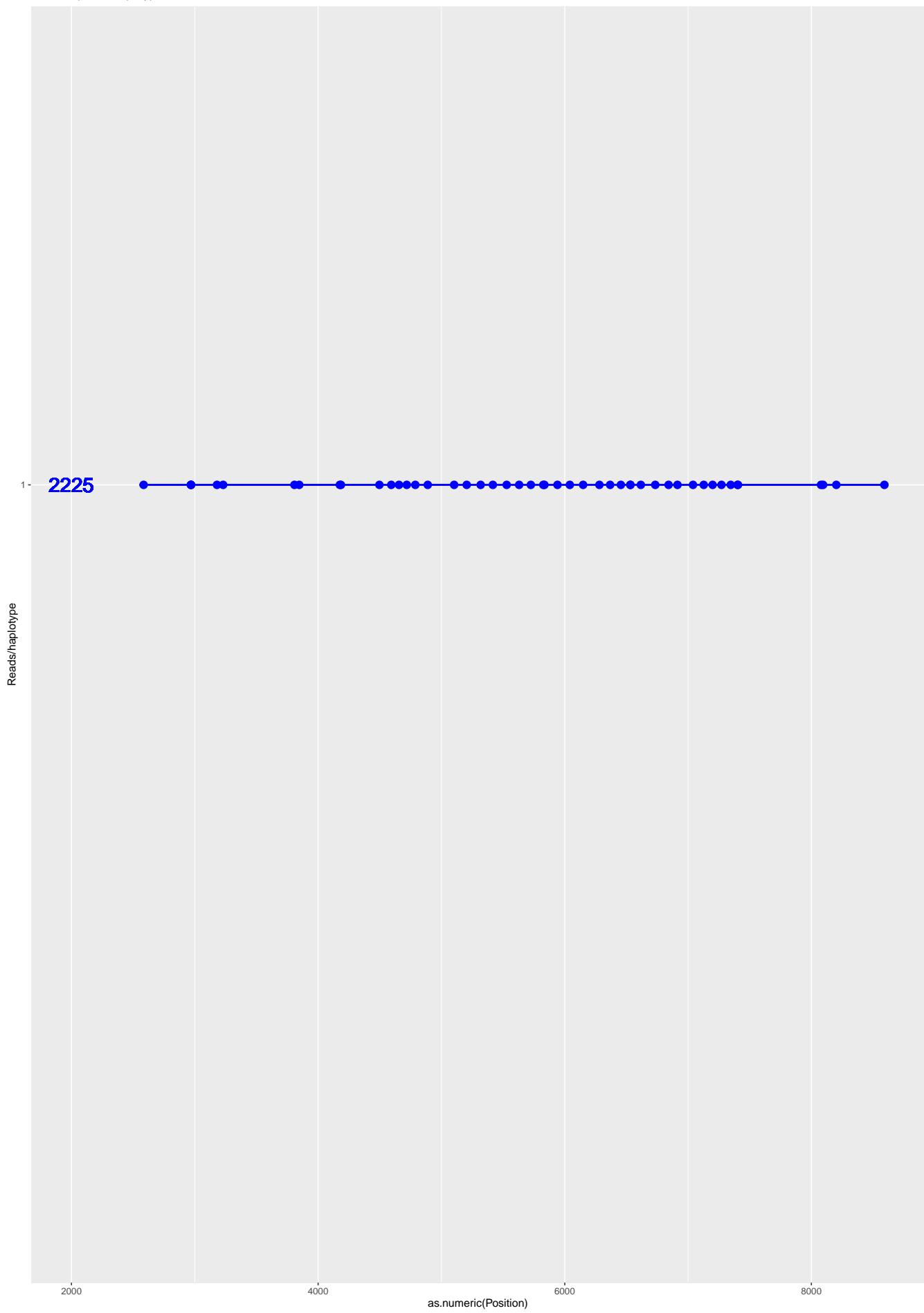


Sample = 4a tetrad = 4 spore = a

Total reads = 2589 PCR=9

haplotypes I began with n[supporting reads] = 2225

most frequent 7 haplotypes.



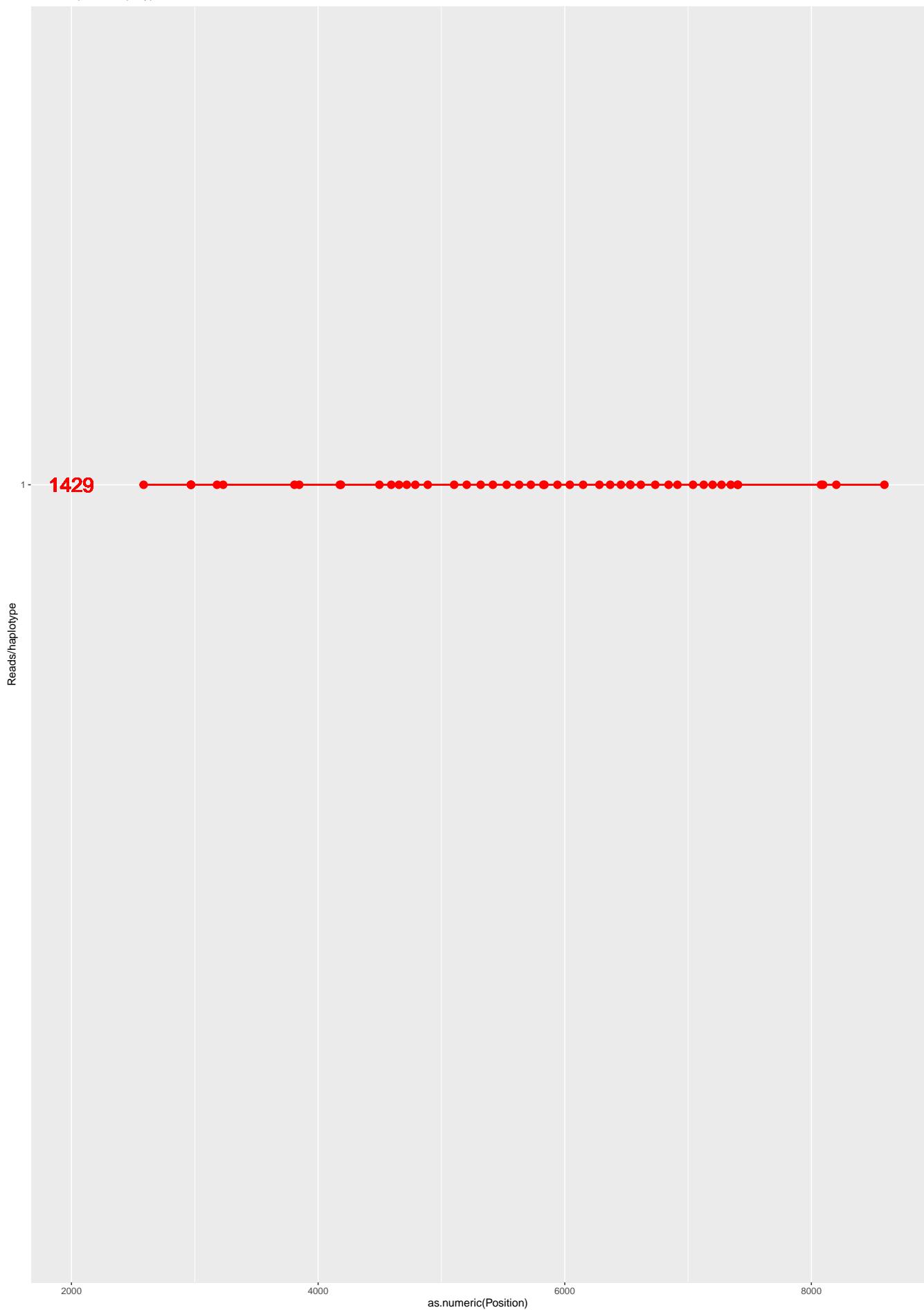
barcode = TCATGAGTCGACACTA & TCATATGTAGTACTCT

Sample = 4b tetrad = 4 spore = b

Total reads = 1491 PCR=10

haplotypes I began with n[supporting reads] = 1429

most frequent 7 haplotypes.



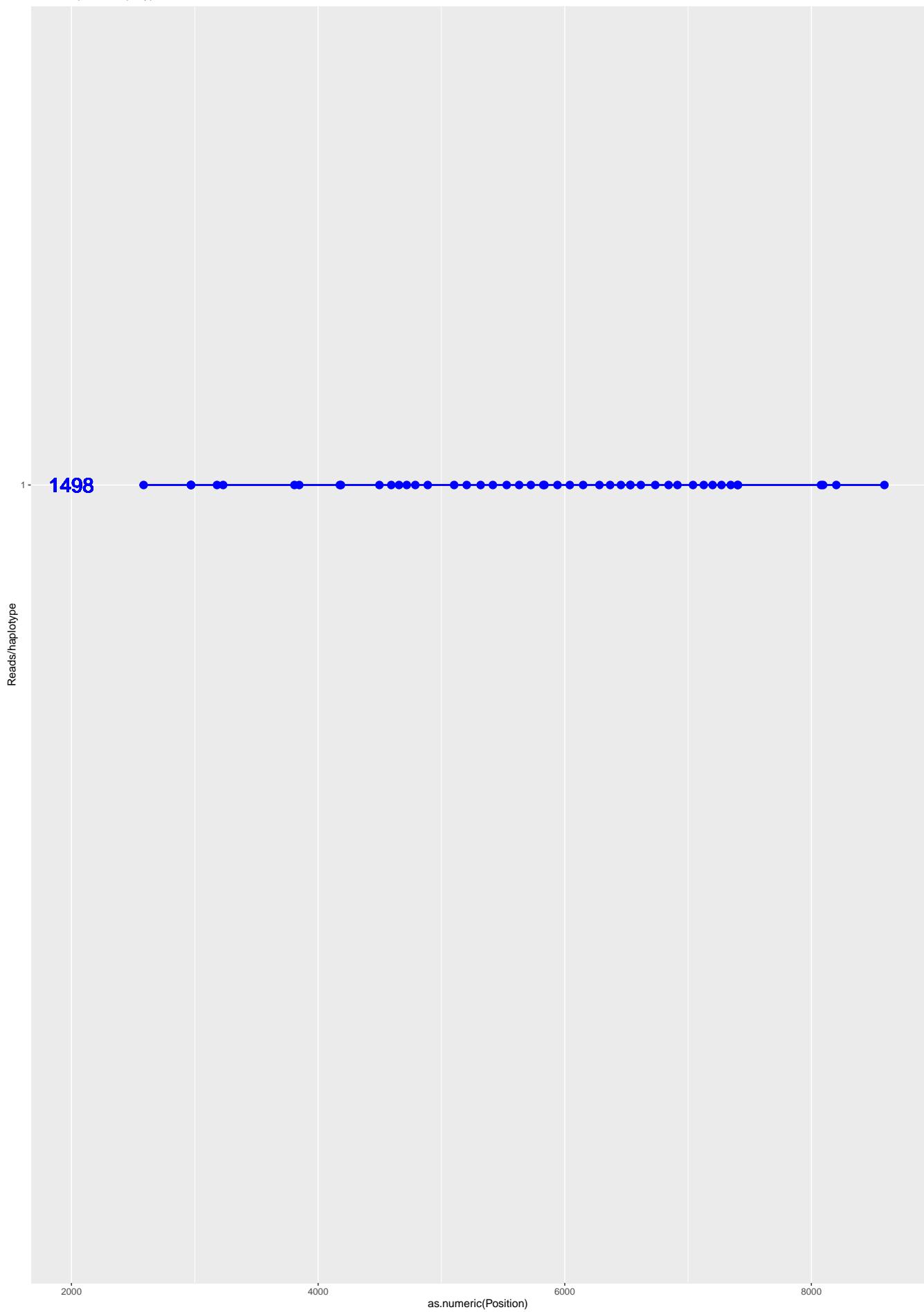
barcode = TCATGAGTCGACACTA & GCGATCTATGCACACG

Sample = 4c tetrad = 4 spore = c

Total reads = 1776 PCR=11

haplotypes I began with n[supporting reads] = 1498

most frequent 7 haplotypes.



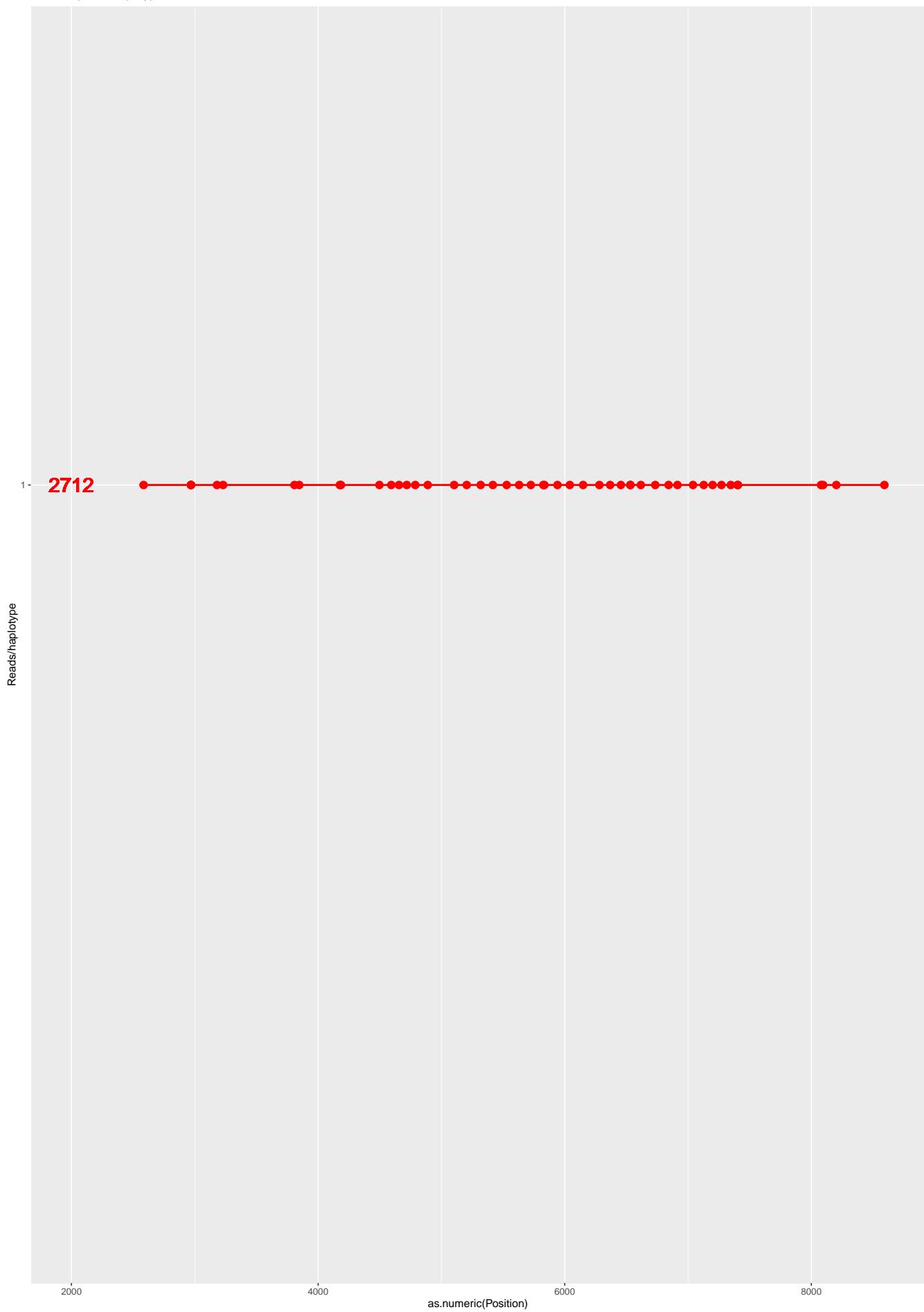
barcode = TCATGAGTCGACACTA & TGCAGTCGAGATACT

Sample = 4d tetrad = 4 spore = d

Total reads = 2821 PCR=12

haplotypes I began with n[supporting reads] = 2712

most frequent 7 haplotypes.

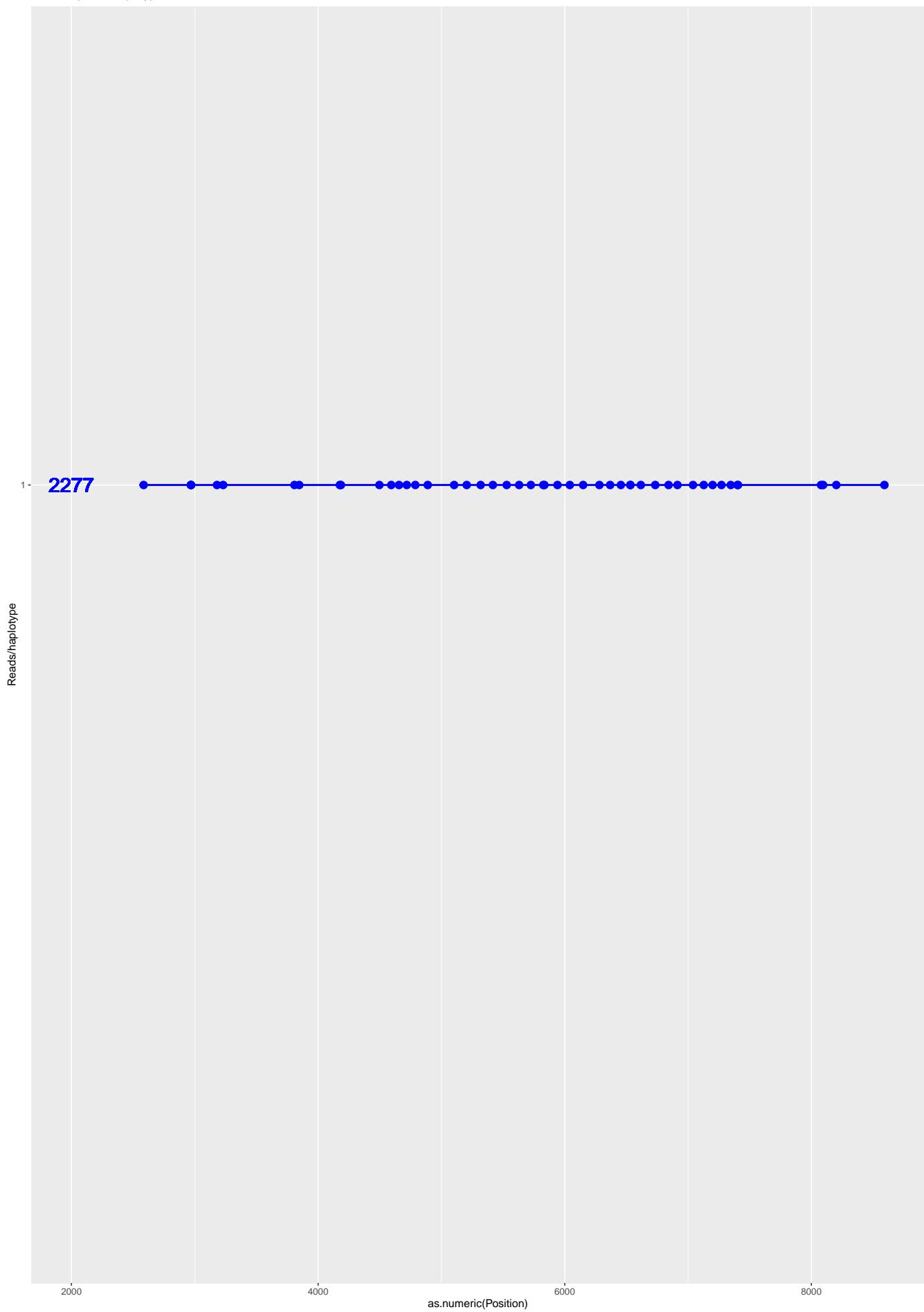


Sample = 5a tetrad = 5 spore = a

Total reads =2639 PCR=13

haplotypes I began with n[supporting reads] = 2277

most frequent 7 haplotypes.



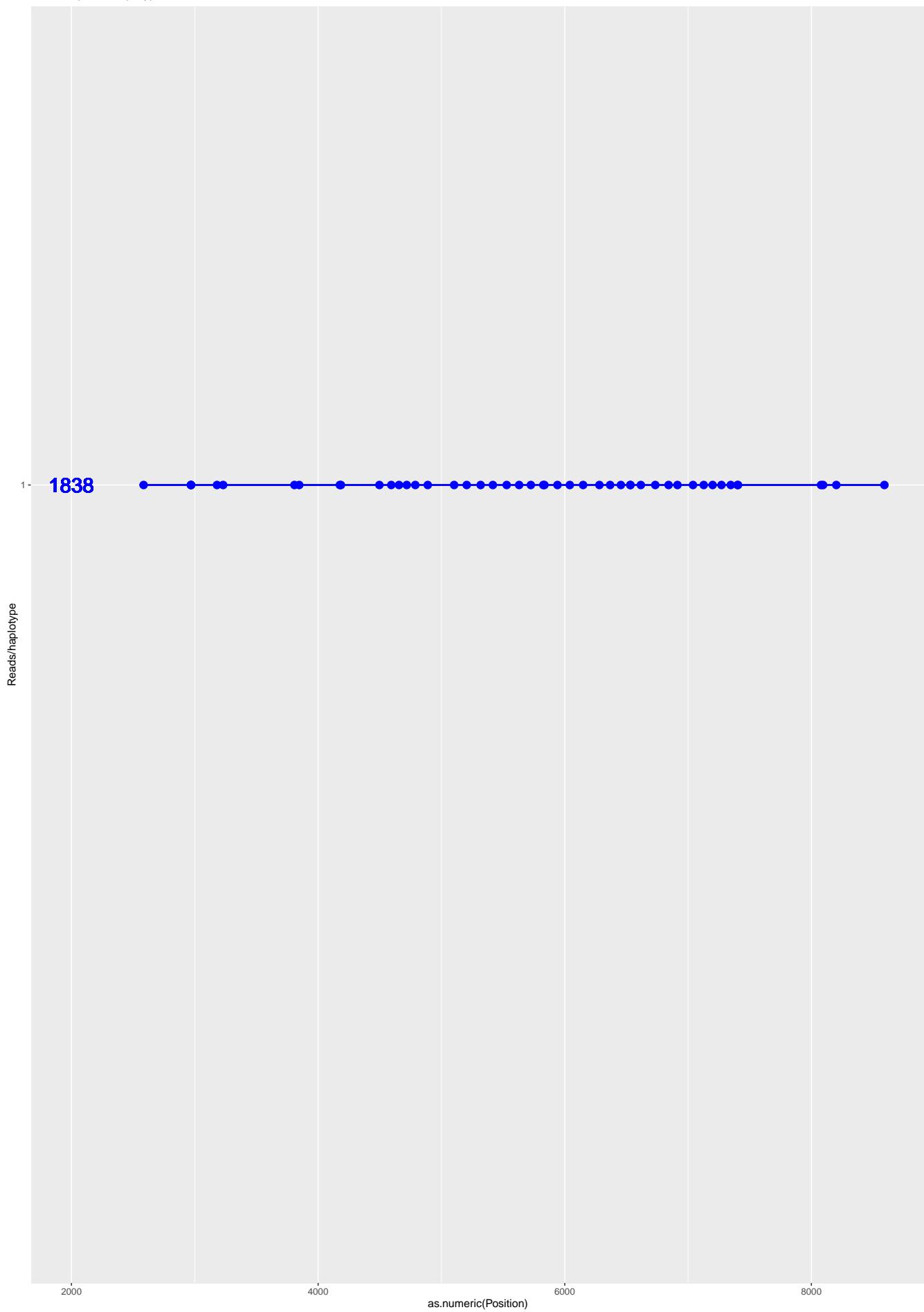
barcode = TCATGAGTCGACACTA & TACAGCGACGTCATCG

Sample = 5b tetrad = 5 spore = b

Total reads = 2150 PCR=14

haplotypes I began with n[supporting reads] = 1838

most frequent 7 haplotypes.

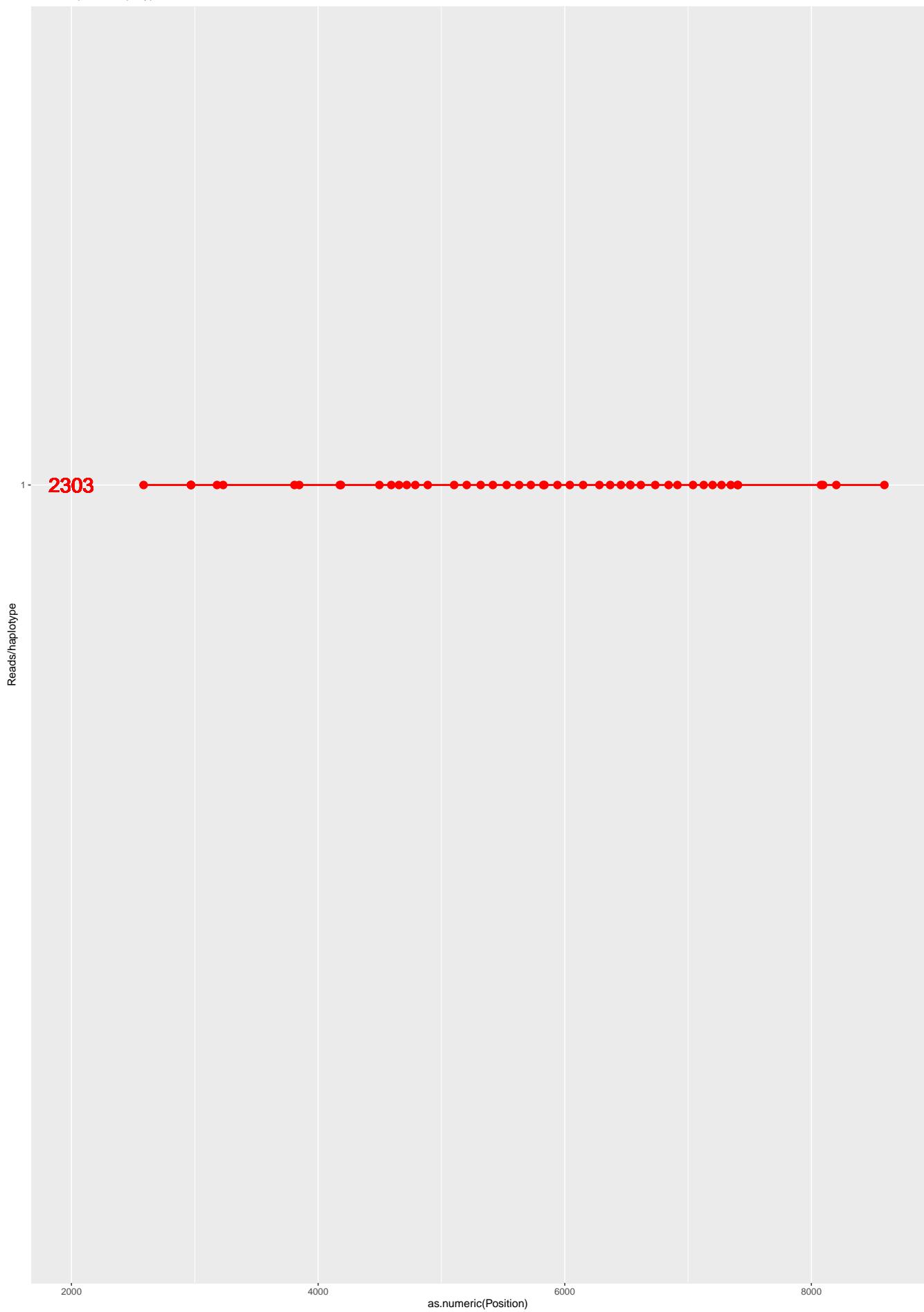


Sample = 5c tetrad = 5 spore = c

Total reads = 2395 PCR=15

haplotypes I began with n[supporting reads] = 2303

most frequent 7 haplotypes.



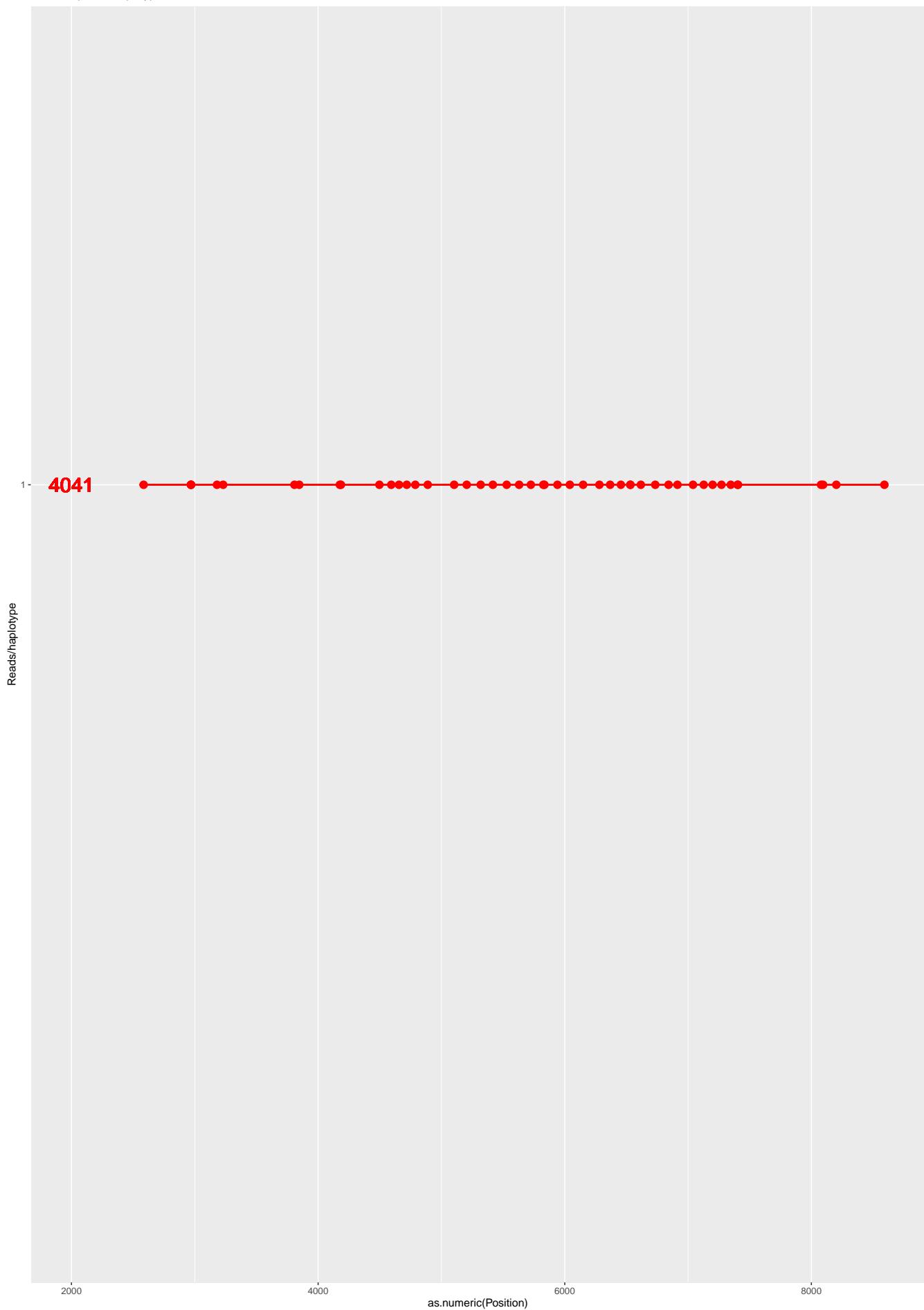
barcode = TCATGAGTCGACACTA & GTCTCTGCGATAACAGC

Sample = 5d tetrad = 5 spore = d

Total reads = 4195 PCR=16

haplotypes I began with n[supporting reads] = 4041

most frequent 7 haplotypes.



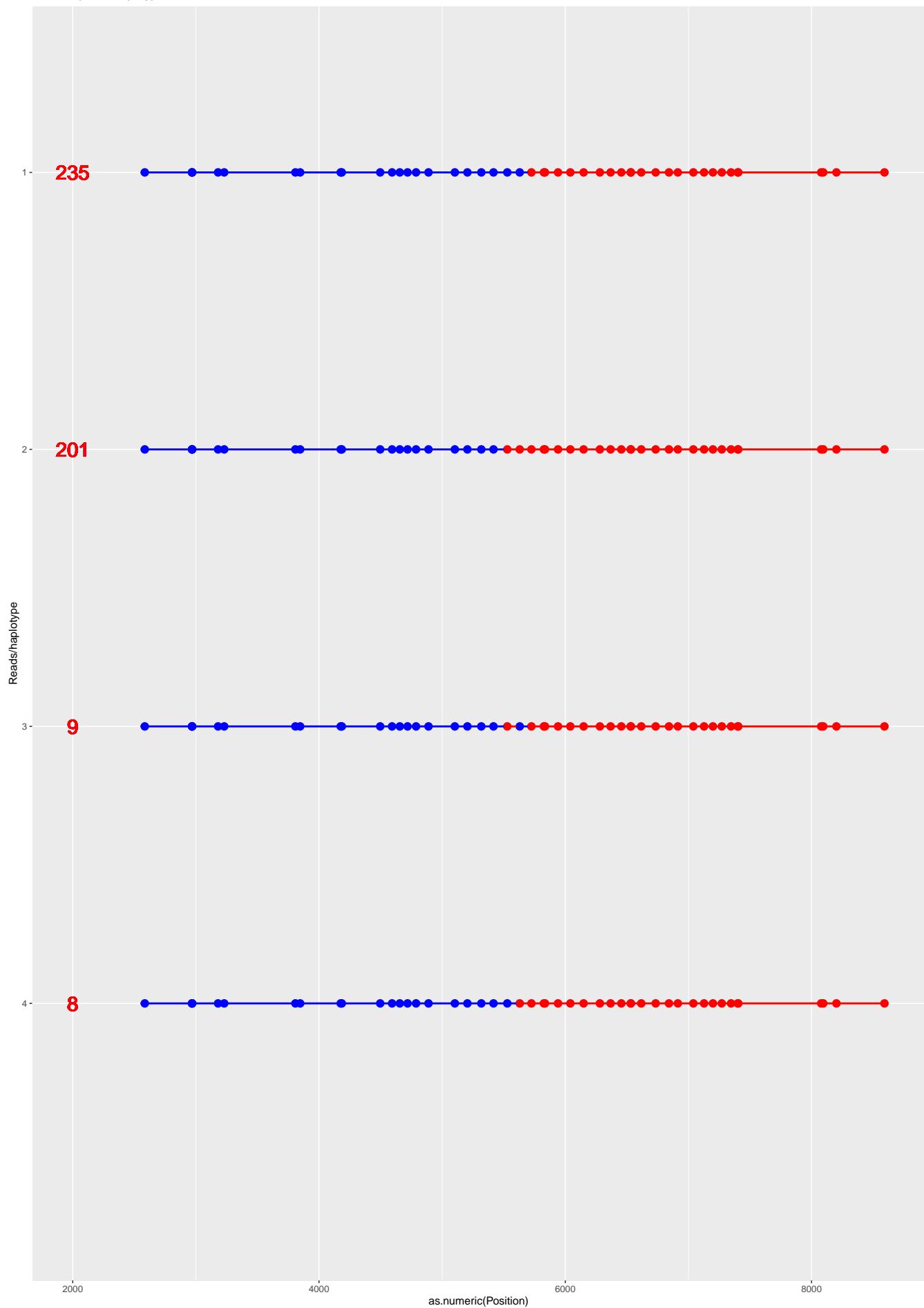
barcode = TCATGAGTCGACACTA & AGTATGAGATAGCTCG

Sample = 6a tetrad = 6 spore = a

Total reads =506 PCR=17

haplotypes I began with n[supporting reads] = 8, 9, 201, 235

most frequent 7 haplotypes.



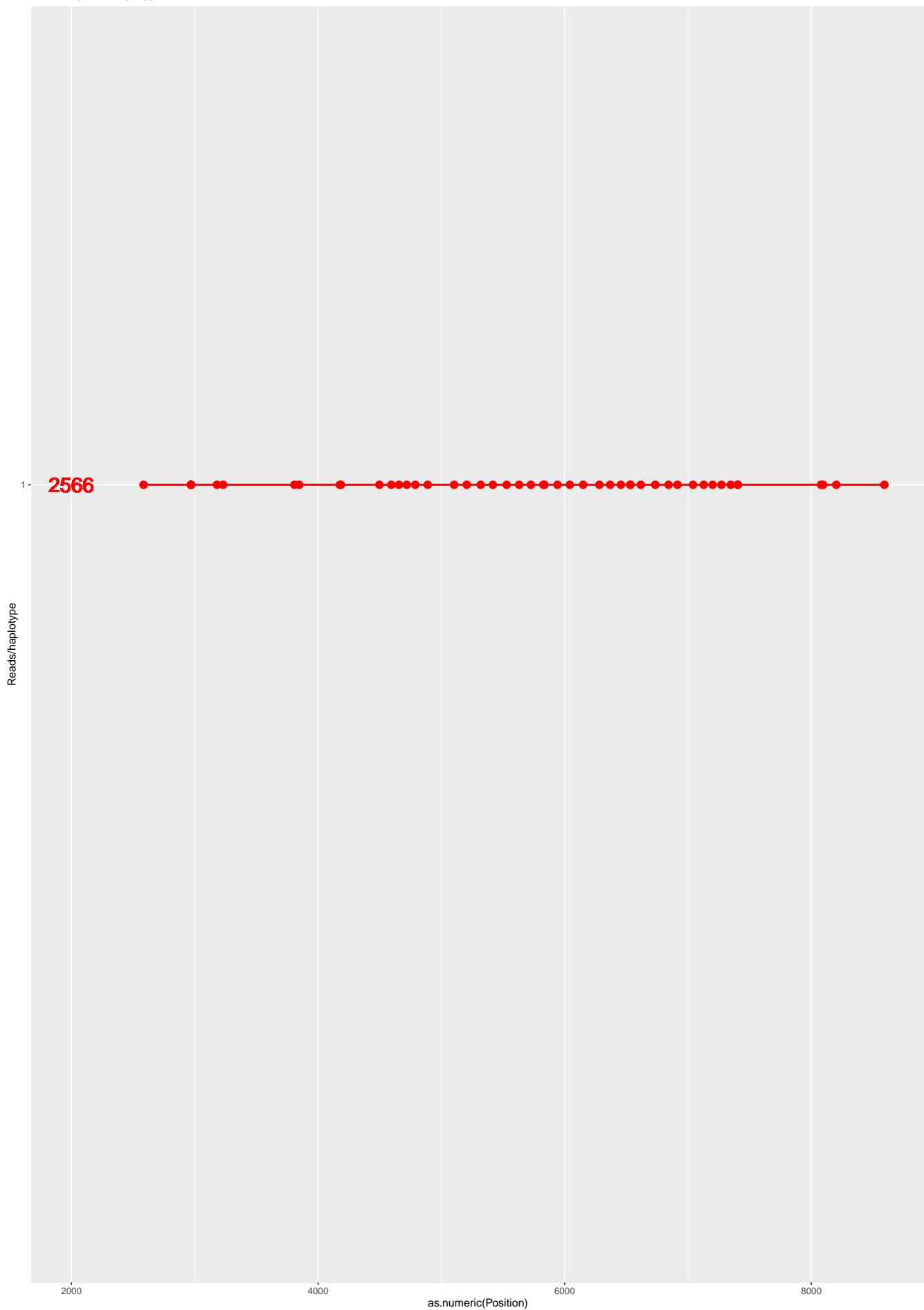
barcode = TATCTATCGTATAACGC & TCATATGTAGTACTCT

Sample = 6b tetrad = 6 spore = b

Total reads = 2662 PCR=18

haplotypes I began with n[supporting reads] = 2566

most frequent 7 haplotypes.



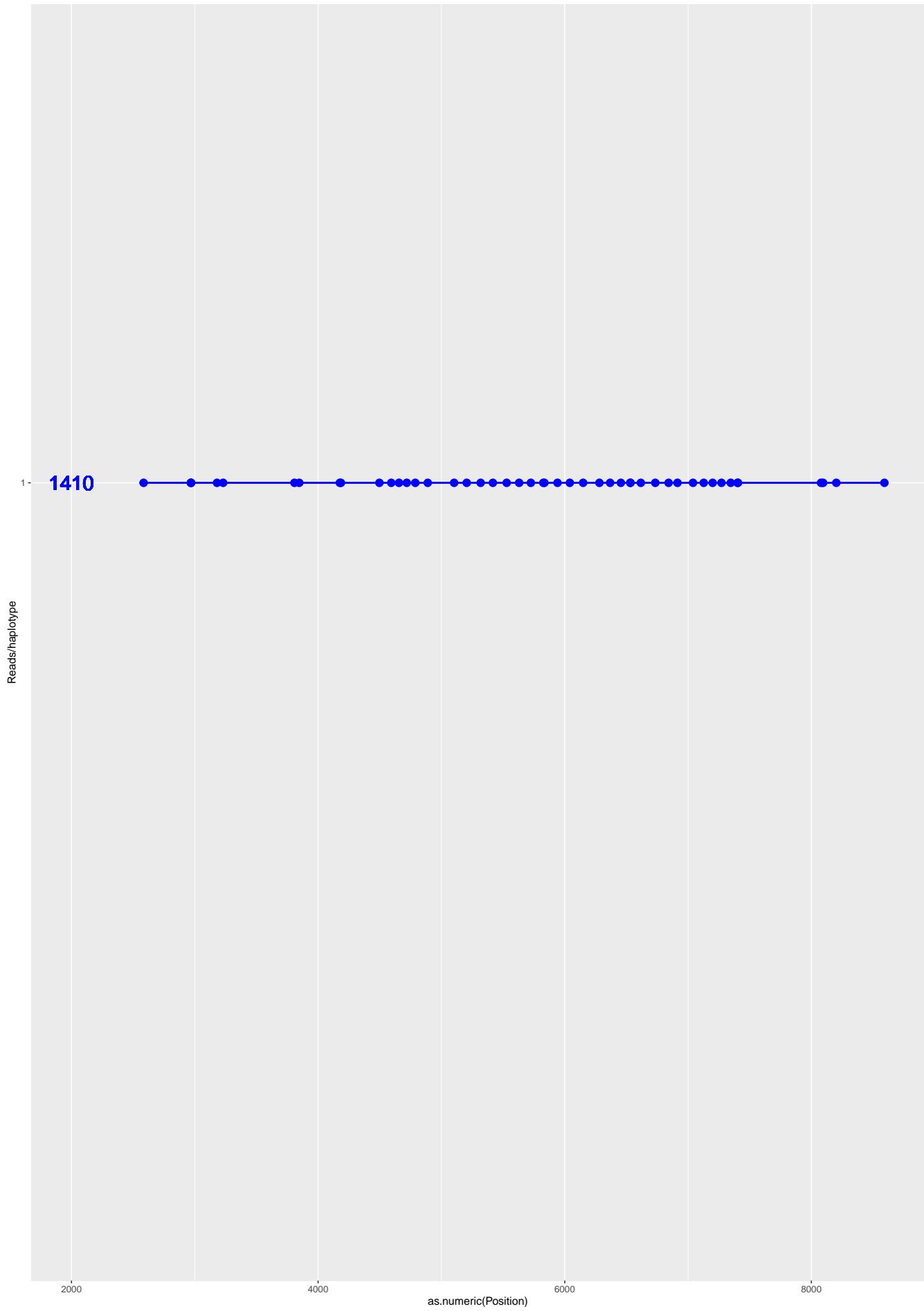
barcode = TATCTATCGTATAACGC & GCGATCTATGCACACG

Sample = 6c tetrad = 6 spore = c

Total reads = 1646 PCR=19

haplotypes I began with n[supporting reads] = 1410

most frequent 7 haplotypes.

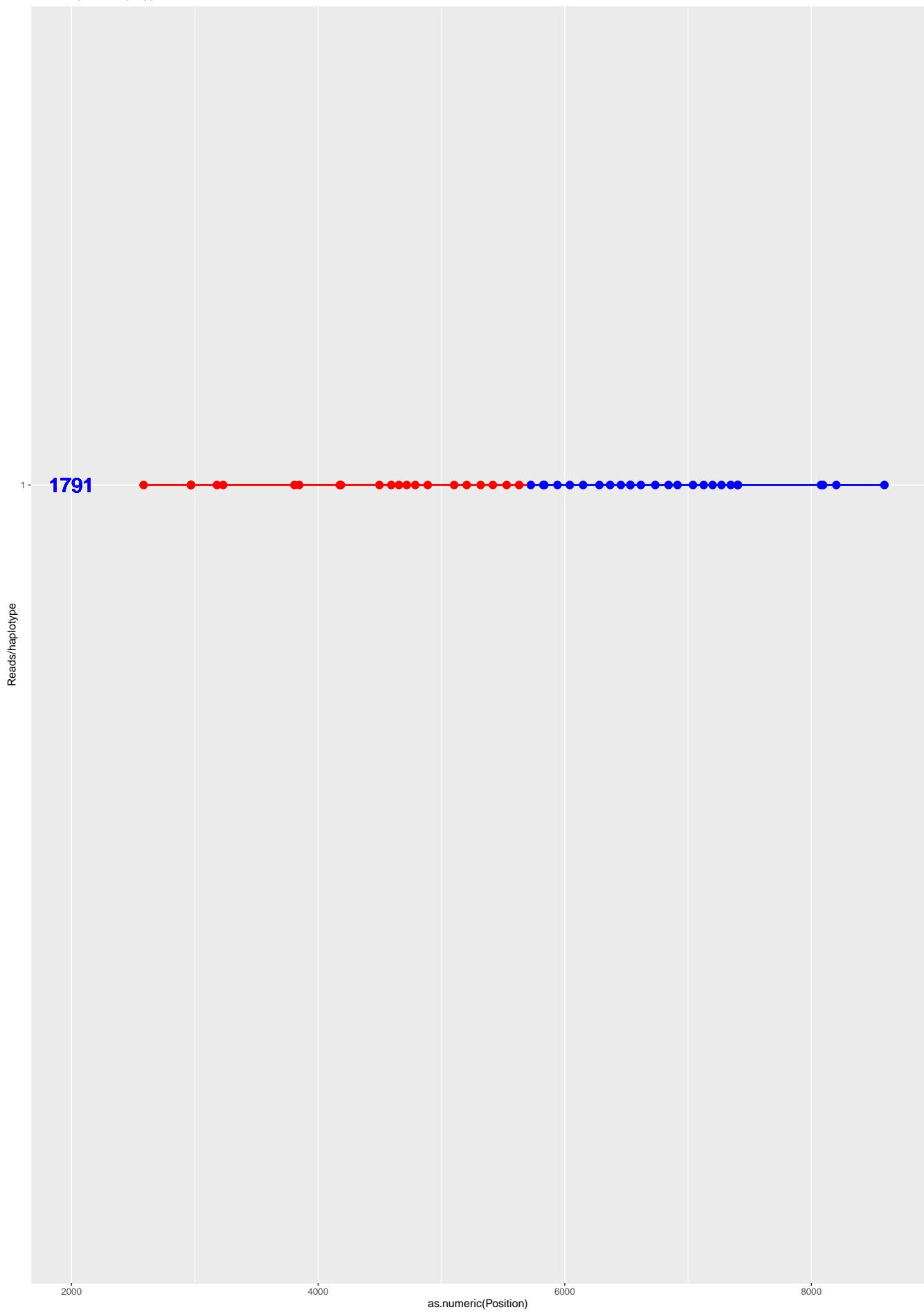


Sample = 6d tetrad = 6 spore = d

Total reads = 1948 PCR=20

haplotypes I began with n[supporting reads] = 1791

most frequent 7 haplotypes.



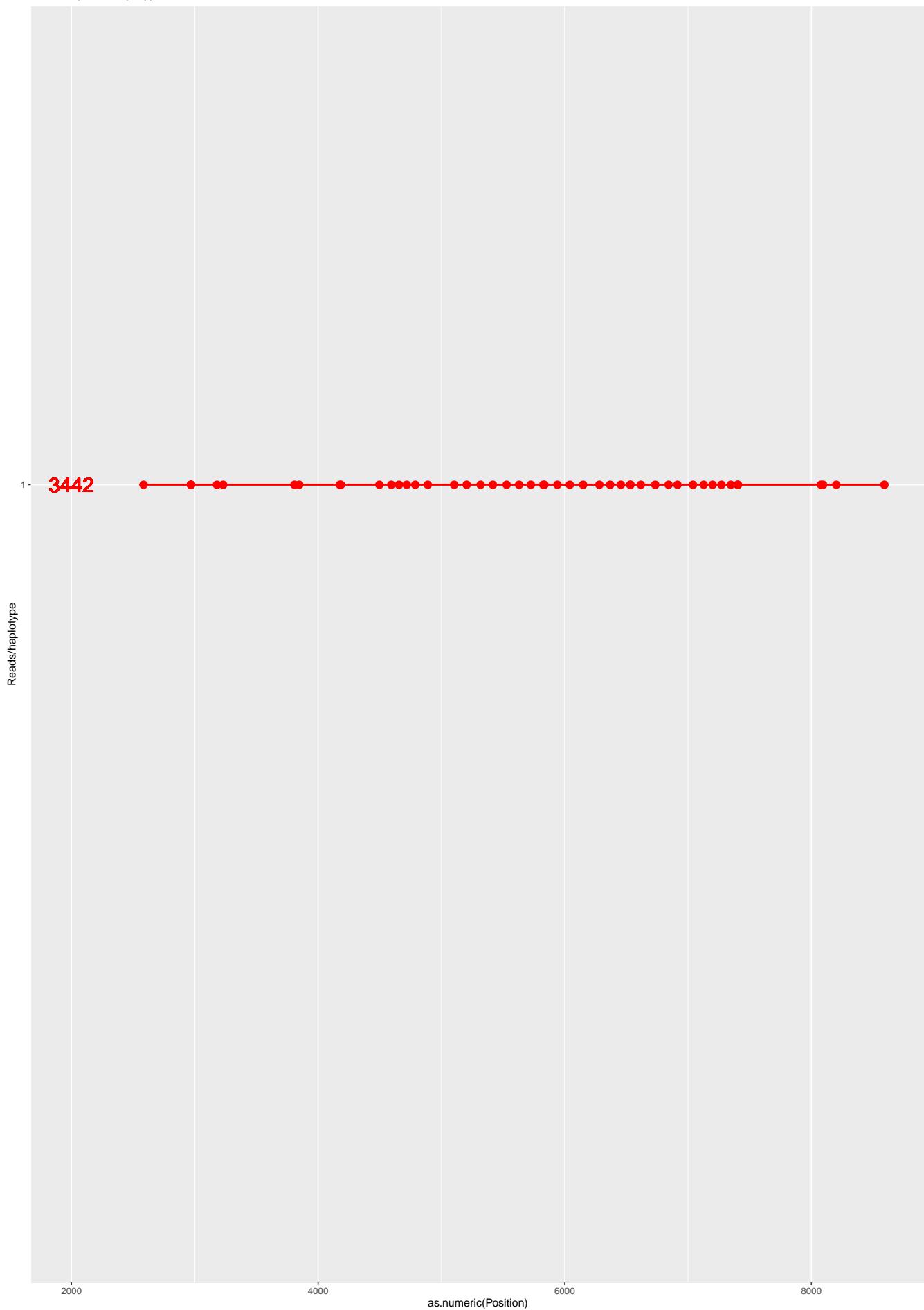
barcode = TATCTATCGTACGC & GACTCTGCGTCGAGTC

Sample = 11a tetrad = 11 spore = a

Total reads = 3605 PCR=21

haplotypes I began with n[supporting reads] = 3442

most frequent 7 haplotypes.



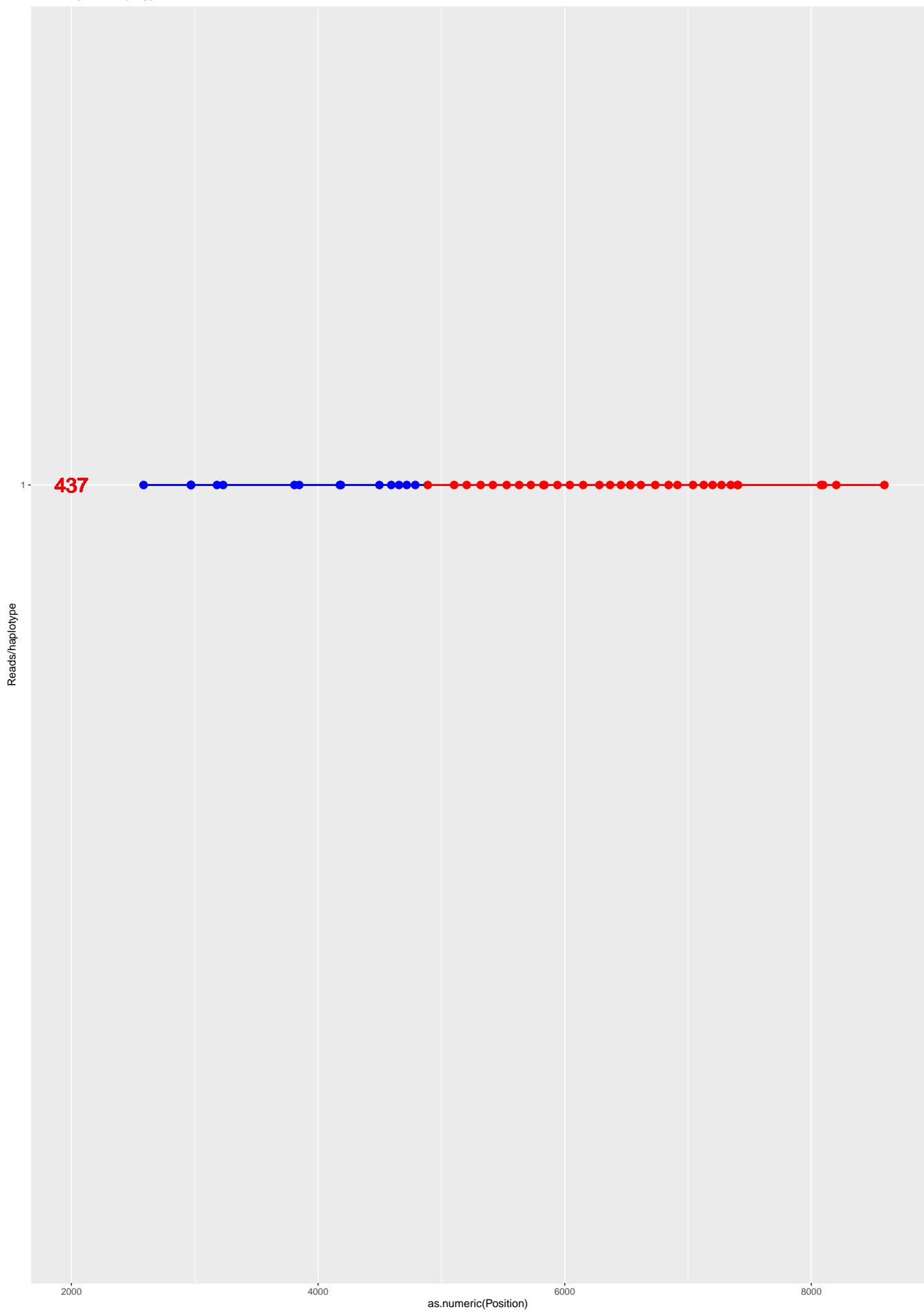
barcode = TATCTATCGTATAACGC & TACAGCGACGTCATCG

Sample = 11b tetrad = 11 spore = b

Total reads = 471 PCR=22

haplotypes I began with n[supporting reads] = 437

most frequent 7 haplotypes.



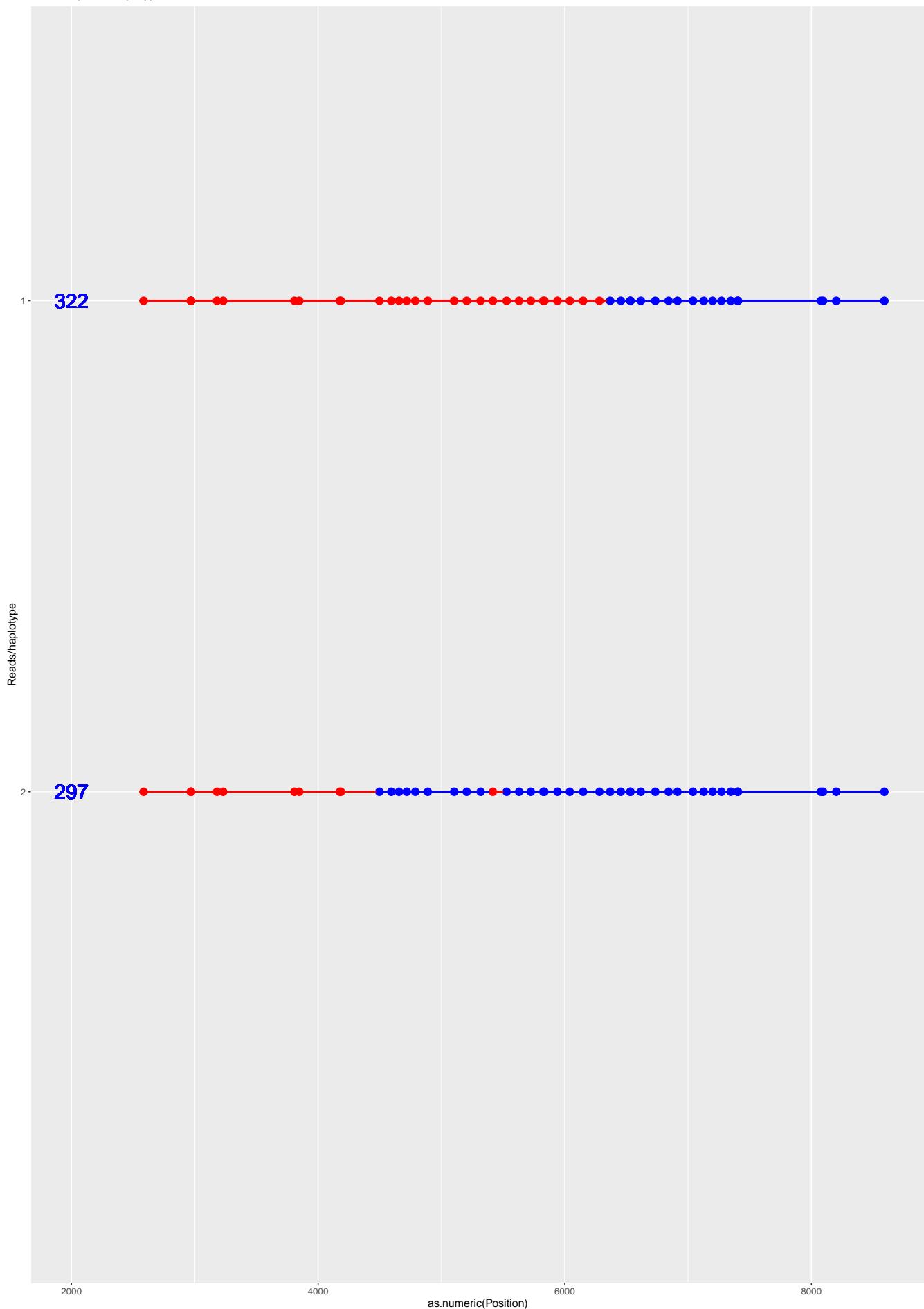
barcode = TATCTATCGTATACGC & GCGCAGACTACGTGTC

Sample = 11c tetrad = 11 spore = c

Total reads = 840 PCR=23

haplotypes I began with n[supporting reads] = 297, 322

most frequent 7 haplotypes.



barcode = TATCTATCGTATAACGC & GTCTCTGCGATAACAGC

Sample = 11d tetrad = 11 spore = d
Total reads = 2386 PCR=24
haplotypes I began with n[supporting reads] = 10, 2042
most frequent 7 haplotypes.

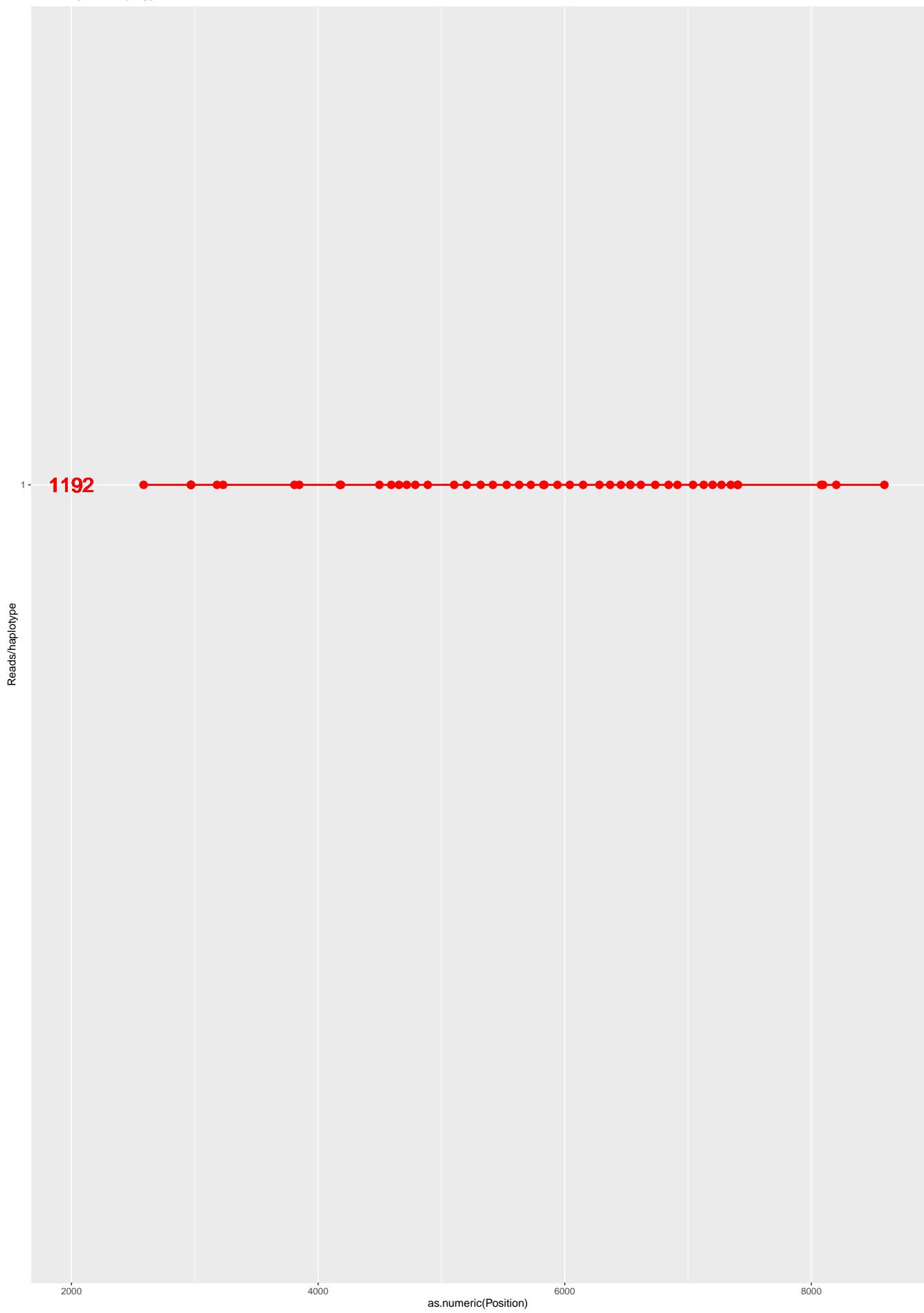


Sample = 12a tetrad = 12 spore = a

Total reads = 1243 PCR=25

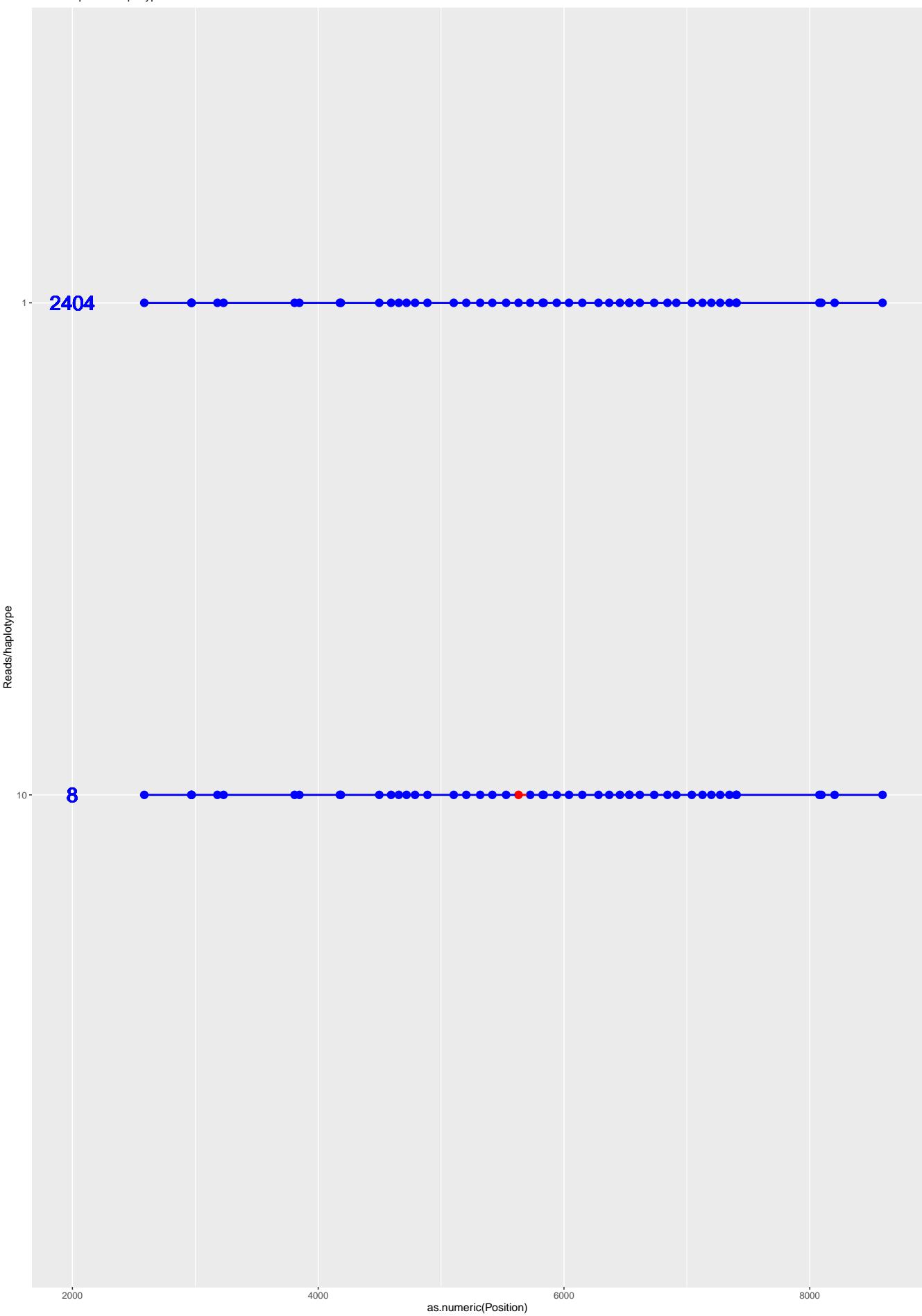
haplotypes I began with n[supporting reads] = 1192

most frequent 7 haplotypes.



barcode = ATCACACTGCATCTGA & TCATATGTAGTACTCT

Sample = 12b tetrad = 12 spore = b
Total reads = 2830 PCR=26
haplotypes I began with [n[supporting reads]] = 8, 2404
most frequent 7 haplotypes.

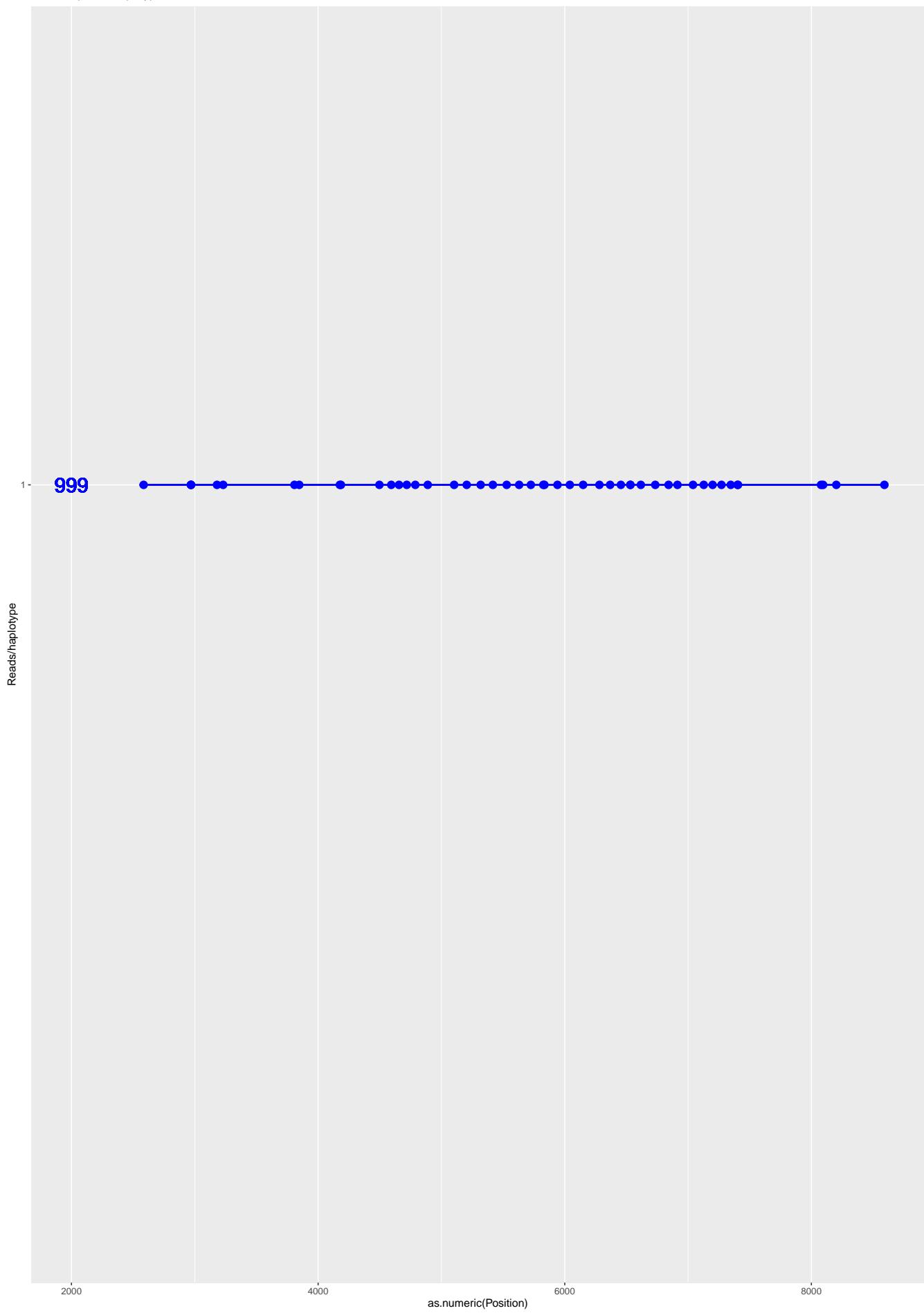


Sample = 12c tetrad = 12 spore = c

Total reads = 1158 PCR=27

haplotypes I began with n[supporting reads] = 999

most frequent 7 haplotypes.



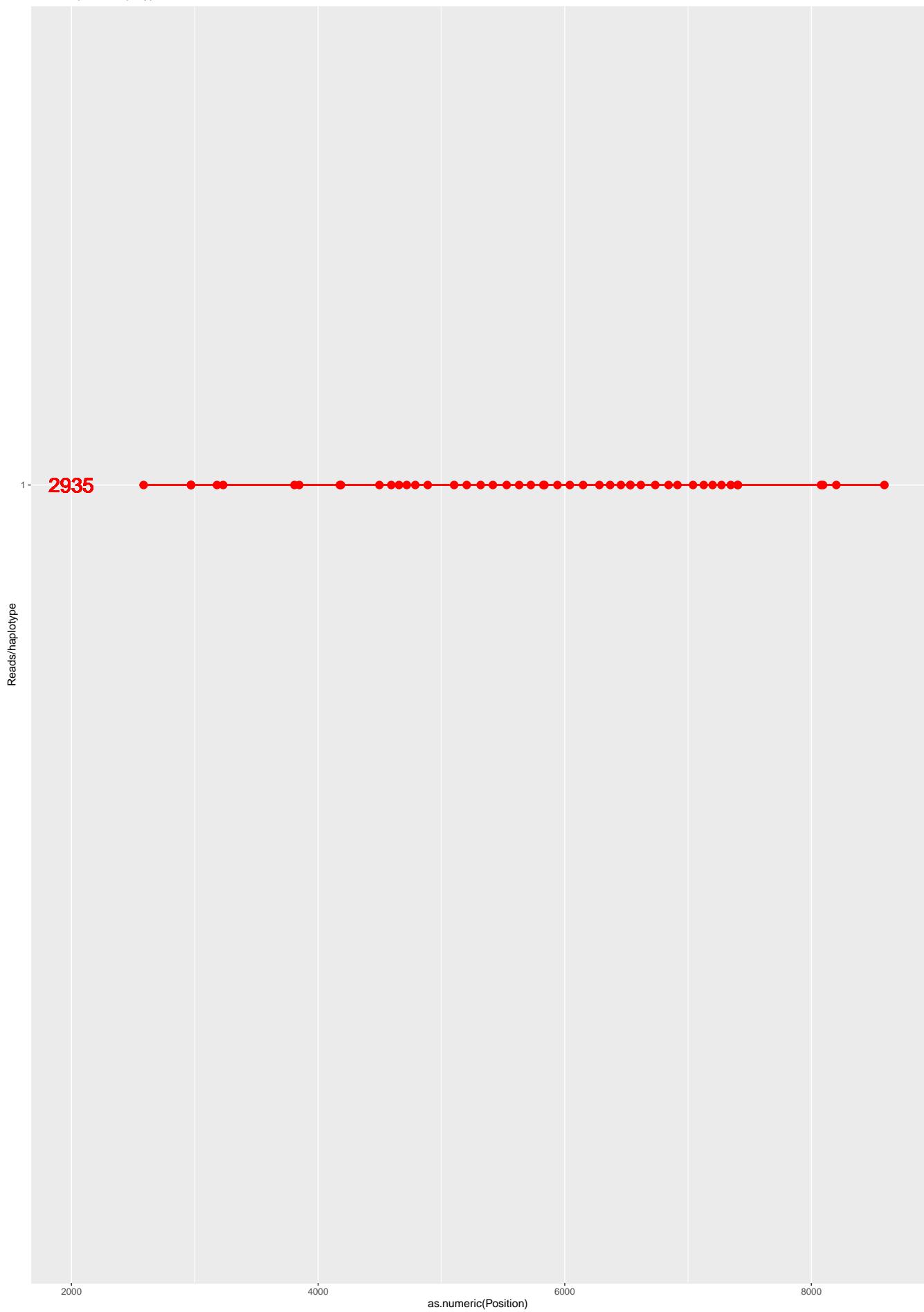
barcode = ATCACACTGCATCTGA & TGCAGTCGAGATACT

Sample = 12d tetrad = 12 spore = d

Total reads = 3061 PCR=28

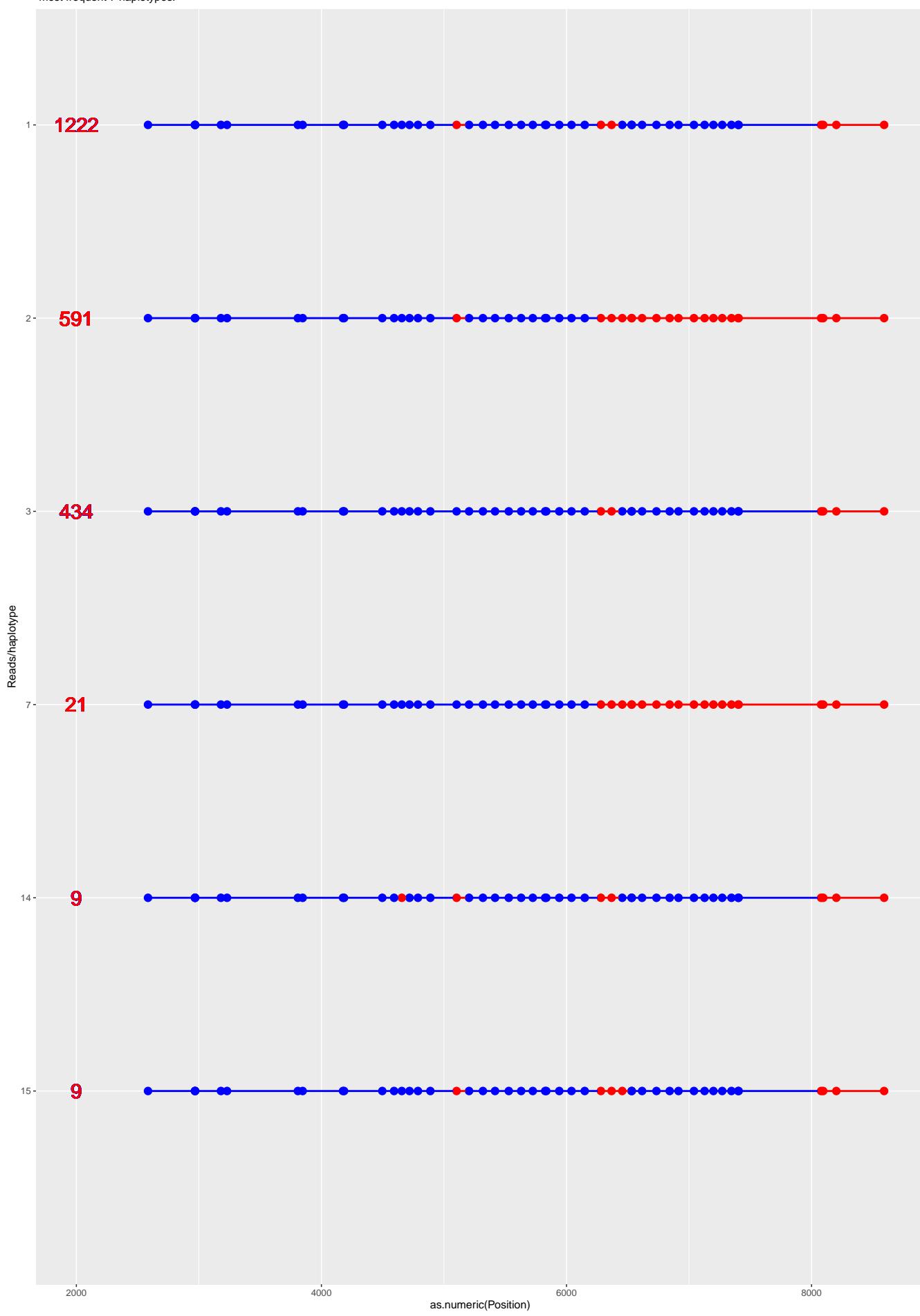
haplotypes I began with n[supporting reads] = 2935

most frequent 7 haplotypes.



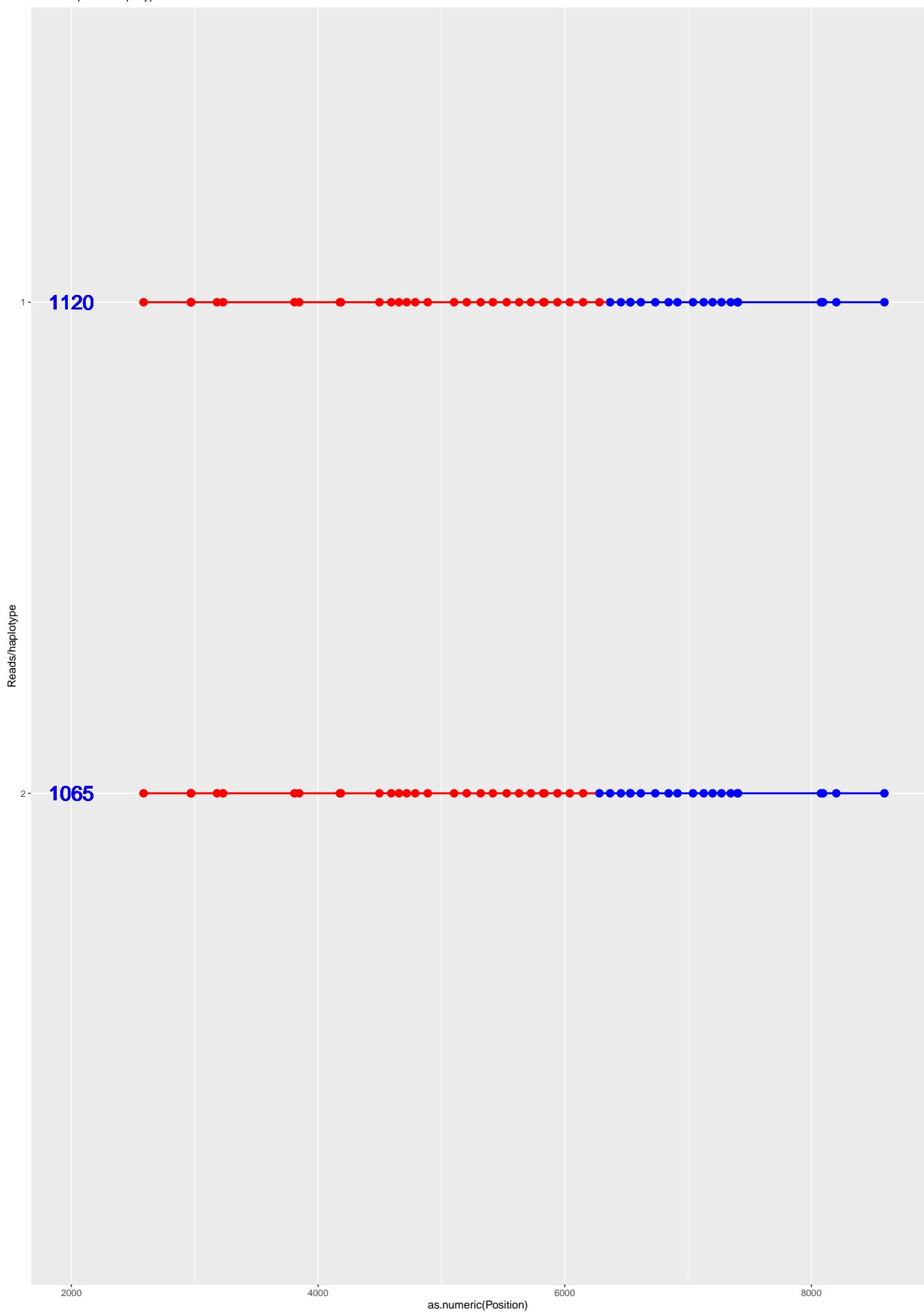
barcode = ATCACACTGCATCTGA & GACTCTGCGTCGAGTC

Sample = 16a tetrad = 16 spore = a
Total reads = 4230 PCR=29
haplotypes I began with [n|supporting reads] = 9, 21, 434, 591, 1222
most frequent 7 haplotypes.



barcode = ATCACACTGCACTGA & TACAGCGACGTCATCG

Sample = 16b tetrad = 16 spore = b
Total reads = 2321 PCR=30
haplotypes I began with n[supporting reads] = 1065, 1120
most frequent 7 haplotypes.



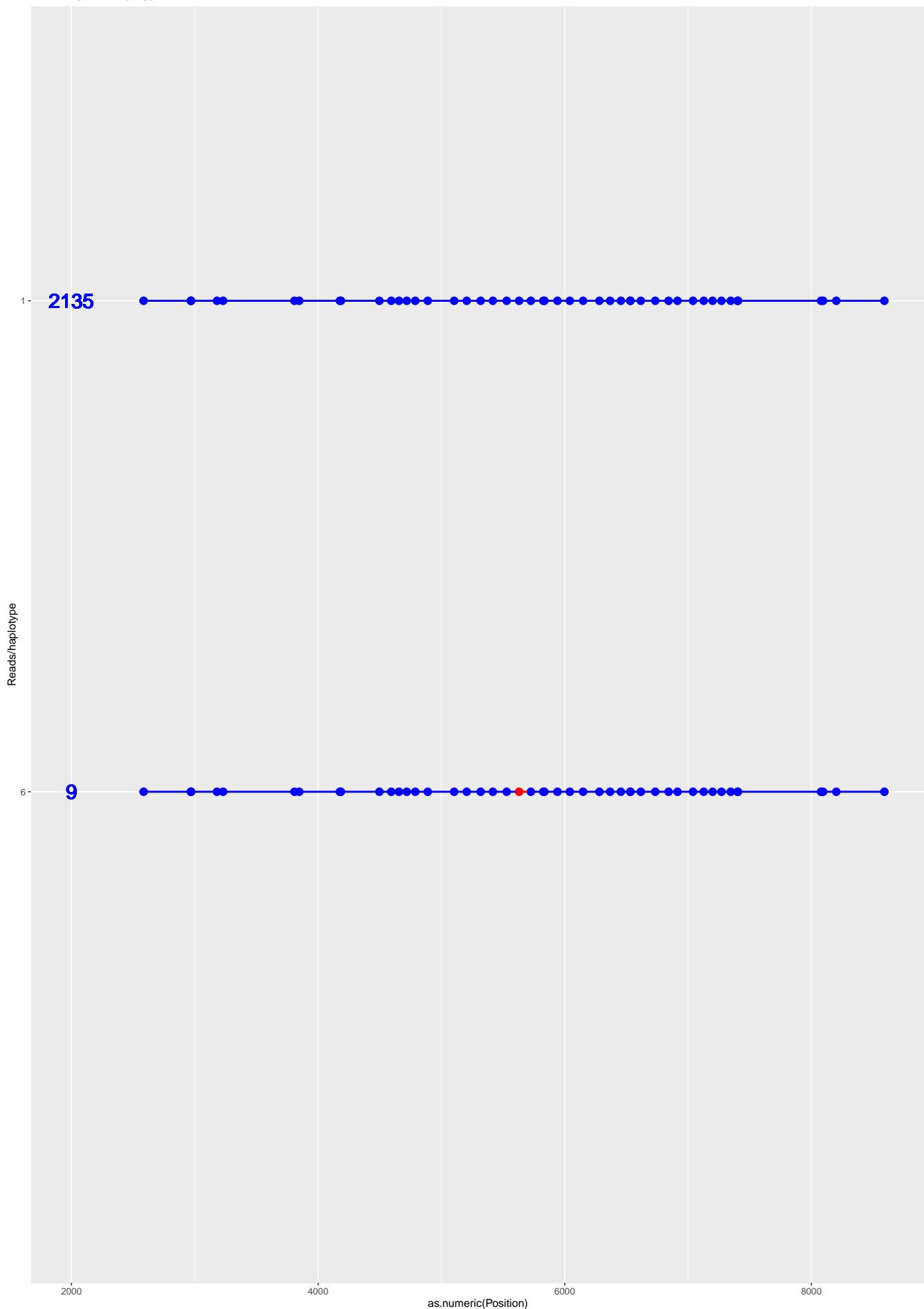
barcode = ATCACACTGCATCTGA & GCGCAGACTACGTGTC

Sample = 16c tetrad = 16 spore = c

Total reads = 2495 PCR=31

haplotypes I began with n[supporting reads] = 9, 2135

most frequent 7 haplotypes.



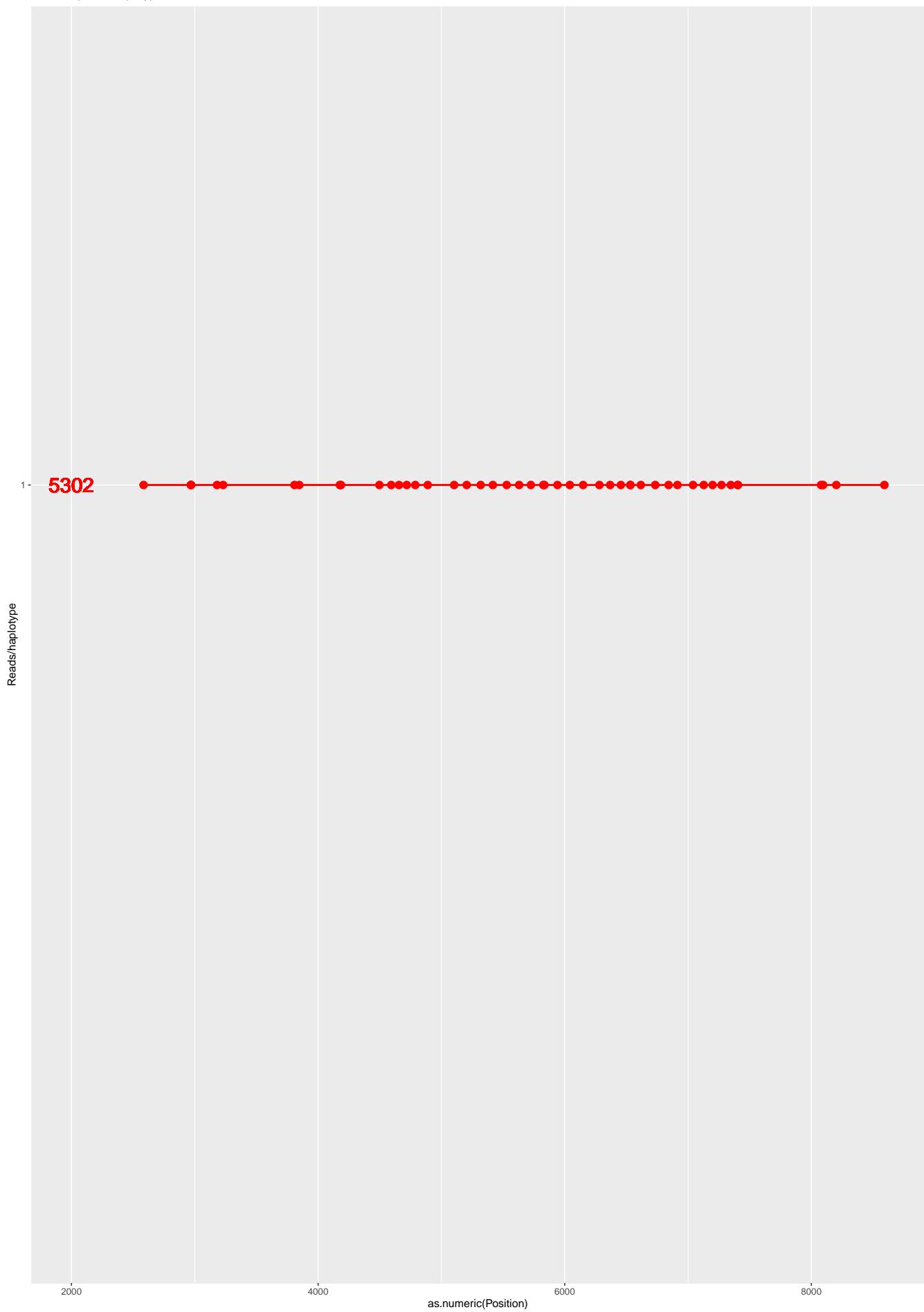
barcode = ATCACACTGCATCTGA & GTCTCTGCGATAACAGC

Sample = 16d tetrad = 16 spore = d

Total reads = 5550 PCR=32

haplotypes I began with n[supporting reads] = 5302

most frequent 7 haplotypes.



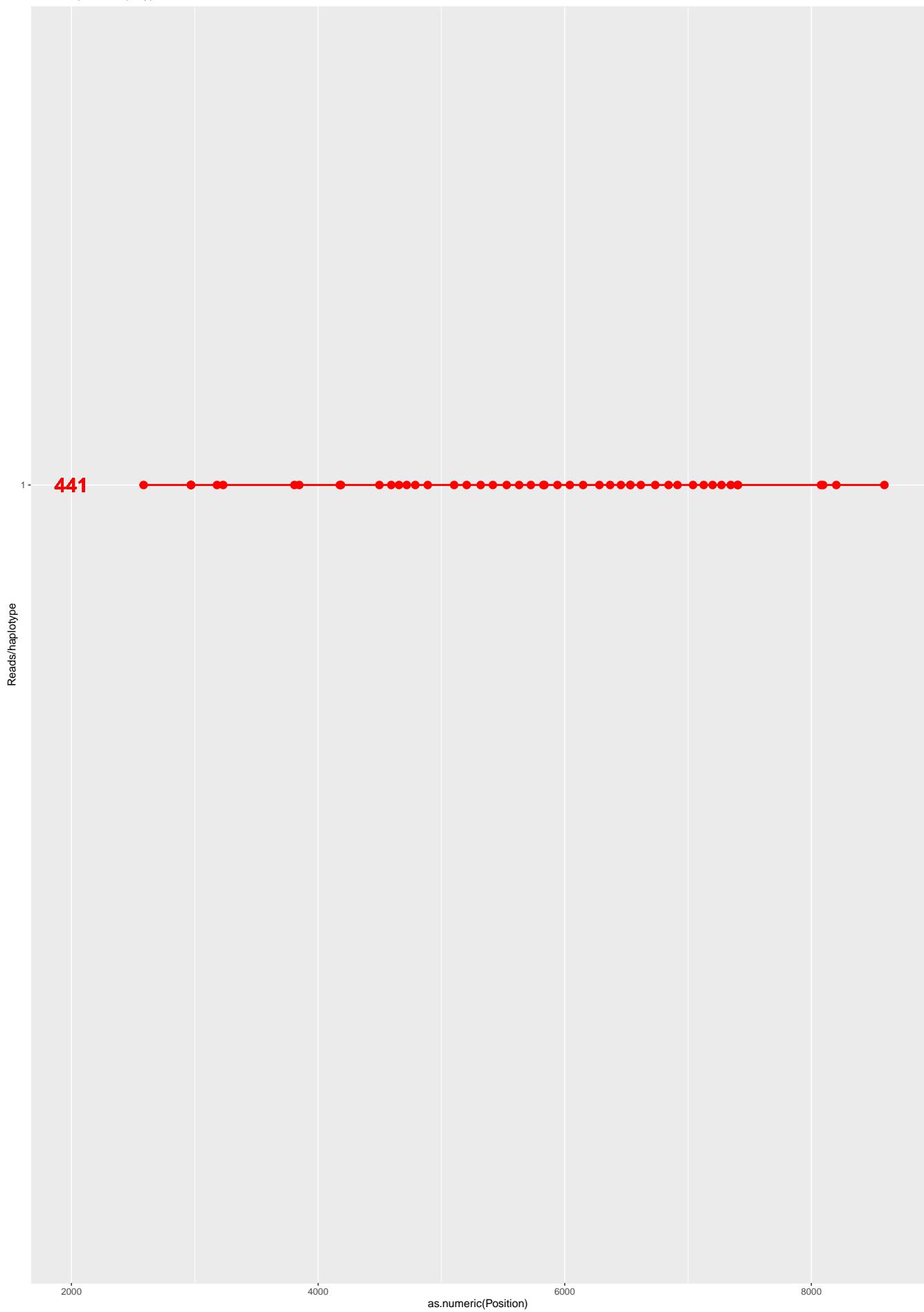
barcode = ATCACACTGCATCTGA & AGTATGAGATAGCTCG

Sample = 18a tetrad = 18 spore = a

Total reads = 456 PCR=33

haplotypes I began with n[supporting reads] = 441

most frequent 7 haplotypes.



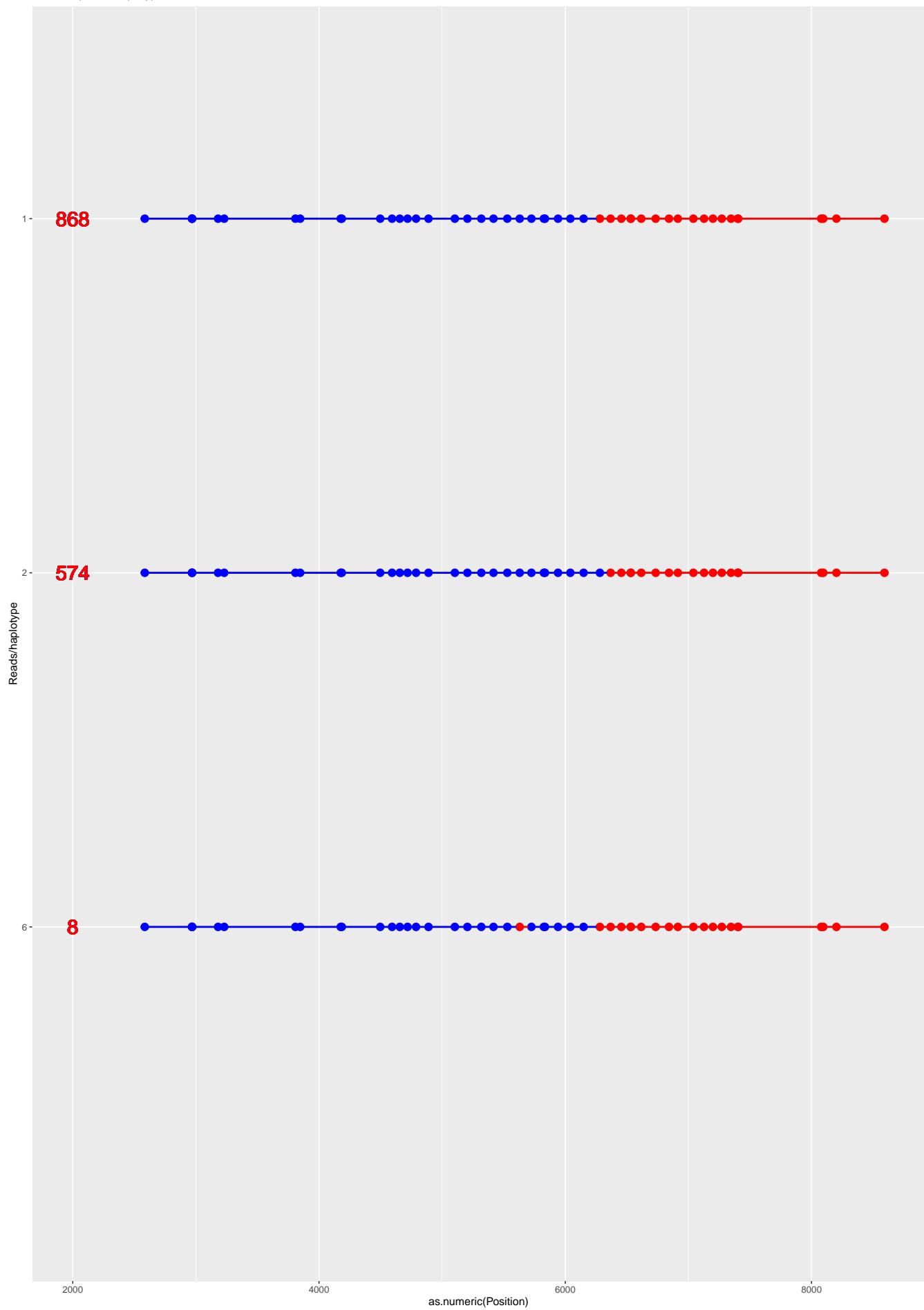
barcode = ACGTACGCTCGTCATA & TCATATGTAGTACTCT

Sample = 18b tetrad = 18 spore = b

Total reads = 1665 PCR=34

haplotypes I began with n[supporting reads] = 8, 574, 868

most frequent 7 haplotypes.

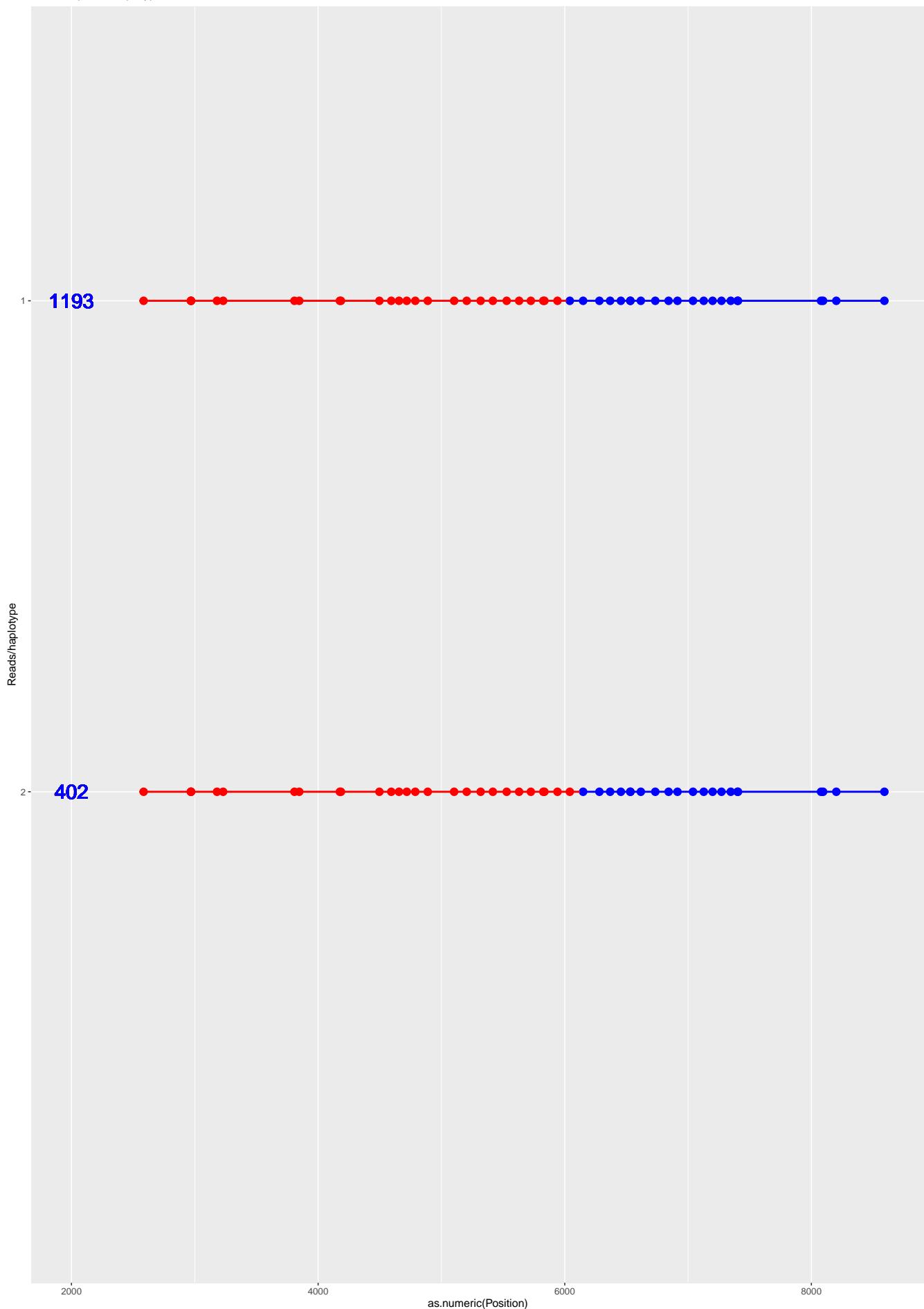


Sample = 18c tetrad = 18 spore = c

Total reads = 1815 PCR=35

haplotypes I began with n[supporting reads] = 402, 1193

most frequent 7 haplotypes.



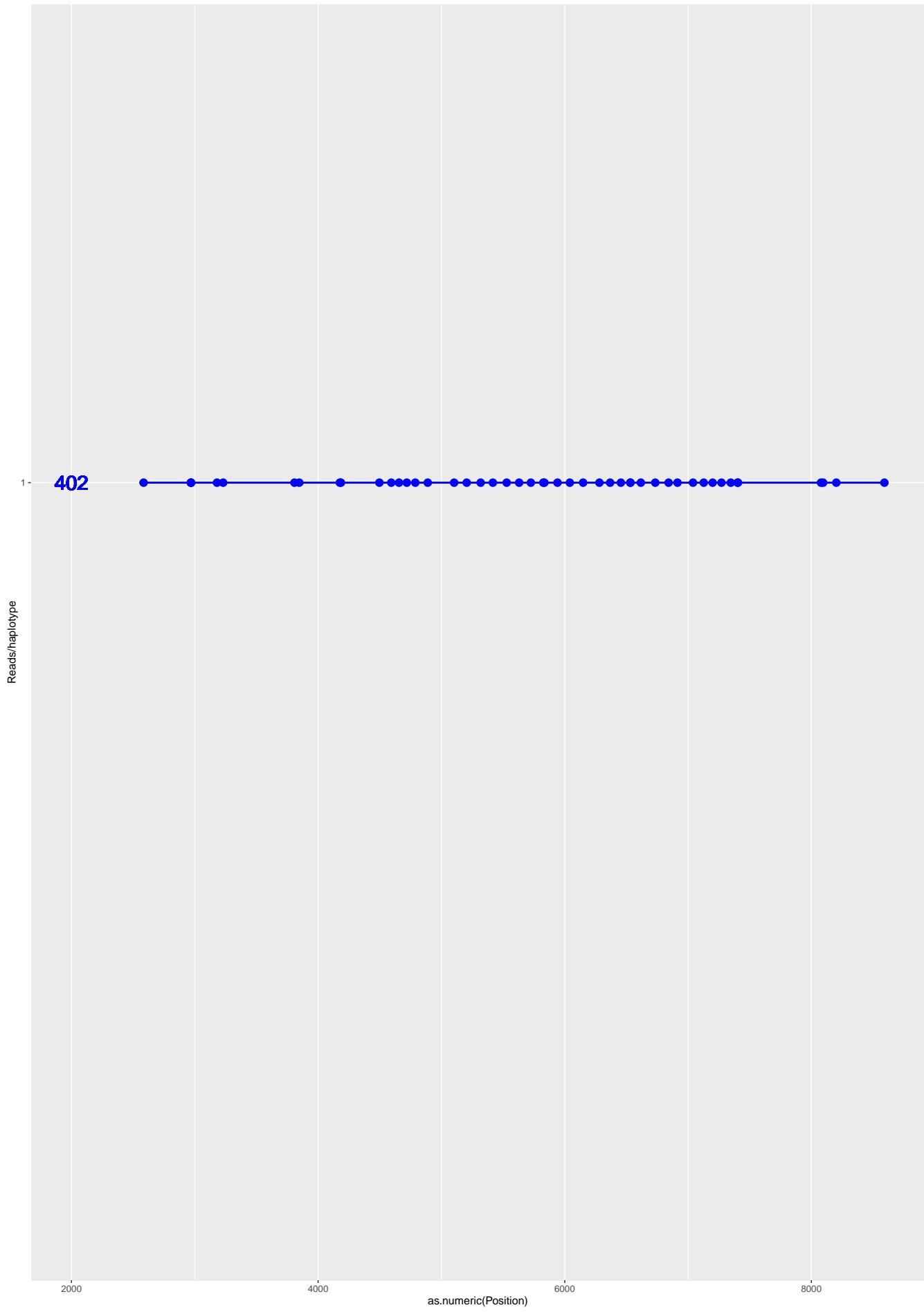
barcode = ACGTACGCTCGTCATA & TGCAGTCGAGATACAT

Sample = 18d tetrad = 18 spore = d

Total reads = 465 PCR=36

haplotypes I began with n[supporting reads] = 402

most frequent 7 haplotypes.



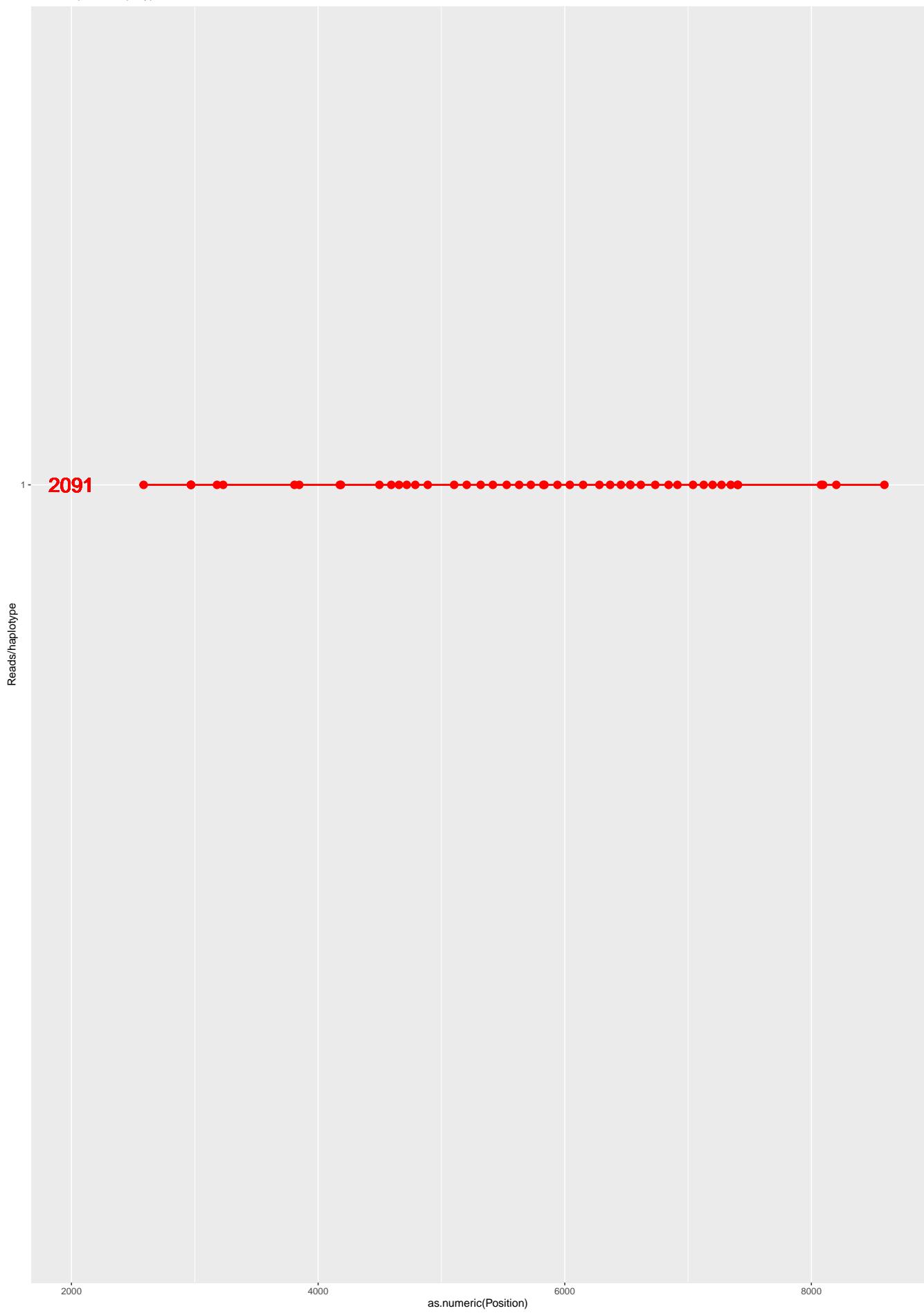
barcode = ACGTACGCTCGTCATA & GACTCTGCGTCGAGTC

Sample = 19a tetrad = 19 spore = a

Total reads = 2187 PCR=37

haplotypes I began with n[supporting reads] = 2091

most frequent 7 haplotypes.



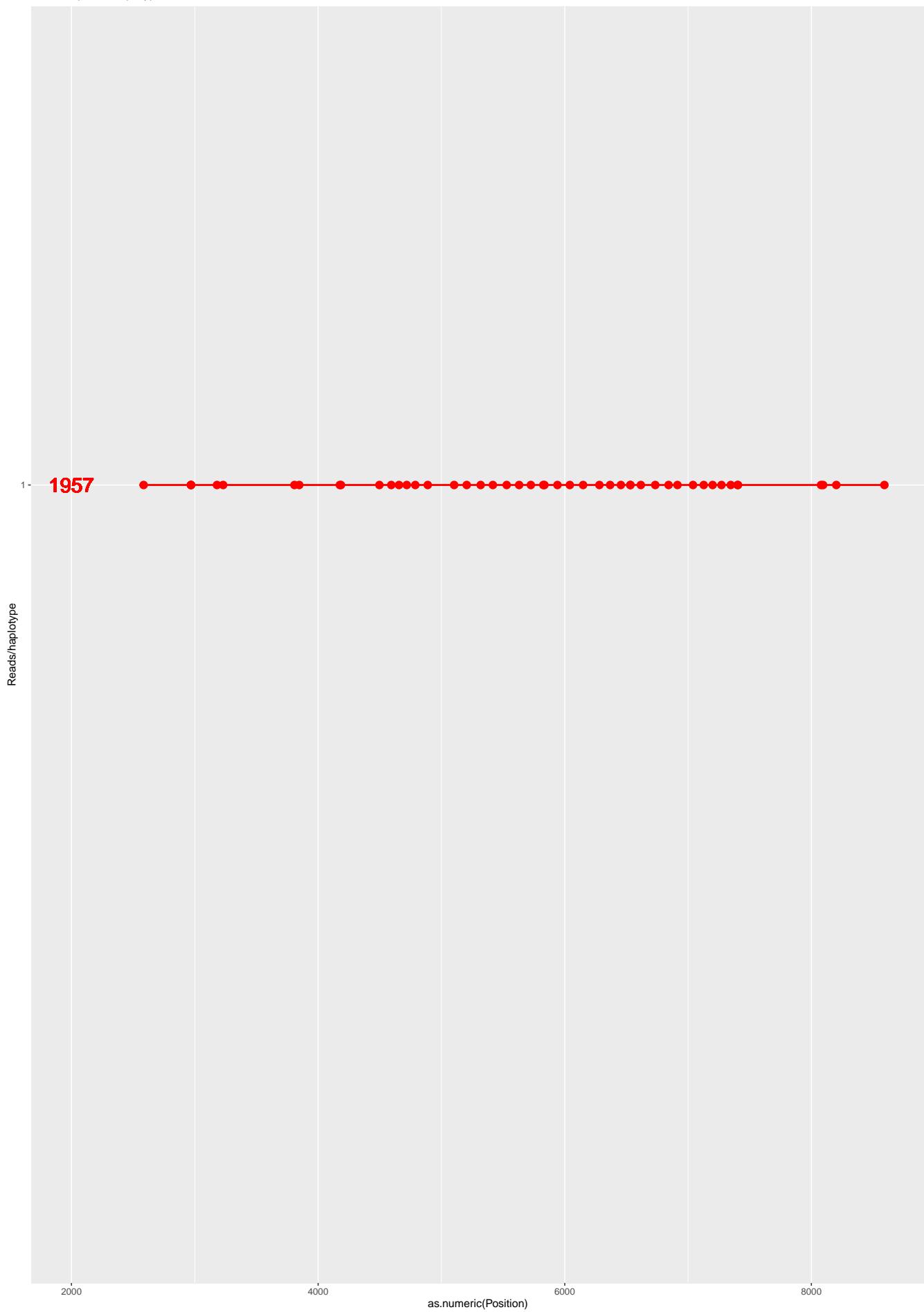
barcode = ACGTACGCTCGTCATA & TACAGCGACGTCATCG

Sample = 19b tetrad = 19 spore = b

Total reads = 2041 PCR=38

haplotypes I began with n[supporting reads] = 1957

most frequent 7 haplotypes.

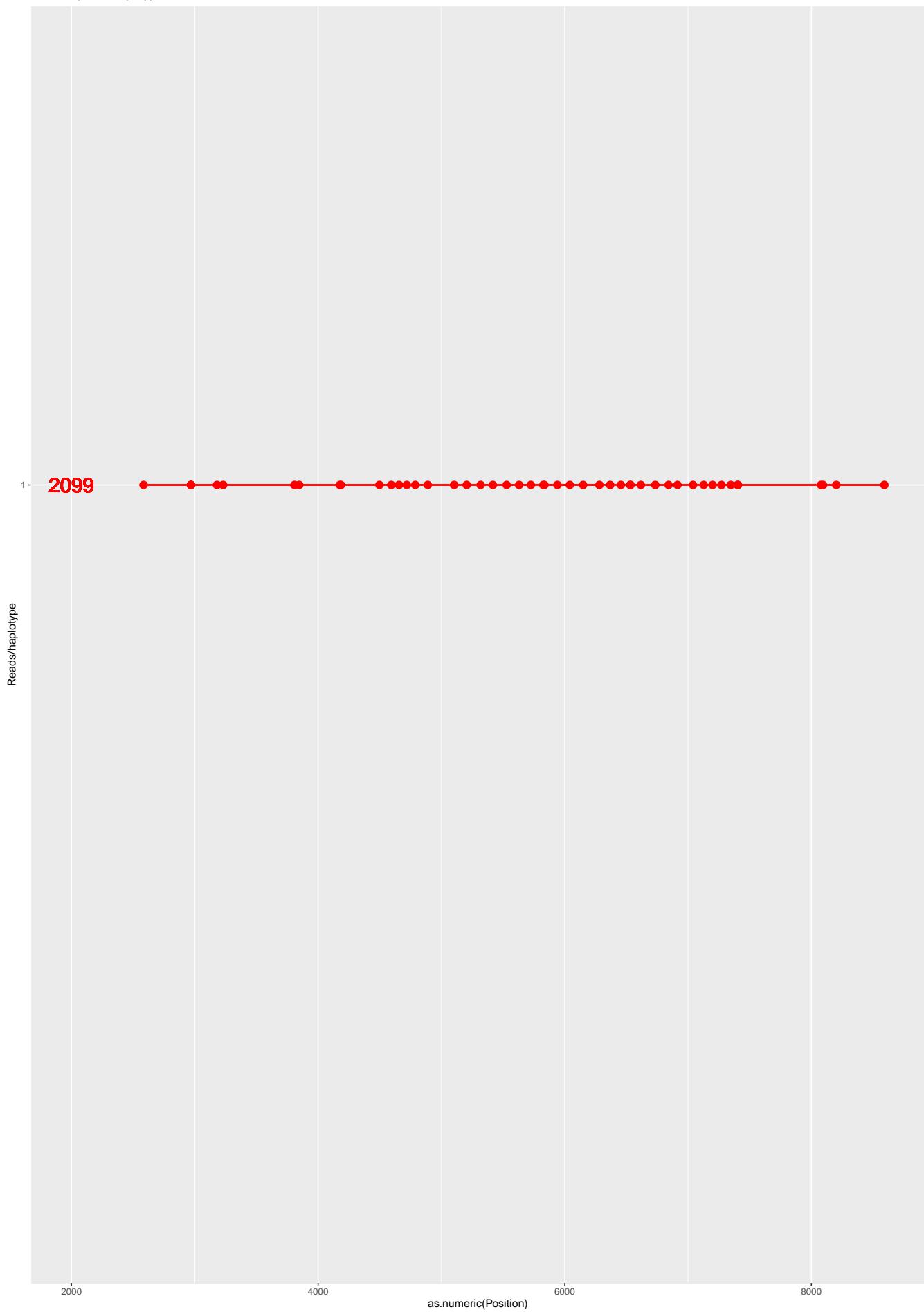


Sample = 19c tetrad = 19 spore = c

Total reads = 2314 PCR=39

haplotypes I began with n[supporting reads] = 2099

most frequent 7 haplotypes.



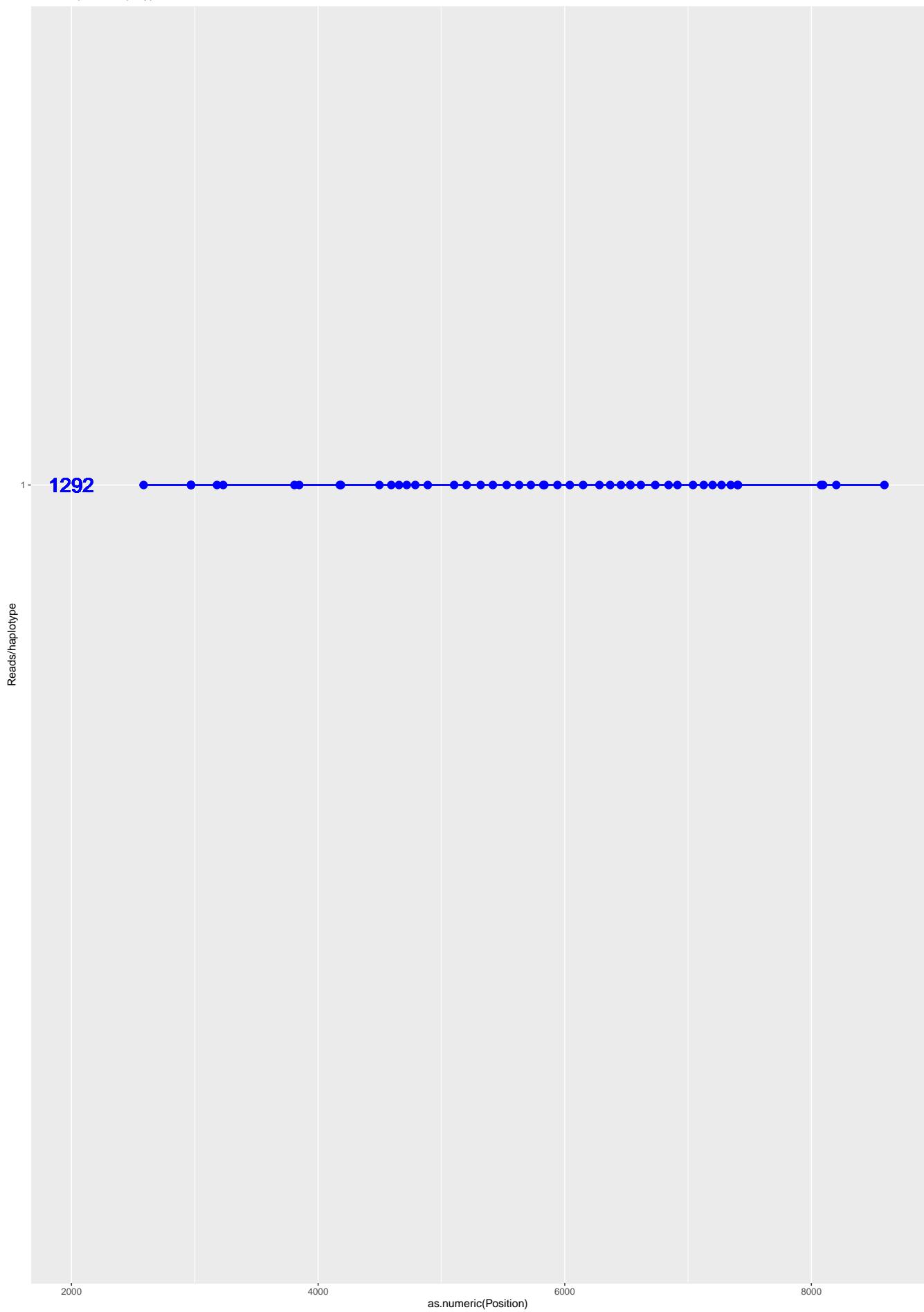
barcode = ACGTACGCTCGTCATA & GTCTCTGCGATACAGC

Sample = 19d tetrad = 19 spore = d

Total reads = 1550 PCR=40

haplotypes I began with n[supporting reads] = 1292

most frequent 7 haplotypes.



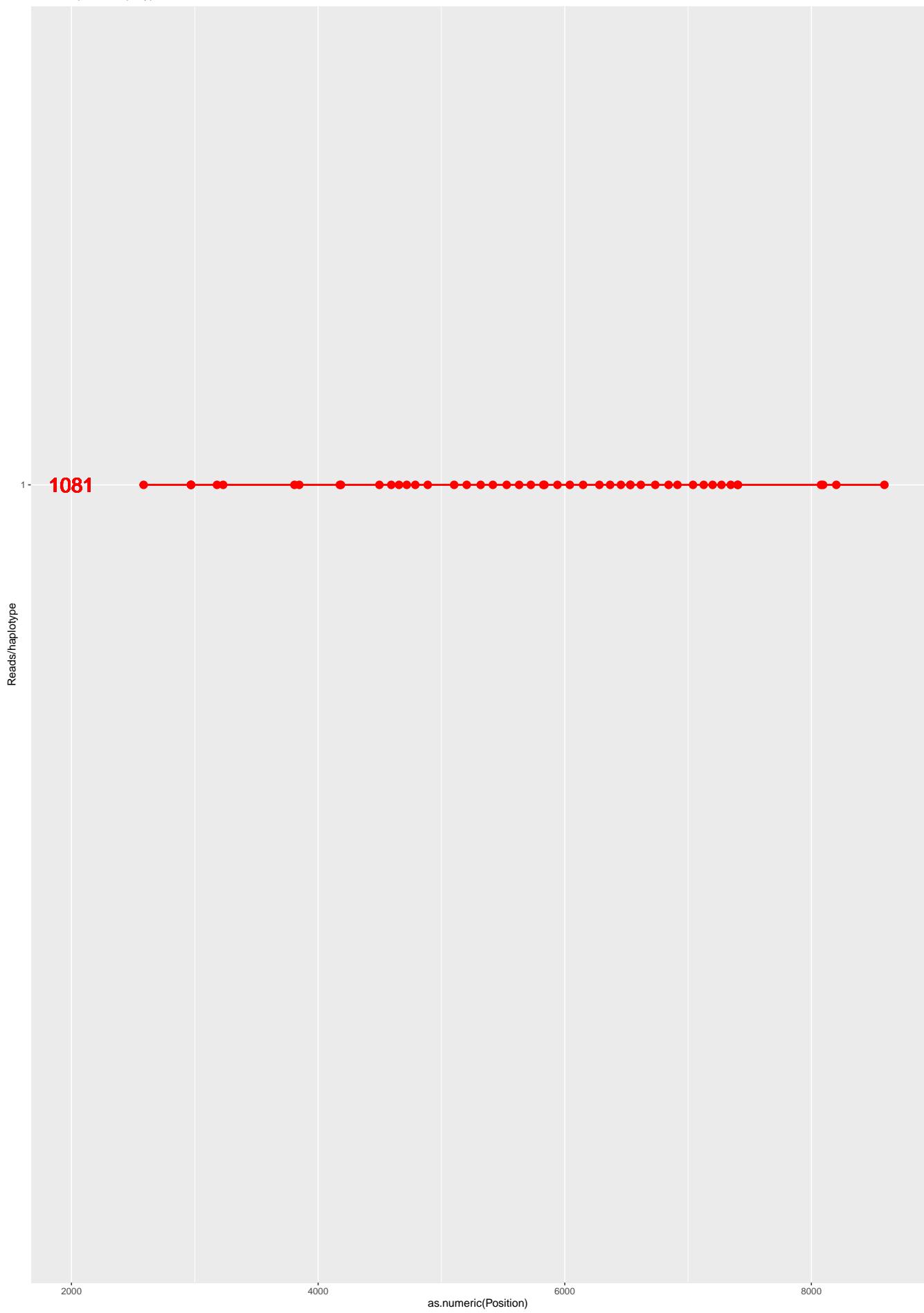
barcode = ACGTACGCTCGTCATA & AGTATGAGATAGCTCG

Sample = 21a tetrad = 21 spore = a

Total reads = 1128 PCR=41

haplotypes I began with n[supporting reads] = 1081

most frequent 7 haplotypes.



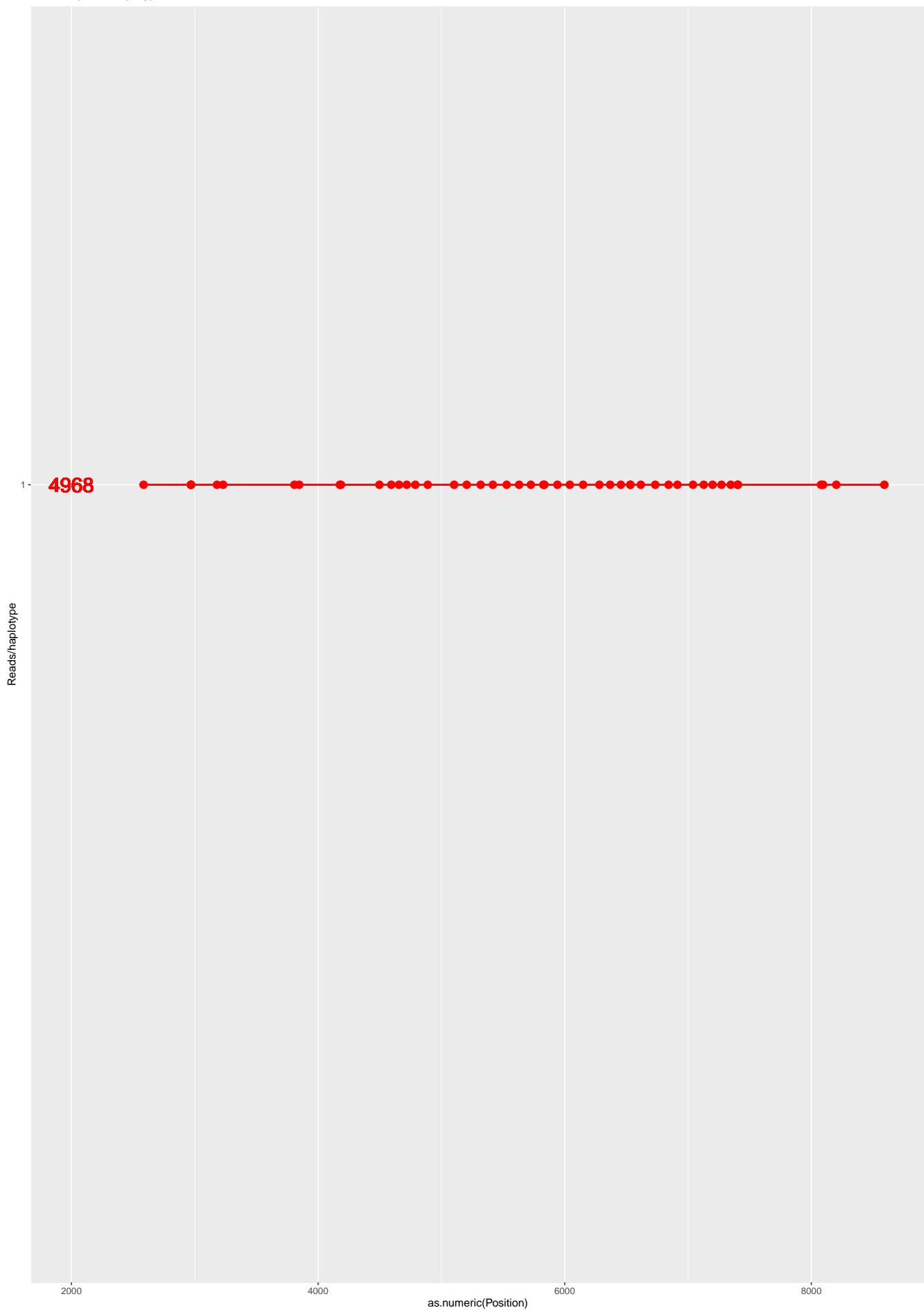
barcode = TGTGAGTCAGTACGCG & TCATATGTAGTACTCT

Sample = 21b tetrad = 21 spore = b

Total reads = 5192 PCR=42

haplotypes I began with n[supporting reads] = 4968

most frequent 7 haplotypes.



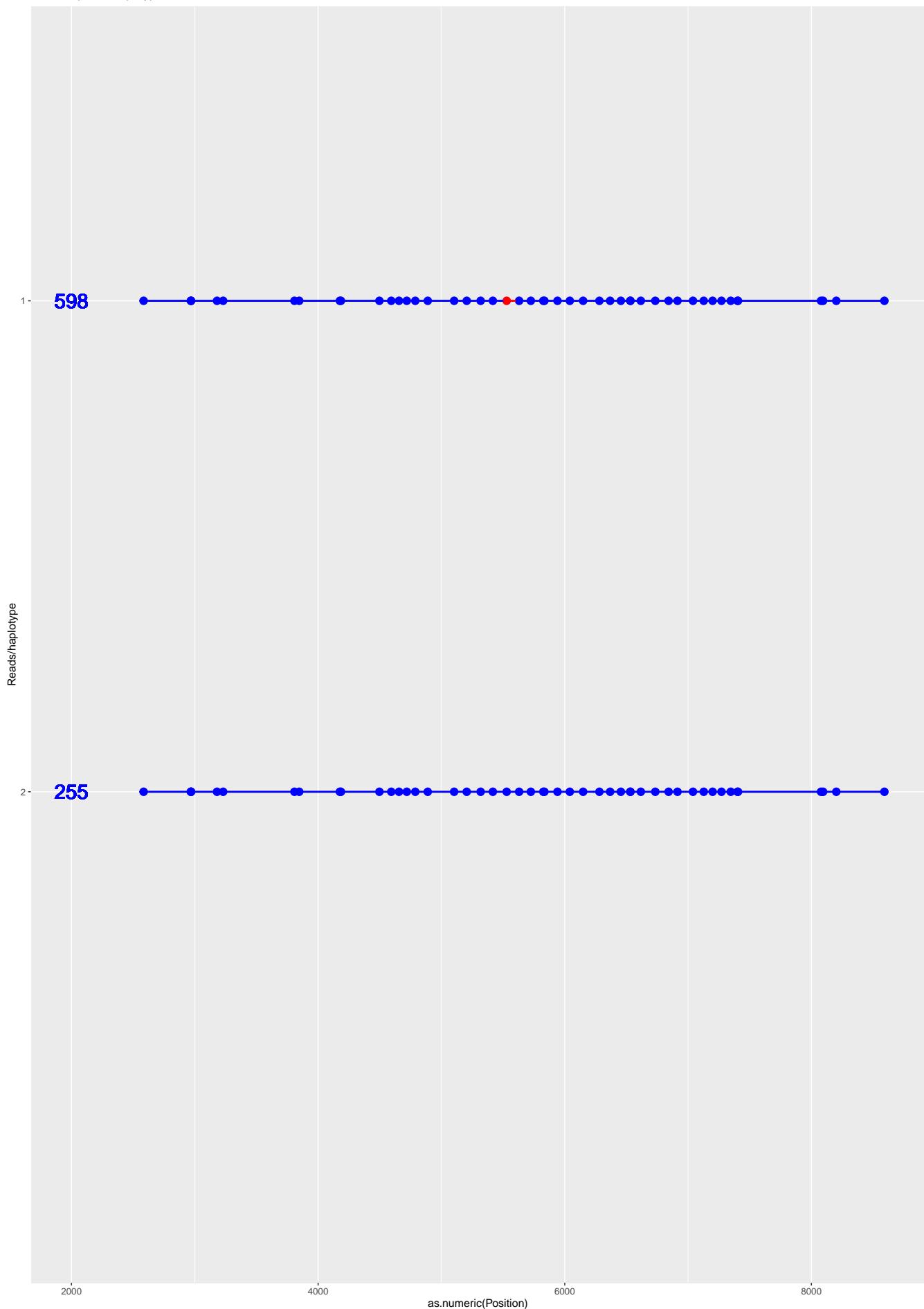
barcode = TGTGAGTCAGTACGCG & GCGATCTATGCACACG

Sample = 21c tetrad = 21 spore = c

Total reads = 986 PCR=43

haplotypes I began with n[supporting reads] = 255, 598

most frequent 7 haplotypes.

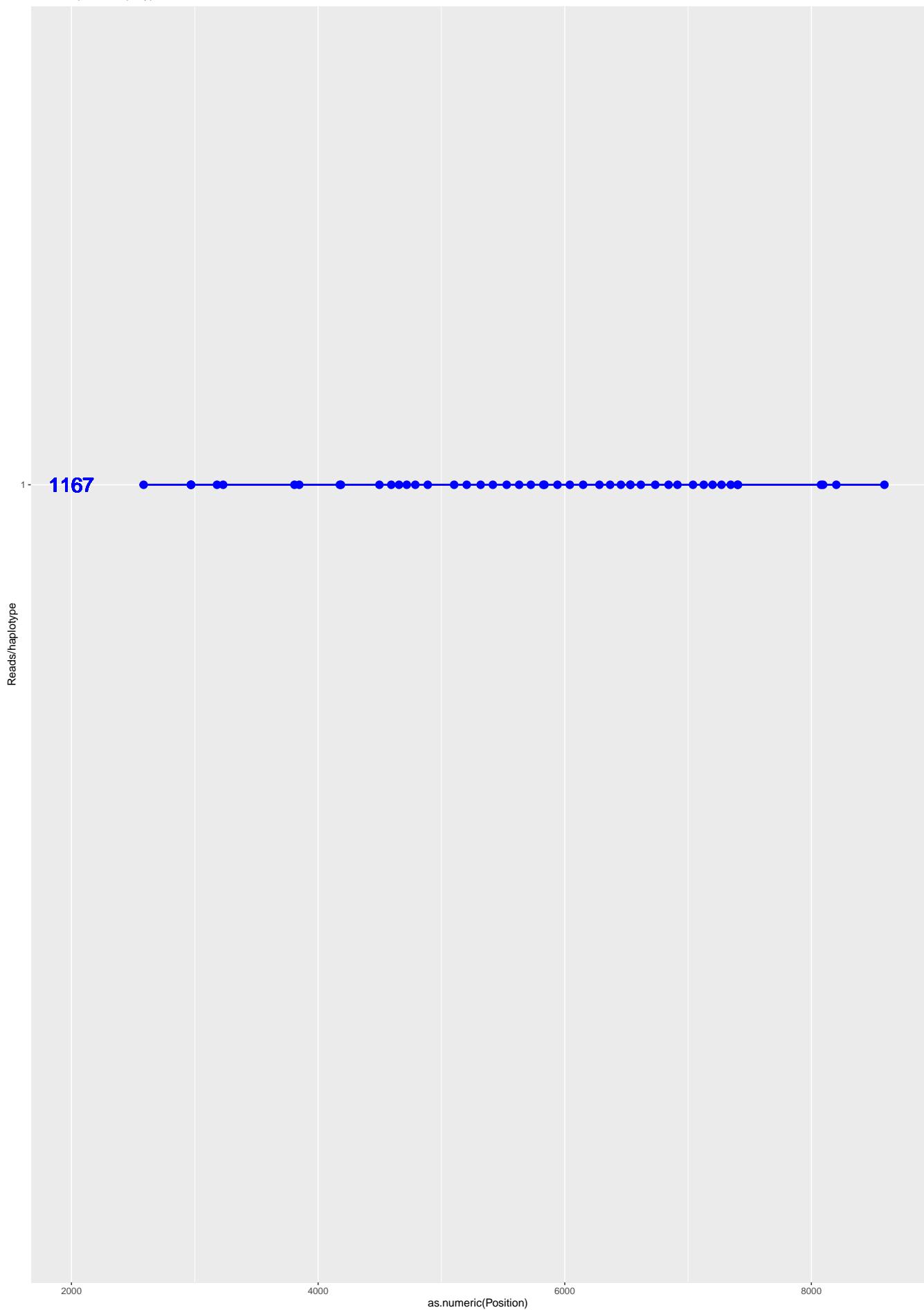


Sample = 21d tetrad = 21 spore = d

Total reads = 1371 PCR=44

haplotypes I began with n[supporting reads] = 1167

most frequent 7 haplotypes.



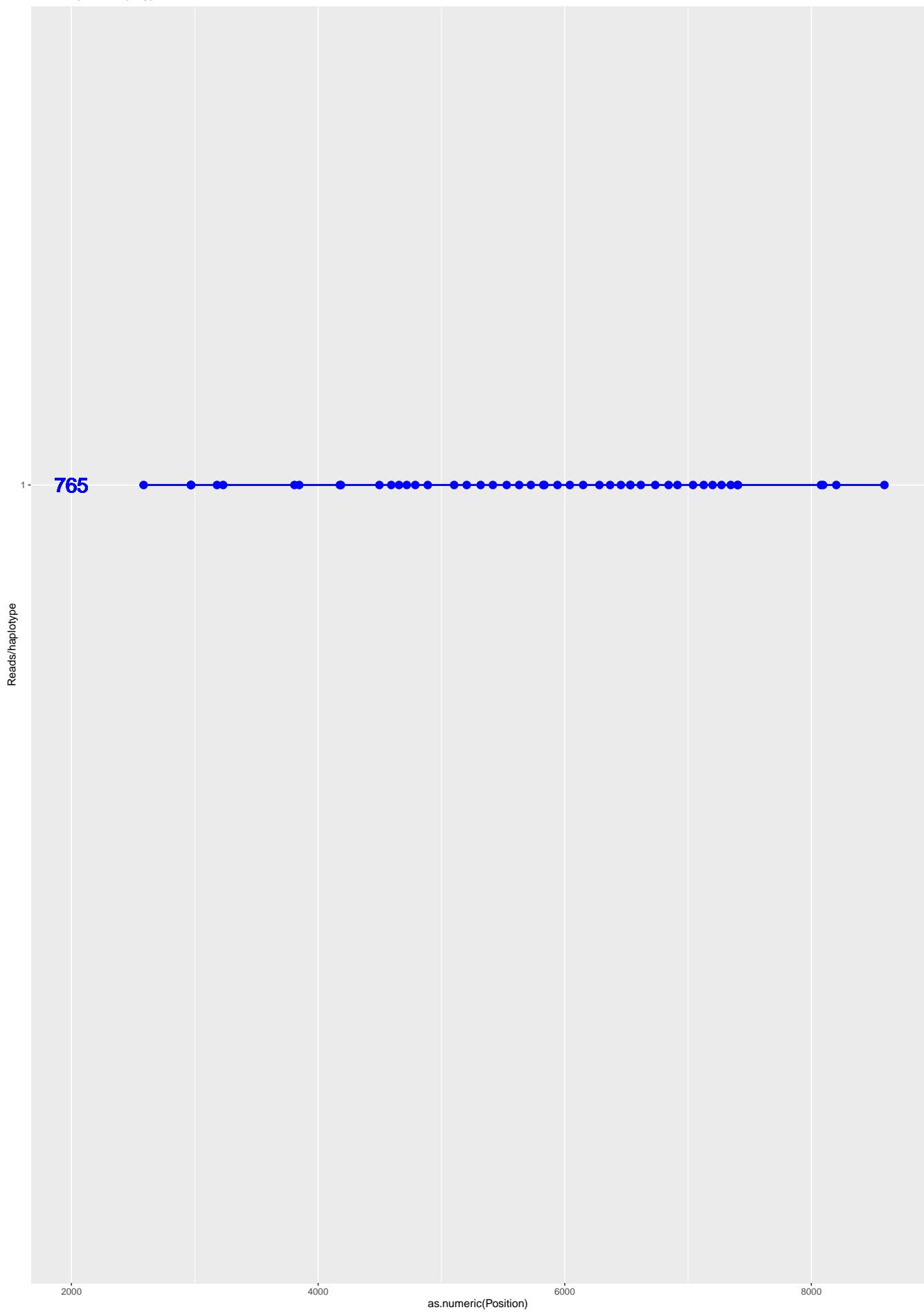
barcode = TGTGAGTCAGTACCGC & GACTCTGCGTCGAGTC

Sample = 22a tetrad = 22 spore = a

Total reads = 881 PCR=45

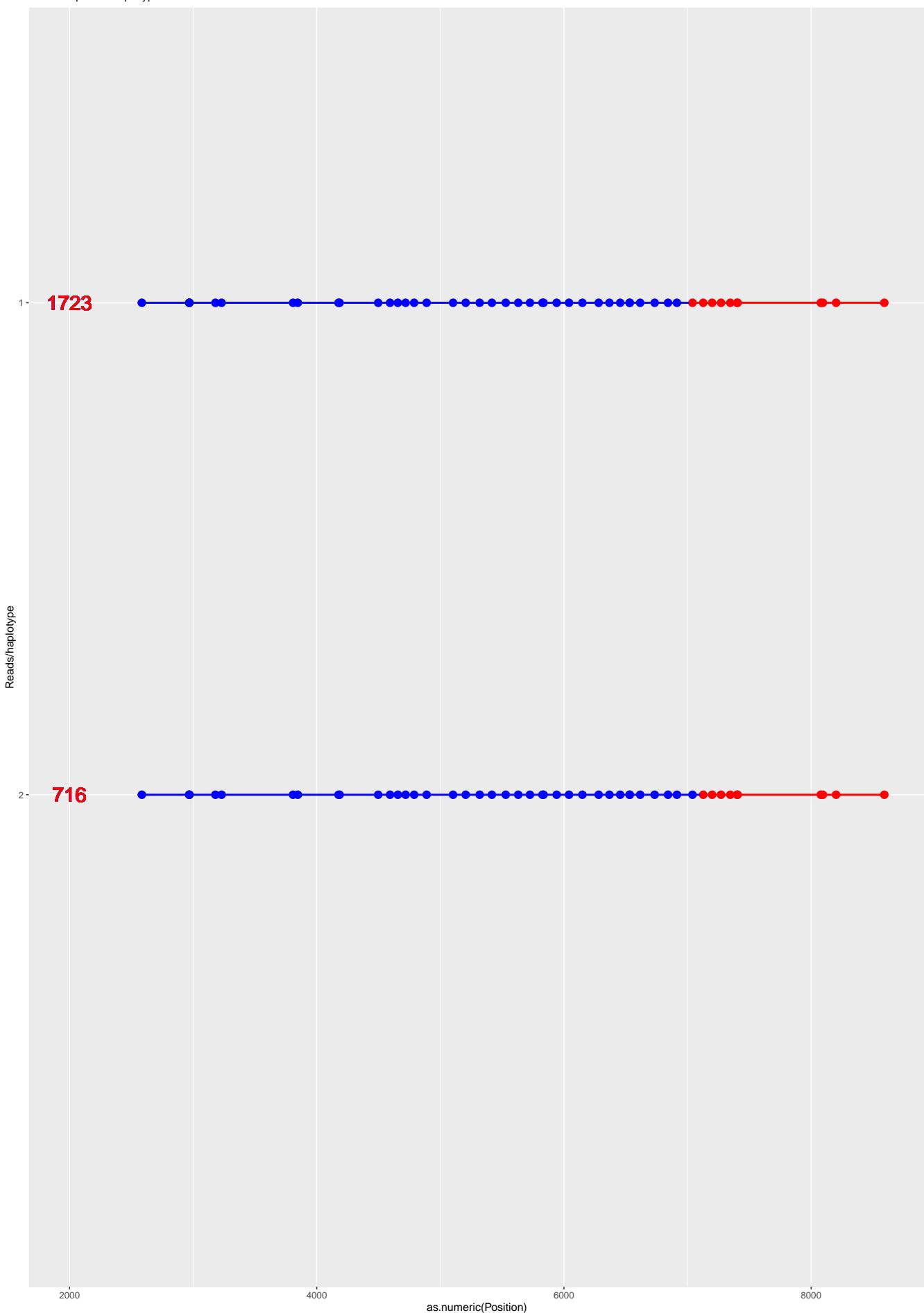
haplotypes I began with n[supporting reads] = 765

most frequent 7 haplotypes.



barcode = TGTGAGTCAGTACGCG & TACAGCGACGTCATCG

Sample = 22b tetrad = 22 spore = b
Total reads = 2871 PCR=46
haplotypes I began with n[supporting reads] = 716, 1723
most frequent 7 haplotypes.



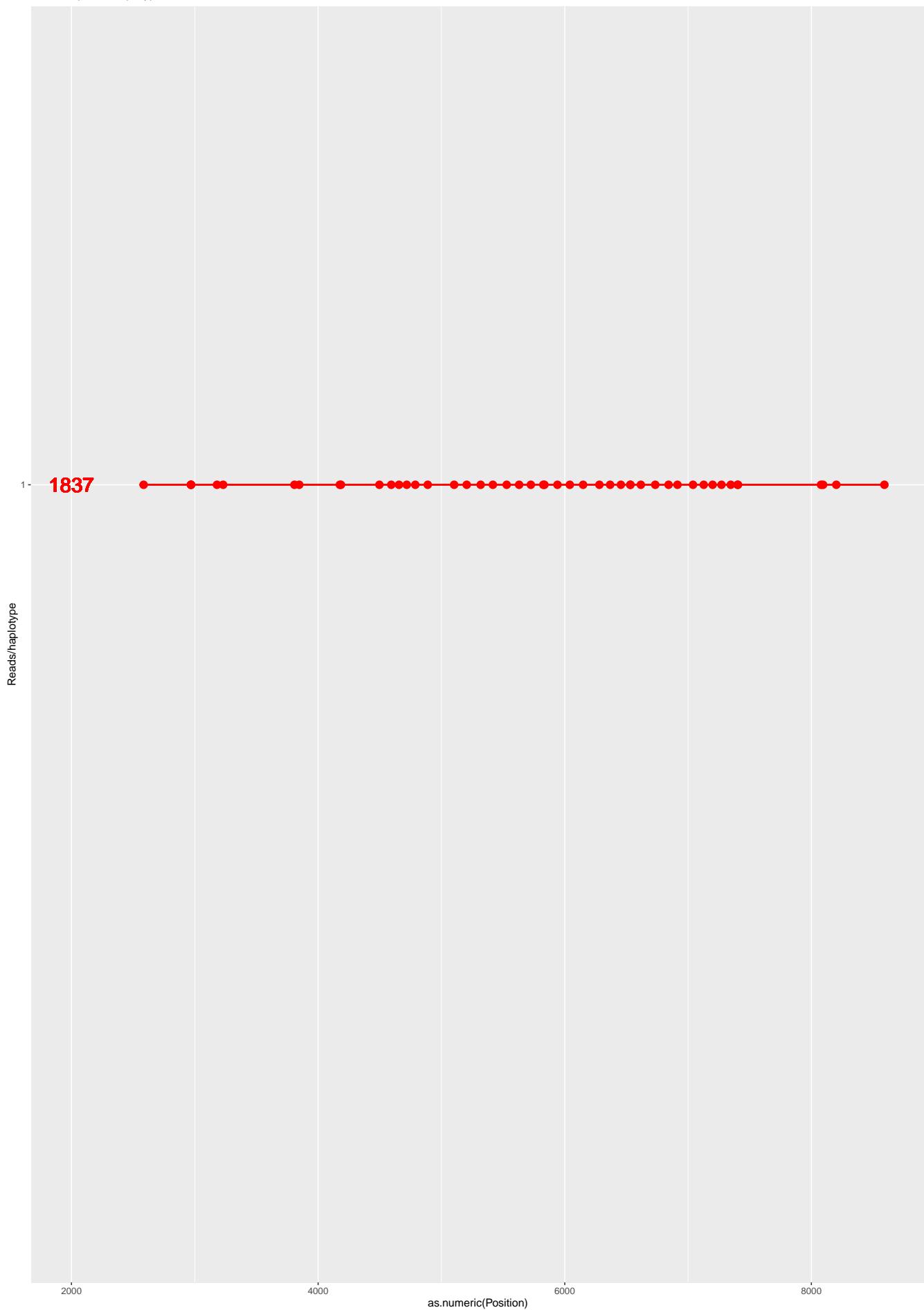
barcode = TGTGAGTCAGTACCGC & GCGCAGACTACGTGTG

Sample = 22c tetrad = 22 spore = c

Total reads = 1925 PCR=47

haplotypes I began with n[supporting reads] = 1837

most frequent 7 haplotypes.



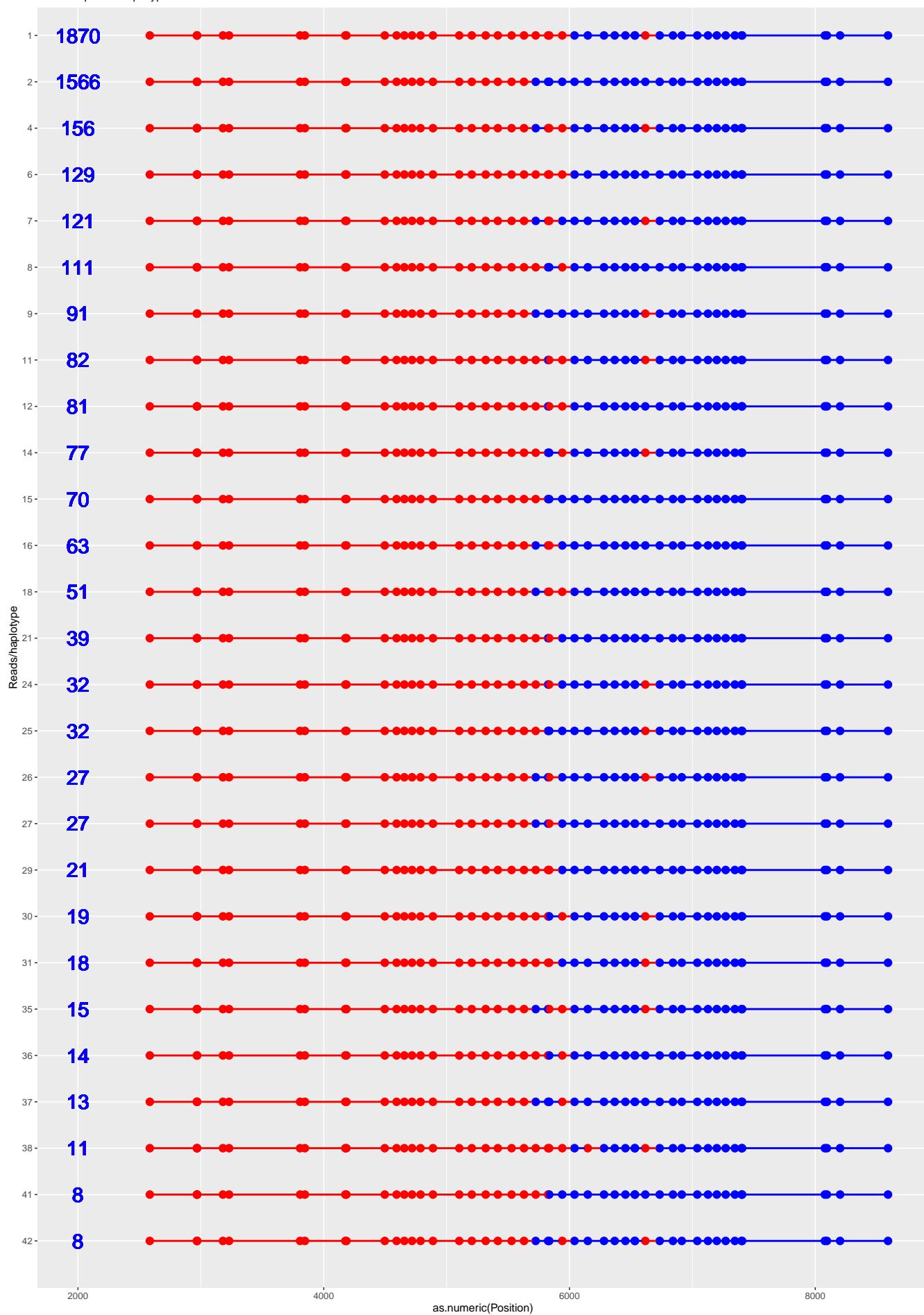
barcode = TGTGAGTCAGTACGGCG & GTCTCTGCGATAACAGC

Sample = 22d tetrad = 22 spore = d

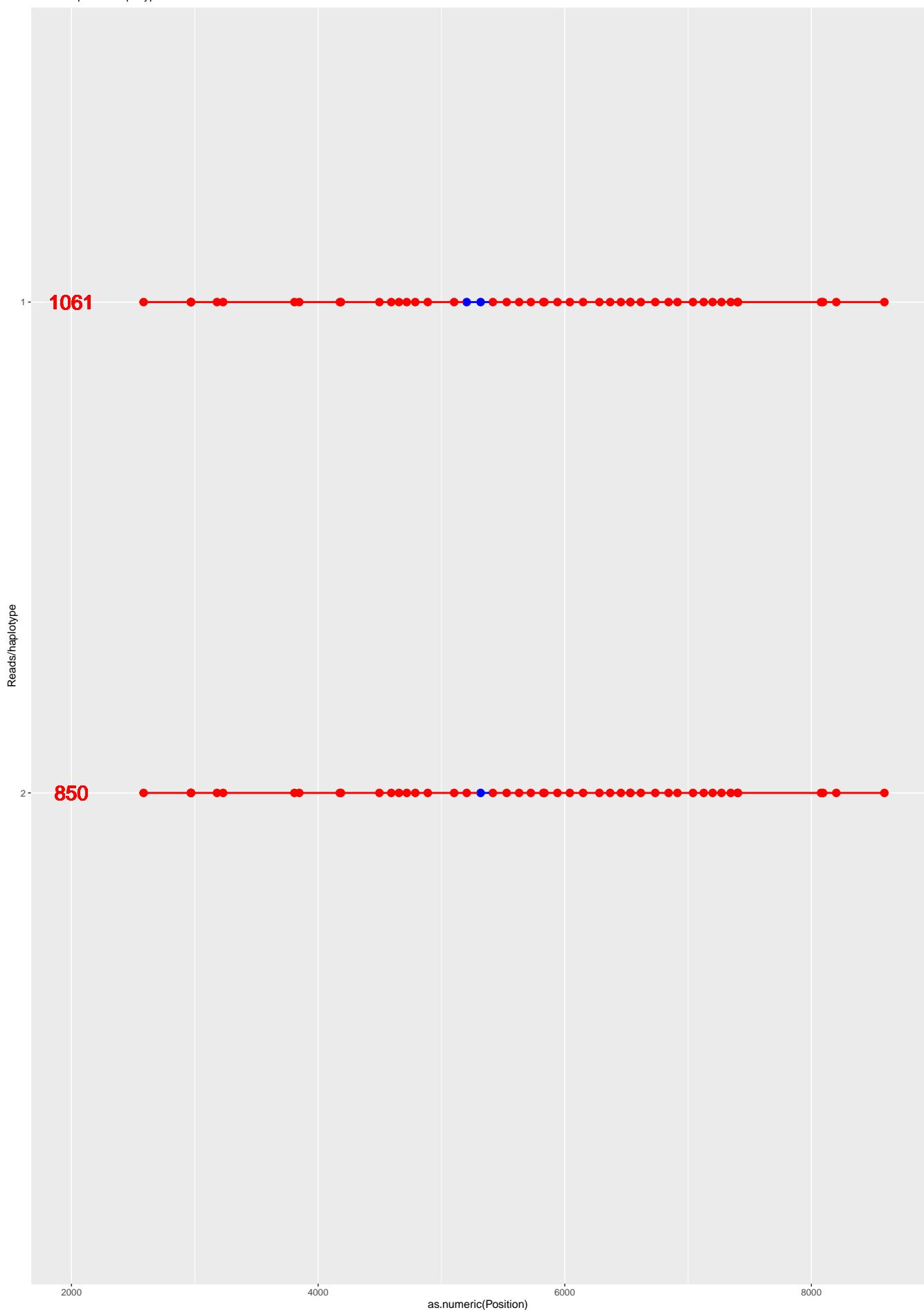
Total reads = 6119 PCR=48

haplotypes I began with [n(supporting reads)] = 8, 11, 13, 14, 15, 18, 19, 21, 27, 32, 39, 51, 63, 70, 77, 81, 82, 91, 111, 121, 129, 156, 1566, 1870

most frequent 7 haplotypes.



Sample = 26a tetrad = 26 spore = a
Total reads = 2122 PCR=49
haplotypes I began with n[supporting reads] = 850, 1061
most frequent 7 haplotypes.



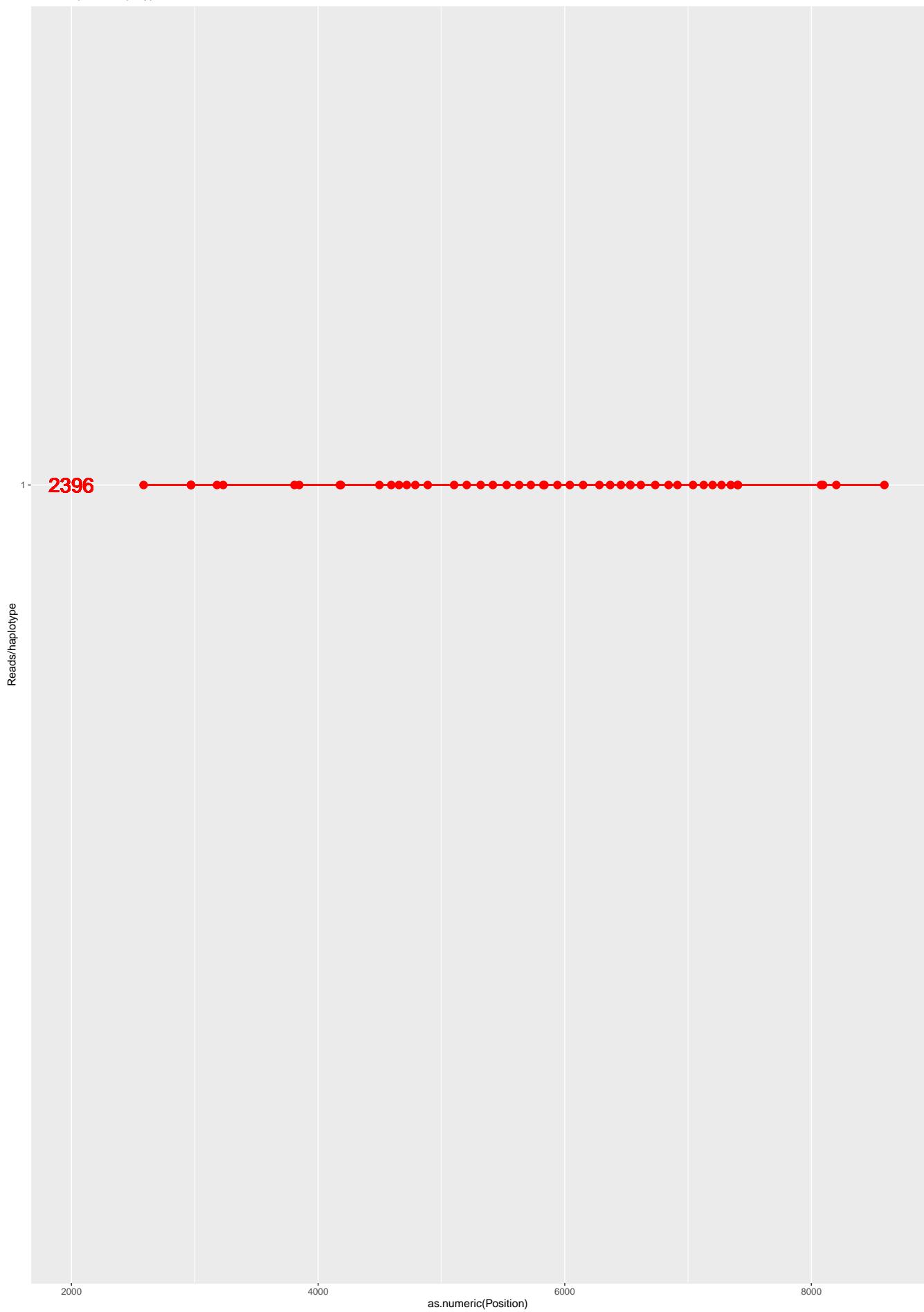
barcode = AGAGACACGATACTCA & TCATATGTAGTACTCT

Sample = 26b tetrad = 26 spore = b

Total reads = 2500 PCR=50

haplotypes I began with n[supporting reads] = 2396

most frequent 7 haplotypes.



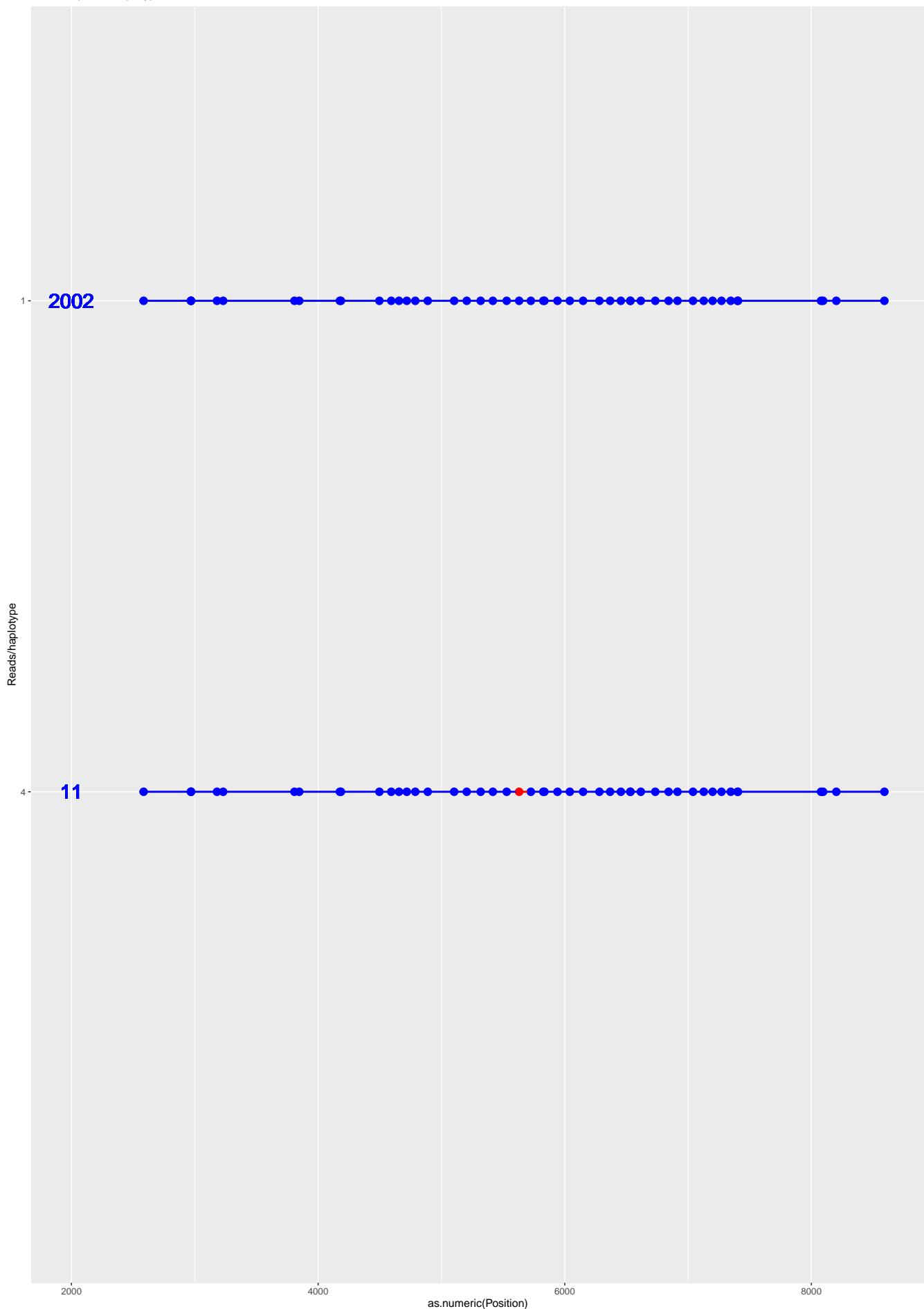
barcode = AGAGACACGATACTCA & GCGATCTATGCACACG

Sample = 26c tetrad = 26 spore = c

Total reads = 2319 PCR=51

haplotypes I began with n[supporting reads] = 11, 2002

most frequent 7 haplotypes.



barcode = AGAGACACGATACTCA & TGCAGTCGAGATACAT

Sample = 26d tetrad = 26 spore = d

Total reads =2997 PCR=52

haplotypes I began with n[supporting reads] = 11, 16, 2567

most frequent 7 haplotypes.



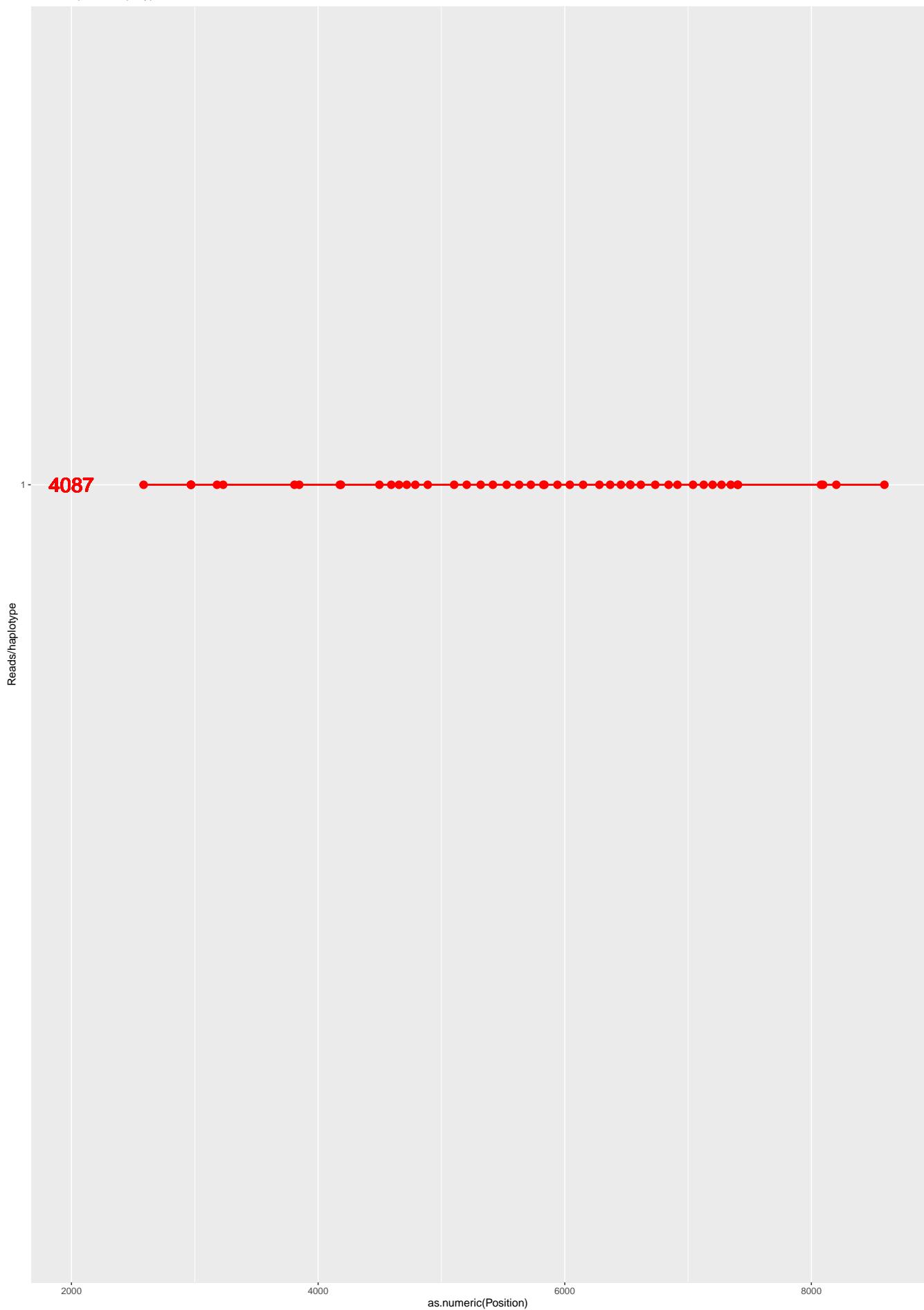
barcode = AGAGACACGATACTCA & GACTCTGCGTCGAGTC

Sample = 29a tetrad = 29 spore = a

Total reads = 4255 PCR=53

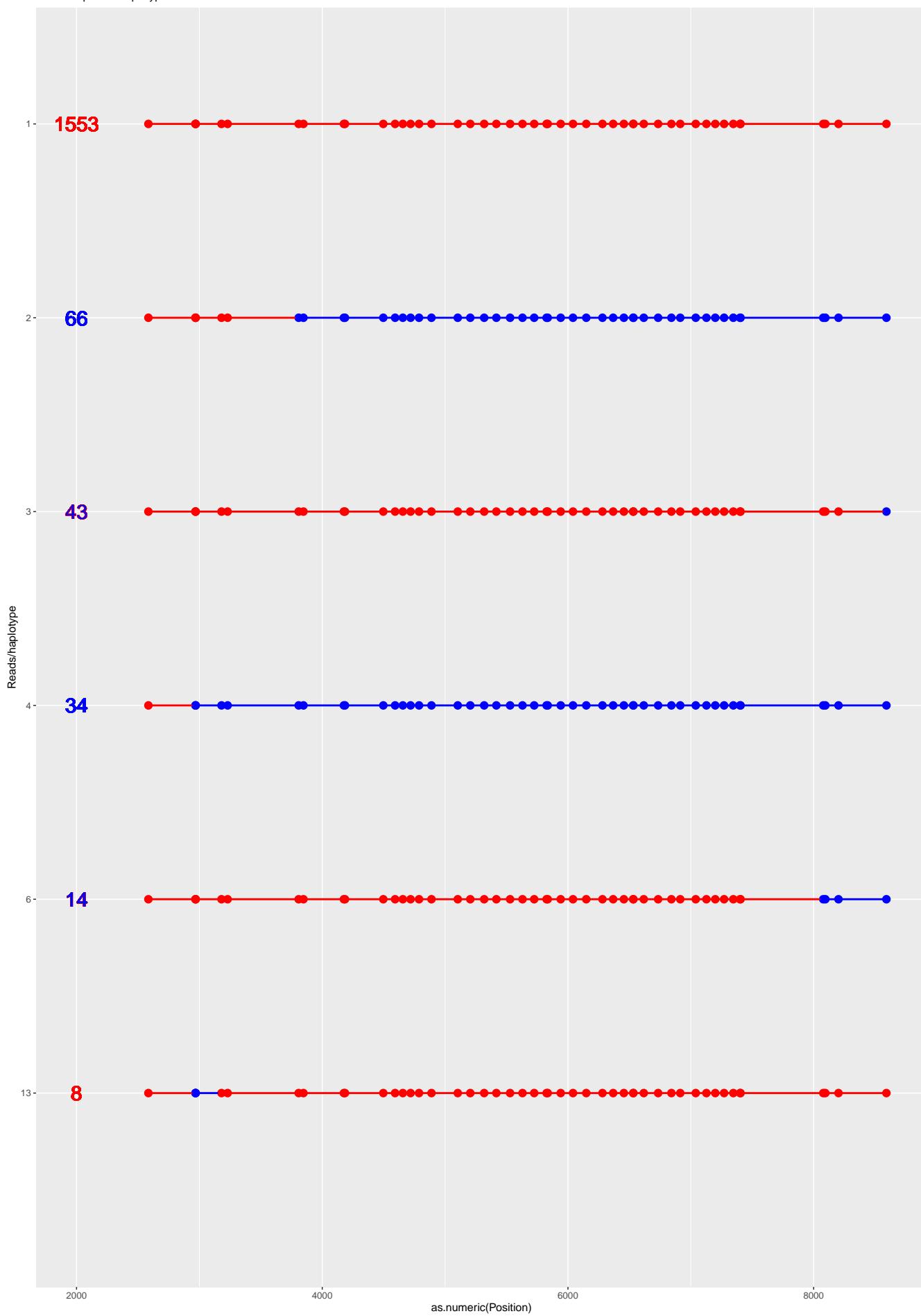
haplotypes I began with n[supporting reads] = 4087

most frequent 7 haplotypes.



barcode = AGAGACACGATACTCA & TACAGCGACGTCATCG

Sample = 29b tetrad = 29 spore = b
Total reads = 3027 PCR=54
haplotypes I began with [n(supporting reads)] = 8, 14, 34, 43, 66, 1553
most frequent 7 haplotypes.



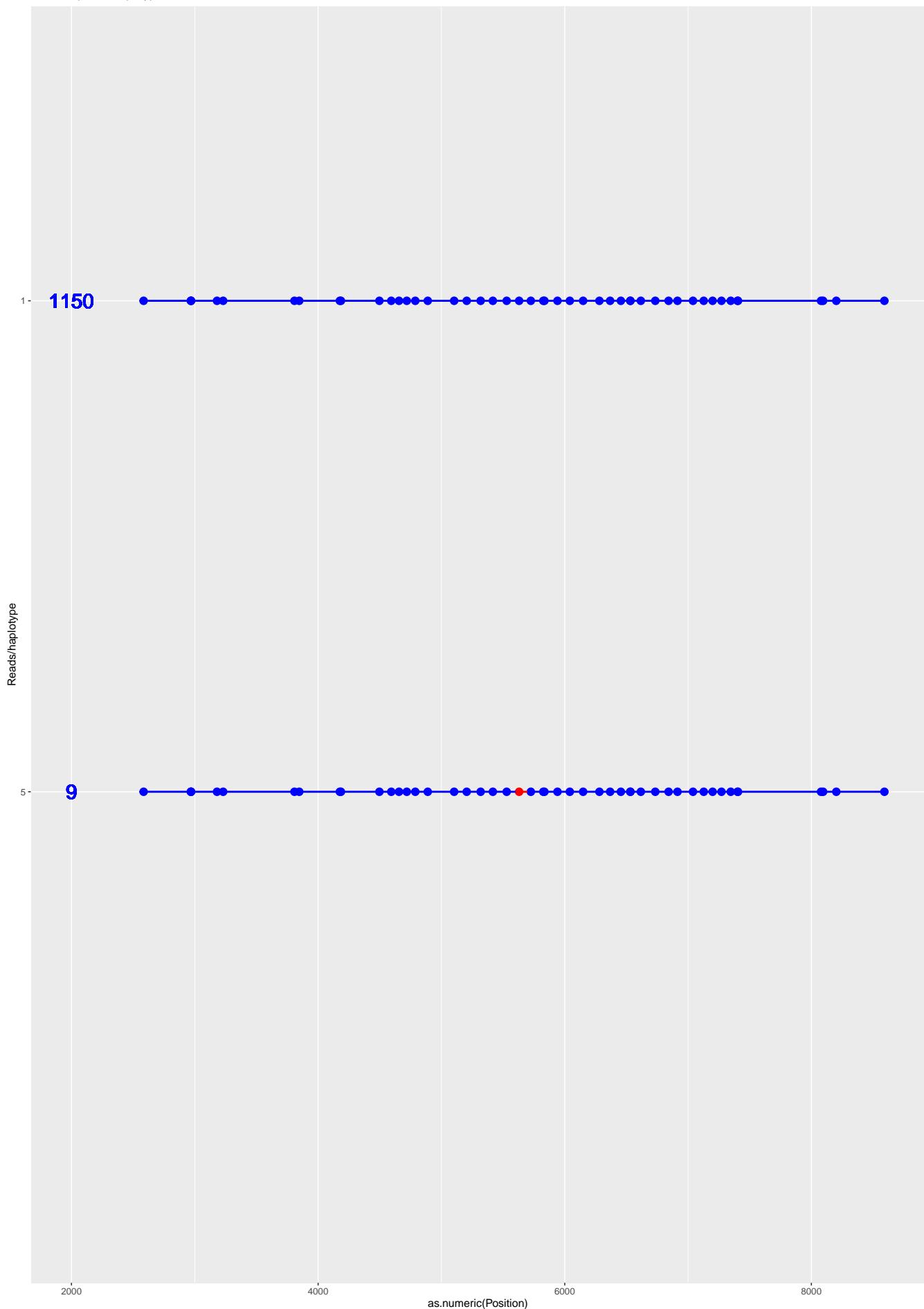
barcode = AGAGACACGATACTCA & GCGCAGACTACGTGTG

Sample = 29c tetrad = 29 spore = c

Total reads = 1346 PCR=55

haplotypes I began with n[supporting reads] = 9, 1150

most frequent 7 haplotypes.



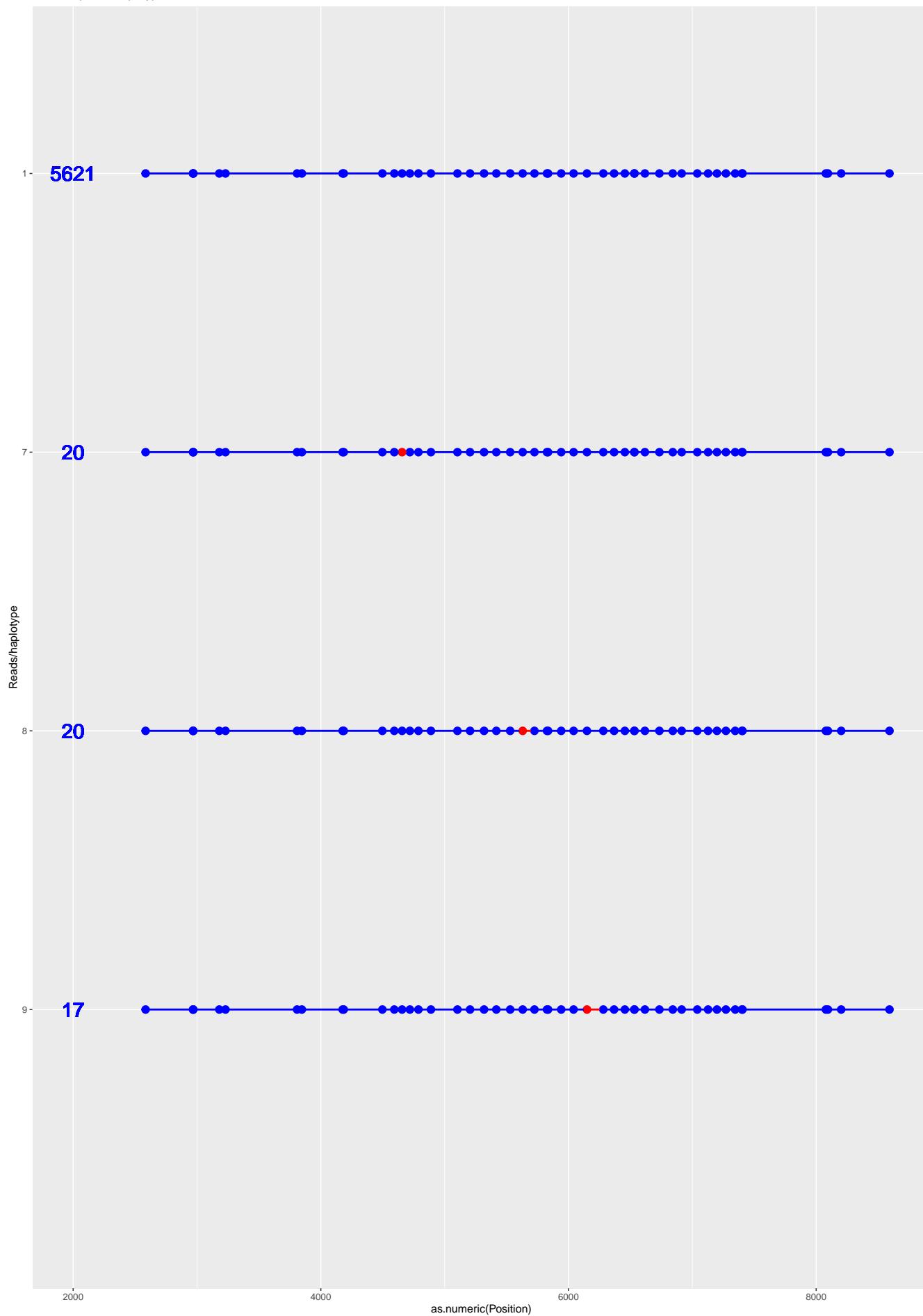
barcode = AGAGACACGATACTCA & GTCTCTGCGATACAGC

Sample = 29d tetrad = 29 spore = d

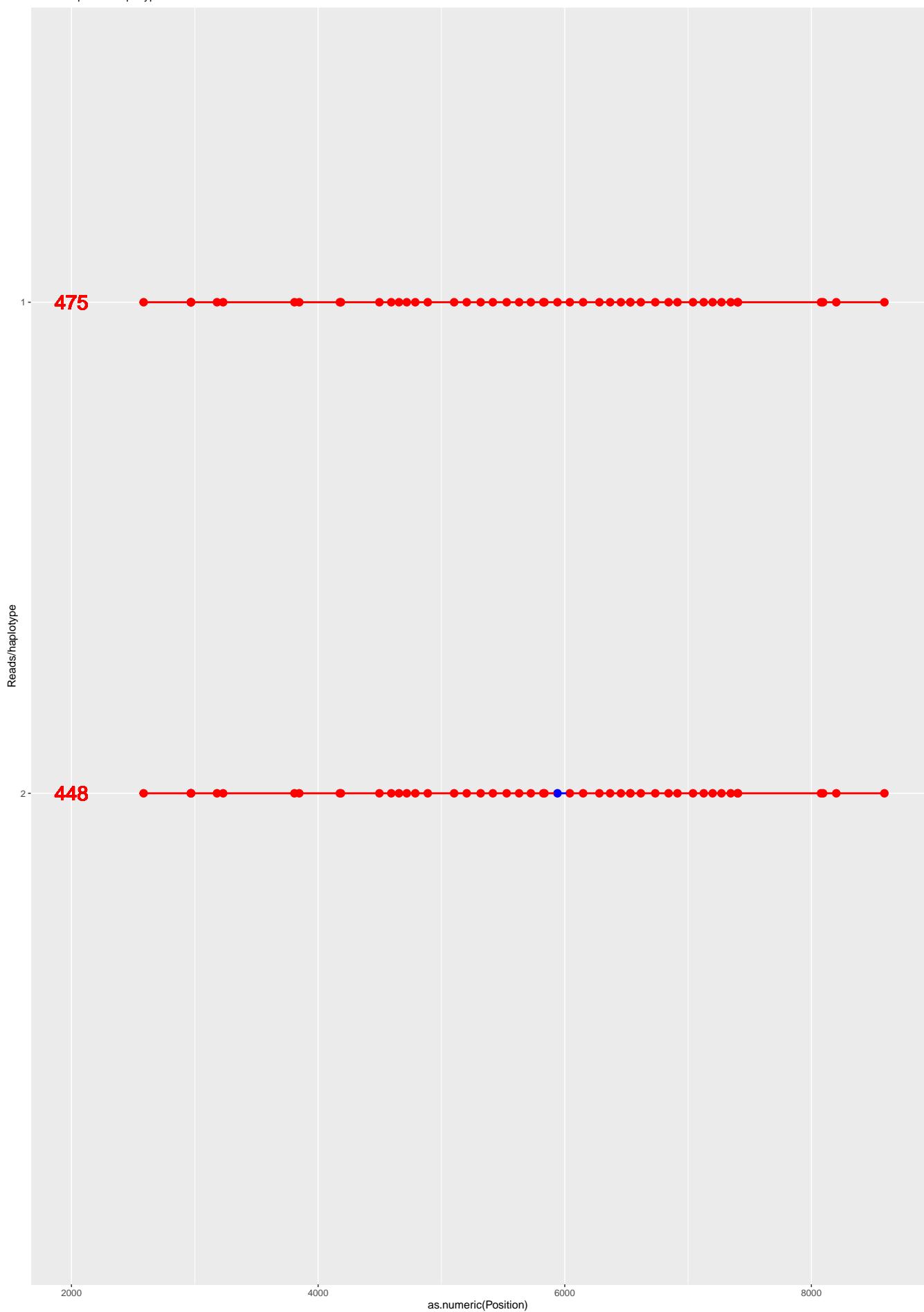
Total reads = 6573 PCR=56

haplotypes I began with n[supporting reads] = 17, 20, 5621

most frequent 7 haplotypes.



Sample = 33a tetrad = 33 spore = a
Total reads = 1043 PCR=57
haplotypes I began with n[supporting reads] = 448, 475
most frequent 7 haplotypes.



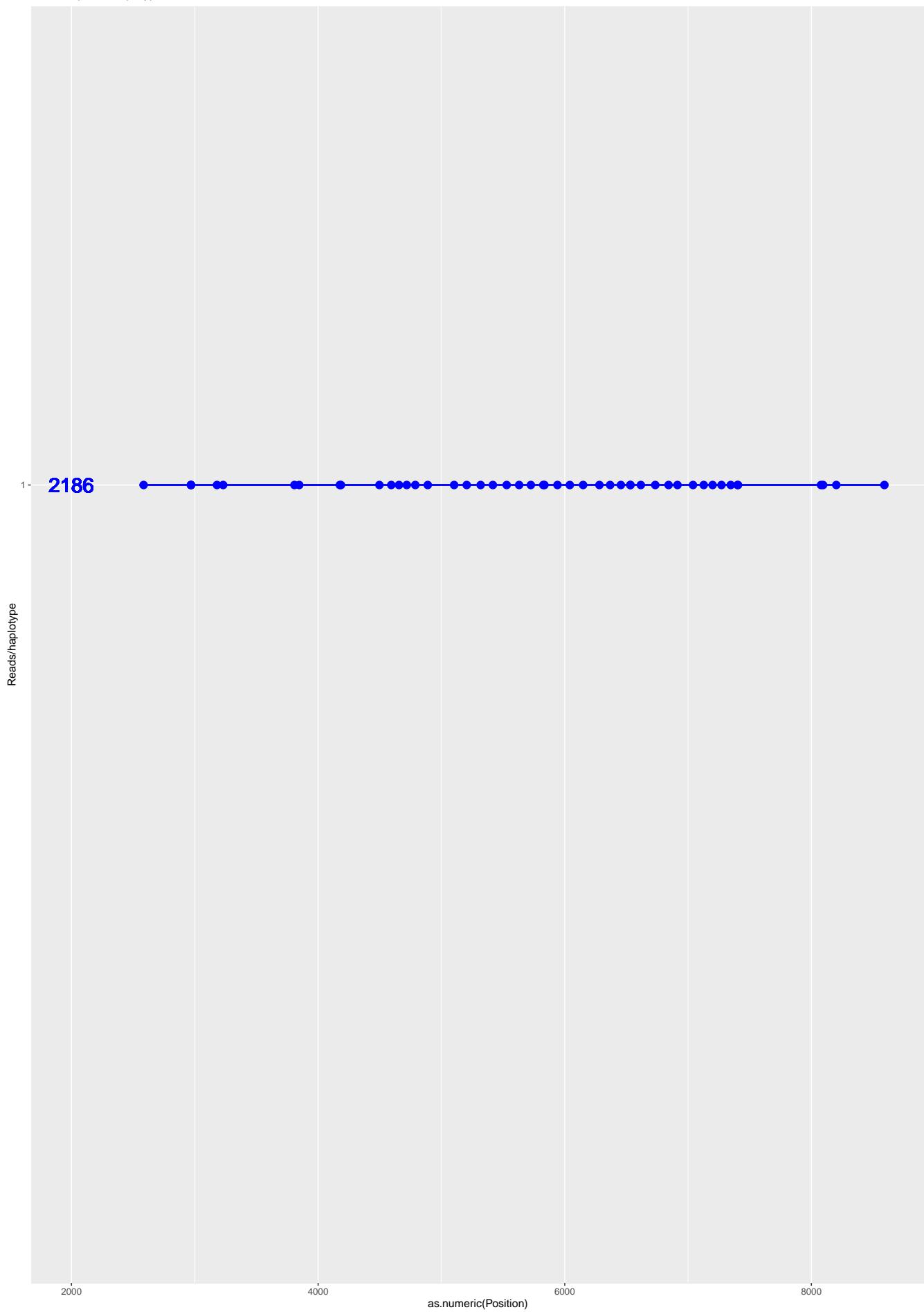
barcode = CTGCTAGAGTCTACAG & TCATATGTAGTACTCT

Sample = 33b tetrad = 33 spore = b

Total reads = 2552 PCR=58

haplotypes I began with n[supporting reads] = 2186

most frequent 7 haplotypes.



