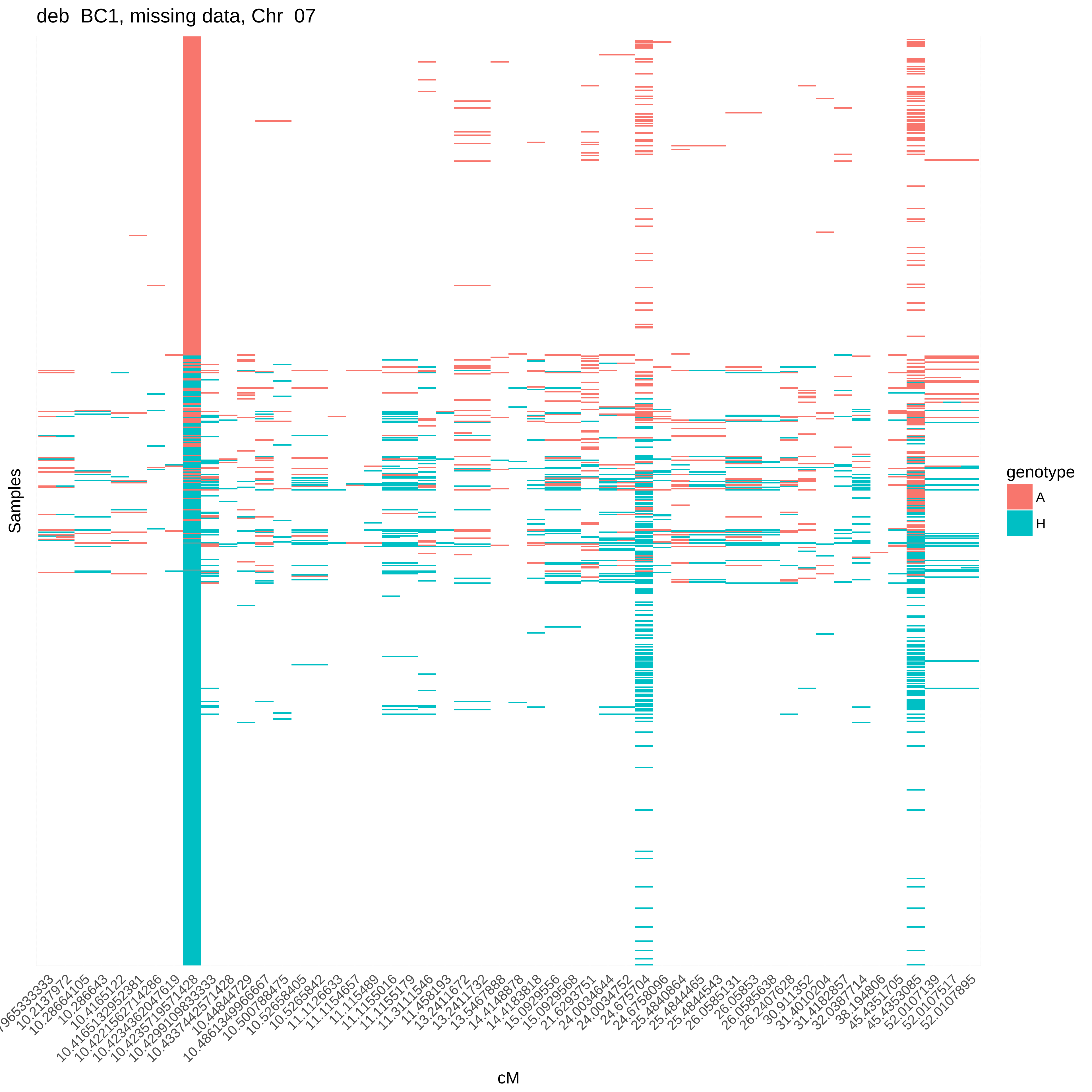
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genotype
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