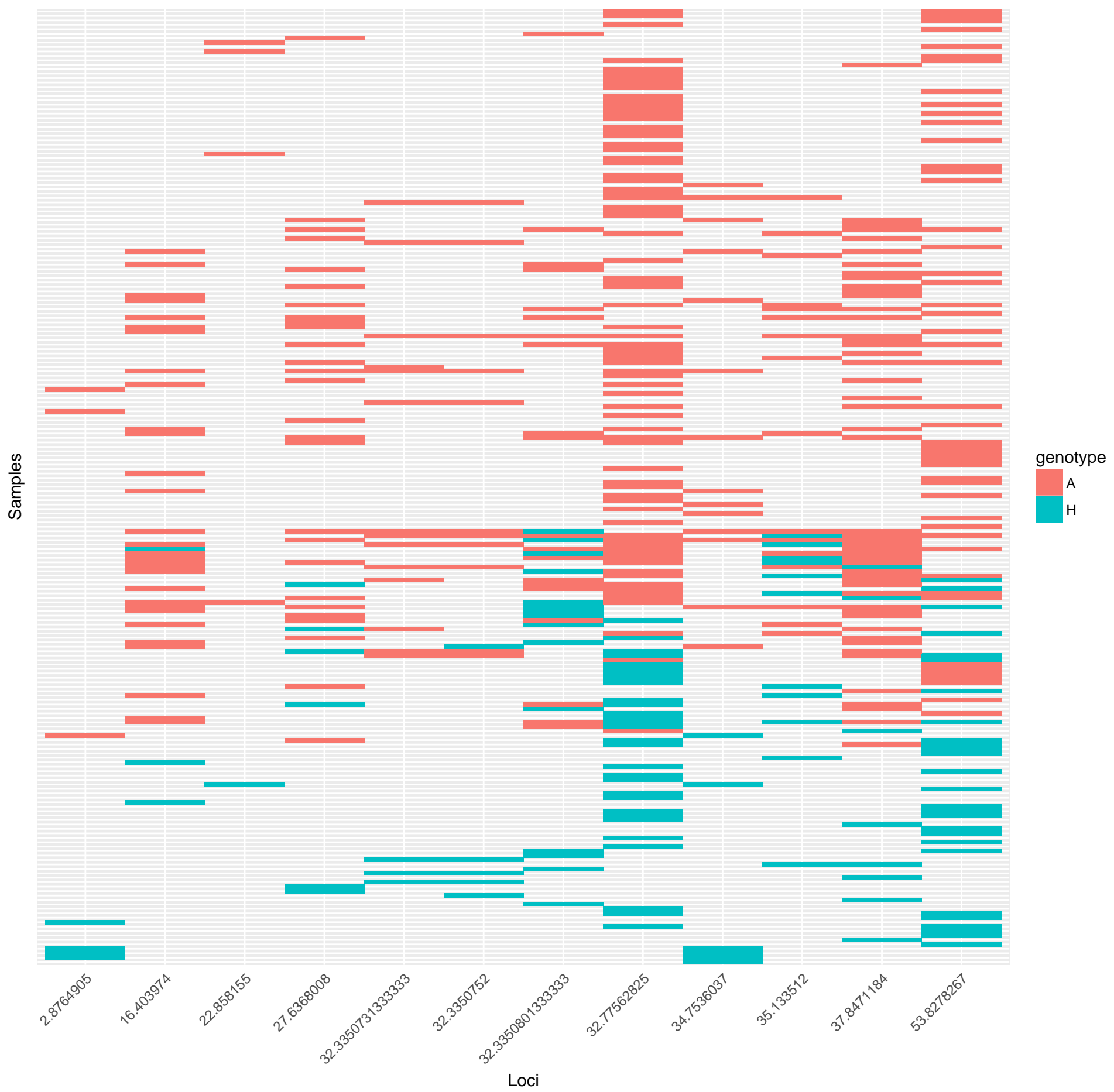
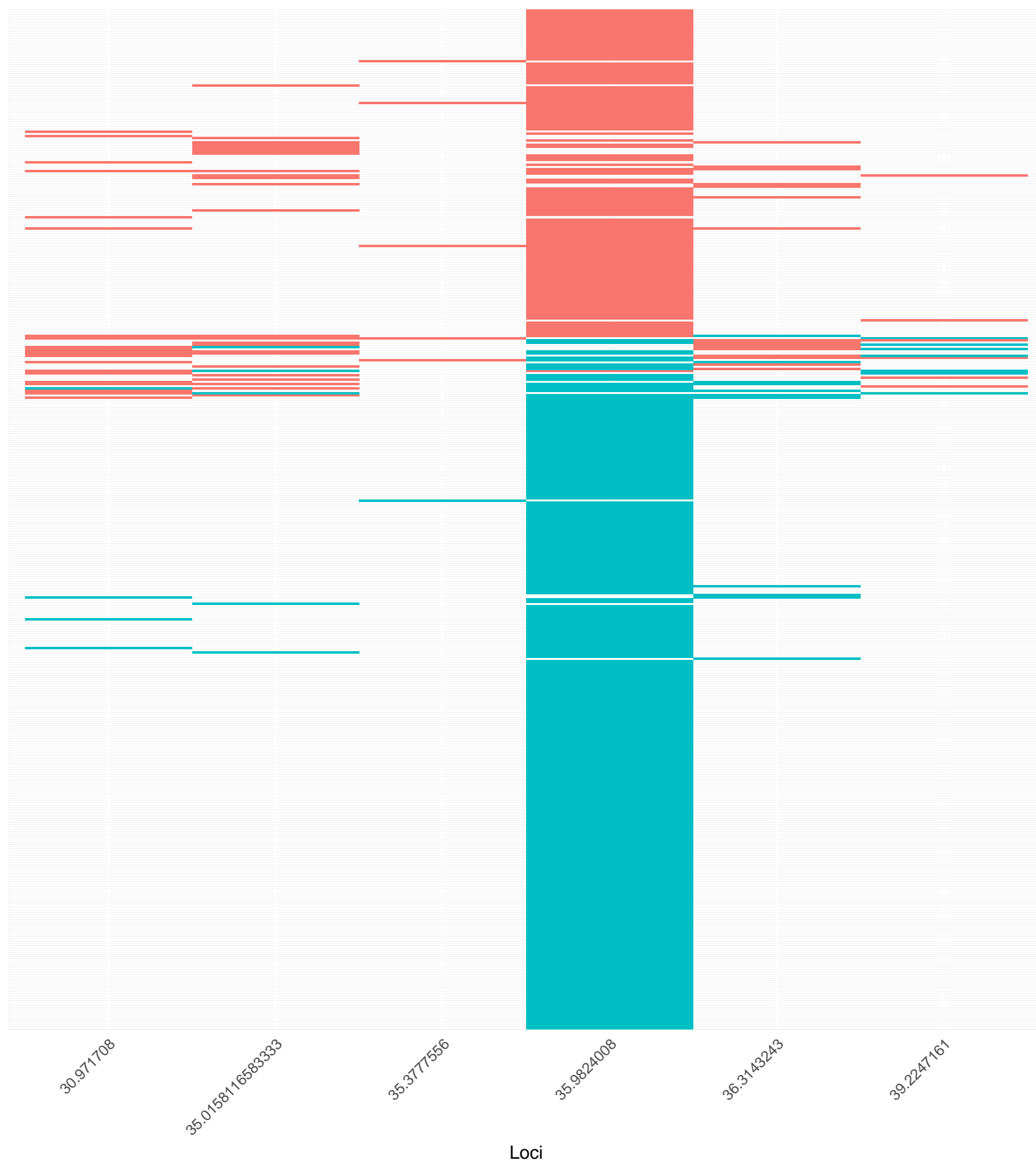


ann1 BC1, missing data, Chr 01



ann1 BC1, missing data, Chr 02



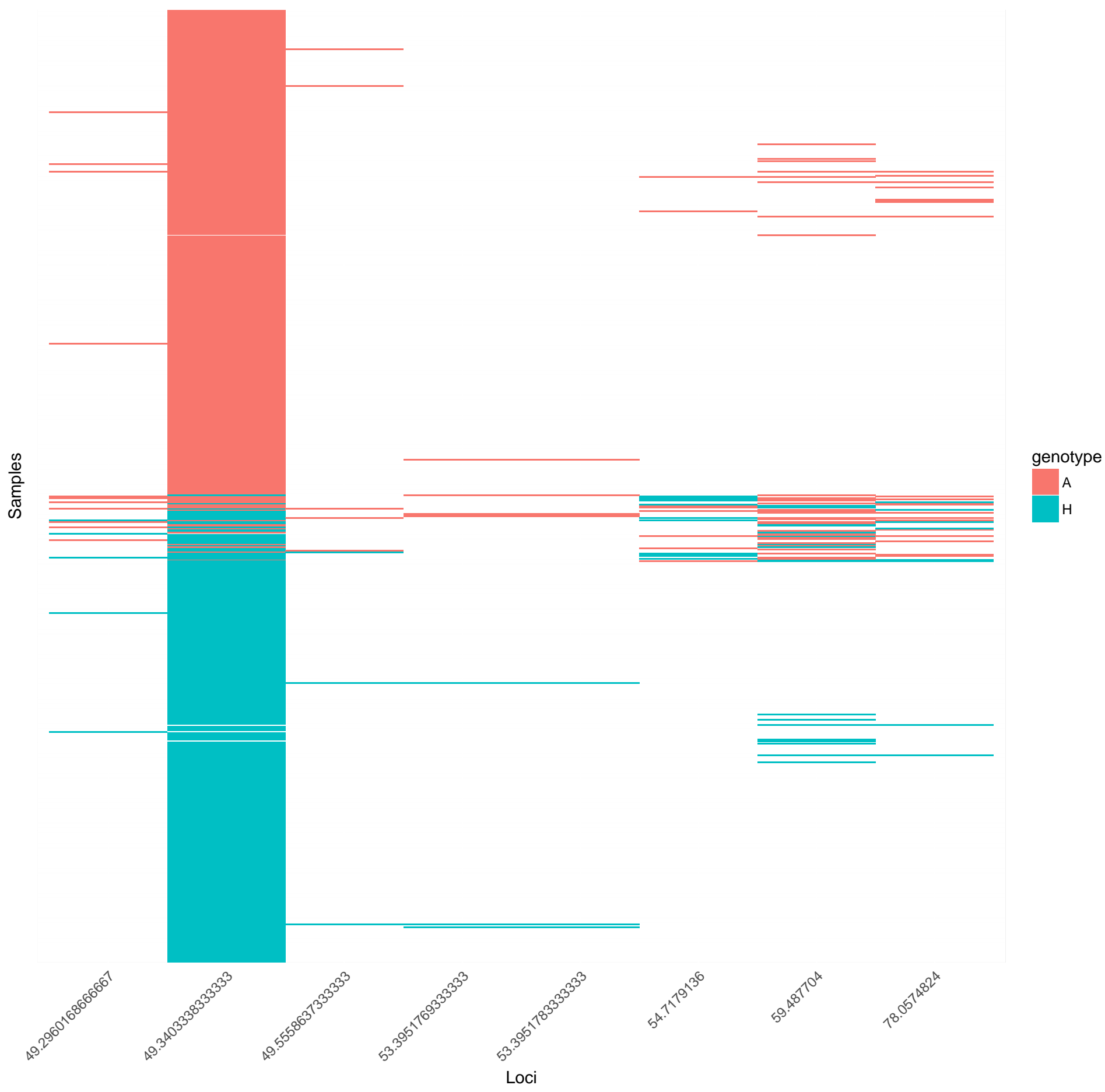
ann1 BC1, missing data, Chr 03



ann1 BC1, missing data, Chr 04



ann1 BC1, missing data, Chr 05



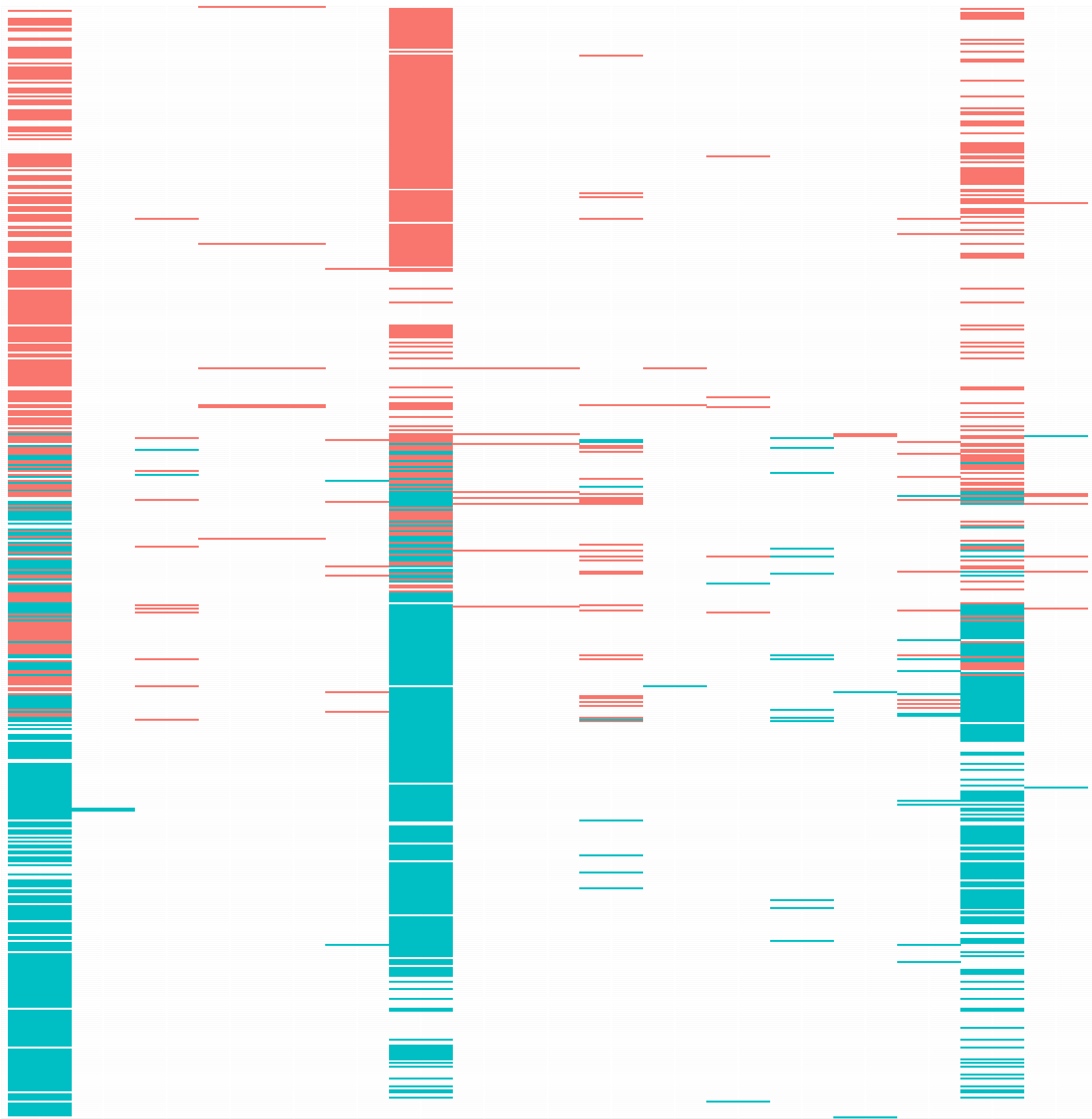
ann1 BC1, missing data, Chr 06

Samples

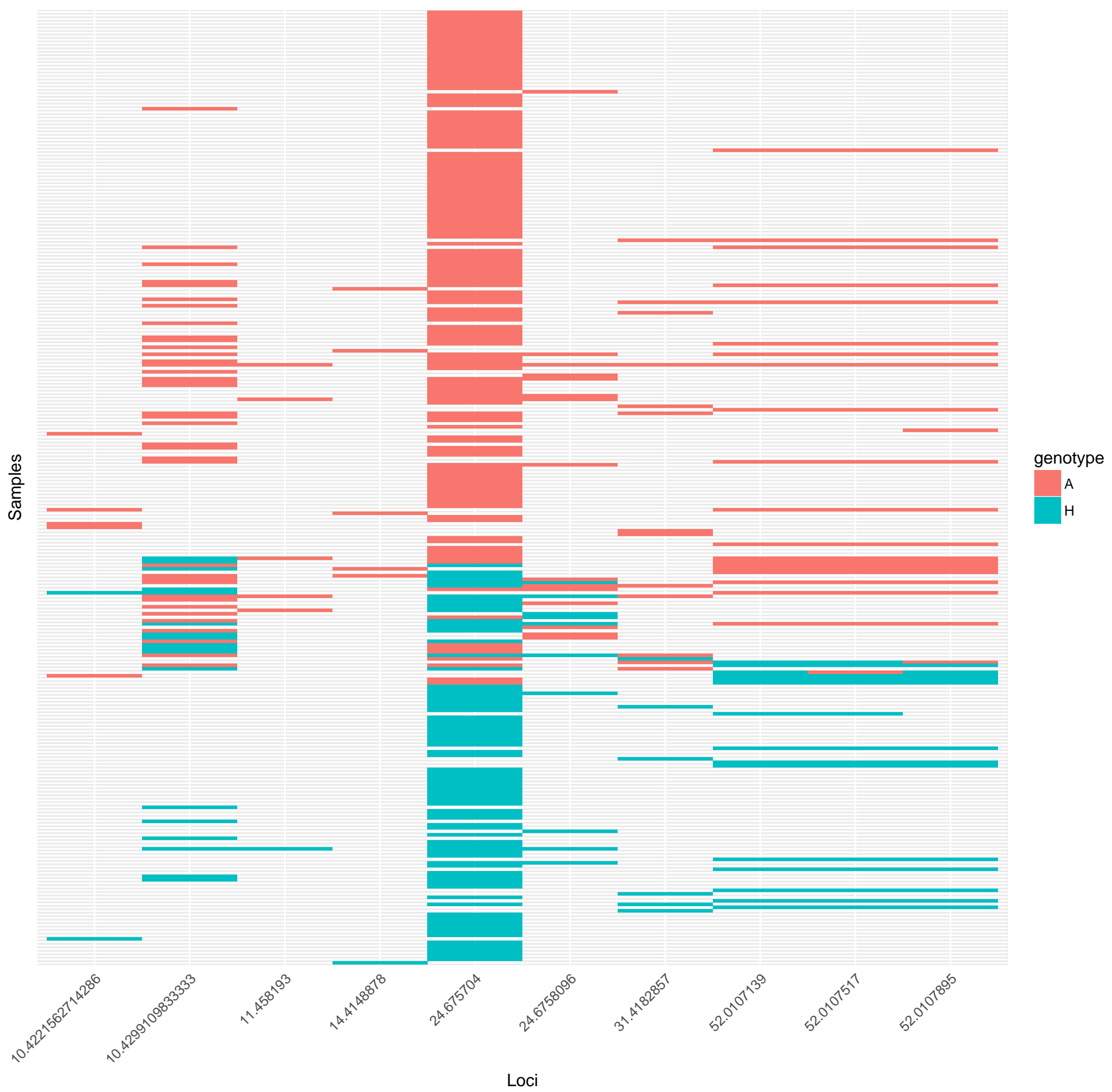
genotype  
A  
H

21.4943937  
22.526416  
30.548933  
31.1032346  
31.1032535  
33.4958333  
34.460529  
36.2194892  
36.2194896  
40.4122246  
43.741684  
44.663665  
46.3594636  
48.9780984  
53.0694161  
53.2315193  
57.1130735