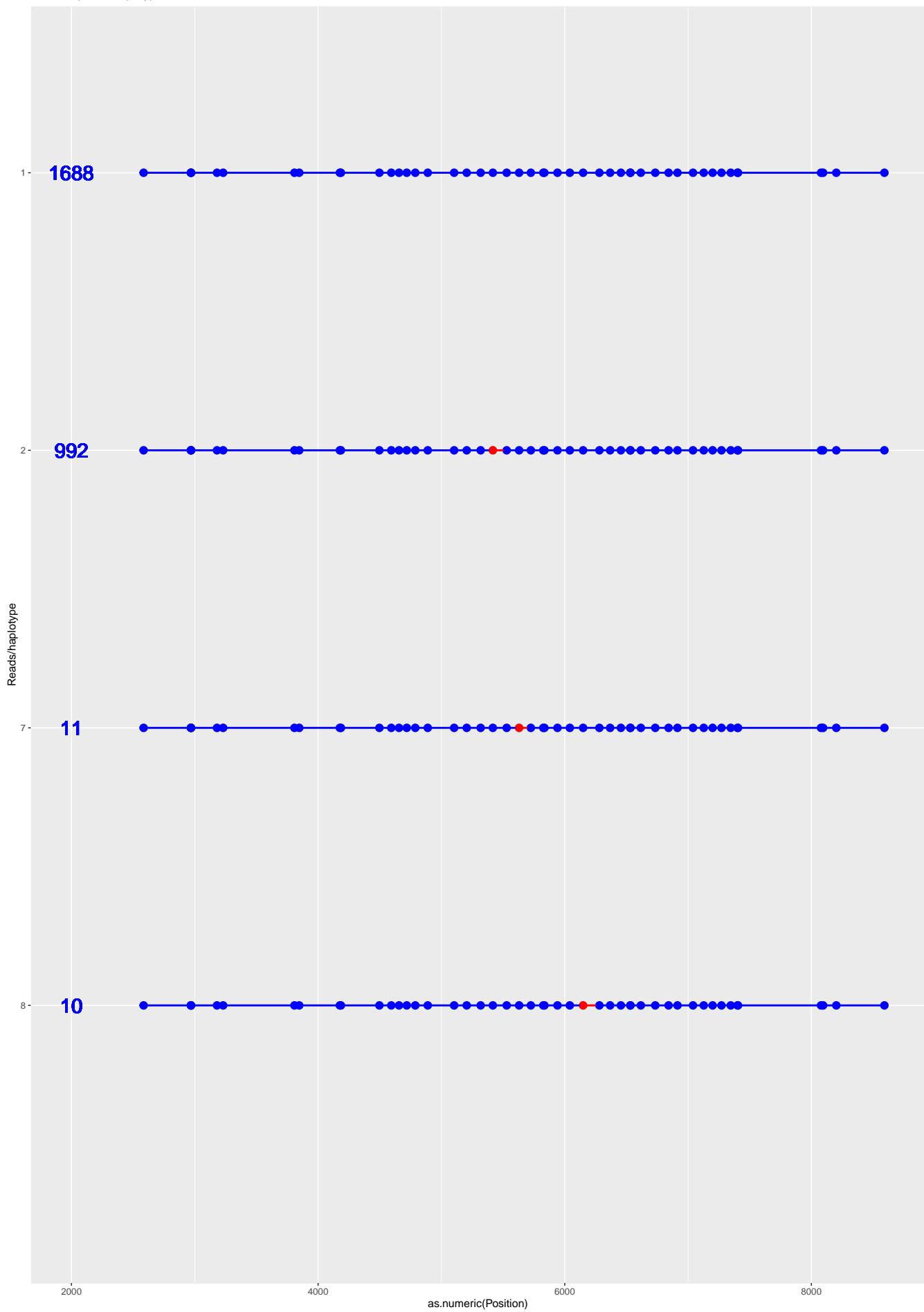
barcode = CTGCTAGAGTCTACAG & GCGATCTATGCACACG

Sample = 33c tetrad = 33 spore = c

Total reads = 3114 PCR=59

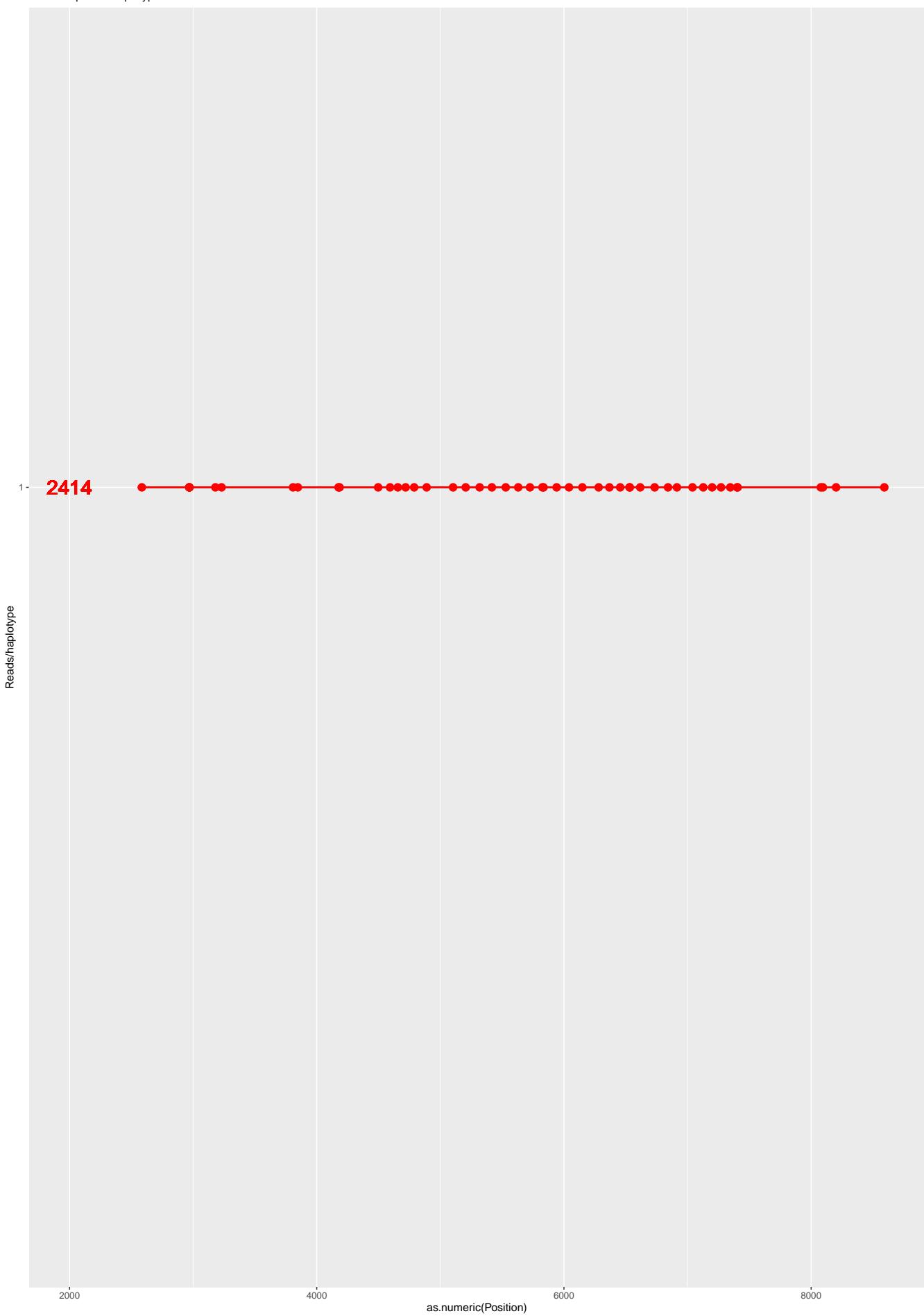
haplotypes I began with n[supporting reads] = 10, 11, 992, 1688

most frequent 7 haplotypes.



barcode = CTGCTAGAGTCTACAG & TGCAGTCGAGATACT

Sample = 33d tetrad = 33 spore = d
Total reads = 2517 PCR=60
haplotypes I began with n[supporting reads] = 2414
most frequent 7 haplotypes.

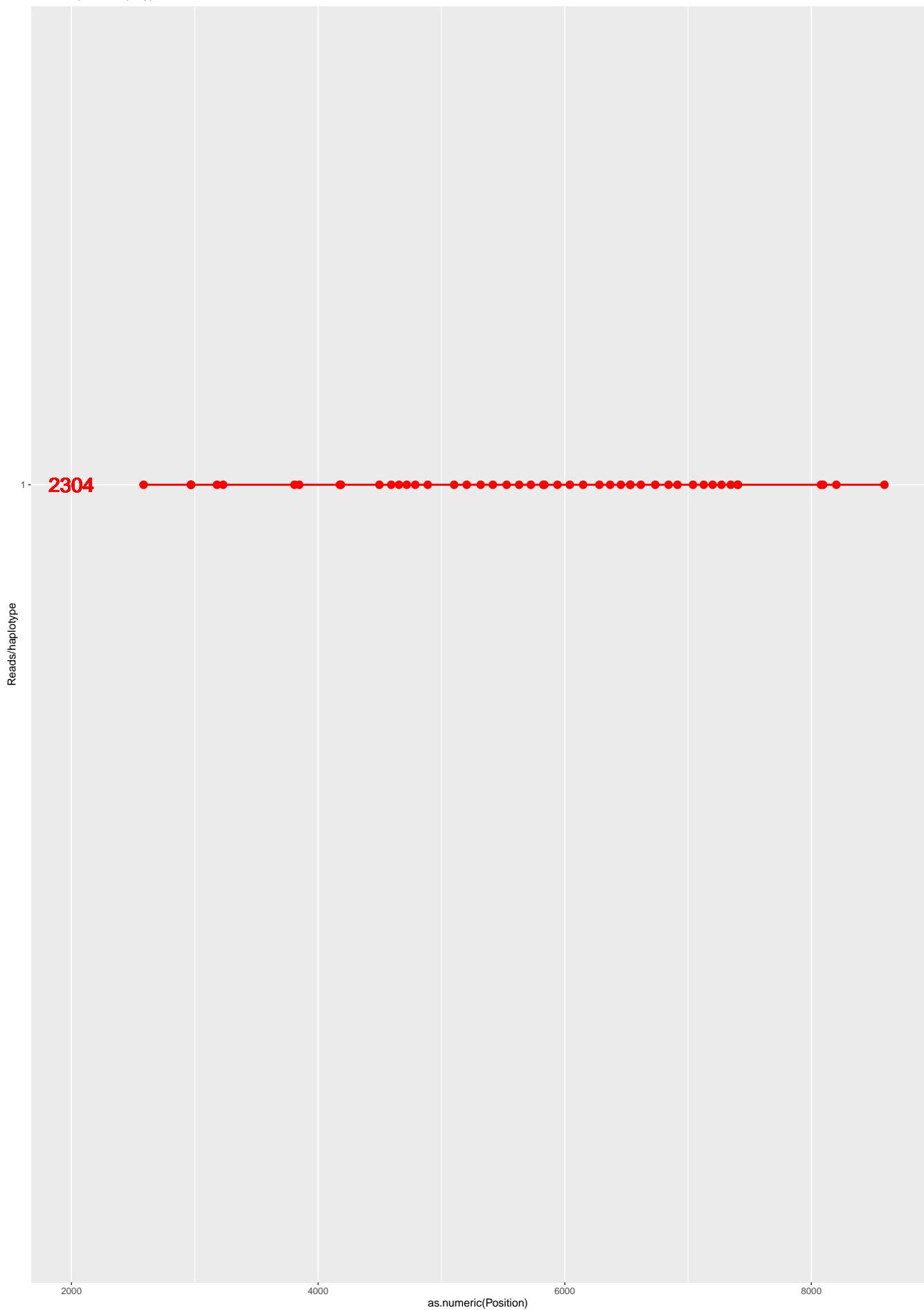


Sample = 34a tetrad = 34 spore = a

Total reads = 2415 PCR=61

haplotypes I began with n[supporting reads] = 2304

most frequent 7 haplotypes.



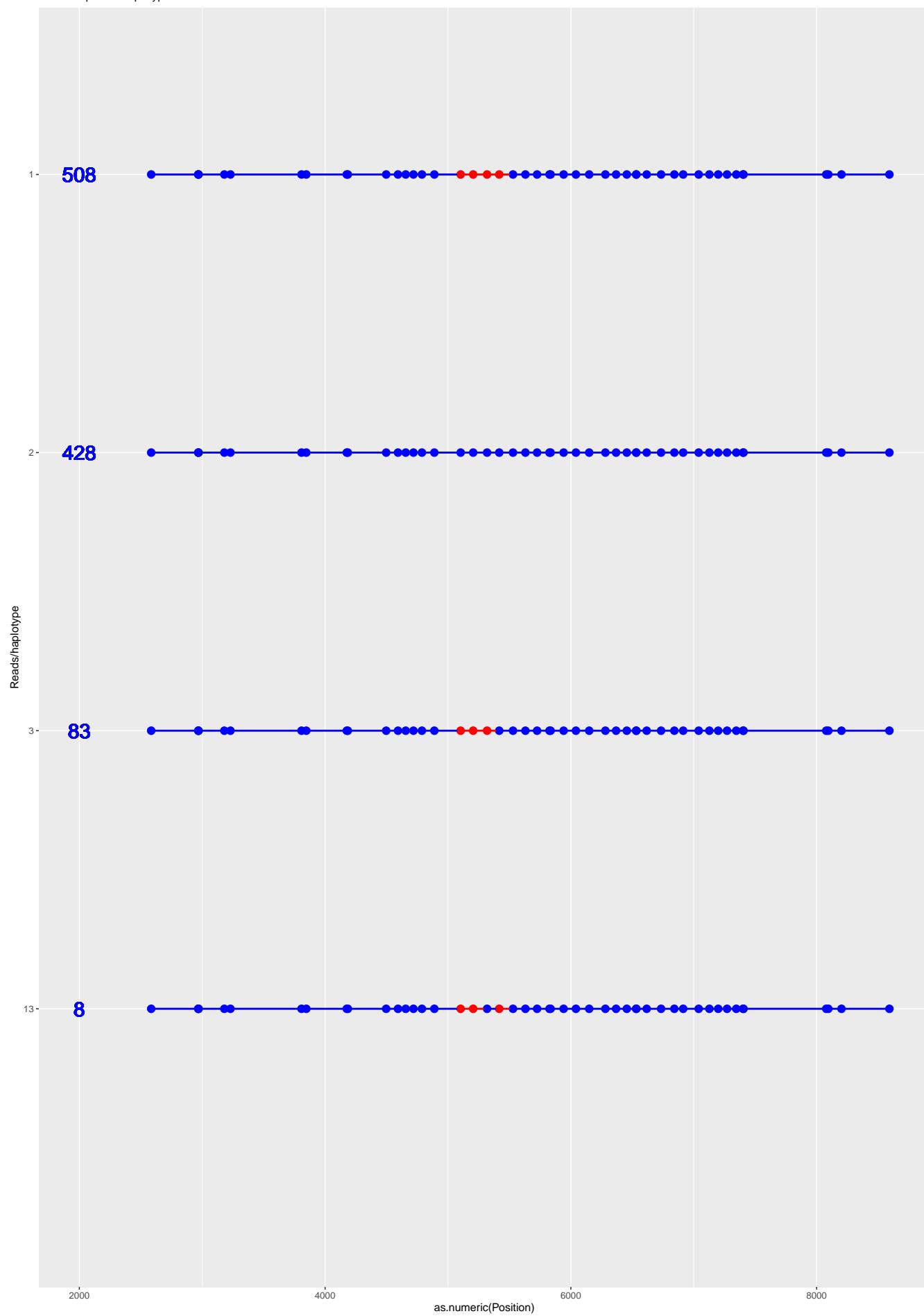
barcode = CTGCTAGAGTCTACAG & TACAGCGACGTCATCG

Sample = 34b tetrad = 34 spore = b

Total reads = 1400 PCR=62

haplotypes I began with [n(supporting reads)] = 8, 83, 428, 508

most frequent 7 haplotypes.

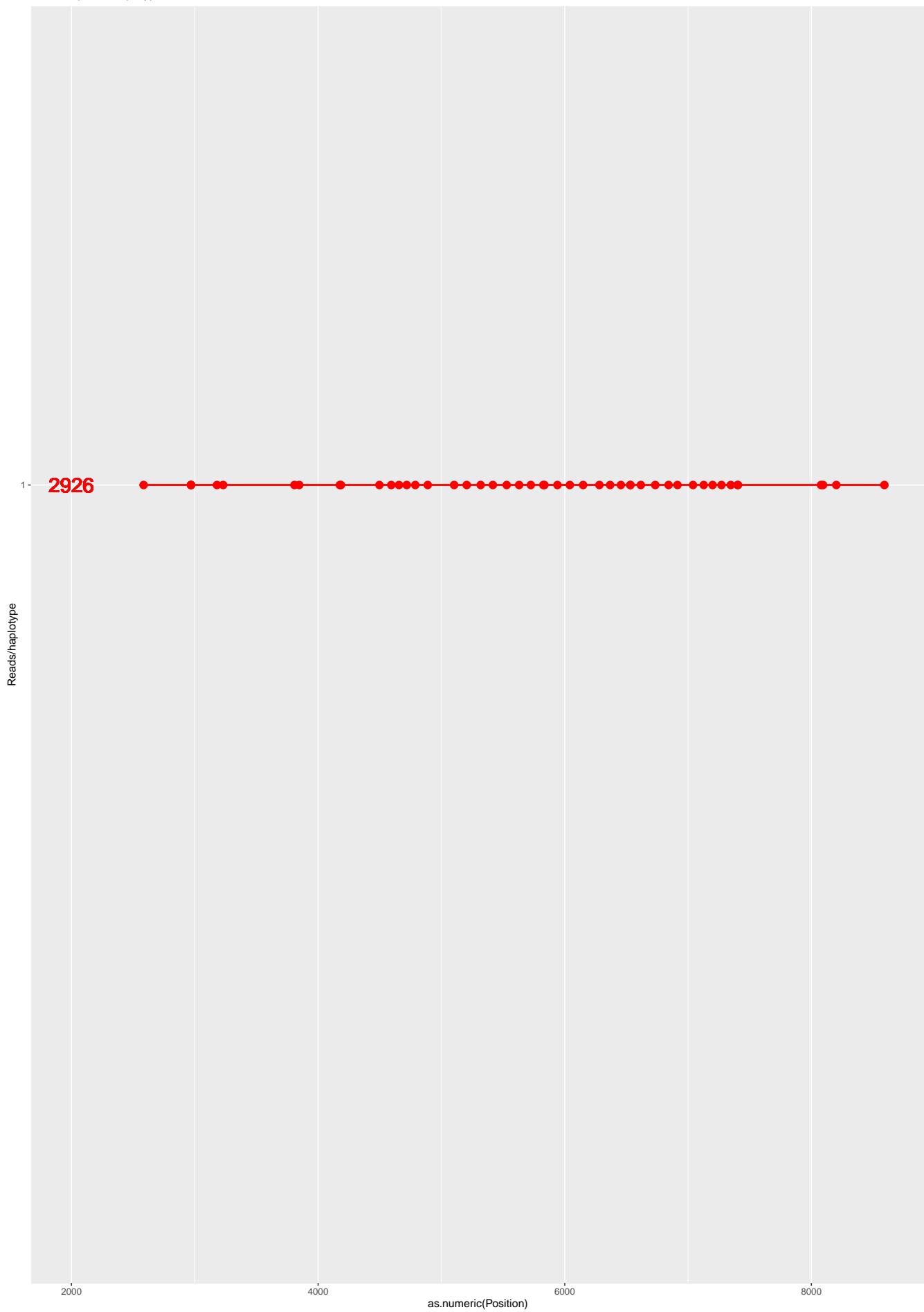


Sample = 34c tetrad = 34 spore = c

Total reads =3068 PCR=63

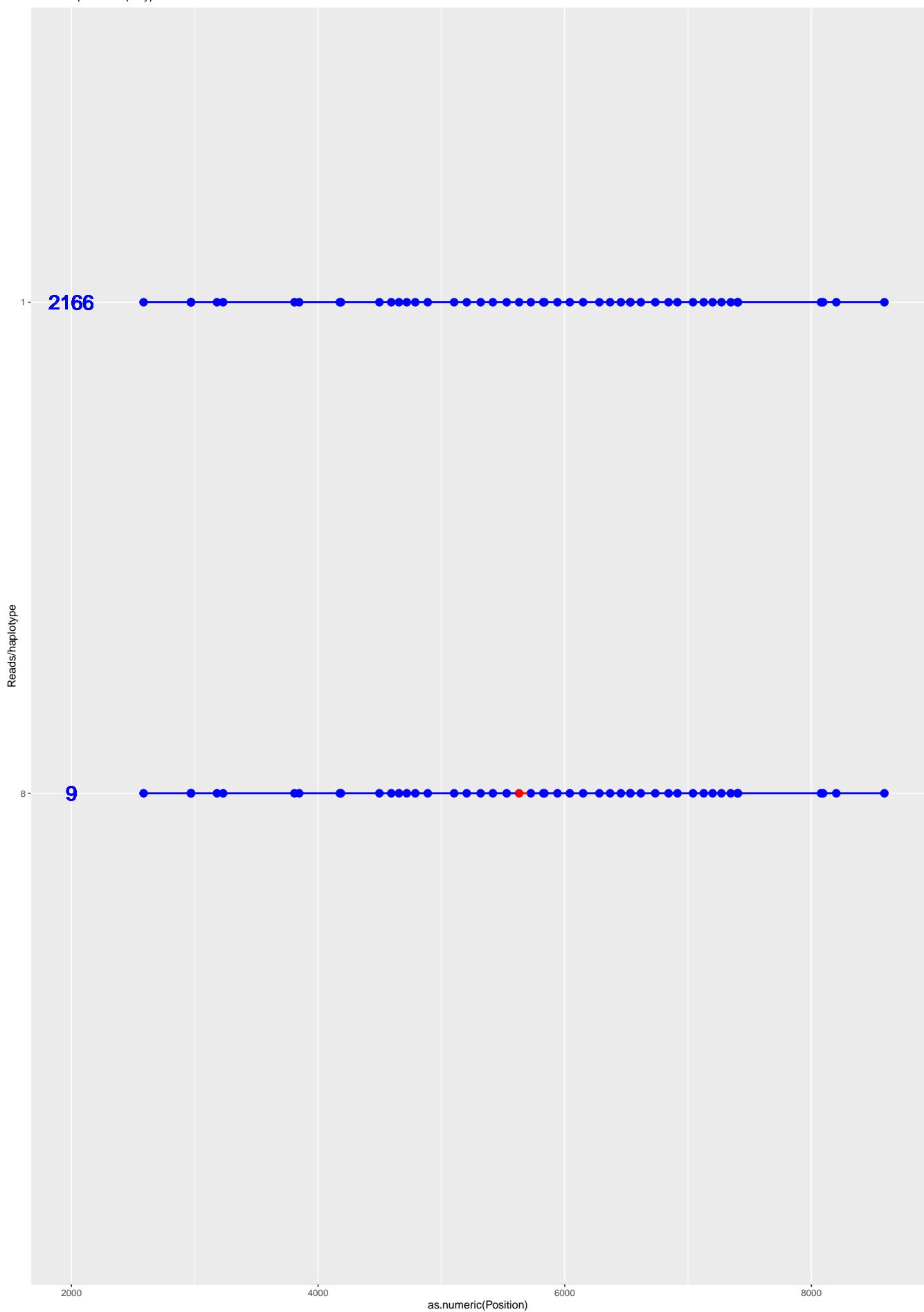
haplotypes I began with n[supporting reads] = 2926

most frequent 7 haplotypes.



barcode = CTGCTAGAGTCTACAG & GTCTCTGCGATACAGC

Sample = 34d tetrad = 34 spore = d
Total reads = 2515 PCR=64
haplotypes I began with n[supporting reads] = 9, 2166
most frequent 7 haplotypes.



barcode = CTGCTAGAGTCTACAG & AGTATGAGATAGCTCG

Sample = 35a tetrad = 35 spore = a

Total reads =2497 PCR=65

haplotypes I began with n[supporting reads] = 8, 9, 2125

most frequent 7 haplotypes.

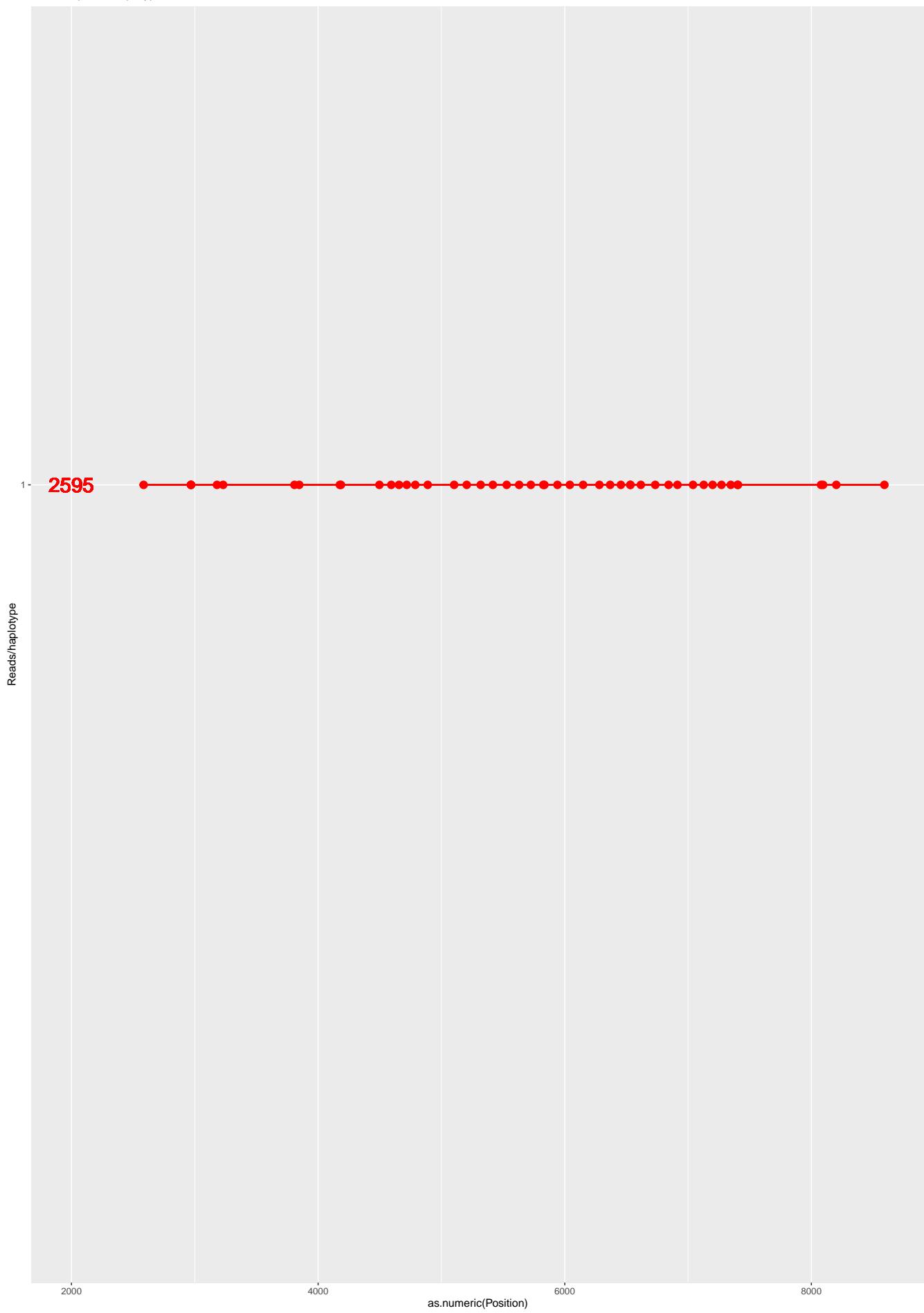


Sample = 35b tetrad = 35 spore = b

Total reads = 2712 PCR=66

haplotypes I began with n[supporting reads] = 2595

most frequent 7 haplotypes.



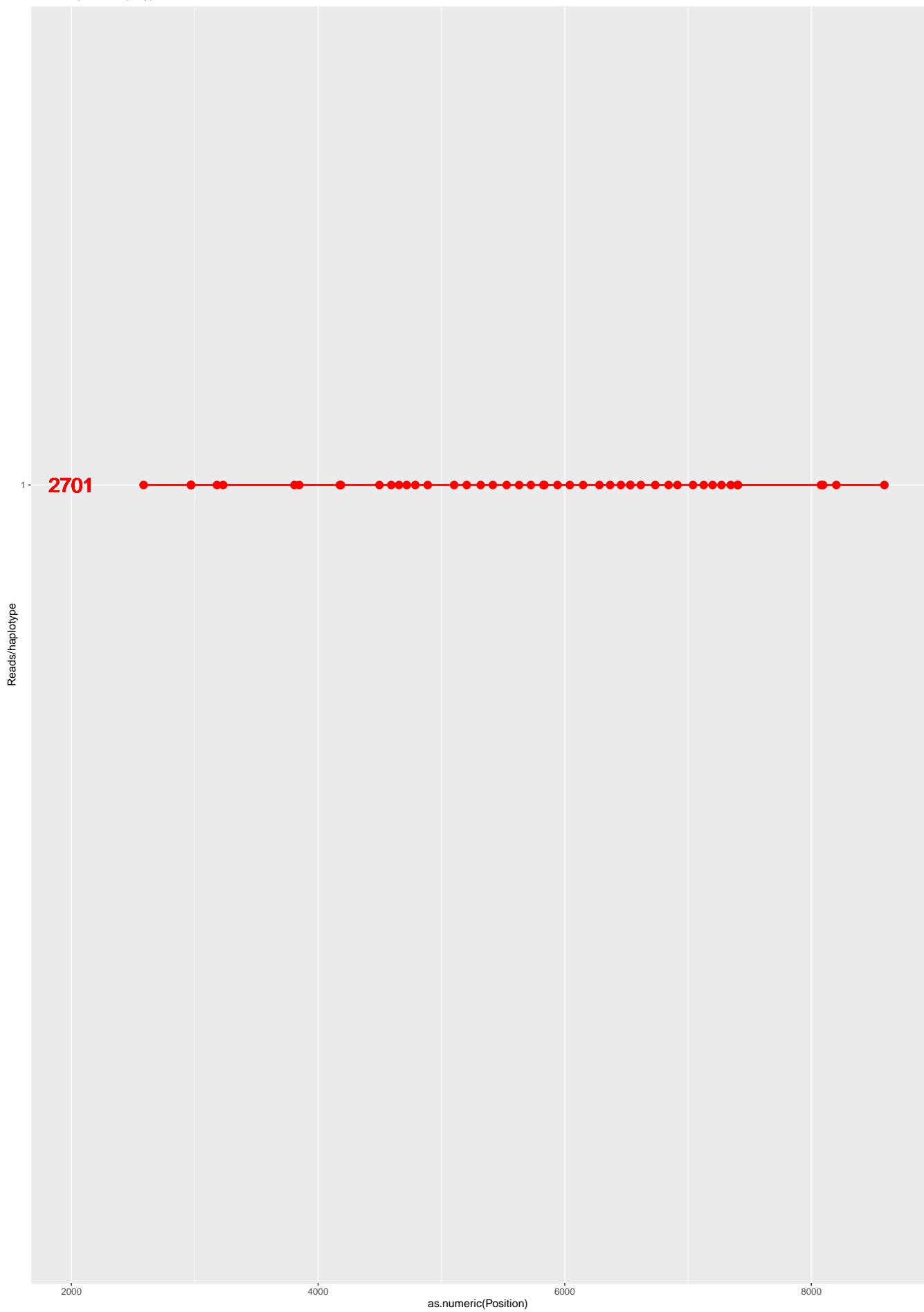
barcode = AGCACTCGCGTCAGTG & GCGATCTATGCACACG

Sample = 35c tetrad = 35 spore = c

Total reads = 2840 PCR=67

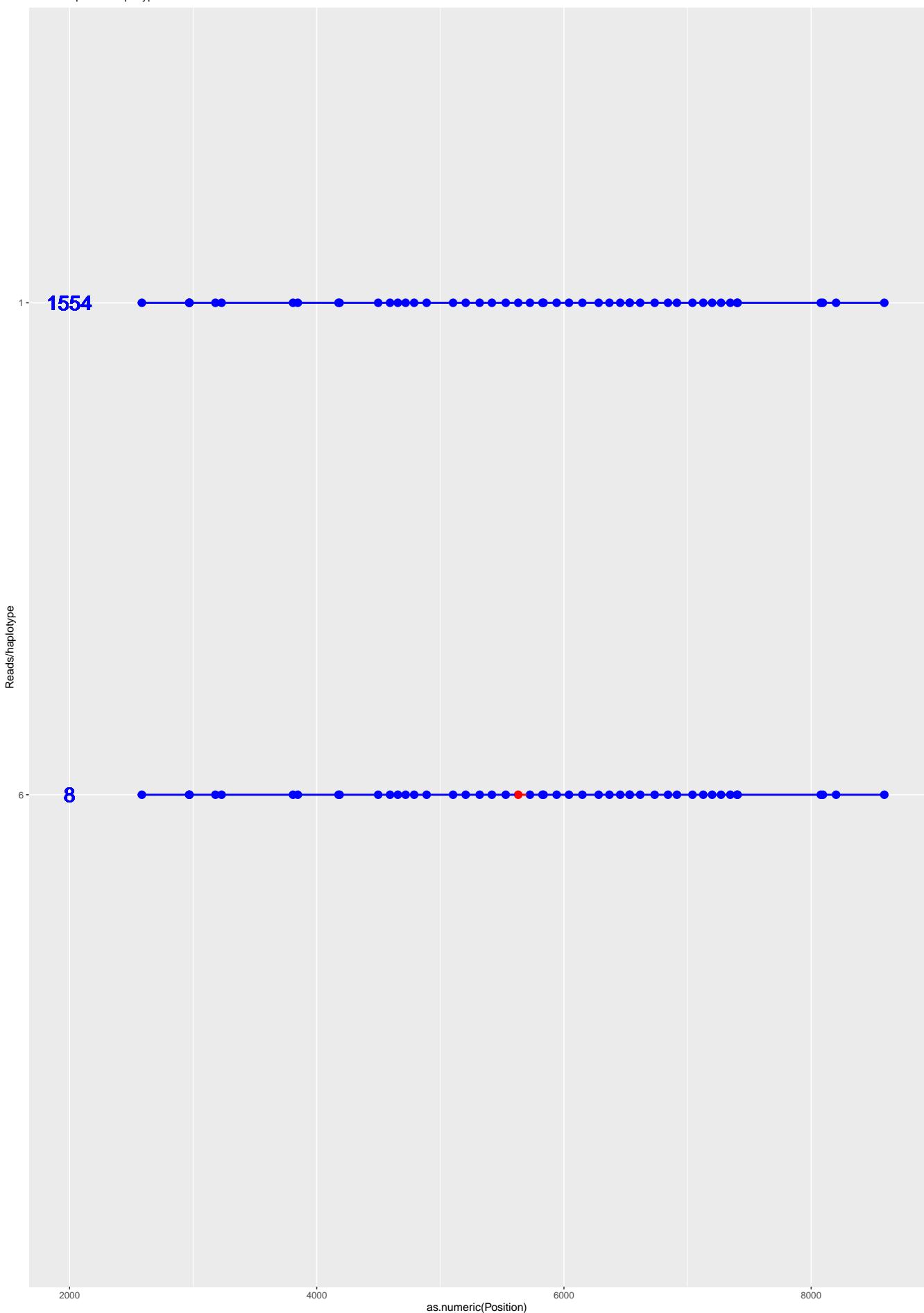
haplotypes I began with n[supporting reads] = 2701

most frequent 7 haplotypes.



barcode = AGCACTCGCGTCAGTG & TGCAGTCGAGATAACAT

Sample = 35d tetrad = 35 spore = d
Total reads = 1825 PCR=68
haplotypes I began with n[supporting reads] = 8, 1554
most frequent 7 haplotypes.



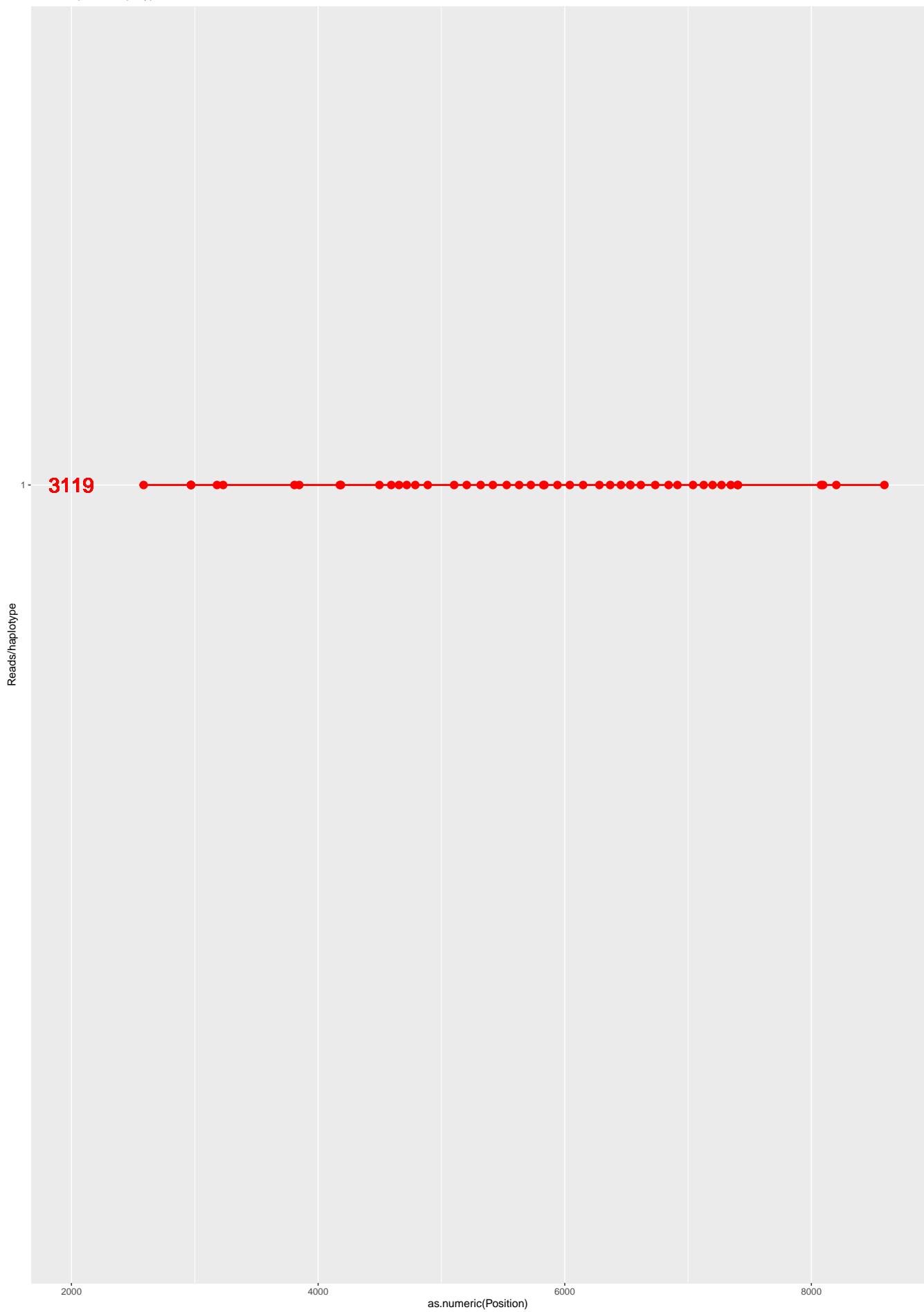
barcode = AGCACTCGCGTCAGTG & GACTCTGCGTCGAGTC

Sample = 36a tetrad = 36 spore = a

Total reads =3251 PCR=69

haplotypes I began with n[supporting reads] = 3119

most frequent 7 haplotypes.



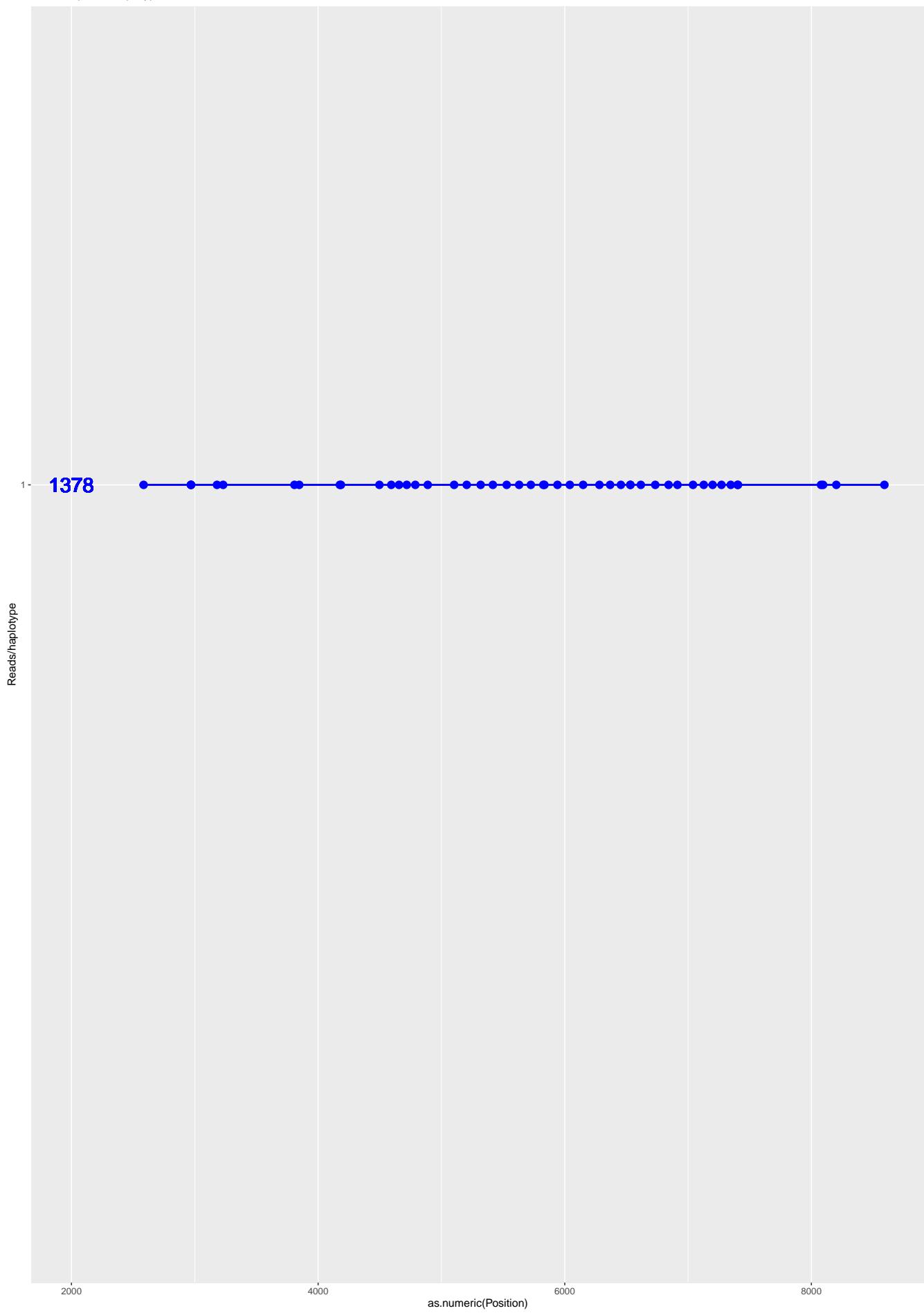
barcode = AGCACTCGCGTCAGTG & TACAGCGACGTCATCG

Sample = 36b tetrad = 36 spore = b

Total reads = 1598 PCR=70

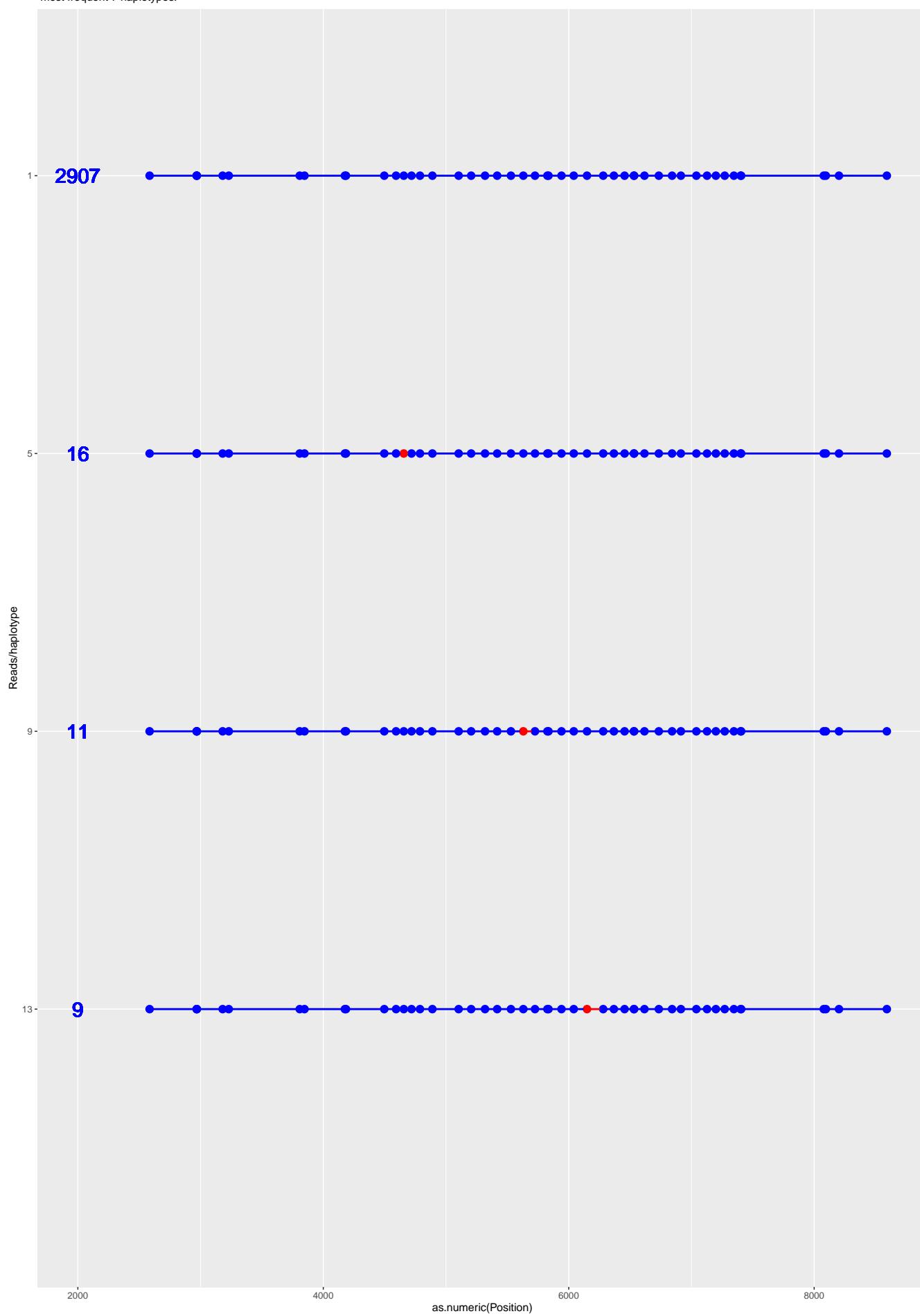
haplotypes I began with n[supporting reads] = 1378

most frequent 7 haplotypes.



barcode = AGCACTCGCGTCAGTG & GCGCAGACTACGTG

Sample = 36c tetrad = 36 spore = c
Total reads = 3420 PCR=71
haplotypes I began with [n:supporting reads] = 9, 11, 16, 2907
most frequent 7 haplotypes.



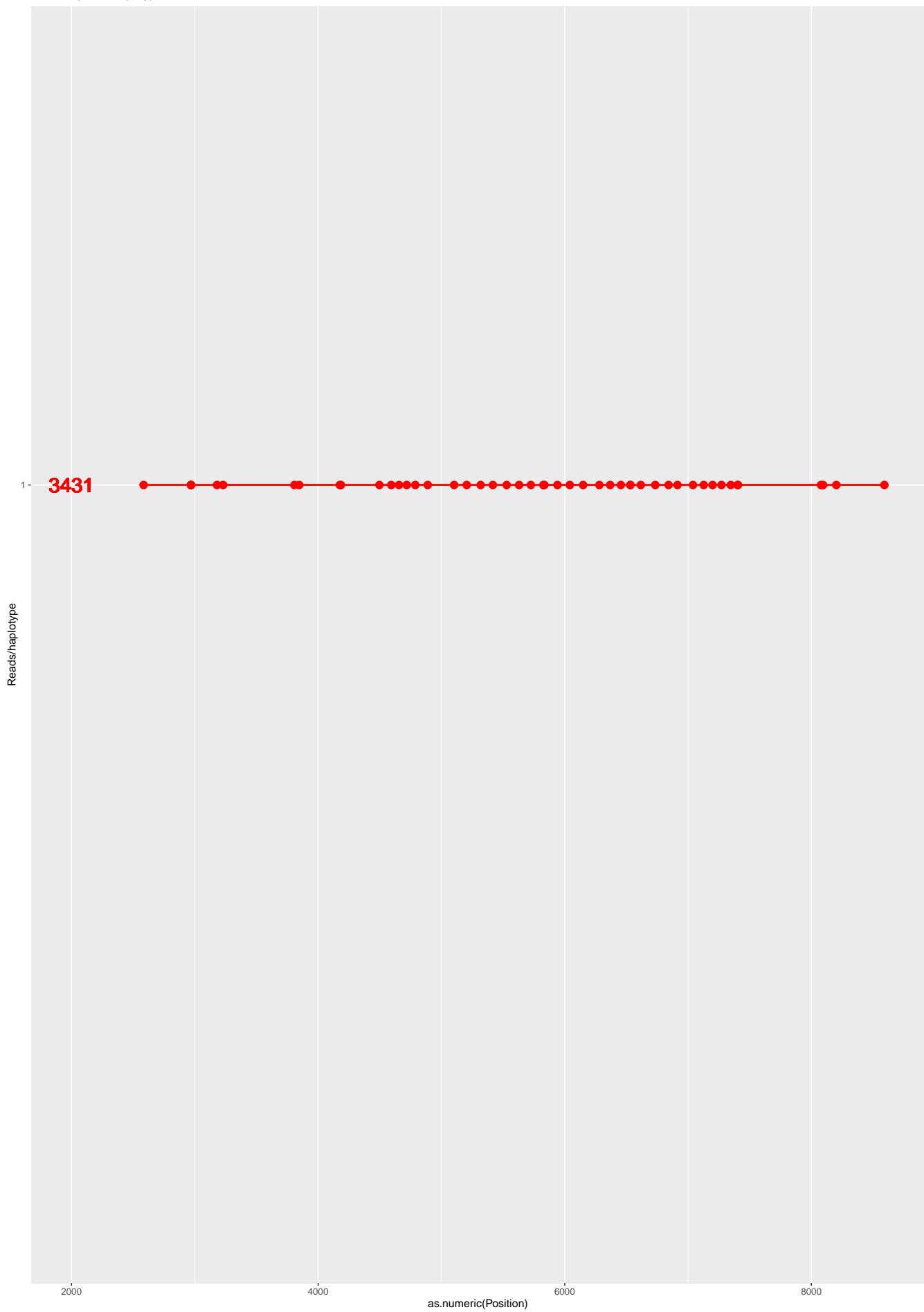
barcode = AGCACTCGCGTCAGTG & GTCTCTGCGATAACAGC

Sample = 36d tetrad = 36 spore = d

Total reads = 3567 PCR=72

haplotypes I began with n[supporting reads] = 3431

most frequent 7 haplotypes.



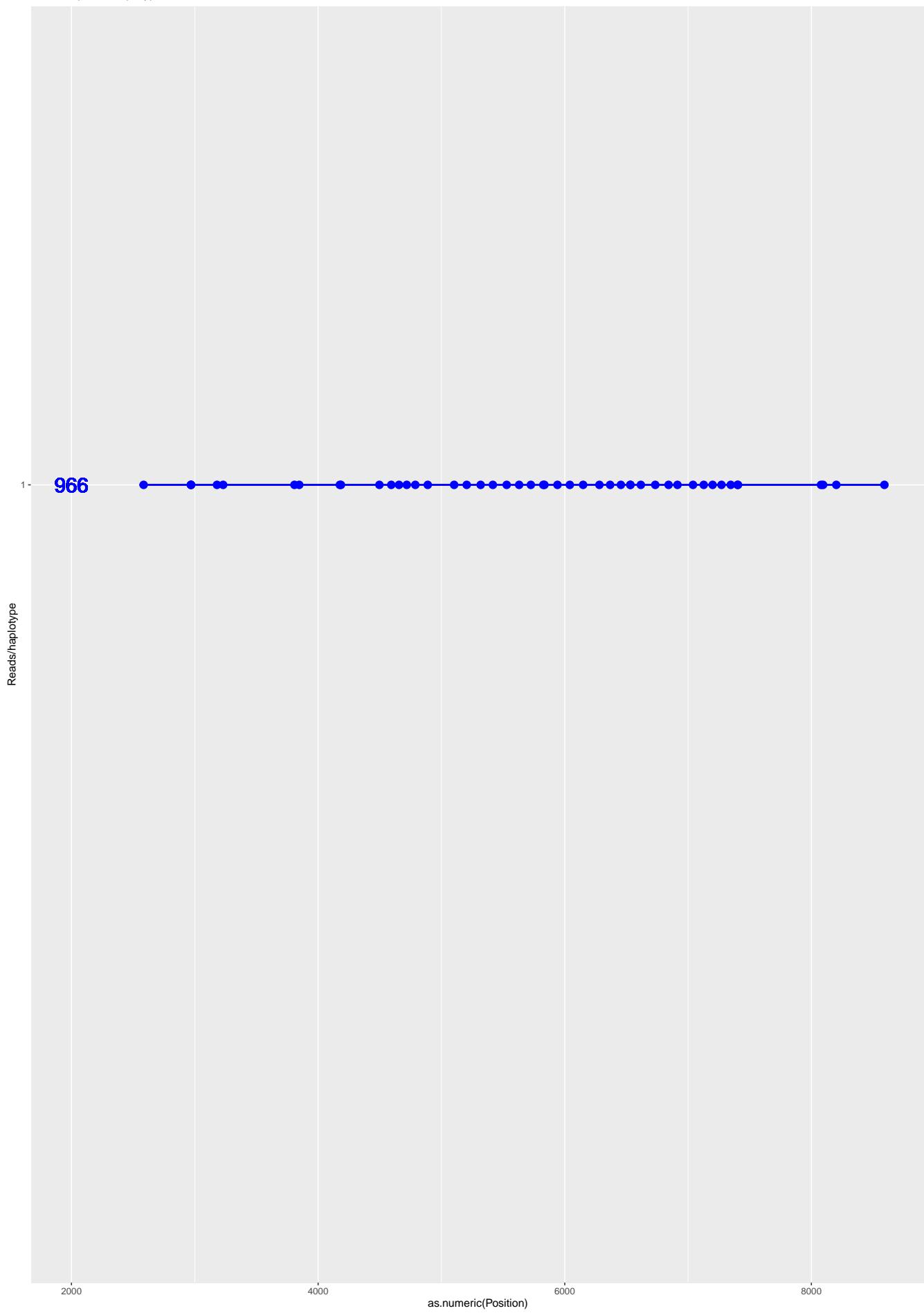
barcode = AGCACTCGCGTCAGTG & AGTATGAGATAGCTCG

Sample = 37a tetrad = 37 spore = a

Total reads = 1151 PCR=73

haplotypes I began with n[supporting reads] = 966

most frequent 7 haplotypes.



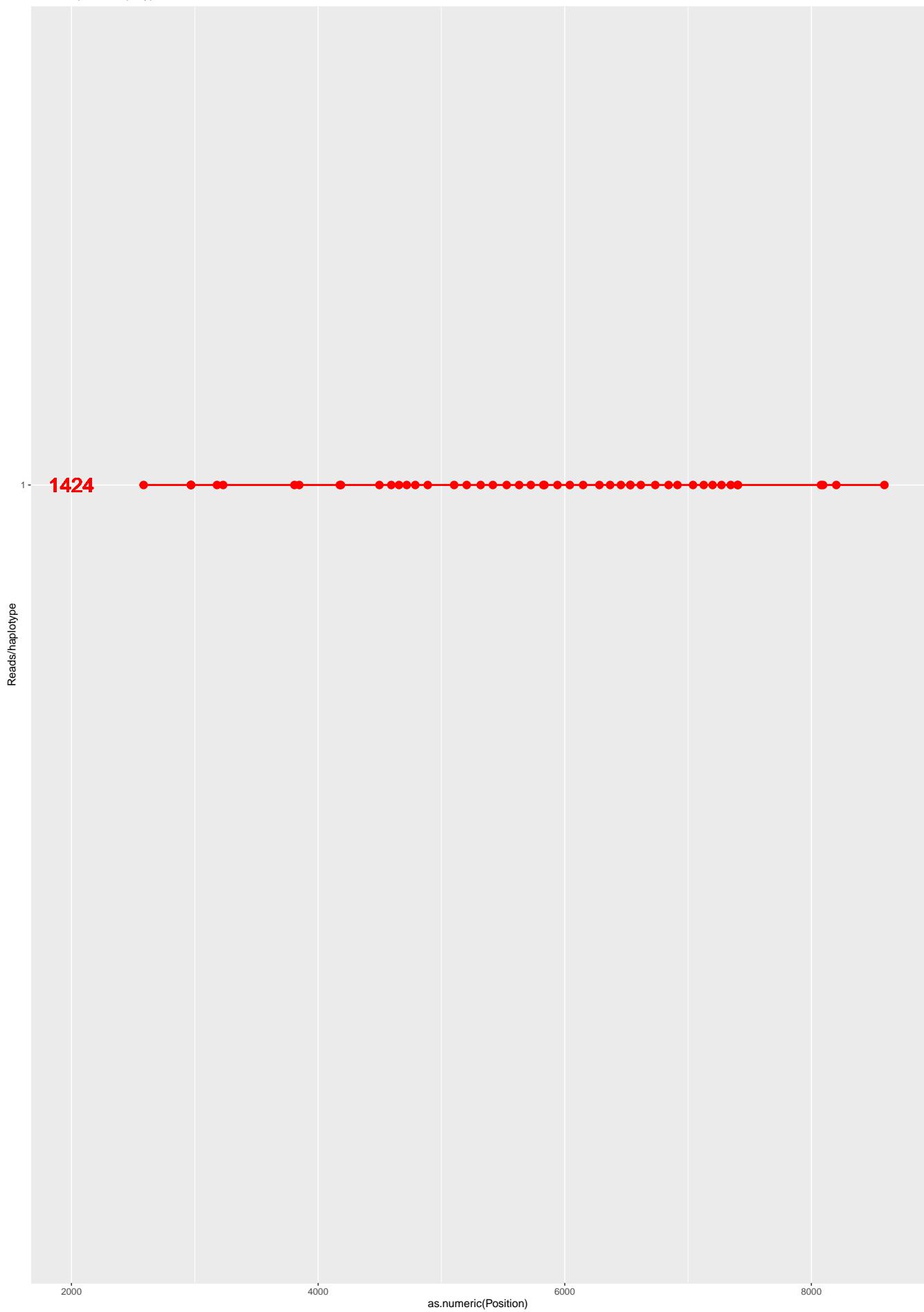
barcode = TCATGCACGTCTCGCT & TCATATGTTAGTACTCT

Sample = 37b tetrad = 37 spore = b

Total reads = 1495 PCR=74

haplotypes I began with n[supporting reads] = 1424

most frequent 7 haplotypes.

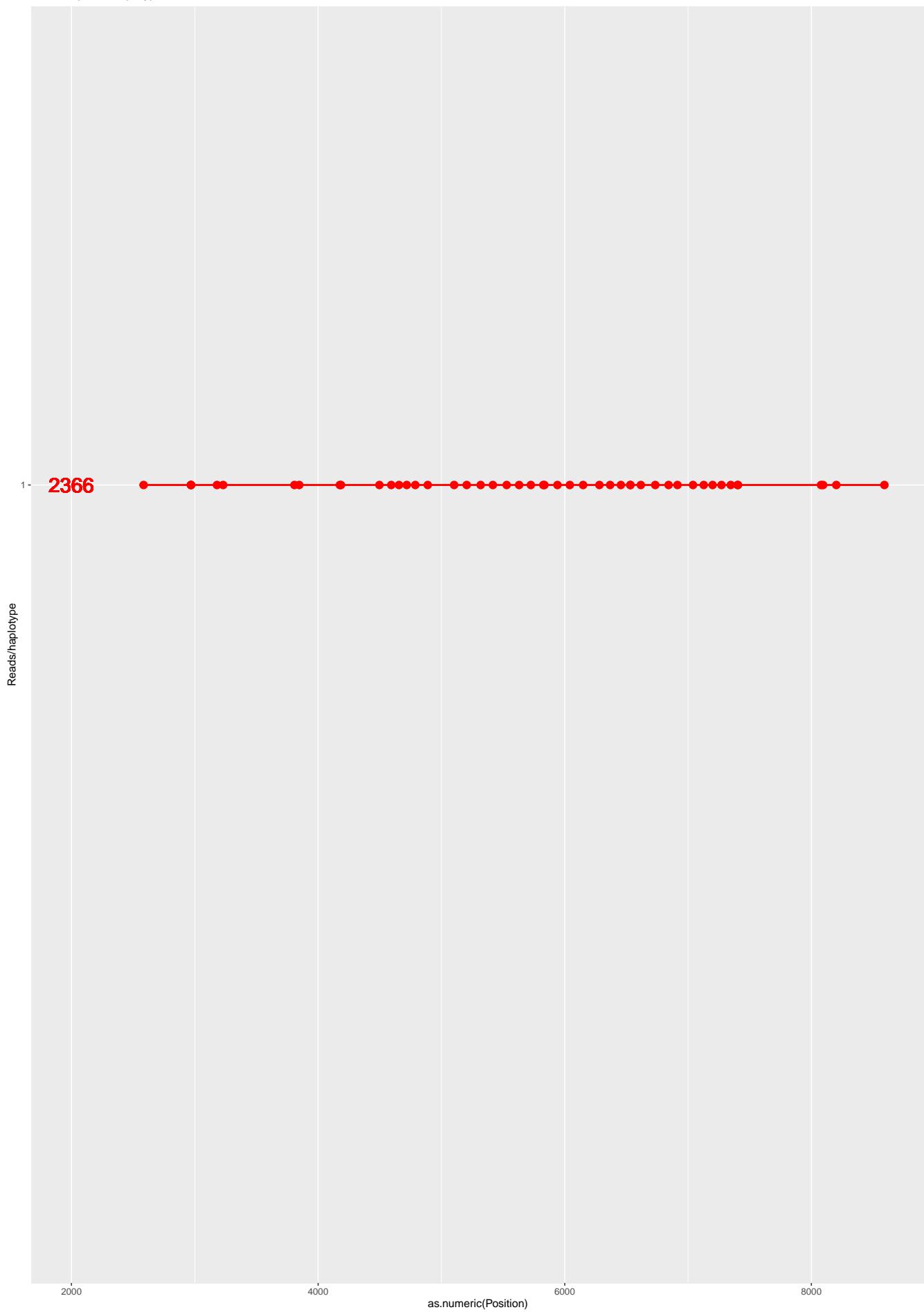


Sample = 37c tetrad = 37 spore = c

Total reads = 2473 PCR=75

haplotypes I began with n[supporting reads] = 2366

most frequent 7 haplotypes.



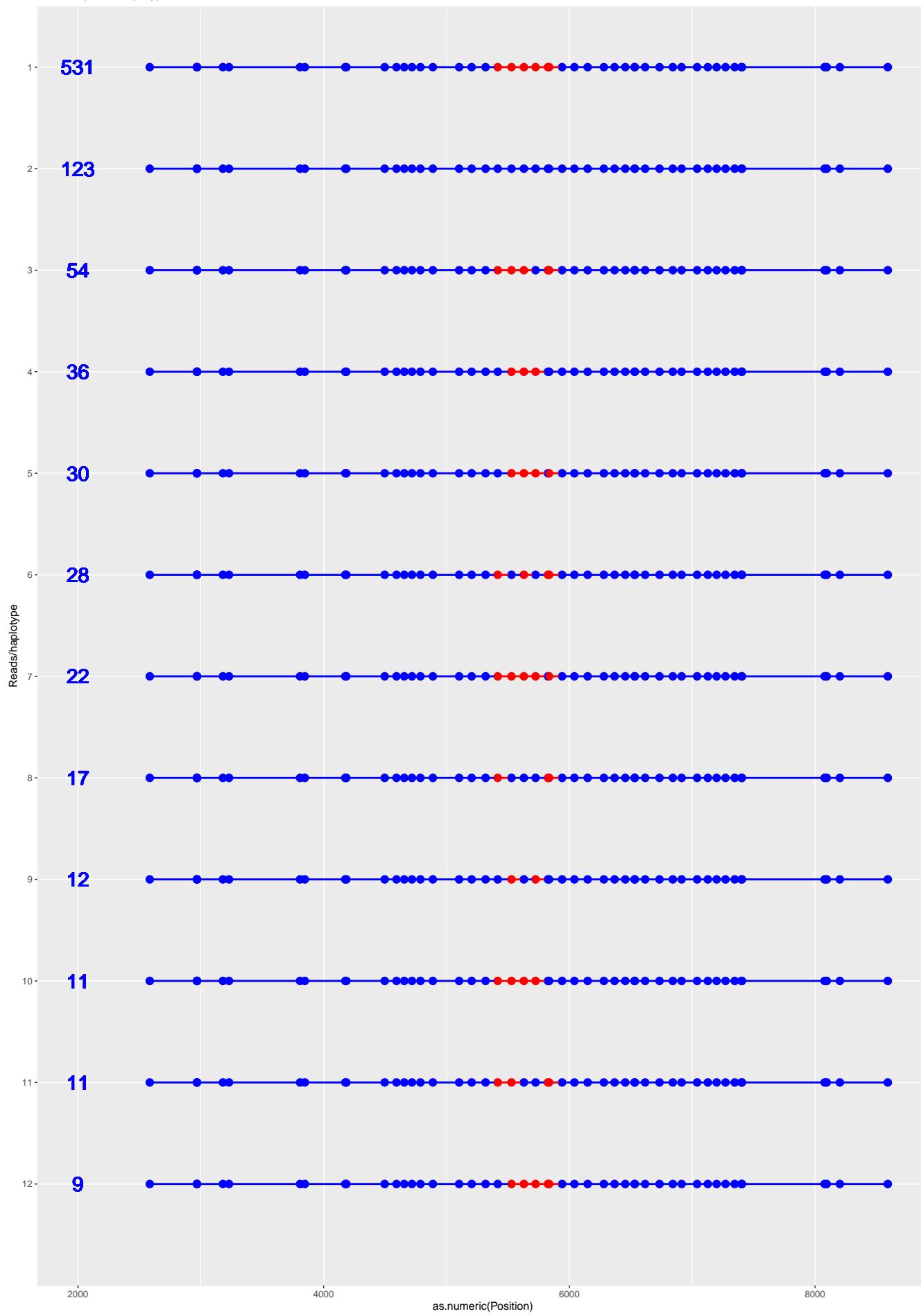
barcode = TCATGCACGTCTCGCT & TGCAGTCGAGATACT

Sample = 37d tetrad = 37 spore = d

Total reads = 1105 PCR=76

haplotypes I began with [n(supporting reads)] = 9, 11, 12, 17, 22, 28, 30, 36, 54, 123, 531

most frequent 7 haplotypes.

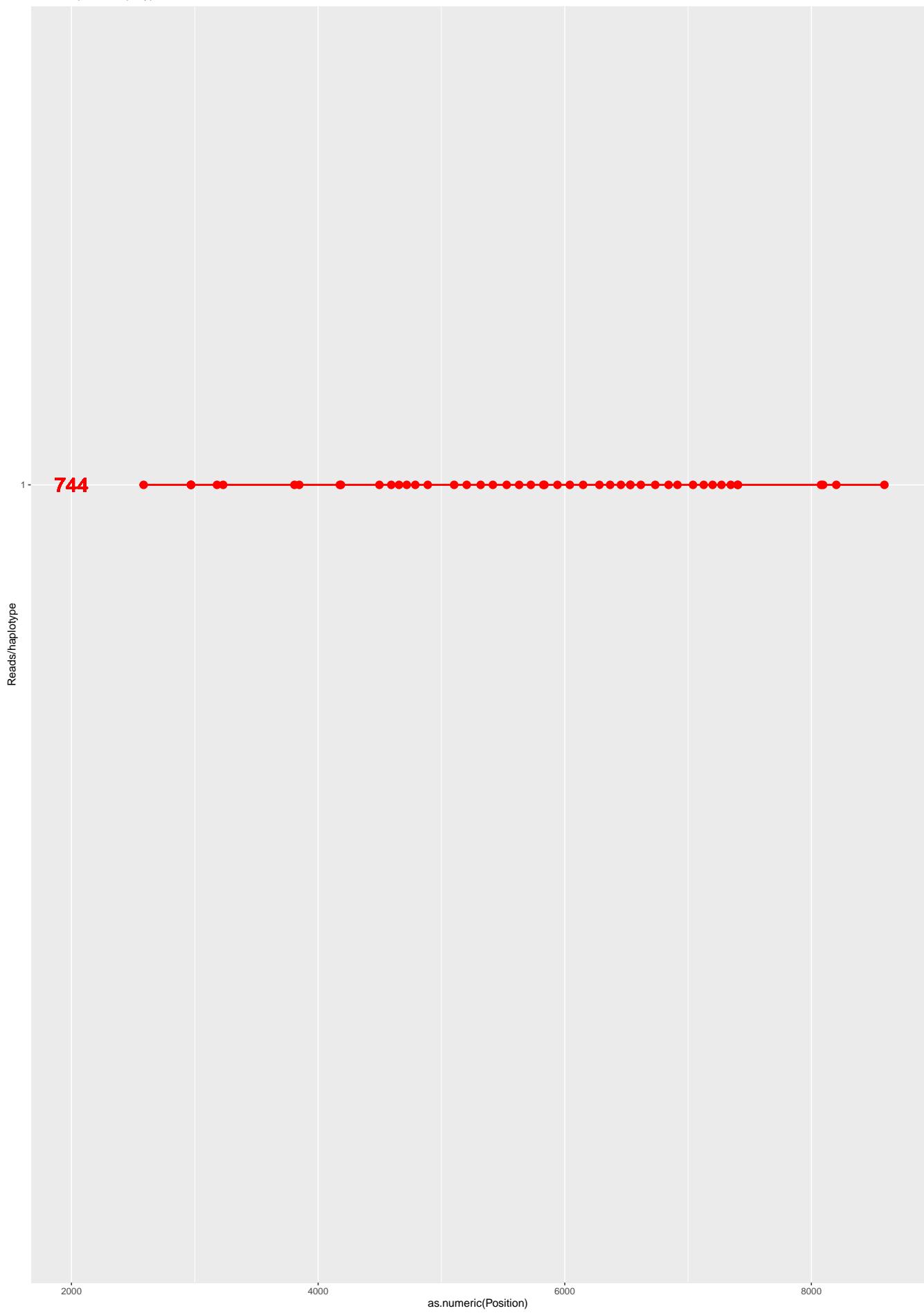


Sample = 39a tetrad = 39 spore = a

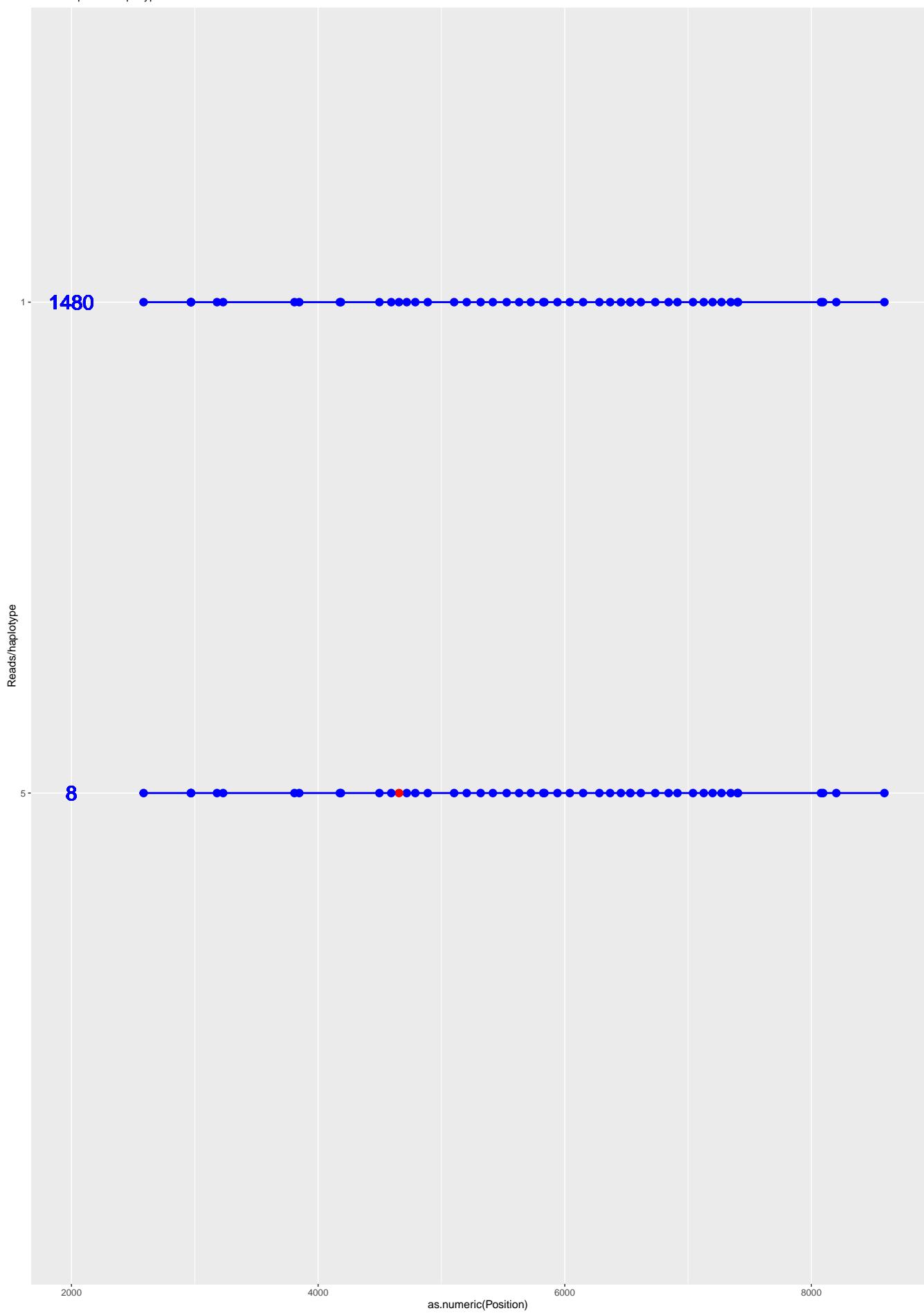
Total reads = 777 PCR=77

haplotypes I began with n[supporting reads] = 744

most frequent 7 haplotypes.



Sample = 39b tetrad = 39 spore = b
Total reads = 1724 PCR=78
haplotypes I began with n[supporting reads] = 8, 1480
most frequent 7 haplotypes.



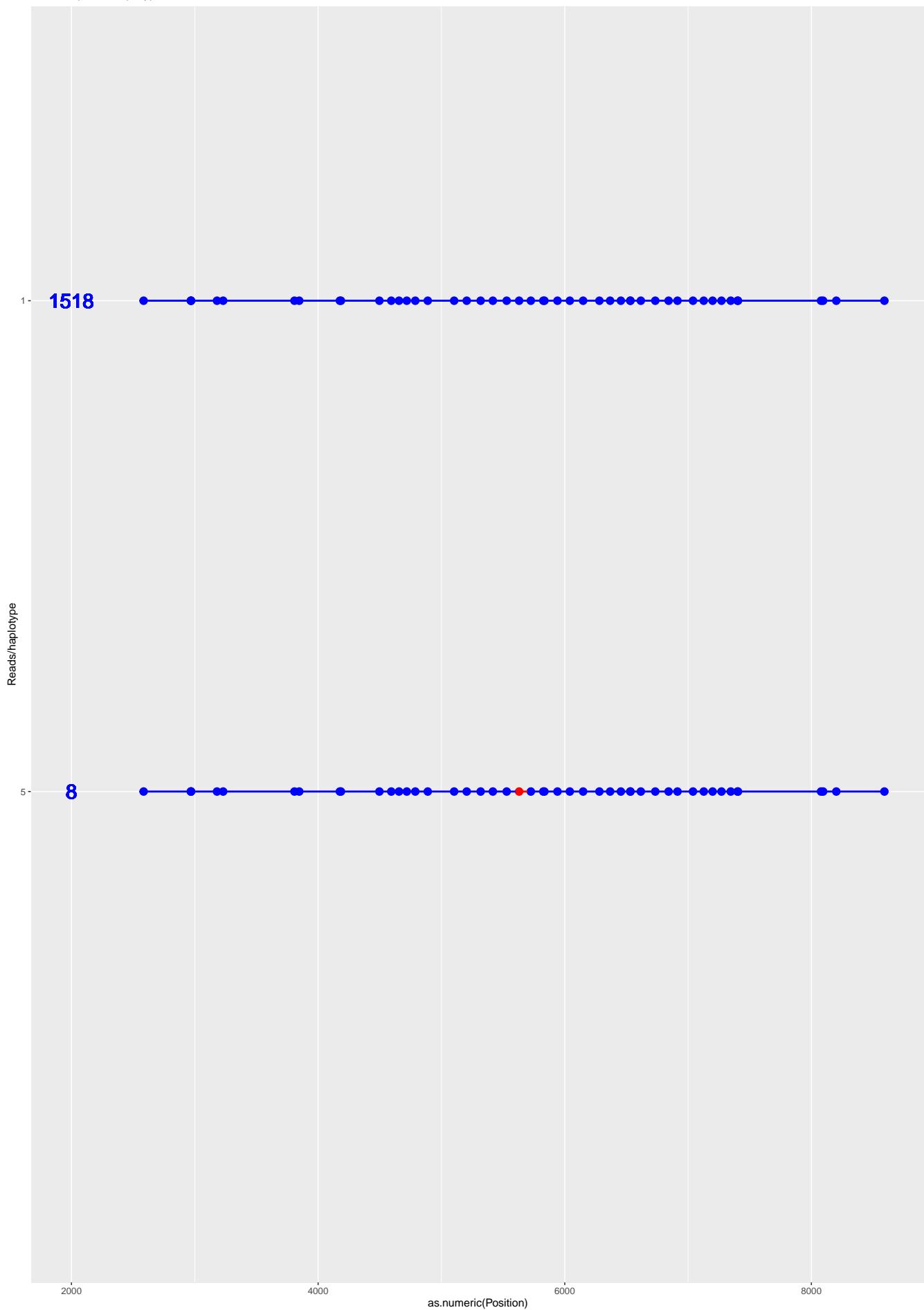
barcode = TCATGCACGTCTCGCT & GCGCAGACTACGTGTC

Sample = 39c tetrad = 39 spore = c

Total reads = 1724 PCR=79

haplotypes I began with n[supporting reads] = 8, 1518

most frequent 7 haplotypes.



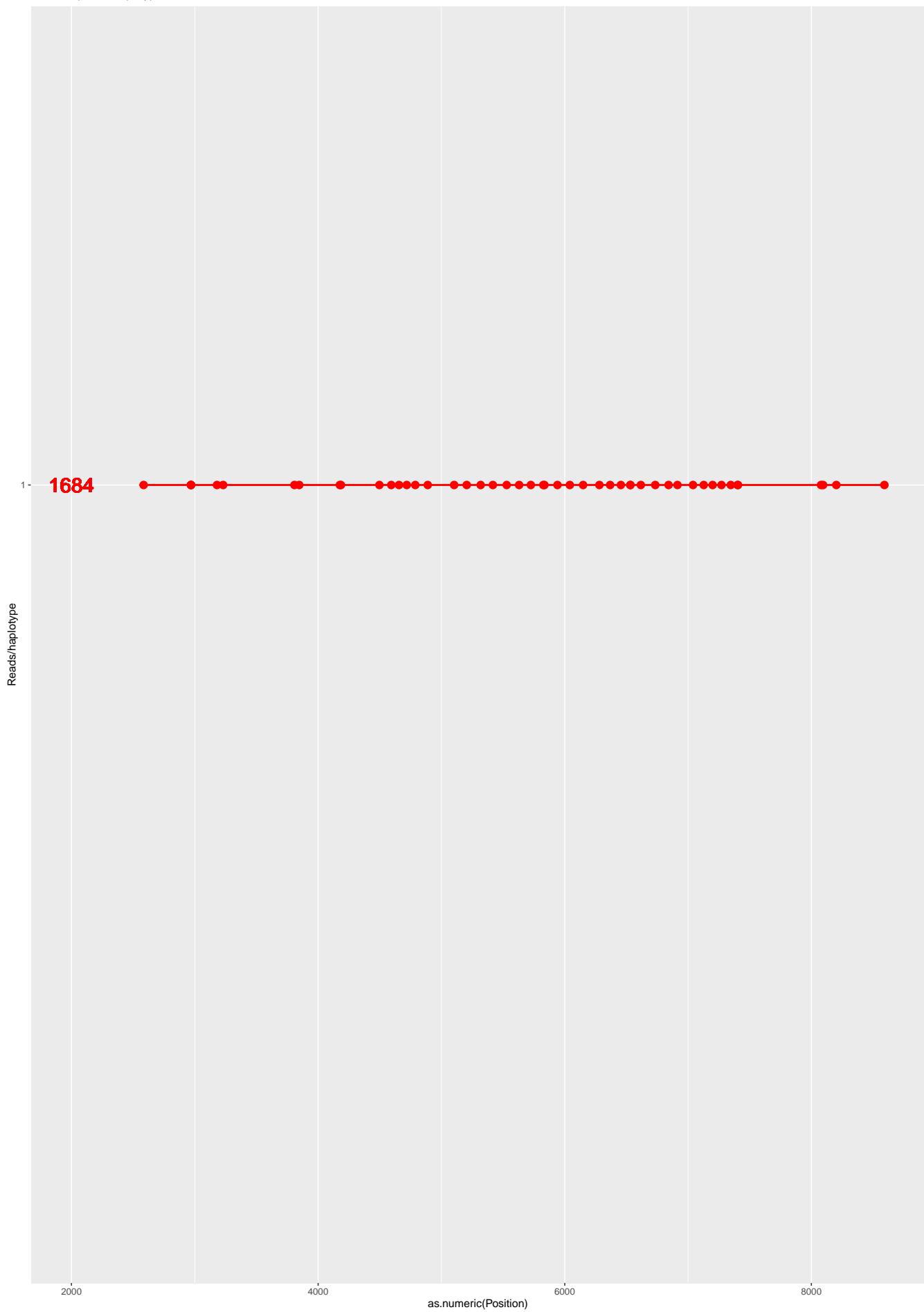
barcode = TCATGCACGTCTCGCT & GTCTCTGCGATAACAGC

Sample = 39d tetrad = 39 spore = d

Total reads = 1768 PCR=80

haplotypes I began with n[supporting reads] = 1684

most frequent 7 haplotypes.



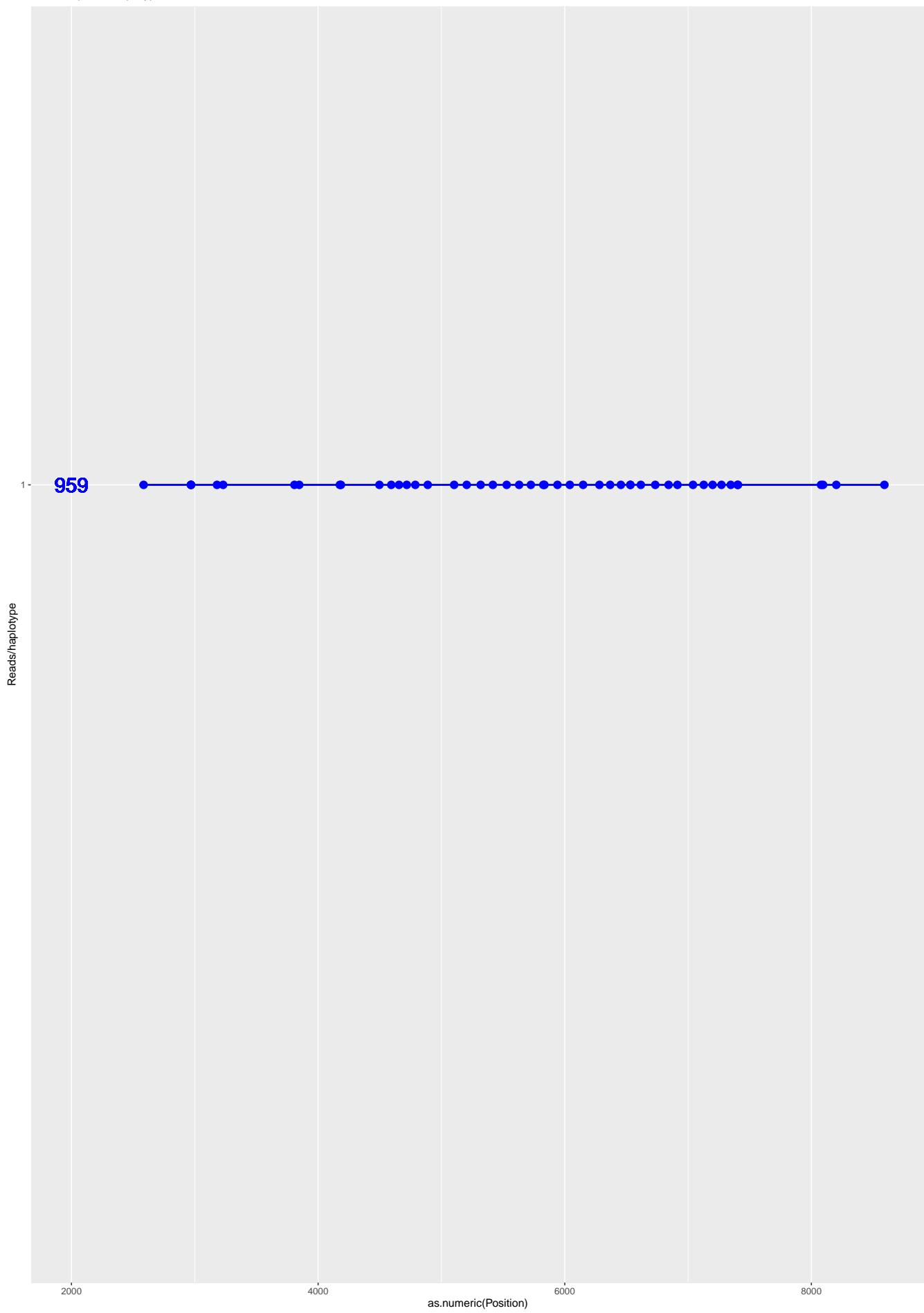
barcode = TCATGCACGTCTCGCT & AGTATGAGATAGCTCG

Sample = 40a tetrad = 40 spore = a

Total reads = 1123 PCR=81

haplotypes I began with n[supporting reads] = 959

most frequent 7 haplotypes.



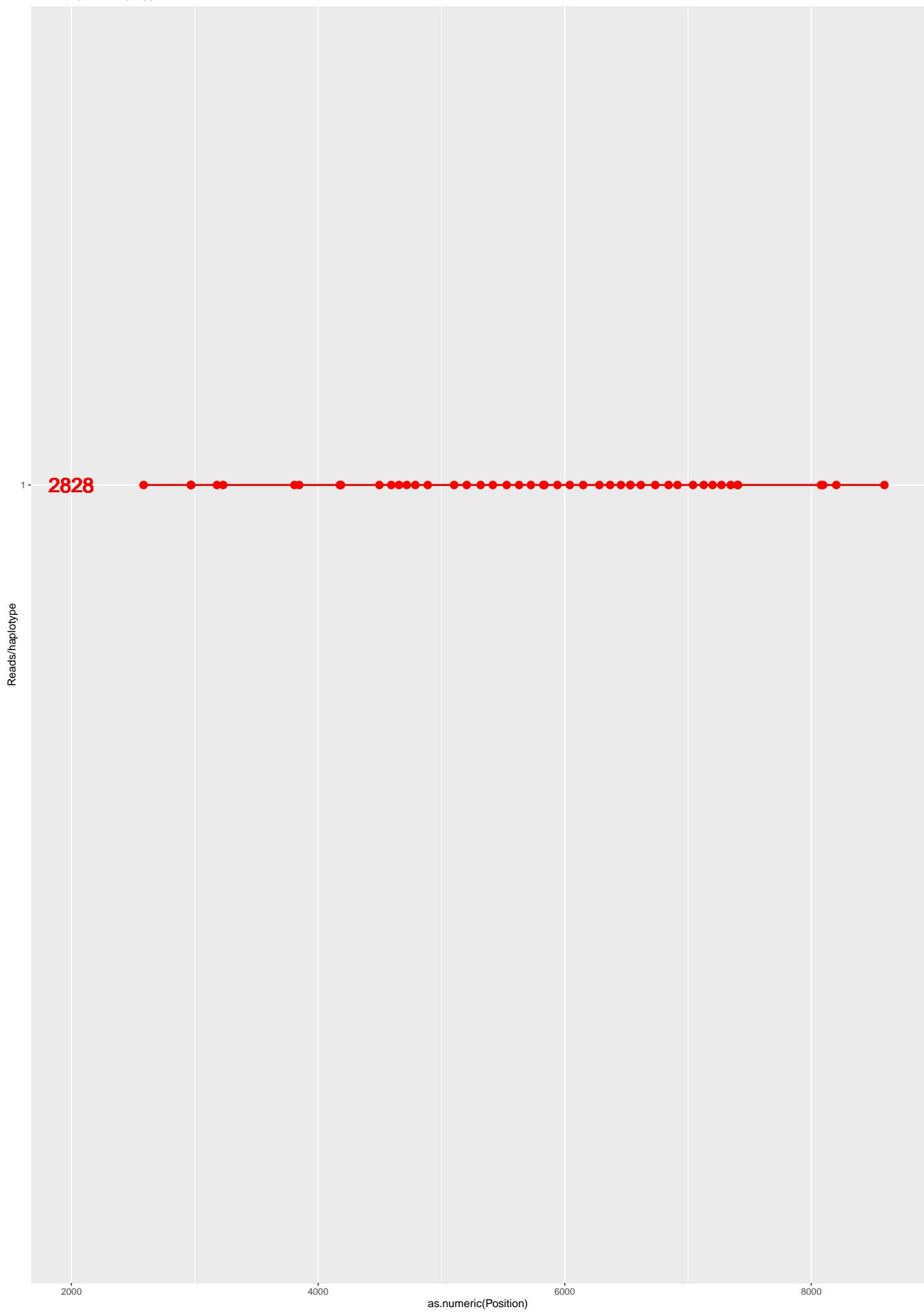
barcode = AGAGCATCTCTGTACT & TCATATGTTAGTACTCT

Sample = 40b tetrad = 40 spore = b

Total reads =2957 PCR=82

haplotypes I began with n[supporting reads] = 2828

most frequent 7 haplotypes.



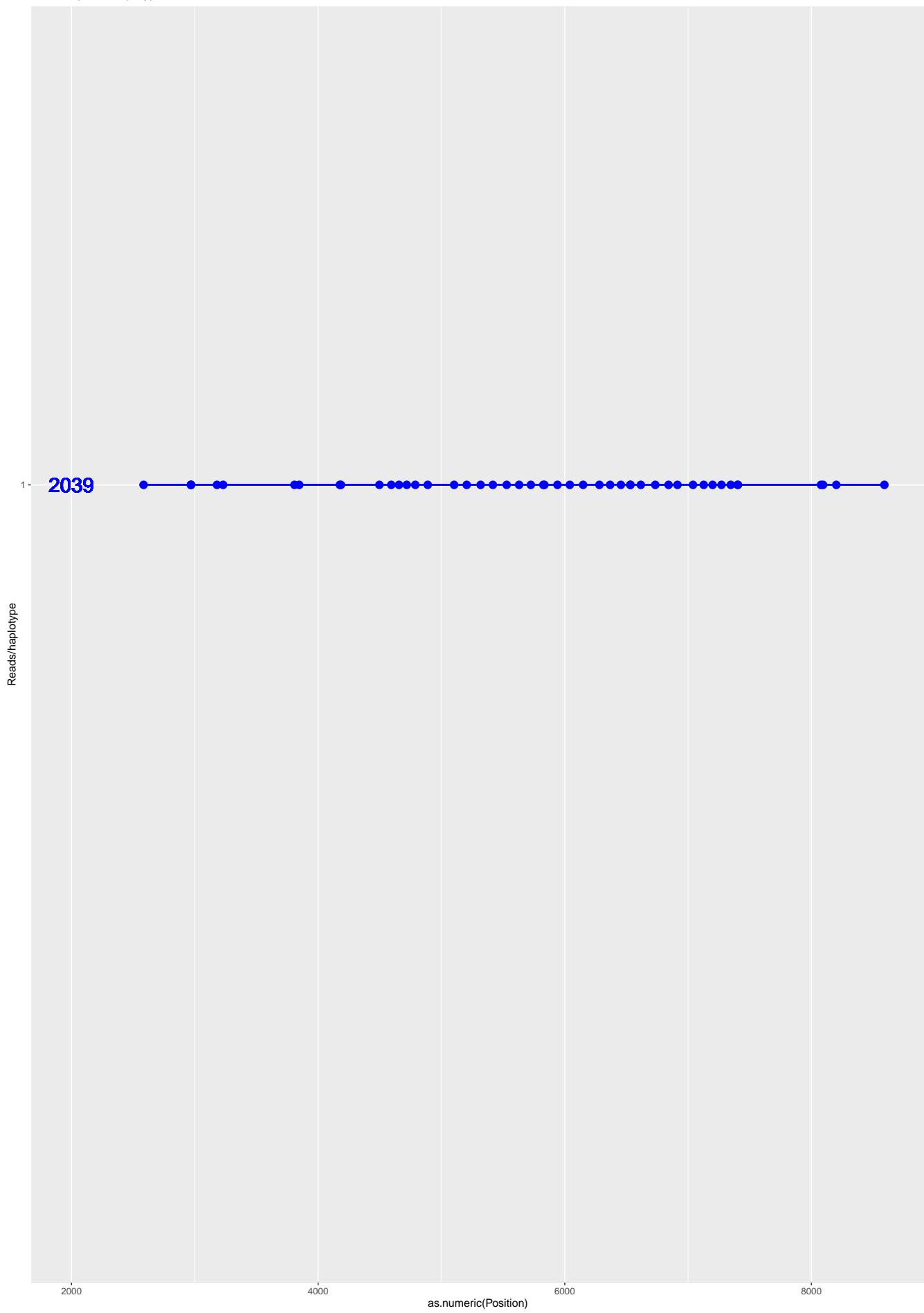
barcode = AGAGCATCTCTGTACT & GCGATCTATGCACACG

Sample = 40c tetrad = 40 spore = c

Total reads = 2329 PCR=83

haplotypes I began with n[supporting reads] = 2039

most frequent 7 haplotypes.



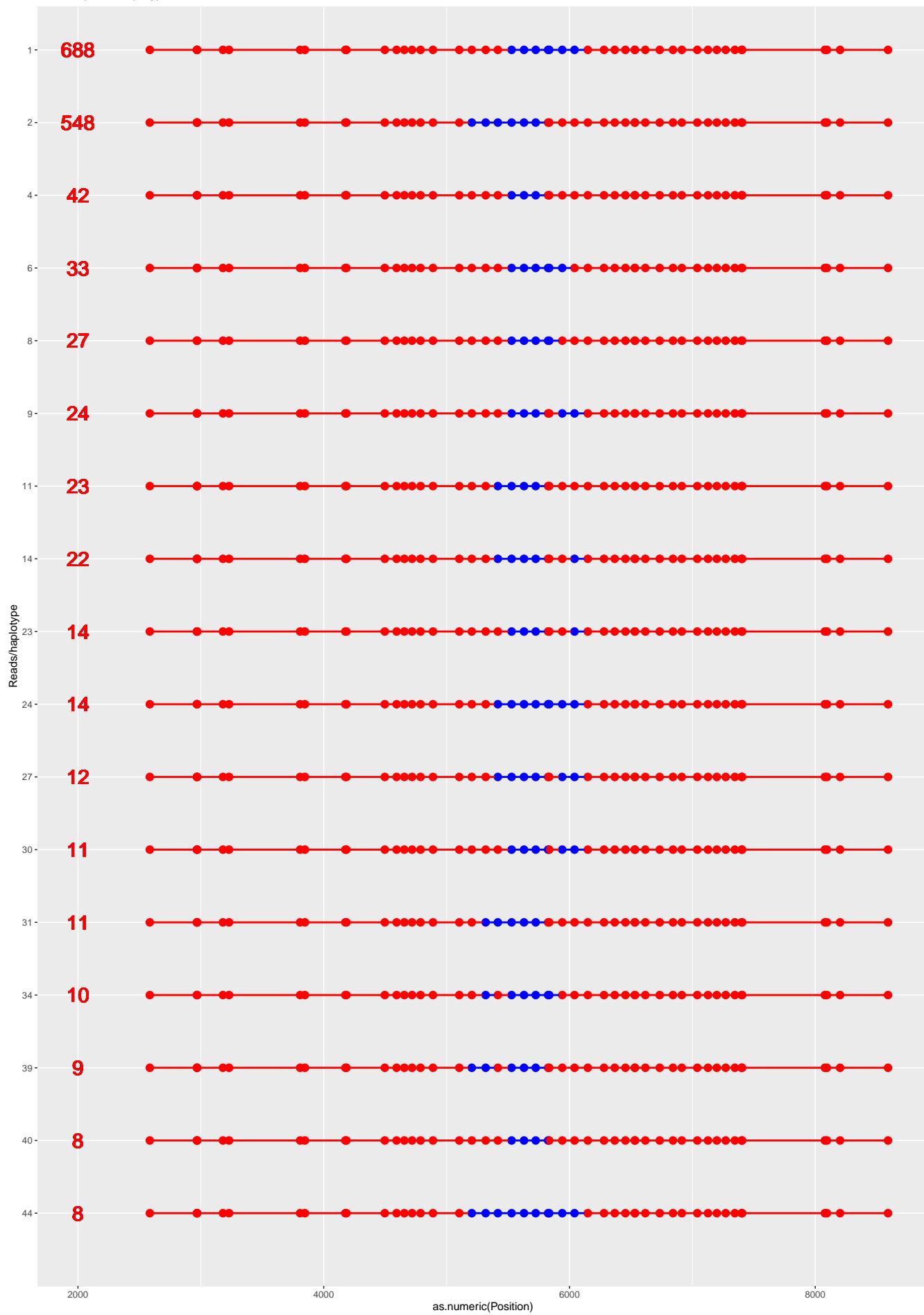
barcode = AGAGCATCTCTGACT & TGCAGTCGAGATACT

Sample = 40d tetrad = 40 spore = d

Total reads = 2427 PCR=84

haplotypes I began with [n(supporting reads)] = 8, 9, 10, 11, 12, 14, 22, 23, 24, 27, 33, 42, 548, 688

most frequent 7 haplotypes.

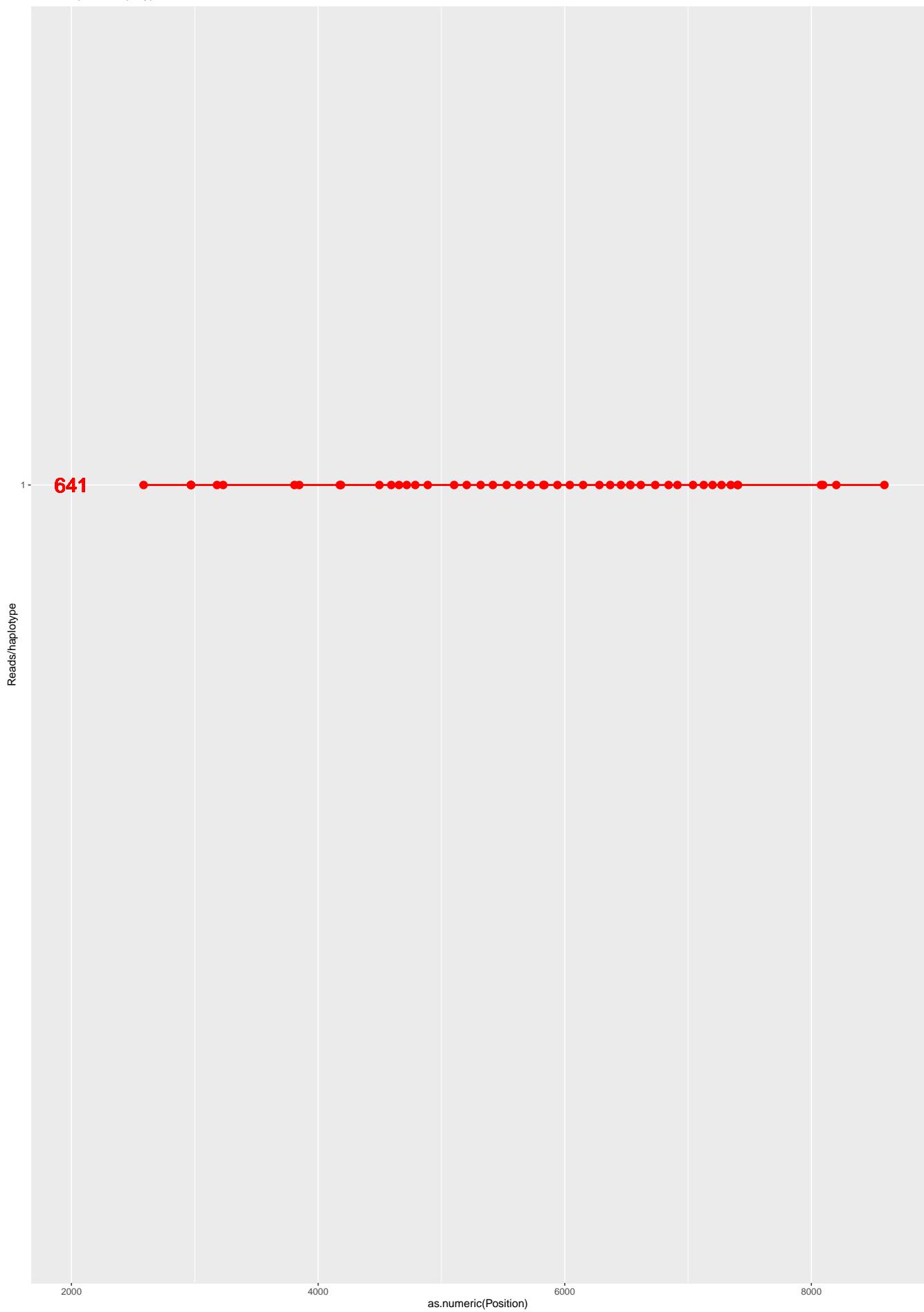


Sample = 42a tetrad = 42 spore = a

Total reads = 661 PCR=89

haplotypes I began with n[supporting reads] = 641

most frequent 7 haplotypes.



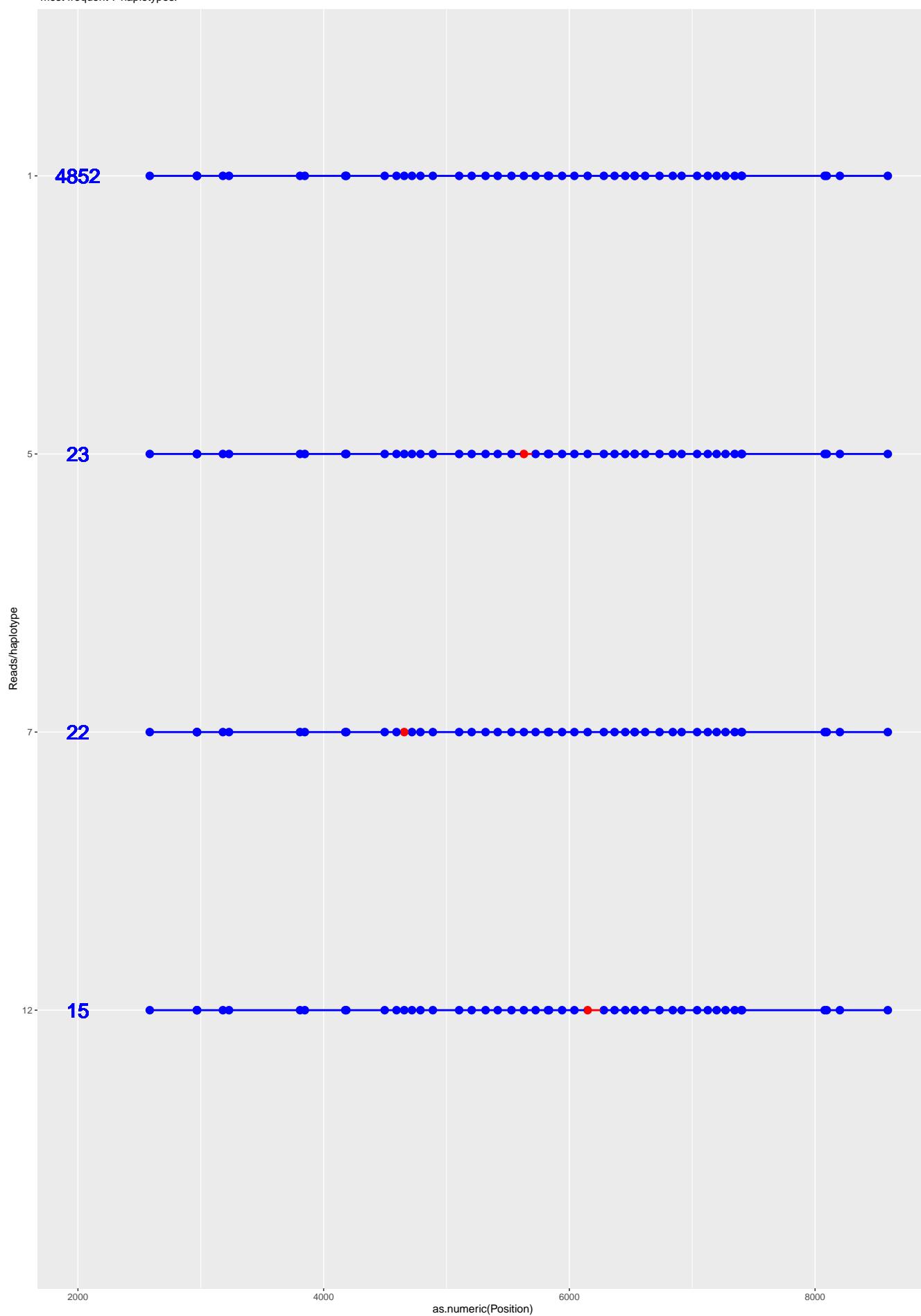
barcode = CGCATCGACTACGCTA & TCATATGTAGTACTCT

Sample = 42b tetrad = 42 spore = b

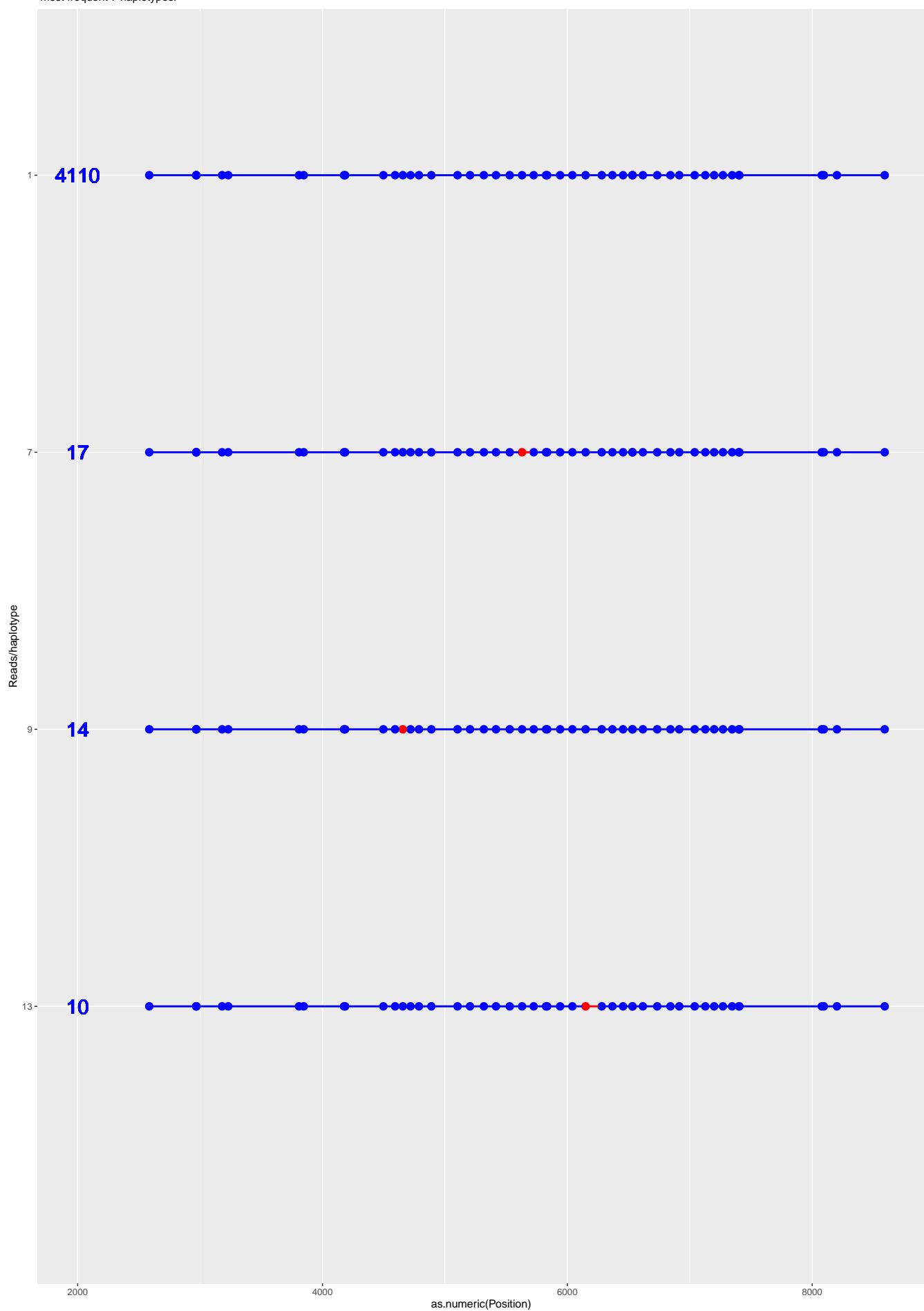
Total reads =5690 PCR=90

haplotypes I began with [n[supporting reads]] = 15, 22, 23, 4852

most frequent 7 haplotypes.



Sample = 42c tetrad = 42 spore = c
Total reads = 4817 PCR=91
haplotypes I began with [n[supporting reads]] = 10, 14, 17, 4110
most frequent 7 haplotypes.

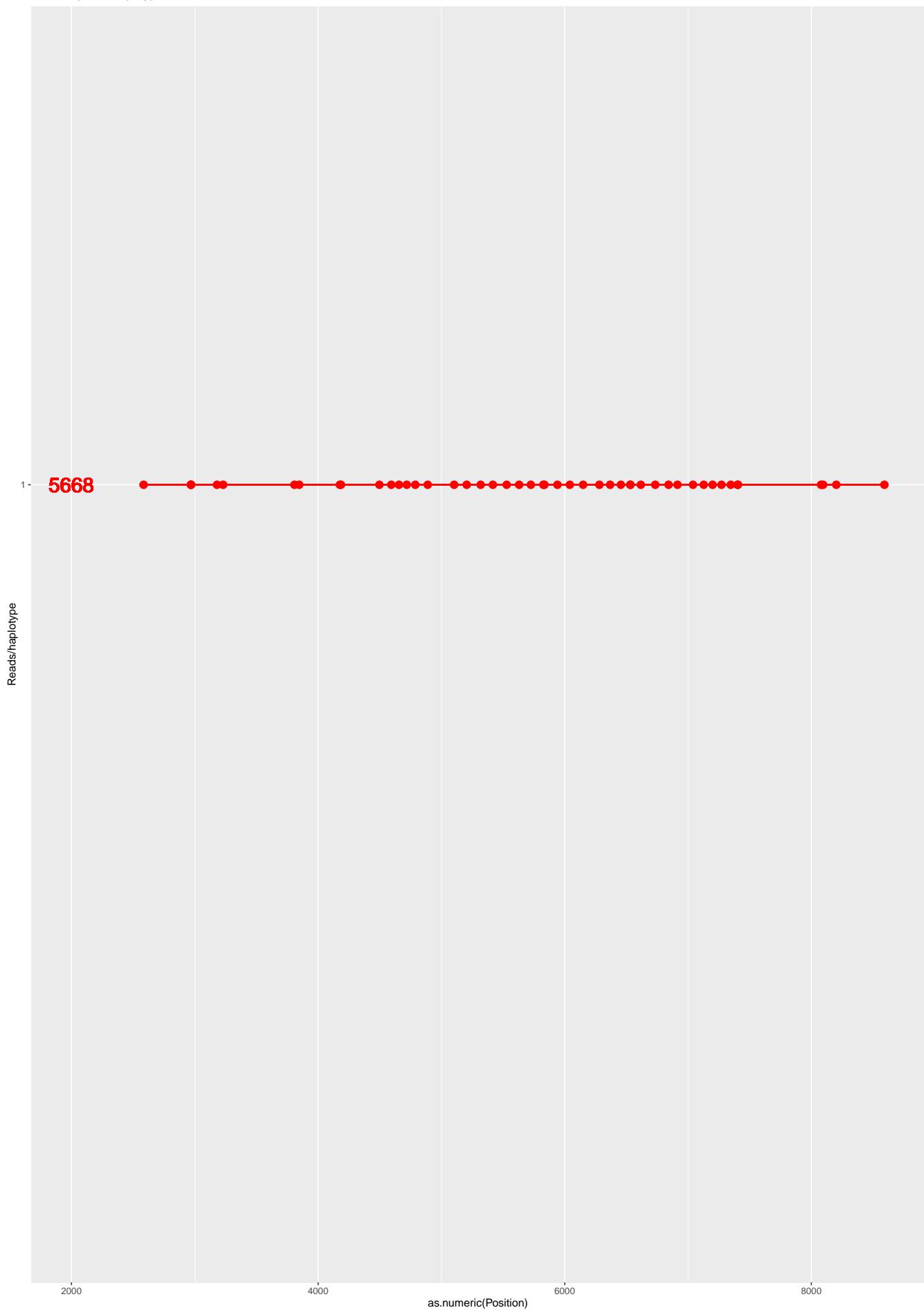


Sample = 42d tetrad = 42 spore = d

Total reads = 5916 PCR=92

haplotypes I began with n[supporting reads] = 5668

most frequent 7 haplotypes.



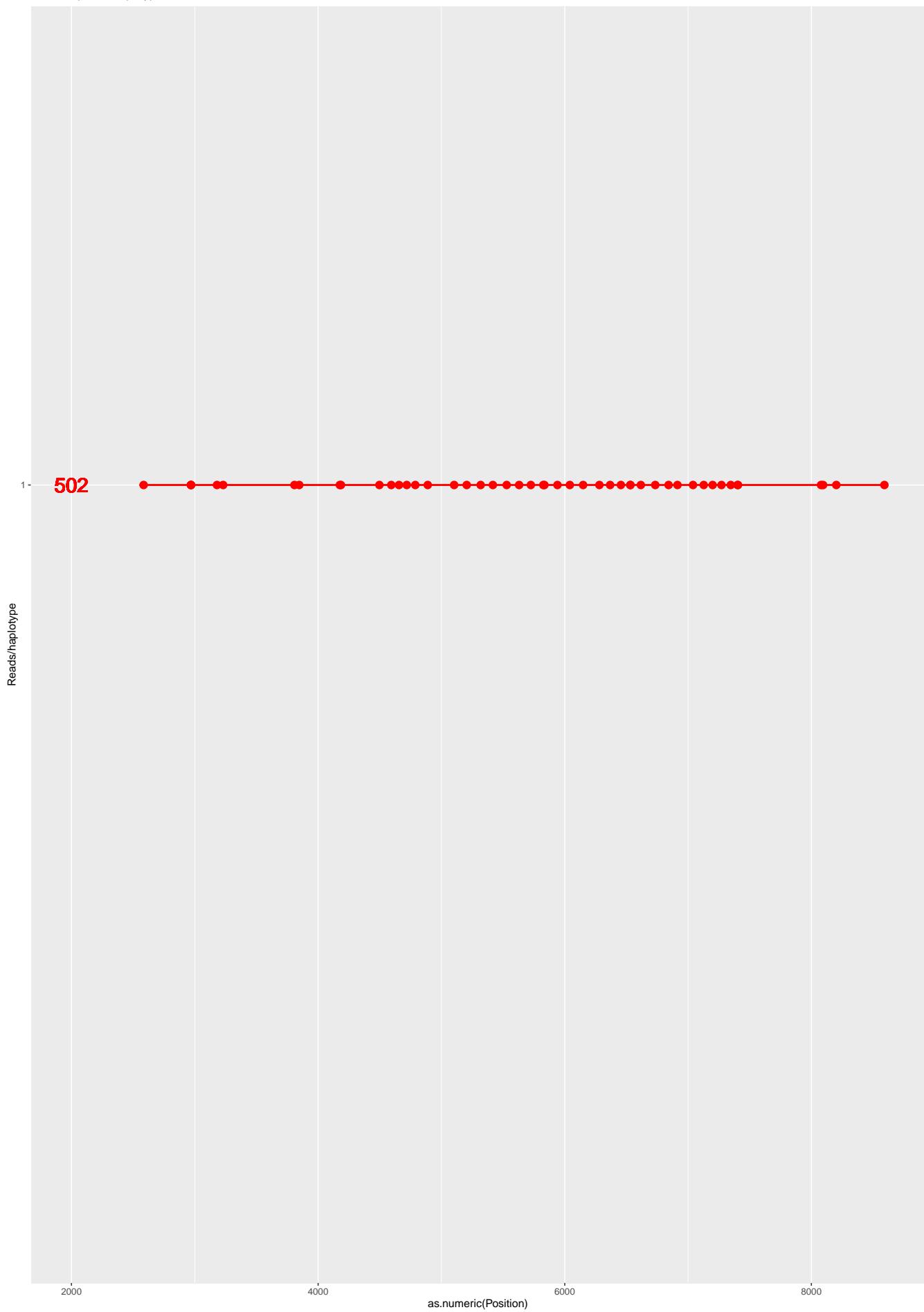
barcode = CGCATCGACTACGCTA & GACTCTGCGTCGAGTC

Sample = 47a tetrad = 47 spore = a

Total reads =528 PCR=101

haplotypes I began with n[supporting reads] = 502

most frequent 7 haplotypes.



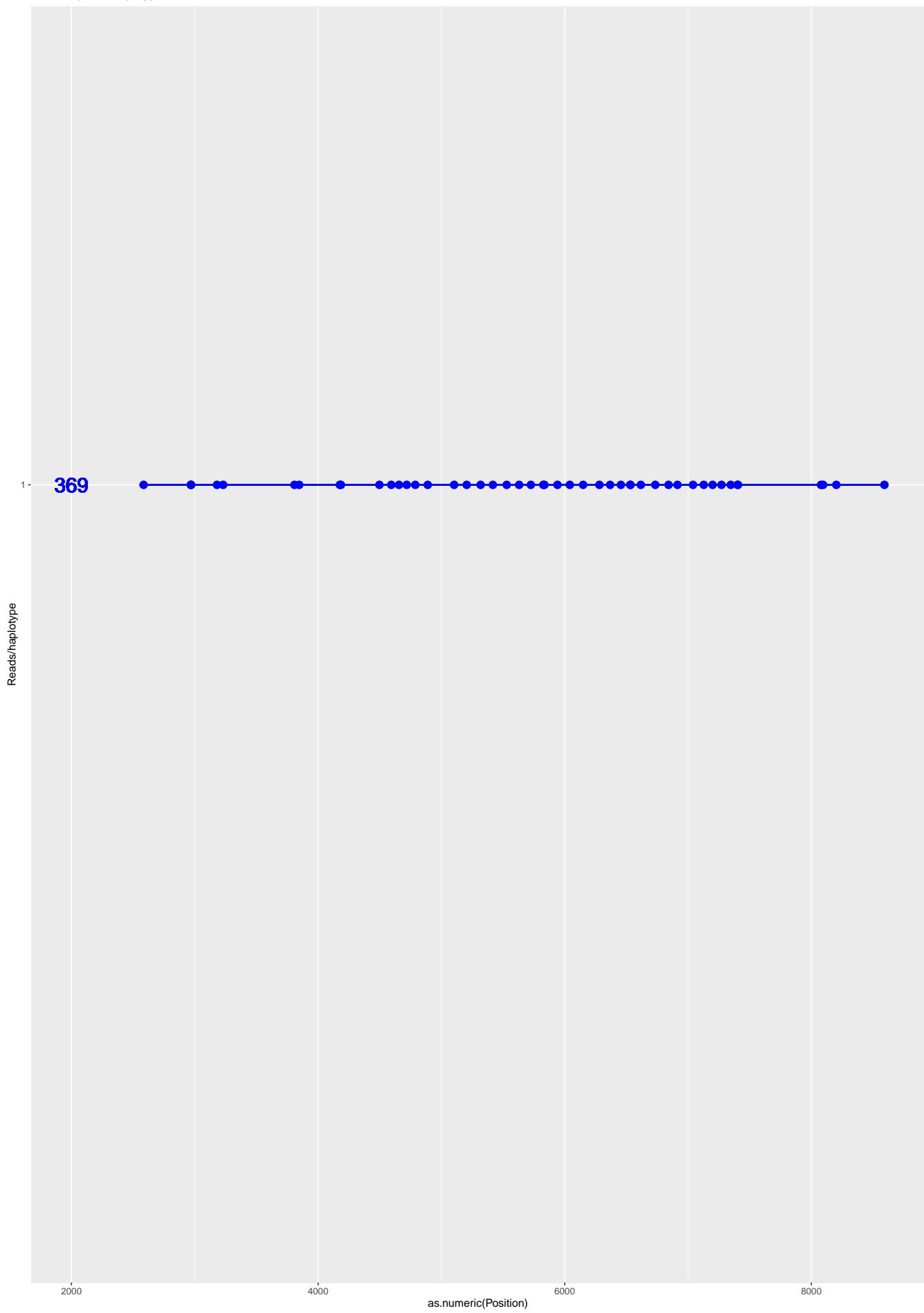
barcode = CGTAGCGTGCTATCAC & TACAGCGACGTCATCG

Sample = 47b tetrad = 47 spore = b

Total reads = 414 PCR=102

haplotypes I began with n[supporting reads] = 369

most frequent 7 haplotypes.



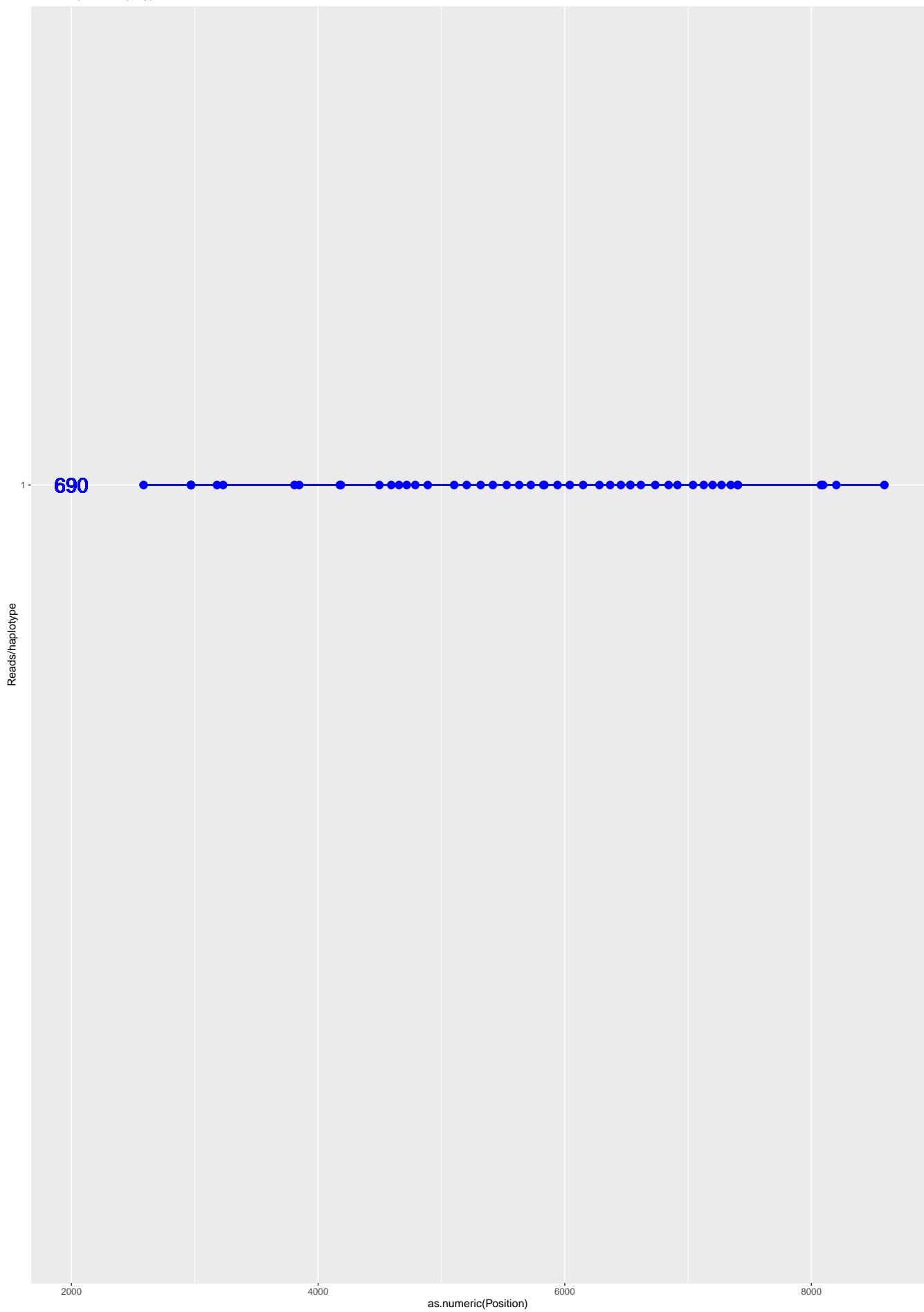
barcode = CGTAGCGTGCTATCAC & GCGCAGACTACGTGTC

Sample = 47c tetrad = 47 spore = c

Total reads = 810 PCR=103

haplotypes I began with n[supporting reads] = 690

most frequent 7 haplotypes.



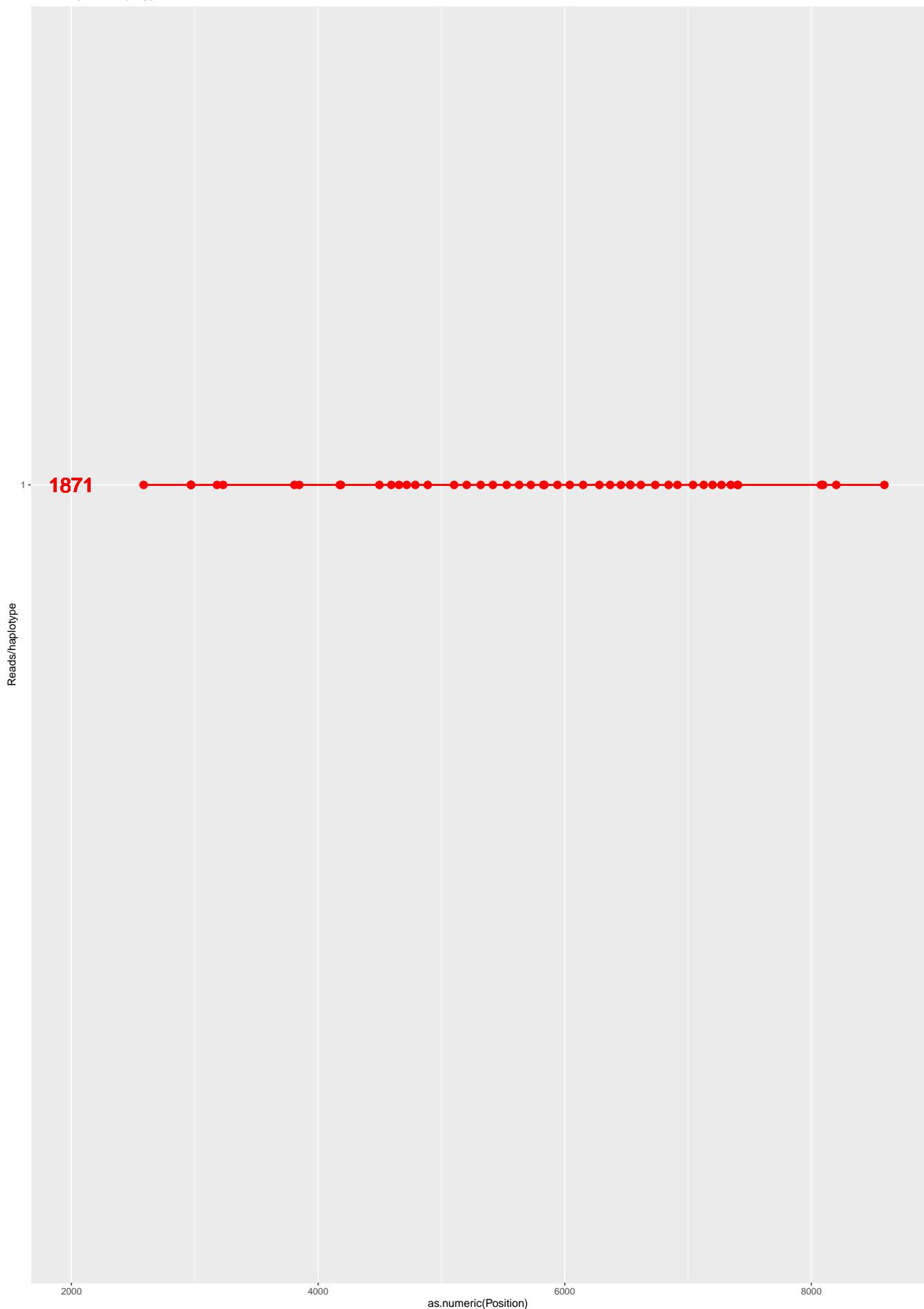
barcode = CGTAGCGTGCTATCAC & GTCTCTGCGATAACAGC

Sample = 47d tetrad = 47 spore = d

Total reads = 1963 PCR=104

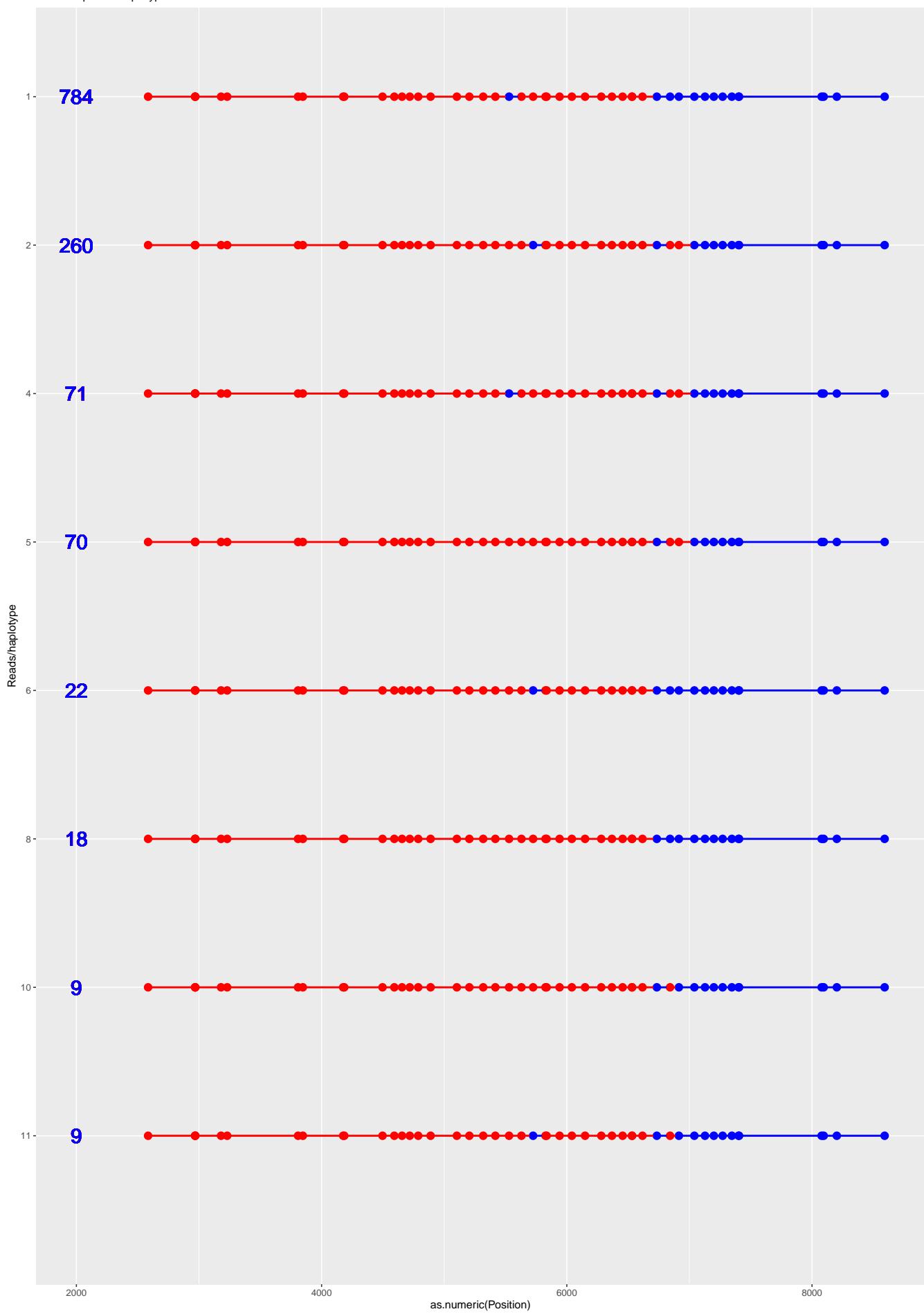
haplotypes I began with n[supporting reads] = 1871

most frequent 7 haplotypes.



barcode = CGTAGCGTGCTATCAC & AGTATGAGATAGCTCG

Sample = 49a tetrad = 49 spore = a
Total reads = 1504 PCR=109
haplotypes I began with [n(supporting reads)] = 9, 18, 22, 70, 71, 260, 784
most frequent 7 haplotypes.

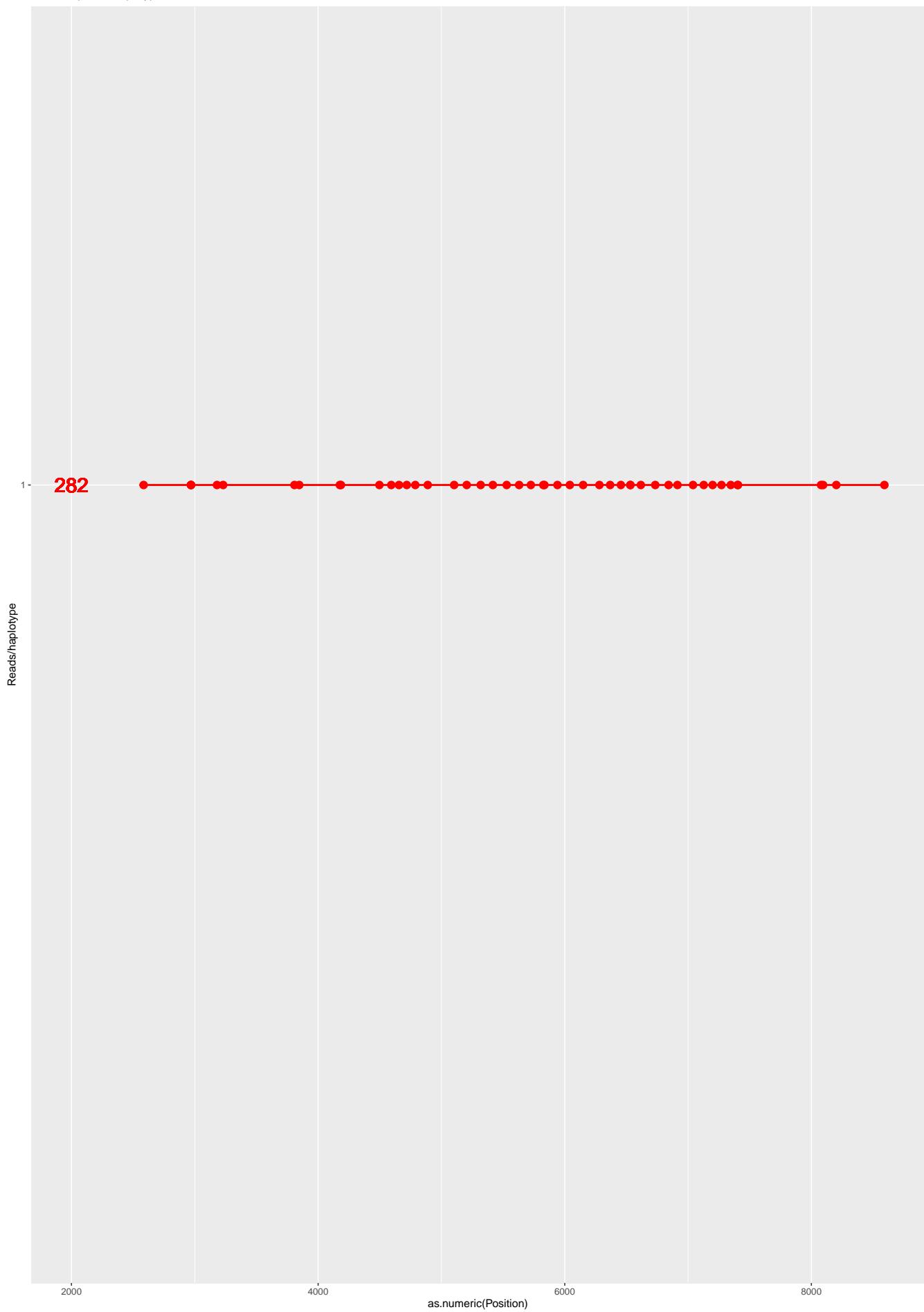


Sample = 49b tetrad = 49 spore = b

Total reads =293 PCR=110

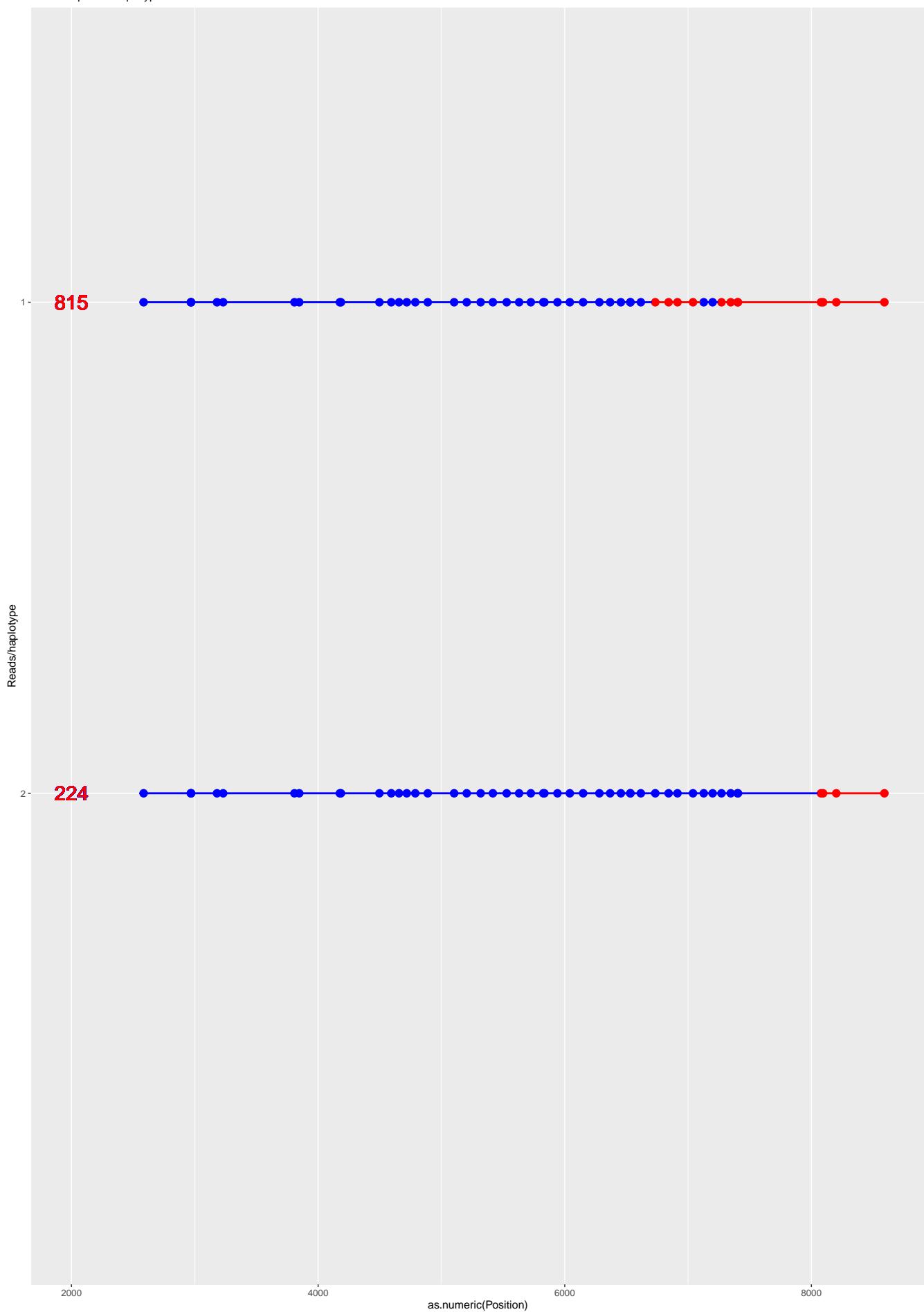
haplotypes I began with n[supporting reads] = 282

most frequent 7 haplotypes.

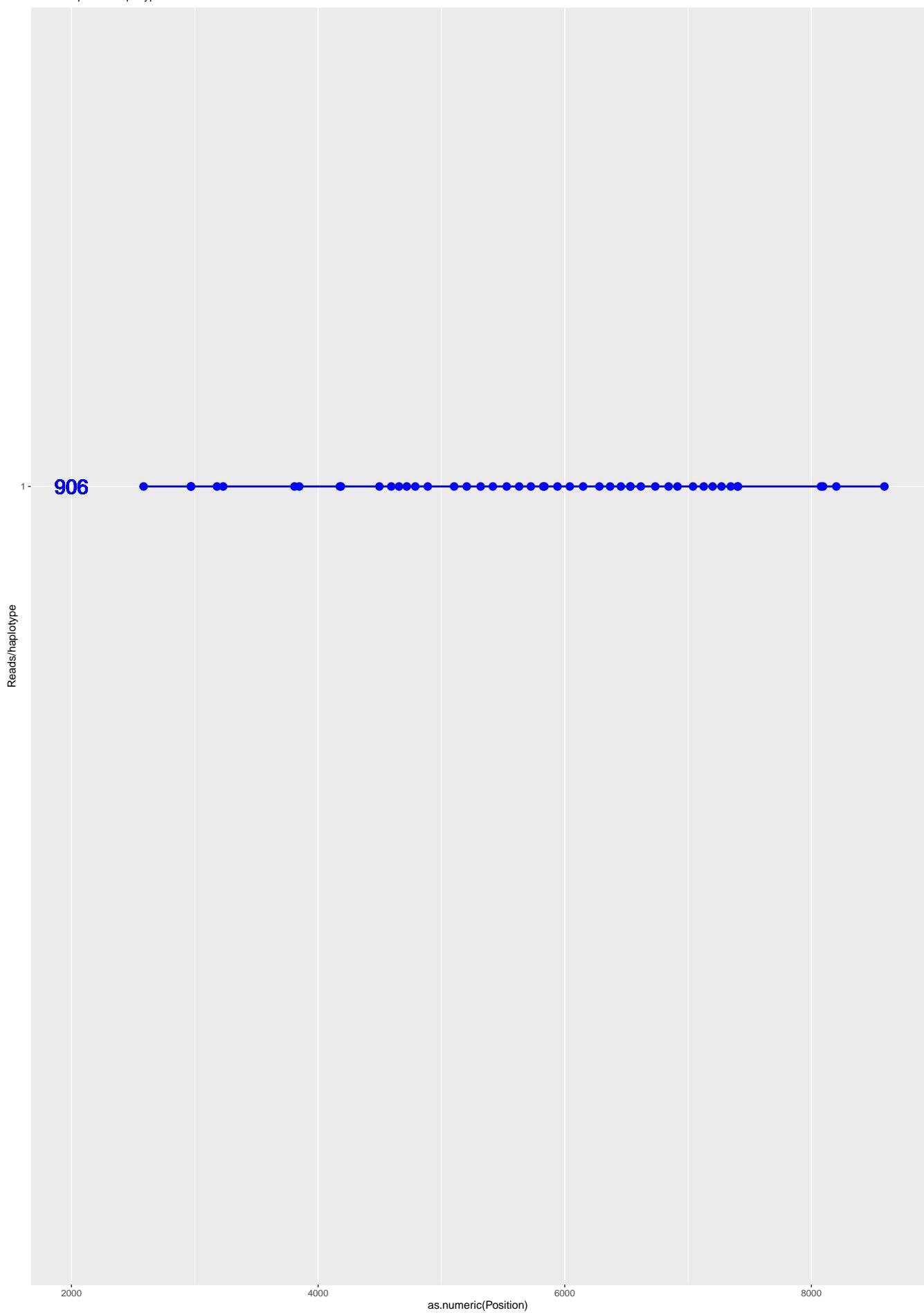


barcode = ATGCTGATGACTGCGA & GCGCAGACTACGTGTG

Sample = 49c tetrad = 49 spore = c
Total reads = 1600 PCR=111
haplotypes I began with n[supporting reads] = 224, 815
most frequent 7 haplotypes.



Sample = 49d tetrad = 49 spore = d
Total reads = 1057 PCR=112
haplotypes I began with n[supporting reads] = 906
most frequent 7 haplotypes.



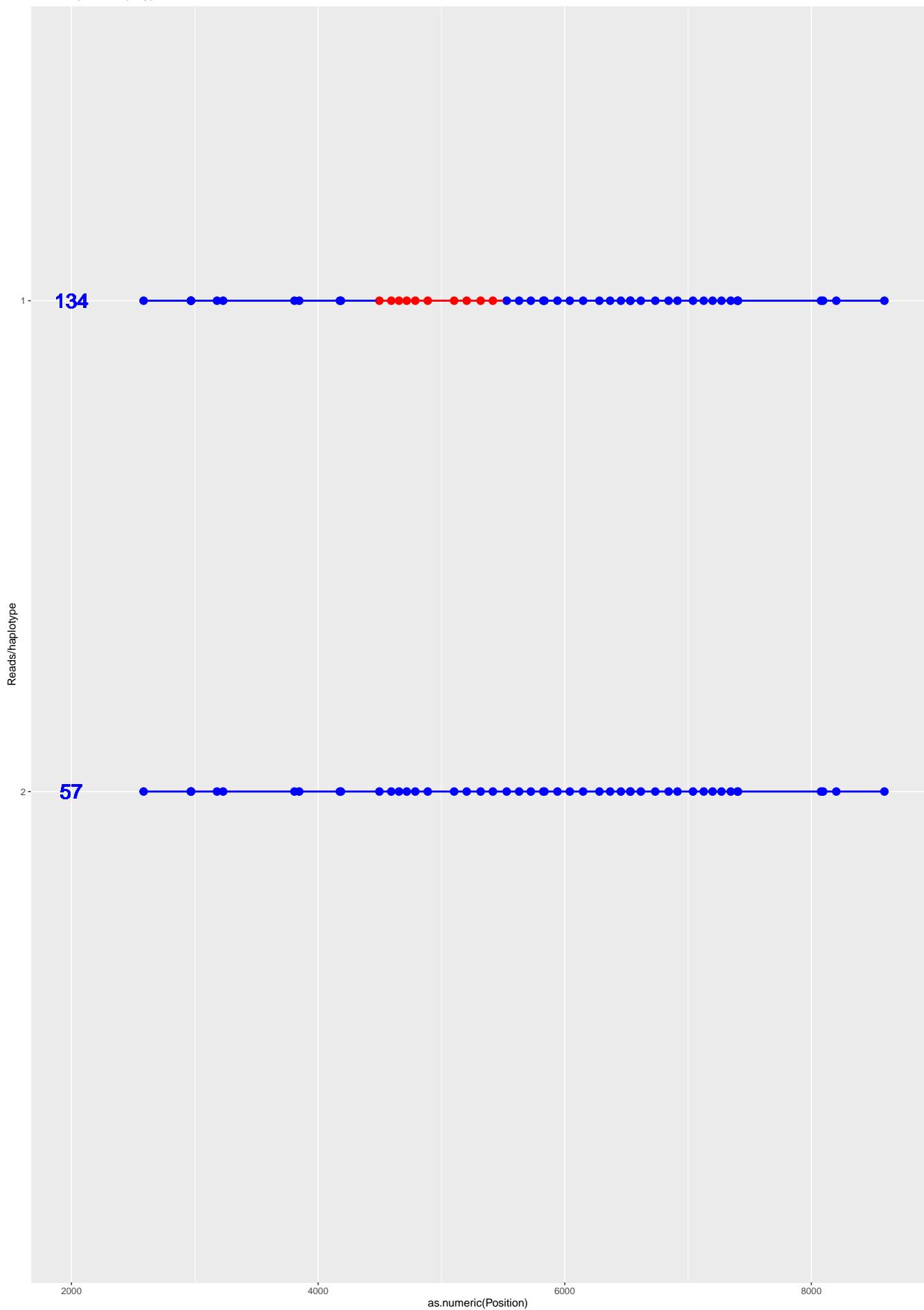
barcode = ATGCTGATGACTGCGA & AGTATGAGATAGCTCG

Sample = 51a tetrad = 51 spore = a

Total reads =378 PCR=117

haplotypes I began with n[supporting reads] = 57, 134

most frequent 7 haplotypes.



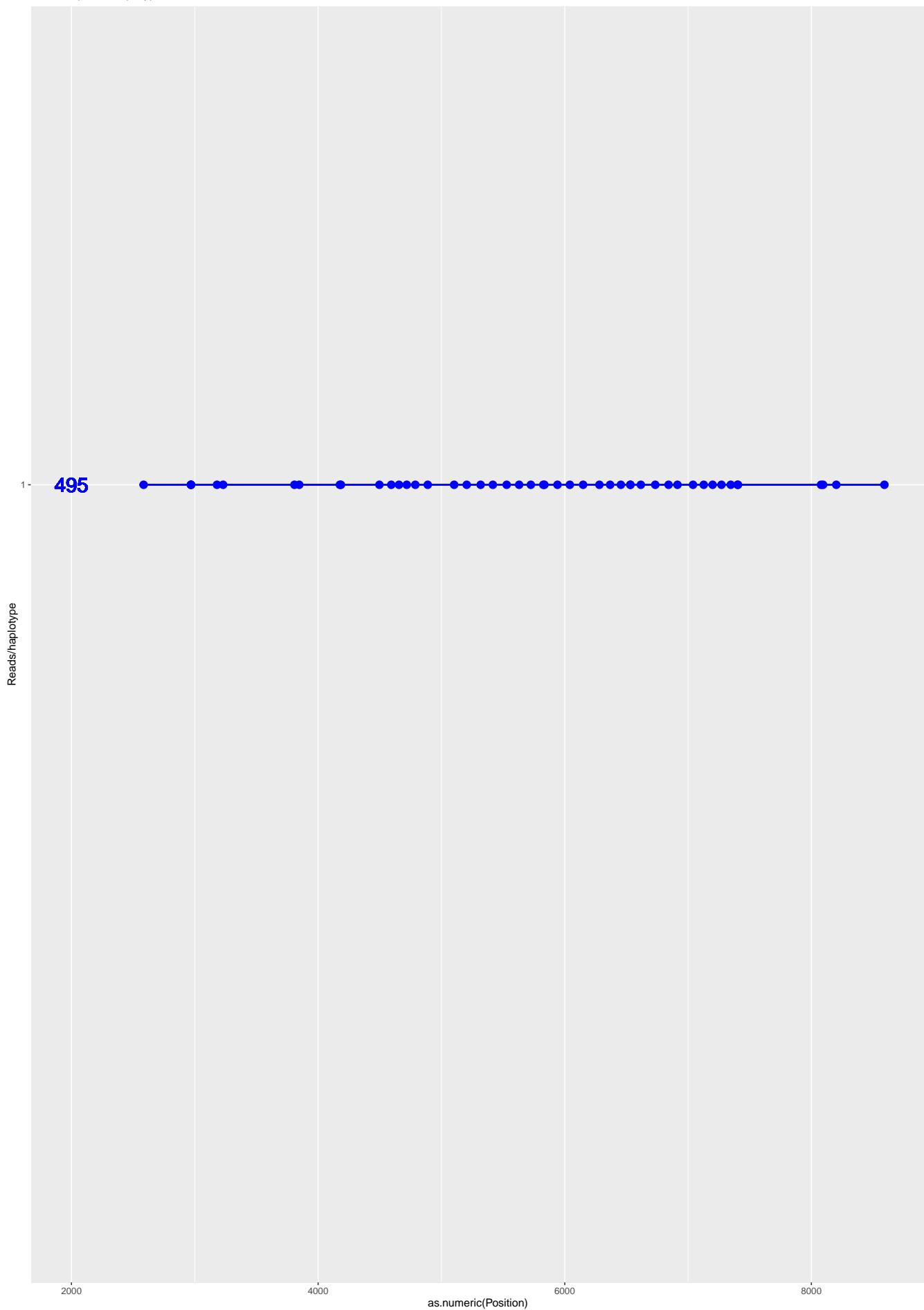
barcode = TGC GTGAGCTGTACAT & TACAGCGACGTCATCG

Sample = 51b tetrad = 51 spore = b

Total reads =582 PCR=118

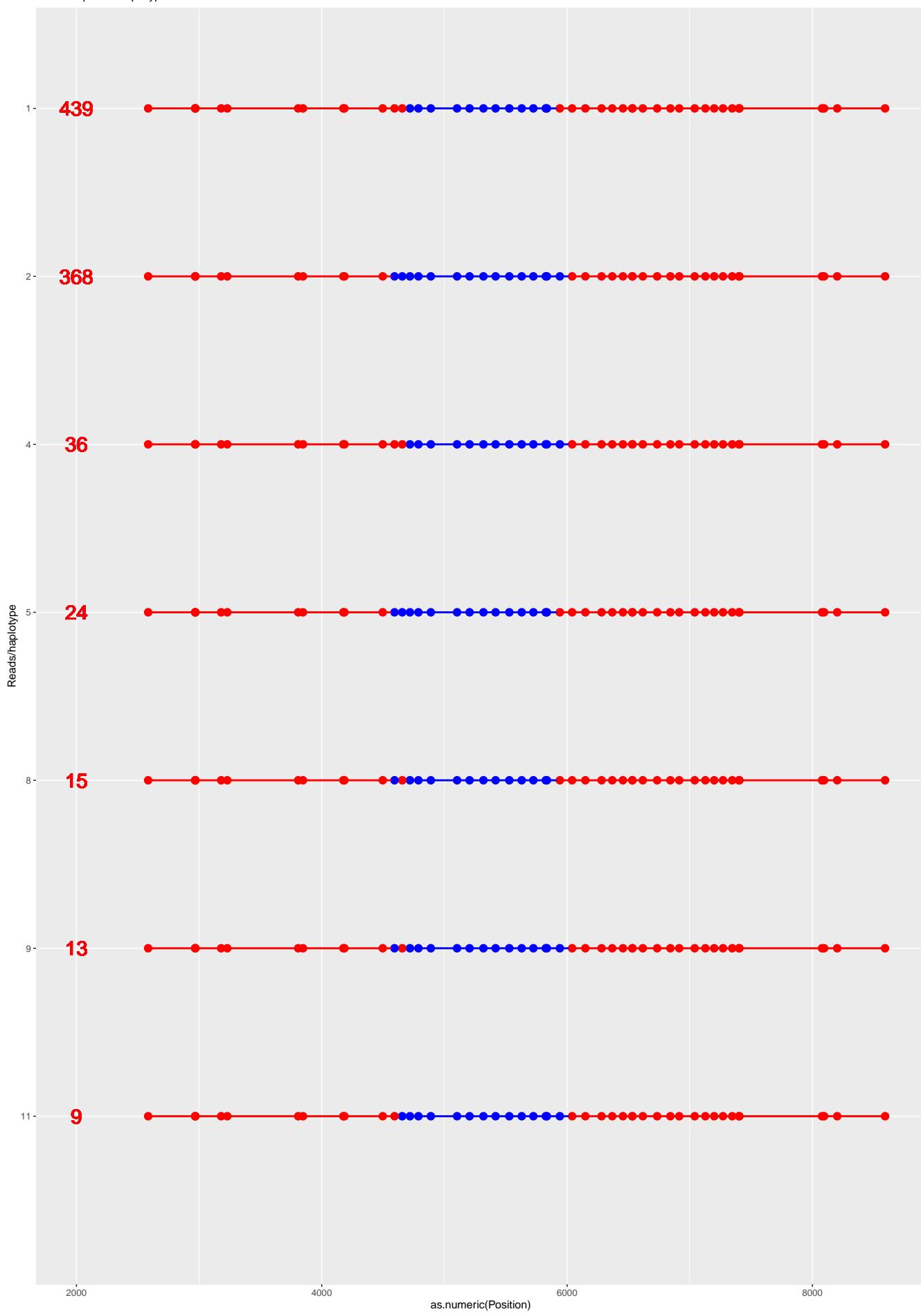
haplotypes I began with n[supporting reads] = 495

most frequent 7 haplotypes.

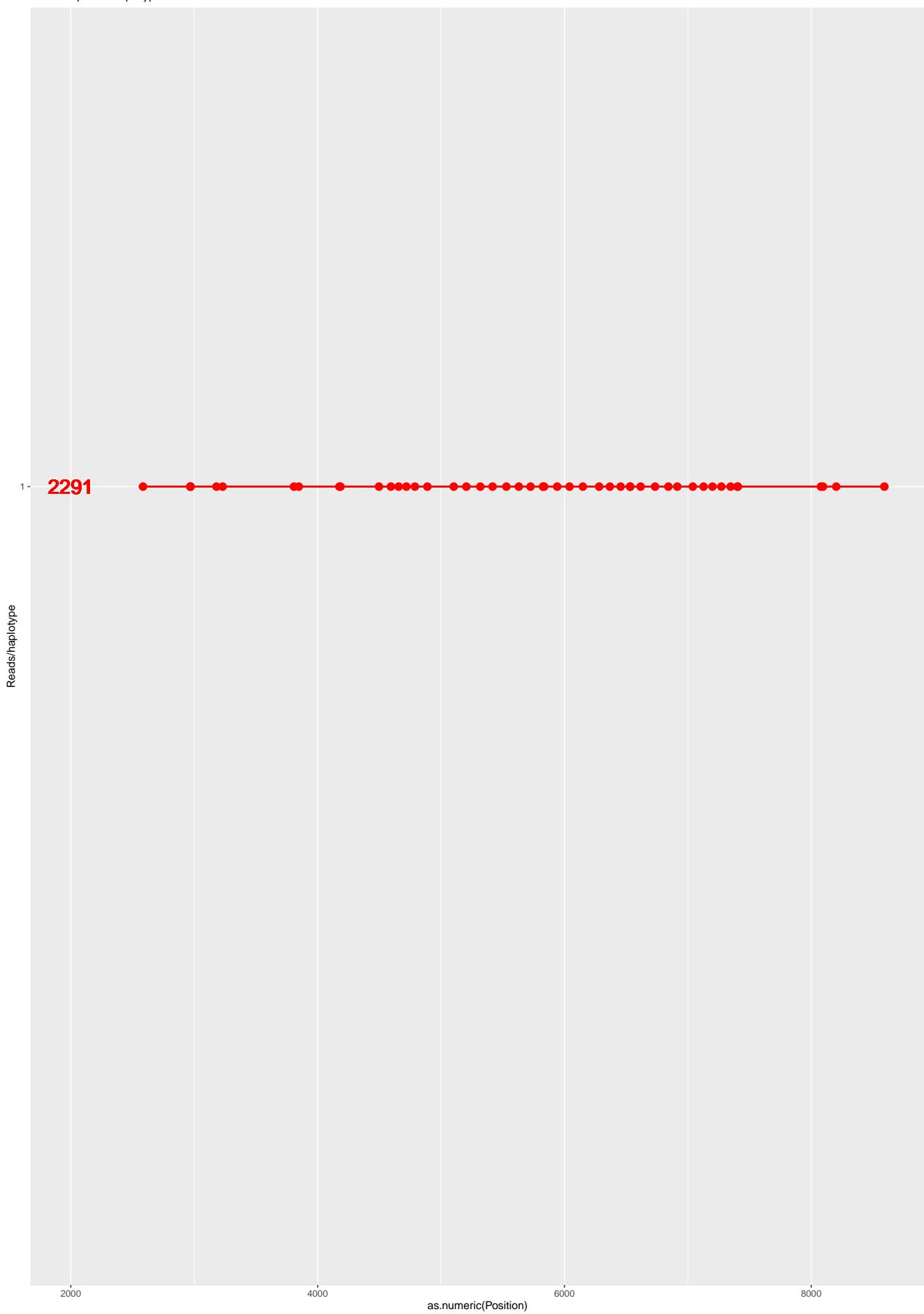


barcode = TGCCTGAGCTGTACAT & GCGCAGACTACGTGTG

Sample = 51c tetrad = 51 spore = c
Total reads = 1091 PCR=119
haplotypes I began with [n|supporting reads] = 9, 13, 15, 24, 36, 368, 439
most frequent 7 haplotypes.



Sample = 51d tetrad = 51 spore = d
Total reads = 2397 PCR=120
haplotypes I began with n[supporting reads] = 2291
most frequent 7 haplotypes.



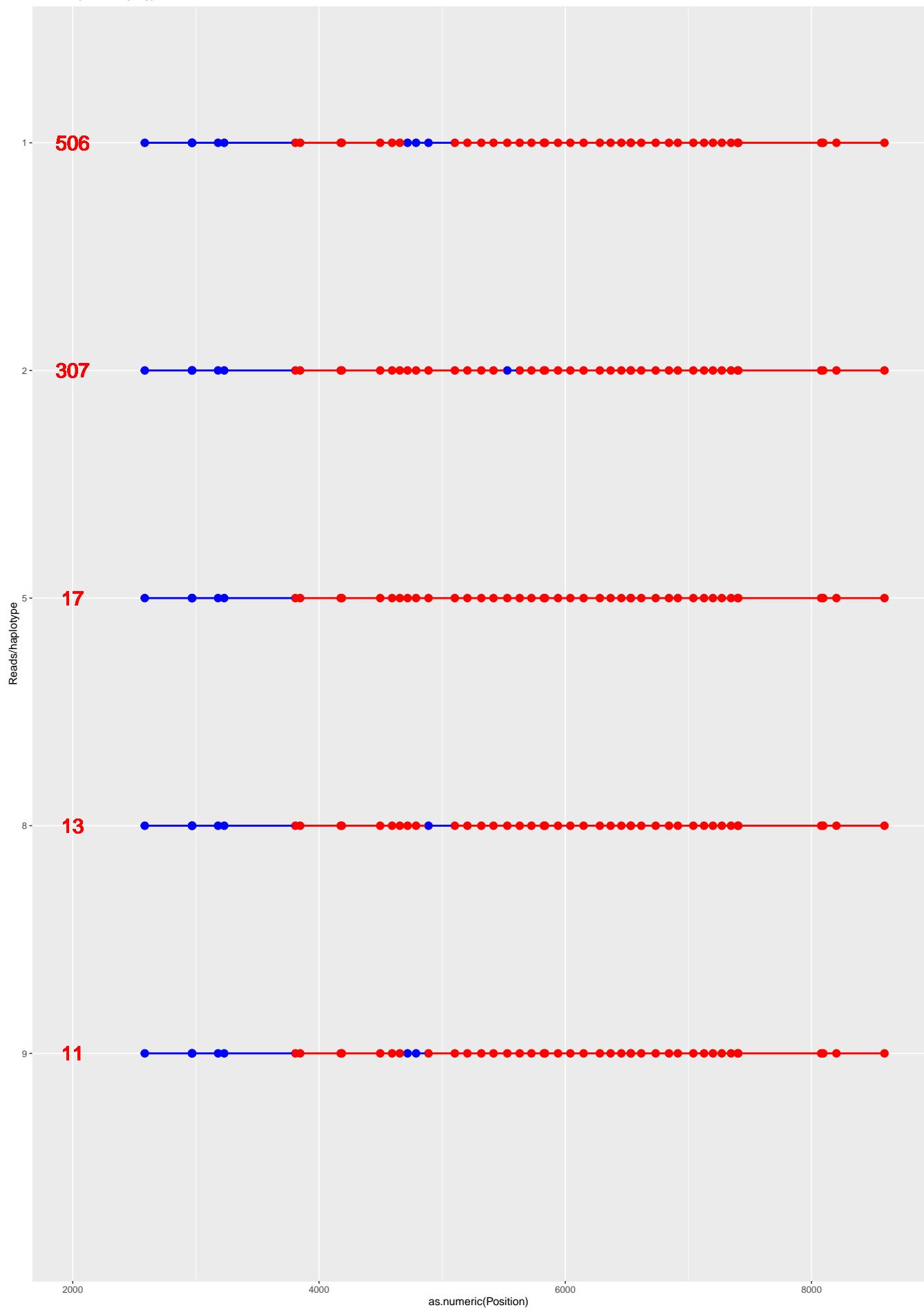
barcode = TGC GTGAGCTGTACAT & AGTATGAGATAGCTCG

Sample = 53a tetrad = 53 spore = a

Total reads = 1093 PCR=125

haplotypes I began with n[supporting reads] = 11, 13, 17, 307, 506

most frequent 7 haplotypes.



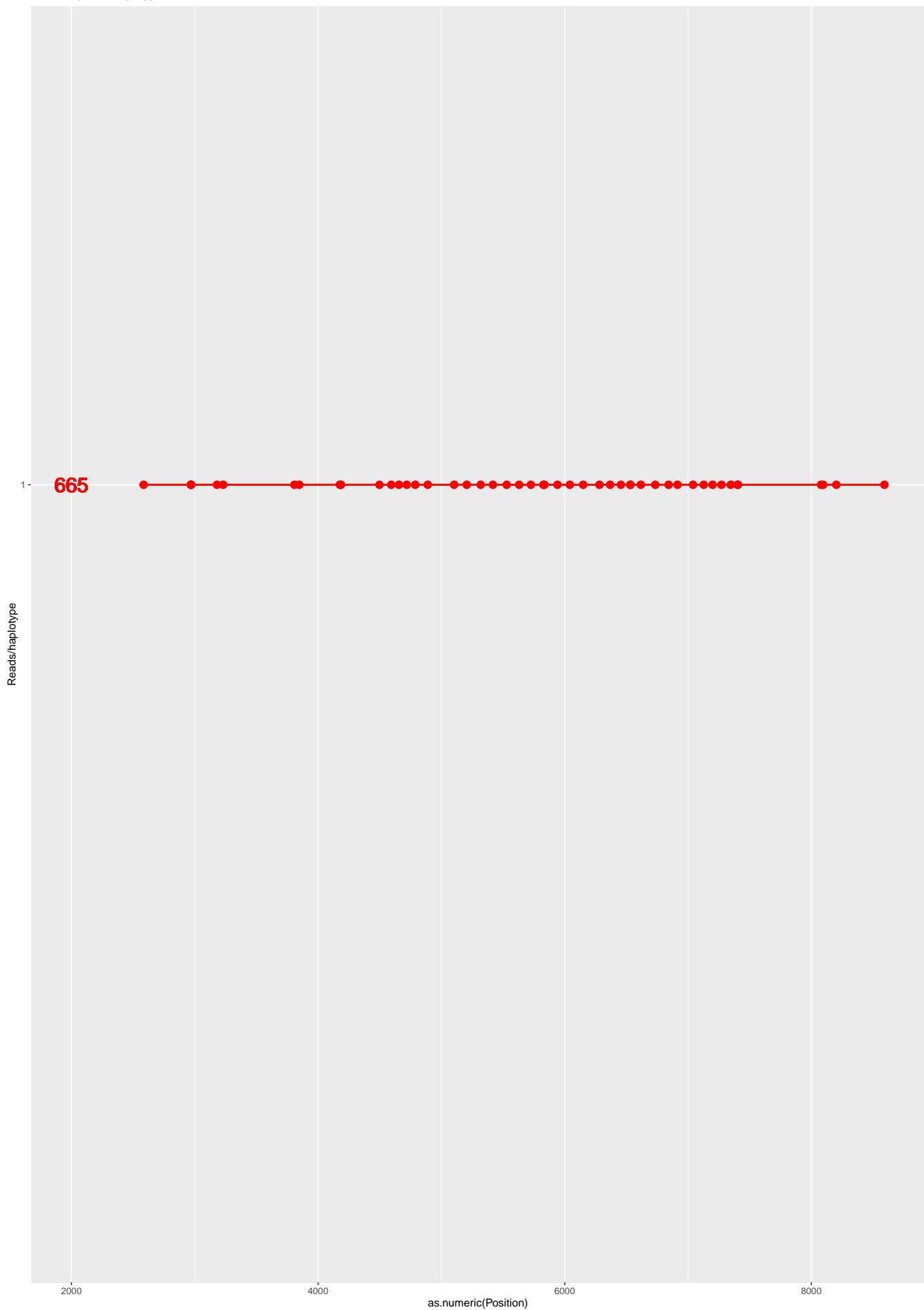
barcode = CGATCATCTATAGACA & TACAGCGACGTCATCG

Sample = 53b tetrad = 53 spore = b

Total reads = 693 PCR=126

haplotypes I began with n[supporting reads] = 665

most frequent 7 haplotypes.



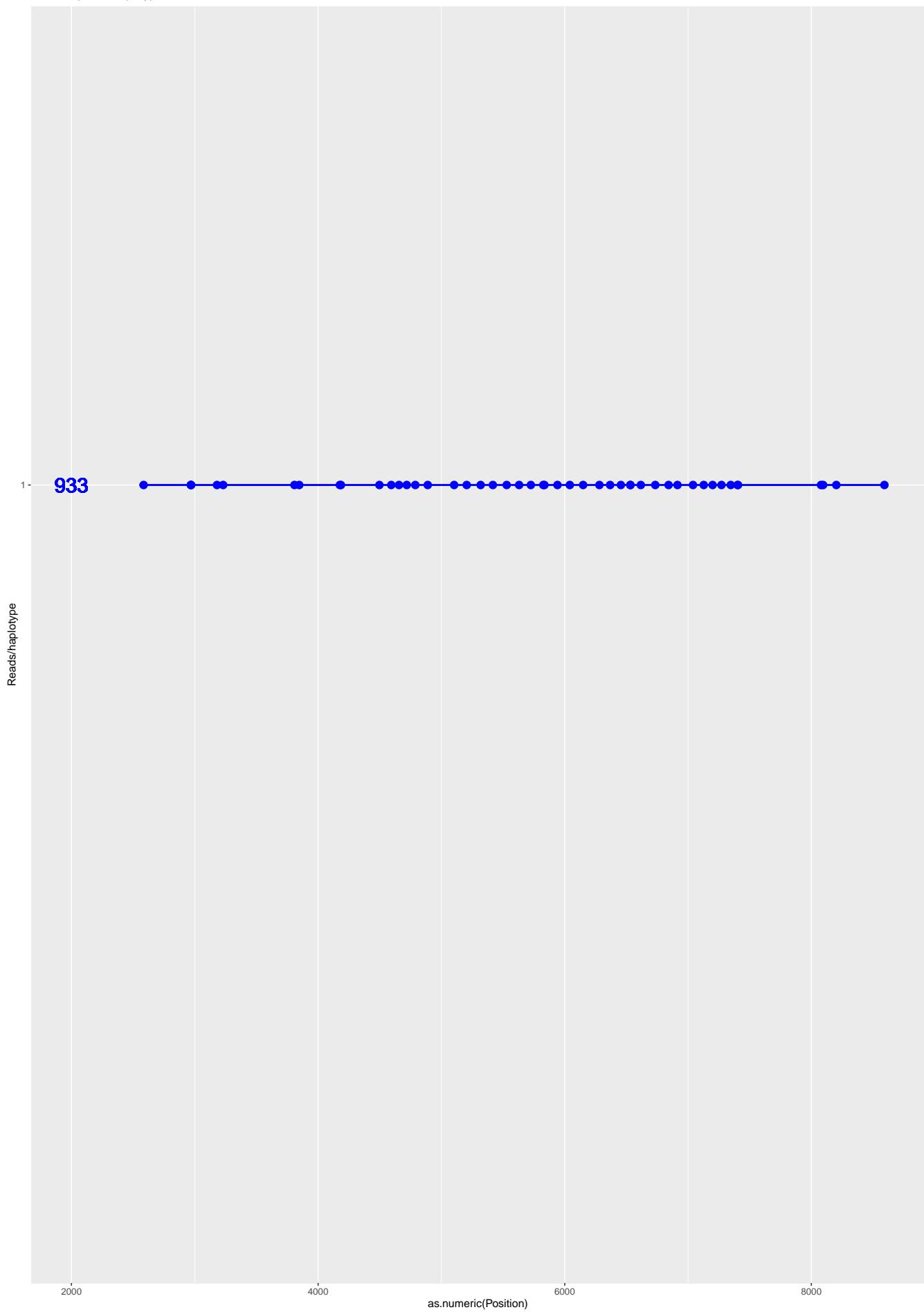
barcode = CGATCATCTATAGACA & GCGCAGACTACGTGTC

Sample = 53c tetrad = 53 spore = c

Total reads = 1078 PCR=127

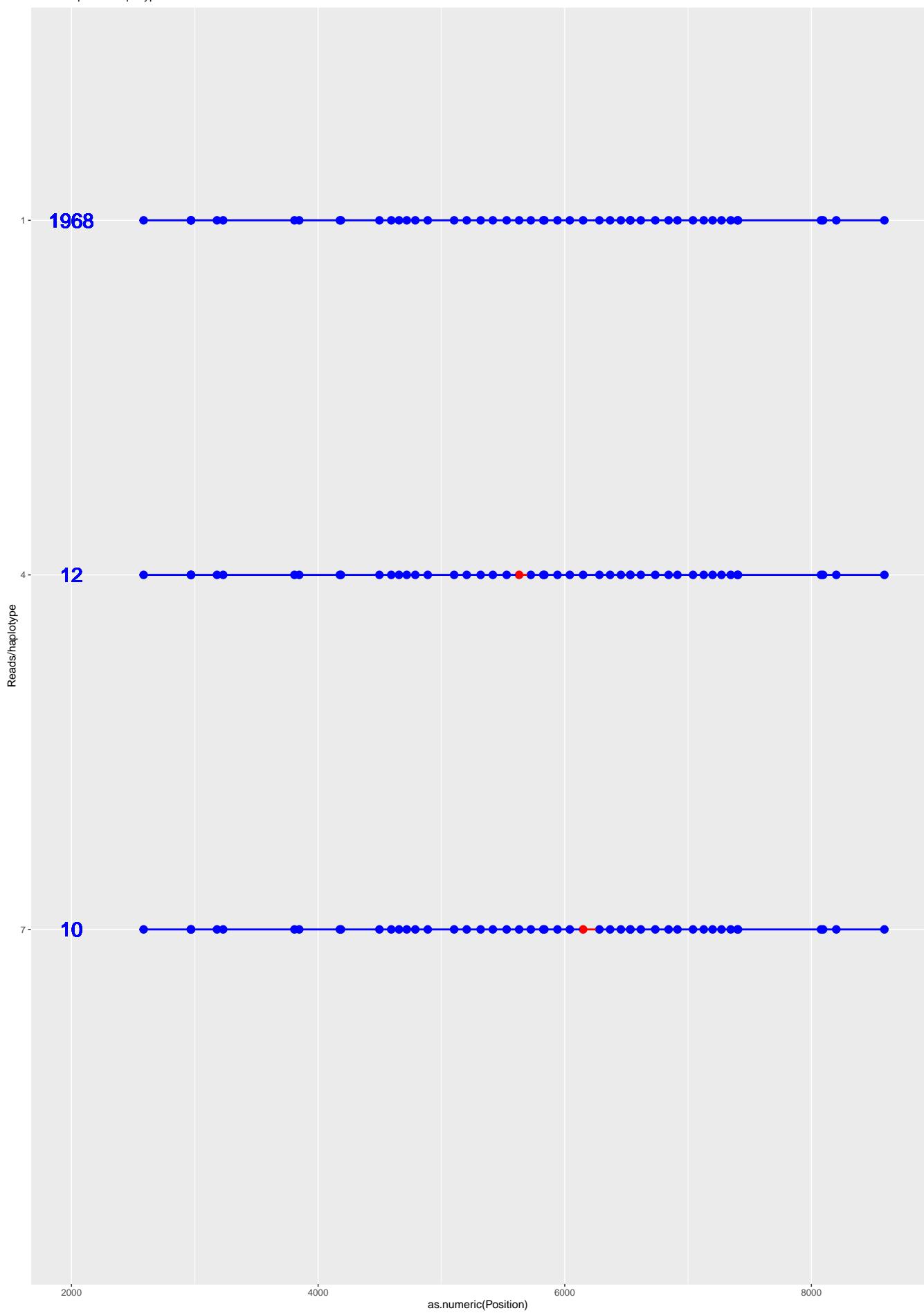
haplotypes I began with n[supporting reads] = 933

most frequent 7 haplotypes.



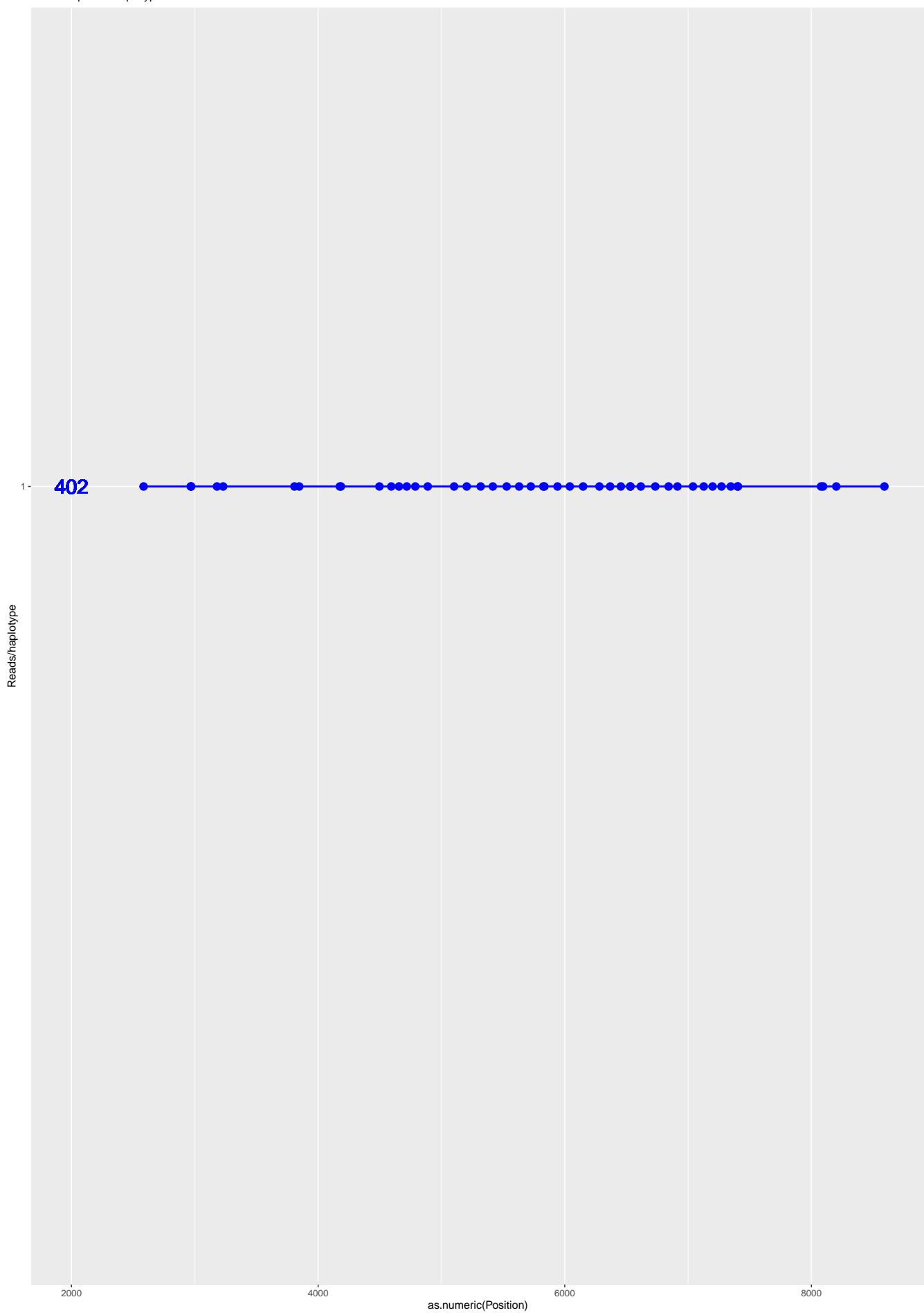
barcode = CGATCATCTATAGACA & GTCTCTGCGATAACAGC

Sample = 53d tetrad = 53 spore = d
Total reads = 2321 PCR=128
haplotypes I began with n[supporting reads] = 10, 12, 1968
most frequent 7 haplotypes.



barcode = CGATCATCTATAGACA & AGTATGAGATAGCTCG

Sample = 55a tetrad = 55 spore = a
Total reads = 478 PCR=133
haplotypes I began with n[supporting reads] = 402
most frequent 7 haplotypes.



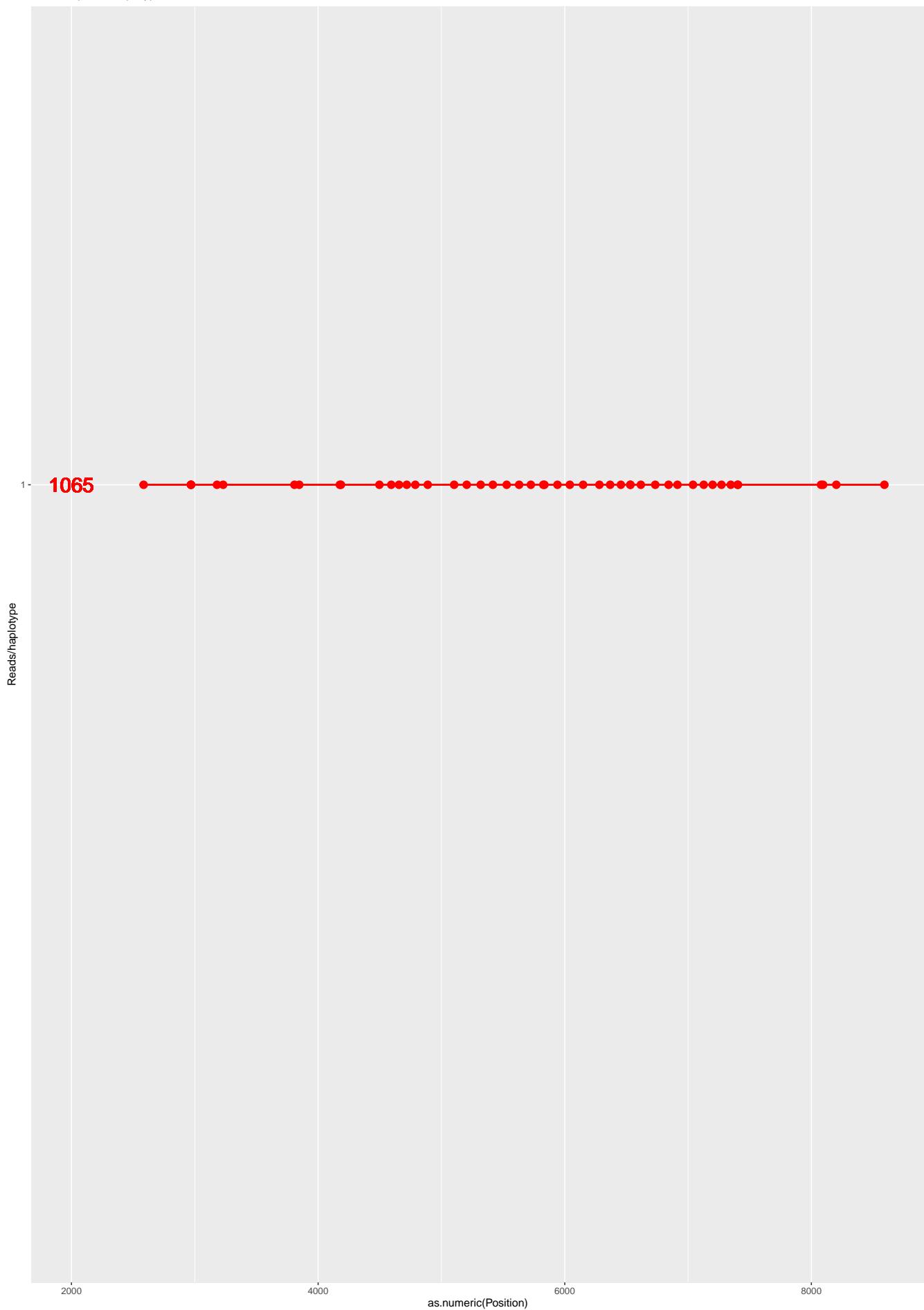
barcode = CGACGTATCTGACAGT & TACAGCGACGTCATCG

Sample = 55b tetrad = 55 spore = b

Total reads = 1112 PCR=134

haplotypes I began with n[supporting reads] = 1065

most frequent 7 haplotypes.



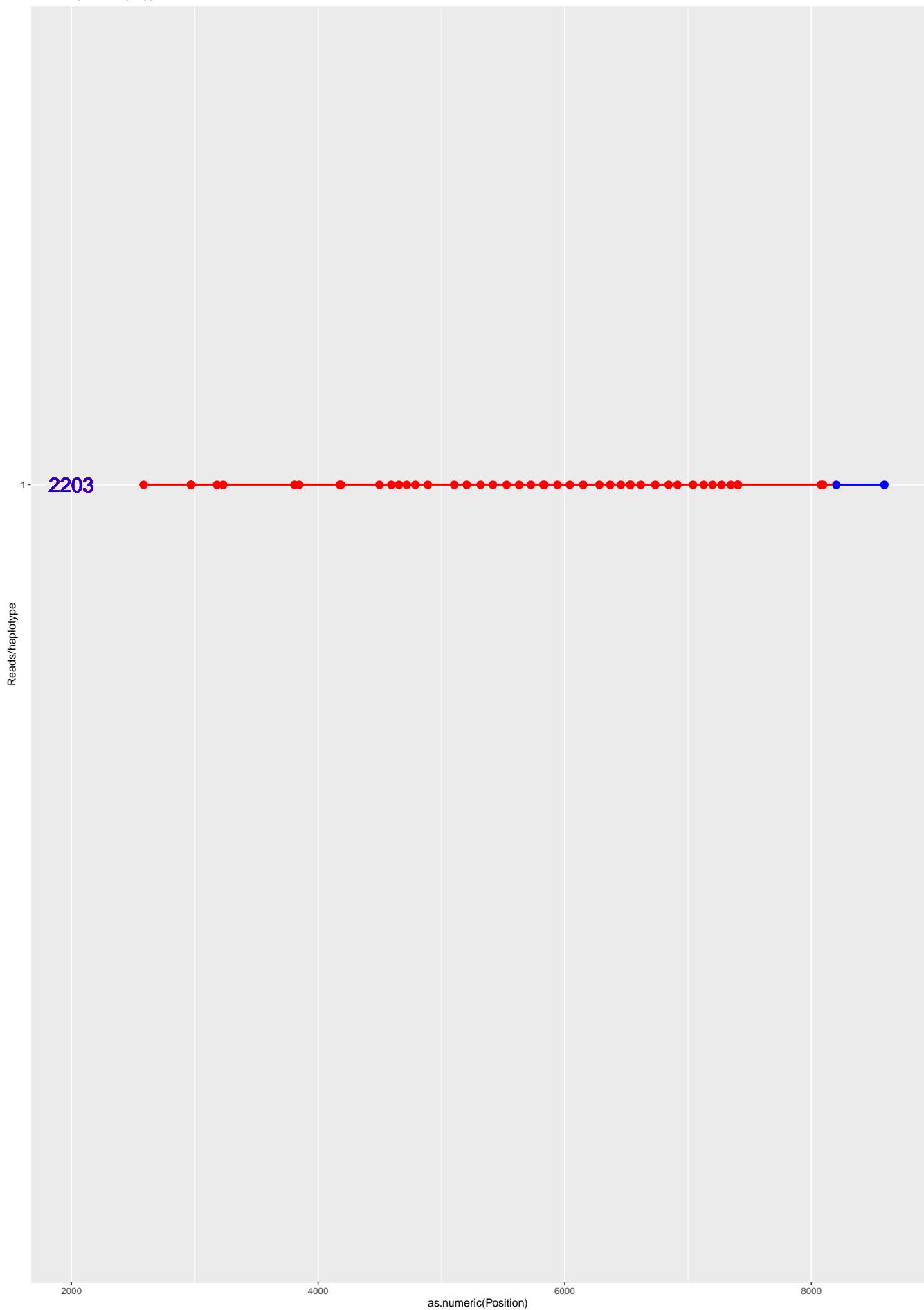
barcode = CGACGTATCTGACAGT & GCGCAGACTACGTGTG

Sample = 55c tetrad = 55 spore = c

Total reads = 2311 PCR=135

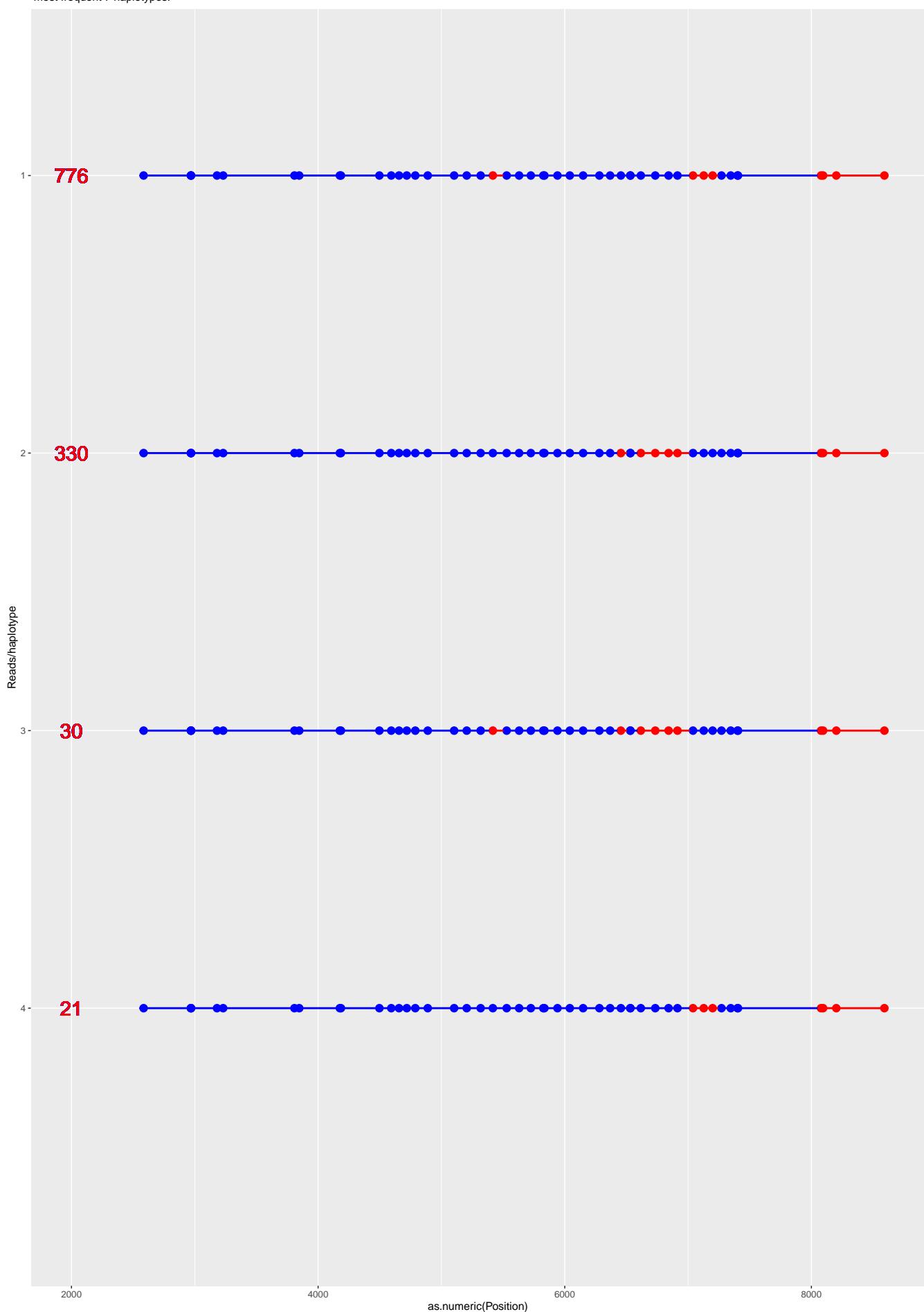
haplotypes I began with n[supporting reads] = 2203

most frequent 7 haplotypes.

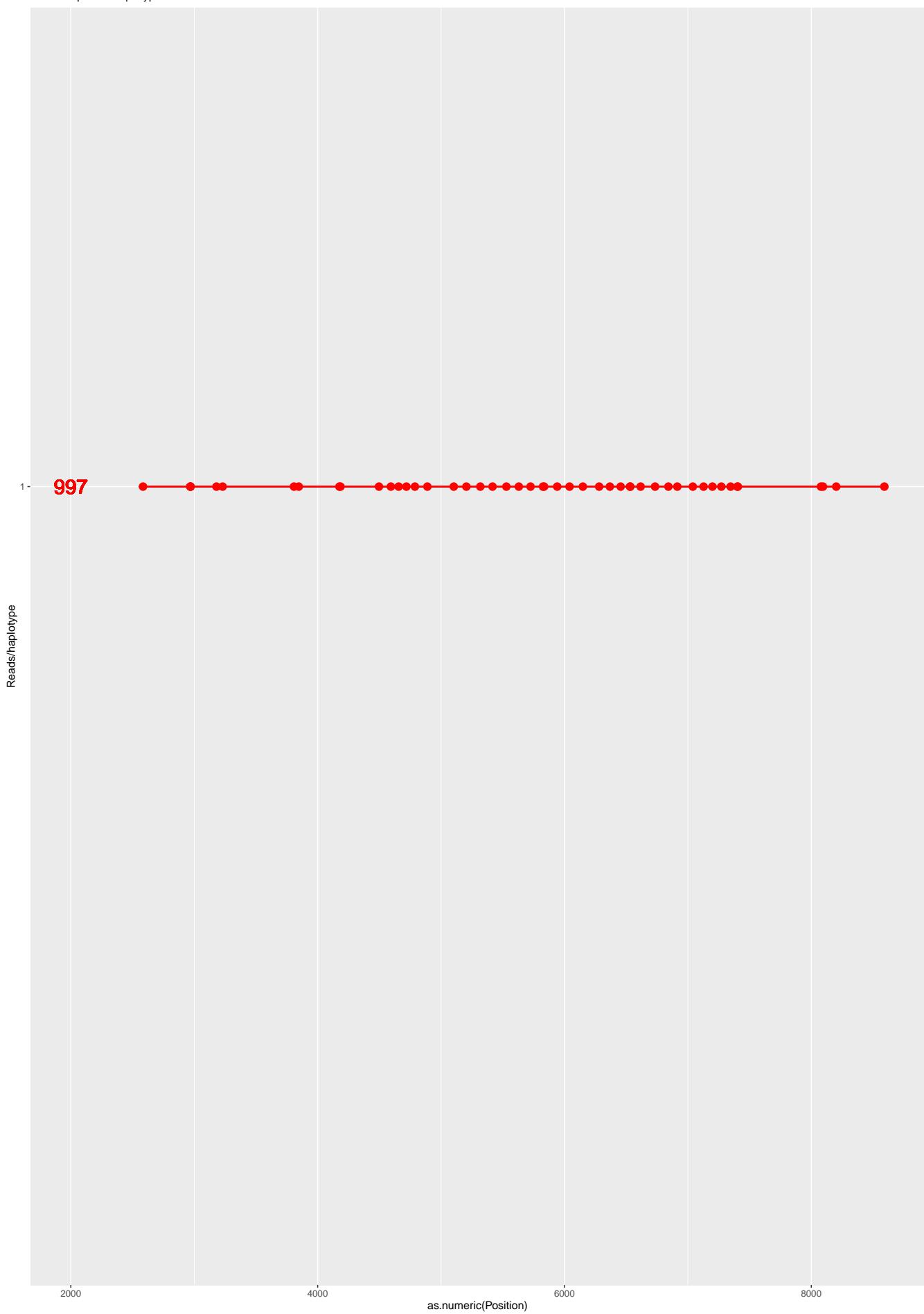


barcode = CGACGTATCTGACAGT & GTCTCTGCGATAACAGC

Sample = 55d tetrad = 55 spore = d
Total reads = 1794 PCR=136
haplotypes I began with n[supporting reads] = 21, 30, 330, 776
most frequent 7 haplotypes.