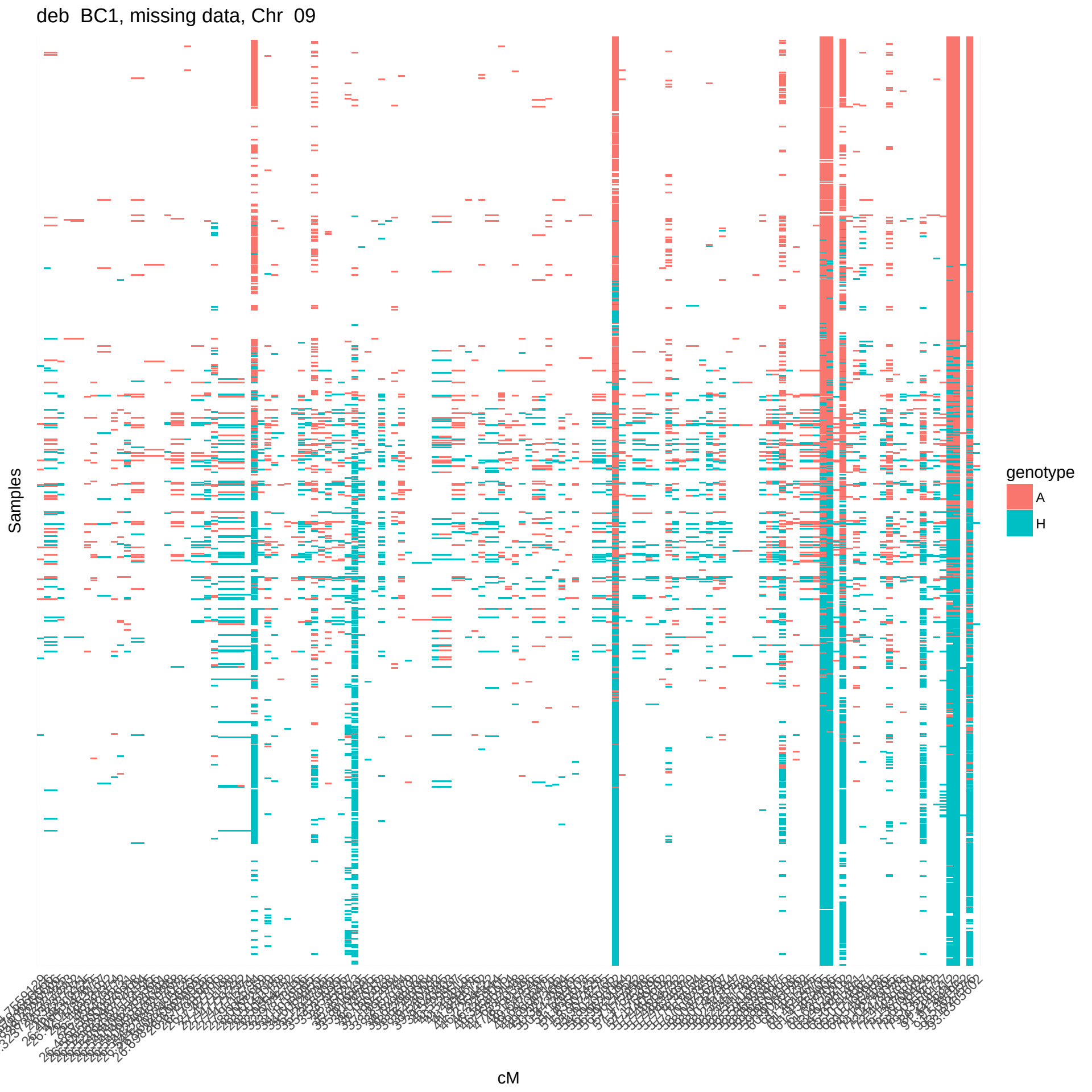
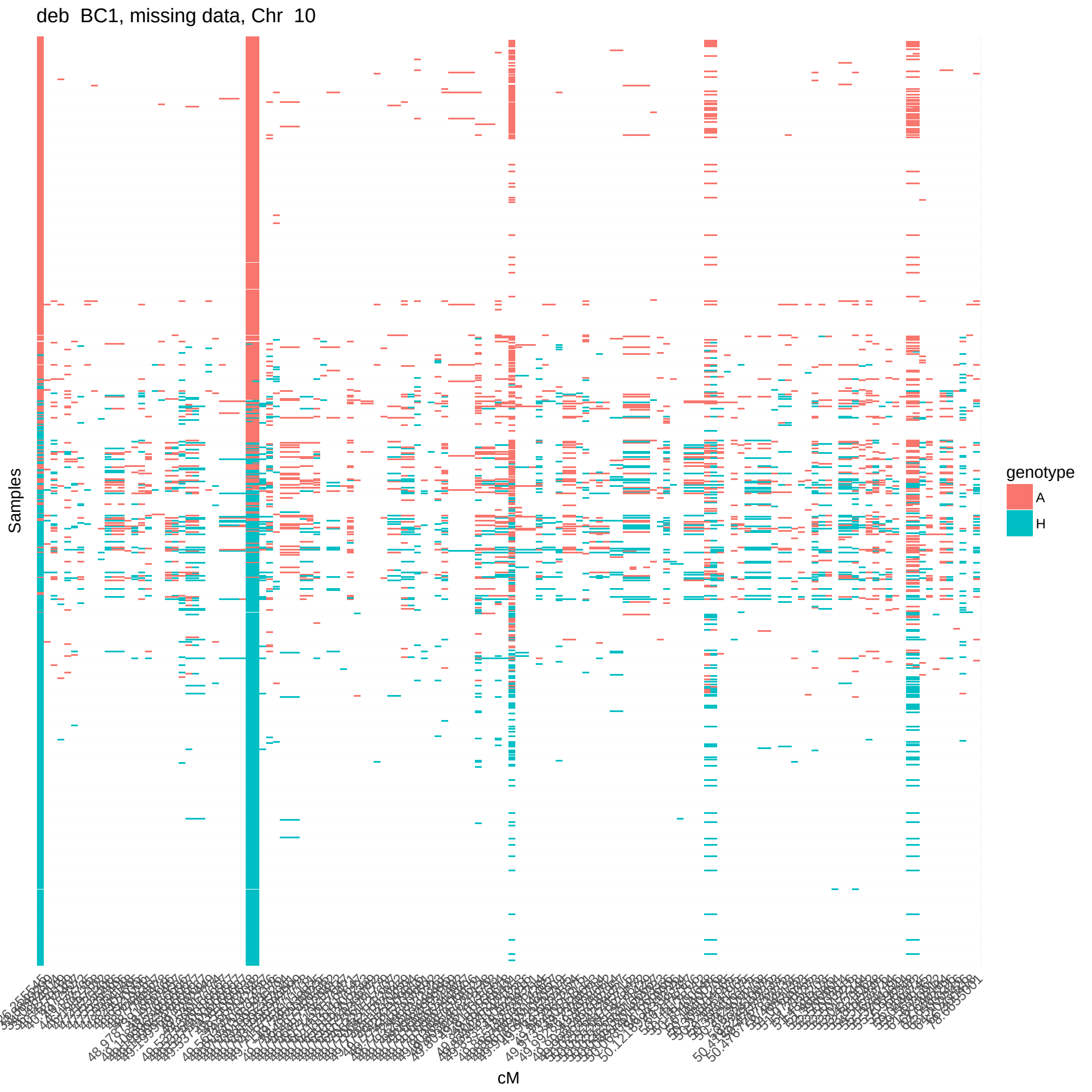
deb BC1, missing data, Chr 08