Loci



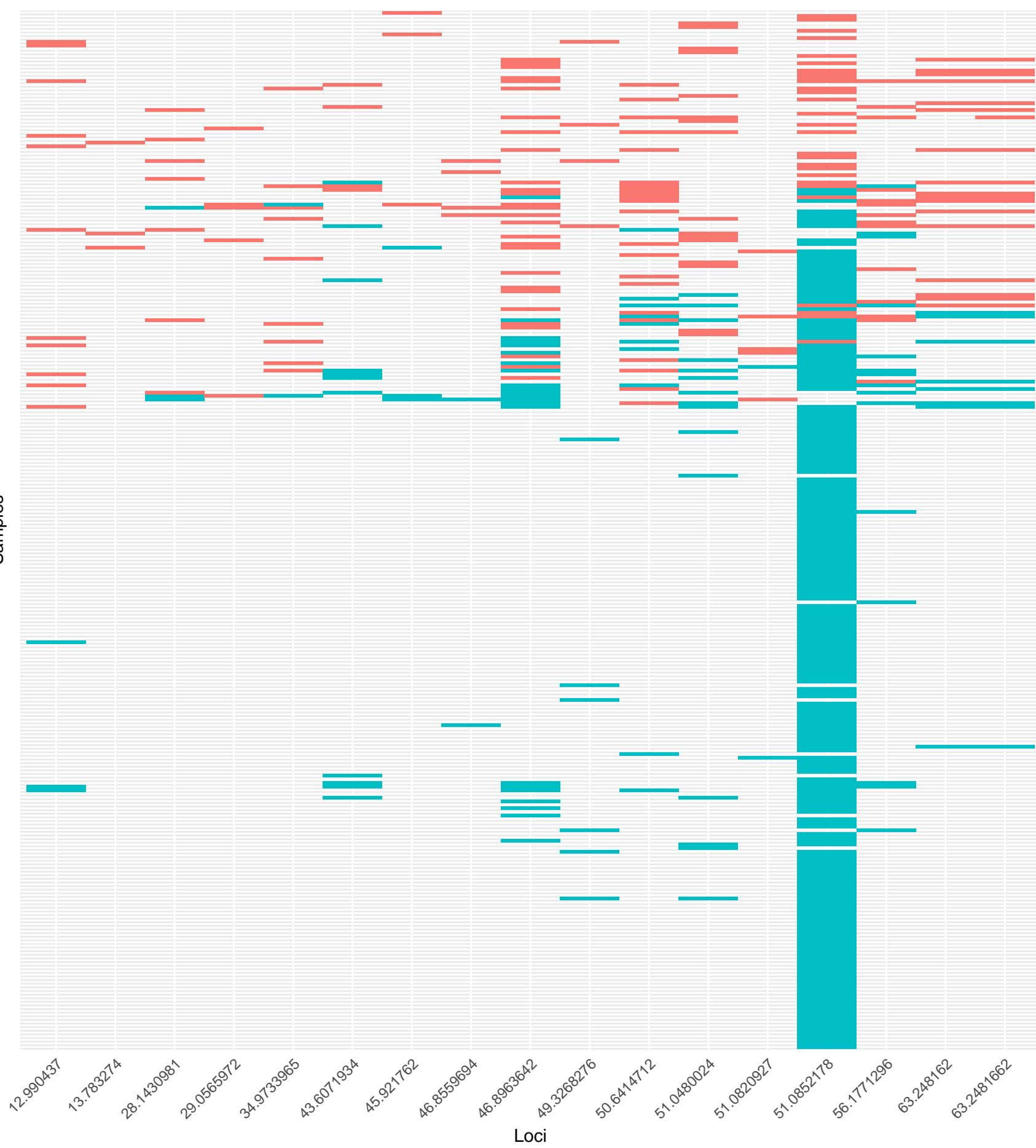
ann1 BC1, missing data, Chr 07



ann1 BC1, missing data, Chr 08

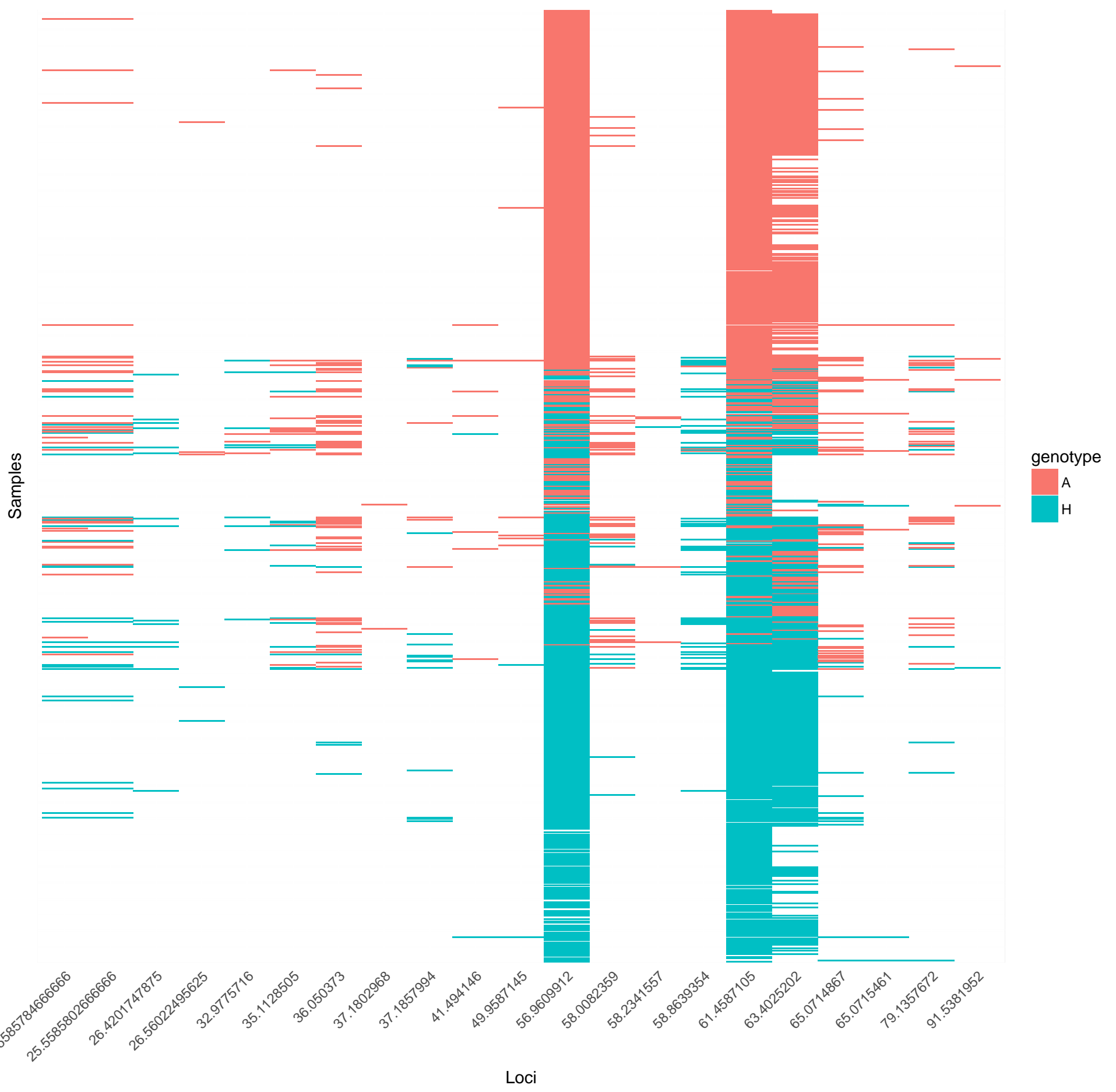
Samples

genotype  
A  
H

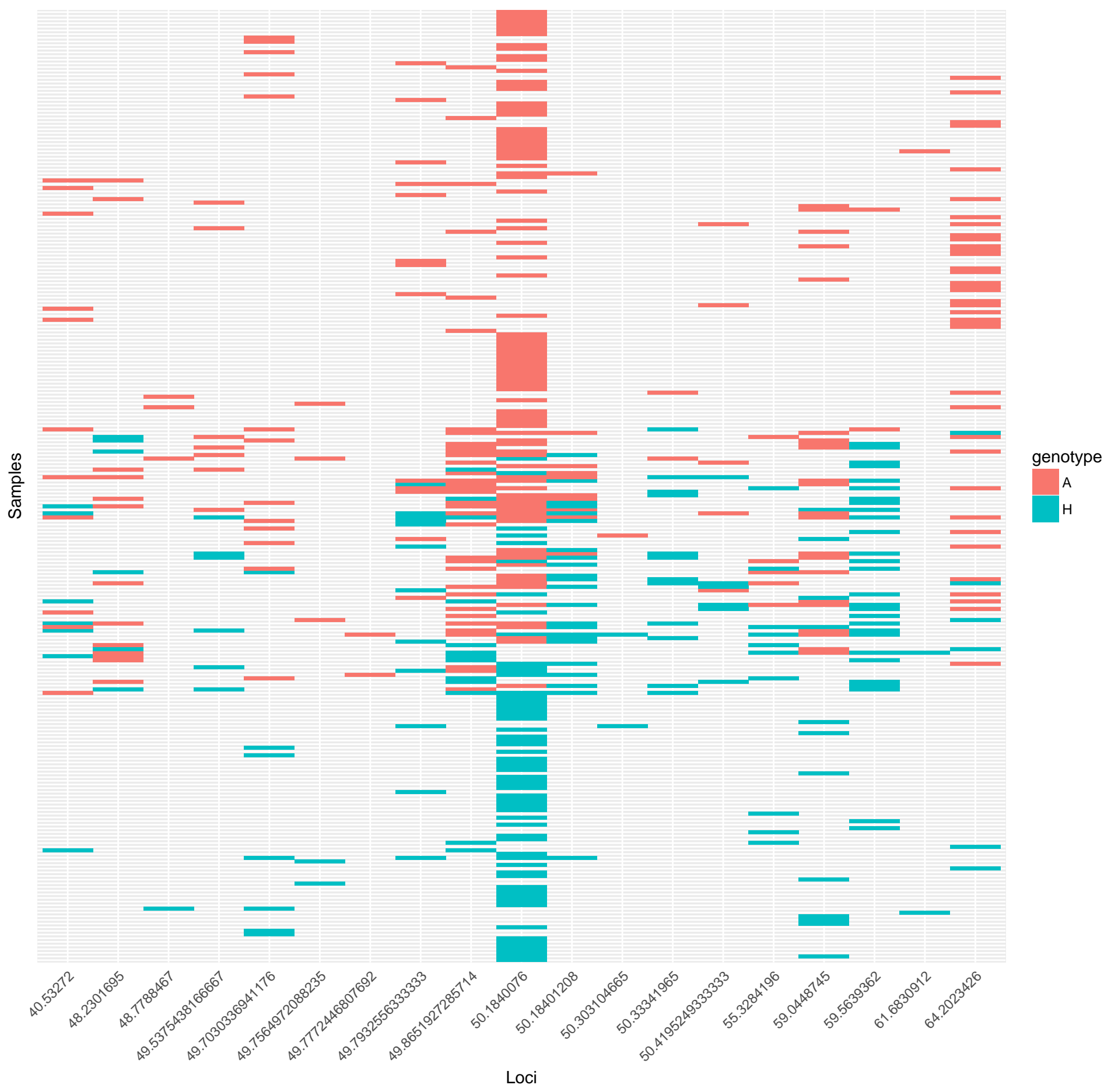


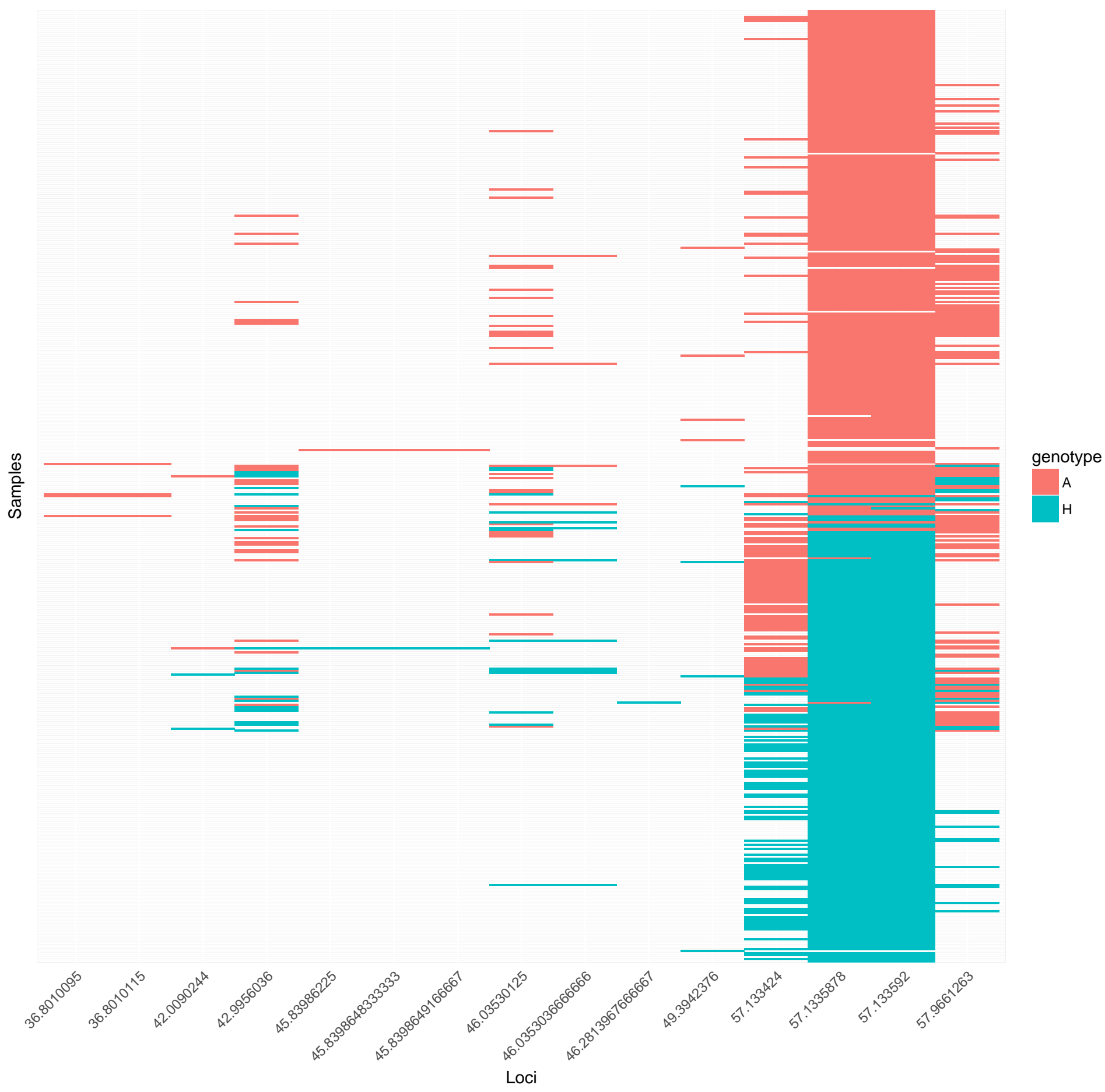


ann1 BC1, missing data, Chr 09

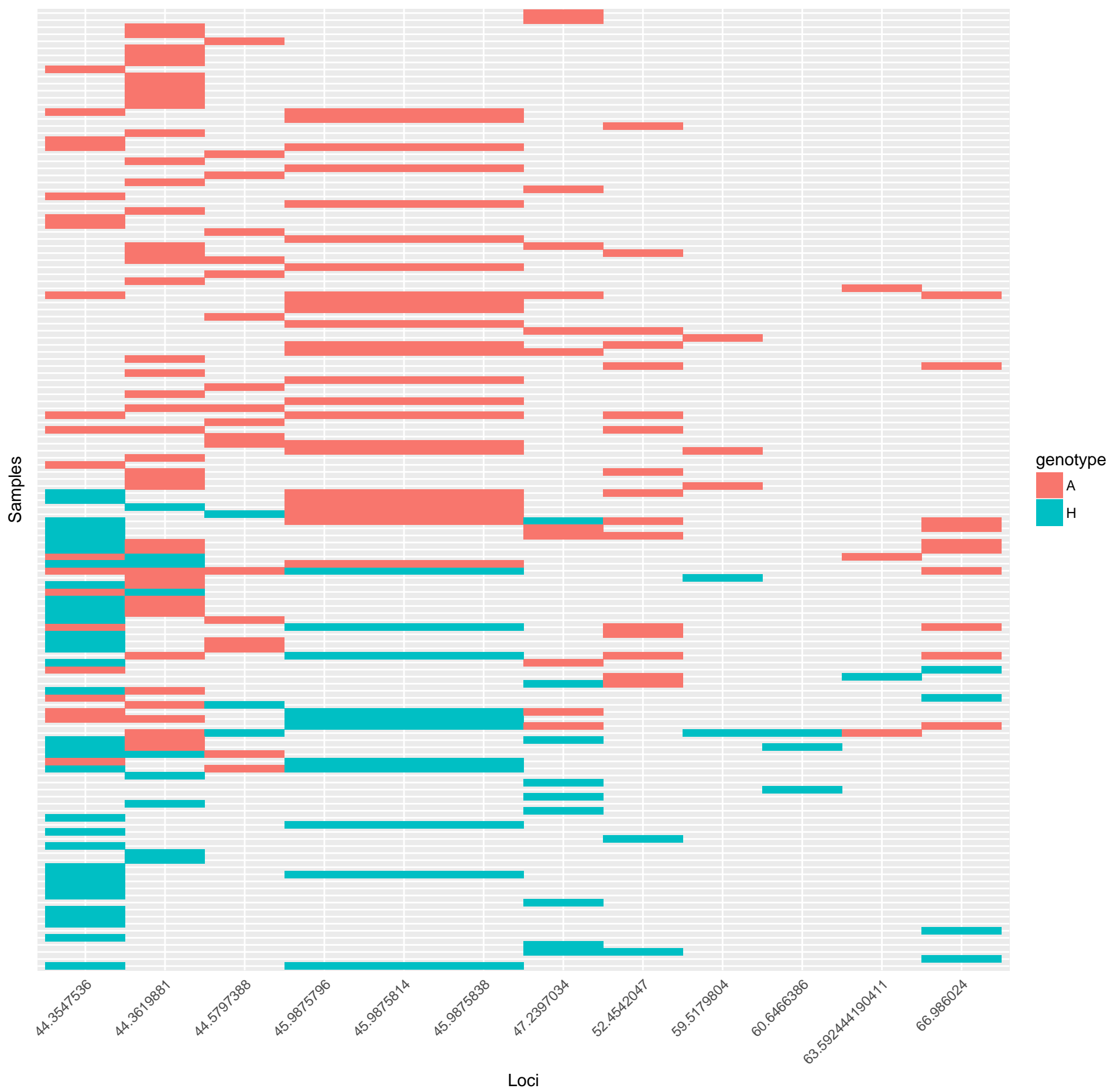


ann1 BC1, missing data, Chr 10

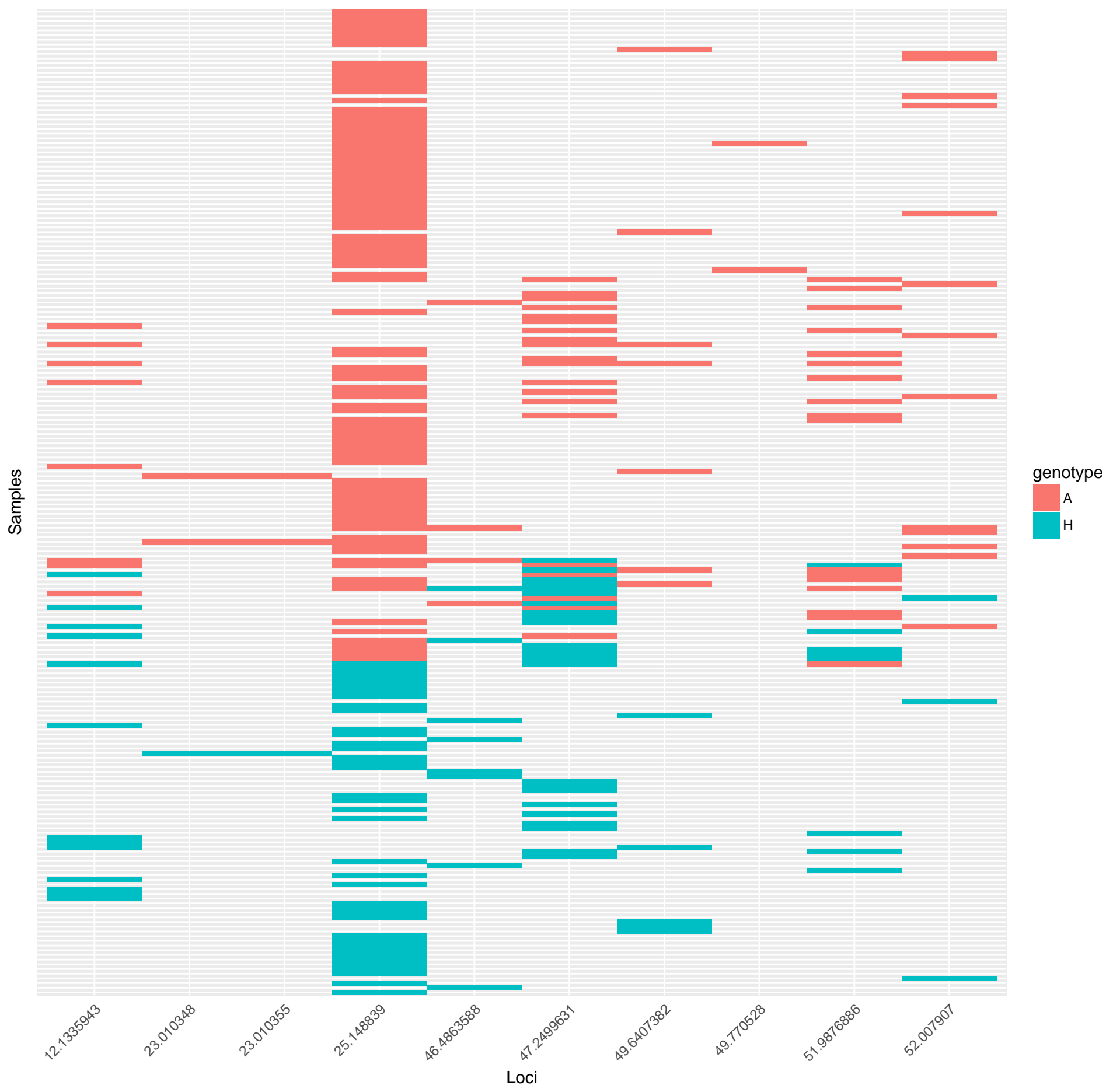




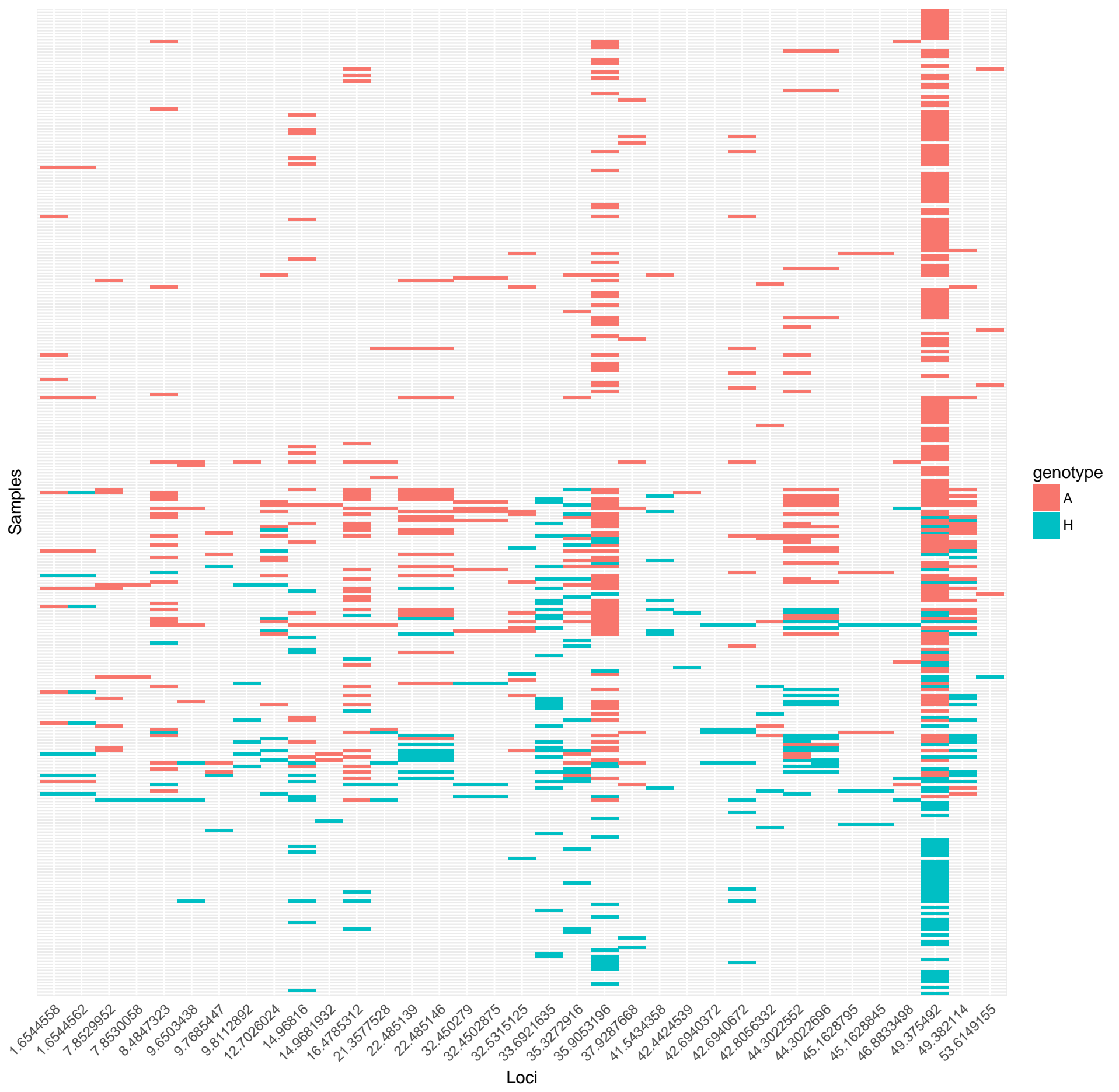
ann1 BC1, missing data, Chr 12



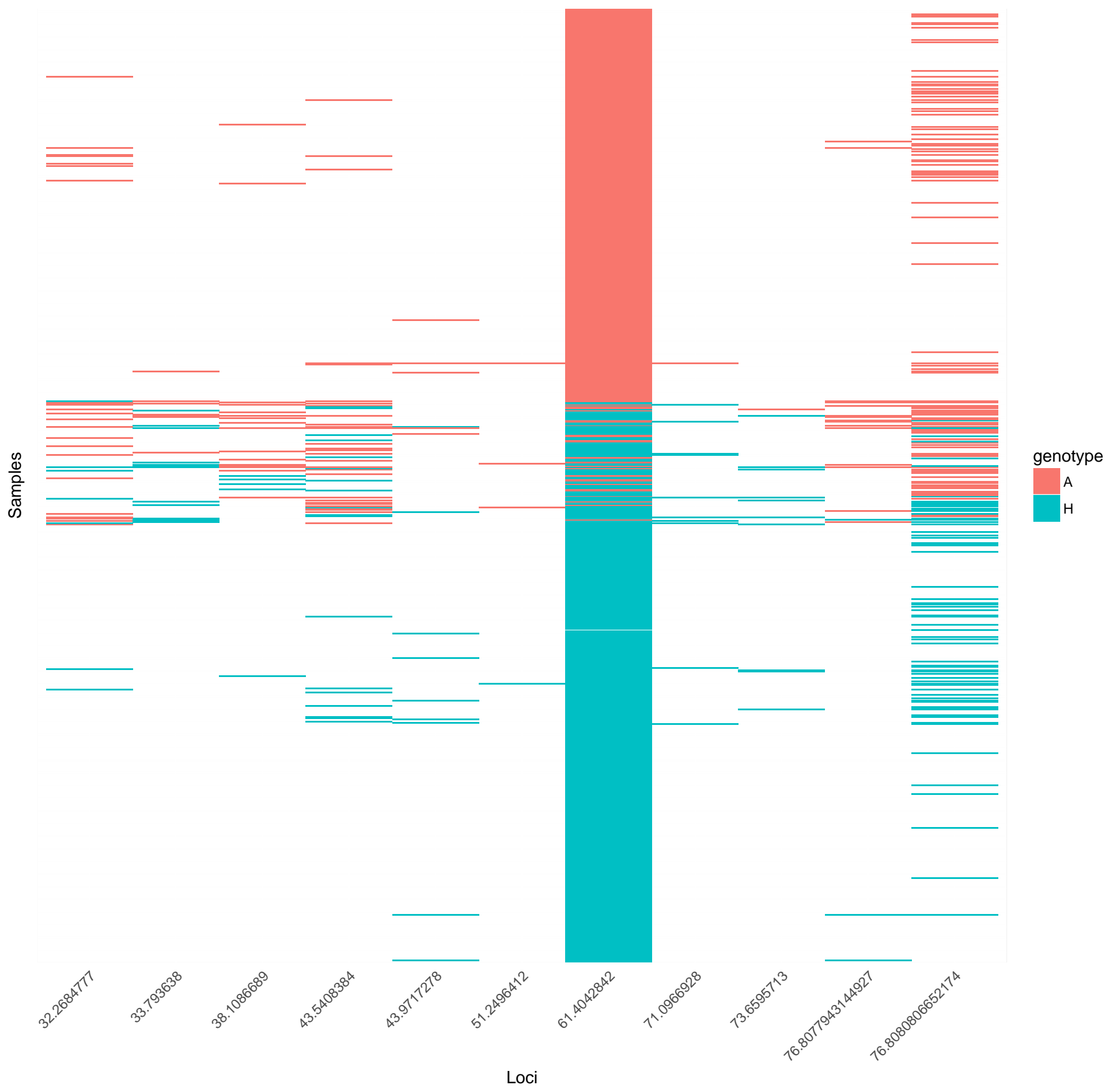
ann1 BC1, missing data, Chr 13



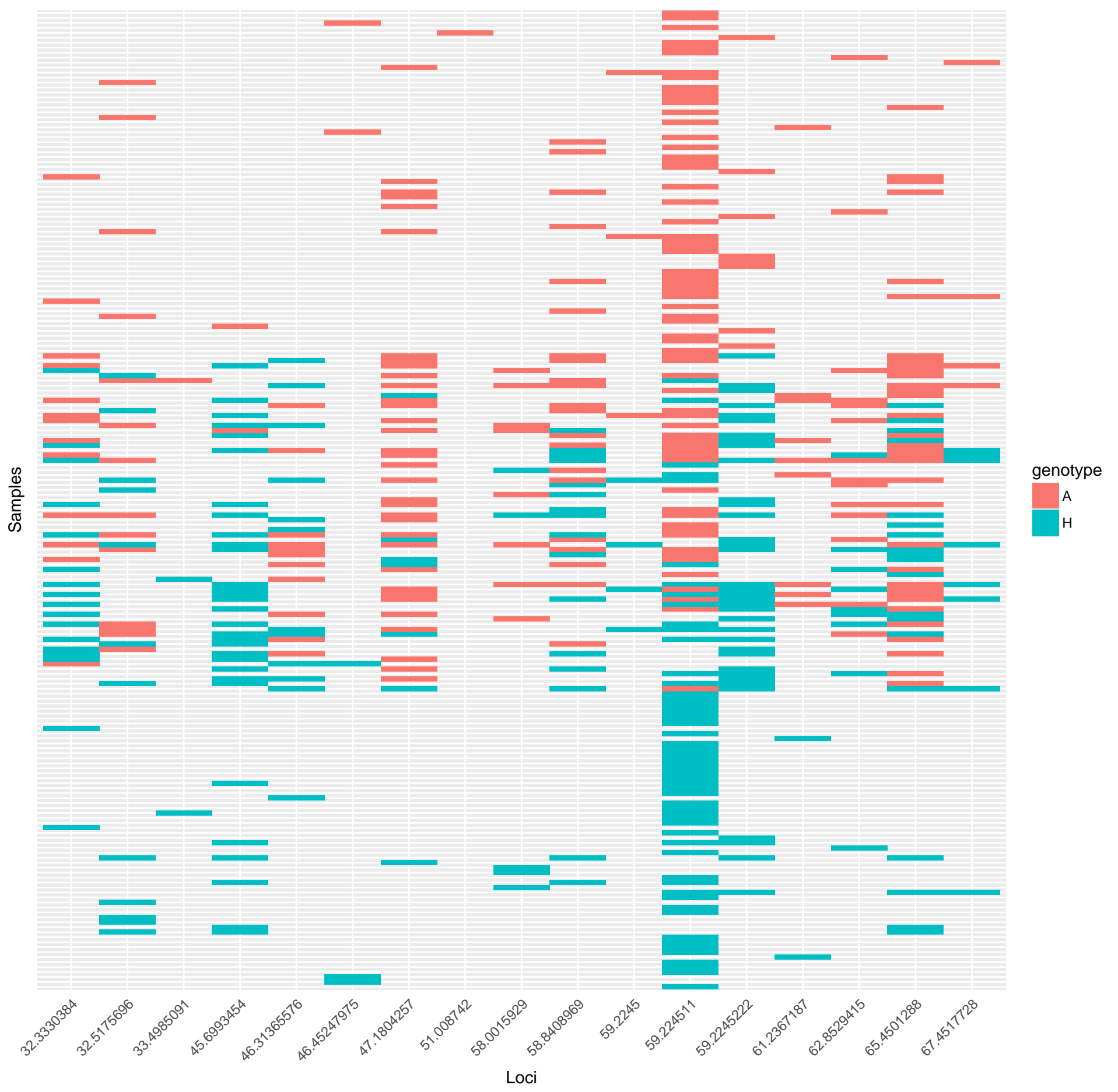
ann1 BC1, missing data, Chr 14



ann1 BC1, missing data, Chr 15

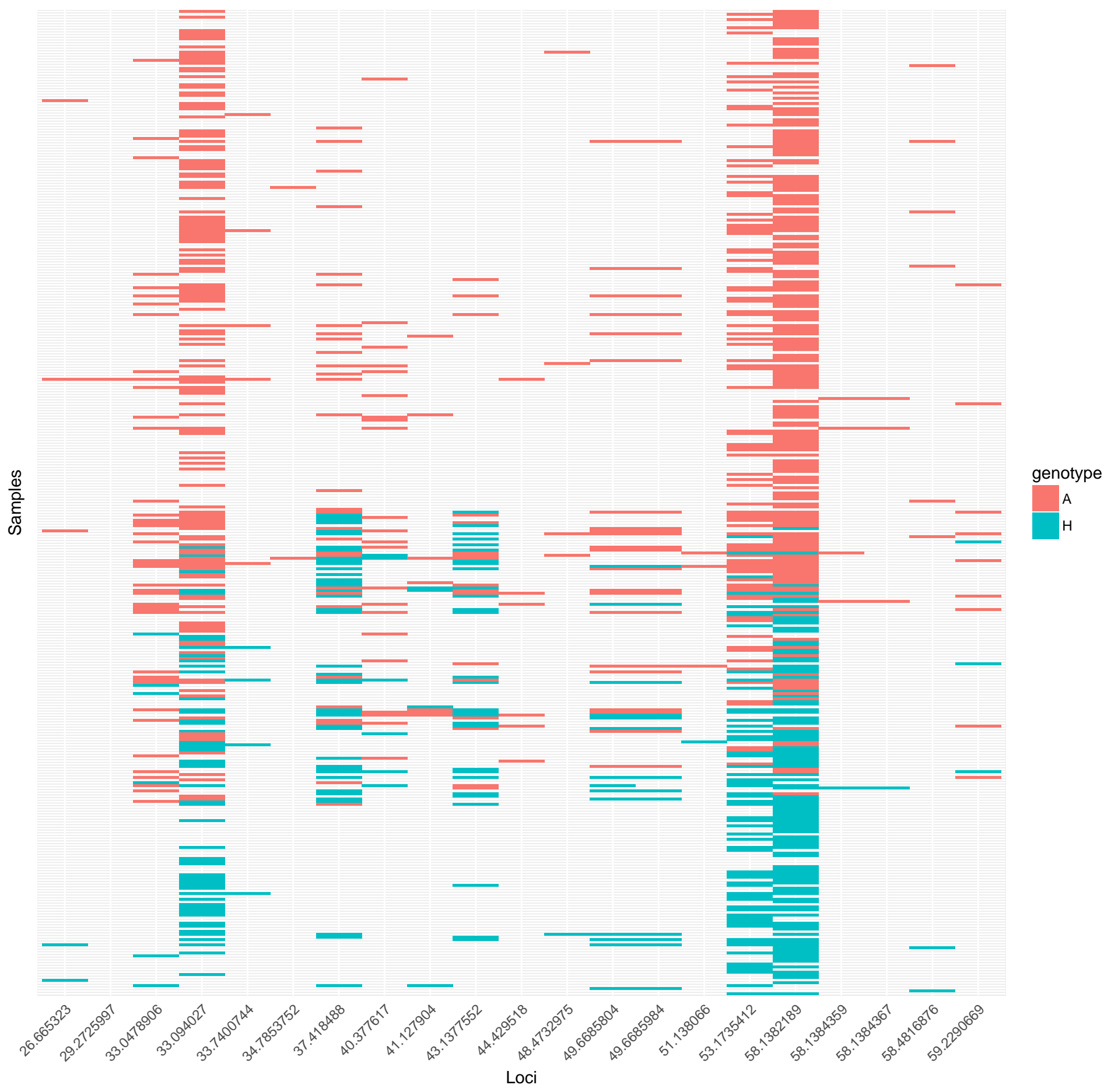


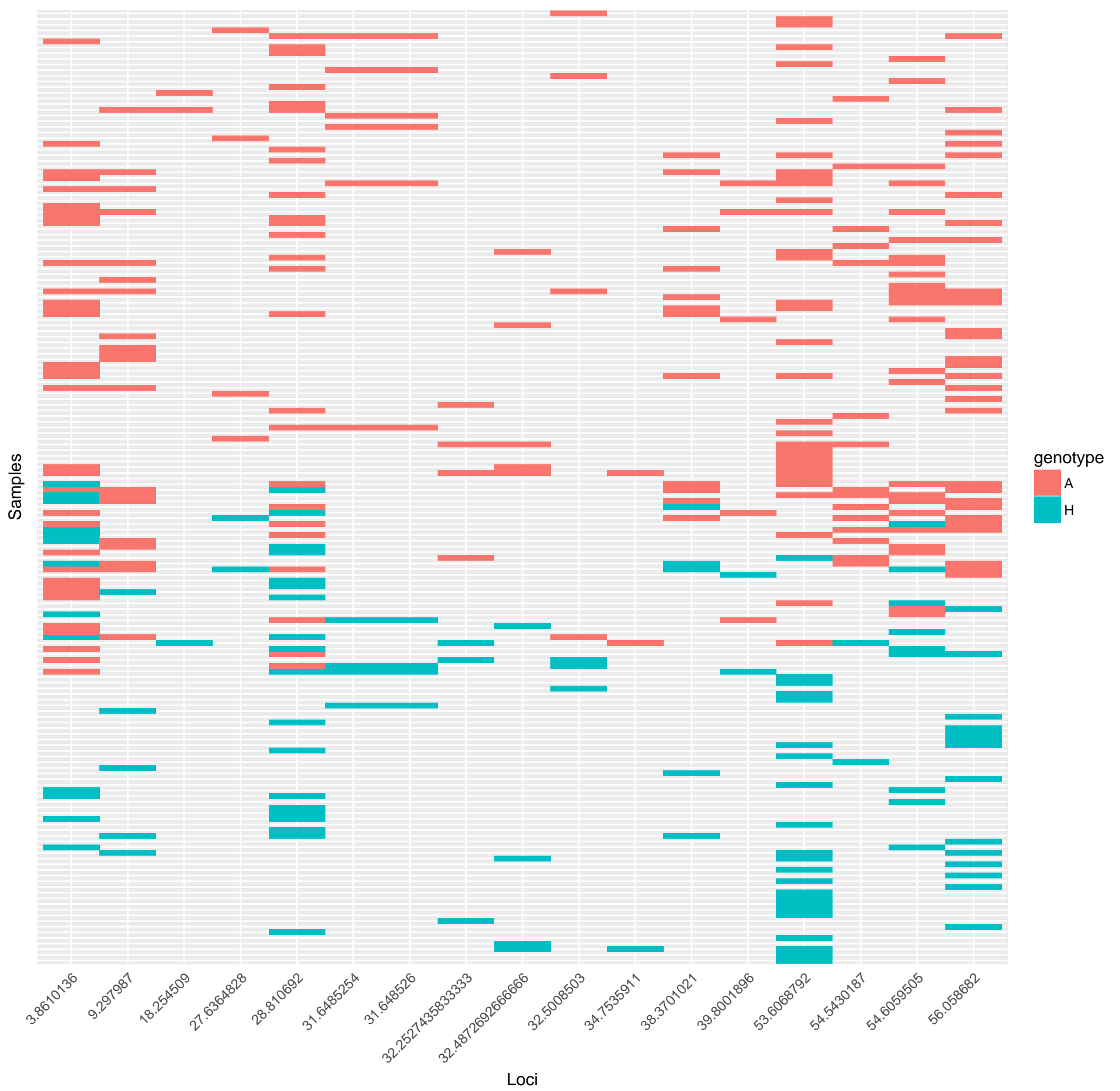