Sample = 58a tetrad = 58 spore = a
Total reads = 1039 PCR=141
haplotypes I began with n[supporting reads] = 997
most frequent 7 haplotypes.

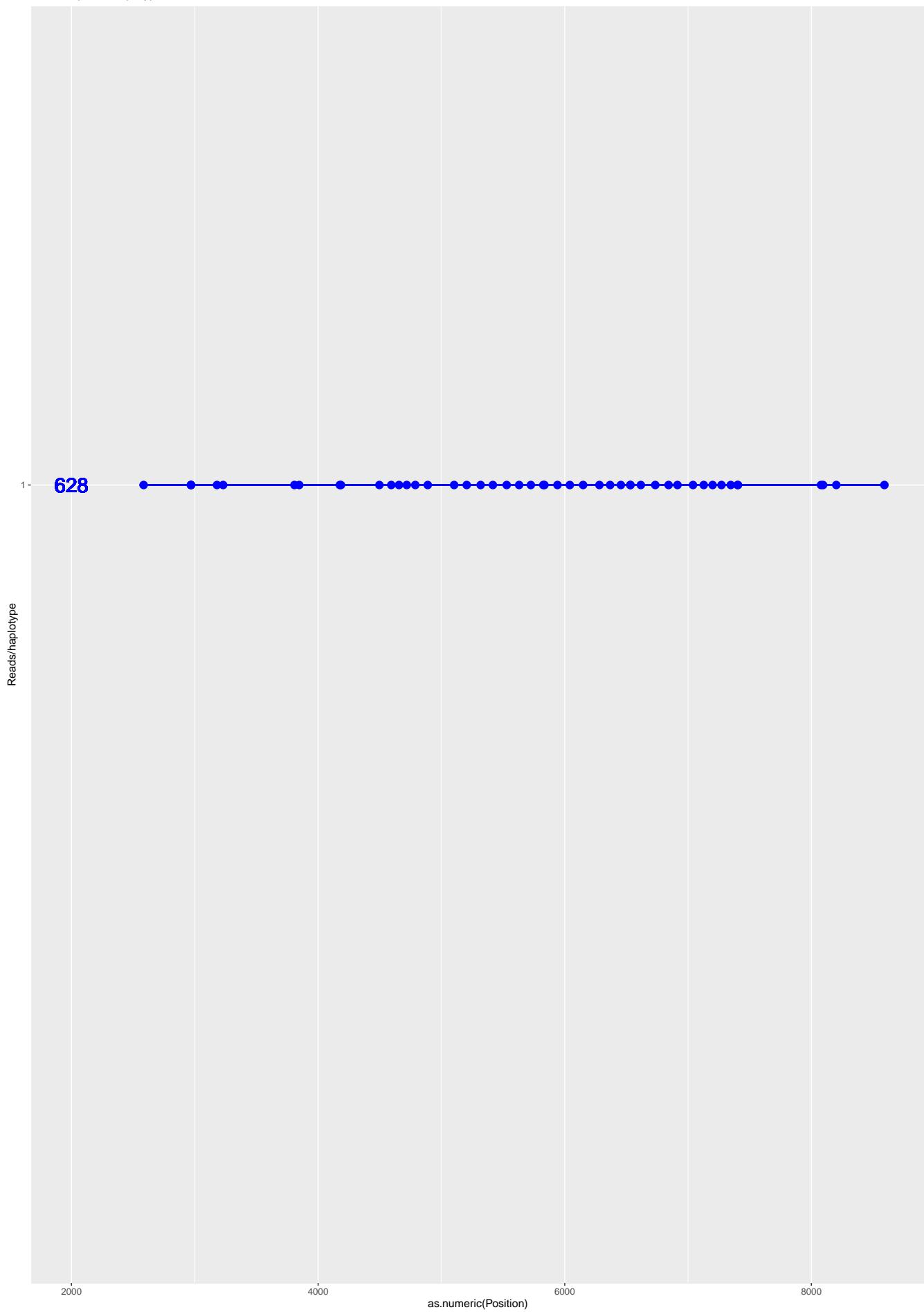


Sample = 58b tetrad = 58 spore = b

Total reads =713 PCR=142

haplotypes I began with n[supporting reads] = 628

most frequent 7 haplotypes.



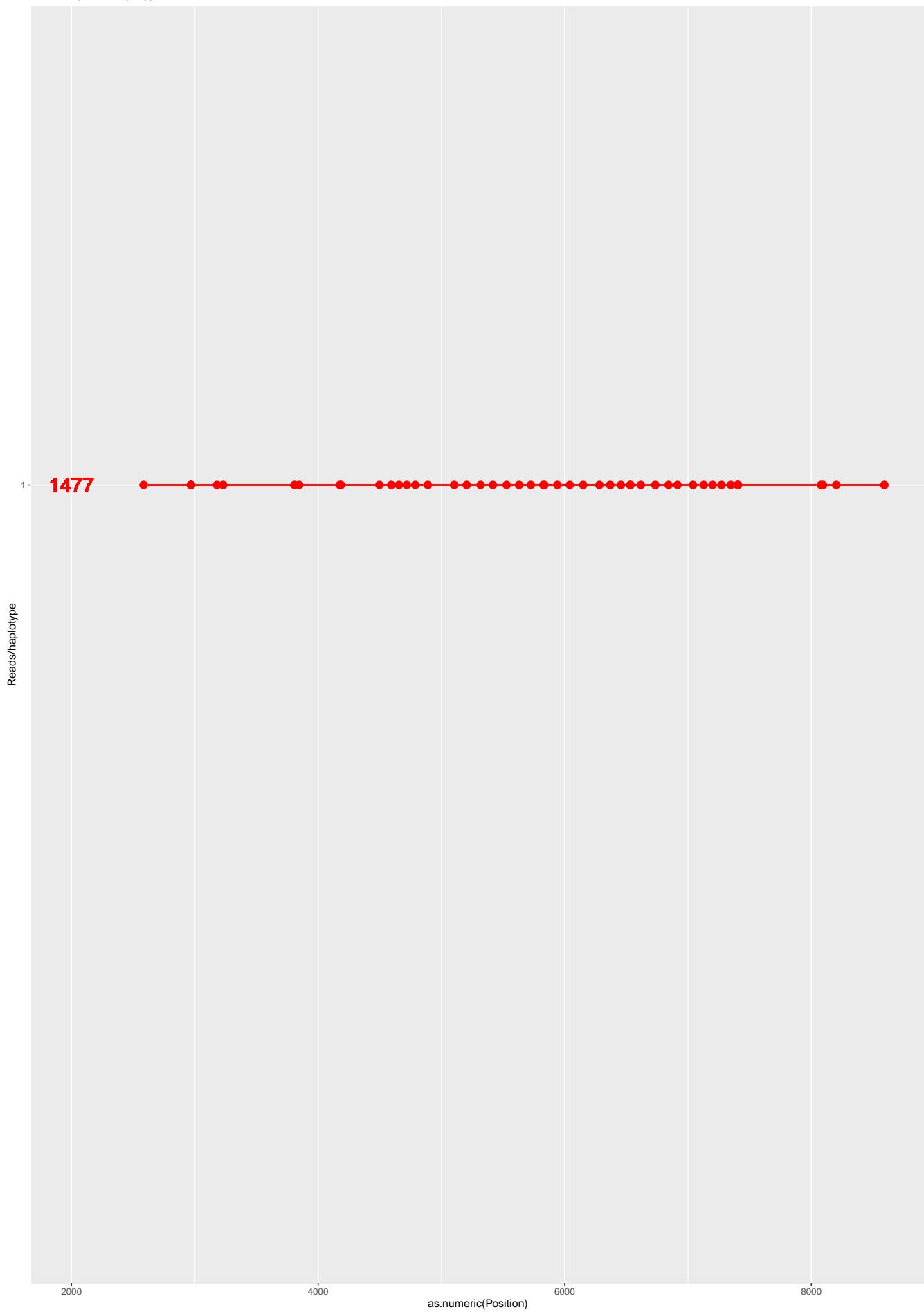
barcode = CACGTCACTAGAGCGA & GCGCAGACTACGTGTG

Sample = 58c tetrad = 58 spore = c

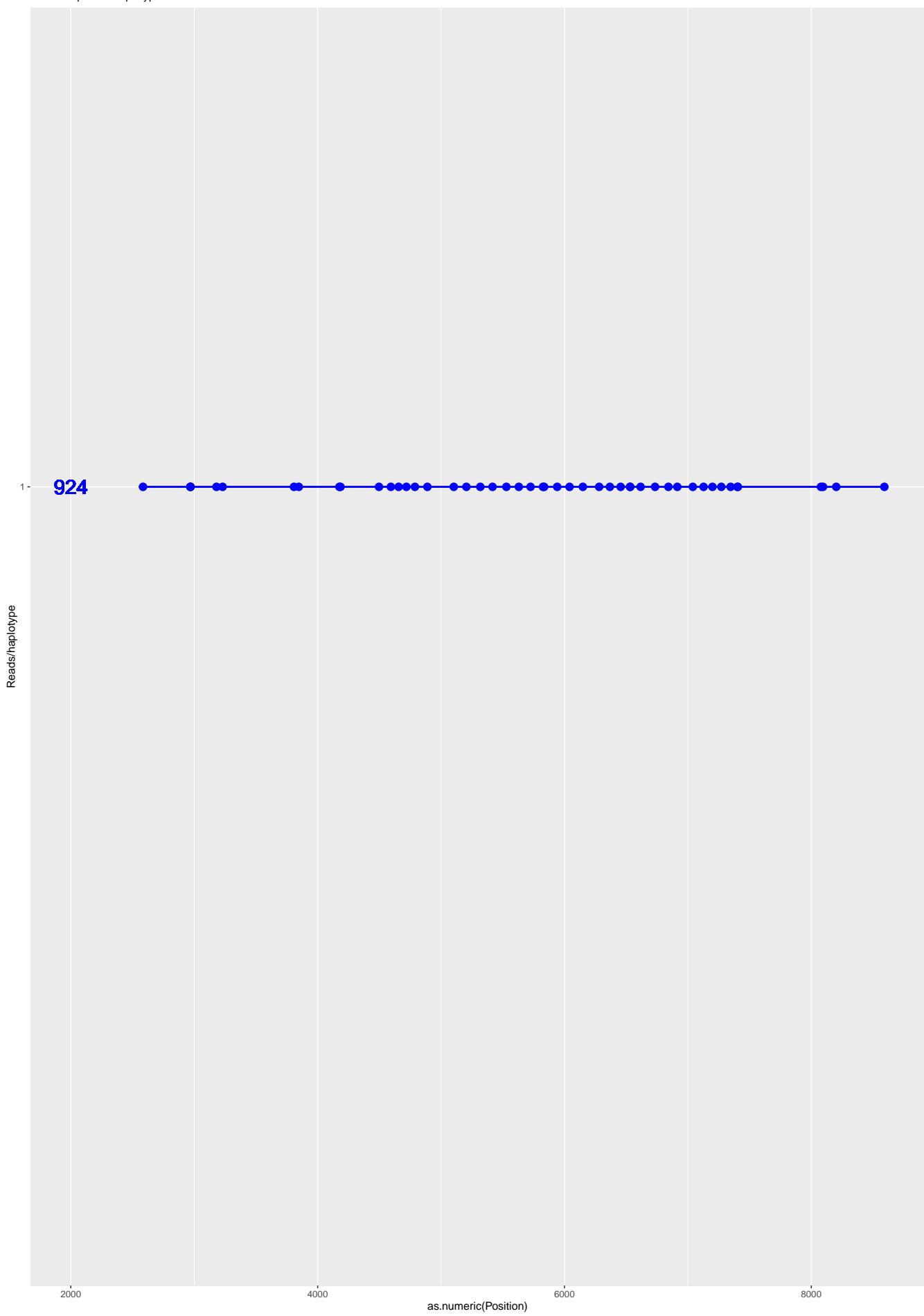
Total reads = 1538 PCR=143

haplotypes I began with n[supporting reads] = 1477

most frequent 7 haplotypes.

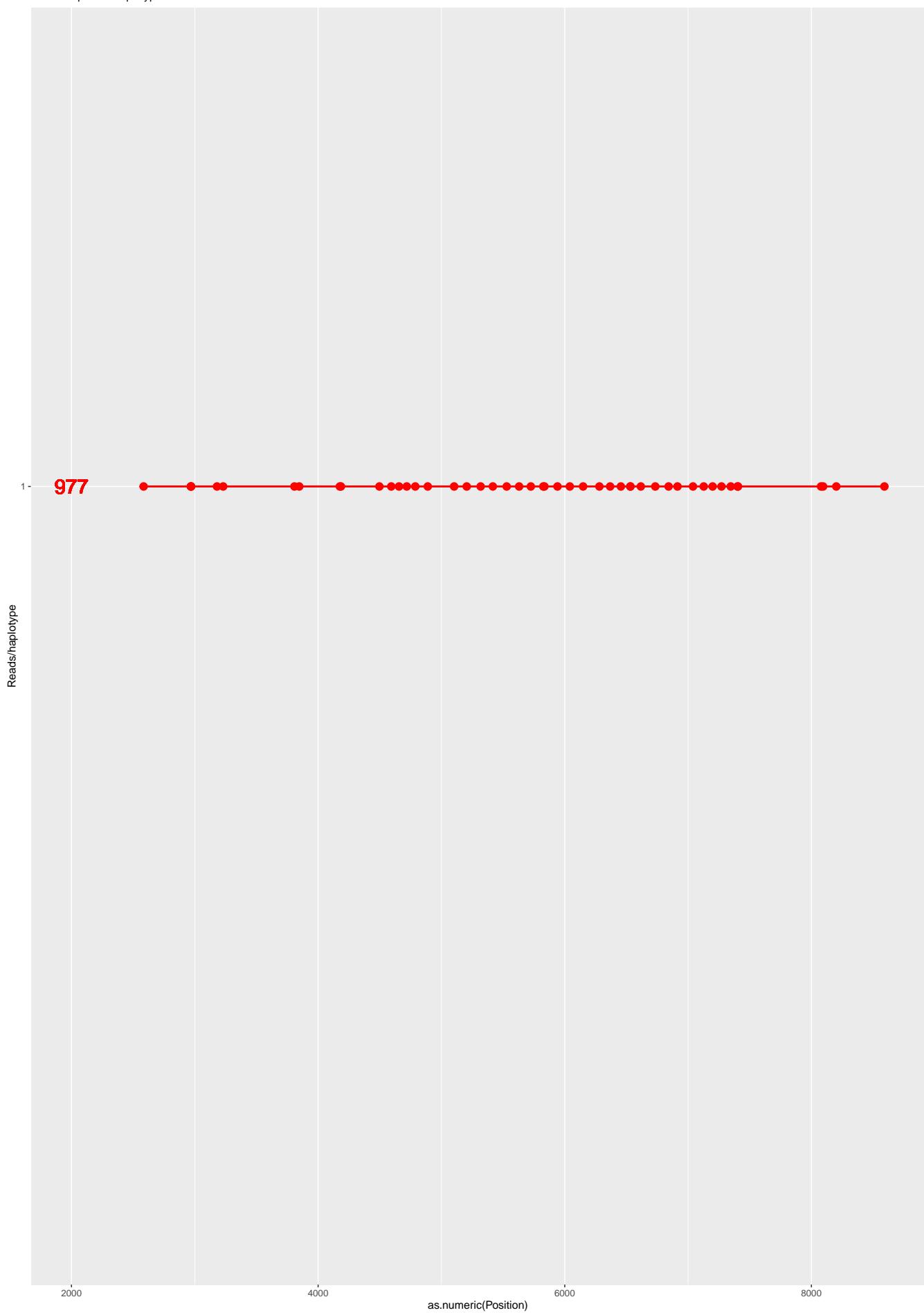


Sample = 58d tetrad = 58 spore = d
Total reads = 1071 PCR=144
haplotypes I began with n[supporting reads] = 924
most frequent 7 haplotypes.



barcode = CACGTCACTAGAGCGA & AGTATGAGATAGCTCG

Sample = 60a tetrad = 60 spore = a
Total reads = 1010 PCR=149
haplotypes I began with n[supporting reads] = 977
most frequent 7 haplotypes.

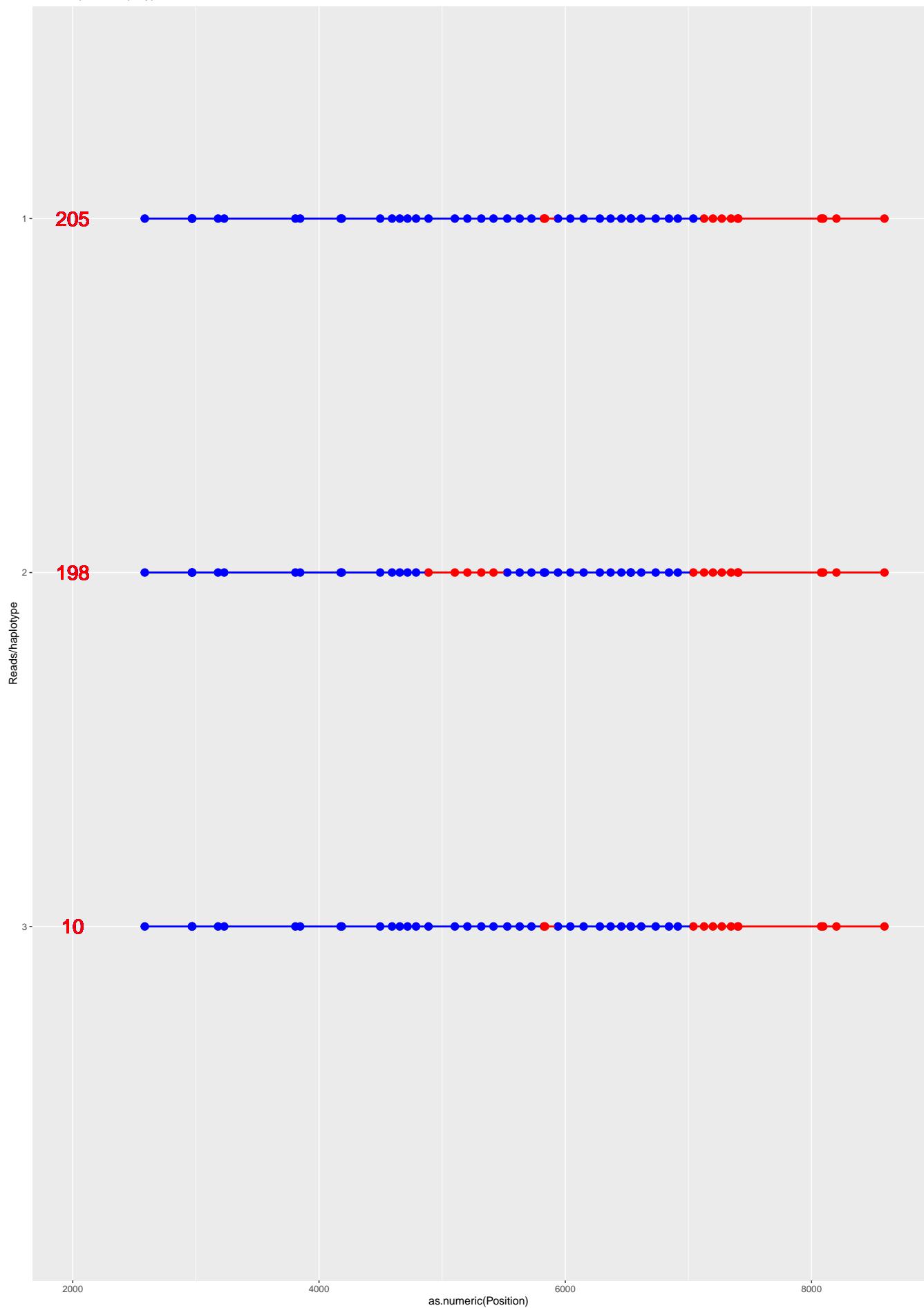


Sample = 60b tetrad = 60 spore = b

Total reads = 633 PCR=150

haplotypes I began with n[supporting reads] = 10, 198, 205

most frequent 7 haplotypes.

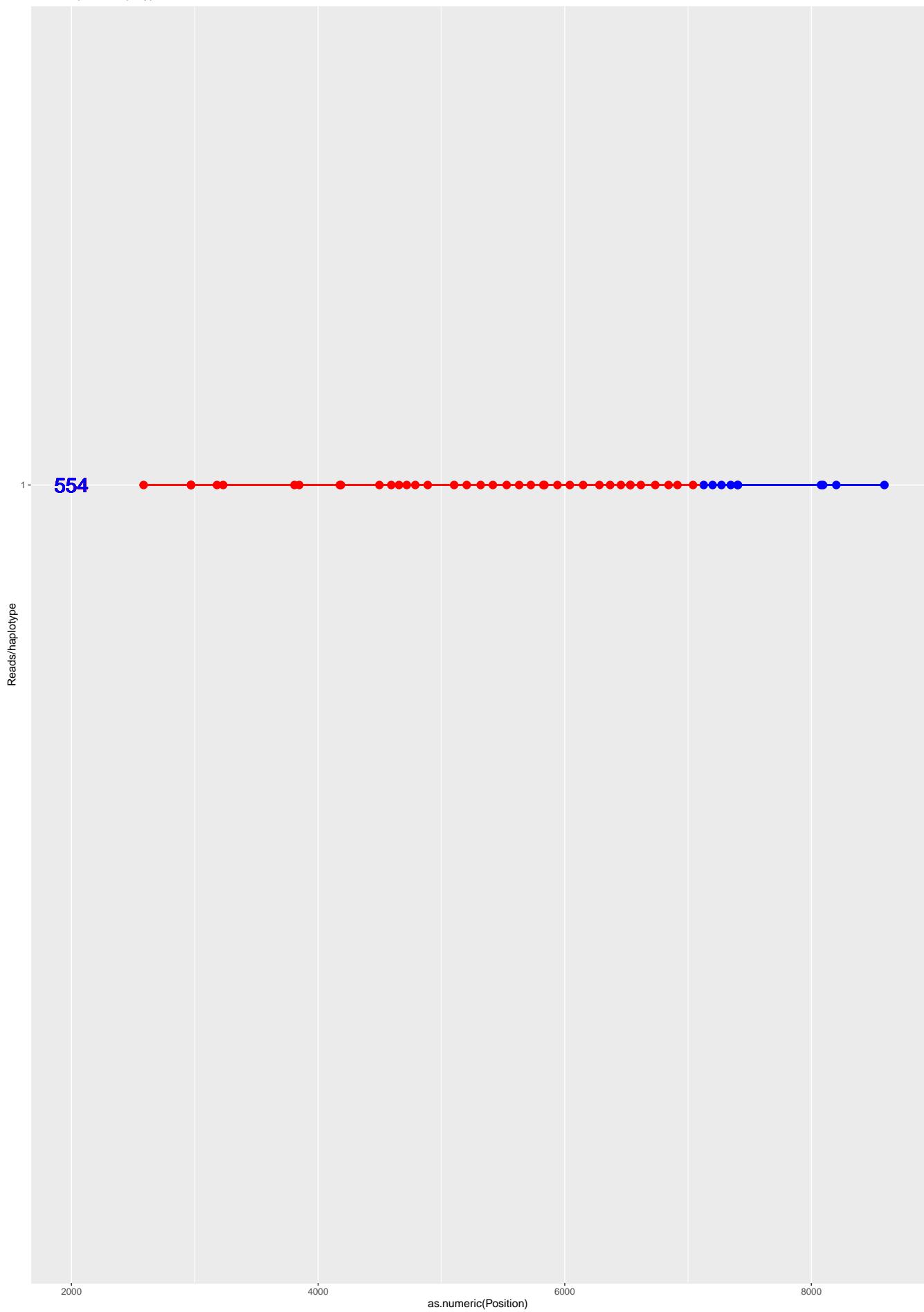


Sample = 60c tetrad = 60 spore = c

Total reads =583 PCR=151

haplotypes I began with n[supporting reads] = 554

most frequent 7 haplotypes.



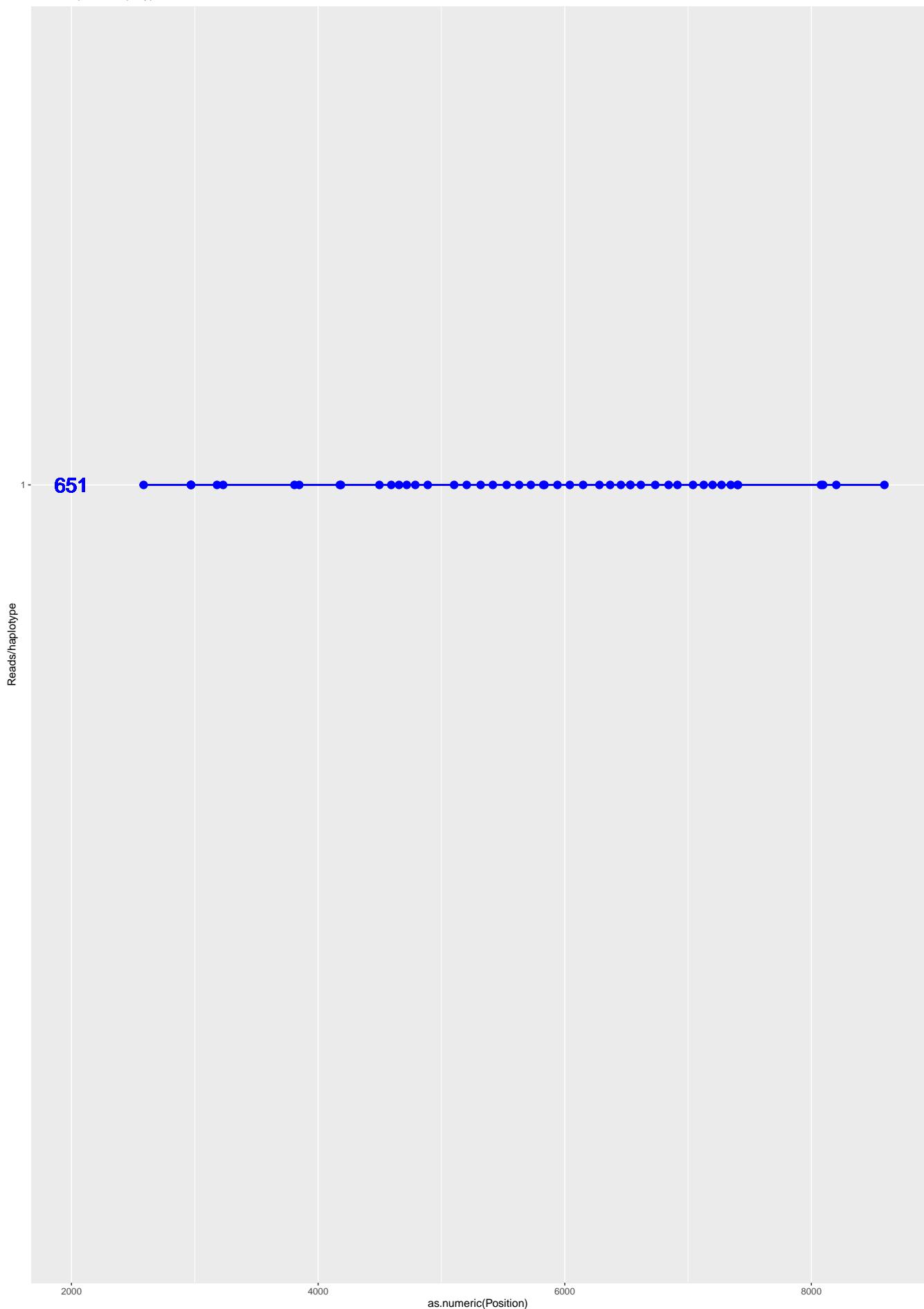
barcode = TGTCGCAGCTACTAGT & GTCTCTGCGATAACAGC

Sample = 60d tetrad = 60 spore = d

Total reads =750 PCR=152

haplotypes I began with n[supporting reads] = 651

most frequent 7 haplotypes.



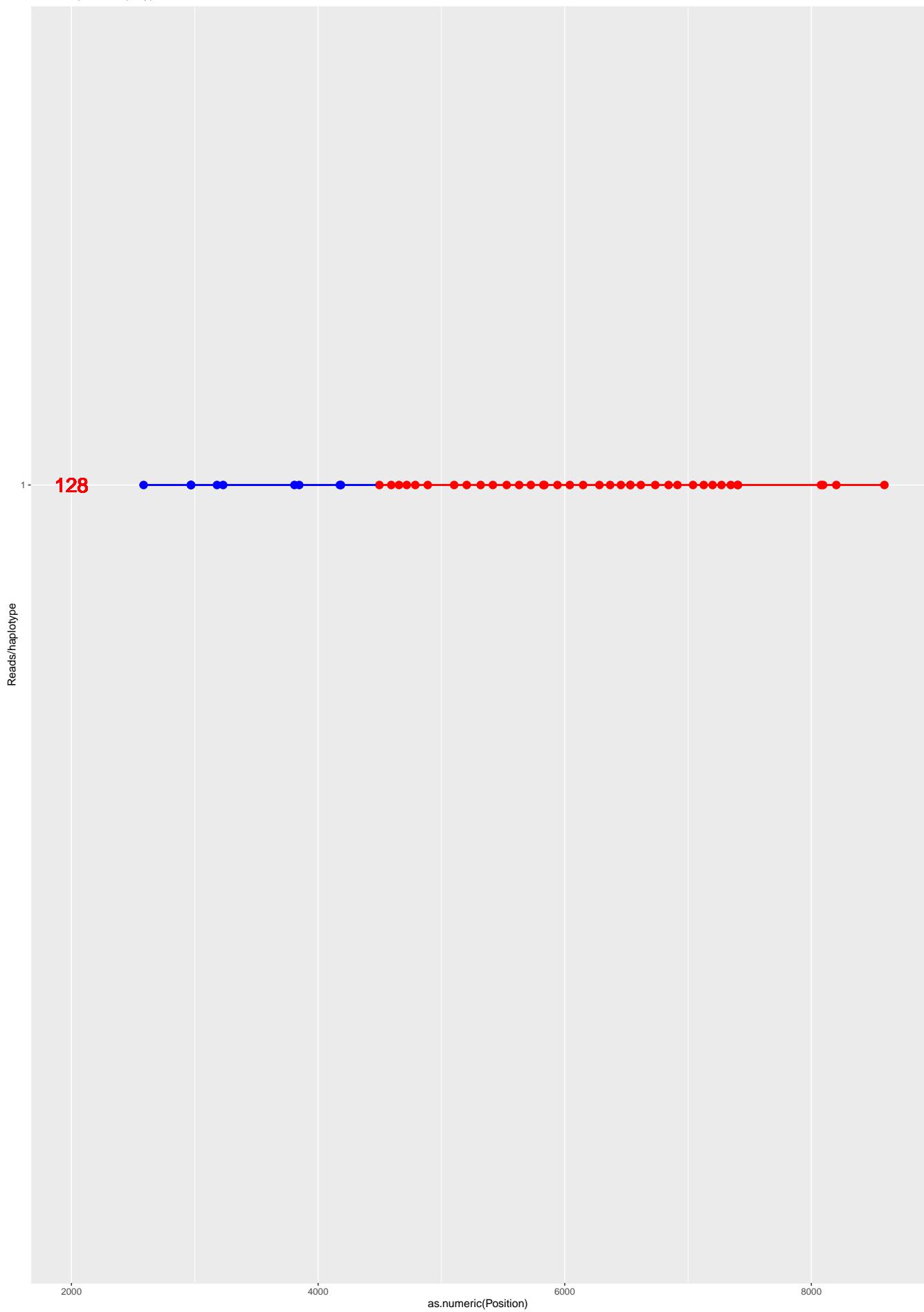
barcode = TGTCGCAGCTACTAGT & AGTATGAGATAGCTCG

Sample = 61a tetrad = 61 spore = a

Total reads =136 PCR=153

haplotypes I began with n[supporting reads] = 128

most frequent 7 haplotypes.



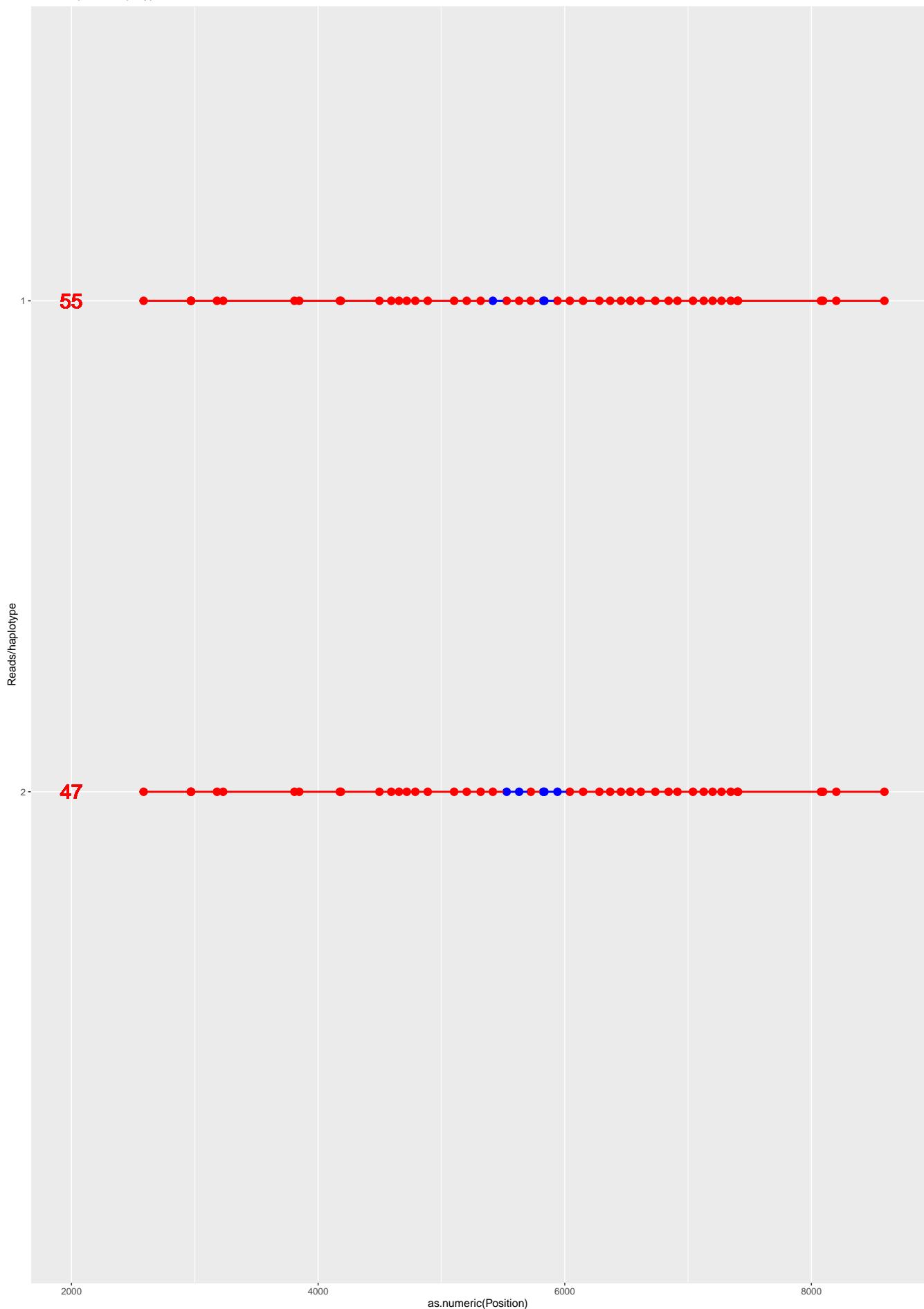
barcode = CATAACGCTGTGTAGCA & TCATATGTAGTACTCT

Sample = 61b tetrad = 61 spore = b

Total reads = 117 PCR=154

haplotypes I began with n[supporting reads] = 47, 55

most frequent 7 haplotypes.



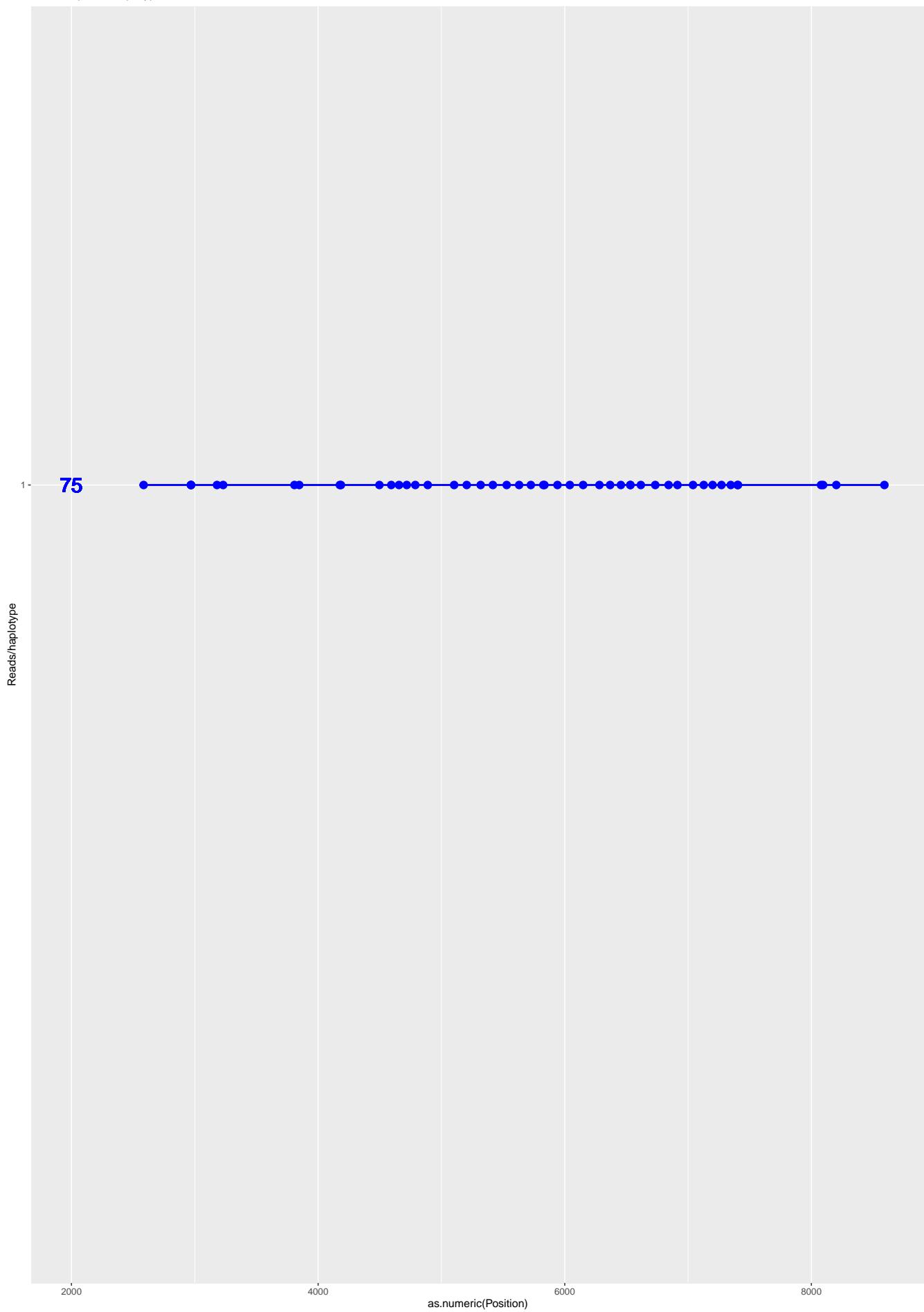
barcode = CATACTGCTGTAGCA & GCGATCTATGCACACG

Sample = 61c tetrad = 61 spore = c

Total reads = 82 PCR=155

haplotypes I began with n[supporting reads] = 75

most frequent 7 haplotypes.



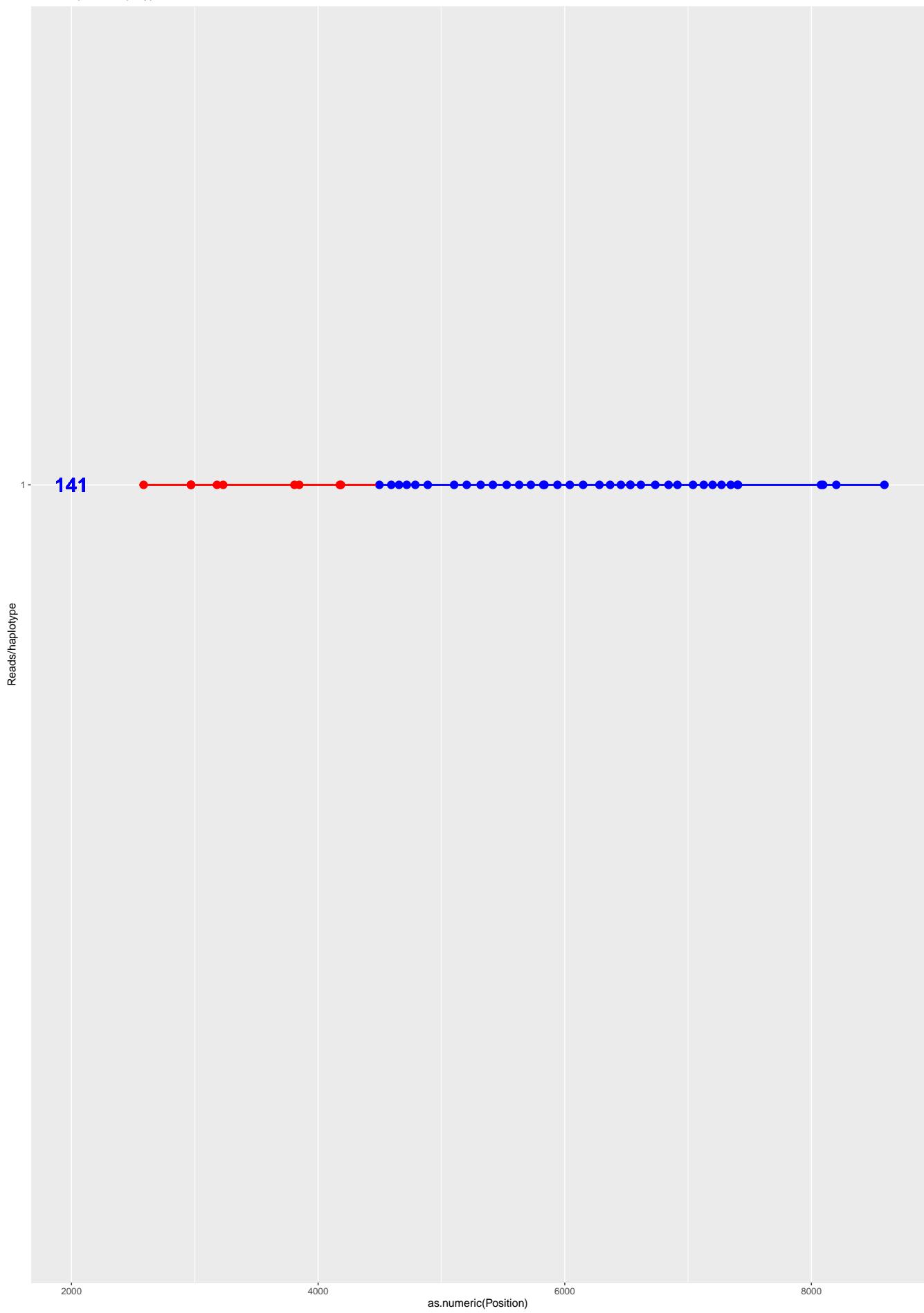
barcode = CATA CGCT GTGT AGCA & TGCAG TCGAG AATACAT

Sample = 61d tetrad = 61 spore = d

Total reads = 155 PCR=156

haplotypes I began with n[supporting reads] = 141

most frequent 7 haplotypes.

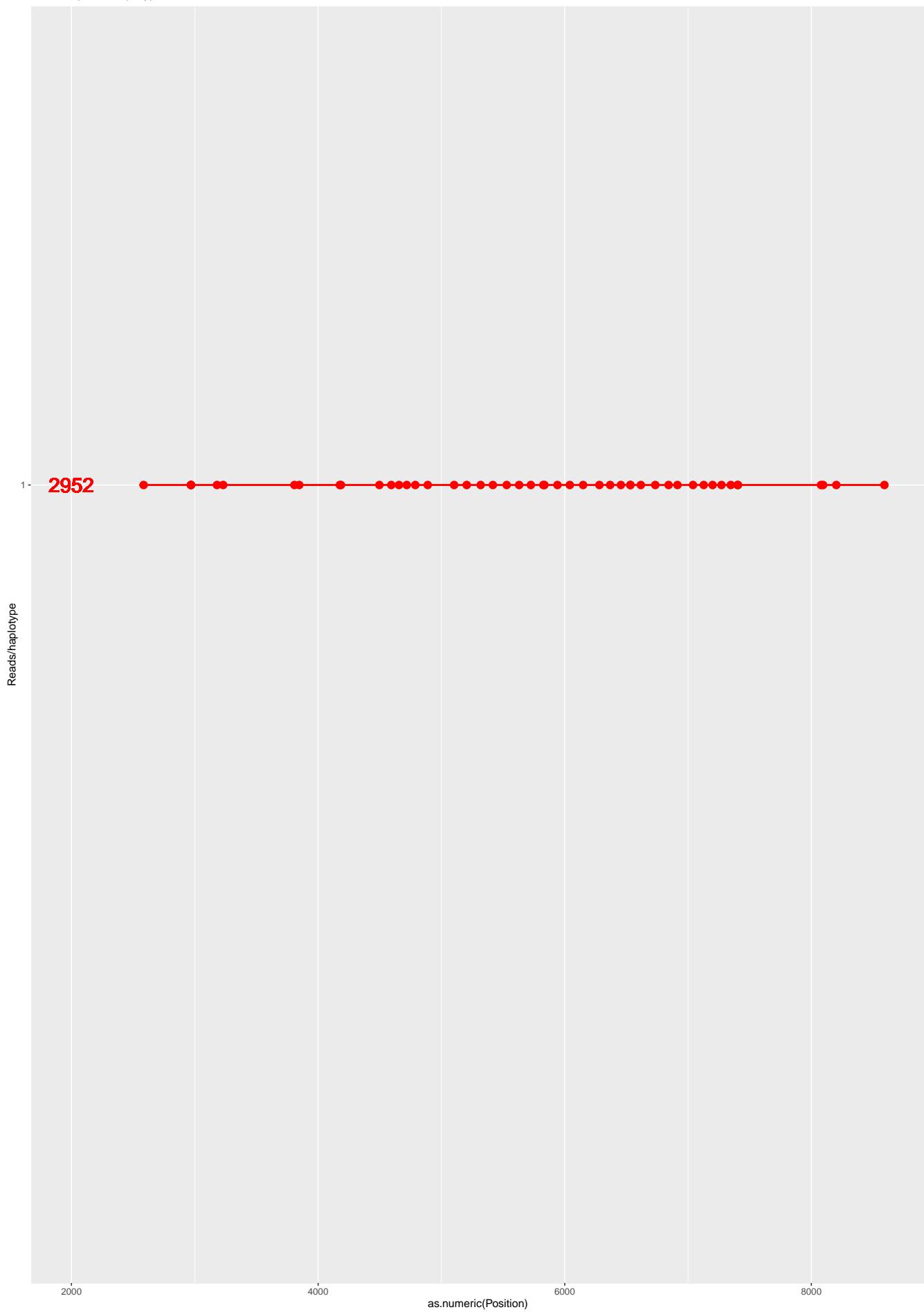


Sample = 62a tetrad = 62 spore = a

Total reads = 3237 PCR=157

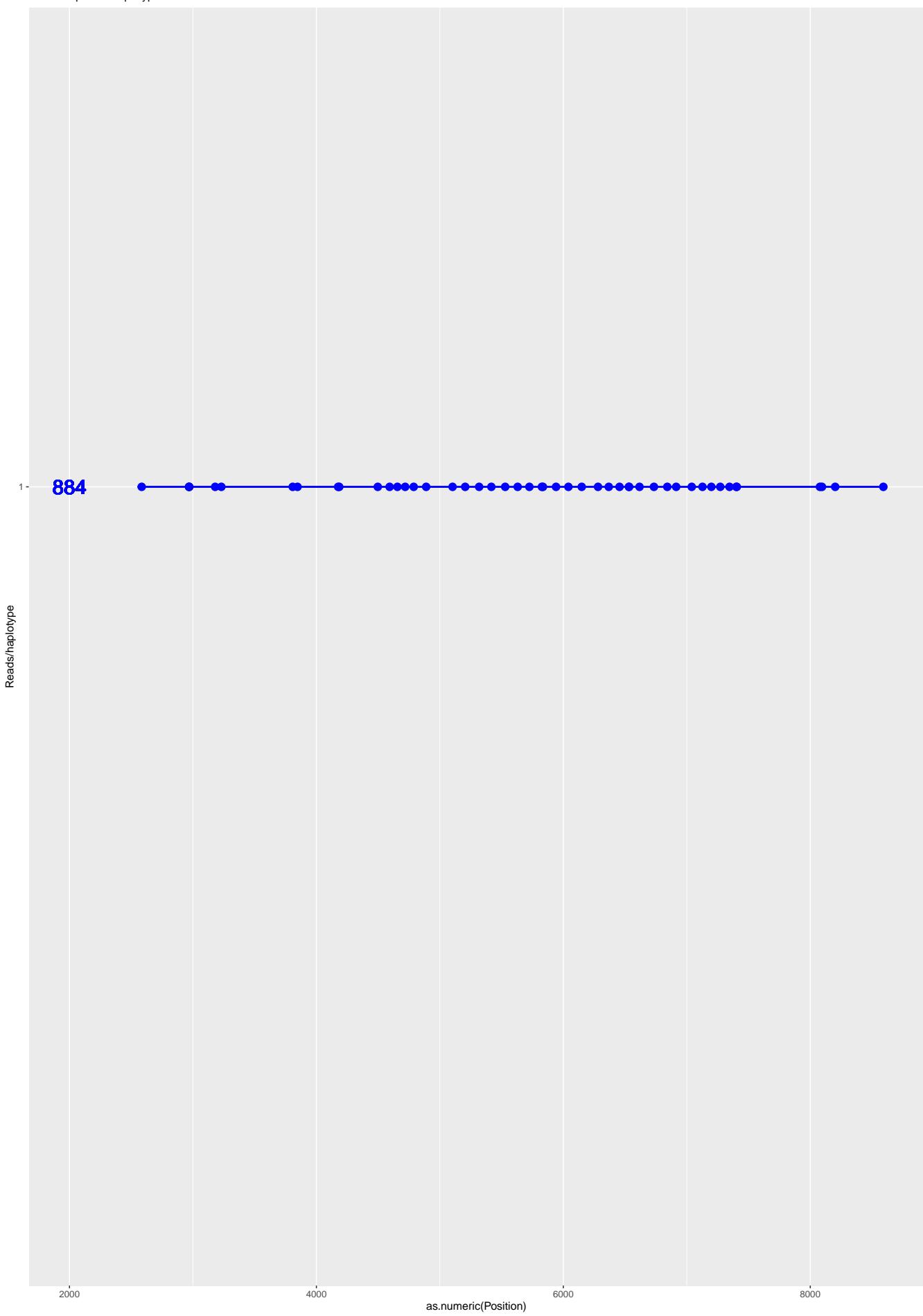
haplotypes I began with n[supporting reads] = 2952

most frequent 7 haplotypes.



barcode = CATAACGCTGTGTAGCA & TACAGCGACGTCATCG

Sample = 62b tetrad = 62 spore = b
Total reads = 1018 PCR=158
haplotypes I began with n[supporting reads] = 884
most frequent 7 haplotypes.



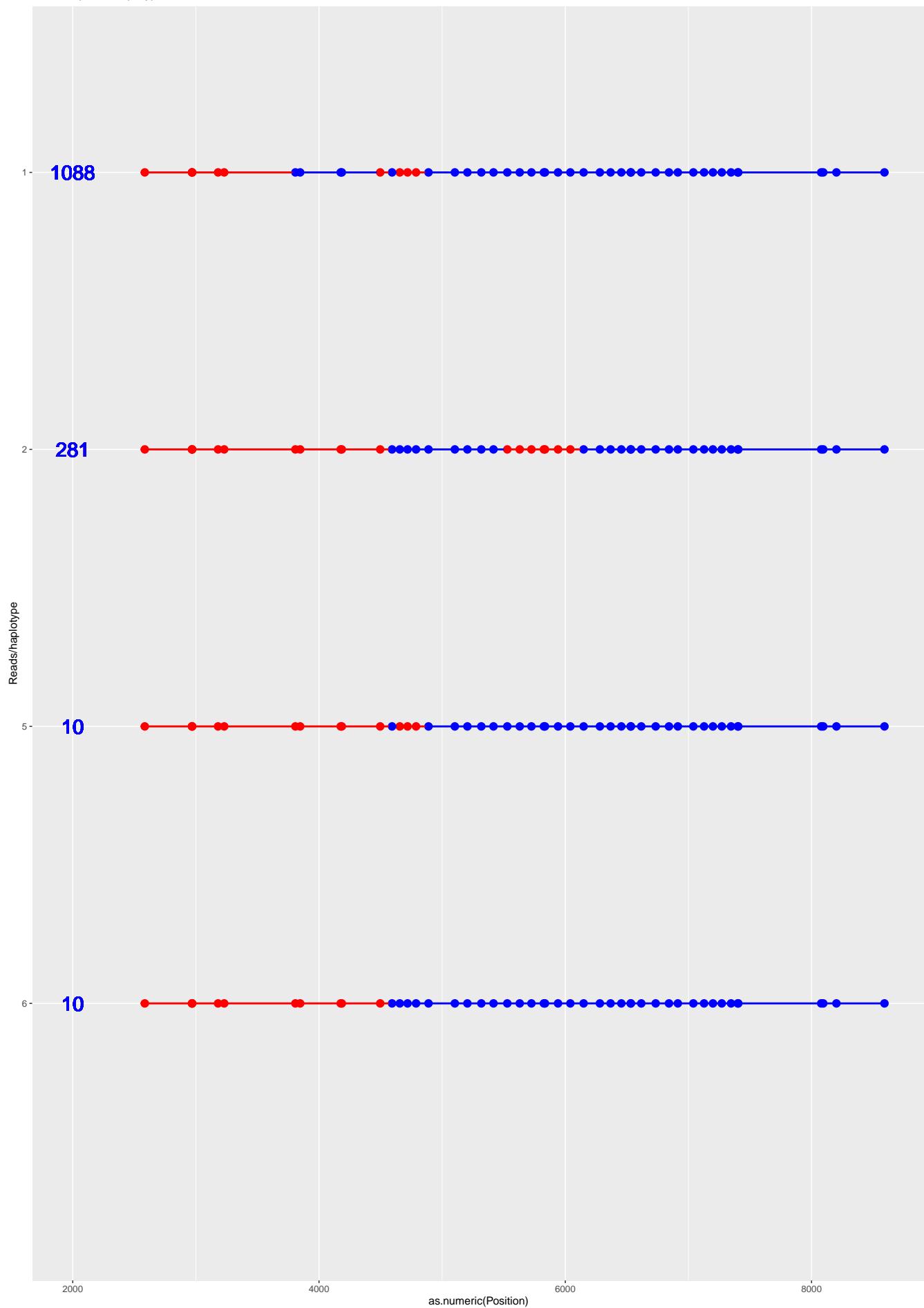
barcode = CATAACGCTGTGTAGCA & GCGCAGACTACGTGTG

Sample = 62c tetrad = 62 spore = c

Total reads = 2495 PCR=159

haplotypes I began with n[supporting reads] = 10, 281, 1088

most frequent 7 haplotypes.

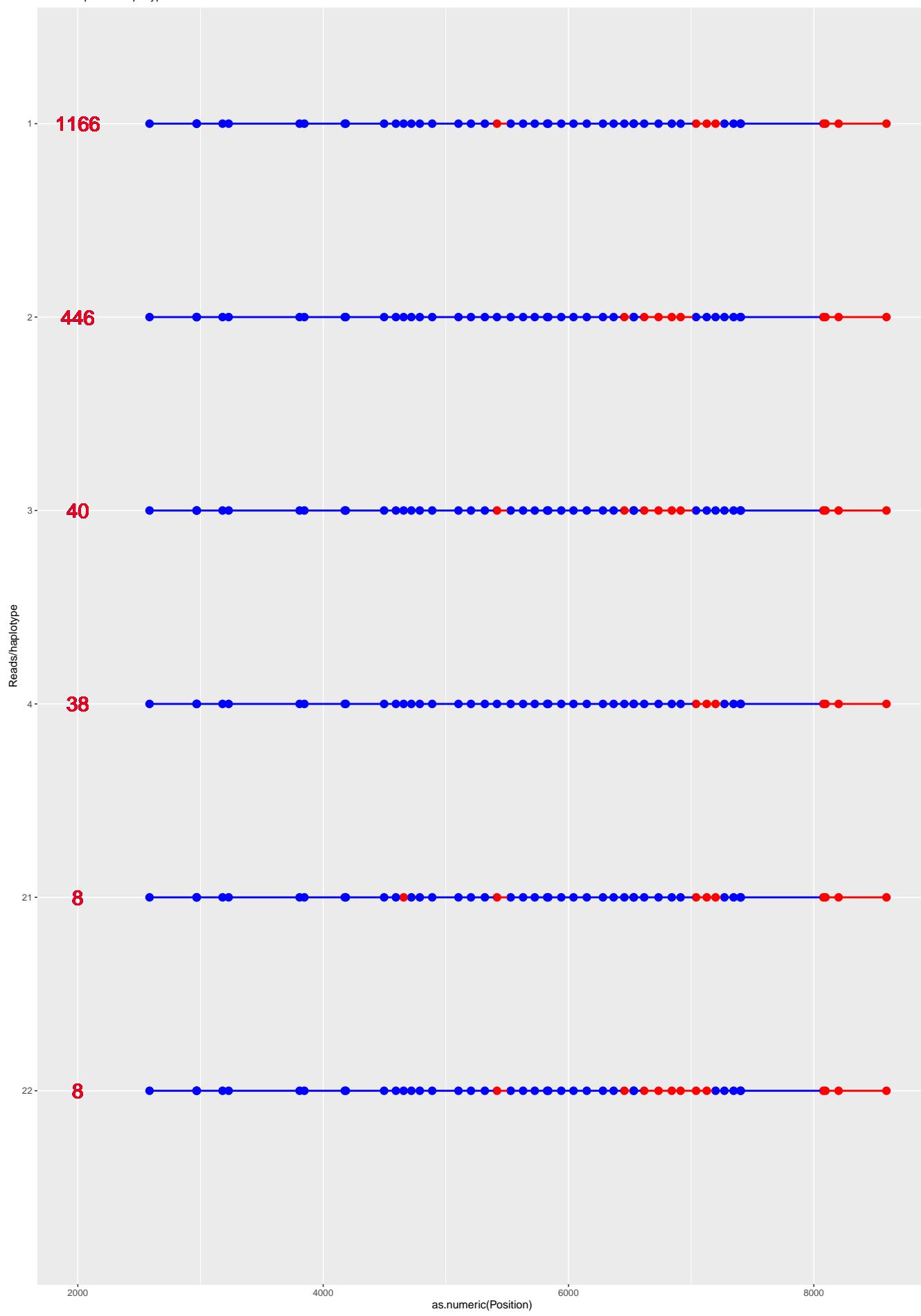


Sample = 62d tetrad = 62 spore = d

Total reads =2985 PCR=160

haplotypes I began with [n(supporting reads)] = 8, 38, 40, 446, 1166

most frequent 7 haplotypes.



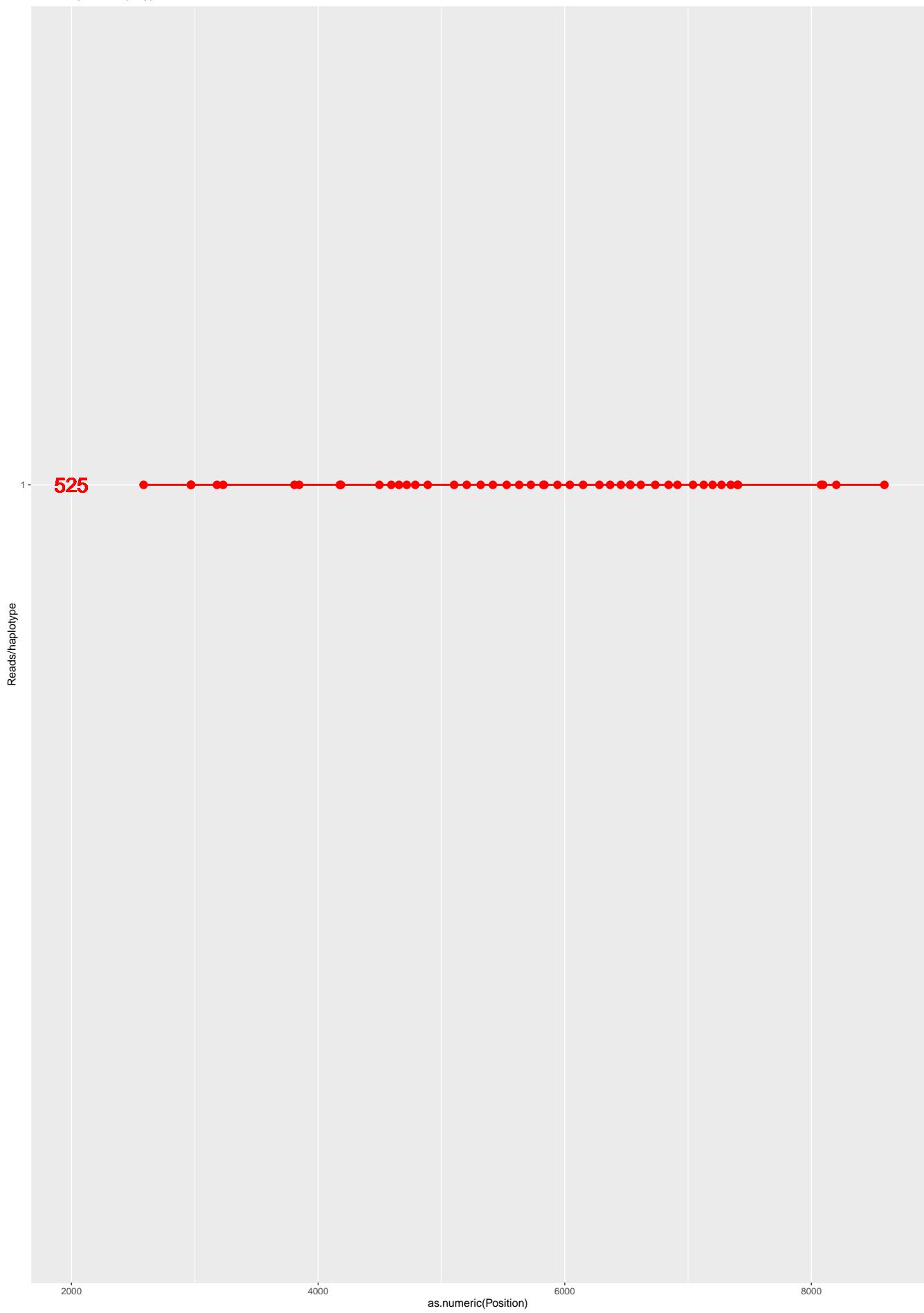
barcode = CATA CGCT GTGT AGCA & AGTATGAGATAGCTCG

Sample = 63a tetrad = 63 spore = a

Total reads =546 PCR=161

haplotypes I began with n[supporting reads] = 525

most frequent 7 haplotypes.



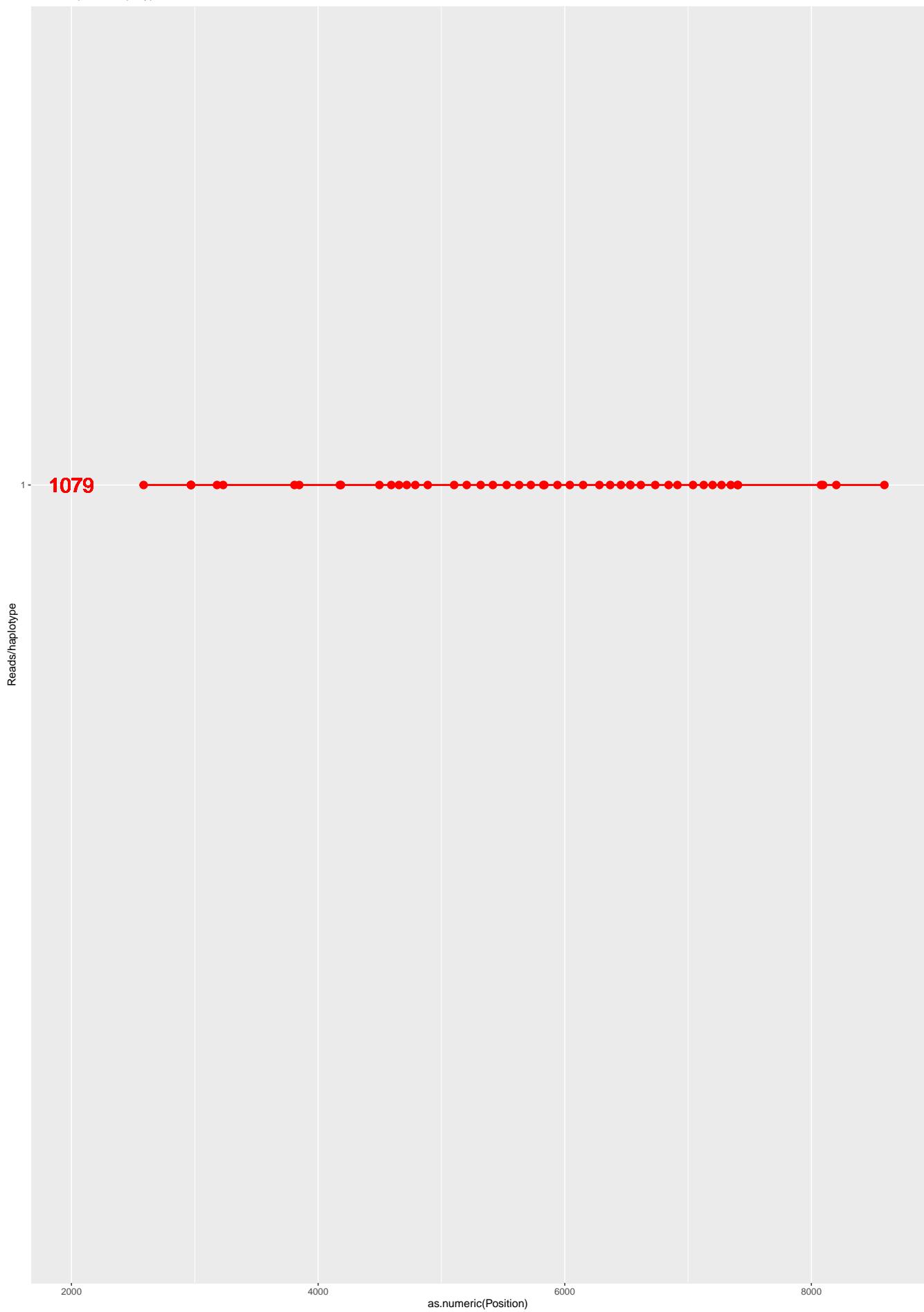
barcode = AGTCGCATGACTGTGT & TCATATGTAGTACTCT

Sample = 63b tetrad = 63 spore = b

Total reads = 1112 PCR=162

haplotypes I began with n[supporting reads] = 1079

most frequent 7 haplotypes.



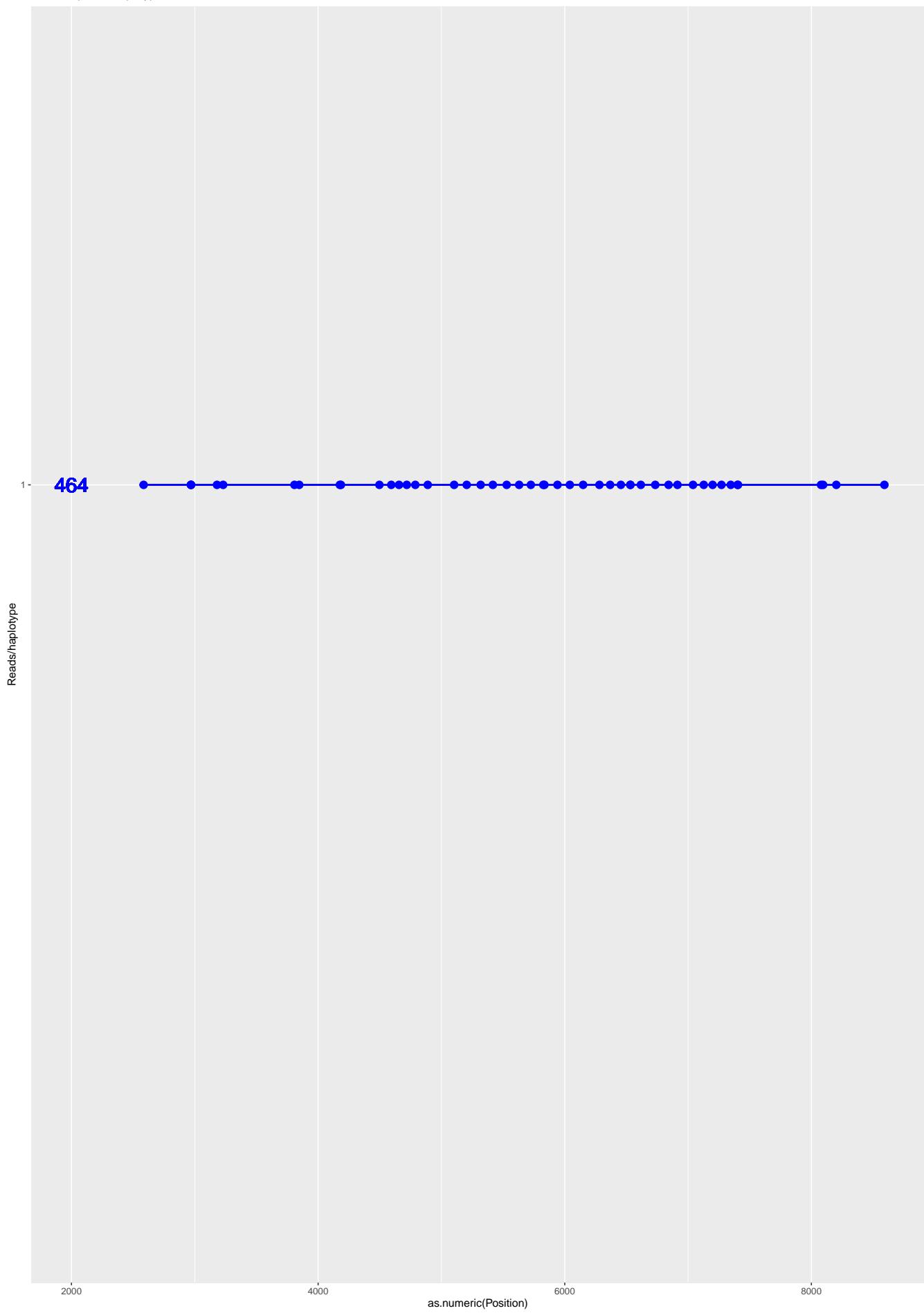
barcode = AGTCGCATGACTGTGT & GCGATCTATGCACACG

Sample = 63c tetrad = 63 spore = c

Total reads =544 PCR=163

haplotypes I began with n[supporting reads] = 464

most frequent 7 haplotypes.



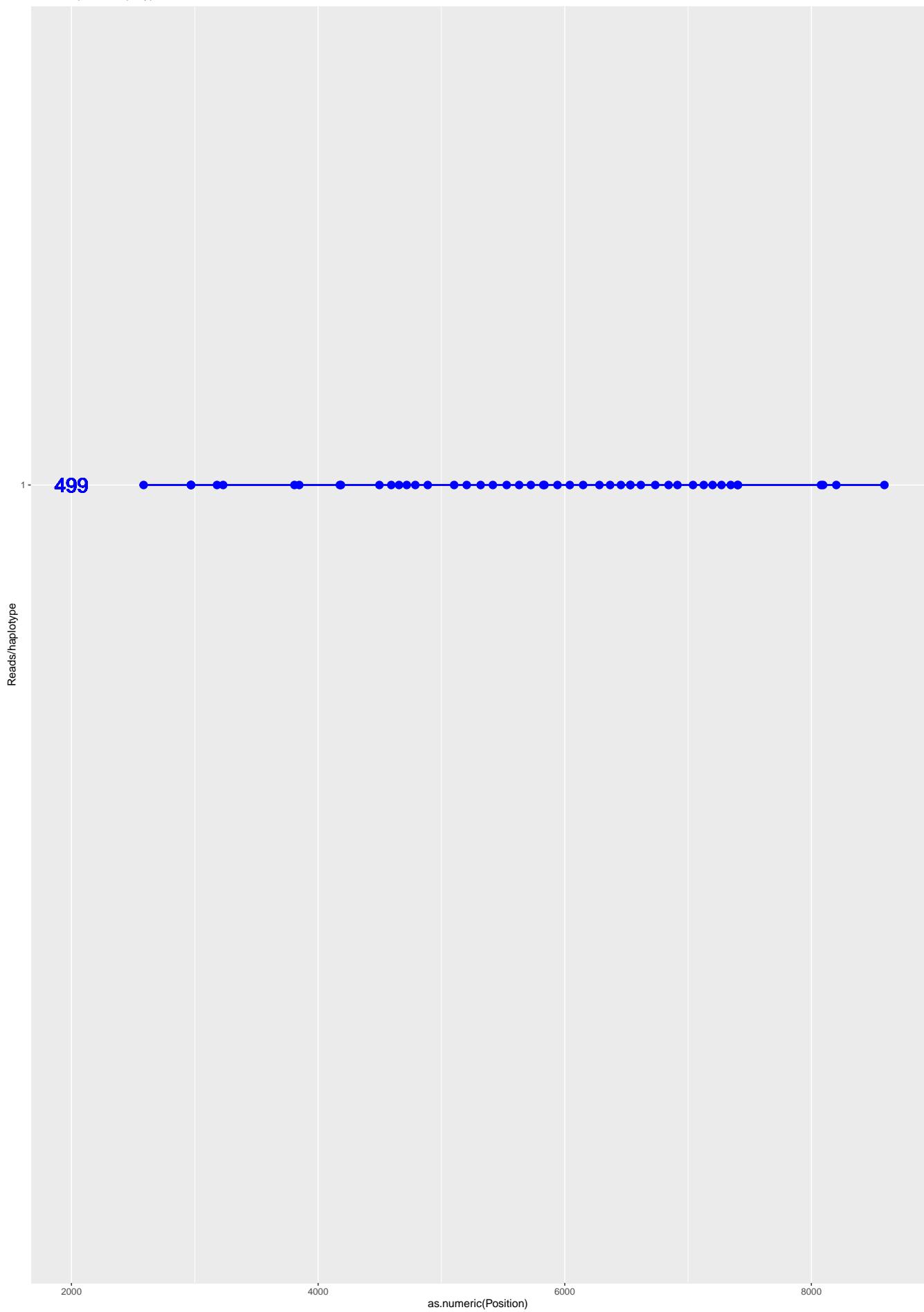
barcode = AGTCGCATGACTGTGT & TGCAGTCGAGATACT

Sample = 63d tetrad = 63 spore = d

Total reads = 592 PCR=164

haplotypes I began with n[supporting reads] = 499

most frequent 7 haplotypes.



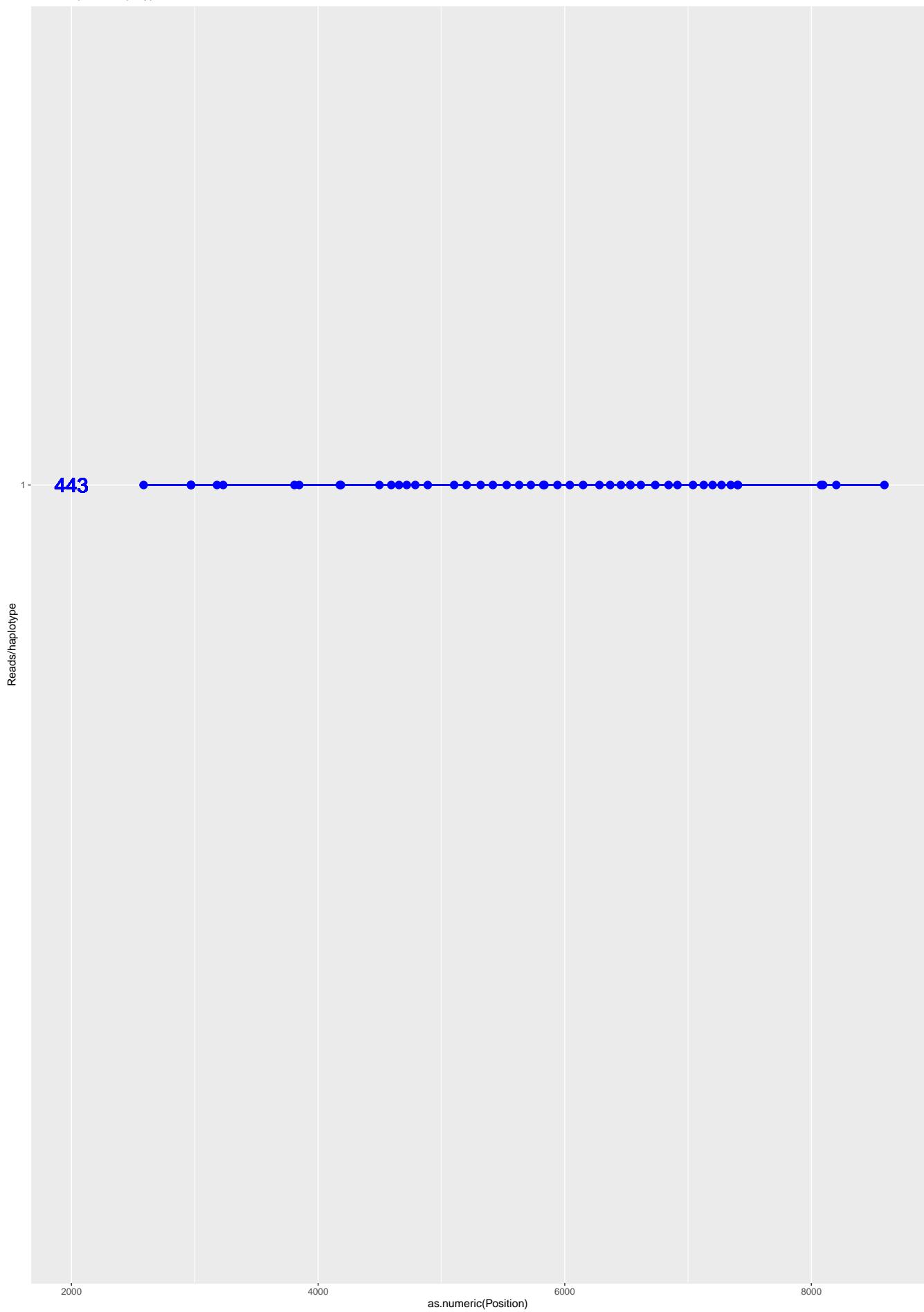
barcode = AGTCGCATGACTGTGT & GACTCTGCGTCGAGTC

Sample = 65a tetrad = 65 spore = a

Total reads = 515 PCR=165

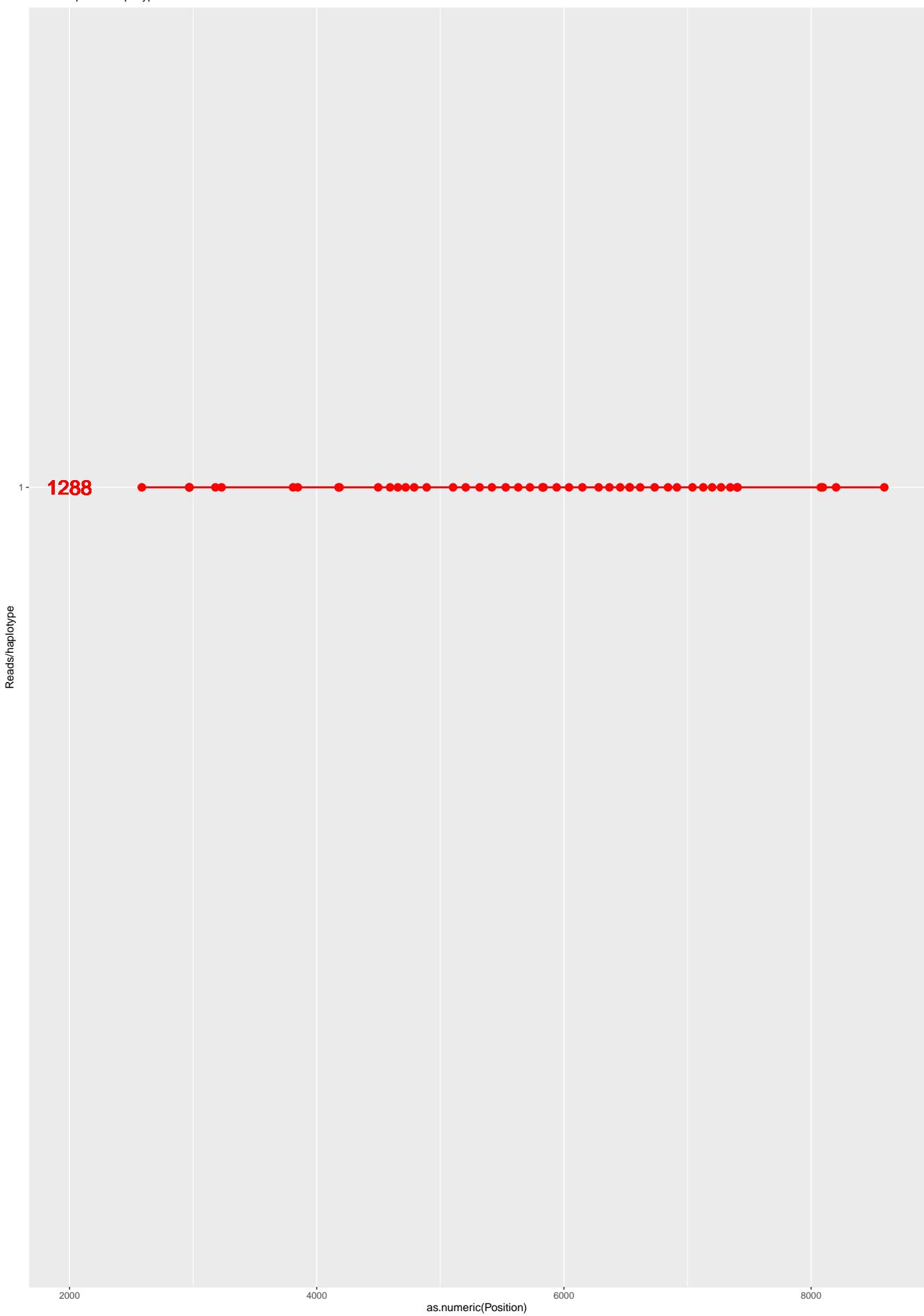
haplotypes I began with n[supporting reads] = 443

most frequent 7 haplotypes.



barcode = AGTCGCATGACTGTGT & TACAGCGACGTCATCG

Sample = 65b tetrad = 65 spore = b
Total reads ≈1337 PCR=166
haplotypes I began with n[supporting reads] = 1288
most frequent 7 haplotypes.



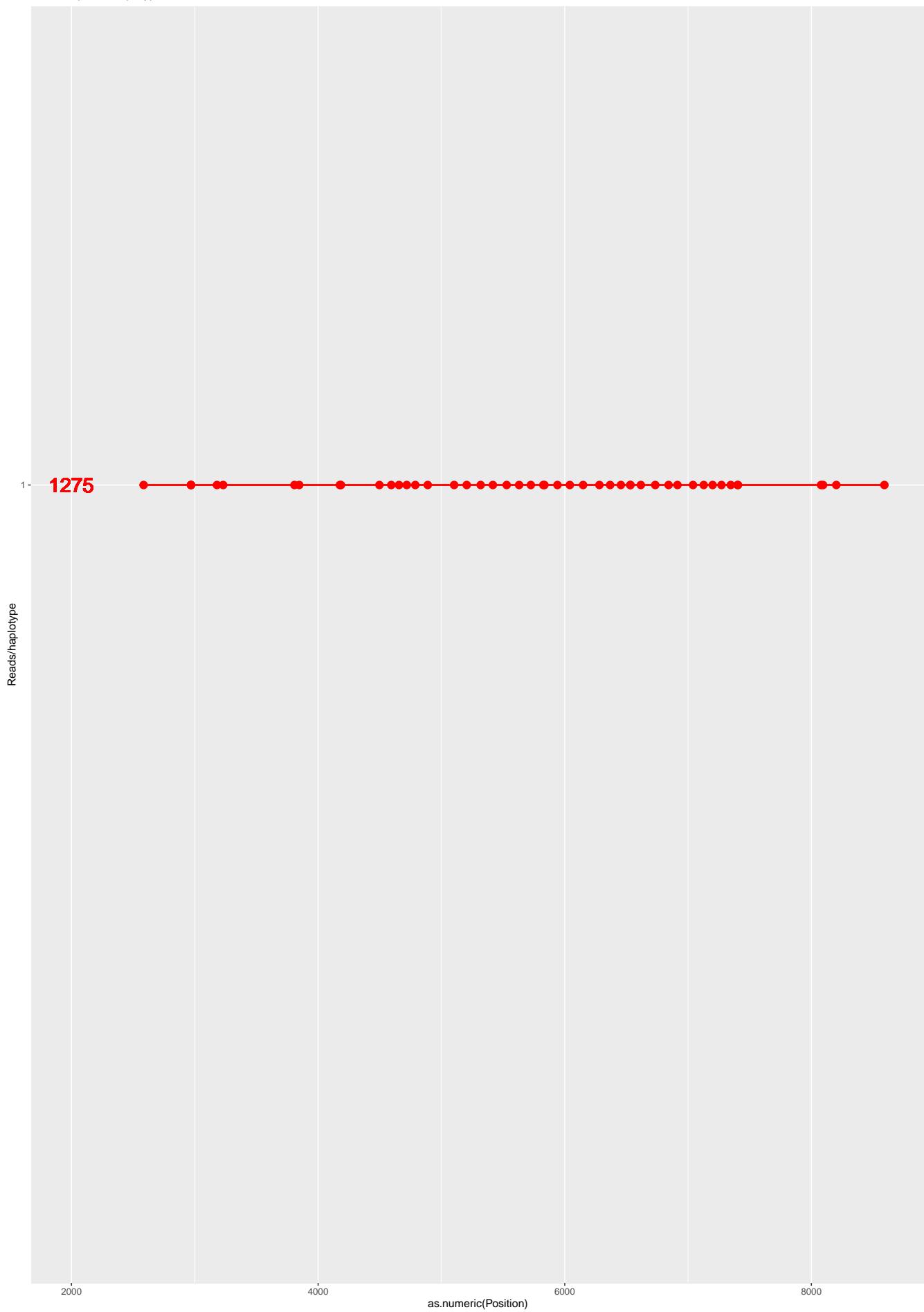
barcode = AGTCGCATGACTGTGT & GCGCAGACTACGTGTG

Sample = 65c tetrad = 65 spore = c

Total reads = 1320 PCR=167

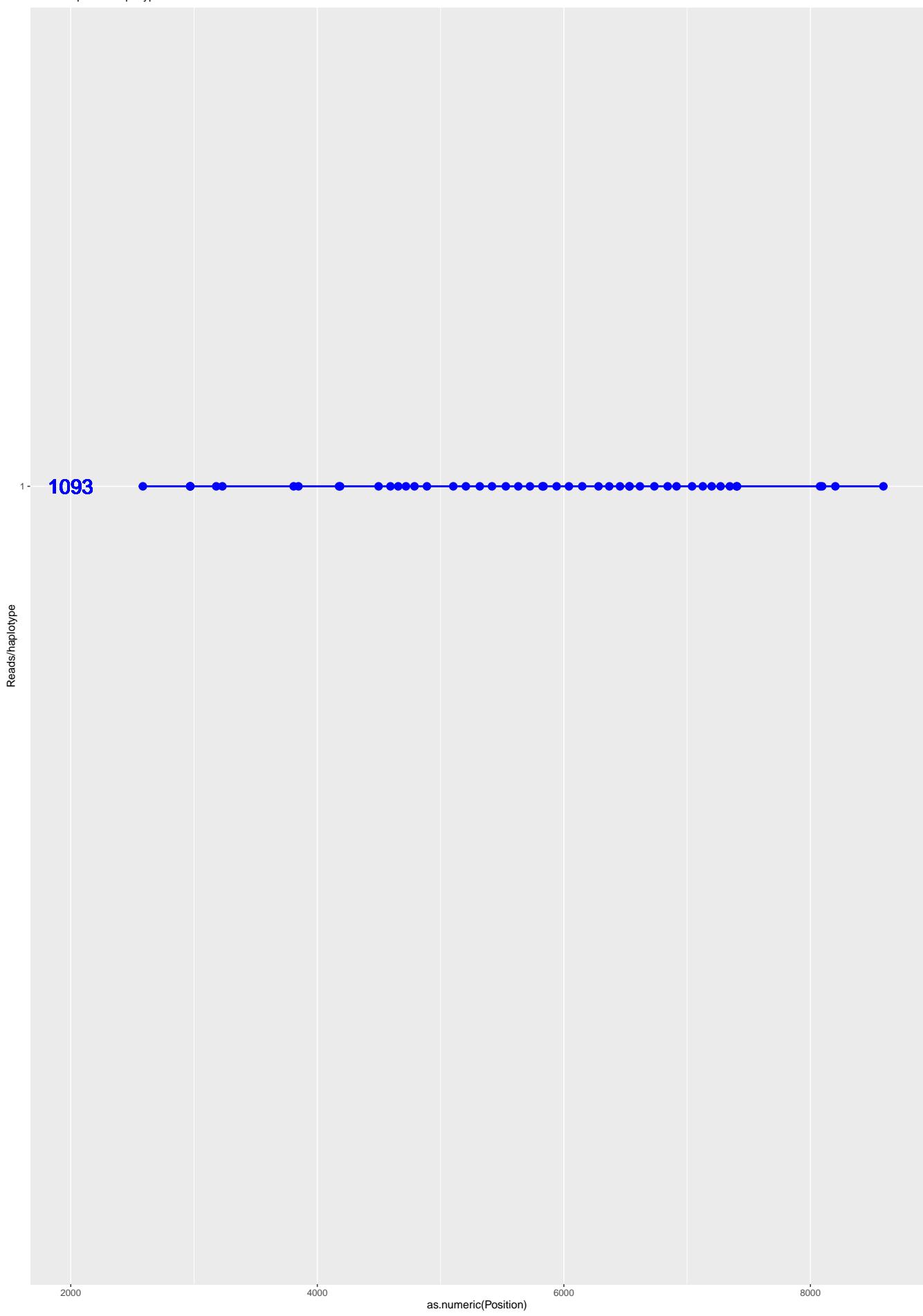
haplotypes I began with n[supporting reads] = 1275

most frequent 7 haplotypes.

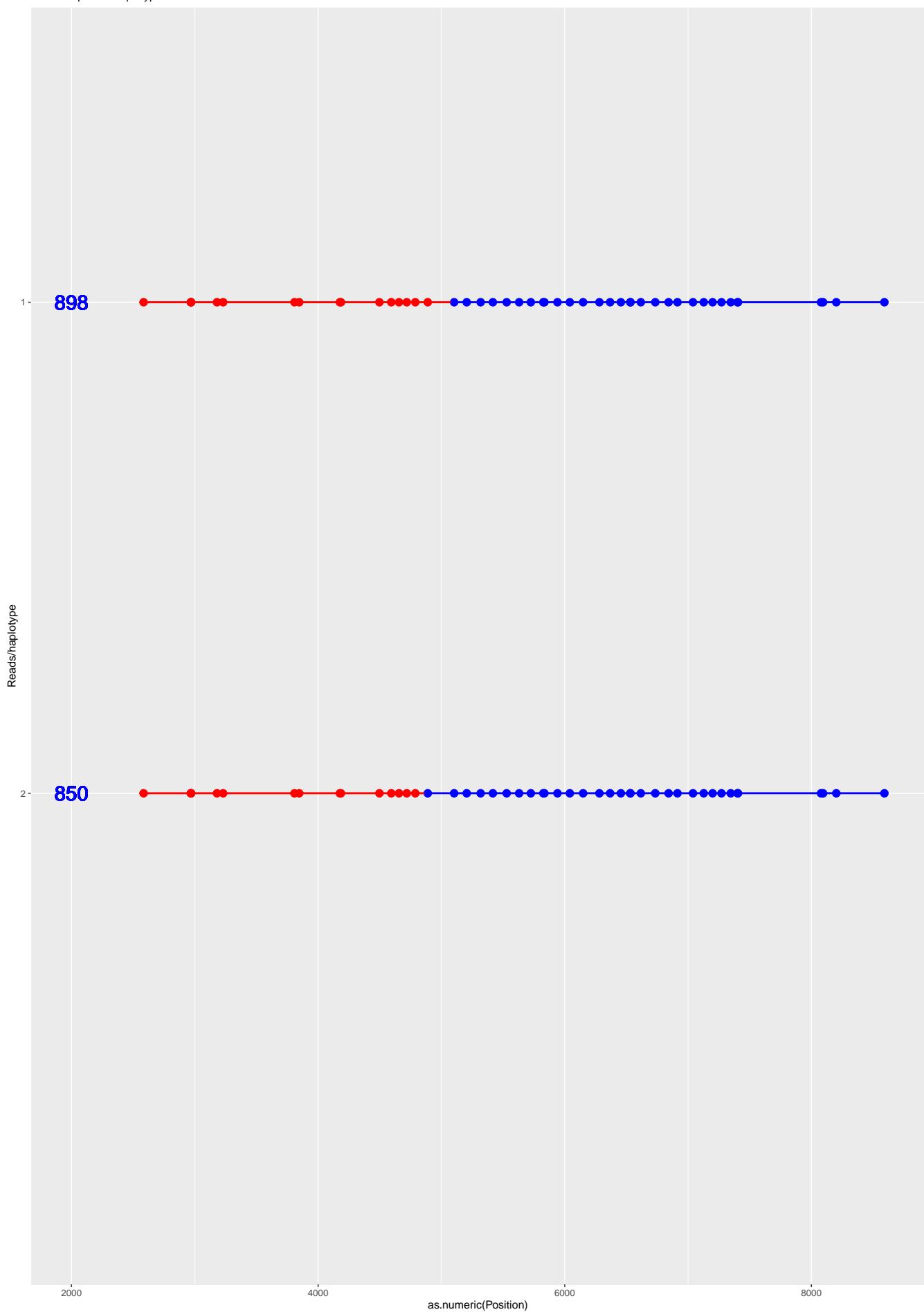


barcode = AGTCGCATGACTGTGT & GTCTCTGCGATAACAGC

Sample = 65d tetrad = 65 spore = d
Total reads = 1266 PCR=168
haplotypes I began with n[supporting reads] = 1093
most frequent 7 haplotypes.



Sample = 67a tetrad = 67 spore = a
Total reads = 2170 PCR=169
haplotypes I began with n[supporting reads] = 850, 898
most frequent 7 haplotypes.



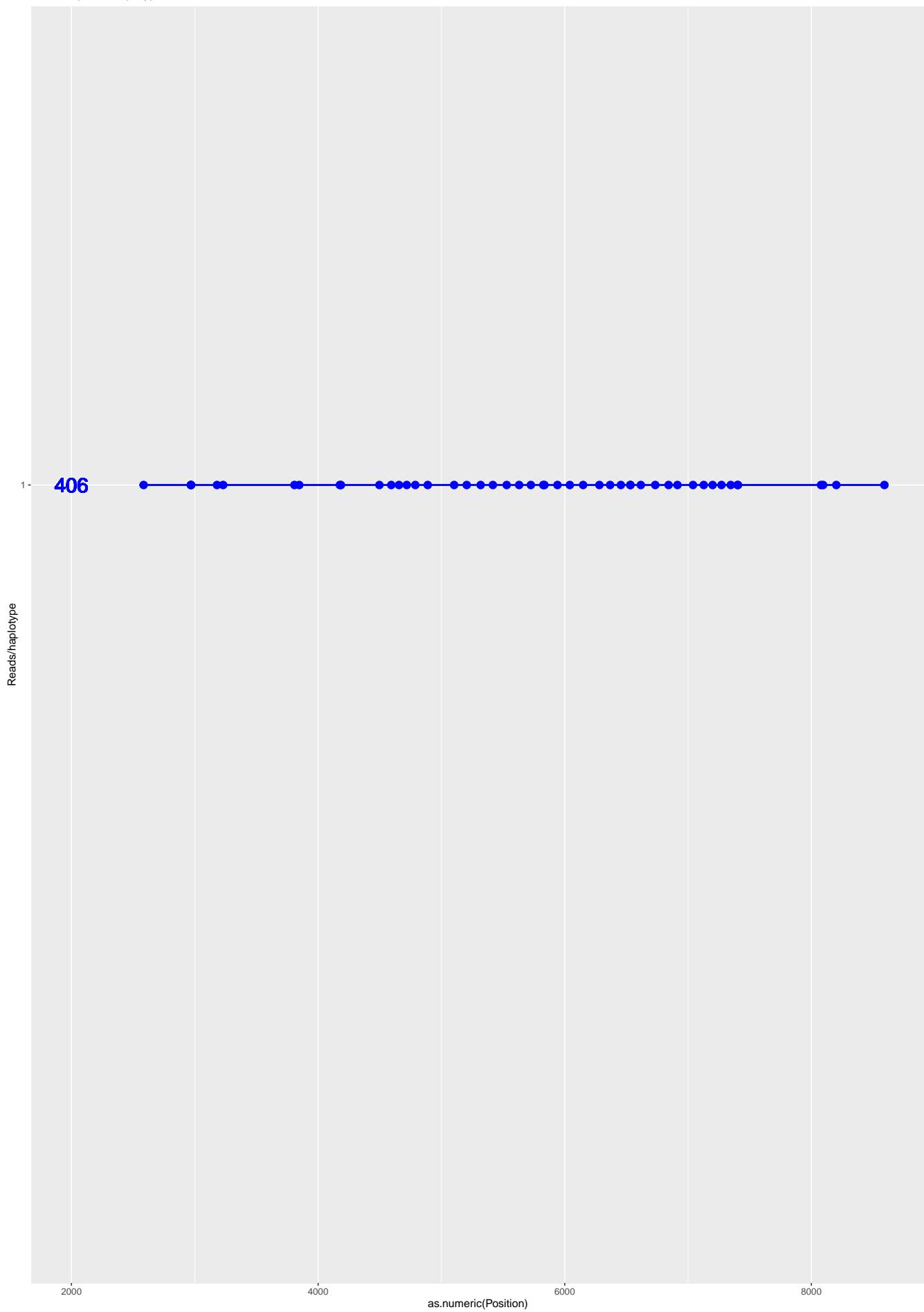
barcode = CAGTACTGCACGATCG & TCATATGTAGTACTCT

Sample = 67b tetrad = 67 spore = b

Total reads = 479 PCR=170

haplotypes I began with n[supporting reads] = 406

most frequent 7 haplotypes.



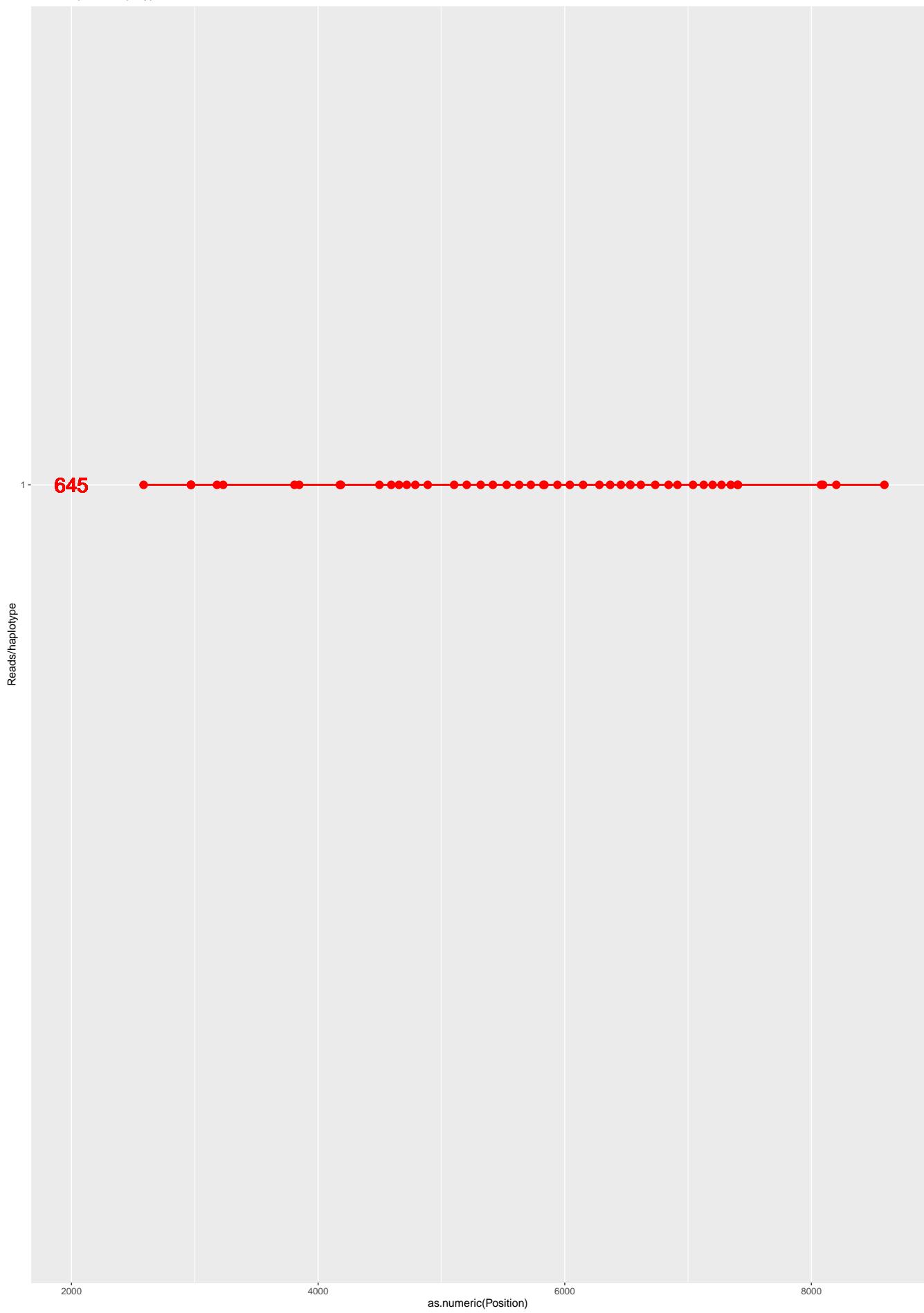
barcode = CAGTACTGCACGATCG & GCGATCTATGCACACG

Sample = 67c tetrad = 67 spore = c

Total reads = 680 PCR=171

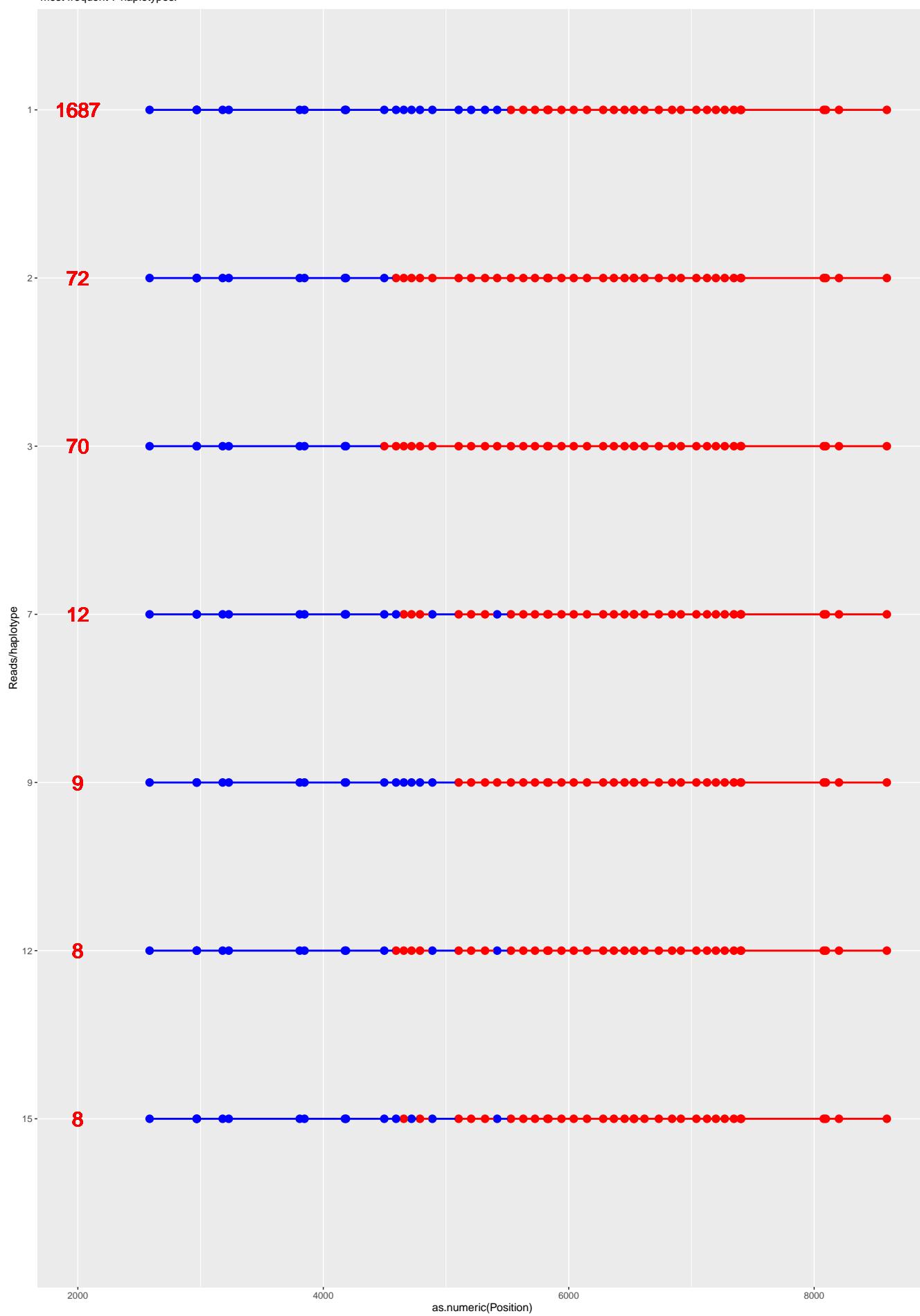
haplotypes I began with n[supporting reads] = 645

most frequent 7 haplotypes.

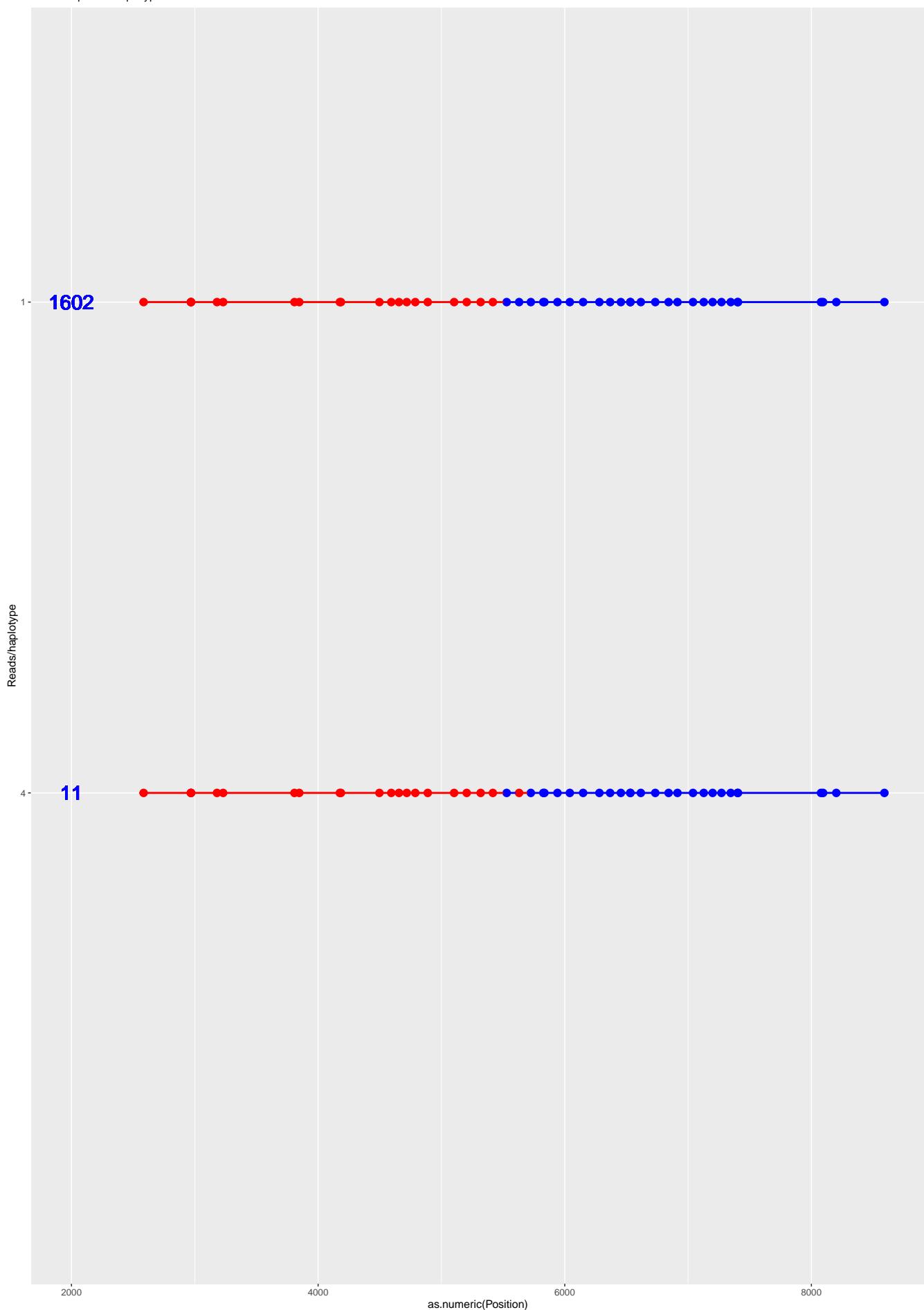


barcode = CAGTACTGCACGATCG & TGCAGTCGAGATACT

Sample = 67d tetrad = 67 spore = d
Total reads = 2780 PCR=172
haplotypes I began with [n|supporting reads] = 8, 9, 12, 70, 72, 1687
most frequent 7 haplotypes.



Sample = 69a tetrad = 69 spore = a
Total reads = 1909 PCR=173
haplotypes I began with n[supporting reads] = 11, 1602
most frequent 7 haplotypes.



barcode = CAGTACTGCACGATCG & TACAGCGACGTCATCG

Sample = 69b tetrad = 69 spore = b
Total reads = 2036 PCR=174
haplotypes I began with n[supporting reads] = 8, 1763
most frequent 7 haplotypes.



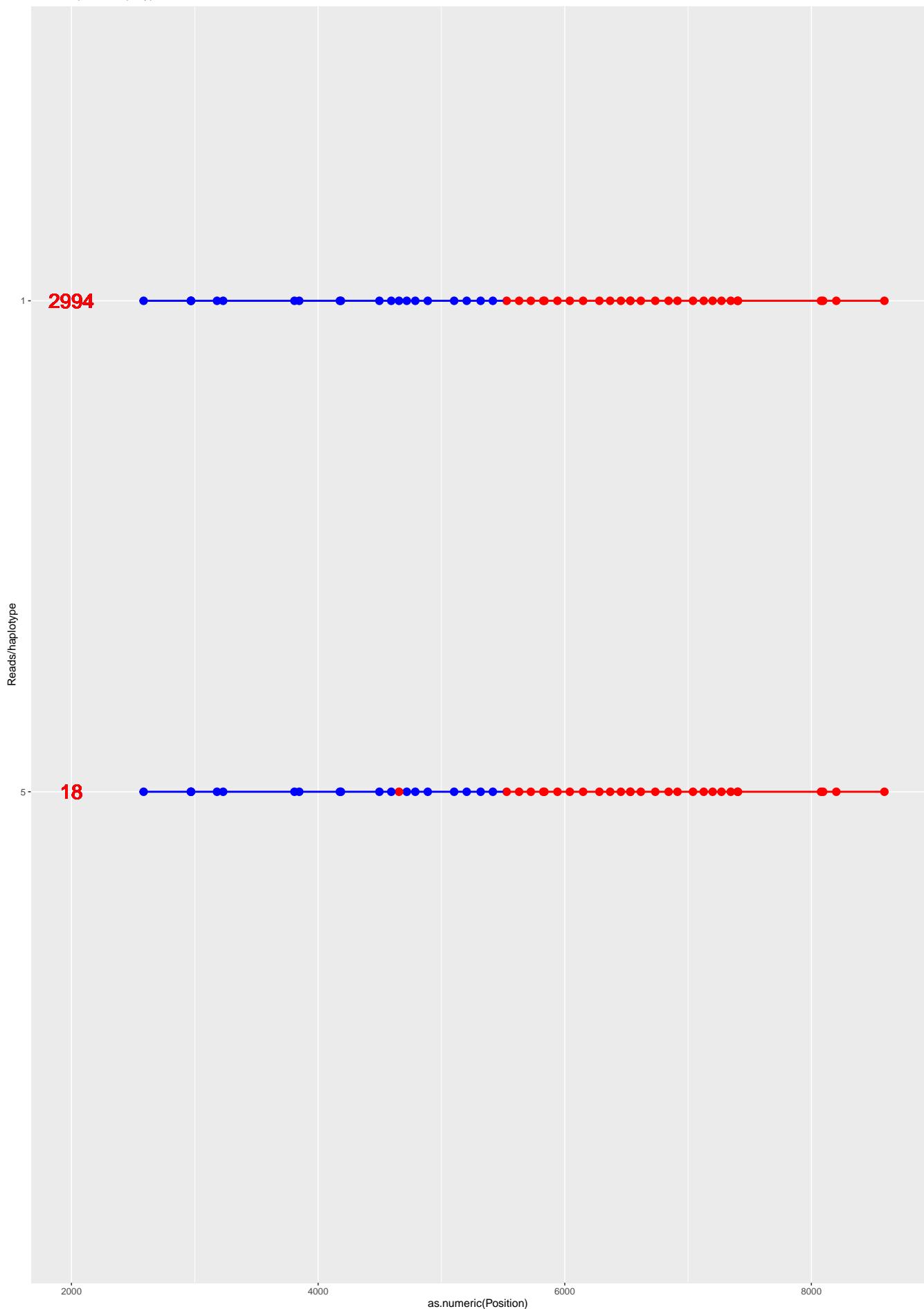
barcode = CAGTACTGCACGATCG & GCGCAGACTACGTGTG

Sample = 69c tetrad = 69 spore = c

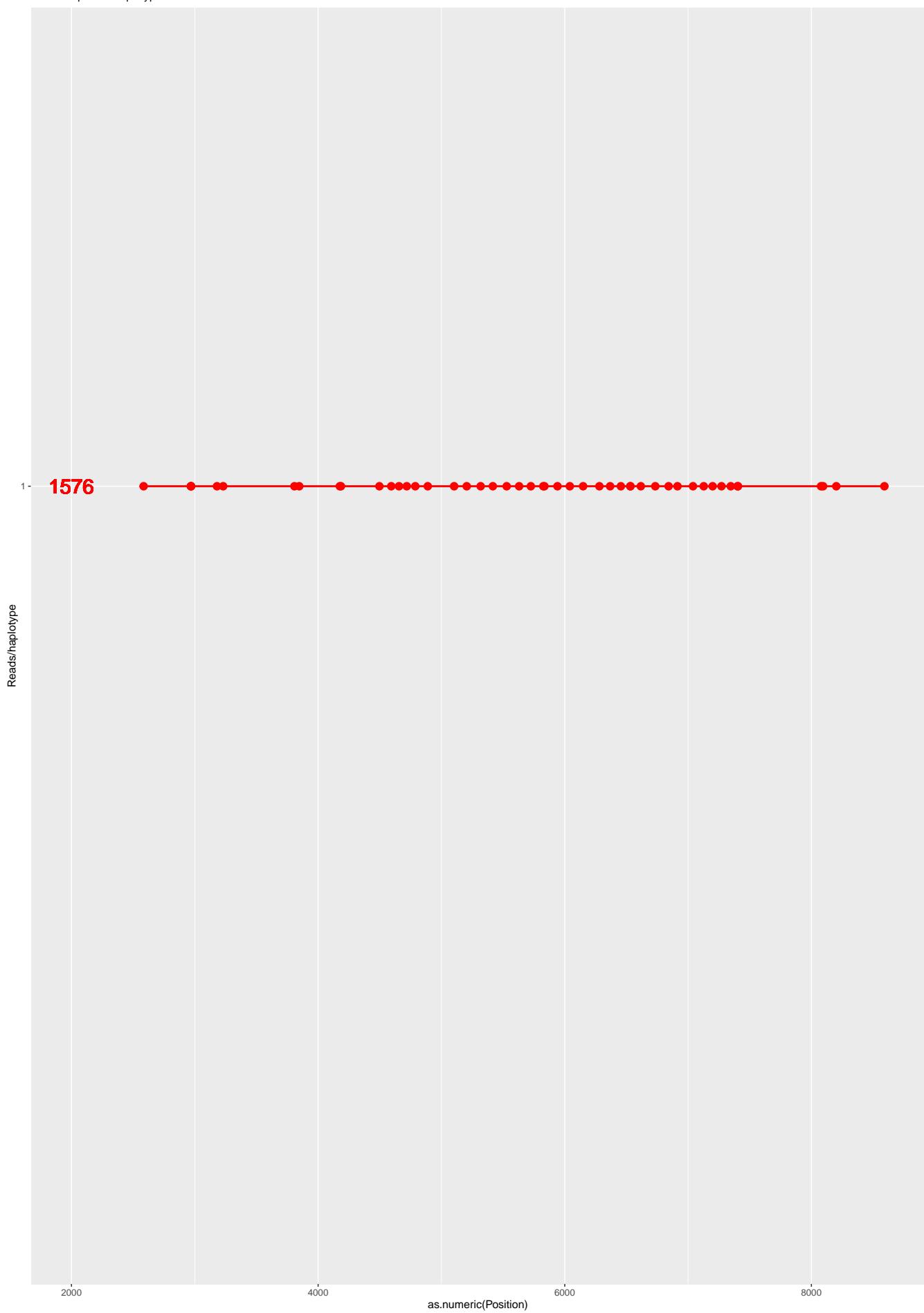
Total reads = 3442 PCR=175

haplotypes I began with n[supporting reads] = 18, 2994

most frequent 7 haplotypes.



Sample = 69d tetrad = 69 spore = d
Total reads = 1644 PCR=176
haplotypes I began with n[supporting reads] = 1576
most frequent 7 haplotypes.



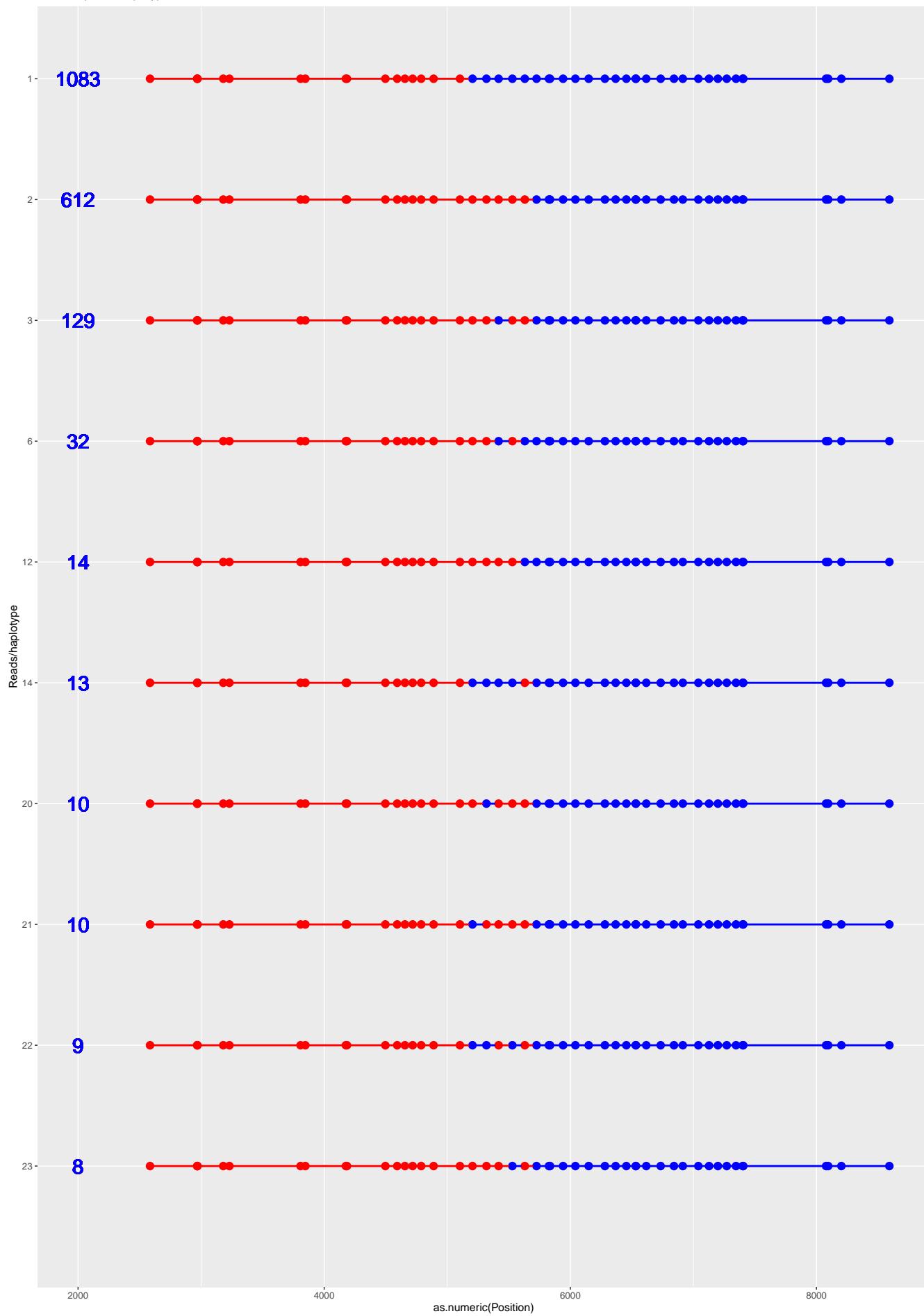
barcode = CAGTACTGCACGATCG & AGTATGAGATAGCTCG

Sample = 72a tetrad = 72 spore = a

Total reads =2491 PCR=181

haplotypes I began with [n(supporting reads)] = 8, 9, 10, 13, 14, 32, 129, 612, 1083

most frequent 7 haplotypes.



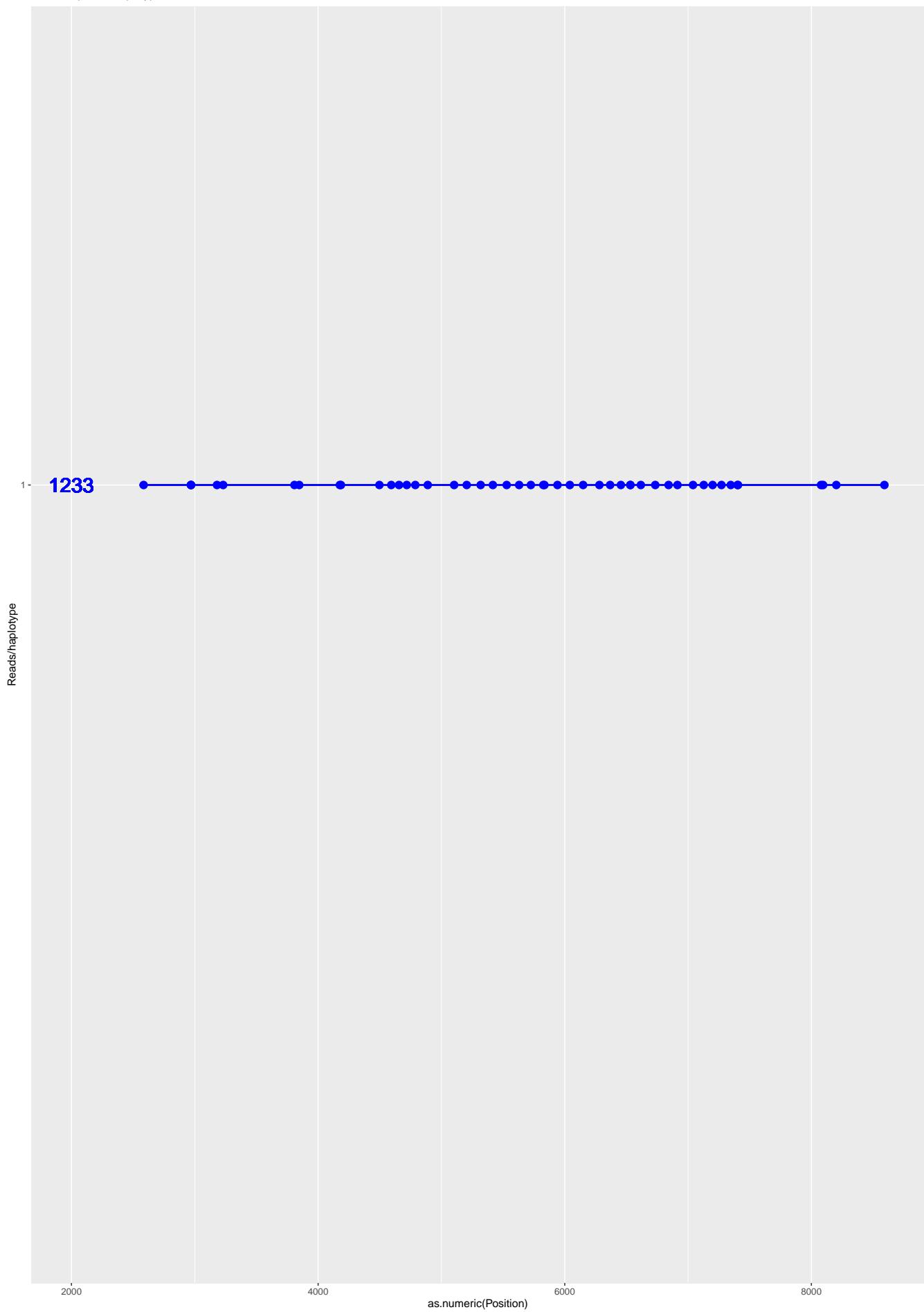
barcode = GTGCTGAGCATCAGAC & TACAGCGACGTATCG

Sample = 72b tetrad = 72 spore = b

Total reads = 1435 PCR=182

haplotypes I began with n[supporting reads] = 1233

most frequent 7 haplotypes.



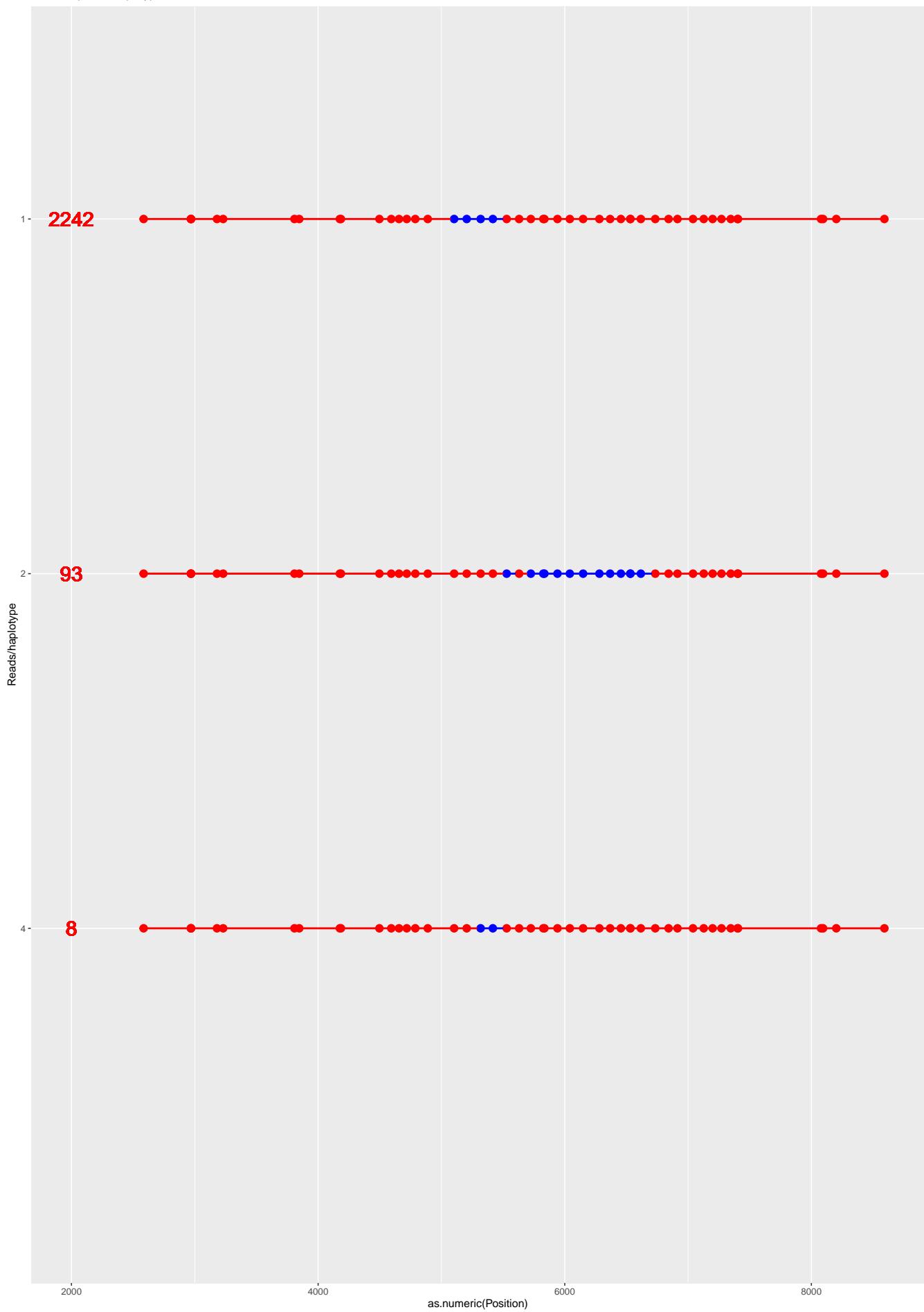
barcode = GTGCTGAGCATCAGAC & GCGCAGACTACGTGTG

Sample = 72c tetrad = 72 spore = c

Total reads = 3197 PCR=183

haplotypes I began with n[supporting reads] = 8, 93, 2242

most frequent 7 haplotypes.

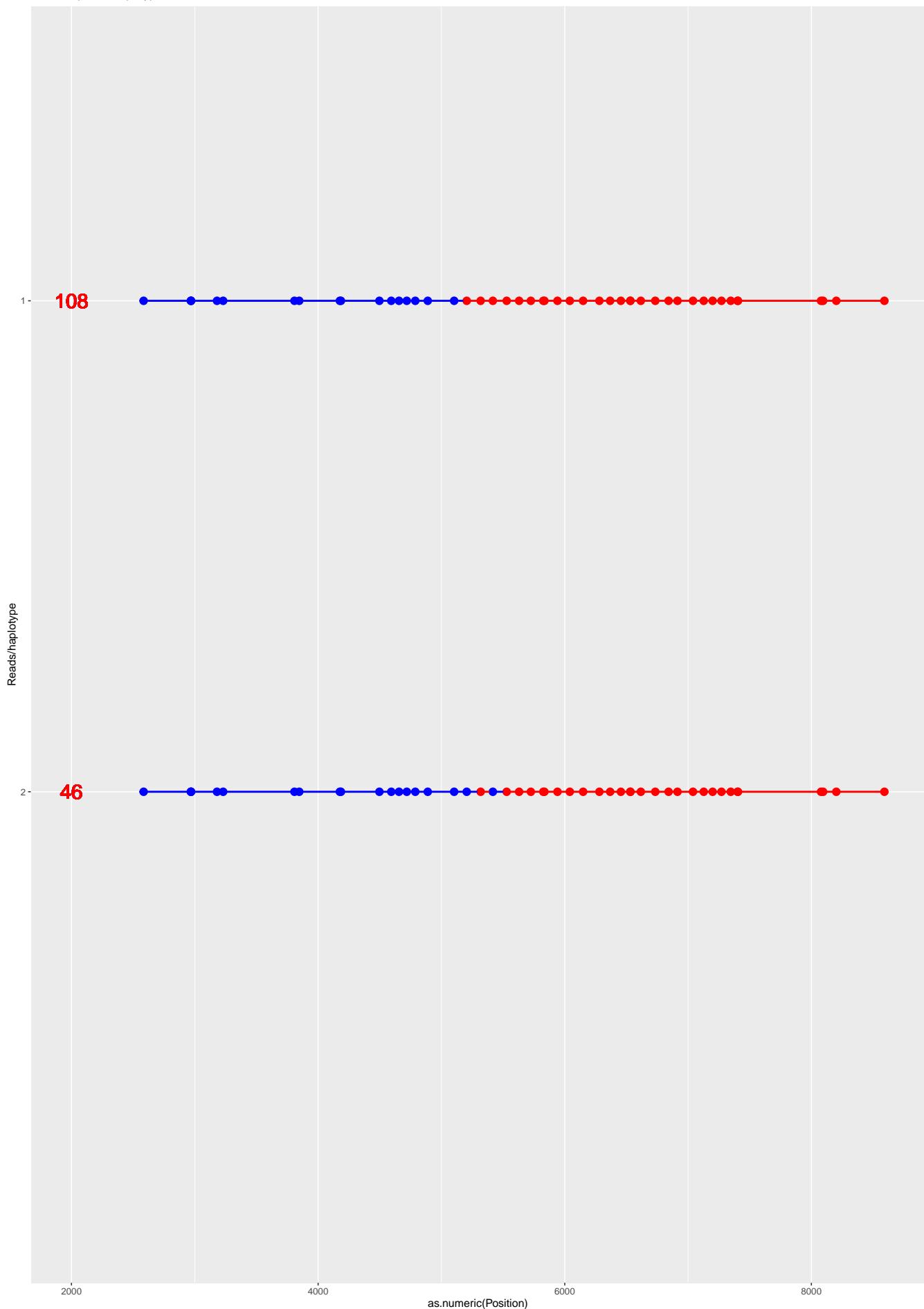


Sample = 72d tetrad = 72 spore = d

Total reads = 182 PCR=184

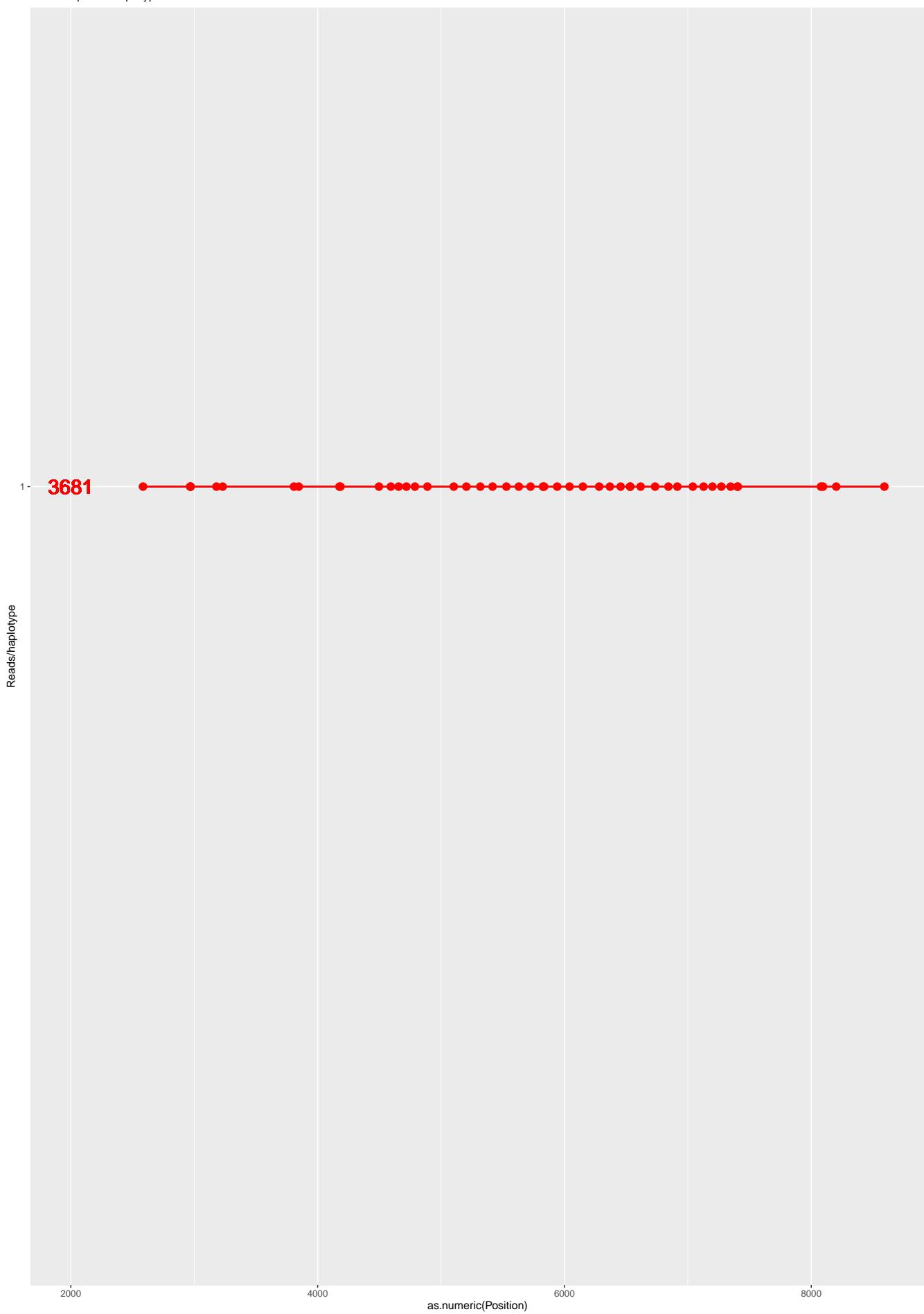
haplotypes I began with n[supporting reads] = 46, 108

most frequent 7 haplotypes.



barcode = GTGCTGAGCAGCATCAGAC & AGTATGAGATAGCTCG

Sample = 75a tetrad = 75 spore = a
Total reads = 3837 PCR=189
haplotypes I began with n[supporting reads] = 3681
most frequent 7 haplotypes.

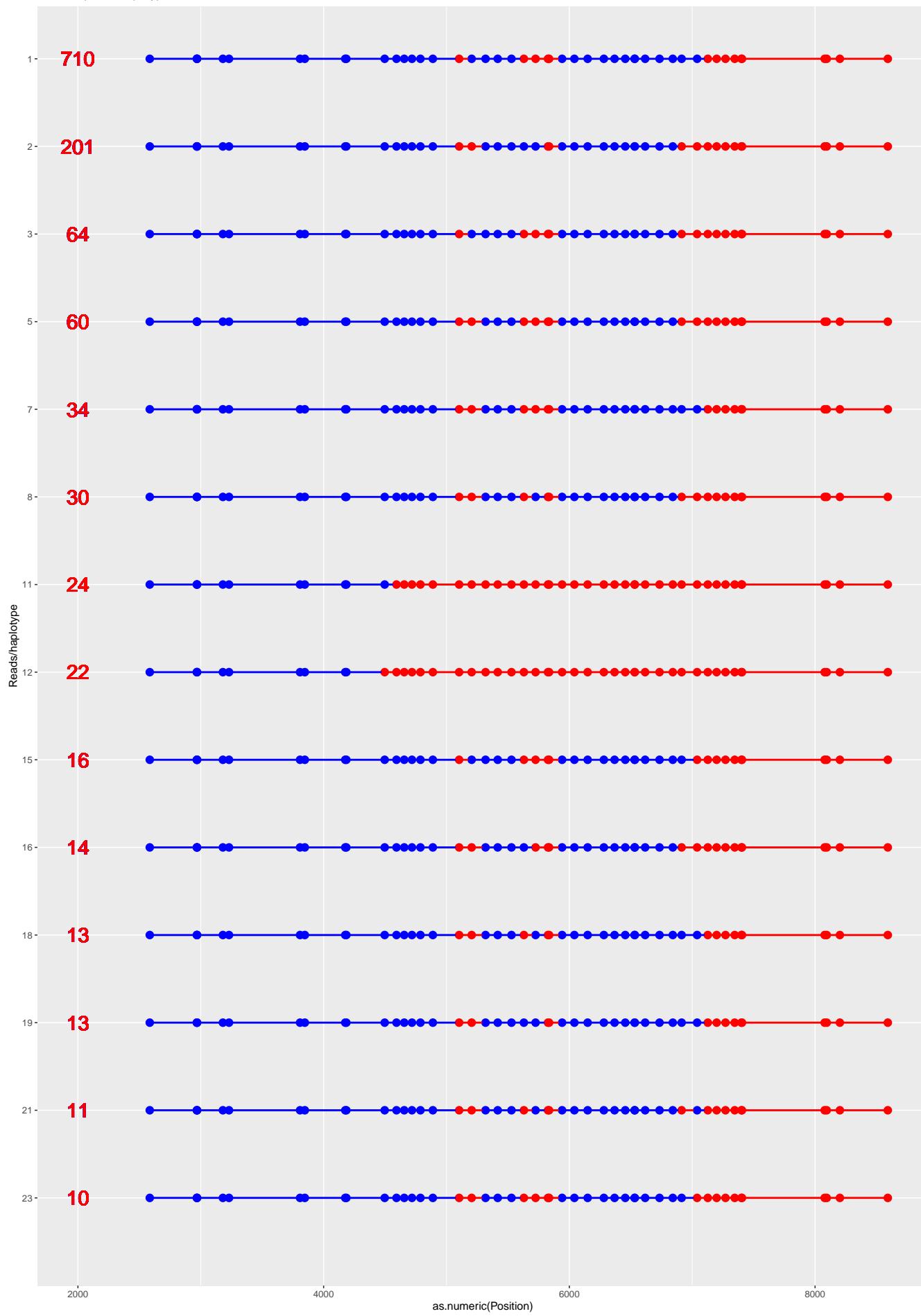


Sample = 75b tetrad = 75 spore = b

Total reads = 2133 PCR=190

haplotypes I began with [n(supporting reads)] = 10, 11, 13, 14, 16, 22, 24, 30, 34, 60, 64, 201, 710

most frequent 7 haplotypes.

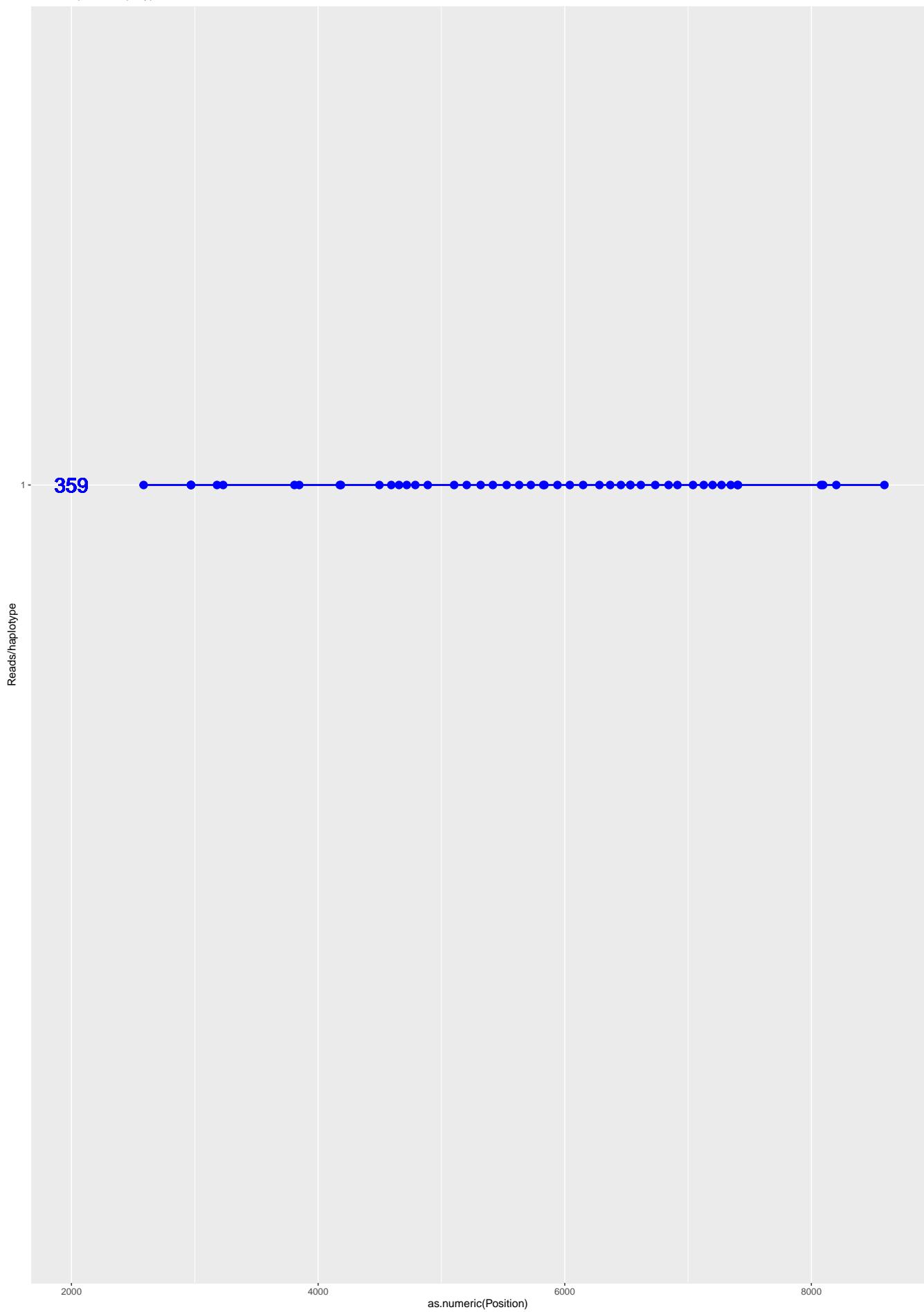


Sample = 75c tetrad = 75 spore = c

Total reads = 416 PCR=191

haplotypes I began with n[supporting reads] = 359

most frequent 7 haplotypes.



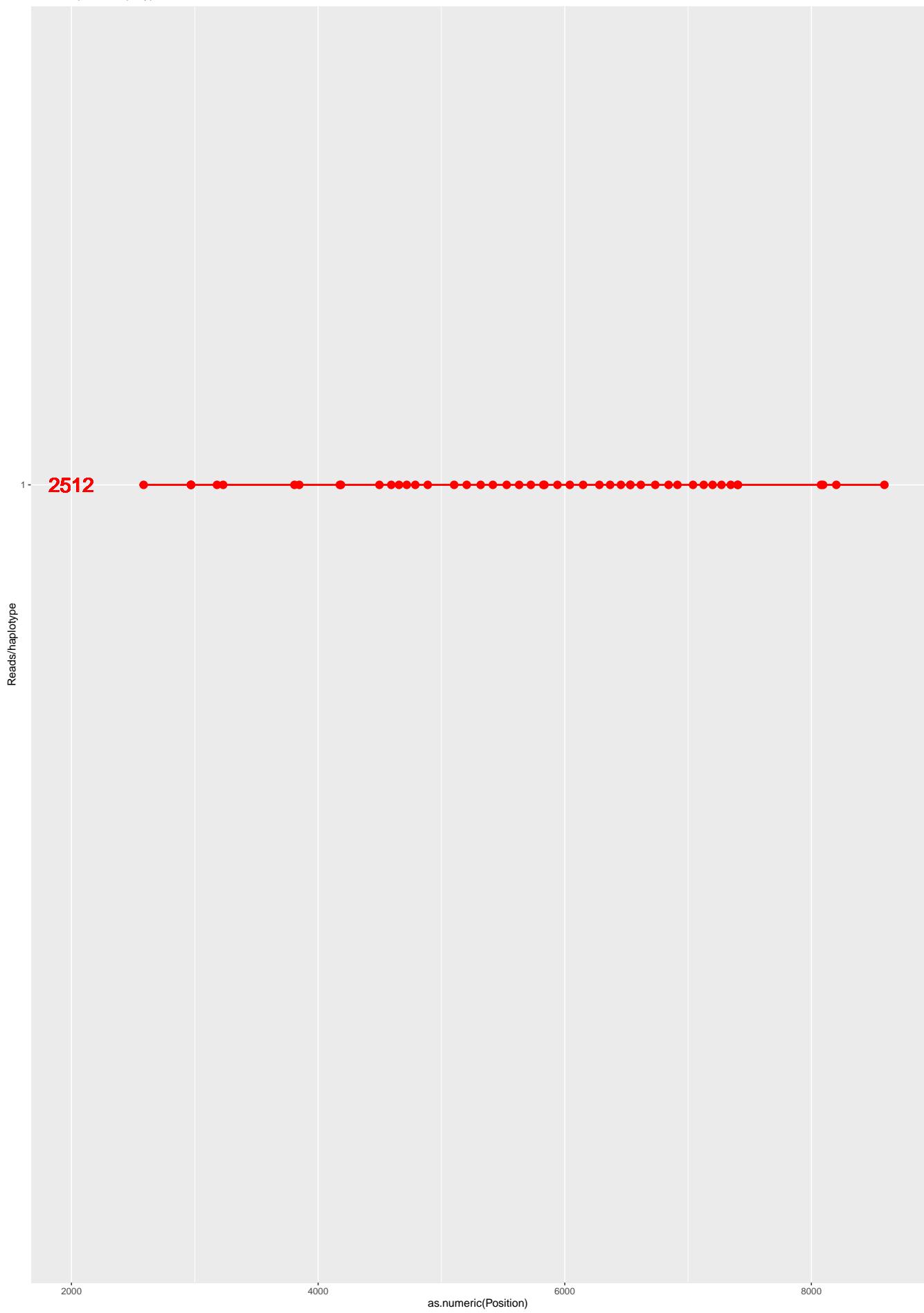
barcode = CACTGATCGATATGCA & GTCTCTGCGATAACAGC

Sample = 75d tetrad = 75 spore = d

Total reads = 2687 PCR=192

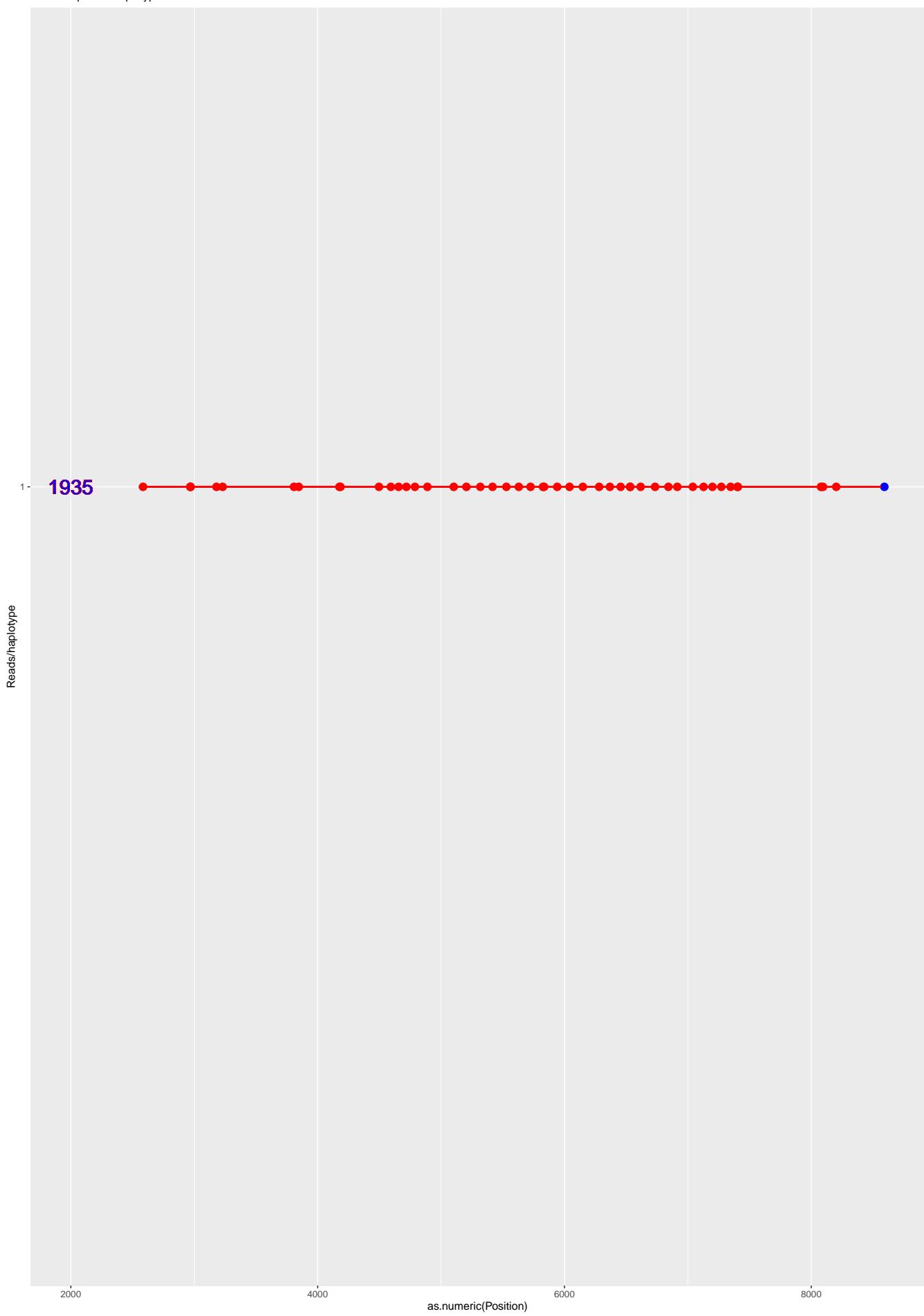
haplotypes I began with n[supporting reads] = 2512

most frequent 7 haplotypes.



barcode = CACTGATCGATATGCA & AGTATGAGATAGCTCG

Sample = 78a tetrad = 78 spore = a
Total reads = 2025 PCR=193
haplotypes I began with n[supporting reads] = 1935
most frequent 7 haplotypes.

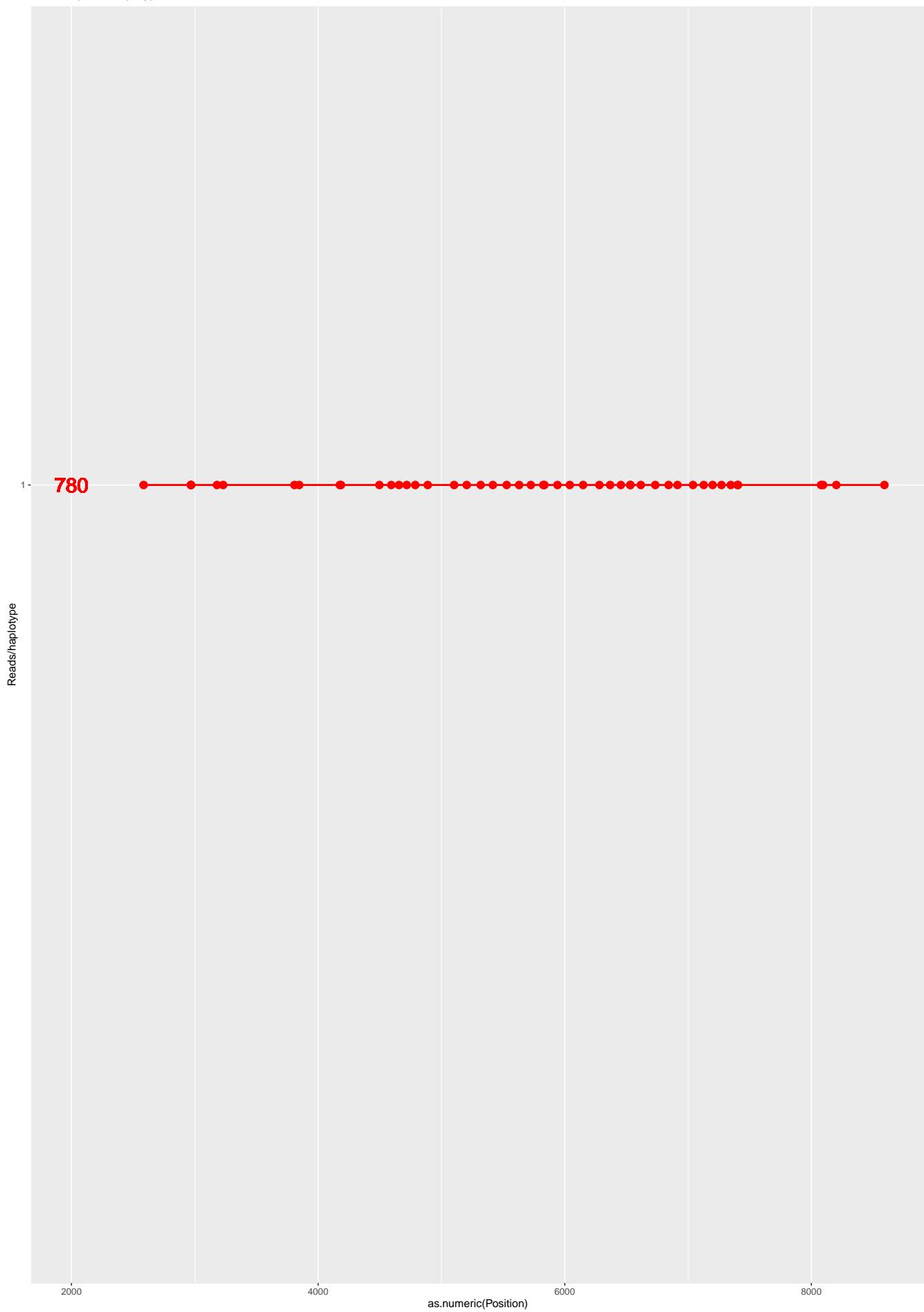


Sample = 78b tetrad = 78 spore = b

Total reads = 813 PCR=194

haplotypes I began with n[supporting reads] = 780

most frequent 7 haplotypes.



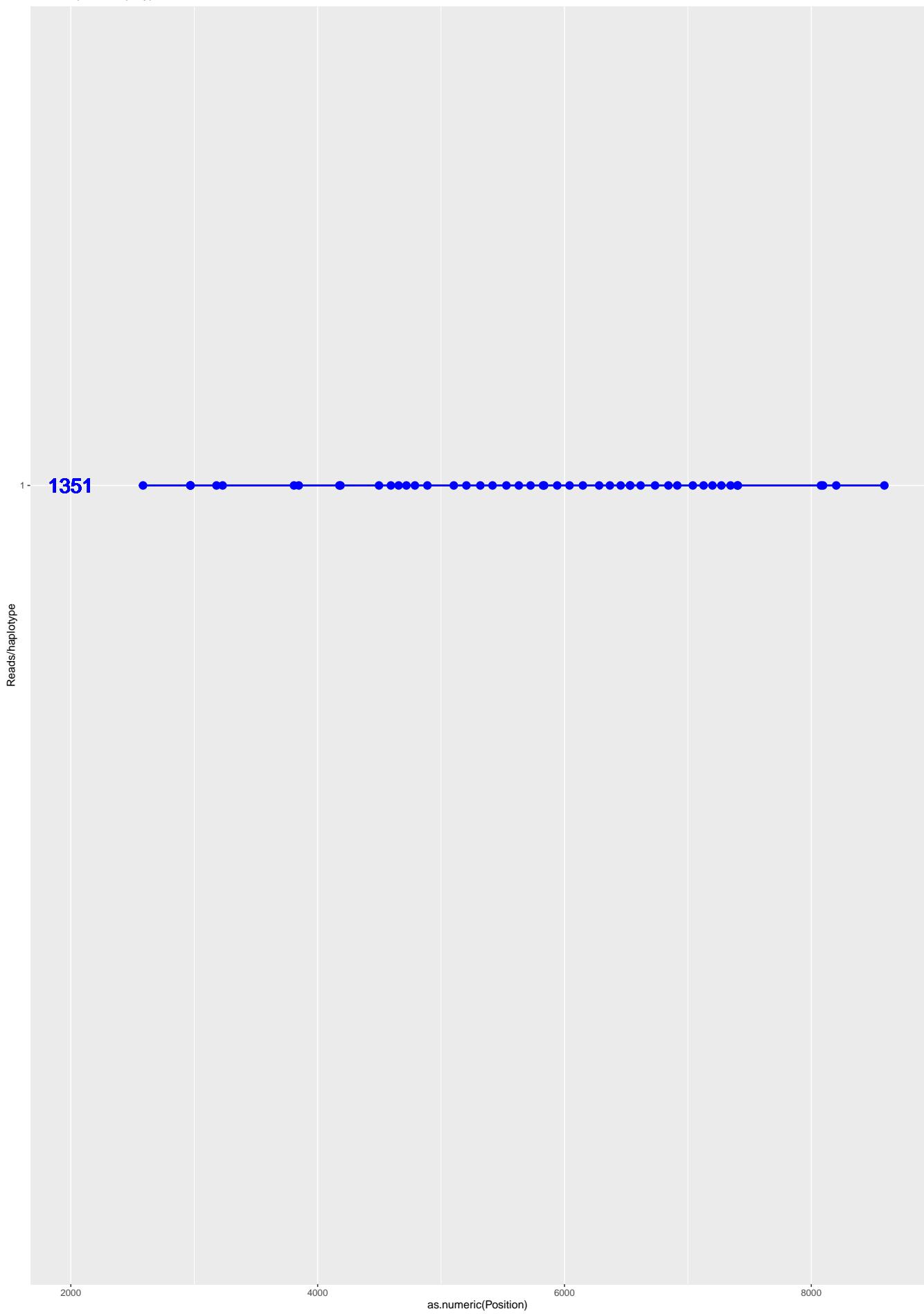
barcode = TACAGTGCTGCTGCG & GCGATCTATGCACACG

Sample = 78c tetrad = 78 spore = c

Total reads = 1574 PCR=195

haplotypes I began with n[supporting reads] = 1351

most frequent 7 haplotypes.



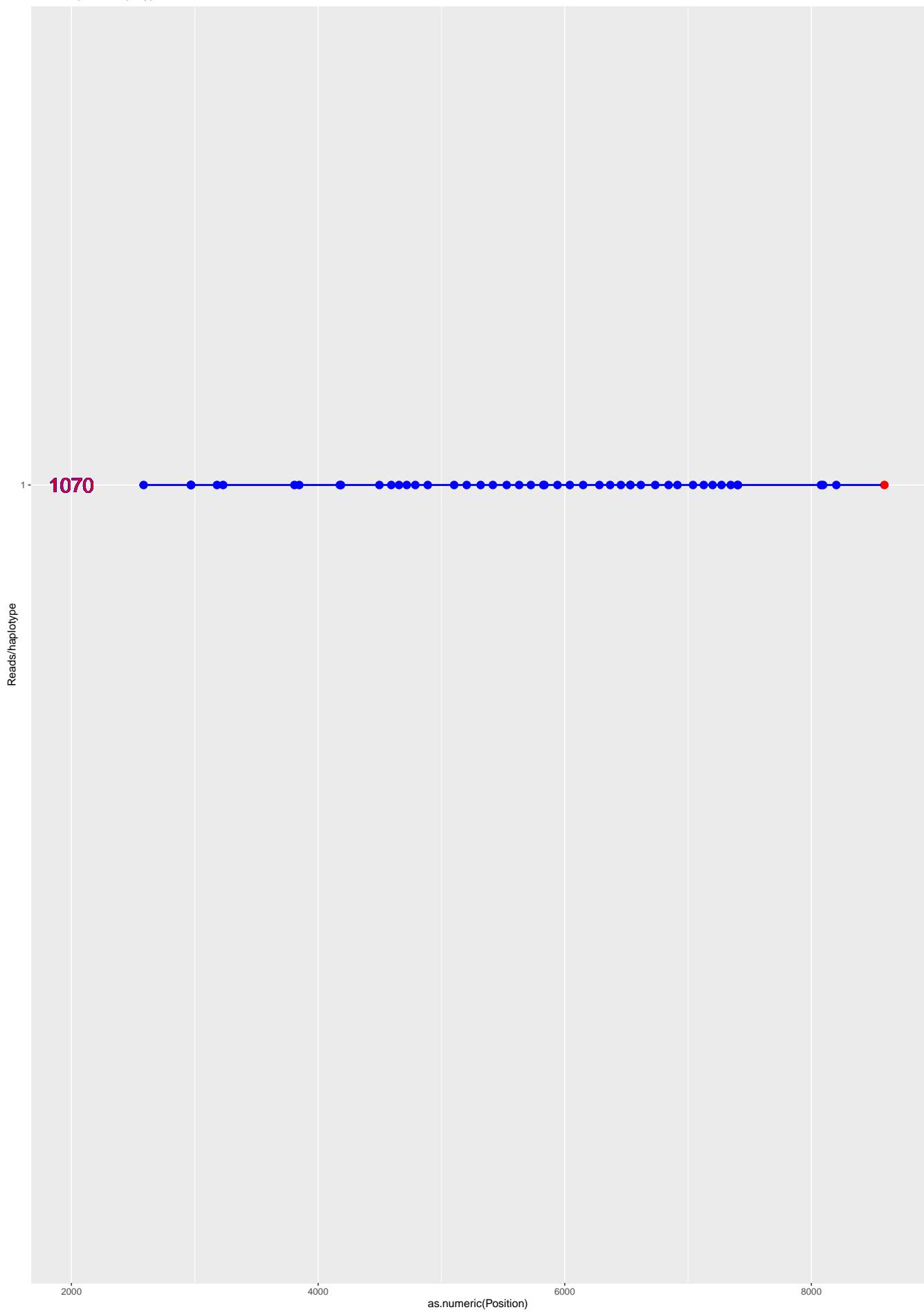
barcode = TACAGTGTCTGCTGCG & TGCAGTCGAGATACT

Sample = 78d tetrad = 78 spore = d

Total reads = 1245 PCR=196

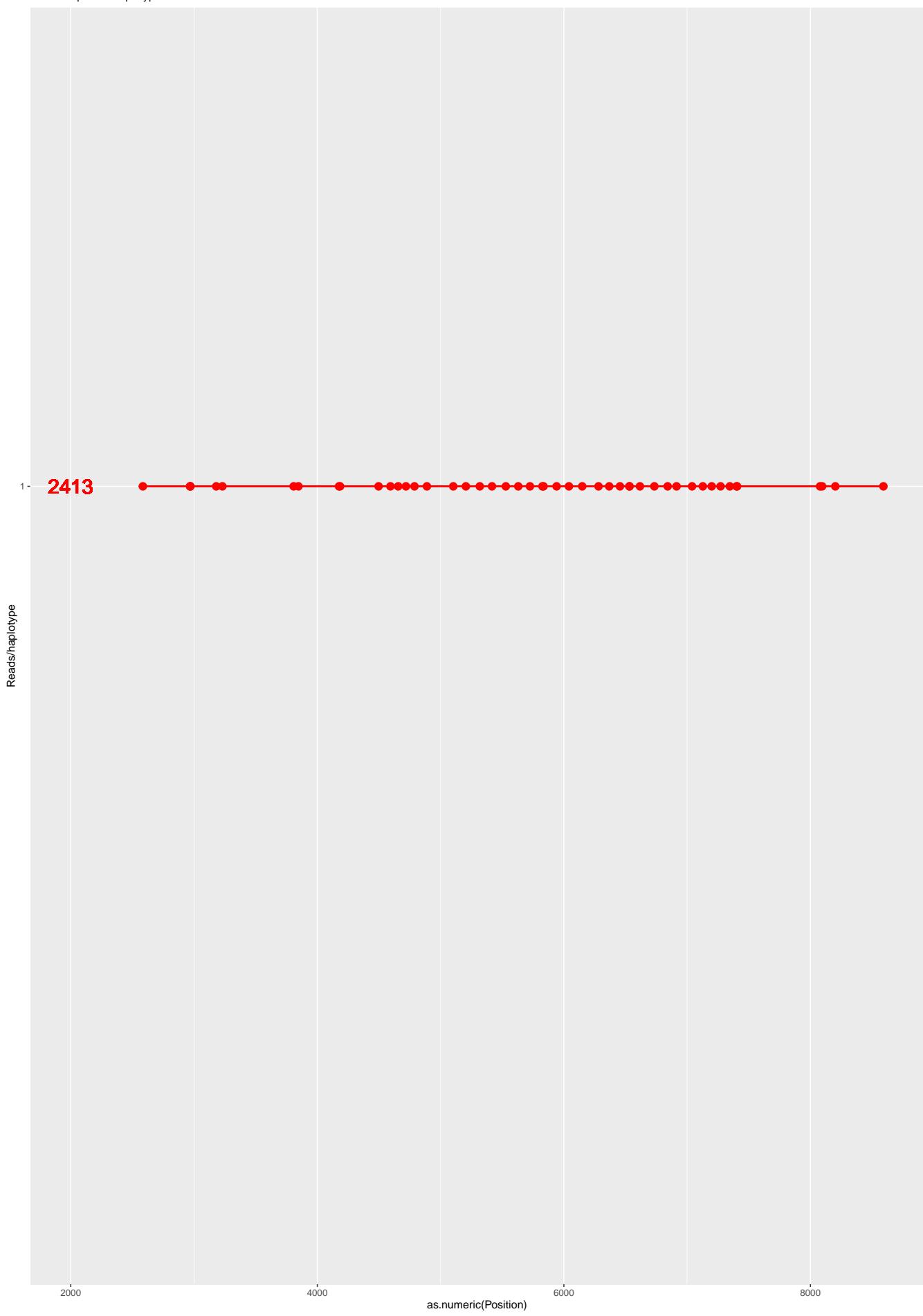
haplotypes I began with n[supporting reads] = 1070

most frequent 7 haplotypes.



barcode = TACAGTGTCTGCTGCG & GACTCTGCGTCGAGTC

Sample = 79a tetrad = 79 spore = a
Total reads = 2530 PCR=197
haplotypes I began with n[supporting reads] = 2413
most frequent 7 haplotypes.

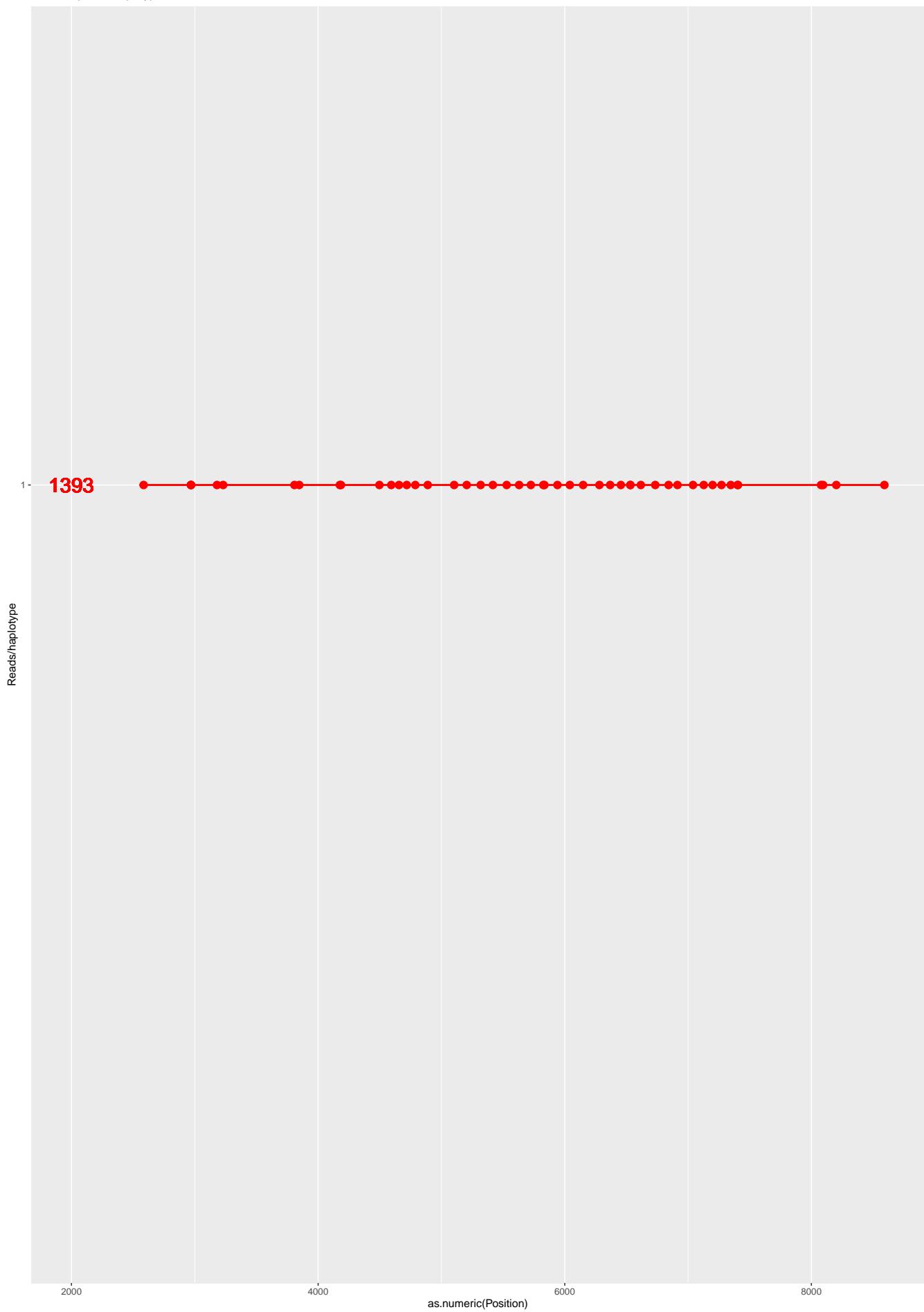


Sample = 79b tetrad = 79 spore = b

Total reads = 1448 PCR=198

haplotypes I began with n[supporting reads] = 1393

most frequent 7 haplotypes.



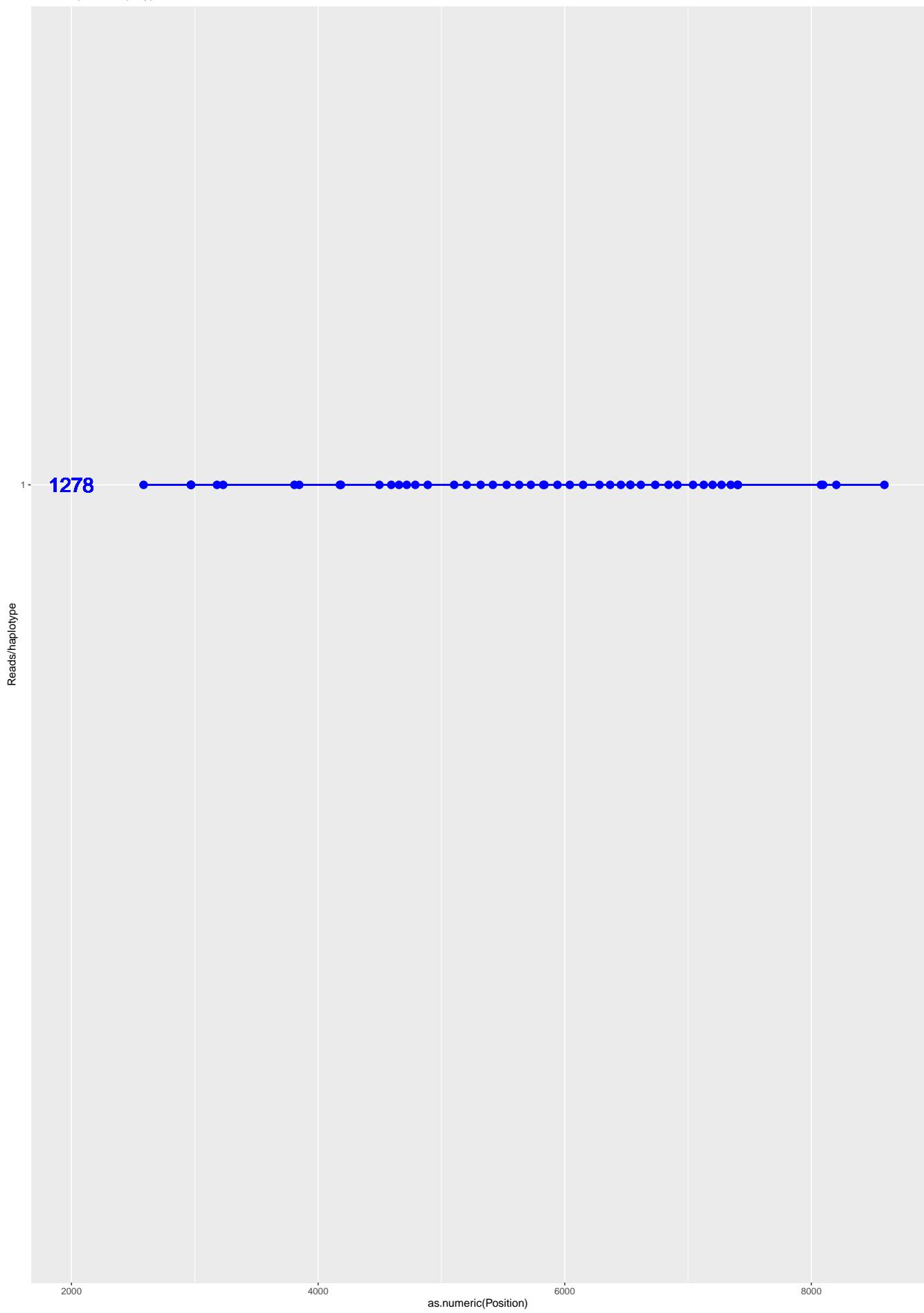
barcode = TACAGTGCTGCTGCG & GCGCAGACTACGTGTG

Sample = 79c tetrad = 79 spore = c

Total reads = 1501 PCR=199

haplotypes I began with n[supporting reads] = 1278

most frequent 7 haplotypes.

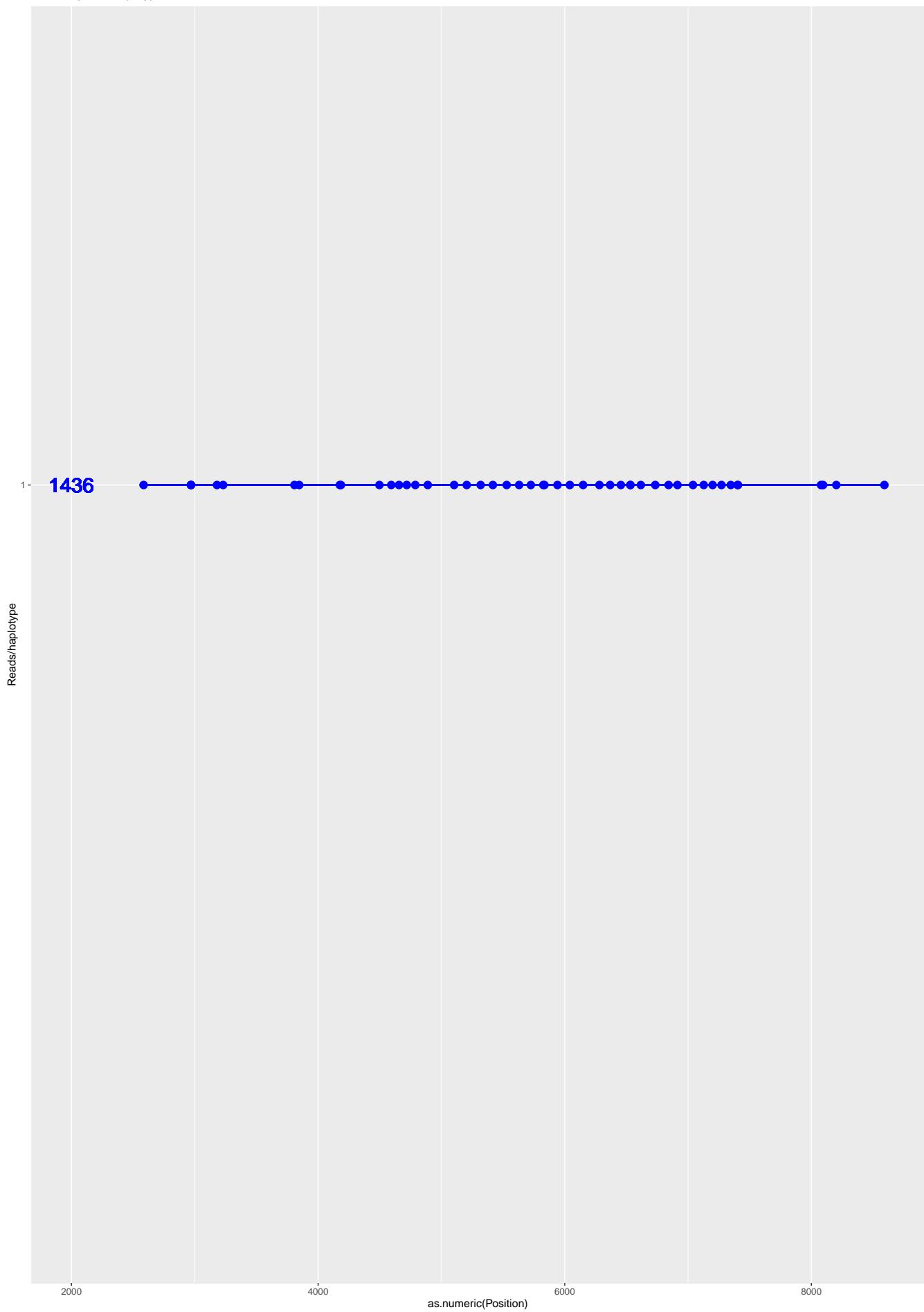


Sample = 79d tetrad = 79 spore = d

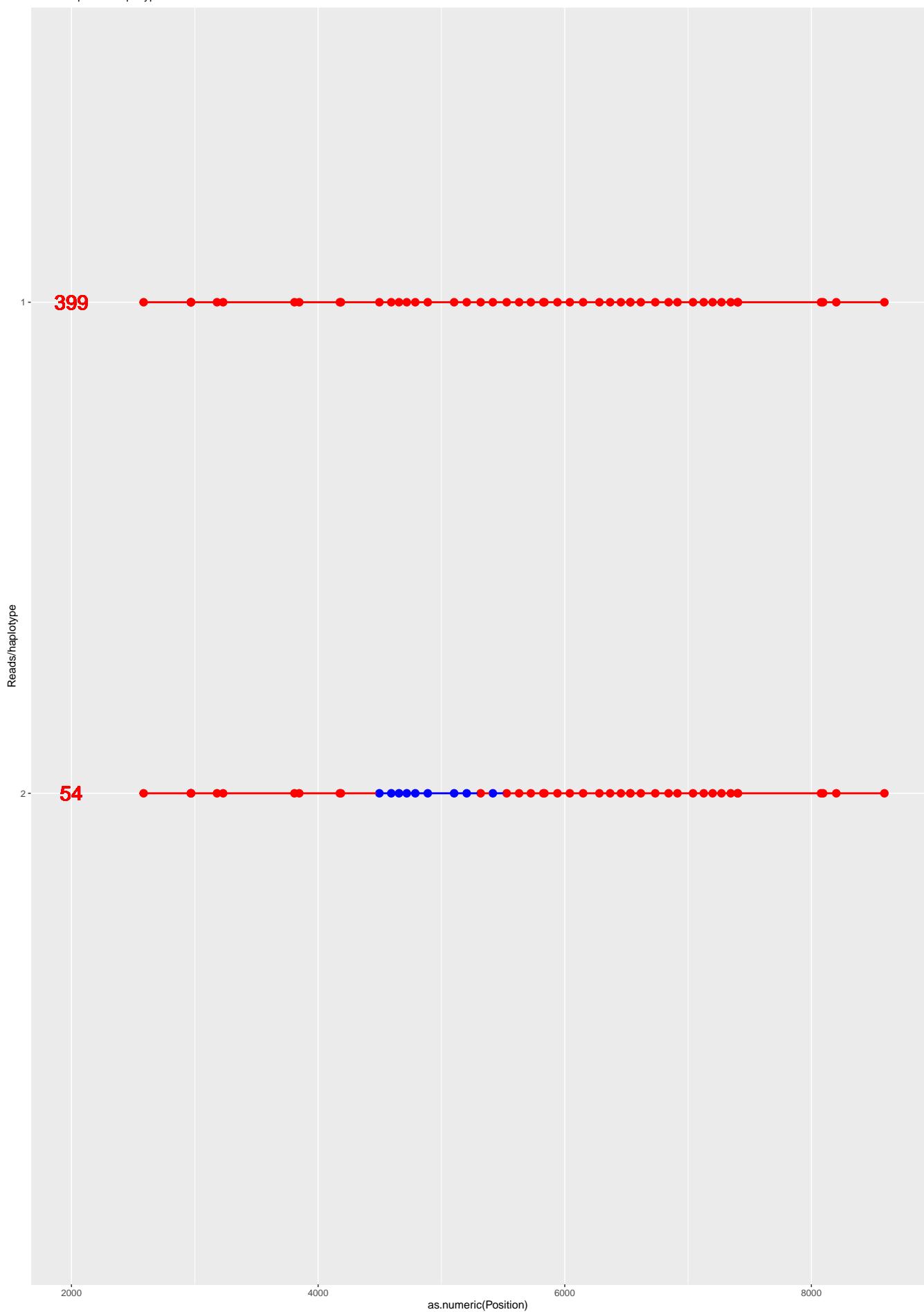
Total reads = 1668 PCR=200

haplotypes I began with n[supporting reads] = 1436

most frequent 7 haplotypes.



Sample = 80a tetrad = 80 spore = a
Total reads = 543 PCR=201
haplotypes I began with n[supporting reads] = 54, 399
most frequent 7 haplotypes.



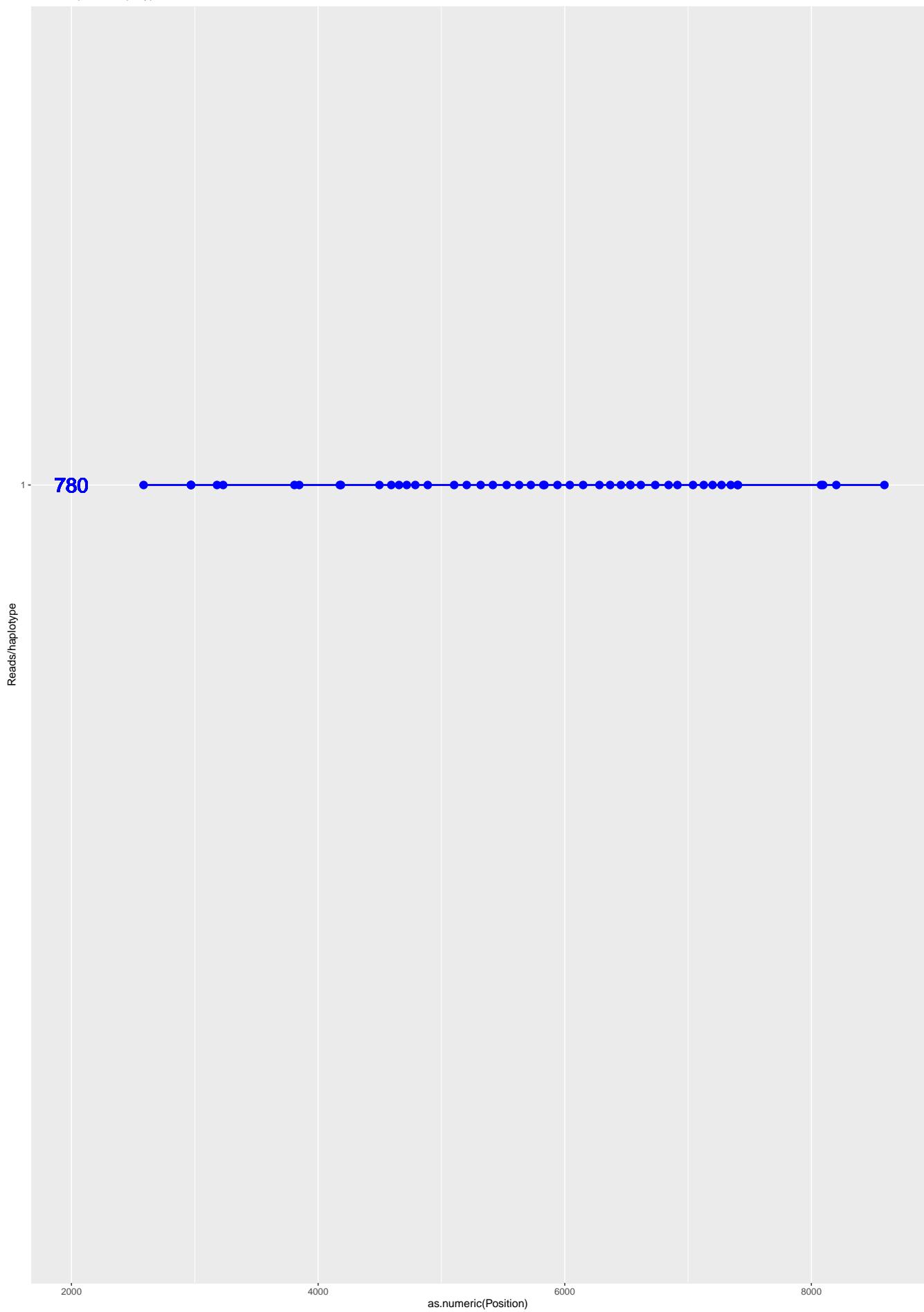
barcode = TACAGATAGTGTAGCG & TCATATGTTAGTACTCT

Sample = 80b tetrad = 80 spore = b

Total reads =923 PCR=202

haplotypes I began with n[supporting reads] = 780

most frequent 7 haplotypes.



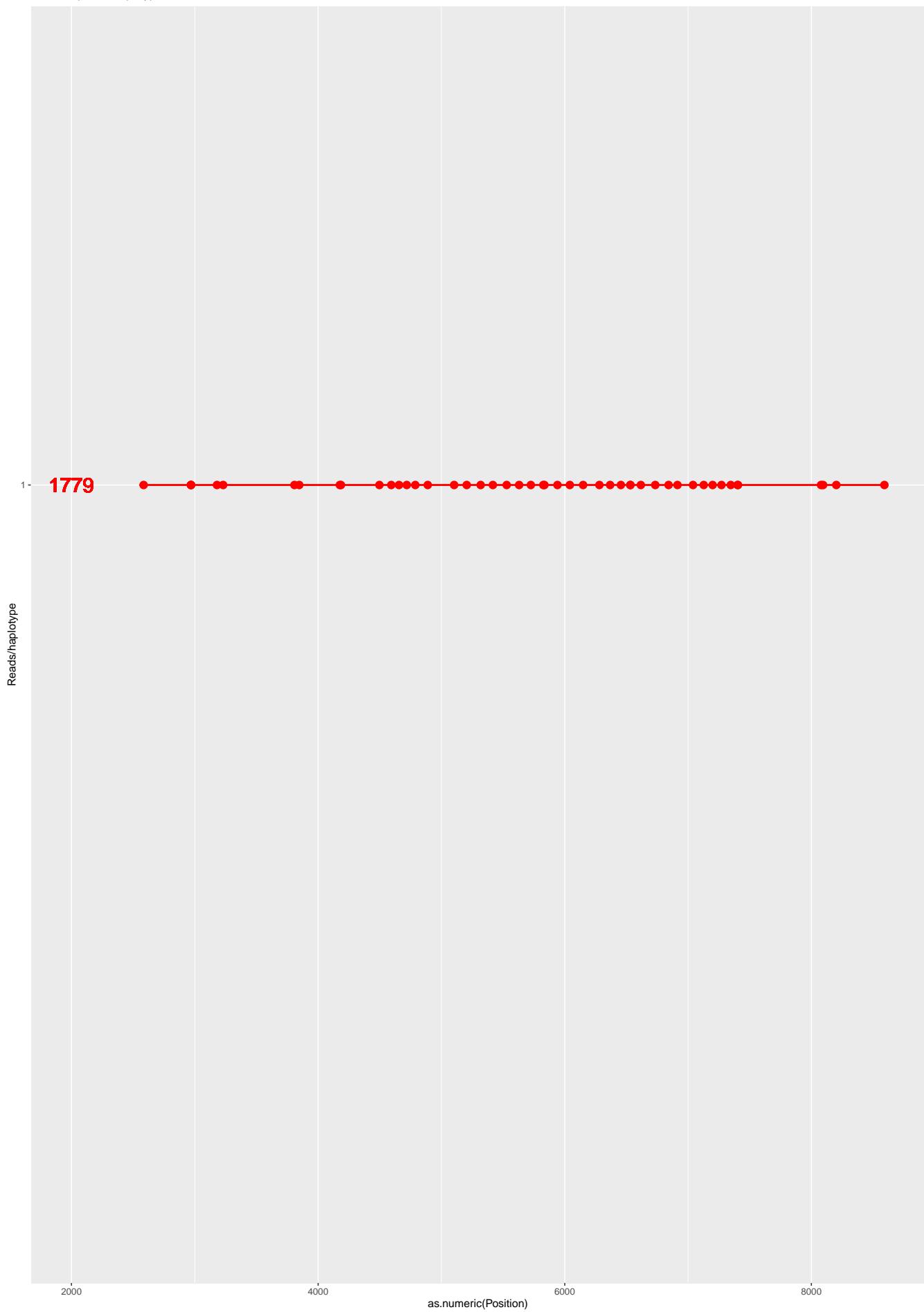
barcode = TACAGATACTGTAGCG & GCGATCTATGCACACG

Sample = 80c tetrad = 80 spore = c

Total reads = 1869 PCR=203

haplotypes I began with n[supporting reads] = 1779

most frequent 7 haplotypes.