Samples
cM
genotype
A
H


deb BC1, missing data, Chr 09
Samples
cM
genotype
A
H


deb BC1, missing data, Chr 10
Samples
cM
genotype
A
H


deb BC1, missing data, Chr 11
Samples
cM
genotype
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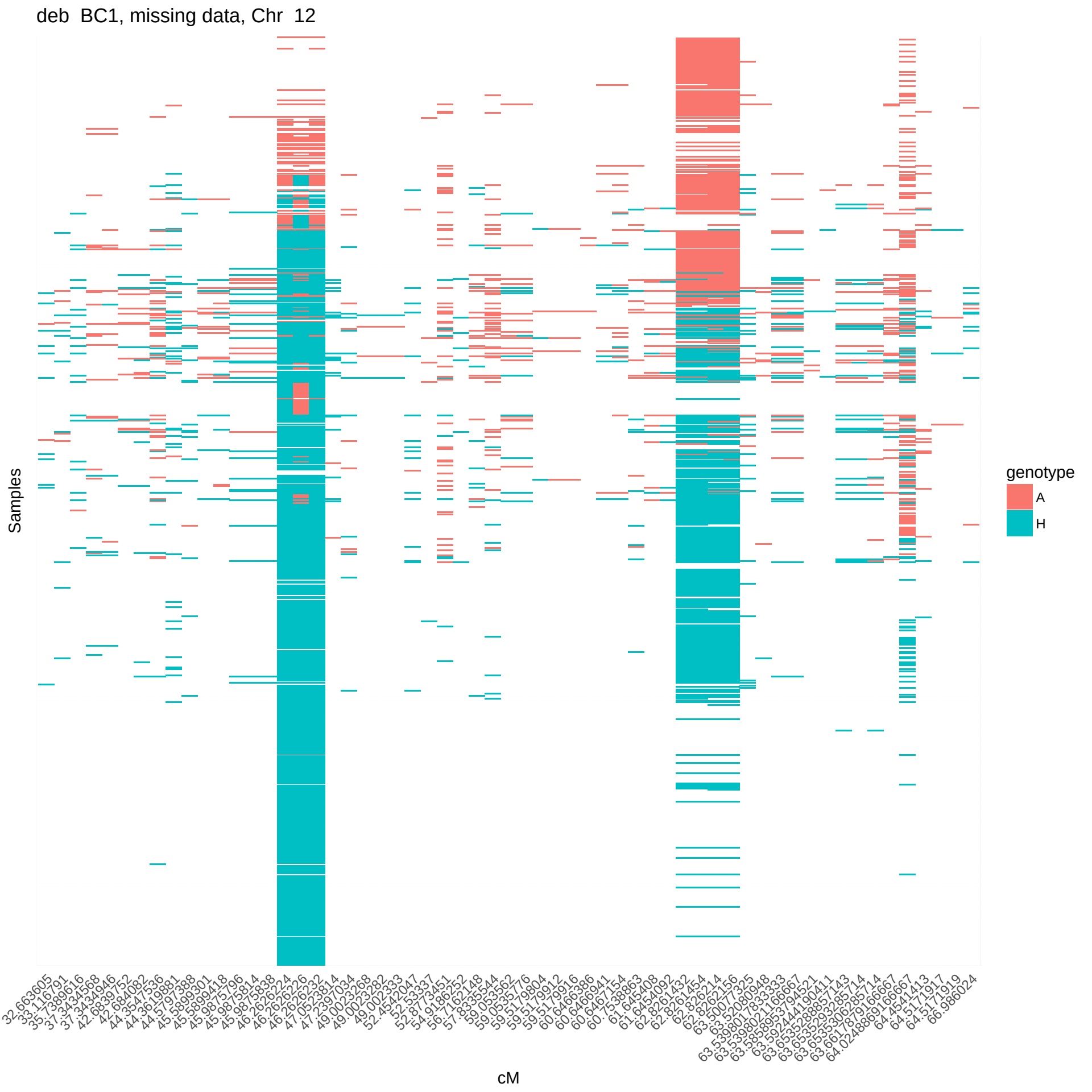
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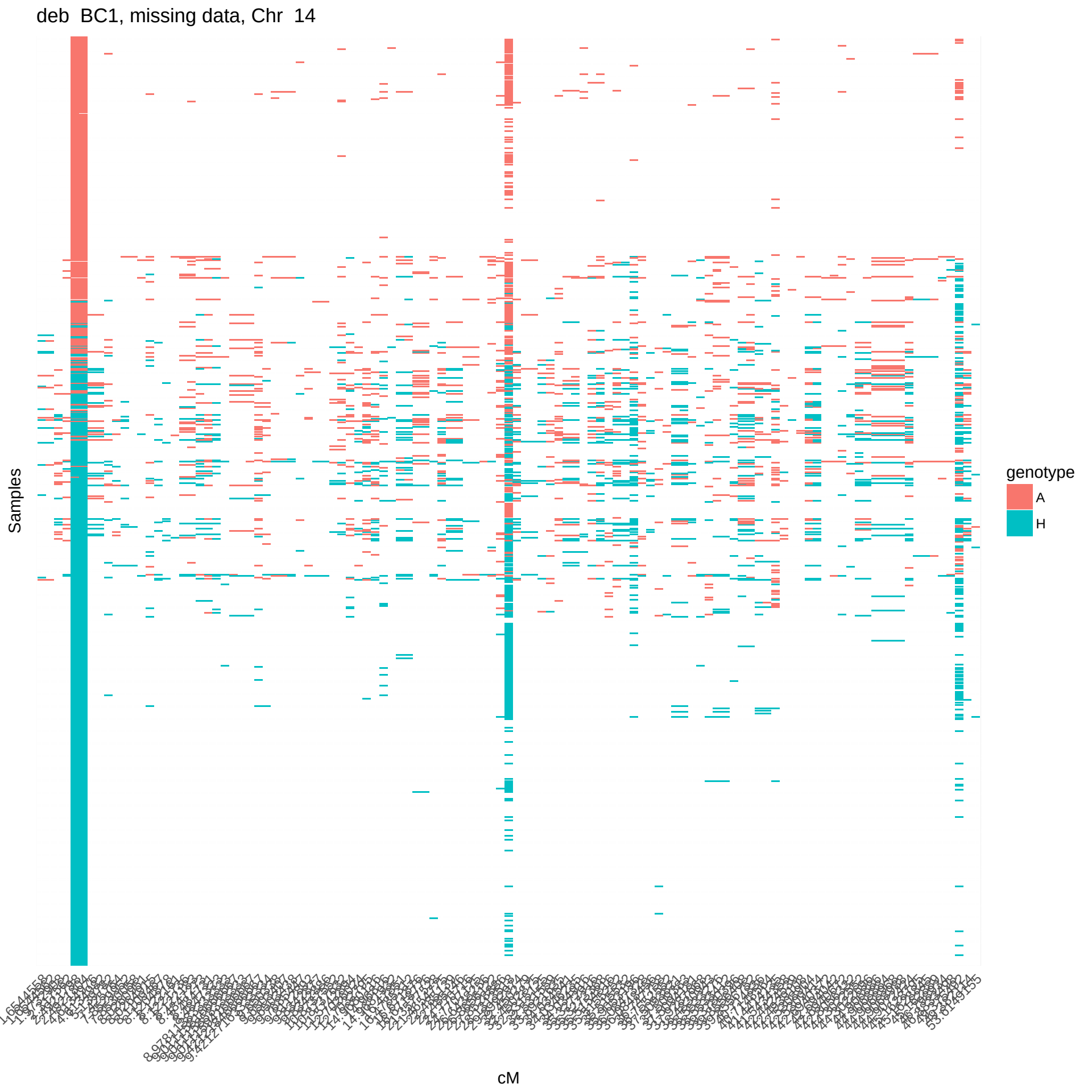