ann1 BC1, missing data, Chr 16





ann1 BC1, missing data, Chr 17





ann2 BC1, missing data, Chr 02

Samples

genotype

A

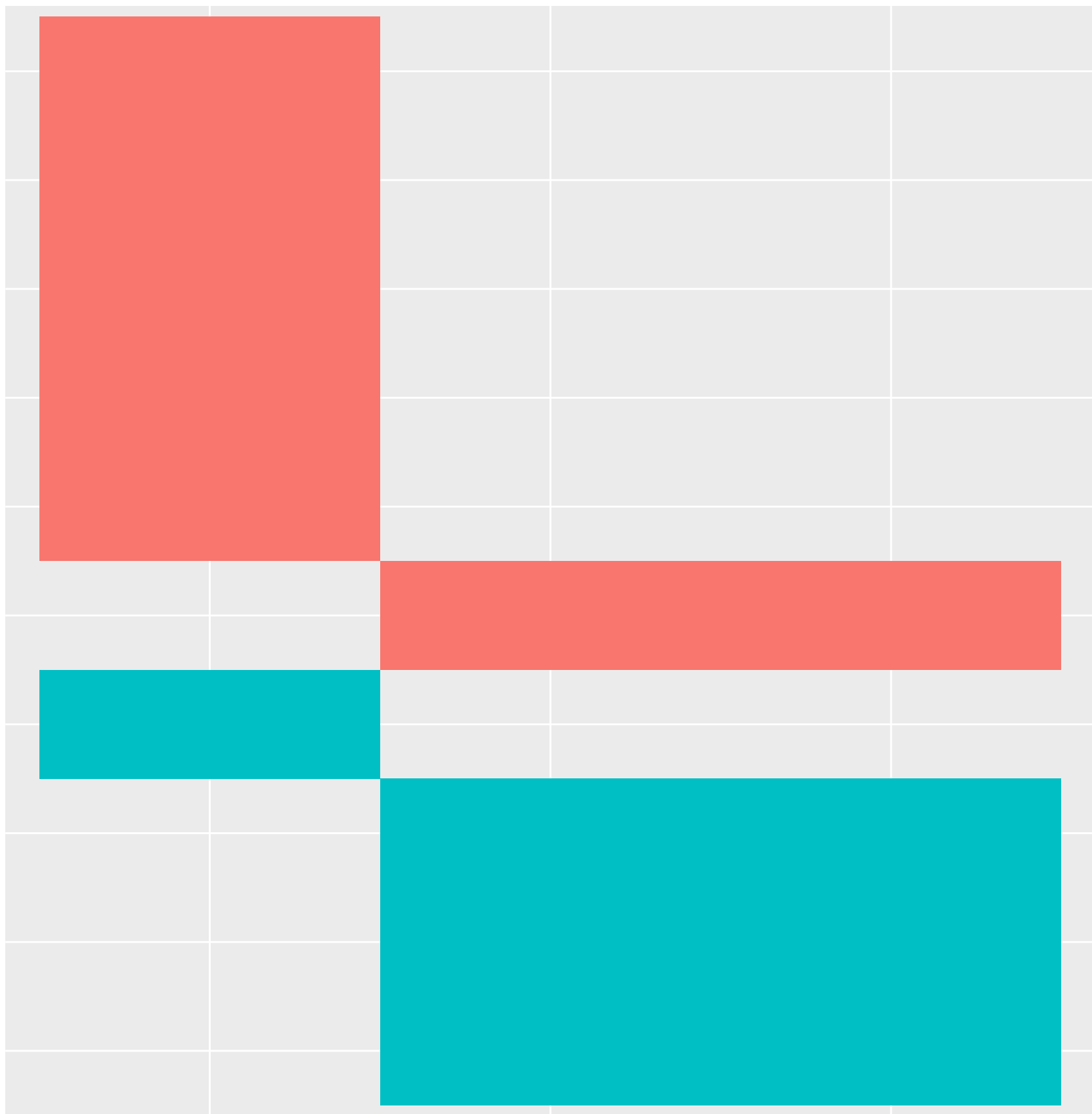
H

39.745247

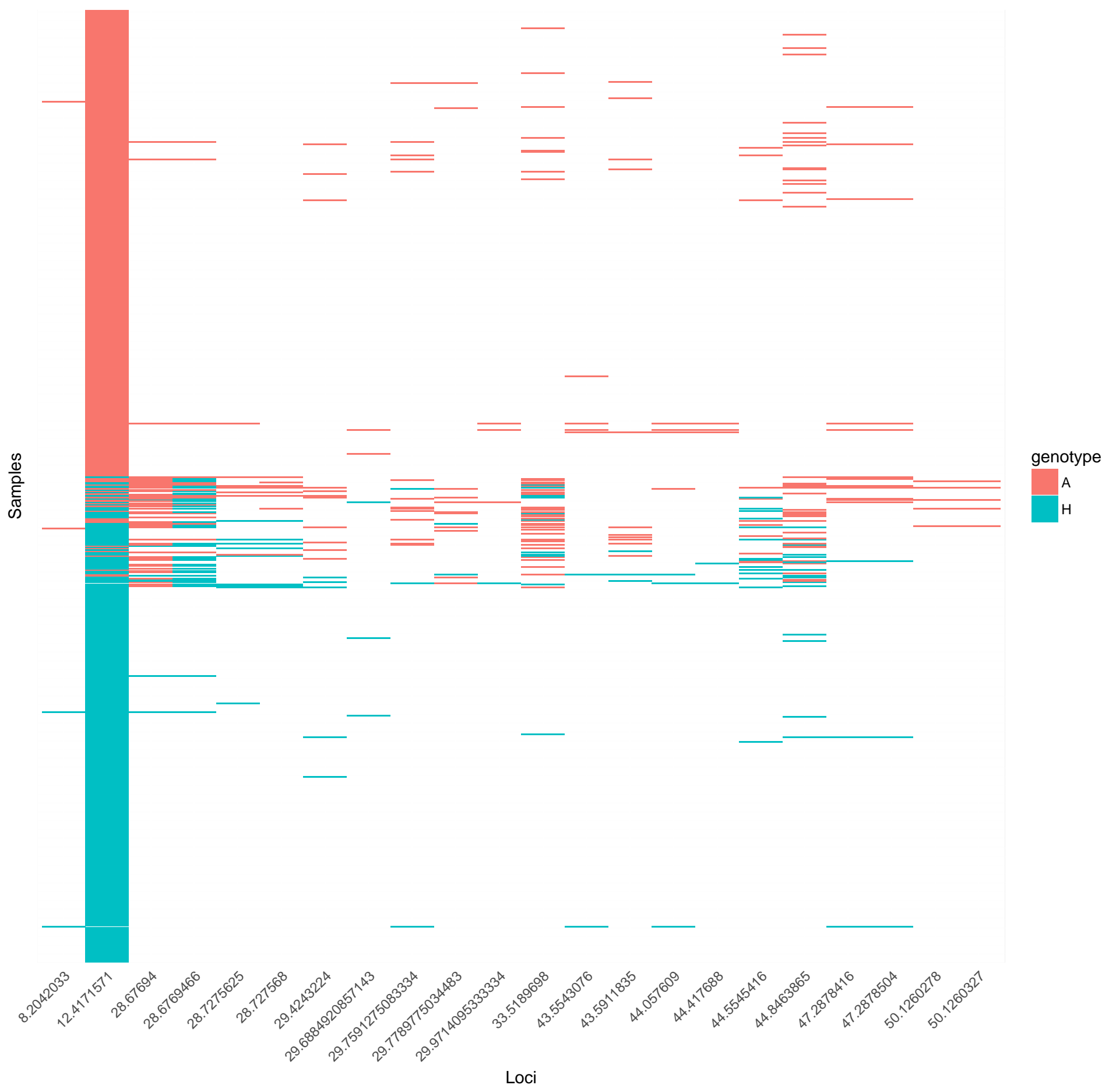
41.8278244

41.8278292

Loci



ann2 BC1, missing data, Chr 03



ann2 BC1, missing data, Chr 04

Samples

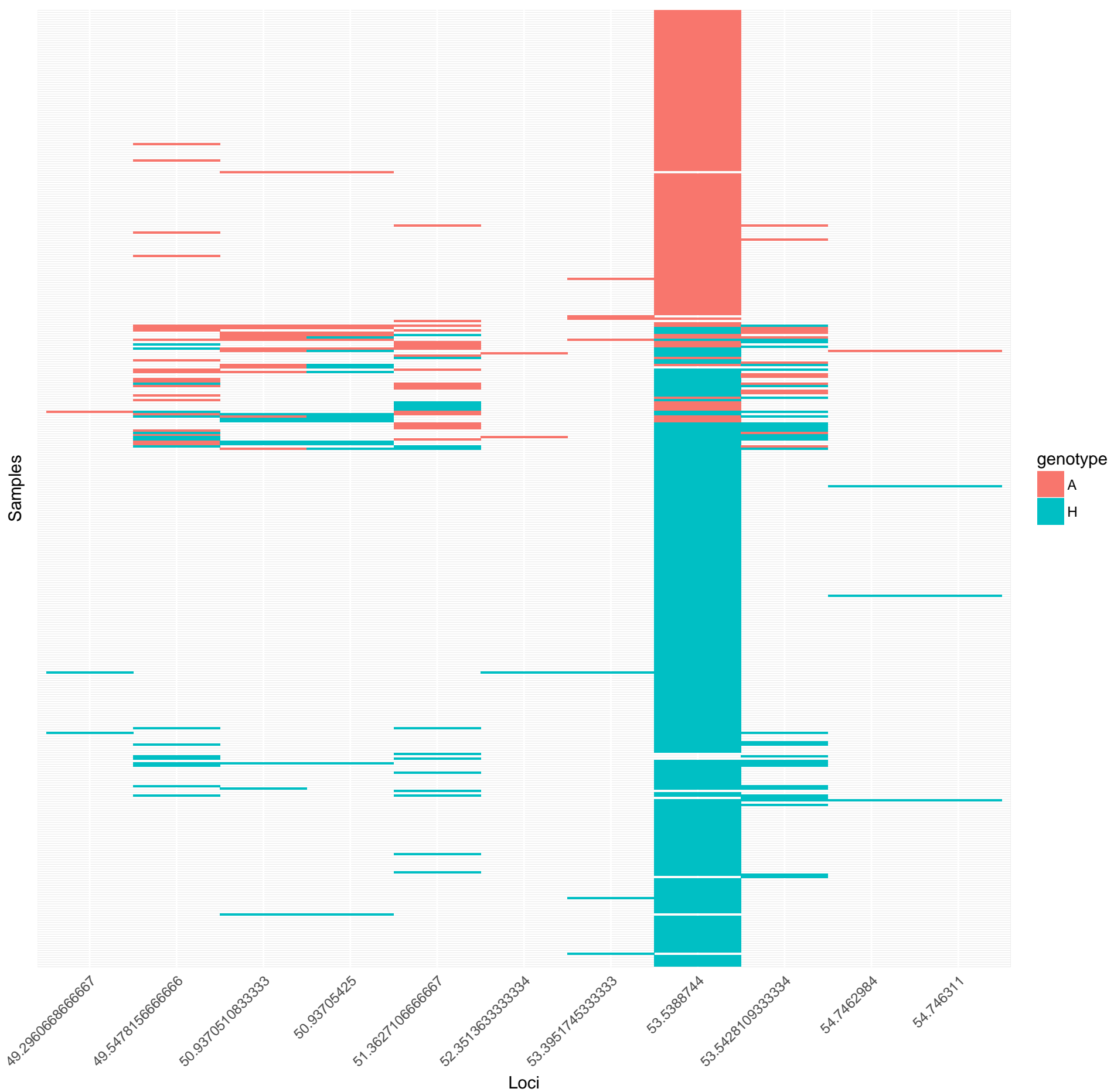
genotype

A

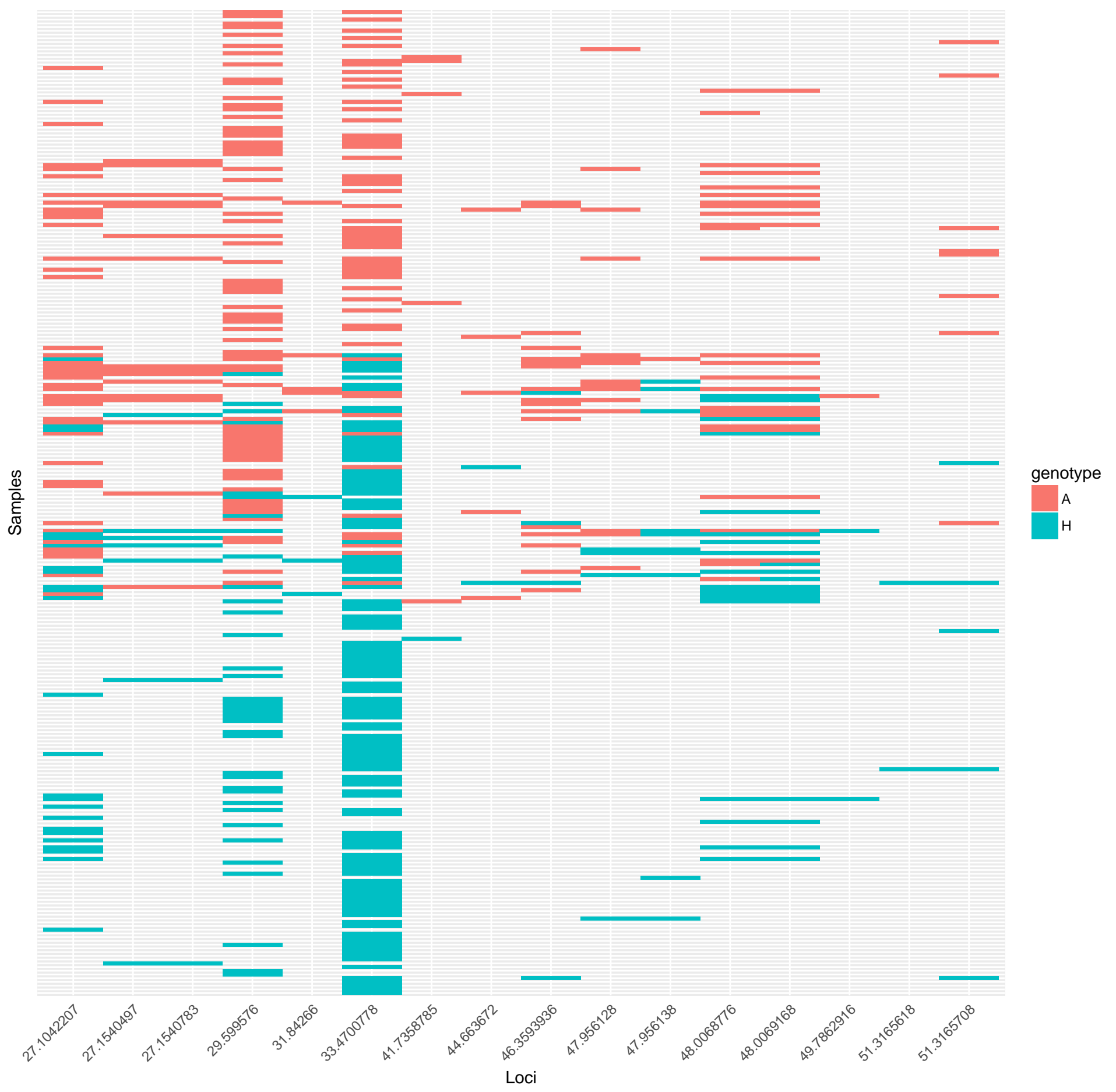
H

21.72941  
43.1834995  
44.3473132  
44.347318  
50.872046022222  
50.872046522222  
51.368922833333  
52.3592871  
52.8329806  
56.5280674  
57.2791111  
58.1533916  
58.1977798  
58.6024899  
59.658007  
59.6580136  
59.658262  
60.477676  
60.4776856  
60.998476  
67.7511728  
70.0523344  
70.84989  
78.0224053