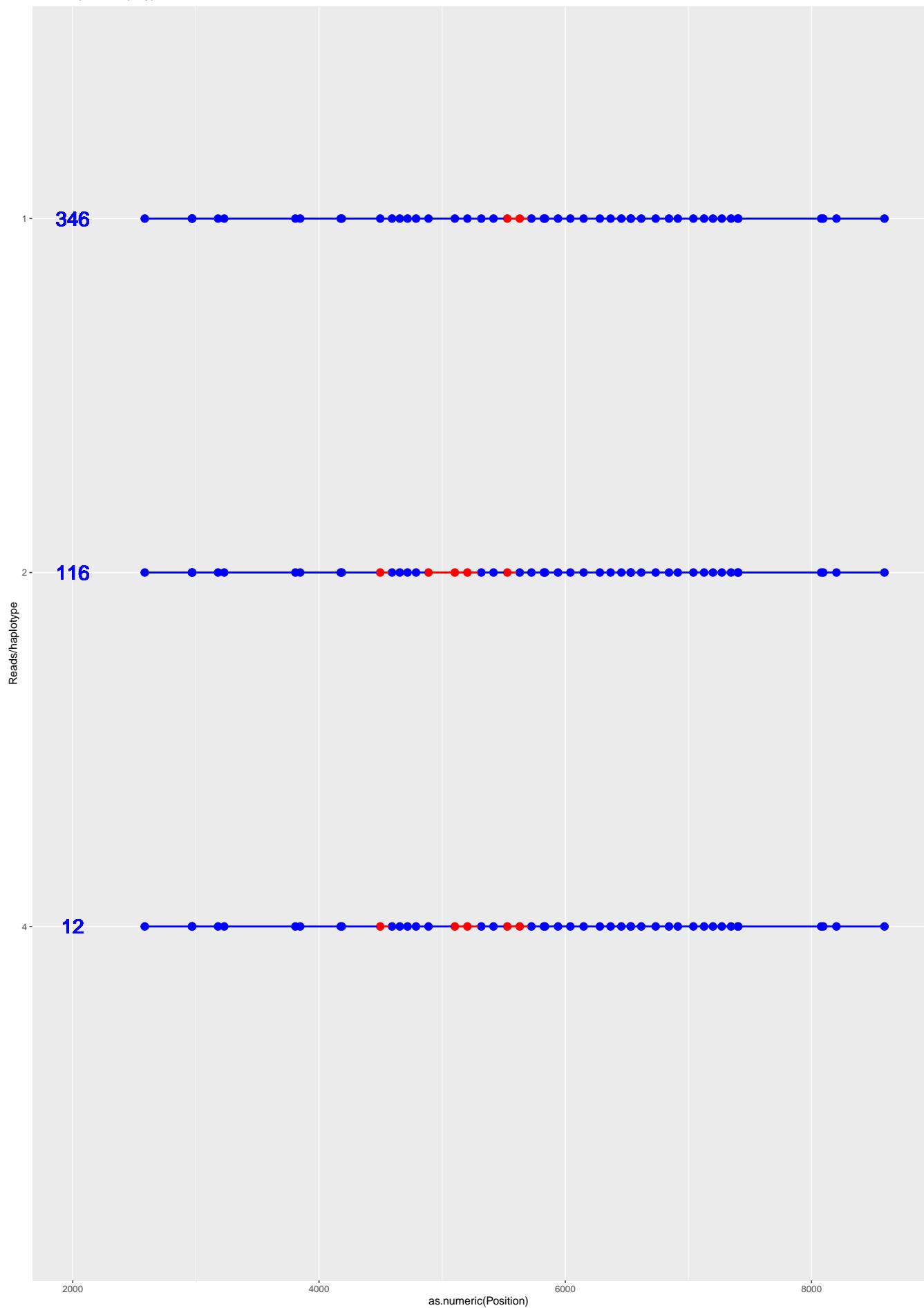
barcode = TACAGATAGTGTAGCG & TGCAGTCGAGATACT

Sample = 80d tetrad = 80 spore = d

Total reads = 633 PCR=204

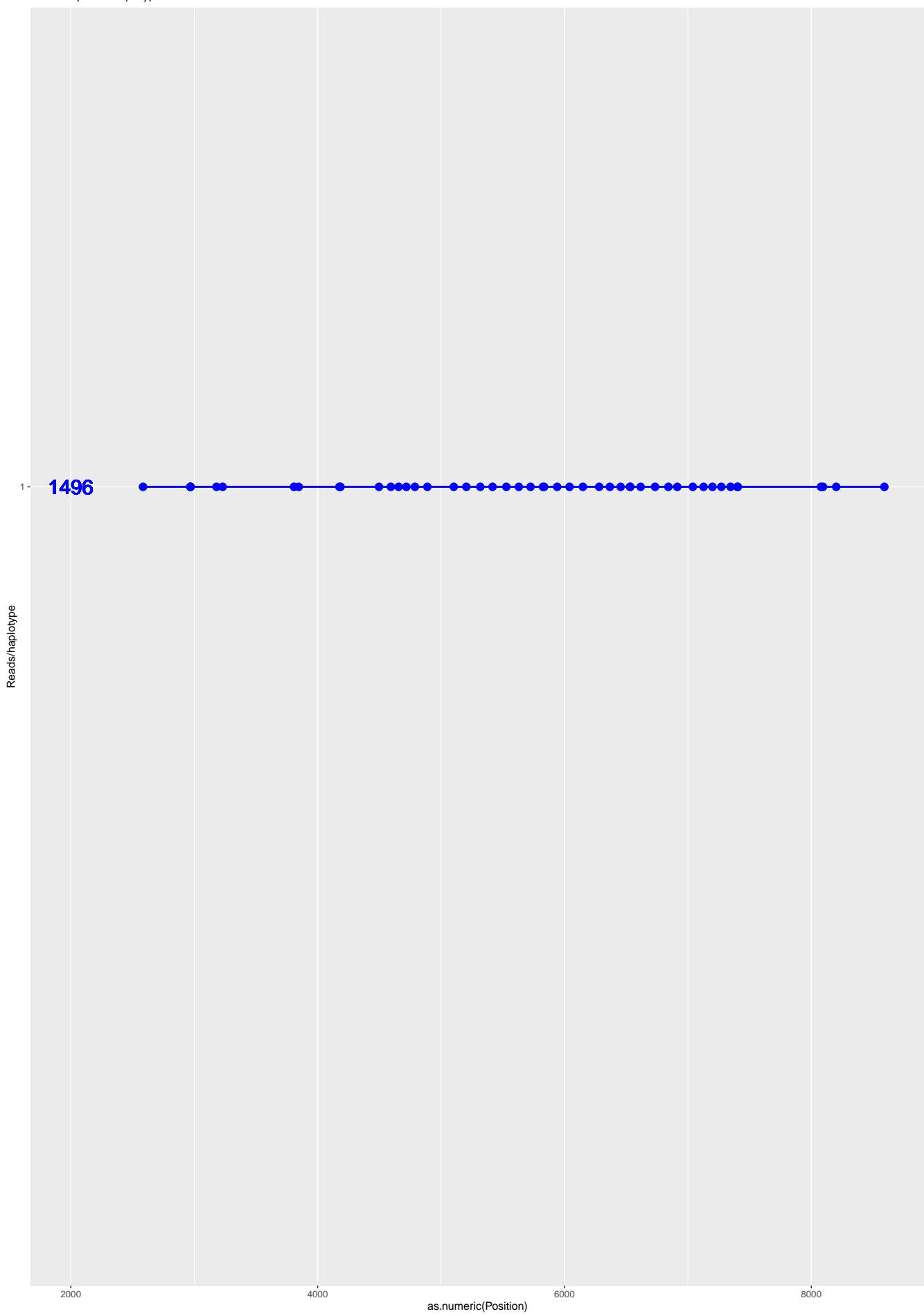
haplotypes I began with n[supporting reads] = 12, 116, 346

most frequent 7 haplotypes.

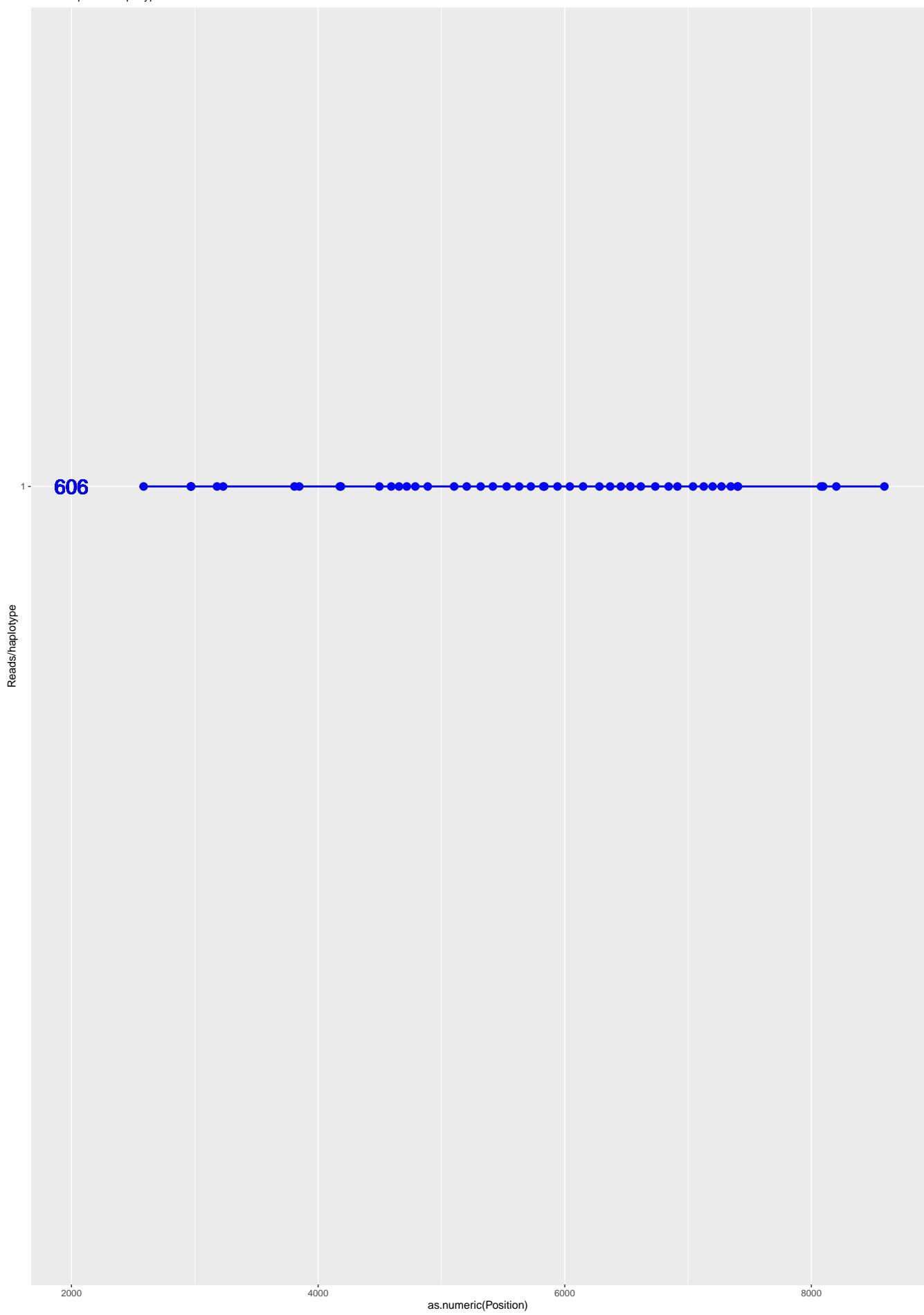


barcode = TACAGATAGTGTAGCG & GACTCTGCGTCGAGTC

Sample = 82a tetrad = 82 spore = a
Total reads = 1759 PCR=205
haplotypes I began with n[supporting reads] = 1496
most frequent 7 haplotypes.



Sample = 82b tetrad = 82 spore = b
Total reads = 737 PCR=206
haplotypes I began with n[supporting reads] = 606
most frequent 7 haplotypes.

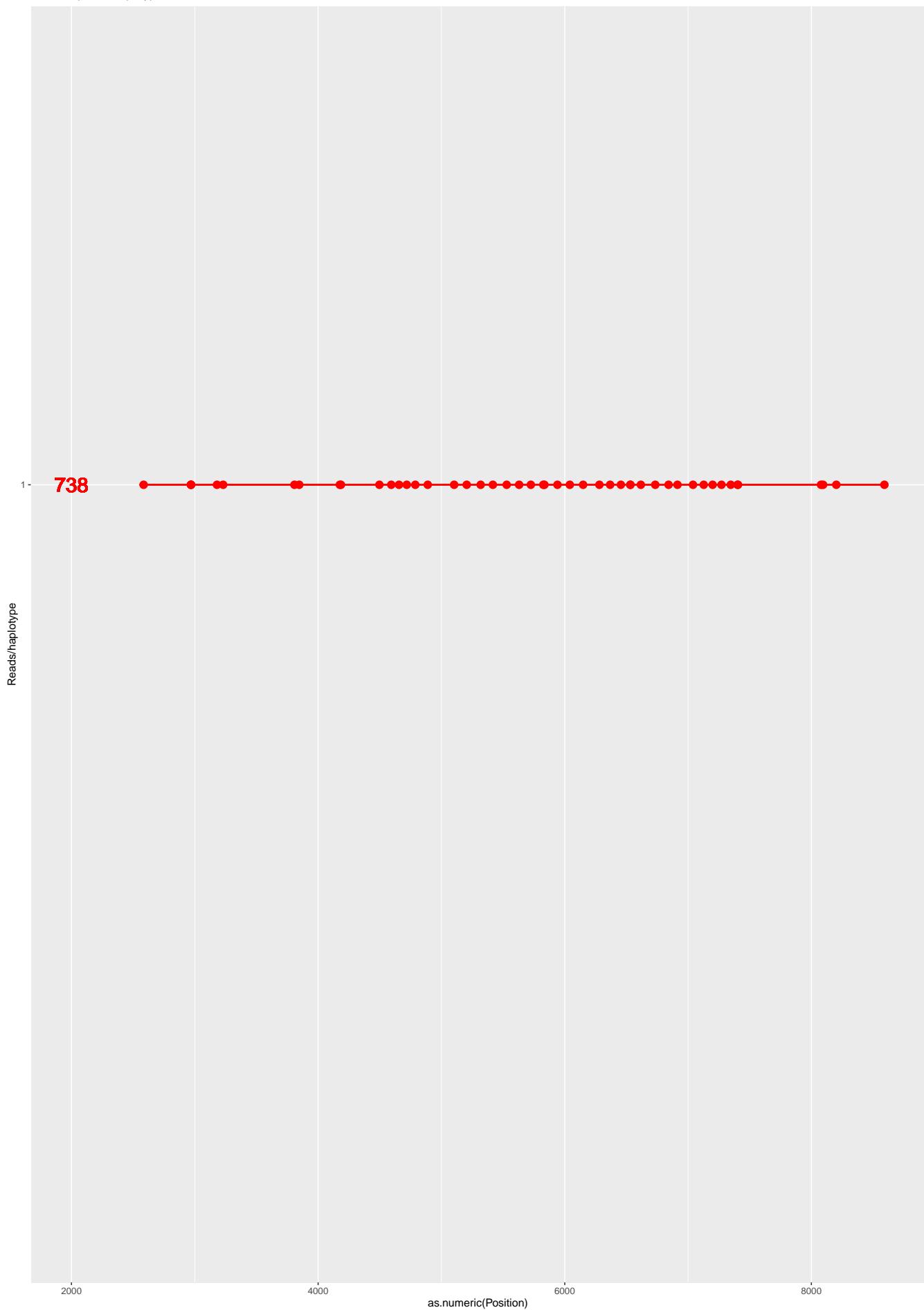


Sample = 82c tetrad = 82 spore = c

Total reads =772 PCR=207

haplotypes I began with n[supporting reads] = 738

most frequent 7 haplotypes.



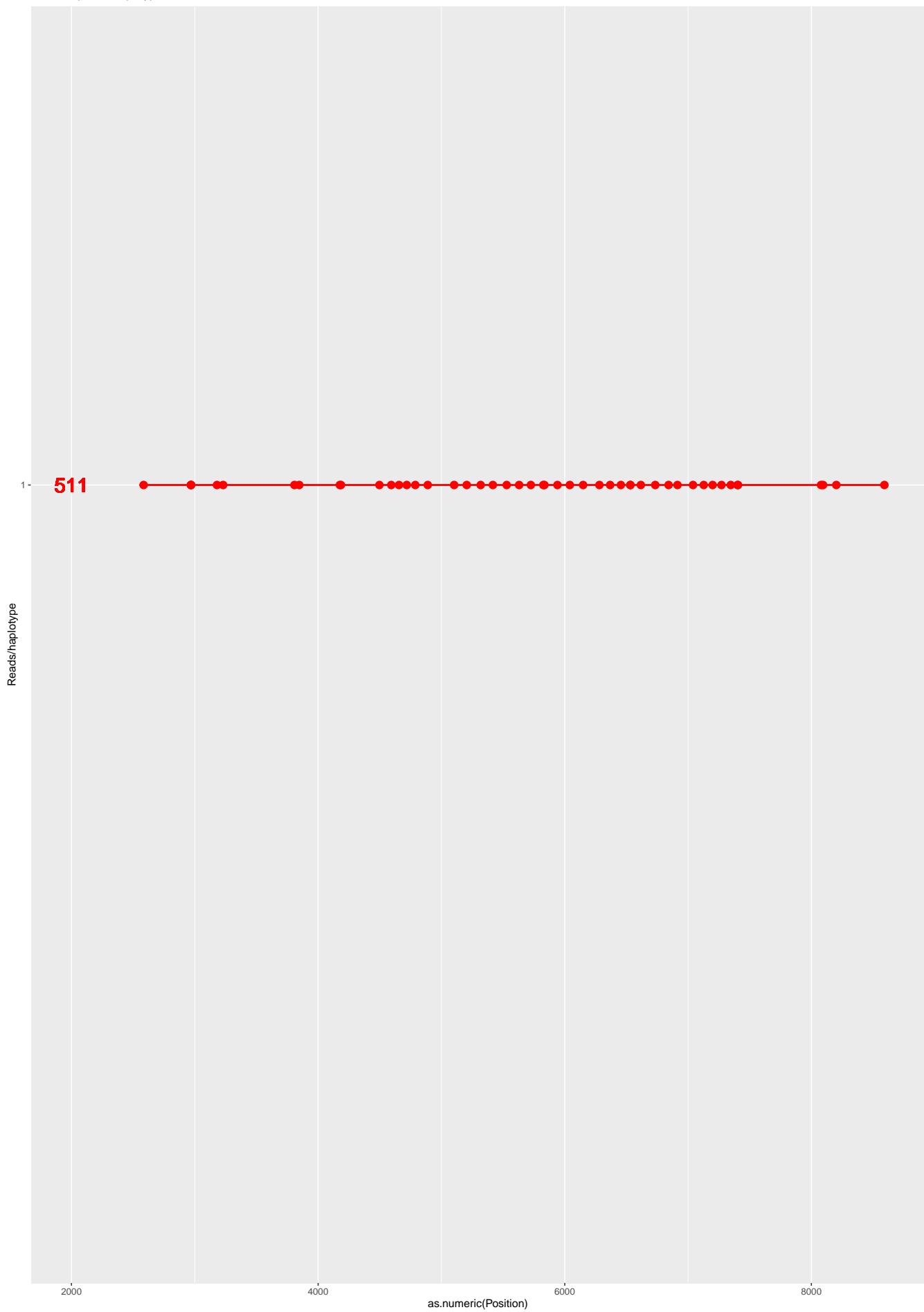
barcode = TACAGATACTGTAGCG & GTCTCTGCGATACAGC

Sample = 82d tetrad = 82 spore = d

Total reads =534 PCR=208

haplotypes I began with n[supporting reads] = 511

most frequent 7 haplotypes.



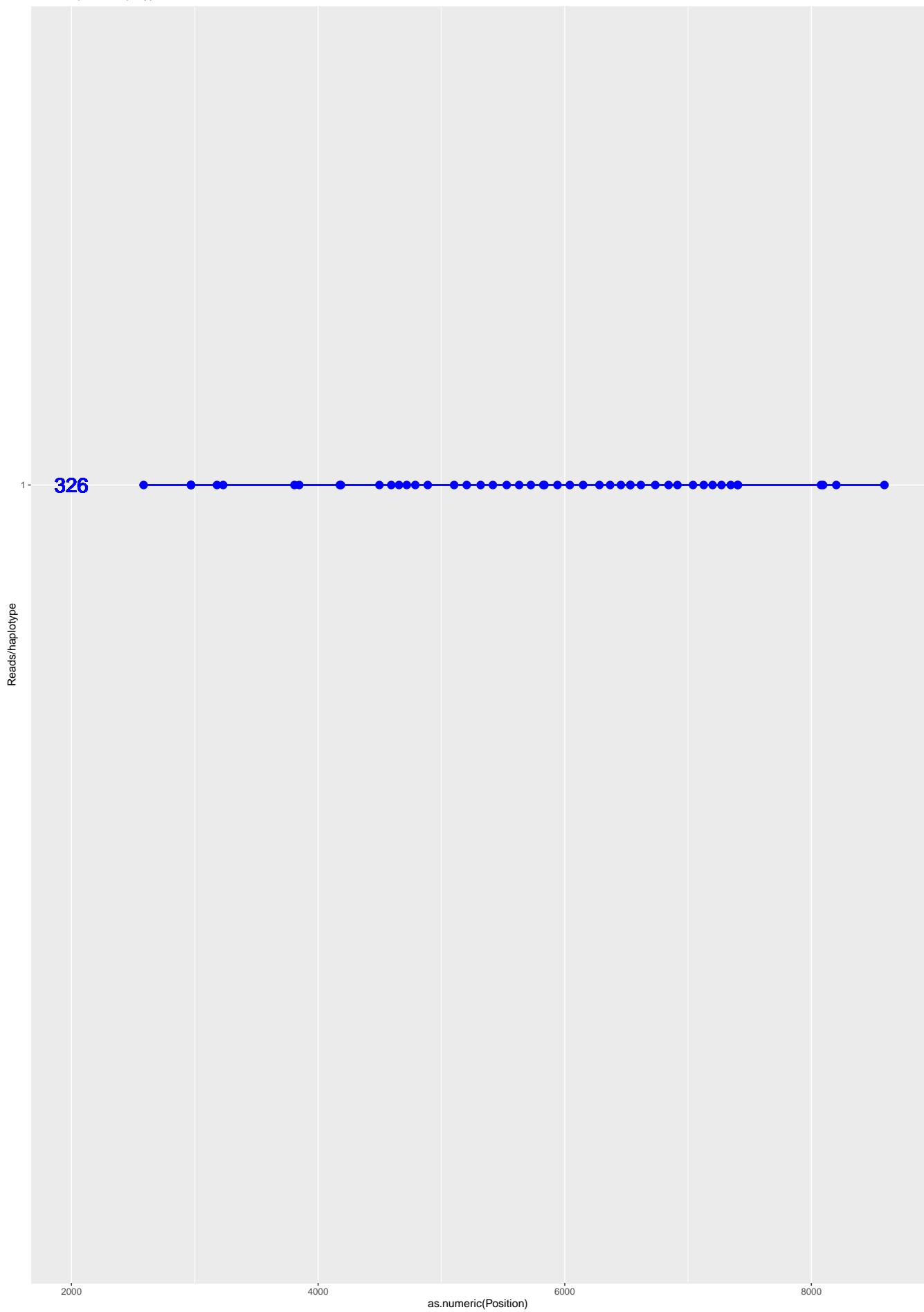
barcode = TACAGATAGTGTAGCG & AGTATGAGATAGCTCG

Sample = 83a tetrad = 83 spore = a

Total reads =383 PCR=209

haplotypes I began with n[supporting reads] = 326

most frequent 7 haplotypes.



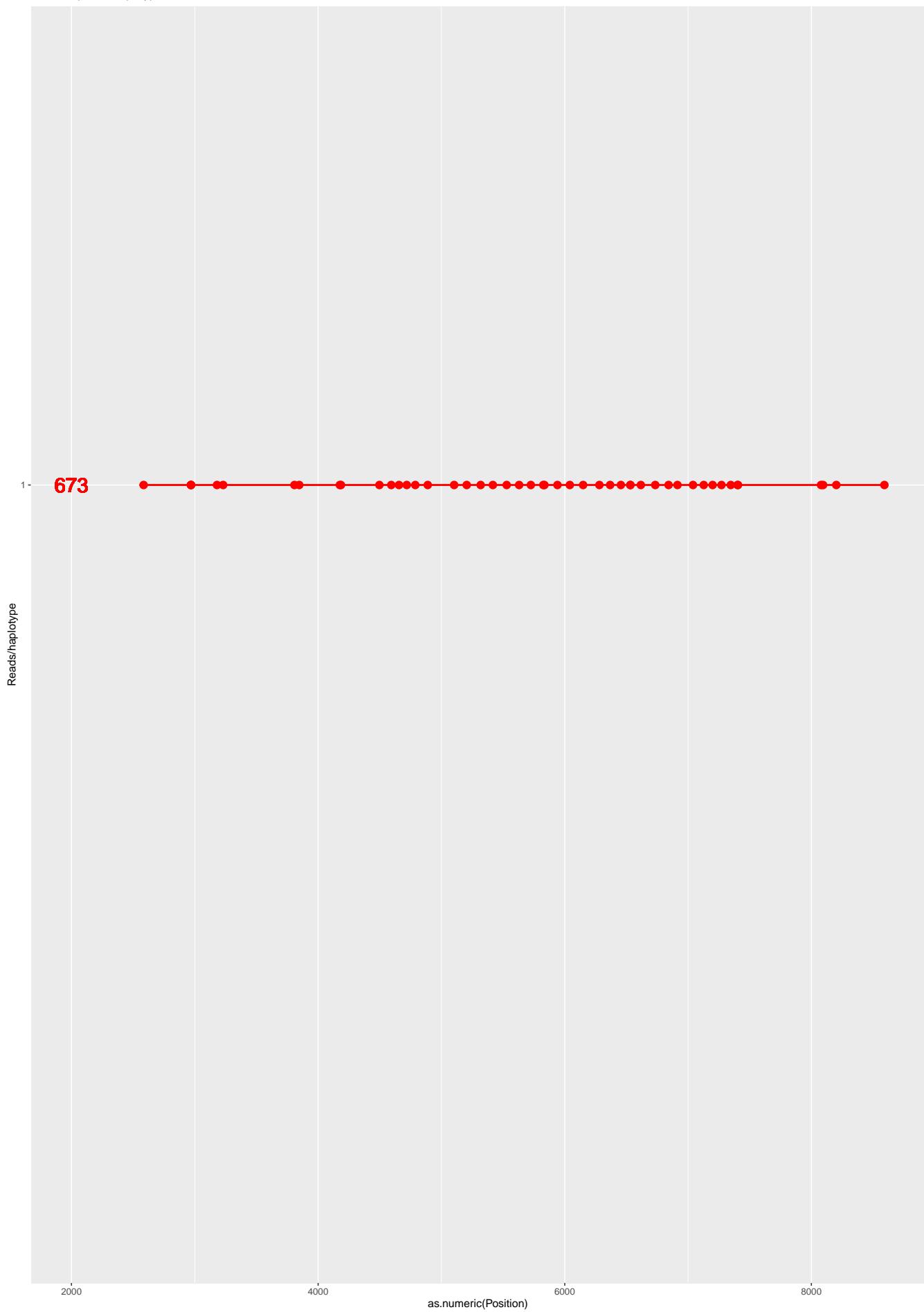
barcode = TCGTAGAGCTCGAGAC & TCATATGAGTACTCT

Sample = 83b tetrad = 83 spore = b

Total reads =706 PCR=210

haplotypes I began with n[supporting reads] = 673

most frequent 7 haplotypes.



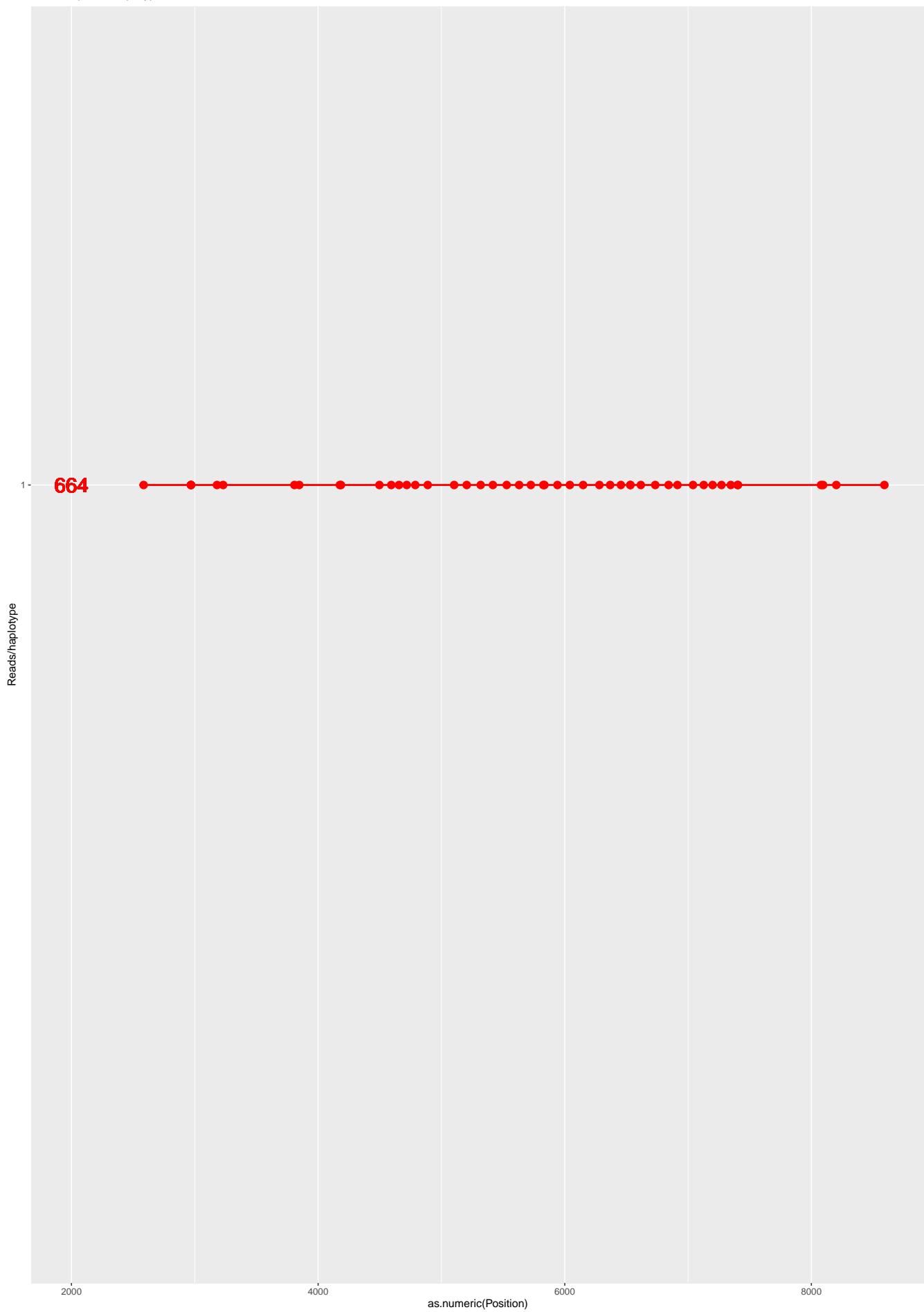
barcode = TCGTAGAGCTGAGAC & GCGATCTATGCACACG

Sample = 83c tetrad = 83 spore = c

Total reads =687 PCR=211

haplotypes I began with n[supporting reads] = 664

most frequent 7 haplotypes.



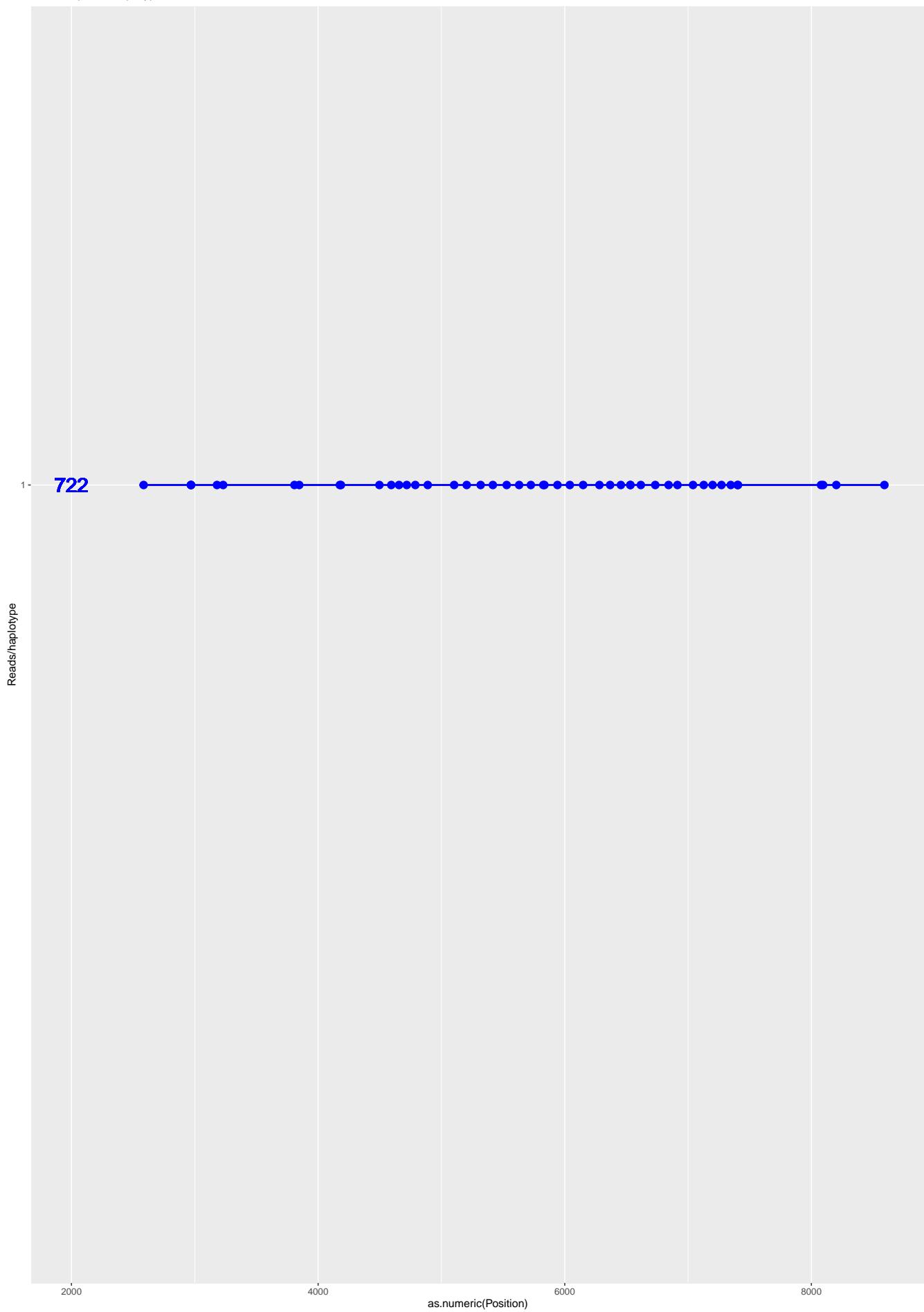
barcode = TCGTAGAGCTGAGAC & TGCAGTCGAGATACT

Sample = 83d tetrad = 83 spore = d

Total reads = 843 PCR=212

haplotypes I began with n[supporting reads] = 722

most frequent 7 haplotypes.



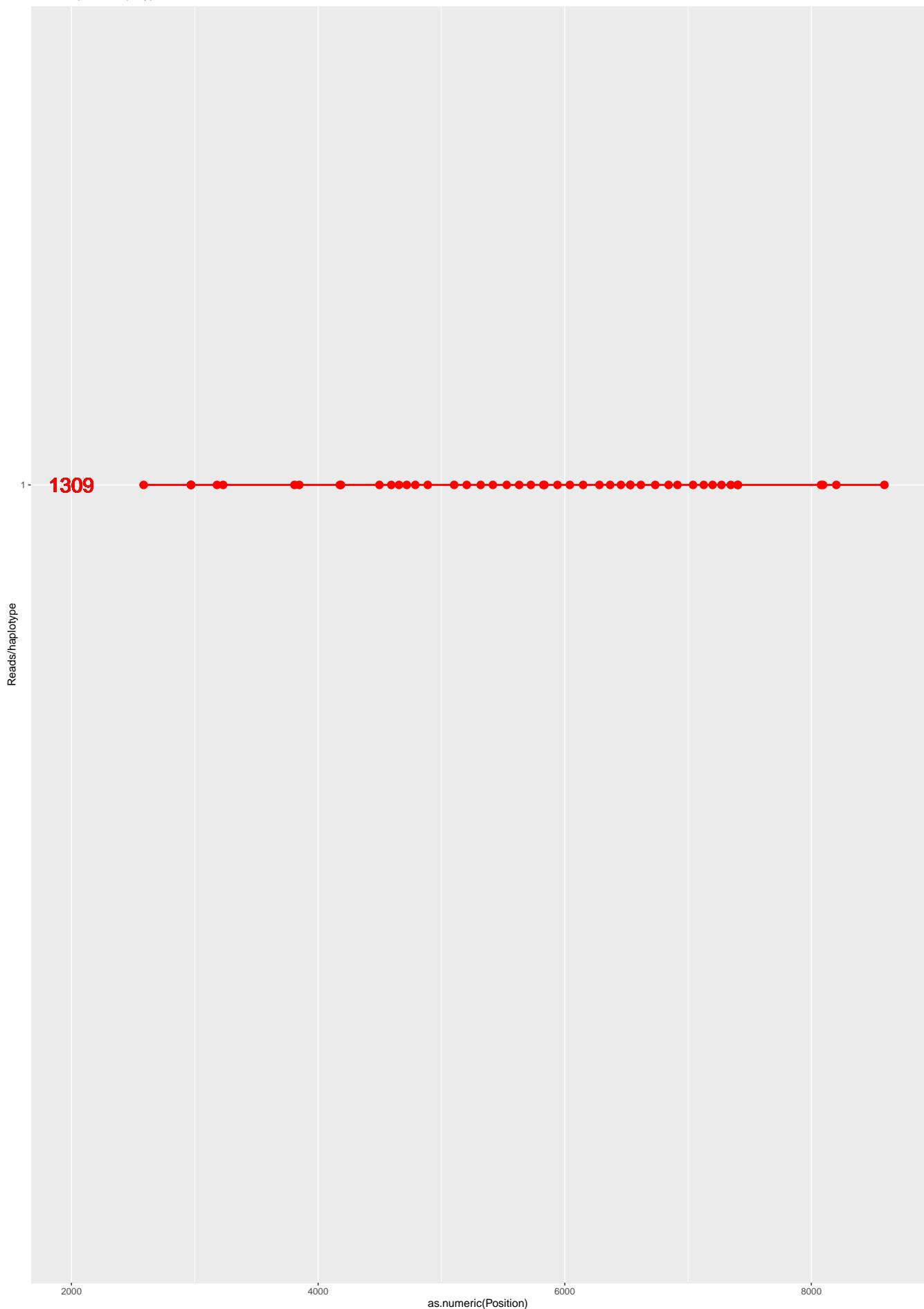
barcode = TCGTAGAGCTCGAGAC & GACTCTGCGTCGAGTC

Sample = 86a tetrad = 86 spore = a

Total reads = 1367 PCR=213

haplotypes I began with n[supporting reads] = 1309

most frequent 7 haplotypes.



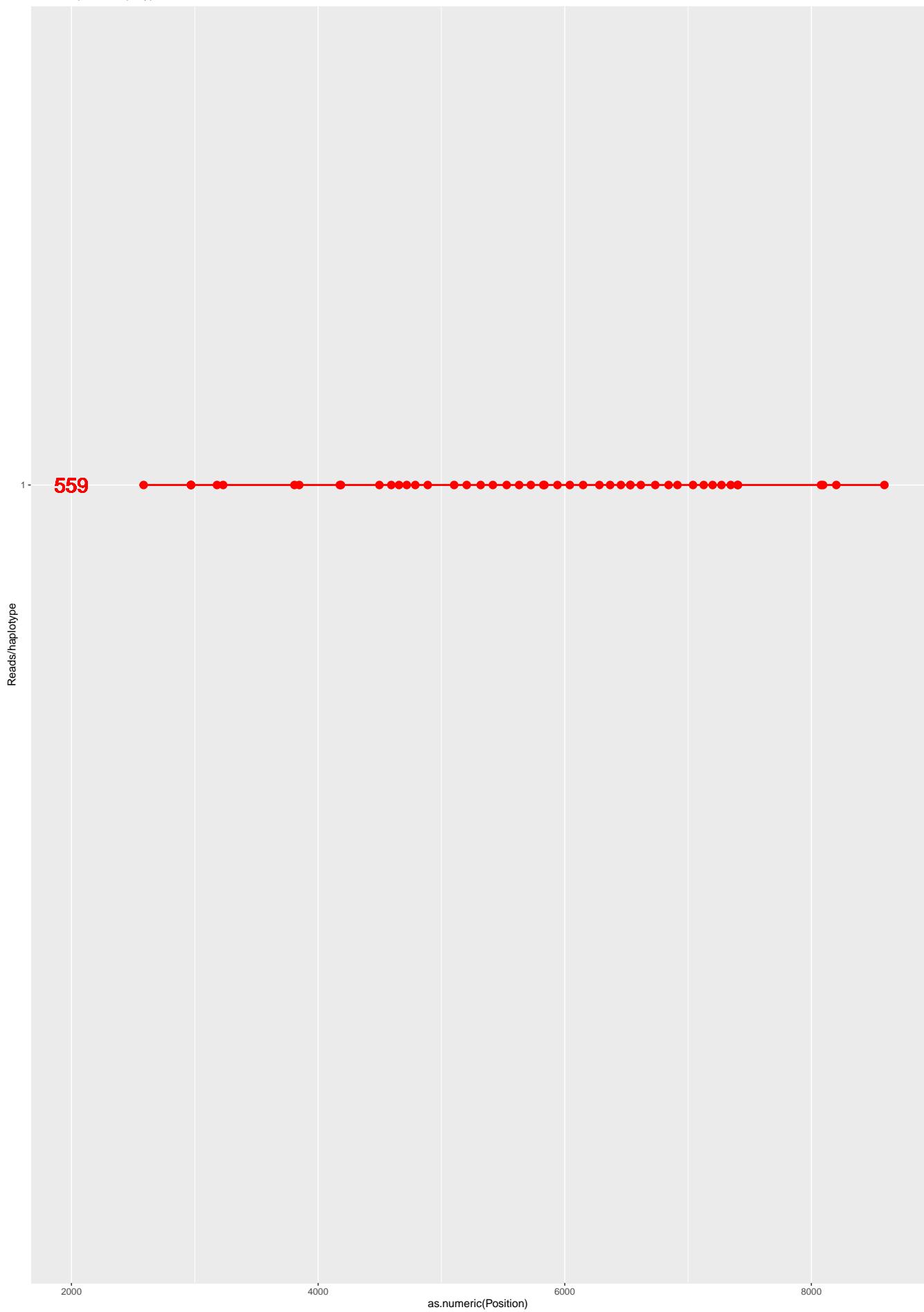
barcode = TCGTAGAGCTCGAGAC & TACAGCGACGTCATCG

Sample = 86b tetrad = 86 spore = b

Total reads =583 PCR=214

haplotypes I began with n[supporting reads] = 559

most frequent 7 haplotypes.



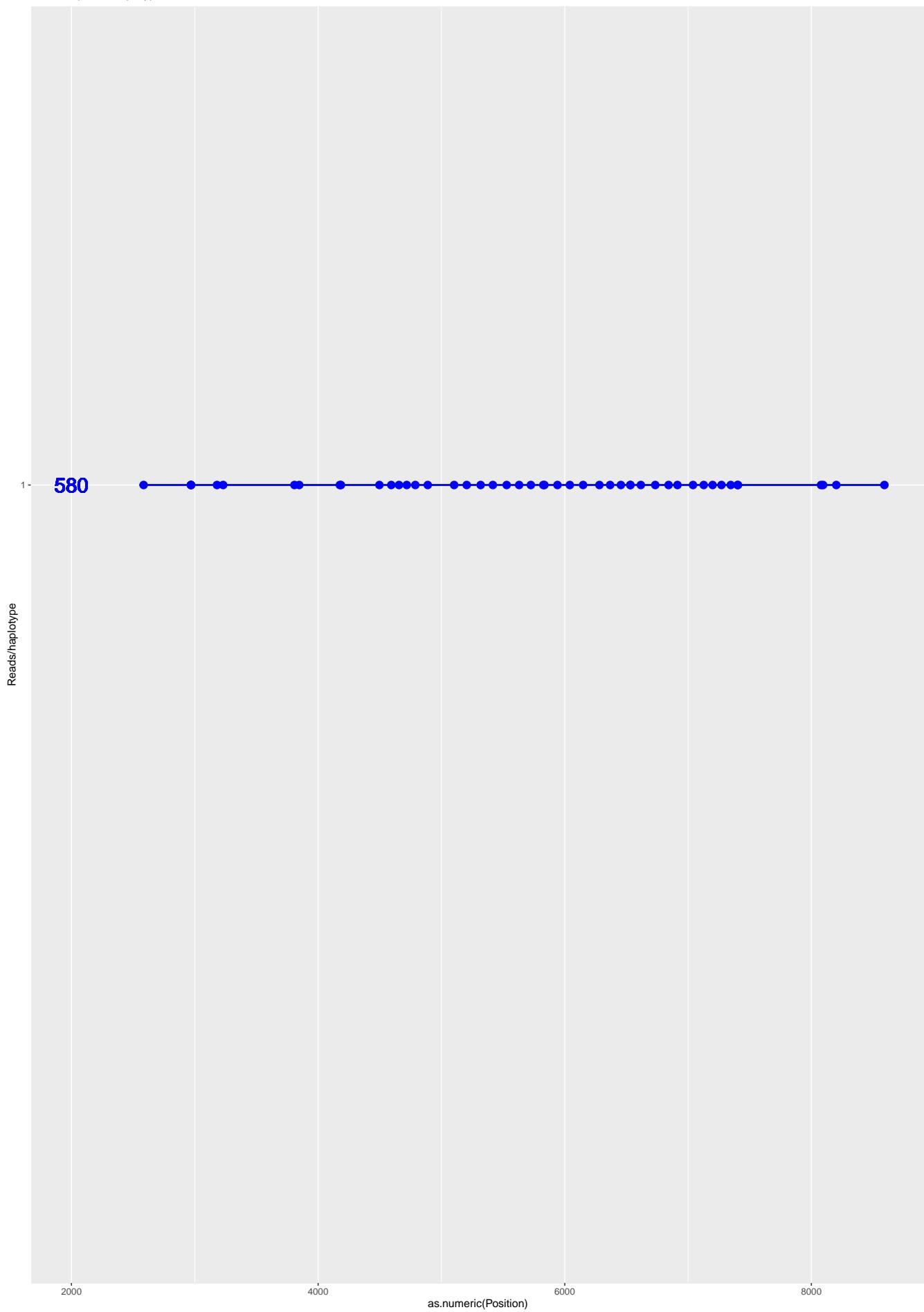
barcode = TCGTAGAGCTCGAGAC & GCGCAGACTACGTGTC

Sample = 86c tetrad = 86 spore = c

Total reads =678 PCR=215

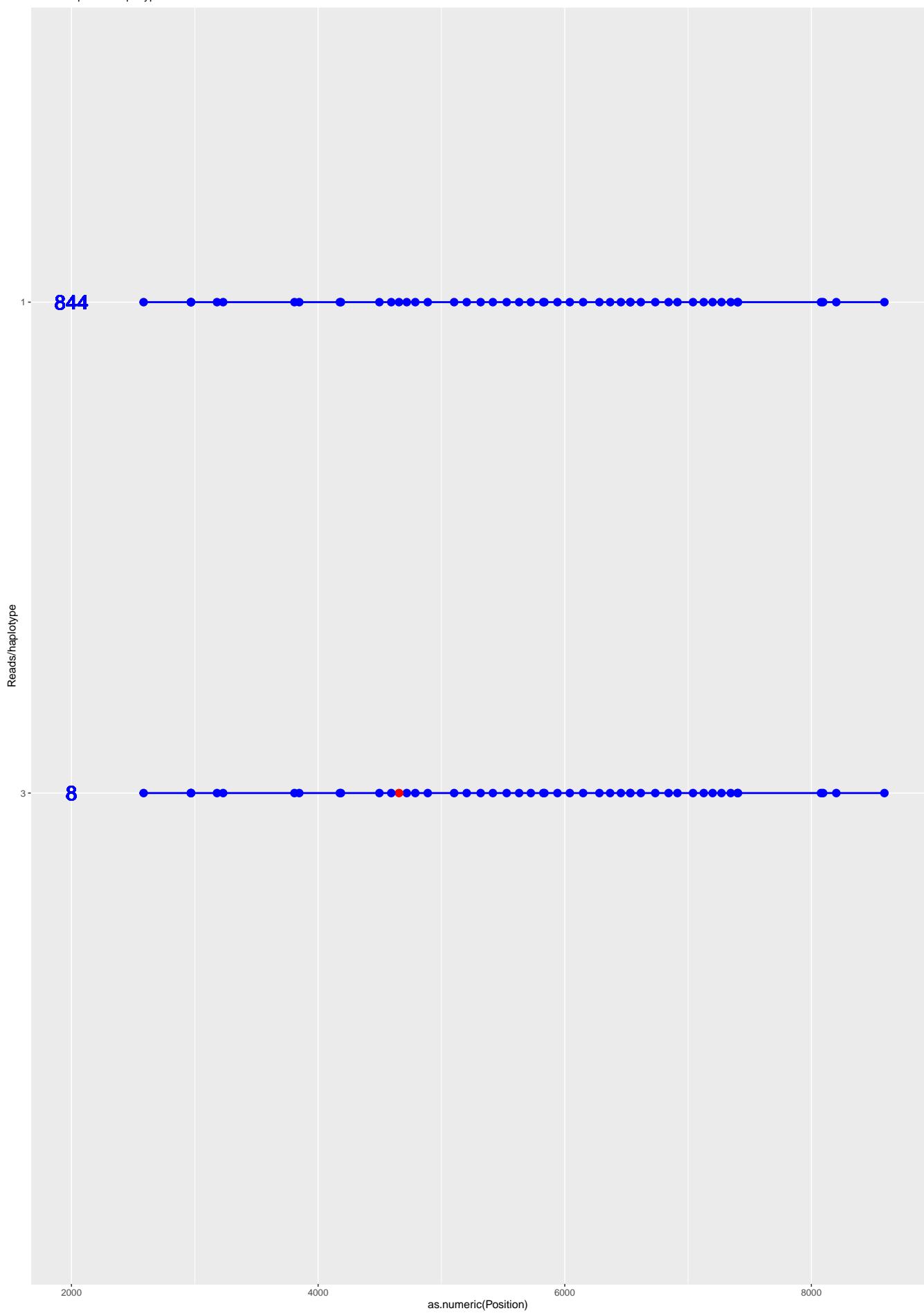
haplotypes I began with n[supporting reads] = 580

most frequent 7 haplotypes.



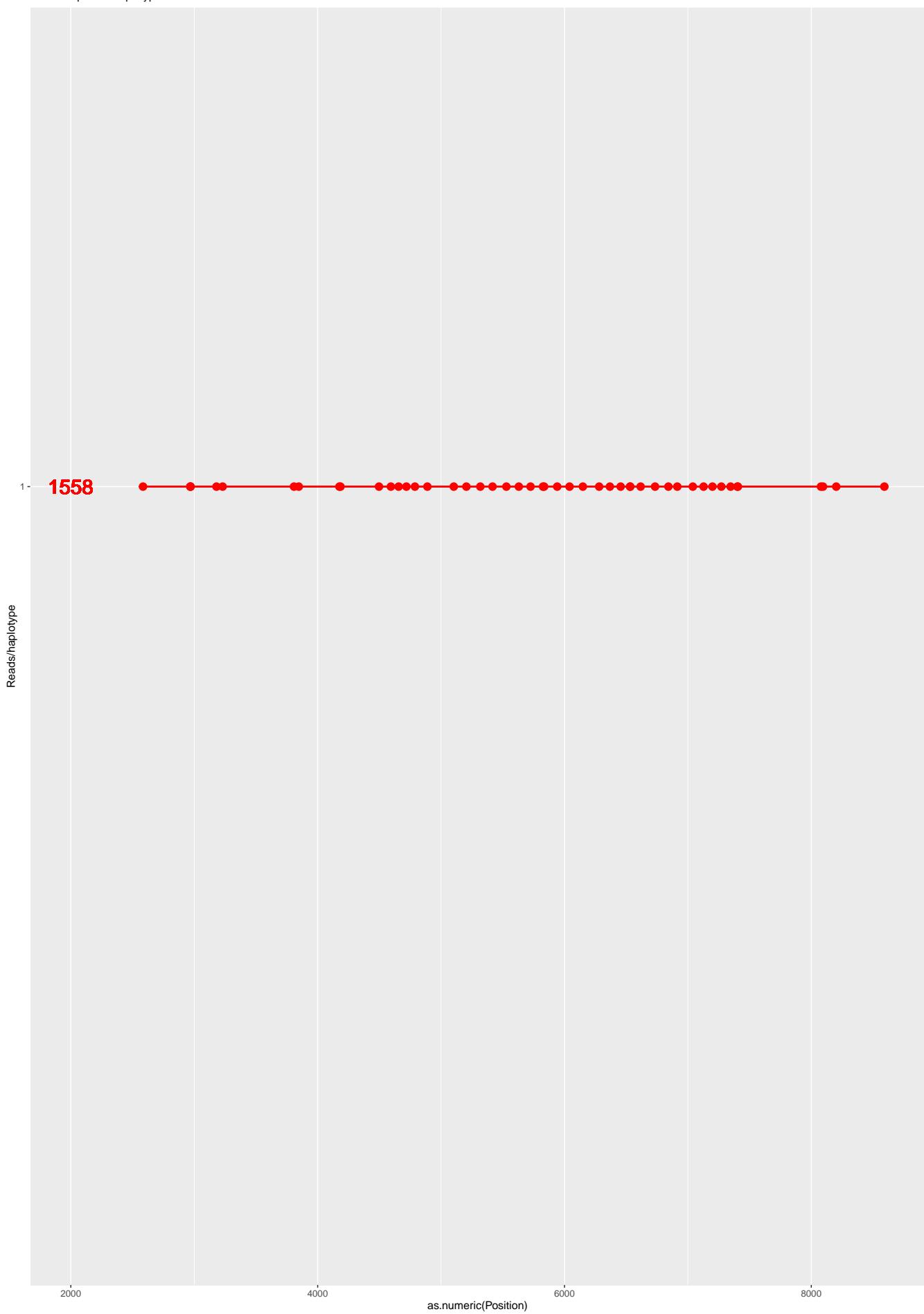
barcode = TCGTAGAGCTCGAGAC & GTCTCTGCGATAACAGC

Sample = 86d tetrad = 86 spore = d
Total reads = 973 PCR=216
haplotypes I began with n[supporting reads] = 8, 844
most frequent 7 haplotypes.



barcode = TCGTAGAGCTGAGAC & AGTATGAGATAGCTCG

Sample = 89a tetrad = 89 spore = a
Total reads = 1625 PCR=217
haplotypes I began with n[supporting reads] = 1558
most frequent 7 haplotypes.



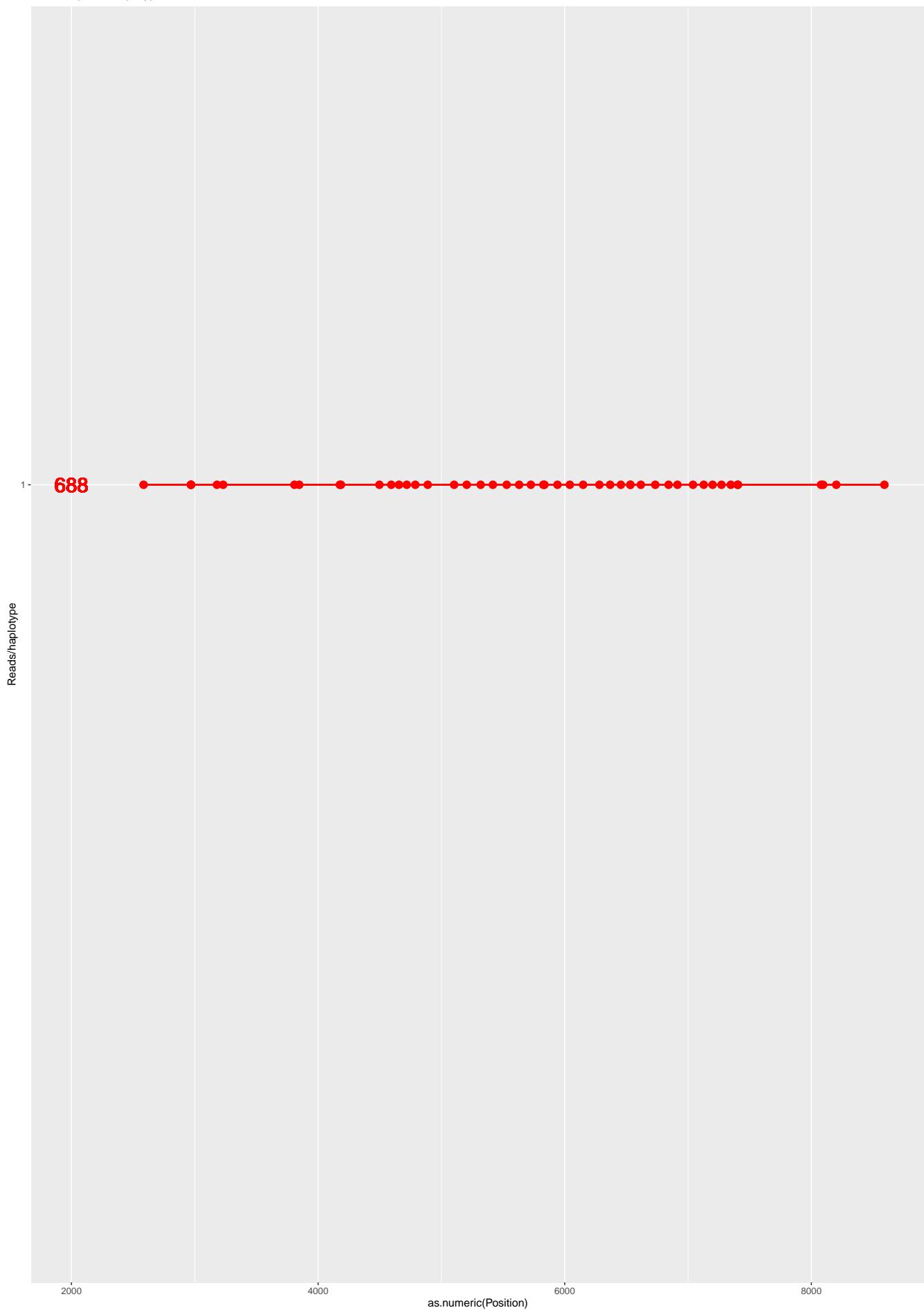
barcode = GAGCTGCGCACTCGAT & TCATATGTAGTACTCT

Sample = 89b tetrad = 89 spore = b

Total reads =724 PCR=218

haplotypes I began with n[supporting reads] = 688

most frequent 7 haplotypes.



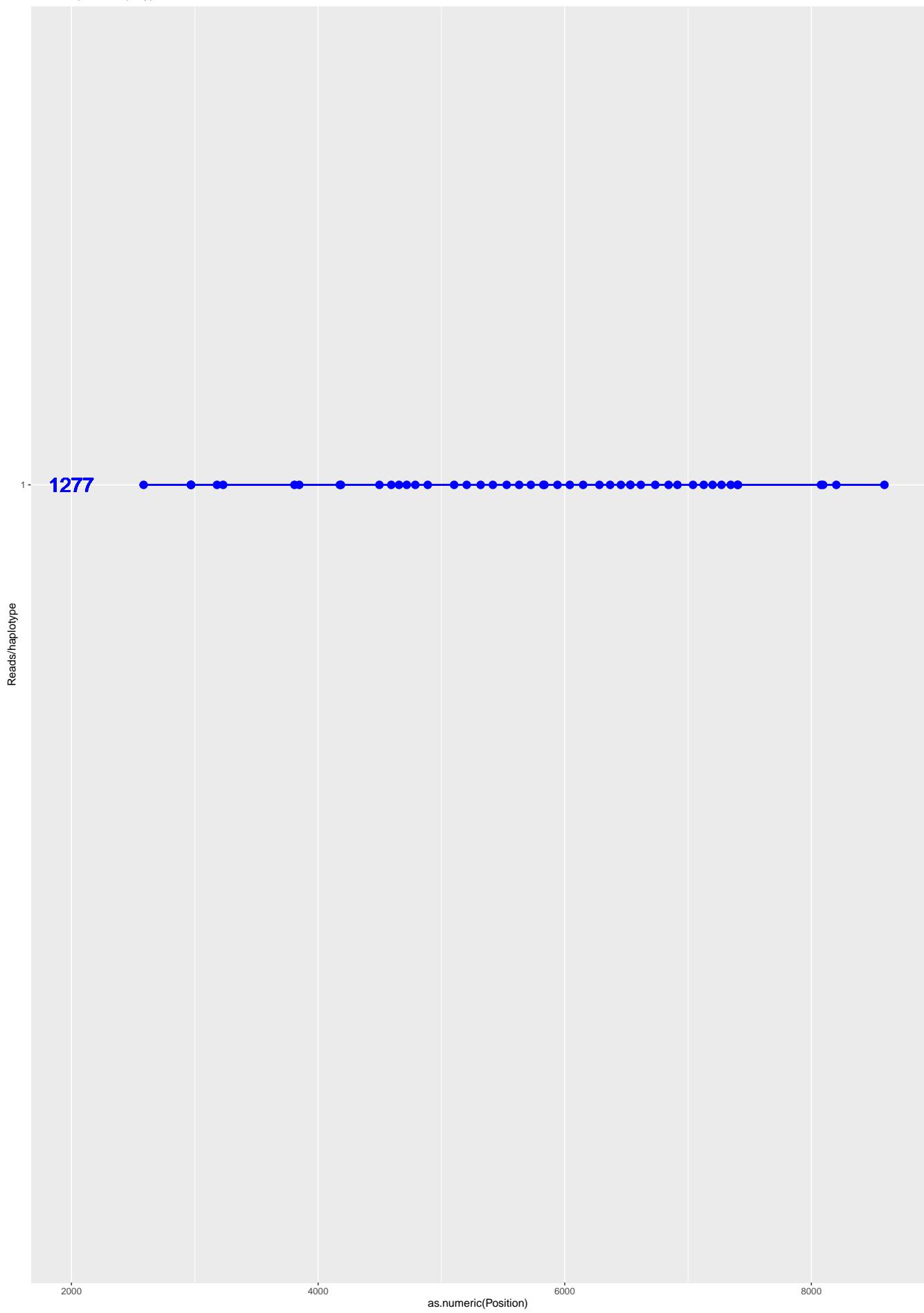
barcode = GAGCTGCGCACTCGAT & GCGATCTATGCACACG

Sample = 89c tetrad = 89 spore = c

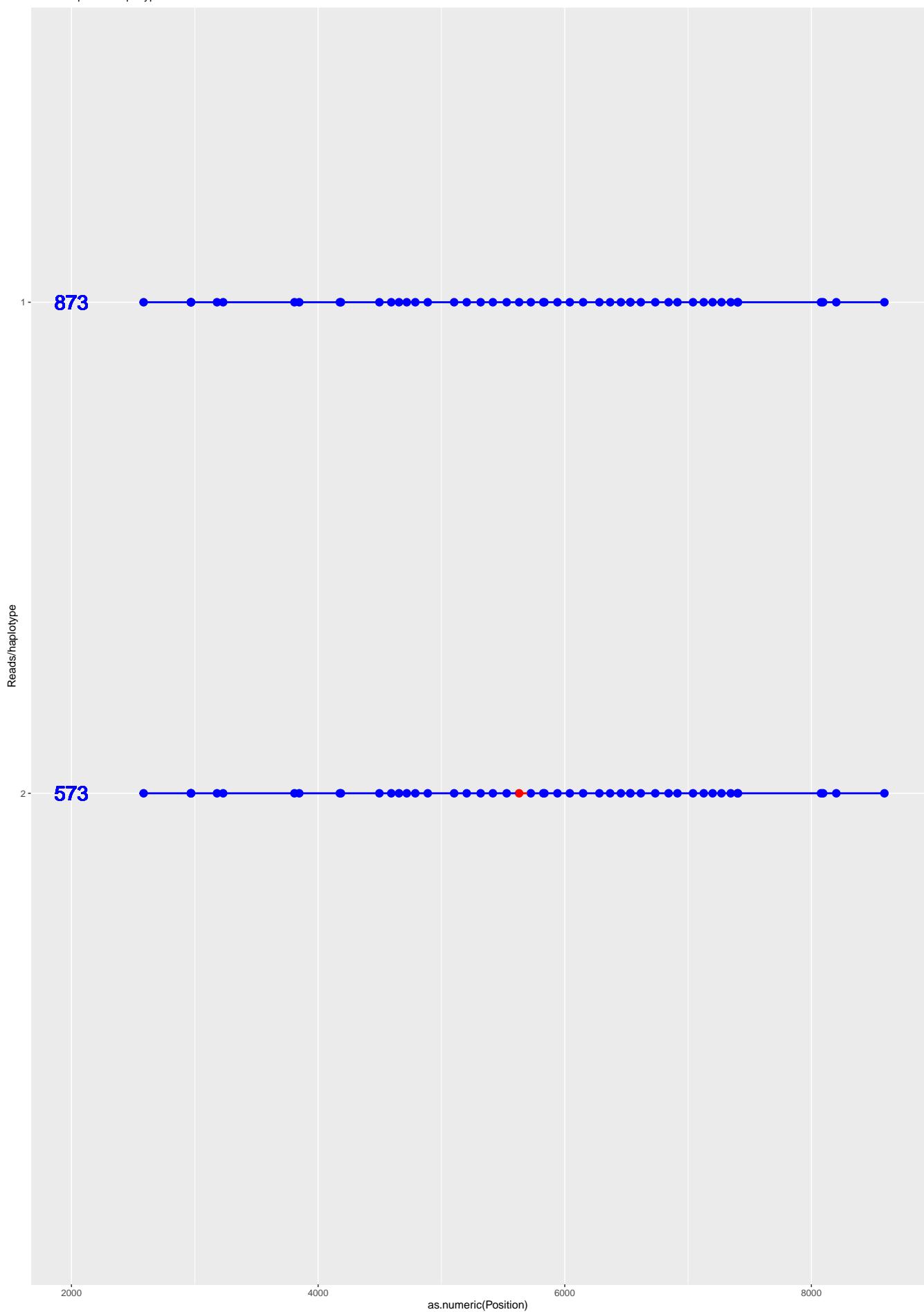
Total reads = 1508 PCR=219

haplotypes I began with n[supporting reads] = 1277

most frequent 7 haplotypes.

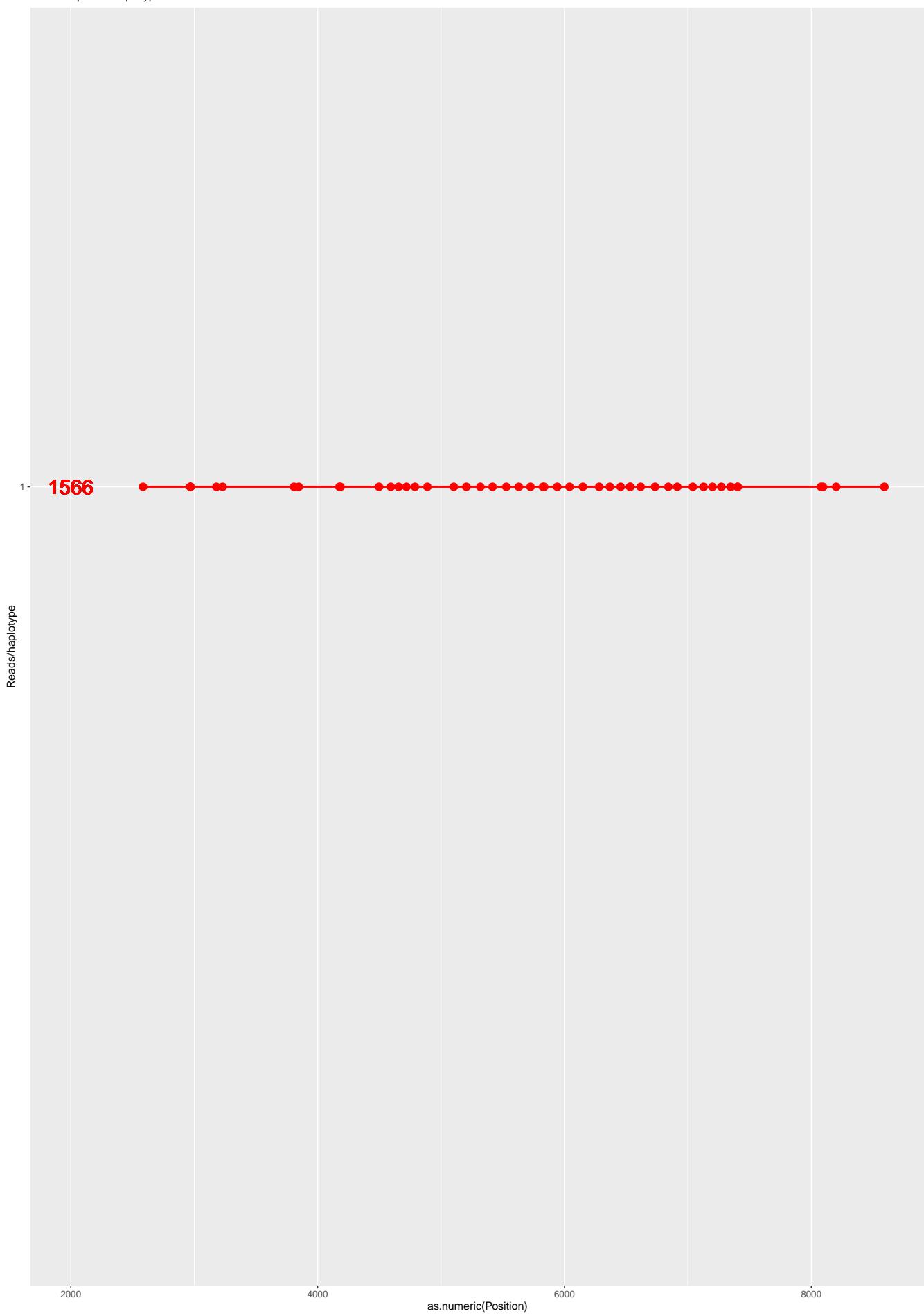


Sample = 89d tetrad = 89 spore = d
Total reads = 1692 PCR=220
haplotypes I began with n[supporting reads] = 573, 873
most frequent 7 haplotypes.



barcode = GAGCTGCGCACTCGAT & GACTCTGCGTCGAGTC

Sample = 92a tetrad = 92 spore = a
Total reads = 1638 PCR=221
haplotypes I began with n[supporting reads] = 1566
most frequent 7 haplotypes.

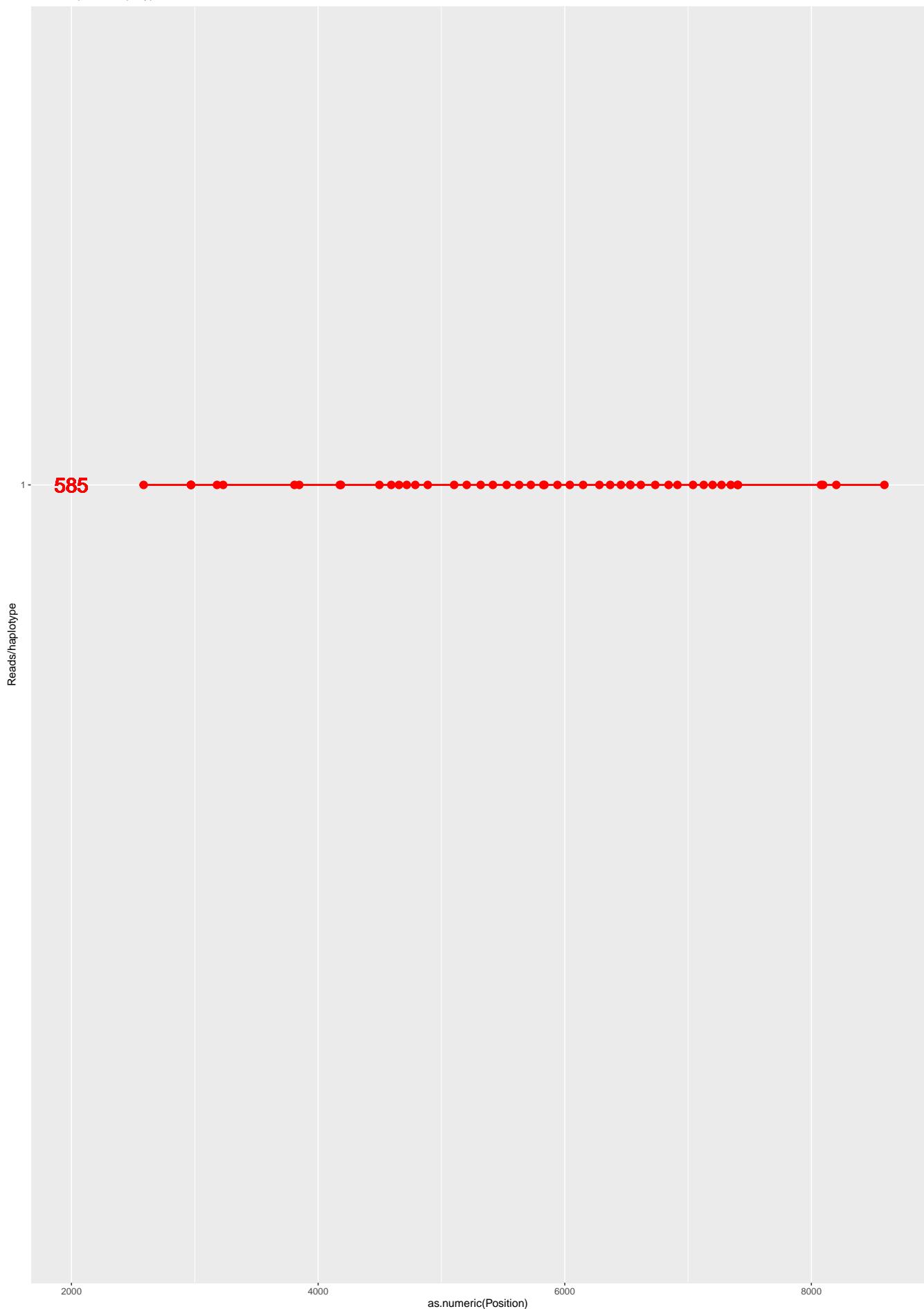


Sample = 92b tetrad = 92 spore = b

Total reads =606 PCR=222

haplotypes I began with n[supporting reads] = 585

most frequent 7 haplotypes.



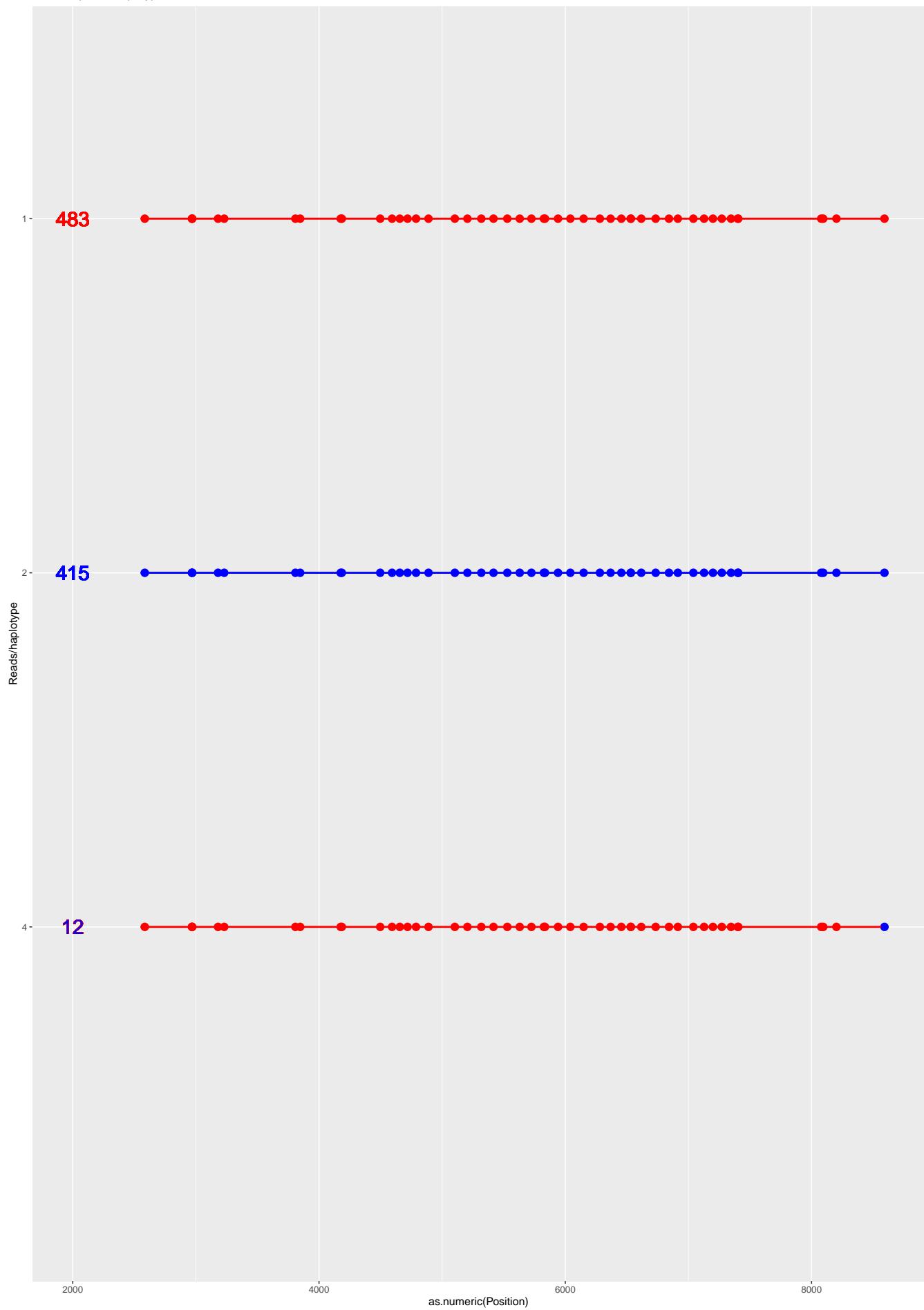
barcode = GAGCTGCGCACTCGAT & GCGCAGACTACGTGTG

Sample = 92c tetrad = 92 spore = c

Total reads = 1649 PCR=223

haplotypes I began with n[supporting reads] = 12, 415, 483

most frequent 7 haplotypes.

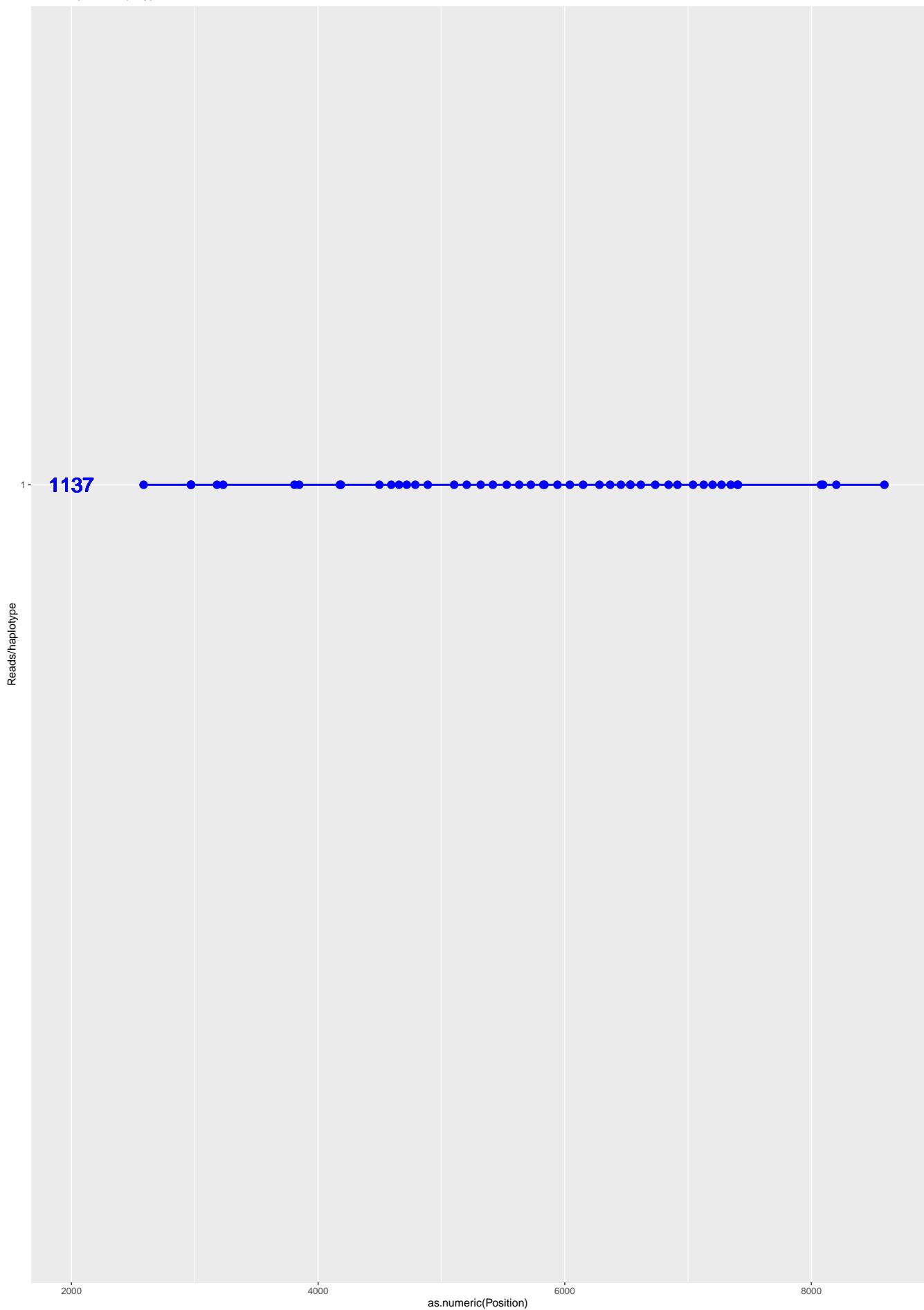


Sample = 92d tetrad = 92 spore = d

Total reads = 1327 PCR=224

haplotypes I began with n[supporting reads] = 1137

most frequent 7 haplotypes.



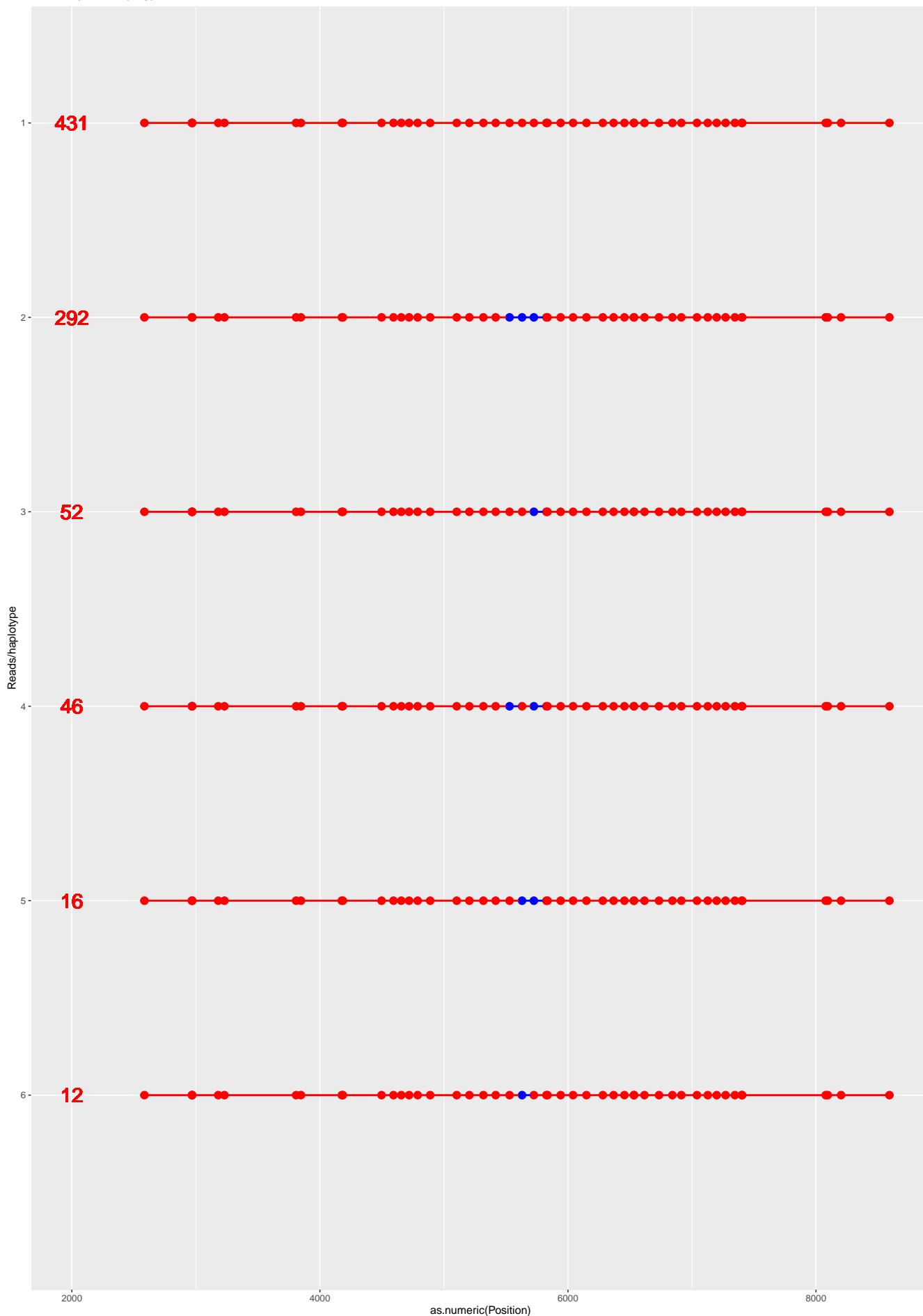
barcode = GAGCTGCGCACTCGAT & AGTATGAGATAGCTCG

Sample = 93a tetrad = 93 spore = a

Total reads = 901 PCR=225

haplotypes I began with n[supporting reads] = 12, 16, 46, 52, 292, 431

most frequent 7 haplotypes.

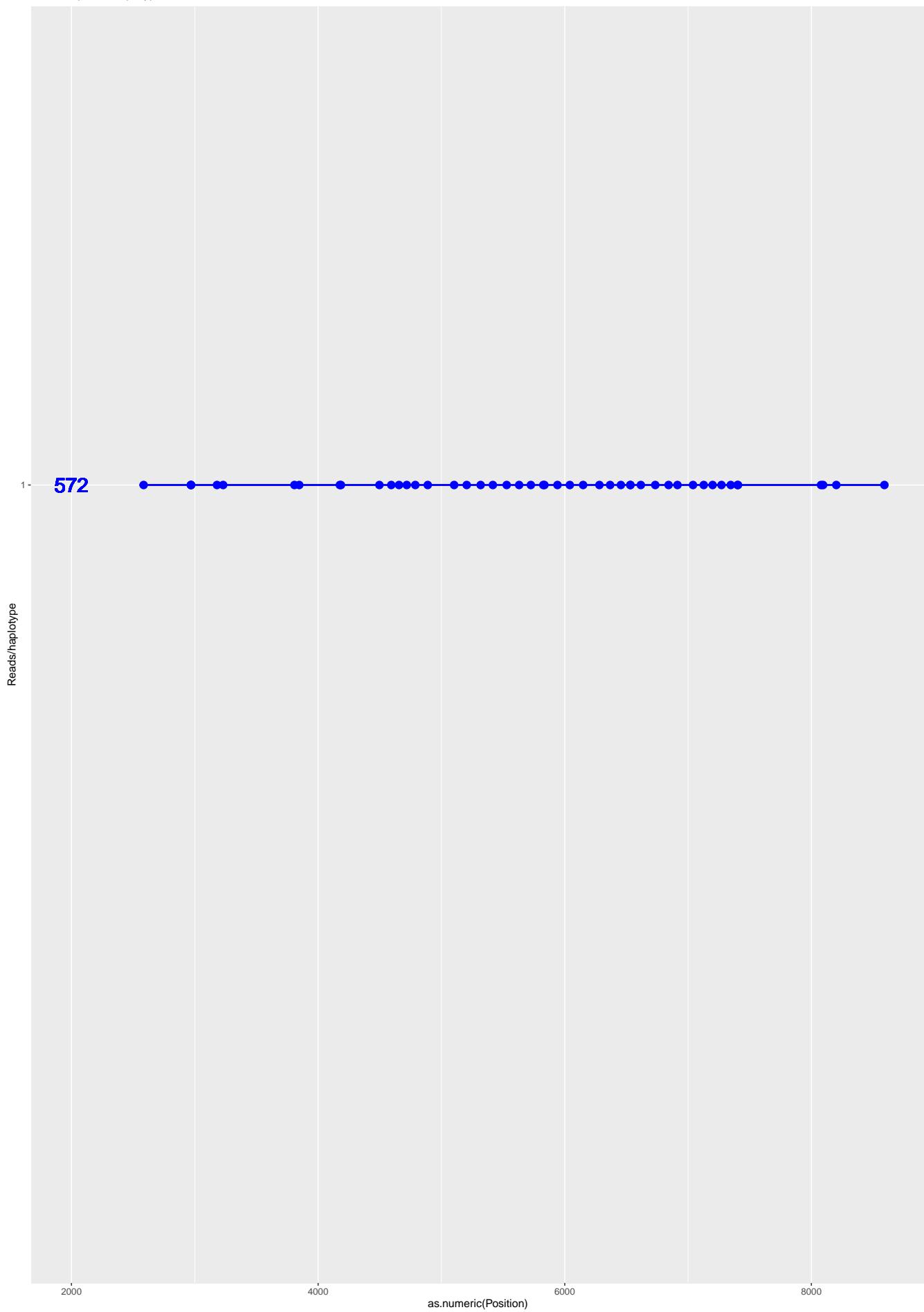


Sample = 93b tetrad = 93 spore = b

Total reads =672 PCR=226

haplotypes I began with n[supporting reads] = 572

most frequent 7 haplotypes.



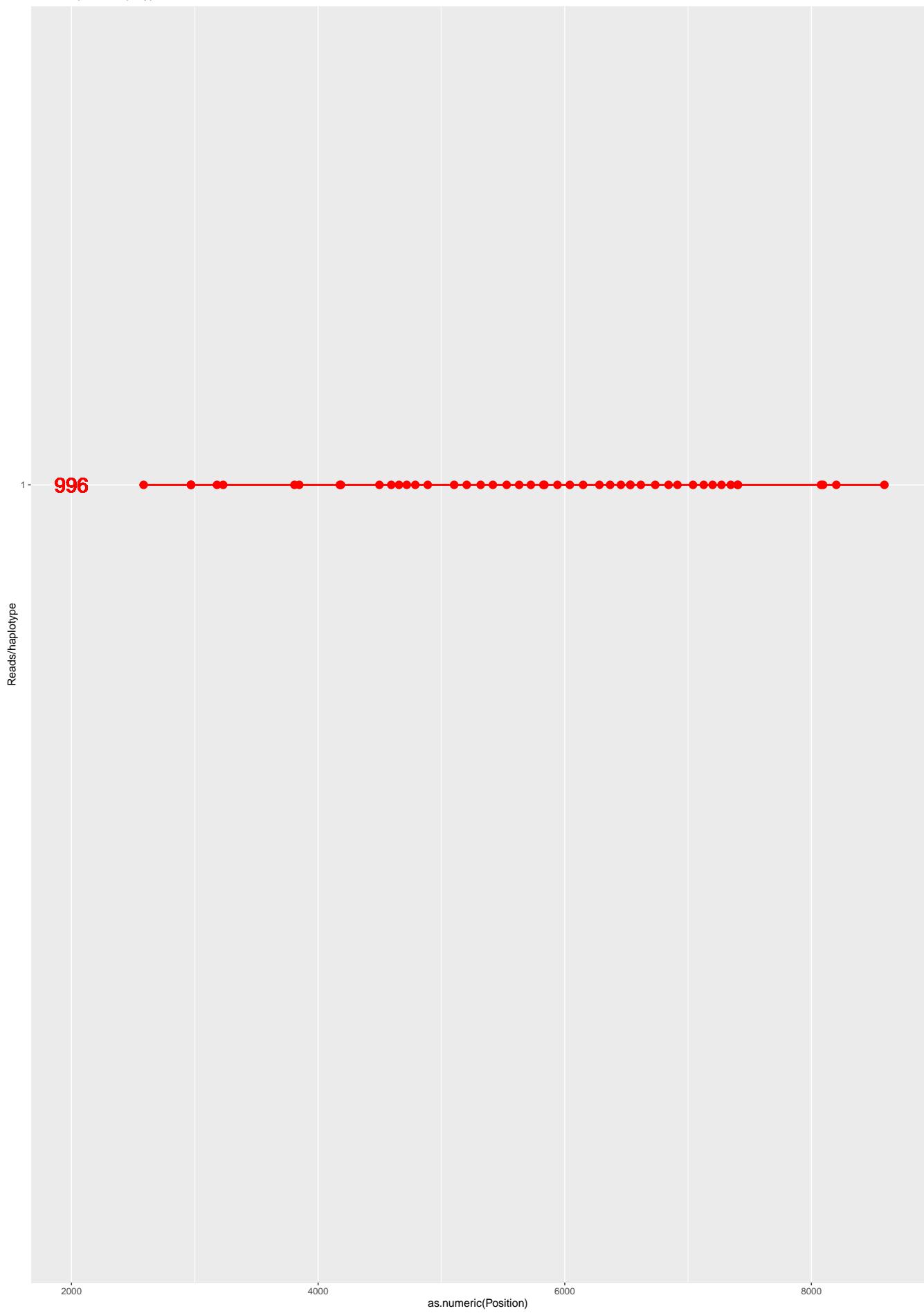
barcode = GCGATGTCGCTATGTG & GCGATCTATGCACACG

Sample = 93c tetrad = 93 spore = c

Total reads = 1032 PCR=227

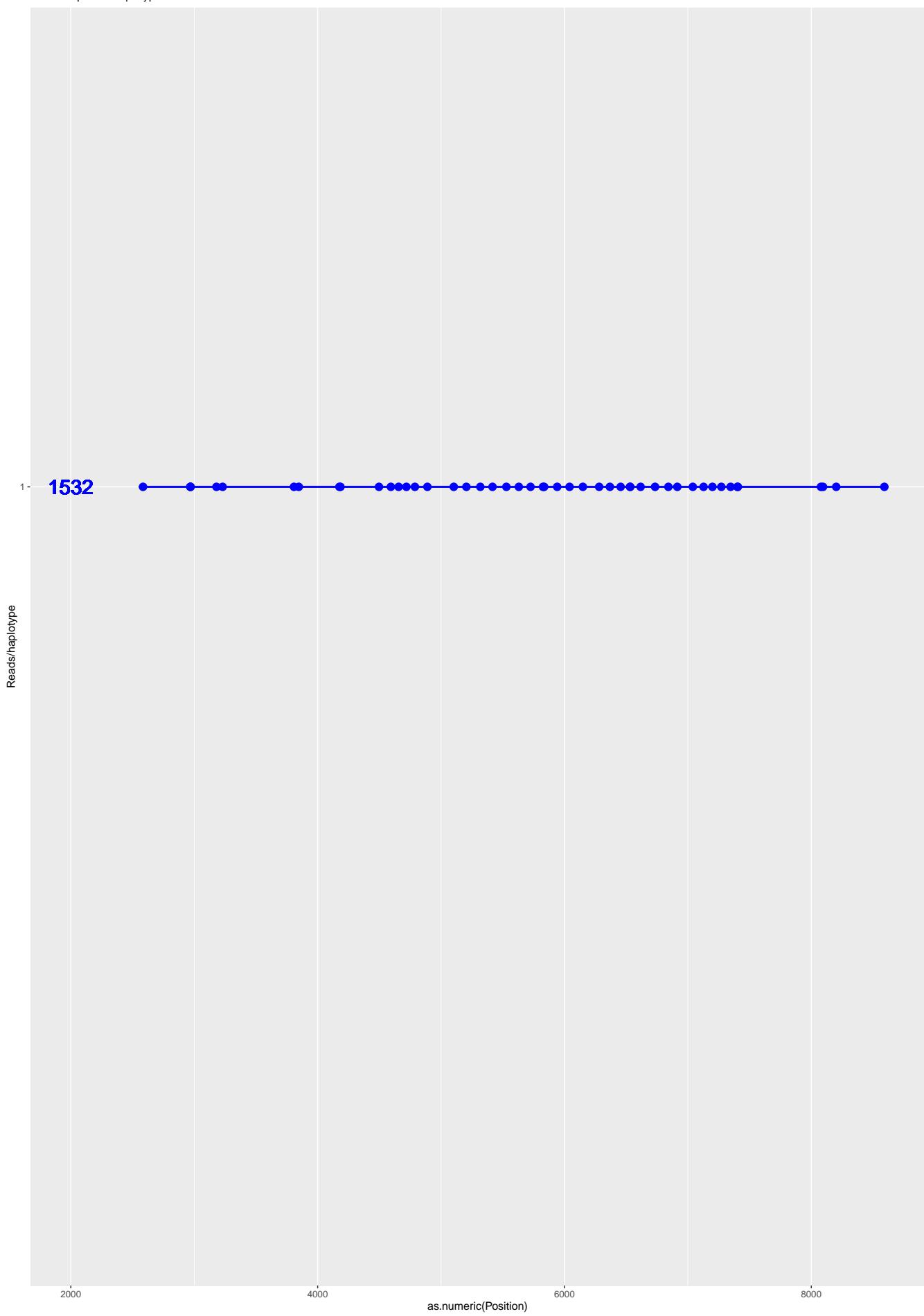
haplotypes I began with n[supporting reads] = 996

most frequent 7 haplotypes.

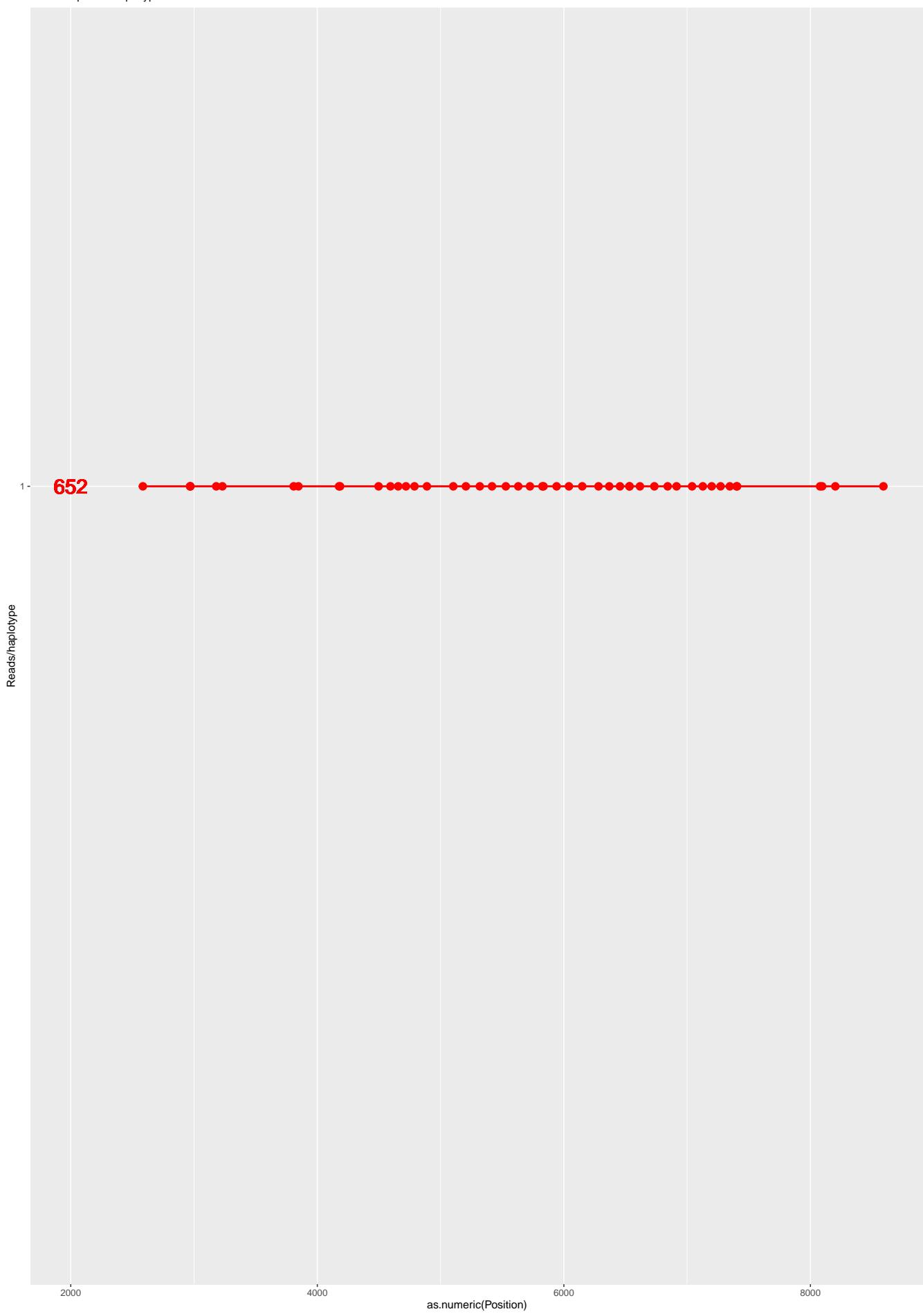


barcode = GCGATGTCGCTATGTG & TGCAGTCGAGATAACAT

Sample = 93d tetrad = 93 spore = d
Total reads = 1779 PCR=228
haplotypes I began with n[supporting reads] = 1532
most frequent 7 haplotypes.



Sample = 94a tetrad = 94 spore = a
Total reads = 679 PCR=229
haplotypes I began with n[supporting reads] = 652
most frequent 7 haplotypes.



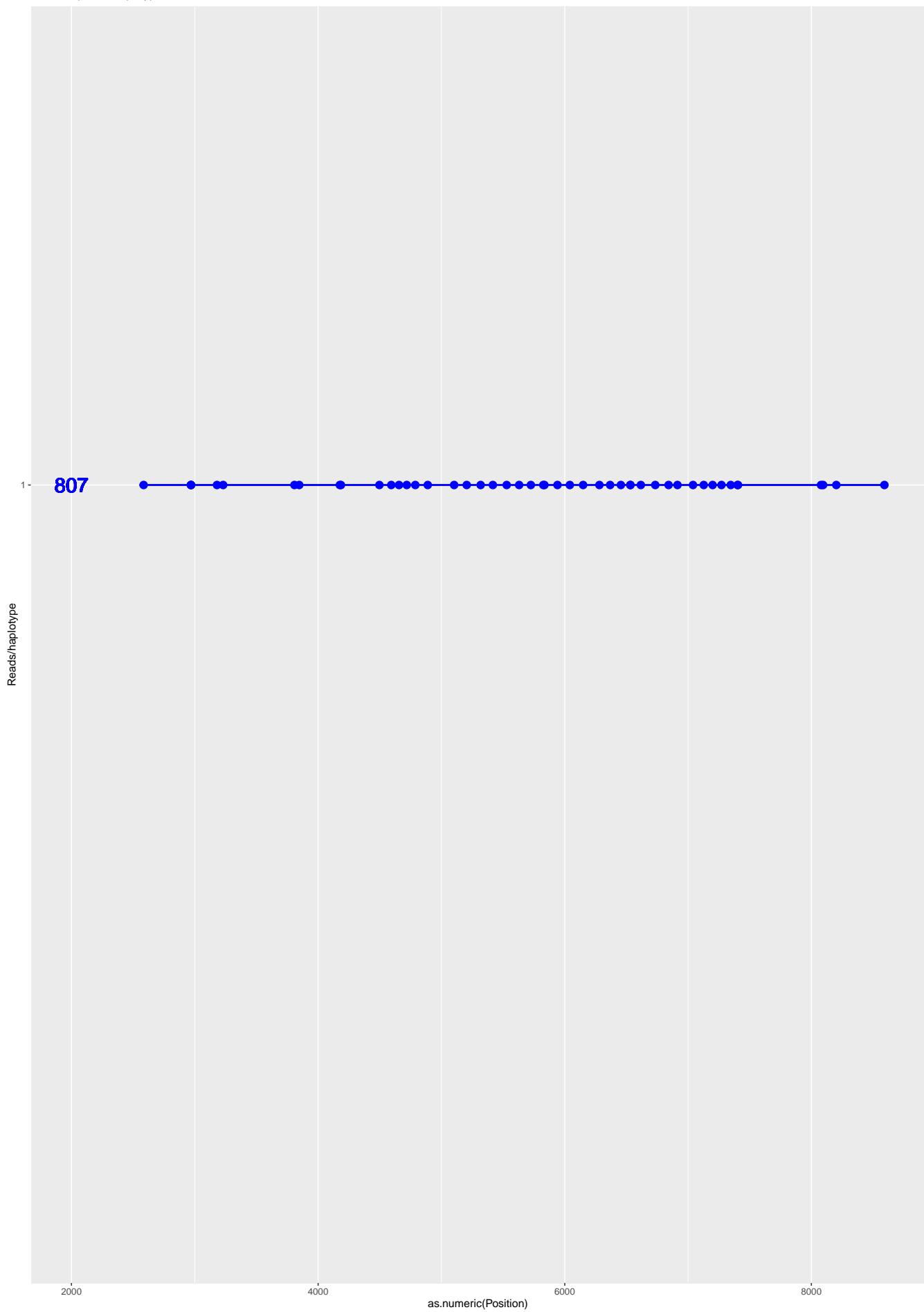
barcode = GCGATGTCGCTATGTG & TACAGCGACGTCATCG

Sample = 94b tetrad = 94 spore = b

Total reads = 950 PCR=230

haplotypes I began with n[supporting reads] = 807

most frequent 7 haplotypes.



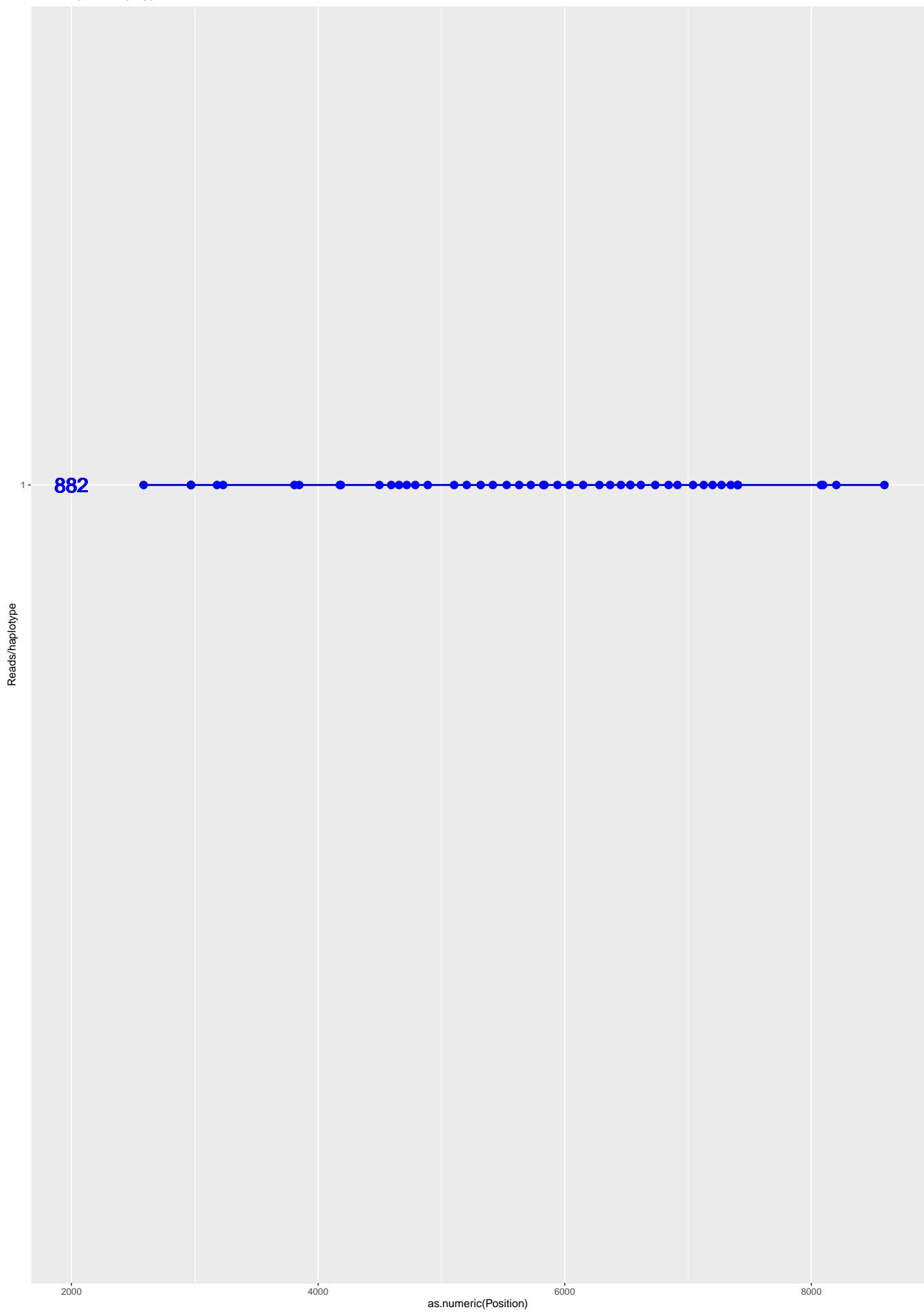
barcode = GCGATGTCGCTATGTG & GCGCAGACTACGTGTG

Sample = 94c tetrad = 94 spore = c

Total reads = 1040 PCR=231

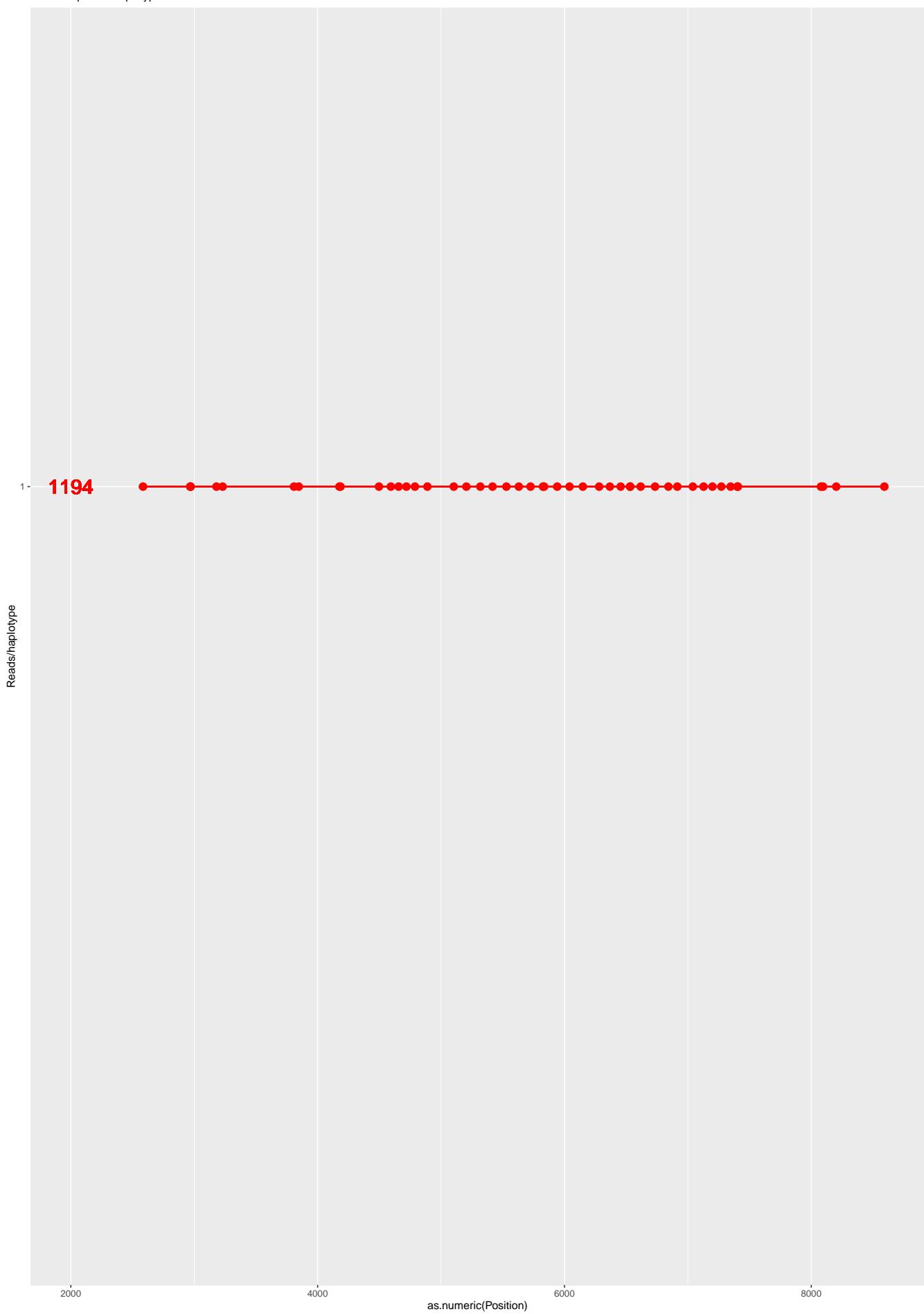
haplotypes I began with n[supporting reads] = 882

most frequent 7 haplotypes.



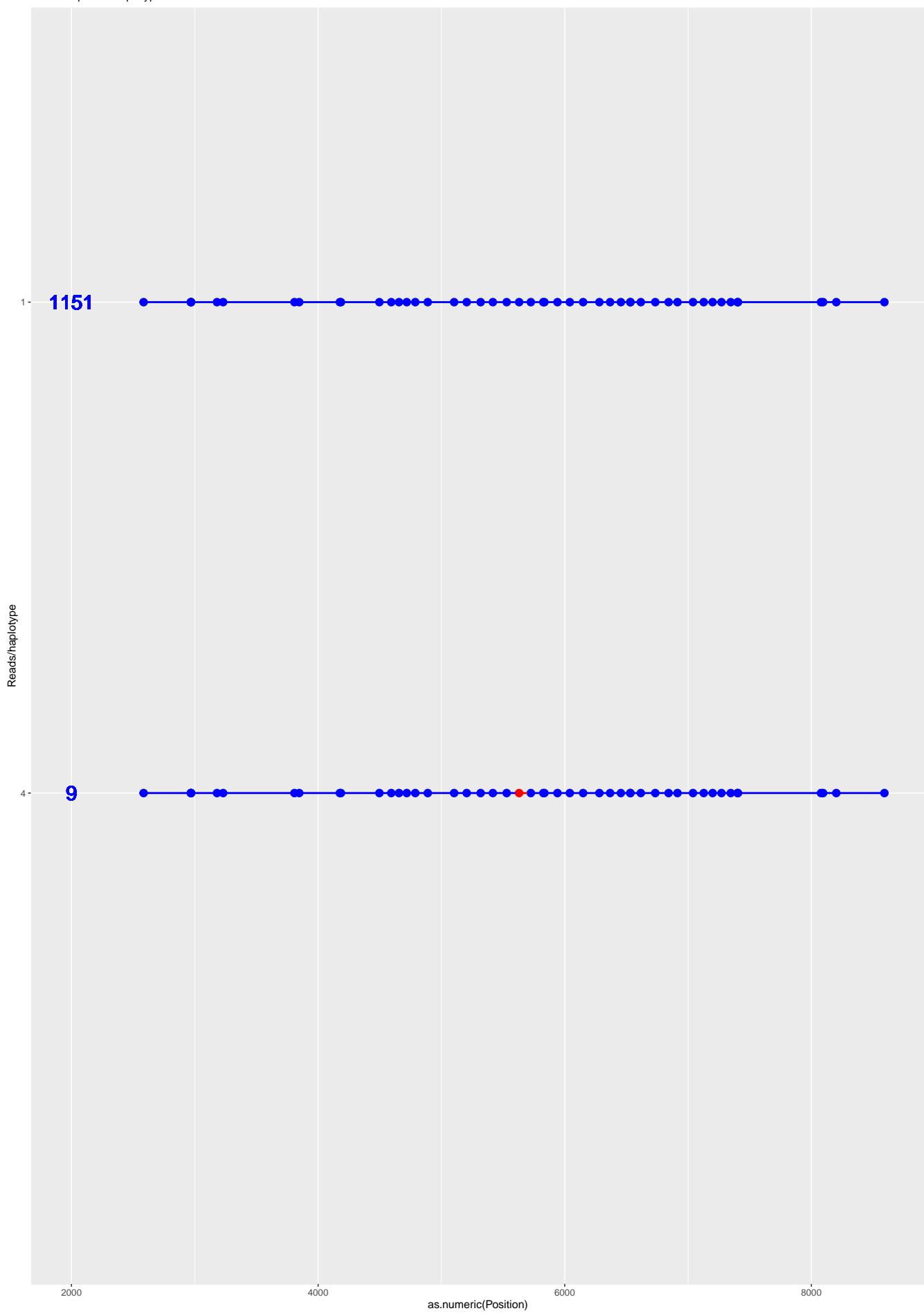
barcode = GCGATGTCGCTATGTG & GTCTCTGCGATAACAGC

Sample = 94d tetrad = 94 spore = d
Total reads = 1256 PCR=232
haplotypes I began with n[supporting reads] = 1194
most frequent 7 haplotypes.



barcode = GCGATGTCGCTATGTG & AGTATGAGATAGCTCG

Sample = 95a tetrad = 95 spore = a
Total reads = 1359 PCR=233
haplotypes I began with n[supporting reads] = 9, 1151
most frequent 7 haplotypes.



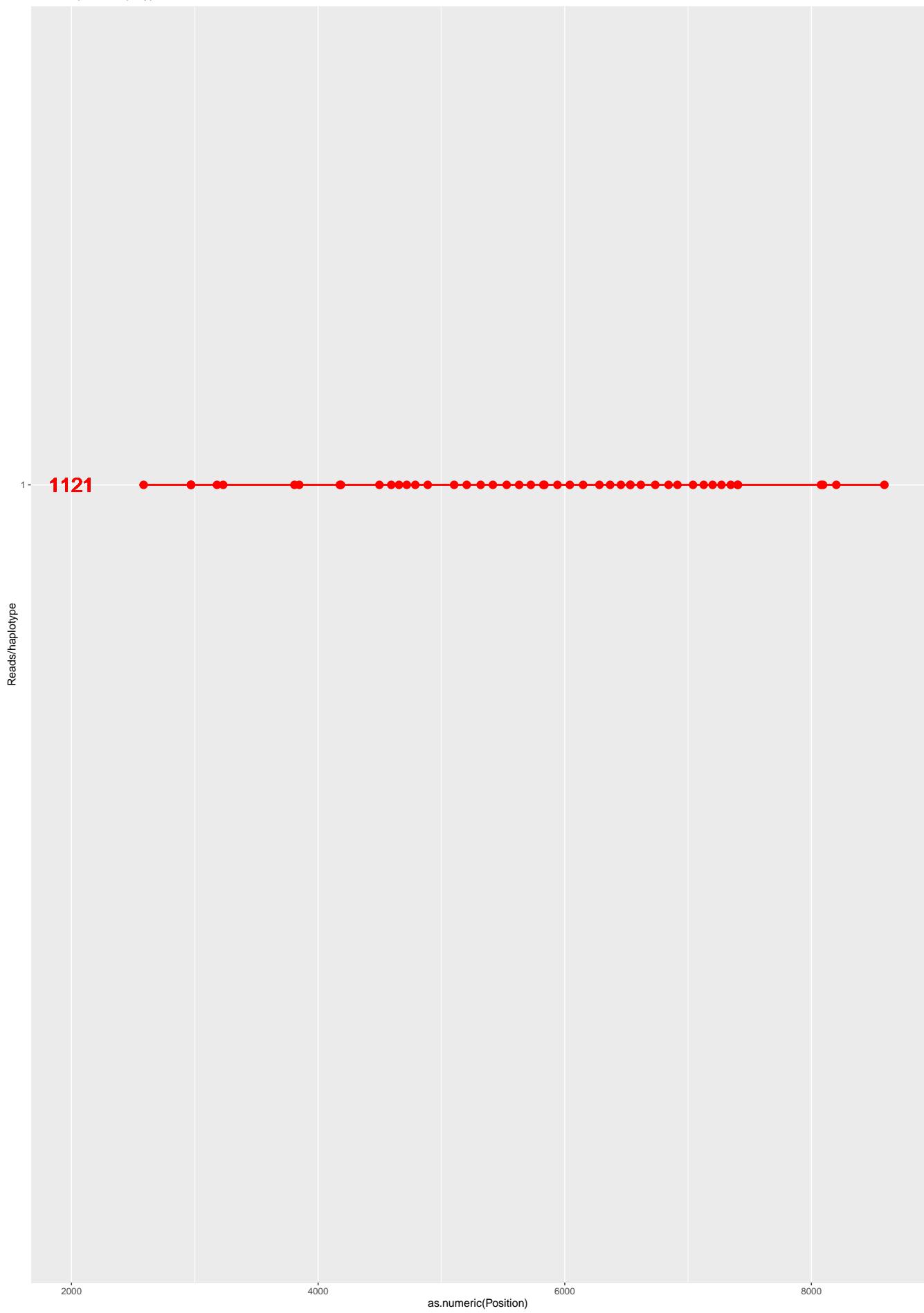
barcode = CGAGAGTCAGCGATA & TCATATGTTAGTACTCT

Sample = 95b tetrad = 95 spore = b

Total reads = 1166 PCR=234

haplotypes I began with n[supporting reads] = 1121

most frequent 7 haplotypes.



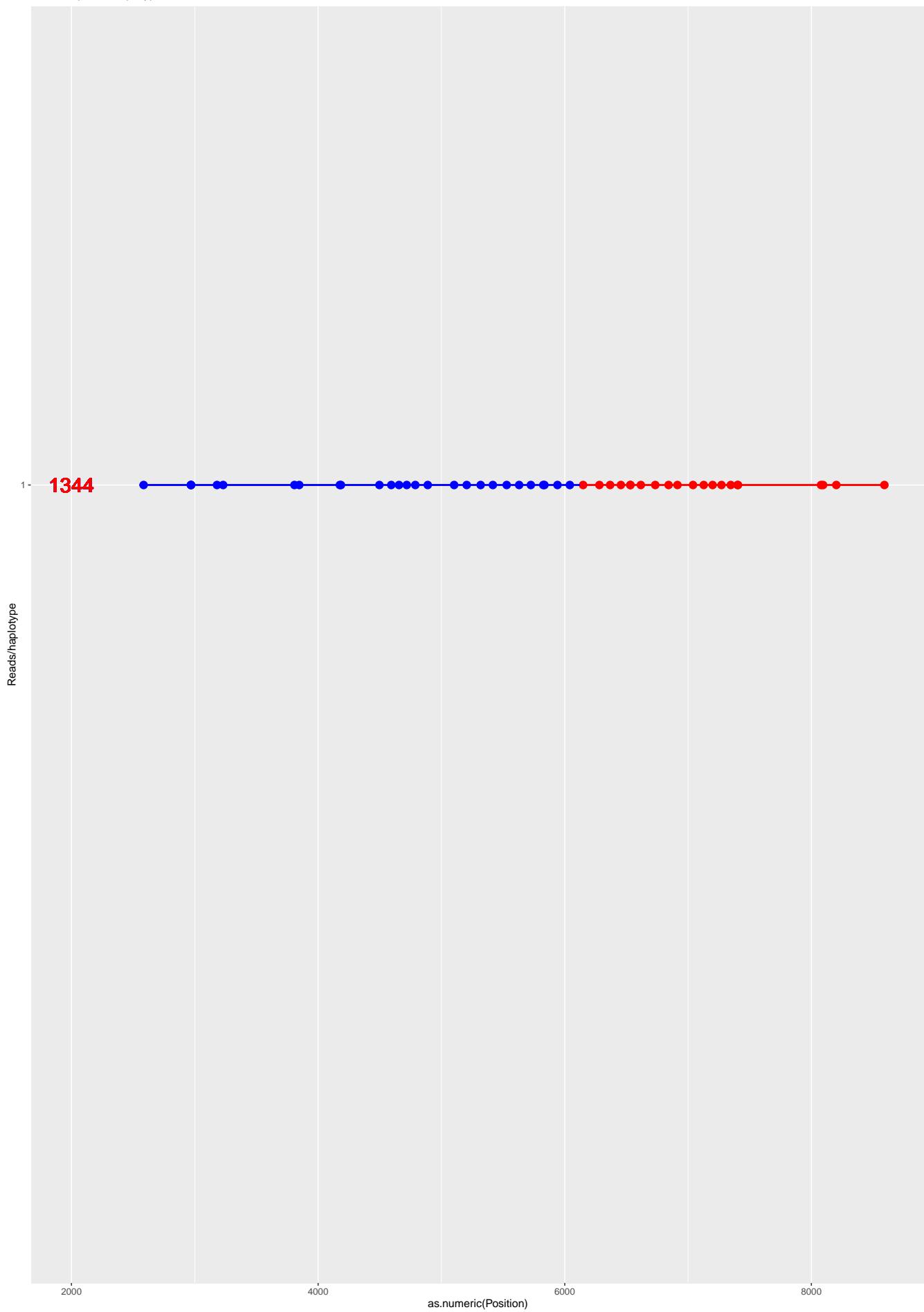
barcode = CGAGAGTCAGCGCATA & GCGATCTATGCACACG

Sample = 95c tetrad = 95 spore = c

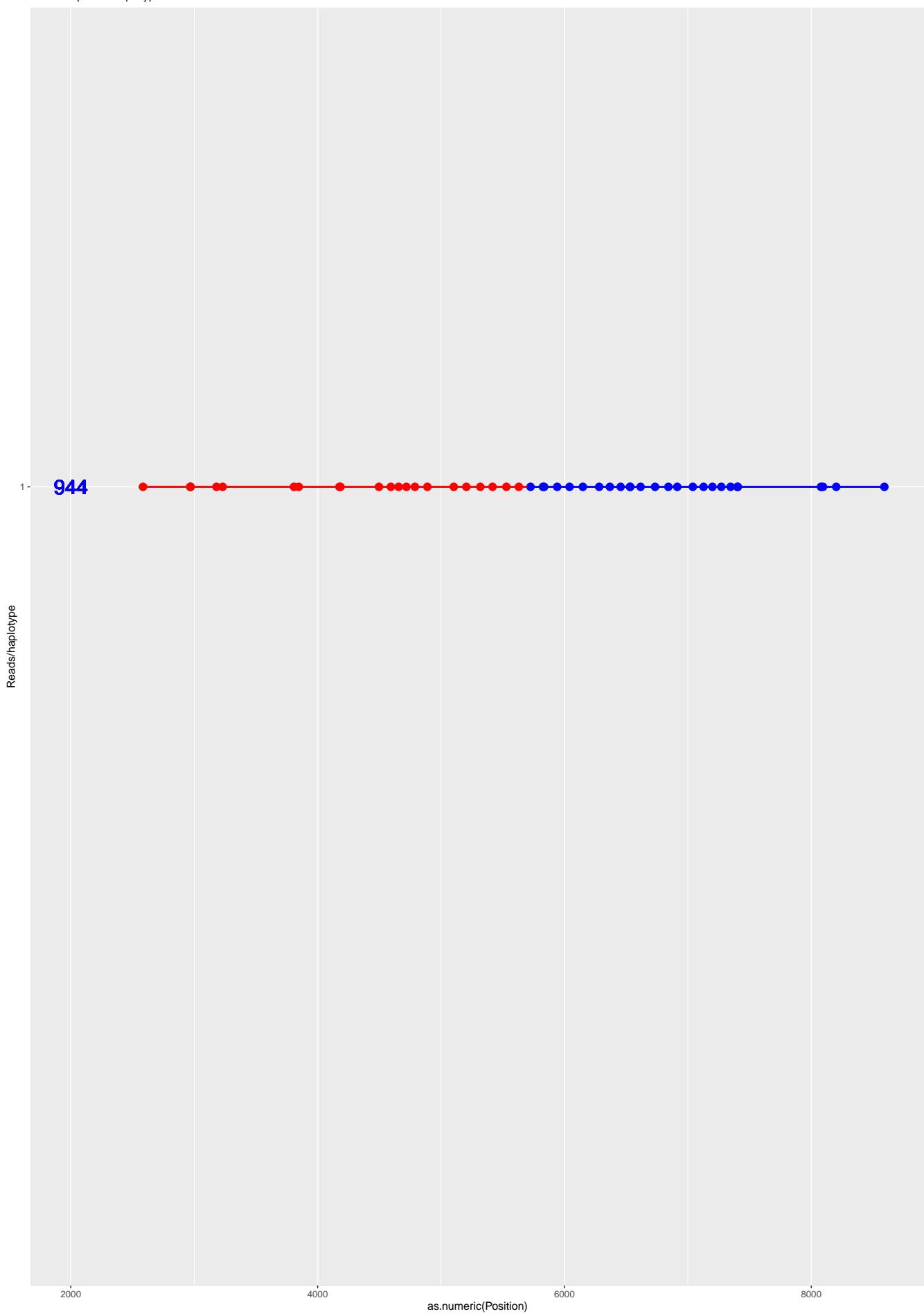
Total reads = 1537 PCR=235

haplotypes I began with n[supporting reads] = 1344

most frequent 7 haplotypes.

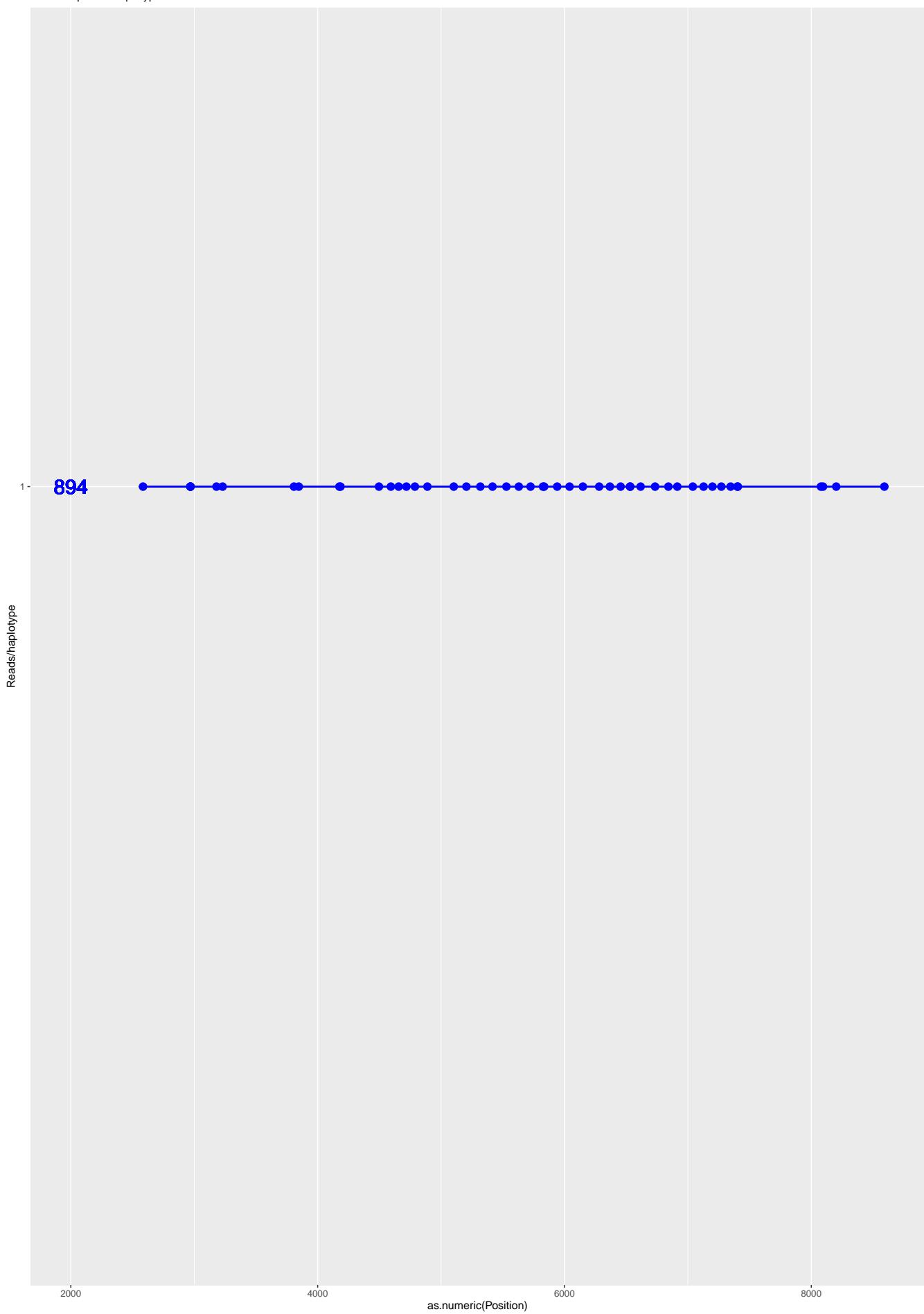


Sample = 95d tetrad = 95 spore = d
Total reads = 1026 PCR=236
haplotypes I began with n[supporting reads] = 944
most frequent 7 haplotypes.



barcode = CGAGAGTCAGCGCATA & GACTCTGCGTCGAGTC

Sample = 97a tetrad = 97 spore = a
Total reads = 1025 PCR=237
haplotypes I began with n[supporting reads] = 894
most frequent 7 haplotypes.

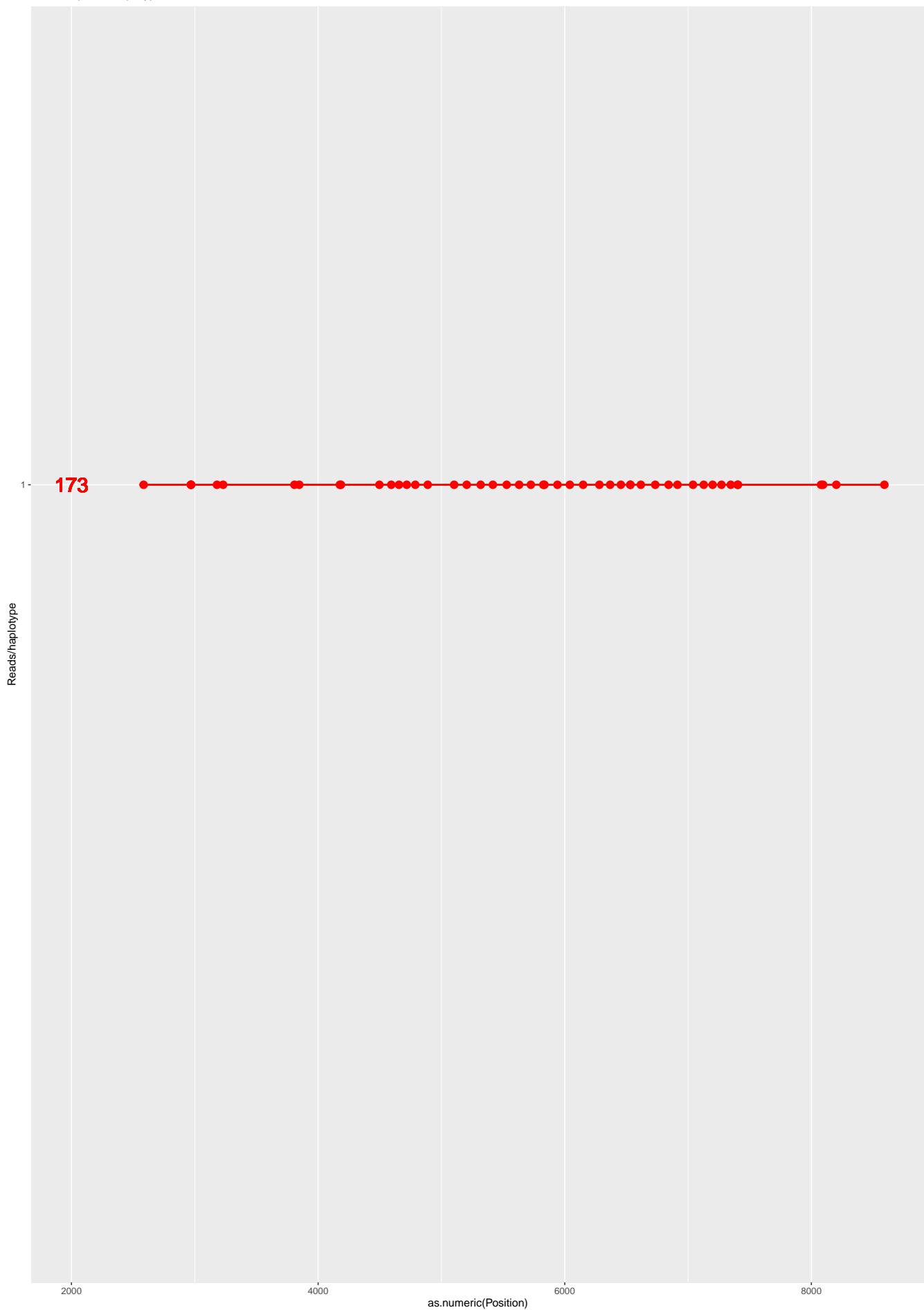


Sample = 97b tetrad = 97 spore = b

Total reads = 182 PCR=238

haplotypes I began with n[supporting reads] = 173

most frequent 7 haplotypes.



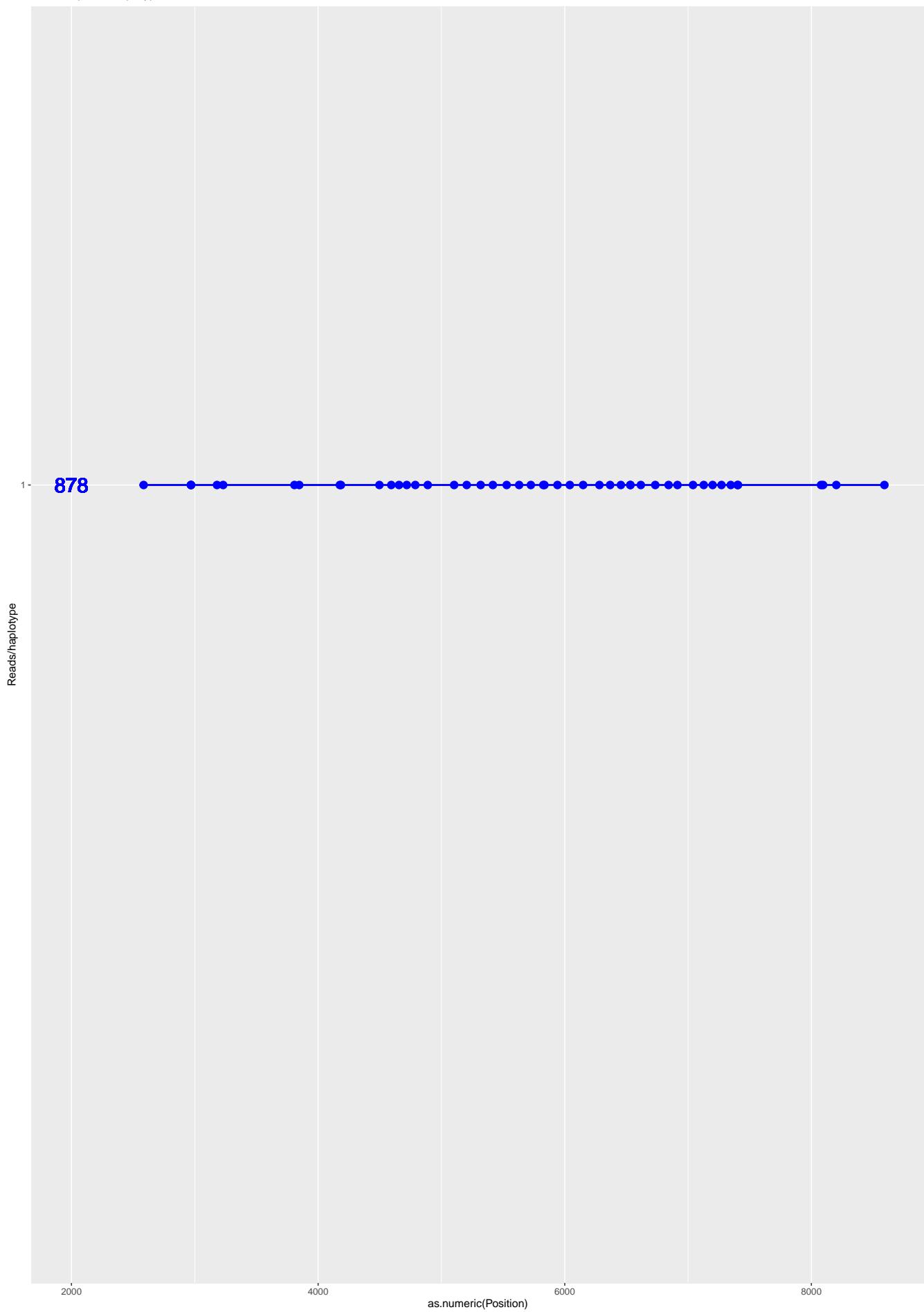
barcode = CGAGAGTCAGCGCATA & GCGCAGACTACGTG

Sample = 97c tetrad = 97 spore = c

Total reads = 1012 PCR=239

haplotypes I began with n[supporting reads] = 878

most frequent 7 haplotypes.



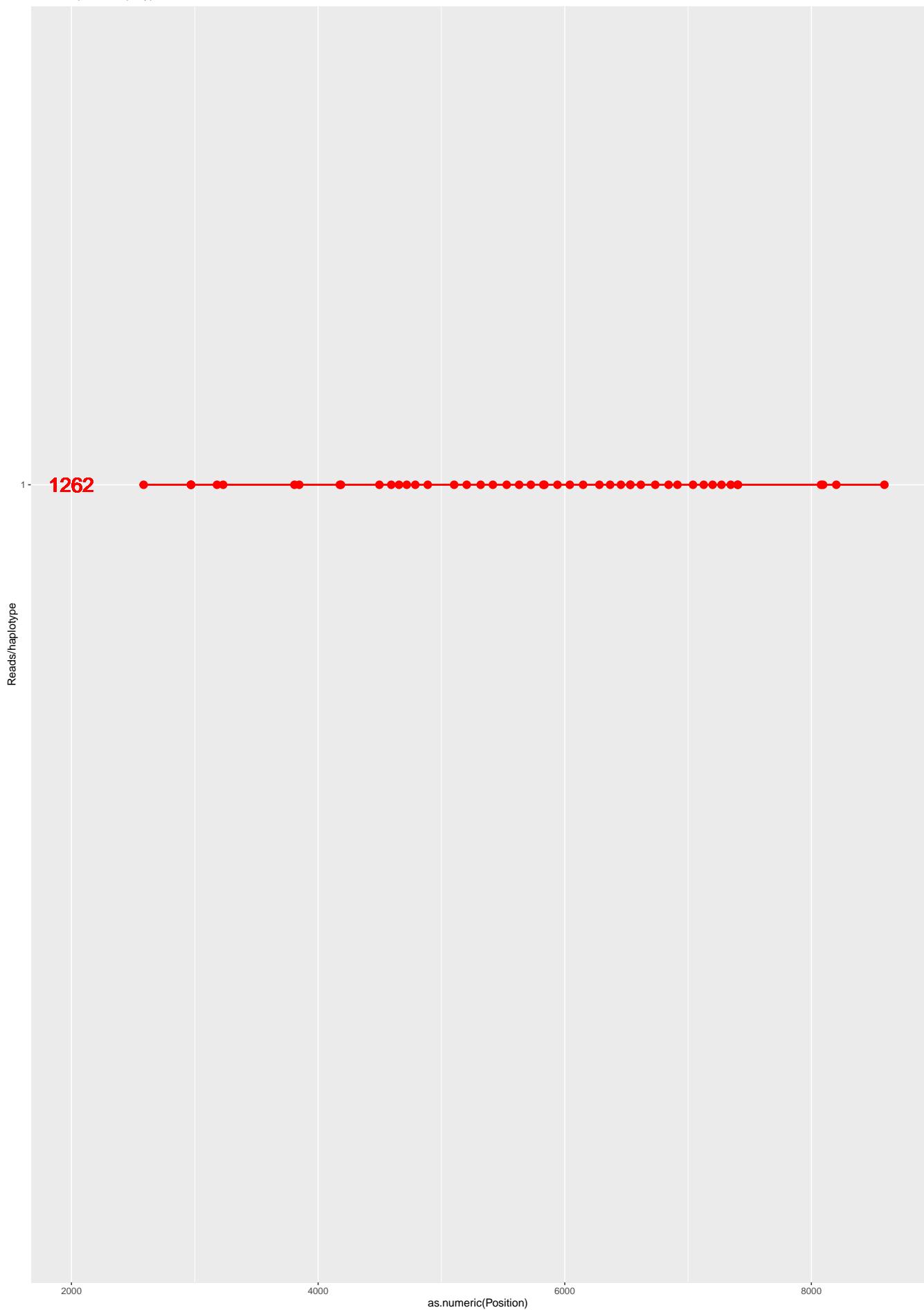
barcode = CGAGAGTCAGCGCATA & GTCTCTGCGATACAGC

Sample = 97d tetrad = 97 spore = d

Total reads = 1323 PCR=240

haplotypes I began with n[supporting reads] = 1262

most frequent 7 haplotypes.



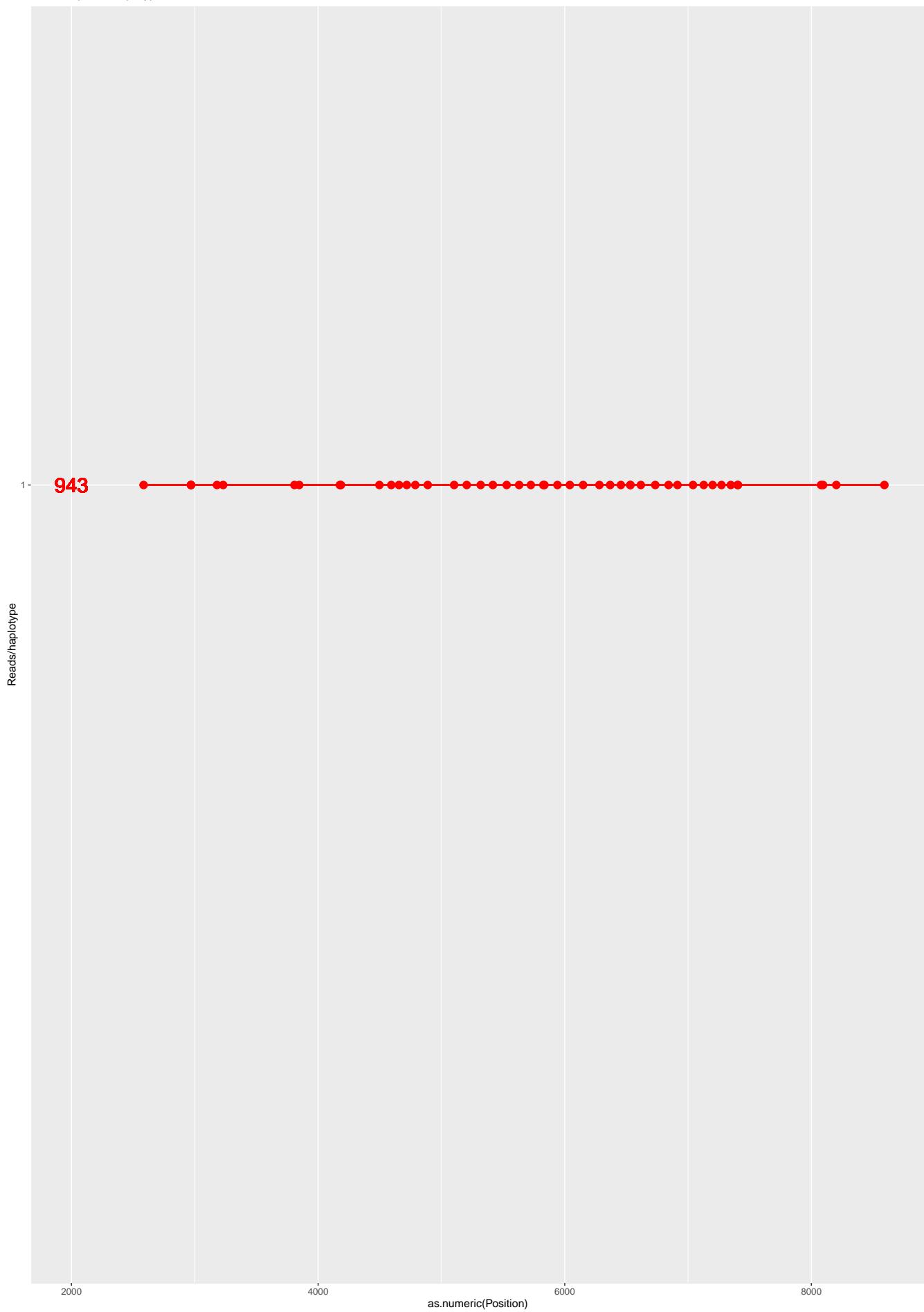
barcode = CGAGAGTCAGCGCATA & AGTATGAGATAGCTCG

Sample = 98a tetrad = 98 spore = a

Total reads = 987 PCR=241

haplotypes I began with n[supporting reads] = 943

most frequent 7 haplotypes.



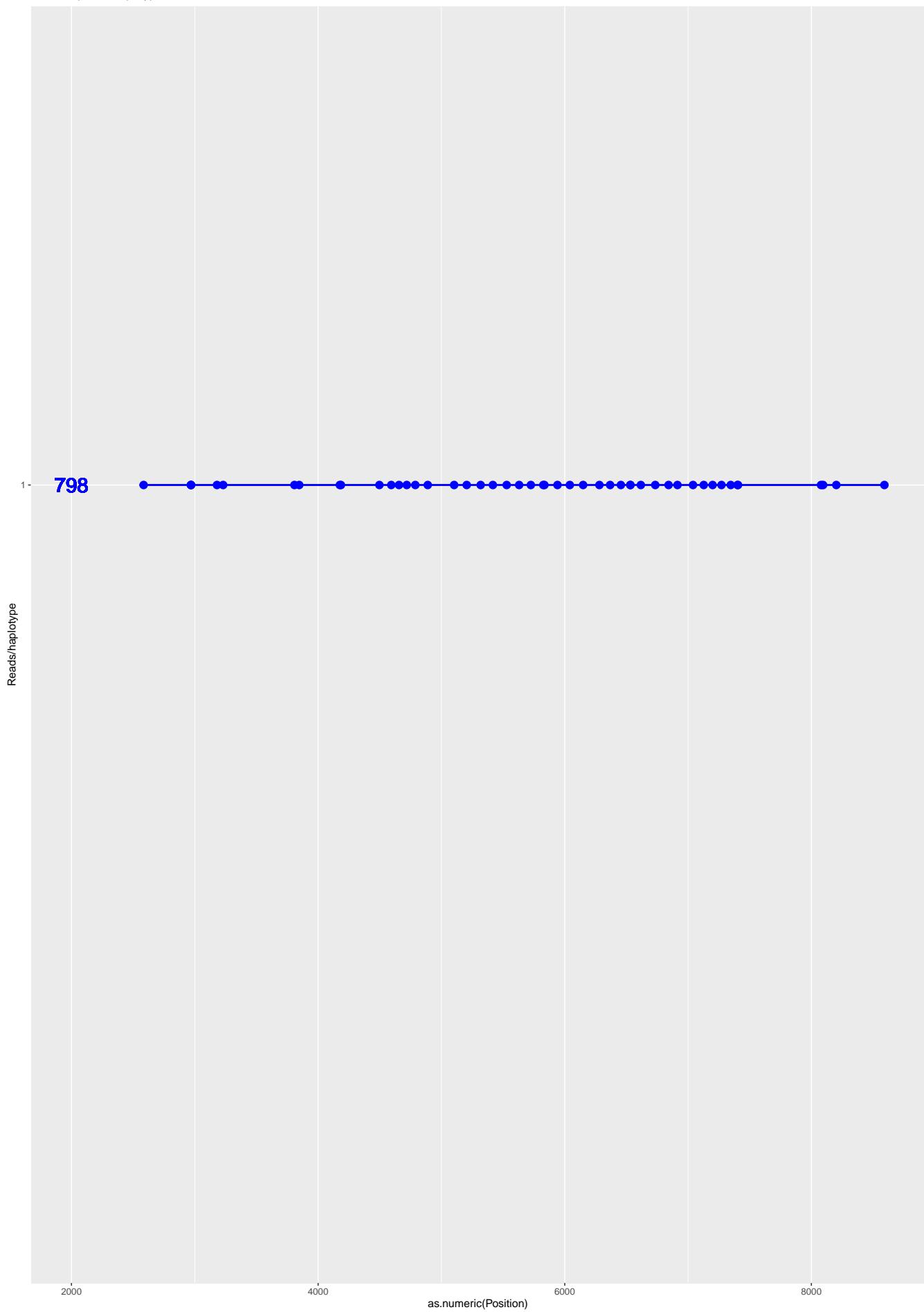
barcode = TCACGATGAGCACGTA & TCATATGTAGTACTCT

Sample = 98b tetrad = 98 spore = b

Total reads = 921 PCR=242

haplotypes I began with n[supporting reads] = 798

most frequent 7 haplotypes.



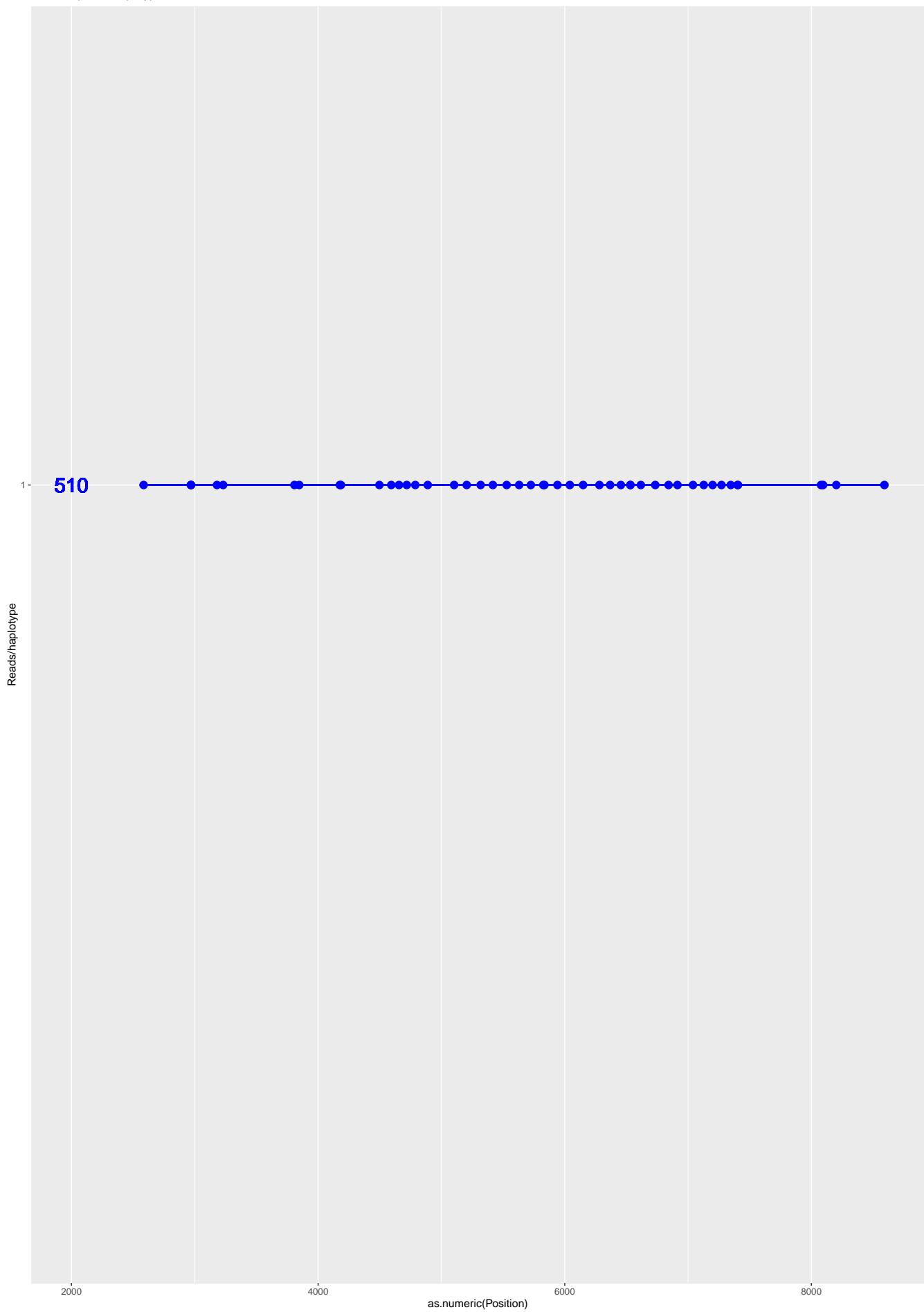
barcode = TCACGATGAGCACGTA & GCGATCTATGCACACG

Sample = 98c tetrad = 98 spore = c

Total reads = 613 PCR=243

haplotypes I began with n[supporting reads] = 510

most frequent 7 haplotypes.



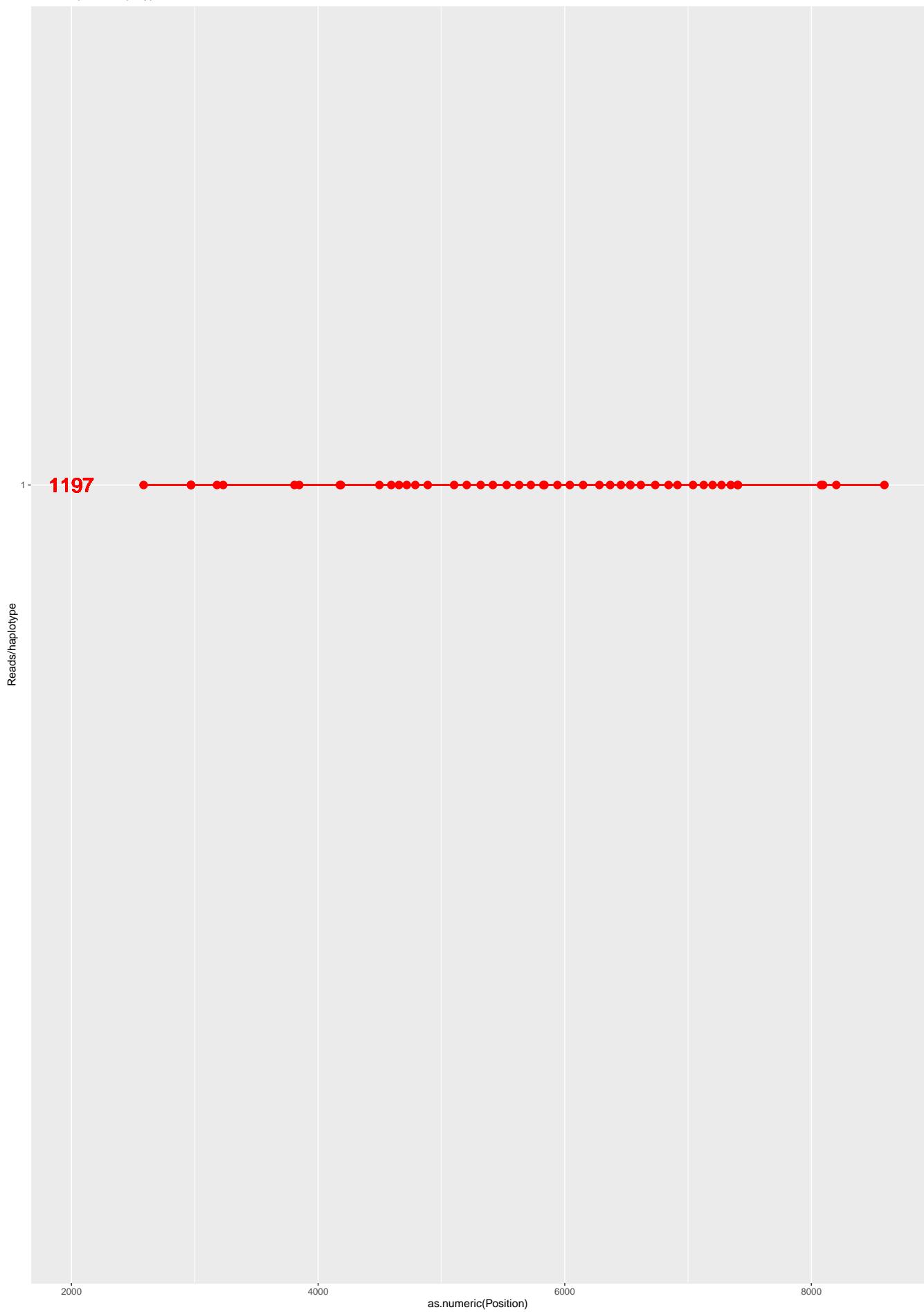
barcode = TCACGATGAGCACGTA & TGCAGTCGAGATACT

Sample = 98d tetrad = 98 spore = d

Total reads = 1261 PCR=244

haplotypes I began with n[supporting reads] = 1197

most frequent 7 haplotypes.



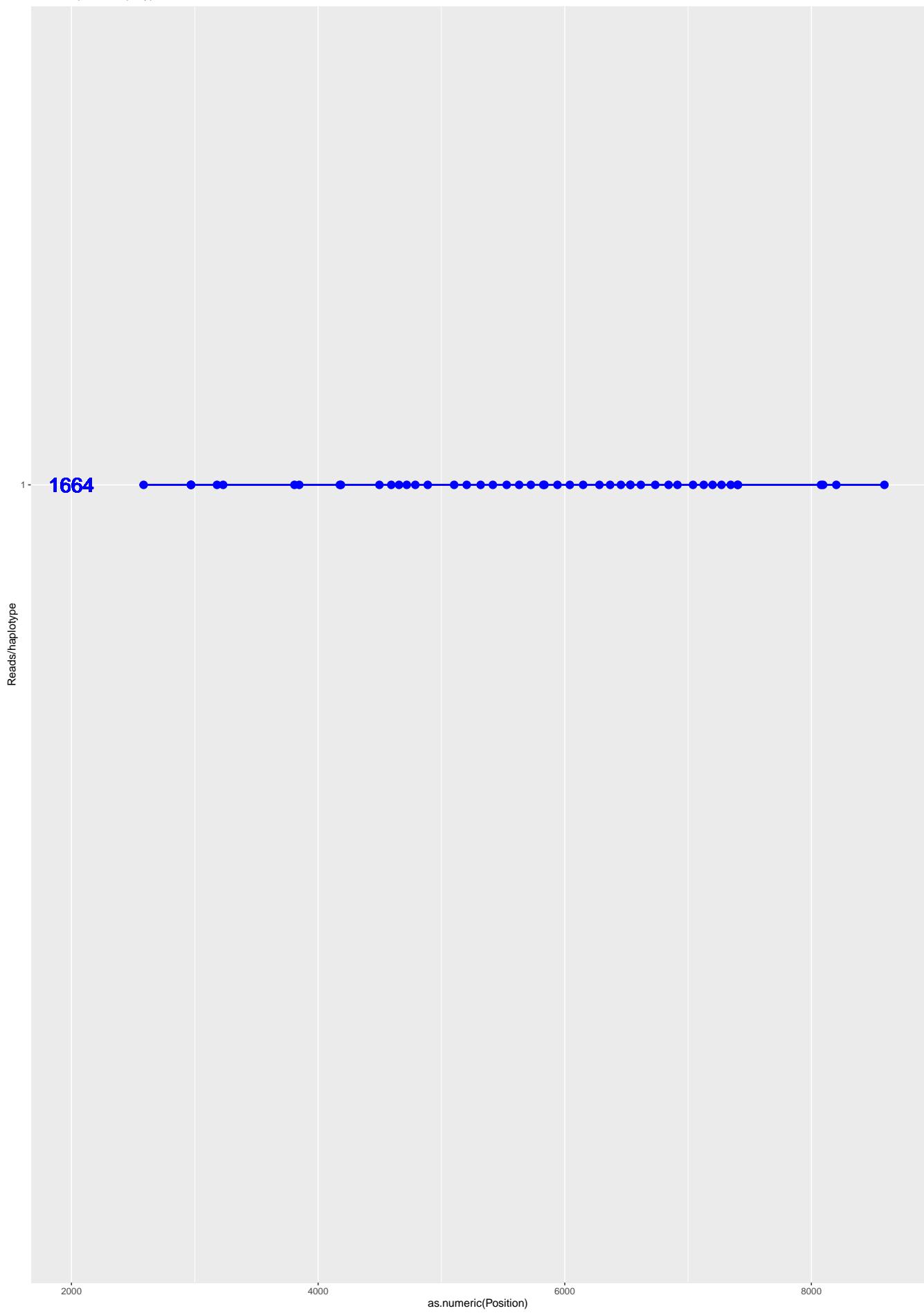
barcode = TCACGATGAGCAGCTA & GACTCTGCGTCGAGTC

Sample = 100a tetrad = 100 spore = a

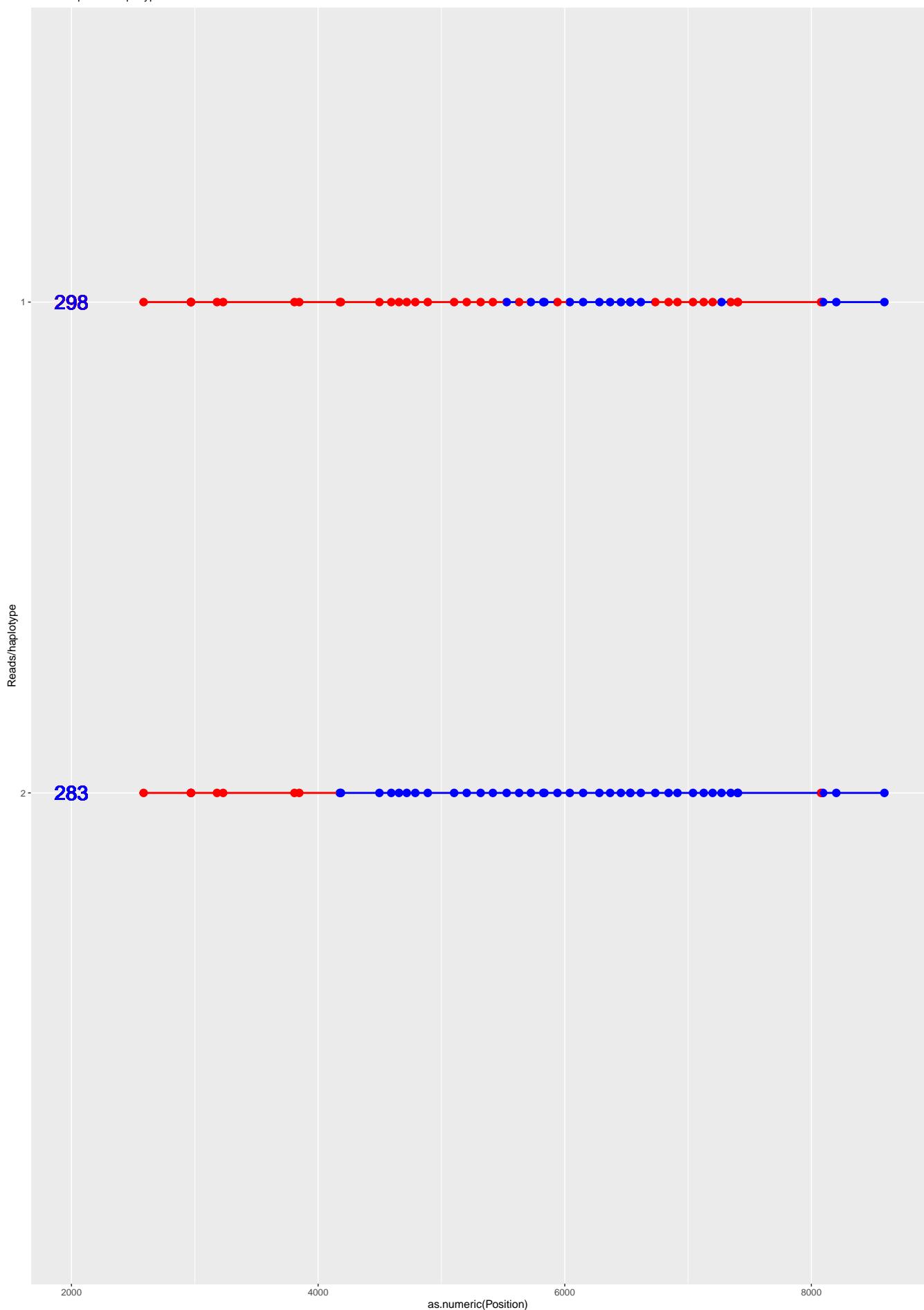
Total reads = 1917 PCR=245

haplotypes I began with n[supporting reads] = 1664

most frequent 7 haplotypes.



Sample = 100b tetrad = 100 spore = b
Total reads = 1406 PCR=246
haplotypes I began with n[supporting reads] = 283, 298
most frequent 7 haplotypes.



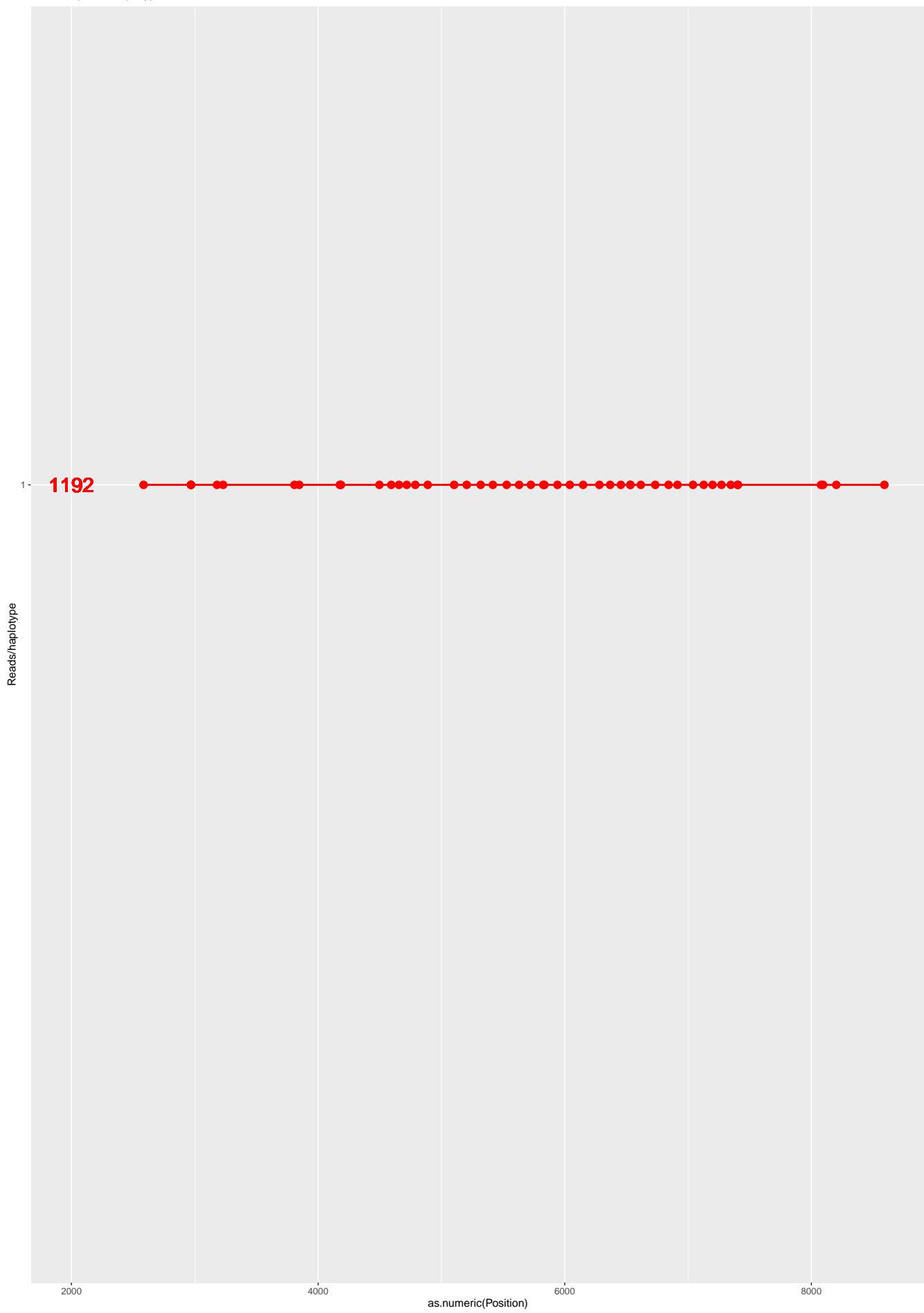
barcode = TCACGATGAGCACGTA & GCGCAGACTACGTGTG

Sample = 100c tetrad = 100 spore = c

Total reads = 1254 PCR=247

haplotypes I began with n[supporting reads] = 1192

most frequent 7 haplotypes.



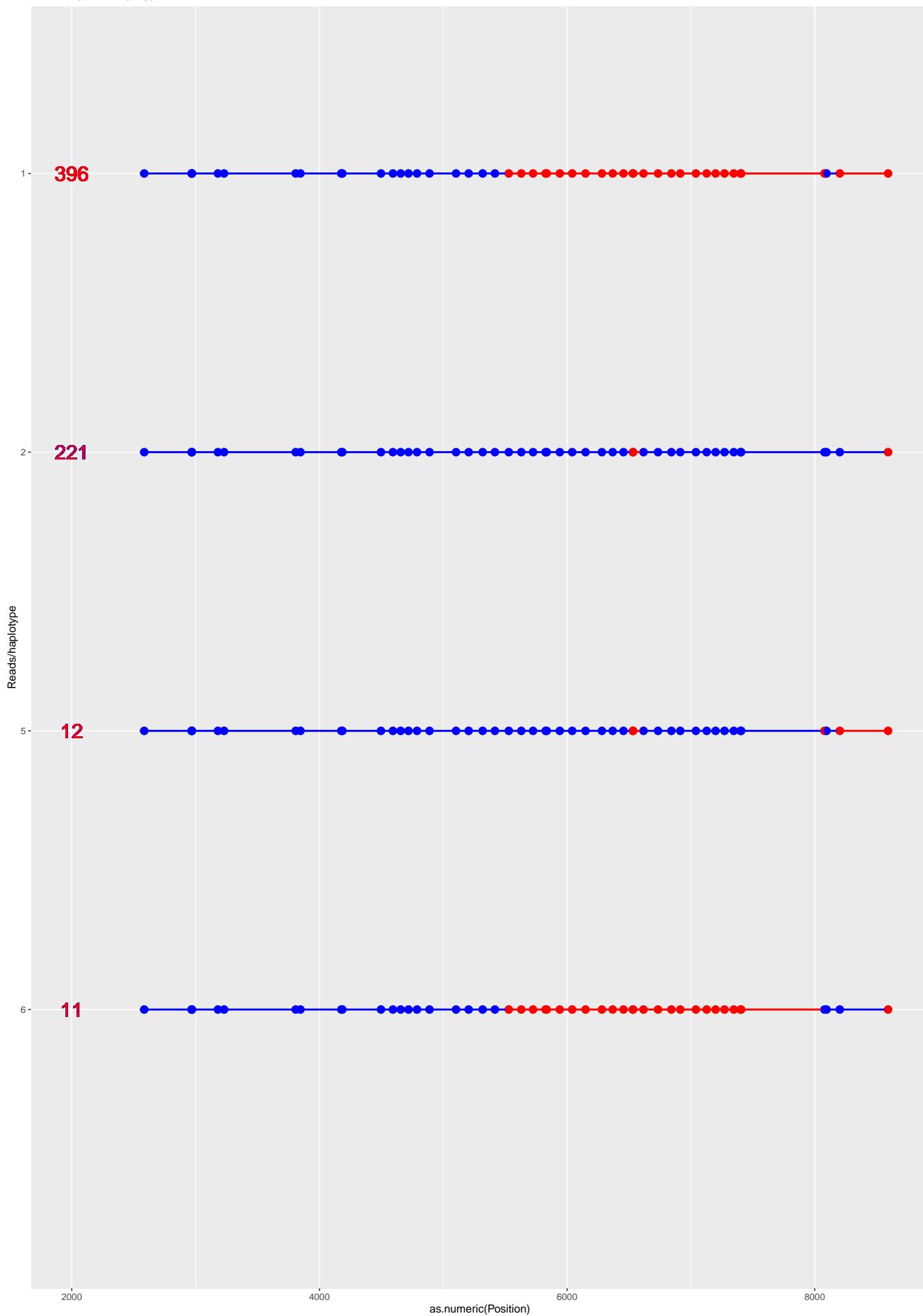
barcode = TCACGATGAGCACGTA & GTCTCTGCGATAACAGC

Sample = 100d tetrad = 100 spore = d

Total reads = 1299 PCR=248

haplotypes I began with n[supporting reads] = 11, 12, 221, 396

most frequent 7 haplotypes.

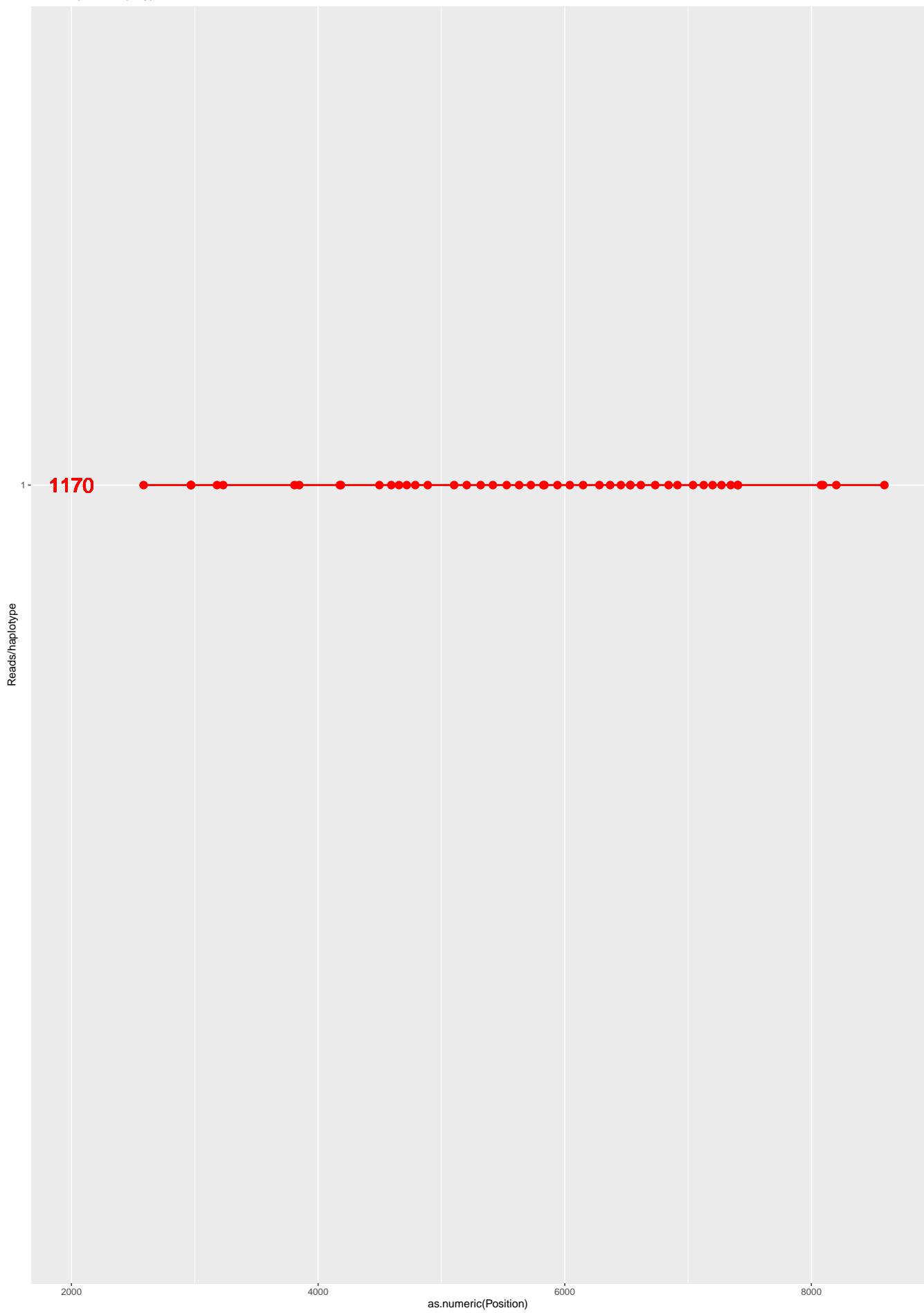


Sample = 103a tetrad = 103 spore = a

Total reads = 1204 PCR=249

haplotypes I began with n[supporting reads] = 1170

most frequent 7 haplotypes.



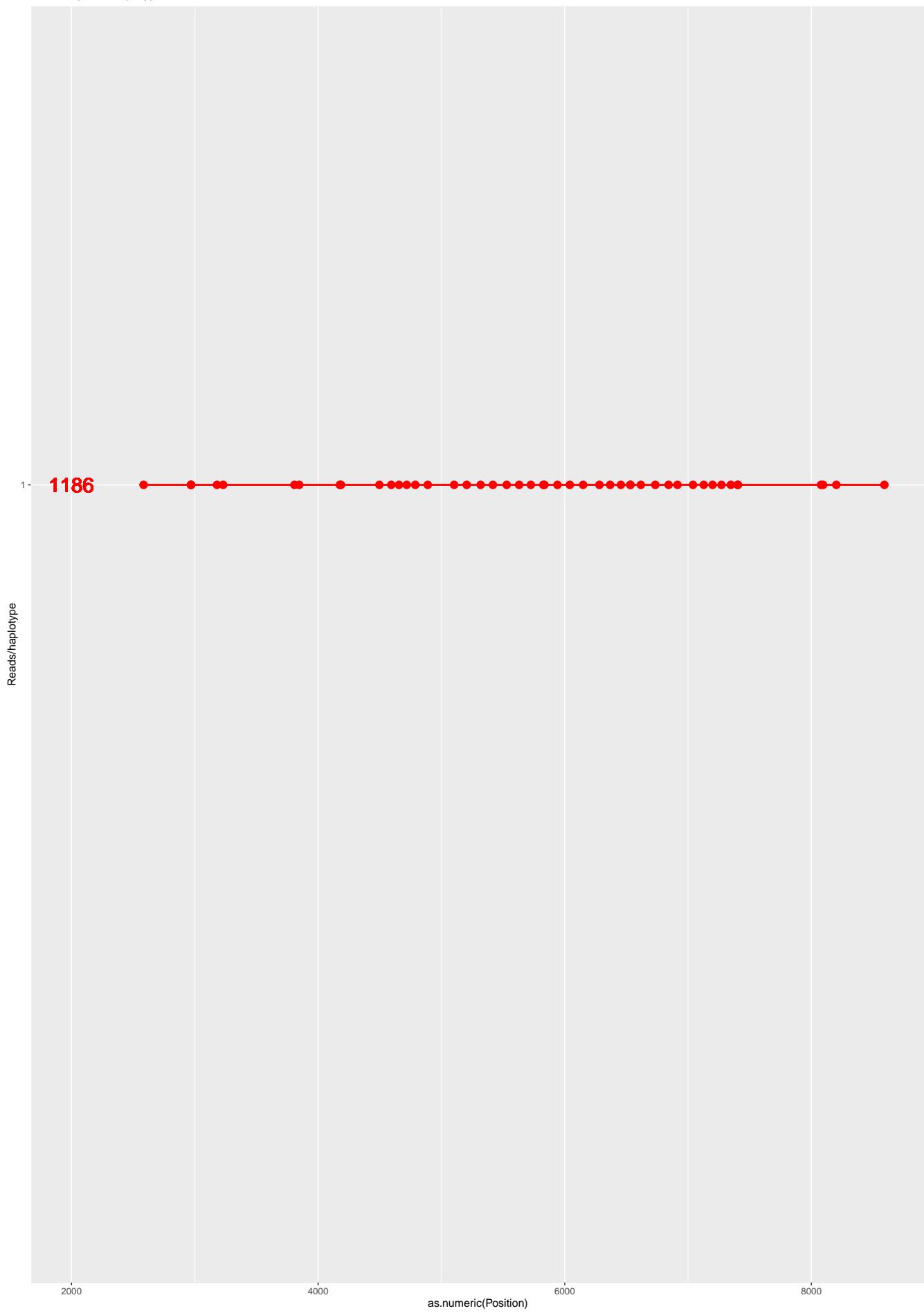
barcode = GACTGAGATCATGATC & TCATATGTAGTACTCT

Sample = 103b tetrad = 103 spore = b

Total reads = 1248 PCR=250

haplotypes I began with n[supporting reads] = 1186

most frequent 7 haplotypes.

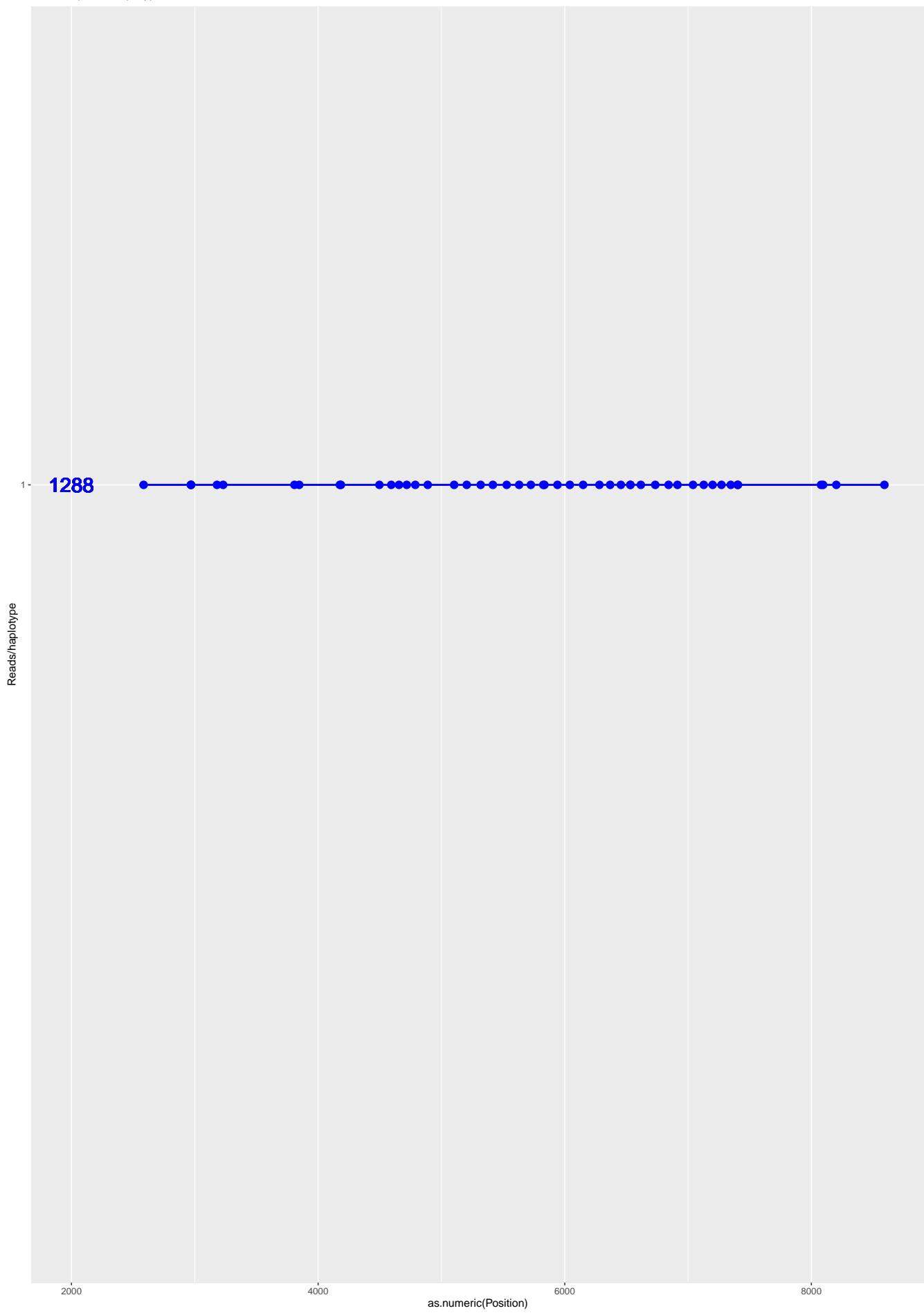


Sample = 103c tetrad = 103 spore = c

Total reads = 1507 PCR=251

haplotypes I began with n[supporting reads] = 1288

most frequent 7 haplotypes.

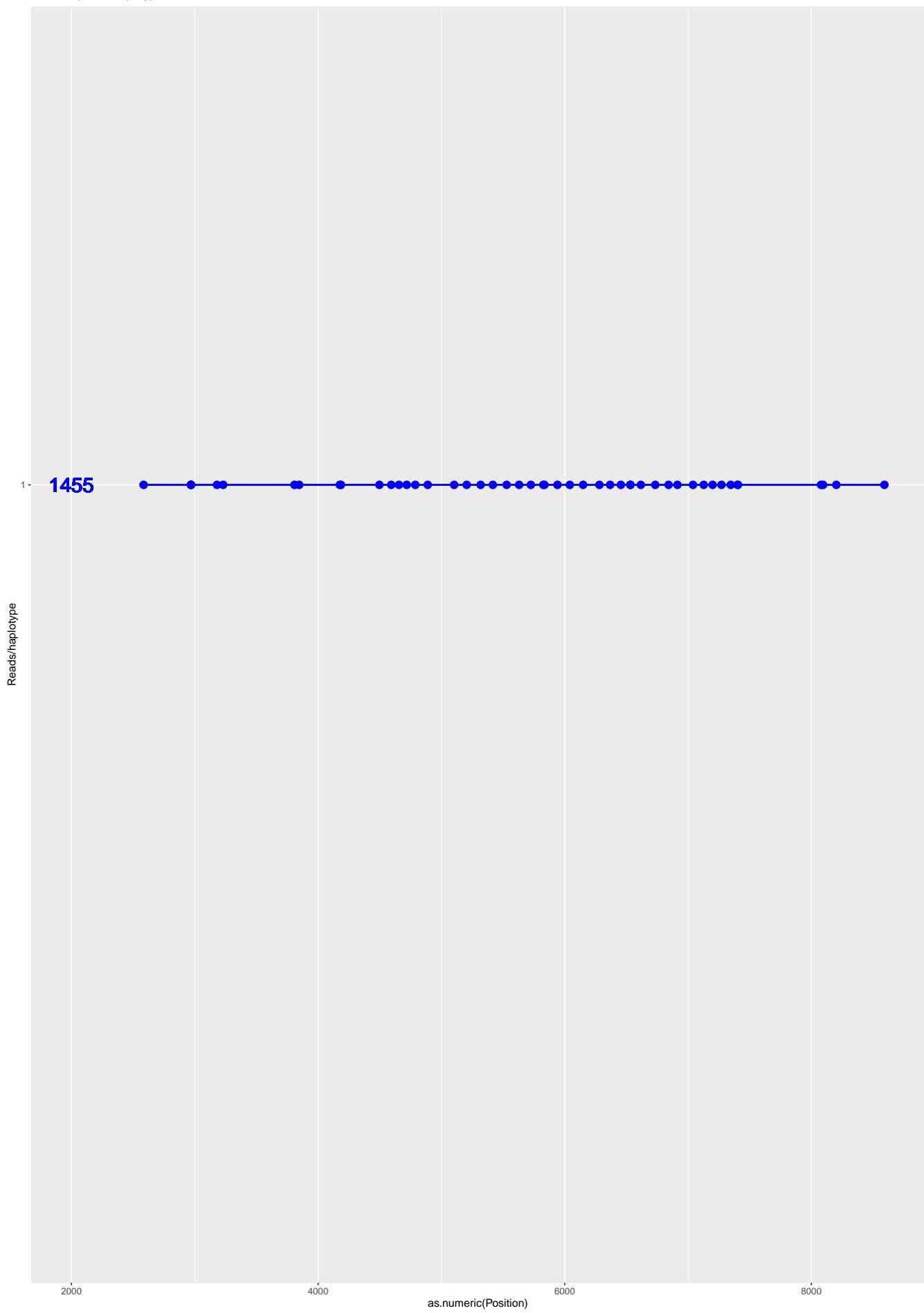


Sample = 103d tetrad = 103 spore = d

Total reads = 1683 PCR=252

haplotypes I began with n[supporting reads] = 1455

most frequent 7 haplotypes.