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Samples
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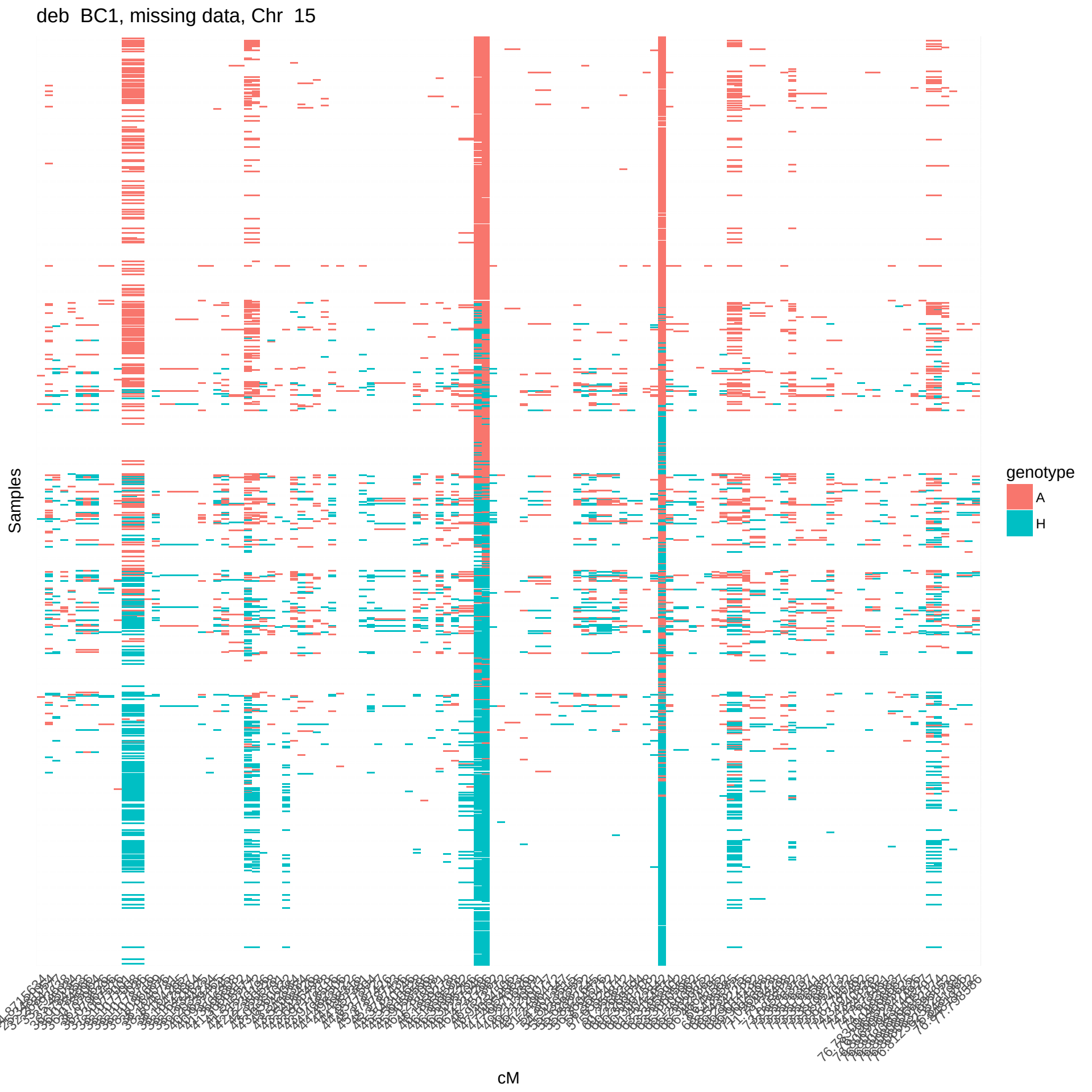