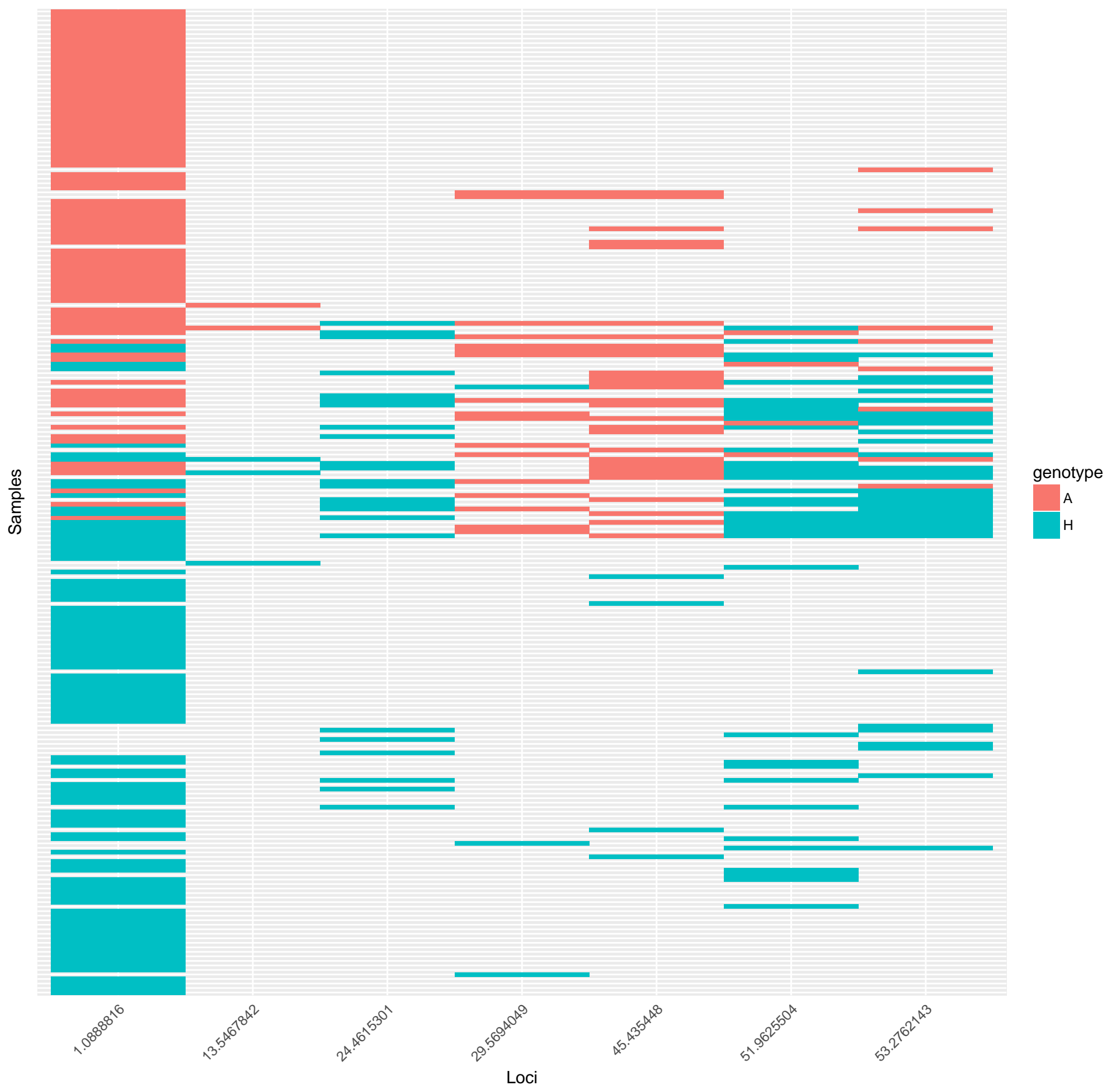
Loci



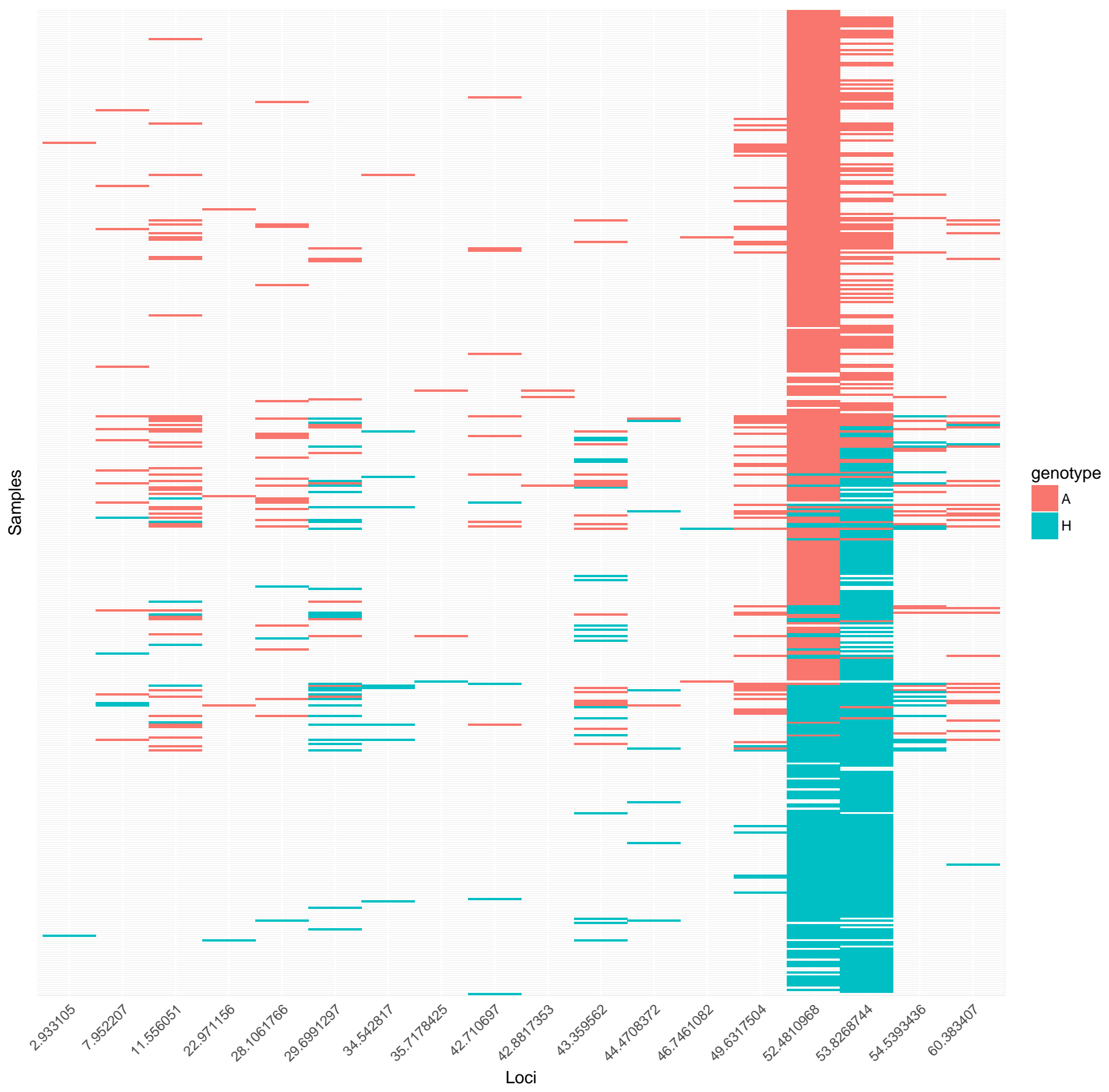
ann2 BC1, missing data, Chr 06



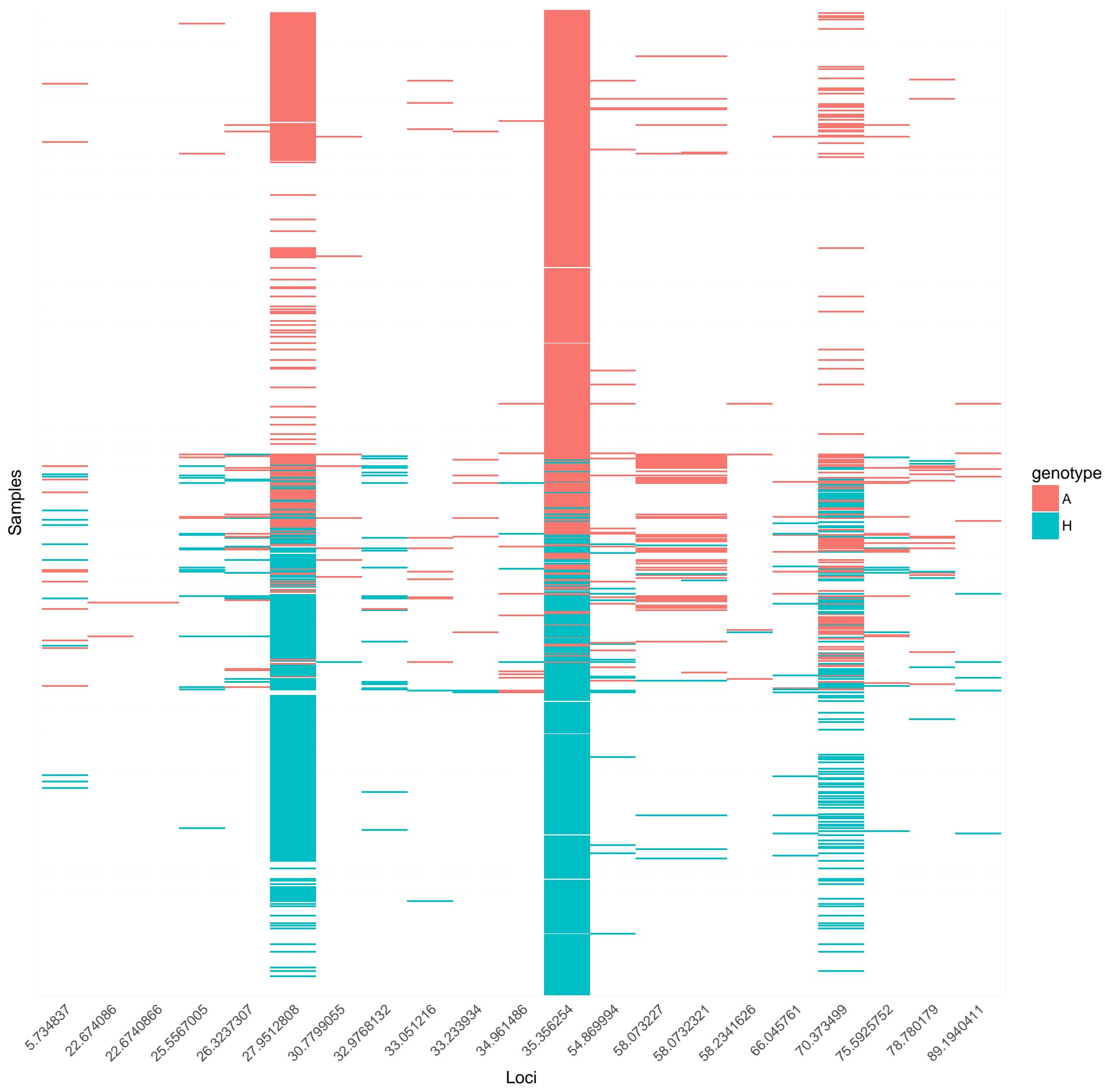
ann2 BC1, missing data, Chr 07

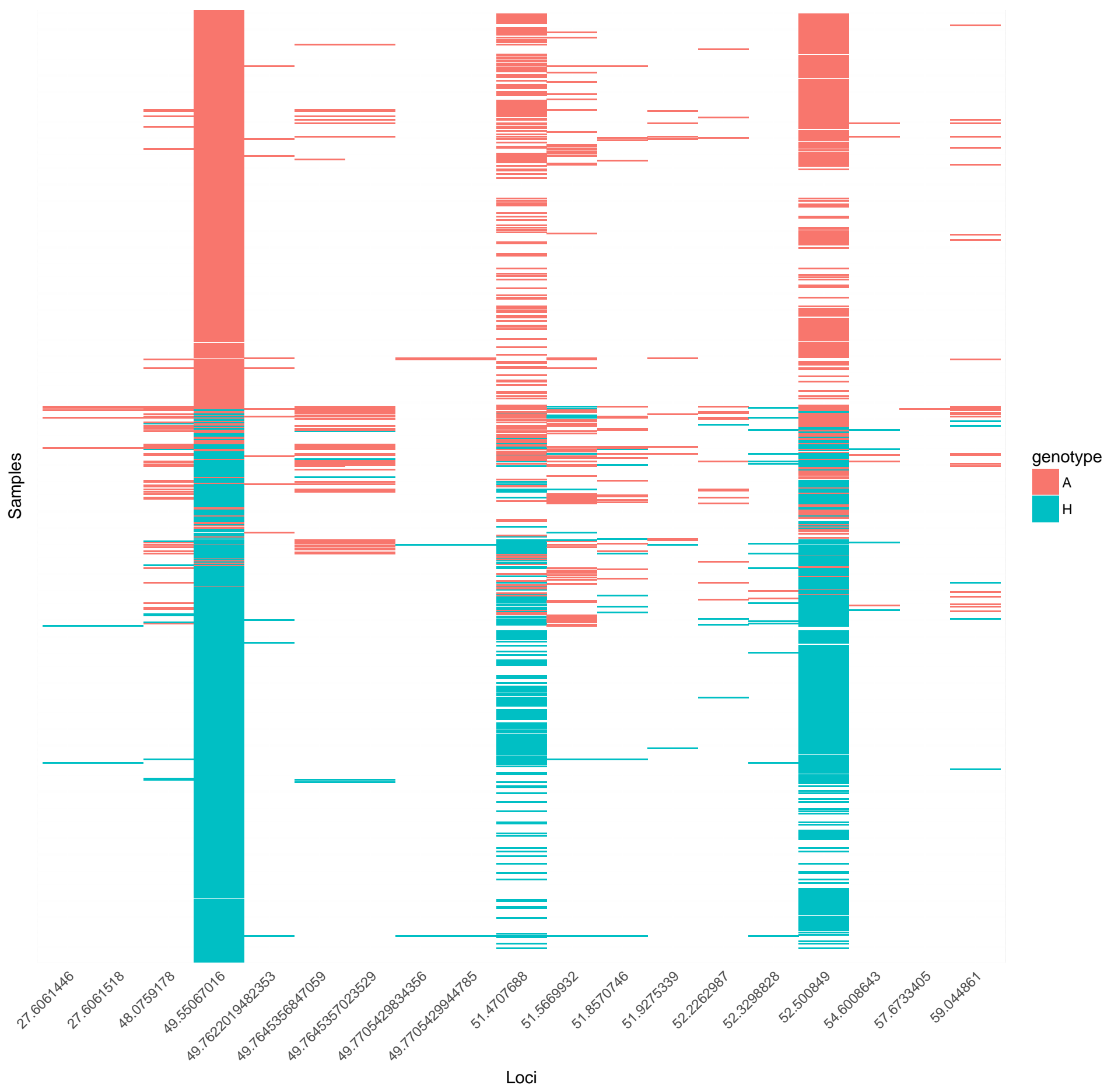




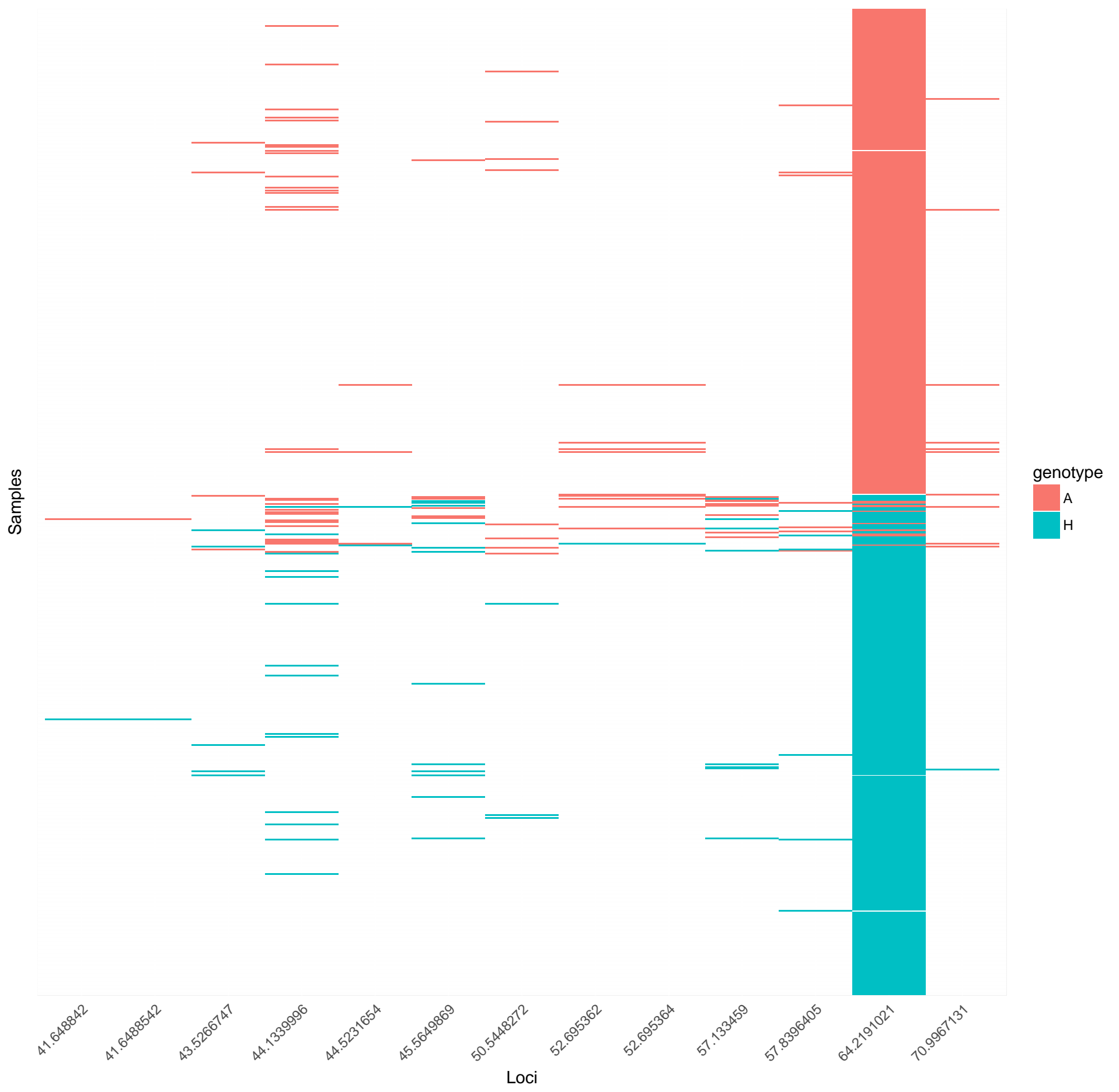


ann2 BC1, missing data, Chr 09

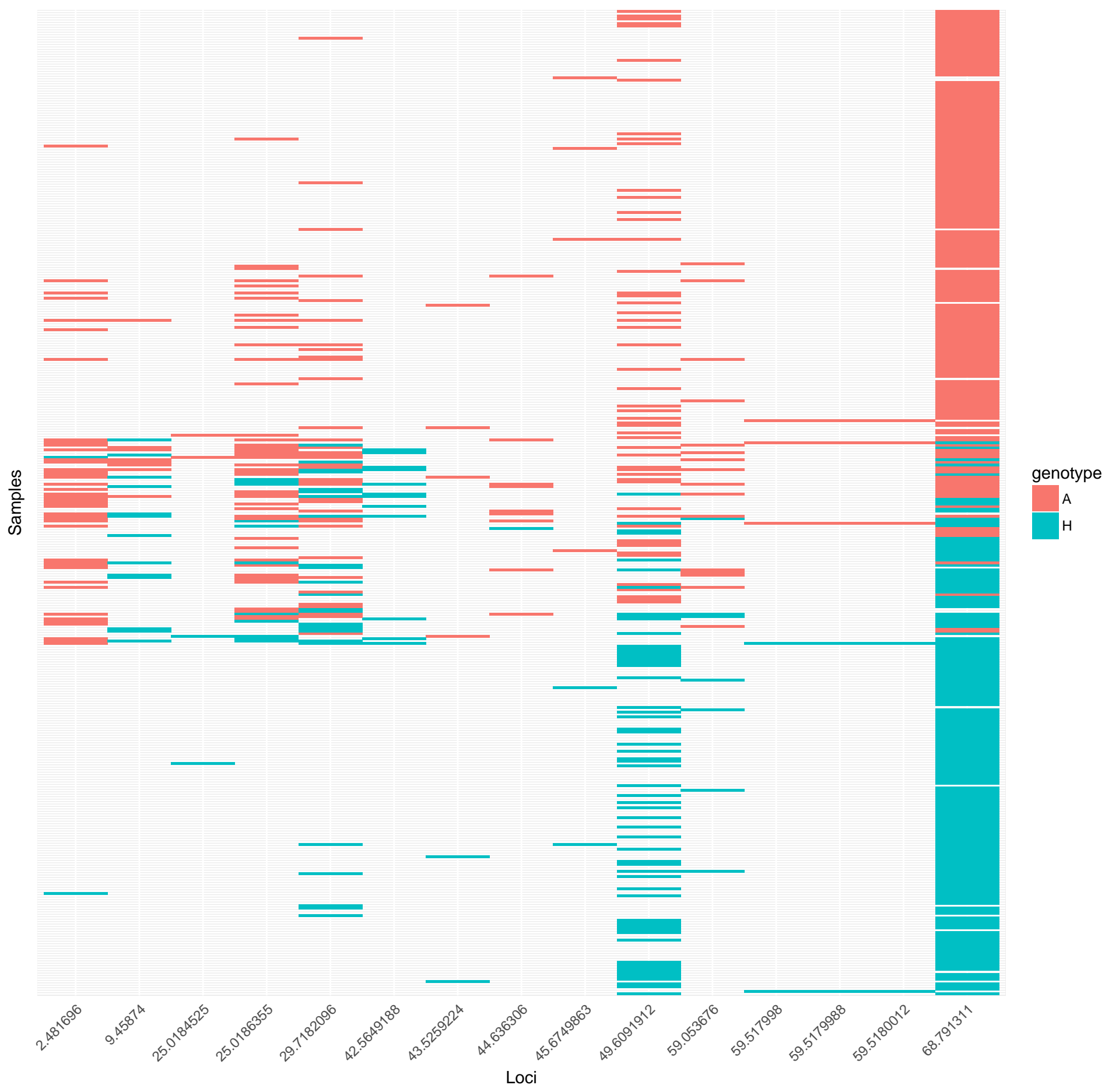




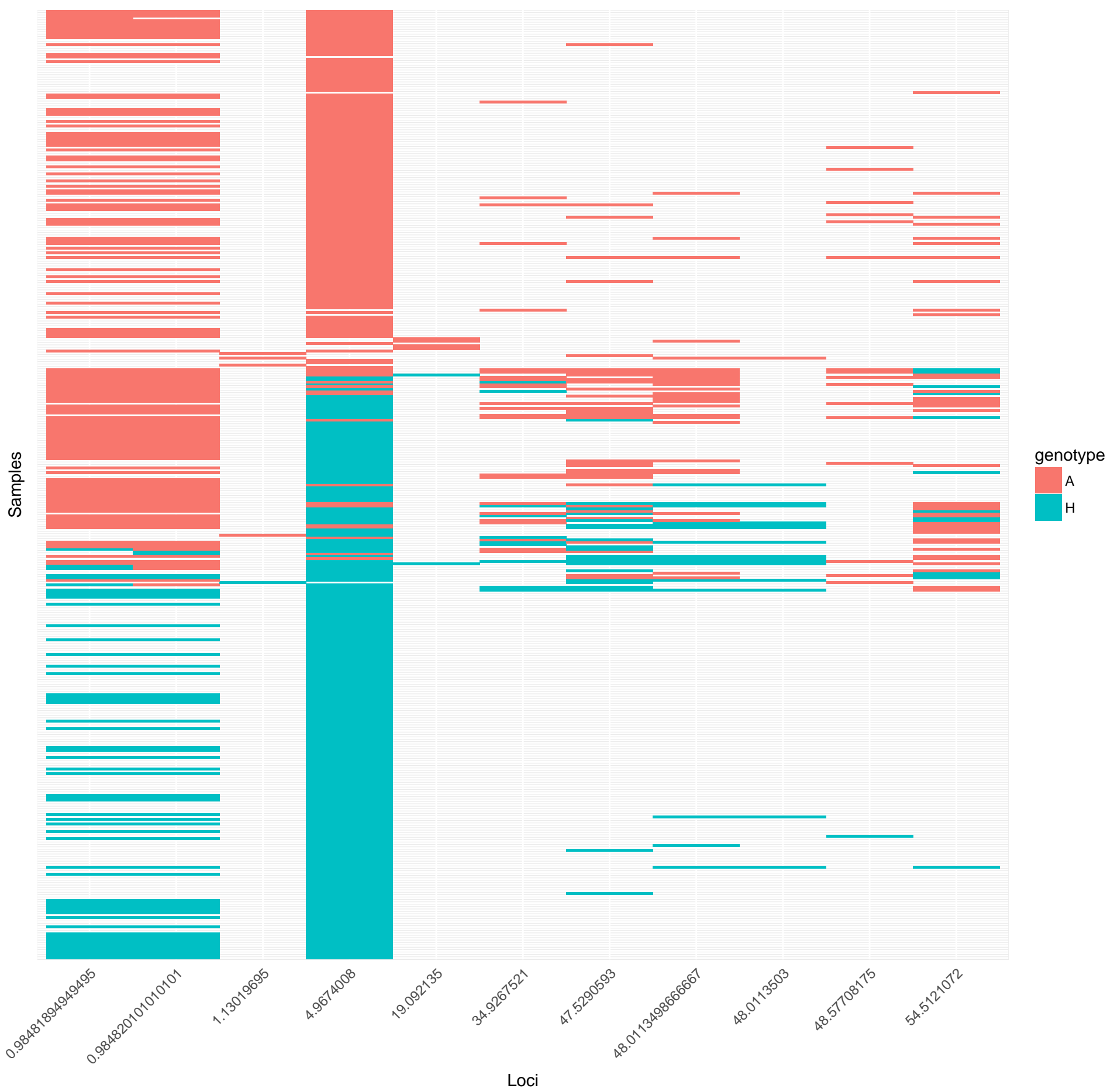
ann2 BC1, missing data, Chr 11



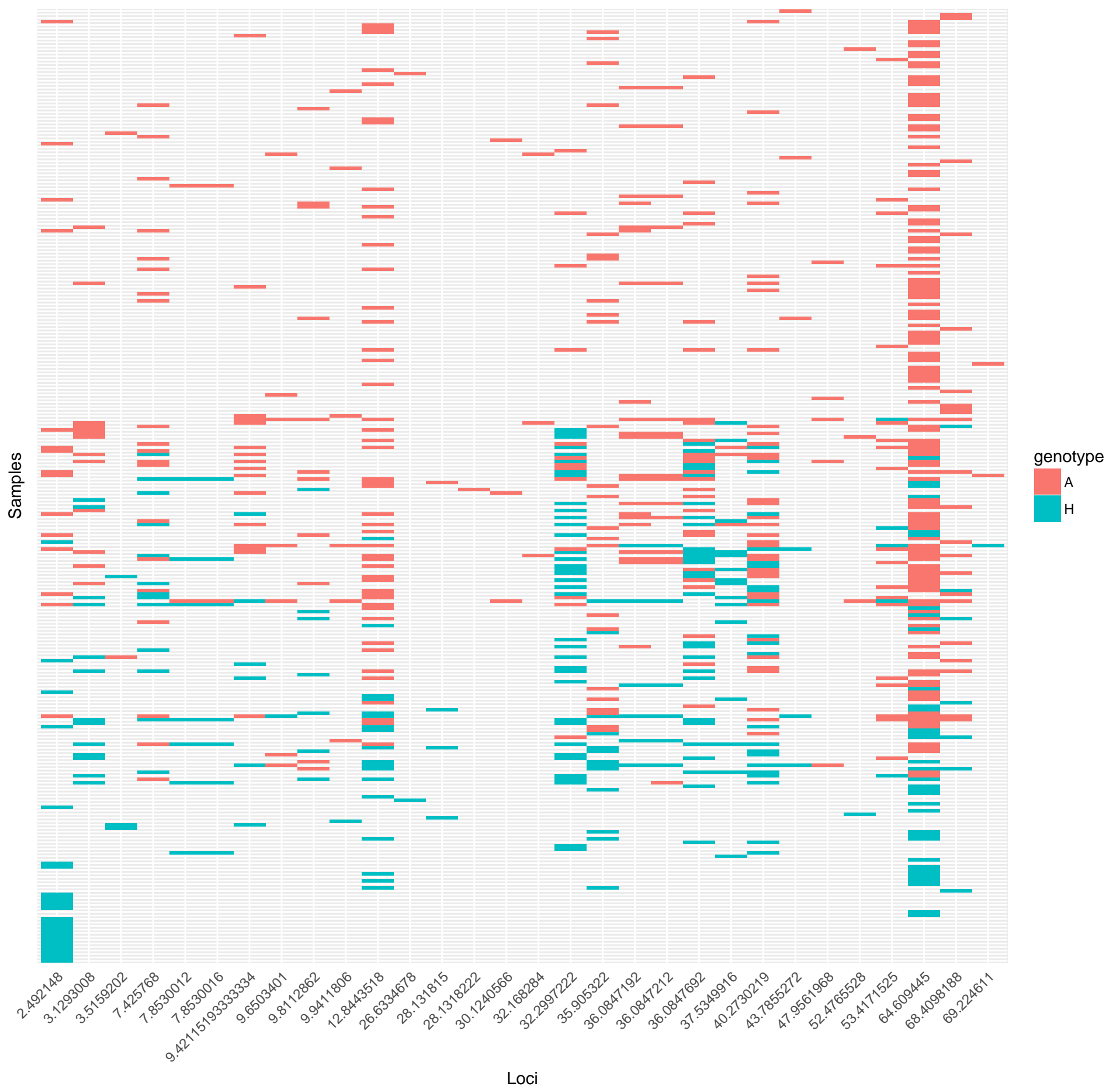
ann2 BC1, missing data, Chr 12



ann2 BC1, missing data, Chr 13

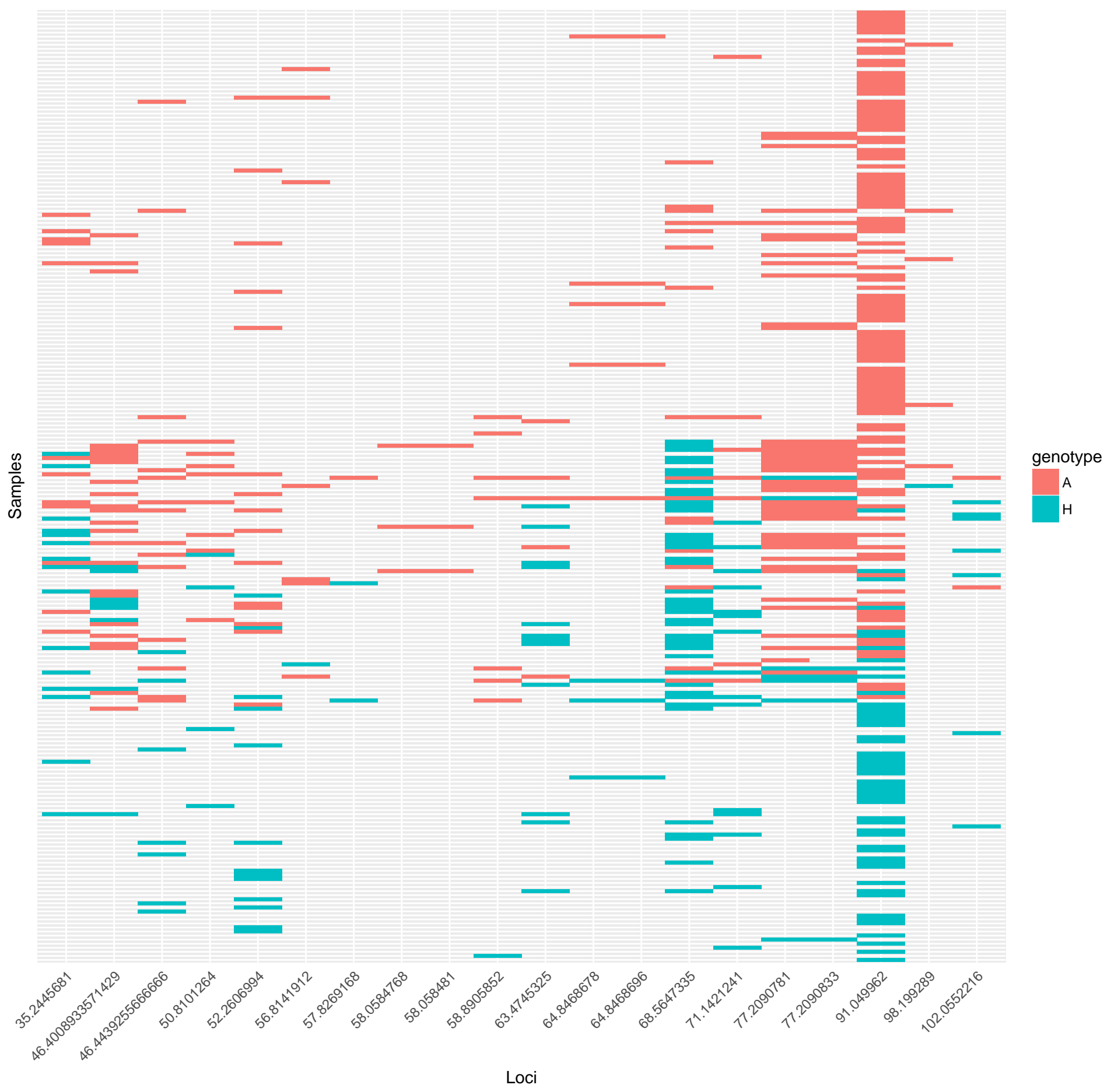