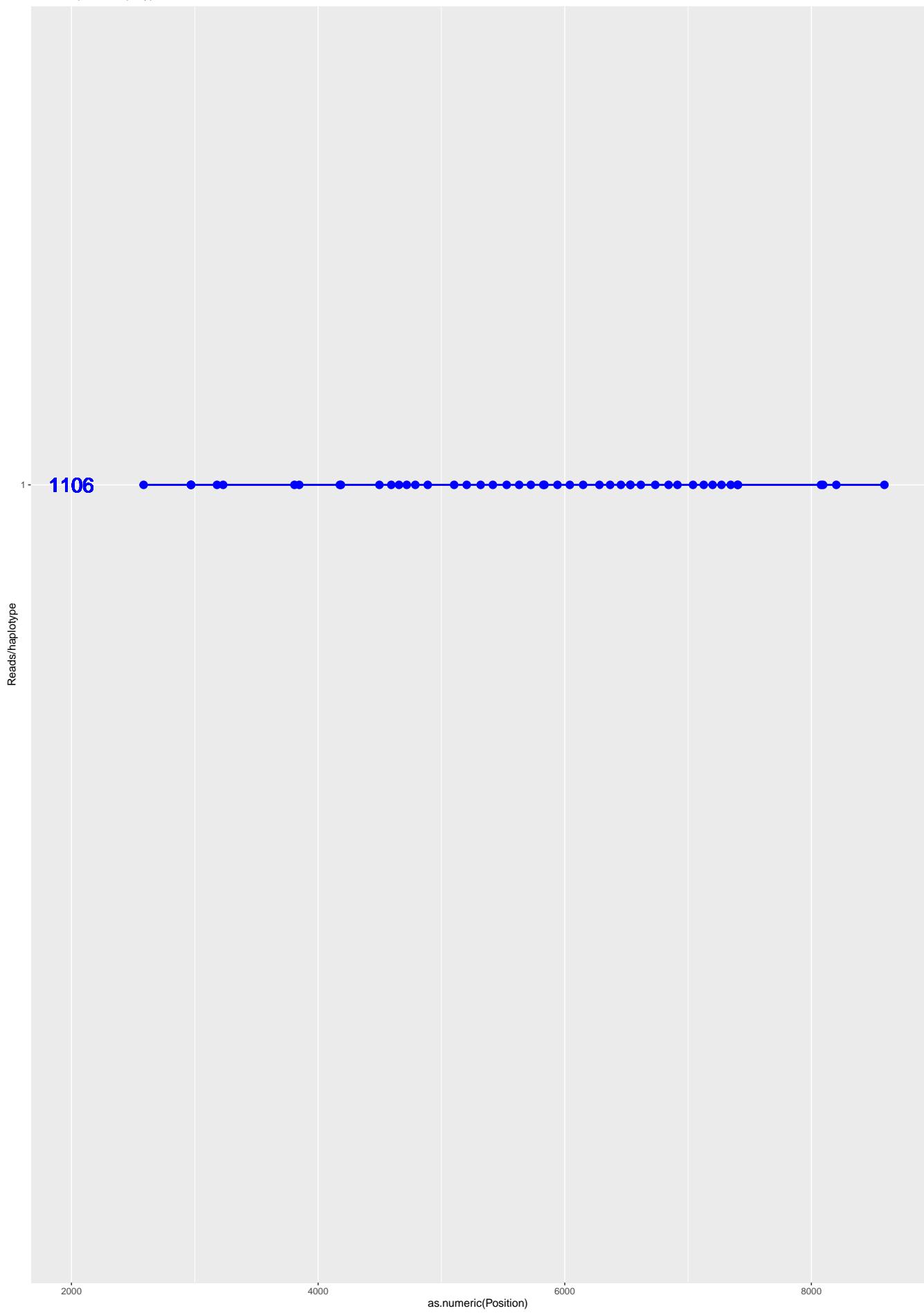


Sample = 104a tetrad = 104 spore = a

Total reads = 1307 PCR=253

haplotypes I began with n[supporting reads] = 1106

most frequent 7 haplotypes.

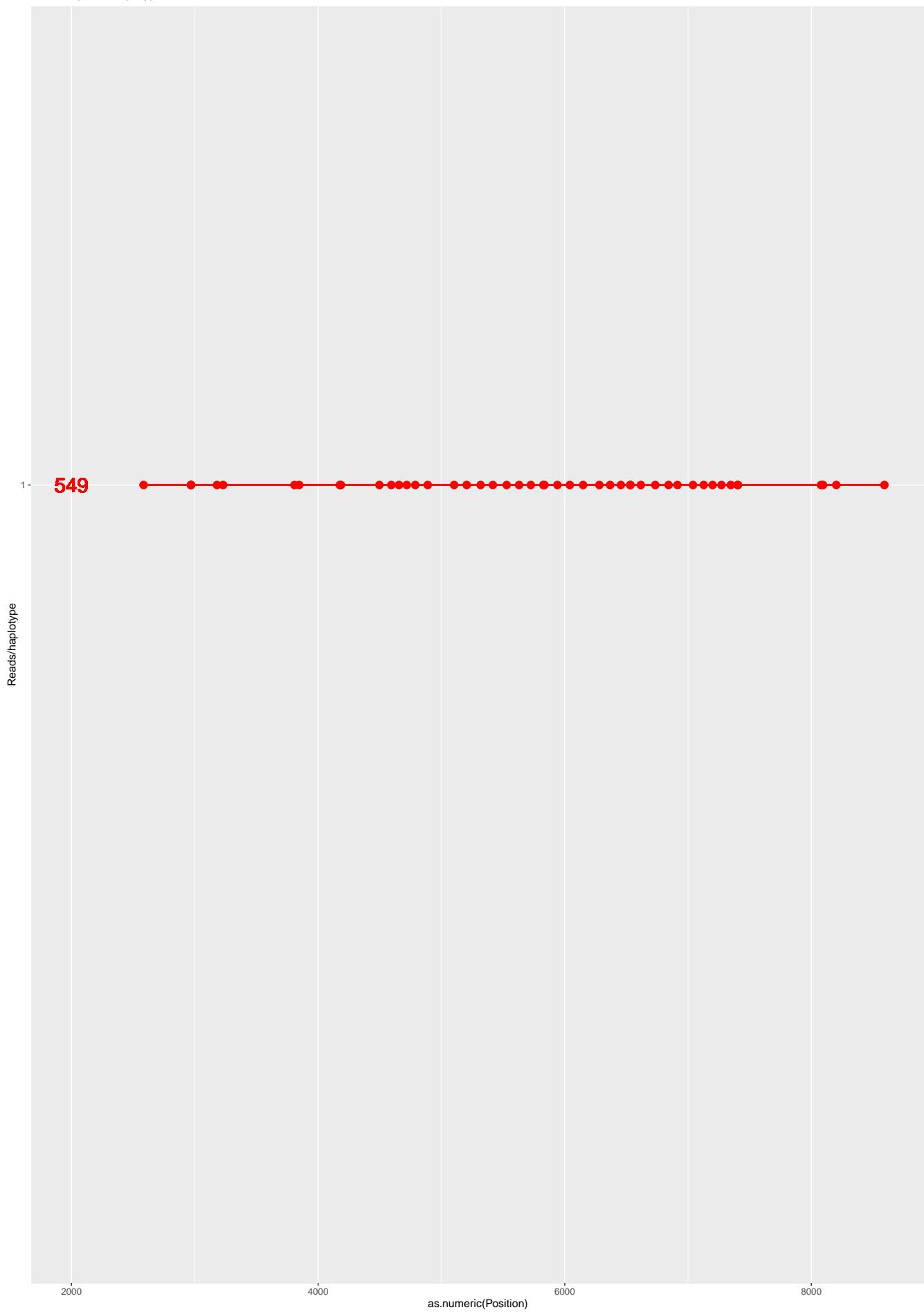


Sample = 104b tetrad = 104 spore = b

Total reads =574 PCR=254

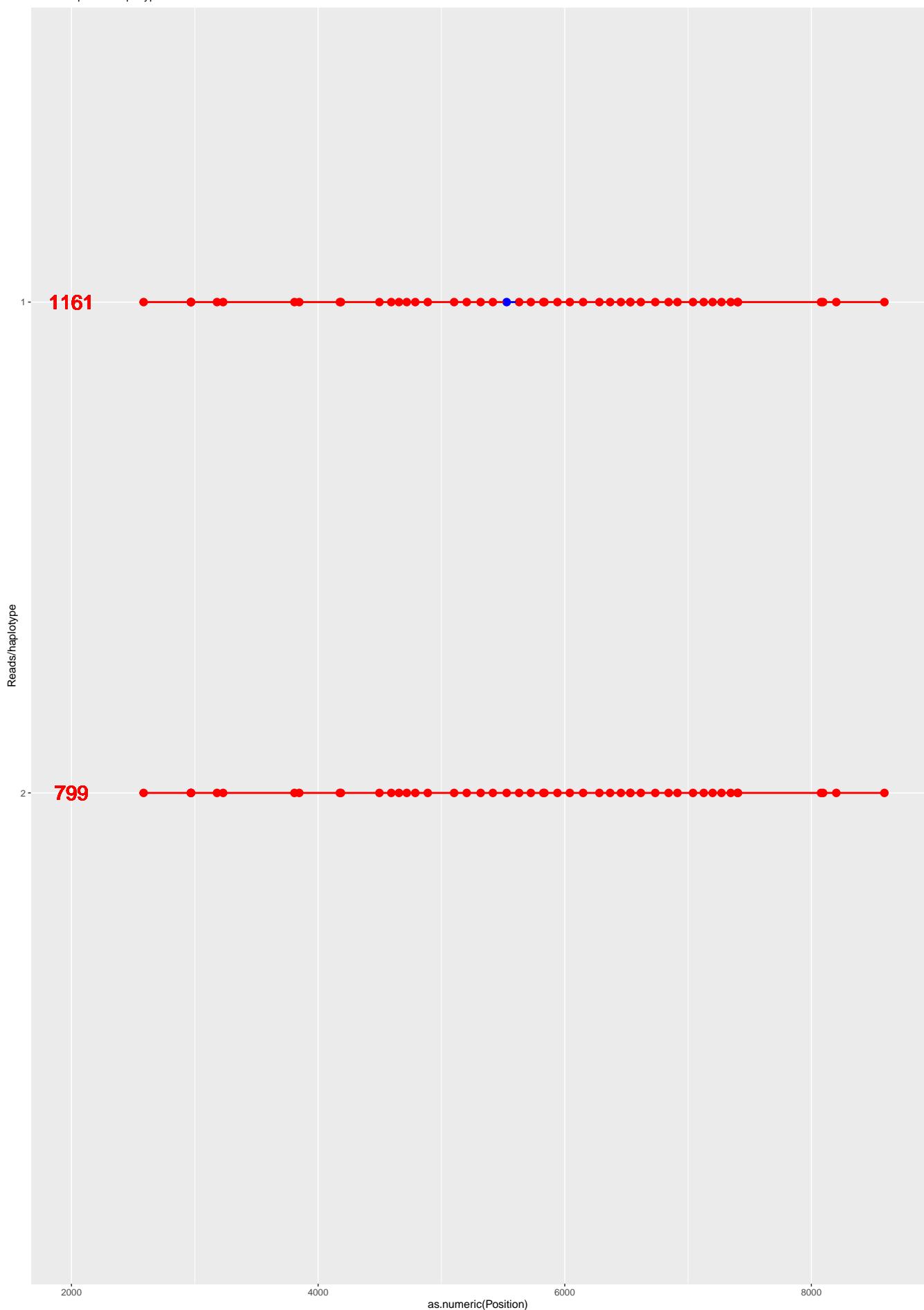
haplotypes I began with n[supporting reads] = 549

most frequent 7 haplotypes.



barcode = GACTGAGATCATGATC & GCGCAGACTACGTGTG

Sample = 104c tetrad = 104 spore = c
Total reads = 2053 PCR=255
haplotypes I began with n[supporting reads] = 799, 1161
most frequent 7 haplotypes.



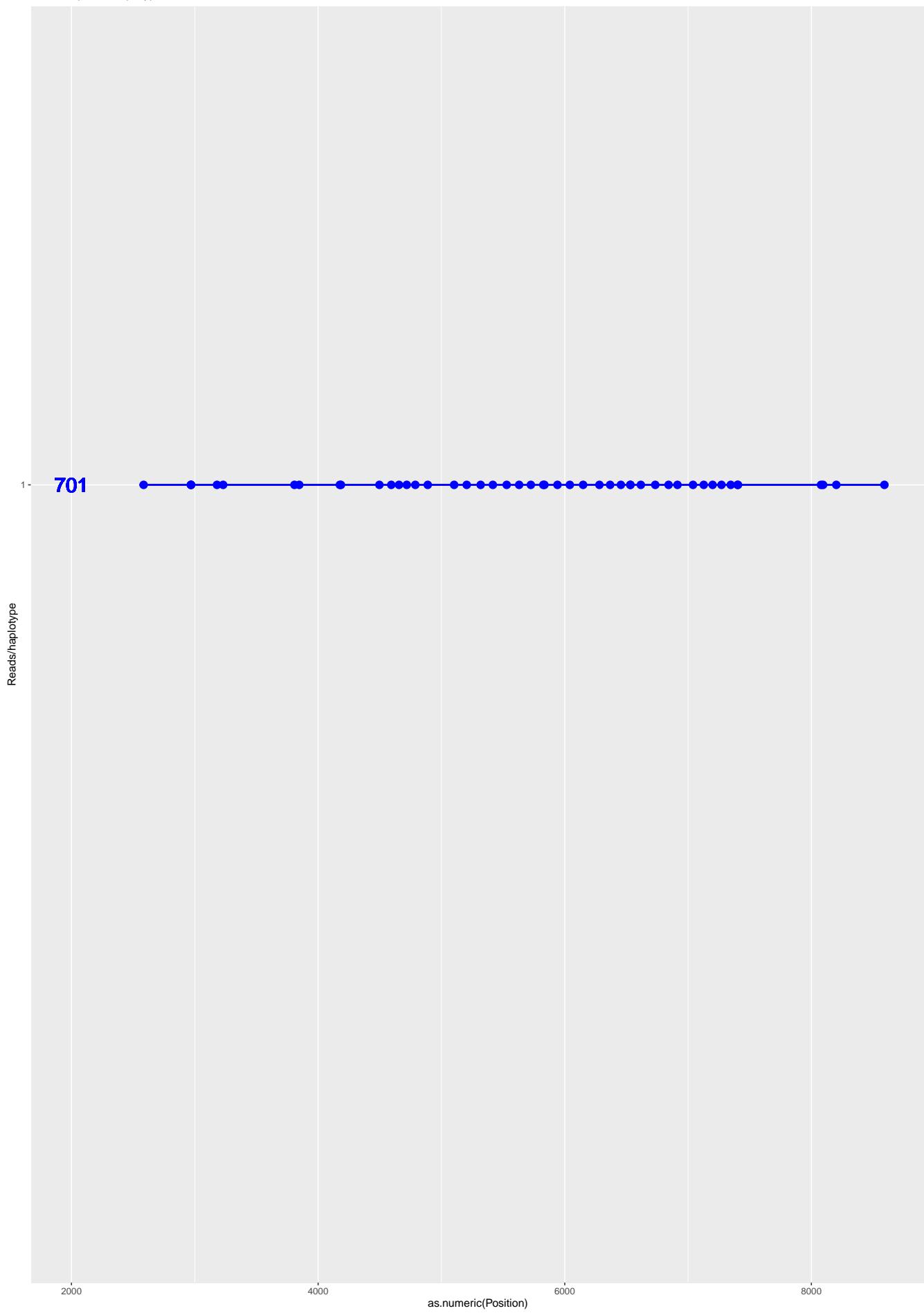
barcode = GACTGAGATCATGATC & GTCTCTGCGATAACAGC

Sample = 104d tetrad = 104 spore = d

Total reads = 819 PCR=256

haplotypes I began with n[supporting reads] = 701

most frequent 7 haplotypes.



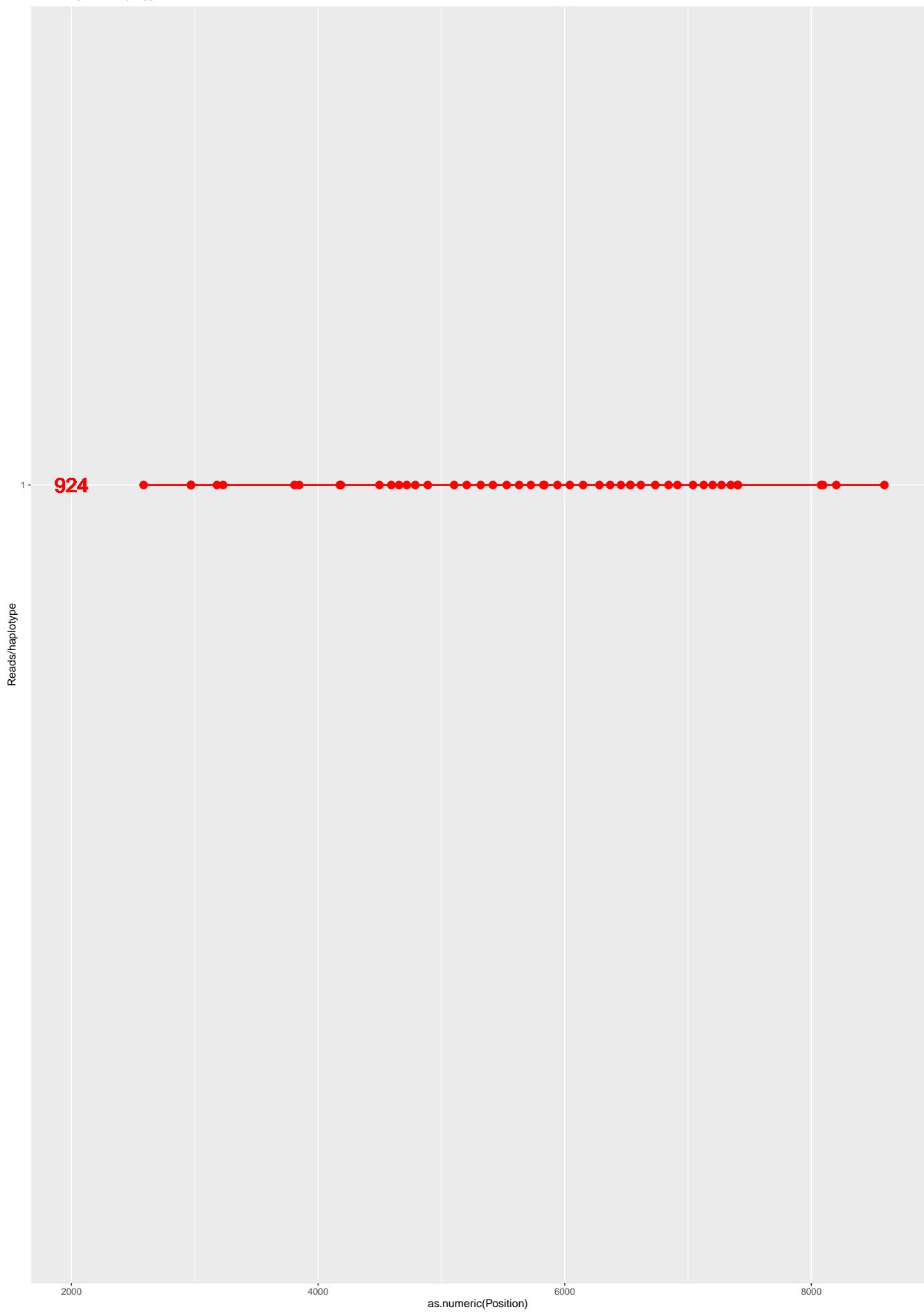
barcode = GACTGAGATCATGATC & AGTATGAGATAGCTCG

Sample = 105a tetrad = 105 spore = a

Total reads = 955 PCR=257

haplotypes I began with n[supporting reads] = 924

most frequent 7 haplotypes.



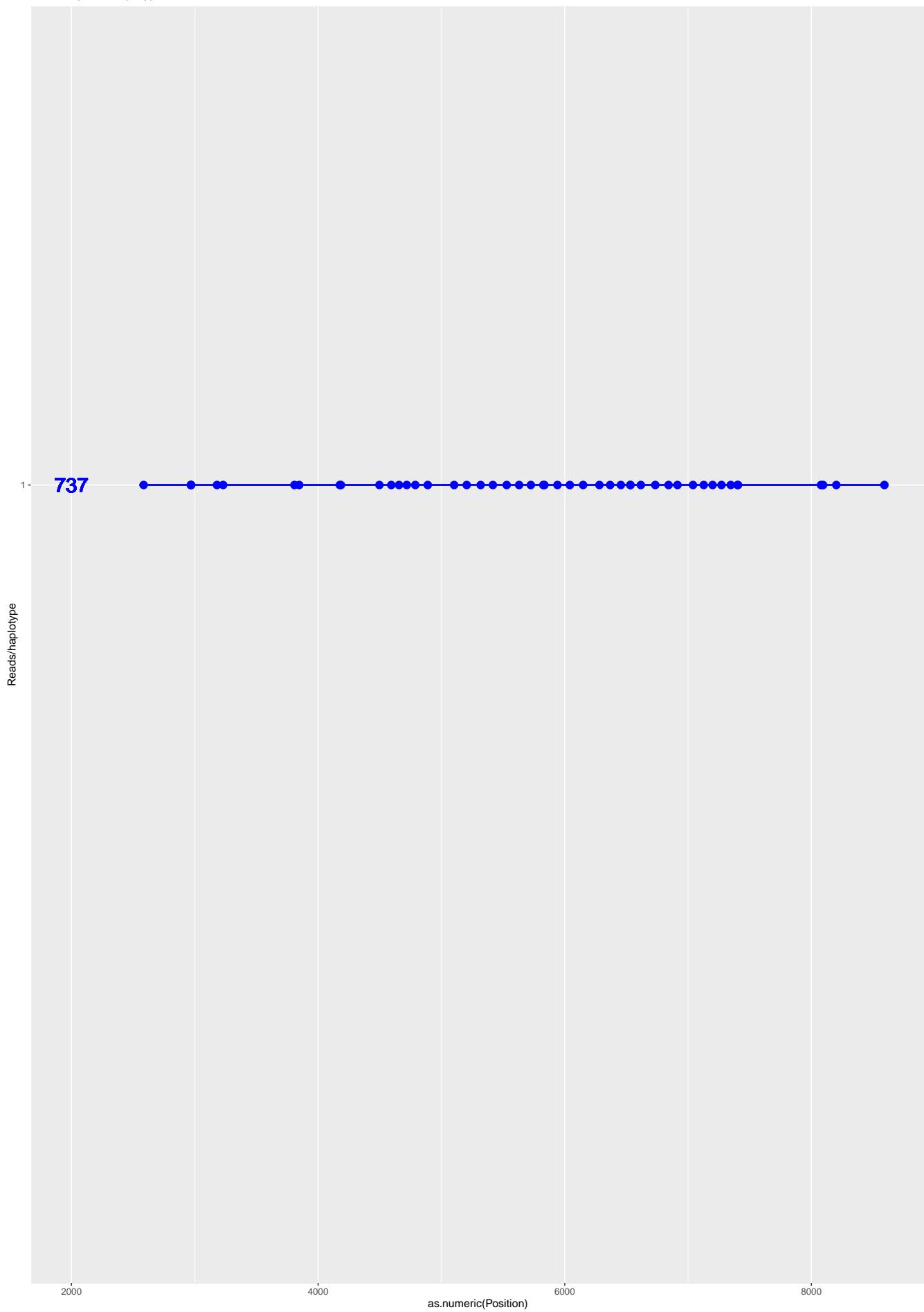
barcode = ACGACATGATACTGCT & TCATATGTAGTACTCT

Sample = 105b tetrad = 105 spore = b

Total reads = 848 PCR=258

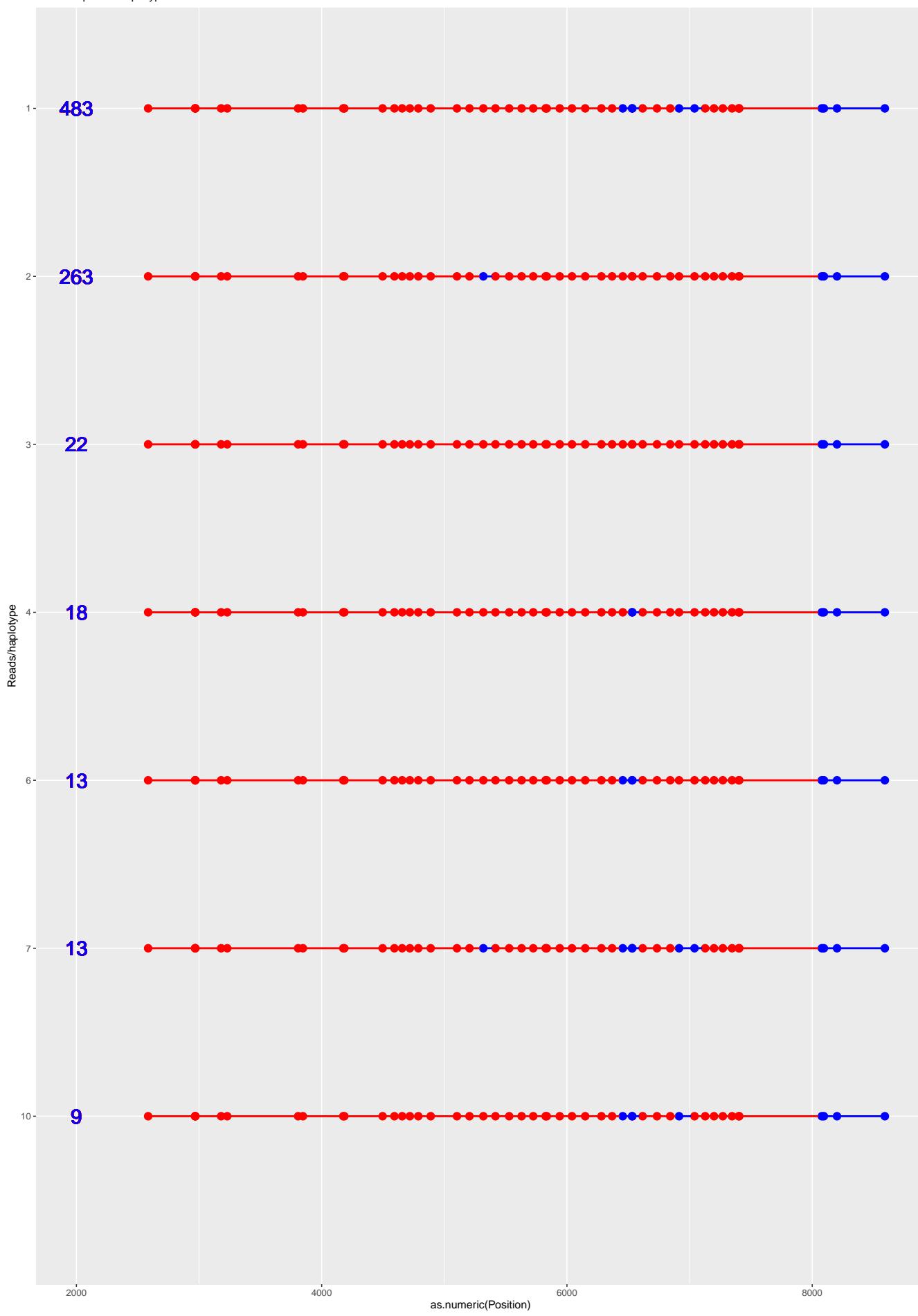
haplotypes I began with n[supporting reads] = 737

most frequent 7 haplotypes.

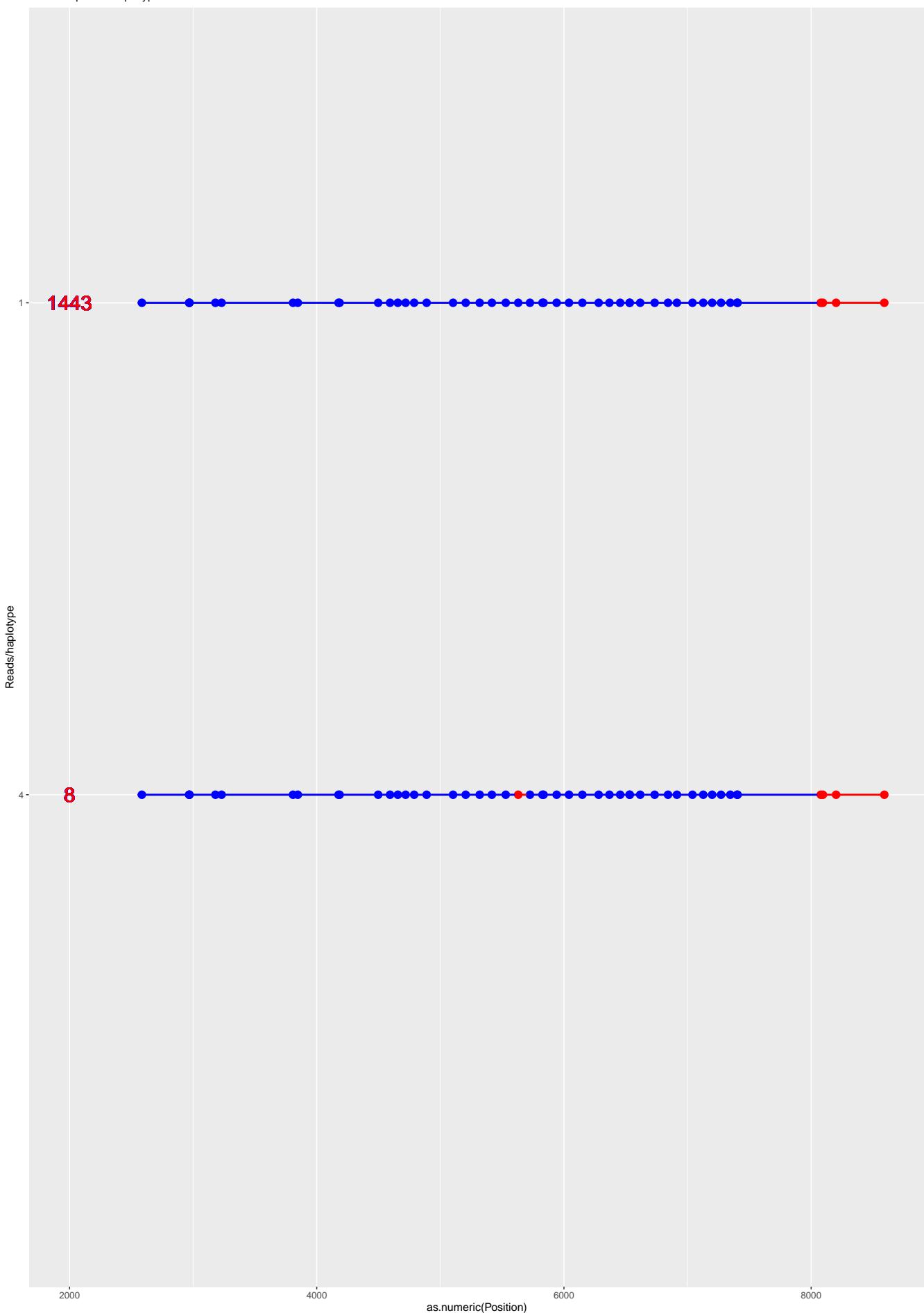


barcode = ACGACATGATACTGCT & GCGATCTATGCACACG

Sample = 105c tetrad = 105 spore = c
 Total reads = 1067 PCR=259
 haplotypes I began with [n|supporting reads] = 9, 13, 18, 22, 263, 483
 most frequent 7 haplotypes.



Sample = 105d tetrad = 105 spore = d
Total reads = 1677 PCR=260
haplotypes I began with n[supporting reads] = 8, 1443
most frequent 7 haplotypes.

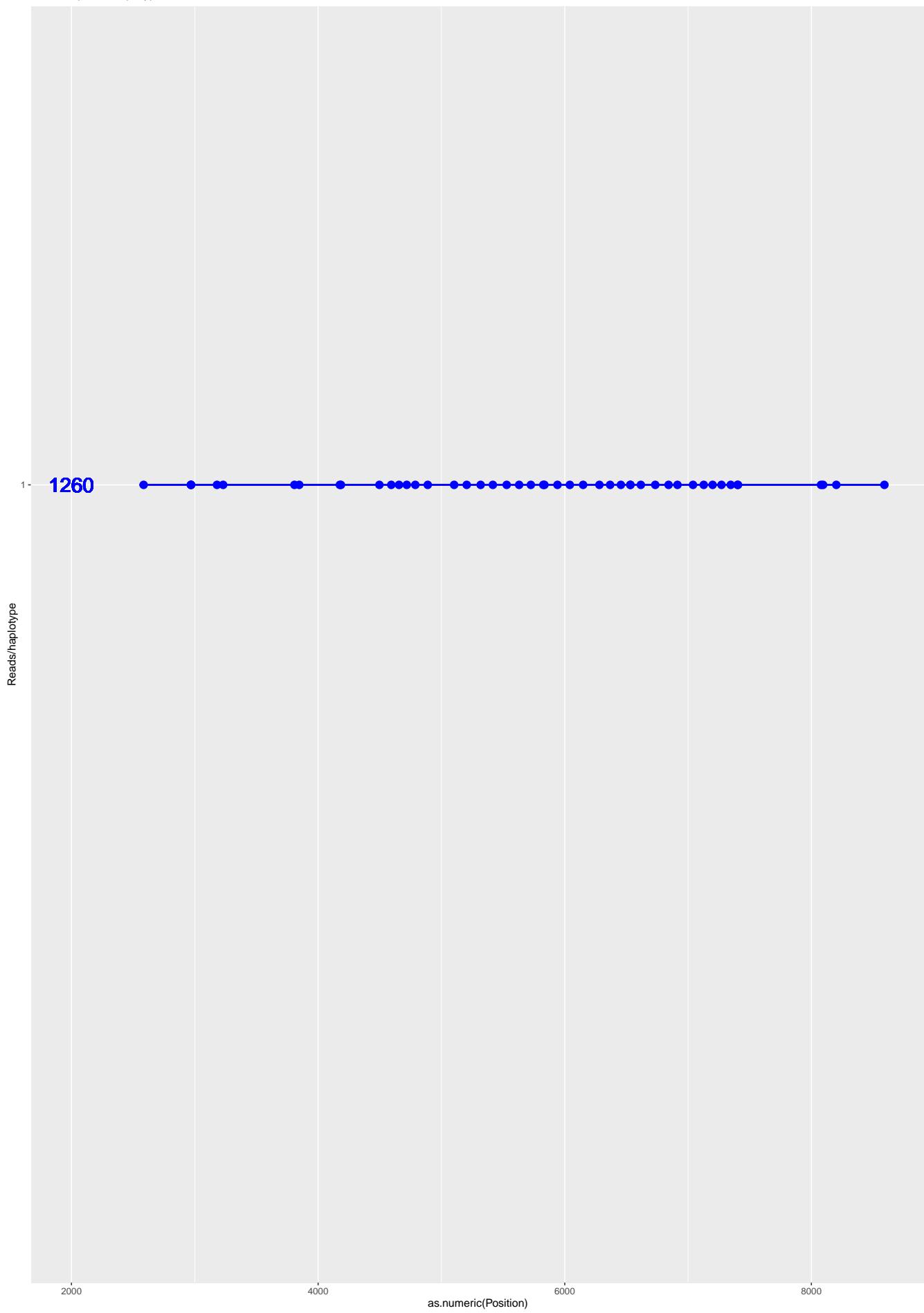


Sample = 106a tetrad = 106 spore = a

Total reads = 1477 PCR=261

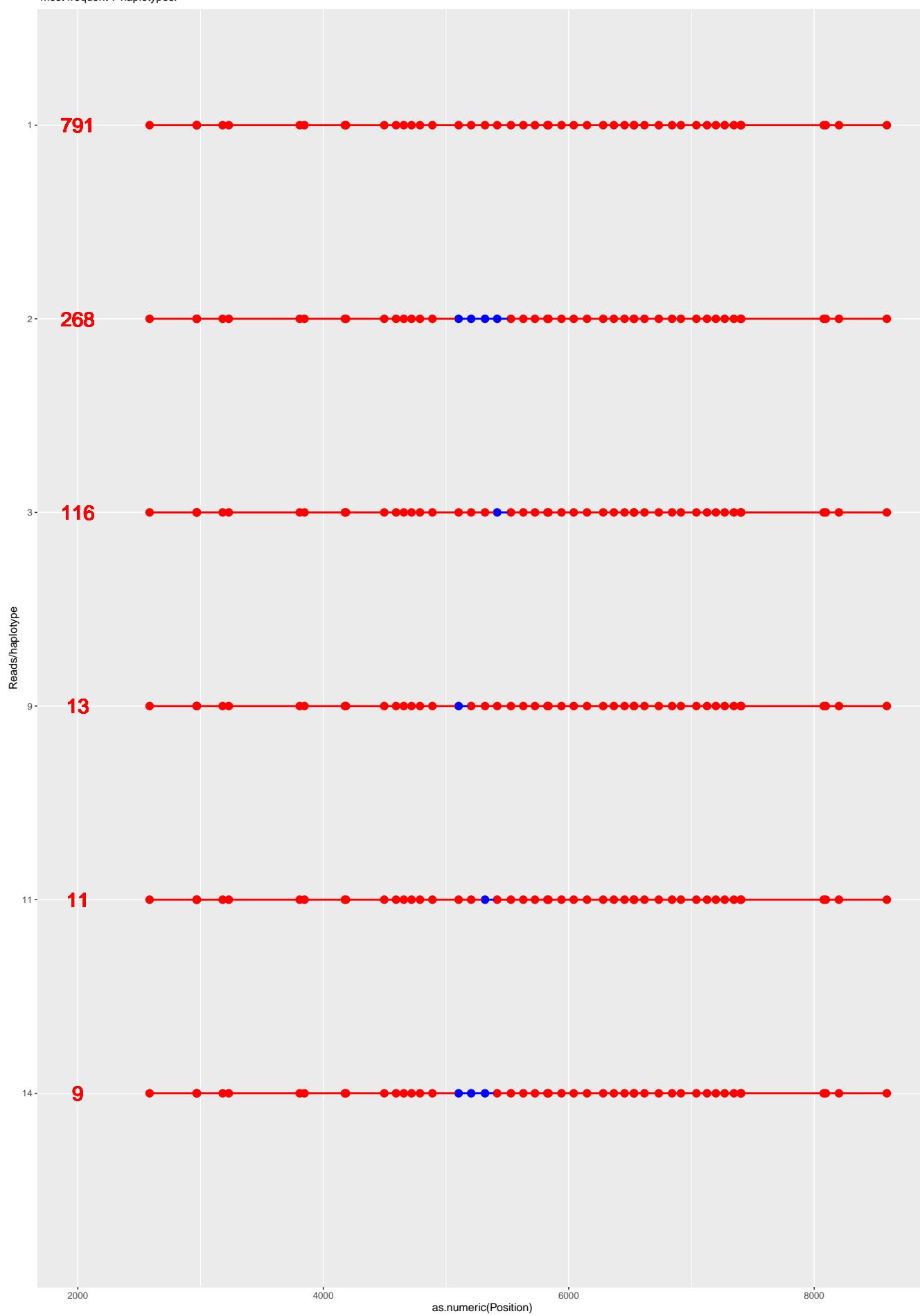
haplotypes I began with n[supporting reads] = 1260

most frequent 7 haplotypes.



barcode = ACGACATGATACTGCT & TACAGCGACGTCATCG

Sample = 106b tetrad = 106 spore = b
Total reads = 1491 PCR=262
haplotypes I began with [n(supporting reads)] = 9, 11, 13, 116, 268, 791
most frequent 7 haplotypes.

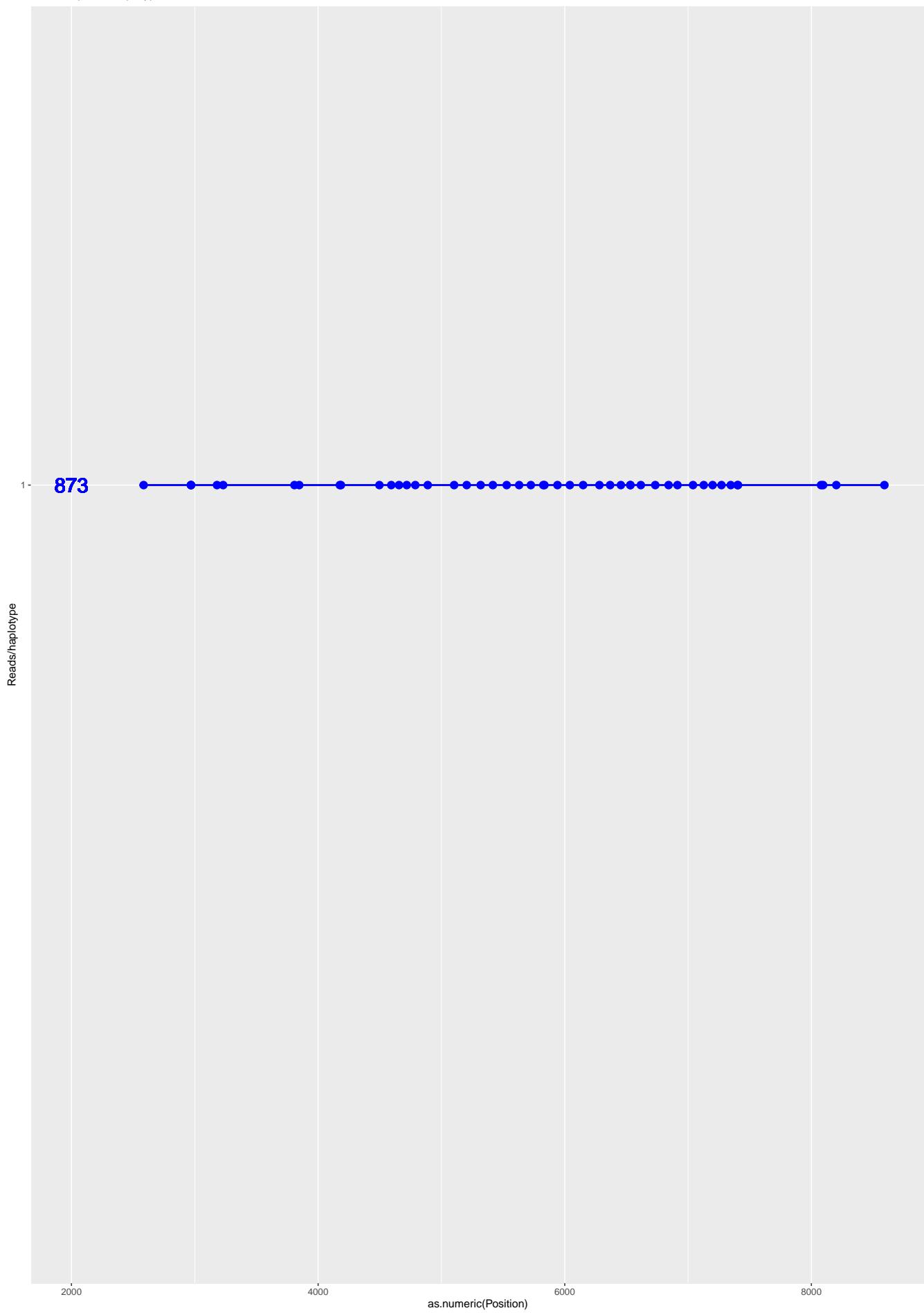


Sample = 106c tetrad = 106 spore = c

Total reads = 1009 PCR=263

haplotypes I began with n[supporting reads] = 873

most frequent 7 haplotypes.



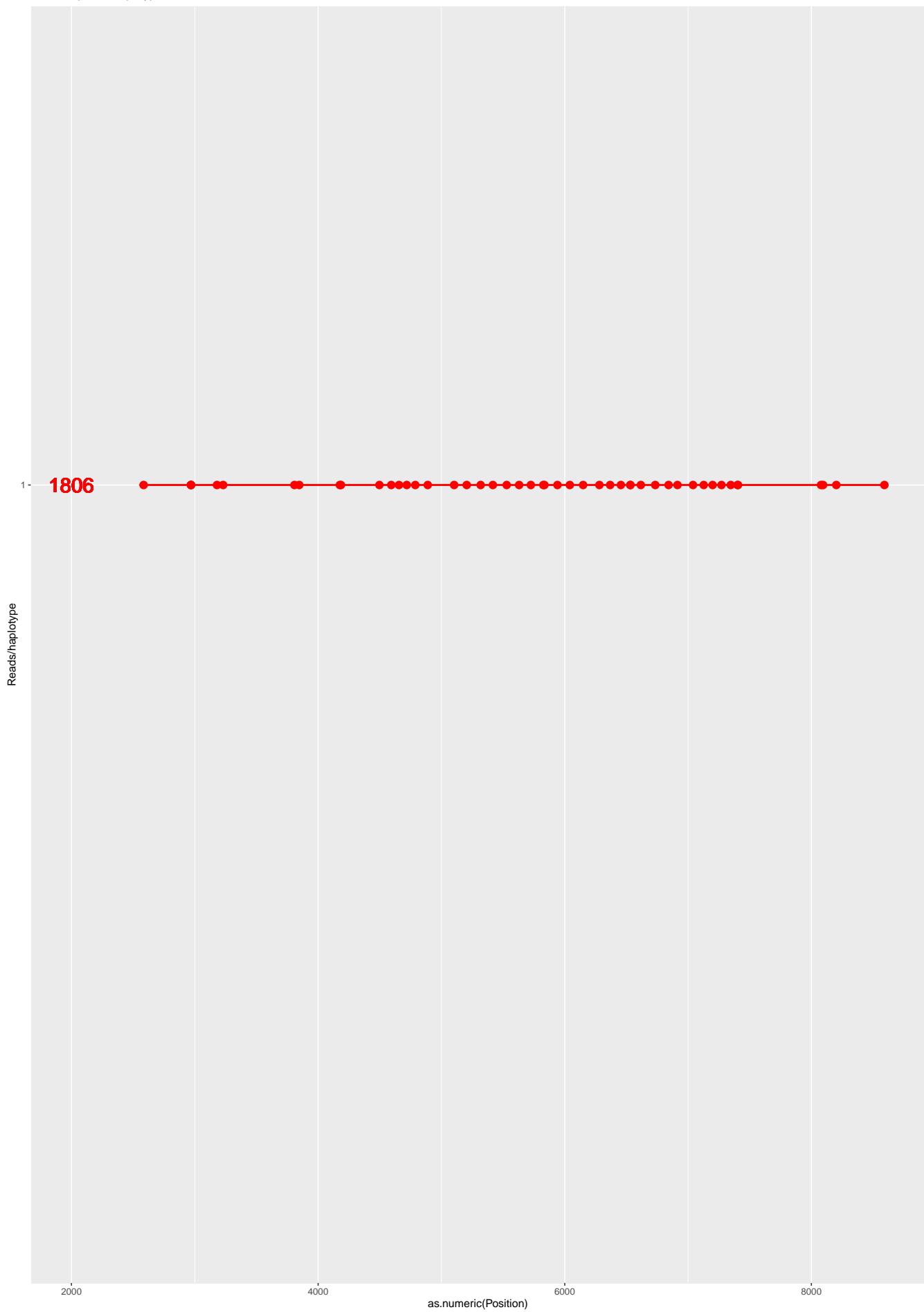
barcode = ACGACATGATACTGCT & GTCTCTGCGATAACAGC

Sample = 106d tetrad = 106 spore = d

Total reads = 1862 PCR=264

haplotypes I began with n[supporting reads] = 1806

most frequent 7 haplotypes.



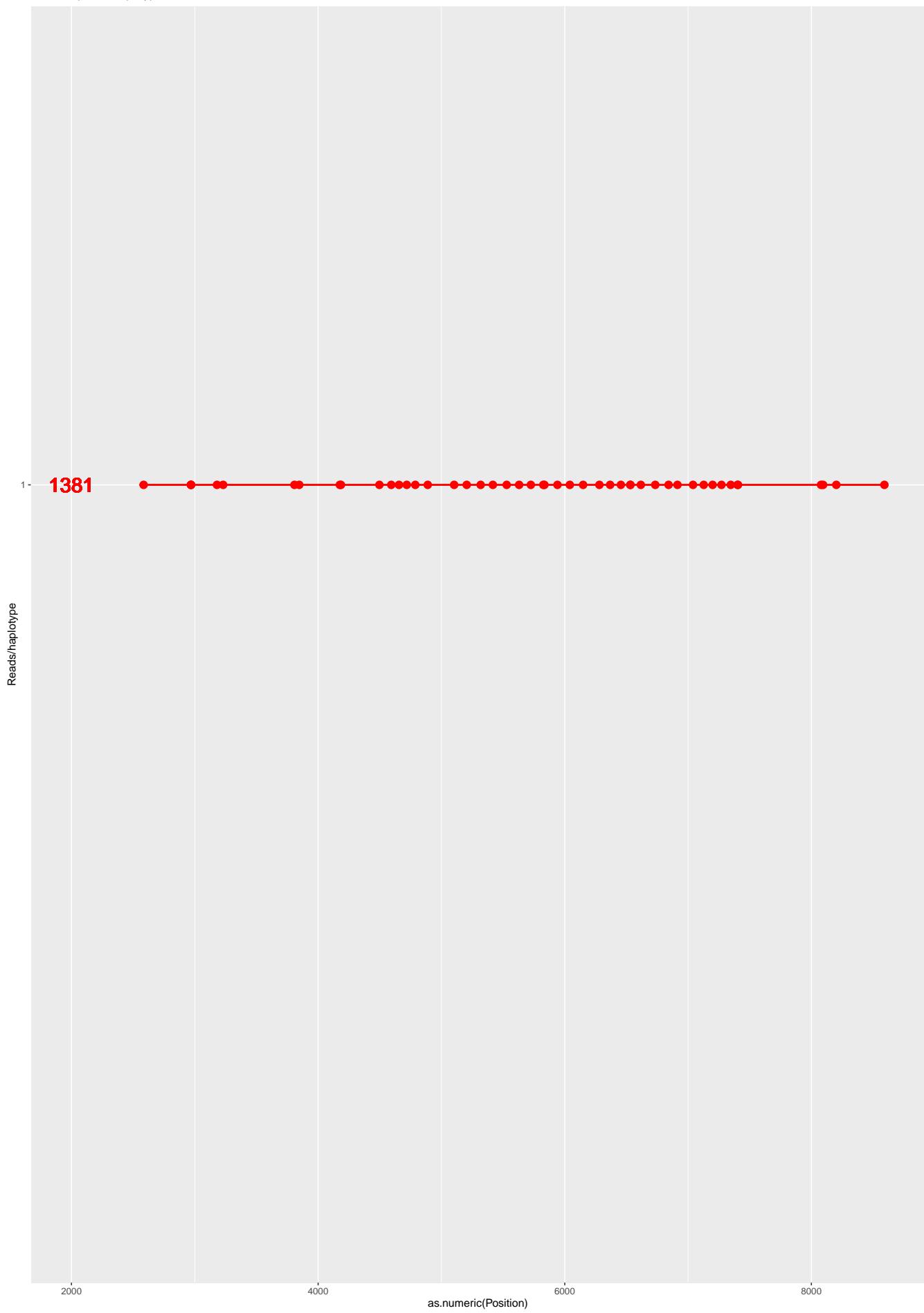
barcode = ACGACATGATACTGCT & AGTATGAGATAGCTCG

Sample = 107a tetrad = 107 spore = a

Total reads = 1437 PCR=265

haplotypes I began with n[supporting reads] = 1381

most frequent 7 haplotypes.



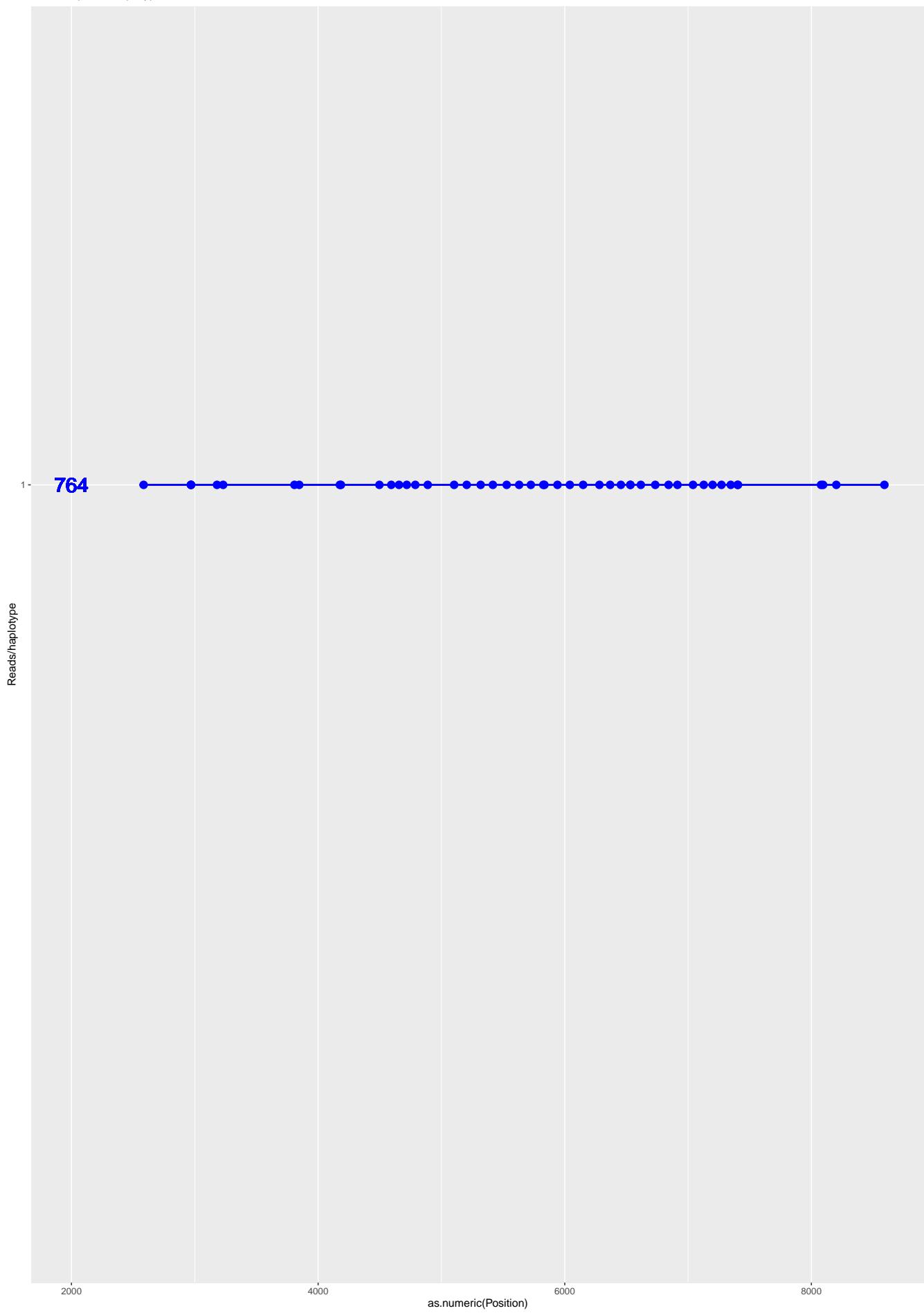
barcode = ATACAGCACAGATGTG & TCATATGTAGTACTCT

Sample = 107b tetrad = 107 spore = b

Total reads = 903 PCR=266

haplotypes I began with n[supporting reads] = 764

most frequent 7 haplotypes.



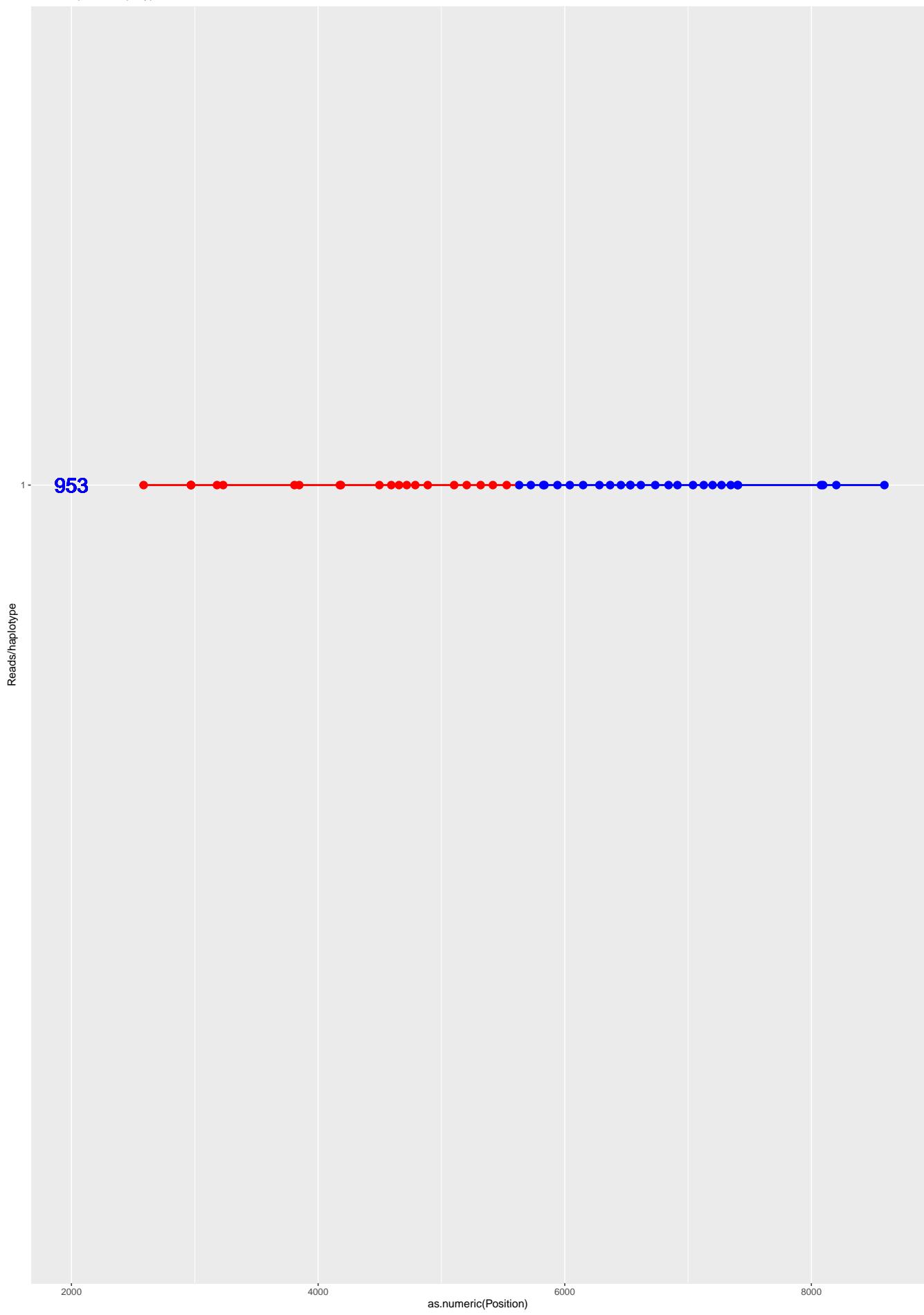
barcode = ATACAGCACAGATGTG & GCGATCTATGCACACG

Sample = 107c tetrad = 107 spore = c

Total reads = 1025 PCR=267

haplotypes I began with n[supporting reads] = 953

most frequent 7 haplotypes.



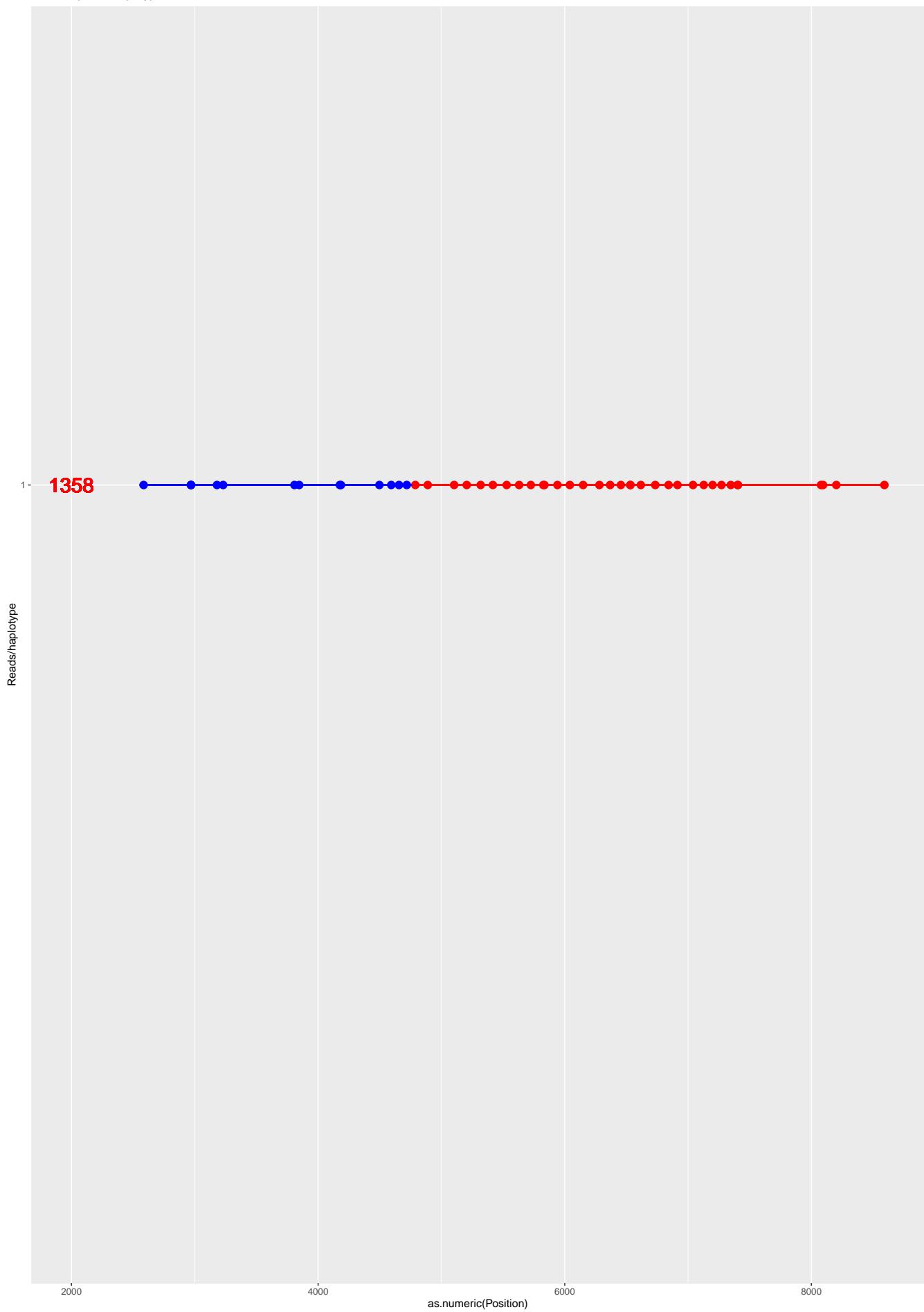
barcode = ATACAGCACAGATGTG & TGCAGTCGAGATACT

Sample = 107d tetrad = 107 spore = d

Total reads = 1448 PCR=268

haplotypes I began with n[supporting reads] = 1358

most frequent 7 haplotypes.



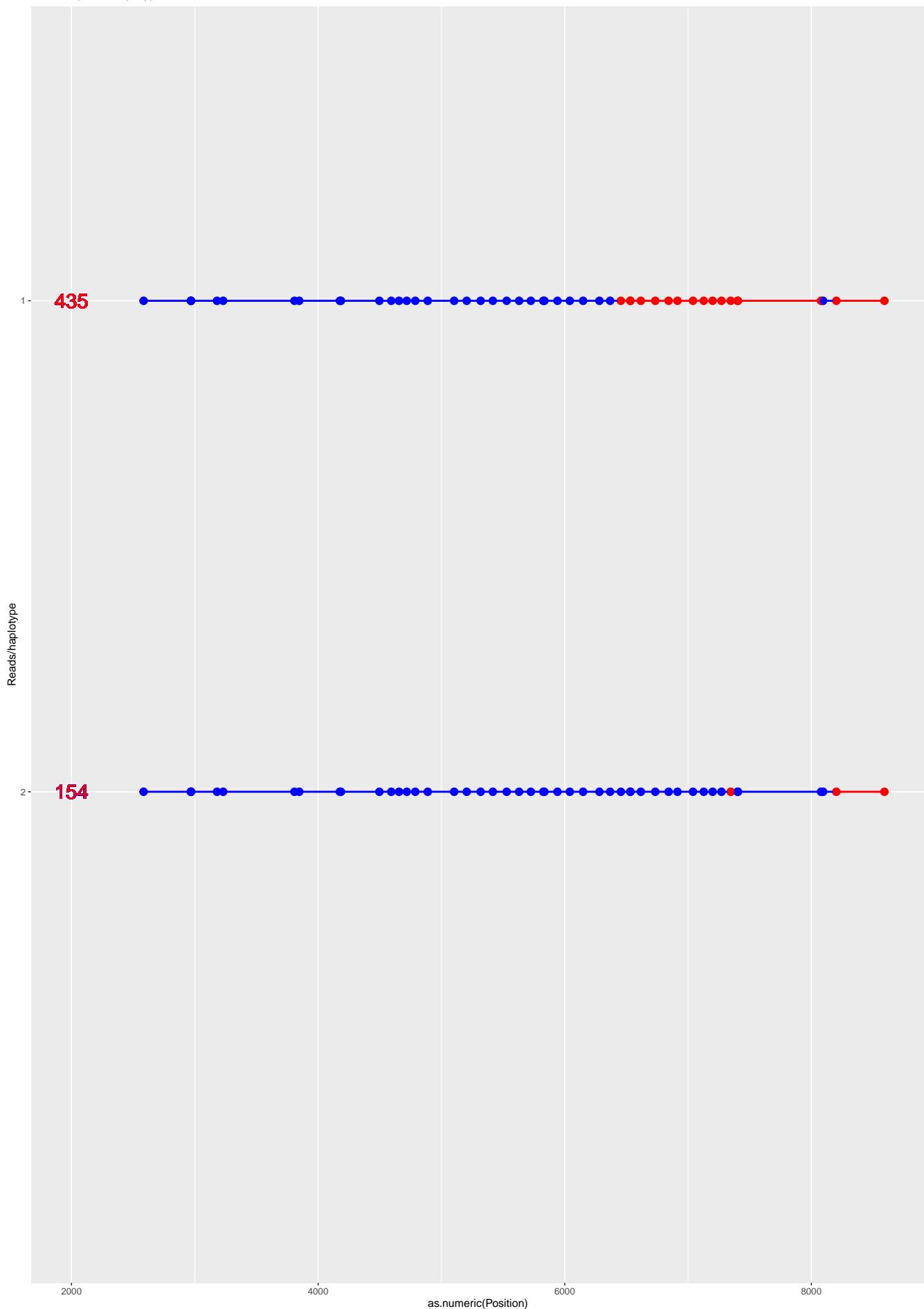
barcode = ATACAGCACAGATGTG & GACTCTGCGTCGAGTC

Sample = 108a tetrad = 108 spore = a

Total reads = 819 PCR=269

haplotypes I began with n[supporting reads] = 154, 435

most frequent 7 haplotypes.



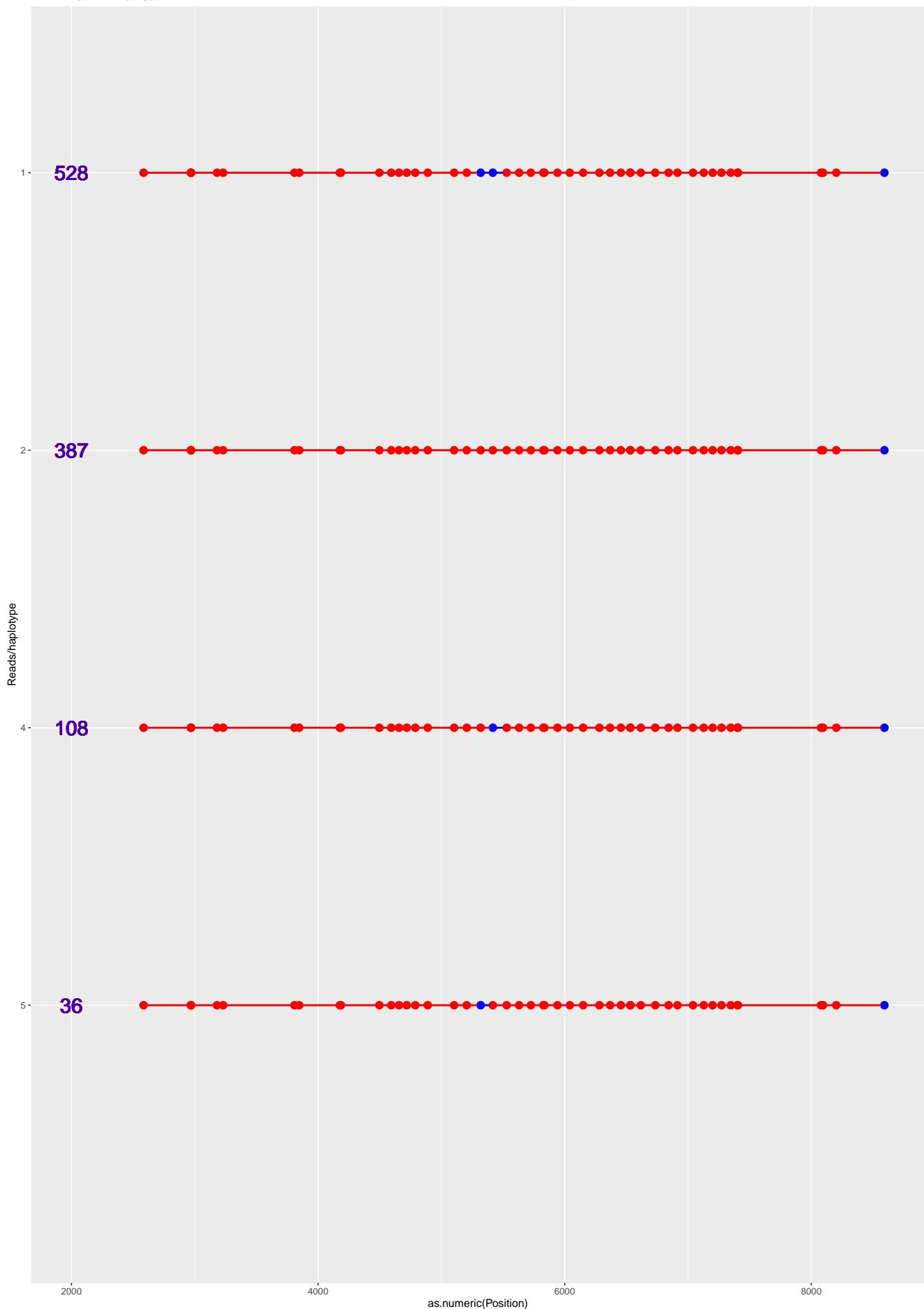
barcode = ATACAGCACAGATGTG & TACAGCGACGTCATCG

Sample = 108b tetrad = 108 spore = b

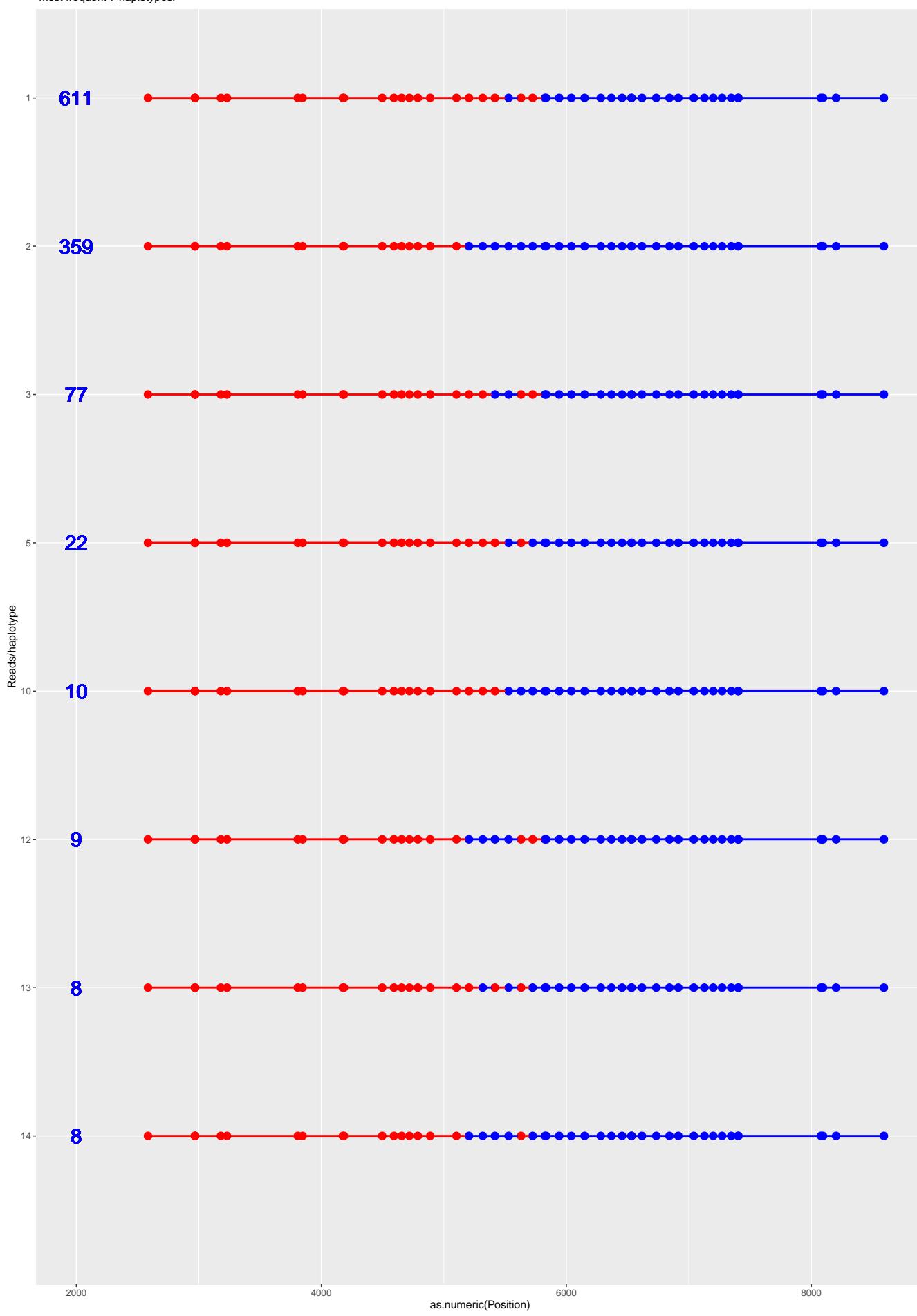
Total reads = 1272 PCR=270

haplotypes I began with n[supporting reads] = 36, 108, 387, 528

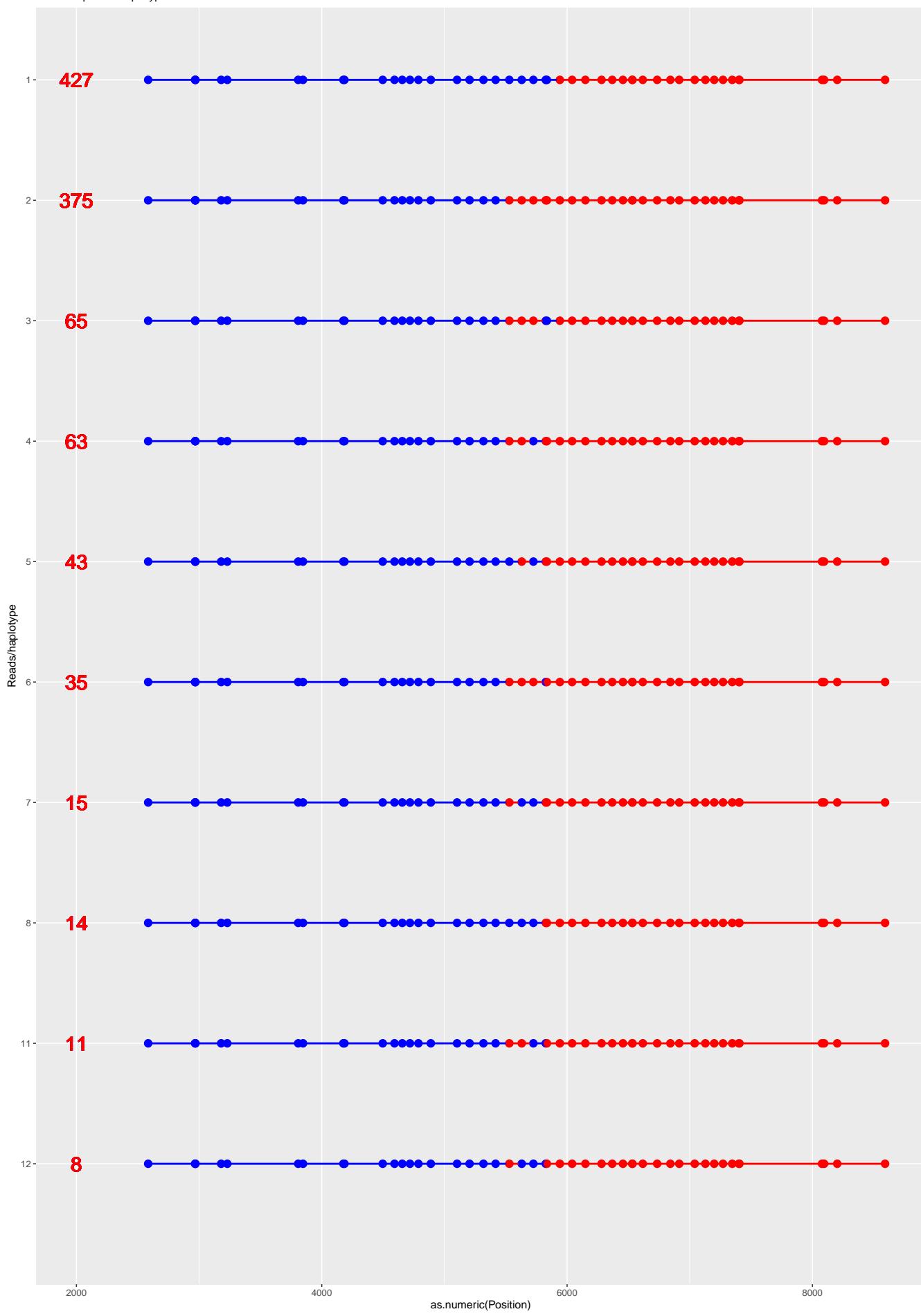
most frequent 7 haplotypes.



Sample = 108c tetrad = 108 spore = c
Total reads = 1376 PCR=271
haplotypes I began with [n(supporting reads)] = 8, 9, 10, 22, 77, 359, 611
most frequent 7 haplotypes.



Sample = 108d tetrad = 108 spore = d
 Total reads = 1288 PCR=272
 haplotypes I began with [n(supporting reads)] = 8, 11, 14, 15, 35, 43, 63, 65, 375, 427
 most frequent 7 haplotypes.



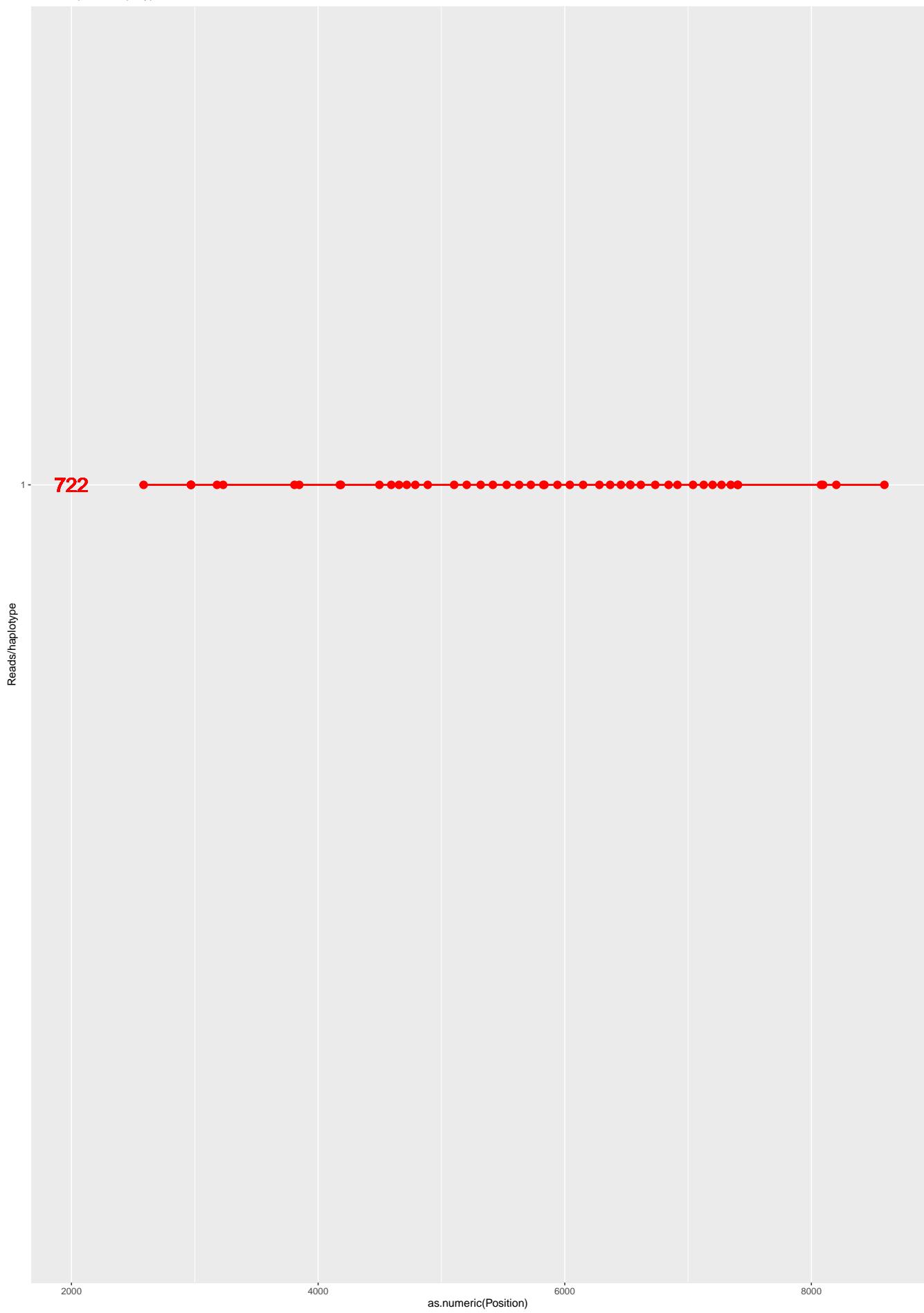
barcode = ATACAGCACAGATGTG & AGTATGAGATAGCTCG

Sample = 110a tetrad = 110 spore = a

Total reads =754 PCR=273

haplotypes I began with n[supporting reads] = 722

most frequent 7 haplotypes.



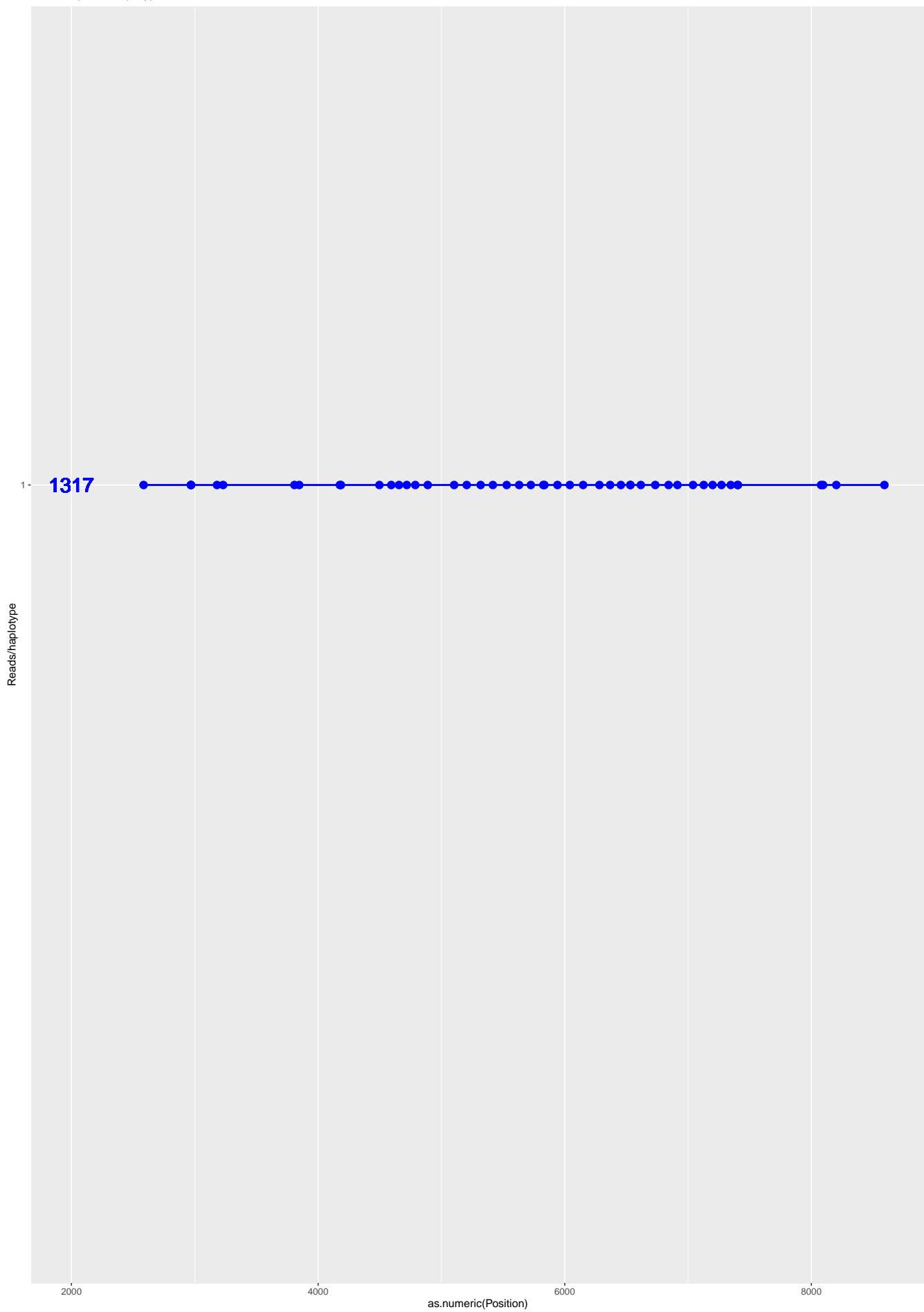
barcode = ACAGTCGATATCTCTC & TCATATGTAGTACTCT

Sample = 110b tetrad = 110 spore = b

Total reads = 1550 PCR=274

haplotypes I began with n[supporting reads] = 1317

most frequent 7 haplotypes.

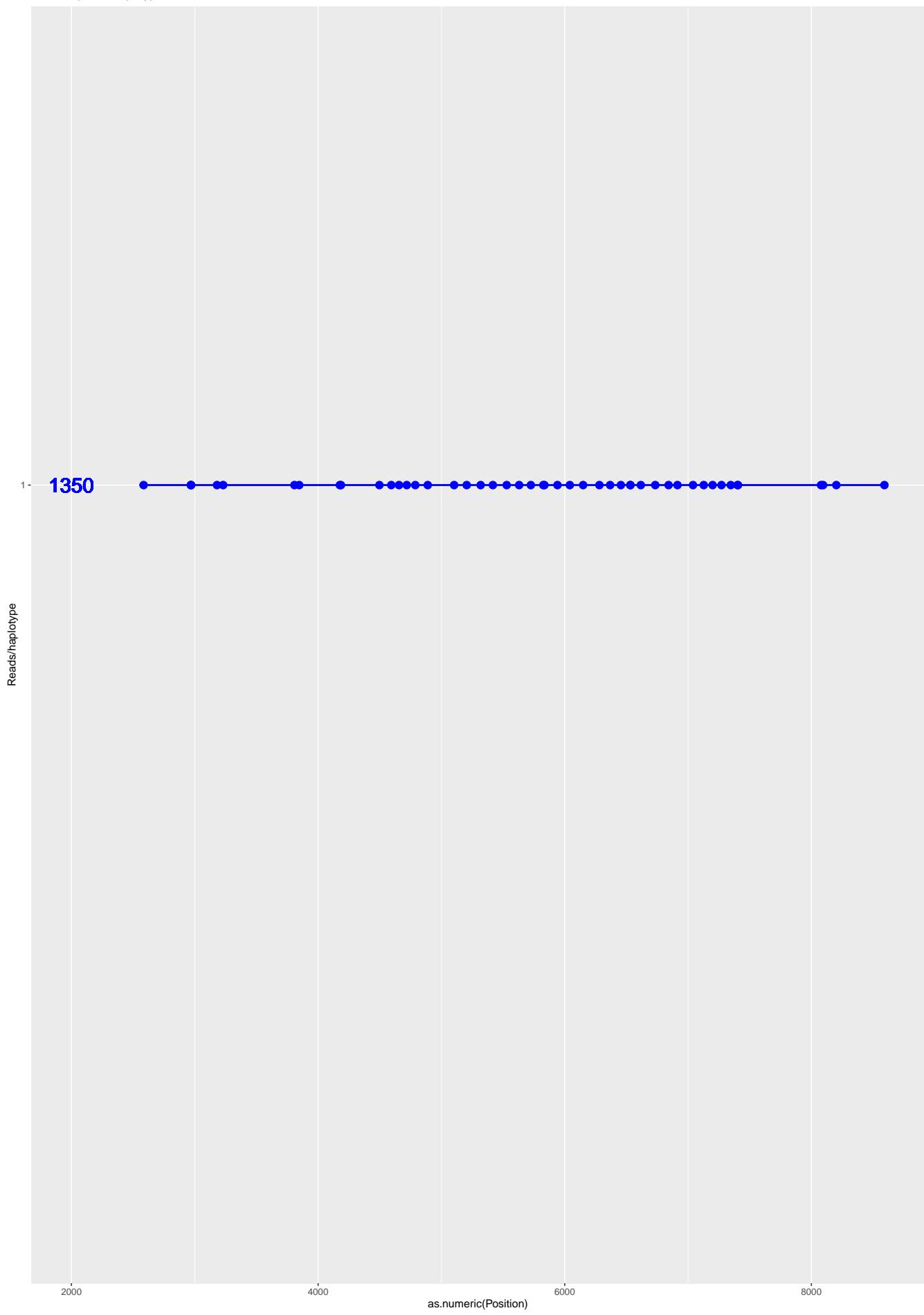


Sample = 110c tetrad = 110 spore = c

Total reads = 1556 PCR=275

haplotypes I began with n[supporting reads] = 1350

most frequent 7 haplotypes.



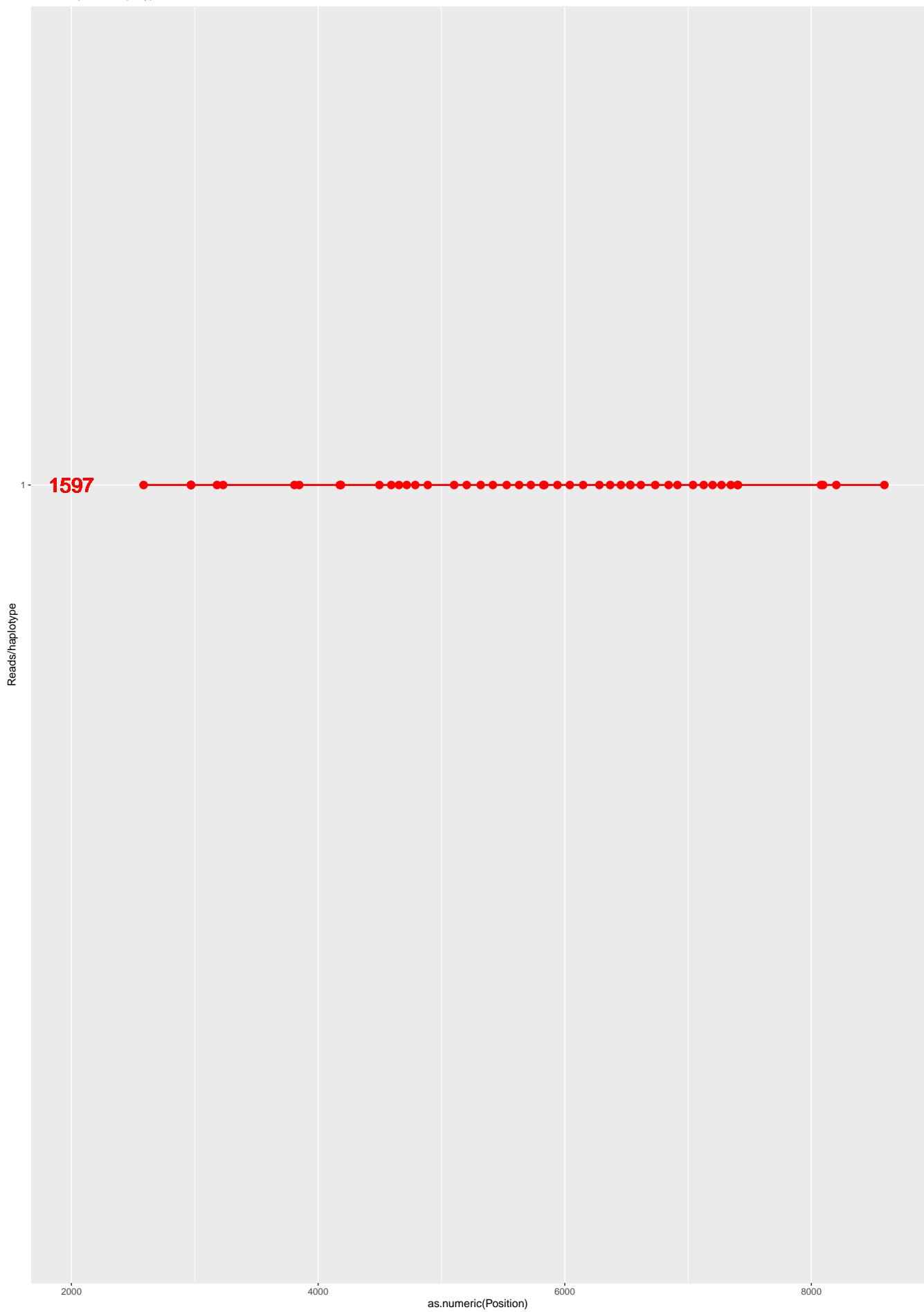
barcode = ACAGTCGATATCTCTC & TGCAGTCGAGATAACAT

Sample = 110d tetrad = 110 spore = d

Total reads = 1674 PCR=276

haplotypes I began with n[supporting reads] = 1597

most frequent 7 haplotypes.

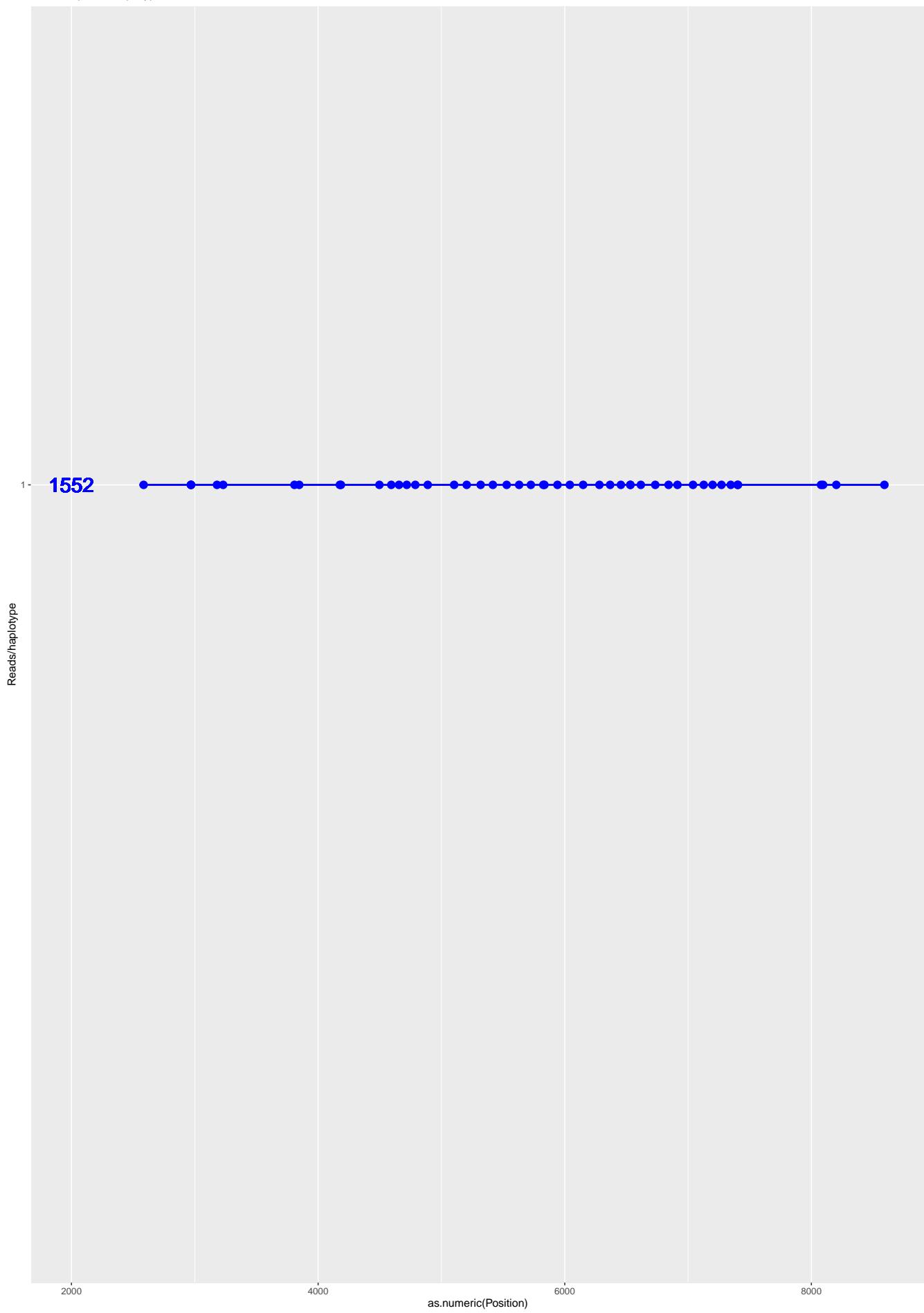


Sample = 112a tetrad = 112 spore = a

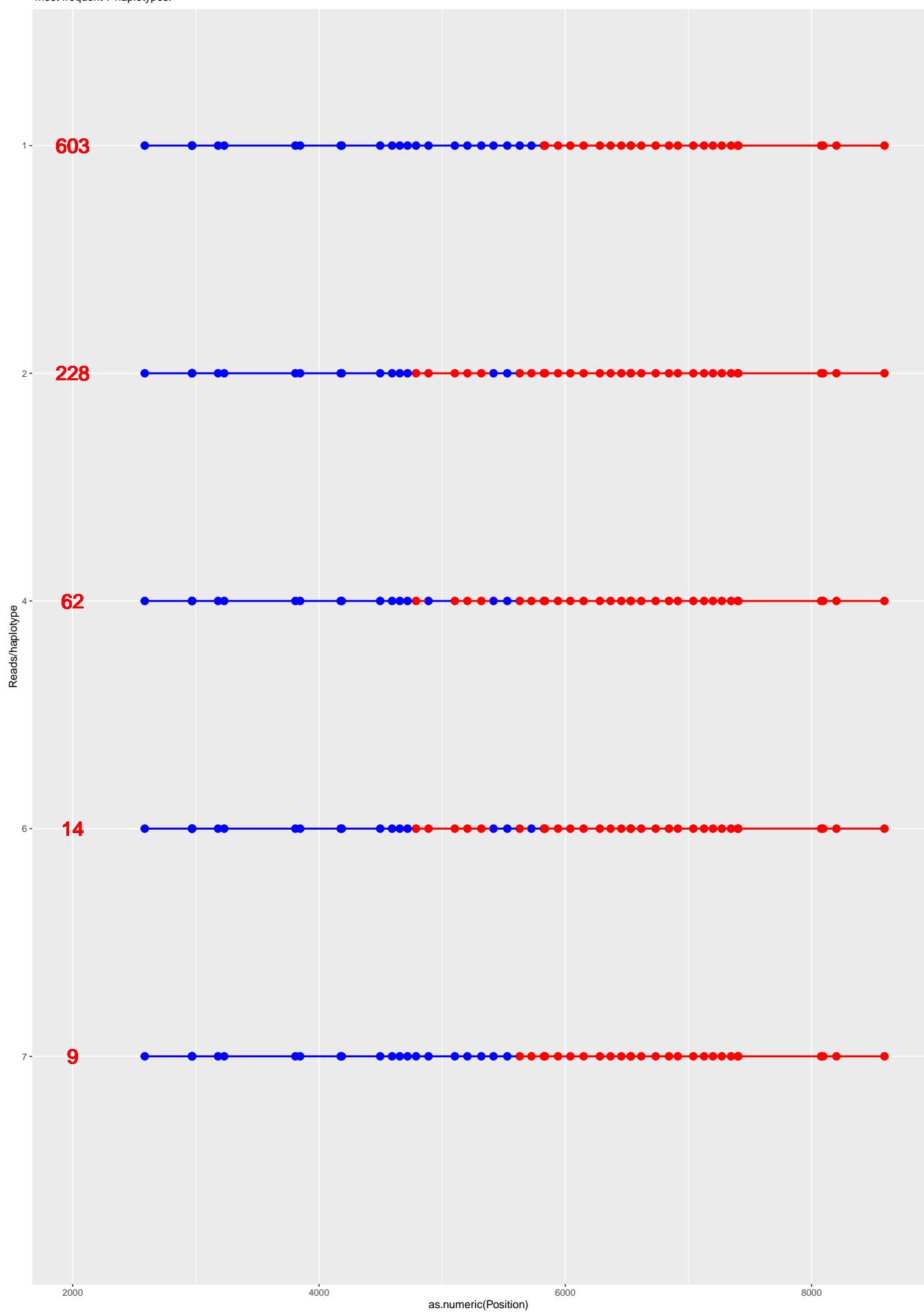
Total reads = 1793 PCR=277

haplotypes I began with n[supporting reads] = 1552

most frequent 7 haplotypes.



Sample = 112b tetrad = 112 spore = b
Total reads = 1416 PCR=278
haplotypes I began with n[supporting reads] = 9, 14, 62, 228, 603
most frequent 7 haplotypes.

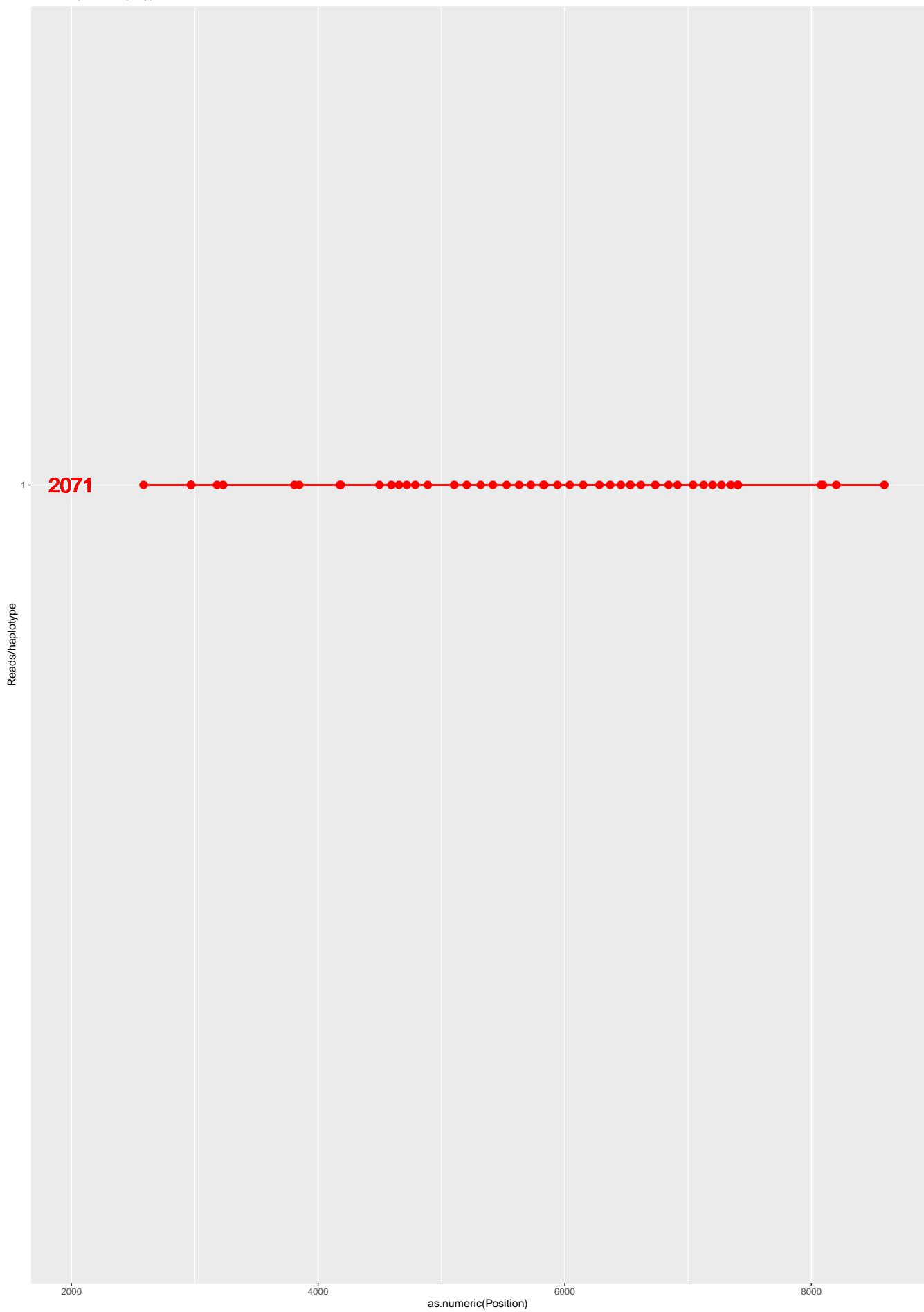


Sample = 112c tetrad = 112 spore = c

Total reads = 2174 PCR=279

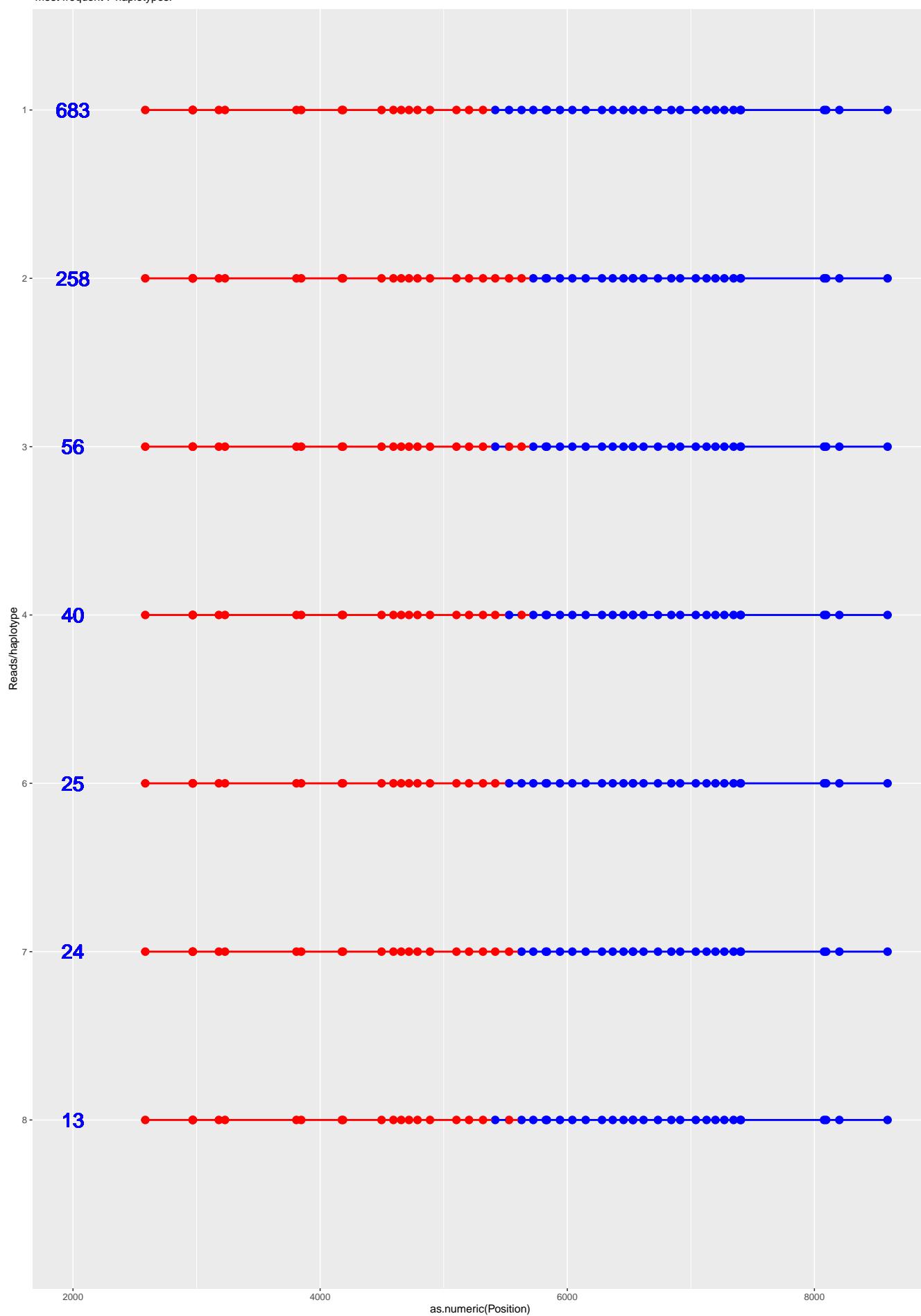
haplotypes I began with n[supporting reads] = 2071

most frequent 7 haplotypes.



barcode = ACAGTCGATATCTCTC & GTCTCTGCGATAACAGC

Sample = 112d tetrad = 112 spore = d
Total reads = 1231 PCR=280
haplotypes I began with n[supporting reads] = 13, 24, 25, 40, 56, 258, 683
most frequent 7 haplotypes.

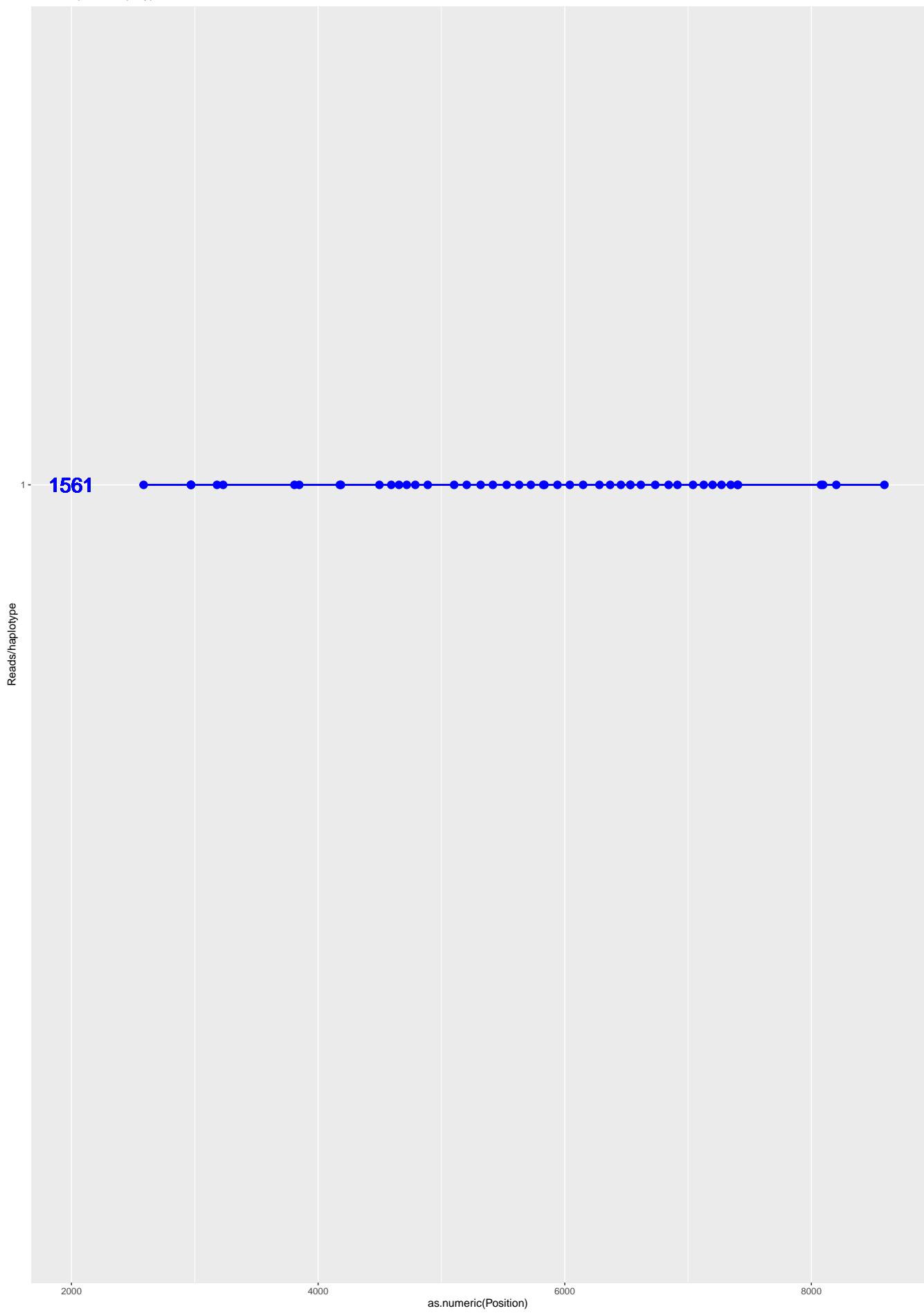


Sample = 114a tetrad = 114 spore = a

Total reads = 1805 PCR=281

haplotypes I began with n[supporting reads] = 1561

most frequent 7 haplotypes.



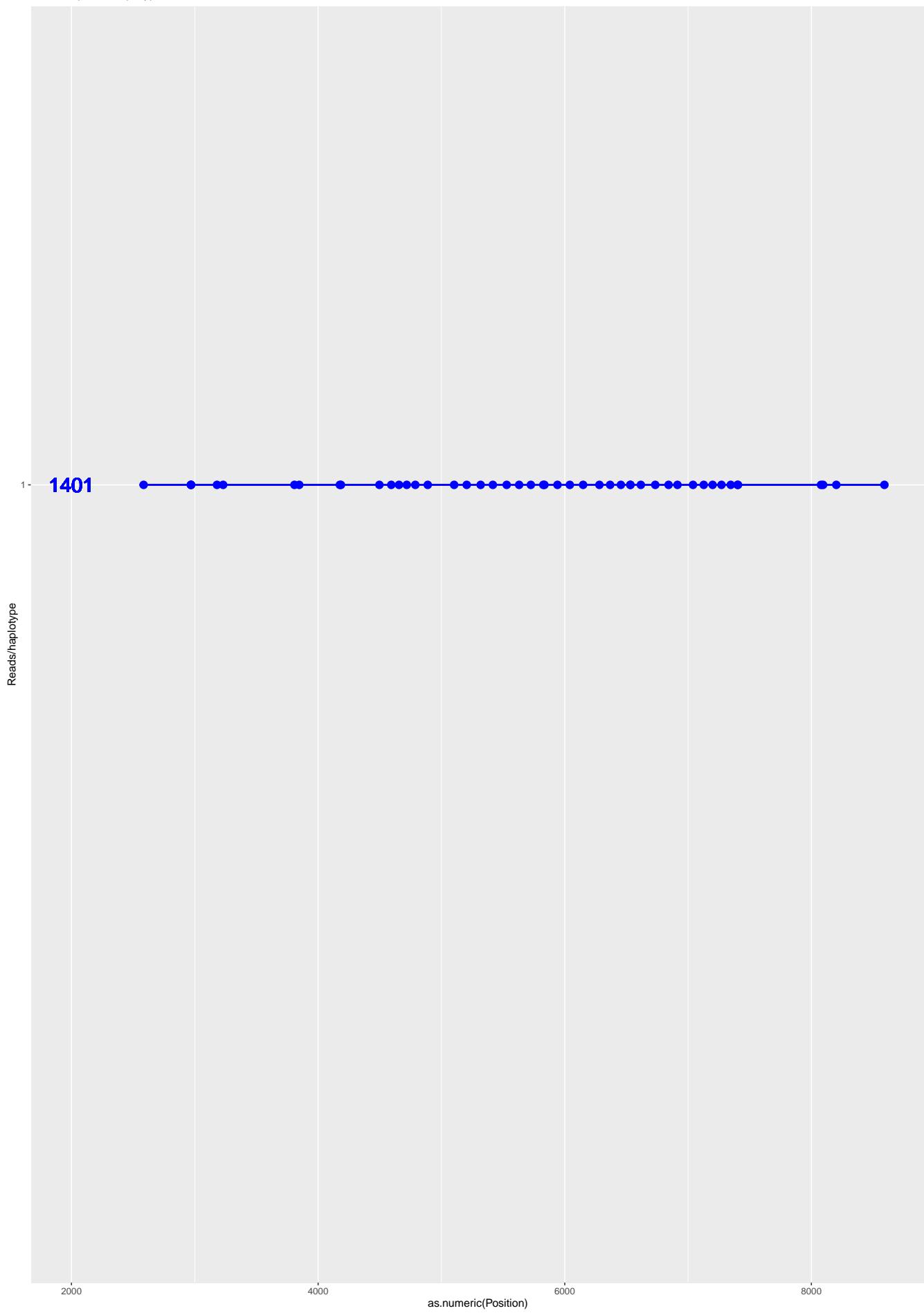
barcode = GCTCGATCACATGACG & TCATATGTAGTACTCT

Sample = 114b tetrad = 114 spore = b

Total reads = 1618 PCR=282

haplotypes I began with n[supporting reads] = 1401

most frequent 7 haplotypes.

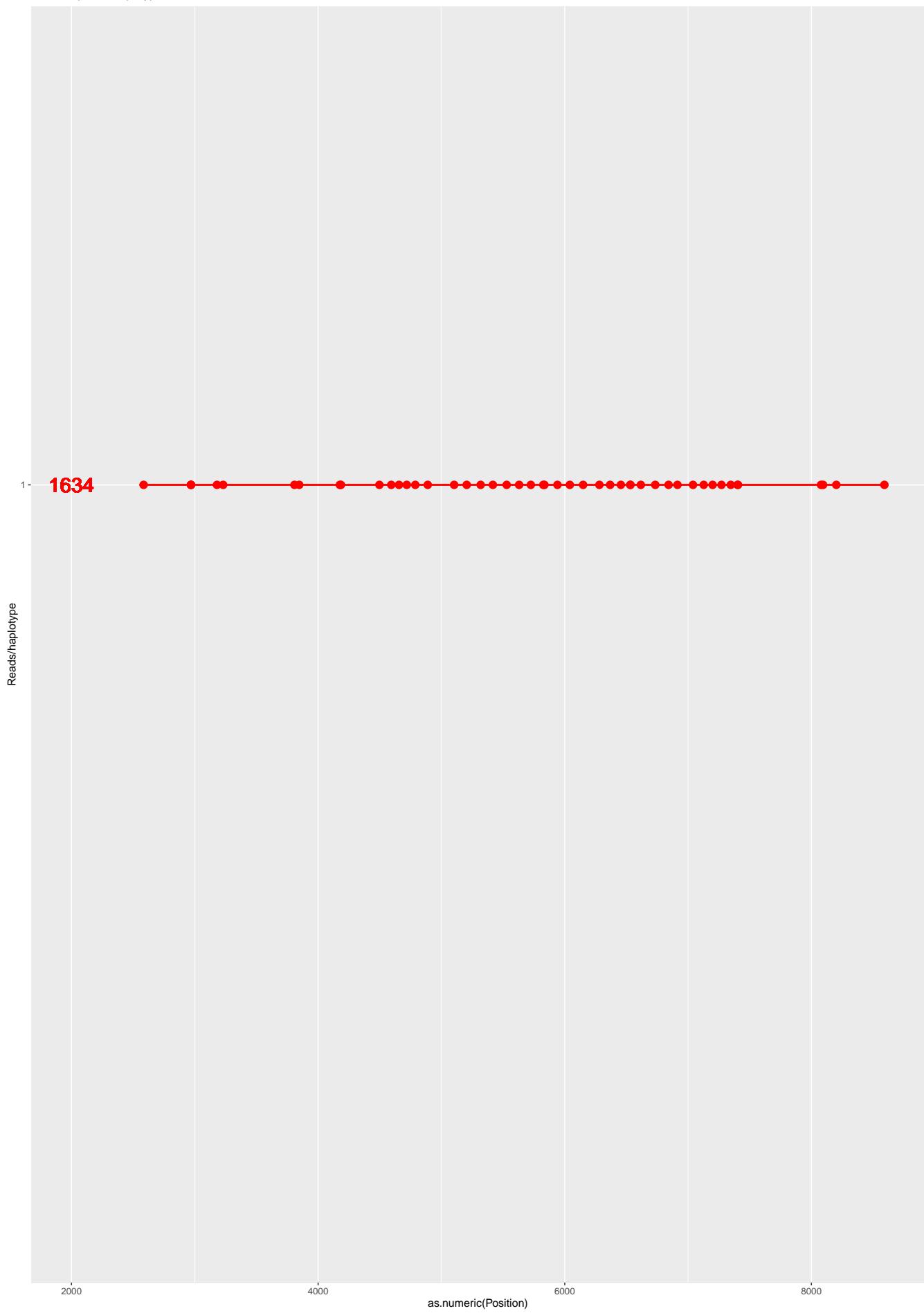


Sample = 114c tetrad = 114 spore = c

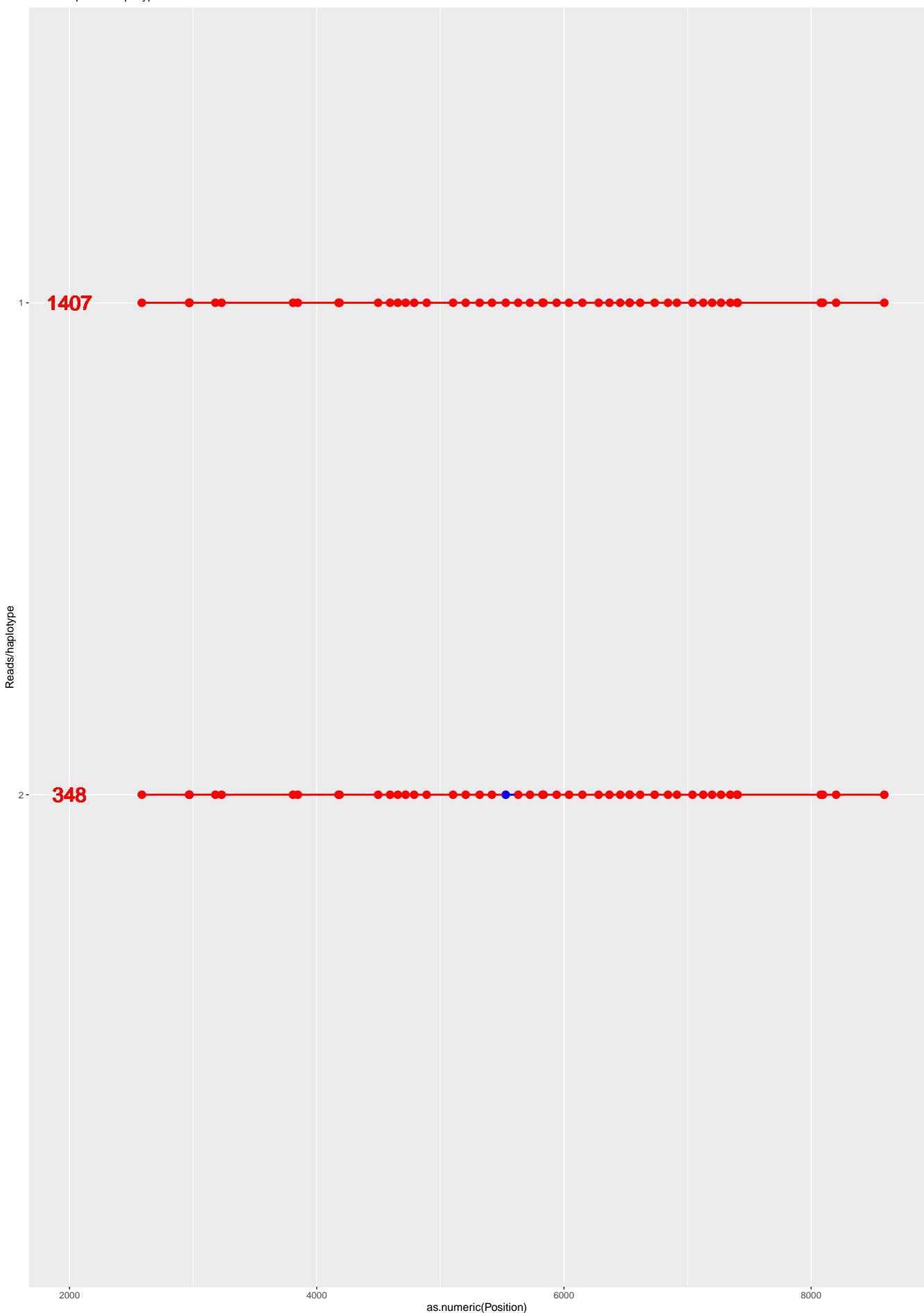
Total reads = 1710 PCR=283

haplotypes I began with n[supporting reads] = 1634

most frequent 7 haplotypes.



Sample = 114d tetrad = 114 spore = d
Total reads = 1836 PCR=284
haplotypes I began with n[supporting reads] = 348, 1407
most frequent 7 haplotypes.



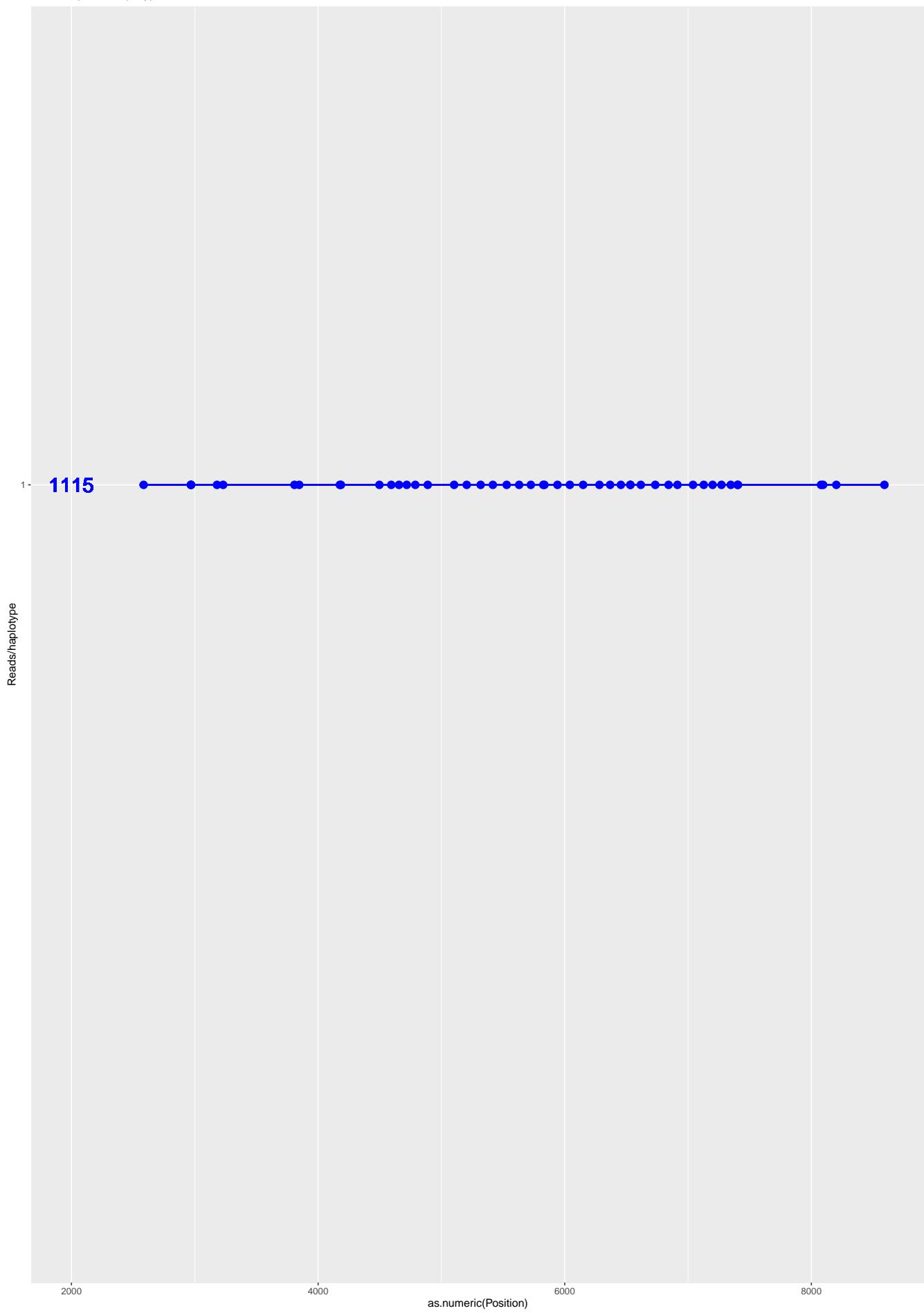
barcode = GCTCGATCACATGACG & GACTCTGCGTCGAGTC

Sample = 115a tetrad = 115 spore = a

Total reads = 1284 PCR=285

haplotypes I began with n[supporting reads] = 1115

most frequent 7 haplotypes.

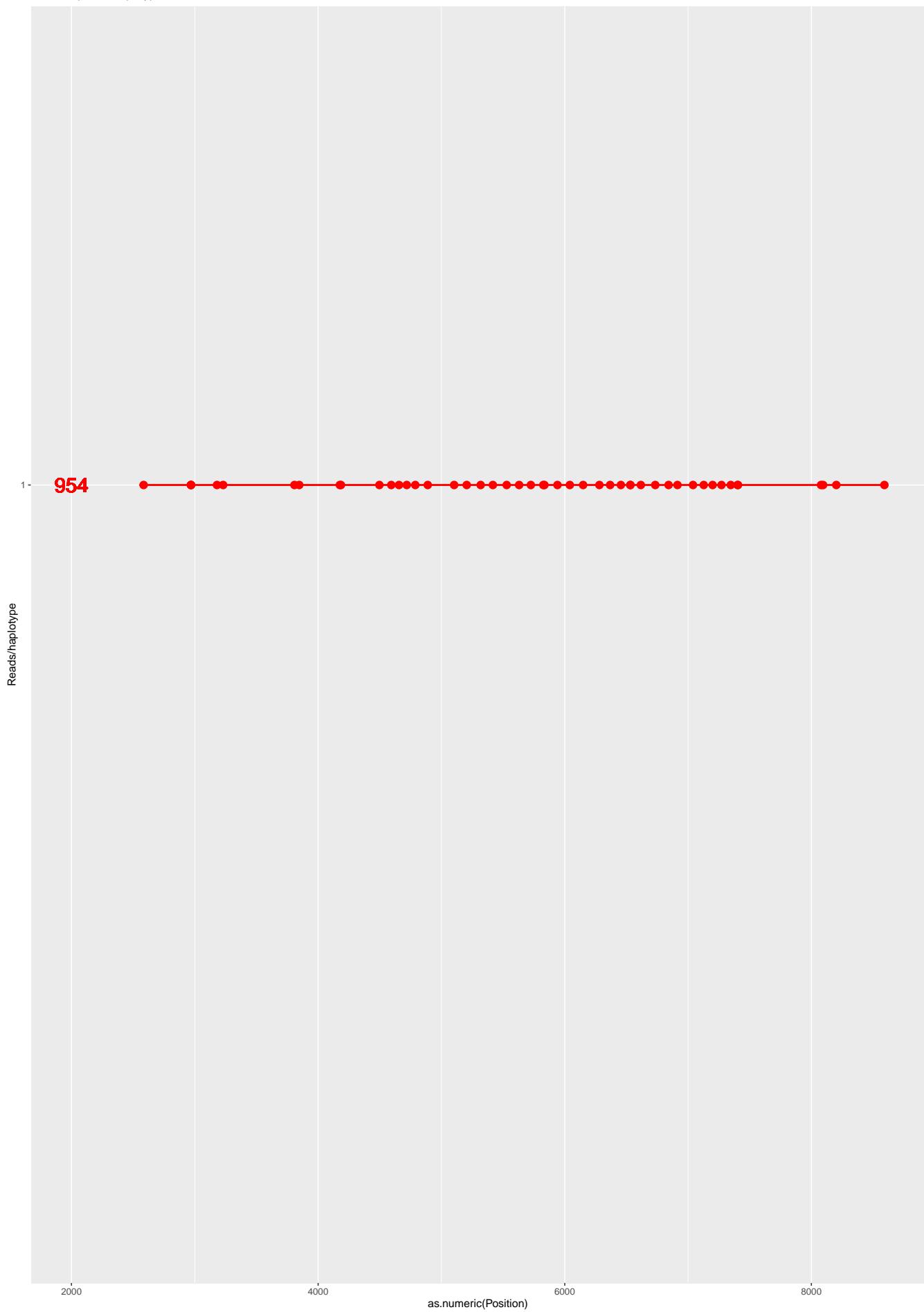


Sample = 115b tetrad = 115 spore = b

Total reads = 997 PCR=286

haplotypes I began with n[supporting reads] = 954

most frequent 7 haplotypes.



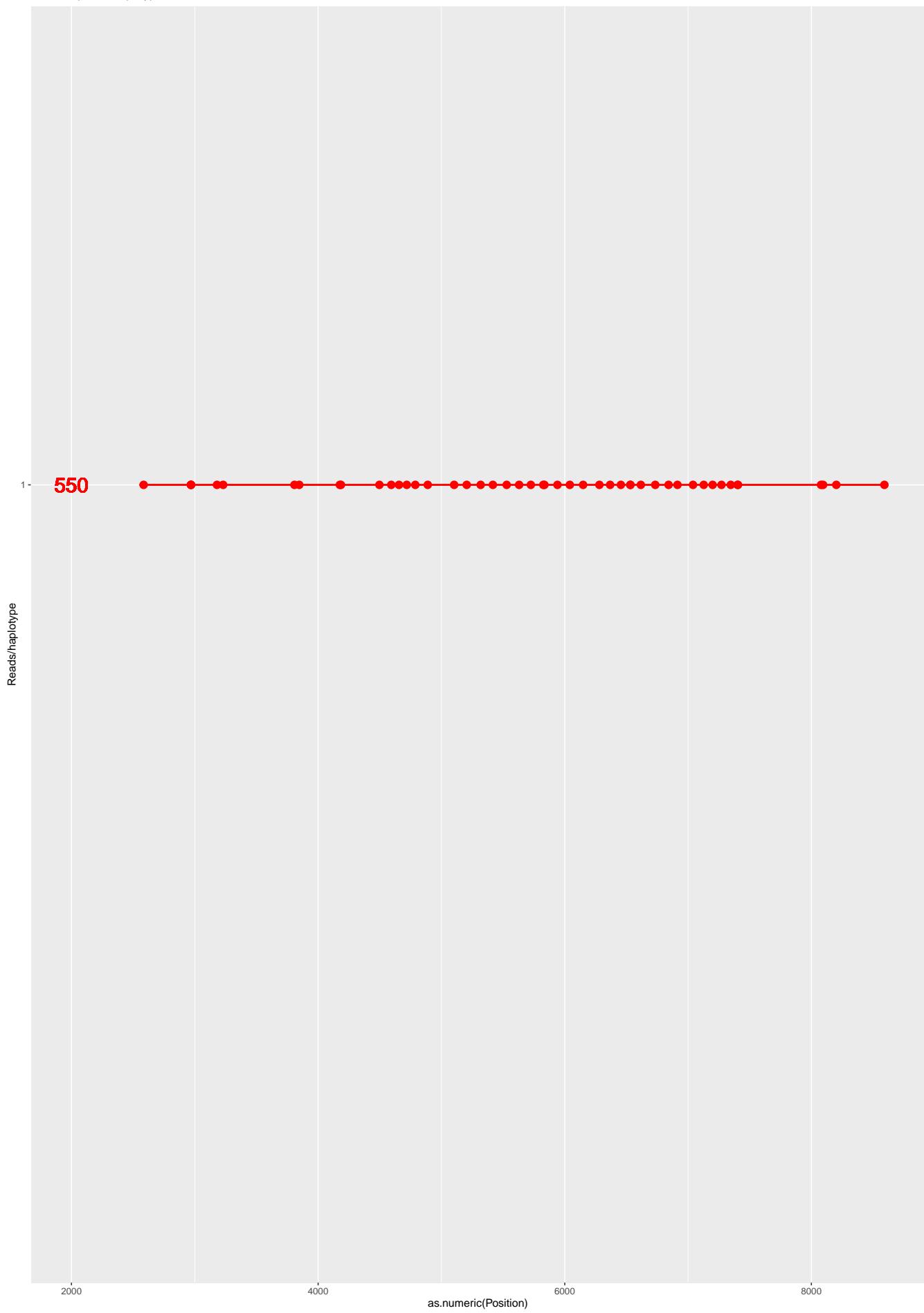
barcode = GCTCGATCACATGACG & GCGCAGACTACGTGTG

Sample = 115c tetrad = 115 spore = c

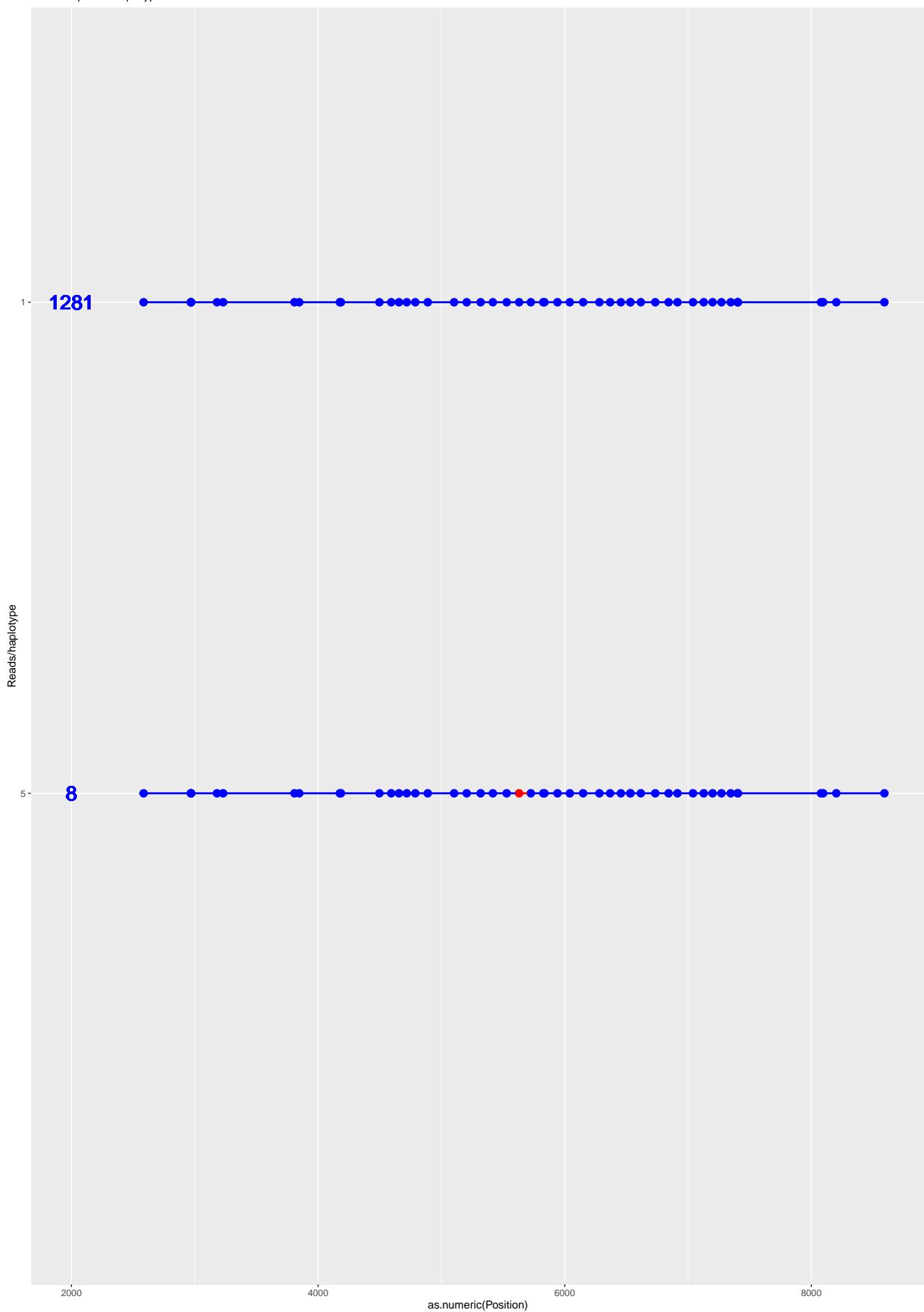
Total reads =571 PCR=287

haplotypes I began with n[supporting reads] = 550

most frequent 7 haplotypes.



Sample = 115d tetrad = 115 spore = d
Total reads = 1497 PCR=288
haplotypes I began with n[supporting reads] = 8, 1281
most frequent 7 haplotypes.



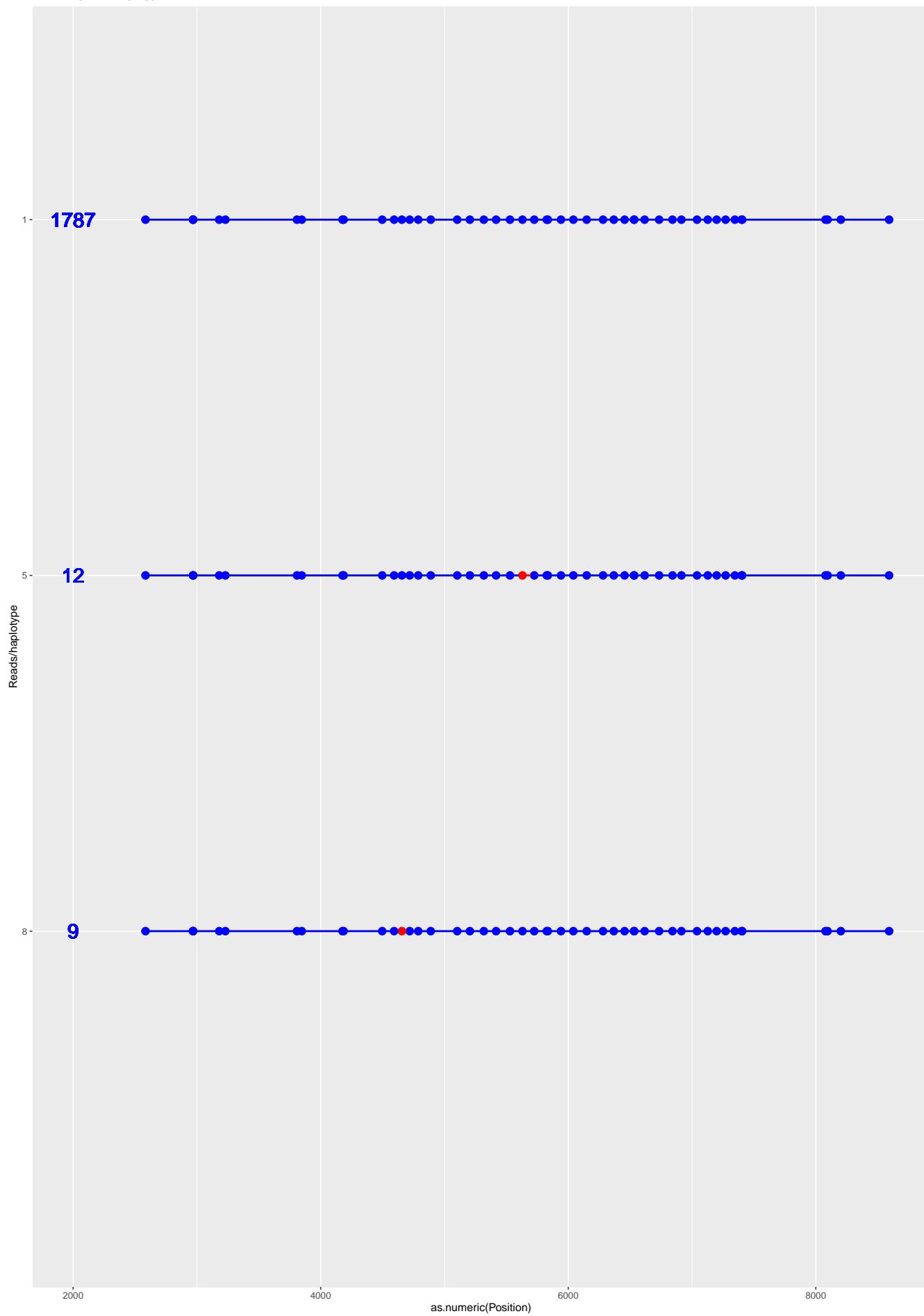
barcode = GCTCGATCACATGACG & AGTATGAGATAGCTCG

Sample = 116a tetrad = 116 spore = a

Total reads = 2098 PCR=289

haplotypes I began with n[supporting reads] = 9, 12, 1787

most frequent 7 haplotypes.



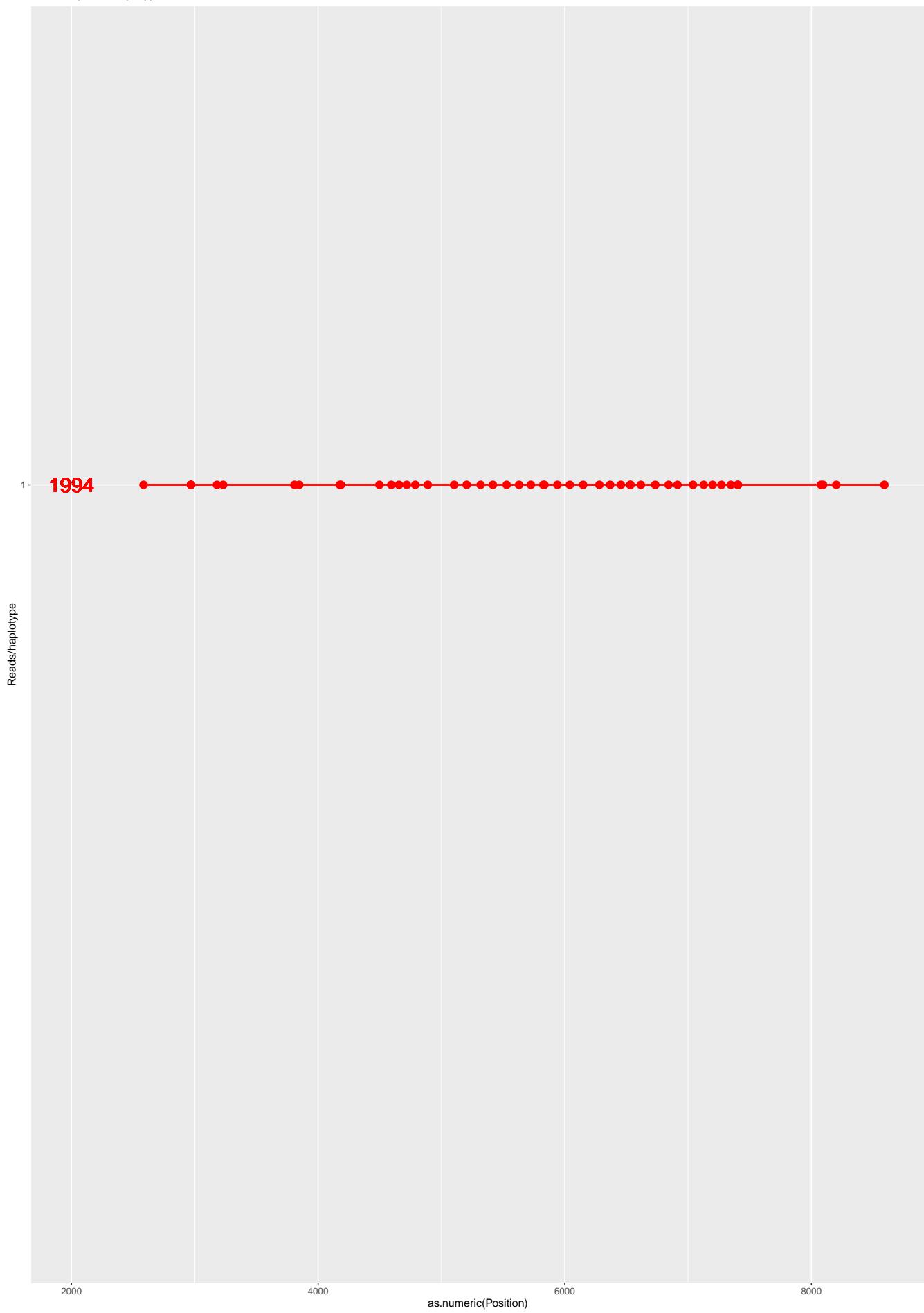
barcode = GCGCTCTGTGTCAGC & GCGACGAGTACTCATG

Sample = 116b tetrad = 116 spore = b

Total reads = 2075 PCR=290

haplotypes I began with n[supporting reads] = 1994

most frequent 7 haplotypes.

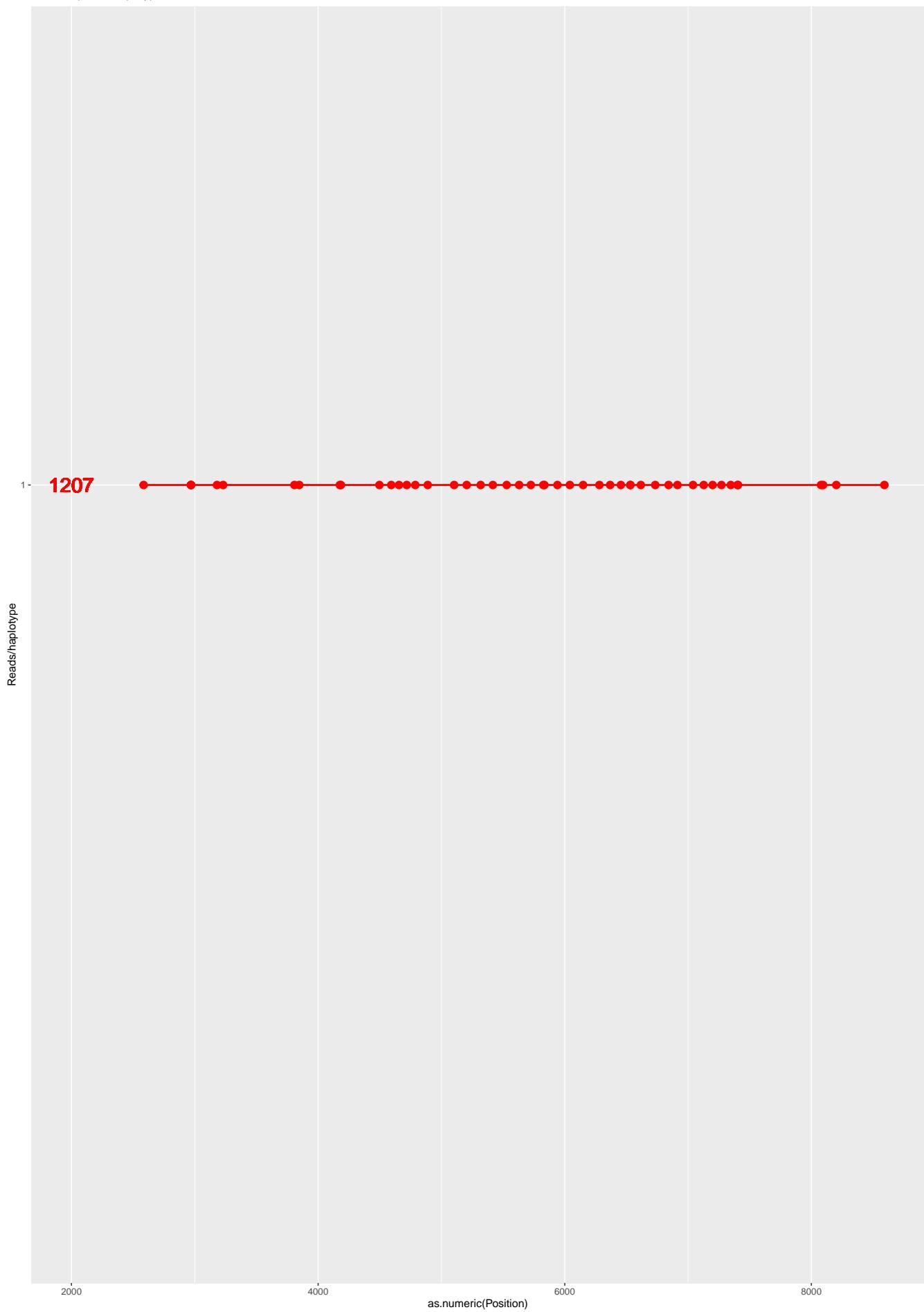


Sample = 116c tetrad = 116 spore = c

Total reads = 1262 PCR=291

haplotypes I began with n[supporting reads] = 1207

most frequent 7 haplotypes.



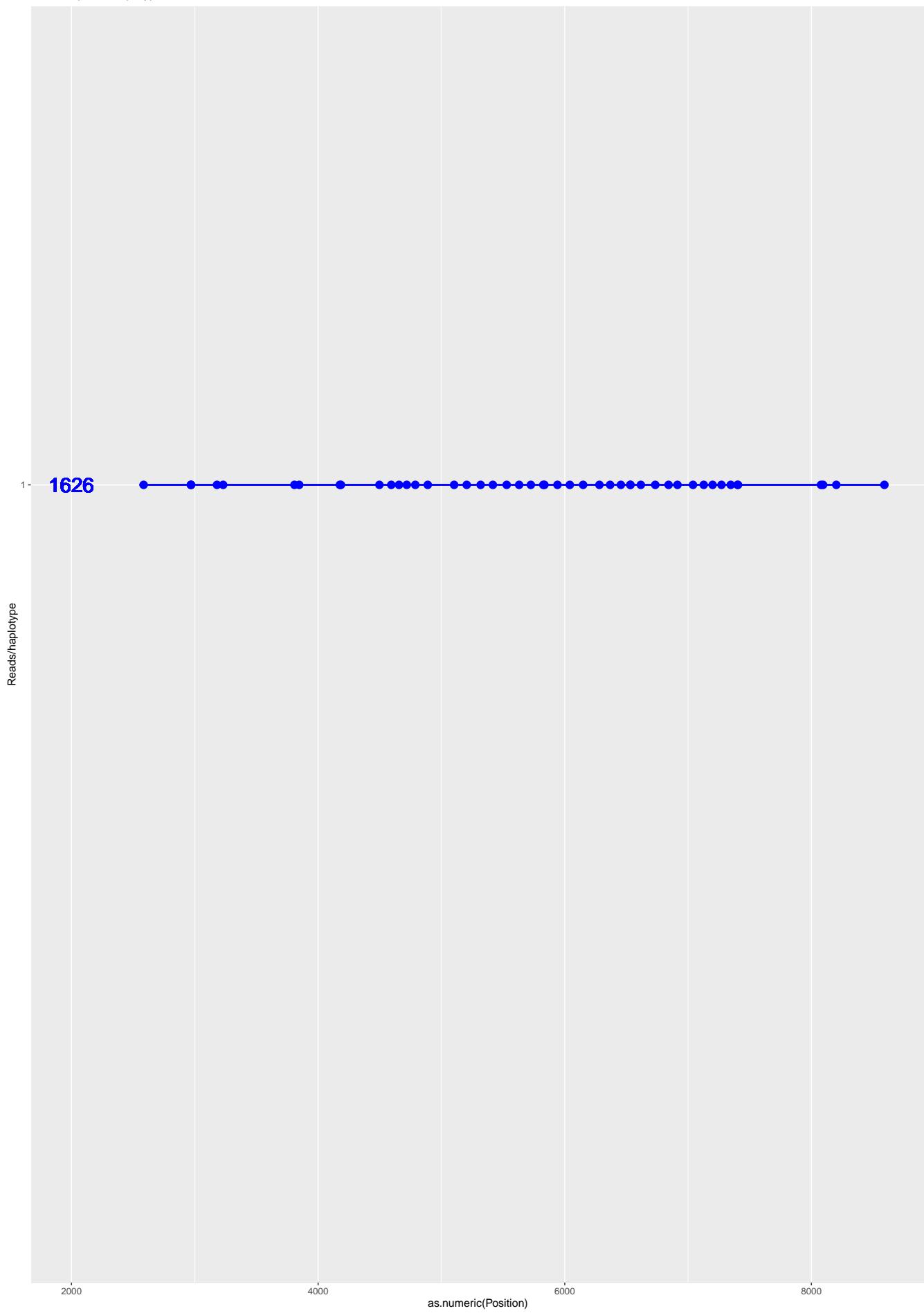
barcode = GCGCTCTGTGTCAGC & ATCATATGATGCGACA

Sample = 116d tetrad = 116 spore = d

Total reads = 1891 PCR=292

haplotypes I began with n[supporting reads] = 1626

most frequent 7 haplotypes.

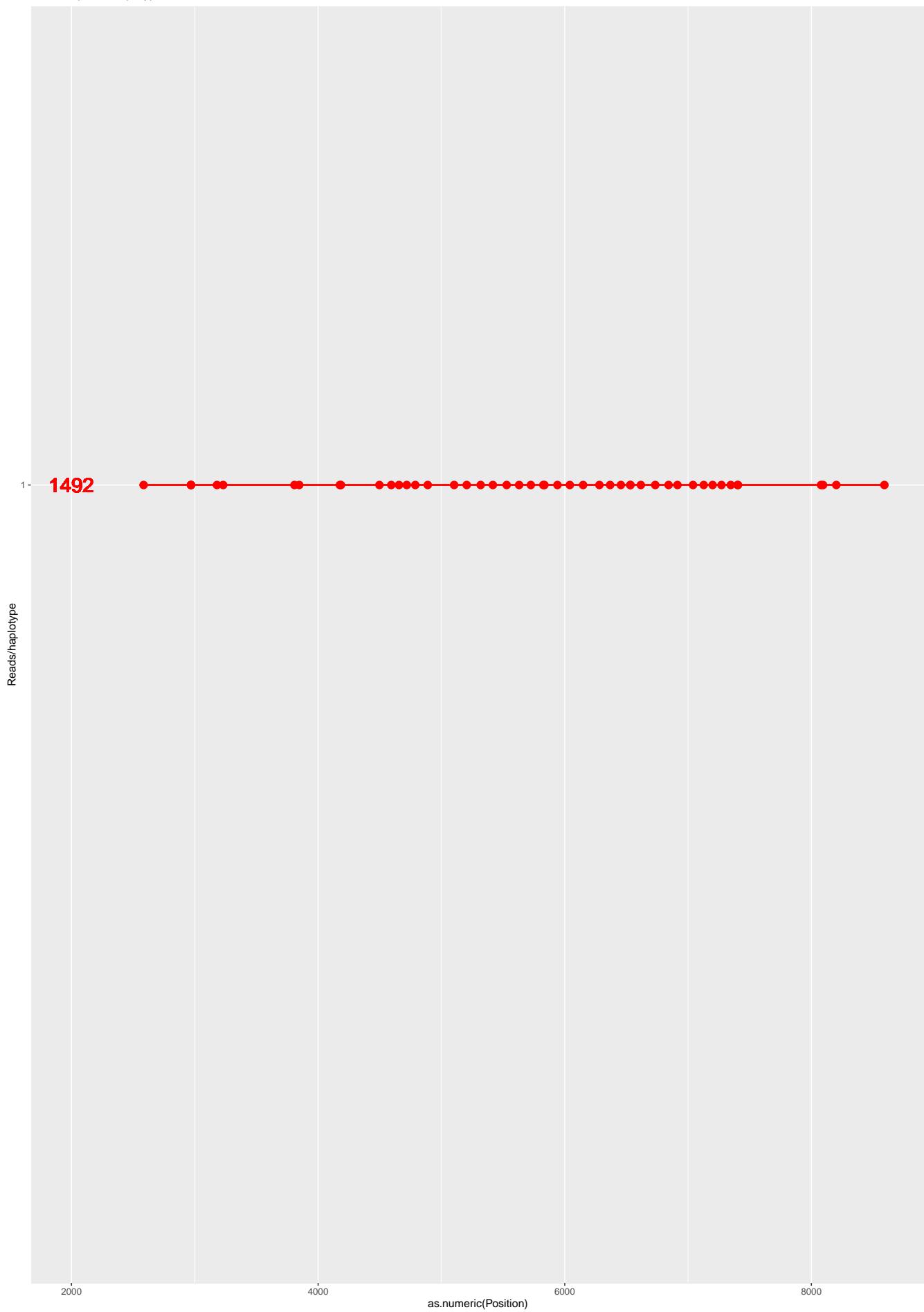


Sample = 117a tetrad = 117 spore = a

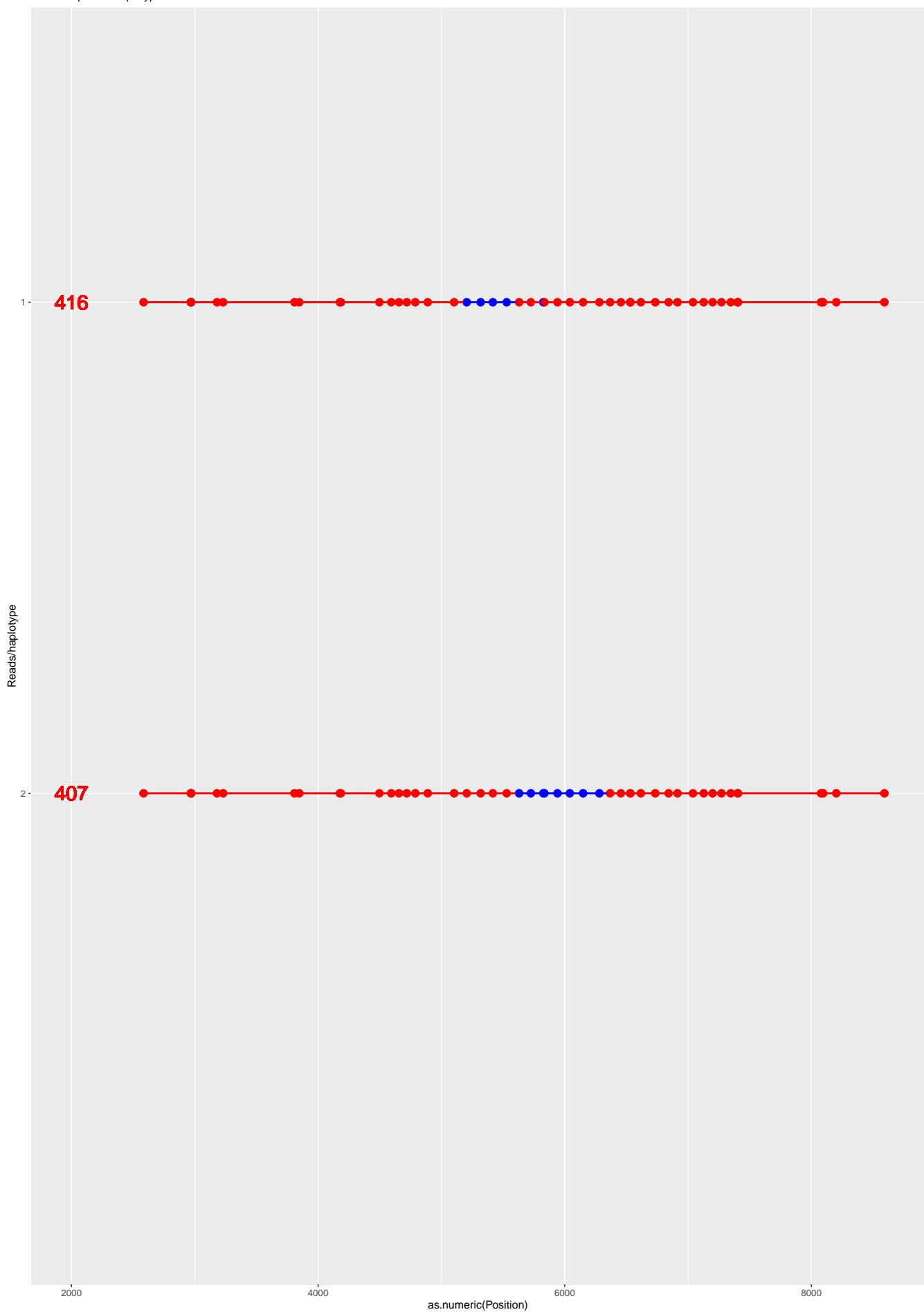
Total reads = 1571 PCR=293

haplotypes I began with n[supporting reads] = 1492

most frequent 7 haplotypes.



Sample = 117b tetrad = 117 spore = b
Total reads = 1182 PCR=294
haplotypes I began with n[supporting reads] = 407, 416
most frequent 7 haplotypes.



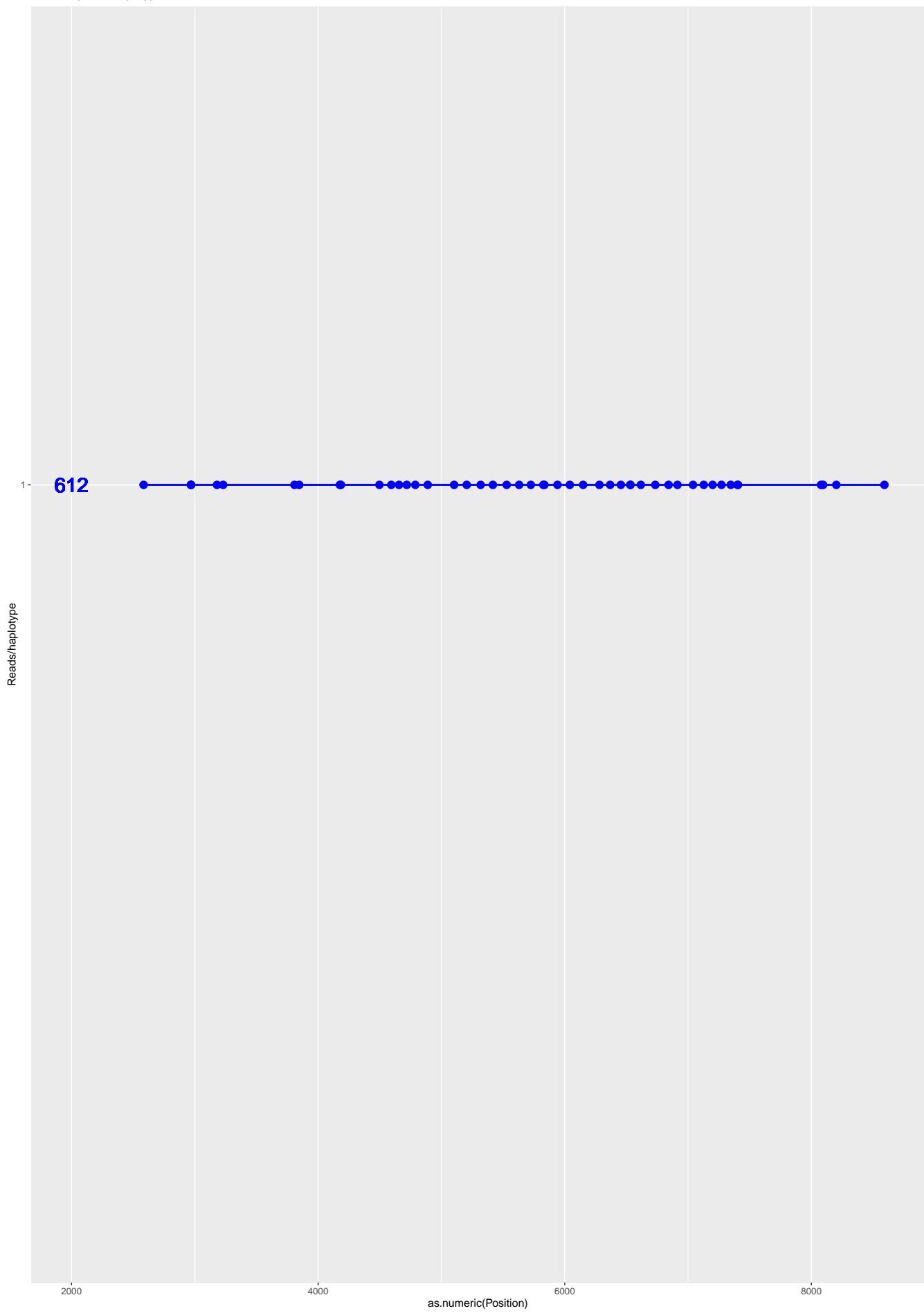
barcode = GCGCTCTGTGTCAGC & TGTGAGACTGCATGTC

Sample = 117c tetrad = 117 spore = c

Total reads = 710 PCR=295

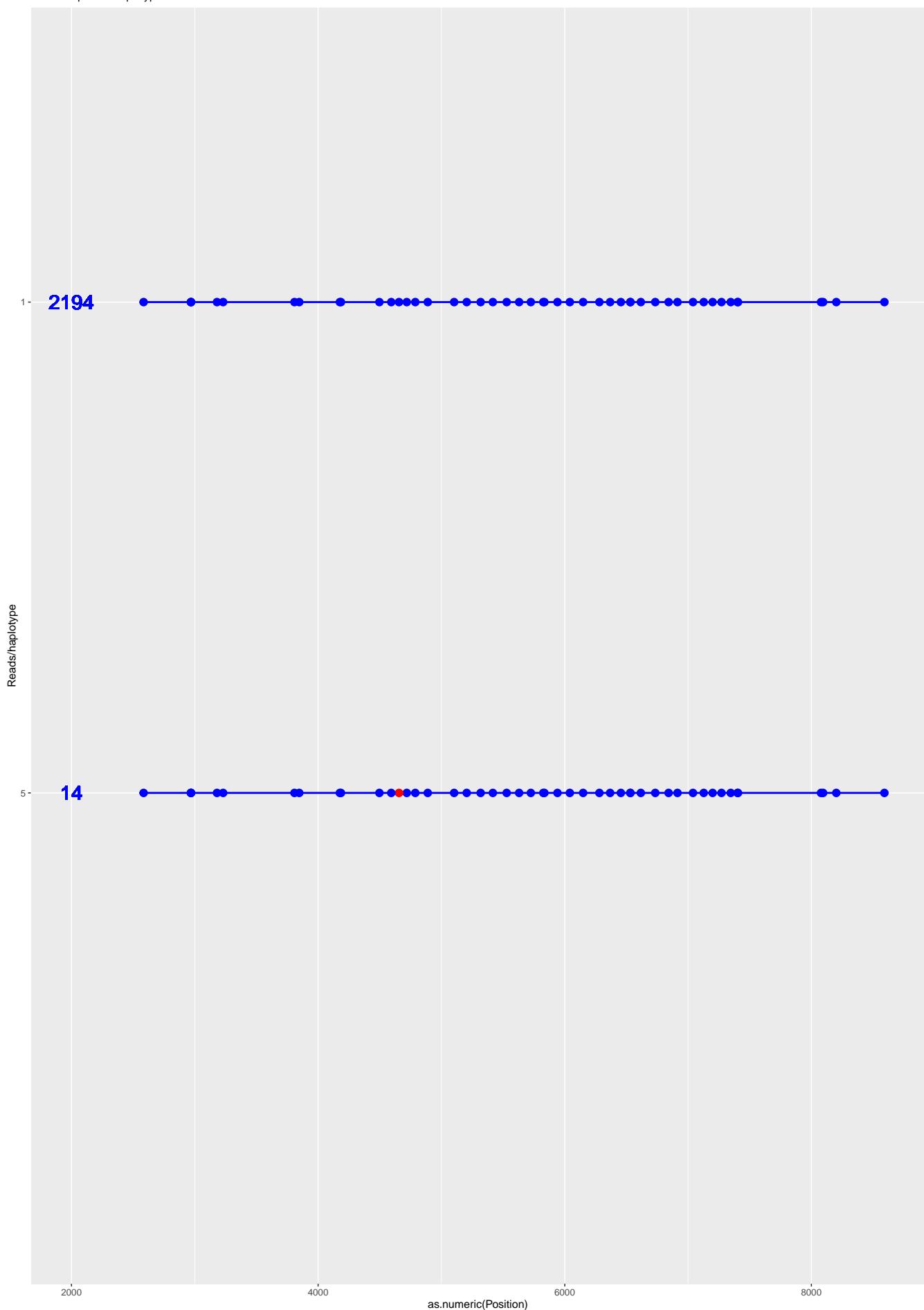
haplotypes I began with n[supporting reads] = 612

most frequent 7 haplotypes.



barcode = GCGCTCTGTGCGCAGC & GCTCAGTGCCTACTG

Sample = 117d tetrad = 117 spore = d
Total reads = 2577 PCR=296
haplotypes I began with n[supporting reads] = 14, 2194
most frequent 7 haplotypes.



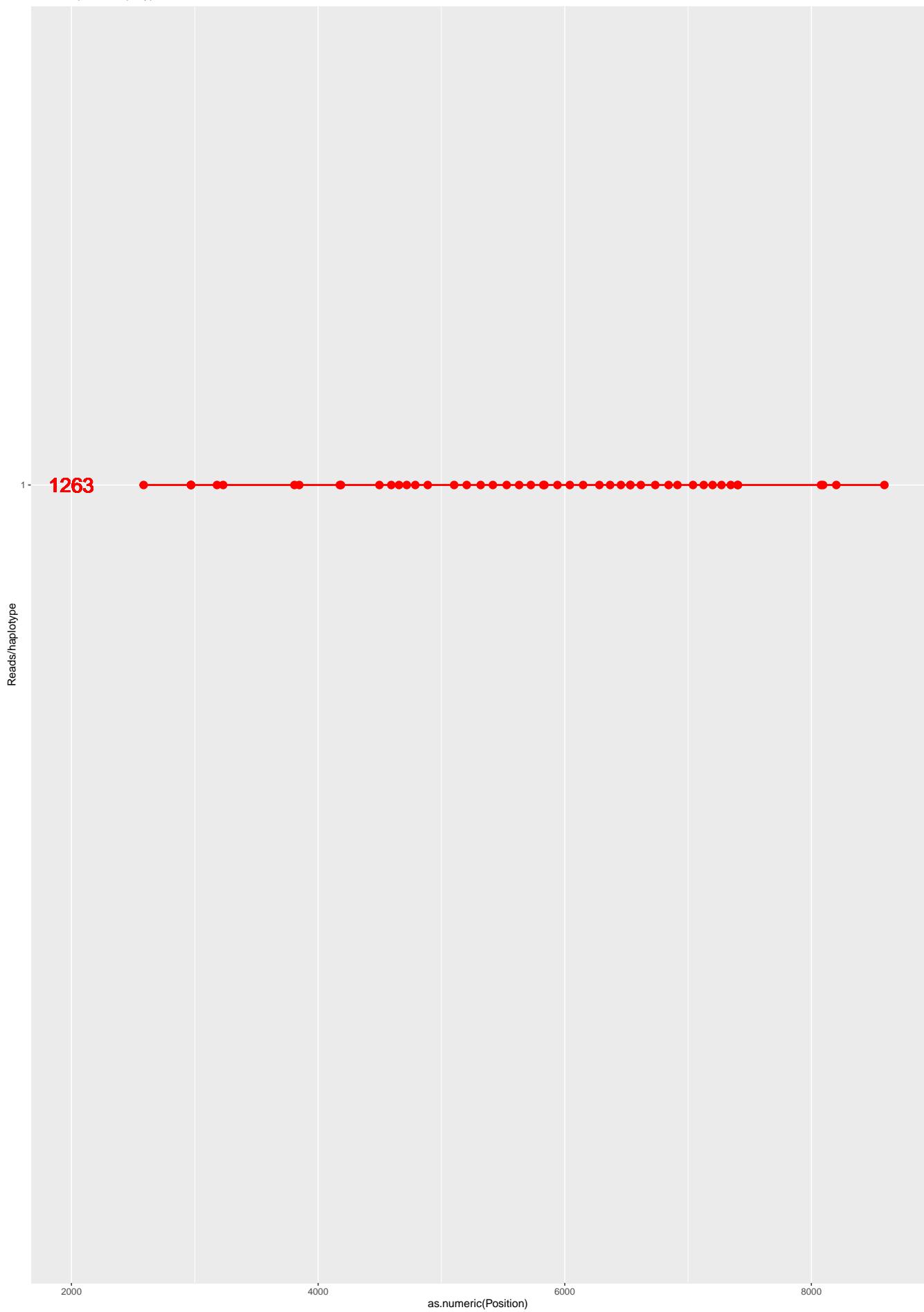
barcode = GCGCTCTGTGTCAGC & ACTATCGCGCACGCAG

Sample = 118a tetrad = 118 spore = a

Total reads = 1320 PCR=297

haplotypes I began with n[supporting reads] = 1263

most frequent 7 haplotypes.



barcode = TCATGAGTCGACACTA & GCGACGAGTACTCATG

Sample = 118b tetrad = 118 spore = b

Total reads = 2597 PCR=298

haplotypes I began with n[supporting reads] = 14, 2259

most frequent 7 haplotypes.

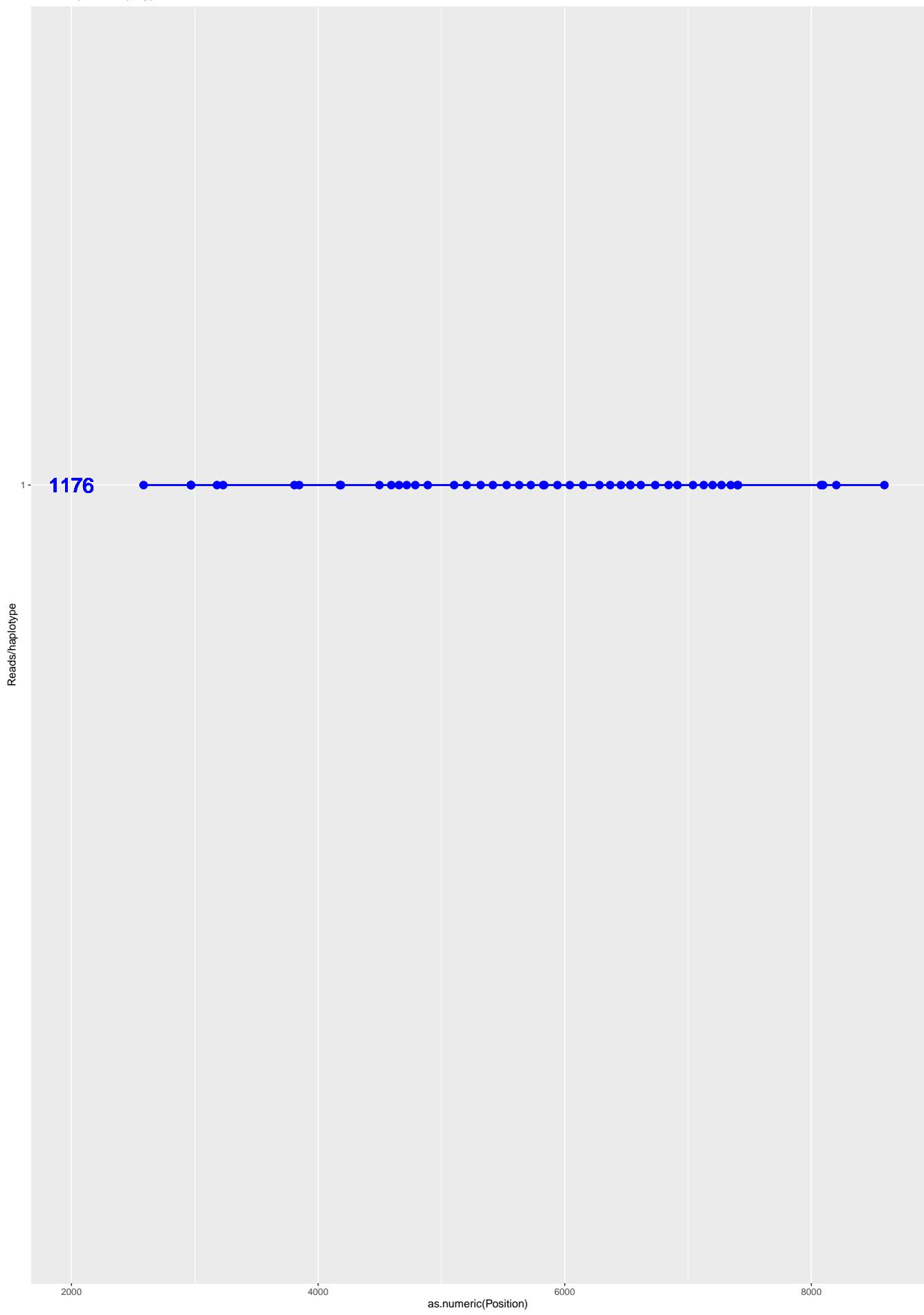


Sample = 118c tetrad = 118 spore = c

Total reads = 1372 PCR=299

haplotypes I began with n[supporting reads] = 1176

most frequent 7 haplotypes.



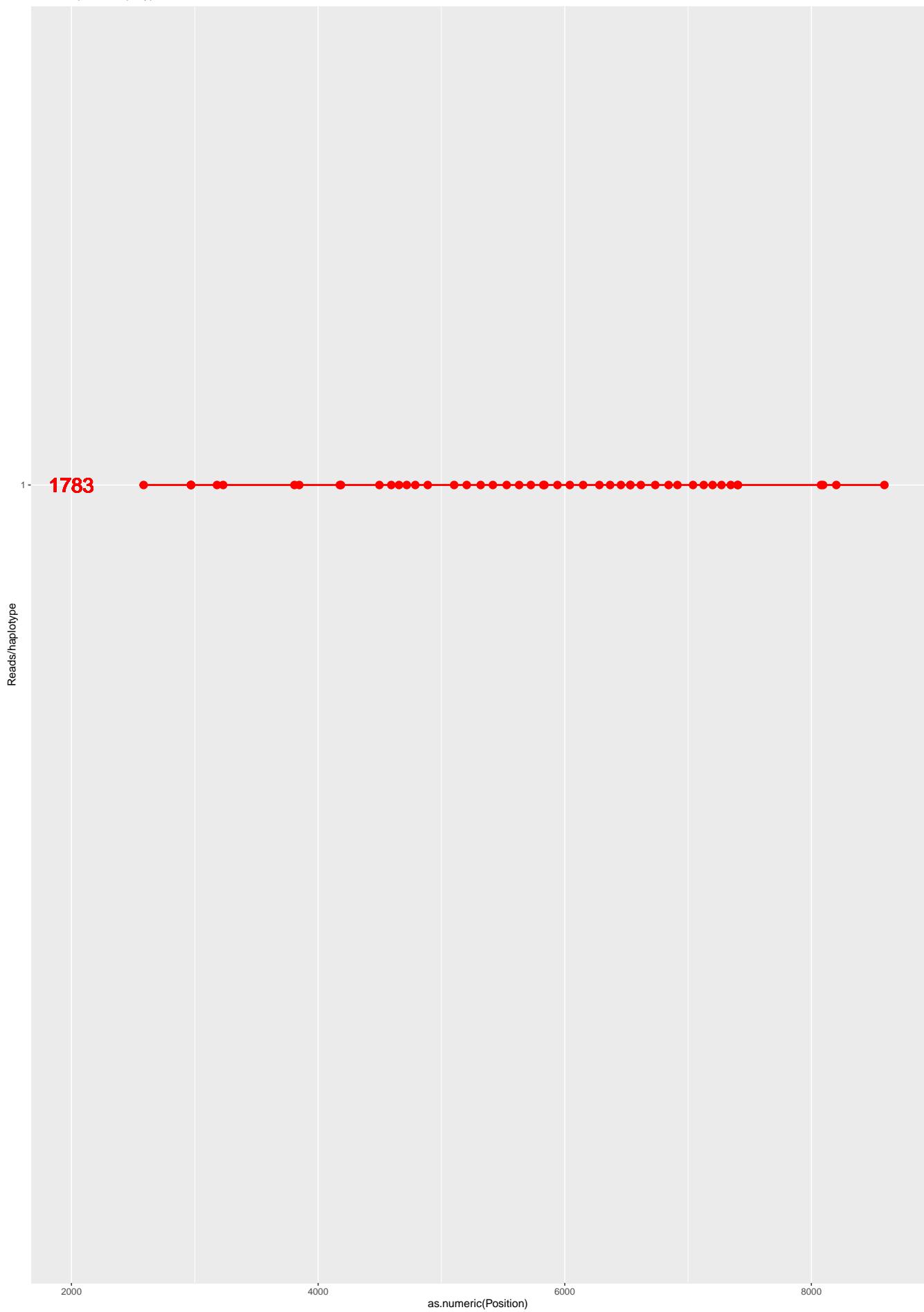
barcode = TCATGAGTCGACACTA & ATCATATGATGCGACA

Sample = 118d tetrad = 118 spore = d

Total reads = 1859 PCR=300

haplotypes I began with n[supporting reads] = 1783

most frequent 7 haplotypes.



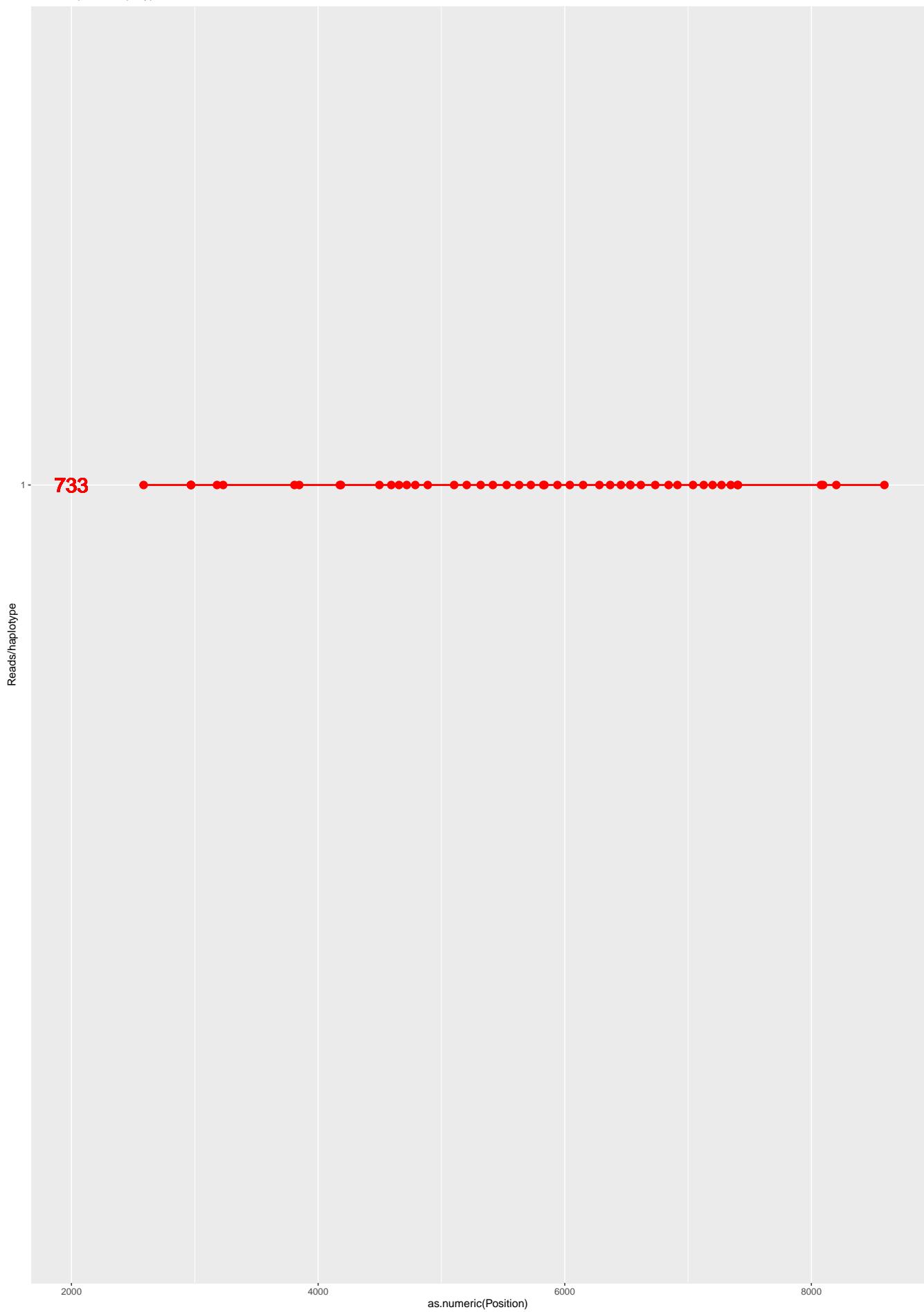
barcode = TCATGAGTCGACACTA & AGACGTAGATCACAGC

Sample = 122a tetrad = 122 spore = a

Total reads =763 PCR=301

haplotypes I began with n[supporting reads] = 733

most frequent 7 haplotypes.



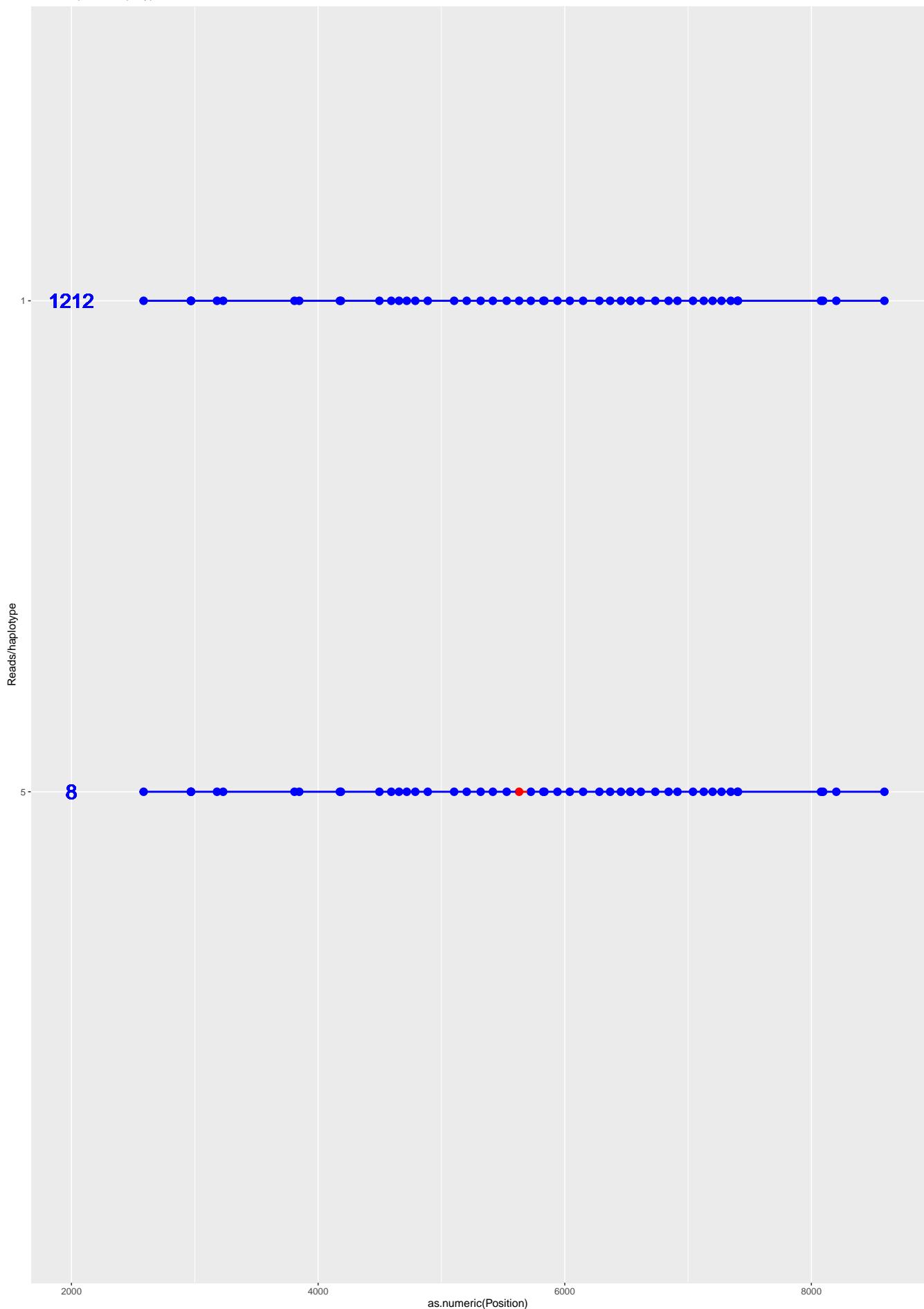
barcode = TCATGAGTCGACACTA & CGTGTCTGCTACTCA

Sample = 122b tetrad = 122 spore = b

Total reads = 1415 PCR=302

haplotypes I began with n[supporting reads] = 8, 1212

most frequent 7 haplotypes.