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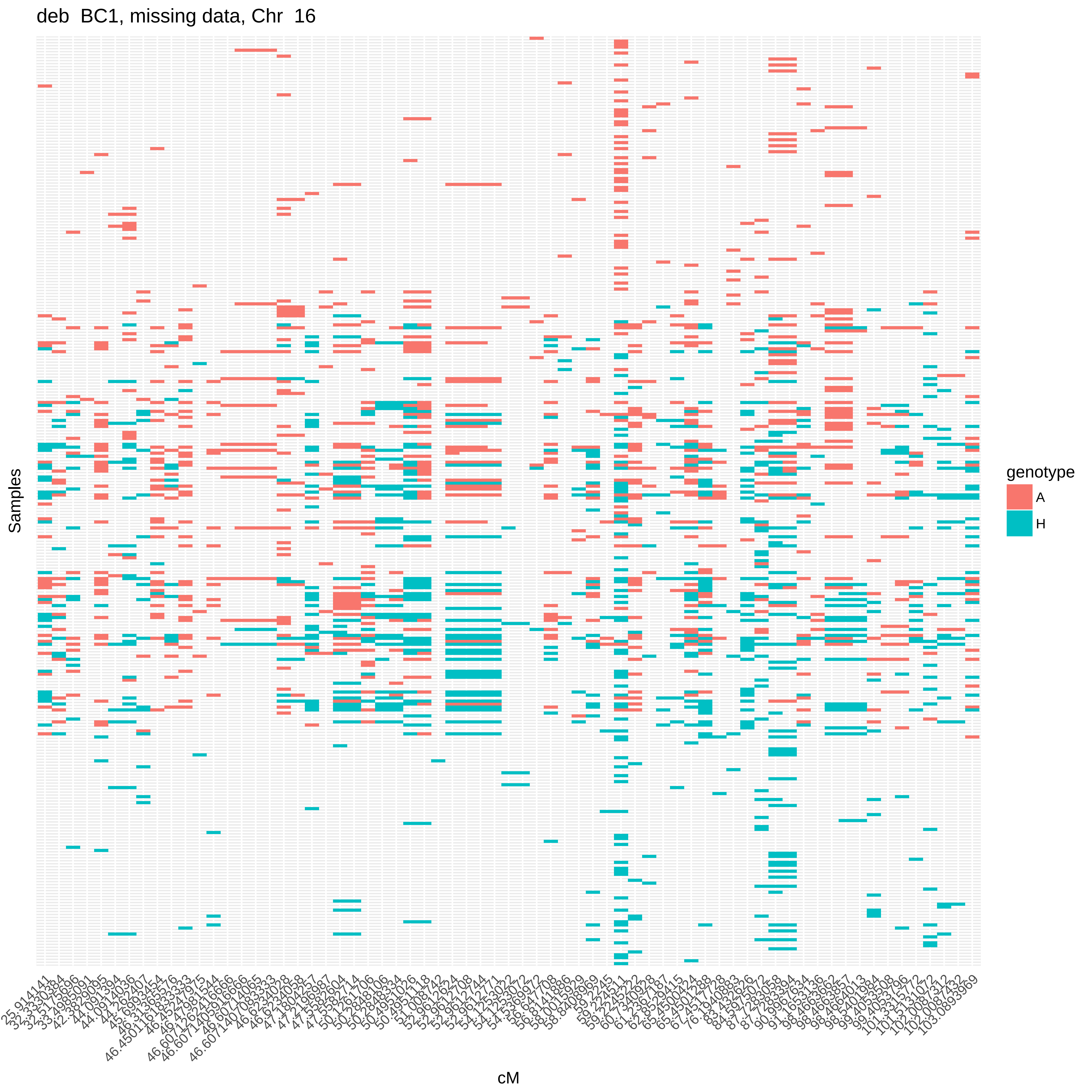