ann2 BC1, missing data, Chr 14

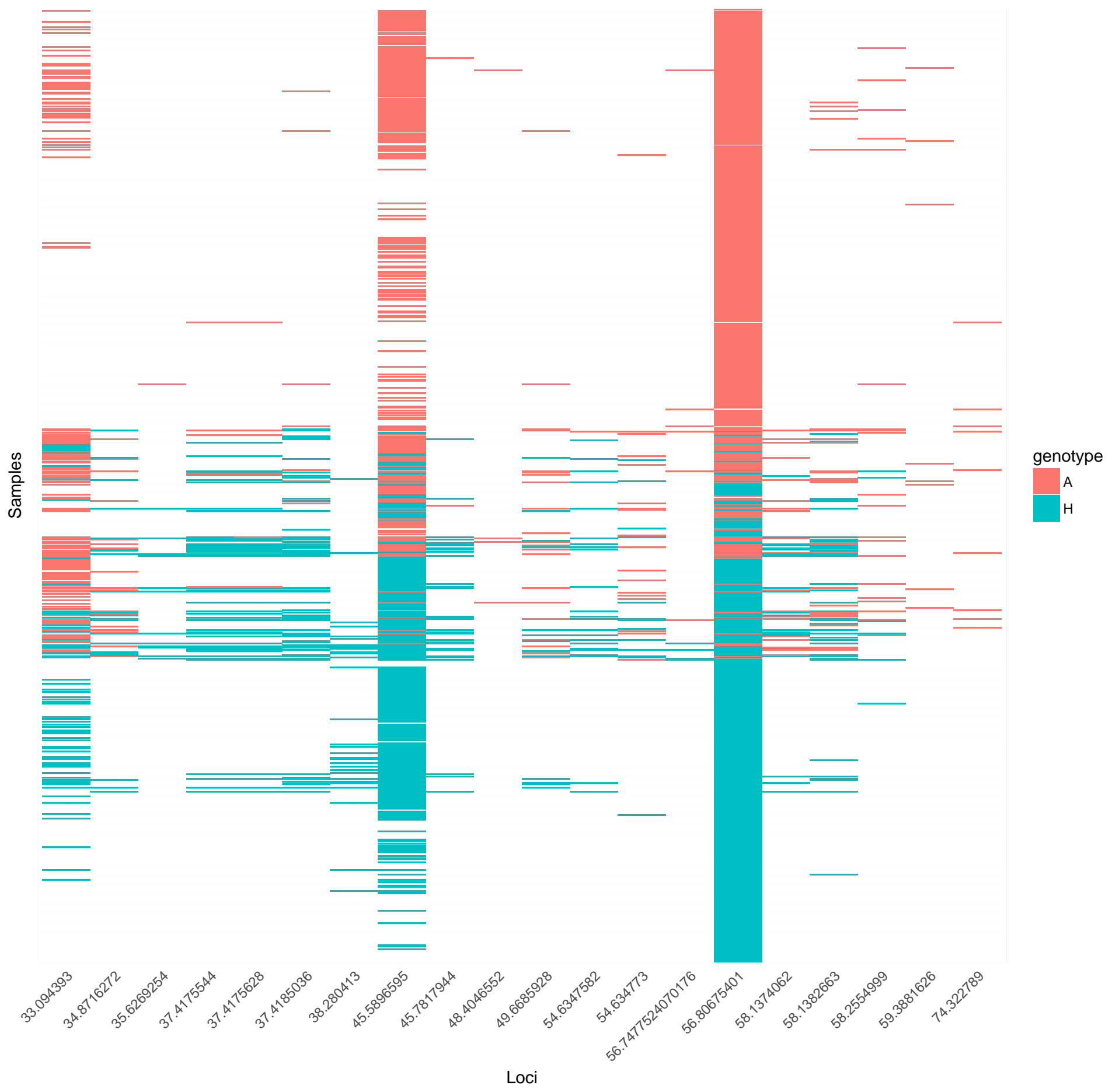


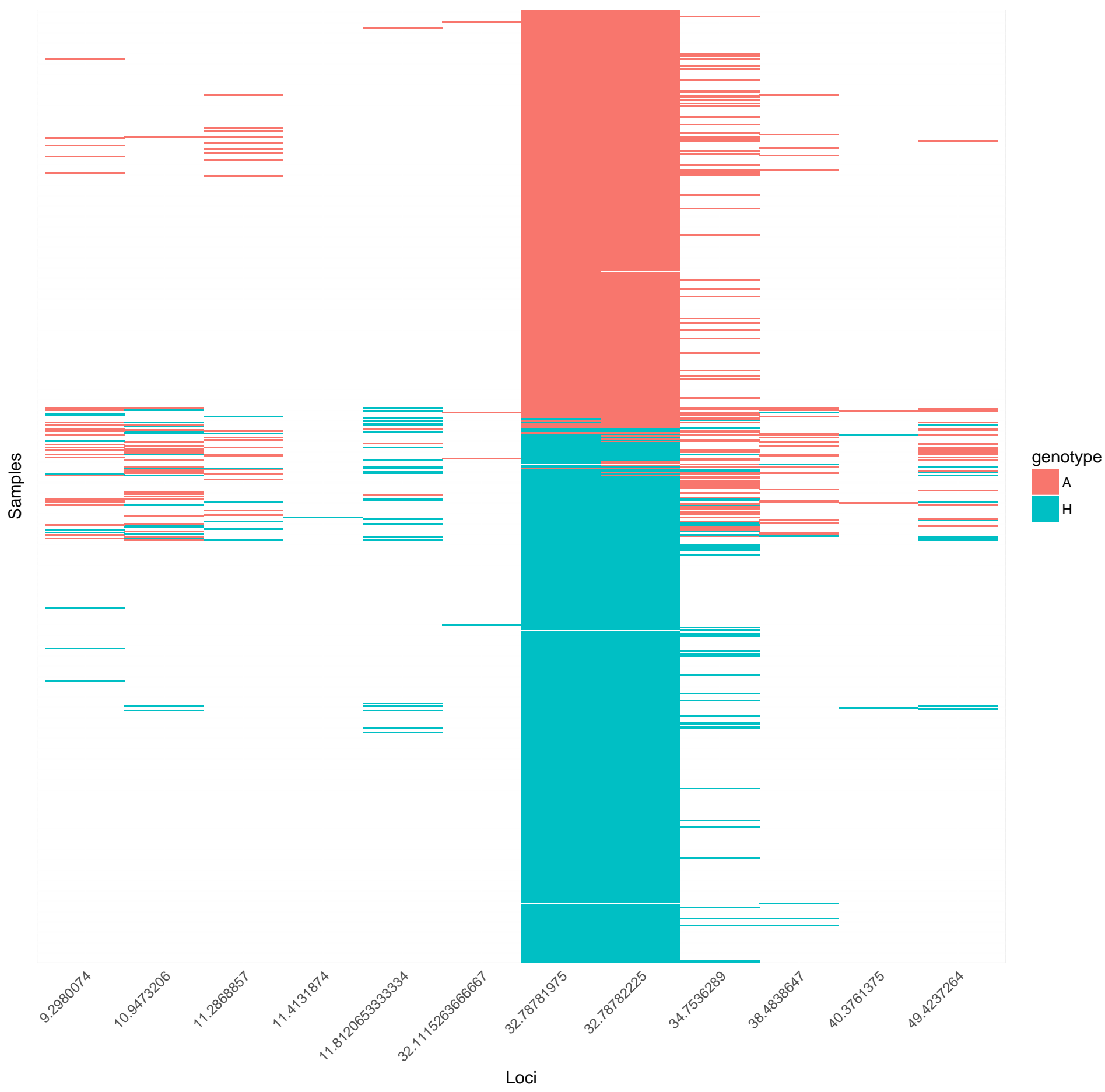




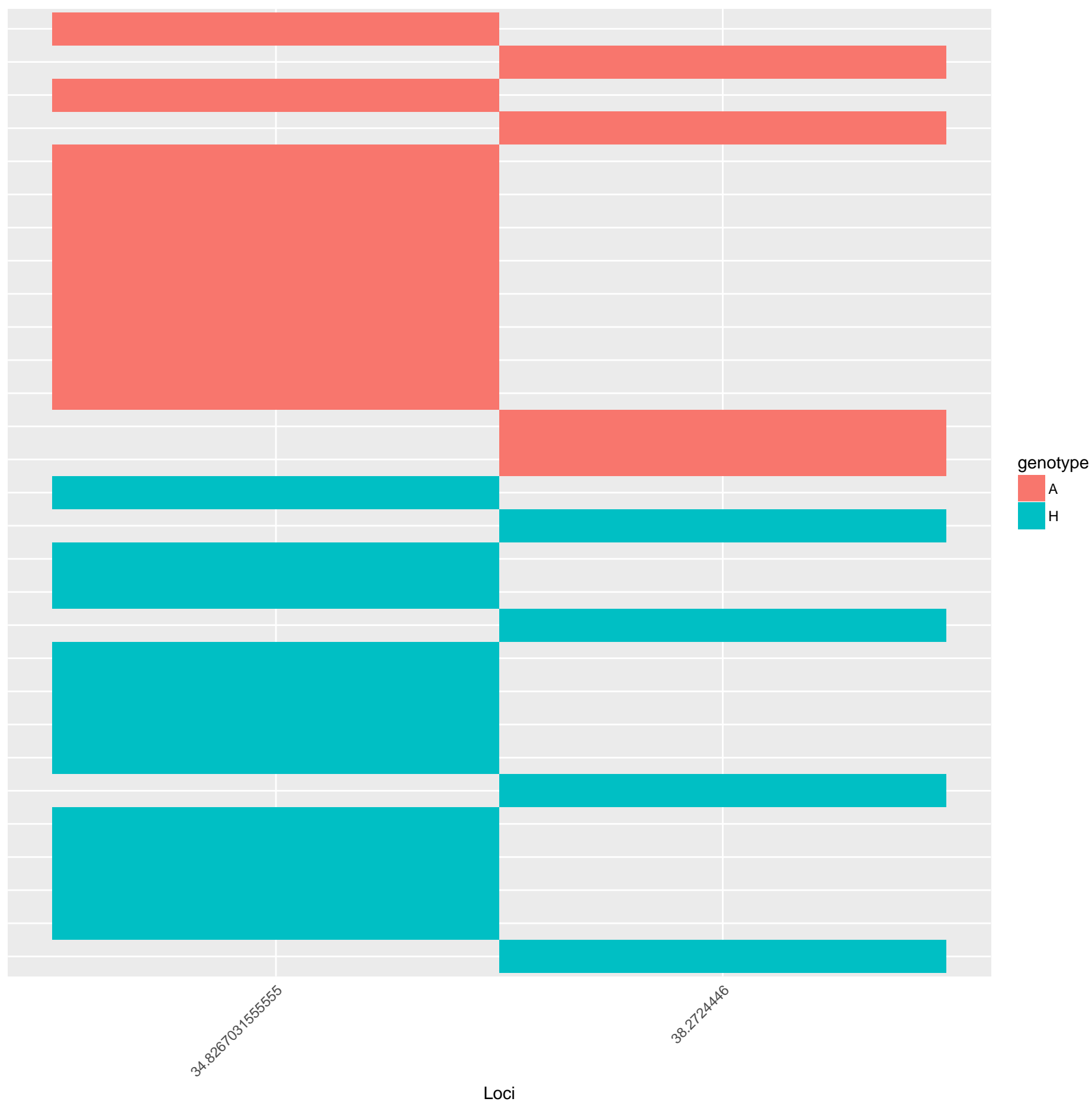


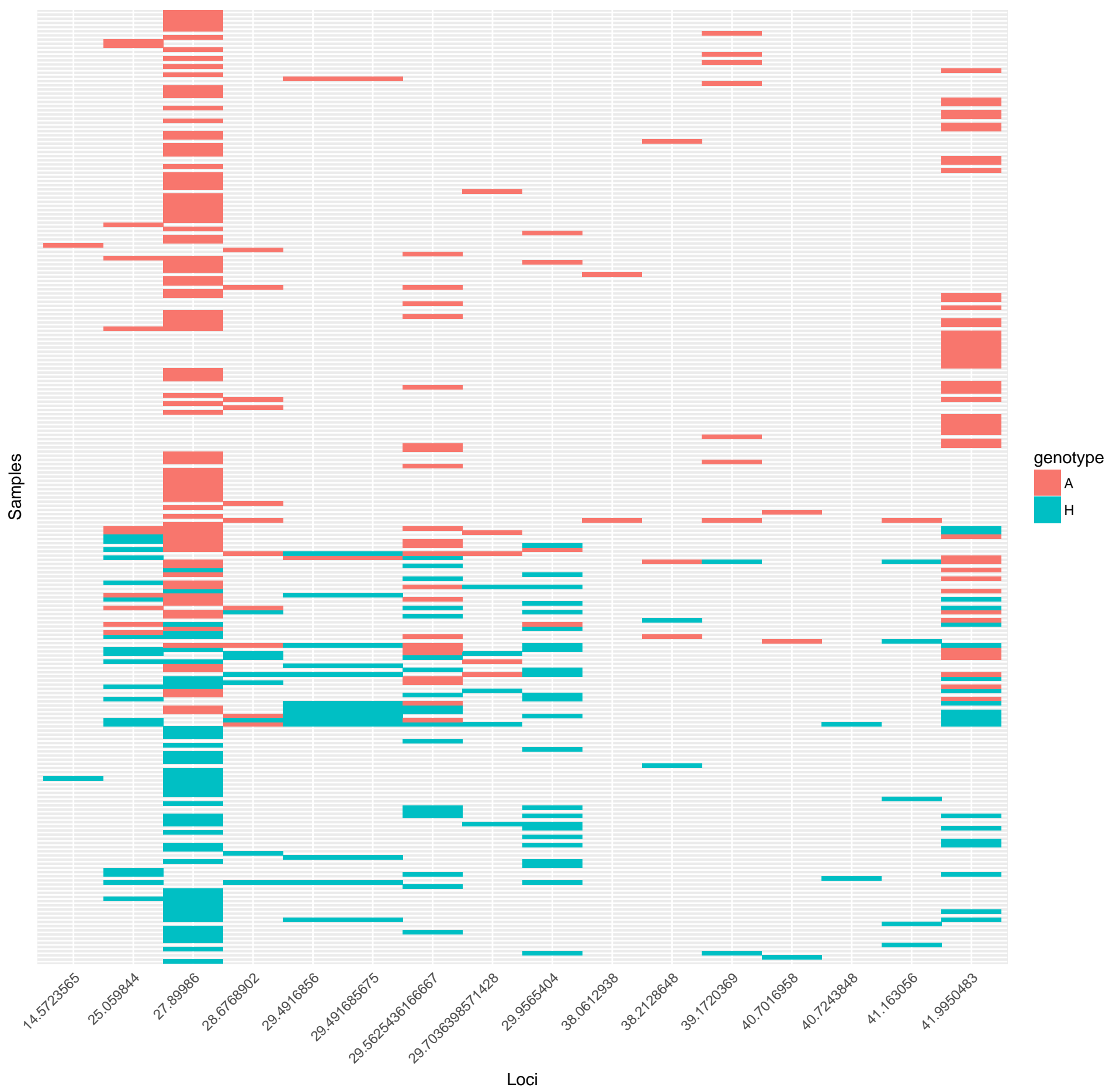
ann2 BC1, missing data, Chr 17





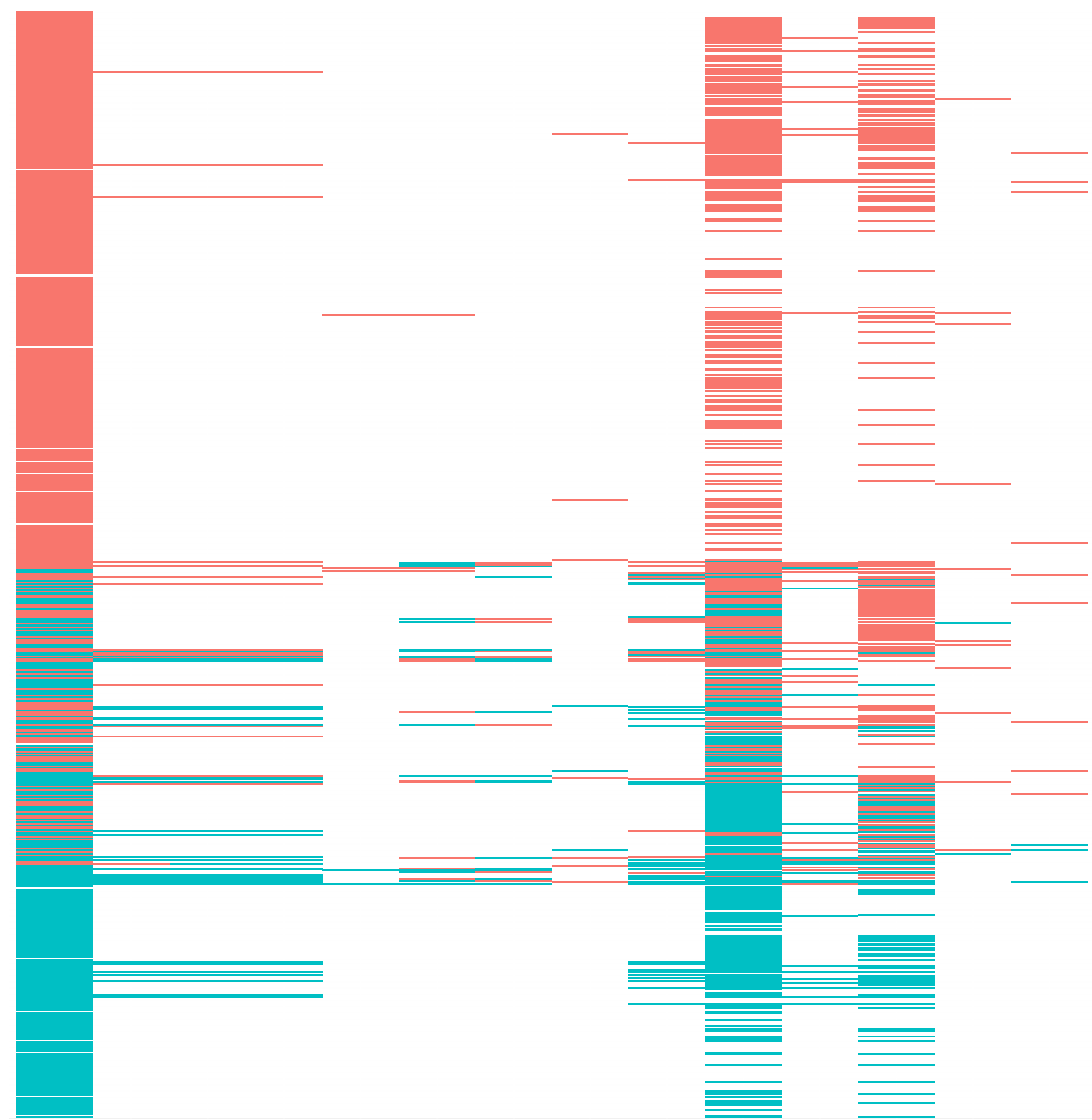
ann3 BC1, missing data, Chr 02





ann3 BC1, missing data, Chr 04

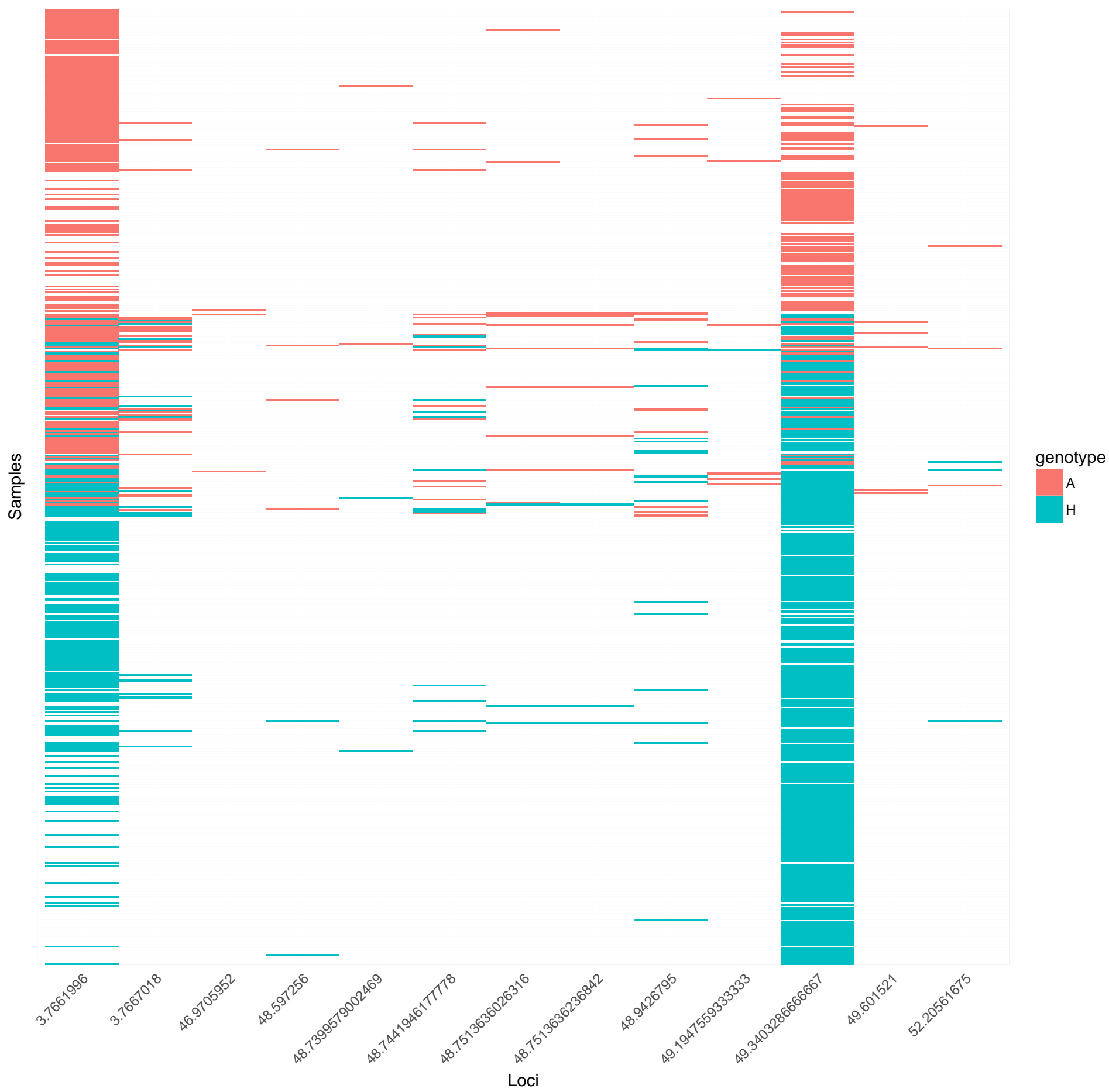
Samples



11.57604 44.9215172 44.9215208 44.921522 52.8328708 52.8328732 52.832878 57.5054016 59.7911699 60.2503828 60.680377 60.9986505 61.002022 70.849848