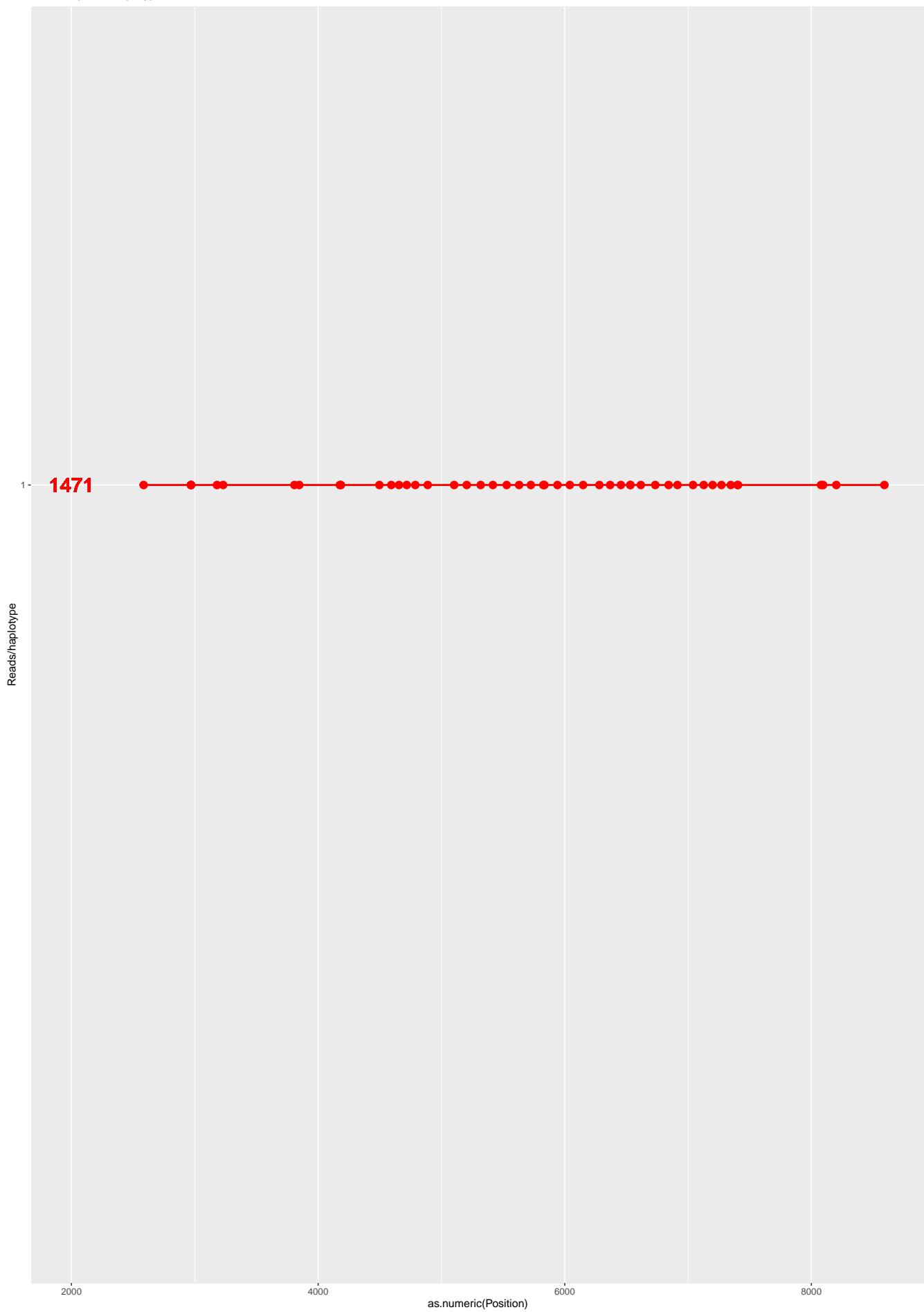


Sample = 122c tetrad = 122 spore = c

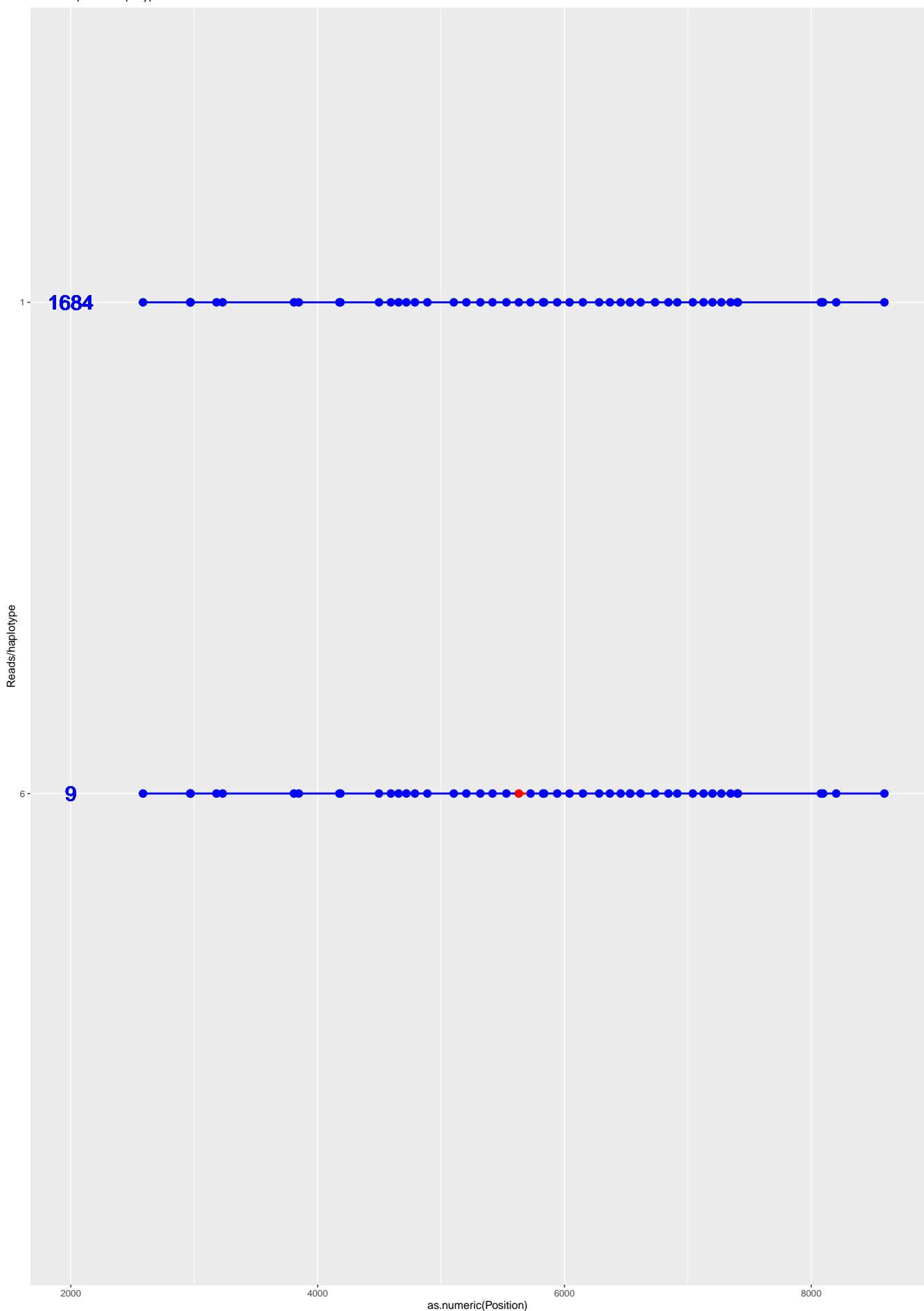
Total reads = 1550 PCR=303

haplotypes I began with n[supporting reads] = 1471

most frequent 7 haplotypes.



Sample = 122d tetrad = 122 spore = d
Total reads = 1954 PCR=304
haplotypes I began with n[supporting reads] = 9, 1684
most frequent 7 haplotypes.



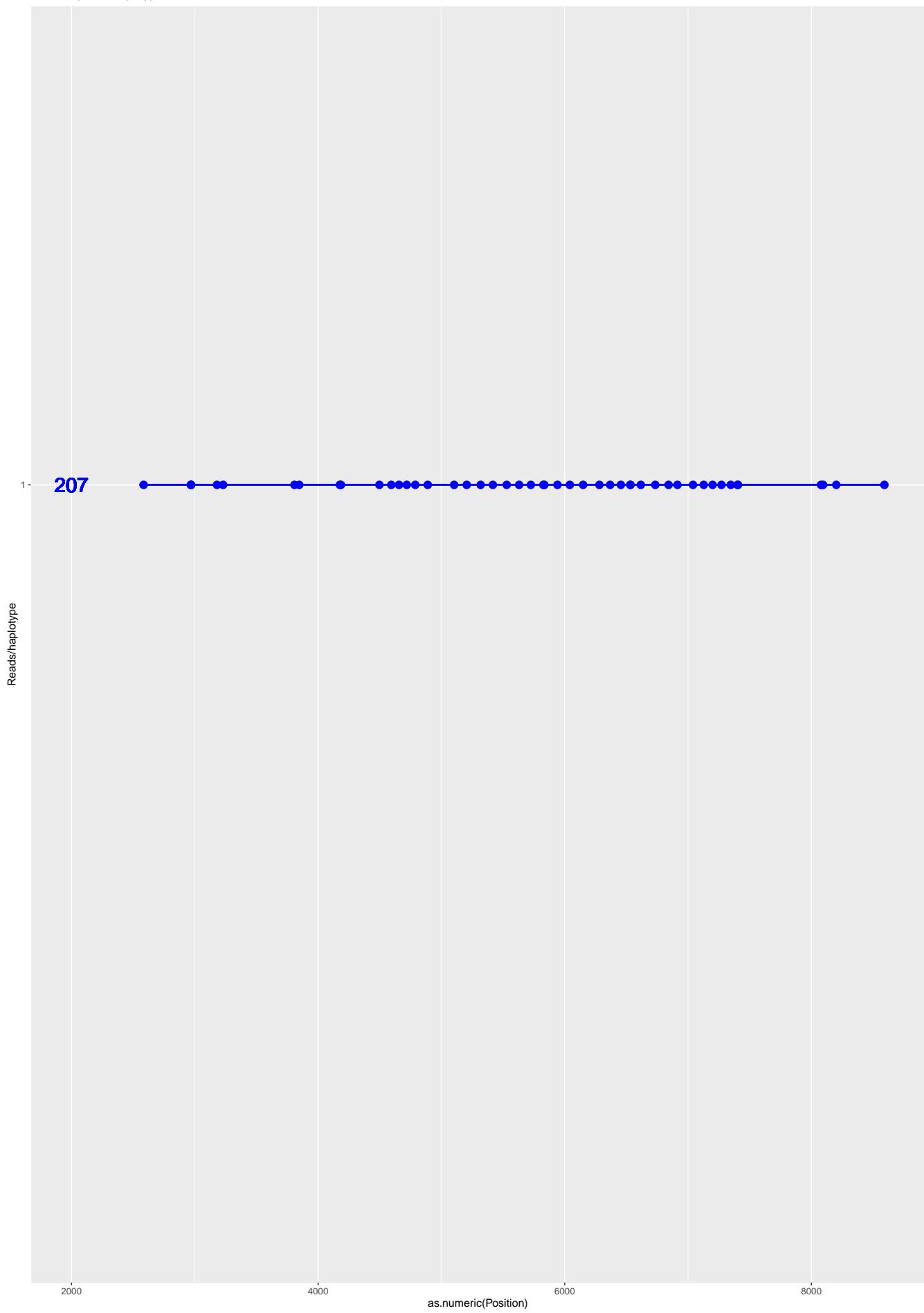
barcode = TCATGAGTCGACACTA & ACTATCGCGCACGCAG

Sample = 123a tetrad = 123 spore = a

Total reads = 234 PCR=305

haplotypes I began with n[supporting reads] = 207

most frequent 7 haplotypes.



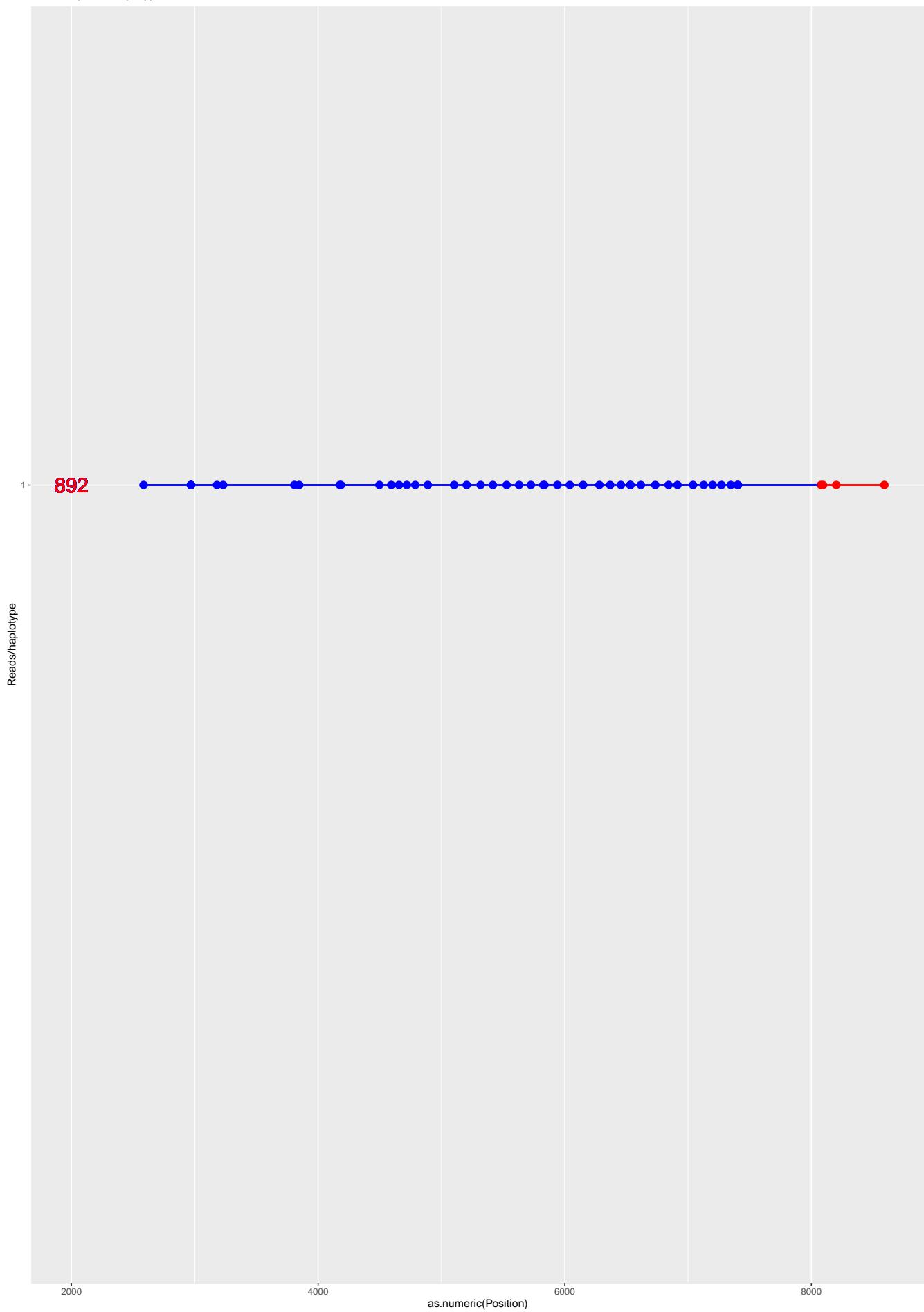
barcode = TATCTATCGTATAACGC & GCGACGAGTACTCATG

Sample = 123b tetrad = 123 spore = b

Total reads = 1028 PCR=306

haplotypes I began with n[supporting reads] = 892

most frequent 7 haplotypes.



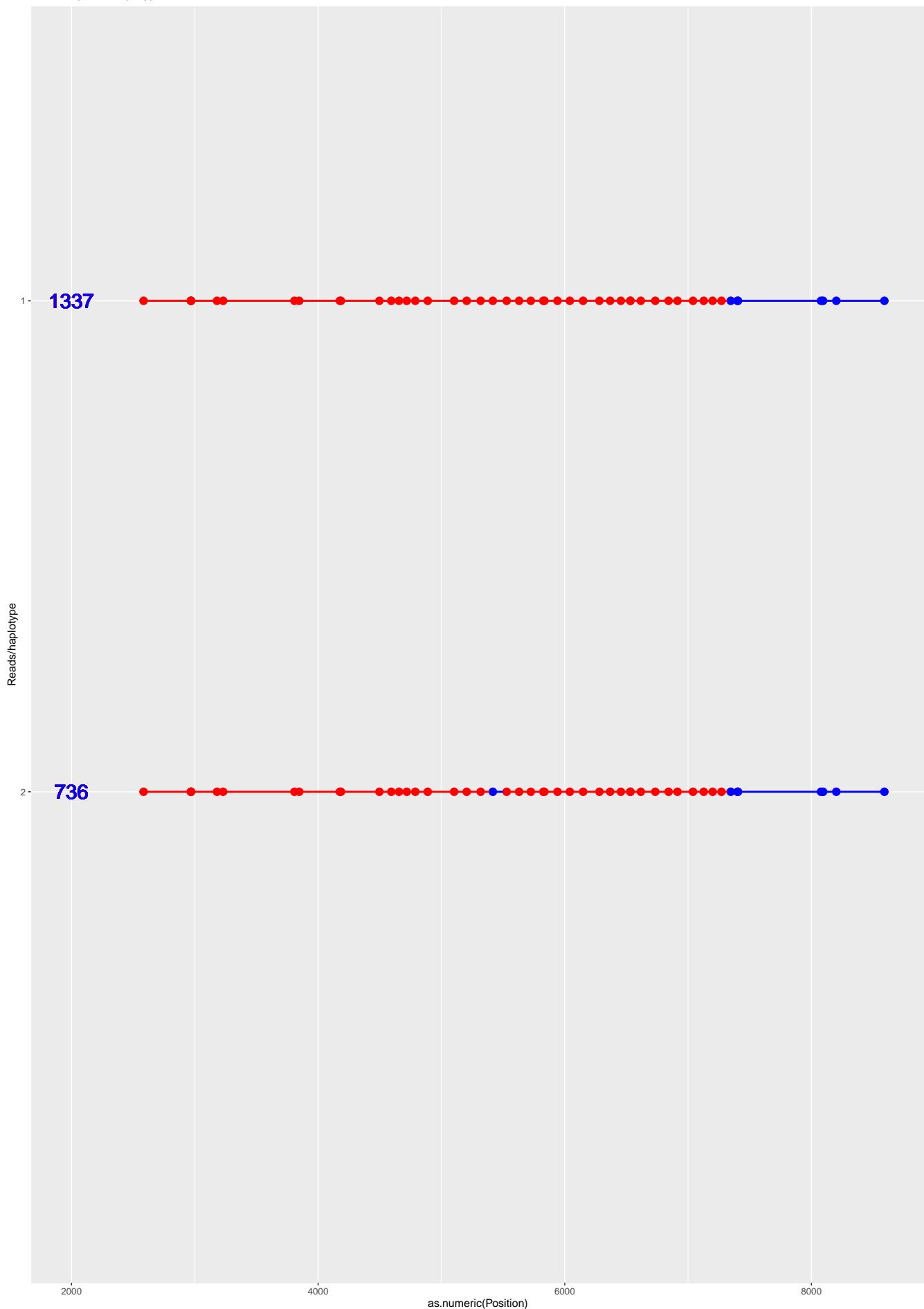
barcode = TATCTATCGTATAACGC & AGTATCACAGTCGCTG

Sample = 123c tetrad = 123 spore = c

Total reads = 2268 PCR=307

haplotypes I began with n[supporting reads] = 736, 1337

most frequent 7 haplotypes.



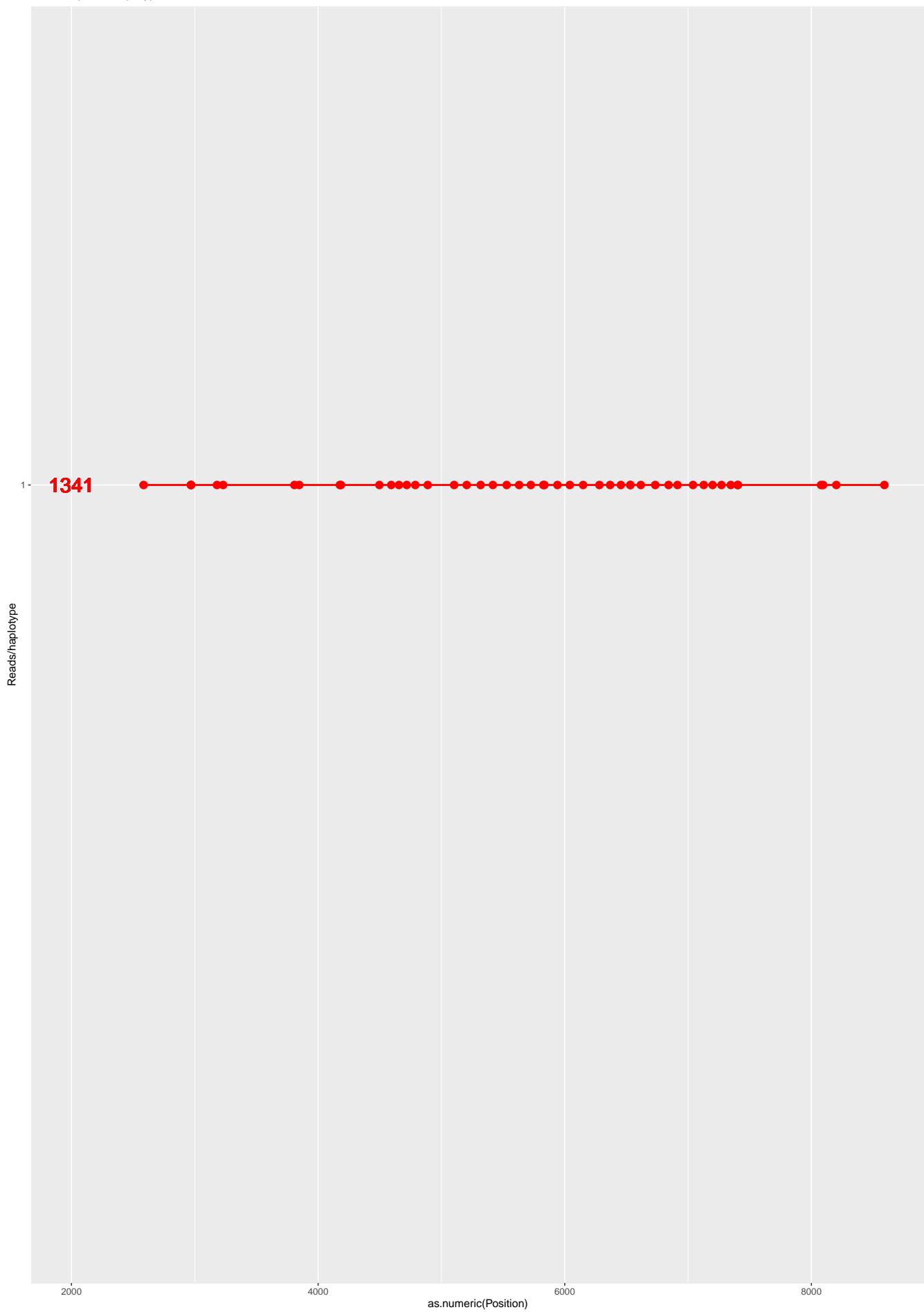
barcode = TATCTATCGTATACGC & ATCATATGATGCGACA

Sample = 123d tetrad = 123 spore = d

Total reads = 1383 PCR=308

haplotypes I began with n[supporting reads] = 1341

most frequent 7 haplotypes.



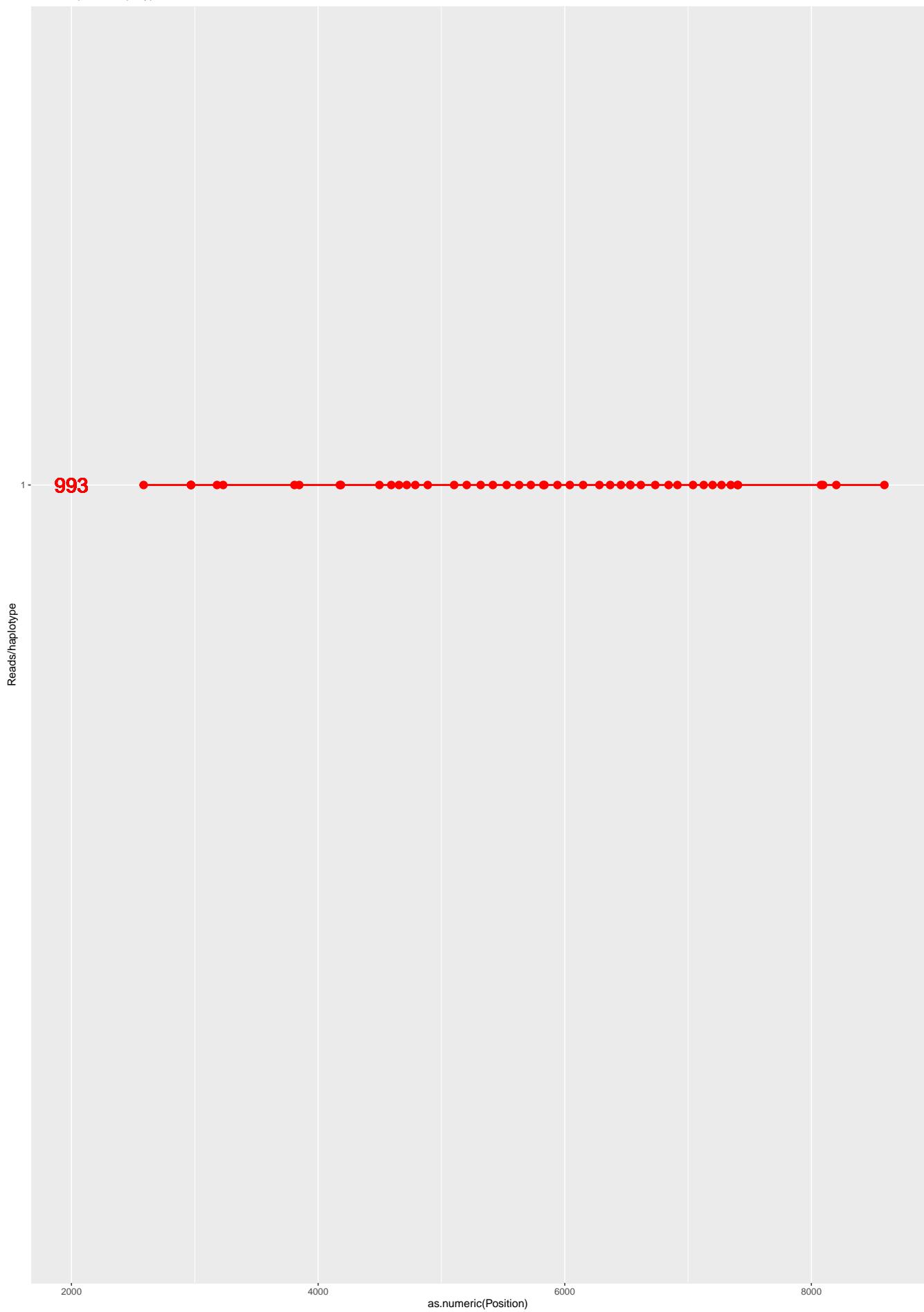
barcode = TATCTATCGTATAACGC & AGACGTTAGATCACAGC

Sample = 124a tetrad = 124 spore = a

Total reads = 1045 PCR=309

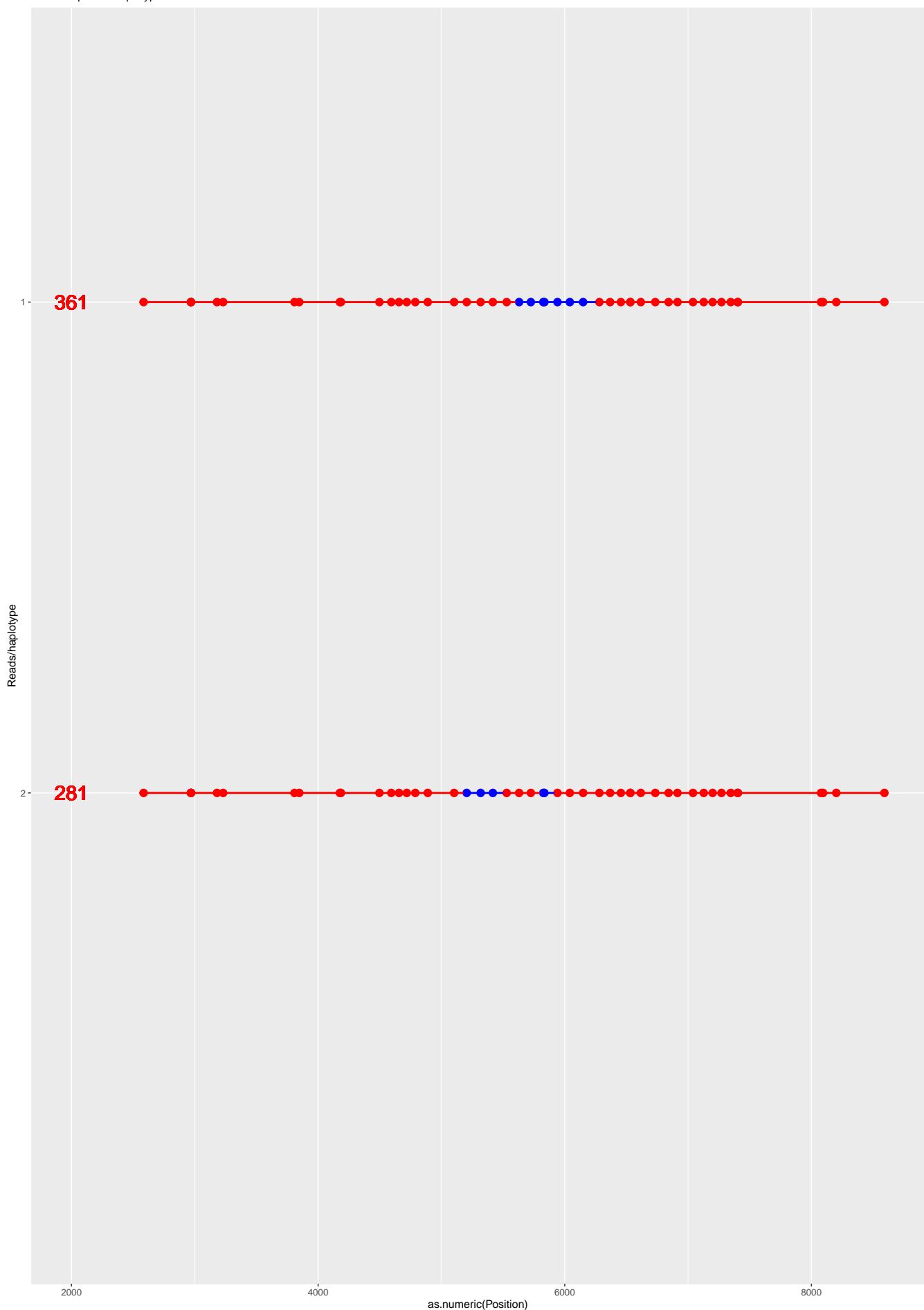
haplotypes I began with n[supporting reads] = 993

most frequent 7 haplotypes.



barcode = TATCTATCGTATAACGC & CGTGTCATGCTACTCA

Sample = 124b tetrad = 124 spore = b
Total reads = 865 PCR=310
haplotypes I began with n[supporting reads] = 281, 361
most frequent 7 haplotypes.



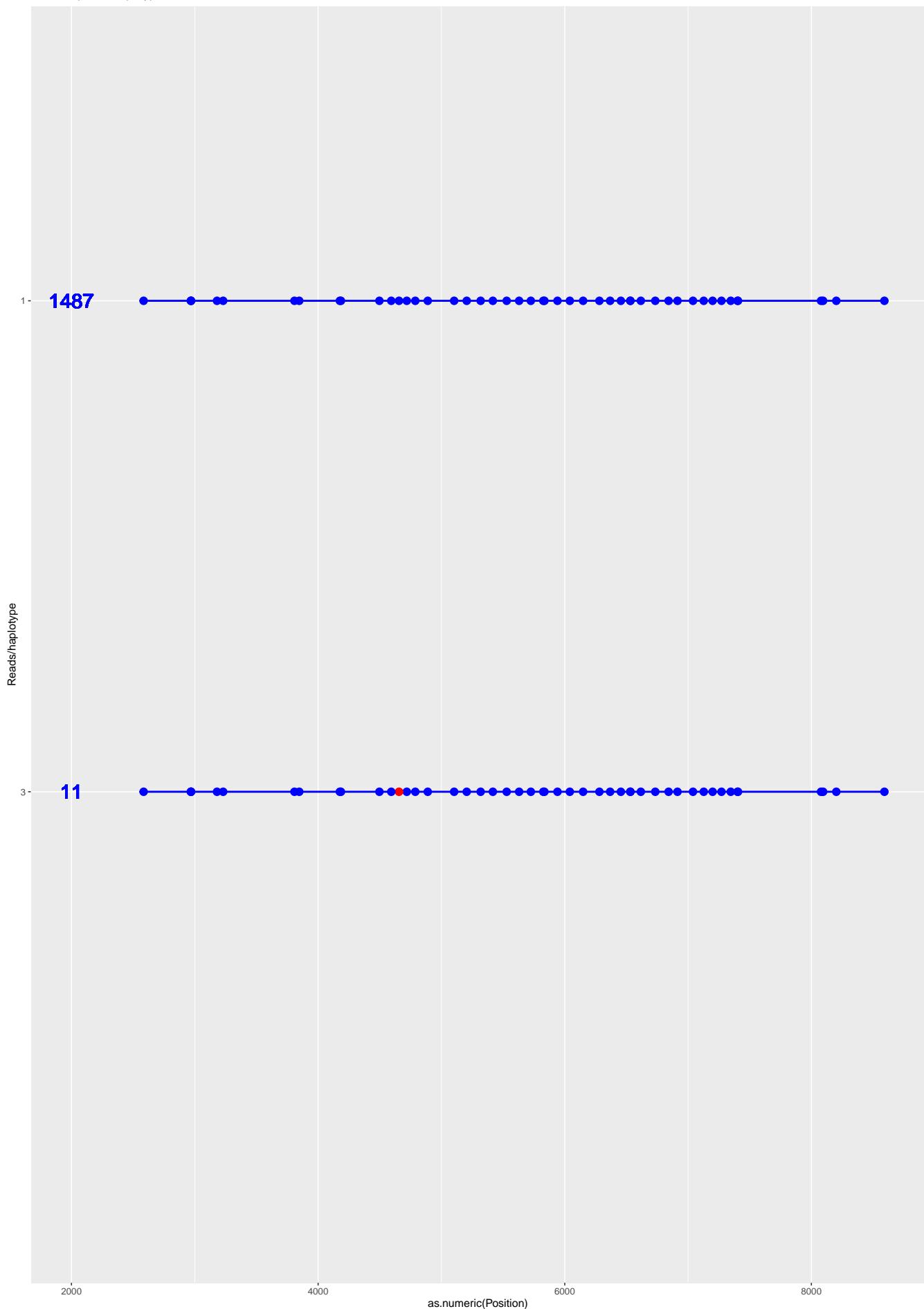
barcode = TATCTATCGTATAACGC & TGTGAGACTGCATGTC

Sample = 124c tetrad = 124 spore = c

Total reads = 1704 PCR=311

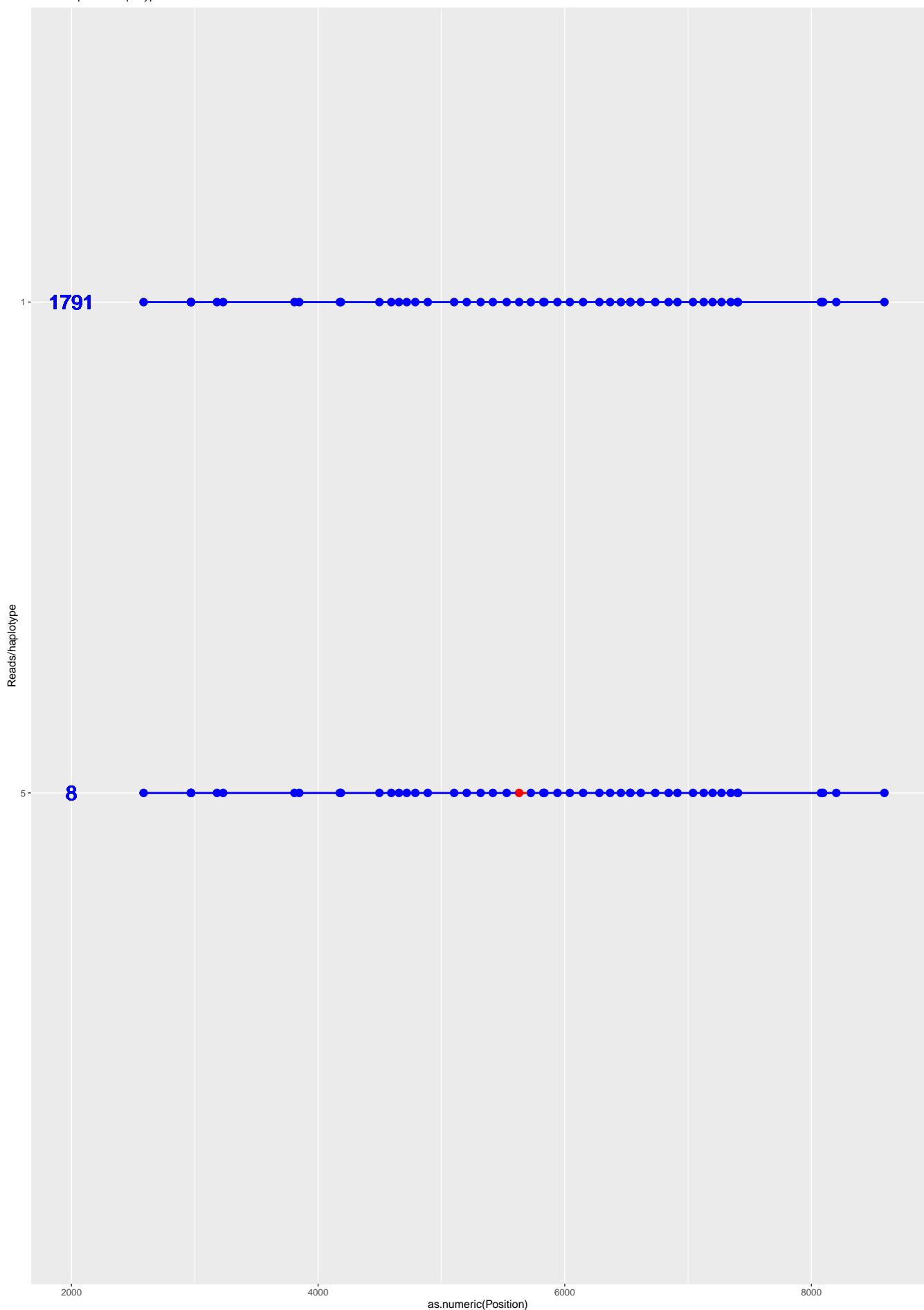
haplotypes I began with n[supporting reads] = 11, 1487

most frequent 7 haplotypes.



barcode = TATCTATCGTATACGC & GCTCAGTGCCTACTG

Sample = 124d tetrad = 124 spore = d
Total reads = 2085 PCR=312
haplotypes I began with n[supporting reads] = 8, 1791
most frequent 7 haplotypes.



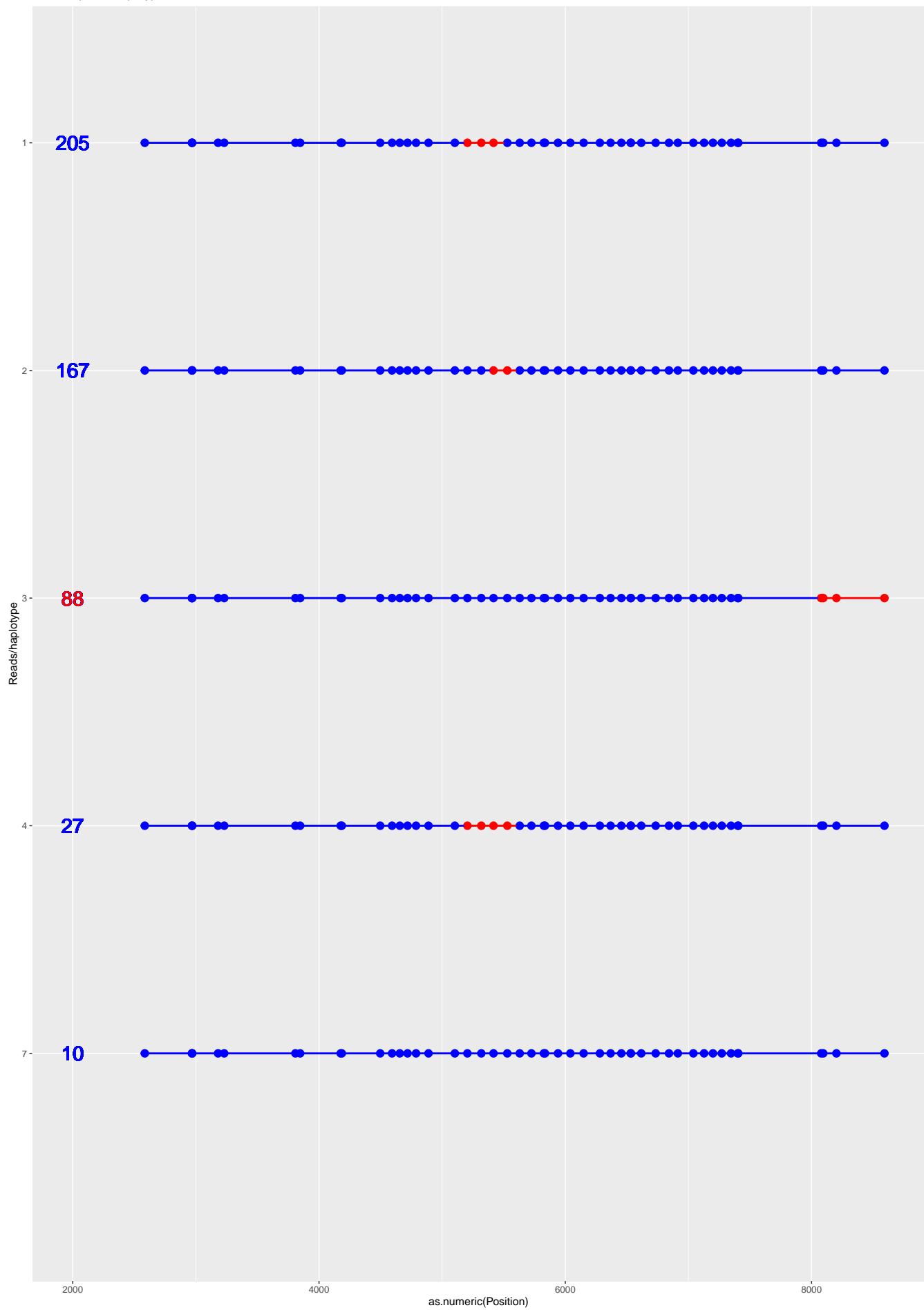
barcode = TATCTATCGTATAACGC & ACTATCGCGCACGCAG

Sample = 126a tetrad = 126 spore = a

Total reads = 727 PCR=313

haplotypes I began with n[supporting reads] = 10, 27, 88, 167, 205

most frequent 7 haplotypes.



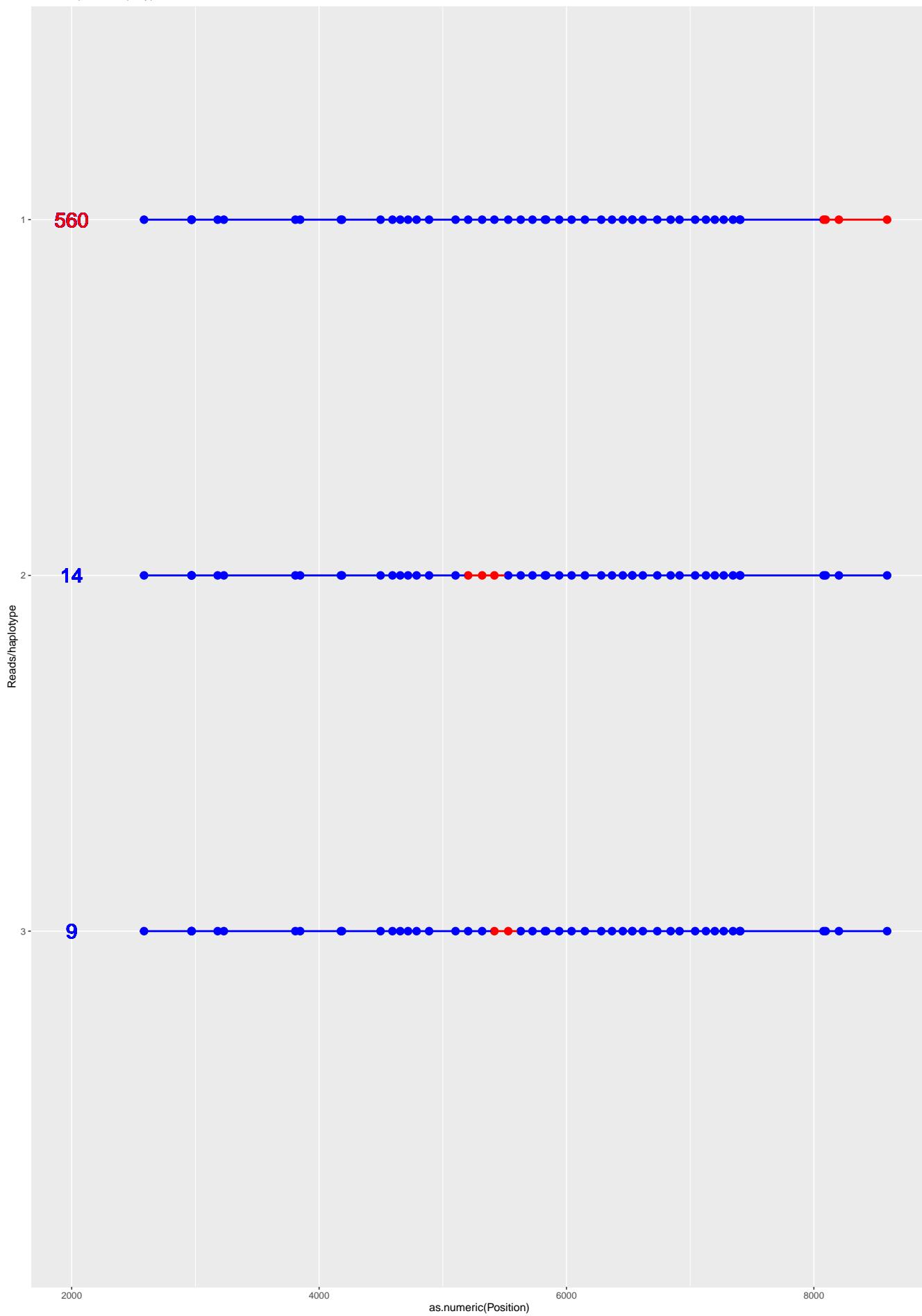
barcode = ATCACACTGCATCTGA & GCGACGAGTACTCATG

Sample = 126b tetrad = 126 spore = b

Total reads = 681 PCR=314

haplotypes I began with n[supporting reads] = 9, 14, 560

most frequent 7 haplotypes.

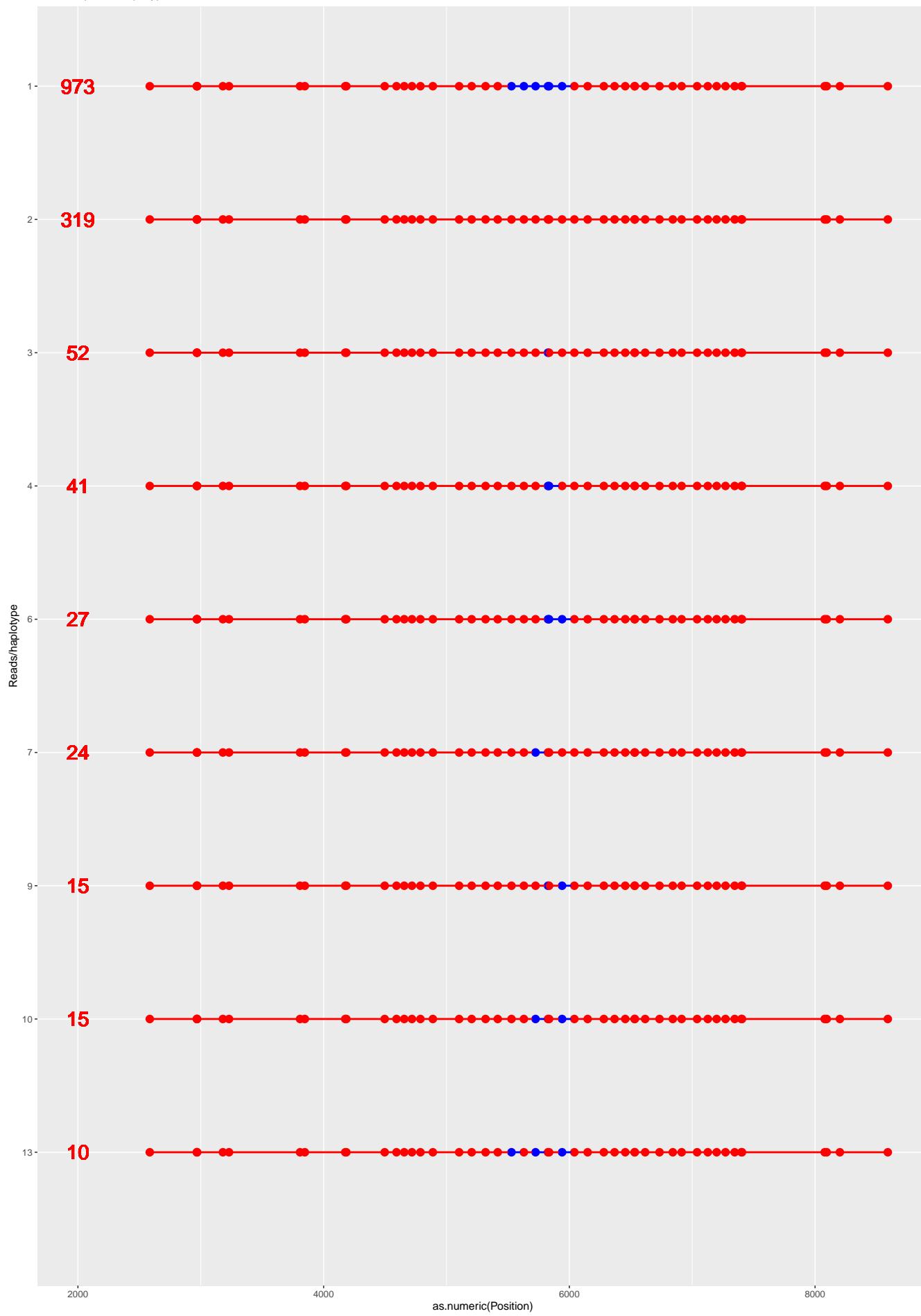


Sample = 126c tetrad = 126 spore = c

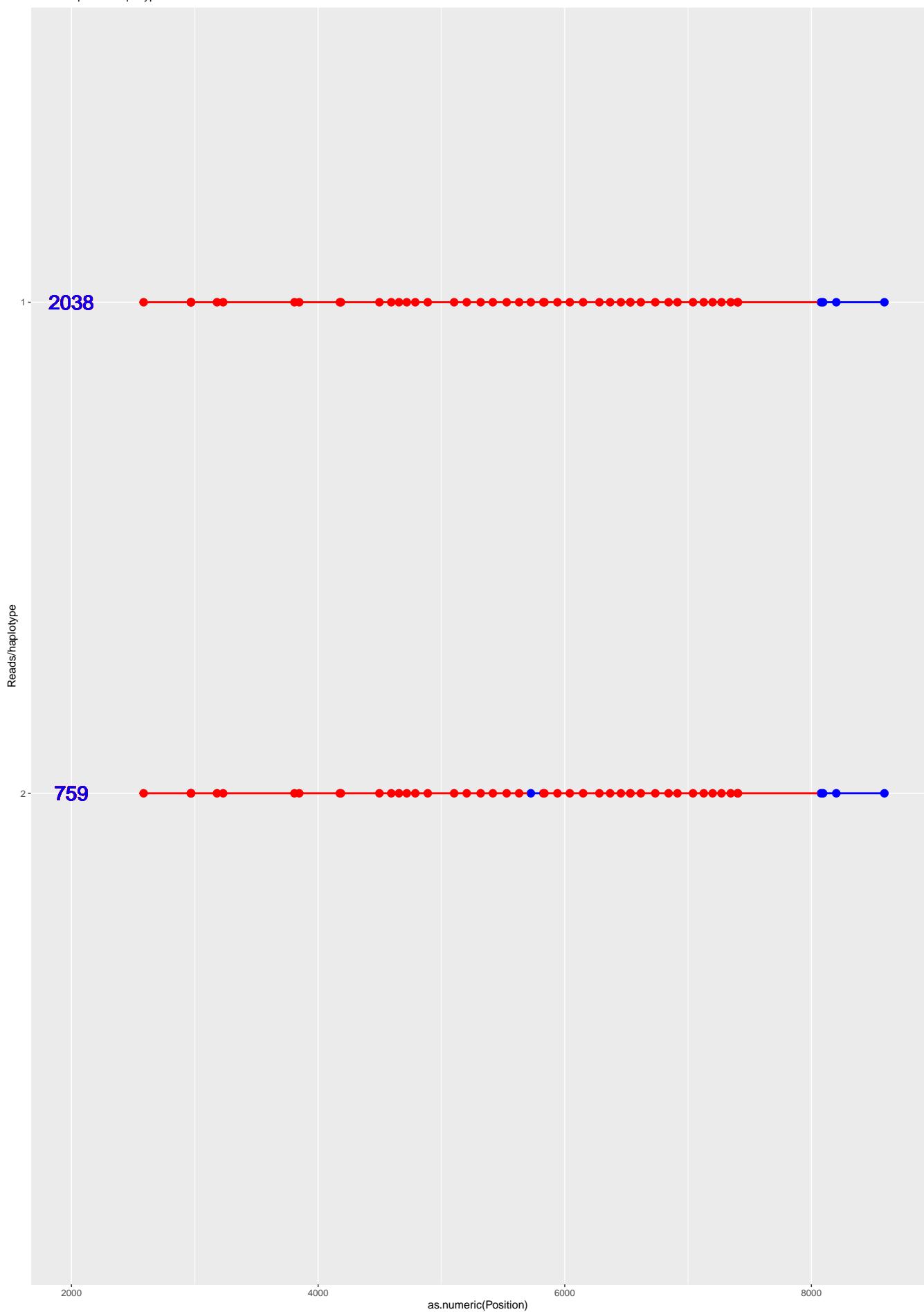
Total reads = 1730 PCR=315

haplotypes I began with [n:supporting reads] = 10, 15, 24, 27, 41, 52, 319, 973

most frequent 7 haplotypes.



Sample = 126d tetrad = 126 spore = d
Total reads = 2963 PCR=316
haplotypes I began with n[supporting reads] = 759, 2038
most frequent 7 haplotypes.



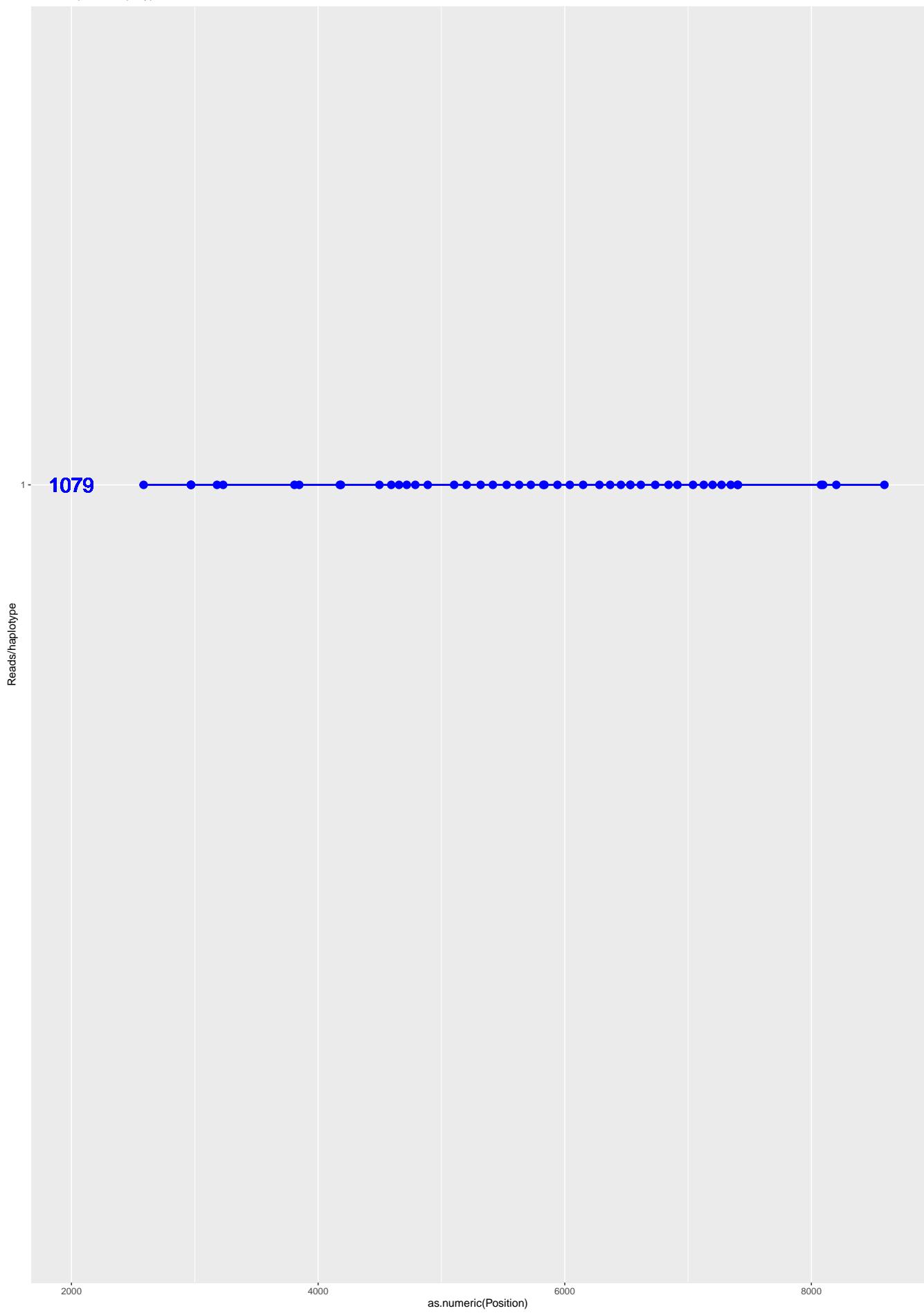
barcode = ATCACACTGCATCTGA & AGACGTTAGATCACAGC

Sample = 128a tetrad = 128 spore = a

Total reads = 1227 PCR=317

haplotypes I began with n[supporting reads] = 1079

most frequent 7 haplotypes.

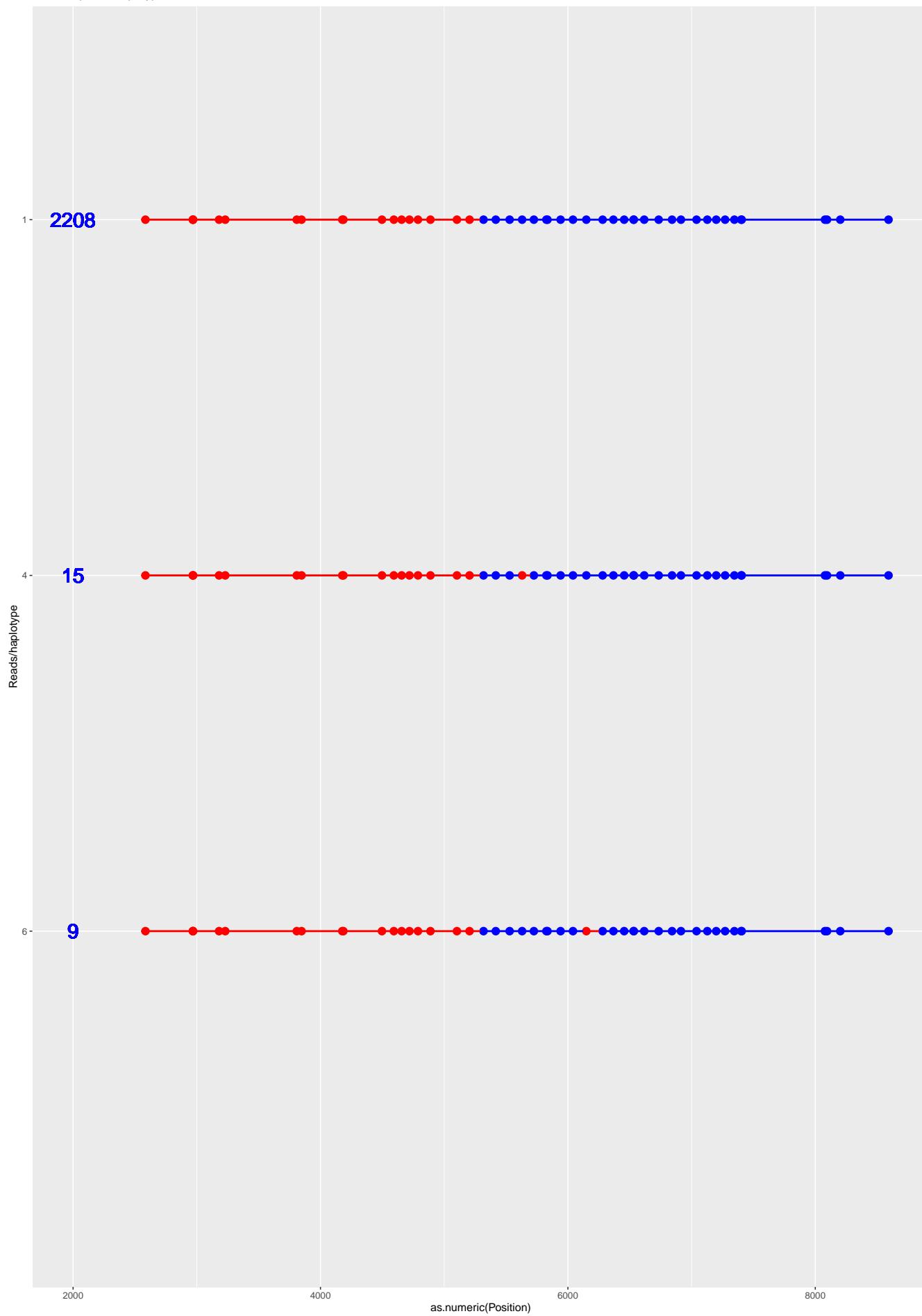


Sample = 128b tetrad = 128 spore = b

Total reads = 2494 PCR=318

haplotypes I began with n[supporting reads] = 9, 15, 2208

most frequent 7 haplotypes.

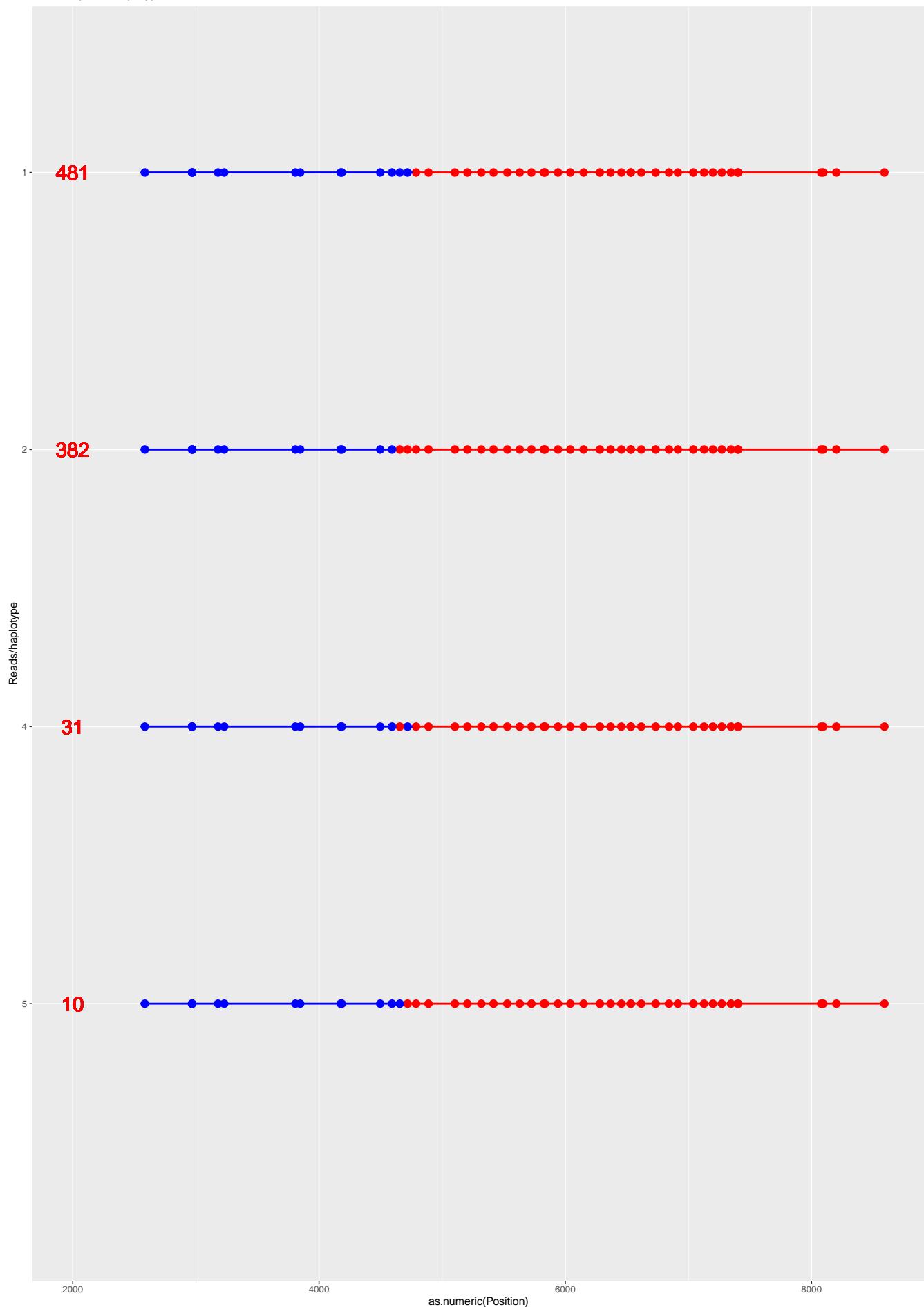


Sample = 128c tetrad = 128 spore = c

Total reads = 1013 PCR=319

haplotypes I began with n[supporting reads] = 10, 31, 382, 481

most frequent 7 haplotypes.



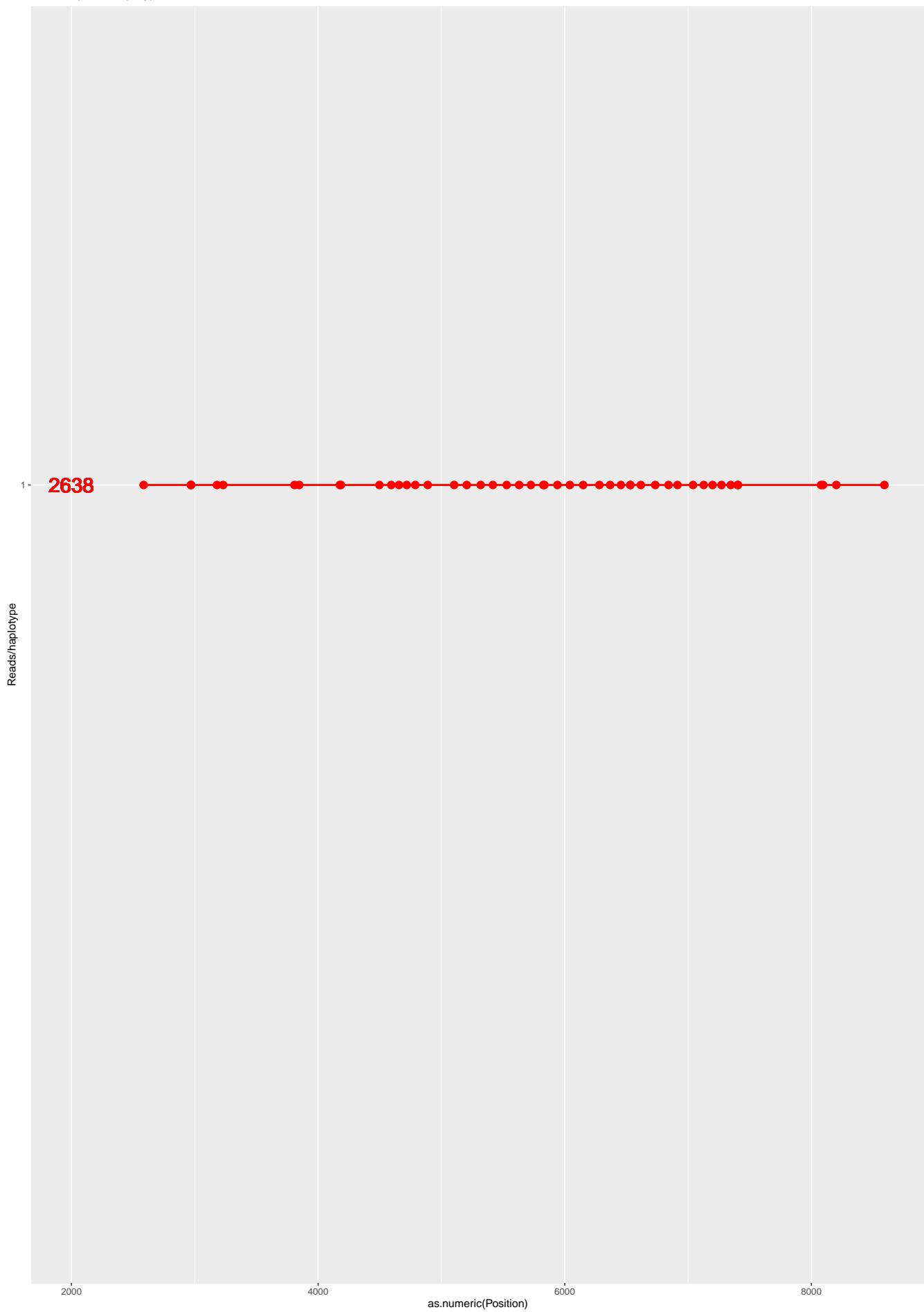
barcode = ATCACACTGCACTGA & GCTCAGTGCCTACTG

Sample = 128d tetrad = 128 spore = d

Total reads =2756 PCR=320

haplotypes I began with n[supporting reads] = 2638

most frequent 7 haplotypes.



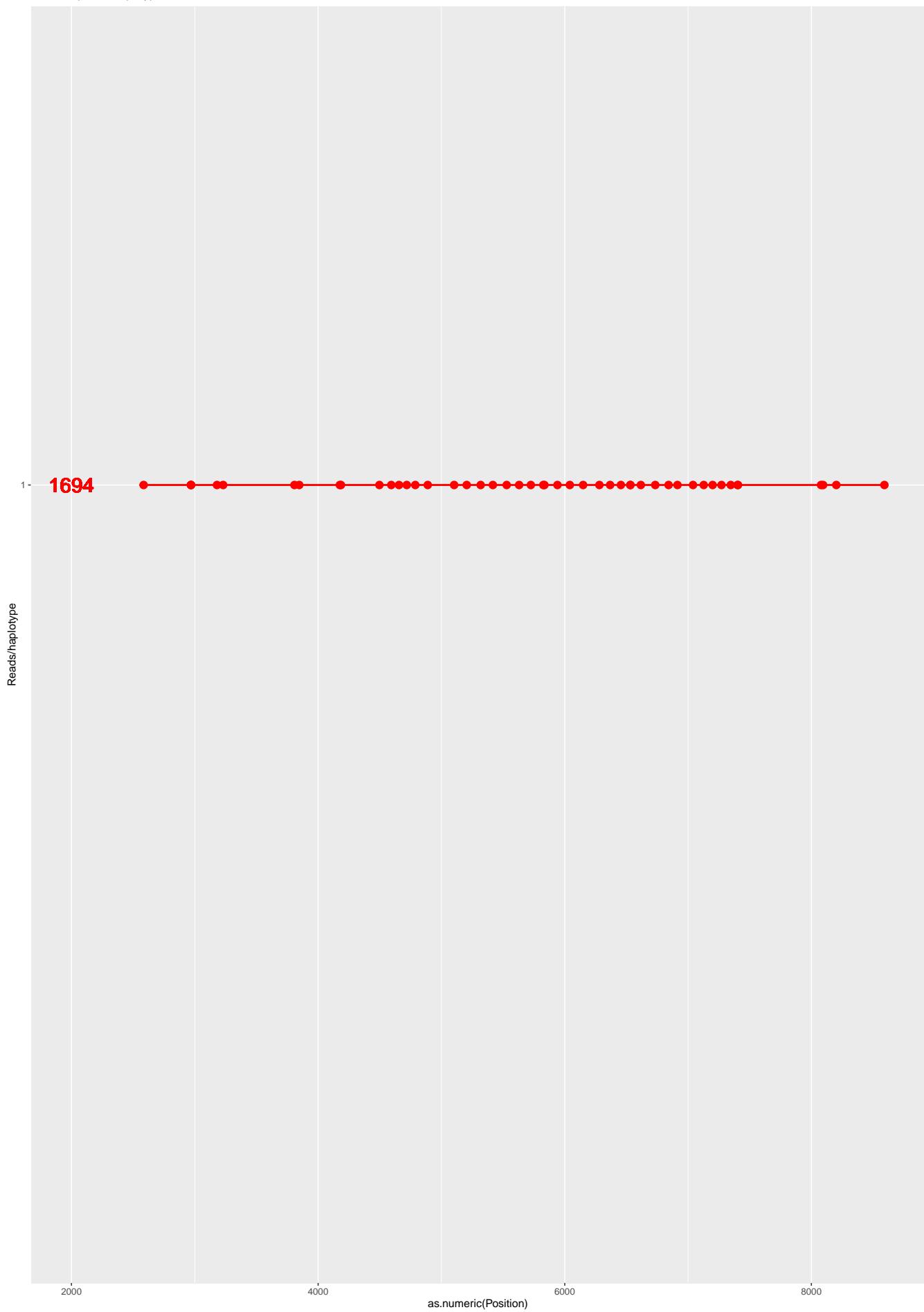
barcode = ATCACACTGCATCTGA & ACTATCGCGACGCAG

Sample = 129a tetrad = 129 spore = a

Total reads = 1761 PCR=321

haplotypes I began with n[supporting reads] = 1694

most frequent 7 haplotypes.

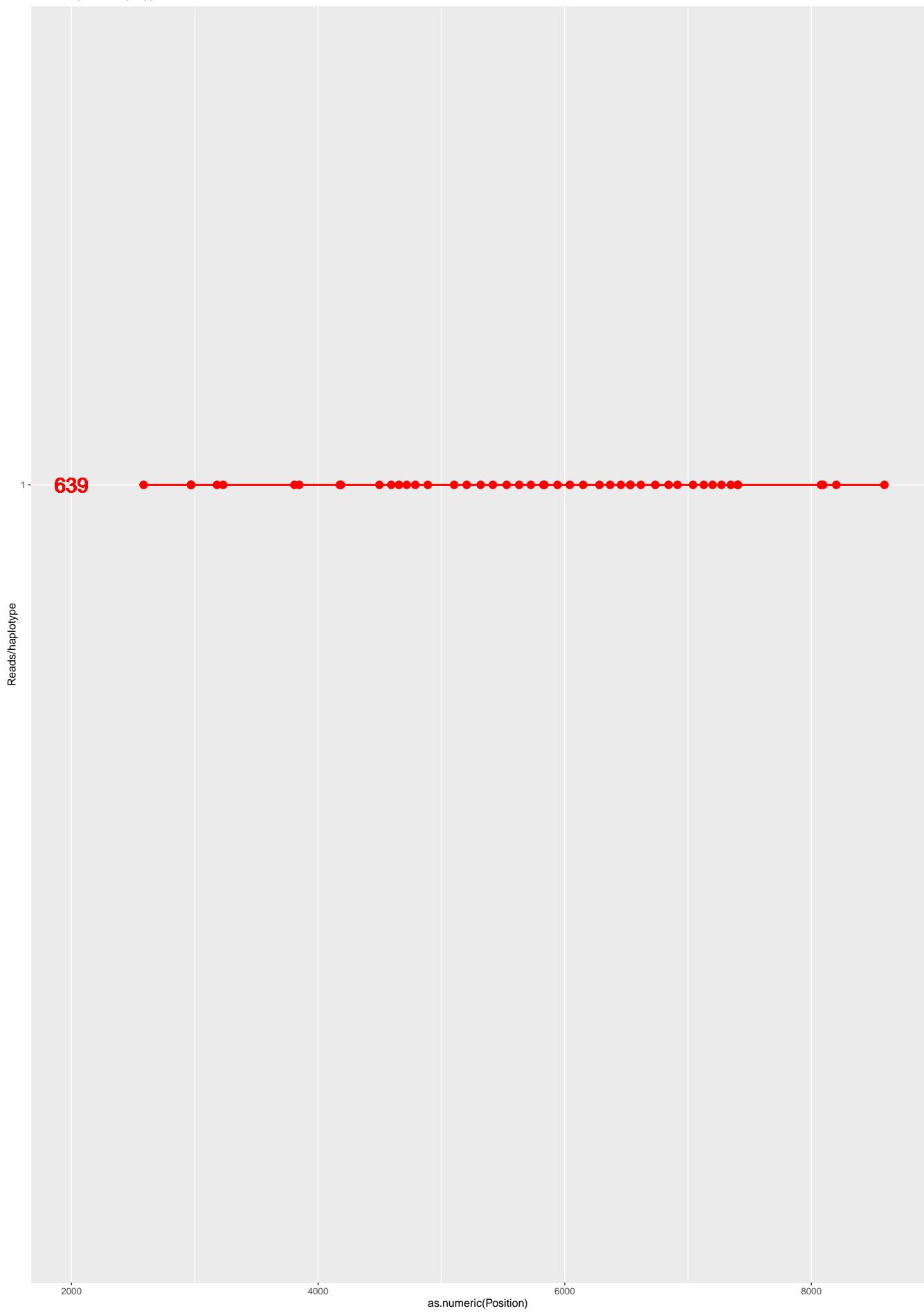


Sample = 129b tetrad = 129 spore = b

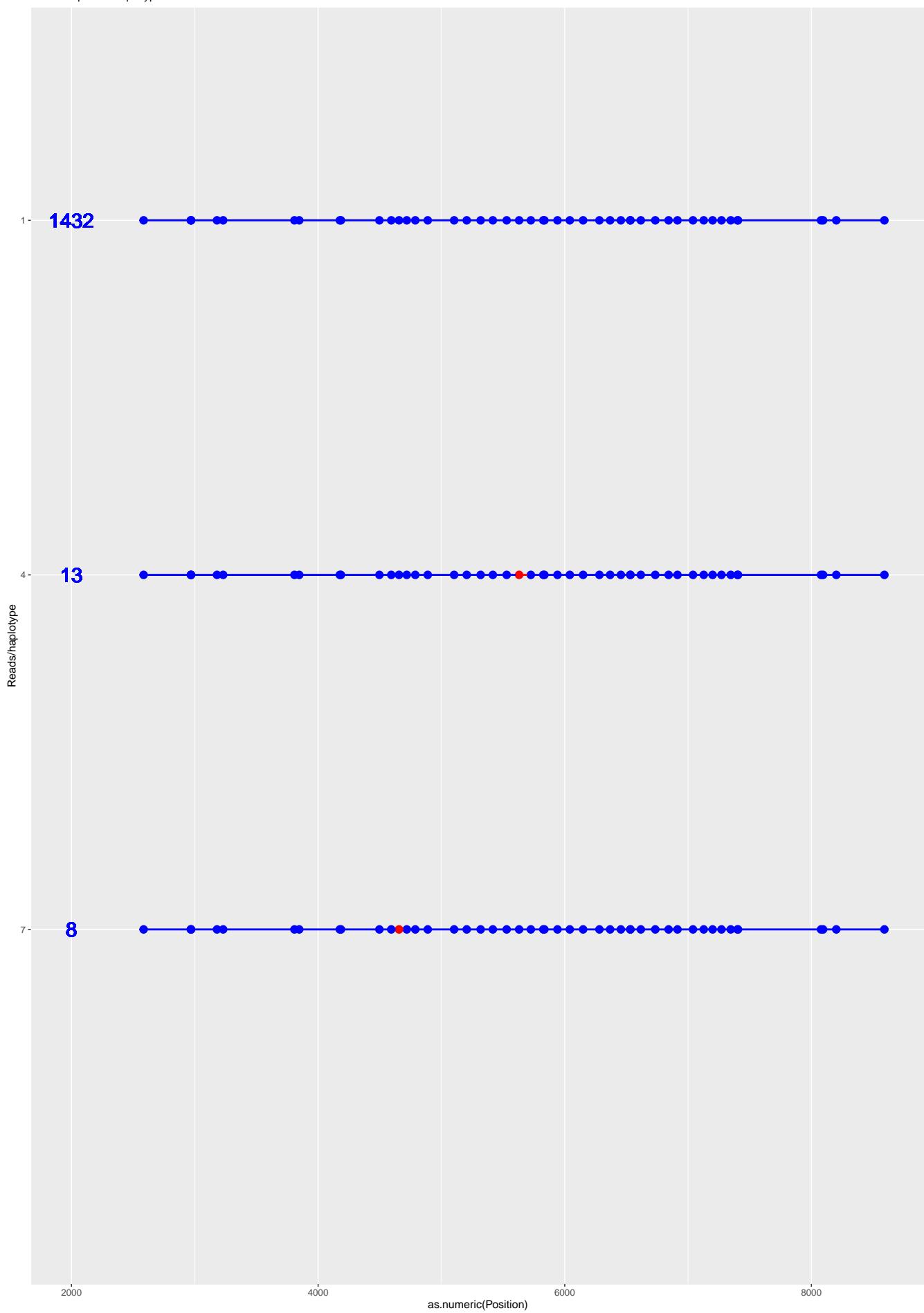
Total reads = 664 PCR=322

haplotypes I began with n[supporting reads] = 639

most frequent 7 haplotypes.



Sample = 129c tetrad = 129 spore = c
Total reads = 1705 PCR=323
haplotypes I began with n[supporting reads] = 8, 13, 1432
most frequent 7 haplotypes.



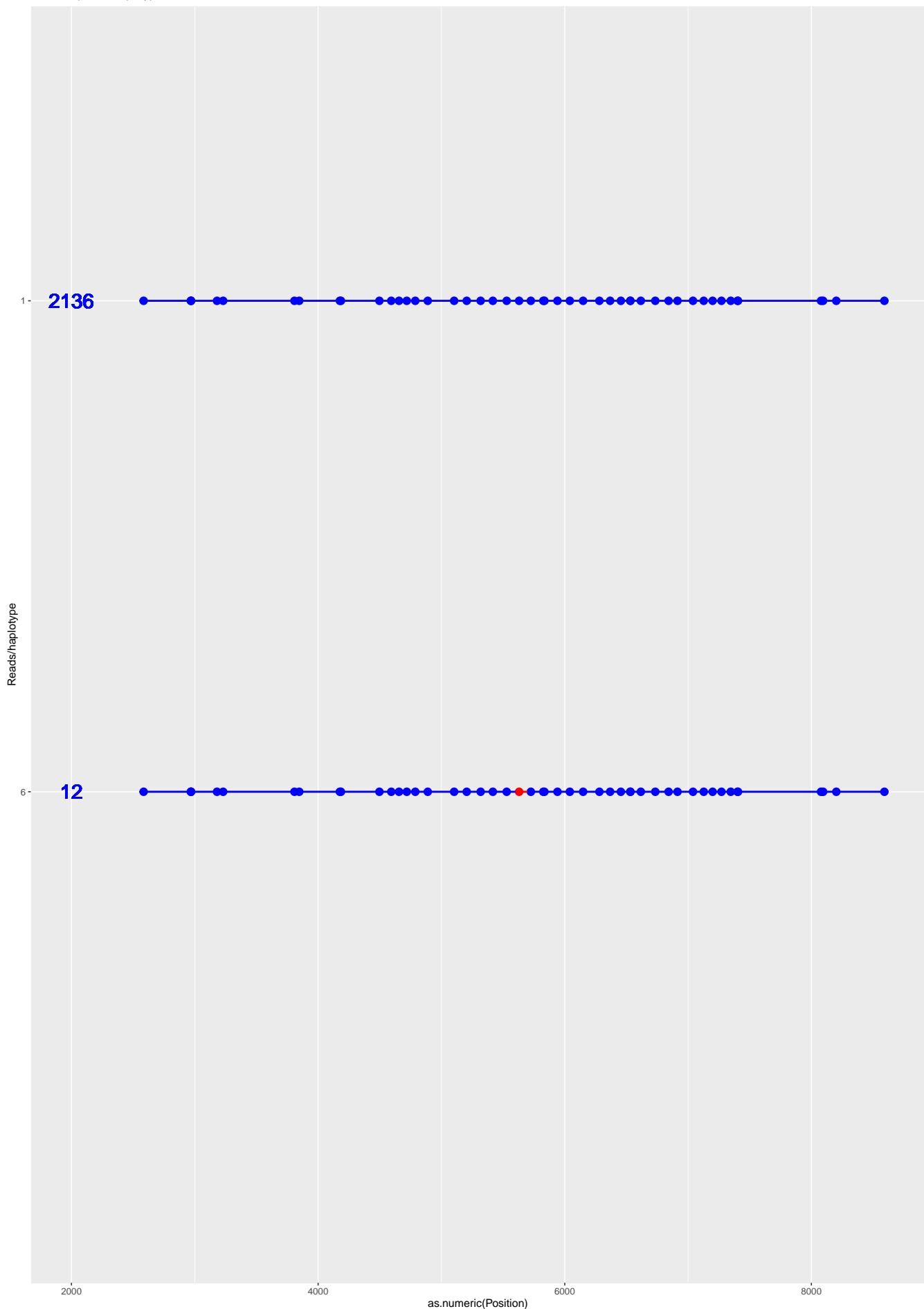
barcode = ACGTACGCTCGTCATA & ATCATATGATGCGACA

Sample = 129d tetrad = 129 spore = d

Total reads = 2477 PCR=324

haplotypes I began with n[supporting reads] = 12, 2136

most frequent 7 haplotypes.

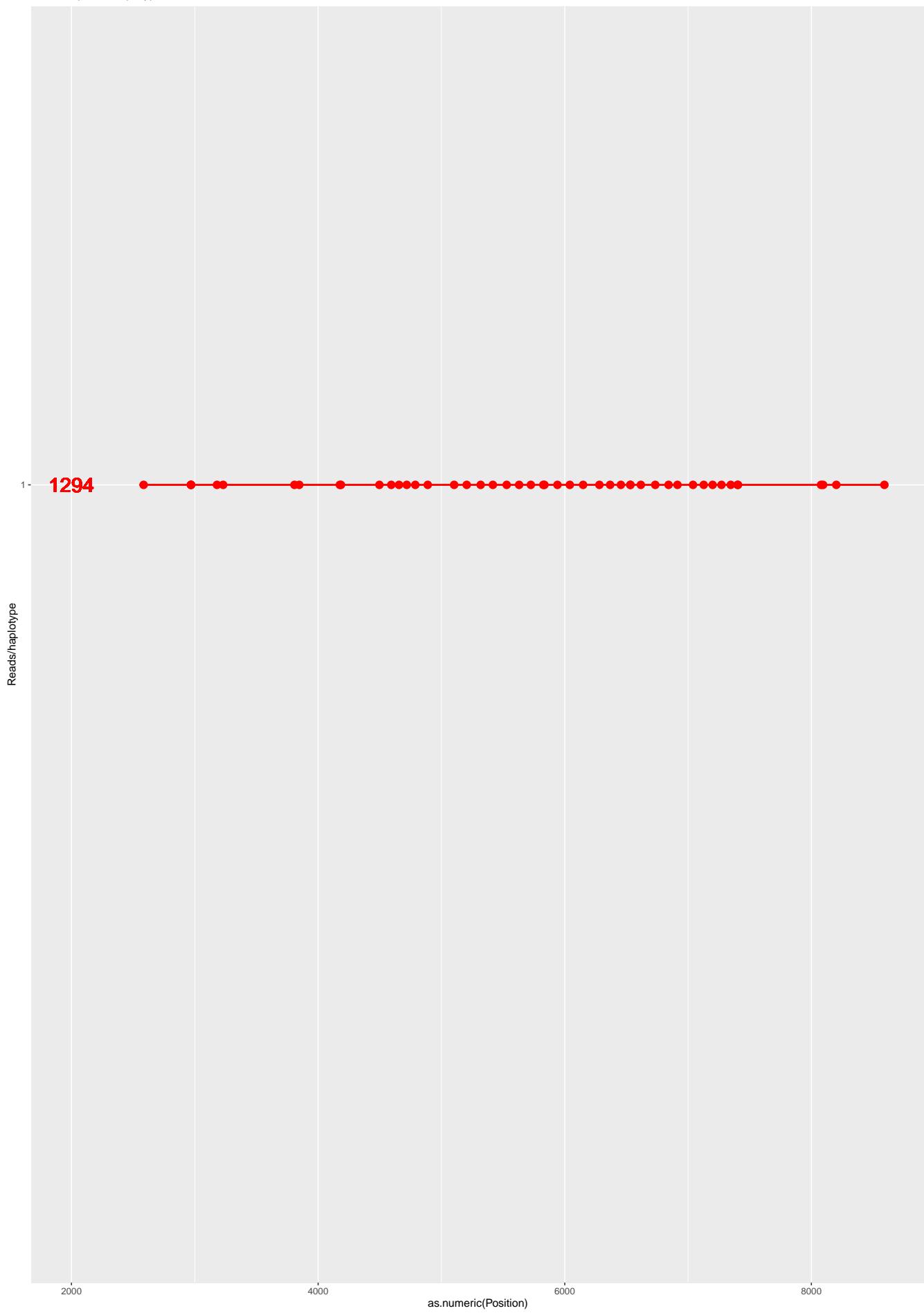


Sample = 130a tetrad = 130 spore = a

Total reads = 1344 PCR=325

haplotypes I began with n[supporting reads] = 1294

most frequent 7 haplotypes.

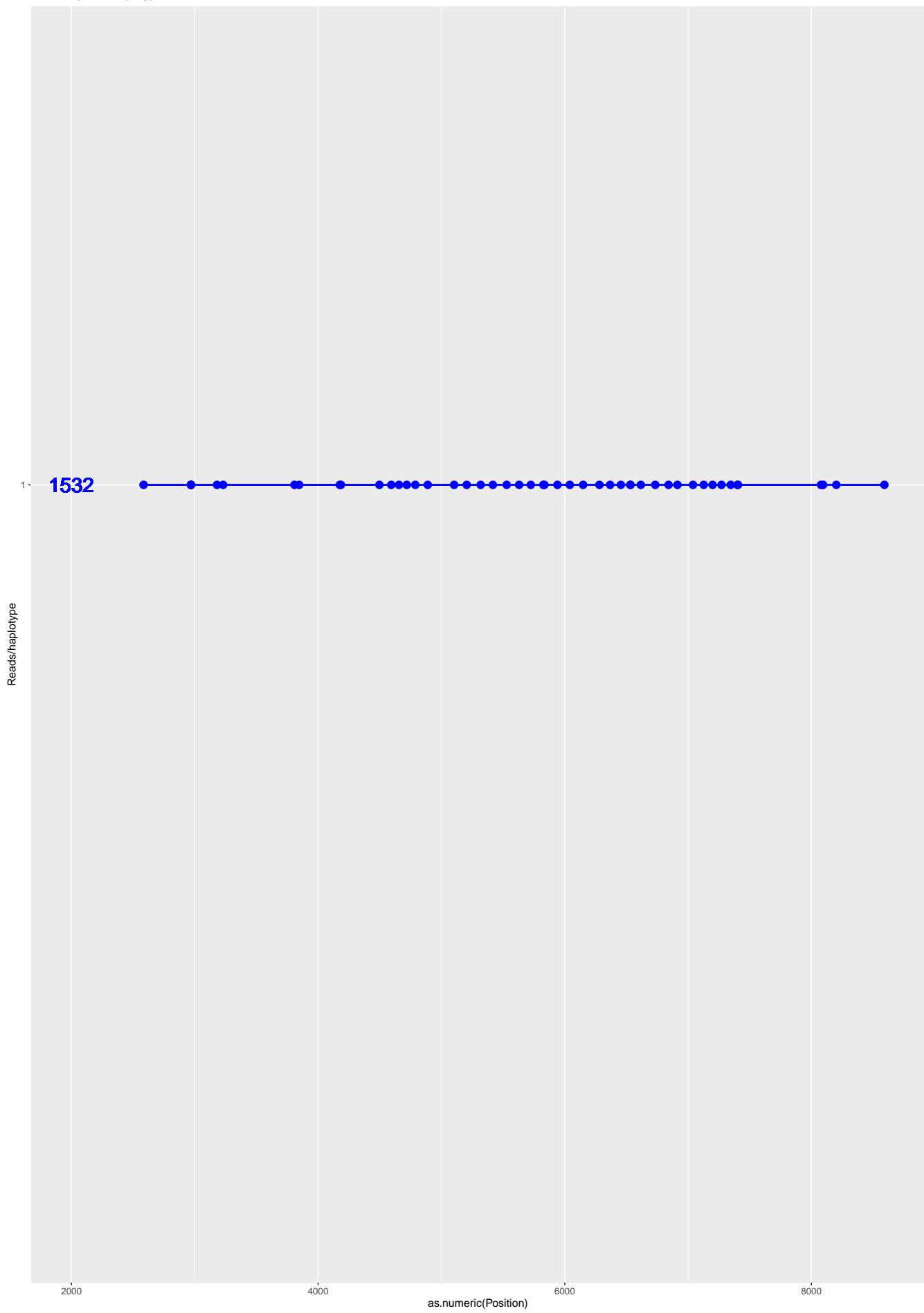


Sample = 130b tetrad = 130 spore = b

Total reads = 1782 PCR=326

haplotypes I began with n[supporting reads] = 1532

most frequent 7 haplotypes.



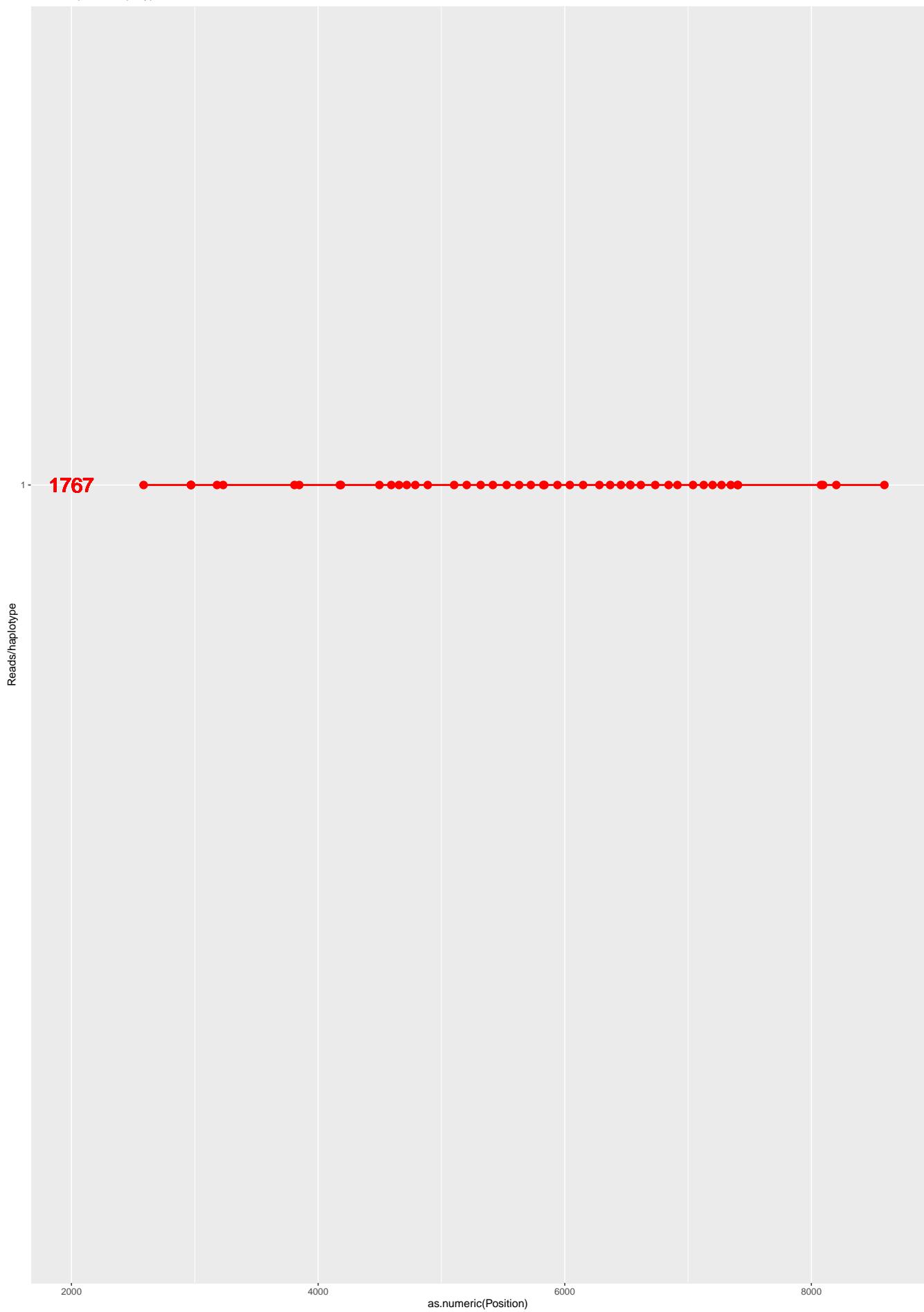
barcode = ACGTACGCTCGTCATA & TGTGAGACTGCATGTC

Sample = 130c tetrad = 130 spore = c

Total reads = 1842 PCR=327

haplotypes I began with n[supporting reads] = 1767

most frequent 7 haplotypes.



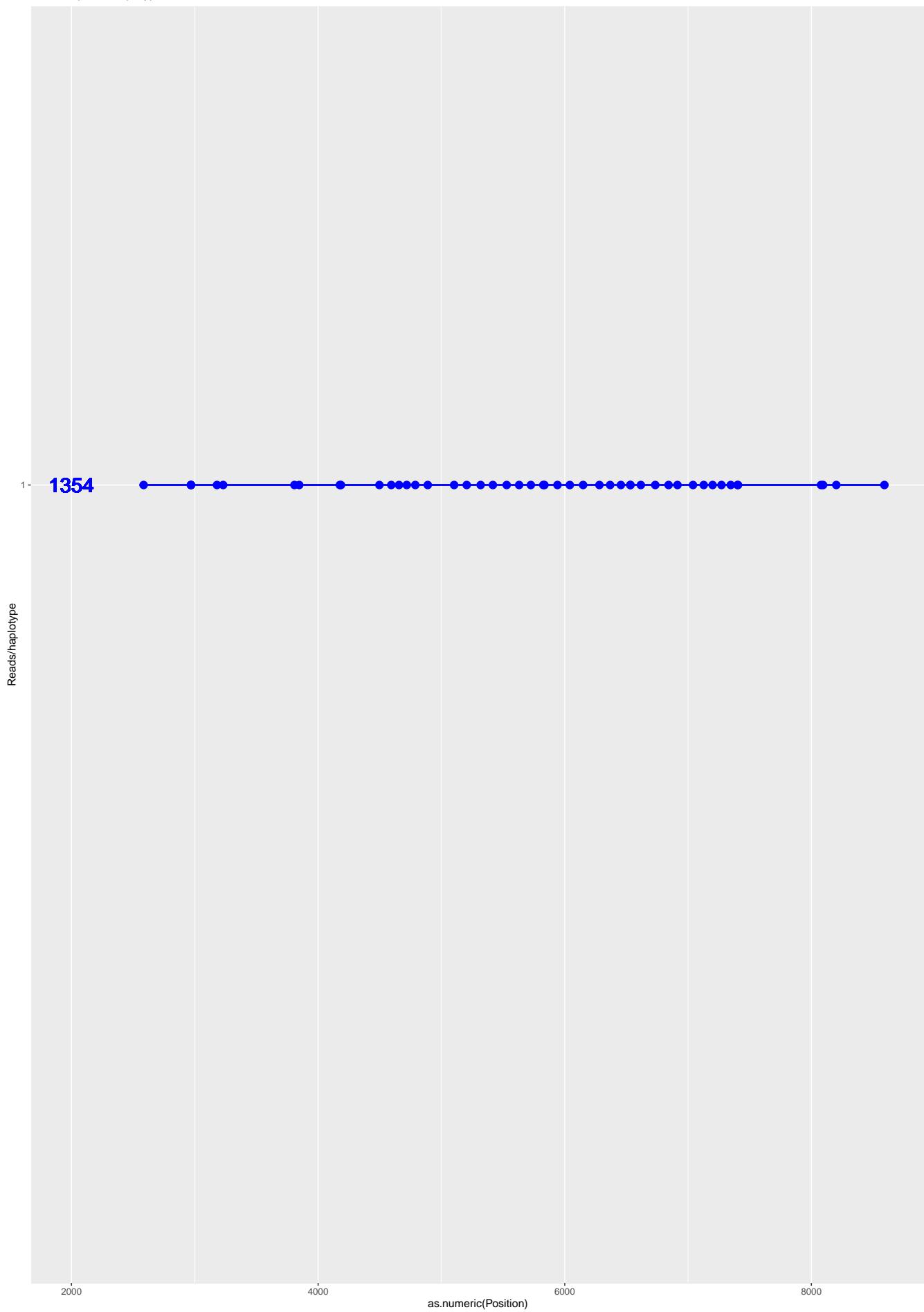
barcode = ACGTACGCTCGTCATA & GCTCAGTGCCTACTG

Sample = 130d tetrad = 130 spore = d

Total reads = 1560 PCR=328

haplotypes I began with n[supporting reads] = 1354

most frequent 7 haplotypes.

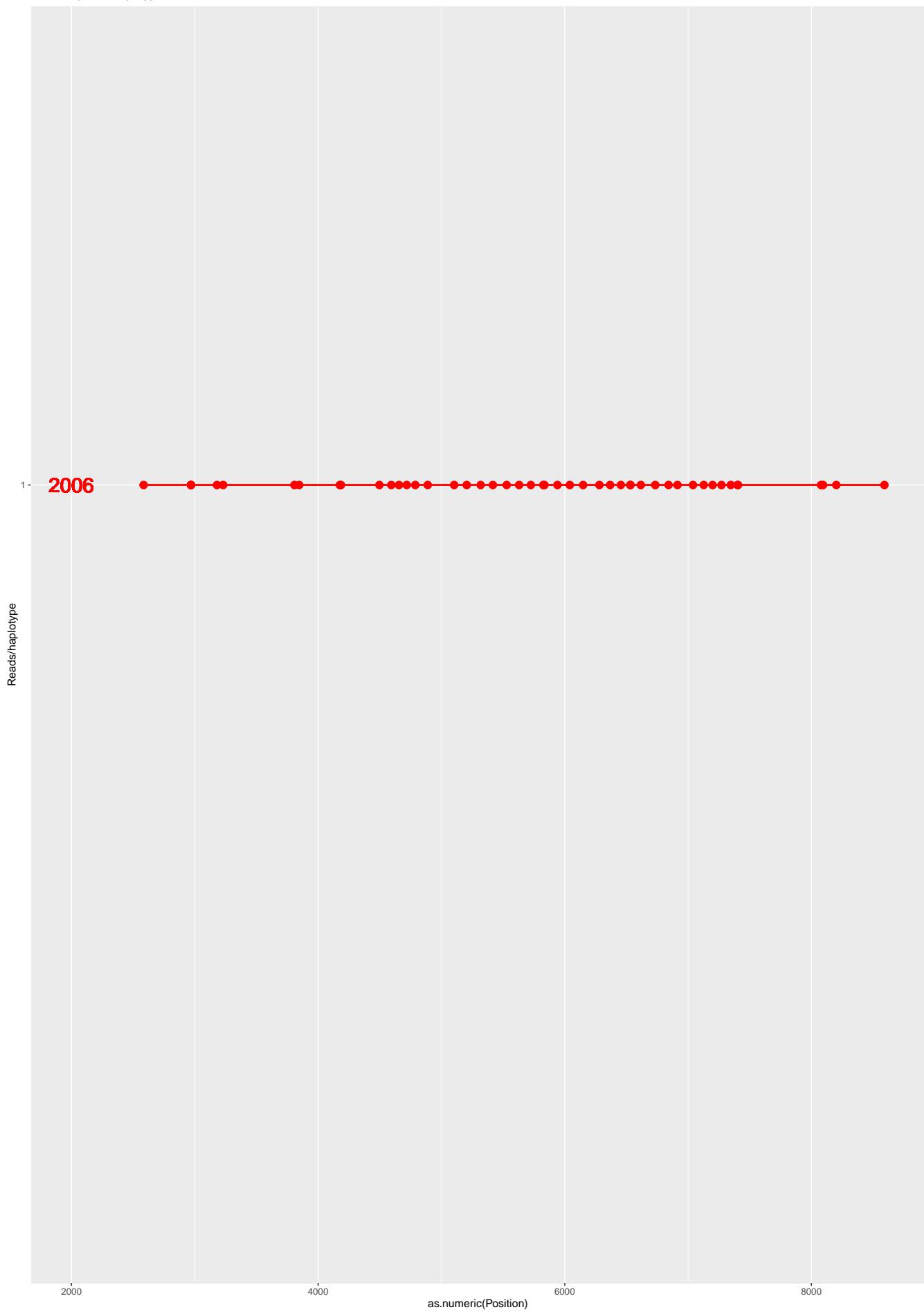


Sample = 131a tetrad = 131 spore = a

Total reads =2067 PCR=329

haplotypes I began with n[supporting reads] = 2006

most frequent 7 haplotypes.



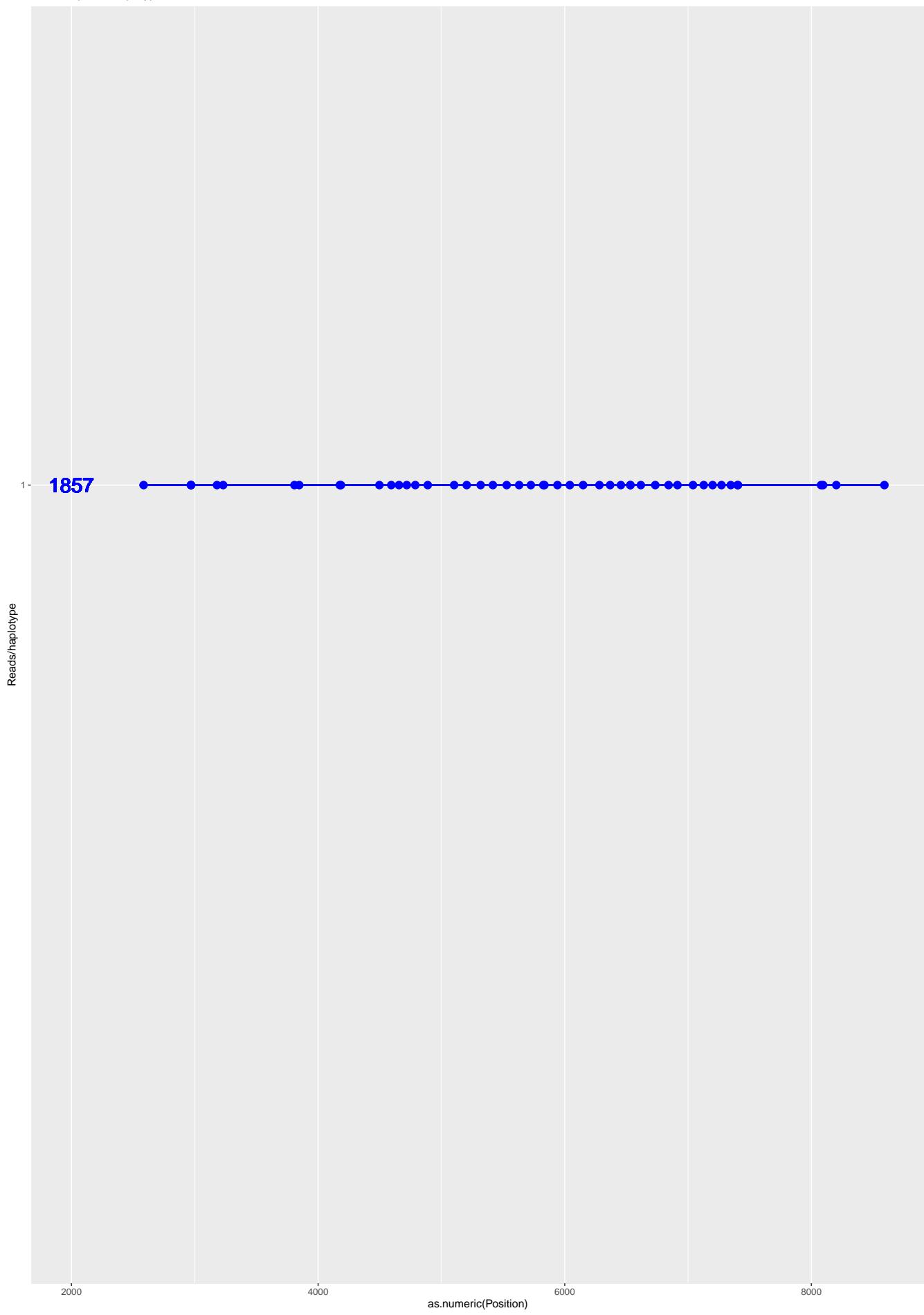
barcode = TGTGAGTCAGTACCGCG & GCGACGAGTACTCATG

Sample = 131b tetrad = 131 spore = b

Total reads = 2164 PCR=330

haplotypes I began with n[supporting reads] = 1857

most frequent 7 haplotypes.



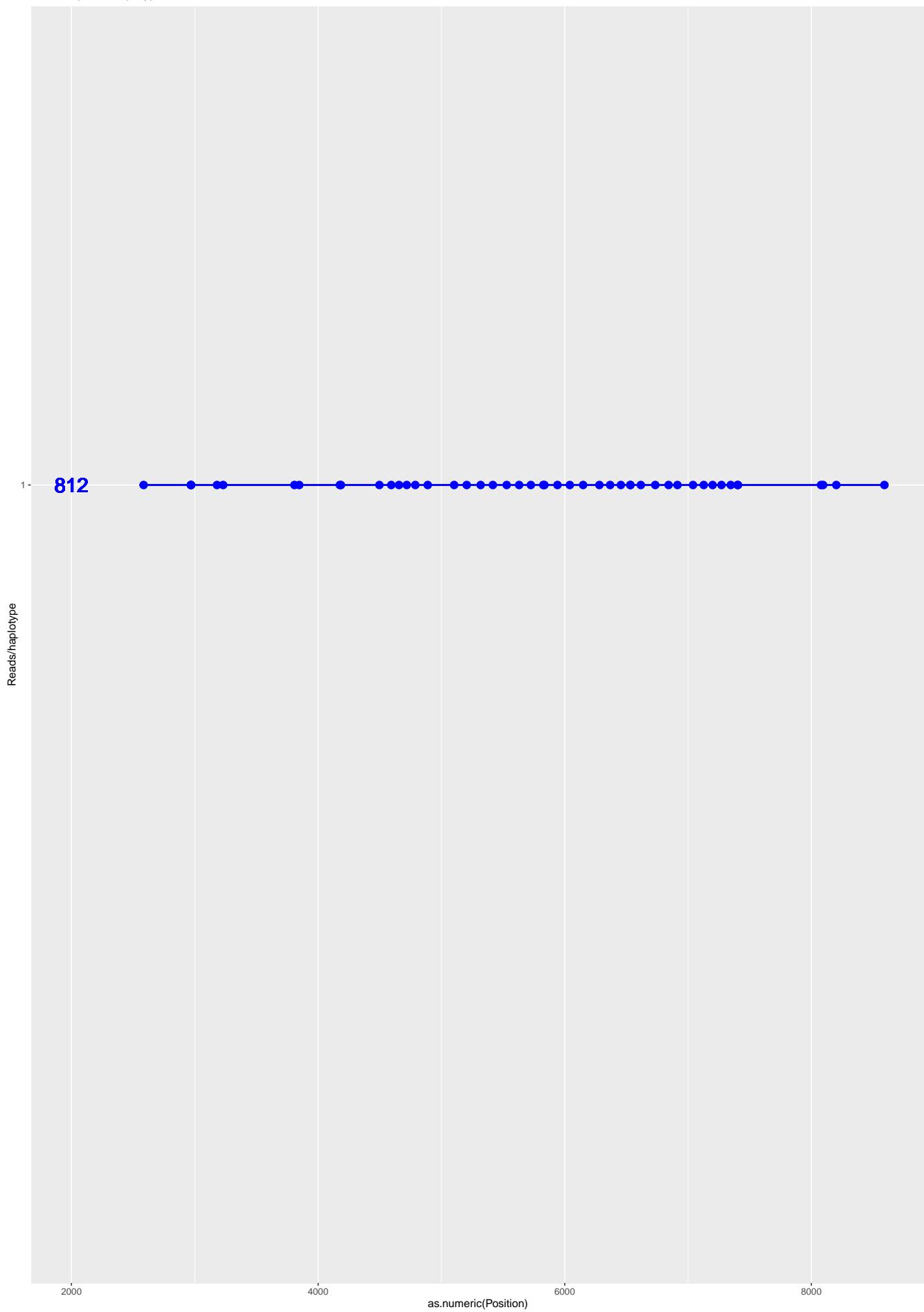
barcode = TGTGAGTCAGTACGCG & AGTATCACAGTCGCTG

Sample = 131c tetrad = 131 spore = c

Total reads = 925 PCR=331

haplotypes I began with n[supporting reads] = 812

most frequent 7 haplotypes.



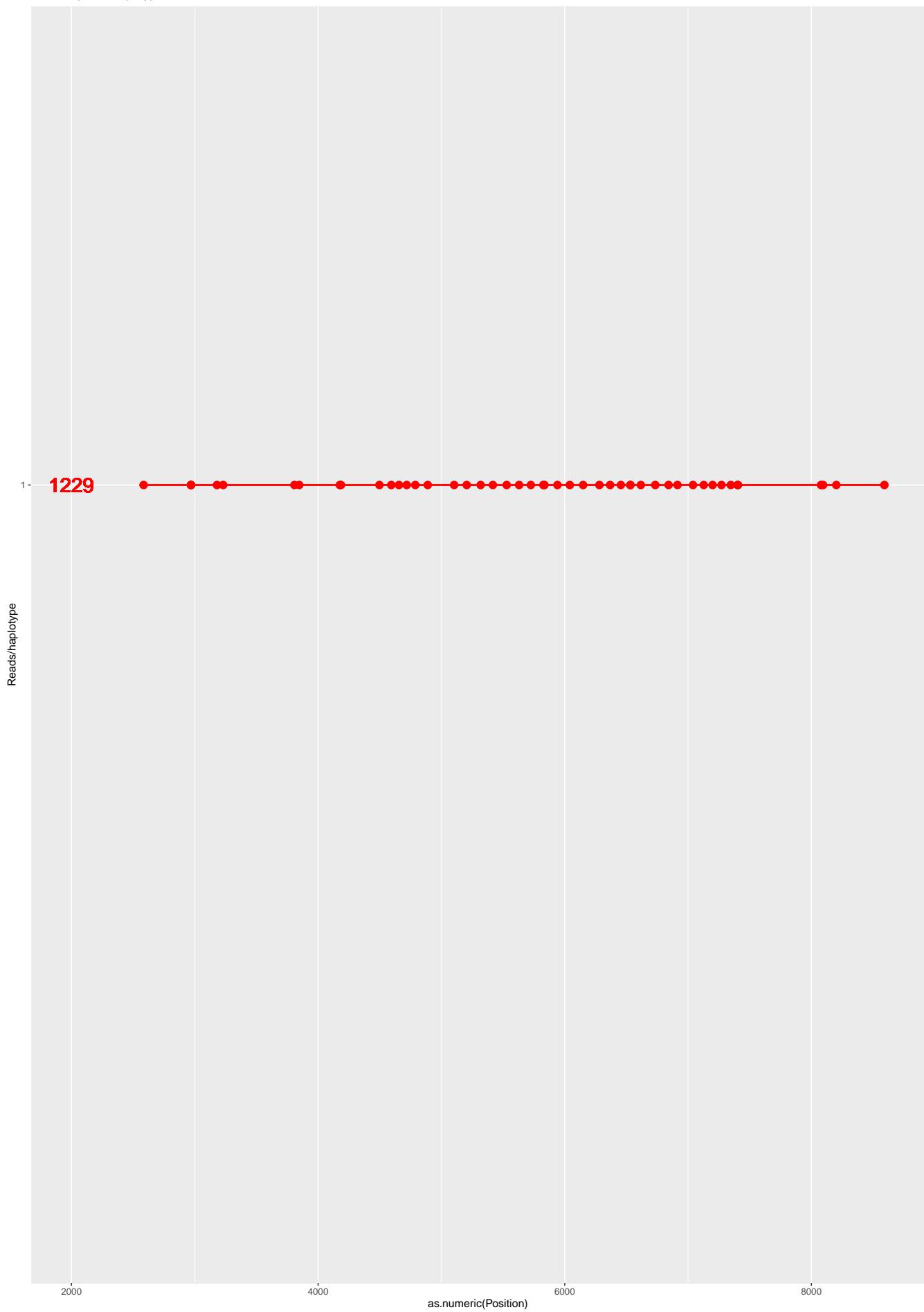
barcode = TGTGAGTCAGTACGCG & ATCATATGATGCGACA

Sample = 131d tetrad = 131 spore = d

Total reads = 1287 PCR=332

haplotypes I began with n[supporting reads] = 1229

most frequent 7 haplotypes.

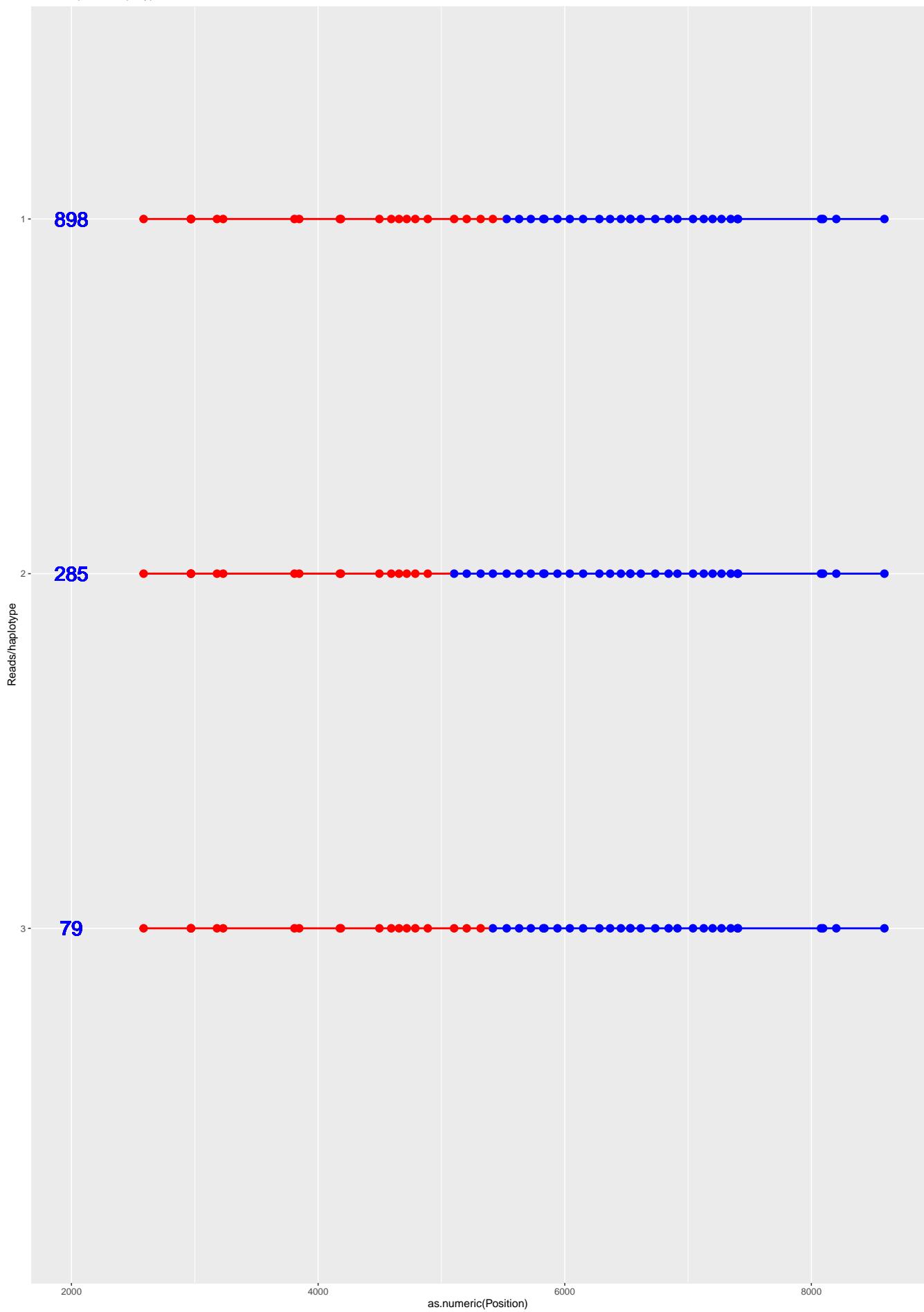


Sample = 133a tetrad = 133 spore = a

Total reads ≈1542 PCR=333

haplotypes I began with n[supporting reads] = 79, 285, 898

most frequent 7 haplotypes.

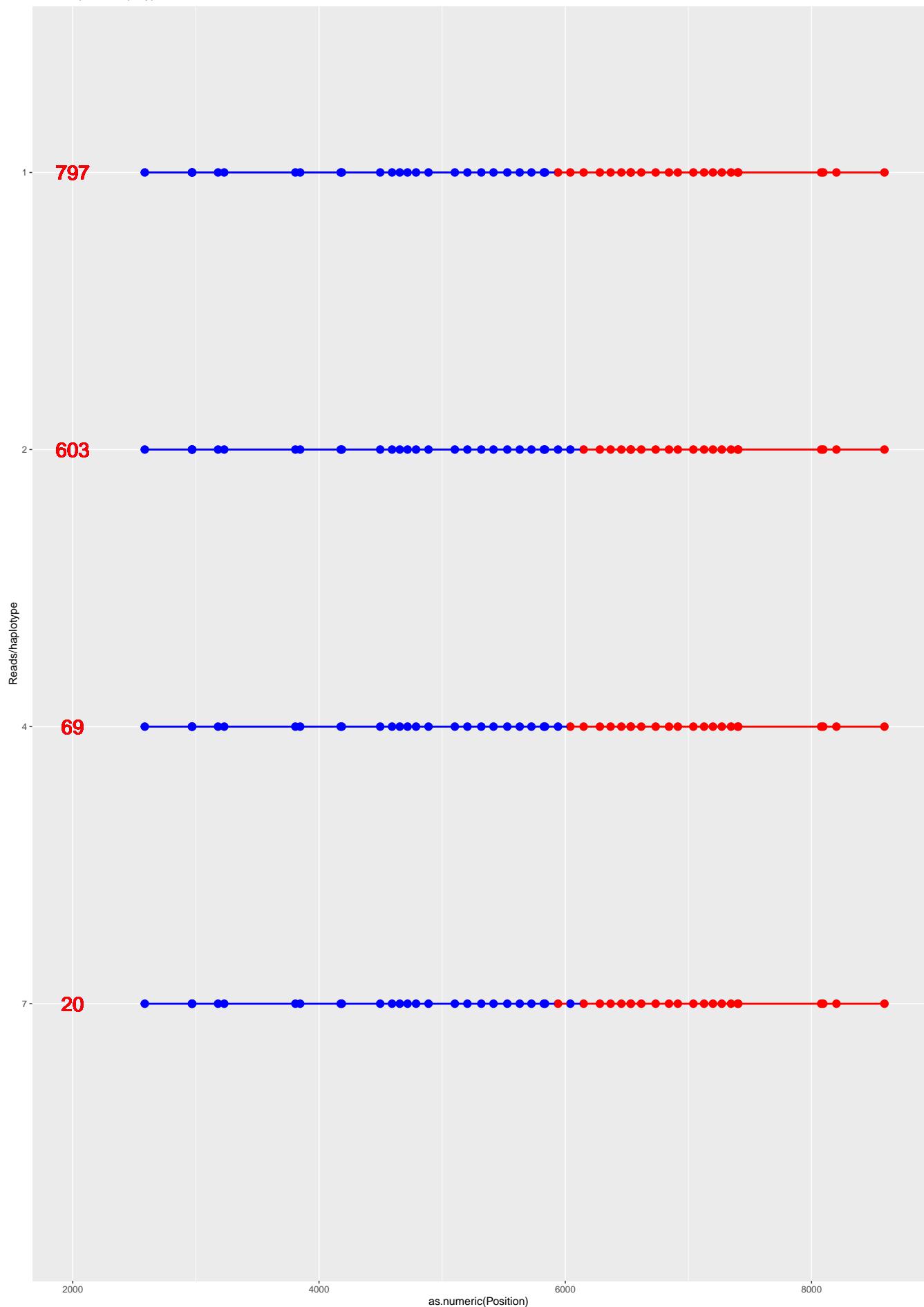


Sample = 133b tetrad = 133 spore = b

Total reads = 1873 PCR=334

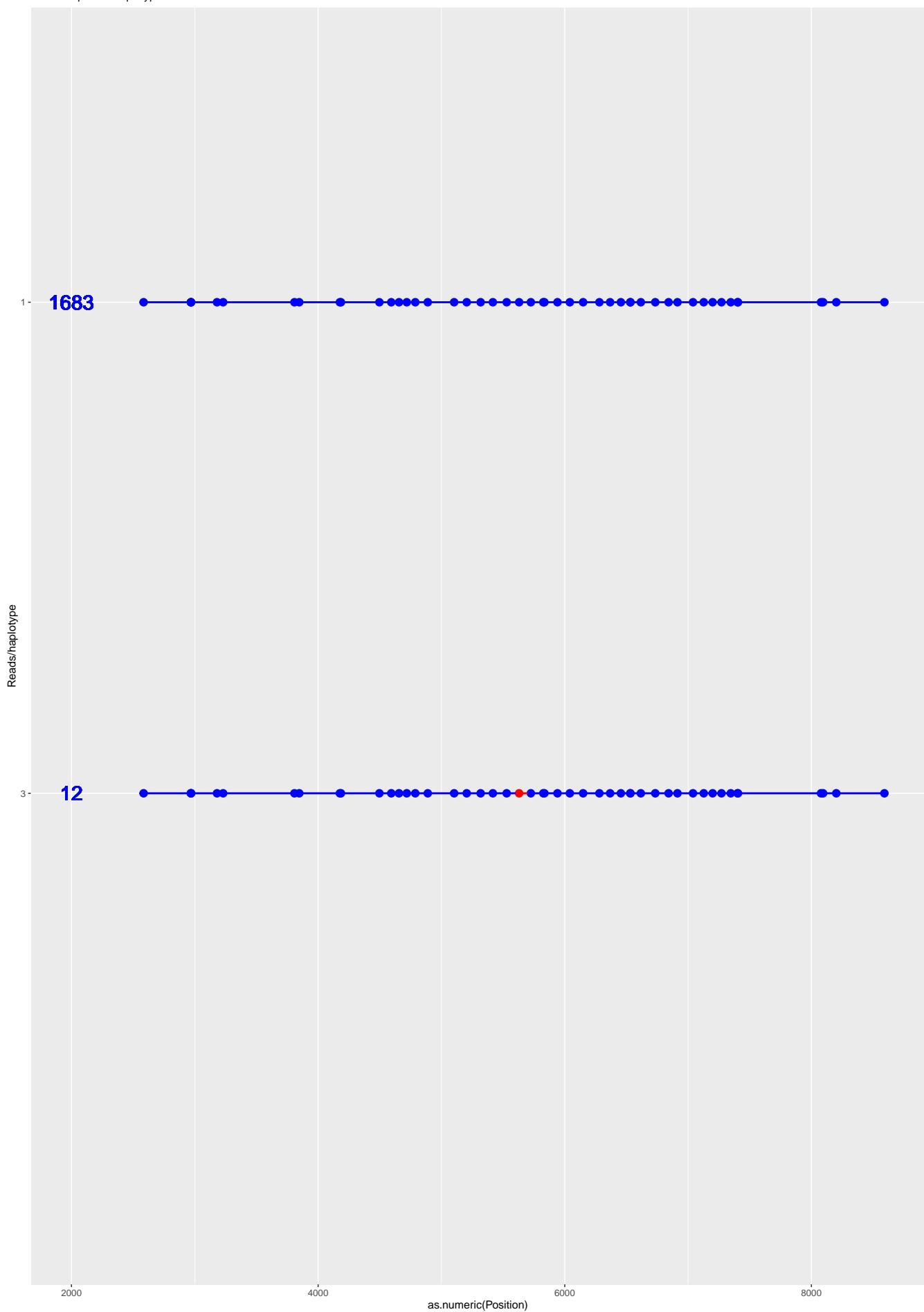
haplotypes I began with n[supporting reads] = 20, 69, 603, 797

most frequent 7 haplotypes.



barcode = TGTGAGTCAGTACCGCG & TGTGAGACTGCATGTC

Sample = 133c tetrad = 133 spore = c
Total reads = 1972 PCR=335
haplotypes I began with n[supporting reads] = 12, 1683
most frequent 7 haplotypes.



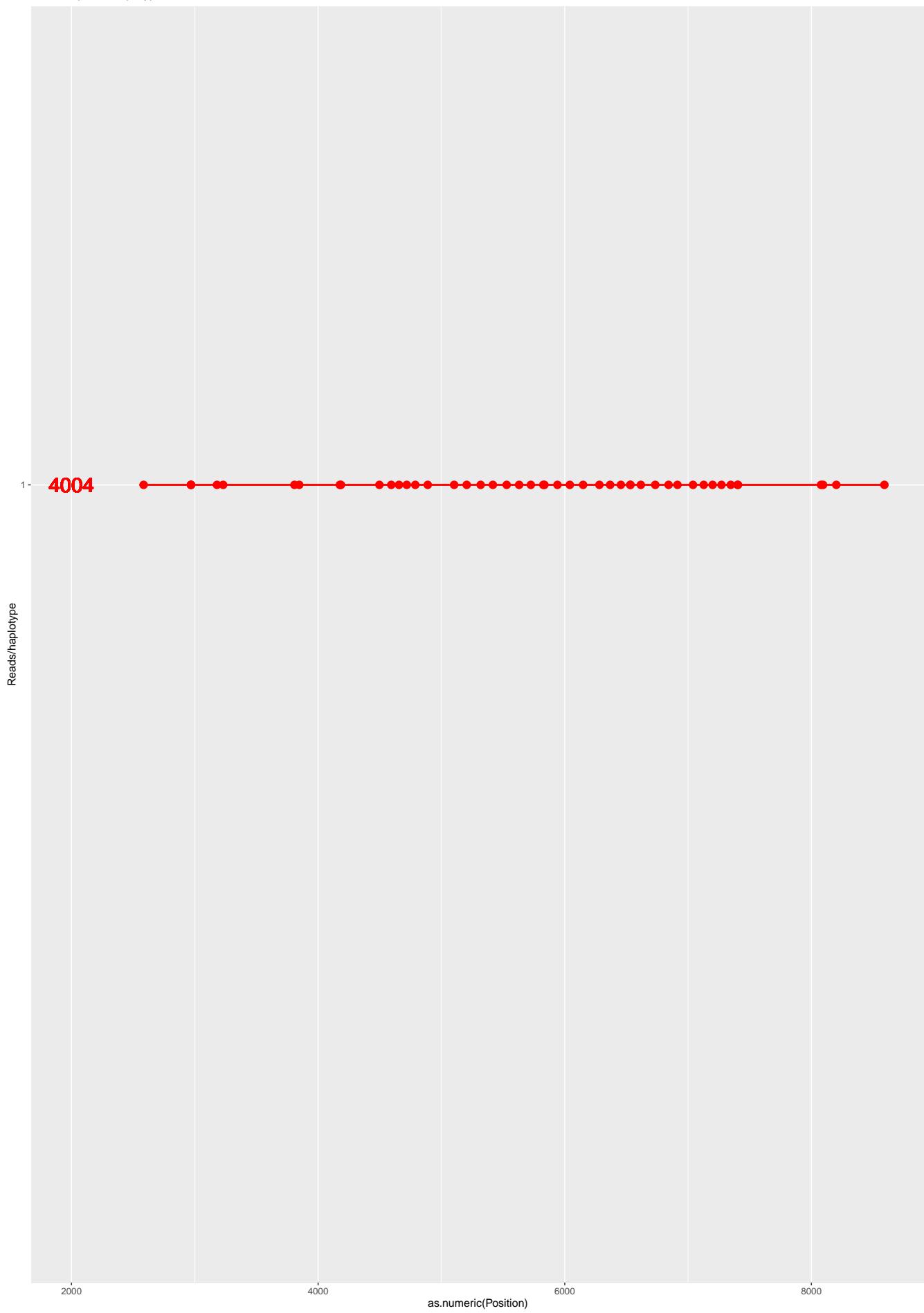
barcode = TGTGAGTCAGTACCGC & GCTCAGTGCCTACTG

Sample = 133d tetrad = 133 spore = d

Total reads = 4187 PCR=336

haplotypes I began with n[supporting reads] = 4004

most frequent 7 haplotypes.



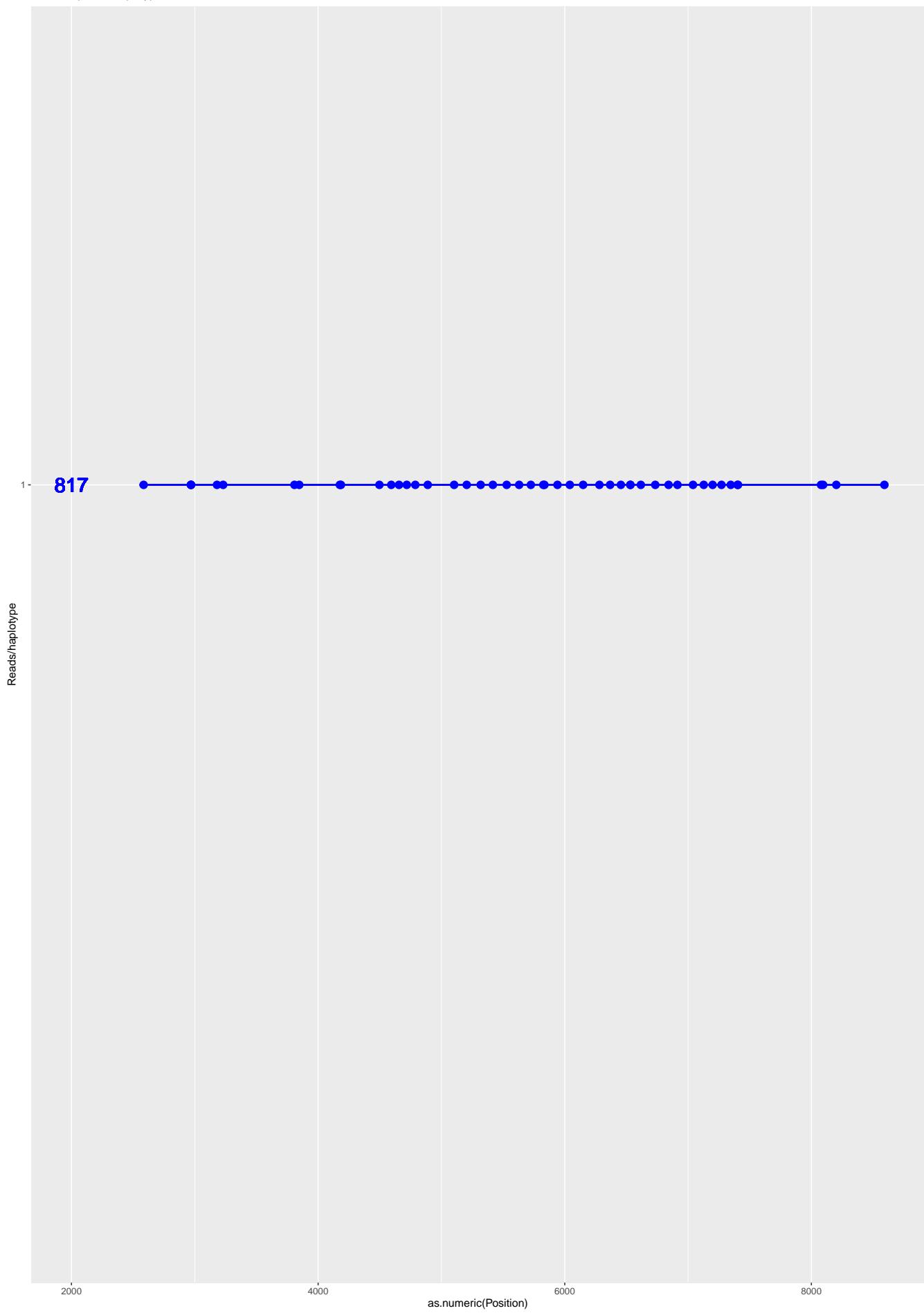
barcode = TGTGAGTCAGTACCGCG & ACTATCGCGCACGCAG

Sample = 134a tetrad = 134 spore = a

Total reads = 961 PCR=337

haplotypes I began with n[supporting reads] = 817

most frequent 7 haplotypes.



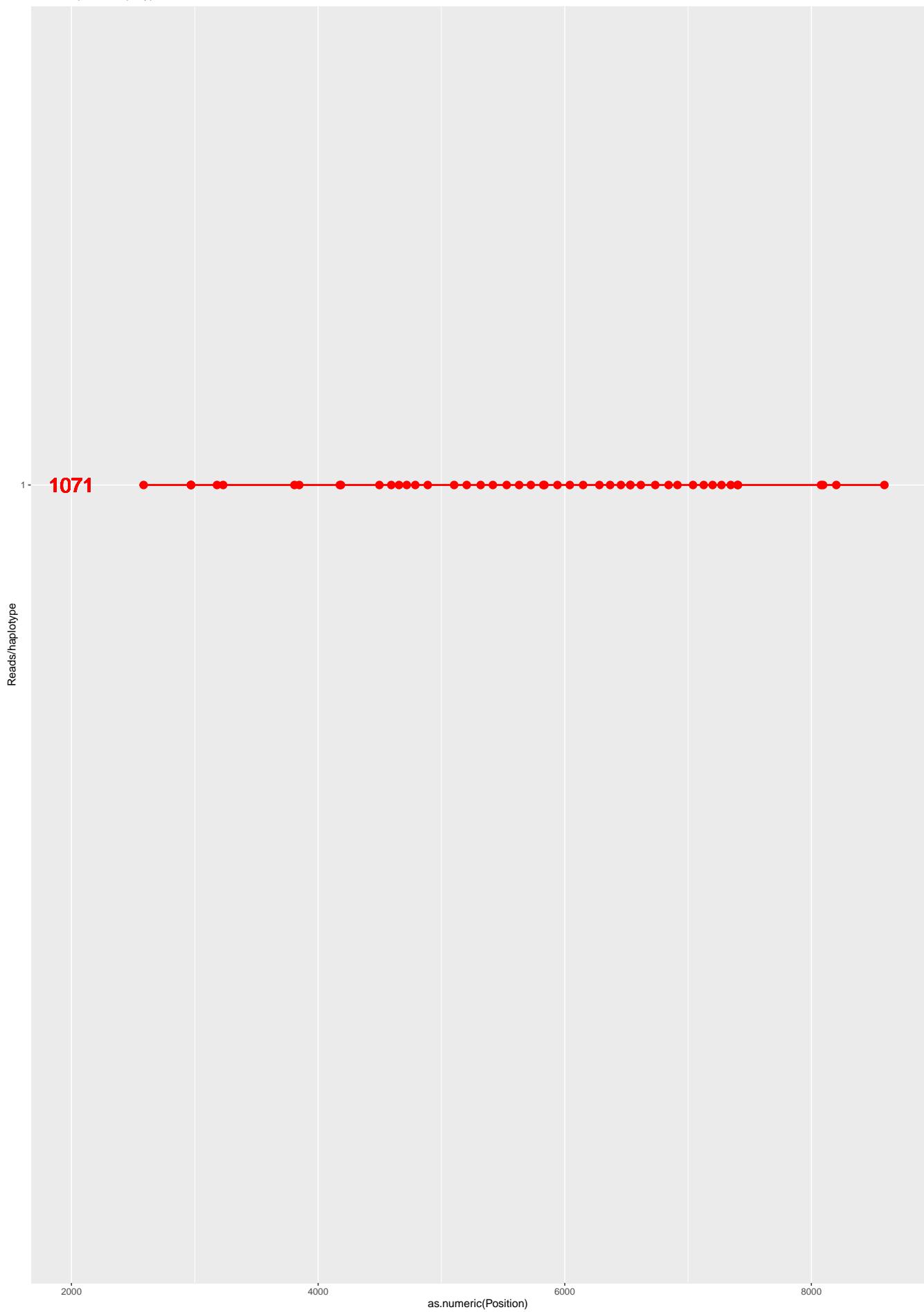
barcode = AGAGACACGATACTCA & GCGACGAGTACTCATG

Sample = 134b tetrad = 134 spore = b

Total reads = 1115 PCR=338

haplotypes I began with n[supporting reads] = 1071

most frequent 7 haplotypes.



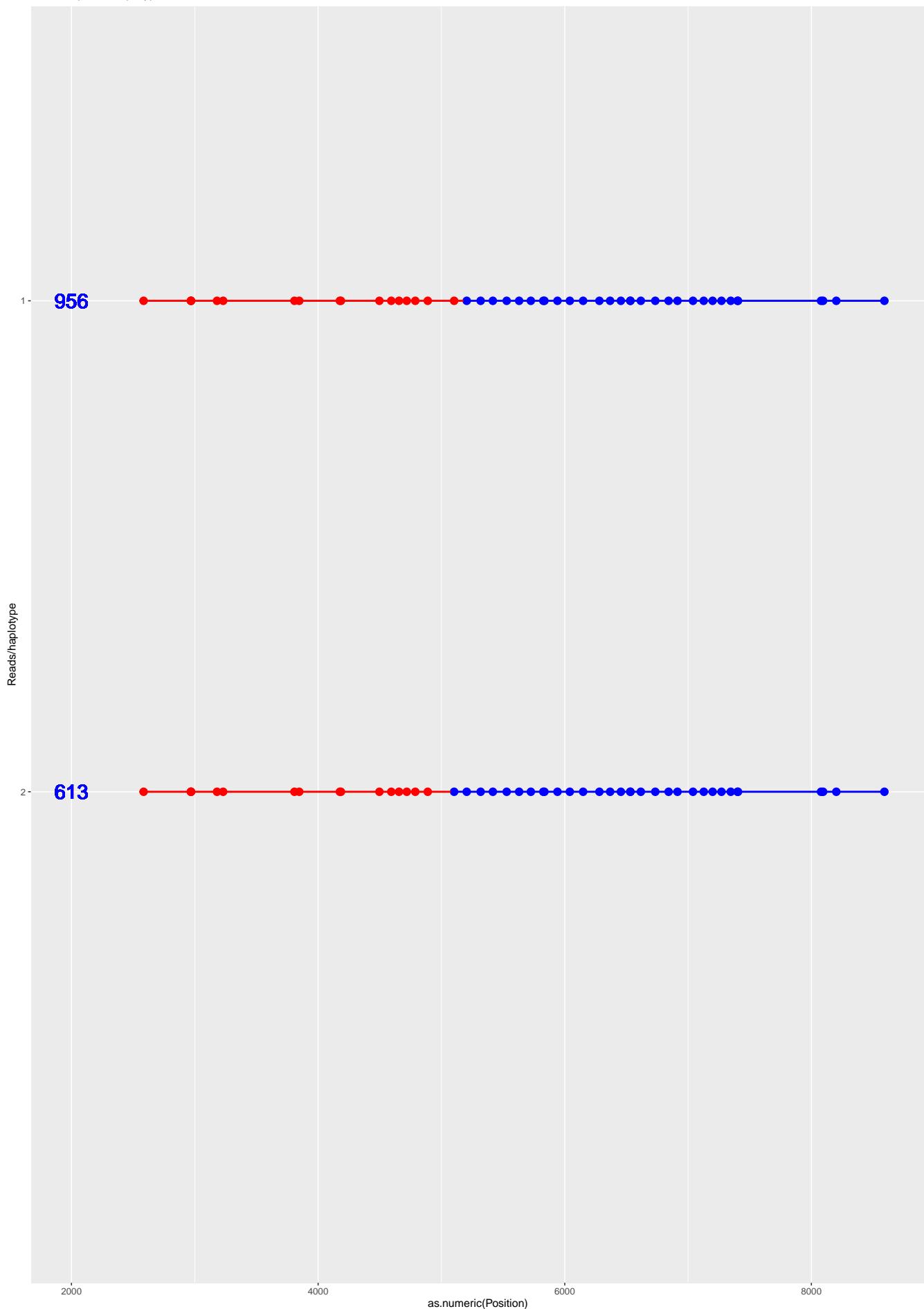
barcode = AGAGACACGATACTCA & AGTATCACAGTCGCTG

Sample = 134c tetrad = 134 spore = c

Total reads = 1869 PCR=339

haplotypes I began with n[supporting reads] = 613, 956

most frequent 7 haplotypes.



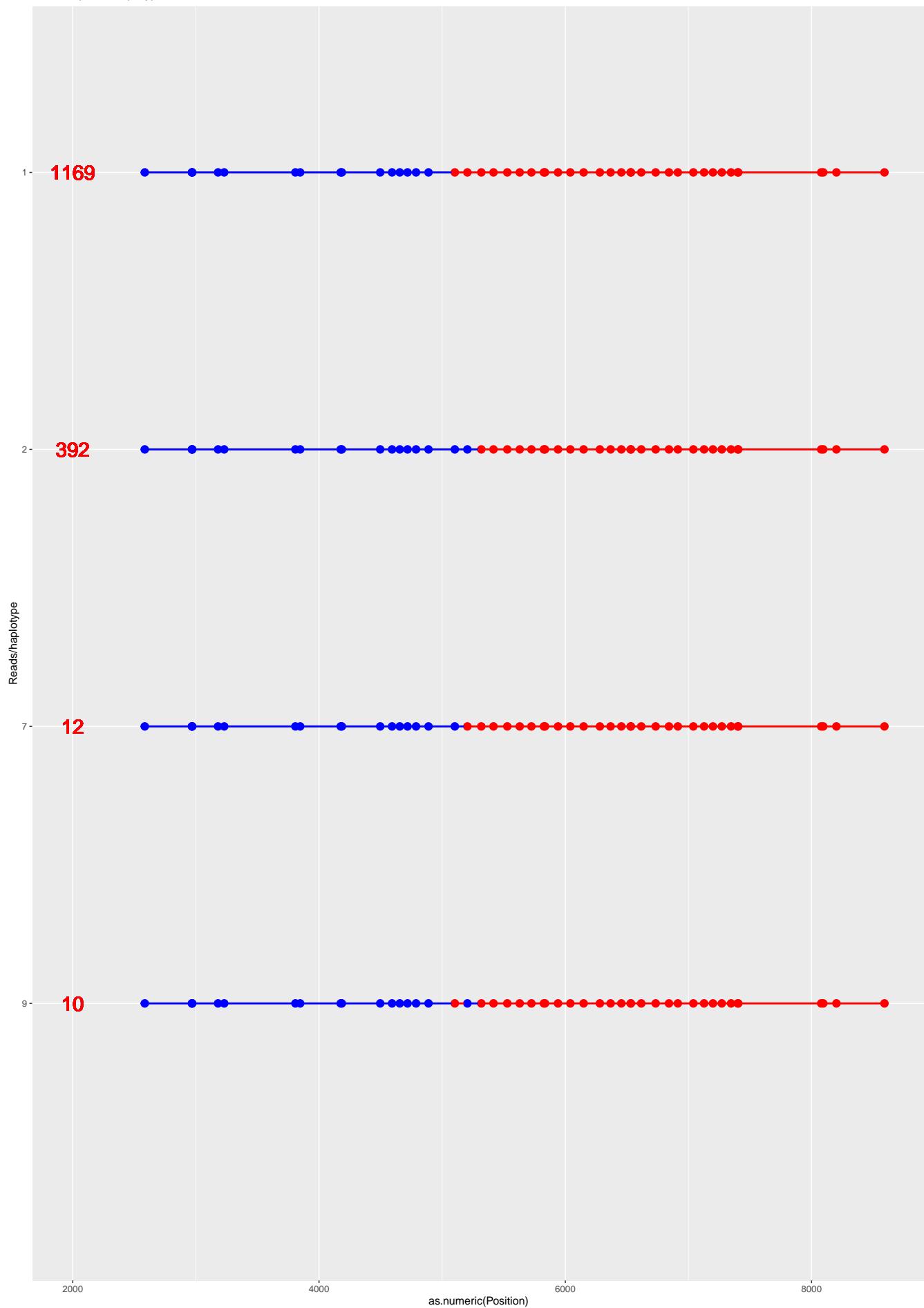
barcode = AGAGACACGATACTCA & ATCATATGATGCGACA

Sample = 134d tetrad = 134 spore = d

Total reads = 1782 PCR=340

haplotypes I began with n[supporting reads] = 10, 12, 392, 1169

most frequent 7 haplotypes.

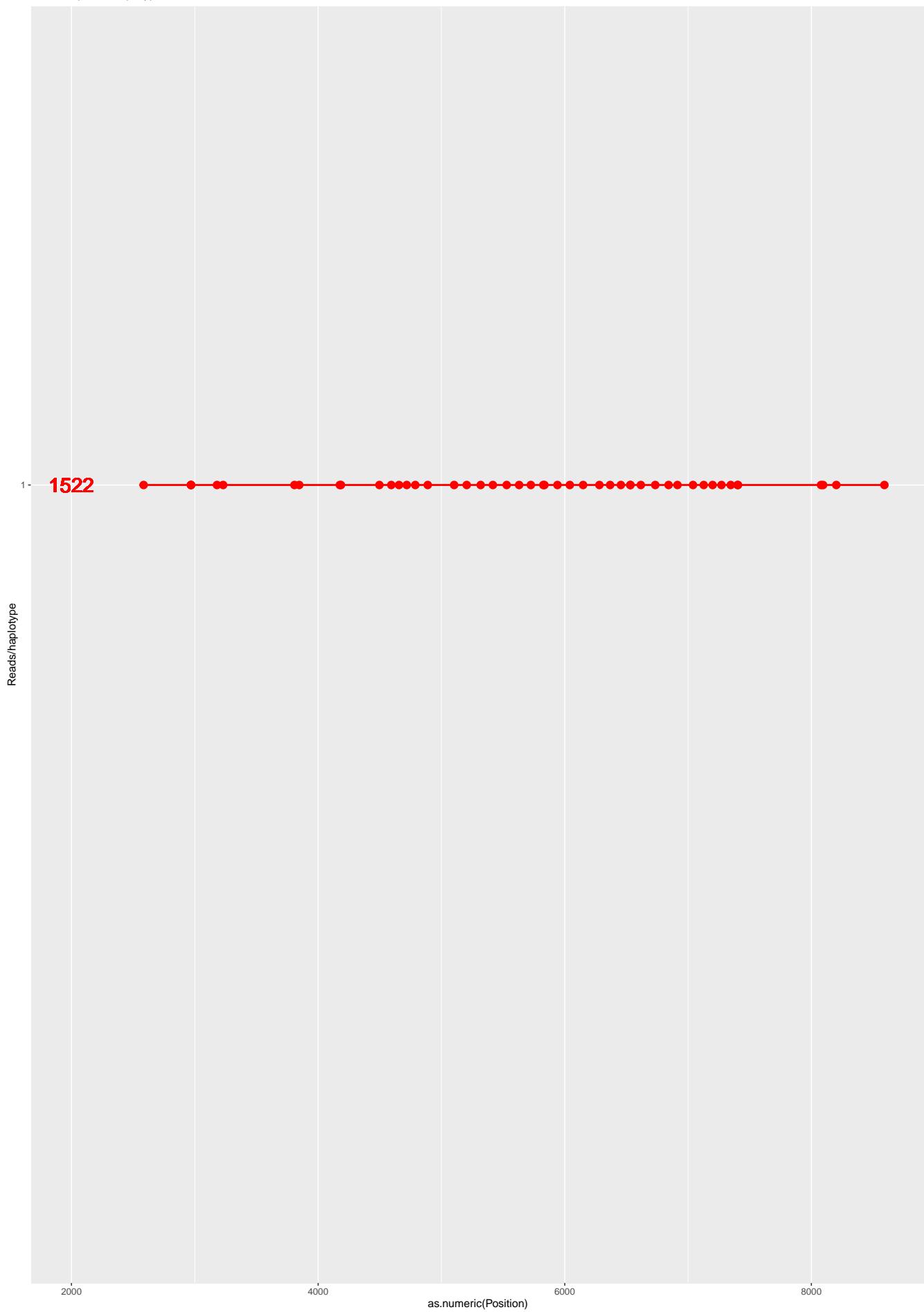


Sample = 137a tetrad = 137 spore = a

Total reads = 1597 PCR=345

haplotypes I began with n[supporting reads] = 1522

most frequent 7 haplotypes.

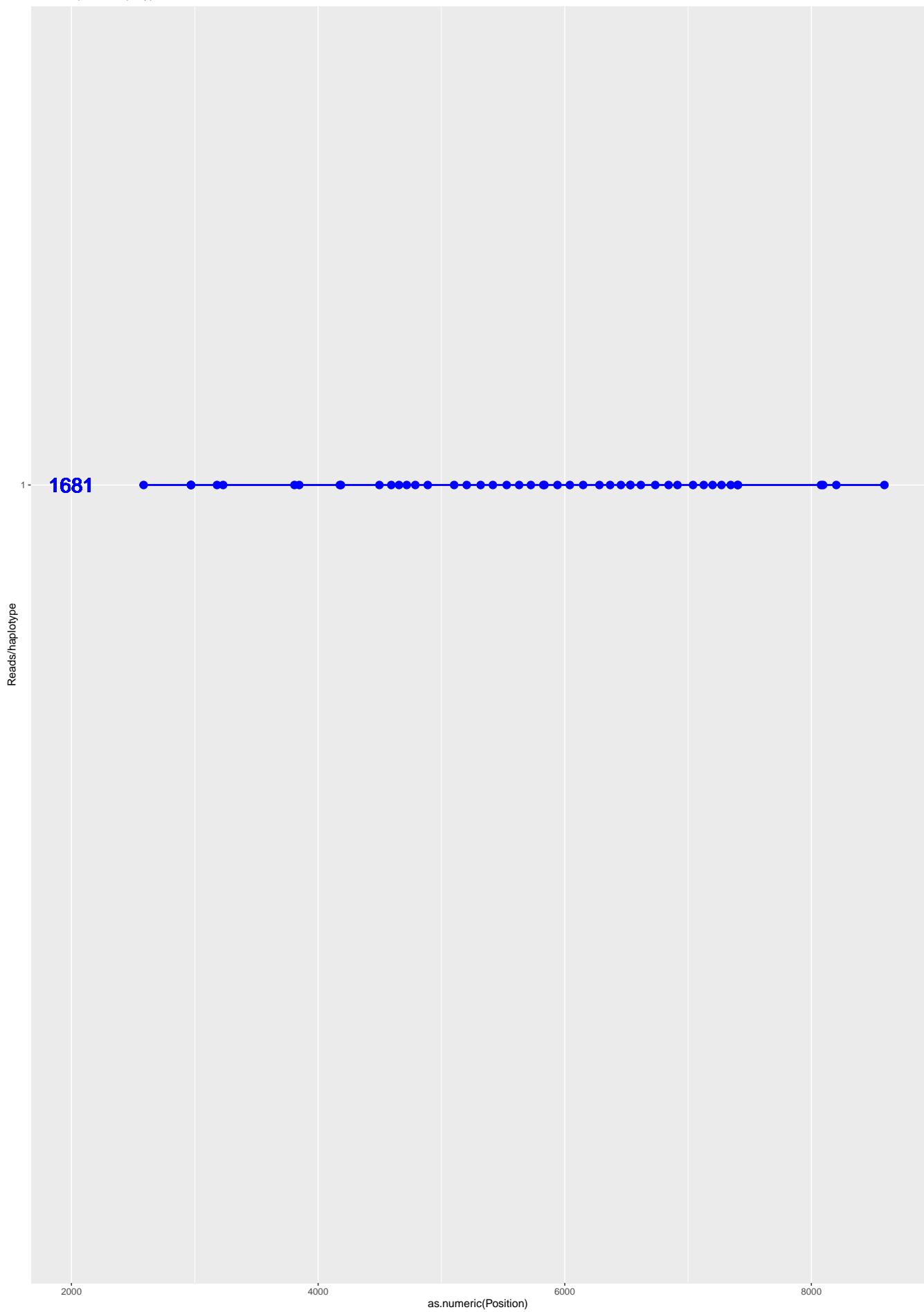


Sample = 137b tetrad = 137 spore = b

Total reads = 1974 PCR=346

haplotypes I began with n[supporting reads] = 1681

most frequent 7 haplotypes.



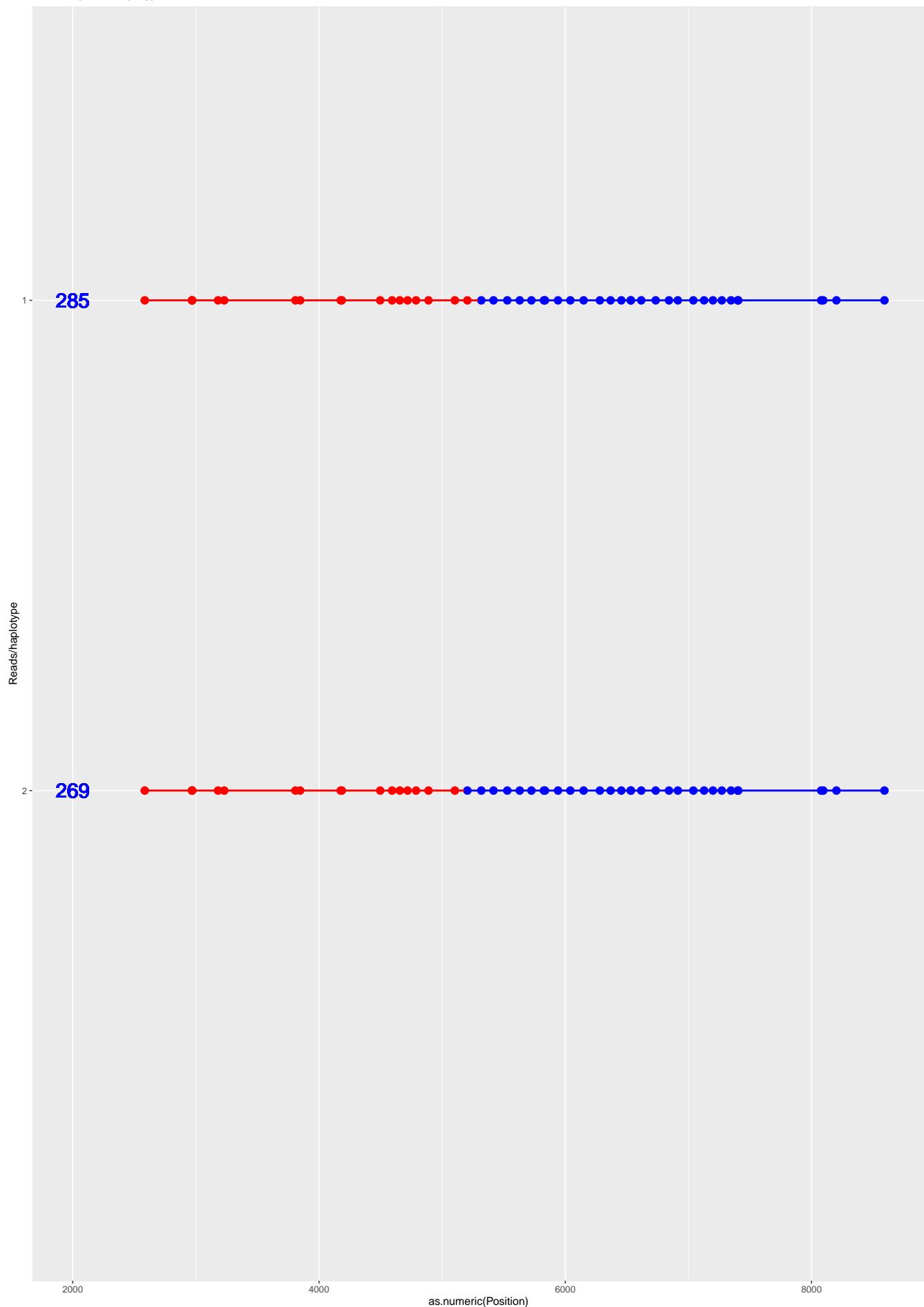
barcode = CTGCTAGAGTCTACAG & AGTATCACAGTCGCTG

Sample = 137c tetrad = 137 spore = c

Total reads = 646 PCR=347

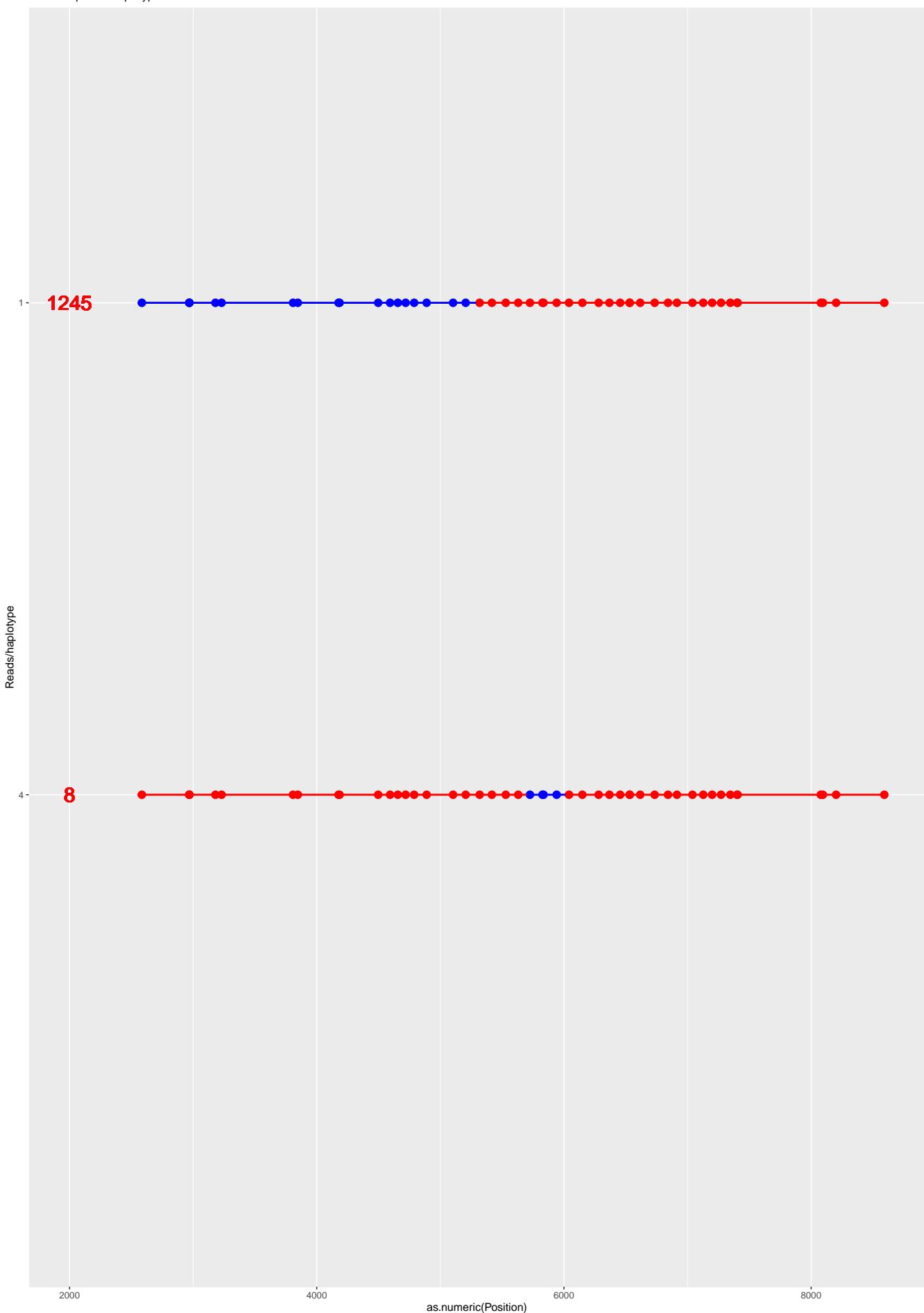
haplotypes I began with n[supporting reads] = 269, 285

most frequent 7 haplotypes.



barcode = CTGCTAGAGTCTACAG & ATCATATGATGCGACA

Sample = 137d tetrad = 137 spore = d
Total reads = 1404 PCR=348
haplotypes I began with n[supporting reads] = 8, 1245
most frequent 7 haplotypes.



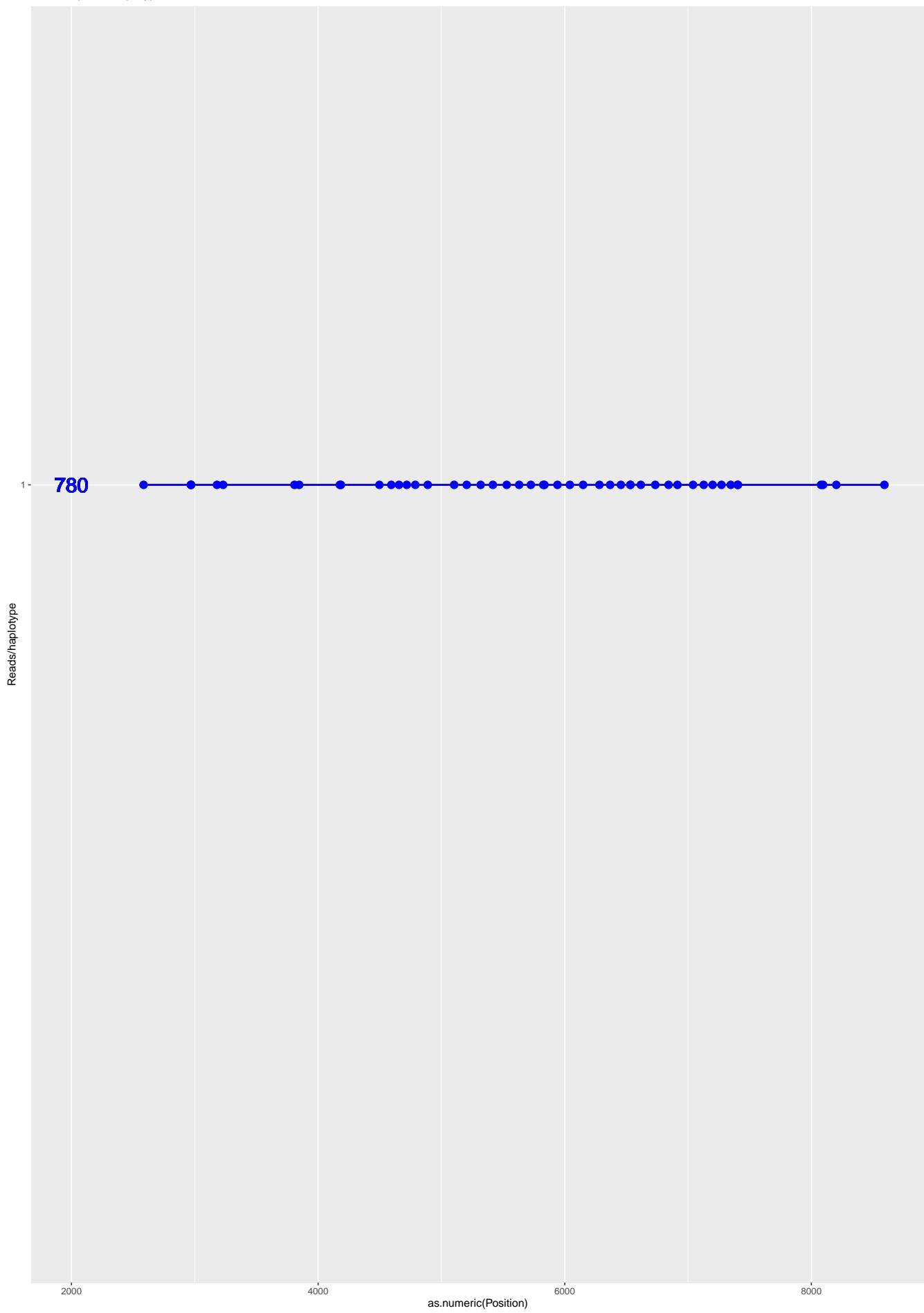
barcode = CTGCTAGAGTCTACAG & AGACGTAGATCACAGC

Sample = 142a tetrad = 142 spore = a

Total reads = 918 PCR=357

haplotypes I began with n[supporting reads] = 780

most frequent 7 haplotypes.

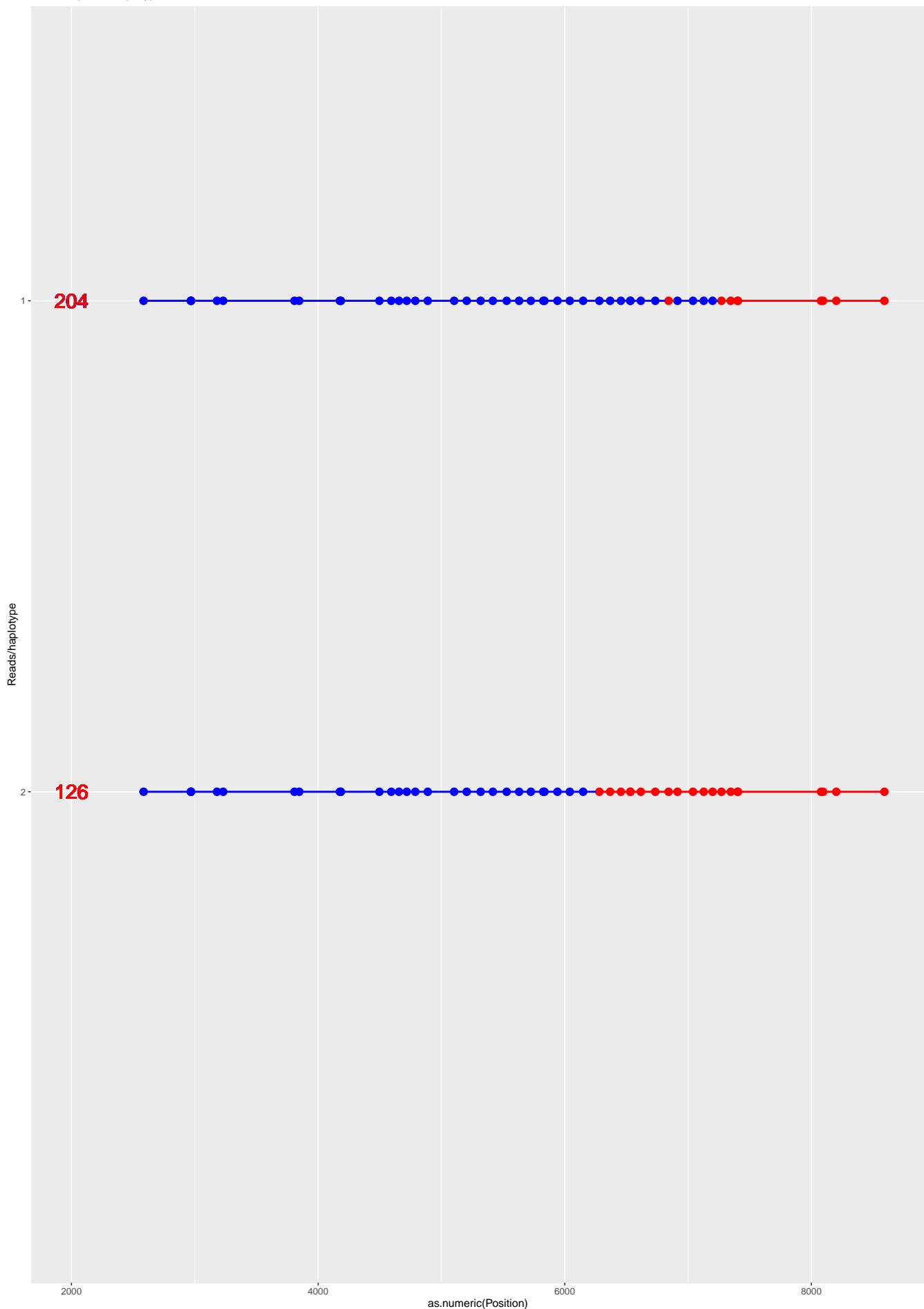


Sample = 142b tetrad = 142 spore = b

Total reads = 426 PCR=358

haplotypes I began with n[supporting reads] = 126, 204

most frequent 7 haplotypes.



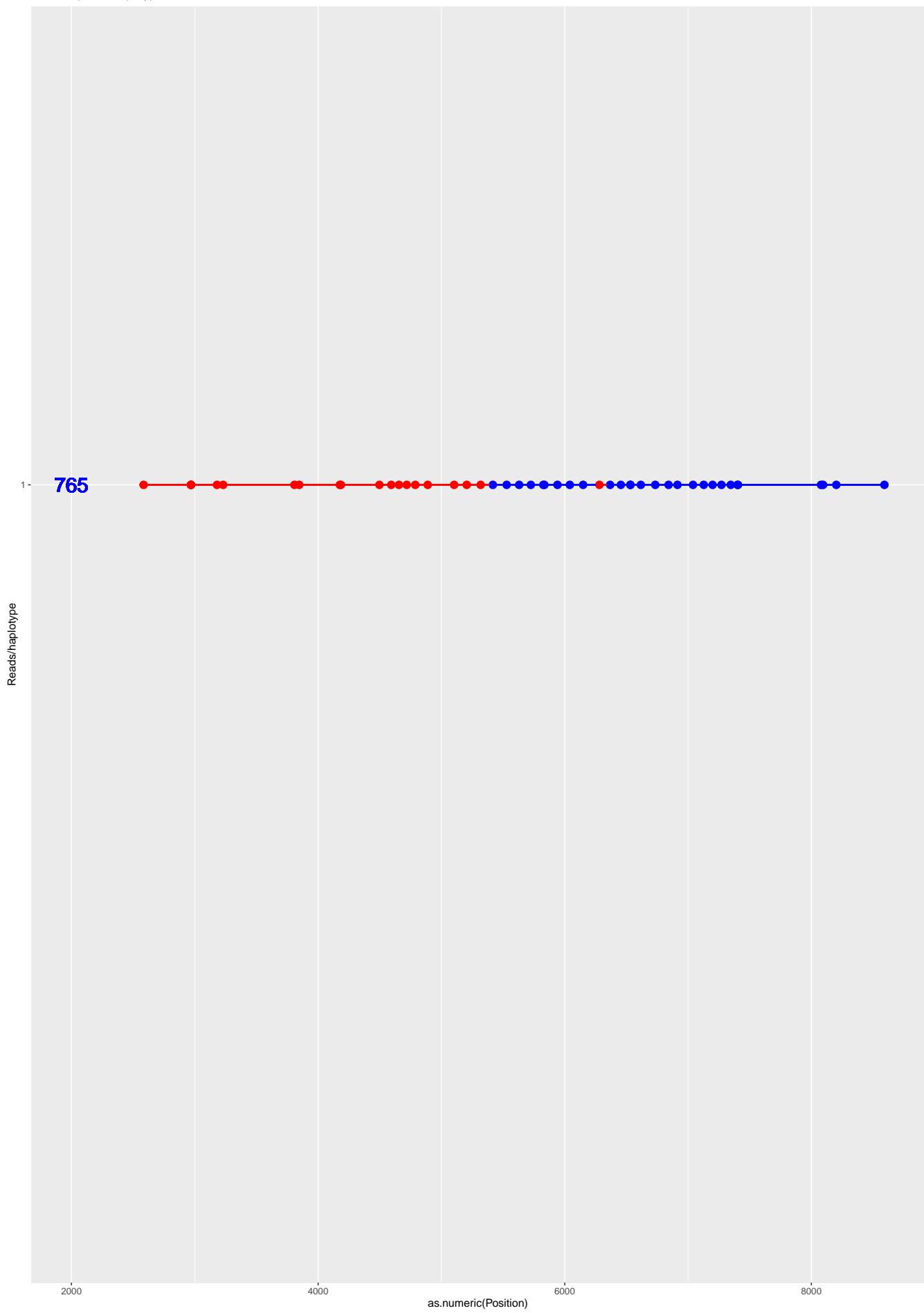
barcode = AGCACTCGCGTCAGTG & TGTGAGACTGCATGTC

Sample = 142c tetrad = 142 spore = c

Total reads = 871 PCR=359

haplotypes I began with n[supporting reads] = 765

most frequent 7 haplotypes.



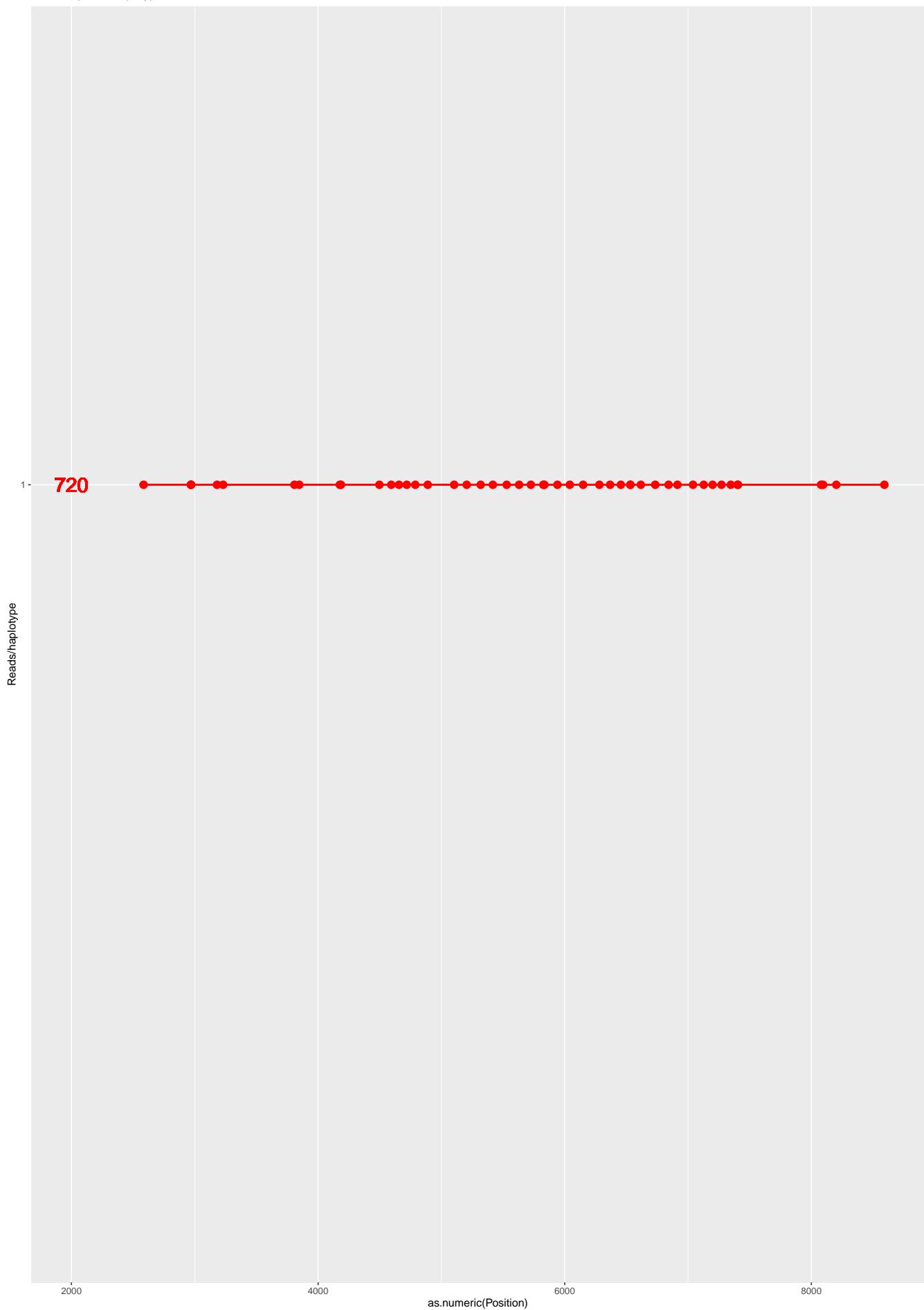
barcode = AGCACTCGCGTCAGTG & GCTCAGTGCCTACTG

Sample = 142d tetrad = 142 spore = d

Total reads =751 PCR=360

haplotypes I began with n[supporting reads] = 720

most frequent 7 haplotypes.



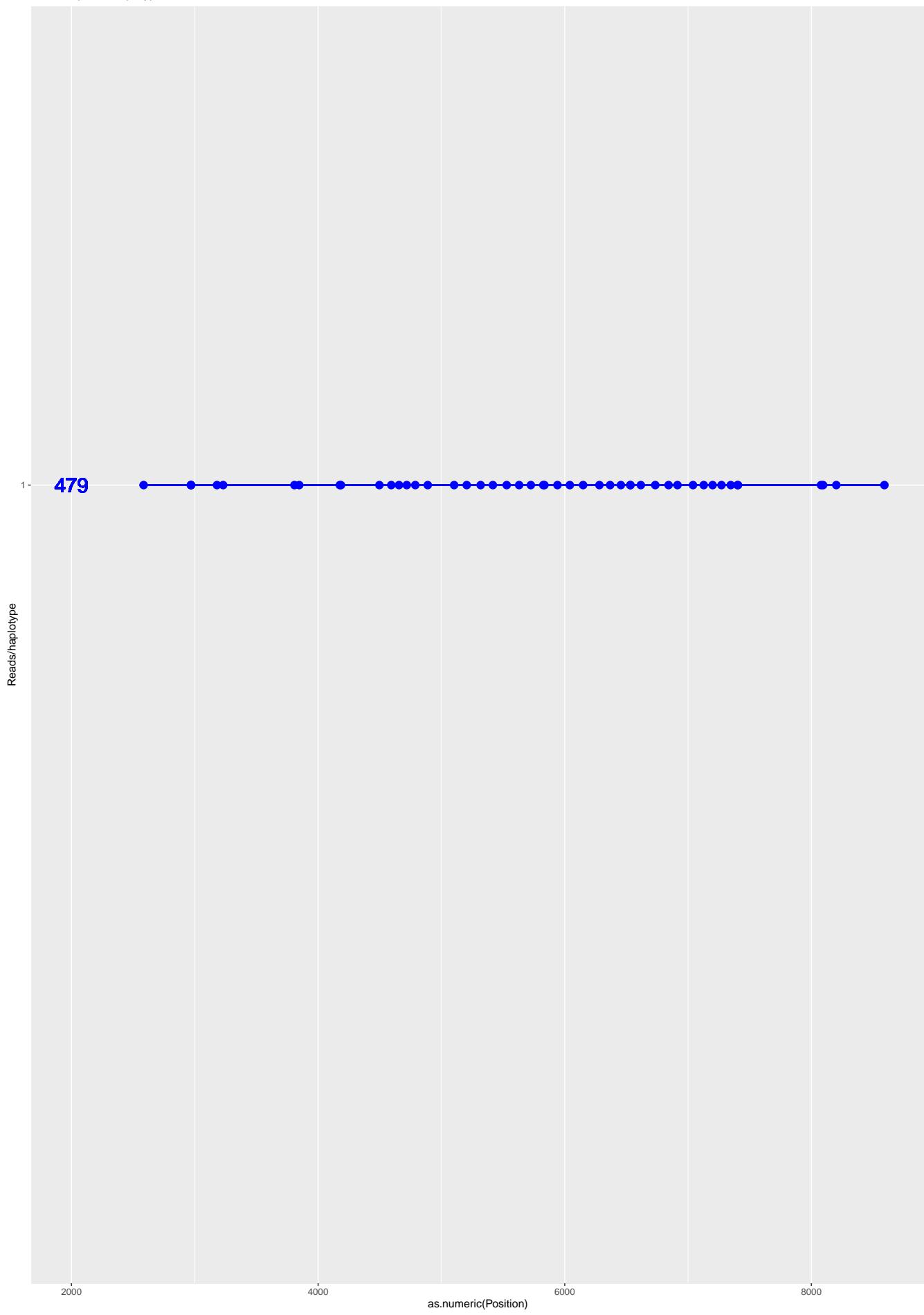
barcode = AGCACTCGCGTCAGTG & ACTATCGCGCACGCAG

Sample = 143a tetrad = 143 spore = a

Total reads =561 PCR=361

haplotypes I began with n[supporting reads] = 479

most frequent 7 haplotypes.



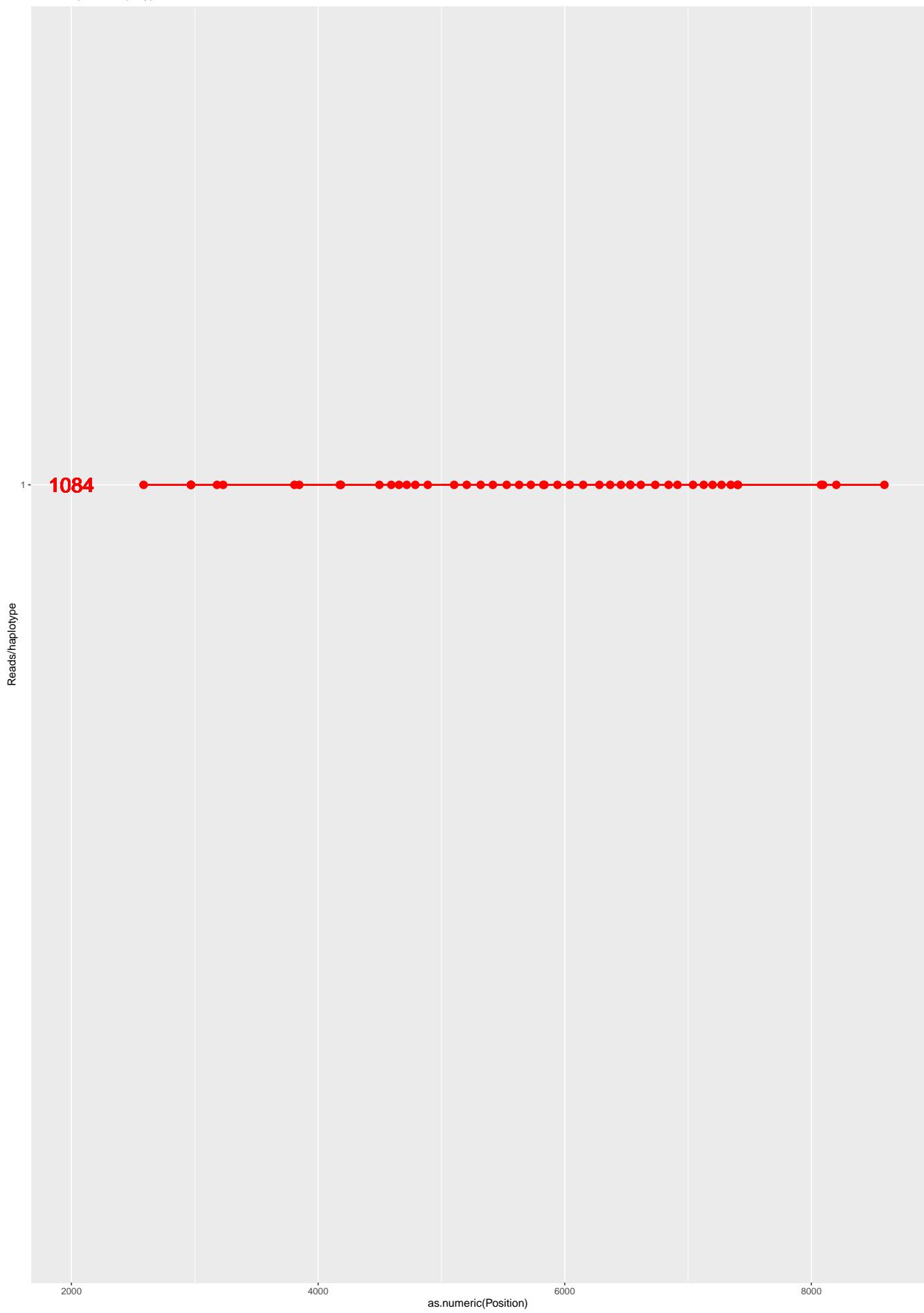
barcode = TCATGCACGTCTCGCT & GCGACGAGTACTCATG

Sample = 143b tetrad = 143 spore = b

Total reads = 1125 PCR=362

haplotypes I began with n[supporting reads] = 1084

most frequent 7 haplotypes.

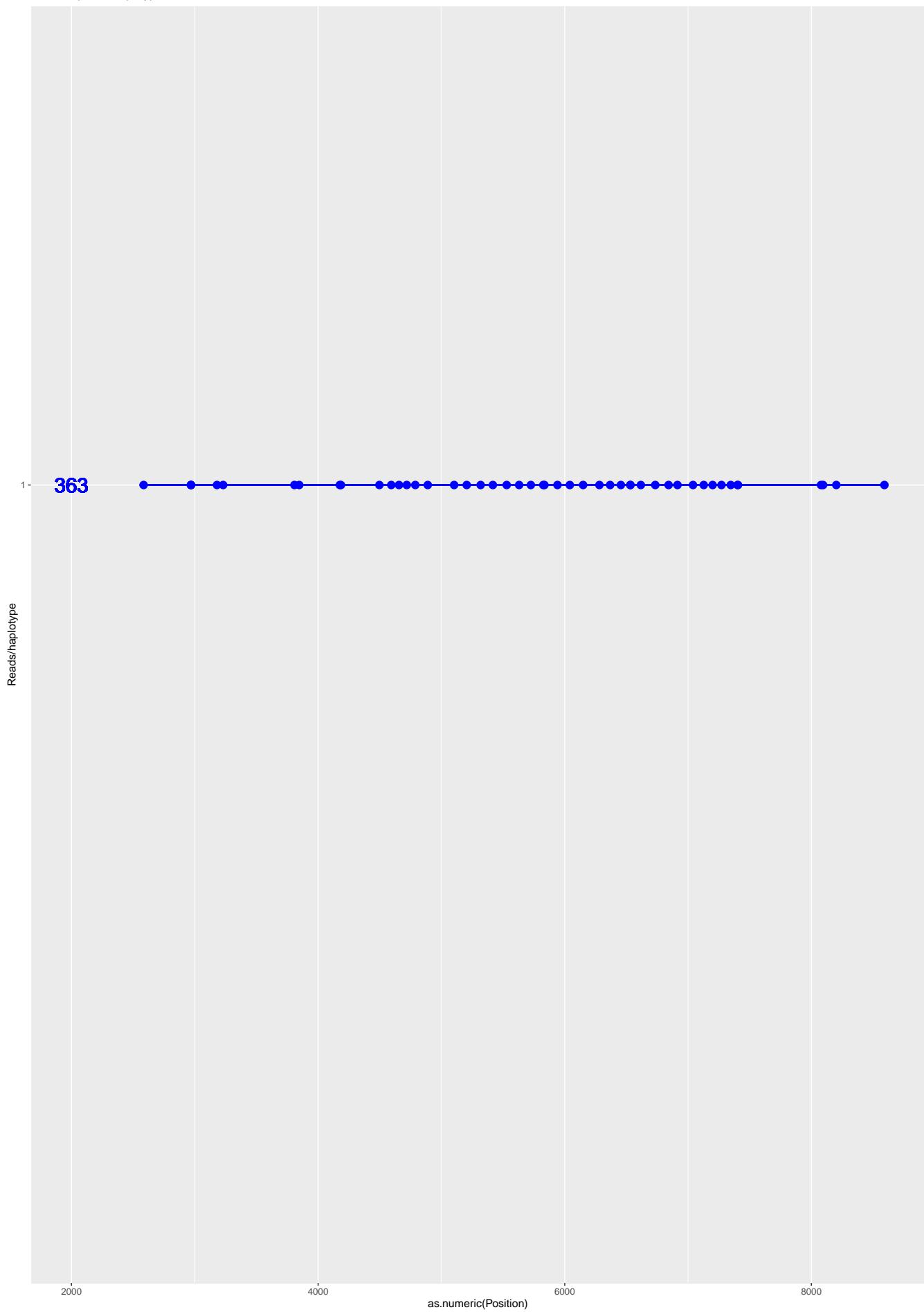


Sample = 143c tetrad = 143 spore = c

Total reads = 417 PCR=363

haplotypes I began with n[supporting reads] = 363

most frequent 7 haplotypes.