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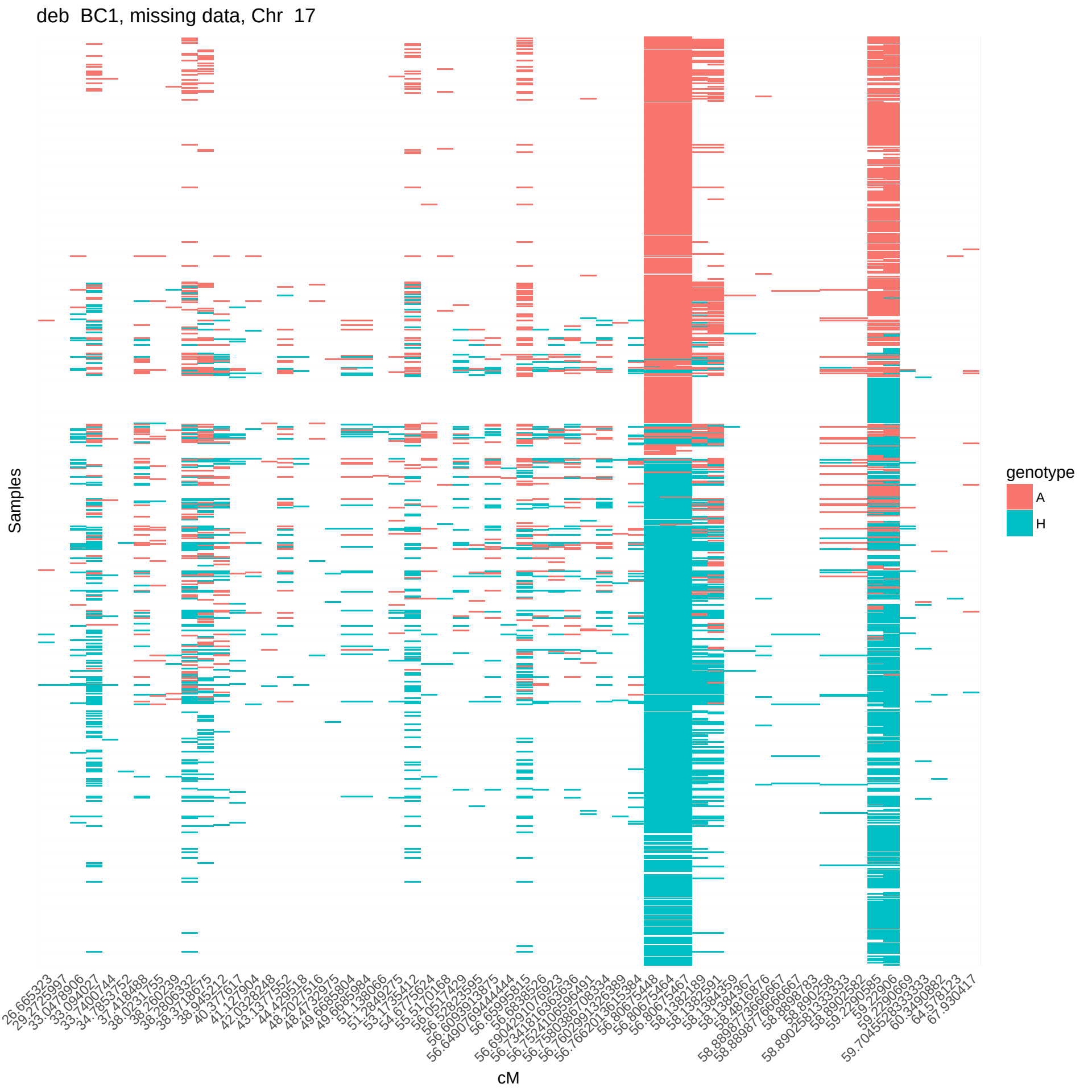
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