Loci

ann3 BC1, missing data, Chr 05



ann3 BC1, missing data, Chr 06

Samples

genotype

A

H

33.8244265

38.829471

40.252105

41.7359055

47.9529332

47.952956

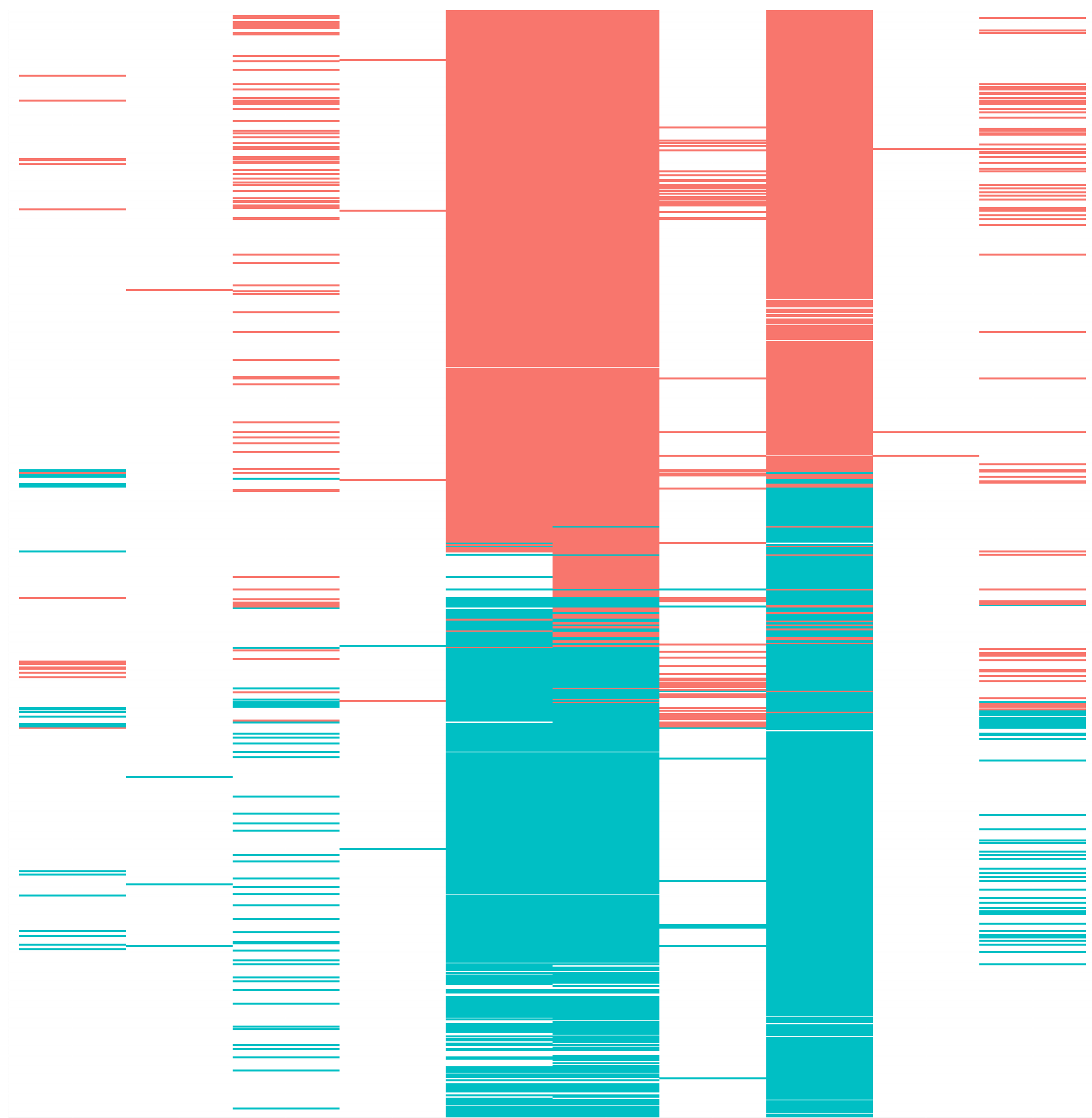
47.952996

49.5611244

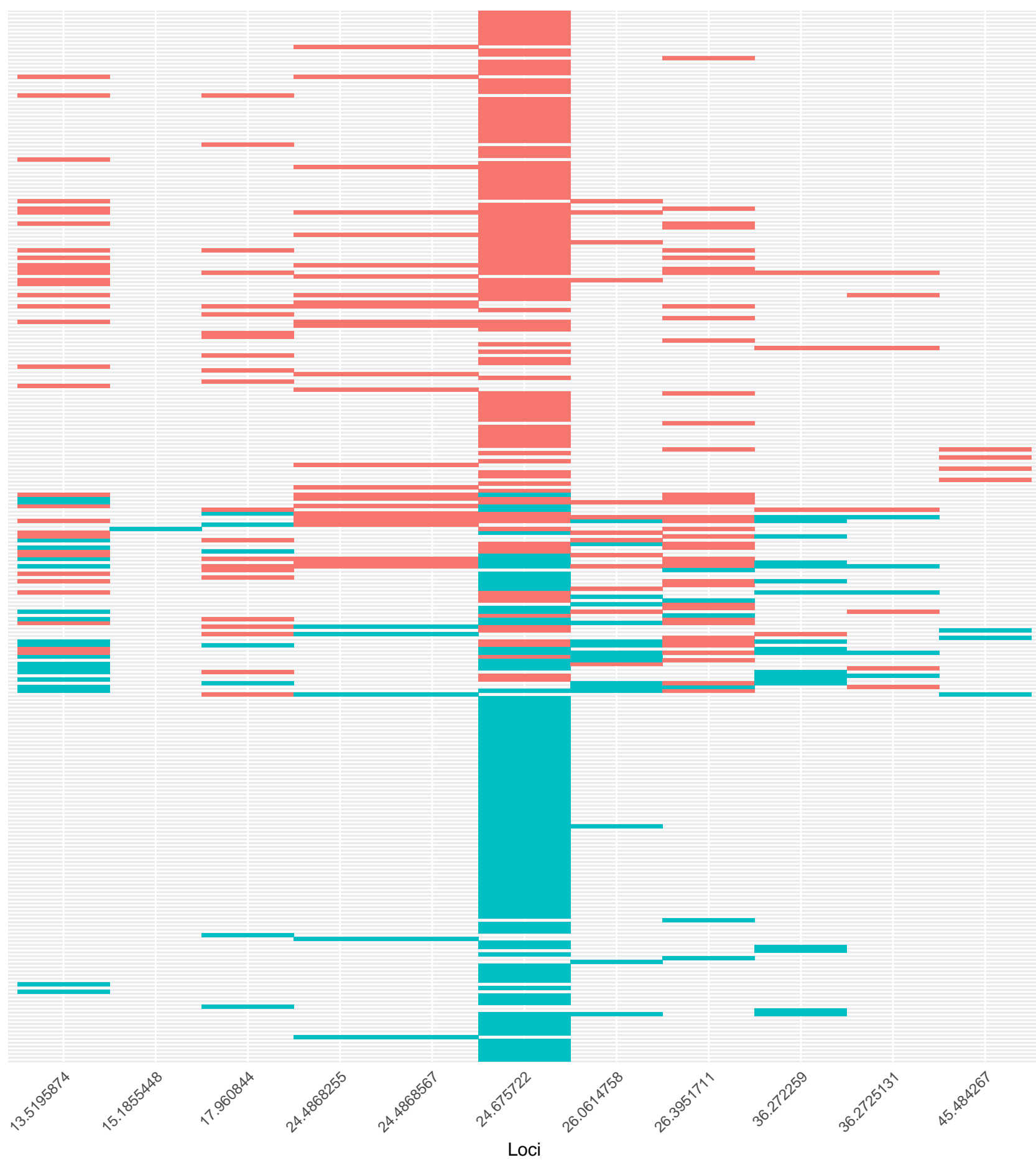
56.335672

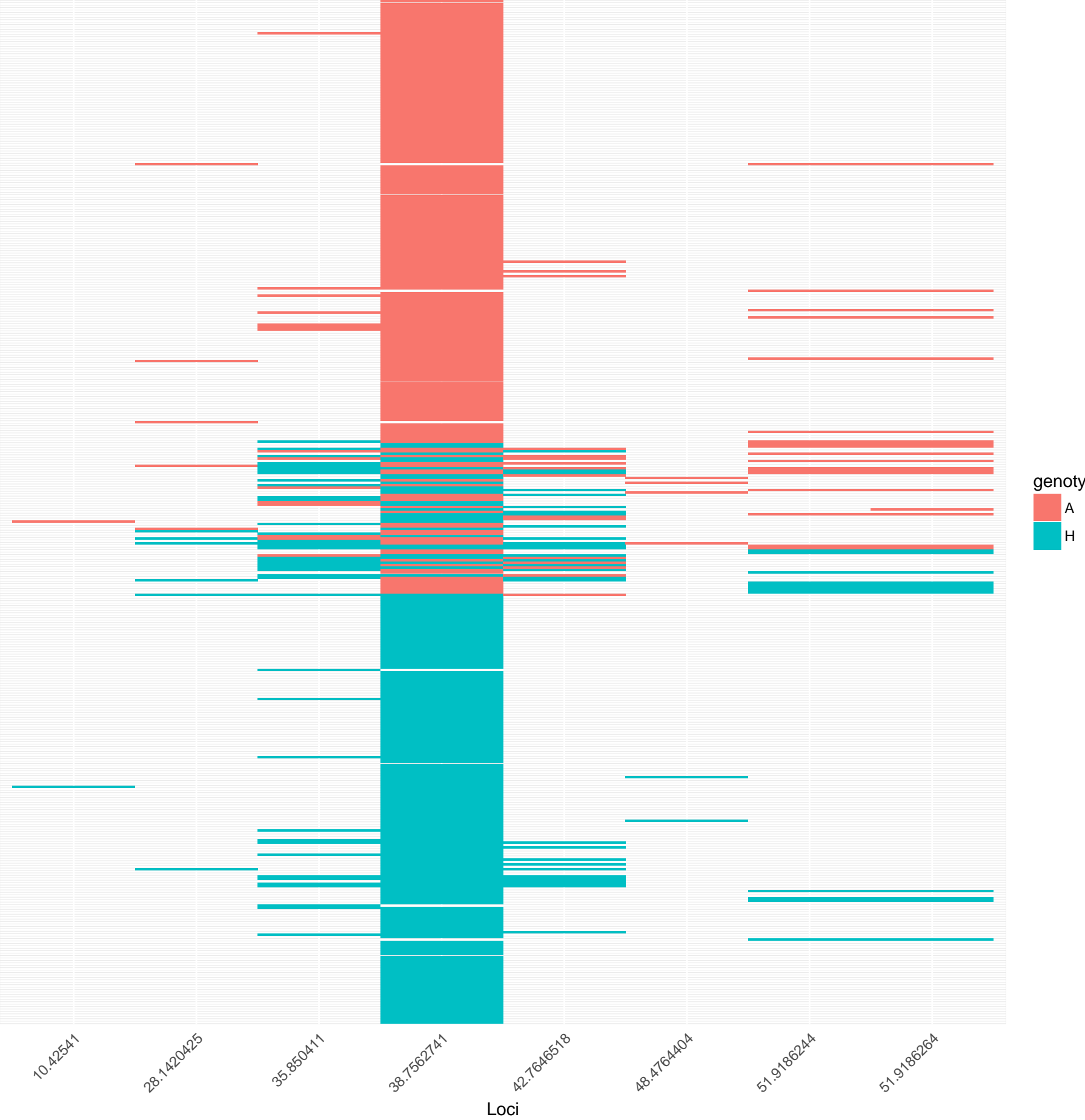
59.69967

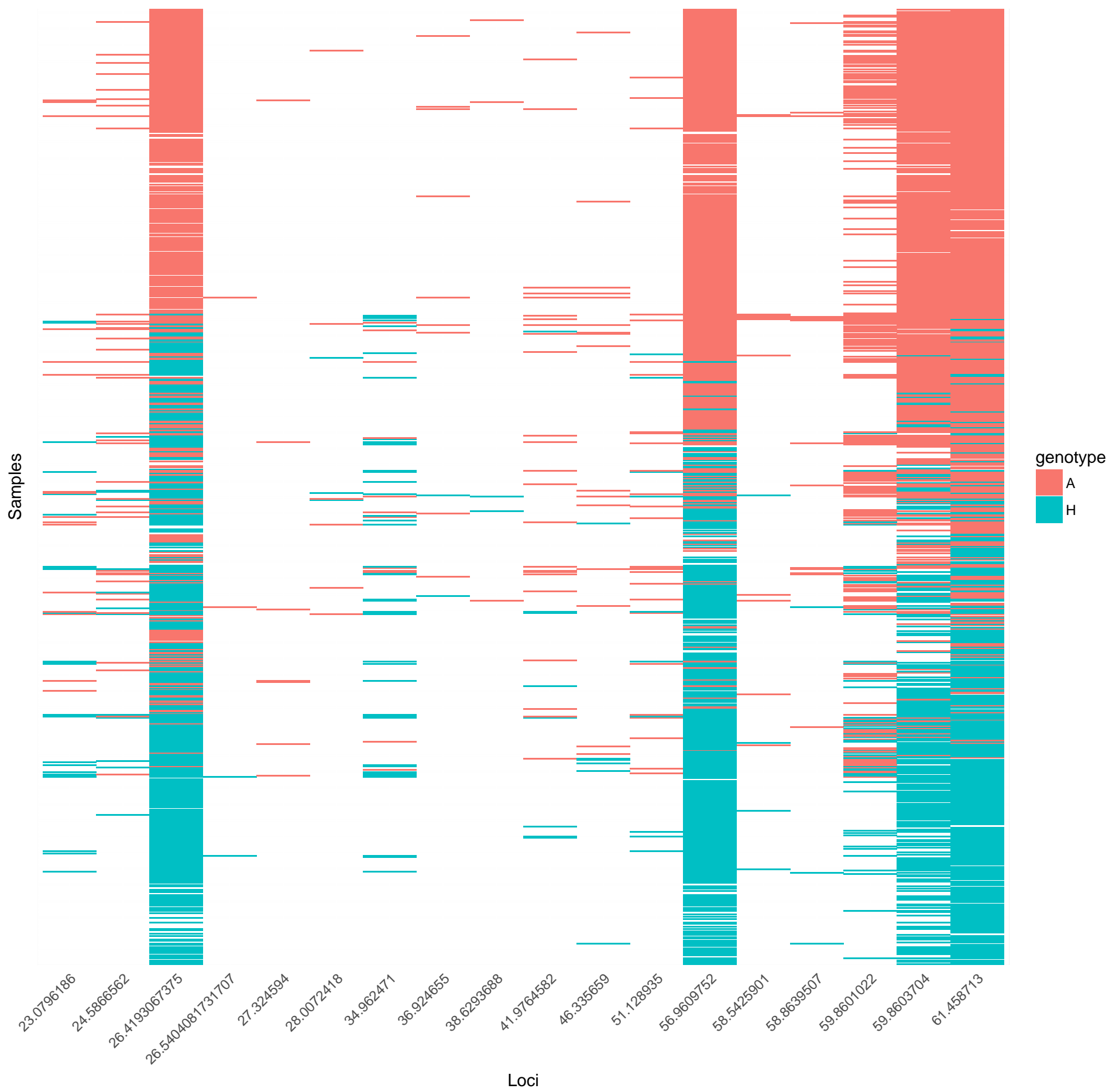
Loci

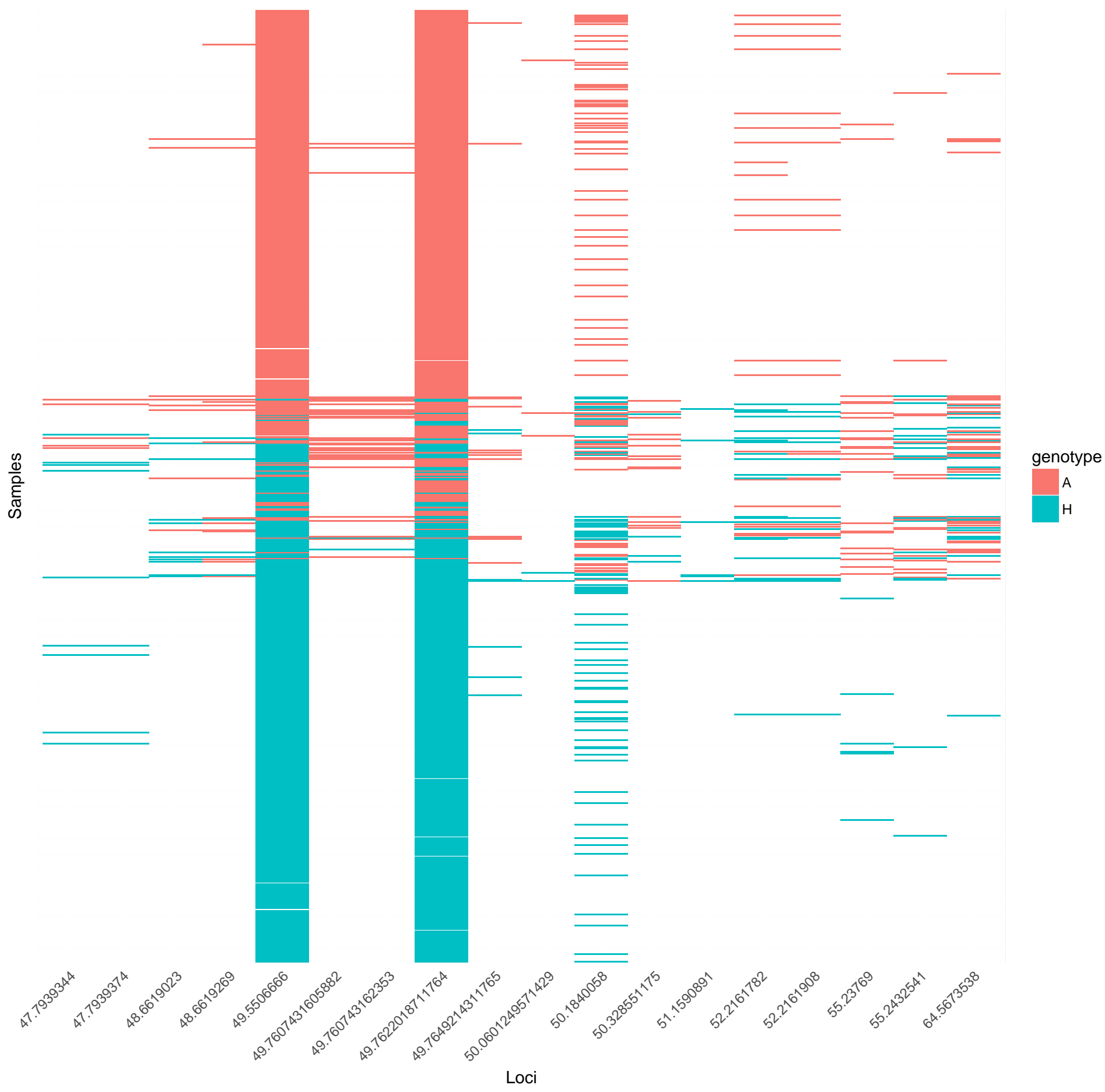












ann3 BC1, missing data, Chr 11

Samples

genotype  
A  
H

44.508278

44.5231464

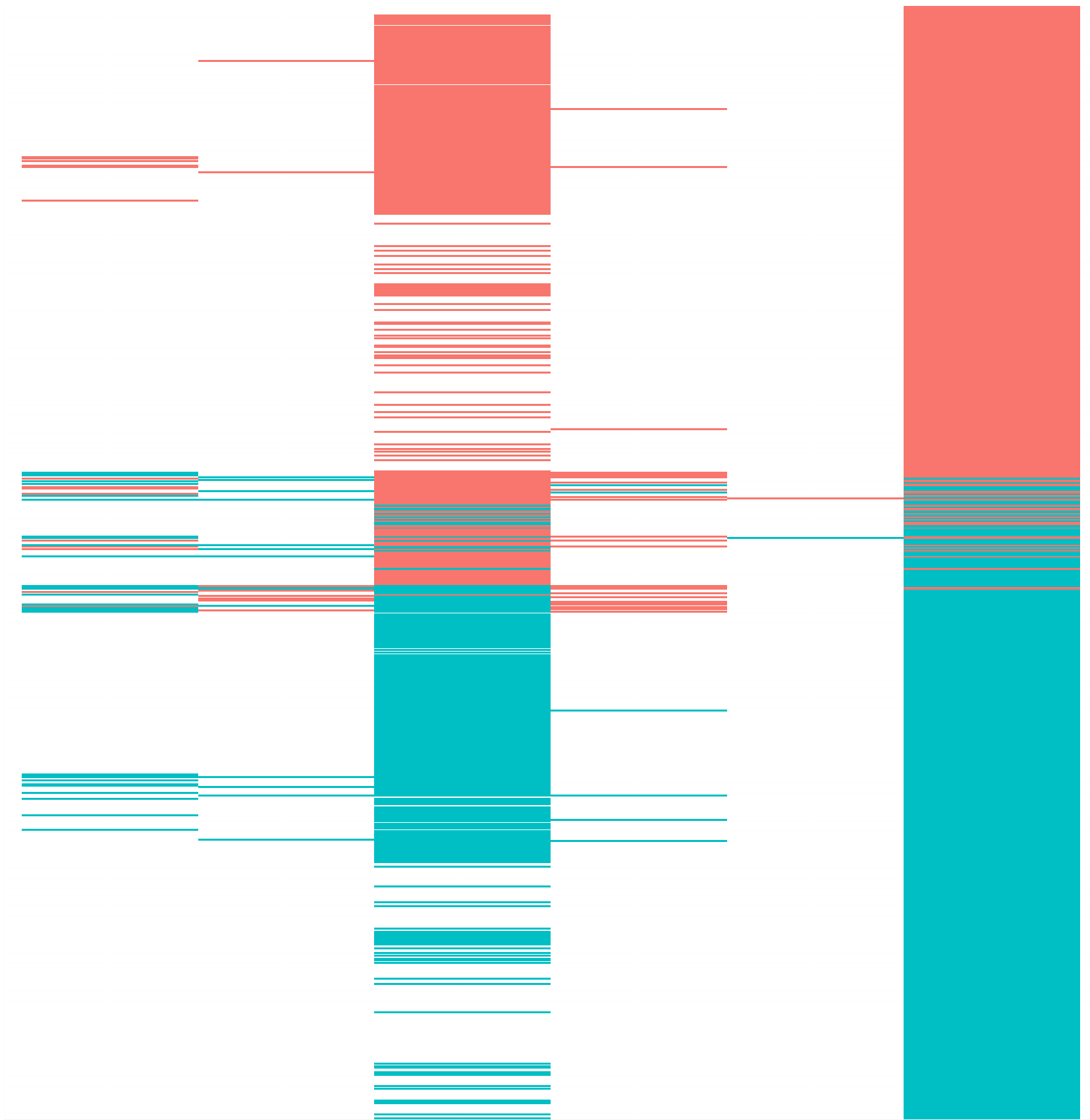
50.5447156

51.776885

51.7907125

64.2190886

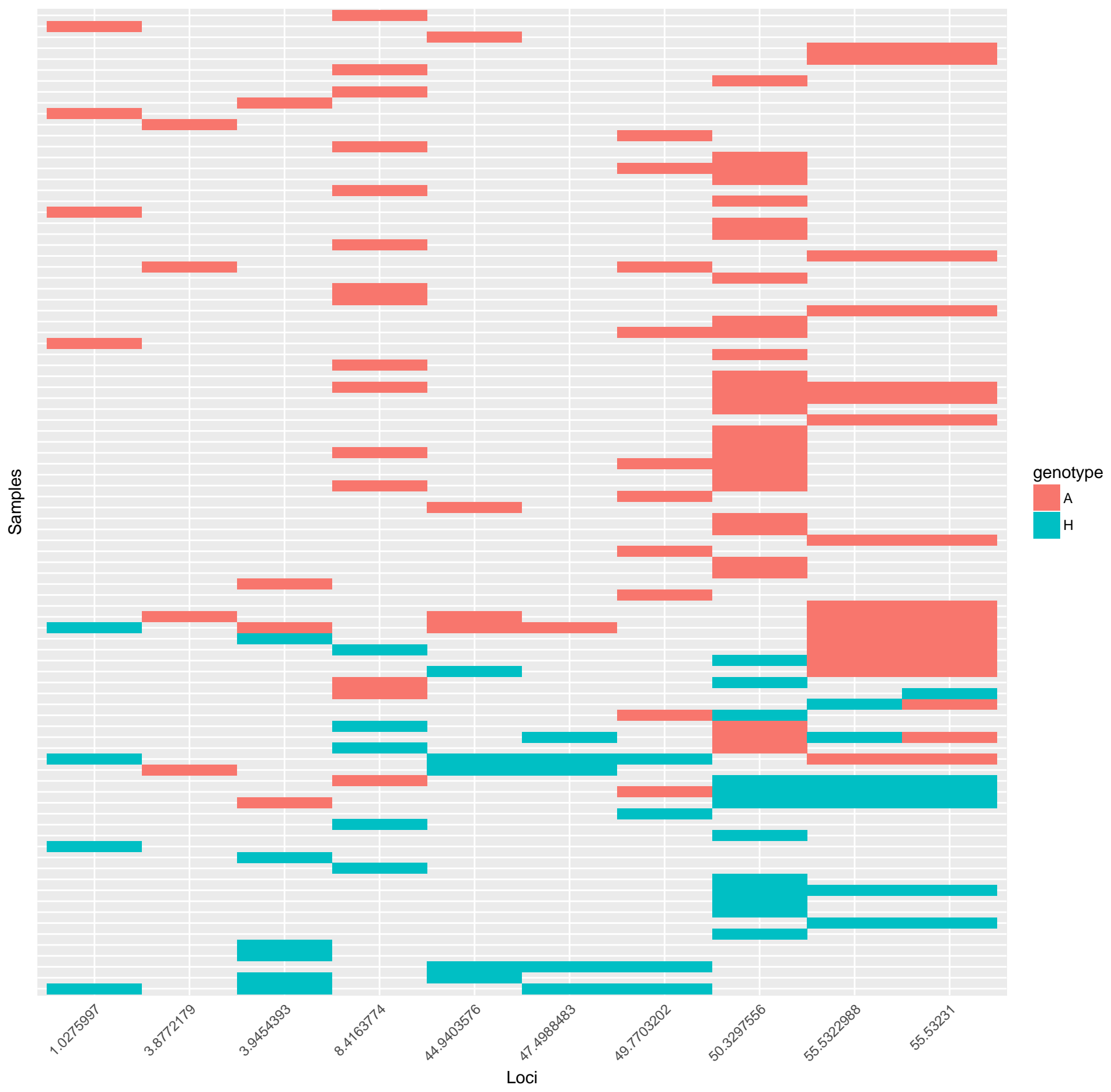
Loci

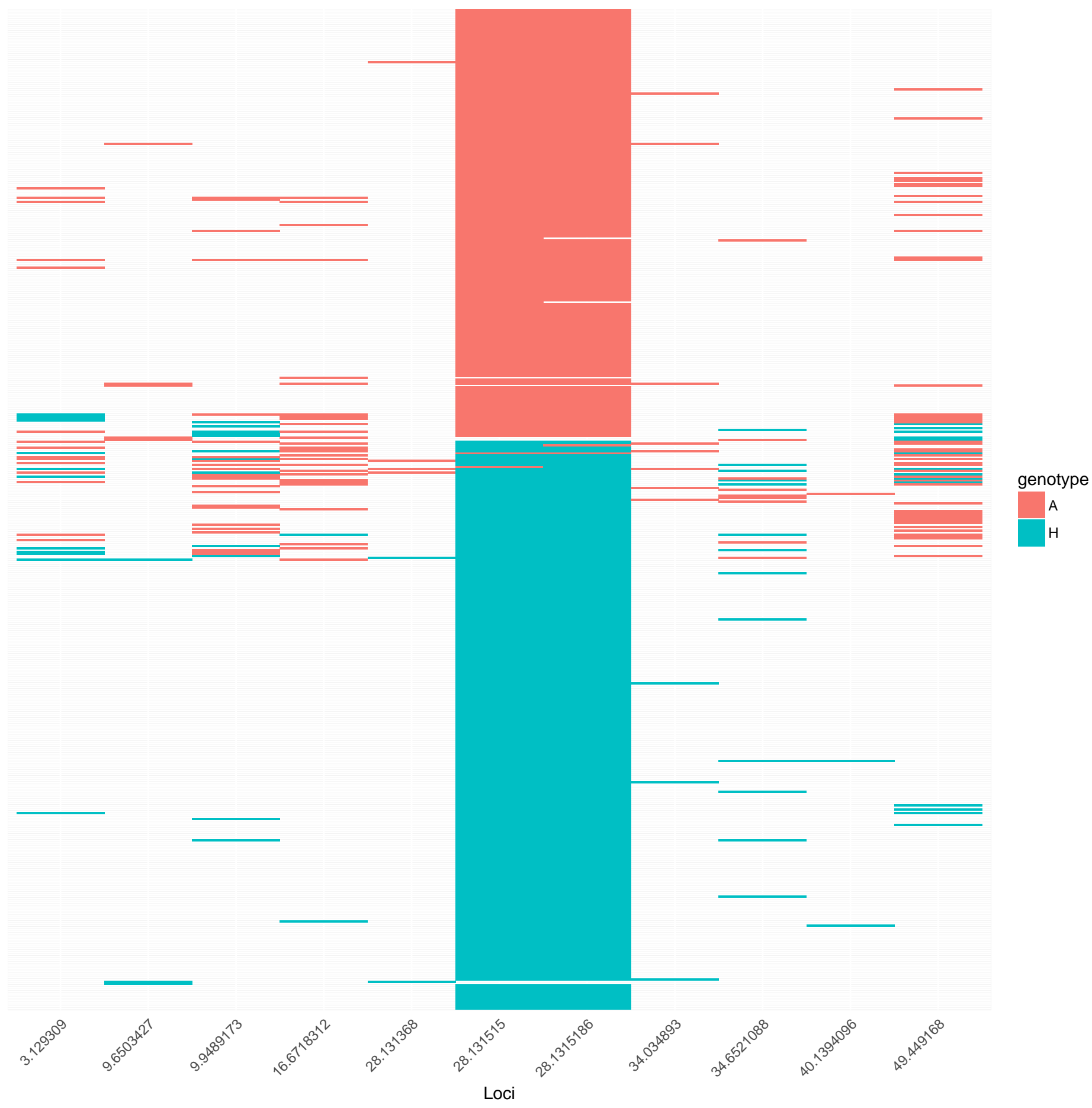


ann3 BC1, missing data, Chr 12