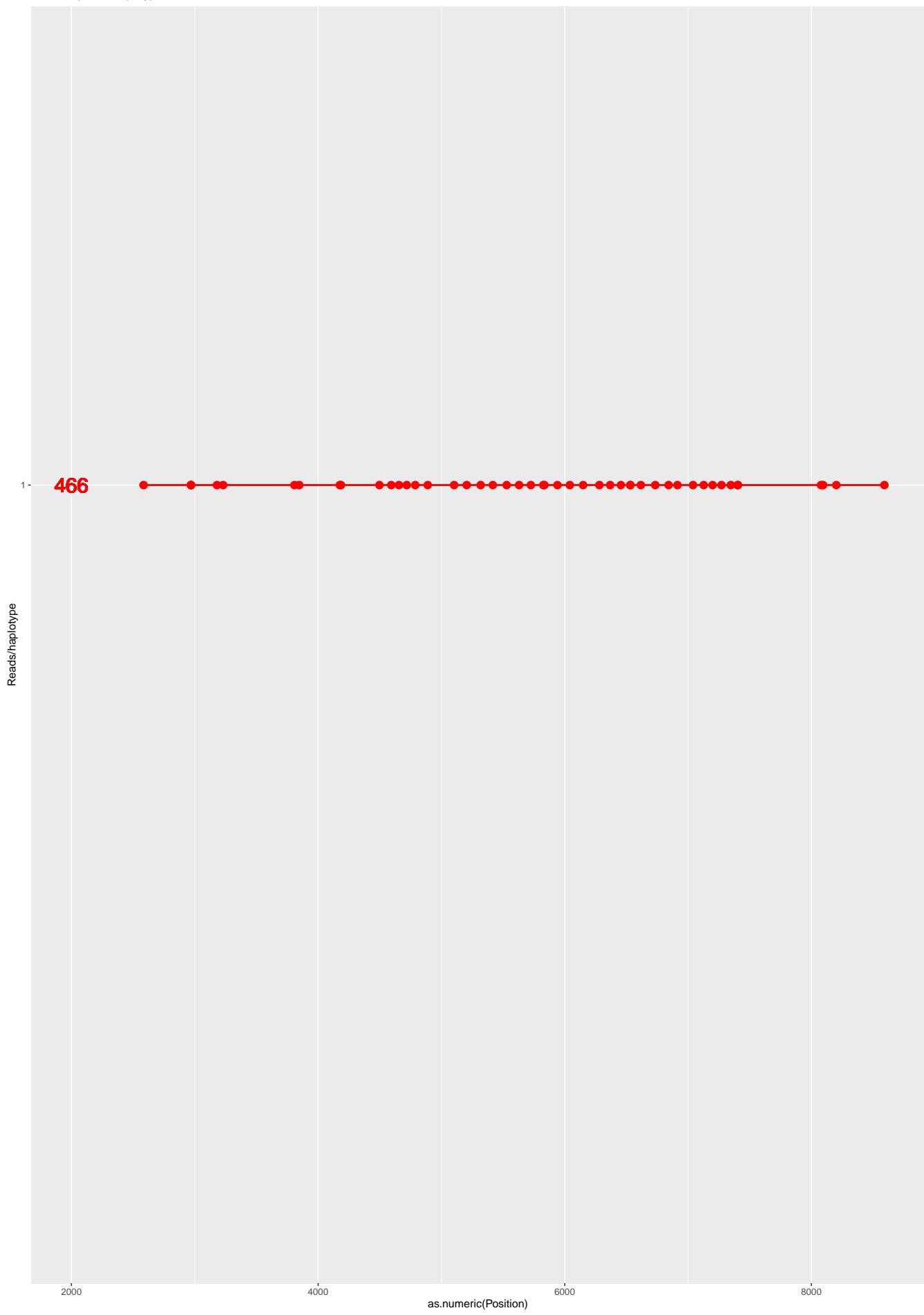
barcode = TCATGCACGTCTCGCT & ATCATATGATGCGACA

Sample = 143d tetrad = 143 spore = d

Total reads = 485 PCR=364

haplotypes I began with n[supporting reads] = 466

most frequent 7 haplotypes.



barcode = TCATGCACGTCTCGCT & AGACGTTAGATCACAGC

Sample = 152a tetrad = 152 spore = a
Total reads = 1731 PCR=385
haplotypes I began with n[supporting reads] = 10, 1472
most frequent 7 haplotypes.

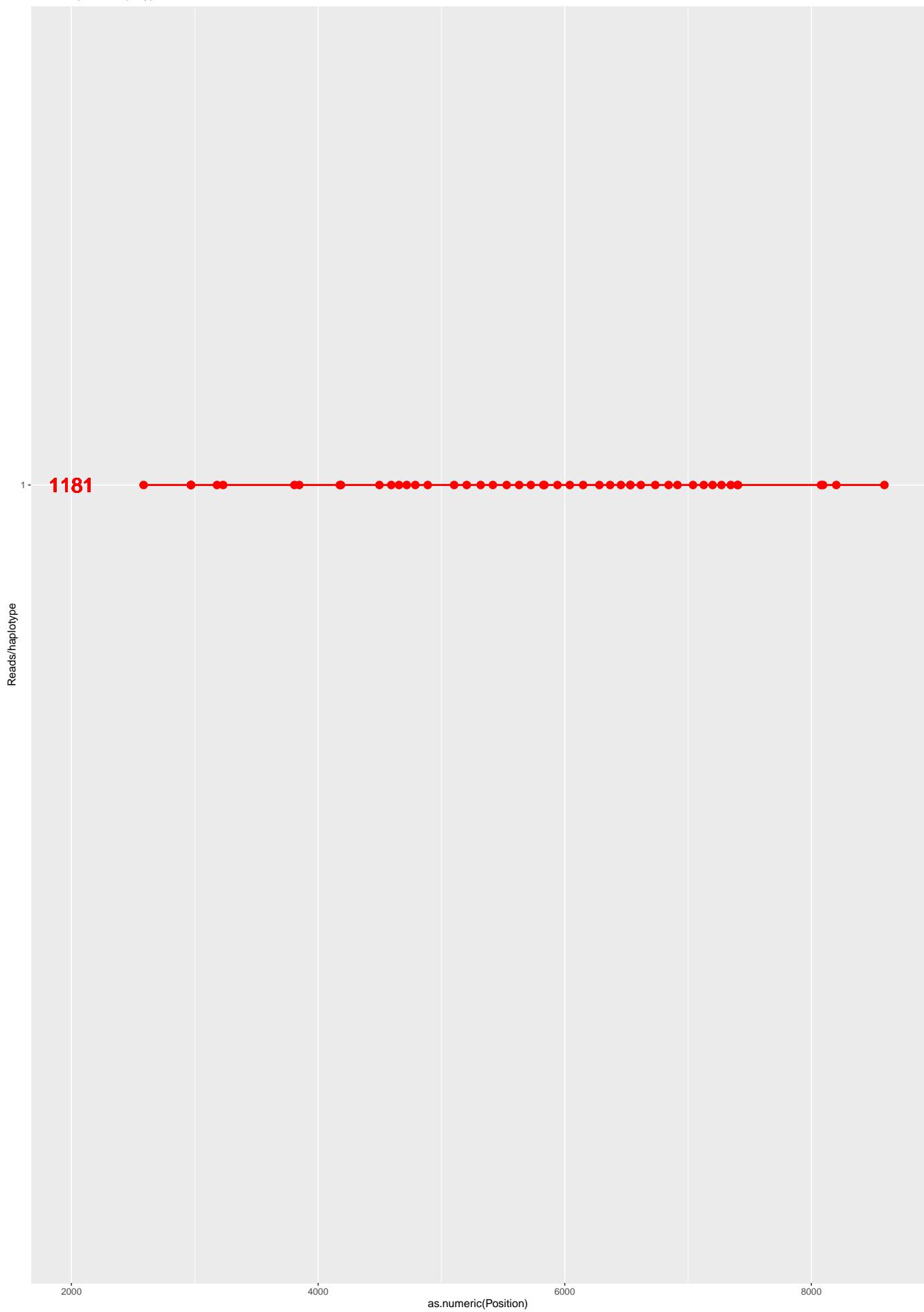


Sample = 152b tetrad = 152 spore = b

Total reads = 1228 PCR=386

haplotypes I began with n[supporting reads] = 1181

most frequent 7 haplotypes.

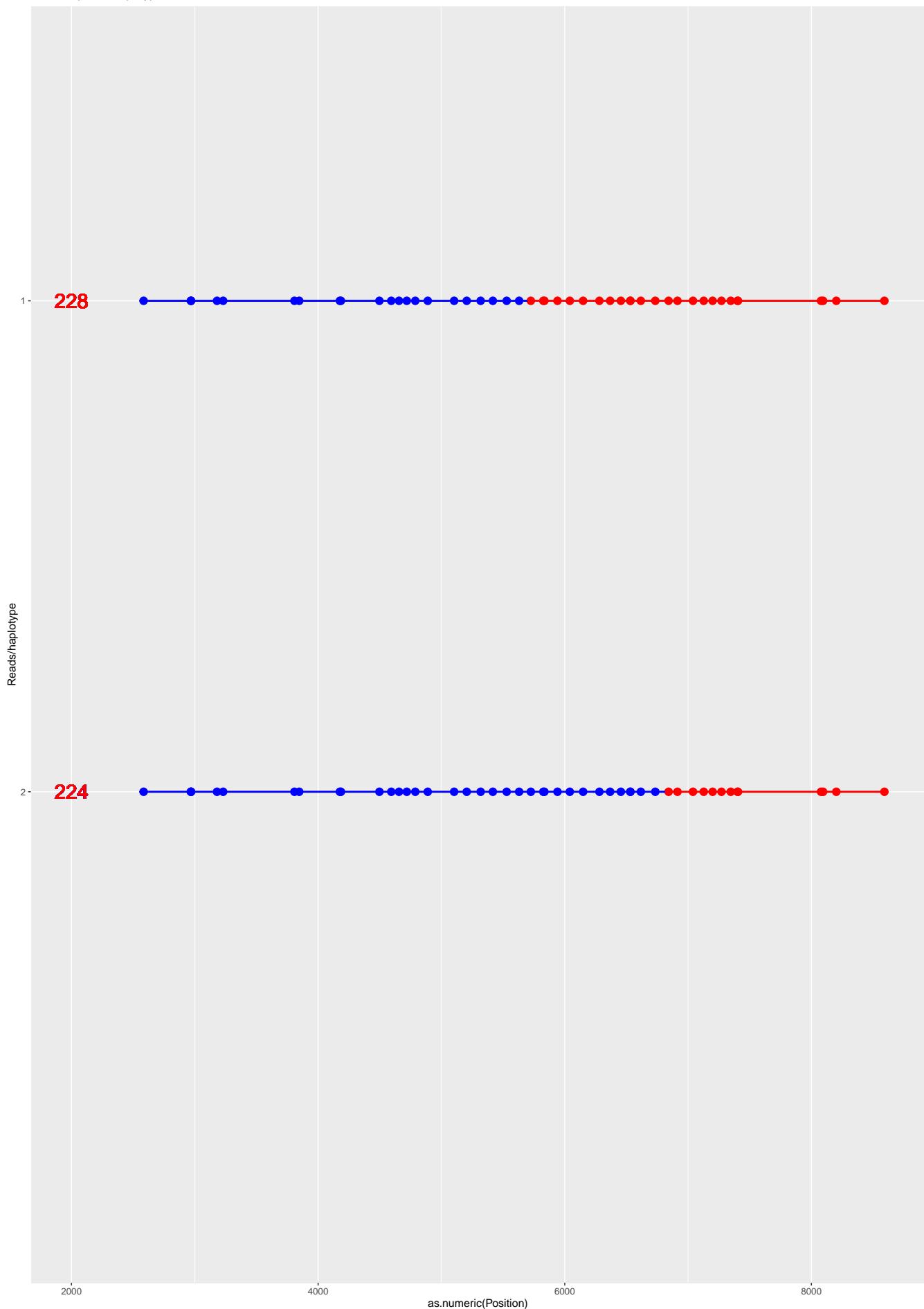


Sample = 152c tetrad = 152 spore = c

Total reads = 635 PCR=387

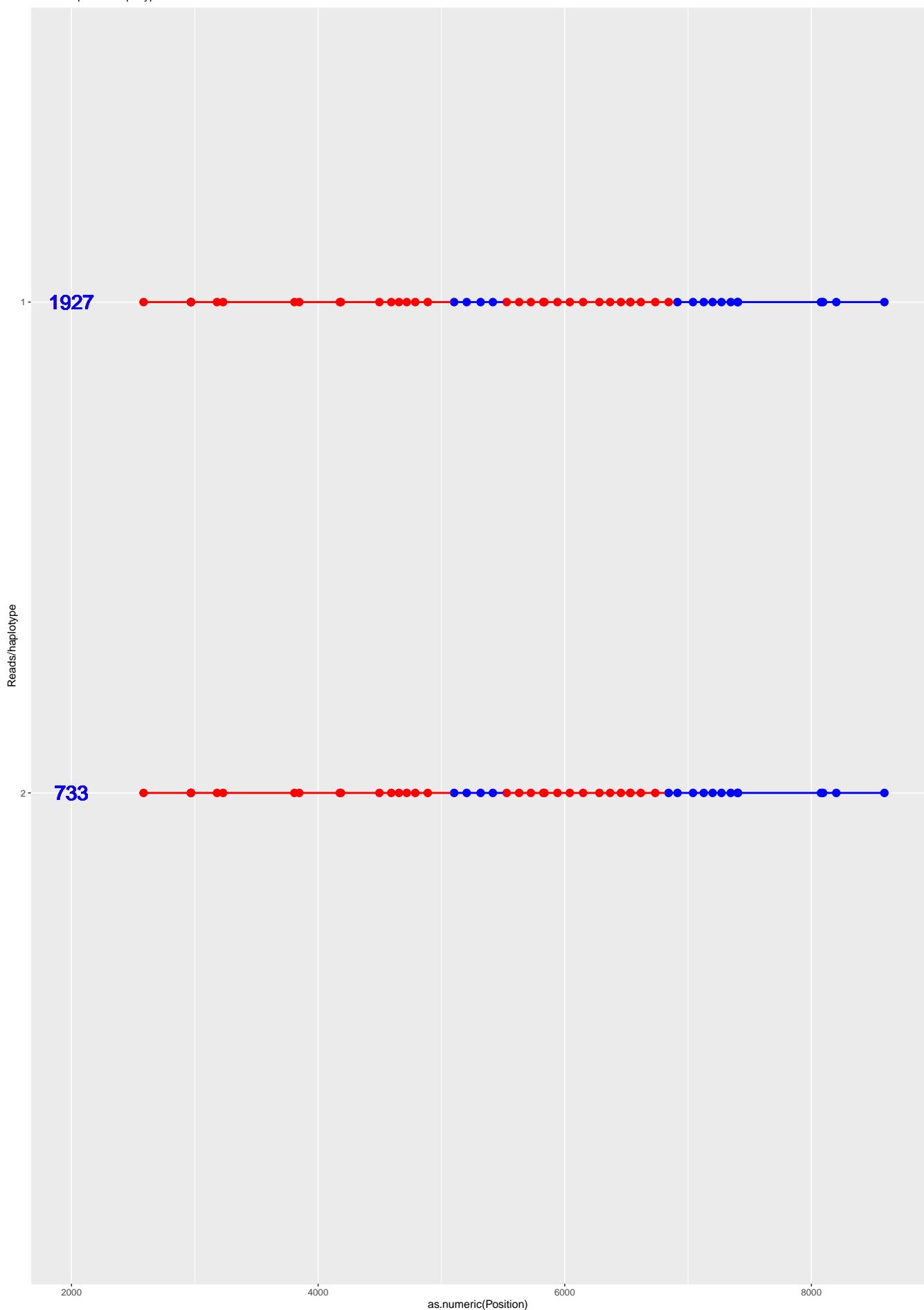
haplotypes I began with n[supporting reads] = 224, 228

most frequent 7 haplotypes.



barcode = CGTAGCGTGCTATCAC & ATCATATGATGCGACA

Sample = 152d tetrad = 152 spore = d
Total reads = 3035 PCR=388
haplotypes I began with n[supporting reads] = 733, 1927
most frequent 7 haplotypes.



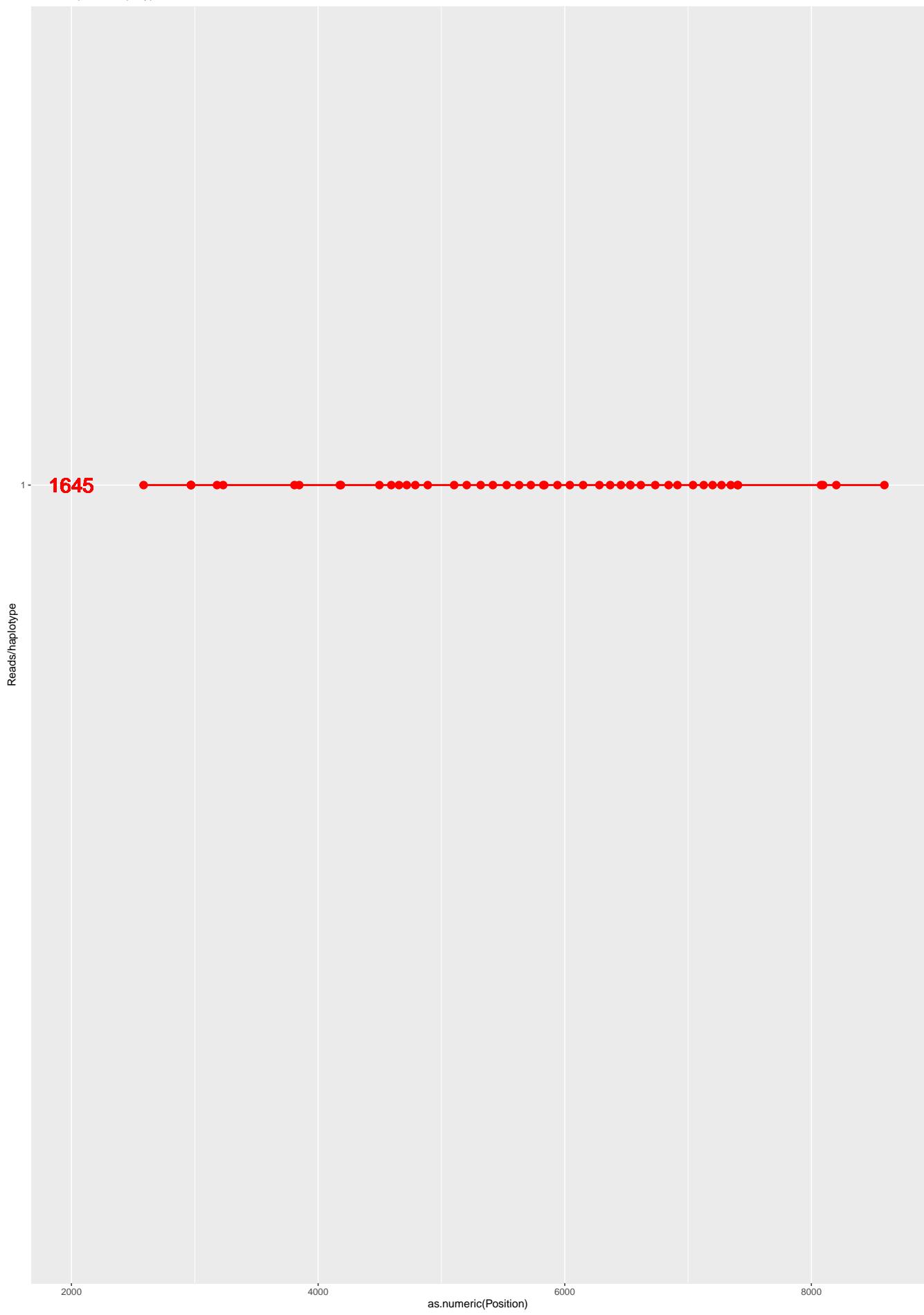
barcode = CGTAGCGTGCTATCAC & AGACGTTAGATCACAGC

Sample = 153a tetrad = 153 spore = a

Total reads = 1703 PCR=389

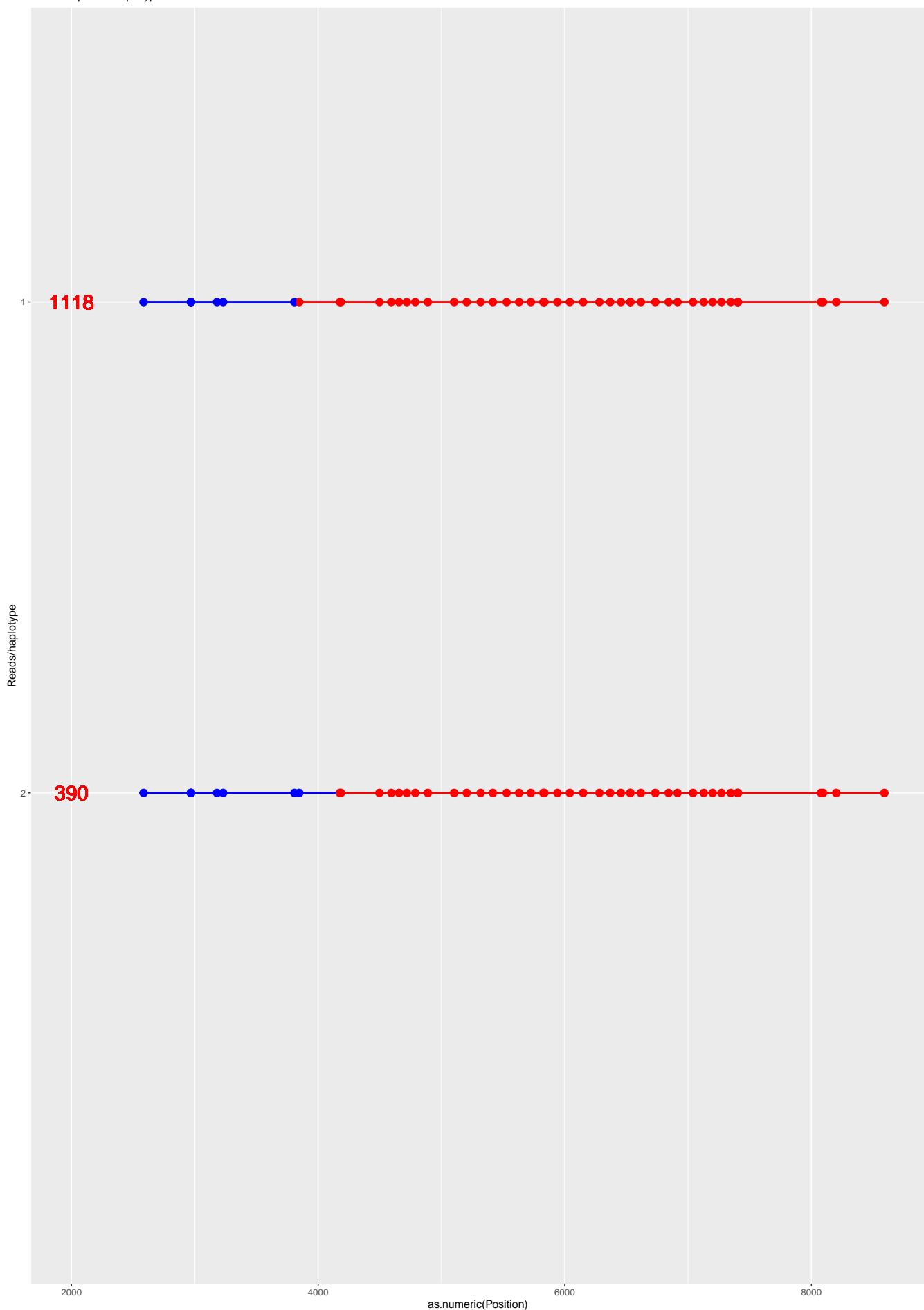
haplotypes I began with n[supporting reads] = 1645

most frequent 7 haplotypes.



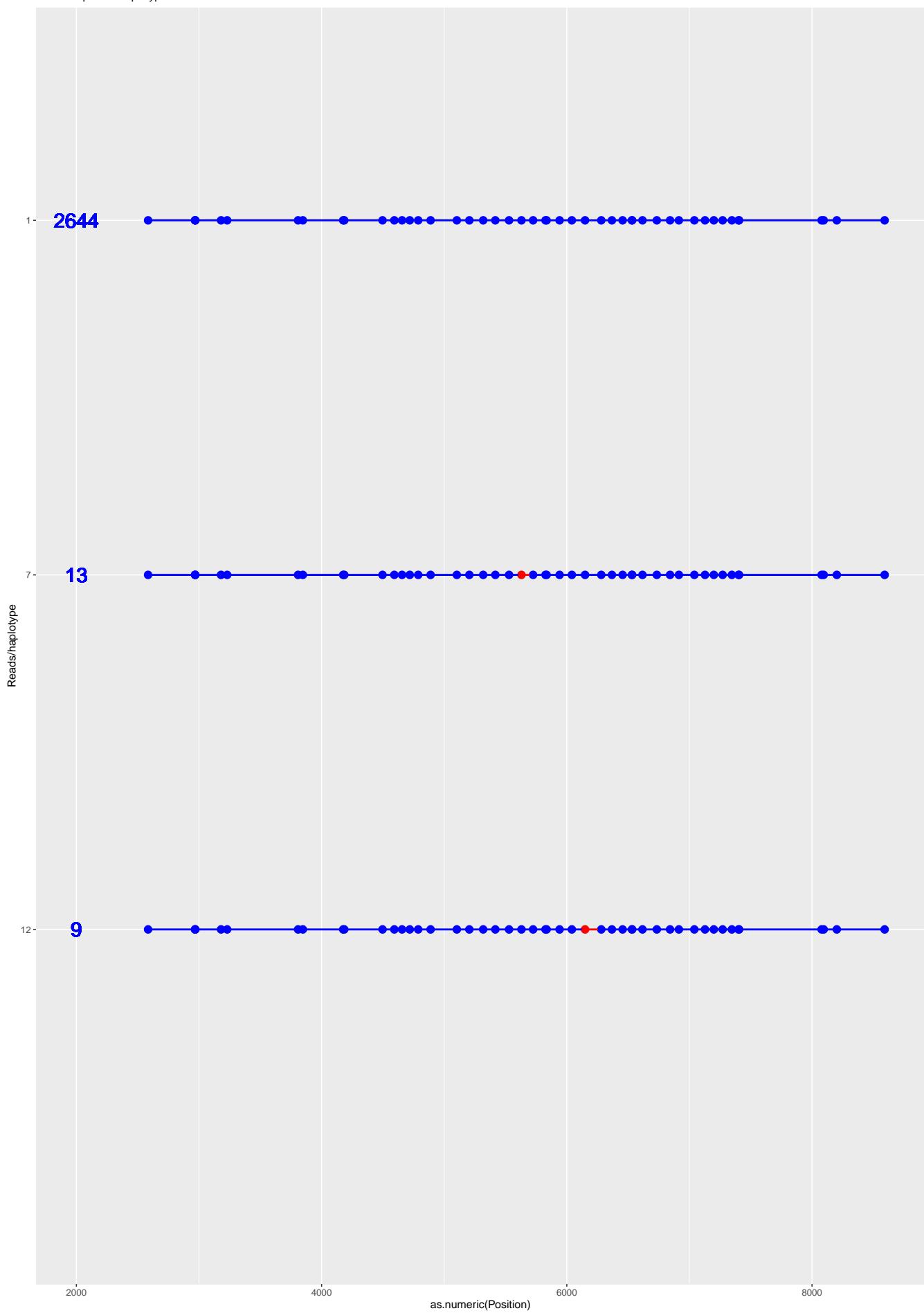
barcode = CGTAGCGTGCTATCAC & CGTGTCACTGCTACTCA

Sample = 153b tetrad = 153 spore = b
Total reads = 1598 PCR=390
haplotypes I began with n[supporting reads] = 390, 1118
most frequent 7 haplotypes.



barcode = CGTAGCGTGCTATCAC & TGTGAGACTGCATGTC

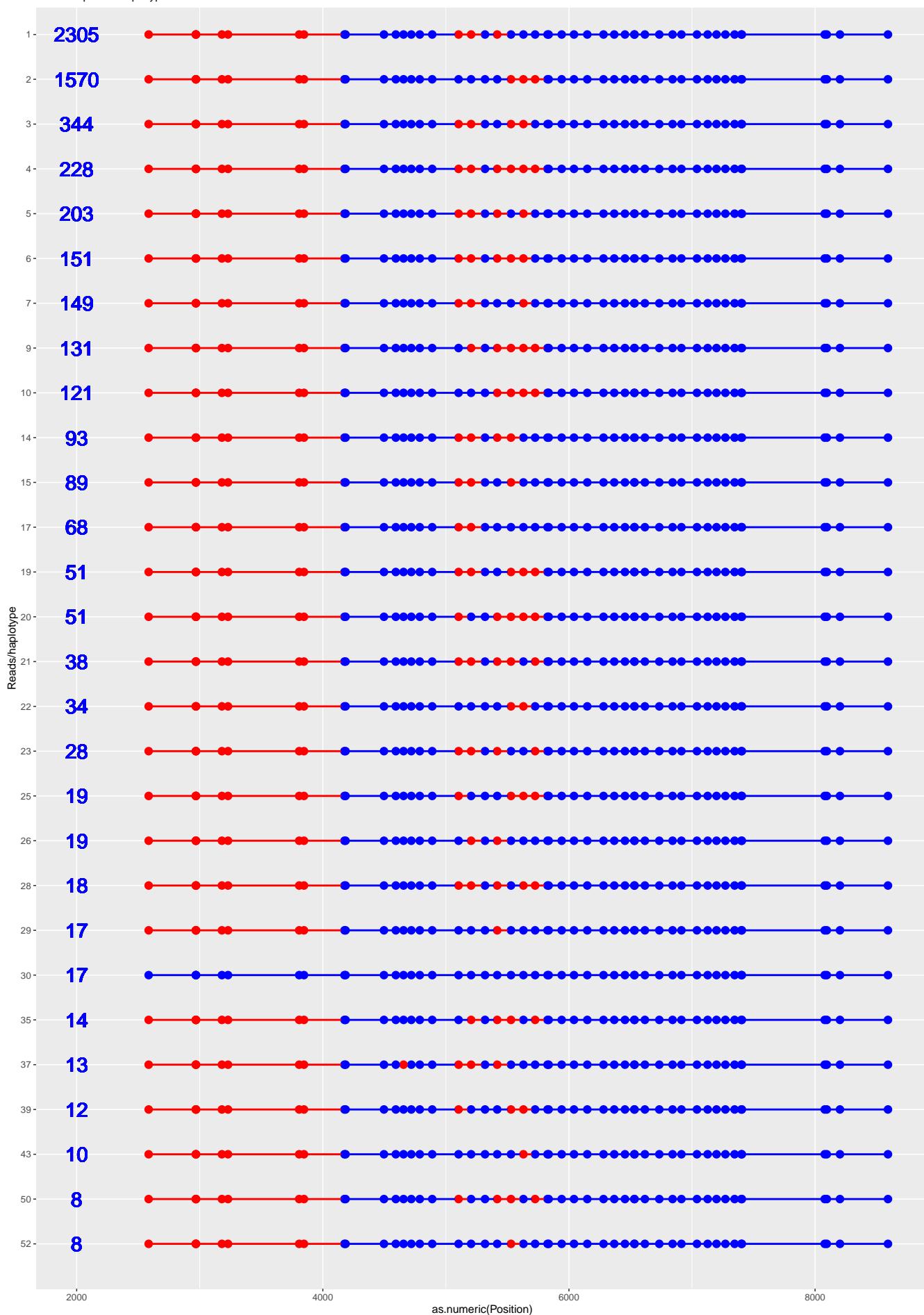
Sample = 153c tetrad = 153 spore = c
Total reads =3121 PCR=391
haplotypes I began with [n|supporting reads] = 9, 13, 2644
most frequent 7 haplotypes.



Sample = 153d tetrad = 153 spore = d

Total reads = 7360 PCR=392

haplotypes I began with [n(supporting reads)] = 8, 10, 12, 13, 14, 17, 18, 19, 28, 34, 38, 51, 68, 89, 93, 121, 131, 149, 151, 203, 228, 344, 1570, 2305
most frequent 7 haplotypes.

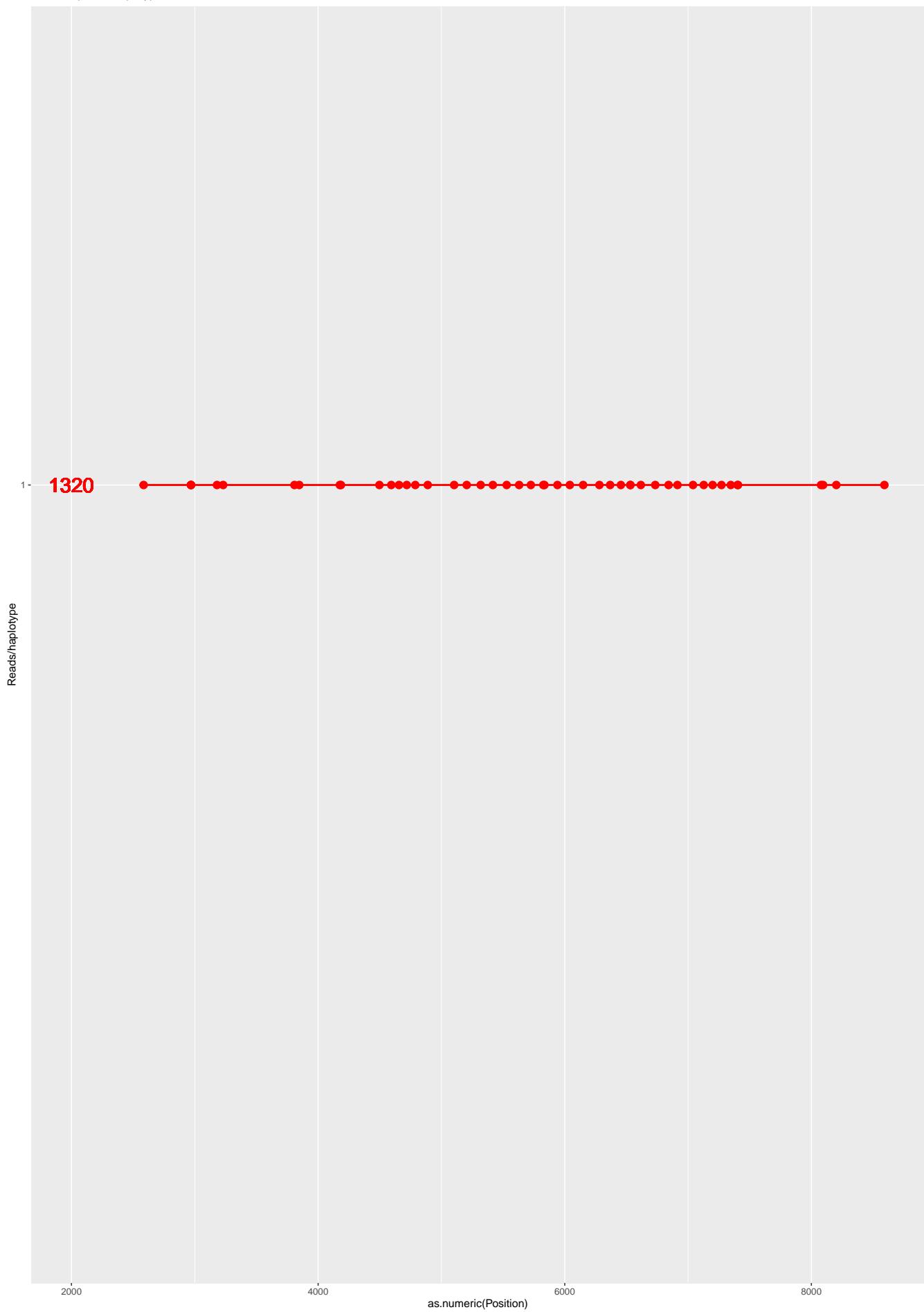


Sample = 157a tetrad = 157 spore = a

Total reads = 1375 PCR=397

haplotypes I began with n[supporting reads] = 1320

most frequent 7 haplotypes.



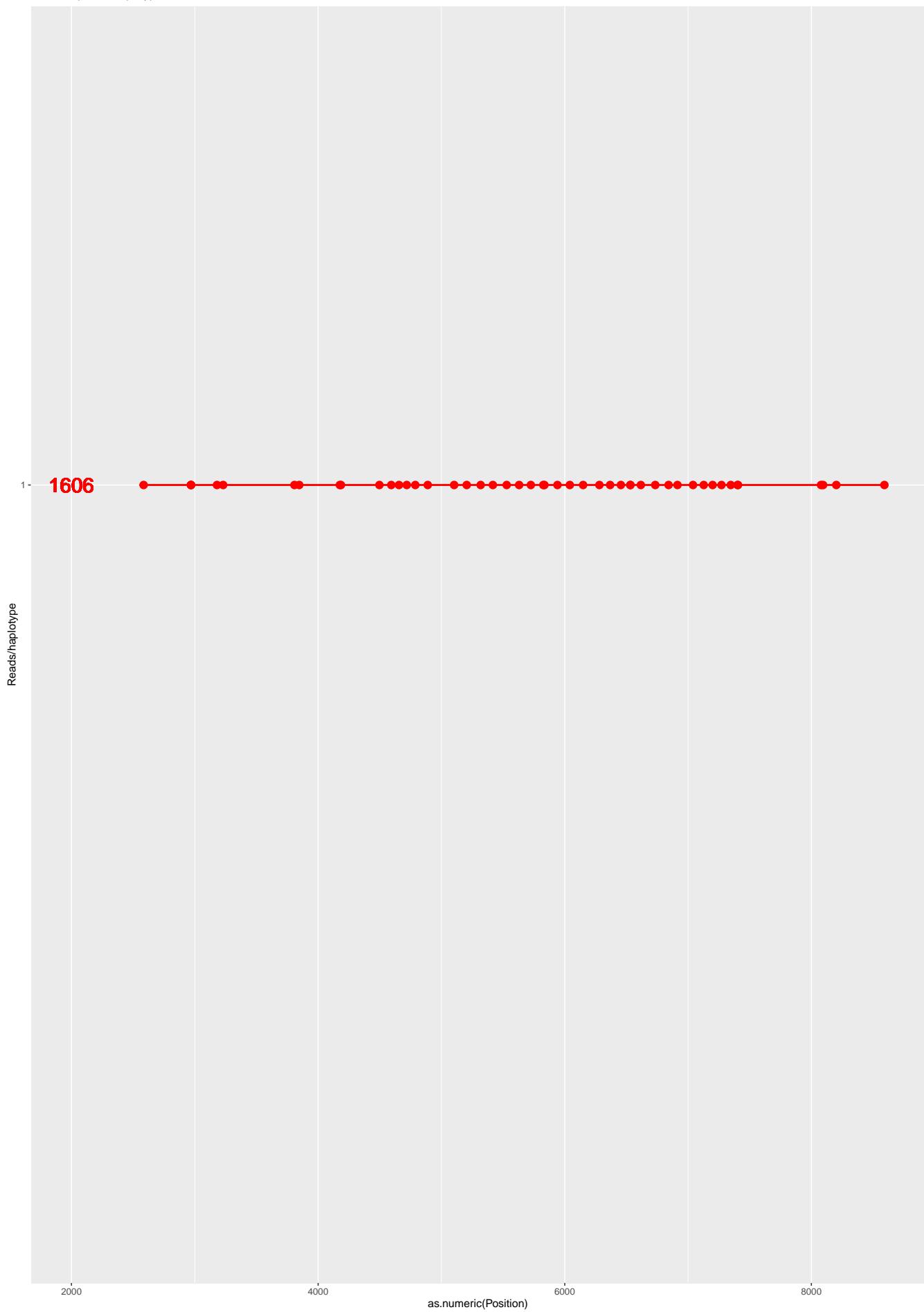
barcode = ATGCTGATGACTGCGA & CGTGTCACTGCTACTCA

Sample = 157b tetrad = 157 spore = b

Total reads = 1682 PCR=398

haplotypes I began with n[supporting reads] = 1606

most frequent 7 haplotypes.

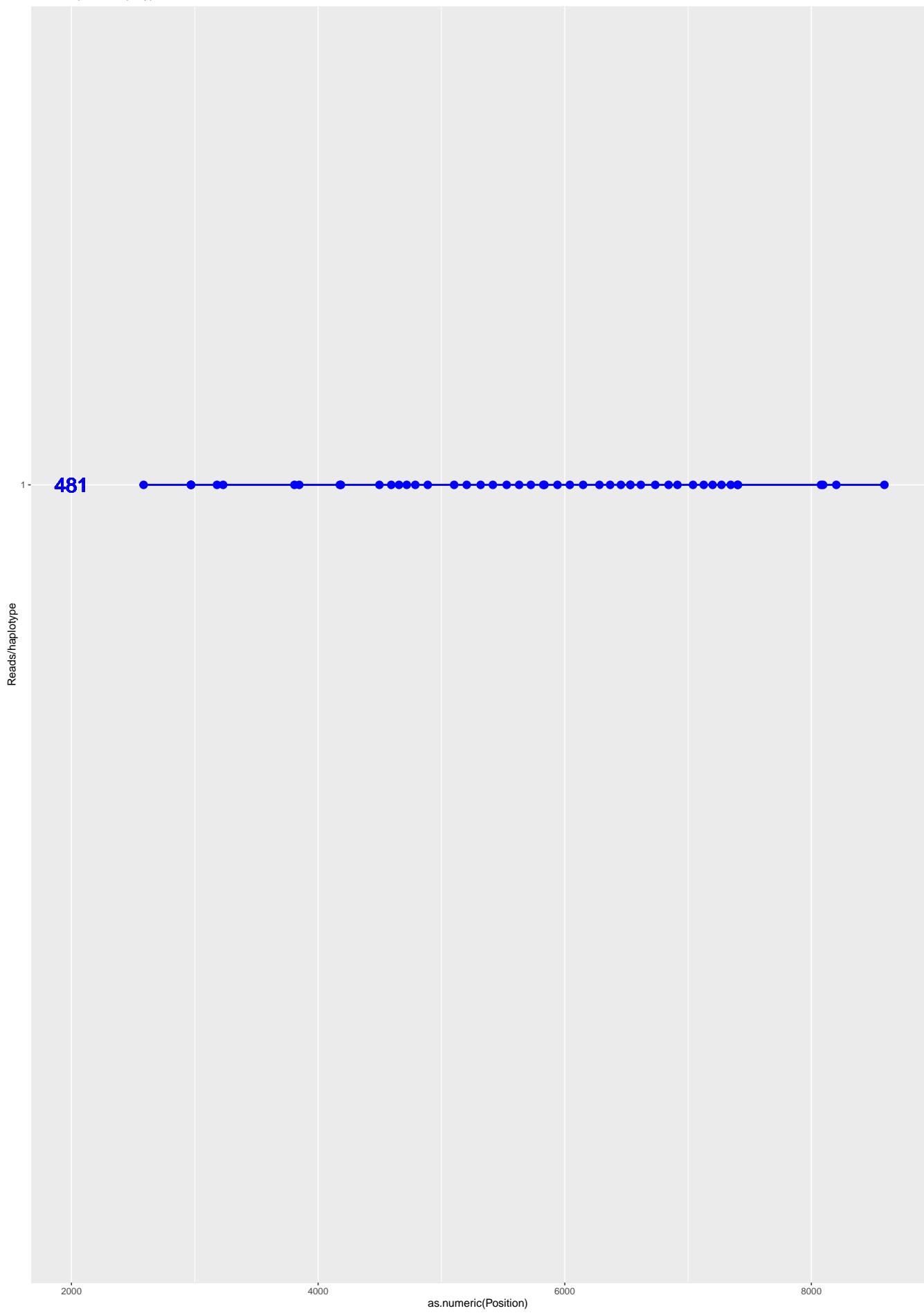


Sample = 157c tetrad = 157 spore = c

Total reads =567 PCR=399

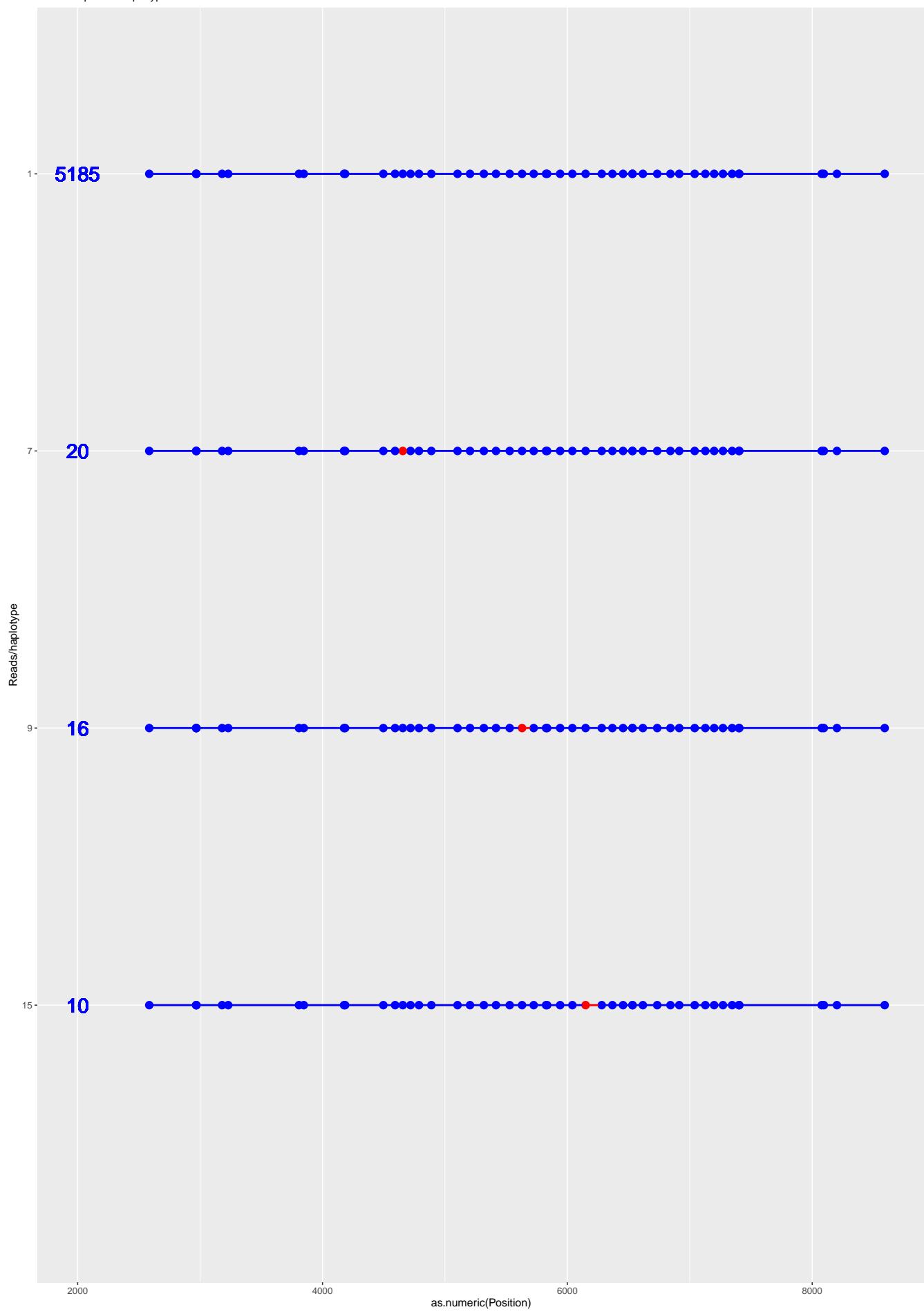
haplotypes I began with n[supporting reads] = 481

most frequent 7 haplotypes.



barcode = ATGCTGATGACTGCGA & GCTCAGTGCCTACTG

Sample = 157d tetrad = 157 spore = d
Total reads = 6024 PCR=400
haplotypes I began with [n:supporting reads] = 10, 16, 20, 5185
most frequent 7 haplotypes.



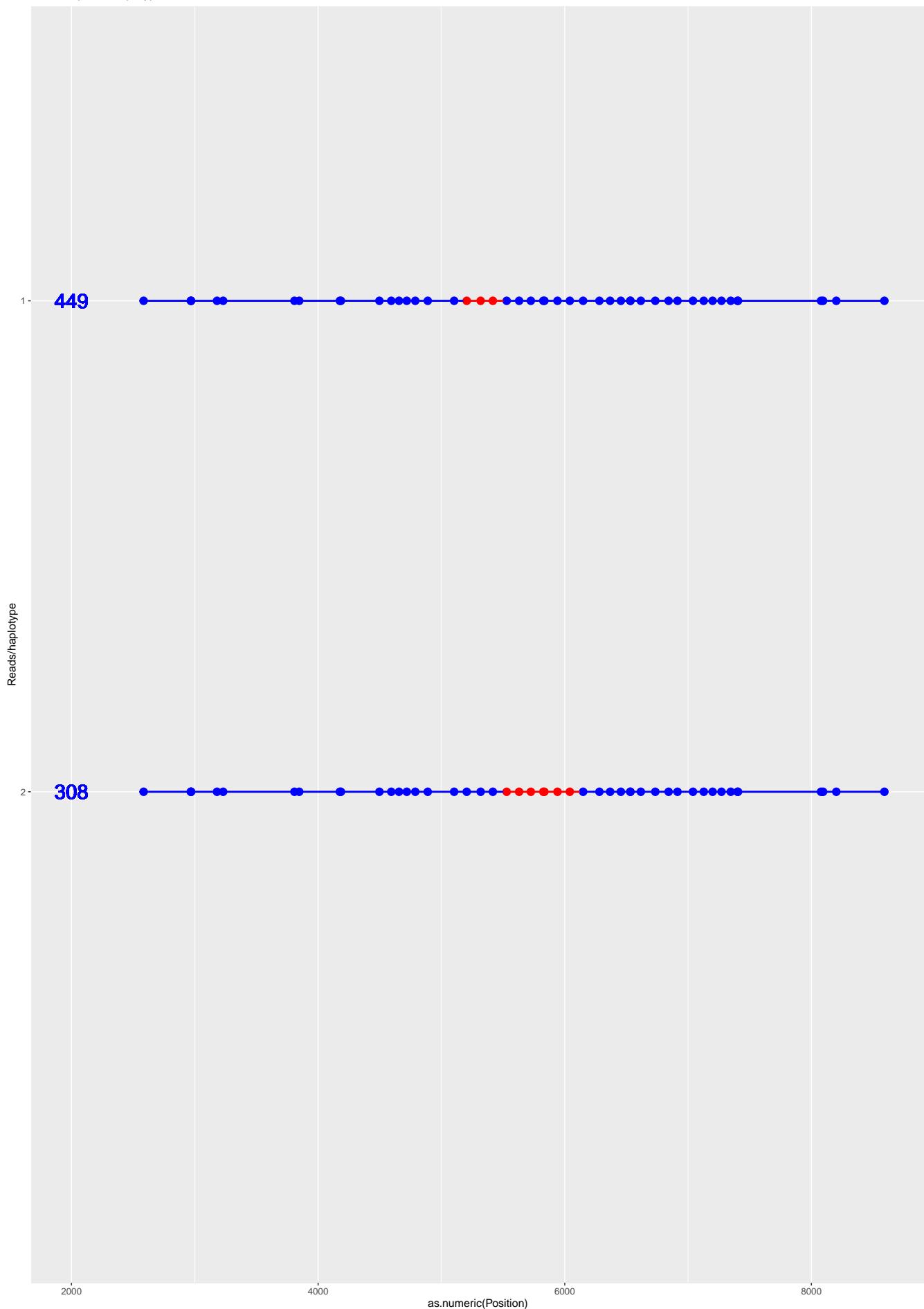
barcode = ATGCTGATGACTGCGA & ACTATCGCGACGCAG

Sample = 158a tetrad = 158 spore = a

Total reads = 1266 PCR=401

haplotypes I began with n[supporting reads] = 308, 449

most frequent 7 haplotypes.



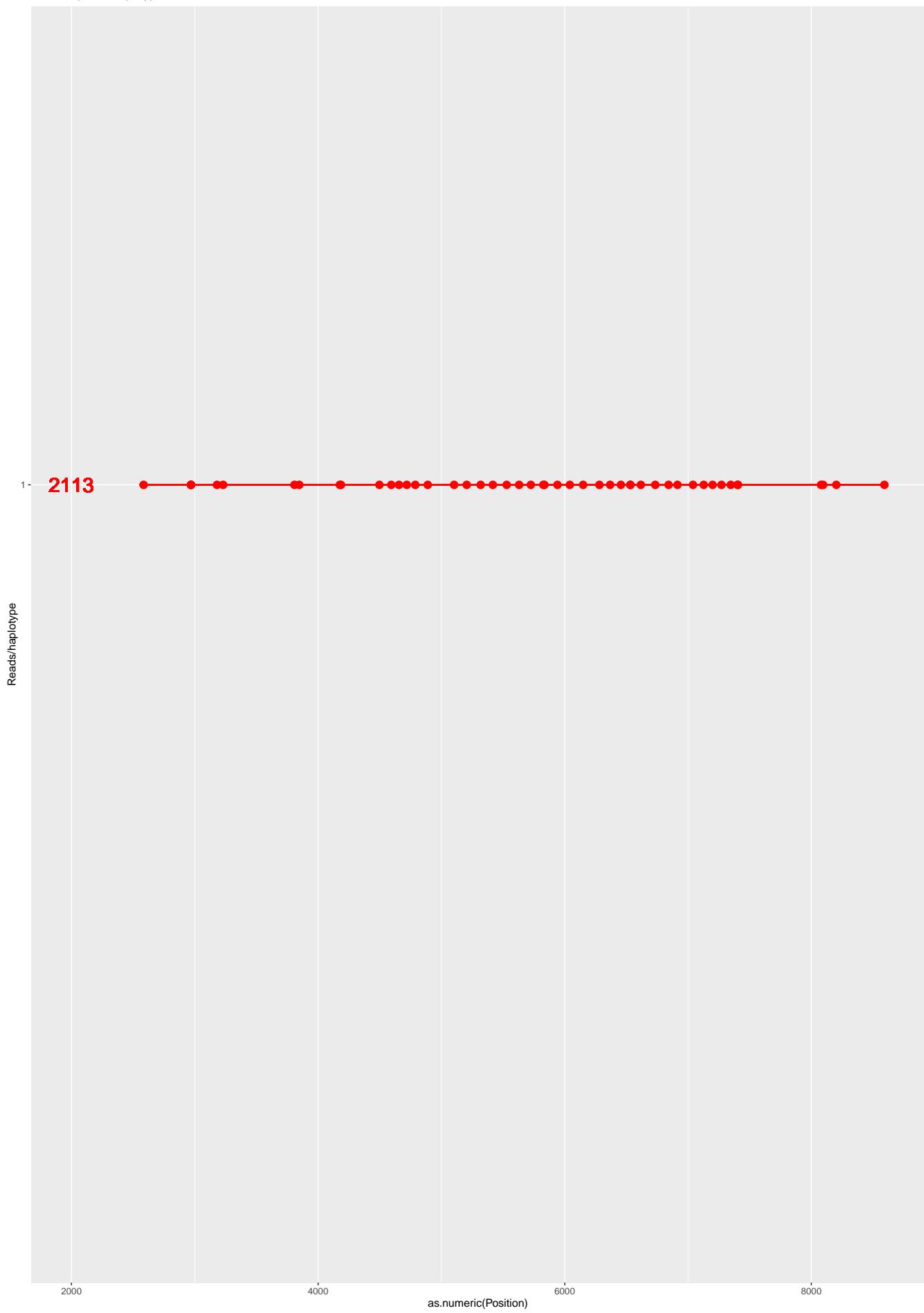
barcode = TGC GTGAGCTGTACAT & GCGACGAGTACTCATG

Sample = 158b tetrad = 158 spore = b

Total reads = 2207 PCR=402

haplotypes I began with n[supporting reads] = 2113

most frequent 7 haplotypes.



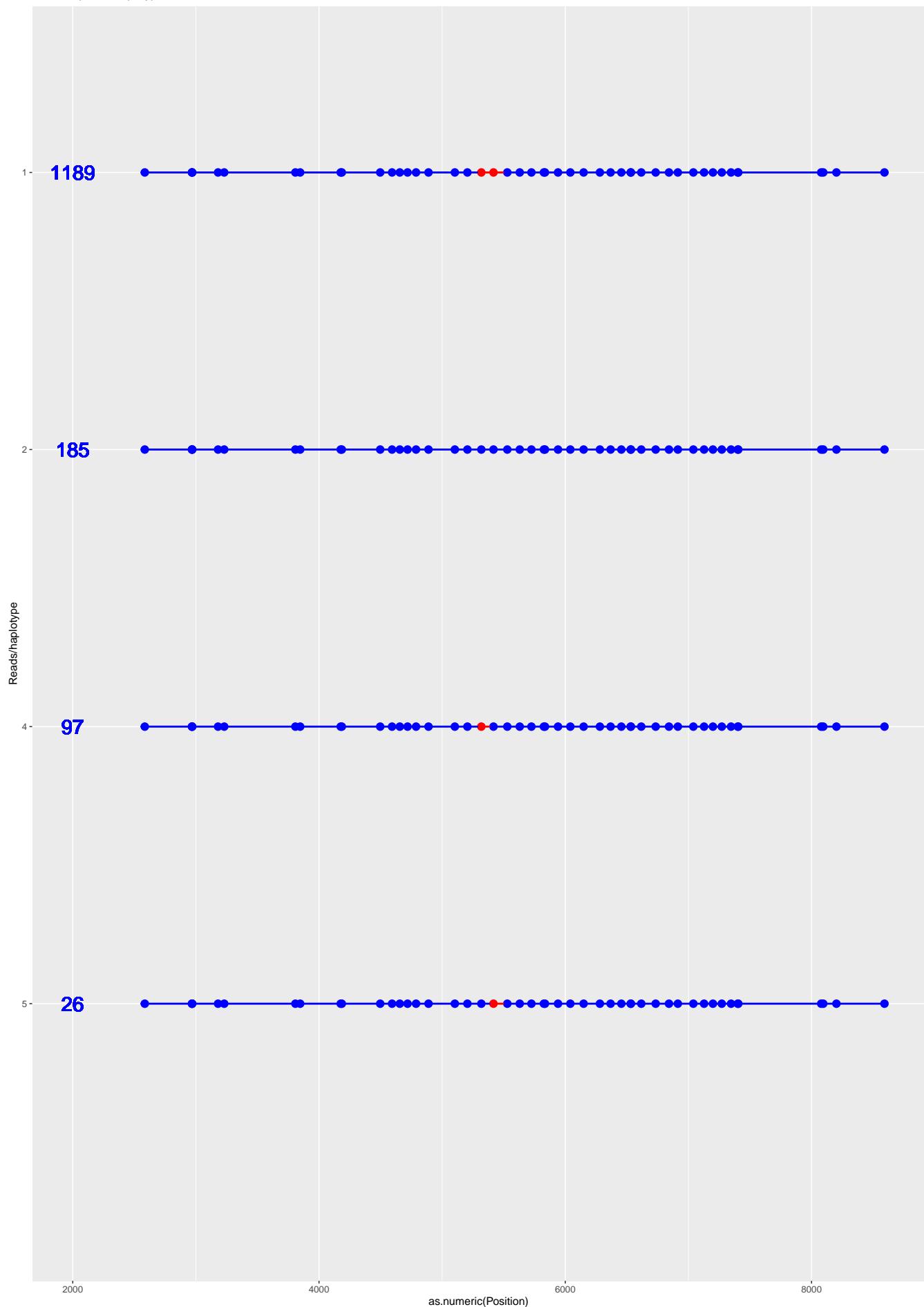
barcode = TGC GTGAGCTGTACAT & AGTATCACAGTCGCTG

Sample = 158c tetrad = 158 spore = c

Total reads = 1833 PCR=403

haplotypes I began with n[supporting reads] = 26, 97, 185, 1189

most frequent 7 haplotypes.

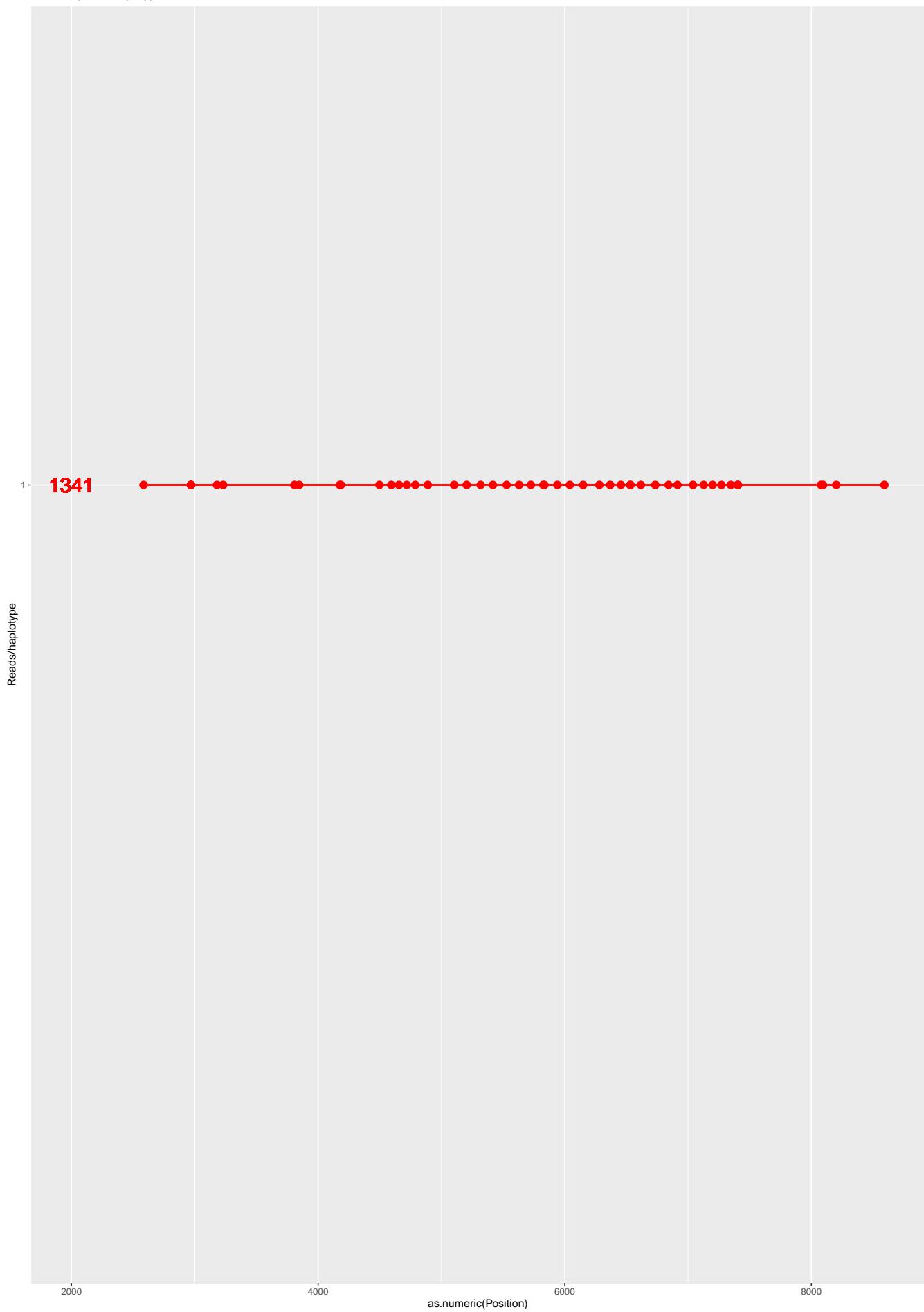


Sample = 158d tetrad = 158 spore = d

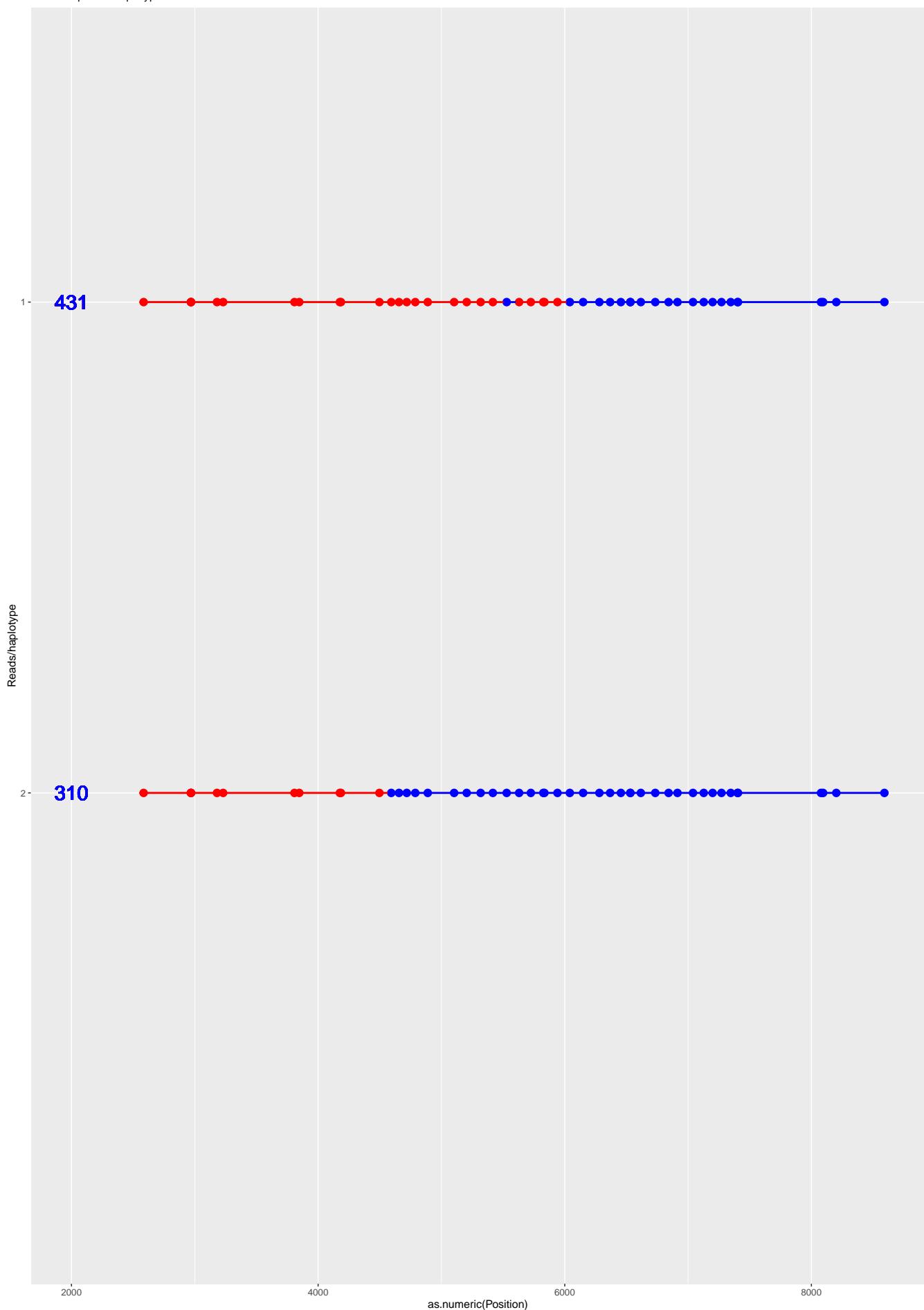
Total reads = 1402 PCR=404

haplotypes I began with n[supporting reads] = 1341

most frequent 7 haplotypes.



Sample = 159a tetrad = 159 spore = a
Total reads = 1221 PCR=405
haplotypes I began with n[supporting reads] = 310, 431
most frequent 7 haplotypes.



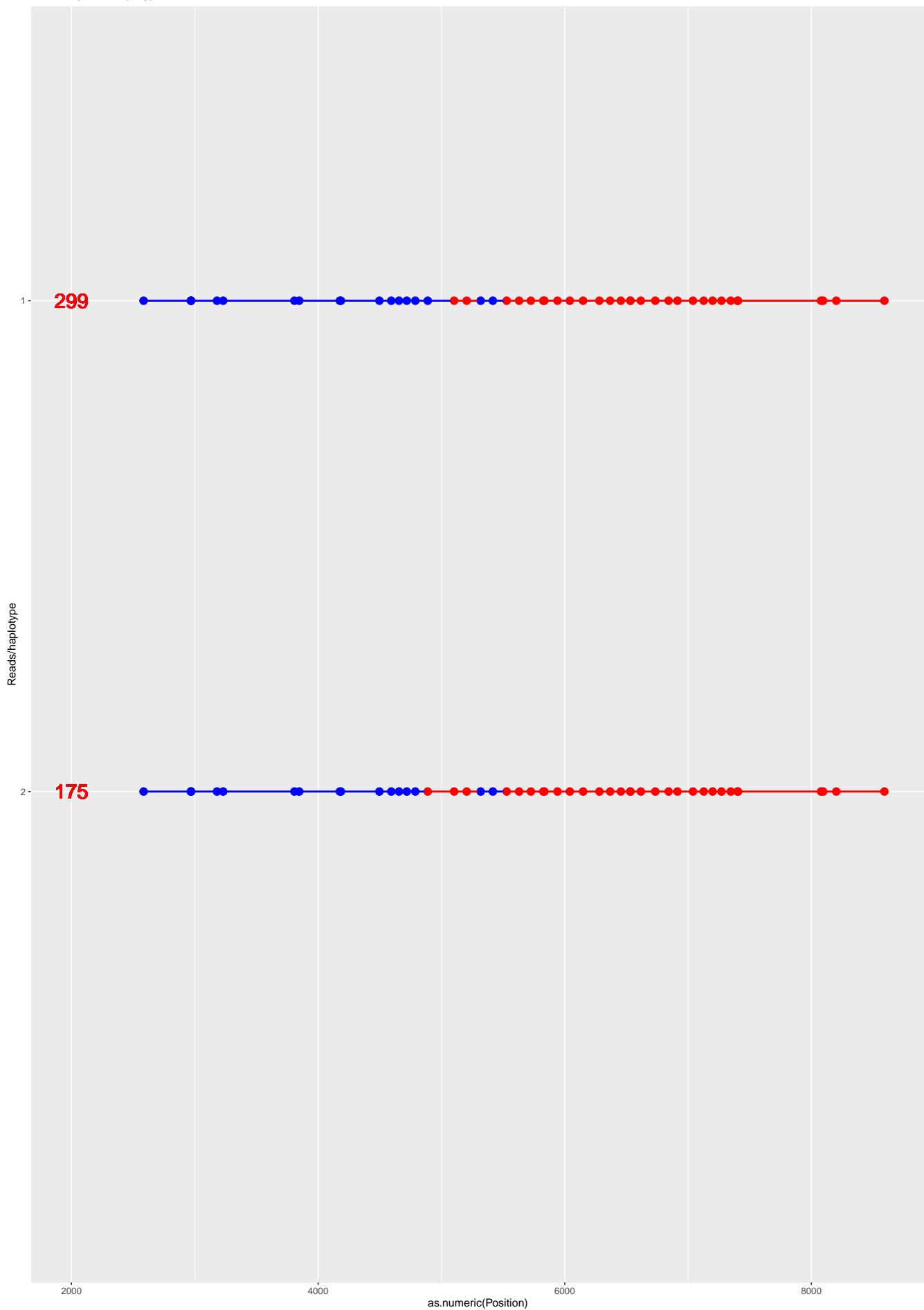
barcode = TGC GTGAGCTGTACAT & CGT GTCATGCTACTCA

Sample = 159b tetrad = 159 spore = b

Total reads =537 PCR=406

haplotypes I began with n[supporting reads] = 175, 299

most frequent 7 haplotypes.



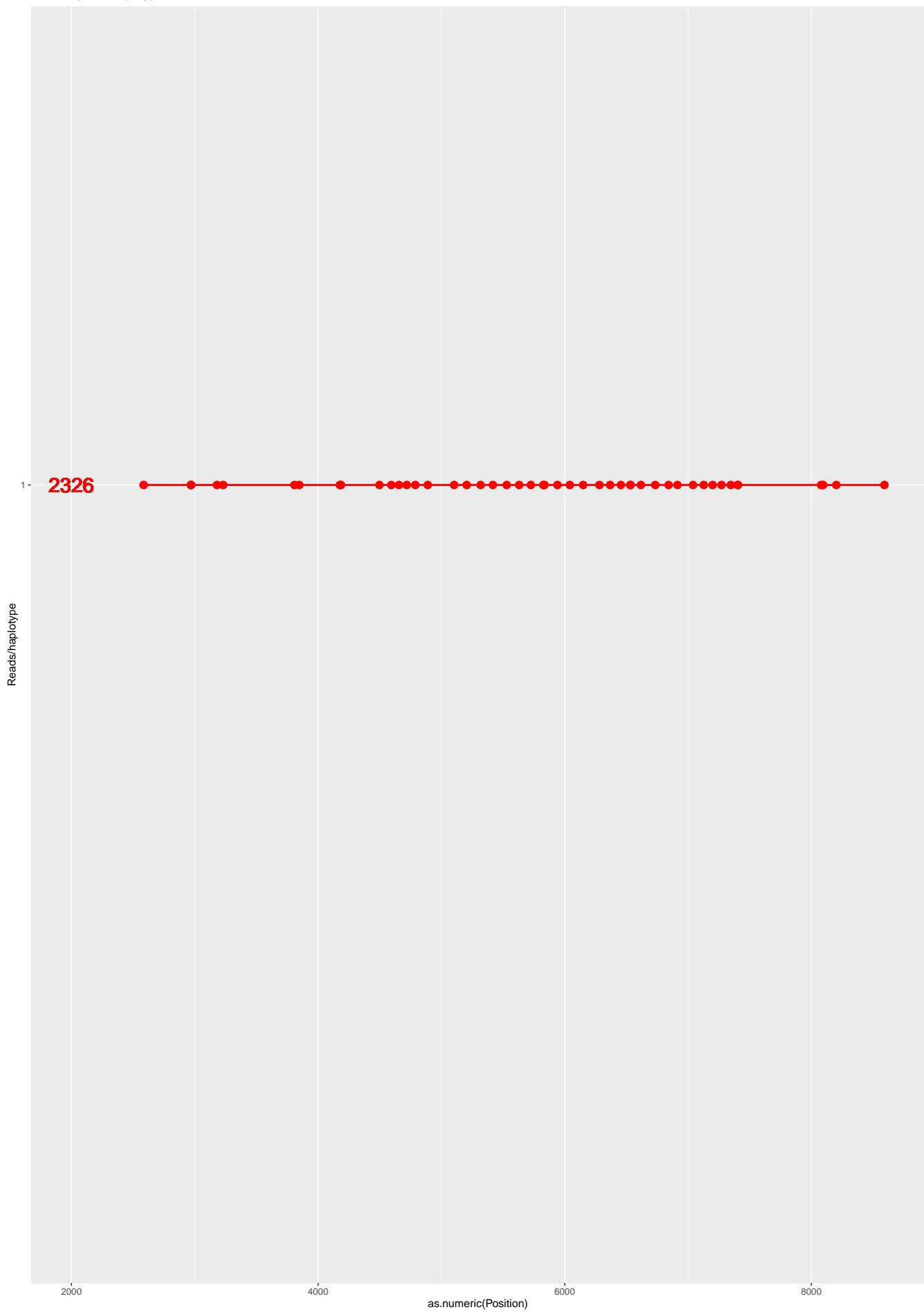
barcode = TGC GTGAGCTGTACAT & TGTGAGACTGCATGTC

Sample = 159c tetrad = 159 spore = c

Total reads = 2435 PCR=407

haplotypes I began with n[supporting reads] = 2326

most frequent 7 haplotypes.



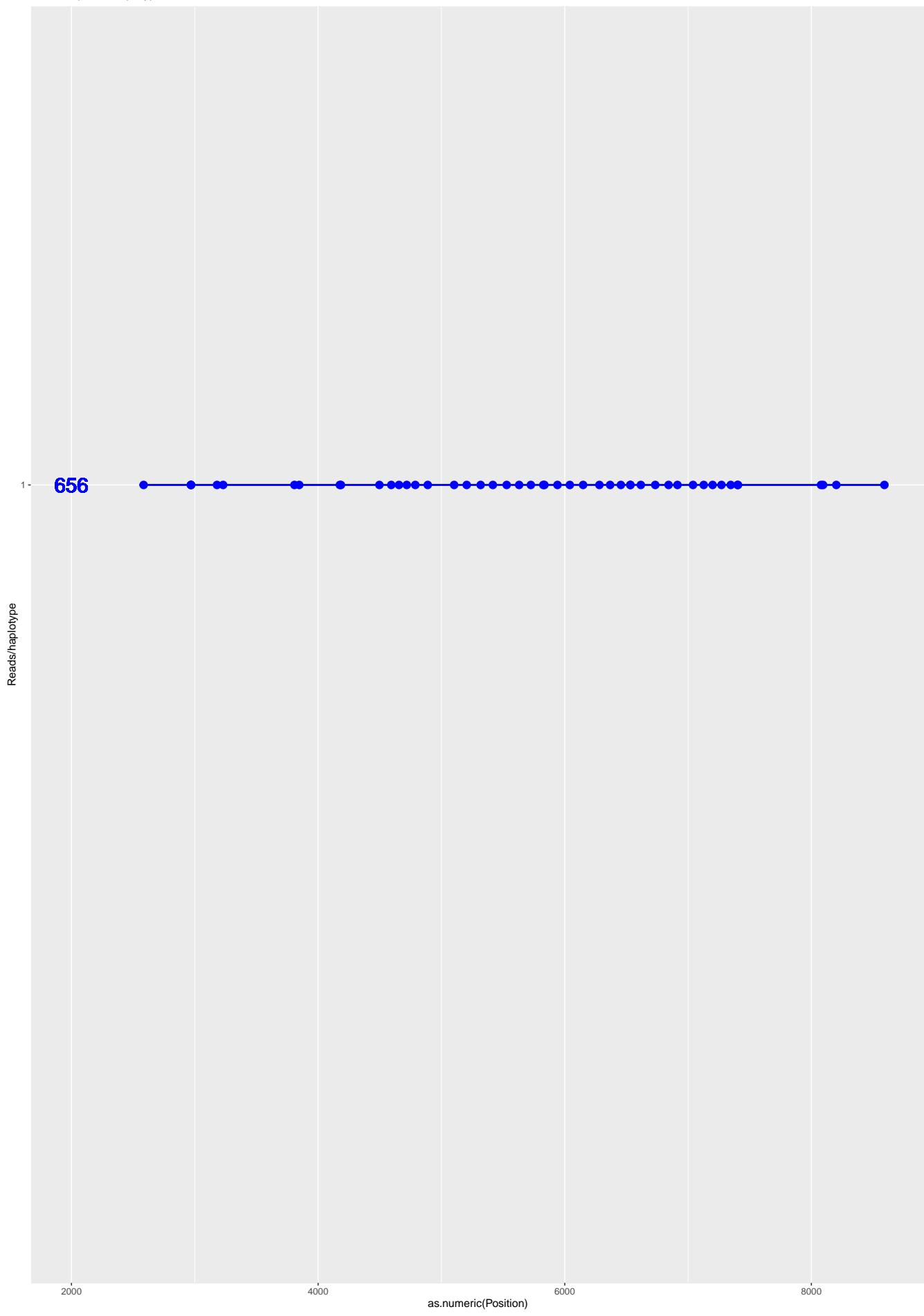
barcode = TGCCTGAGCTGTACAT & GCTCAGTGCCTACTG

Sample = 159d tetrad = 159 spore = d

Total reads = 783 PCR=408

haplotypes I began with n[supporting reads] = 656

most frequent 7 haplotypes.



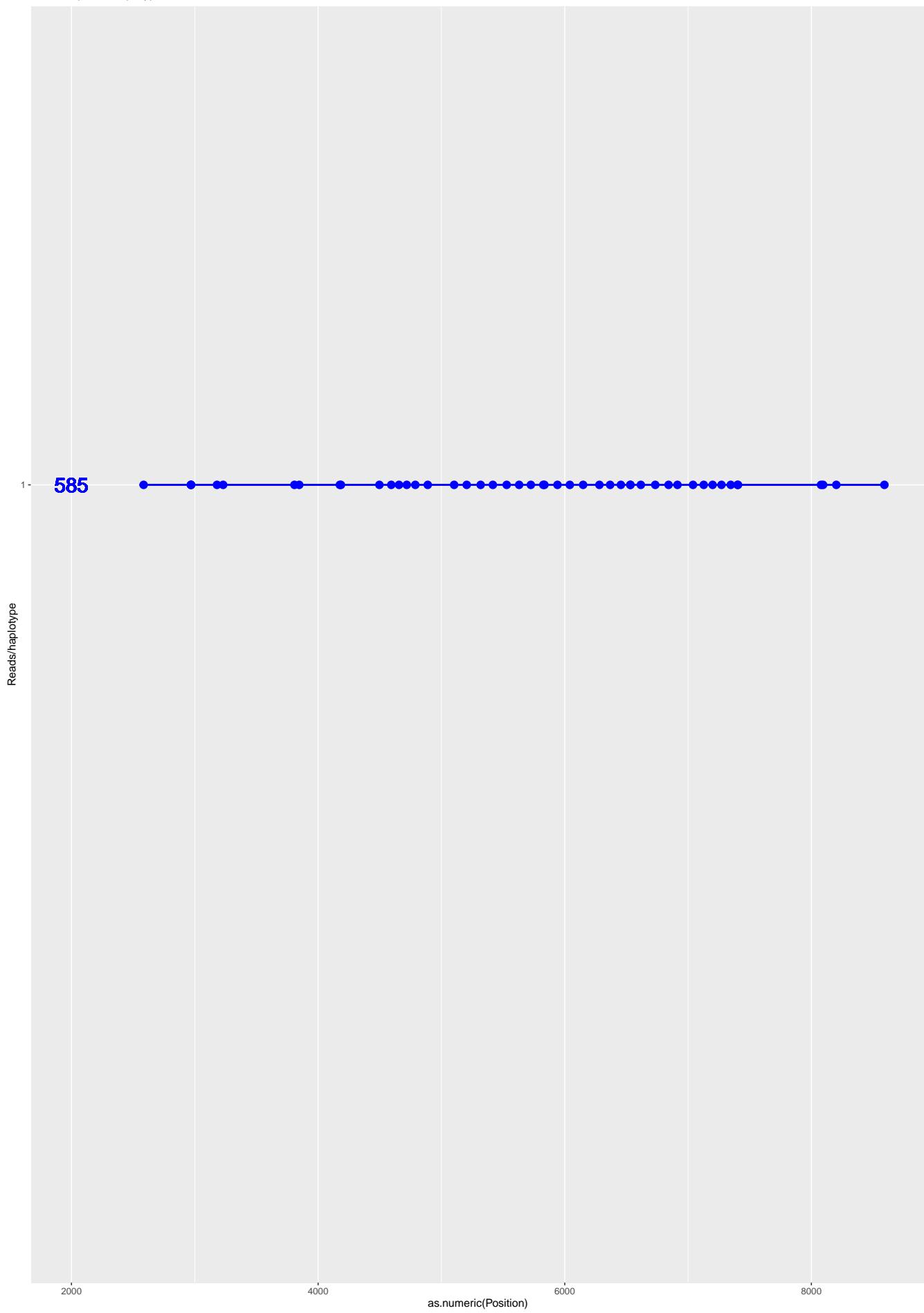
barcode = TGCCTGAGCTGTACAT & ACTATCGCGCACGCAG

Sample = 160a tetrad = 160 spore = a

Total reads = 668 PCR=409

haplotypes I began with n[supporting reads] = 585

most frequent 7 haplotypes.



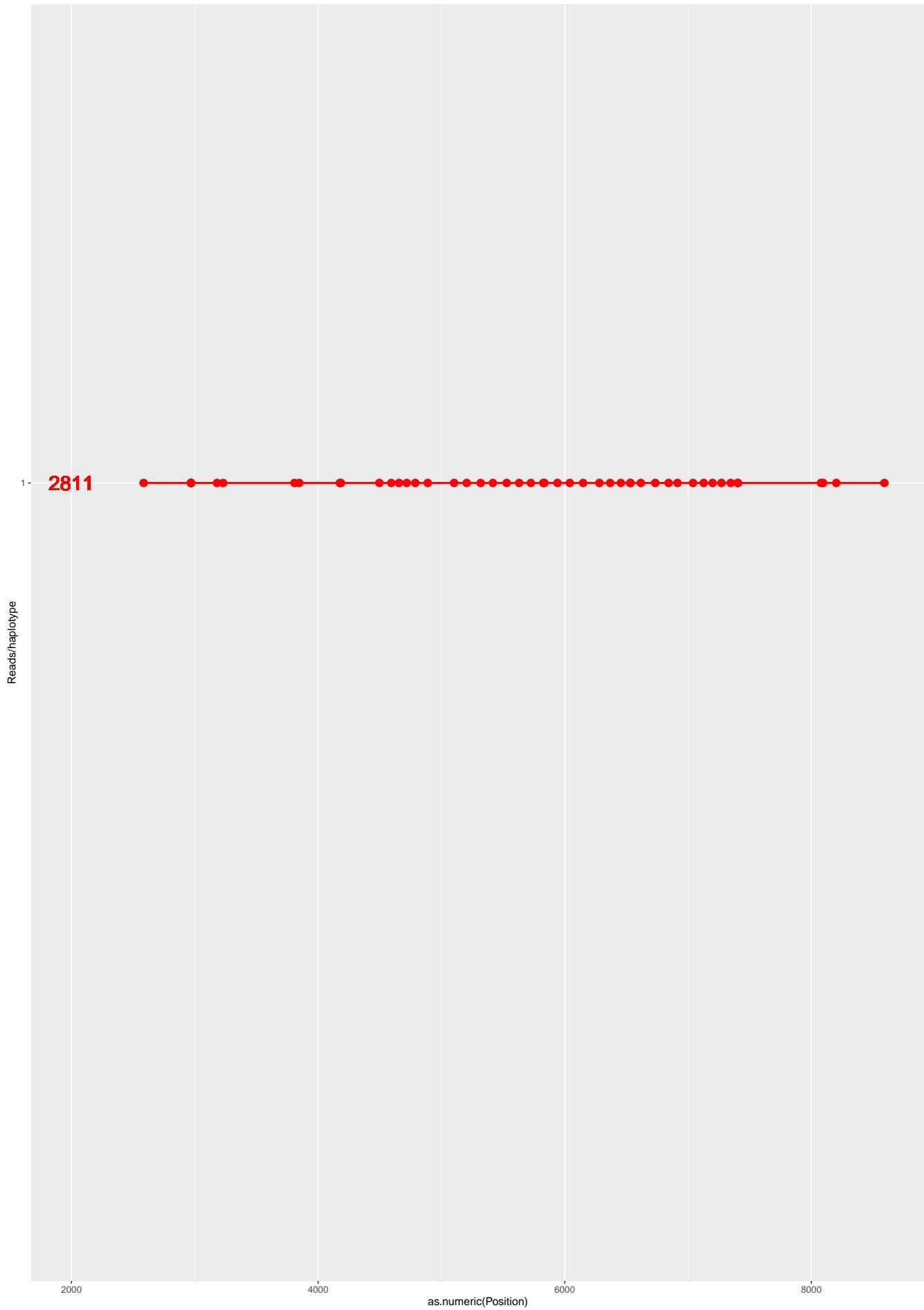
barcode = CGATCATCTATAGACA & GCGACGAGTACTCATG

Sample = 160b tetrad = 160 spore = b

Total reads = 2914 PCR=410

haplotypes I began with n[supporting reads] = 2811

most frequent 7 haplotypes.



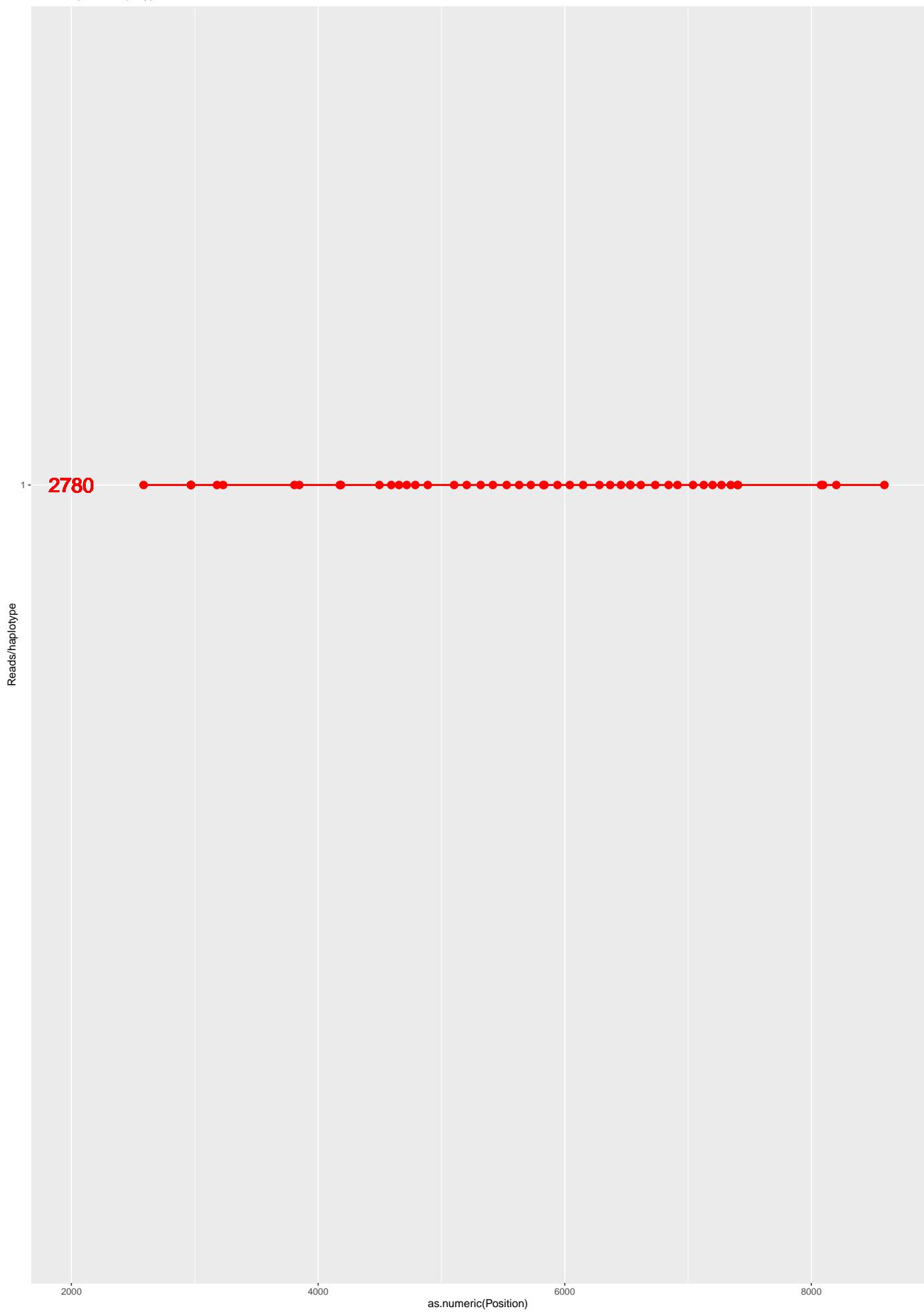
barcode = CGATCATCTATAAGACA & AGTATCACAGTCGCTG

Sample = 160c tetrad = 160 spore = c

Total reads = 2894 PCR=411

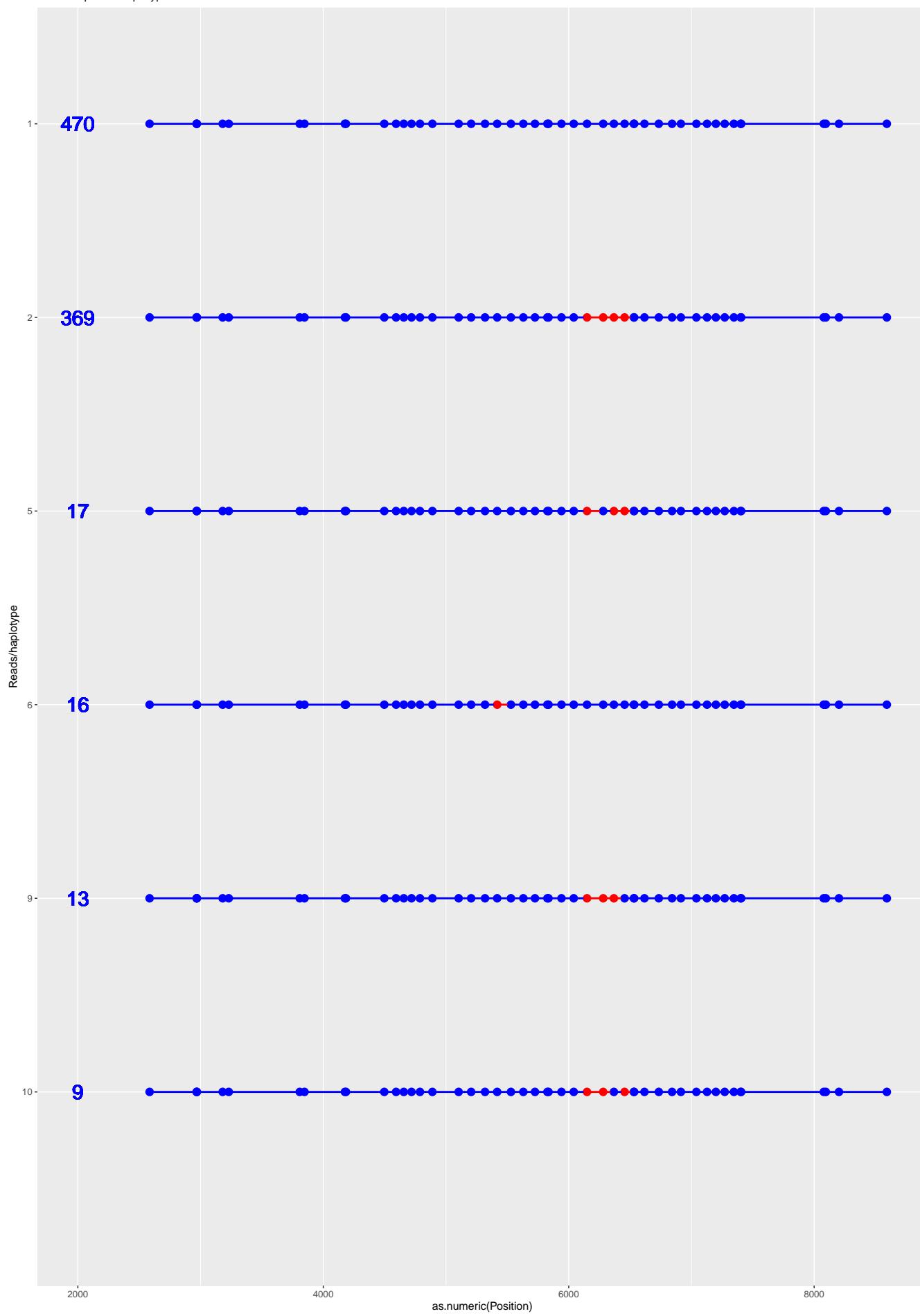
haplotypes I began with n[supporting reads] = 2780

most frequent 7 haplotypes.



barcode = CGATCATCTATAGACA & ATCATATGATGCGACA

Sample = 160d tetrad = 160 spore = d
Total reads = 1187 PCR=412
haplotypes I began with [n|supporting reads] = 9, 13, 16, 17, 369, 470
most frequent 7 haplotypes.



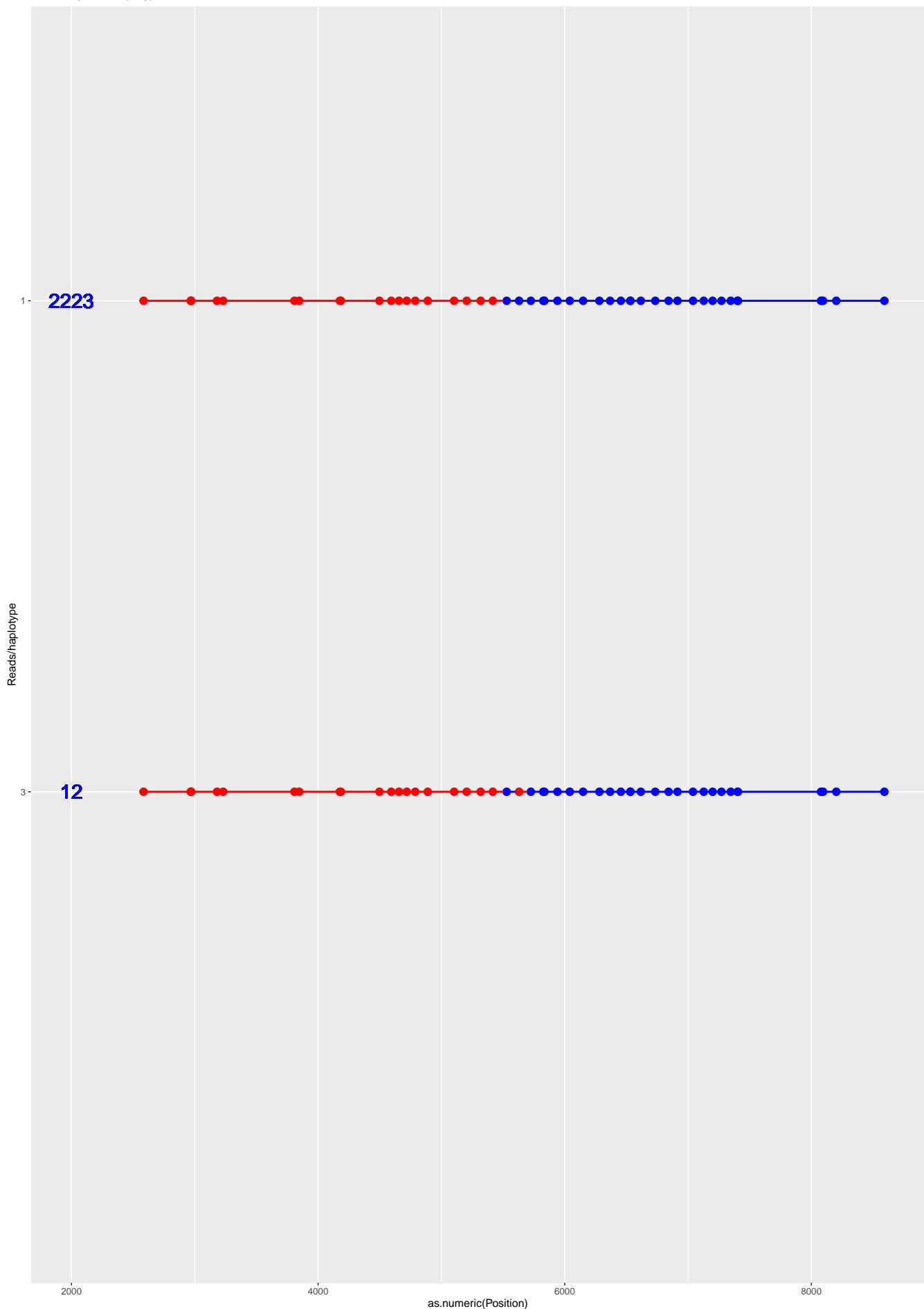
barcode = CGATCATCTATAGACA & AGACGTTAGATCACAGC

Sample = 161a tetrad = 161 spore = a

Total reads = 2420 PCR=413

haplotypes I began with n[supporting reads] = 12, 2223

most frequent 7 haplotypes.



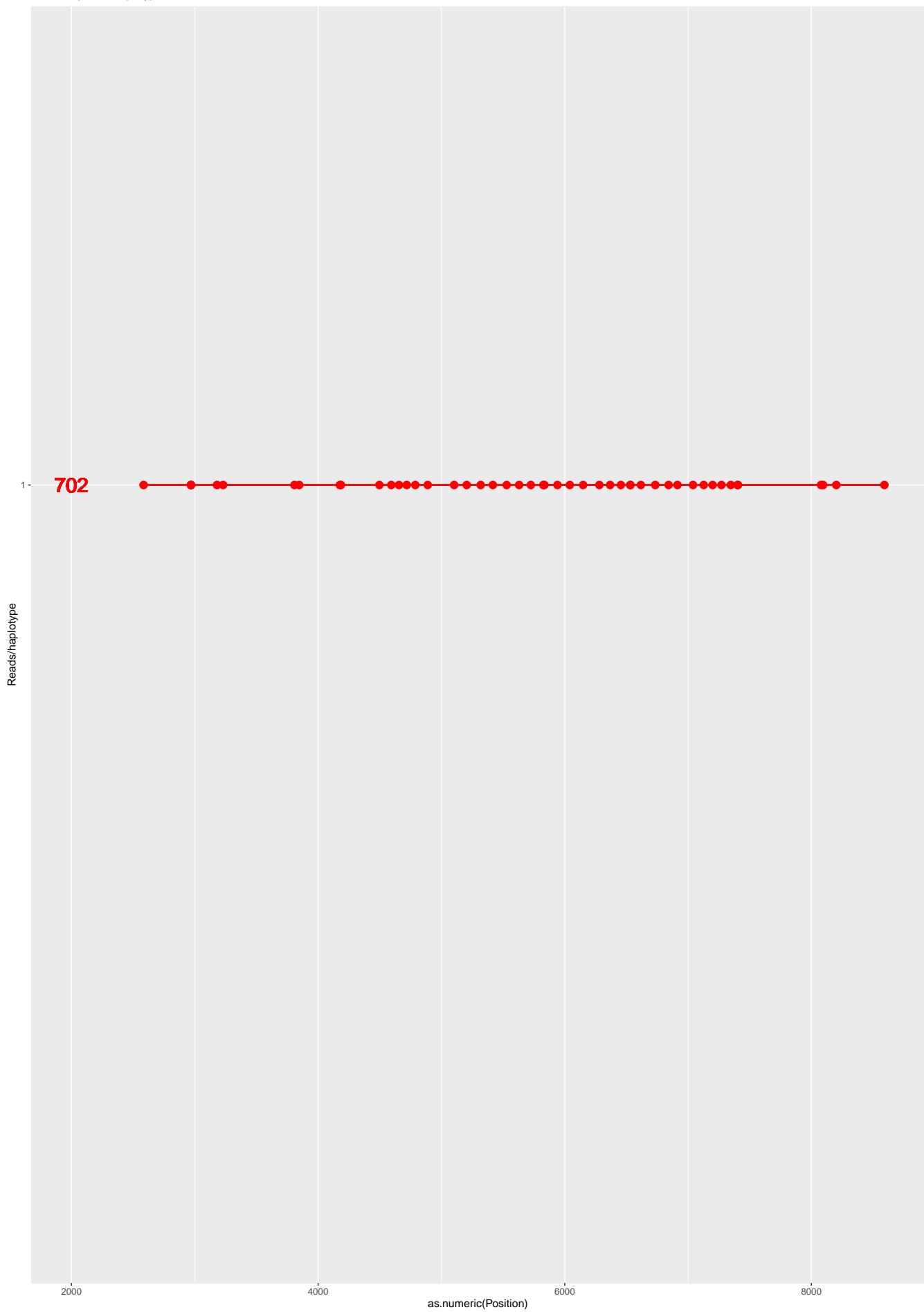
barcode = CGATCATCTATAGACA & CGTGTCACTGCTACTCA

Sample = 161b tetrad = 161 spore = b

Total reads =734 PCR=414

haplotypes I began with n[supporting reads] = 702

most frequent 7 haplotypes.



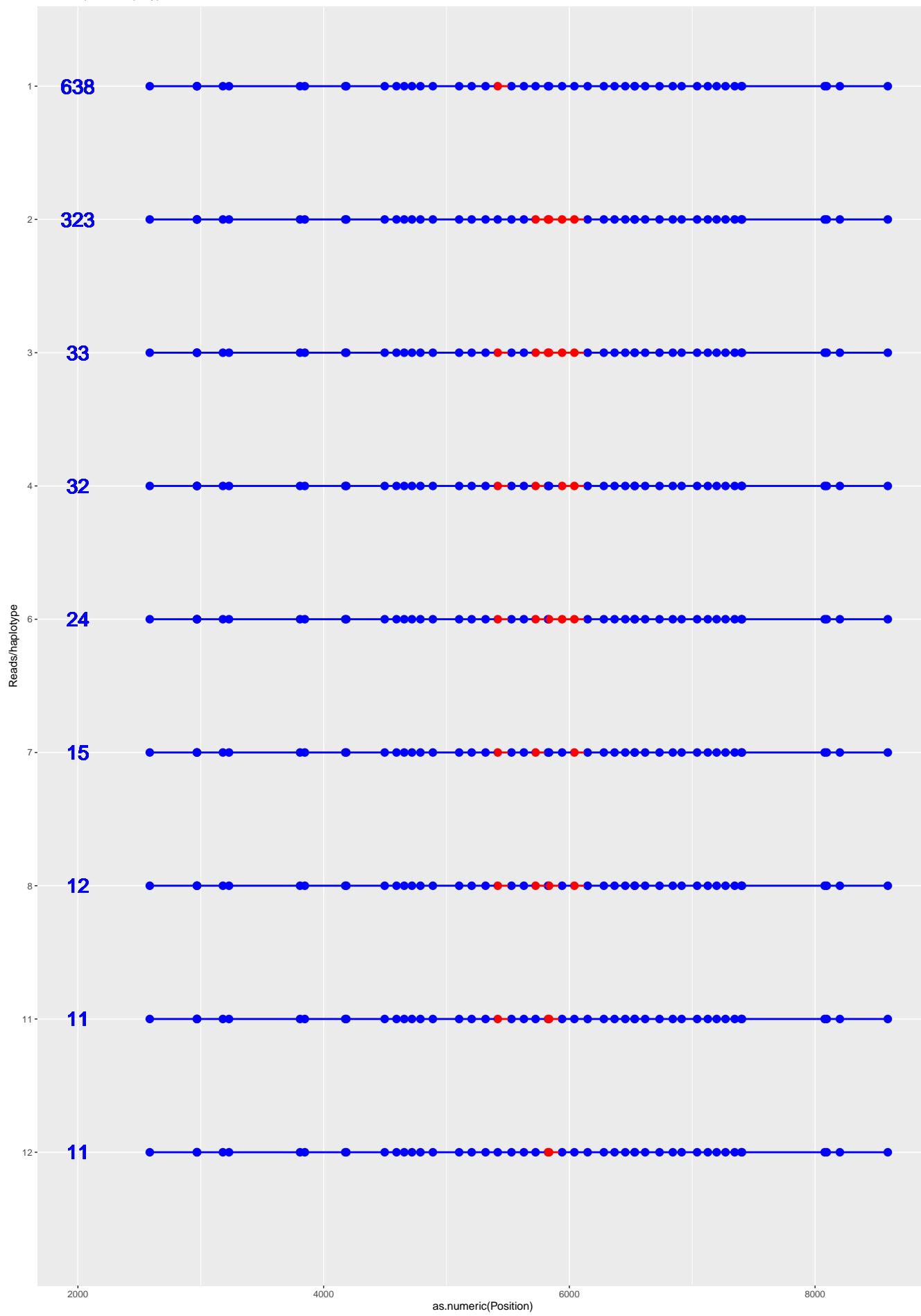
barcode = CGATCATCTATAGACA & TGTGAGACTGCATGTC

Sample = 161c tetrad = 161 spore = c

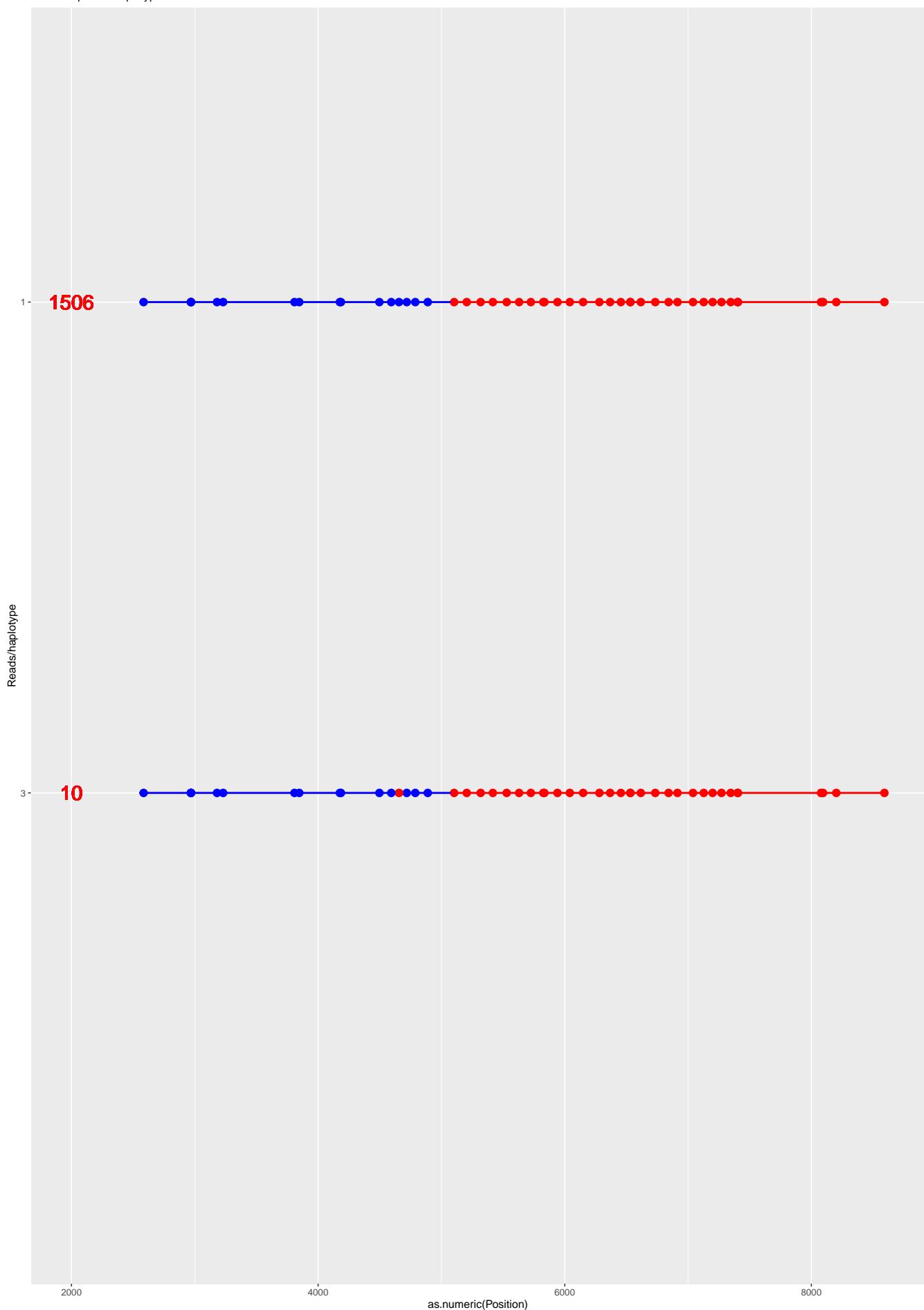
Total reads = 1478 PCR=415

haplotypes I began with [n(supporting reads)] = 11, 12, 15, 24, 32, 33, 323, 638

most frequent 7 haplotypes.



Sample = 161d tetrad = 161 spore = d
Total reads = 1607 PCR=416
haplotypes I began with n[supporting reads] = 10, 1506
most frequent 7 haplotypes.



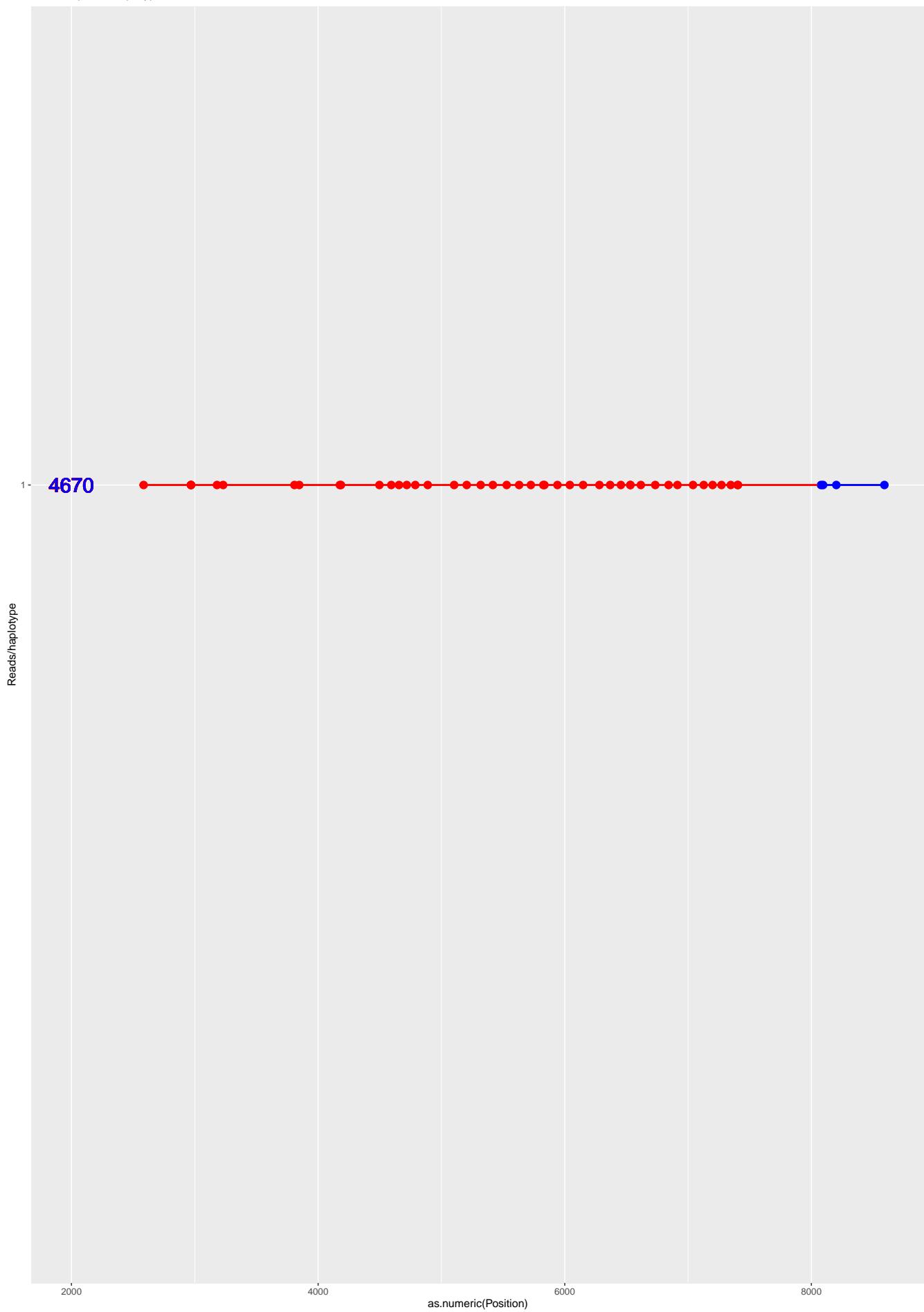
barcode = CGATCATCTATAGACA & ACTATCGCGCACGCAG

Sample = 162a tetrad = 162 spore = a

Total reads = 4920 PCR=417

haplotypes I began with n[supporting reads] = 4670

most frequent 7 haplotypes.



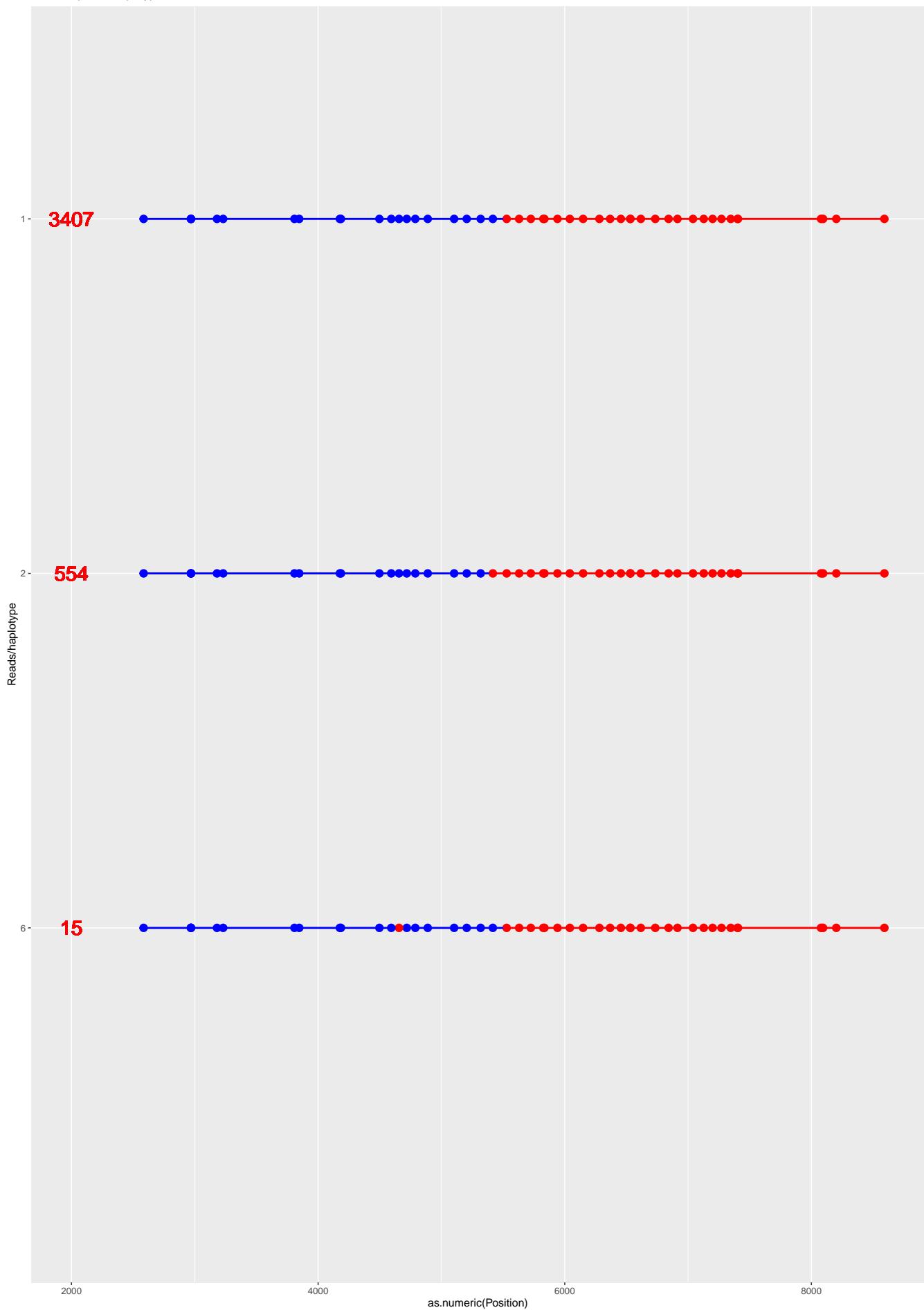
barcode = CGACGTATCTGACAGT & GCGACGAGTACTCATG

Sample = 162b tetrad = 162 spore = b

Total reads = 4460 PCR=418

haplotypes I began with n[supporting reads] = 15, 554, 3407

most frequent 7 haplotypes.

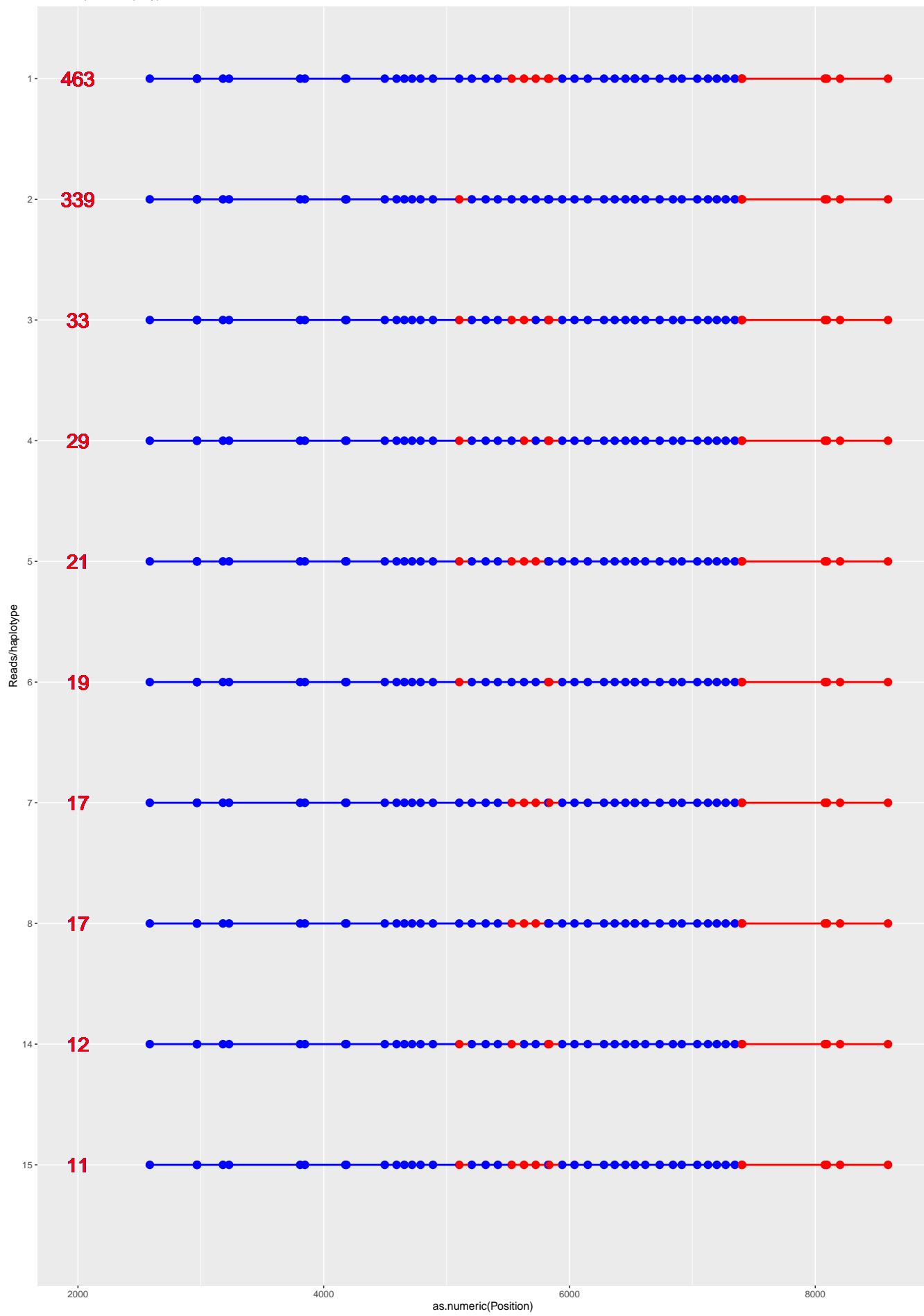


Sample = 162c tetrad = 162 spore = c

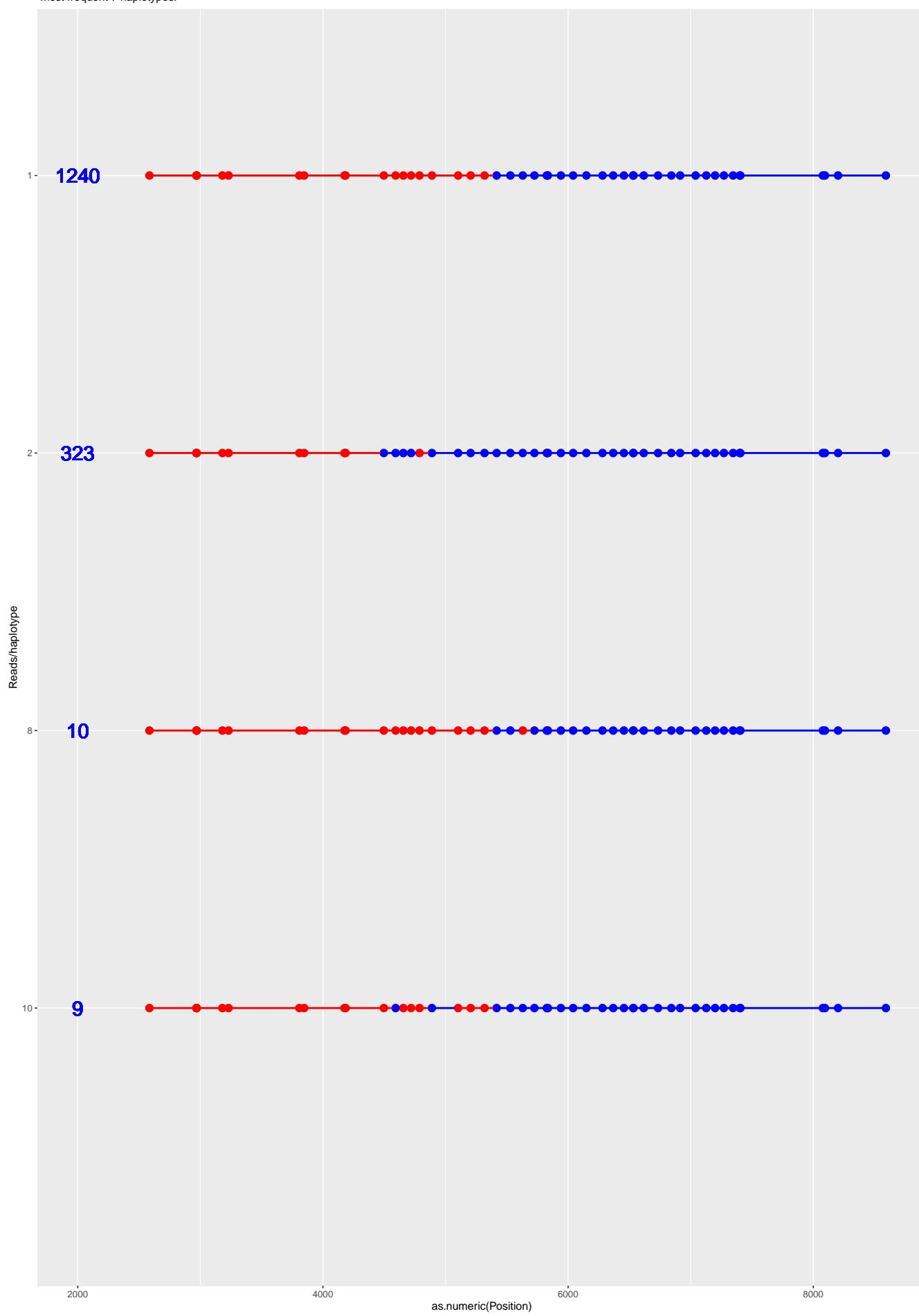
Total reads = 1229 PCR=419

haplotypes I began with [n|supporting reads] = 11, 12, 17, 19, 21, 29, 33, 339, 463

most frequent 7 haplotypes.



Sample = 162d tetrad = 162 spore = d
Total reads = 2174 PCR=420
haplotypes I began with [n|supporting reads] = 9, 10, 323, 1240
most frequent 7 haplotypes.

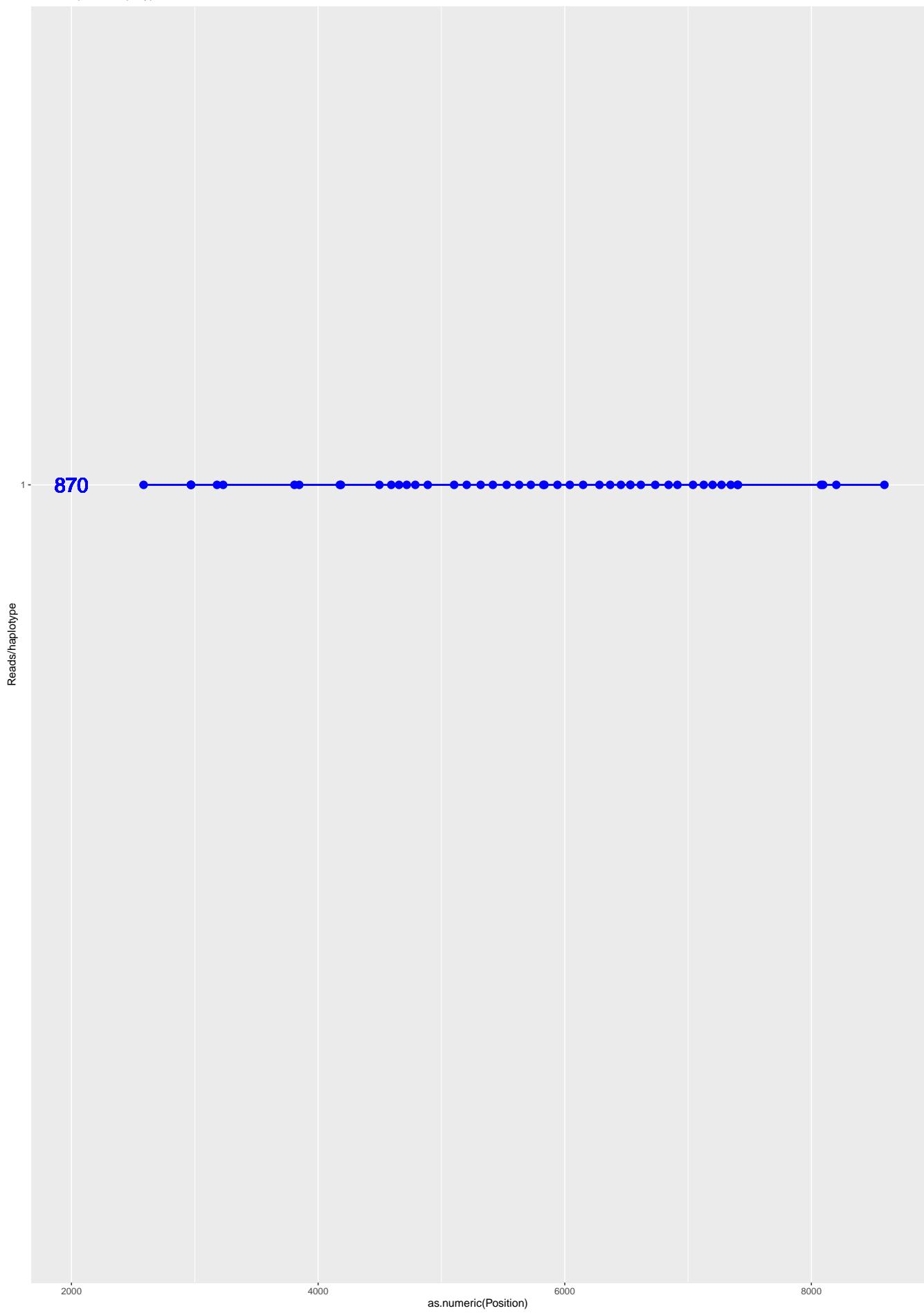


Sample = 163a tetrad = 163 spore = a

Total reads = 1020 PCR=421

haplotypes I began with n[supporting reads] = 870

most frequent 7 haplotypes.



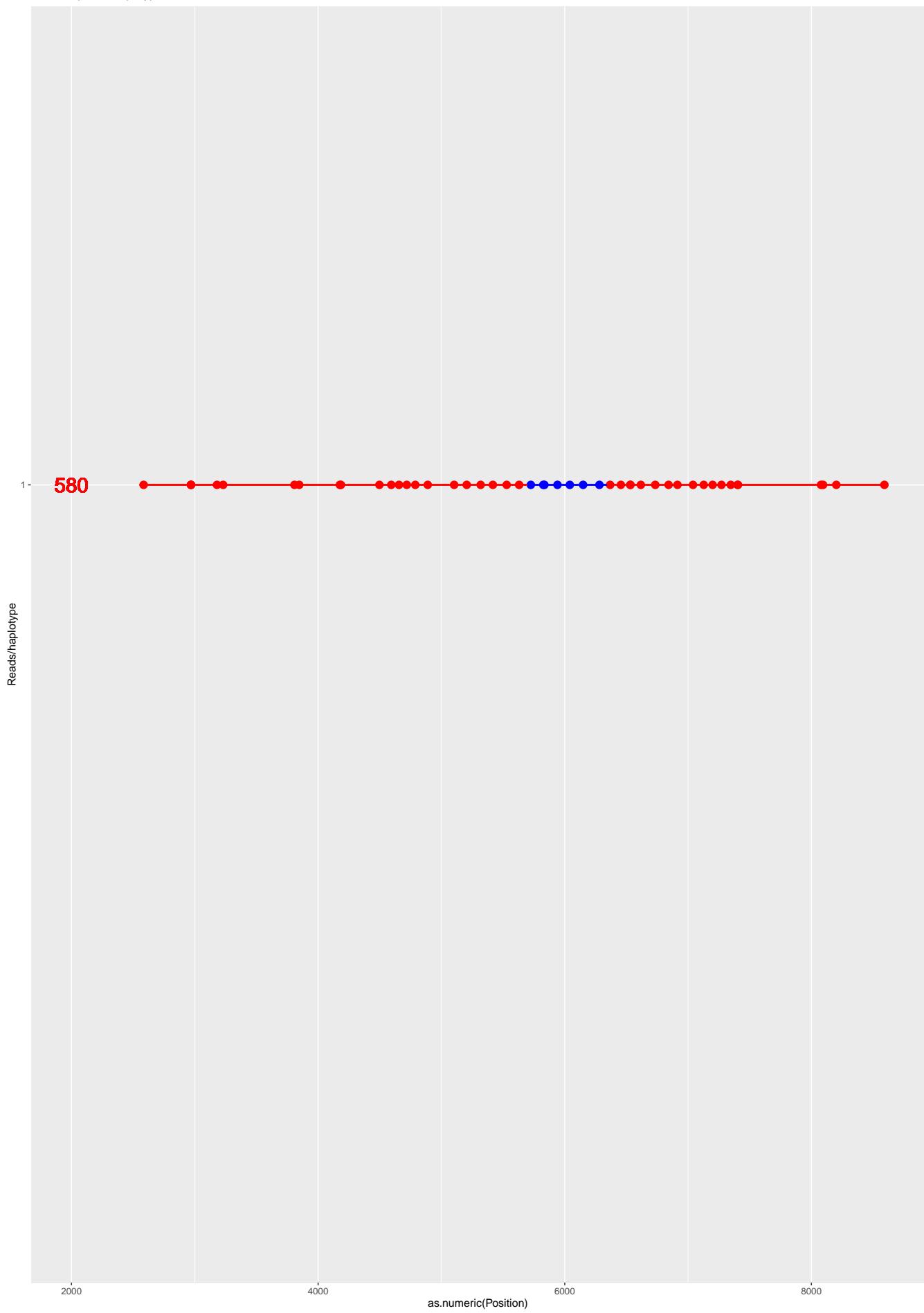
barcode = CGACGTATCTGACAGT & CGTGTCACTGCTACTCA

Sample = 163b tetrad = 163 spore = b

Total reads = 609 PCR=422

haplotypes I began with n[supporting reads] = 580

most frequent 7 haplotypes.



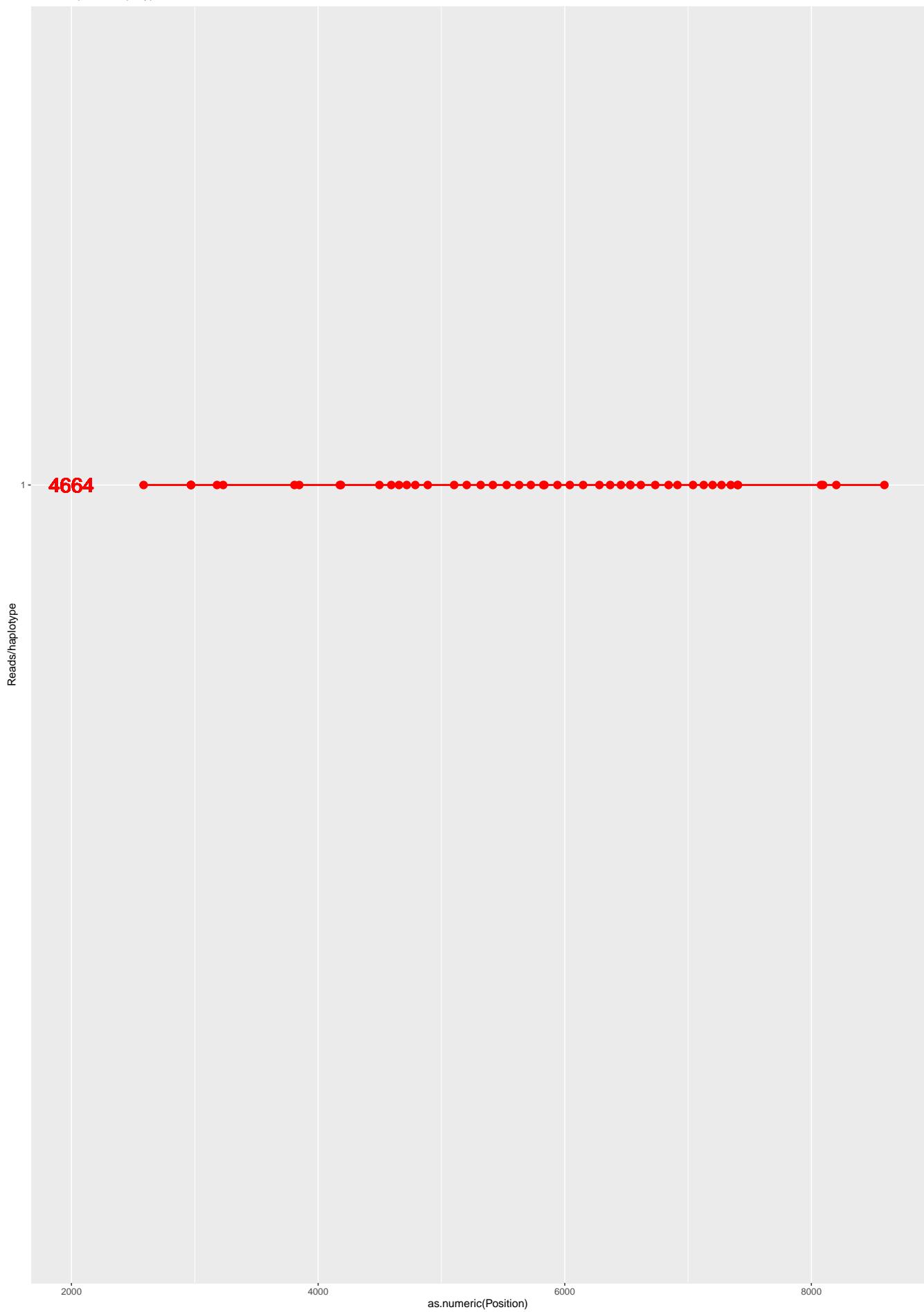
barcode = CGACGTATCTGACAGT & TGTGAGACTGCATGTC

Sample = 163c tetrad = 163 spore = c

Total reads = 4852 PCR=423

haplotypes I began with n[supporting reads] = 4664

most frequent 7 haplotypes.



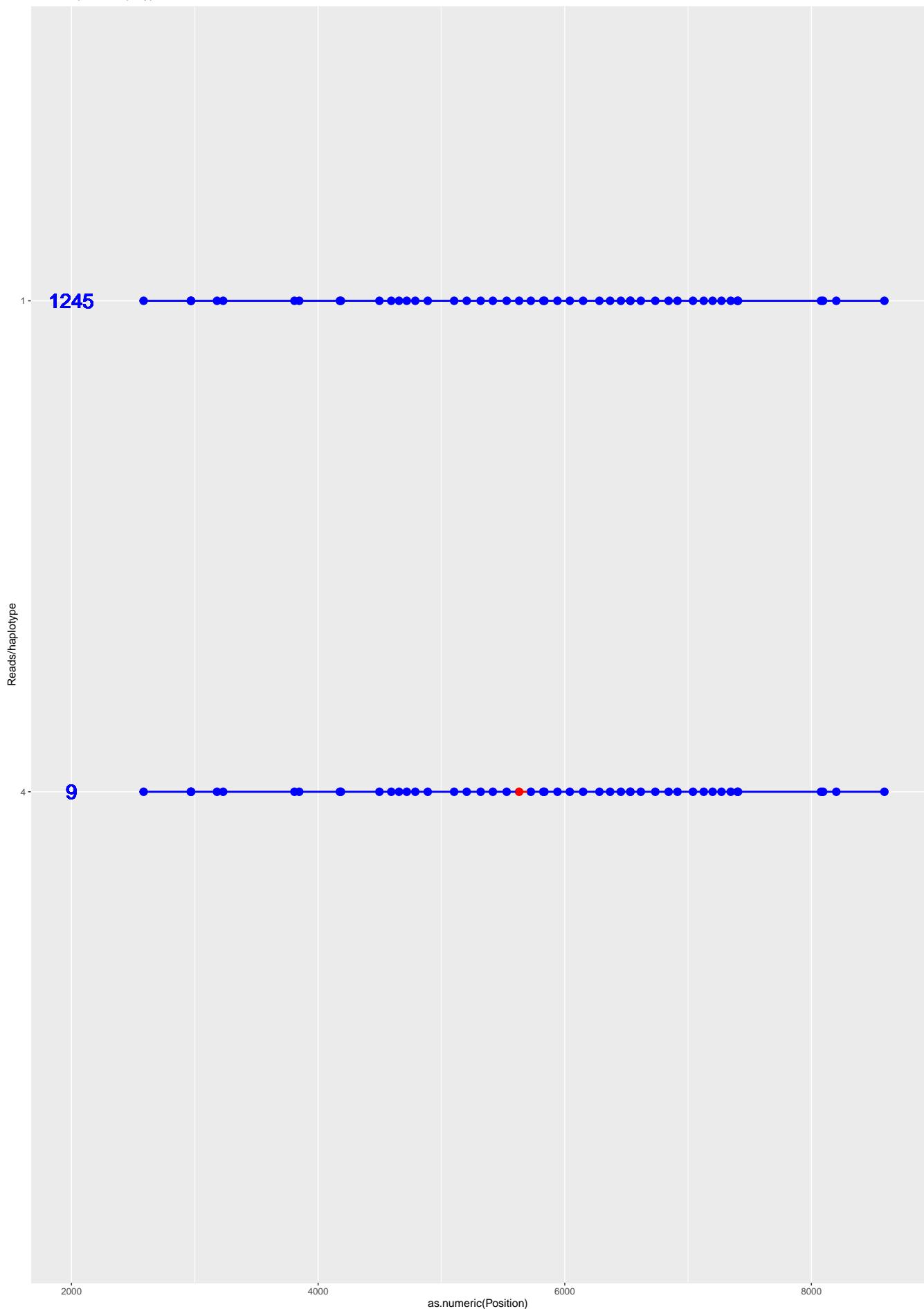
barcode = CGACGTATCTGACAGT & GCTCAGTGCCTACTG

Sample = 163d tetrad = 163 spore = d

Total reads = 1468 PCR=424

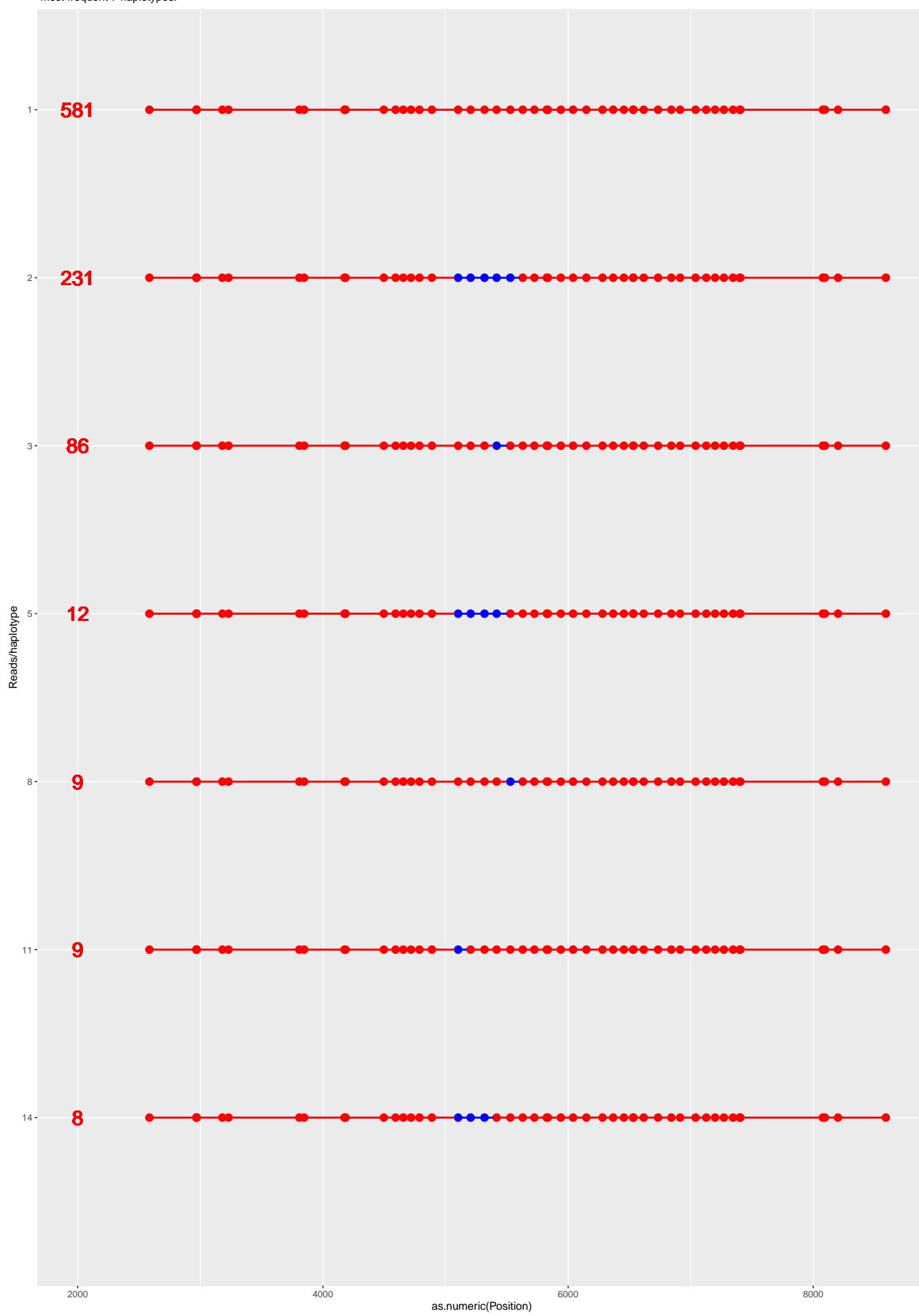
haplotypes I began with n[supporting reads] = 9, 1245

most frequent 7 haplotypes.



barcode = CGACGTATCTGACAGT & ACTATCGCGCACGCAG

Sample = 168a tetrad = 168 spore = a
 Total reads = 1195 PCR=429
 haplotypes I began with [n|supporting reads] = 8, 9, 12, 86, 231, 581
 most frequent 7 haplotypes.

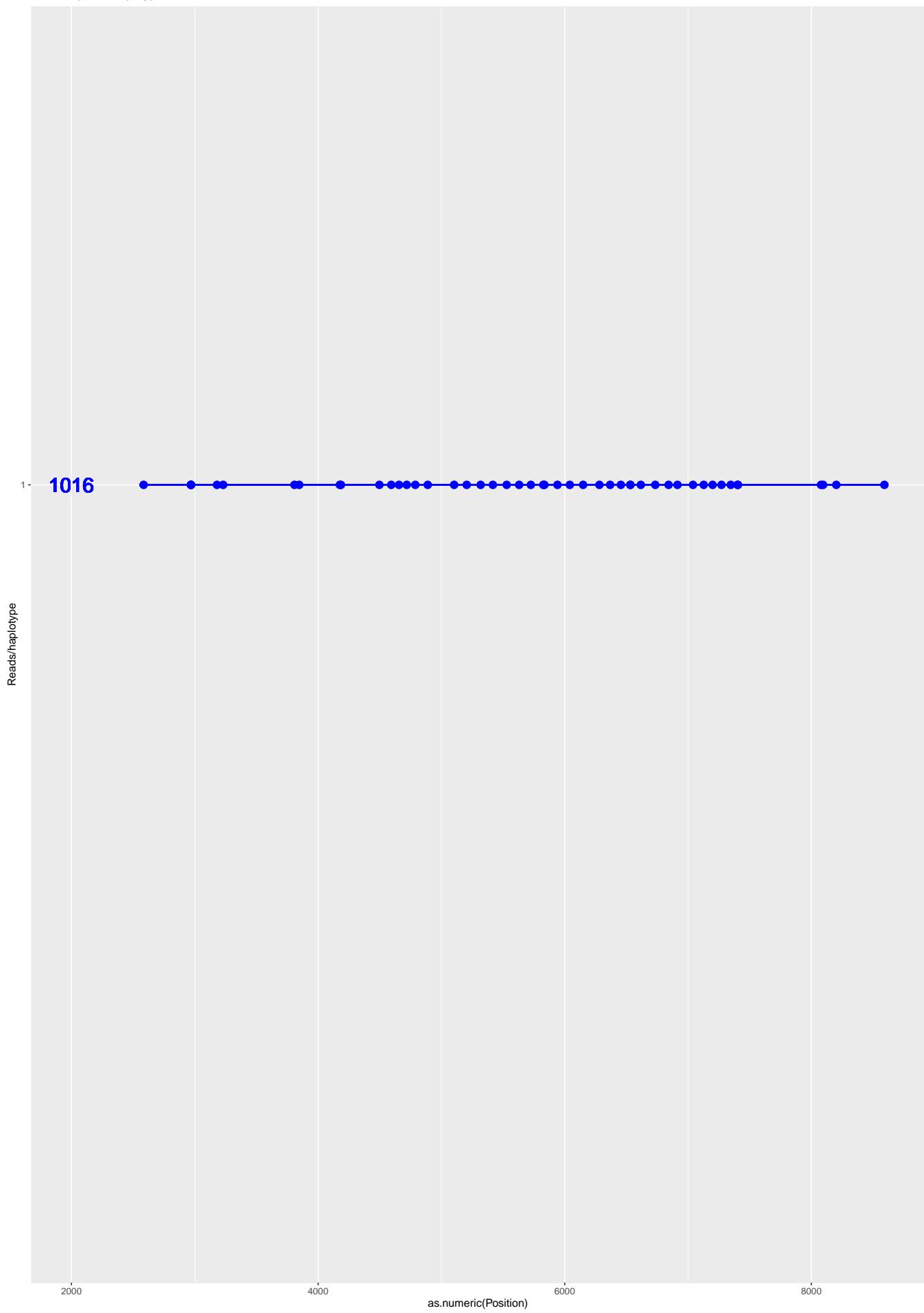


Sample = 168b tetrad = 168 spore = b

Total reads = 1184 PCR=430

haplotypes I began with n[supporting reads] = 1016

most frequent 7 haplotypes.

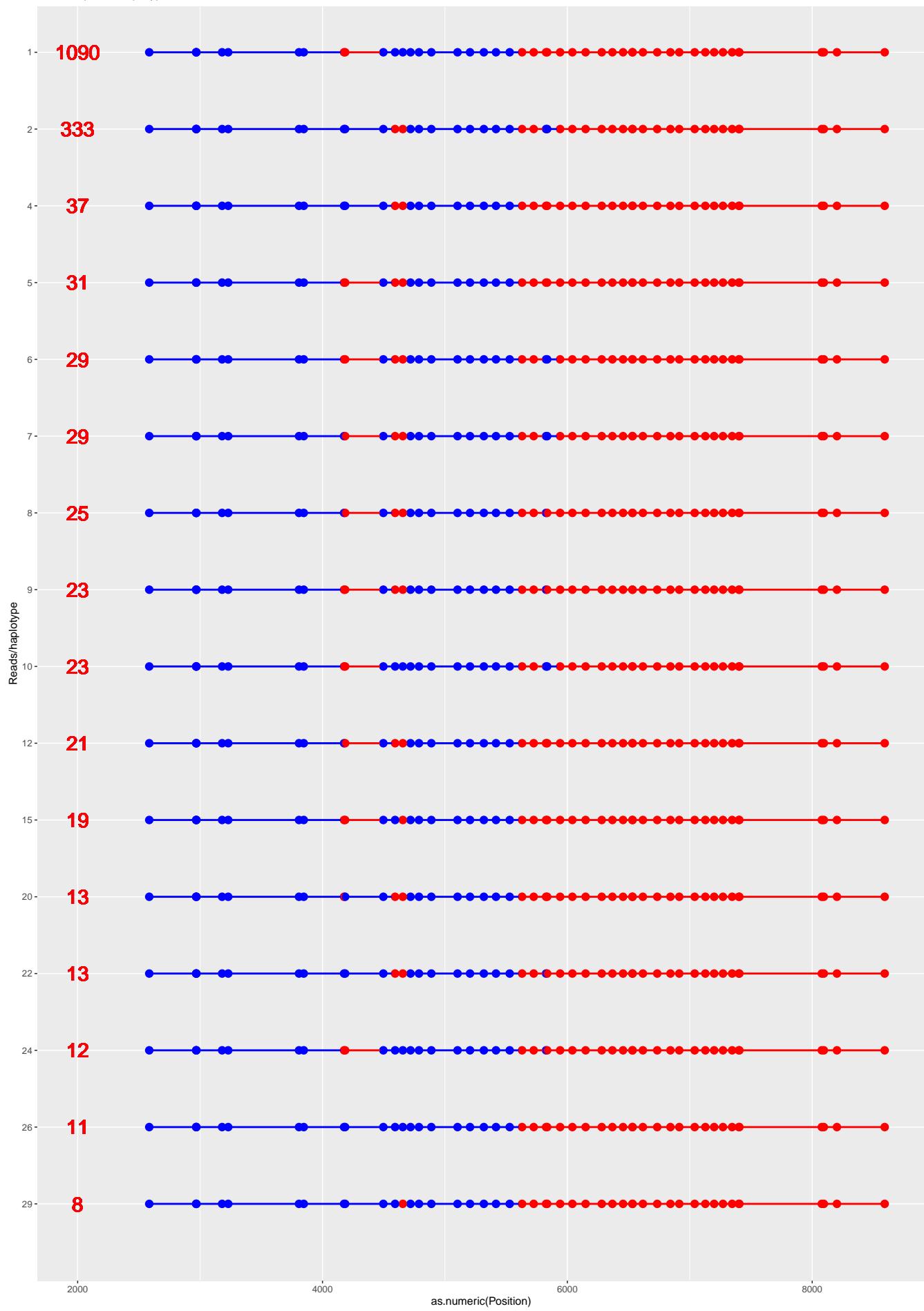


Sample = 168c tetrad = 168 spore = c

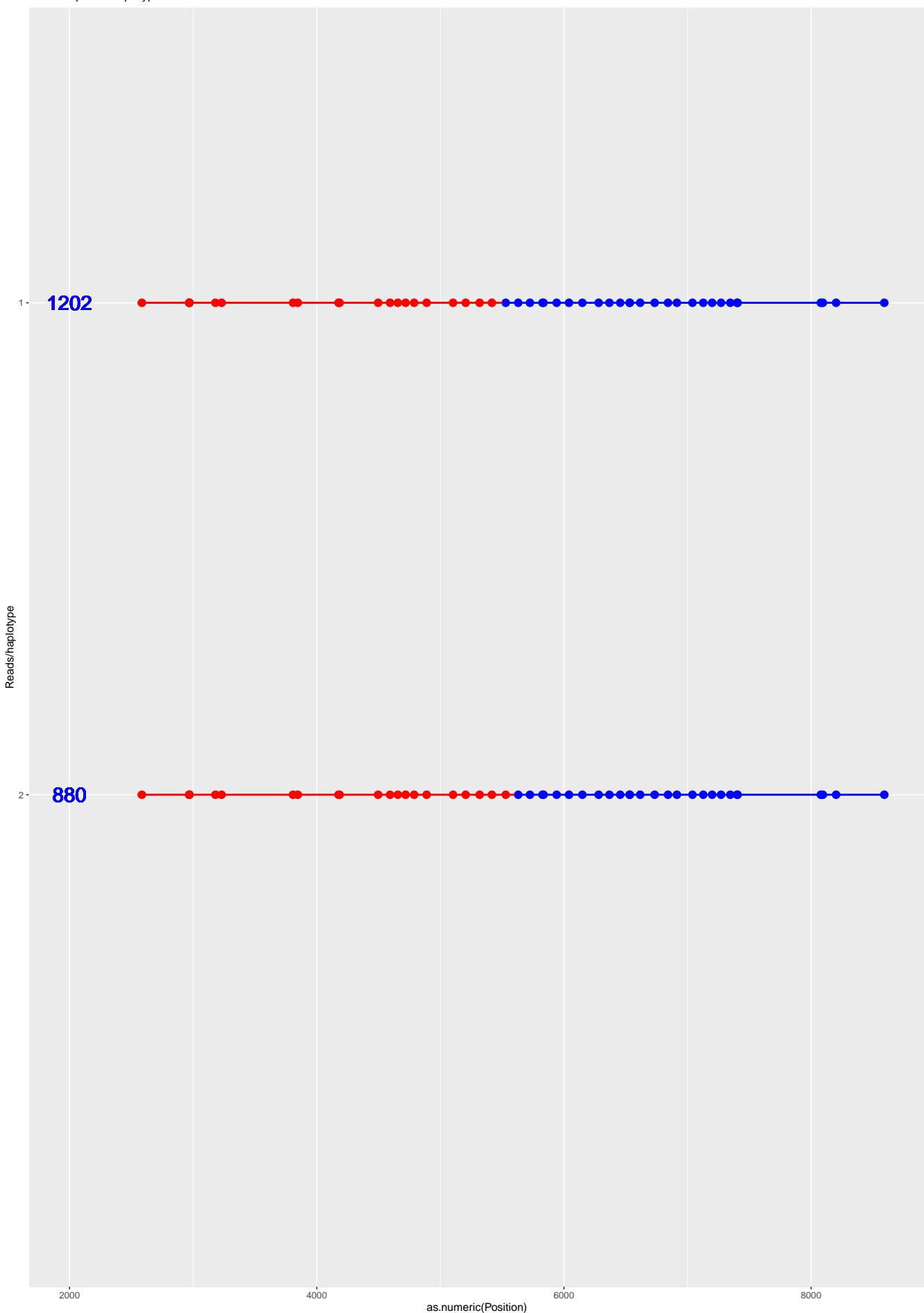
Total reads = 2306 PCR=431

haplotypes I began with [n(supporting reads)] = 8, 11, 12, 13, 19, 21, 23, 25, 29, 31, 37, 333, 1090

most frequent 7 haplotypes.



Sample = 168d tetrad = 168 spore = d
Total reads = 2278 PCR=432
haplotypes I began with n[supporting reads] = 880, 1202
most frequent 7 haplotypes.

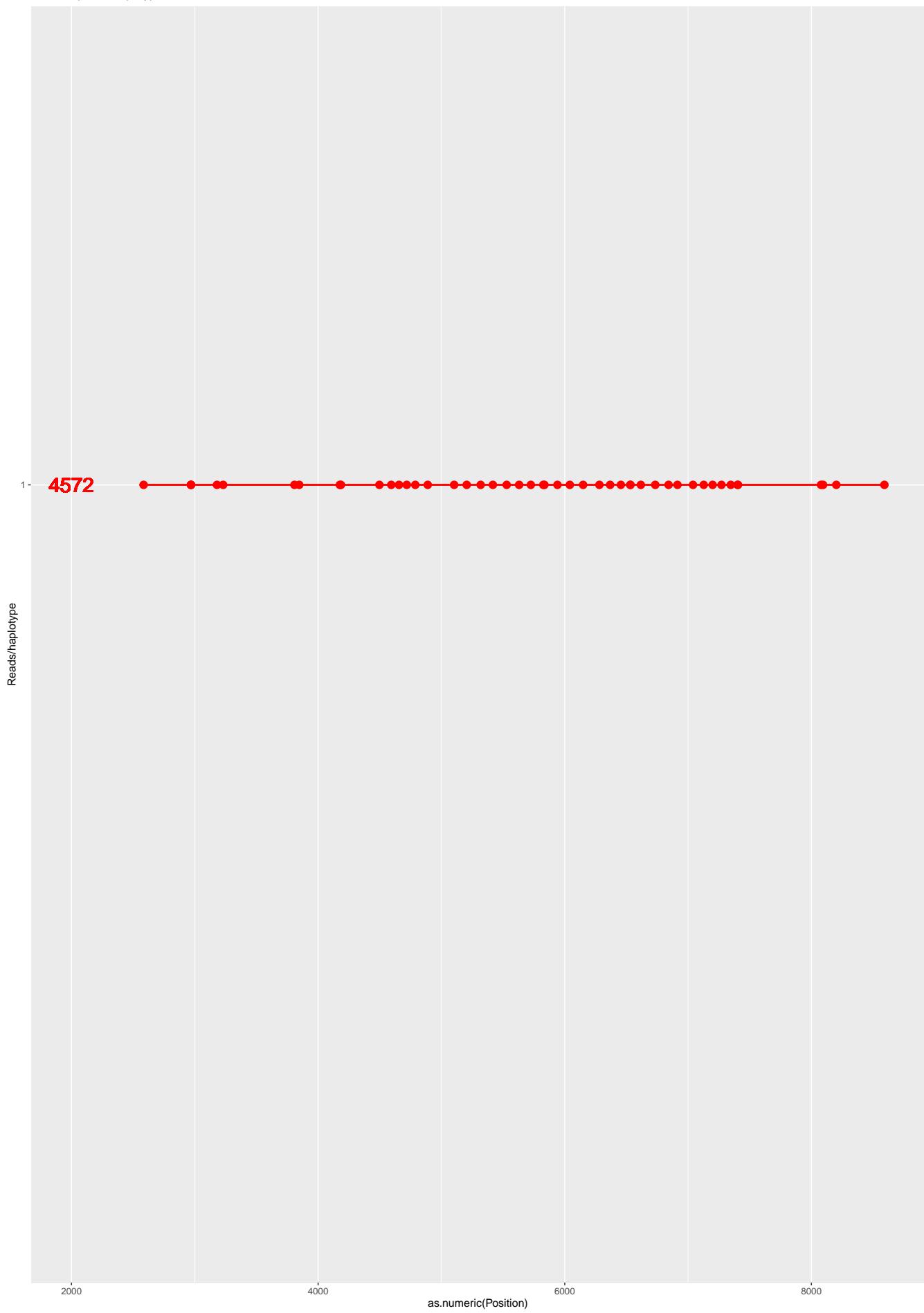


Sample = 175a tetrad = 175 spore = a

Total reads = 4745 PCR=449

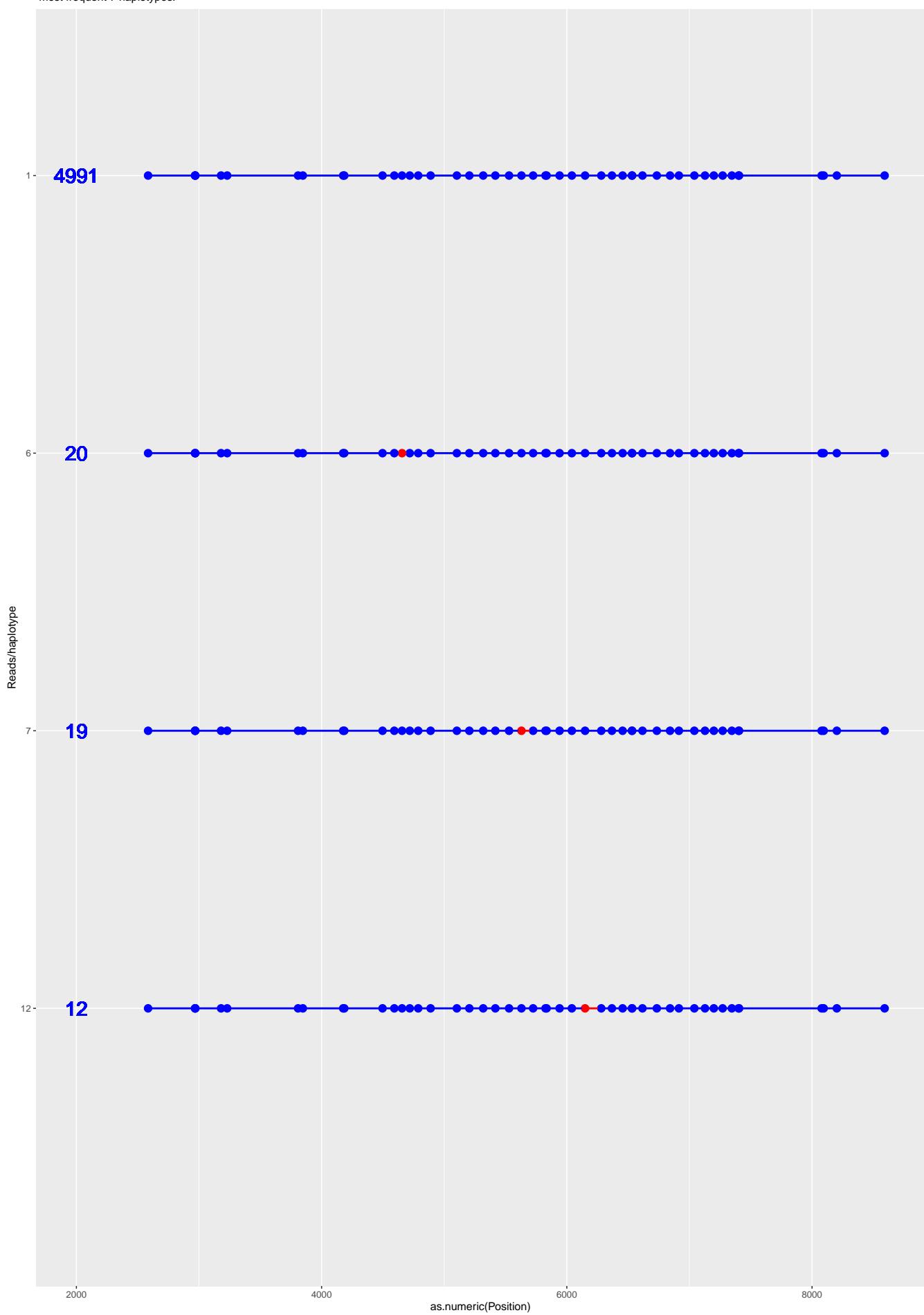
haplotypes I began with n[supporting reads] = 4572

most frequent 7 haplotypes.



barcode = AGTCGCATGACTGTGT & GCGACGAGTACTCATG

Sample = 175b tetrad = 175 spore = b
Total reads = 5797 PCR=450
haplotypes I began with [n|supporting reads] = 12, 19, 20, 4991
most frequent 7 haplotypes.



Sample = 175c tetrad = 175 spore = c
Total reads = 3108 PCR=451
haplotypes I began with [n|supporting reads] = 8, 18, 2676
most frequent 7 haplotypes.

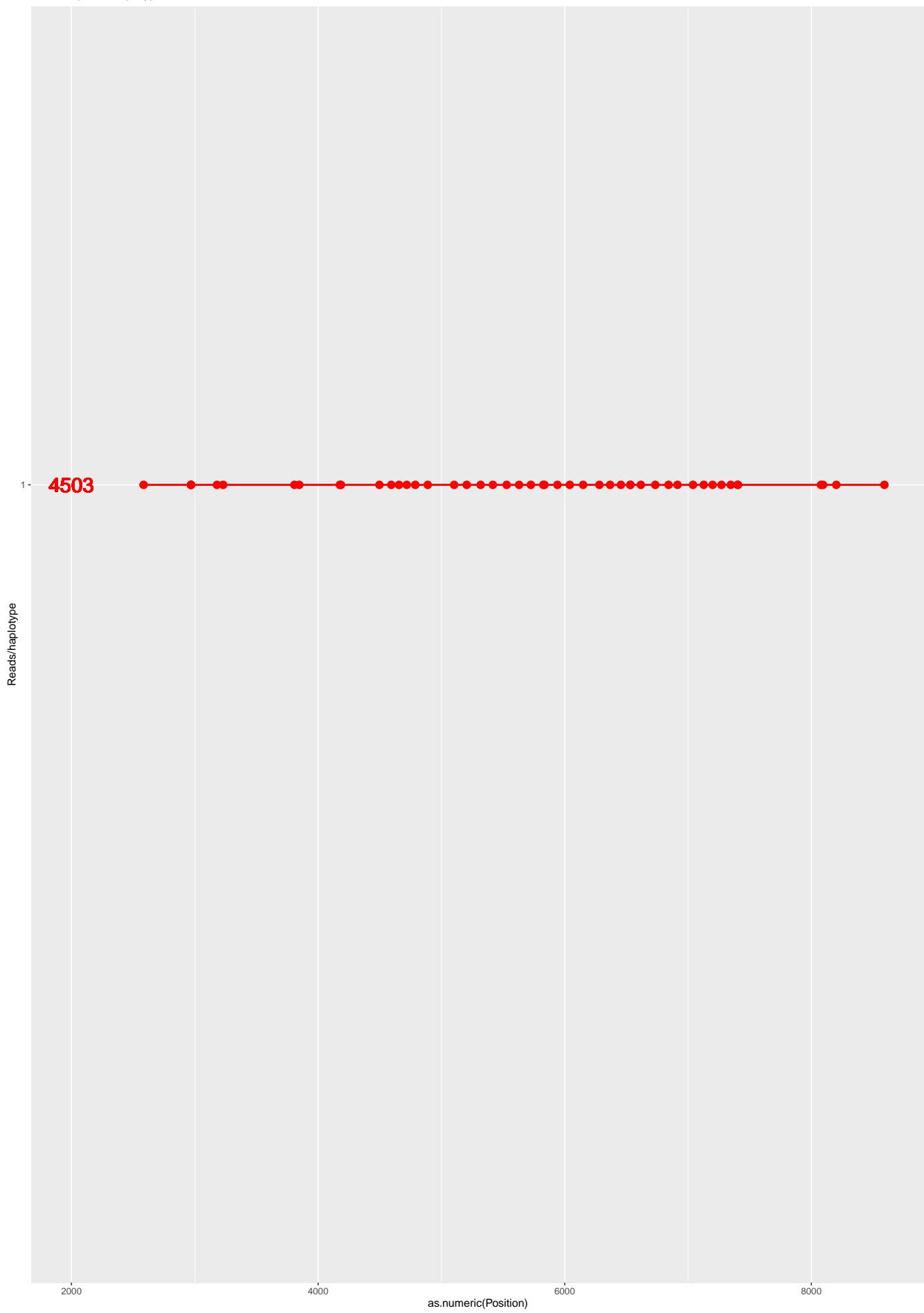


Sample = 175d tetrad = 175 spore = d

Total reads = 4704 PCR=452

haplotypes I began with n[supporting reads] = 4503

most frequent 7 haplotypes.



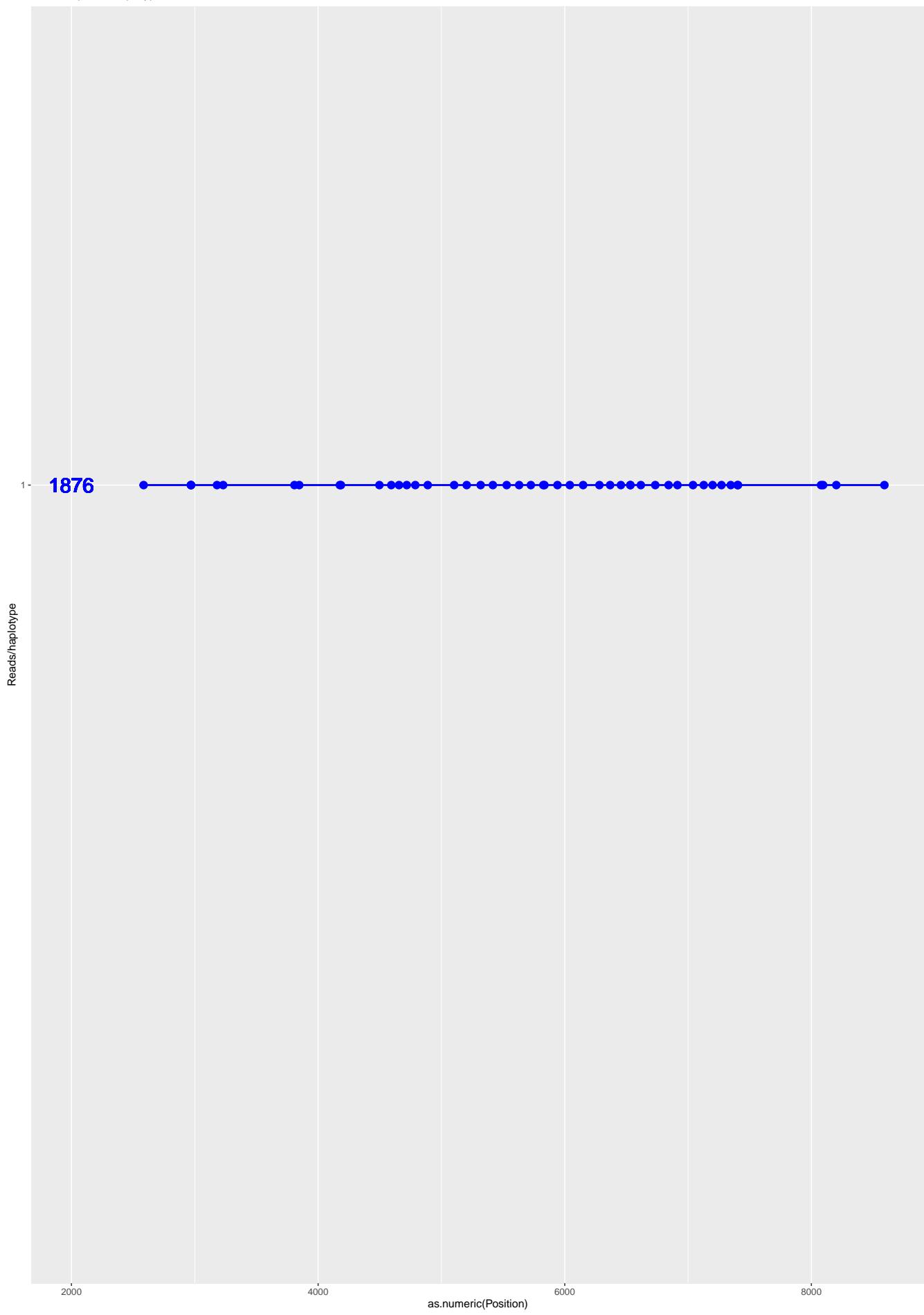
barcode = AGTCGCATGACTGTGT & AGACGTTAGATCACAGC

Sample = 177a tetrad = 177 spore = a

Total reads = 2196 PCR=457

haplotypes I began with n[supporting reads] = 1876

most frequent 7 haplotypes.



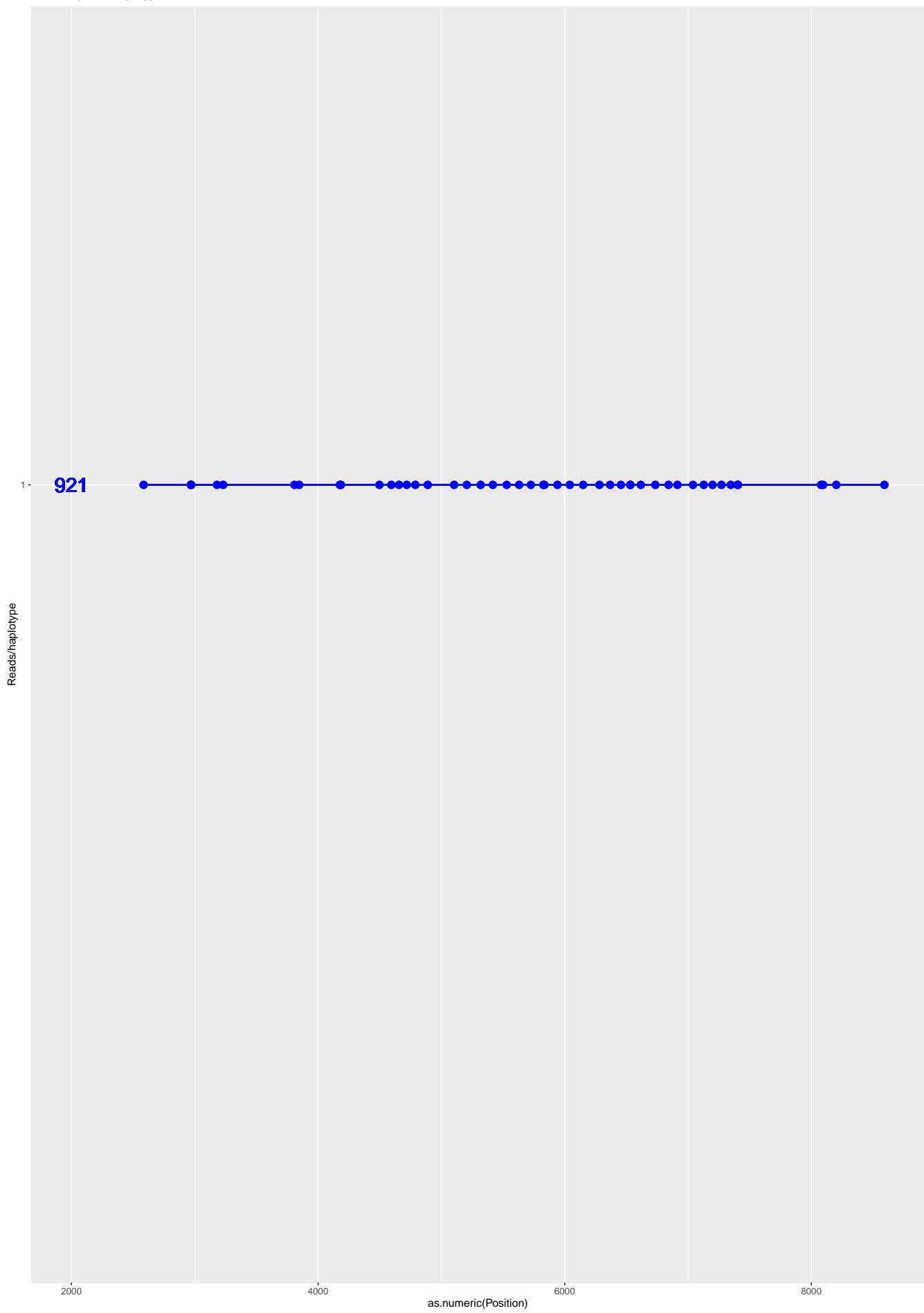
barcode = CAGTACTGCACGATCG & GCGACGAGTACTCATG

Sample = 177b tetrad = 177 spore = b

Total reads = 1089 PCR=458

haplotypes I began with n[supporting reads] = 921

most frequent 7 haplotypes.



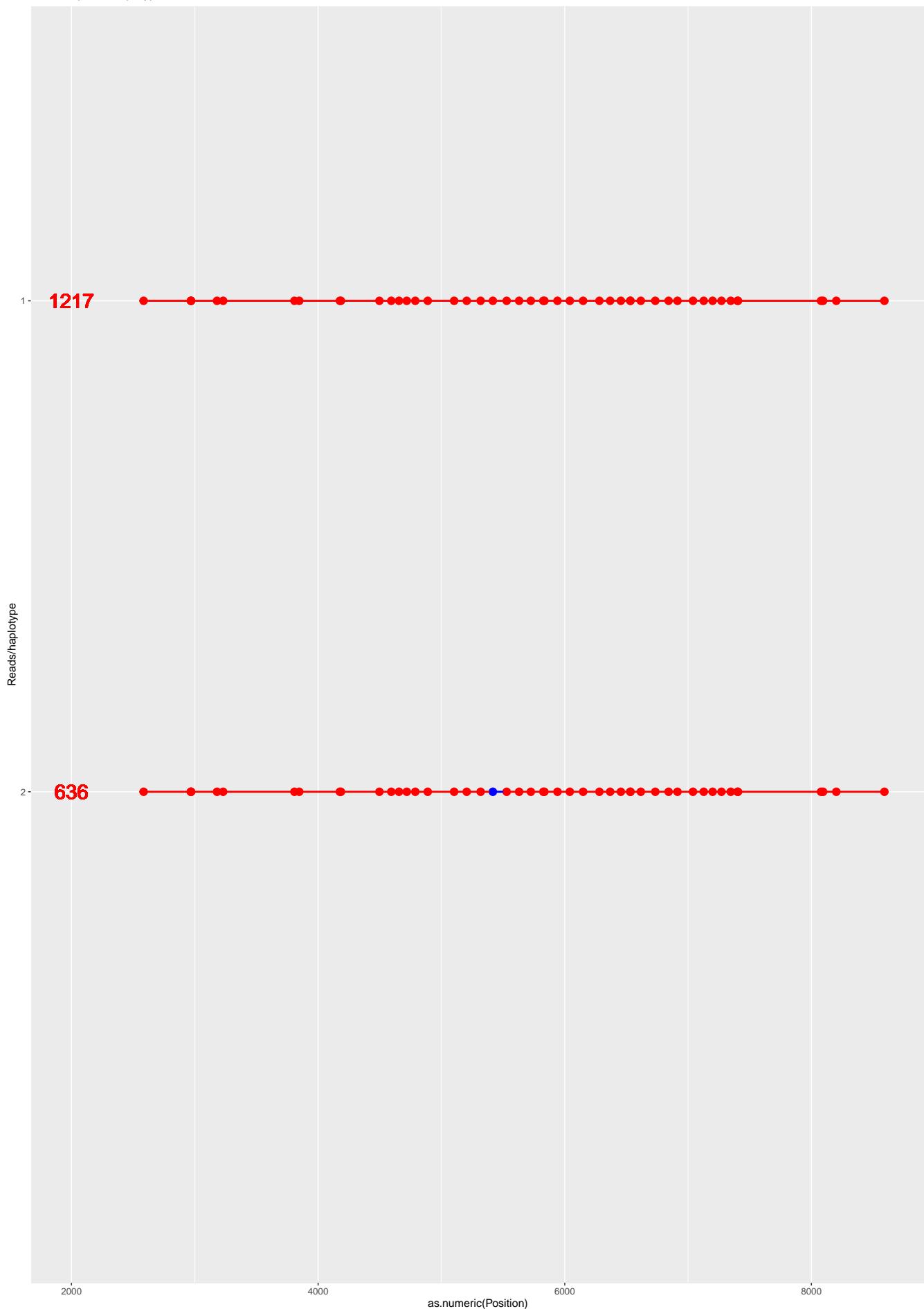
barcode = CAGTACTGCACGATCG & AGTATCACAGTCGCTG

Sample = 177c tetrad = 177 spore = c

Total reads = 1974 PCR=459

haplotypes I began with n[supporting reads] = 636, 1217

most frequent 7 haplotypes.



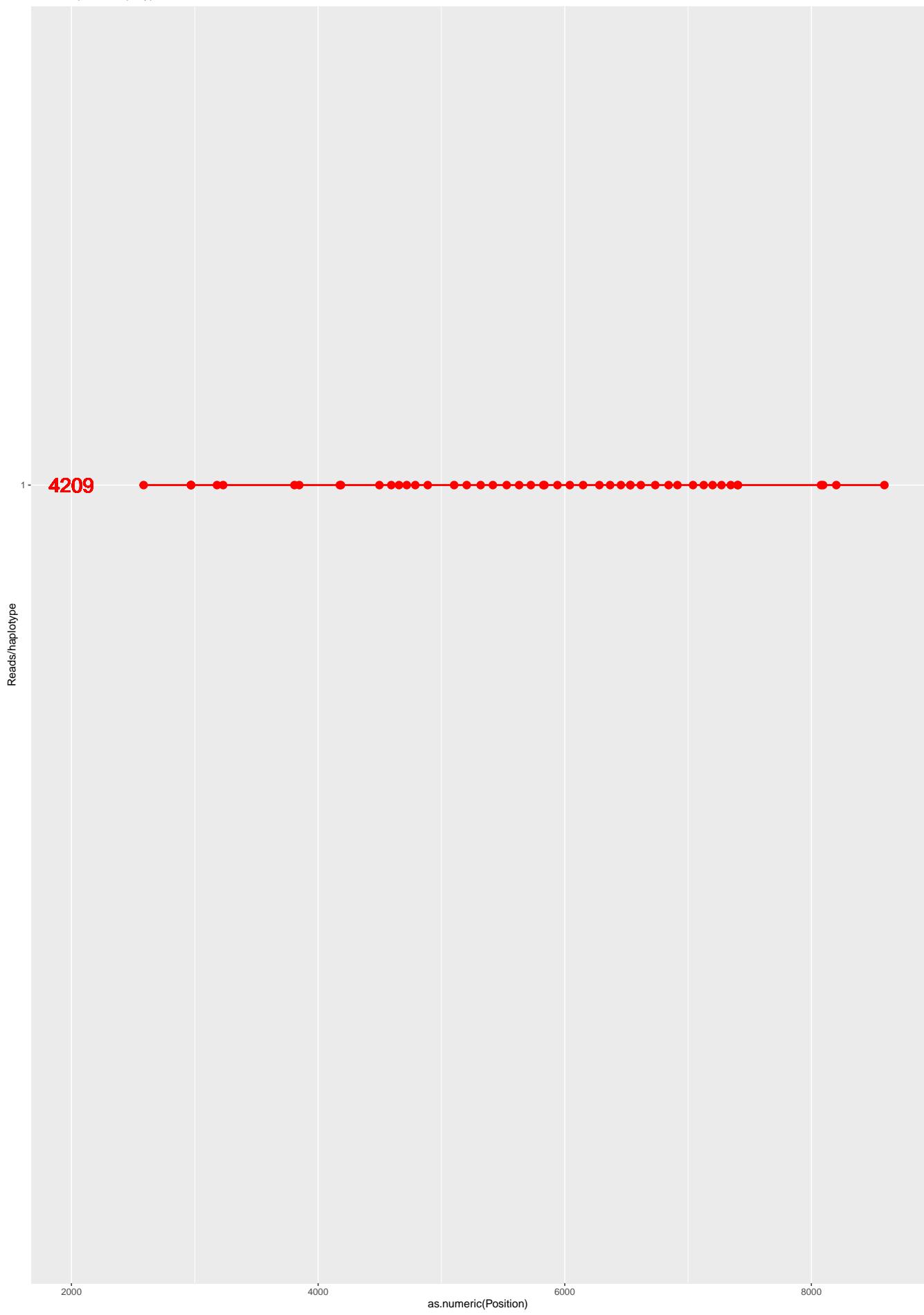
barcode = CAGTACTGCACGATCG & ATCATATGATGCGACA

Sample = 177d tetrad = 177 spore = d

Total reads = 4367 PCR=460

haplotypes I began with n[supporting reads] = 4209

most frequent 7 haplotypes.



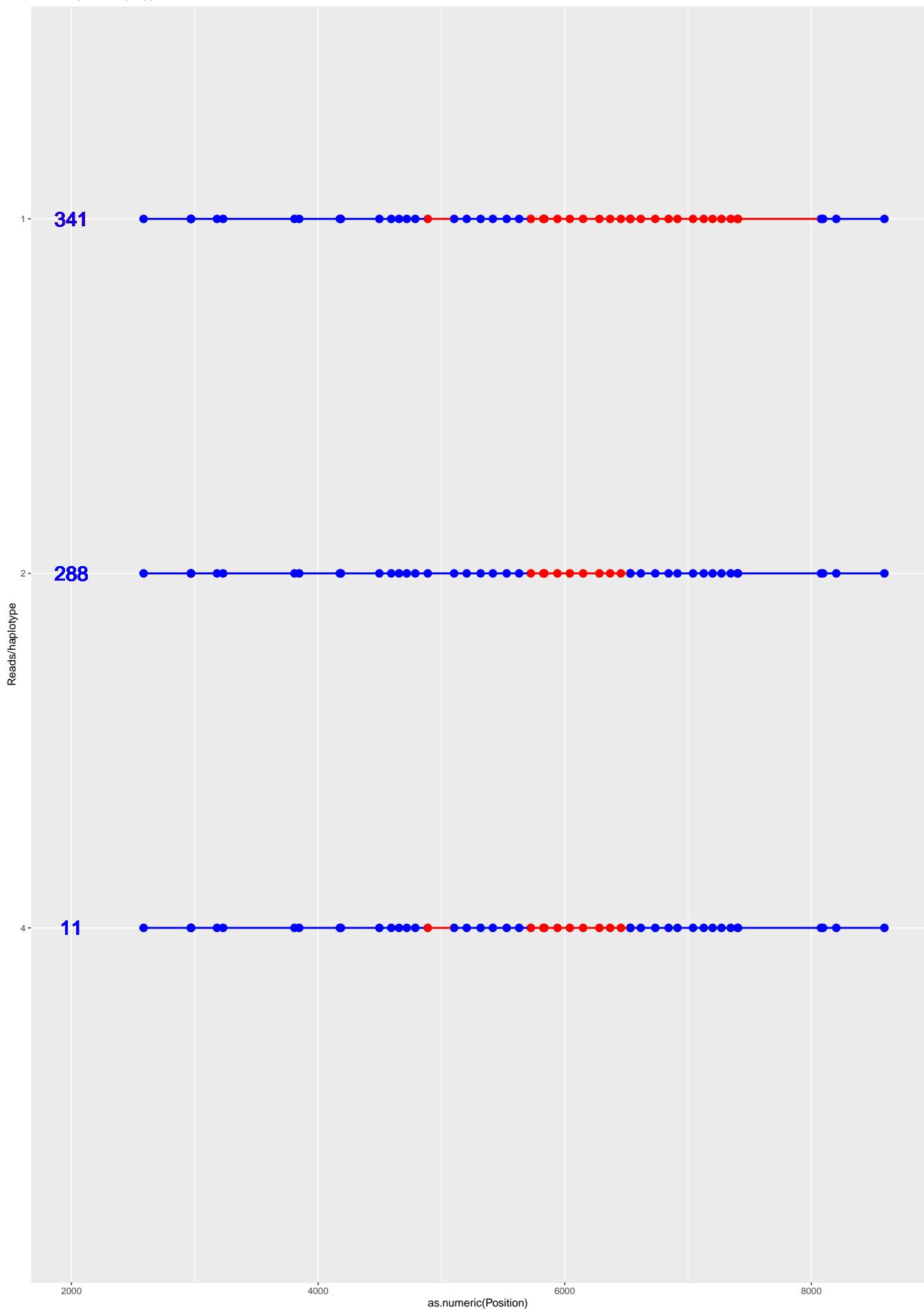
barcode = CAGTACTGCACGATCG & AGACGTAGATCACAGC

Sample = 178a tetrad = 178 spore = a

Total reads = 833 PCR=461

haplotypes I began with n[supporting reads] = 11, 288, 341

most frequent 7 haplotypes.



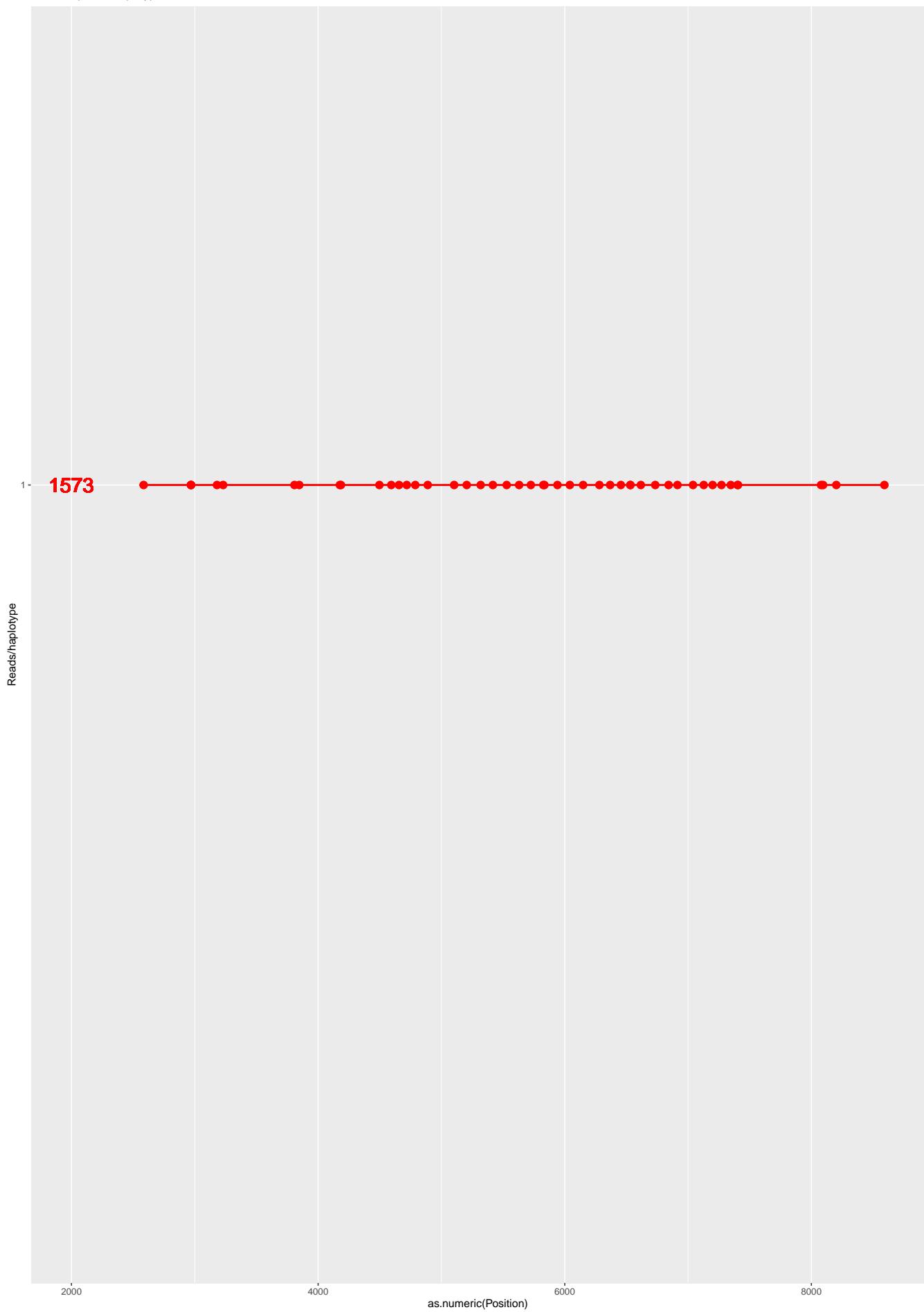
barcode = CAGTACTGCACGATCG & CGTGTCACTGCTACTCA

Sample = 178b tetrad = 178 spore = b

Total reads = 1638 PCR=462

haplotypes I began with n[supporting reads] = 1573

most frequent 7 haplotypes.