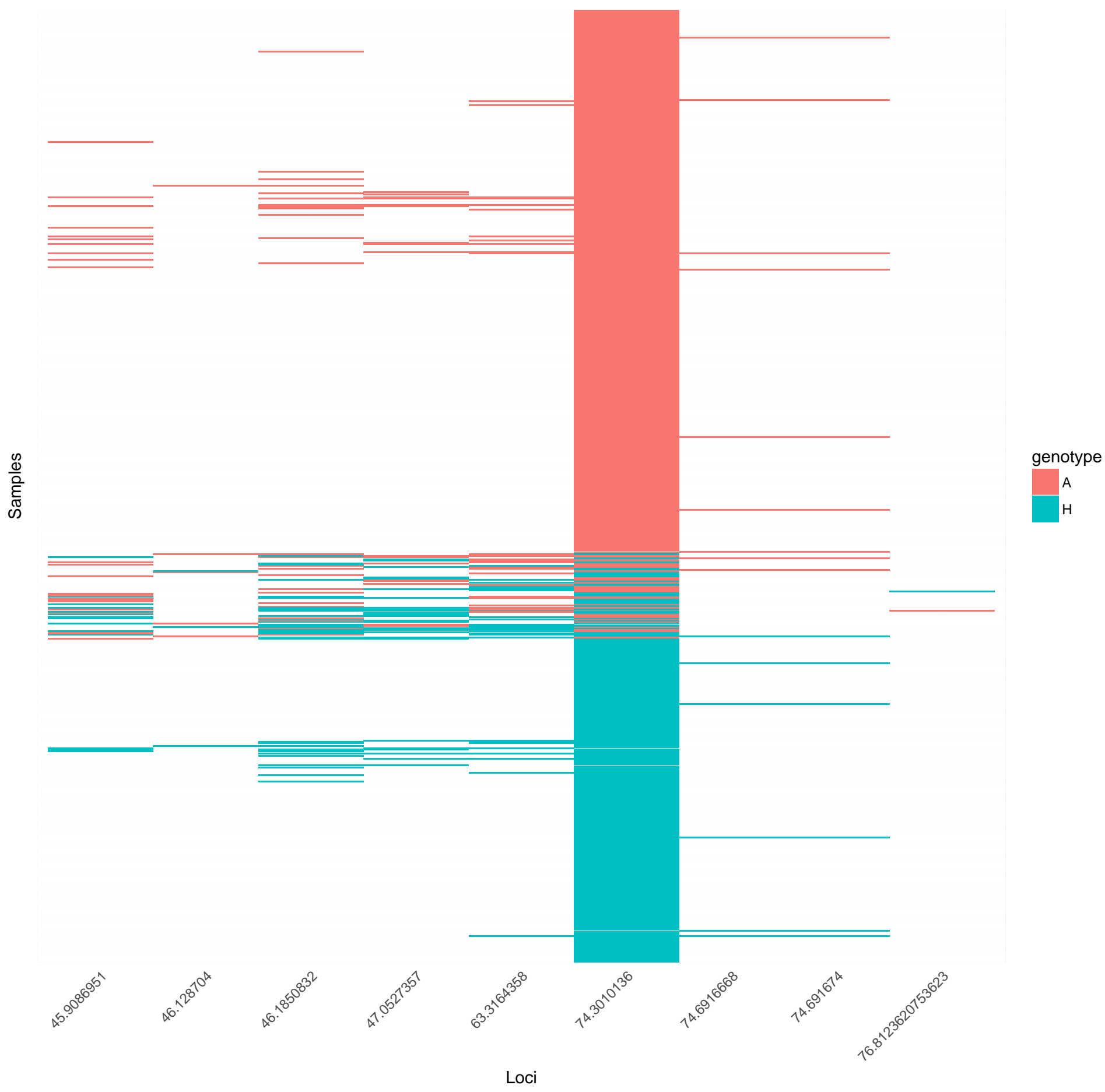


ann3 BC1, missing data, Chr 13

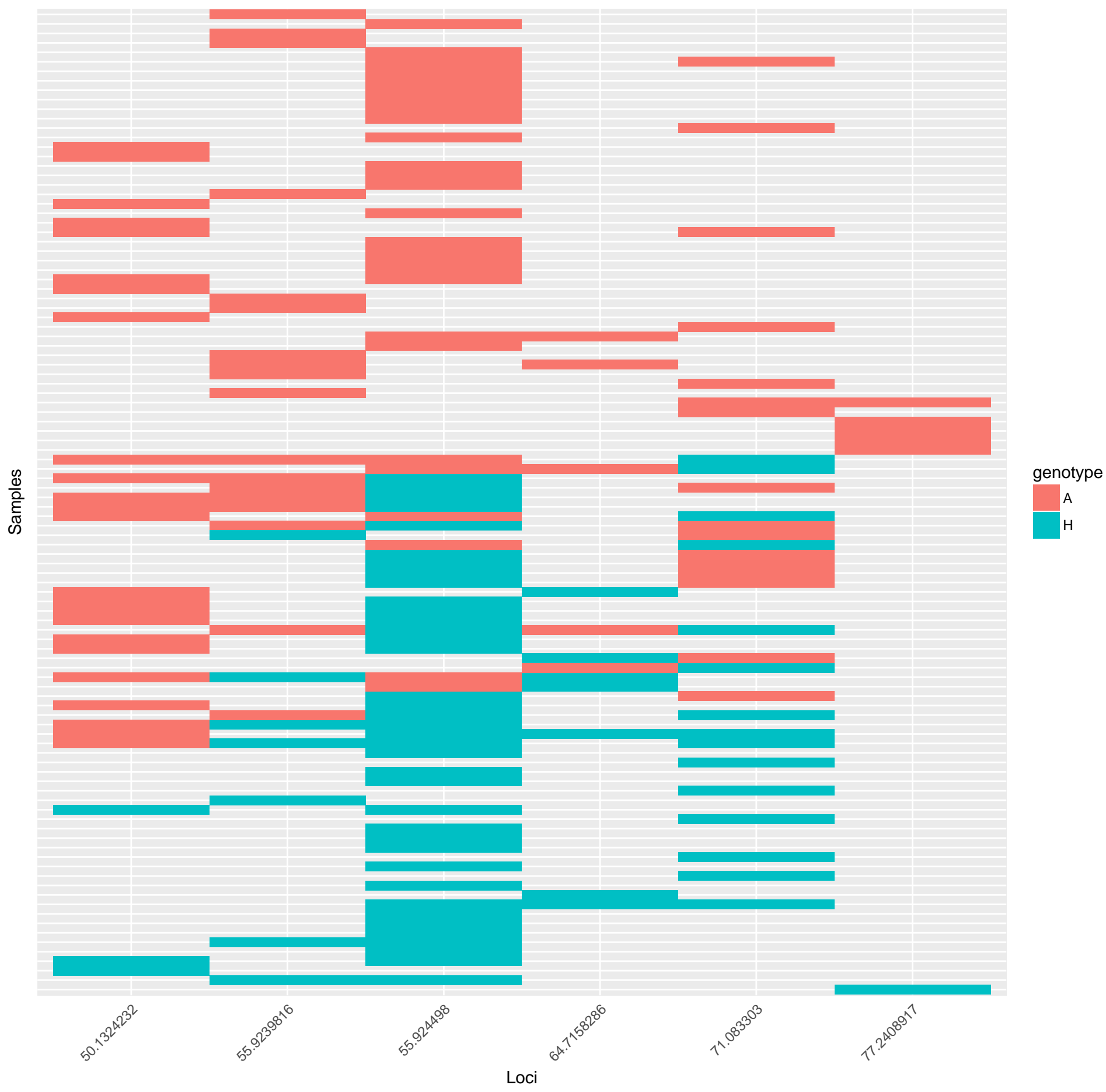


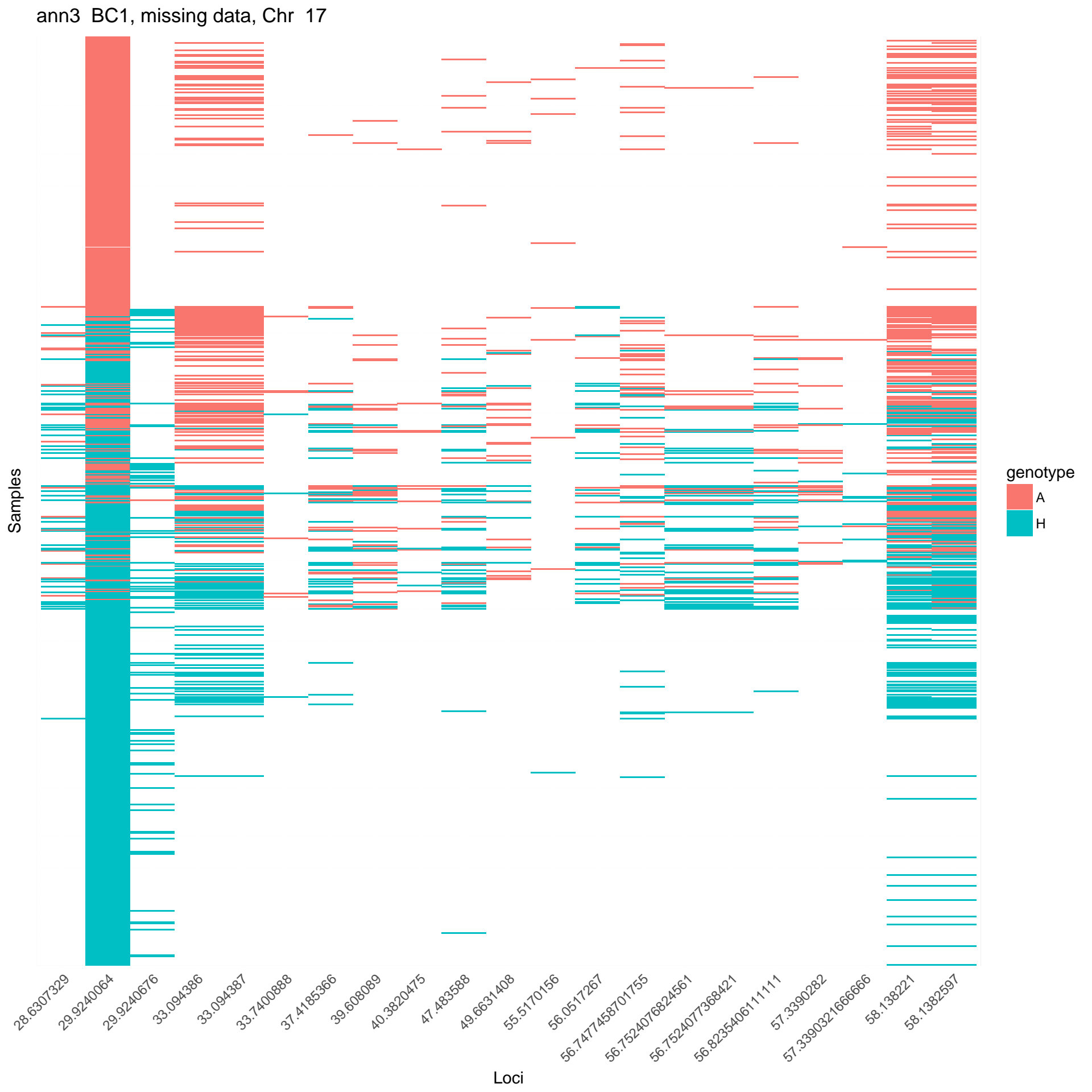






ann3 BC1, missing data, Chr 16





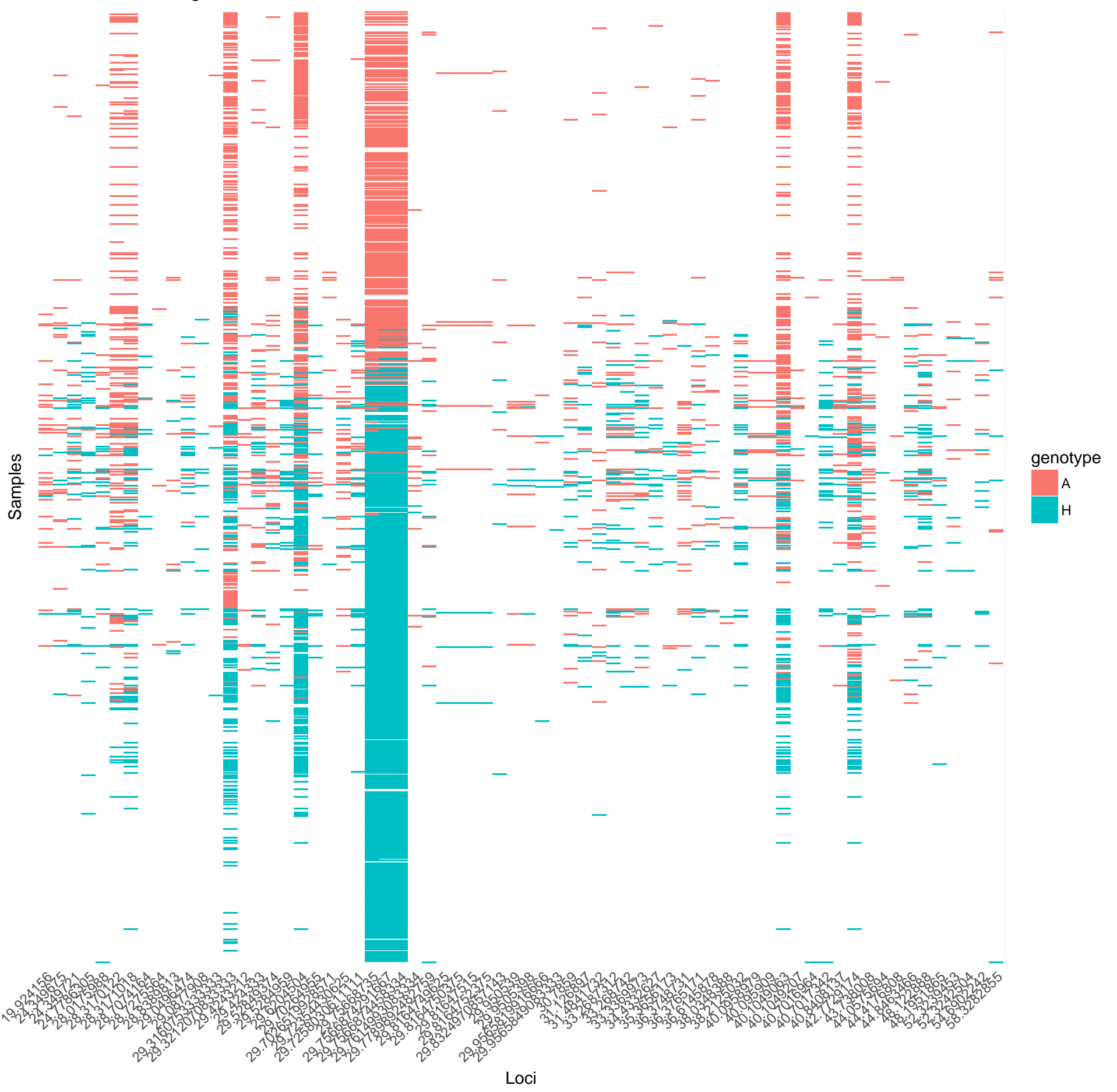
The image displays a 2D Fourier transform of a 1D signal. The horizontal axis (x-axis) represents spatial frequency in cycles per inch, ranging from 0 to 43.37041. The vertical axis (y-axis) represents temporal frequency in cycles per second, ranging from 1 to 43. The plot is filled with a dense grid of horizontal lines, colored red and teal. A prominent vertical teal line is visible at approximately 32.741 cycles per inch. The overall pattern suggests a complex, periodic signal with multiple frequency components.

A  
H

deb BC1, missing data, Chr 02



deb BC1, missing data, Chr 03





A  
H

A  
H

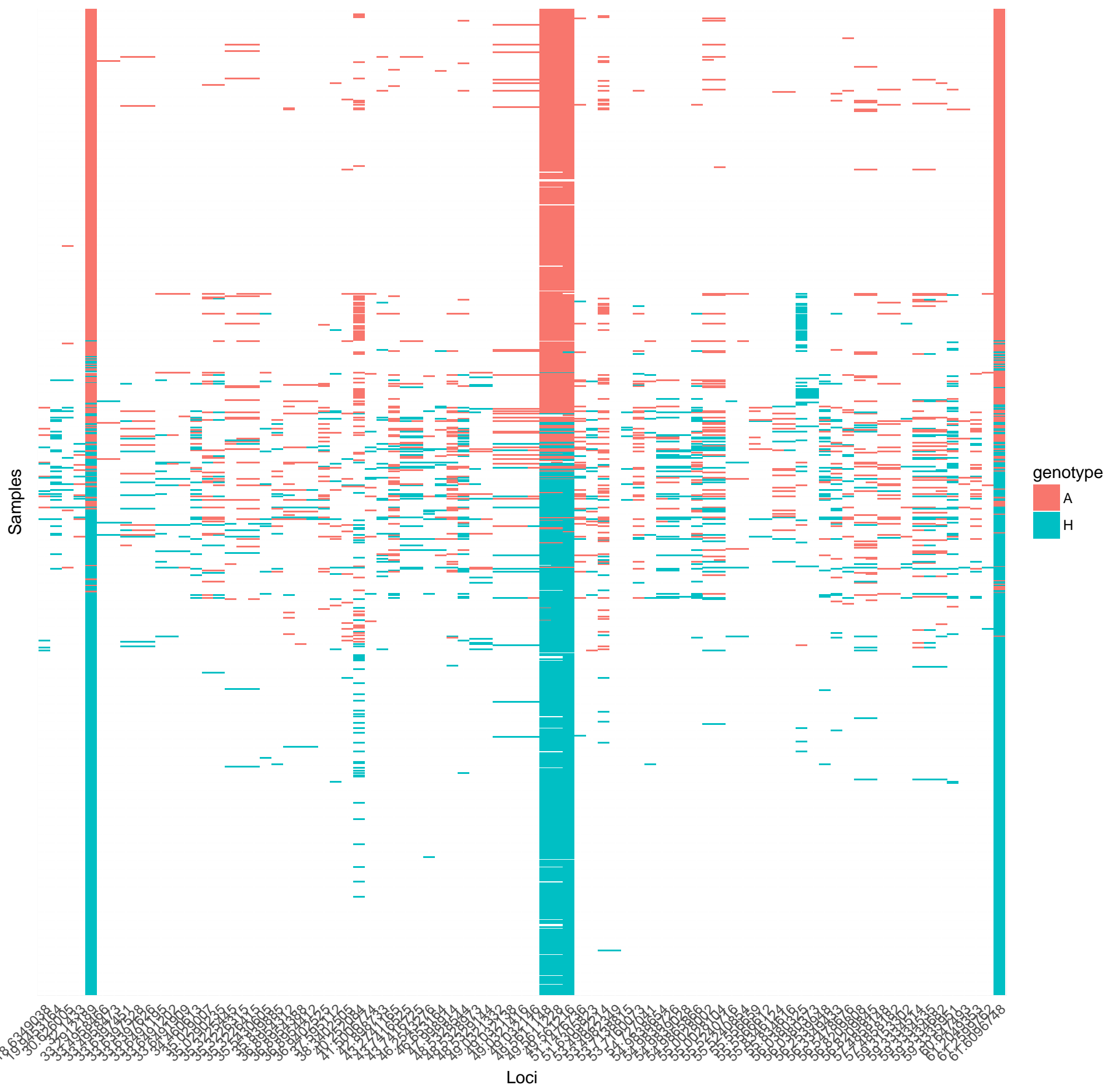
A

H

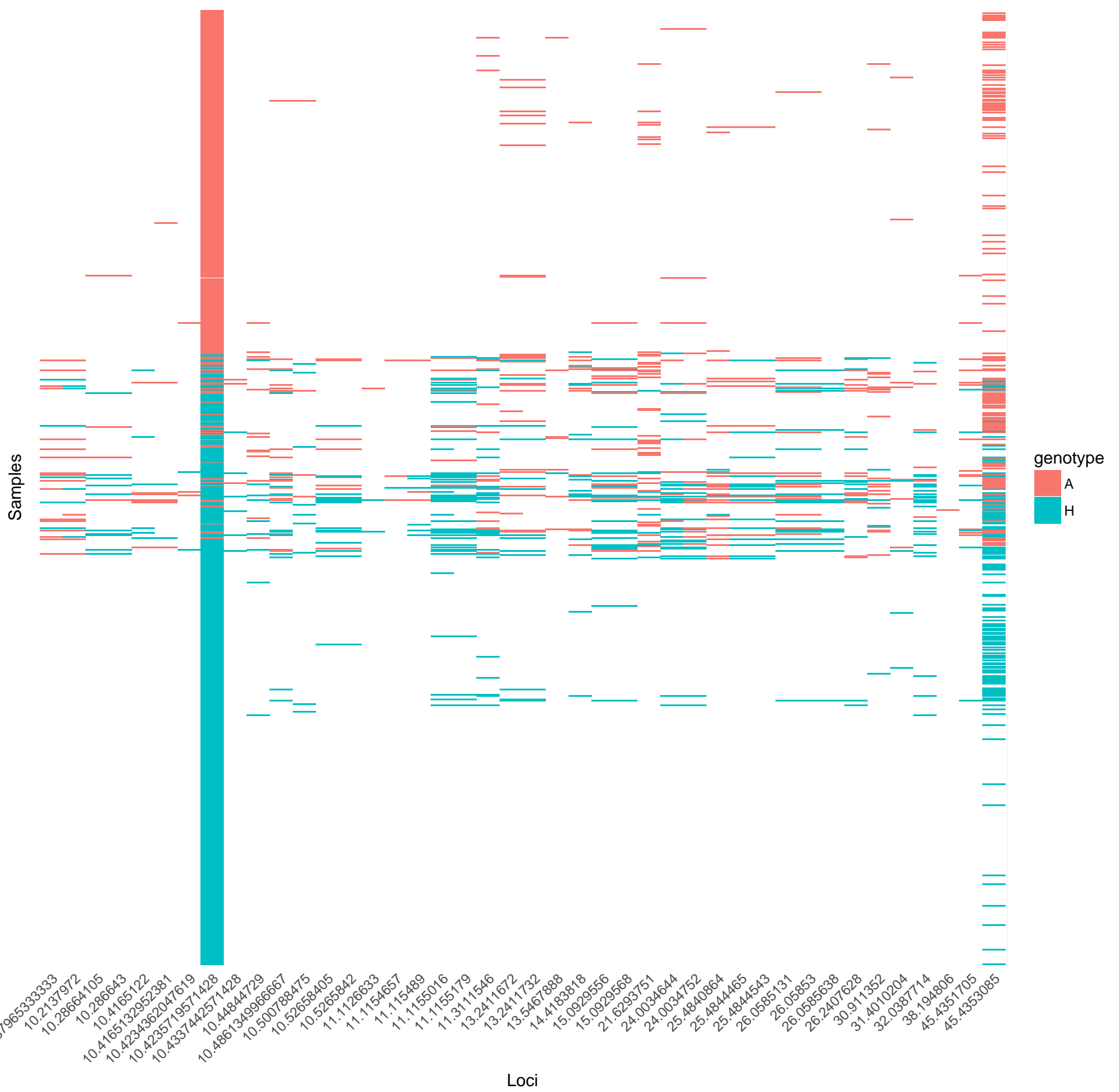
Loci



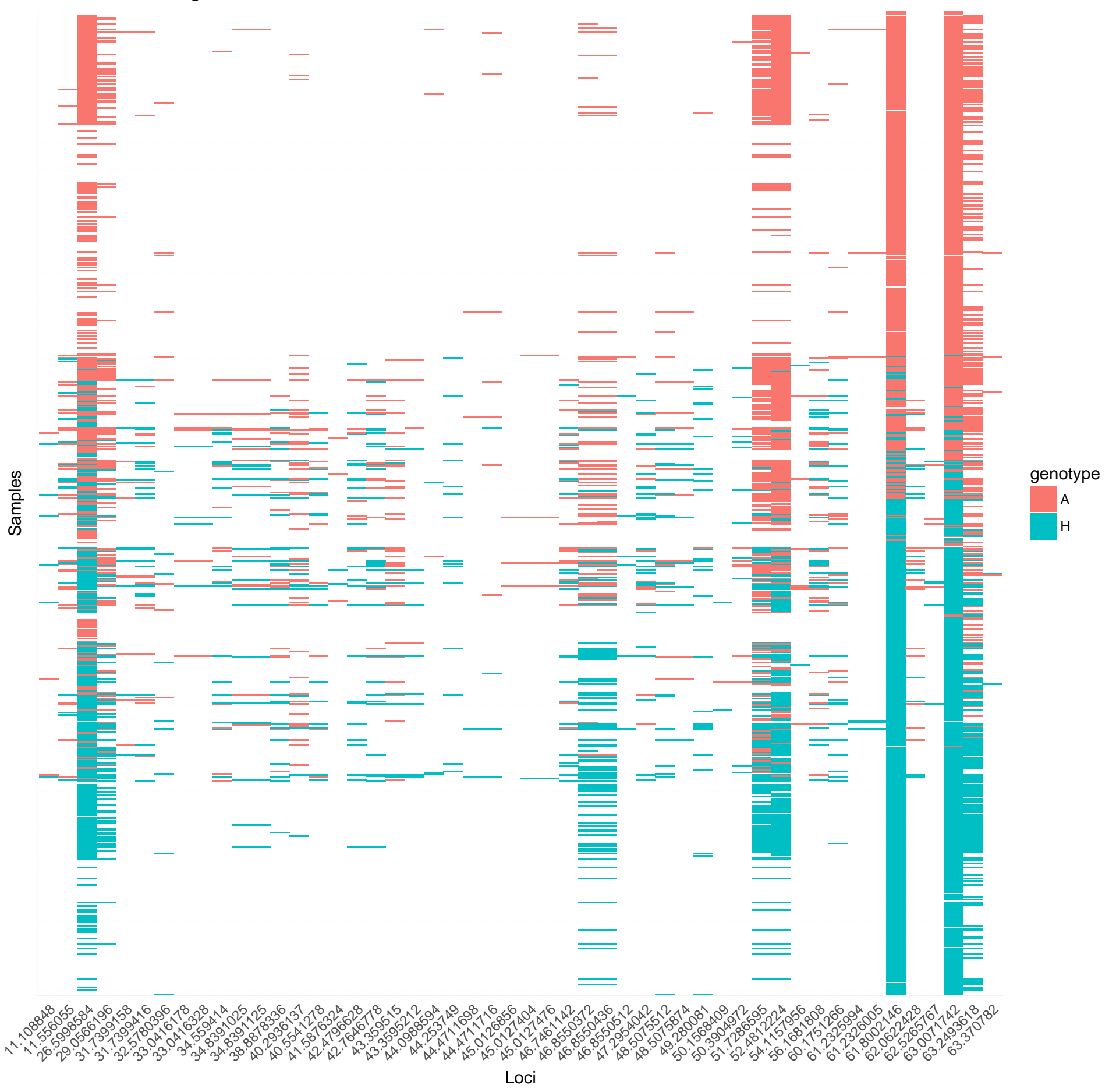
deb BC1, missing data, Chr 06



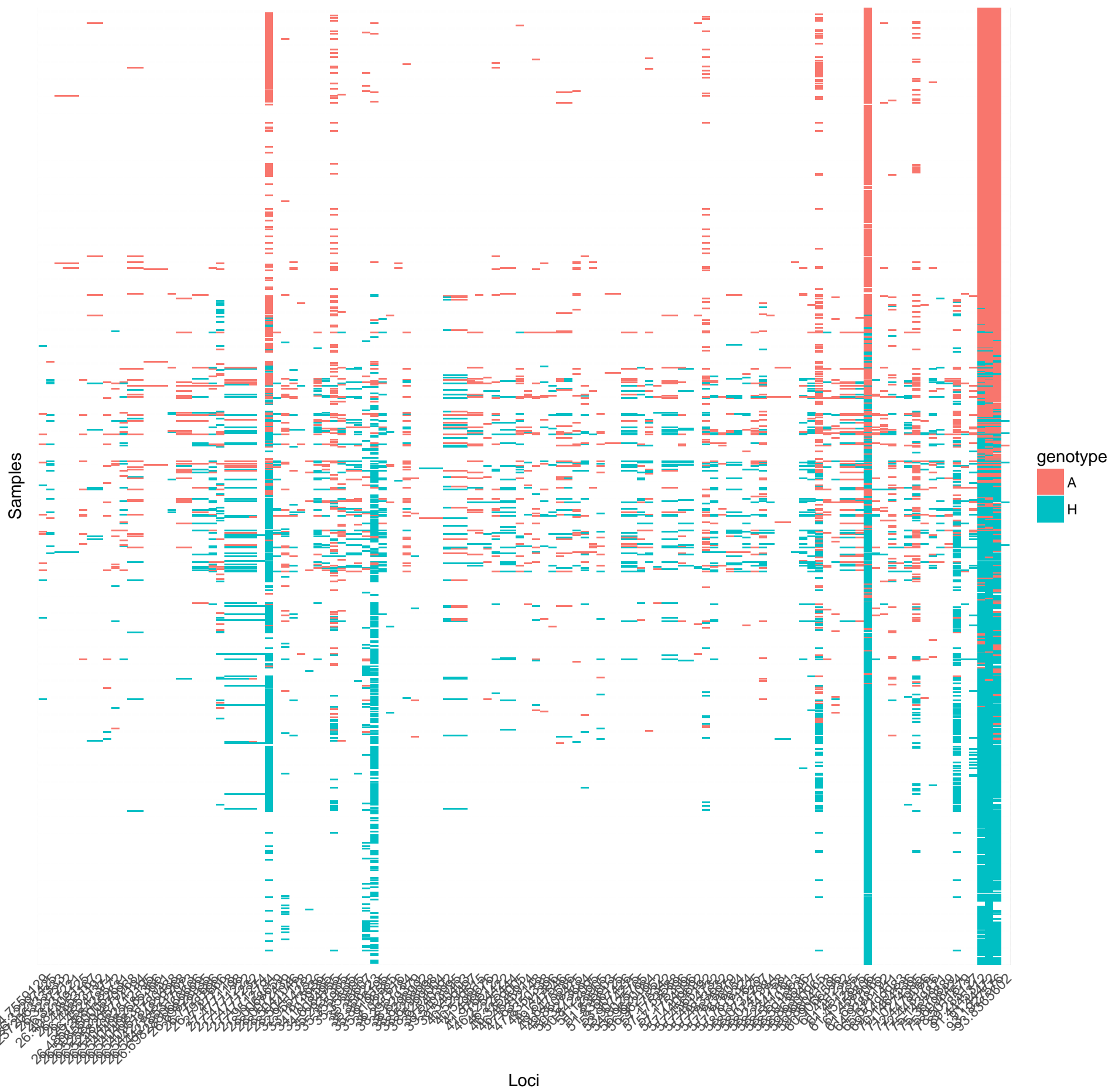
deb BC1, missing data, Chr 07



deb BC1, missing data, Chr 08



deb BC1, missing data, Chr 09



deb BC1, missing data, Chr 10

Samples

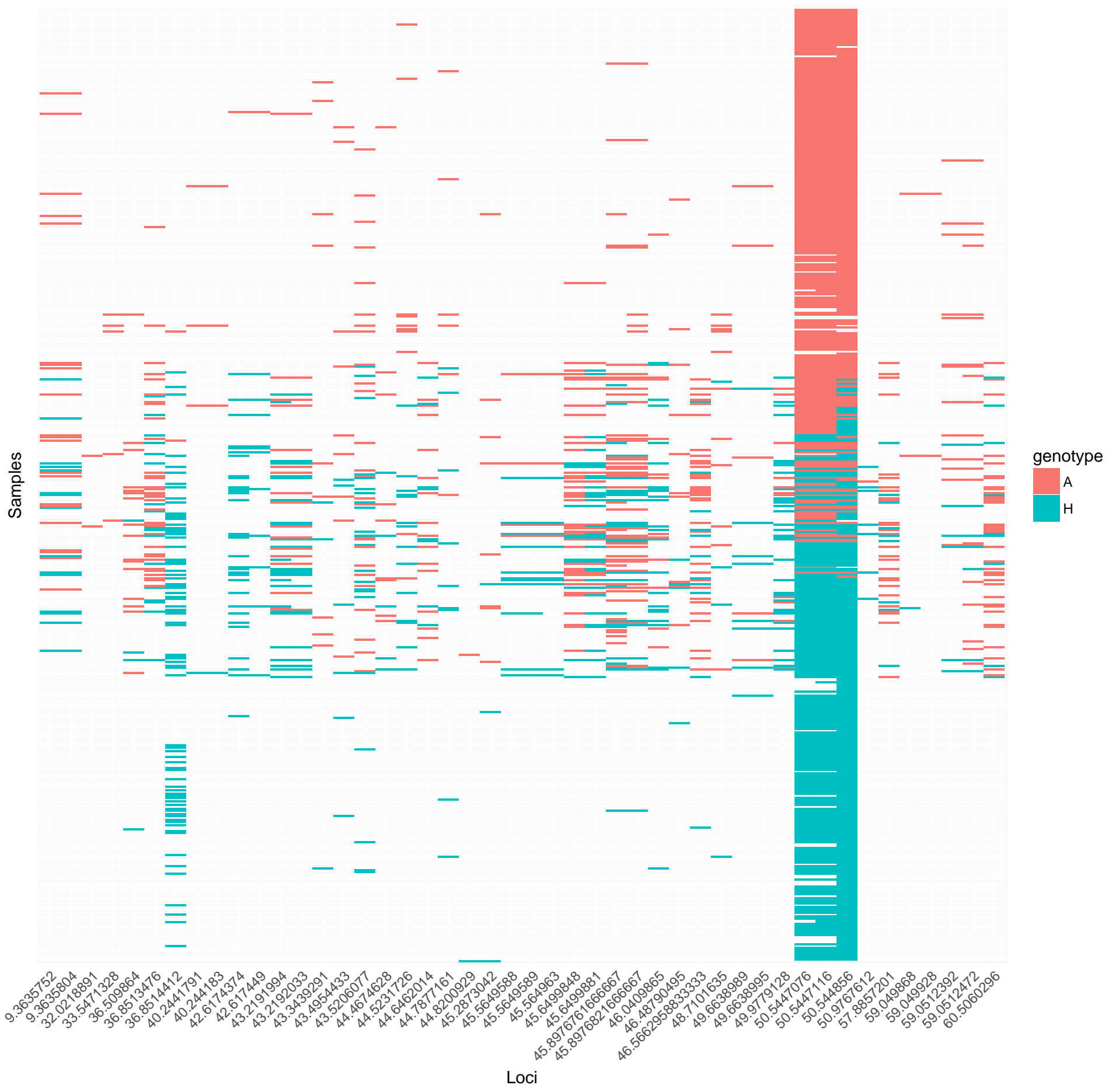
genotype

A

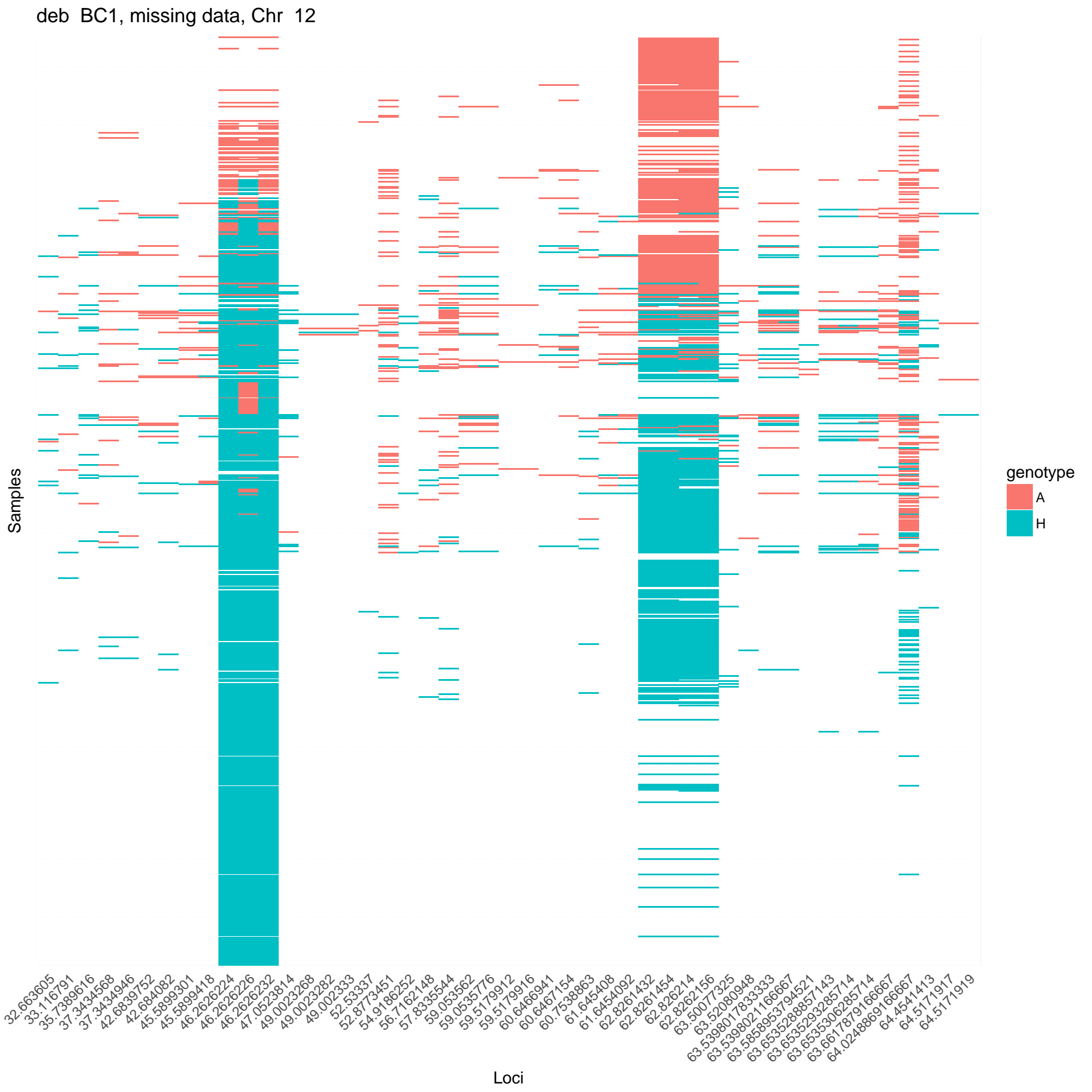
H

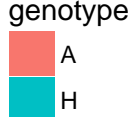
Loci

deb BC1, missing data, Chr 11



deb BC1, missing data, Chr 12

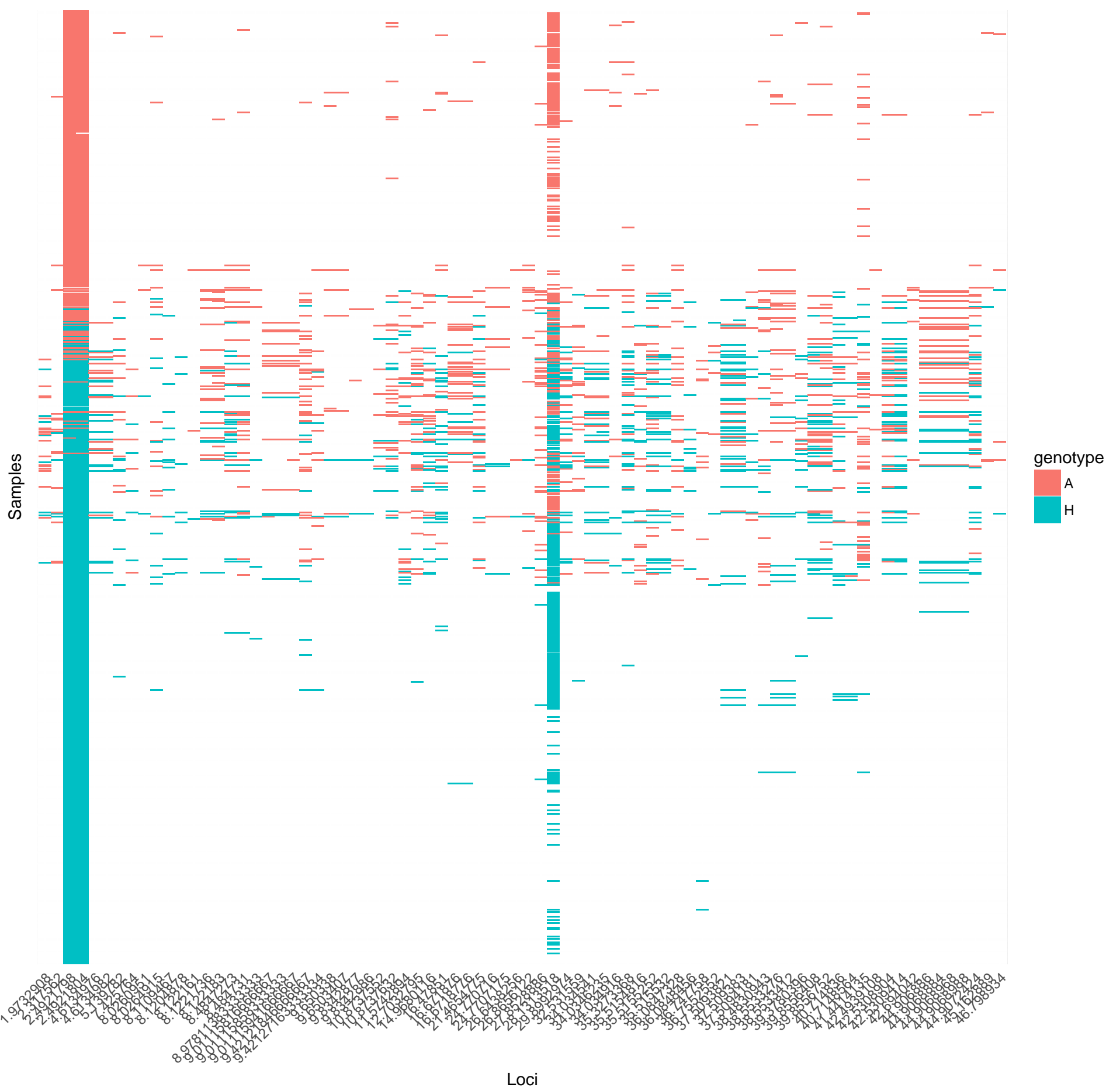




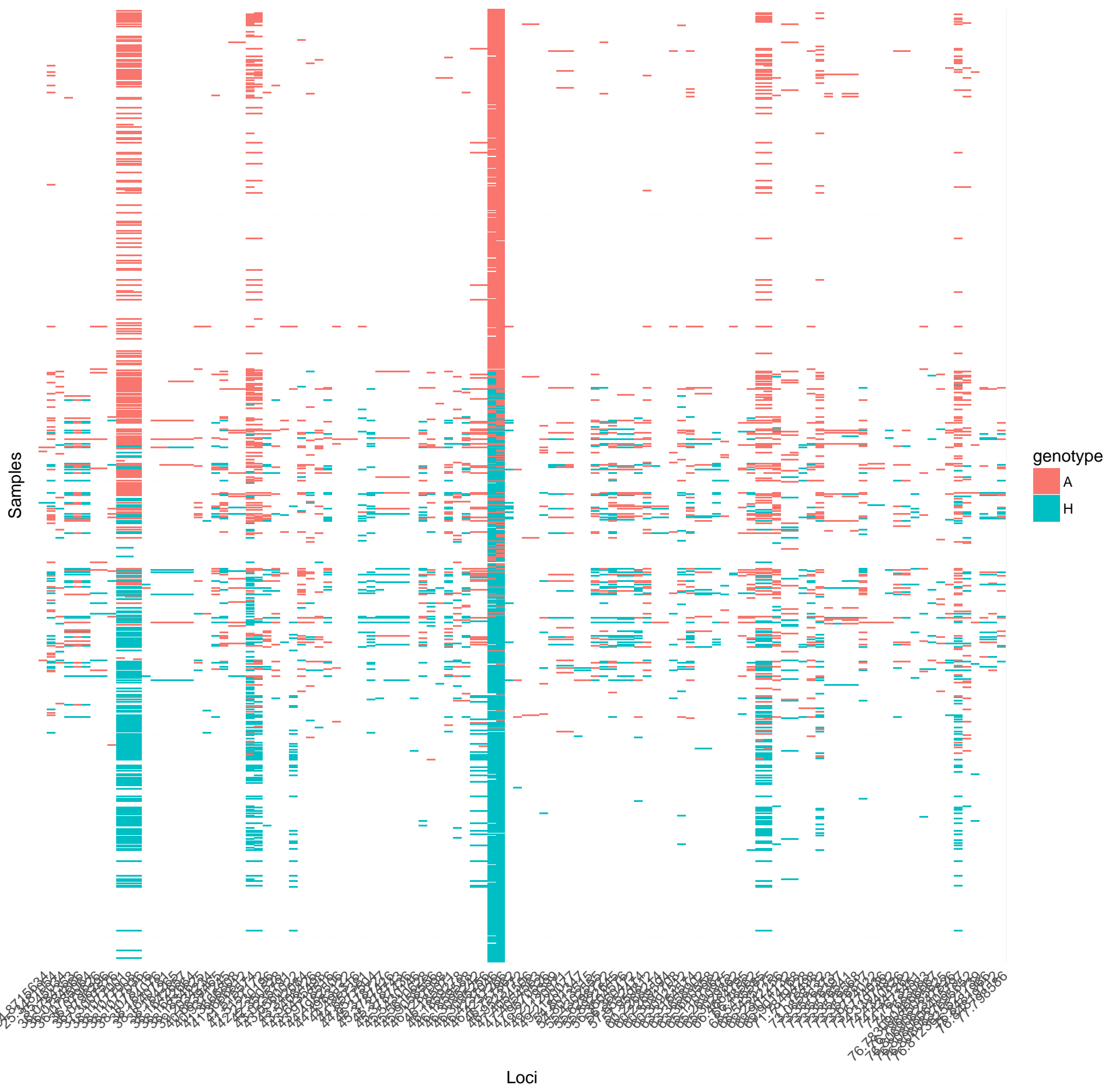
Loci



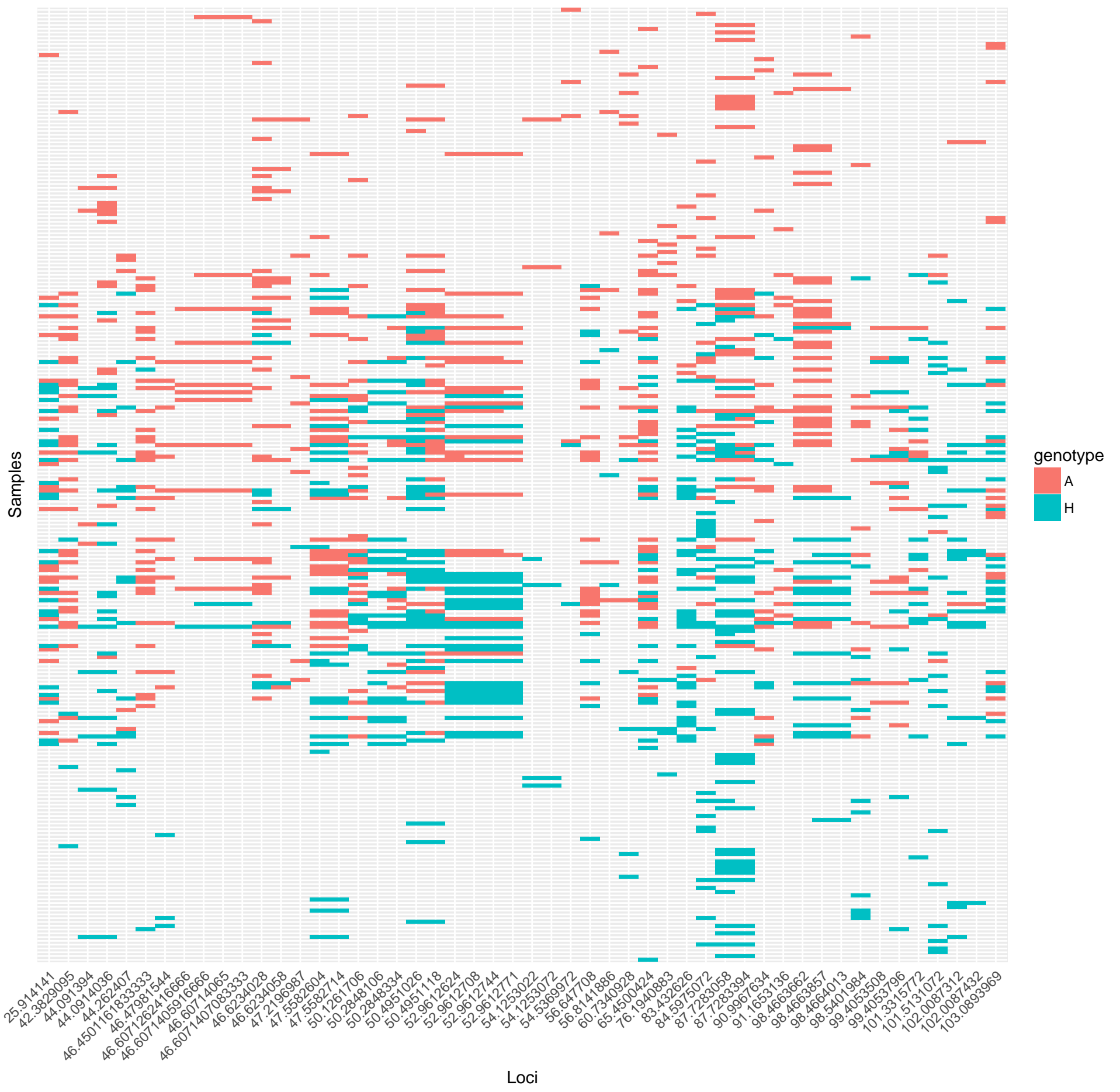
deb BC1, missing data, Chr 14



deb BC1, missing data, Chr 15



deb BC1, missing data, Chr 16



deb BC1, missing data, Chr 17