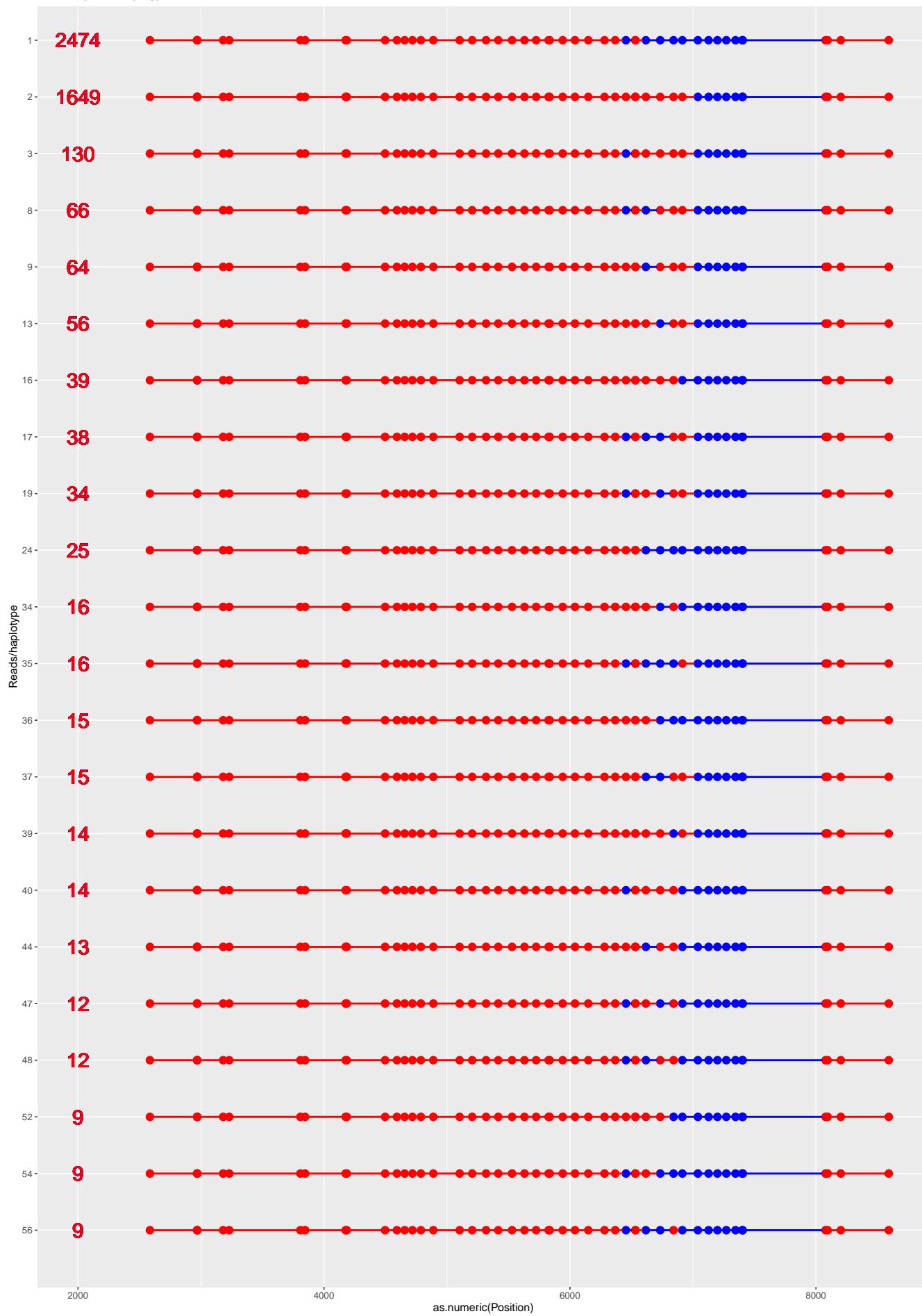
barcode = CAGTAACGACGATCG & TGTGAGACTGCATGTC

Sample = 178c tetrad = 178 spore = c

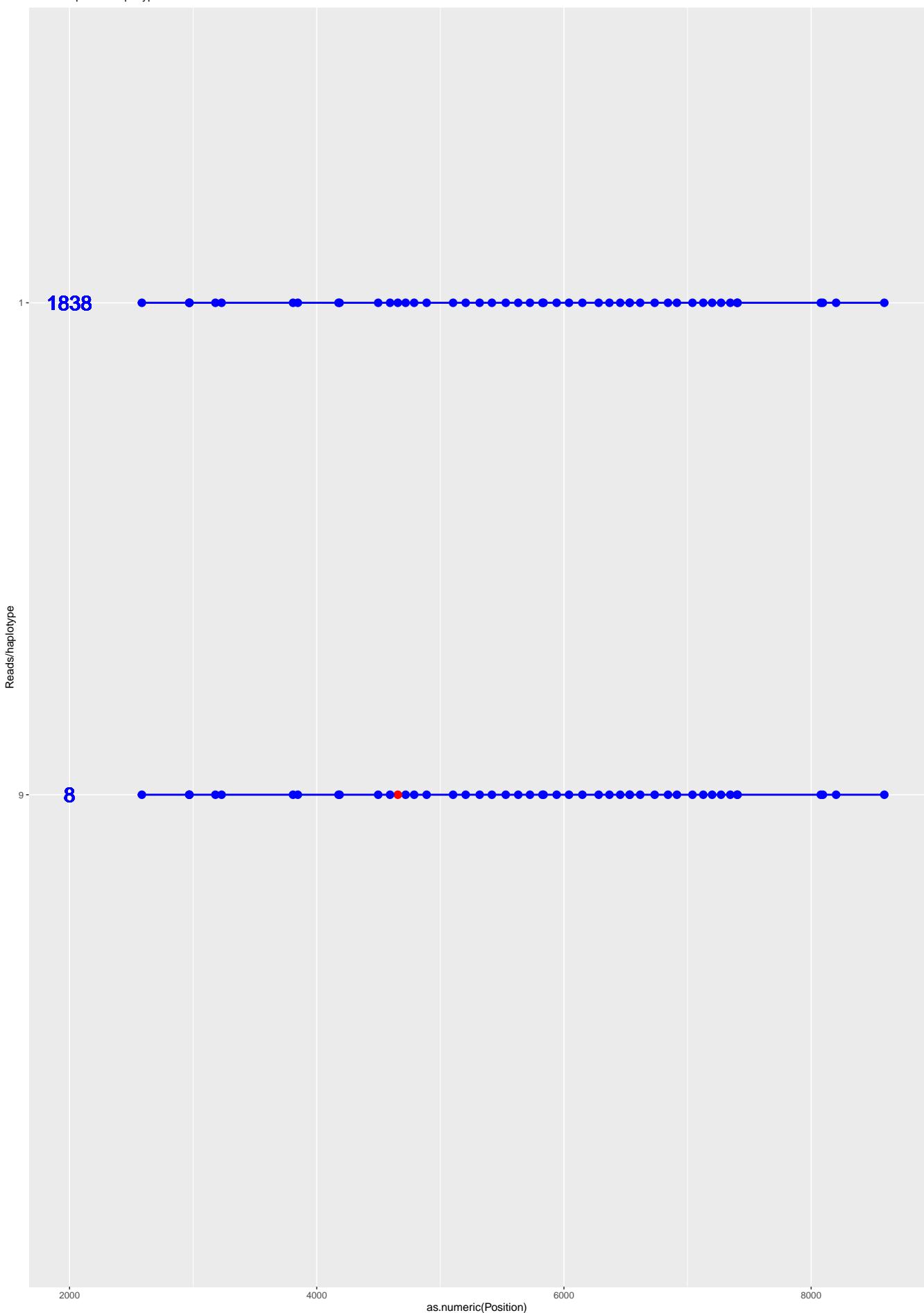
Total reads = 6353 PCR=463

haplotypes I began with [n:supporting reads] = 9, 12, 13, 14, 15, 16, 25, 34, 38, 39, 56, 64, 66, 130, 1649, 2474

most frequent 7 haplotypes.



Sample = 178d tetrad = 178 spore = d
Total reads = 2123 PCR=464
haplotypes I began with n[supporting reads] = 8, 1838
most frequent 7 haplotypes.



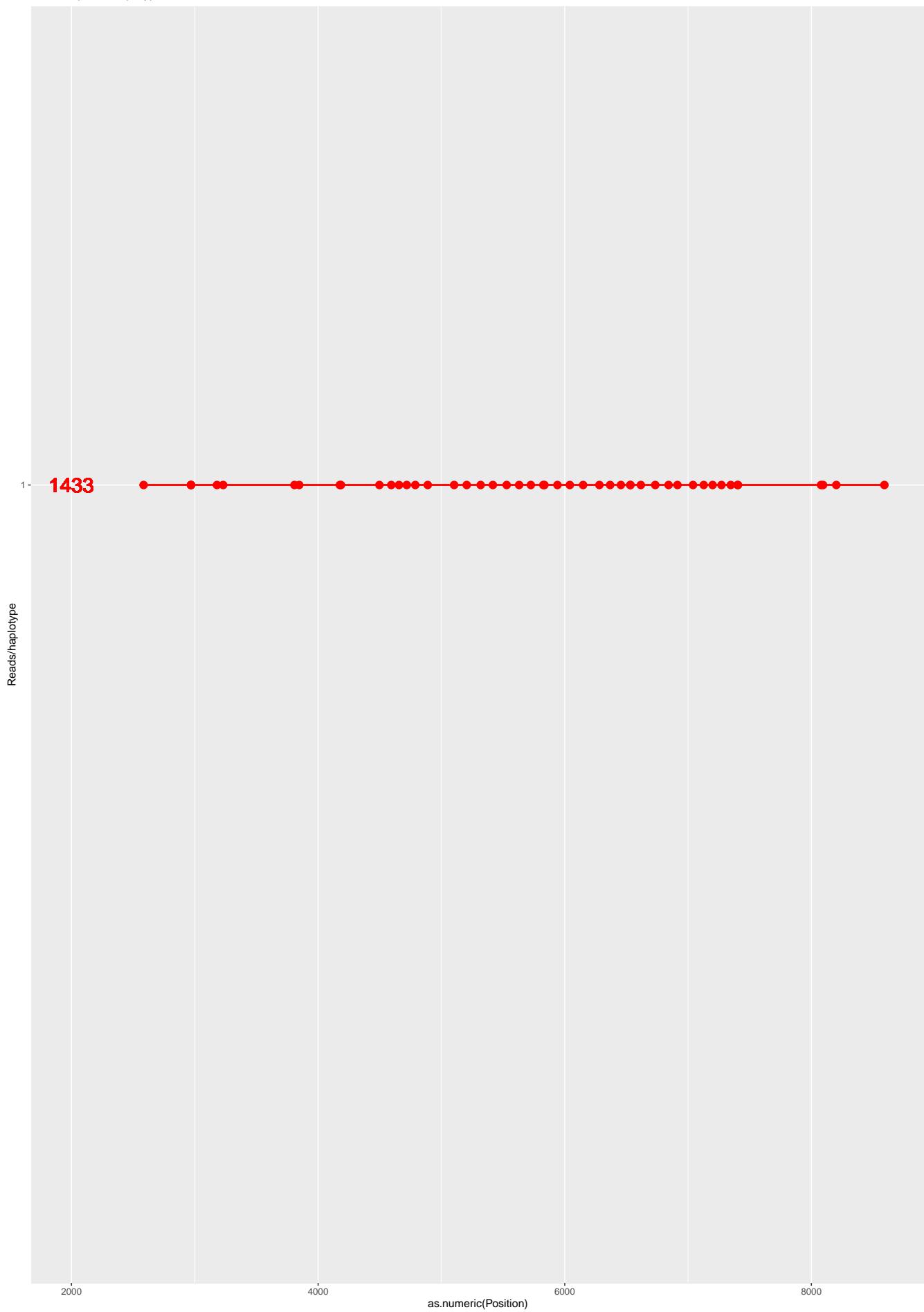
barcode = CAGTACTGCACGATCG & ACTATCGCGCACGCAG

Sample = 184a tetrad = 184 spore = a

Total reads = 1484 PCR=477

haplotypes I began with n[supporting reads] = 1433

most frequent 7 haplotypes.



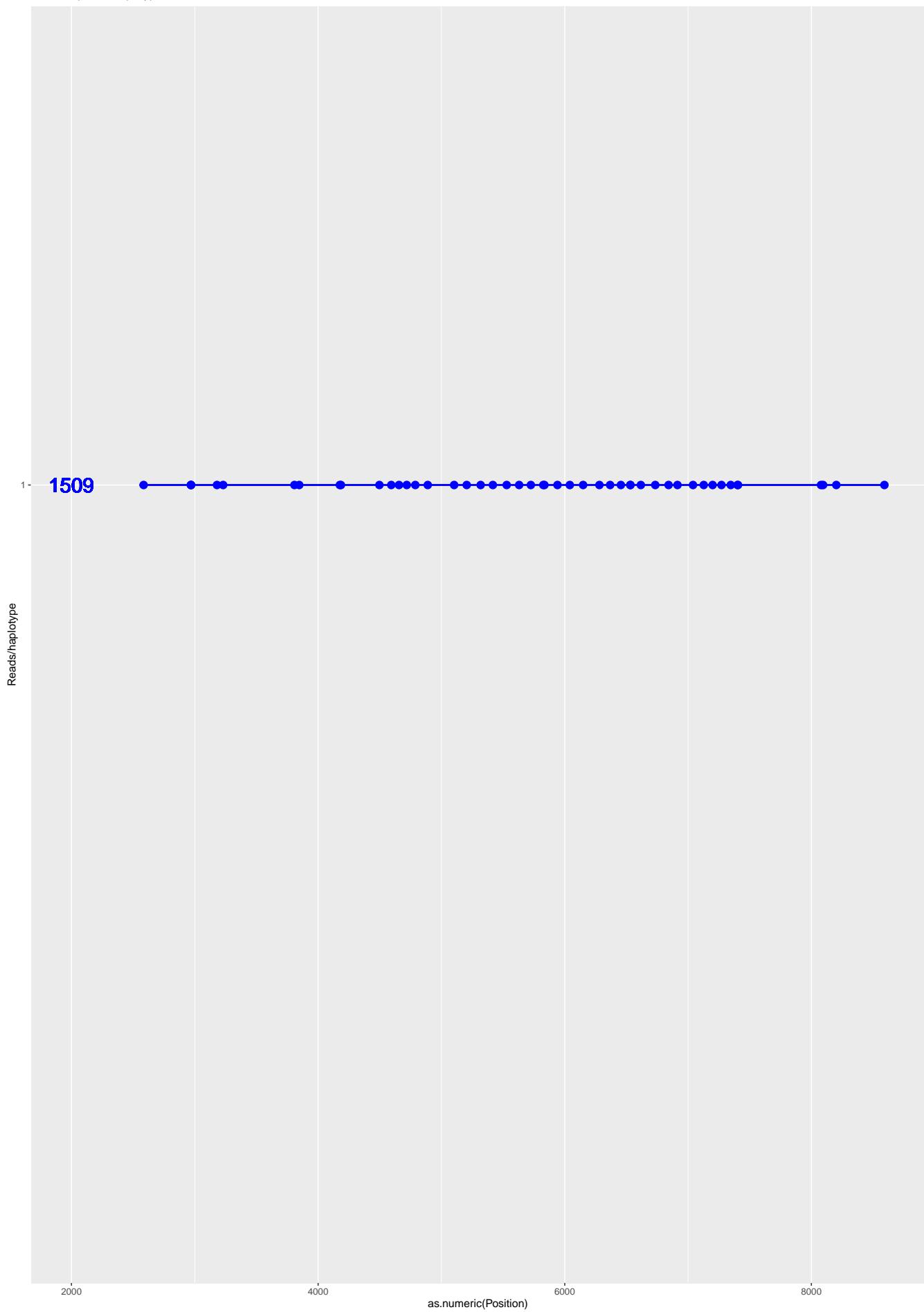
barcode = CACTGATCGATATGCA & CGTGTCTAGCTACTCA

Sample = 184b tetrad = 184 spore = b

Total reads = 1775 PCR=478

haplotypes I began with n[supporting reads] = 1509

most frequent 7 haplotypes.



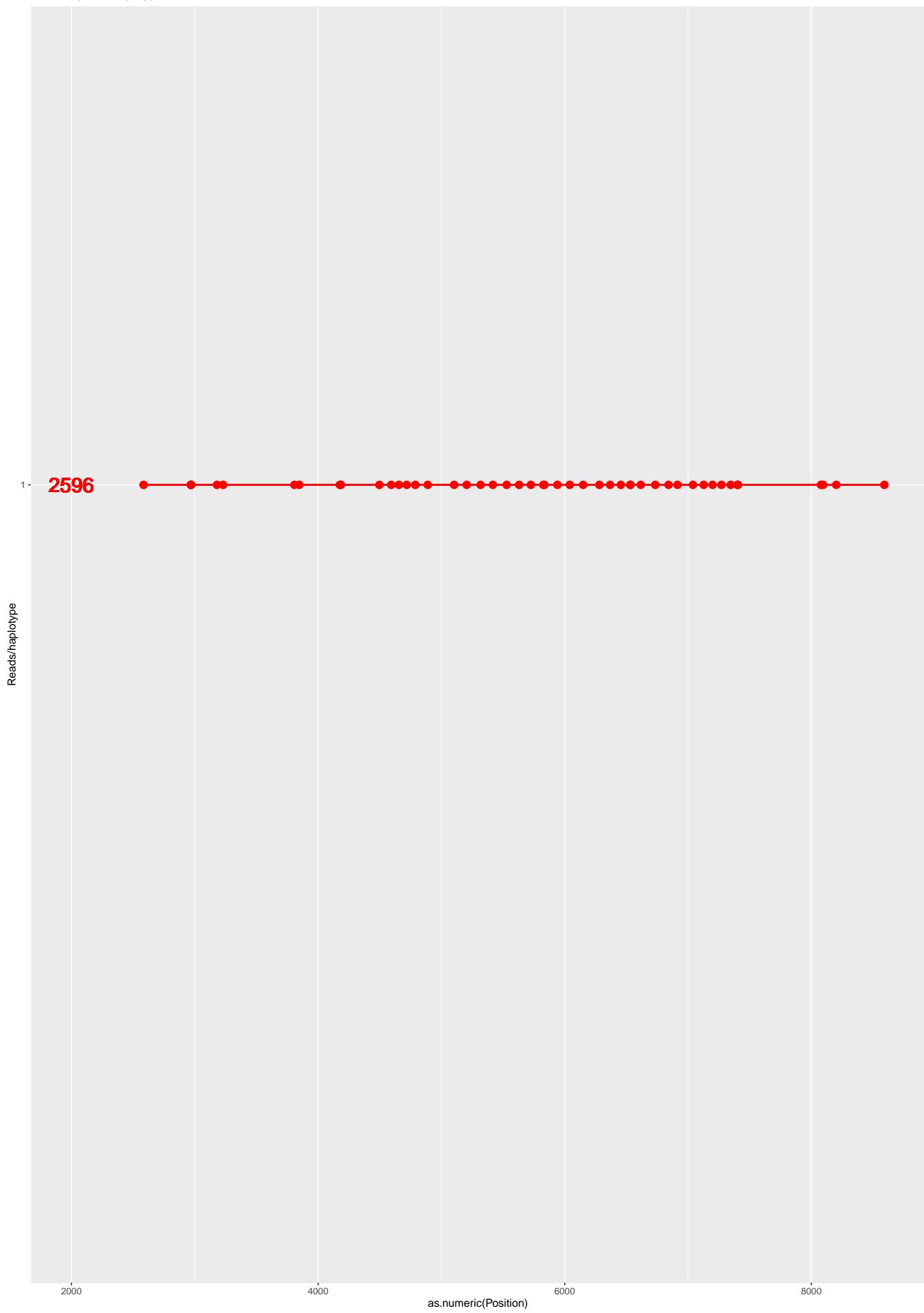
barcode = CACTGATCGATATGCA & TGTGAGACTGCATGTC

Sample = 184c tetrad = 184 spore = c

Total reads = 2728 PCR=479

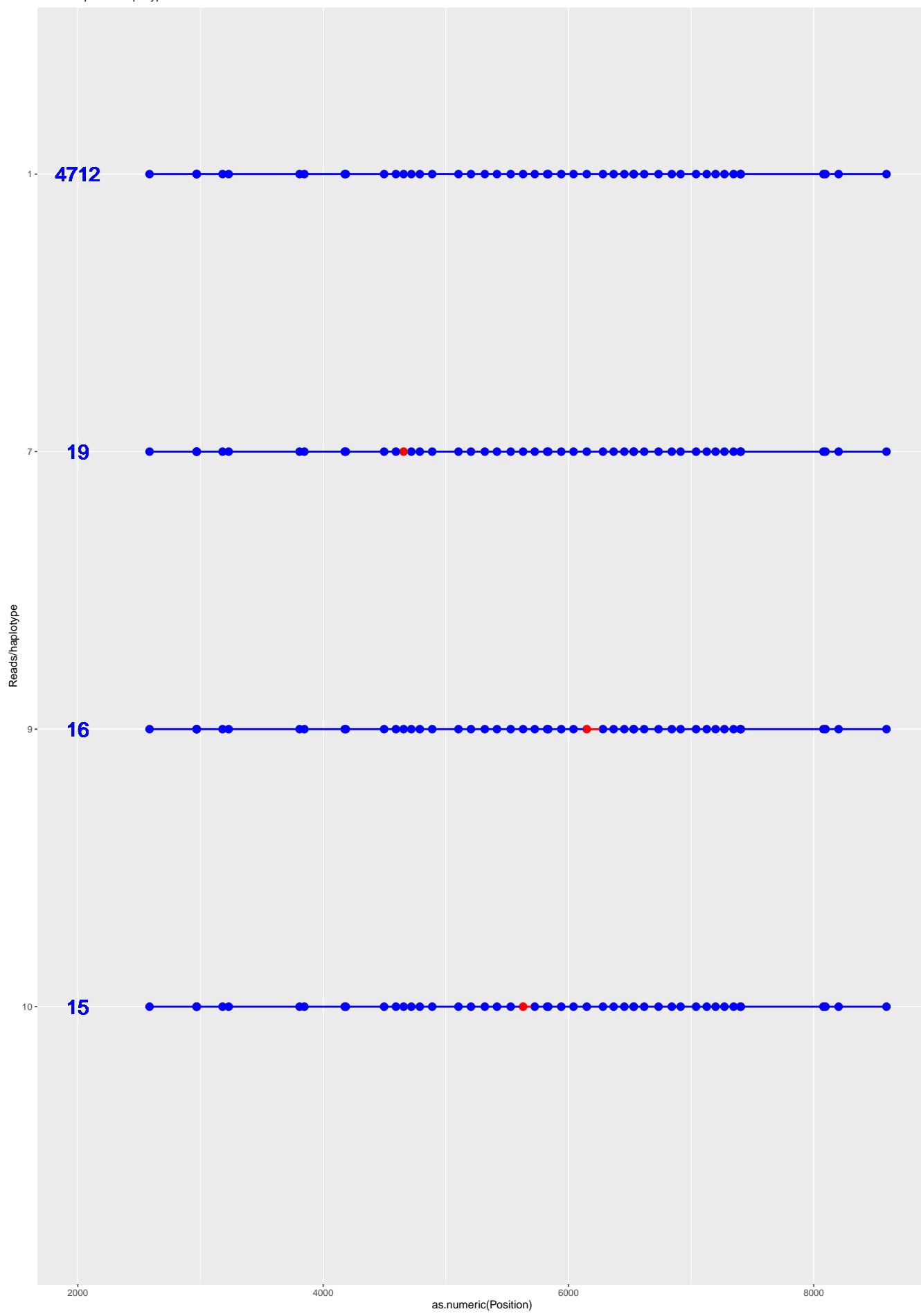
haplotypes I began with n[supporting reads] = 2596

most frequent 7 haplotypes.



barcode = CACTGATCGATATGCA & GCTCAGTGCCTACTG

Sample = 184d tetrad = 184 spore = d
Total reads = 5485 PCR=480
haplotypes I began with [n:supporting reads] = 15, 16, 19, 4712
most frequent 7 haplotypes.

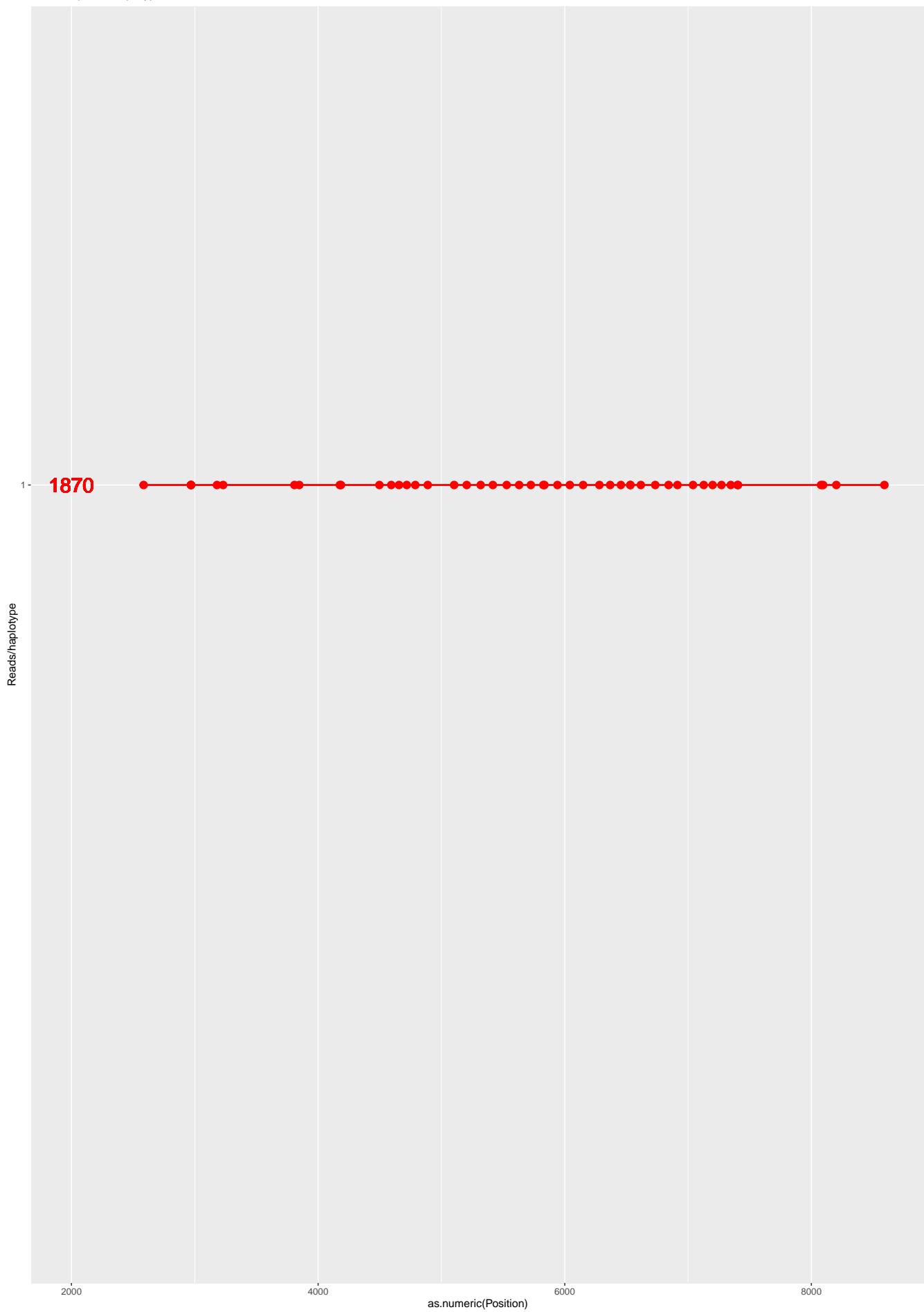


Sample = 185a tetrad = 185 spore = a

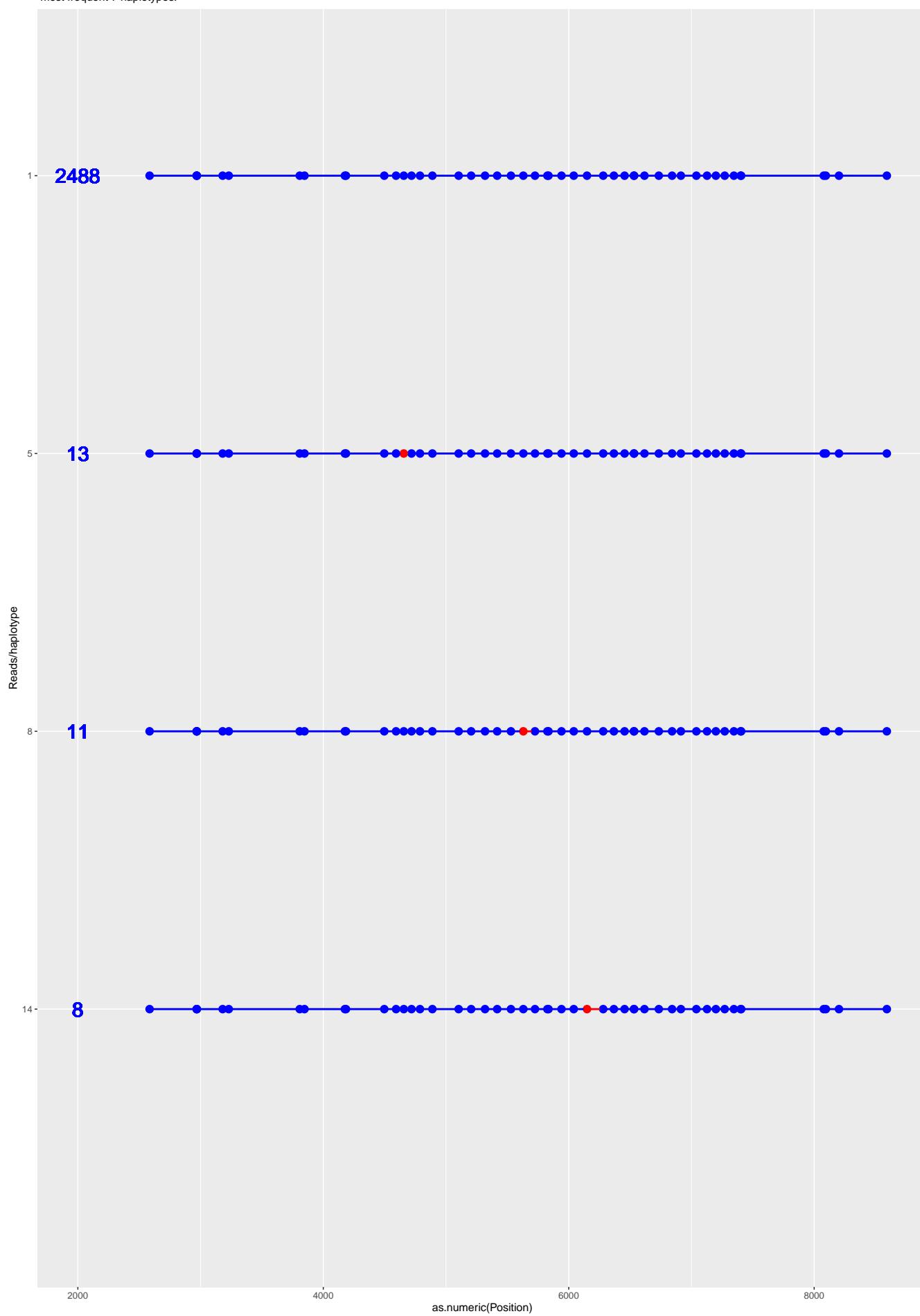
Total reads = 1966 PCR=481

haplotypes I began with n[supporting reads] = 1870

most frequent 7 haplotypes.



Sample = 185b tetrad = 185 spore = b
Total reads = 2936 PCR=482
haplotypes I began with [n|supporting reads] = 8, 11, 13, 2488
most frequent 7 haplotypes.



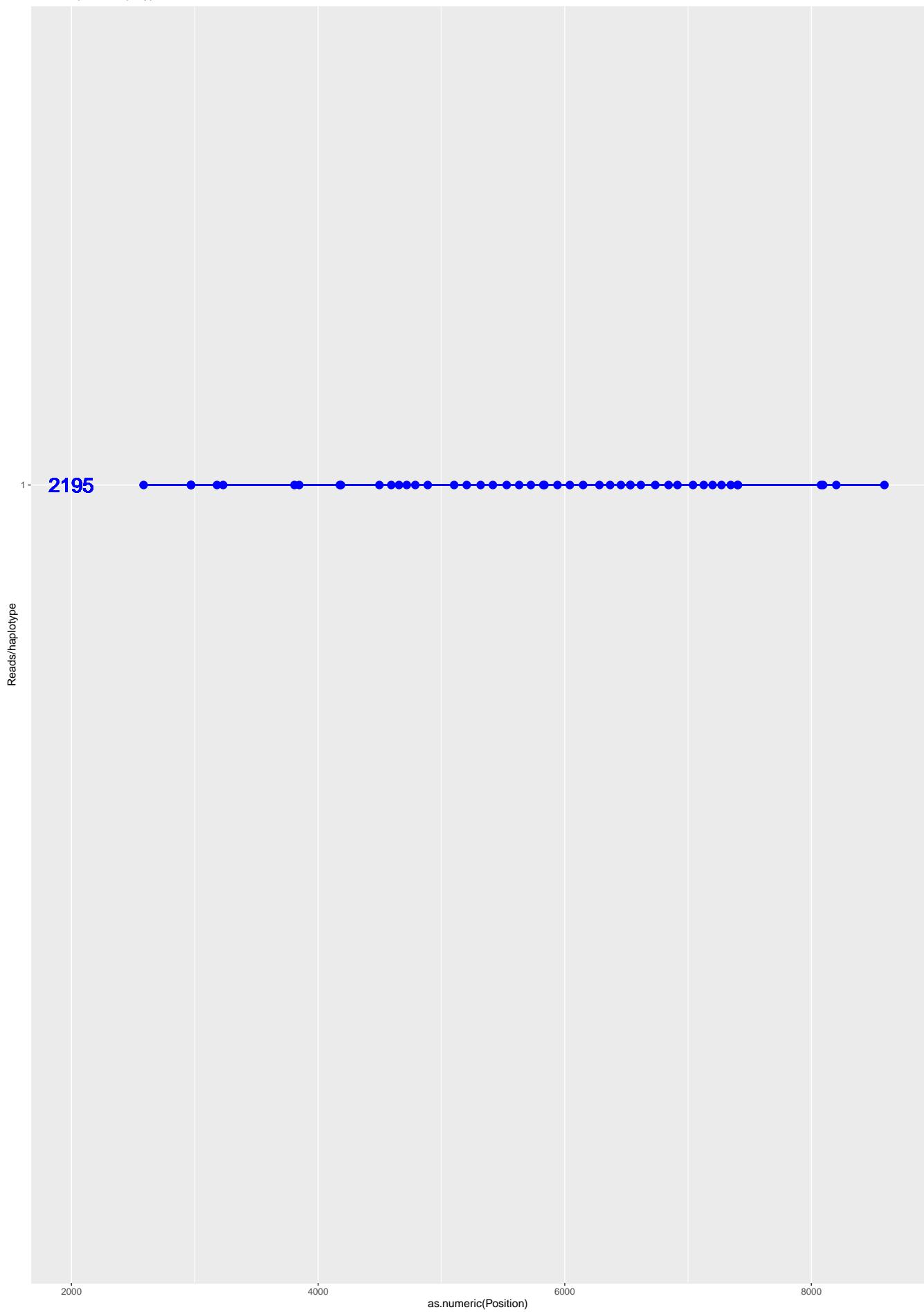
barcode = TACAGTGTCTGCTGCG & AGTATCACAGTCGCTG

Sample = 185c tetrad = 185 spore = c

Total reads = 2594 PCR=483

haplotypes I began with n[supporting reads] = 2195

most frequent 7 haplotypes.



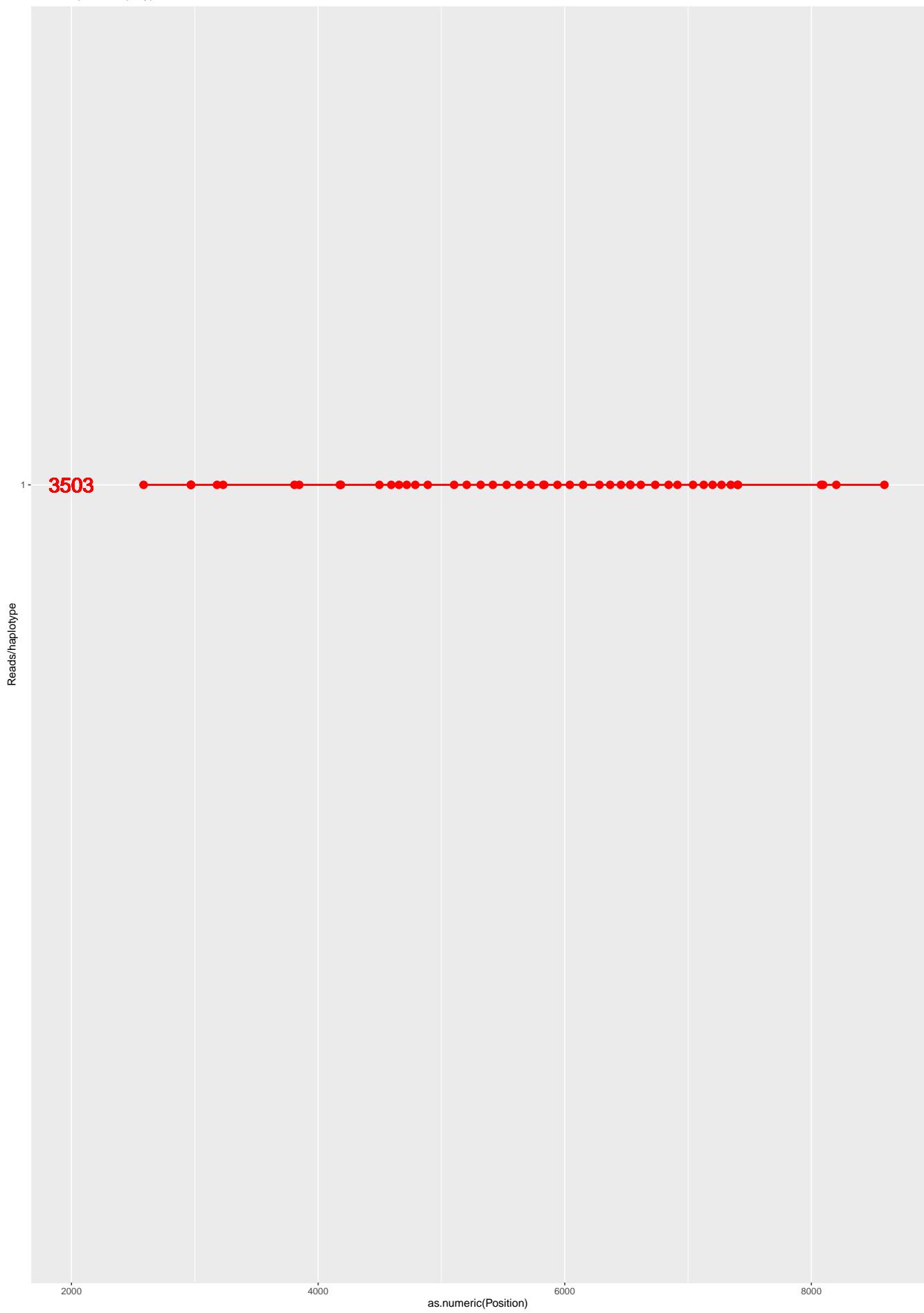
barcode = TACAGTGCTGCTGCG & ATCATATGATGCGACA

Sample = 185d tetrad = 185 spore = d

Total reads = 3645 PCR=484

haplotypes I began with n[supporting reads] = 3503

most frequent 7 haplotypes.

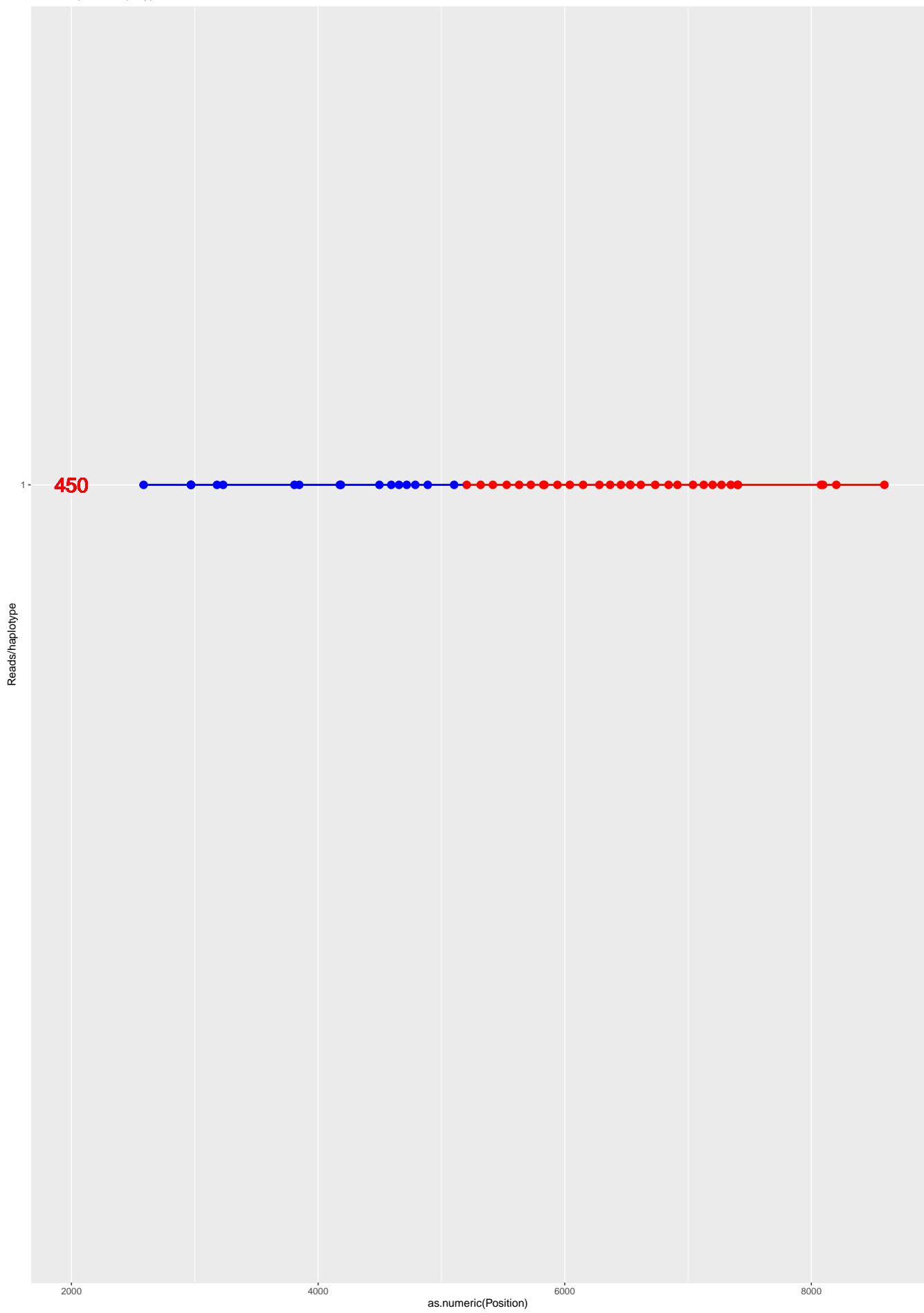


Sample = 186a tetrad = 186 spore = a

Total reads = 487 PCR=485

haplotypes I began with n[supporting reads] = 450

most frequent 7 haplotypes.



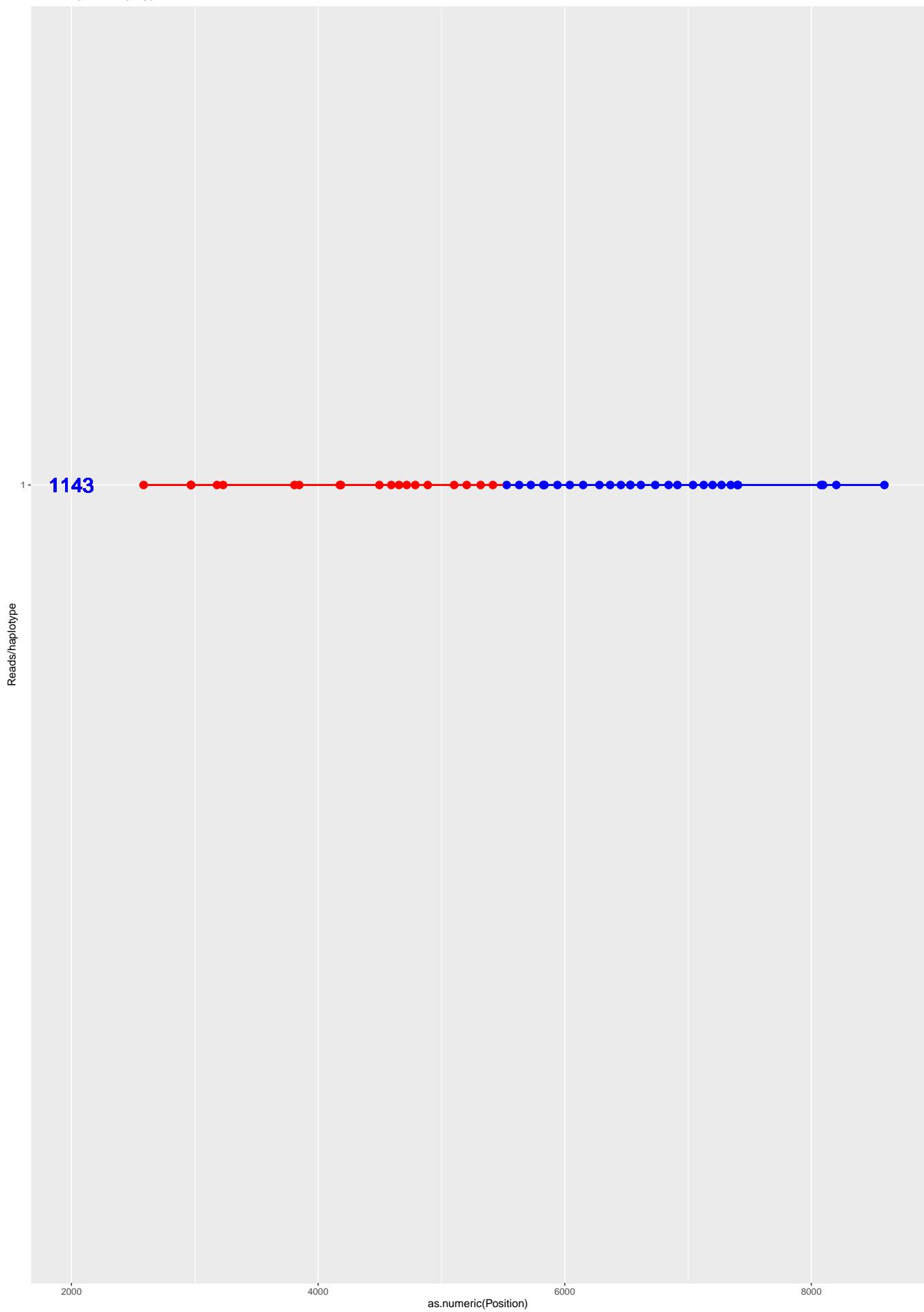
barcode = TACAGTGTCTGCTGCG & CGTGTCACTGCTACTCA

Sample = 186b tetrad = 186 spore = b

Total reads = 1247 PCR=486

haplotypes I began with n[supporting reads] = 1143

most frequent 7 haplotypes.



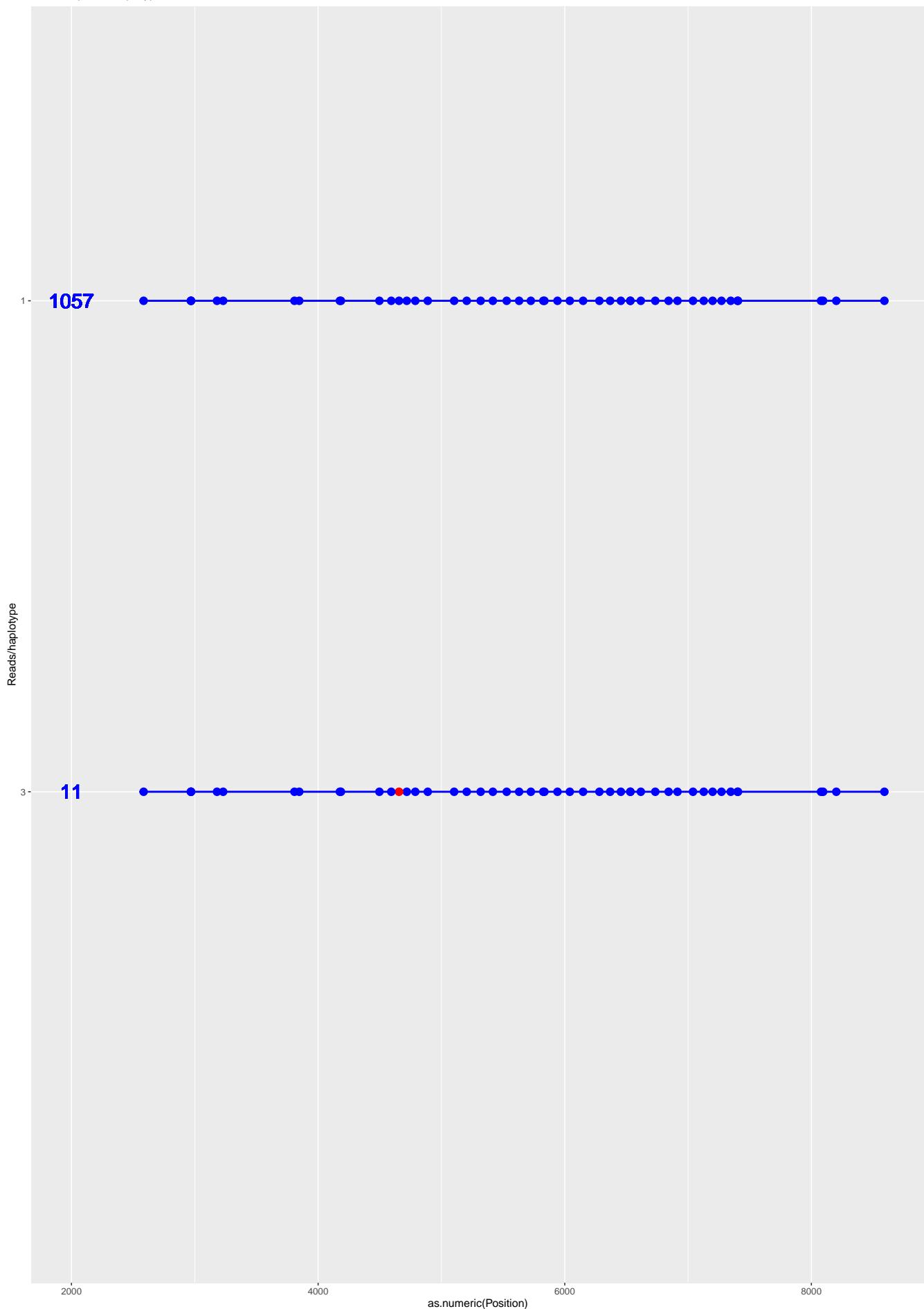
barcode = TACAGTGCTGCTGCG & TGTGAGACTGCATGTC

Sample = 186c tetrad = 186 spore = c

Total reads = 1269 PCR=487

haplotypes I began with n[supporting reads] = 11, 1057

most frequent 7 haplotypes.



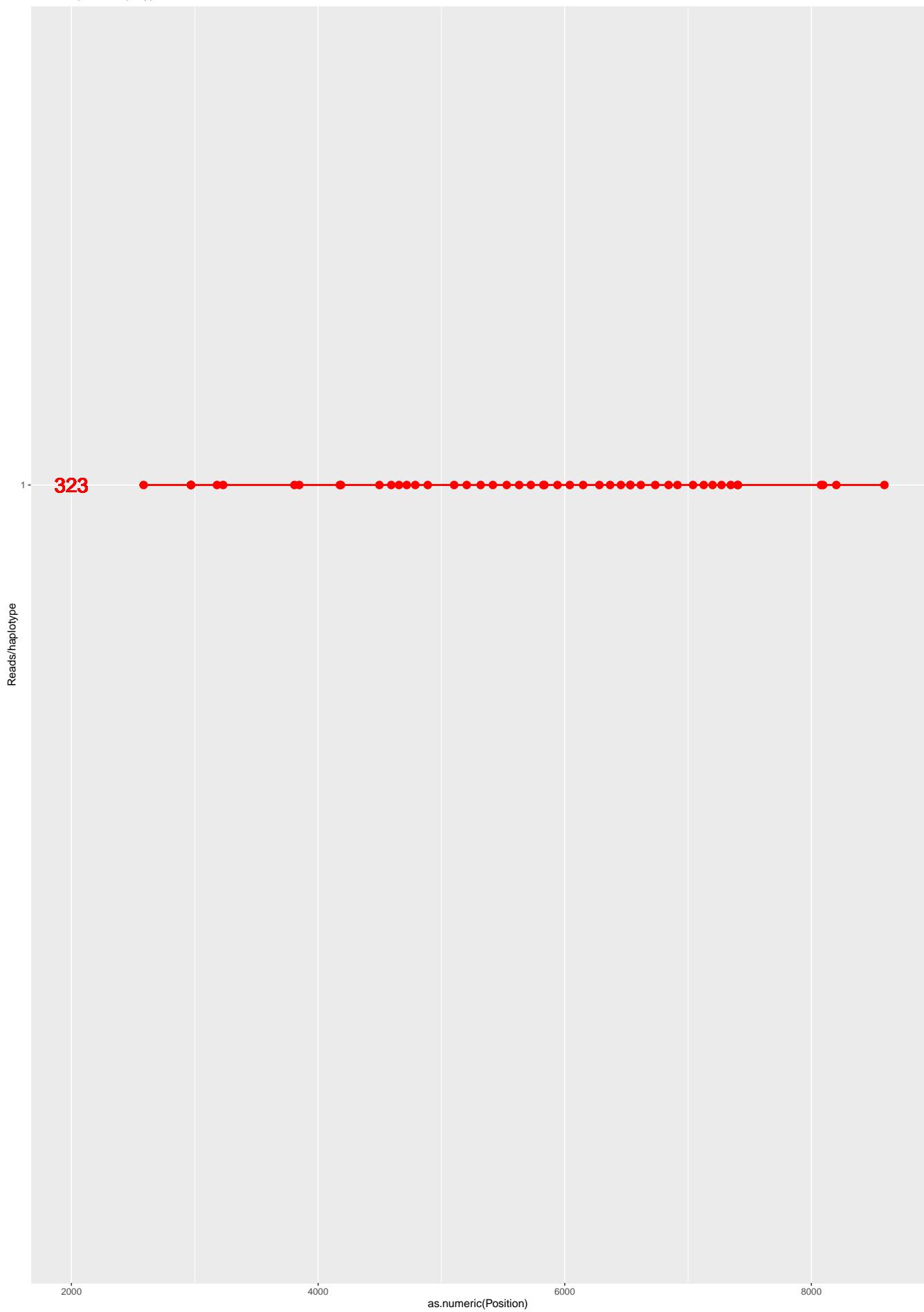
barcode = TACAGTGCTGCTGCG & GCTCAGTGCCTACTG

Sample = 186d tetrad = 186 spore = d

Total reads =336 PCR=488

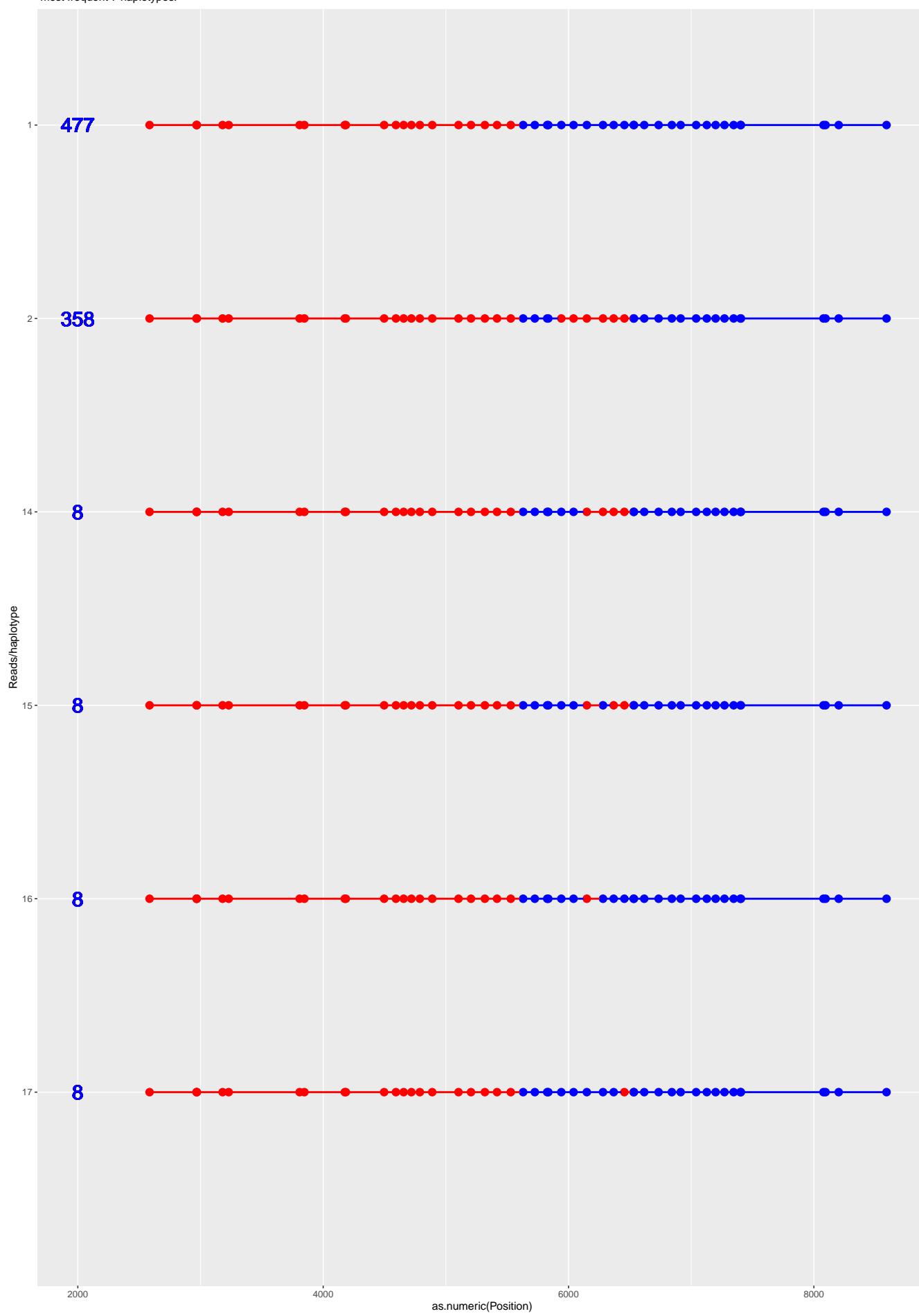
haplotypes I began with n[supporting reads] = 323

most frequent 7 haplotypes.



barcode = TACAGTGCTGCTGCG & ACTATCGCGCACGCAG

Sample = 187a tetrad = 187 spore = a
Total reads = 1483 PCR=489
haplotypes I began with [n(supporting reads)] = 8, 358, 477
most frequent 7 haplotypes.



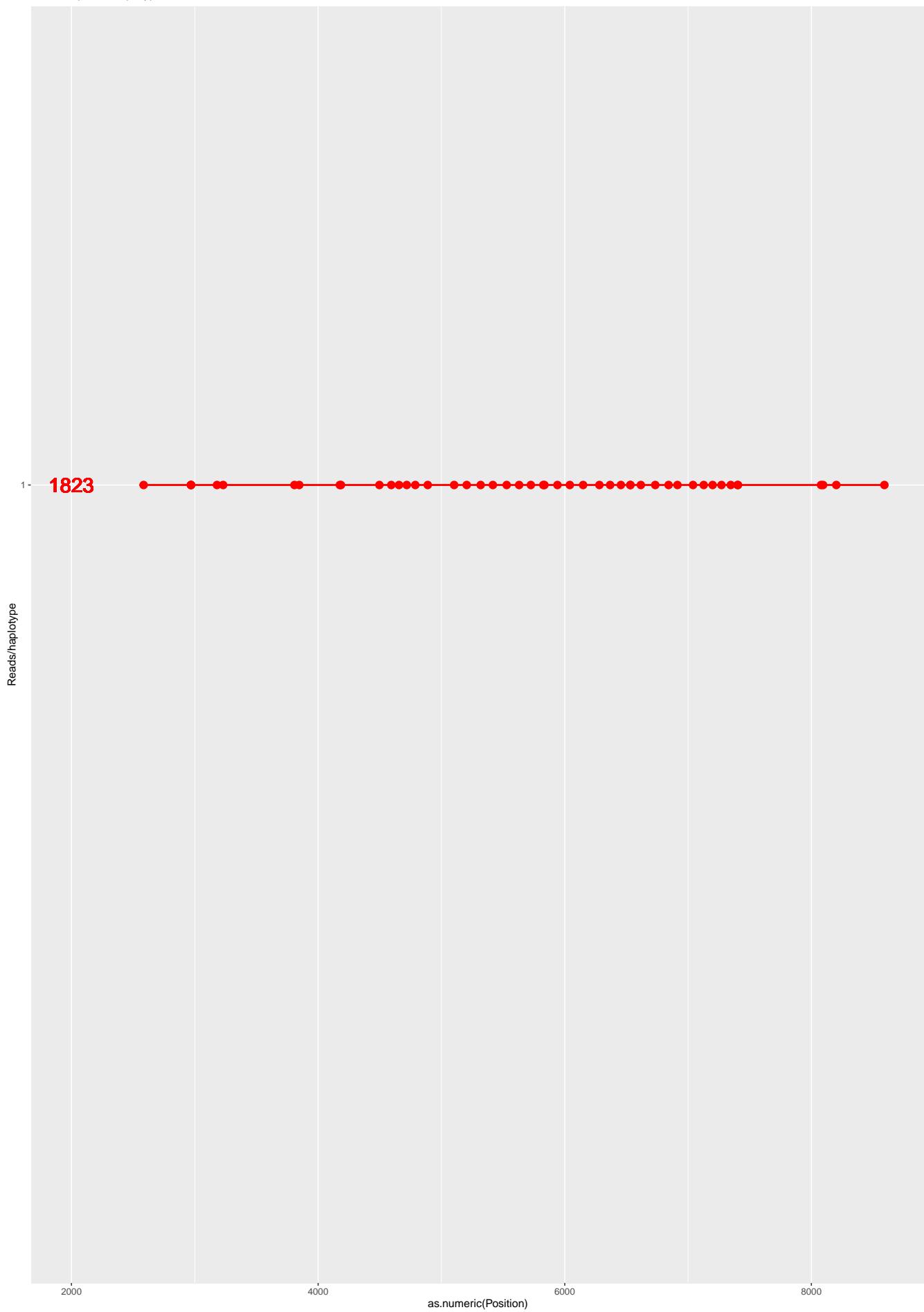
barcode = TACAGATAGTGTAGCG & GCGACGAGTACTCATG

Sample = 187b tetrad = 187 spore = b

Total reads = 1913 PCR=490

haplotypes I began with n[supporting reads] = 1823

most frequent 7 haplotypes.

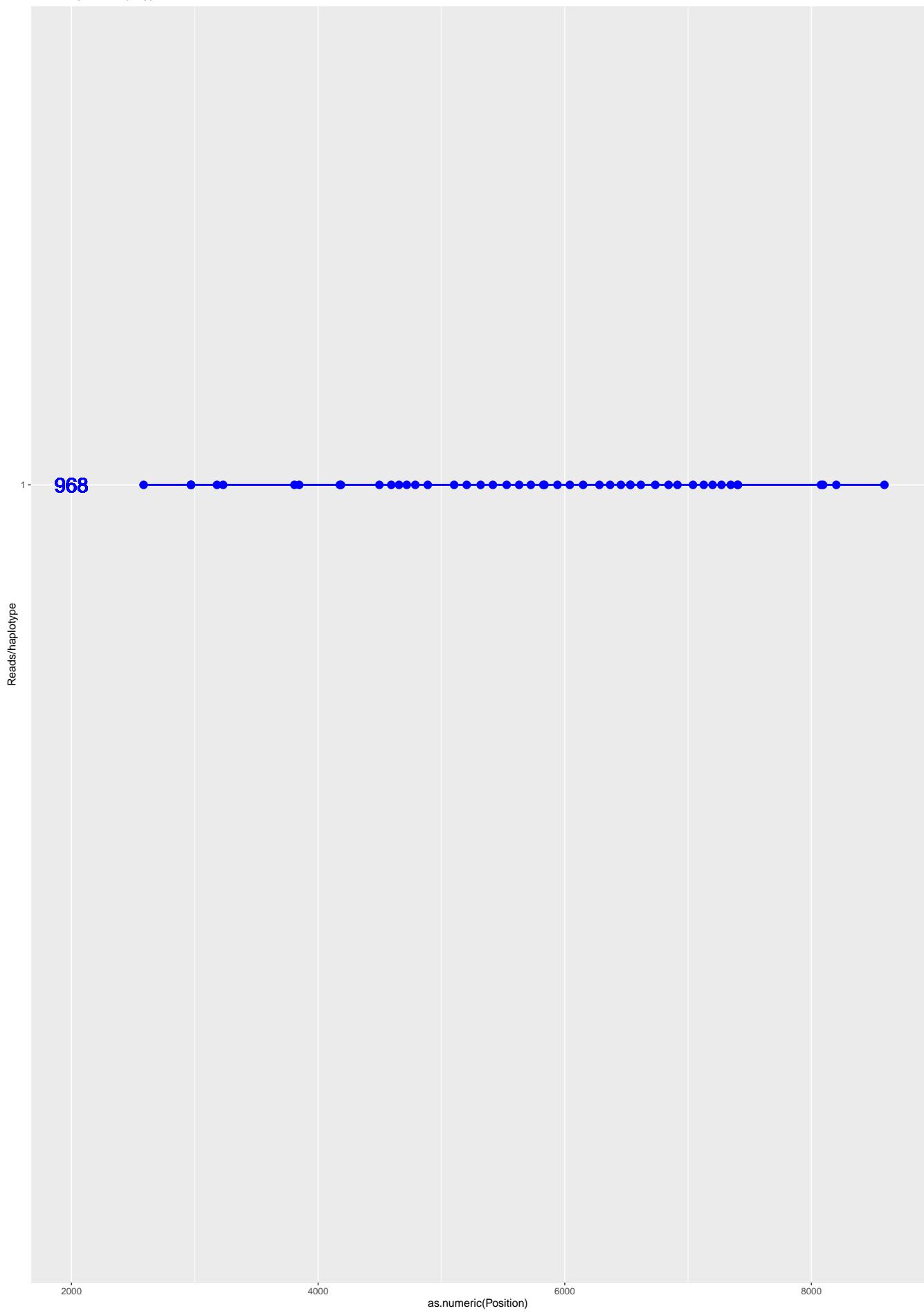


Sample = 187c tetrad = 187 spore = c

Total reads = 1147 PCR=491

haplotypes I began with n[supporting reads] = 968

most frequent 7 haplotypes.



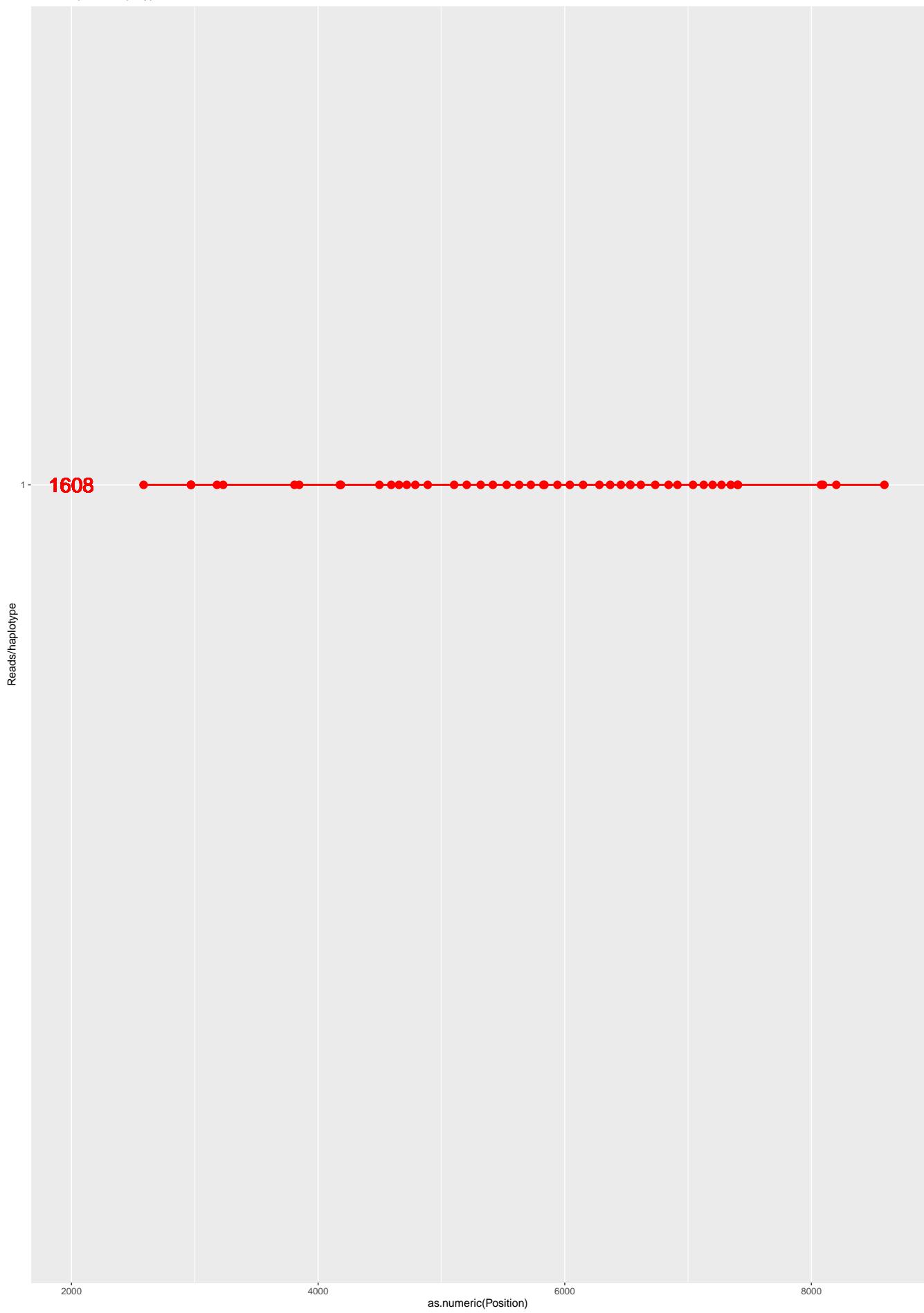
barcode = TACAGATAGTGTAGCG & ATCATATGATGCGACA

Sample = 187d tetrad = 187 spore = d

Total reads = 1687 PCR=492

haplotypes I began with n[supporting reads] = 1608

most frequent 7 haplotypes.

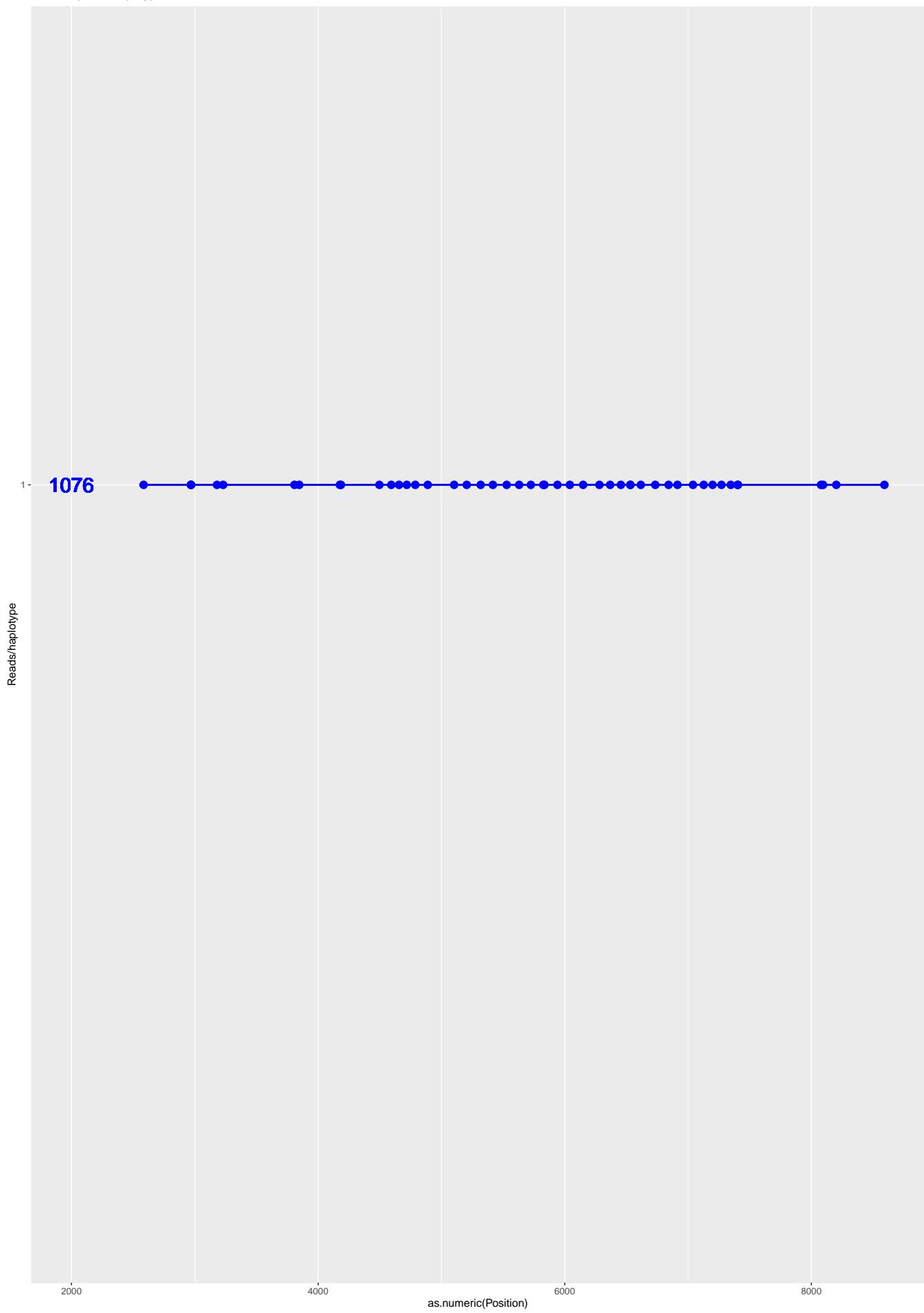


Sample = 188a tetrad = 188 spore = a

Total reads = 1265 PCR=493

haplotypes I began with n[supporting reads] = 1076

most frequent 7 haplotypes.



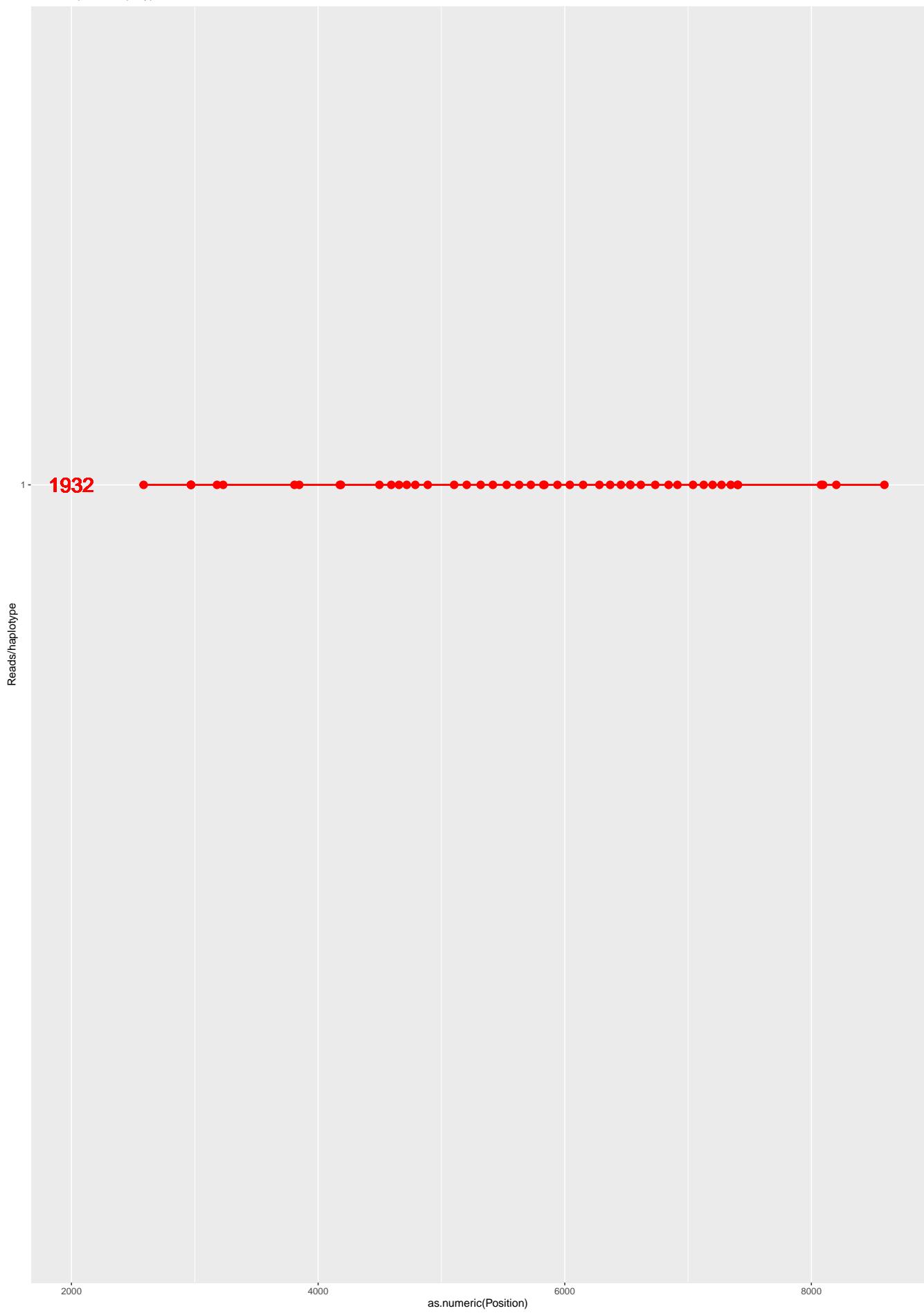
barcode = TACAGATAAGTGTAGCG & CGTGTCATGCTACTCA

Sample = 188b tetrad = 188 spore = b

Total reads = 2015 PCR=494

haplotypes I began with n[supporting reads] = 1932

most frequent 7 haplotypes.

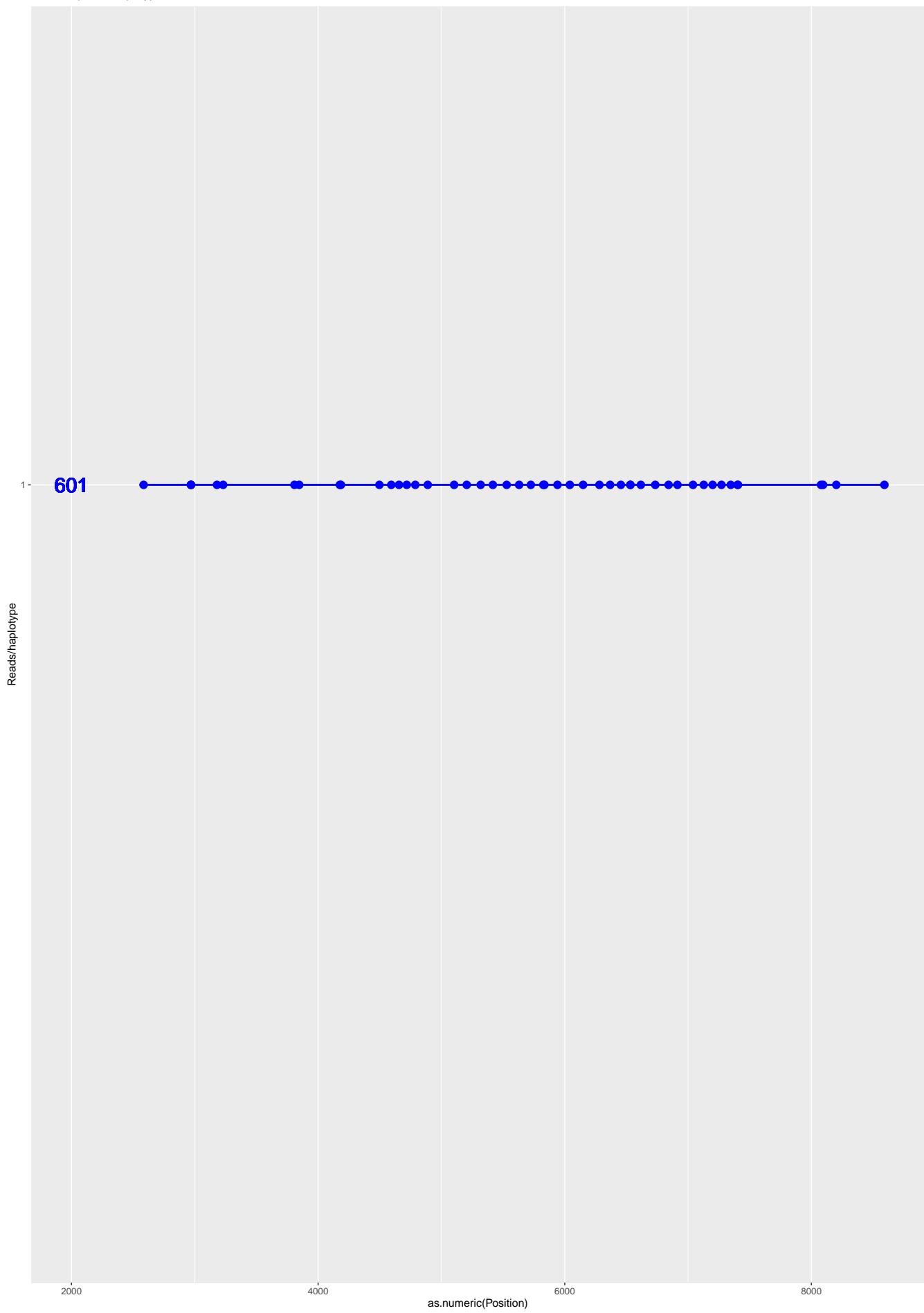


Sample = 188c tetrad = 188 spore = c

Total reads =704 PCR=495

haplotypes I began with n[supporting reads] = 601

most frequent 7 haplotypes.



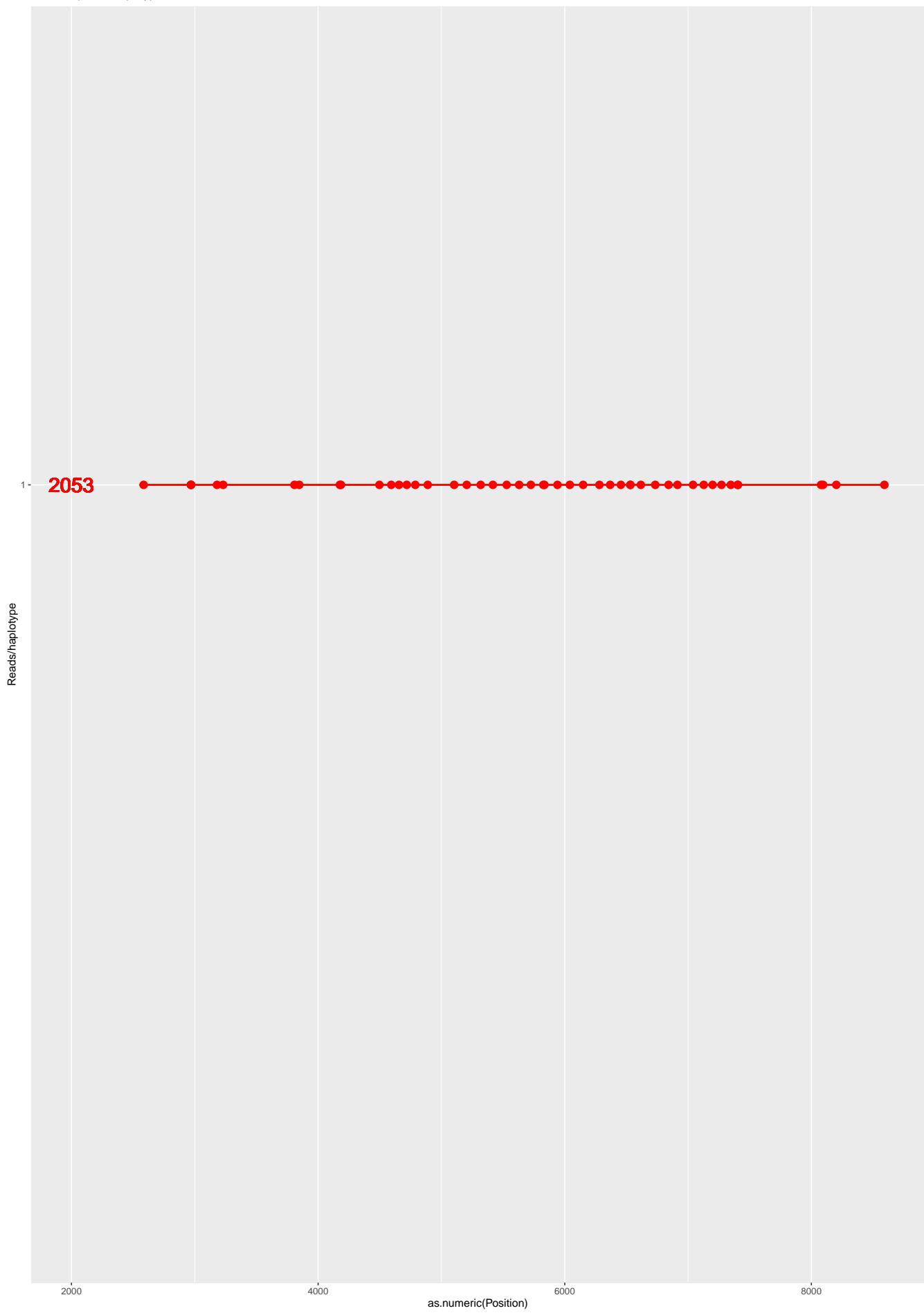
barcode = TACAGATAGTGTAGCG & GCTCAGTGCCTACTG

Sample = 188d tetrad = 188 spore = d

Total reads = 2150 PCR=496

haplotypes I began with n[supporting reads] = 2053

most frequent 7 haplotypes.



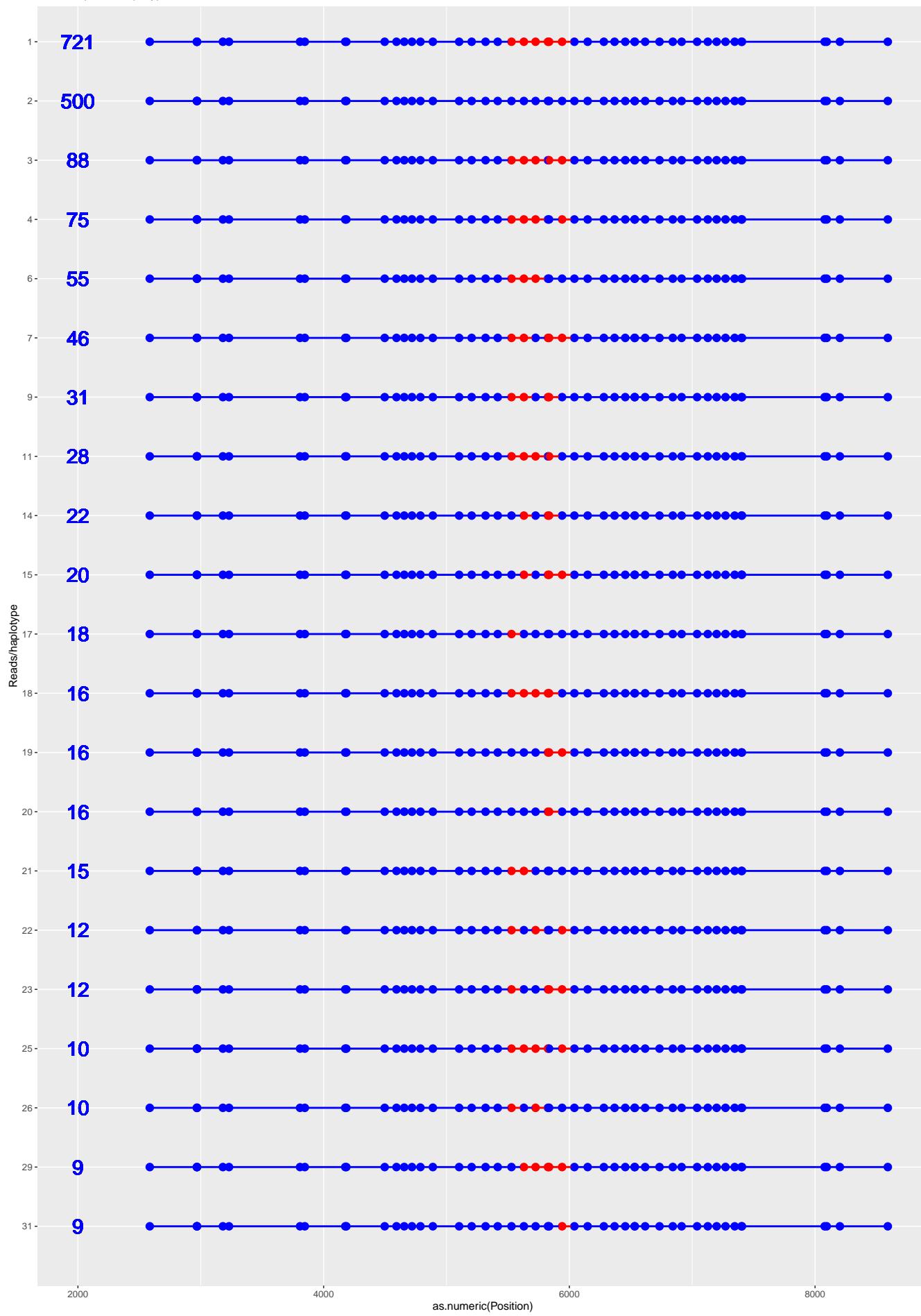
barcode = TACAGATAGTGTAGCG & ACTATCGCGCACGCAG

Sample = 191a tetrad = 191 spore = a

Total reads =2408 PCR=501

haplotypes I began with [n|supporting reads] = 9, 10, 12, 15, 16, 18, 20, 22, 28, 31, 46, 55, 75, 88, 500, 721

most frequent 7 haplotypes.



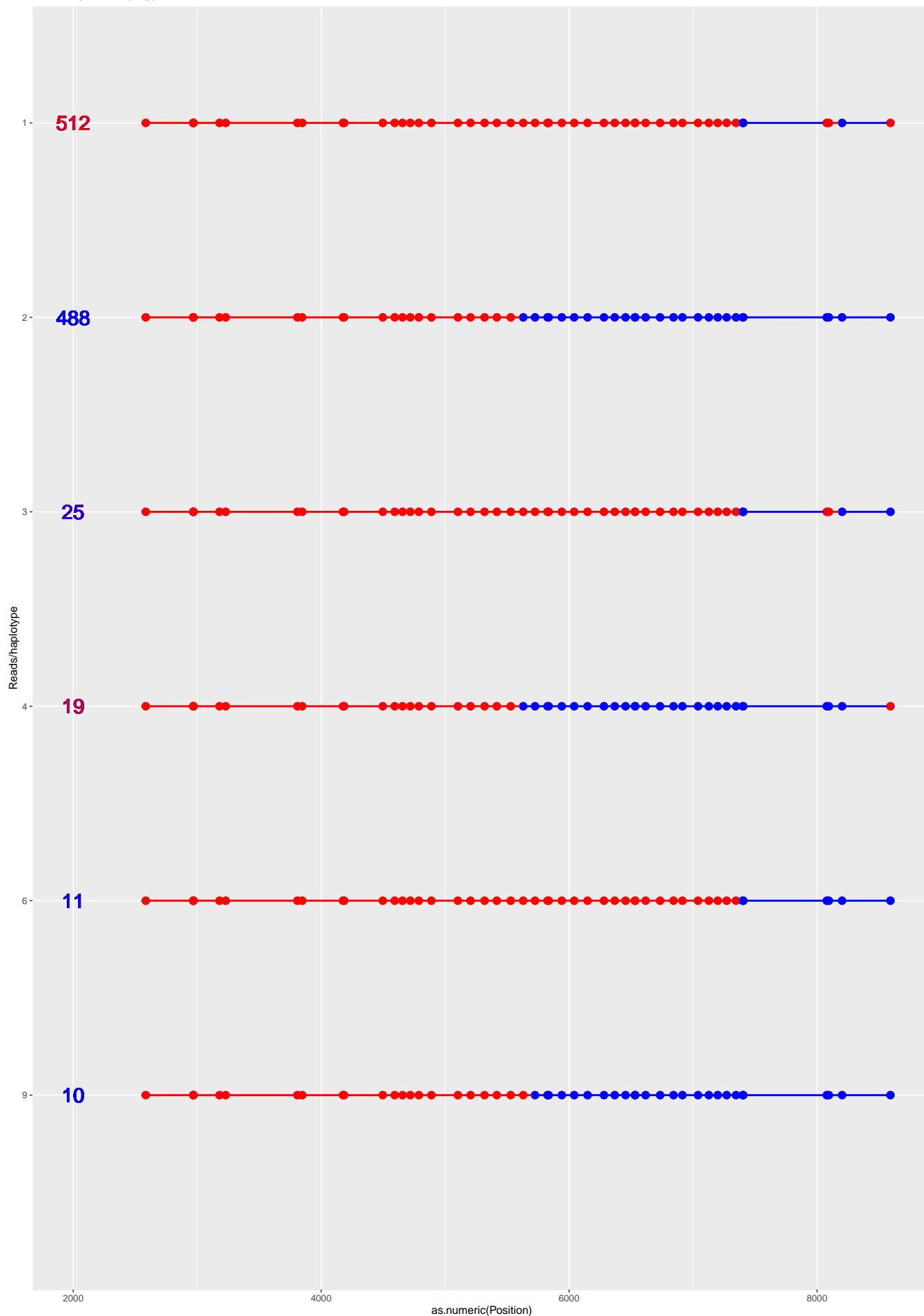
barcode = TCGTAGAGCTGAGAC & CGTGTCACTGACTCA

Sample = 191b tetrad = 191 spore = b

Total reads = 2037 PCR=502

haplotypes I began with n[supporting reads] = 10, 11, 19, 25, 488, 512

most frequent 7 haplotypes.



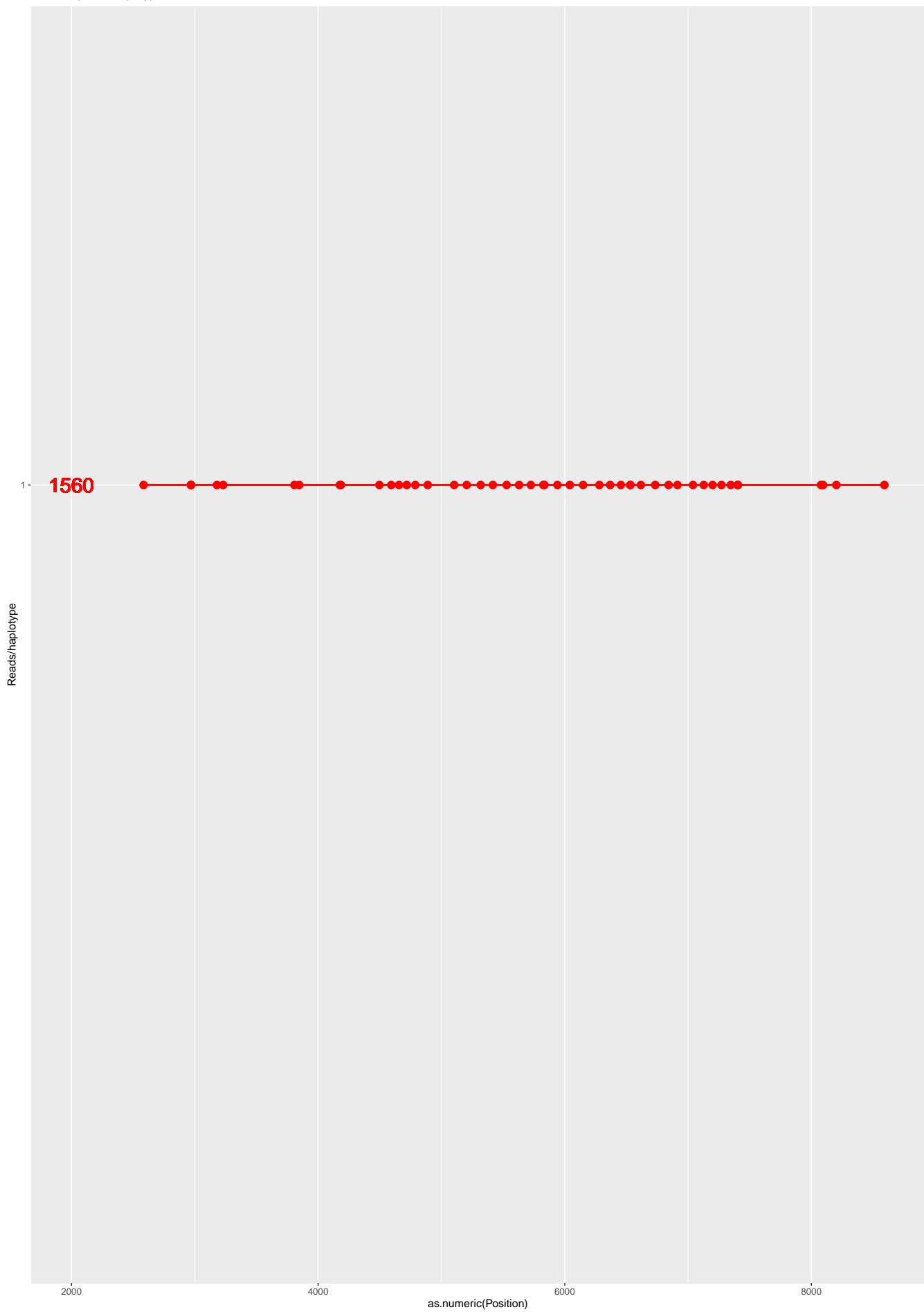
barcode = TCGTAGAGCTCGAGAC & TGTGAGACTGCATGTC

Sample = 191c tetrad = 191 spore = c

Total reads = 1618 PCR=503

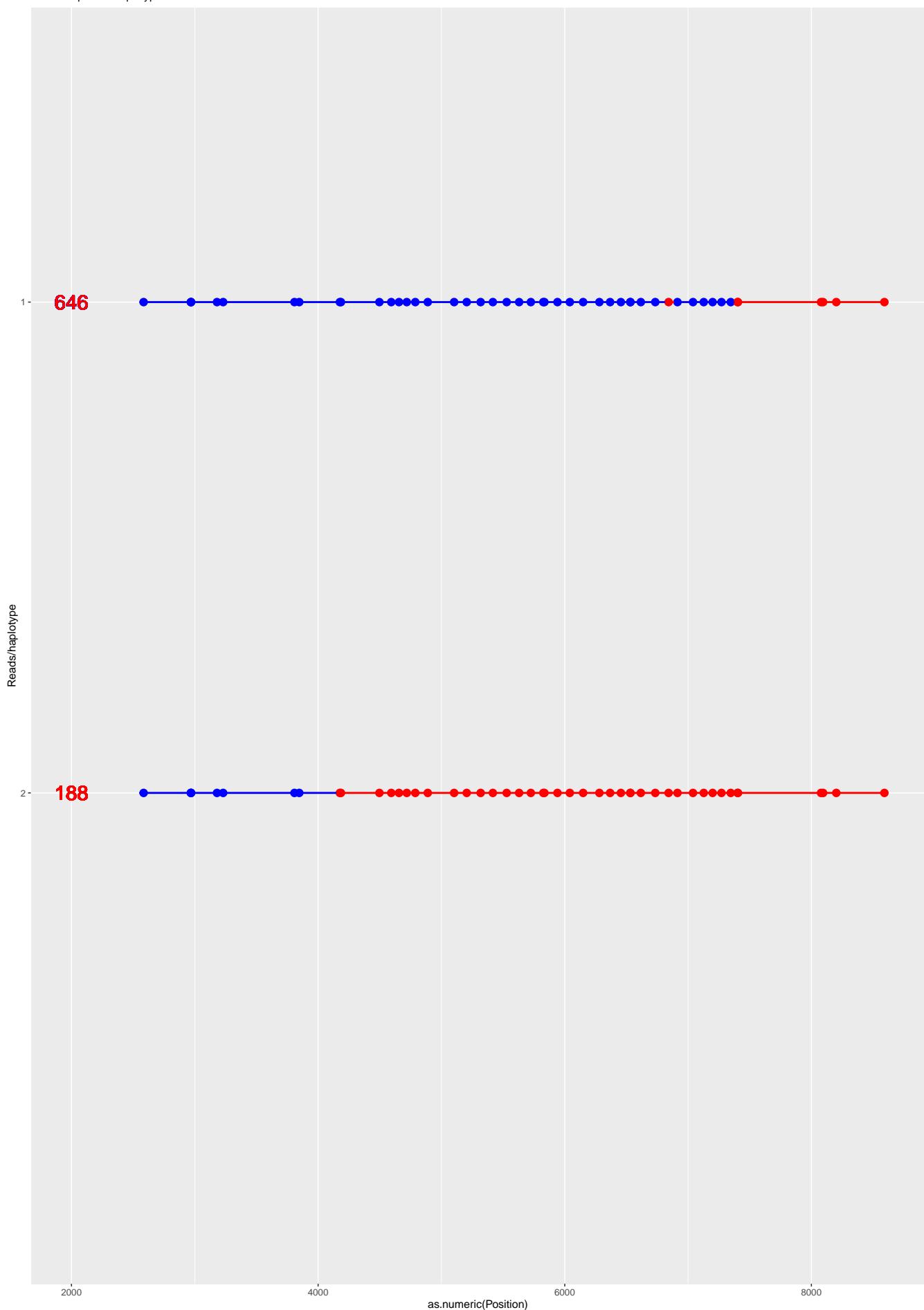
haplotypes I began with n[supporting reads] = 1560

most frequent 7 haplotypes.



barcode = TCGTAGAGCTCGAGAC & GCTCAGTGCCTACTG

Sample = 191d tetrad = 191 spore = d
Total reads = 1958 PCR=504
haplotypes I began with n[supporting reads] = 188, 646
most frequent 7 haplotypes.



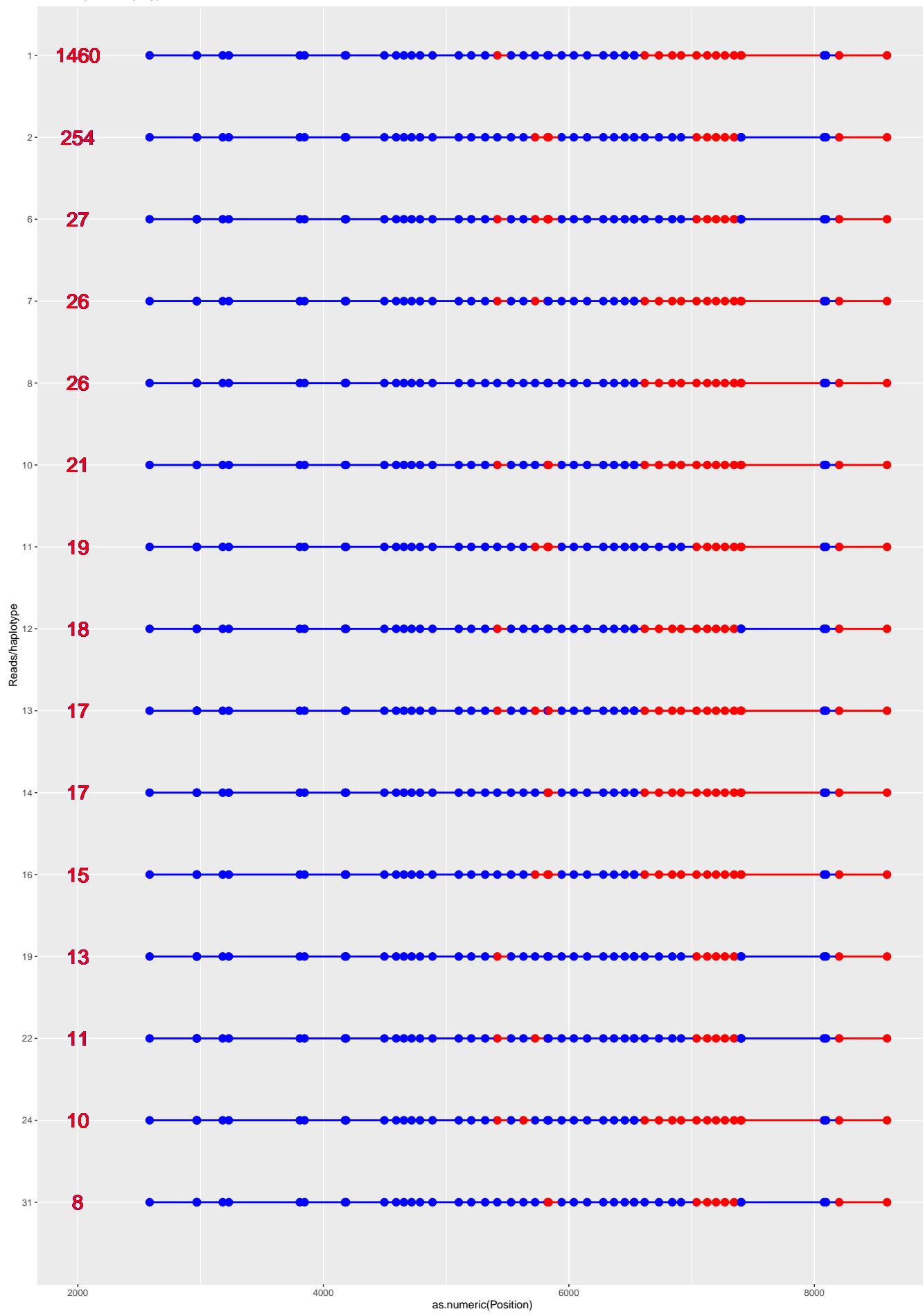
barcode = TCGTAGAGCTCGAGAC & ACTATCGCGCACGCAG

Sample = 195a tetrad = 195 spore = a

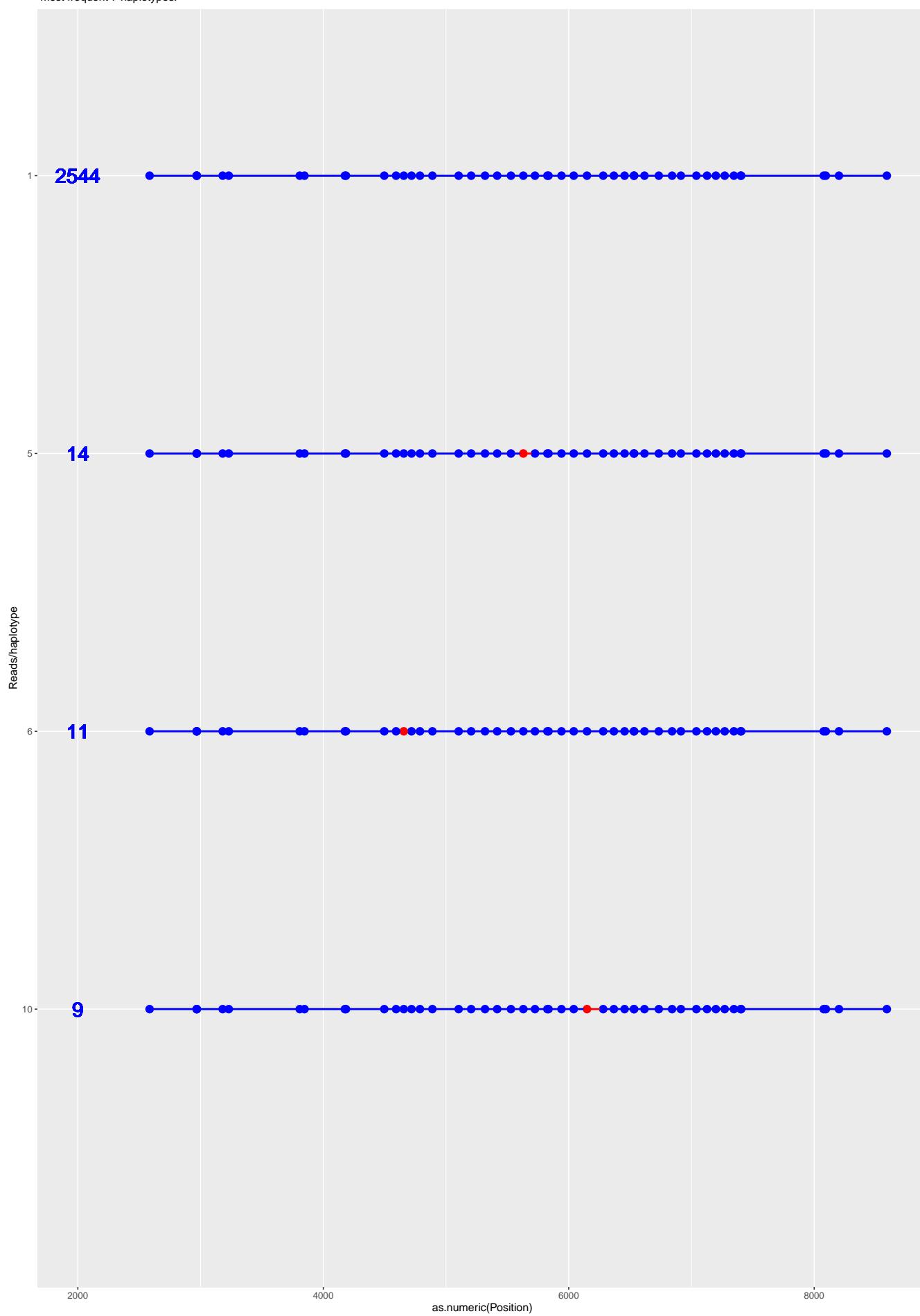
Total reads = 3192 PCR=509

haplotypes I began with [n(supporting reads)] = 8, 10, 11, 13, 15, 17, 18, 19, 21, 26, 27, 254, 1460

most frequent 7 haplotypes.



Sample = 195b tetrad = 195 spore = b
Total reads = 3013 PCR=510
haplotypes I began with [n(supporting reads)] = 9, 11, 14, 2544
most frequent 7 haplotypes.



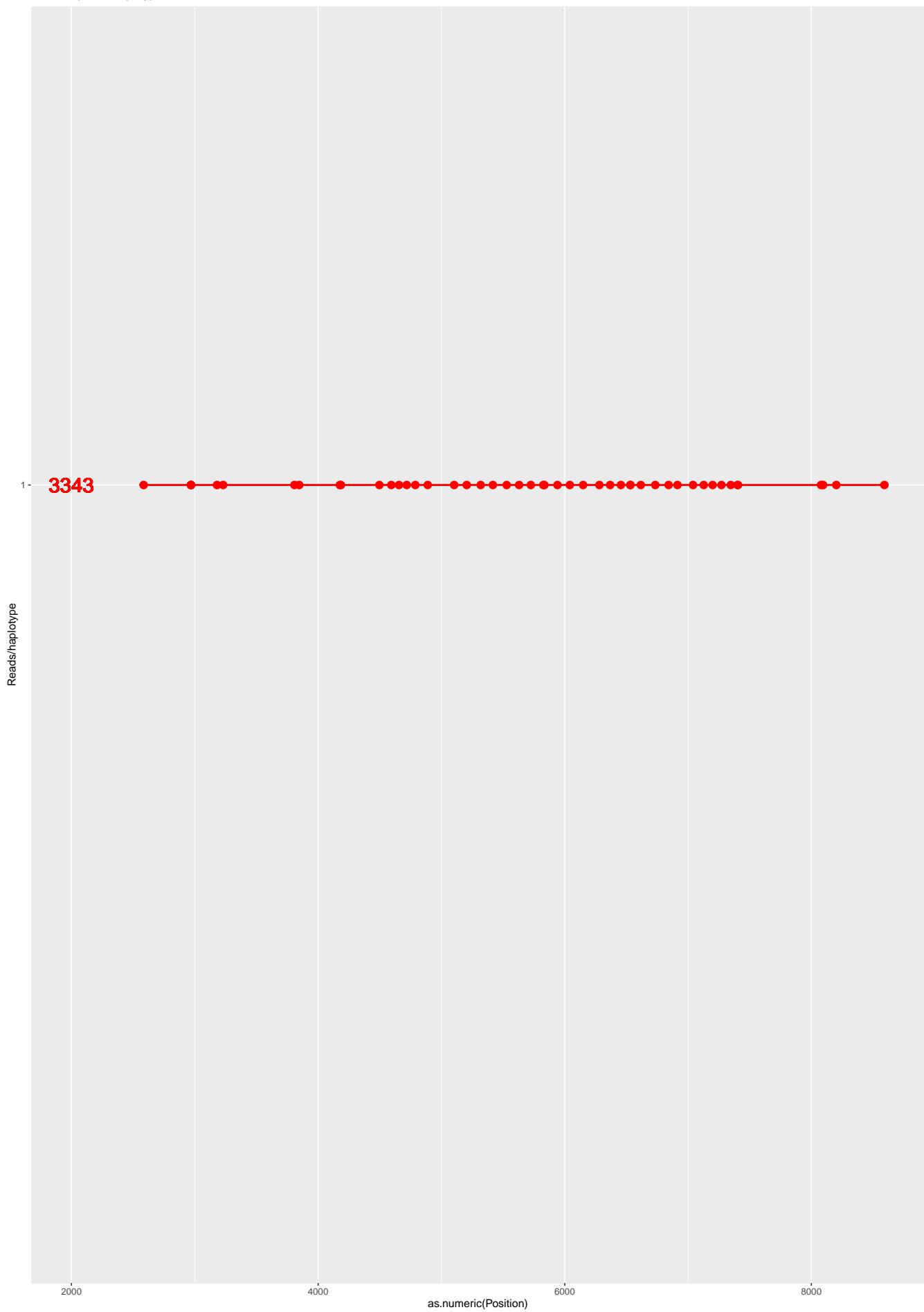
barcode = GAGCTGCGCAGTCGAT & TGTGAGACTGCATGTC

Sample = 195c tetrad = 195 spore = c

Total reads = 3476 PCR=511

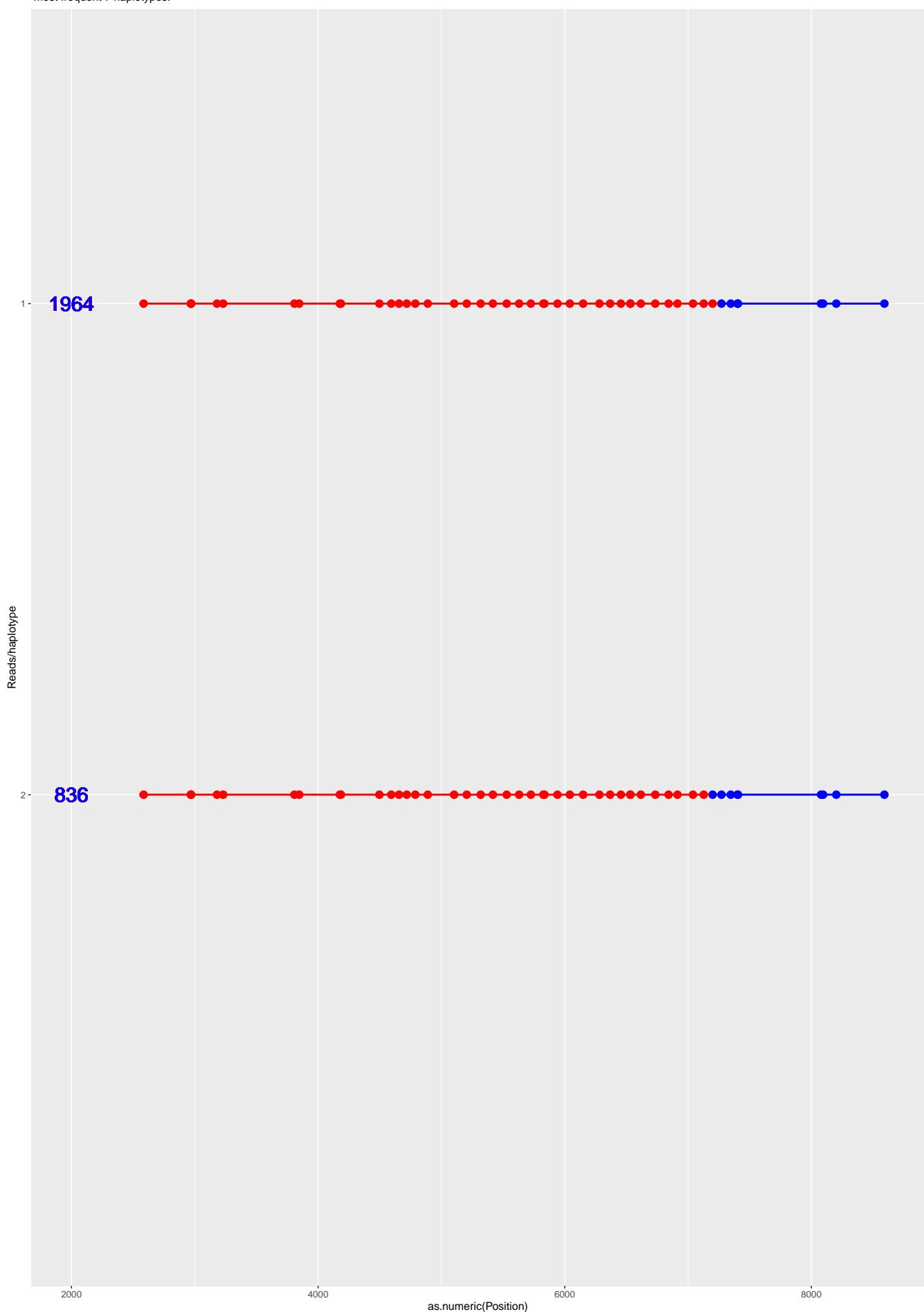
haplotypes I began with n[supporting reads] = 3343

most frequent 7 haplotypes.



barcode = GAGCTGCGCACTCGAT & GCTCAGTGCCTACTG

Sample = 195d tetrad = 195 spore = d
Total reads = 3059 PCR=512
haplotypes I began with n[supporting reads] = 836, 1964
most frequent 7 haplotypes.



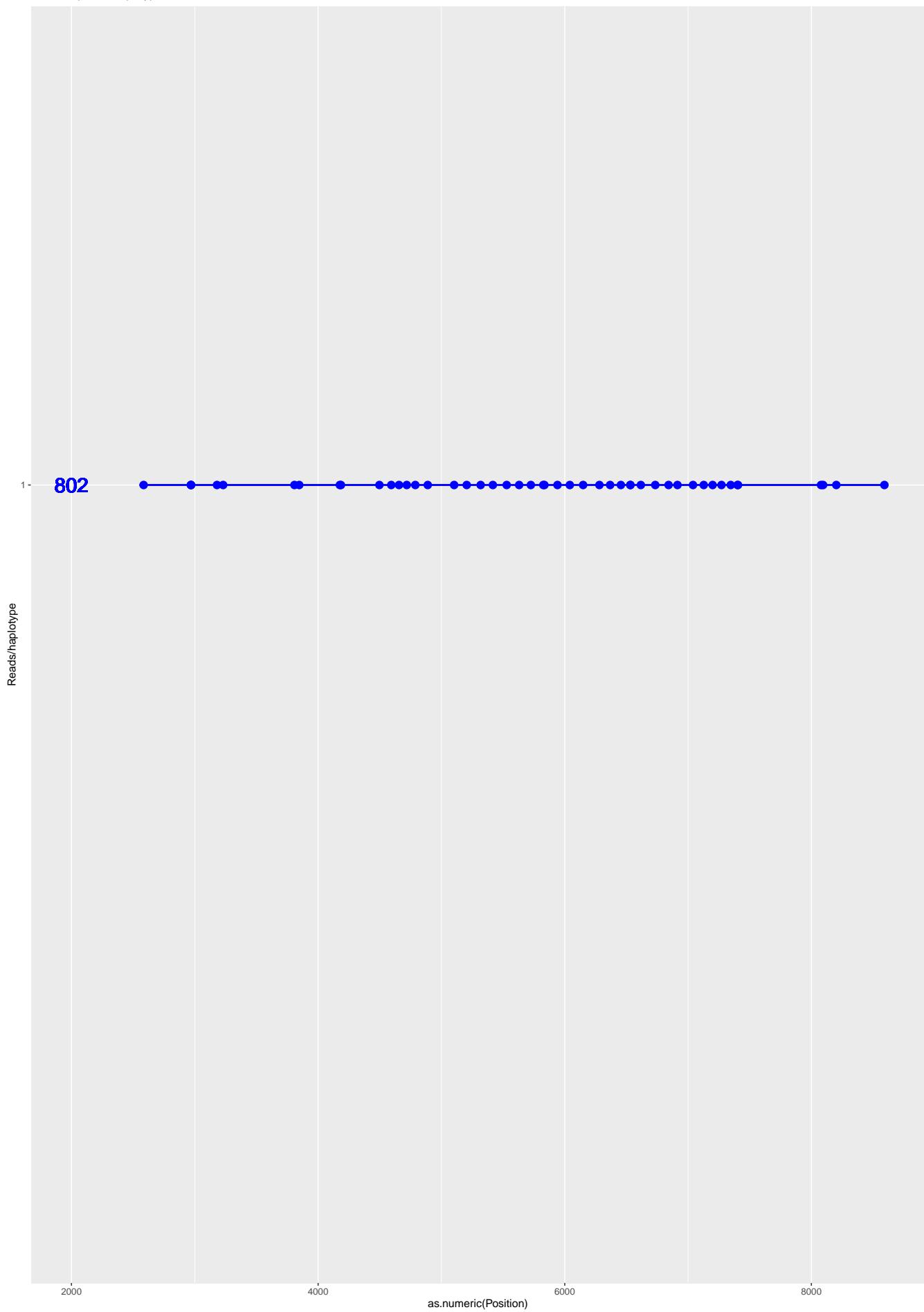
barcode = GAGCTGCGCACTCGAT & ACTATCGCGCACGCAG

Sample = 196a tetrad = 196 spore = a

Total reads = 925 PCR=513

haplotypes I began with n[supporting reads] = 802

most frequent 7 haplotypes.



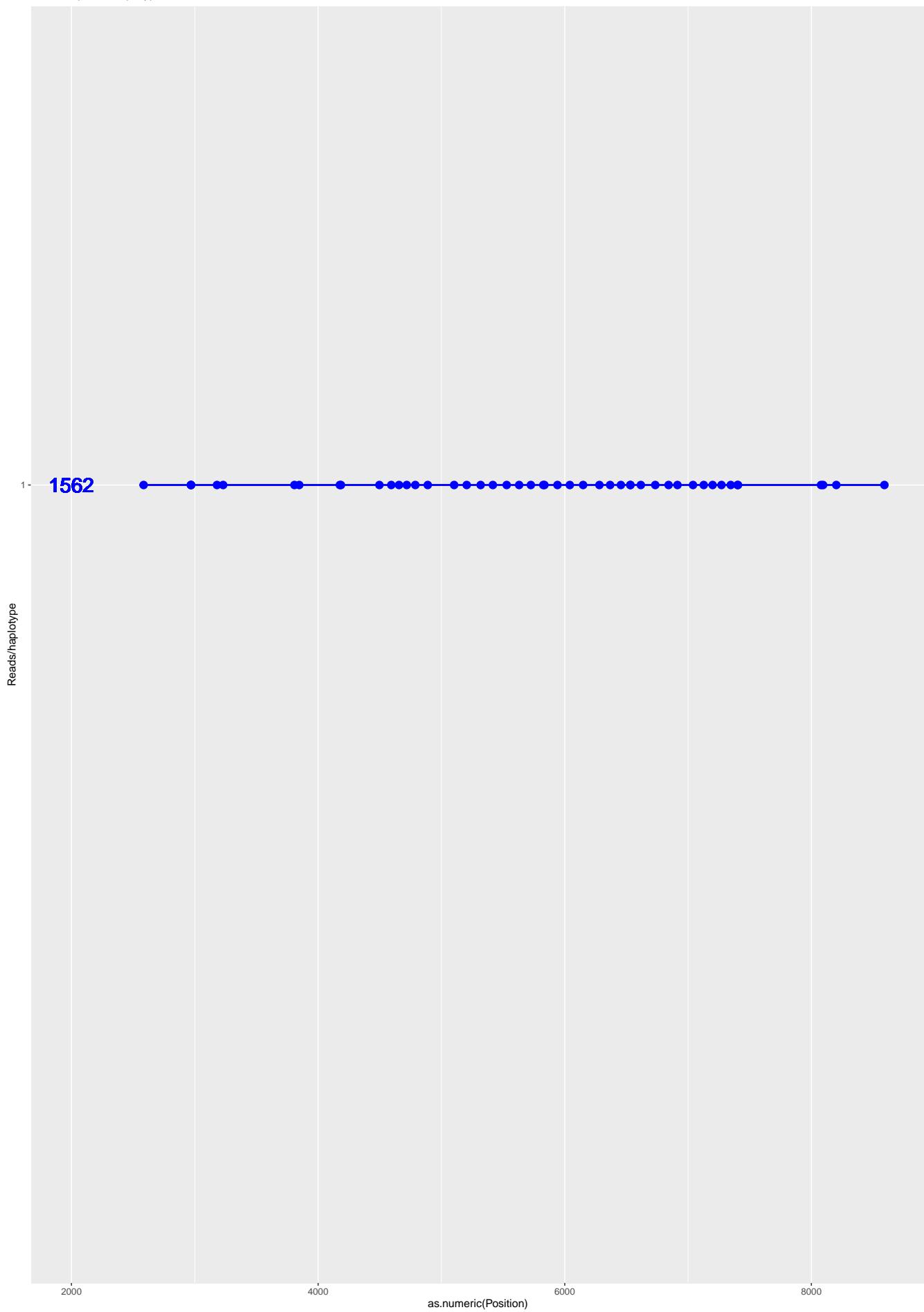
barcode = GCGATGTCGCTATGTG & GCGACGAGTACTCATG

Sample = 196b tetrad = 196 spore = b

Total reads = 1799 PCR=514

haplotypes I began with n[supporting reads] = 1562

most frequent 7 haplotypes.



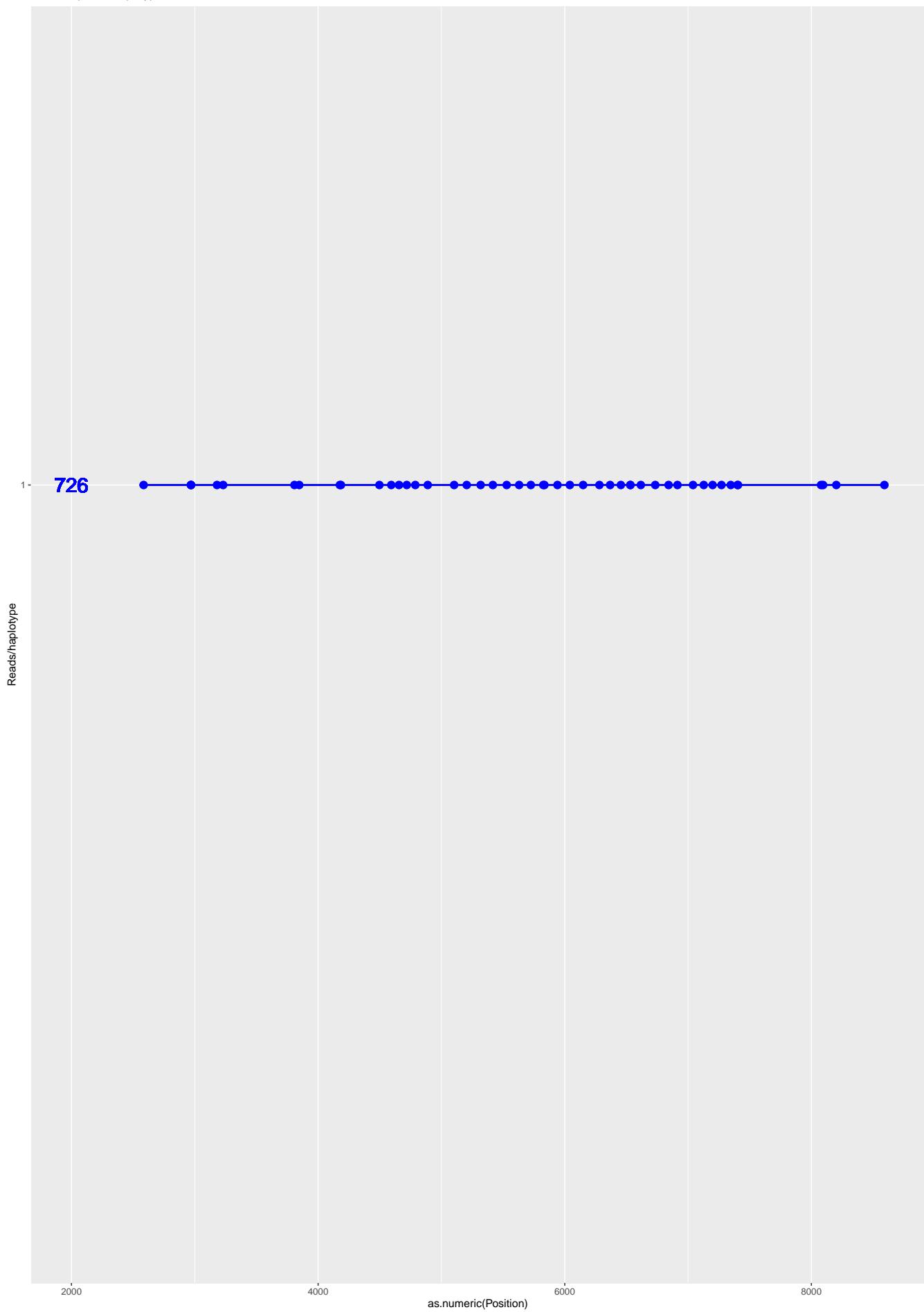
barcode = GCGATGTCGCTATGTG & AGTATCACAGTCGCTG

Sample = 196c tetrad = 196 spore = c

Total reads = 847 PCR=515

haplotypes I began with n[supporting reads] = 726

most frequent 7 haplotypes.



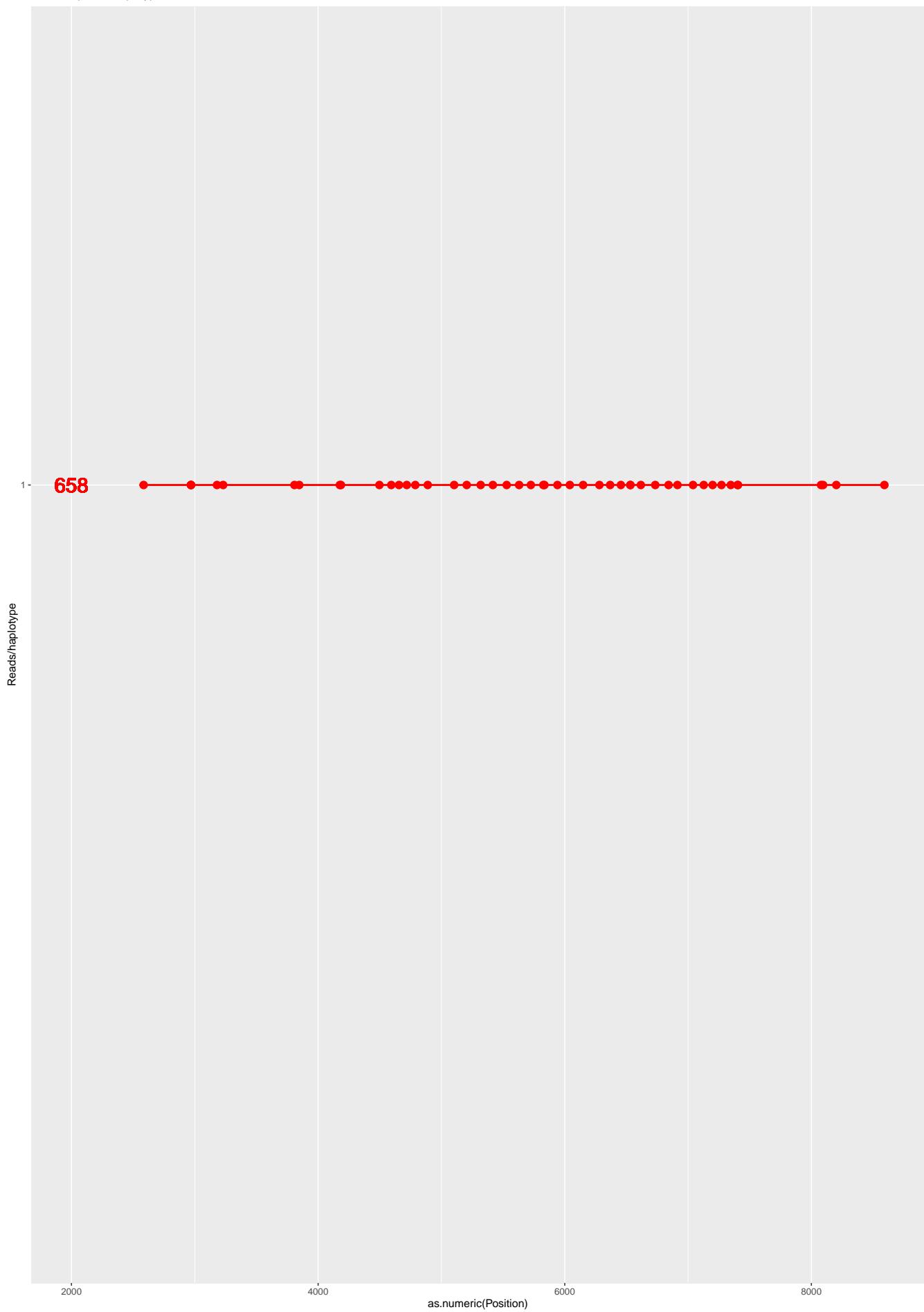
barcode = GCGATGTCGCTATGTG & ATCATATGATGCGACA

Sample = 196d tetrad = 196 spore = d

Total reads = 691 PCR=516

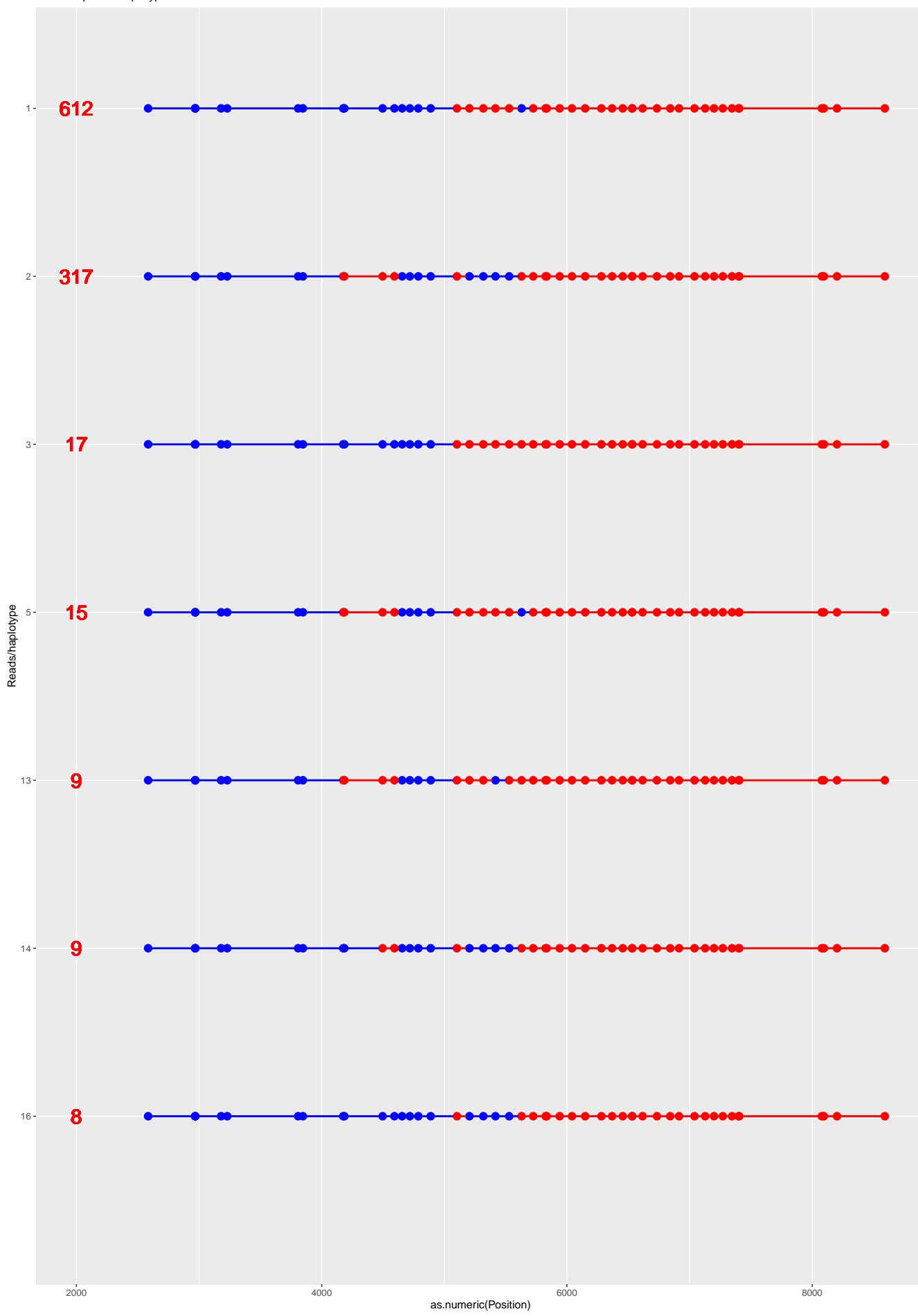
haplotypes I began with n[supporting reads] = 658

most frequent 7 haplotypes.



barcode = GCGATGTCGCTATGTG & AGACGTTAGATCACAGC

Sample = 197a tetrad = 197 spore = a
 Total reads = 1697 PCR=517
 haplotypes I began with [n(supporting reads)] = 8, 9, 15, 17, 317, 612
 most frequent 7 haplotypes.

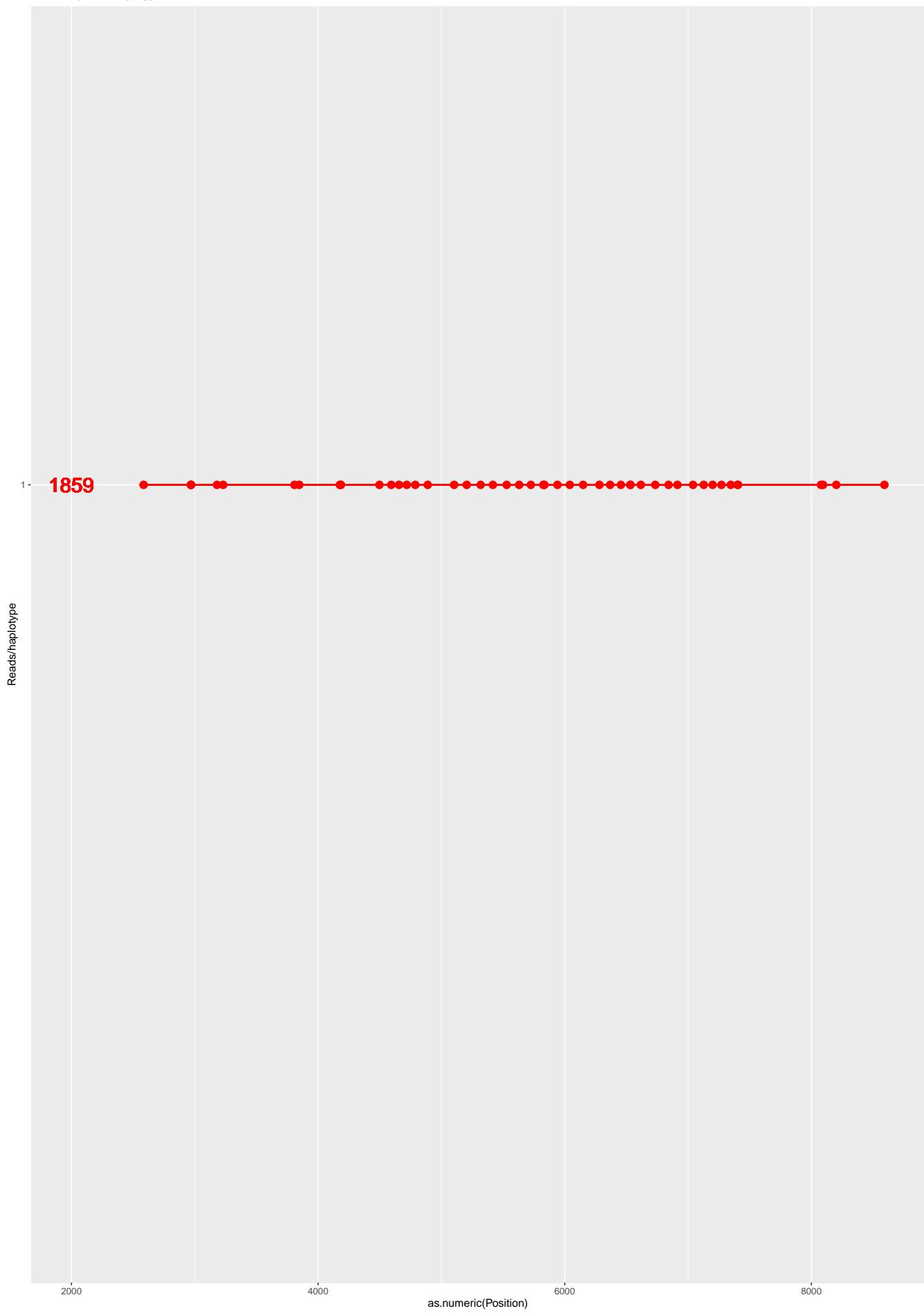


Sample = 197b tetrad = 197 spore = b

Total reads = 1949 PCR=518

haplotypes I began with n[supporting reads] = 1859

most frequent 7 haplotypes.

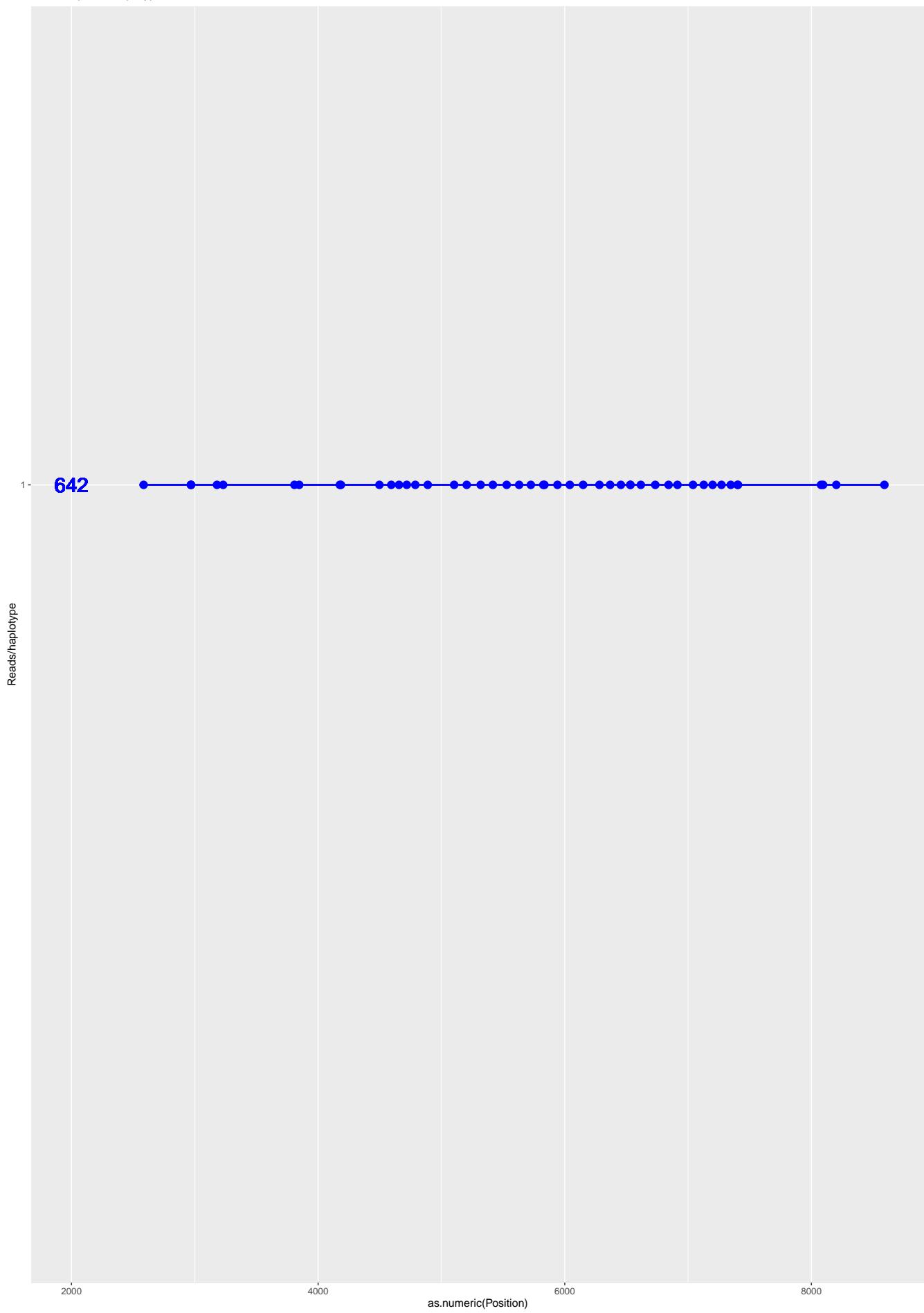


Sample = 197c tetrad = 197 spore = c

Total reads =766 PCR=519

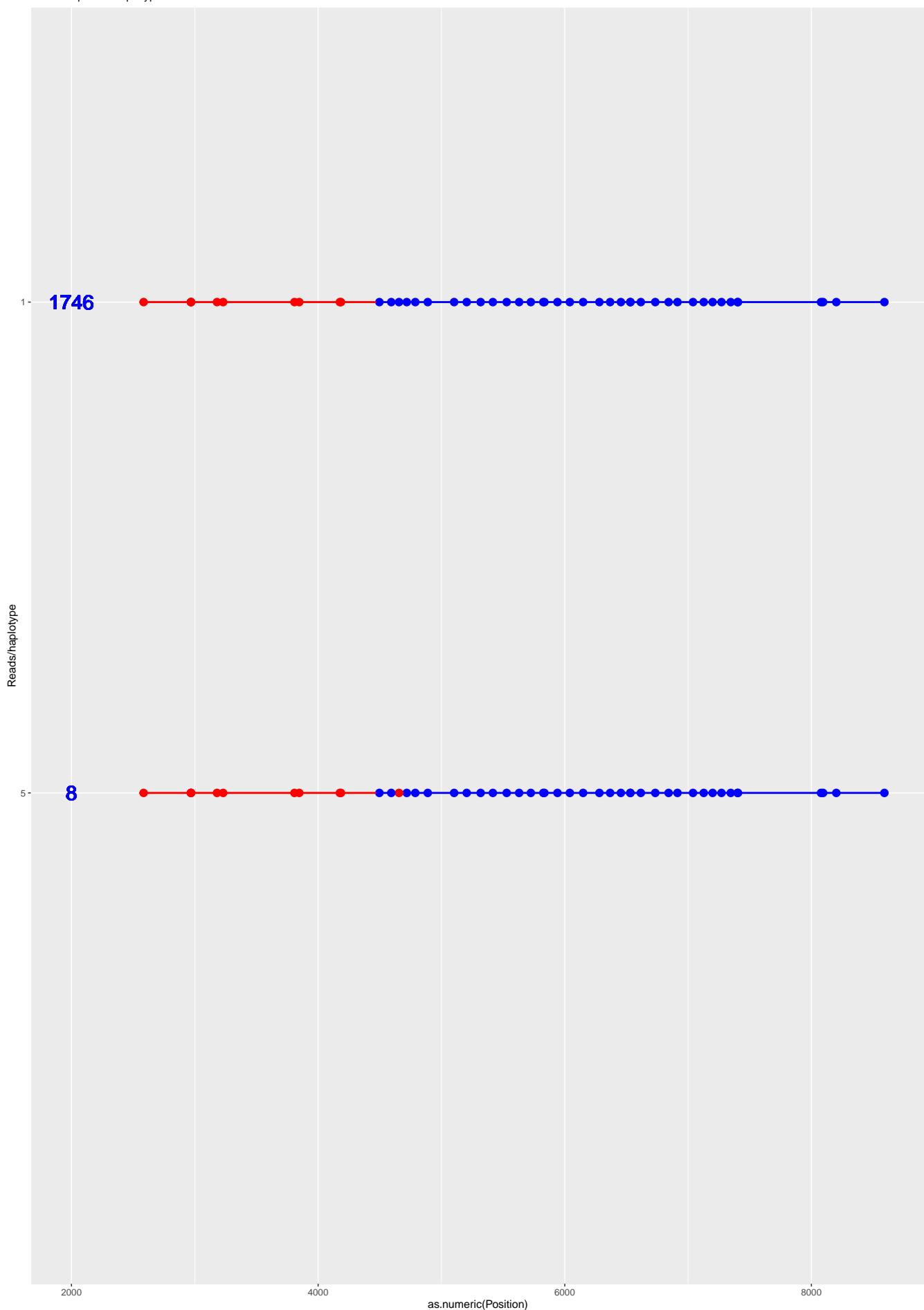
haplotypes I began with n[supporting reads] = 642

most frequent 7 haplotypes.

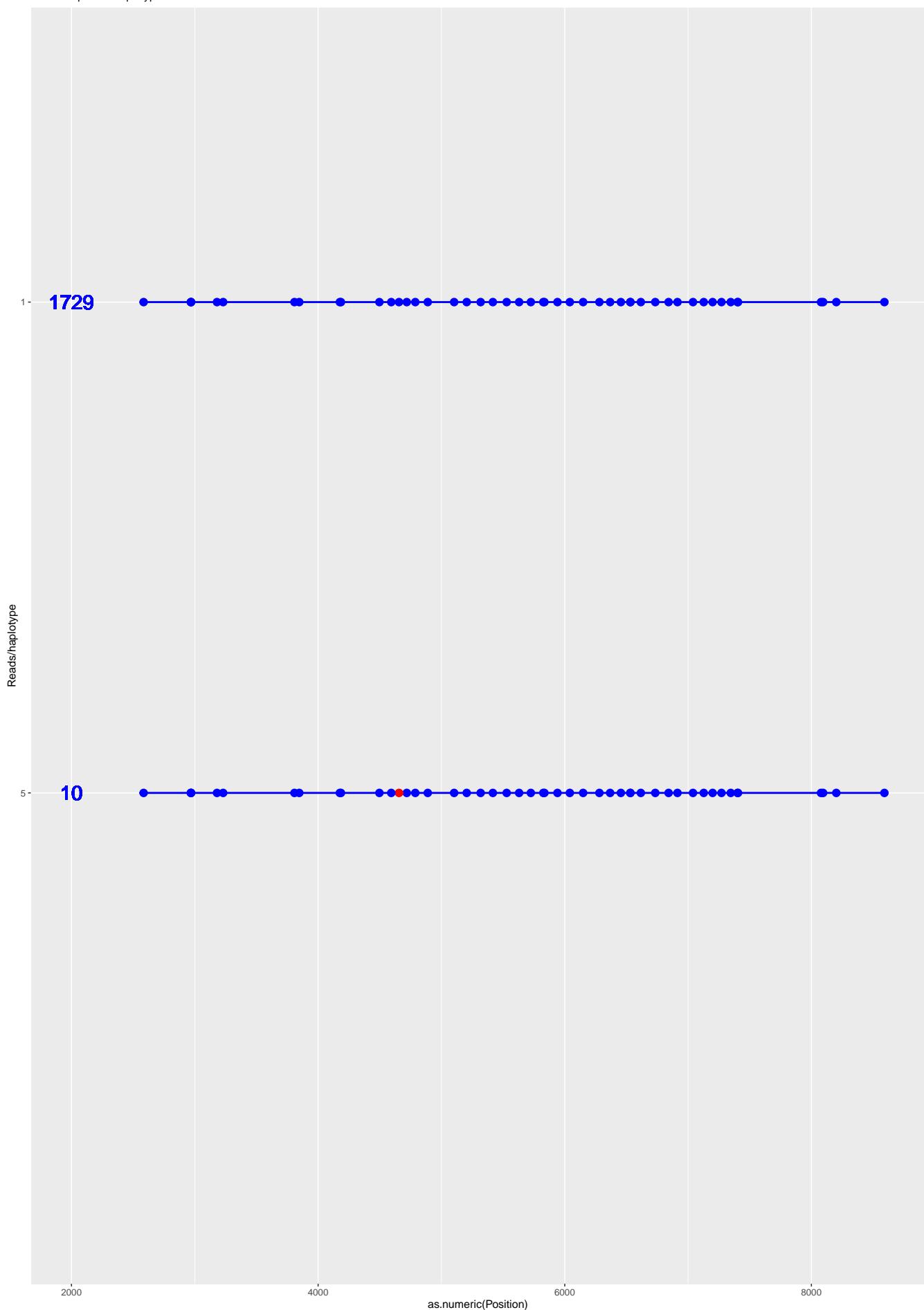


barcode = GCGATGTCGCTATGTG & GCTCAGTGCCTACTG

Sample = 197d tetrad = 197 spore = d
Total reads = 1995 PCR=520
haplotypes I began with n[supporting reads] = 8, 1746
most frequent 7 haplotypes.



Sample = 198a tetrad = 198 spore = a
Total reads = 2010 PCR=521
haplotypes I began with n[supporting reads] = 10, 1729
most frequent 7 haplotypes.



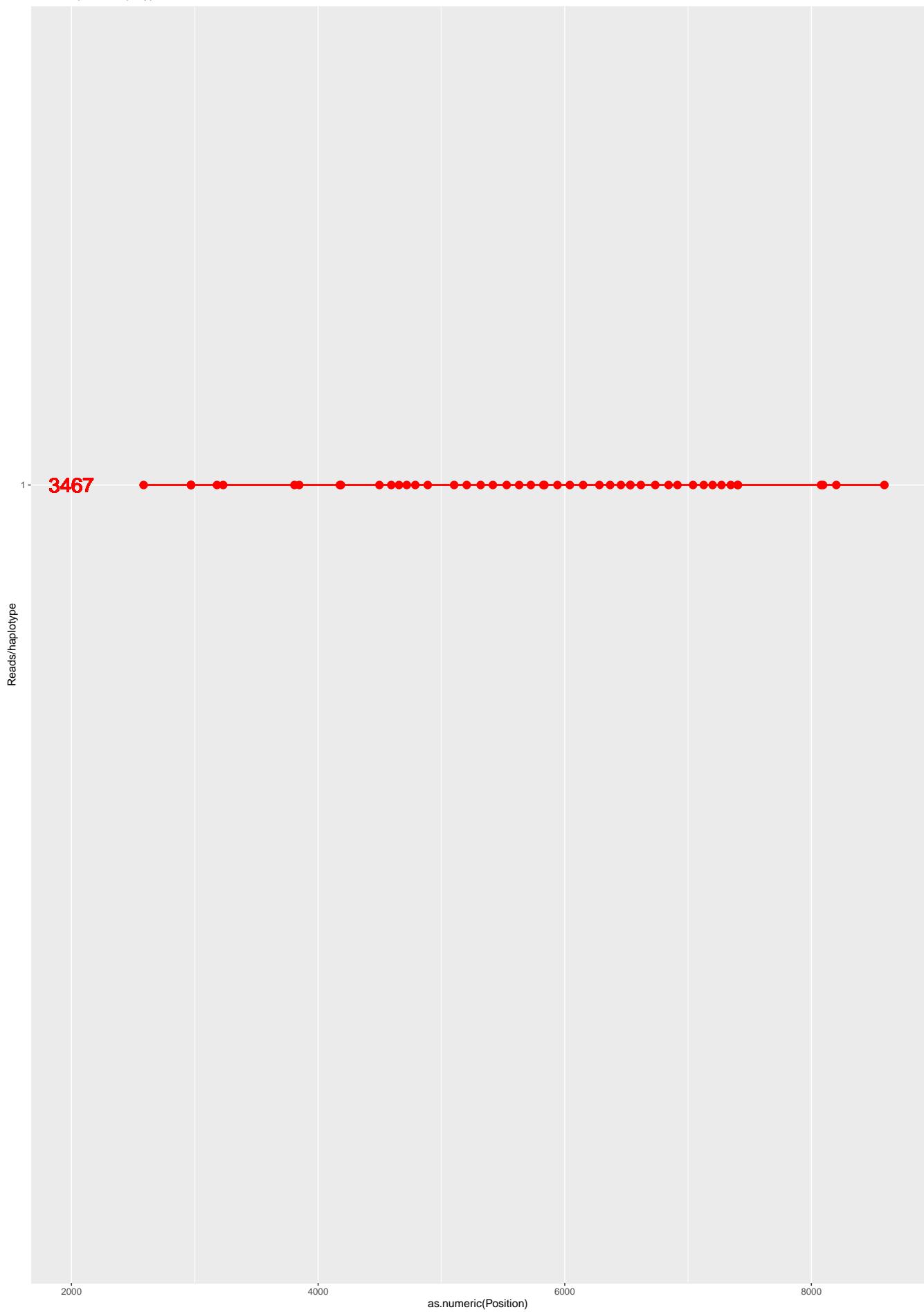
barcode = CGAGAGTCAGCGCATA & GCGACGAGTACTCATG

Sample = 198b tetrad = 198 spore = b

Total reads =3621 PCR=522

haplotypes I began with n[supporting reads] = 3467

most frequent 7 haplotypes.



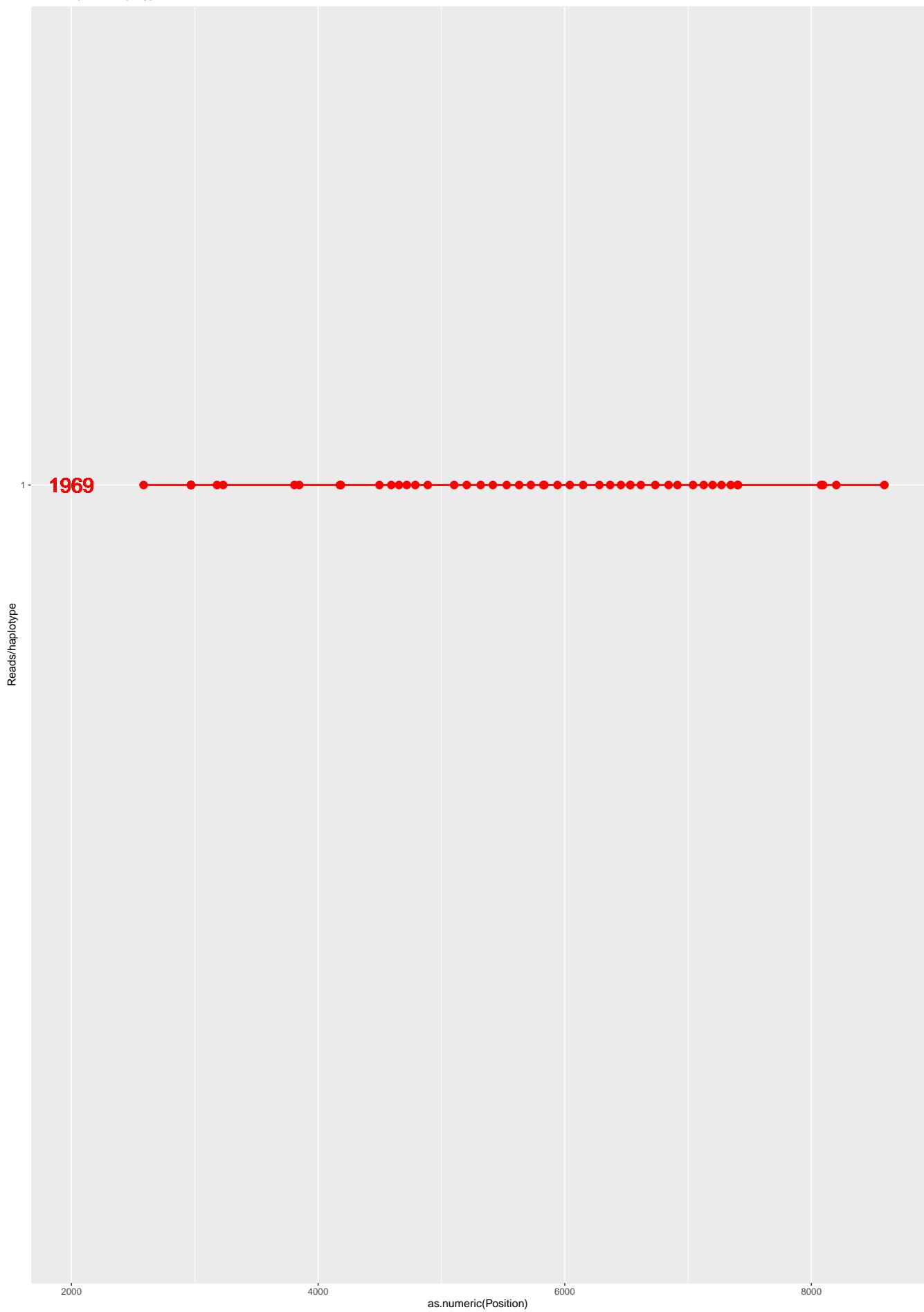
barcode = CGAGAGTCAGCGCATA & AGTATCACAGTCGCTG

Sample = 198c tetrad = 198 spore = c

Total reads = 2042 PCR=523

haplotypes I began with n[supporting reads] = 1969

most frequent 7 haplotypes.



Sample = 198d tetrad = 198 spore = d

Total reads = 4321 PCR=524

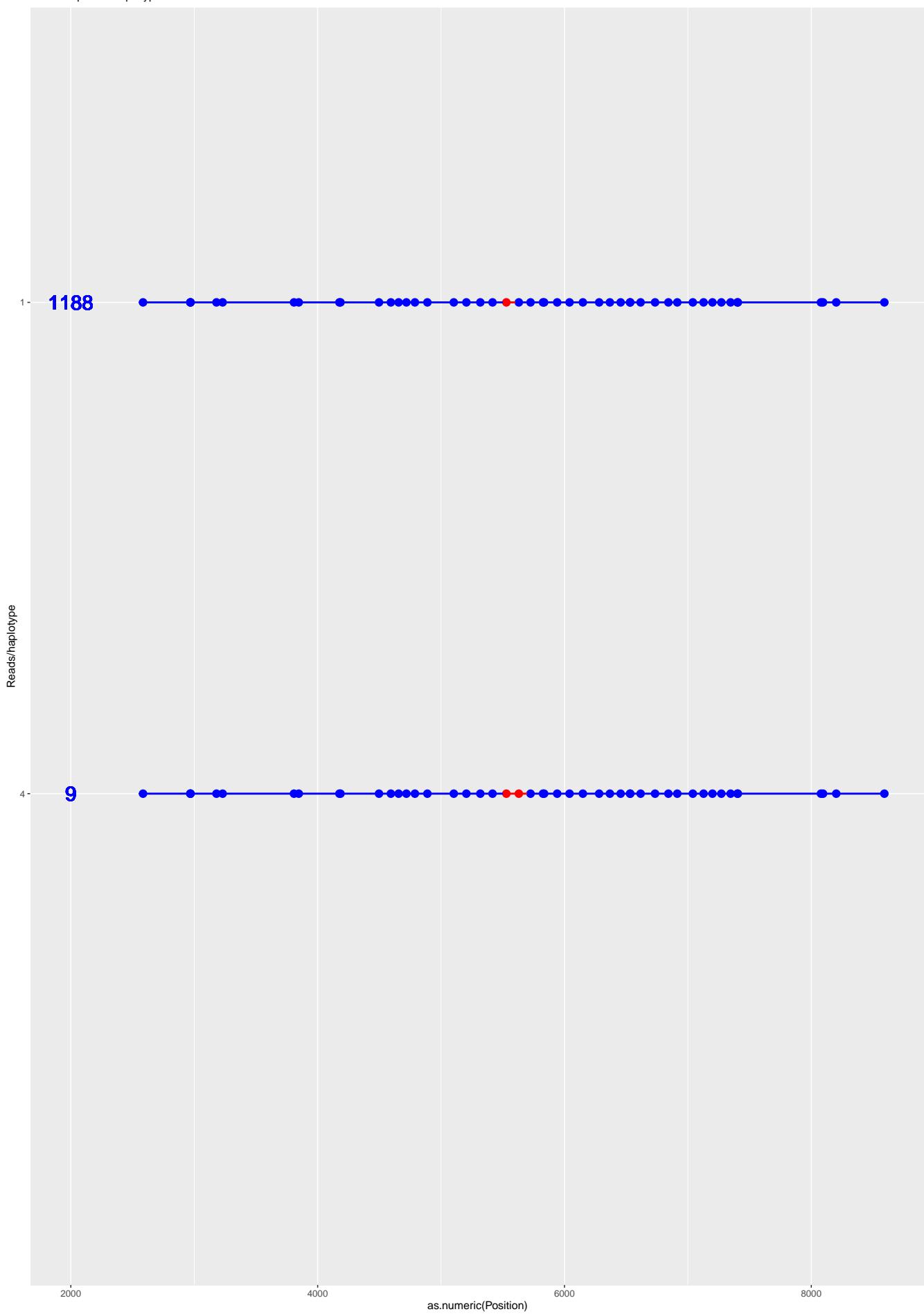
haplotypes I began with n[supporting reads] = 16, 17, 3682

most frequent 7 haplotypes.



barcode = CGAGAGTCAGCGCATA & AGACGTTAGATCACAGC

Sample = 201a tetrad = 201 spore = a
Total reads = 1410 PCR=529
haplotypes I began with n[supporting reads] = 9, 1188
most frequent 7 haplotypes.



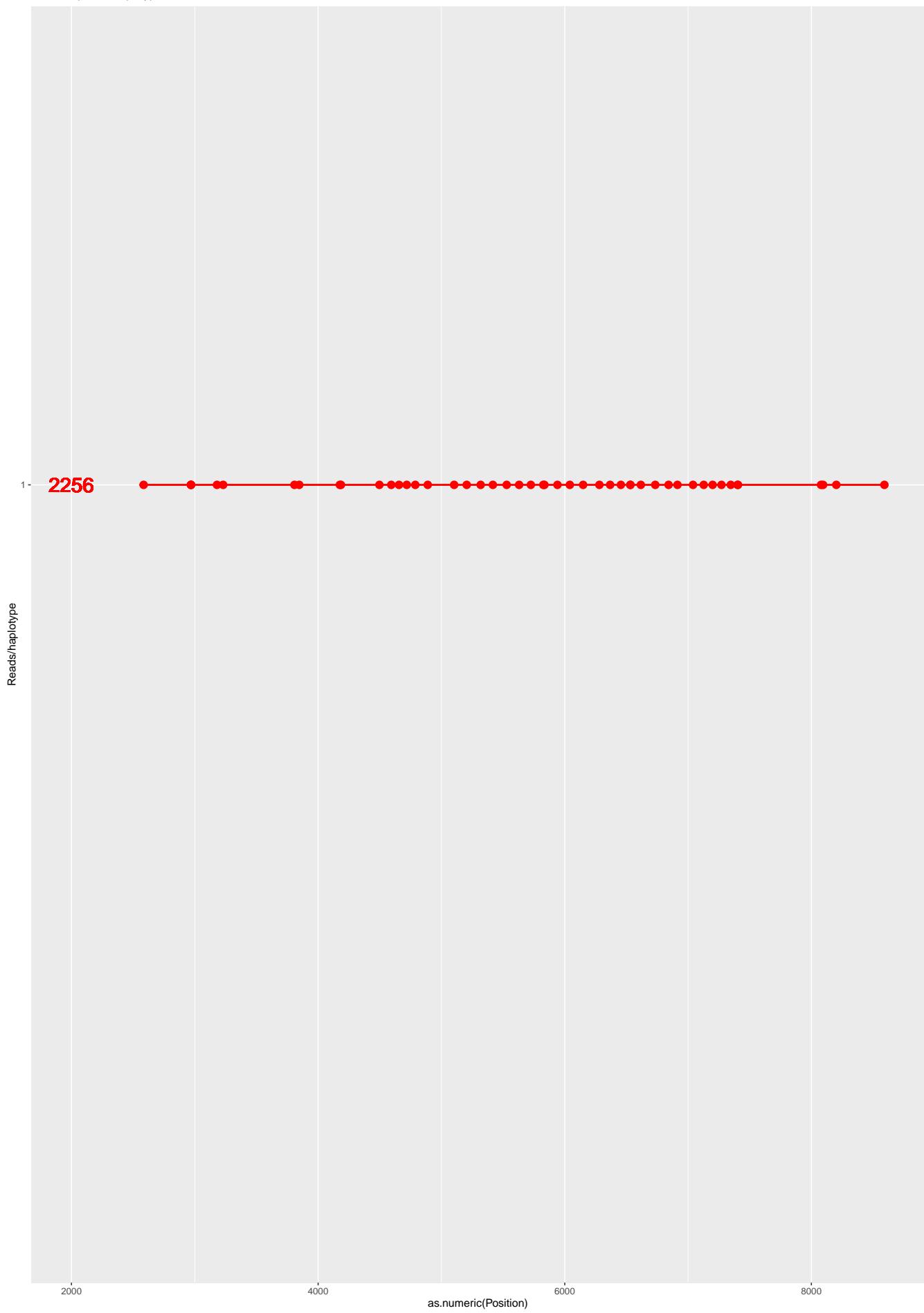
barcode = TCACGATGAGCACGTA & GCGACGAGTACTCATG

Sample = 201b tetrad = 201 spore = b

Total reads = 2365 PCR=530

haplotypes I began with n[supporting reads] = 2256

most frequent 7 haplotypes.



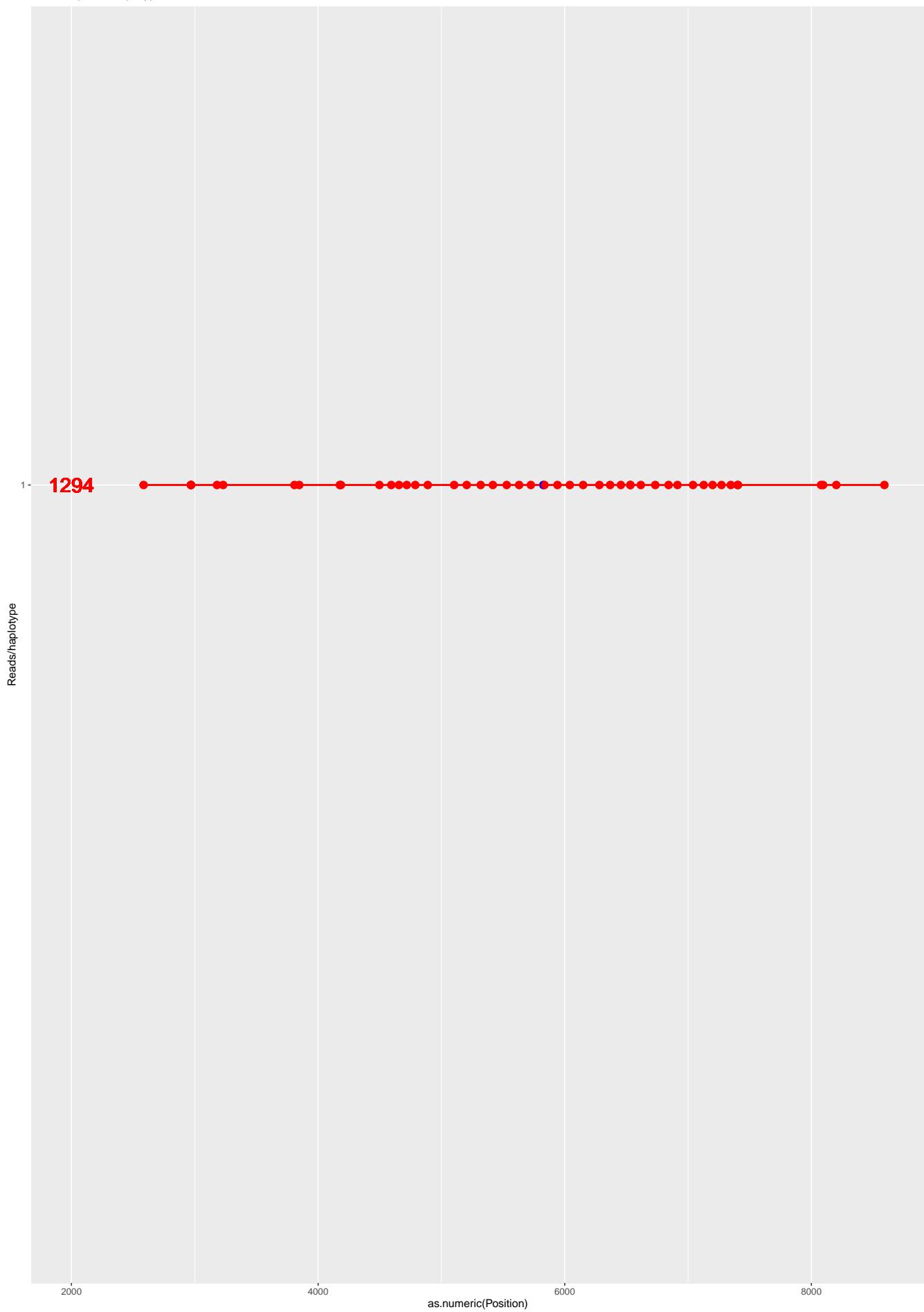
barcode = TCACGATGAGCACGTA & AGTATCACAGTCGCTG

Sample = 201c tetrad = 201 spore = c

Total reads = 1361 PCR=531

haplotypes I began with n[supporting reads] = 1294

most frequent 7 haplotypes.



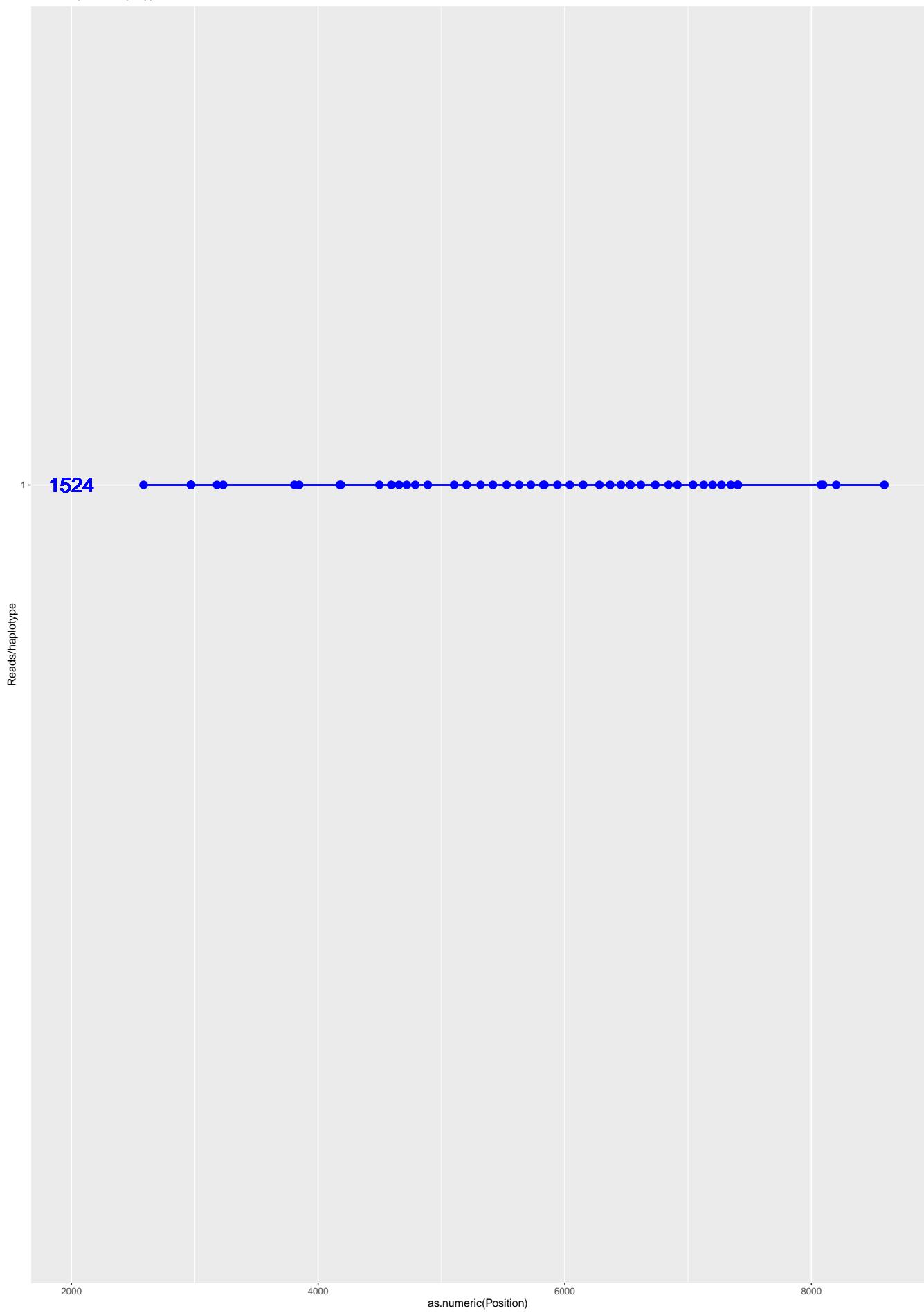
barcode = TCACGATGAGCACGTA & ATCATATGATGCGACA

Sample = 201d tetrad = 201 spore = d

Total reads = 1800 PCR=532

haplotypes I began with n[supporting reads] = 1524

most frequent 7 haplotypes.

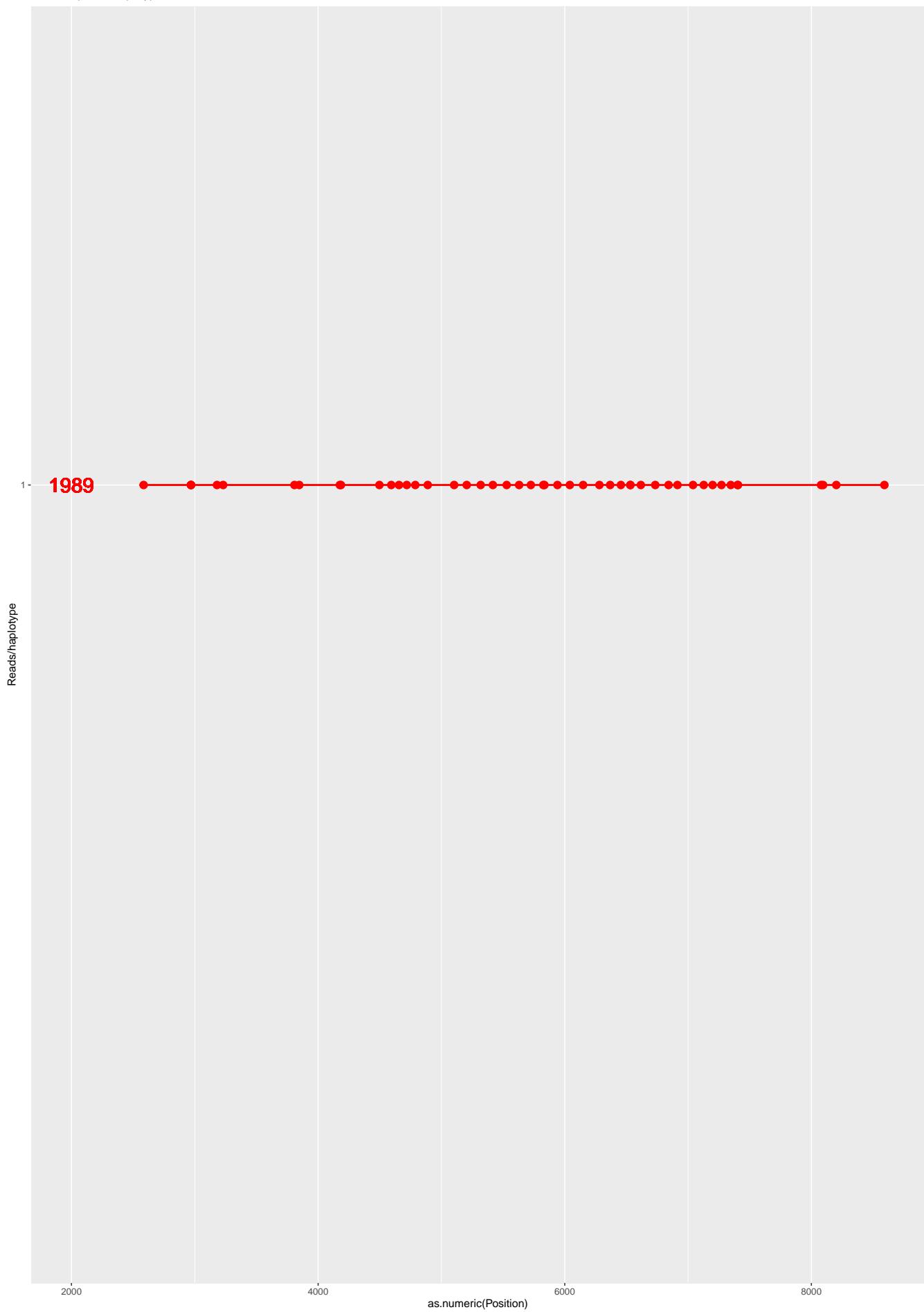


Sample = 204a tetrad = 204 spore = a

Total reads = 2076 PCR=533

haplotypes I began with n[supporting reads] = 1989

most frequent 7 haplotypes.



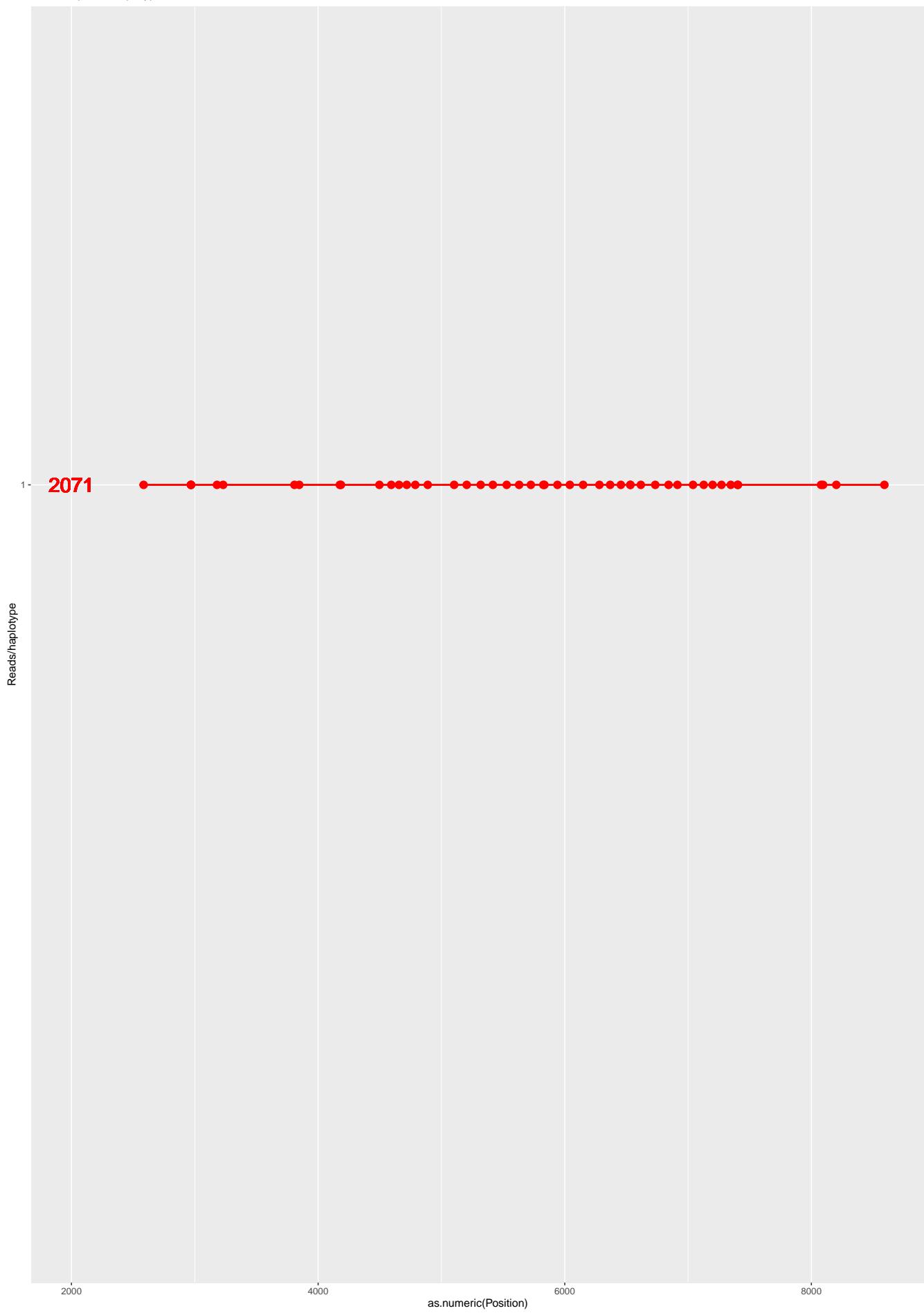
barcode = TCACGATGAGCACGTA & CGTGTCACTGCTACTCA

Sample = 204b tetrad = 204 spore = b

Total reads = 2149 PCR=534

haplotypes I began with n[supporting reads] = 2071

most frequent 7 haplotypes.



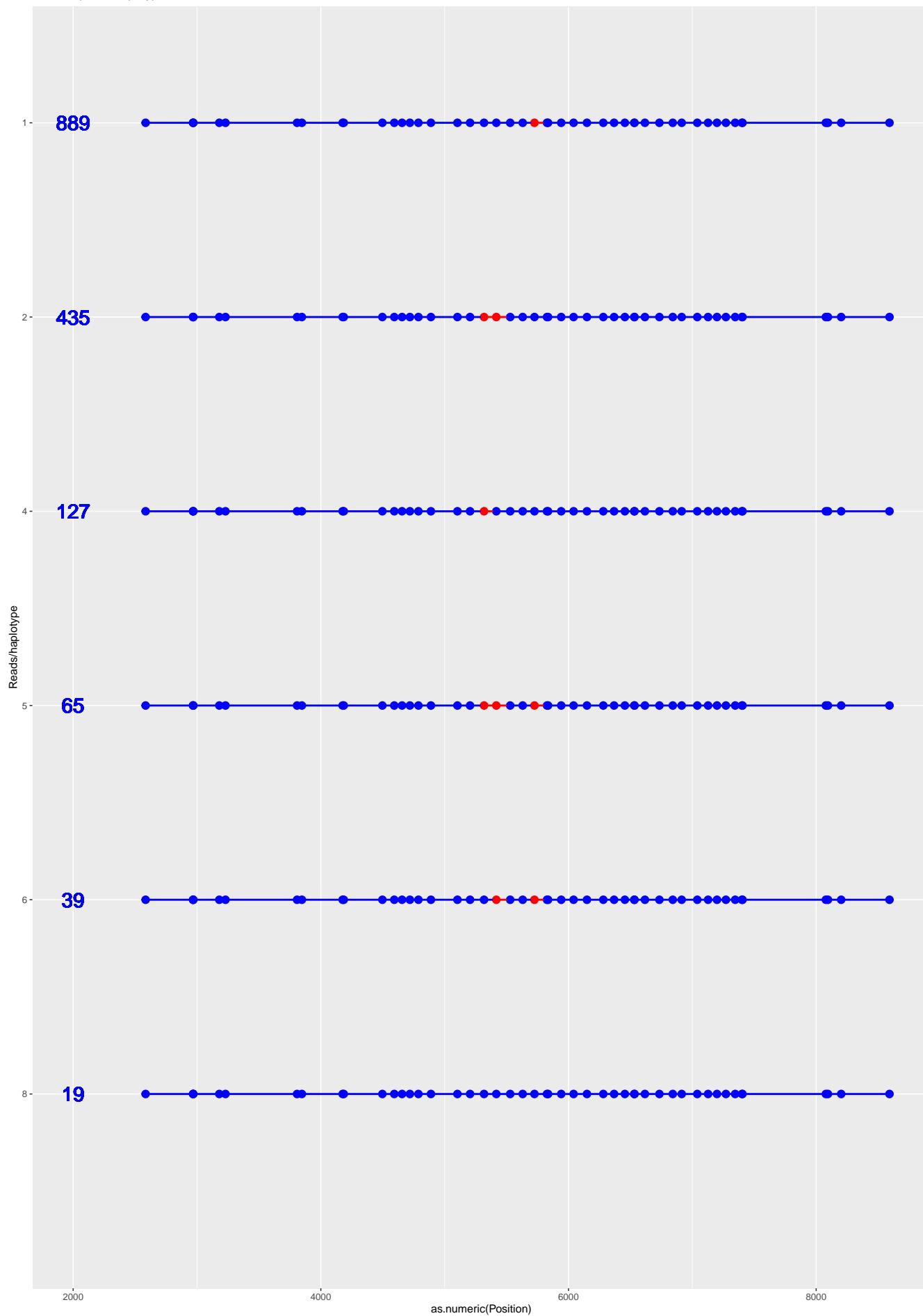
barcode = TCACGATGAGCACGTA & TGTGAGACTGCATGTC

Sample = 204c tetrad = 204 spore = c

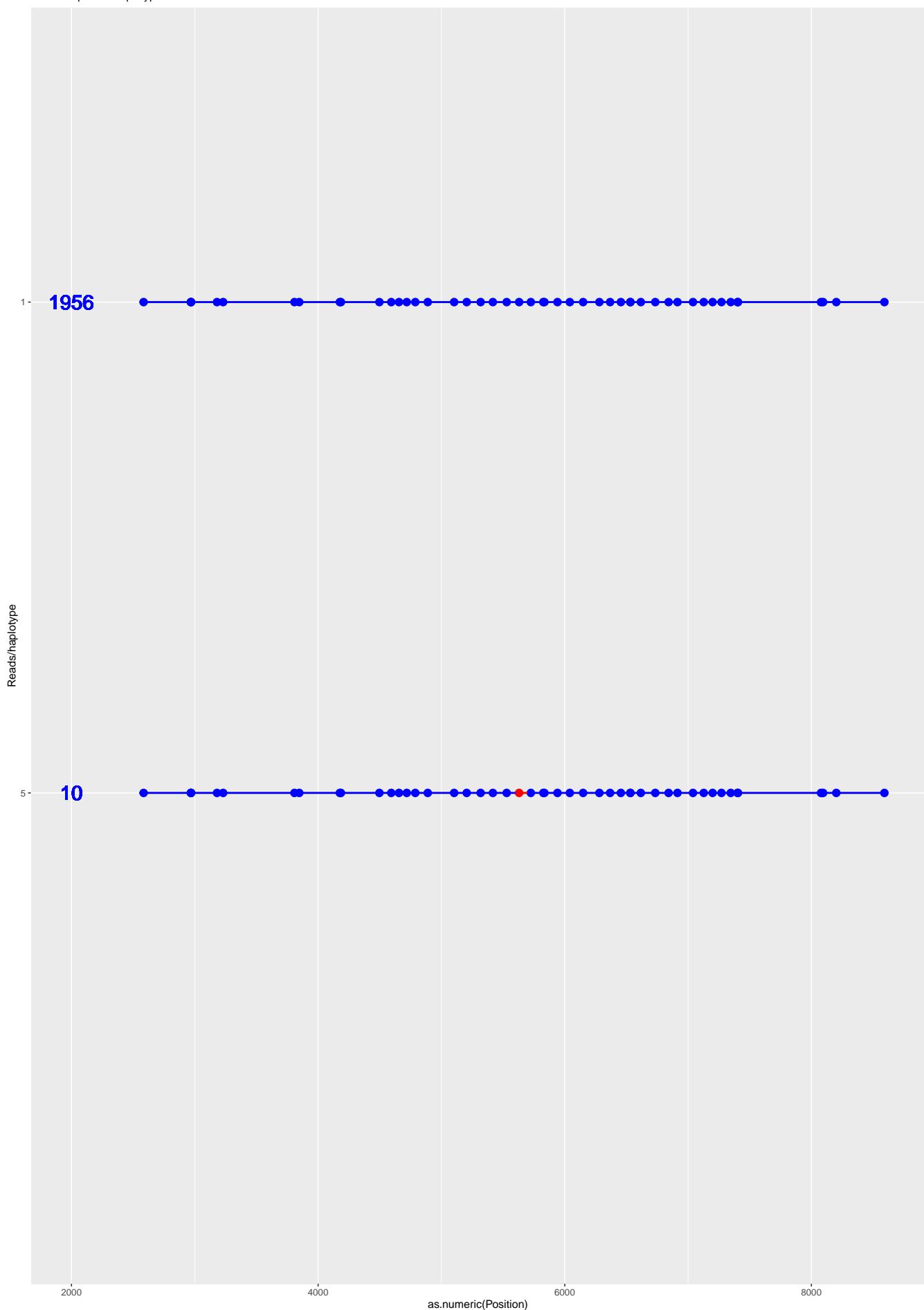
Total reads = 2038 PCR=535

haplotypes I began with n[supporting reads] = 19, 39, 65, 127, 435, 889

most frequent 7 haplotypes.



Sample = 204d tetrad = 204 spore = d
Total reads = 2274 PCR=536
haplotypes I began with n[supporting reads] = 10, 1956
most frequent 7 haplotypes.

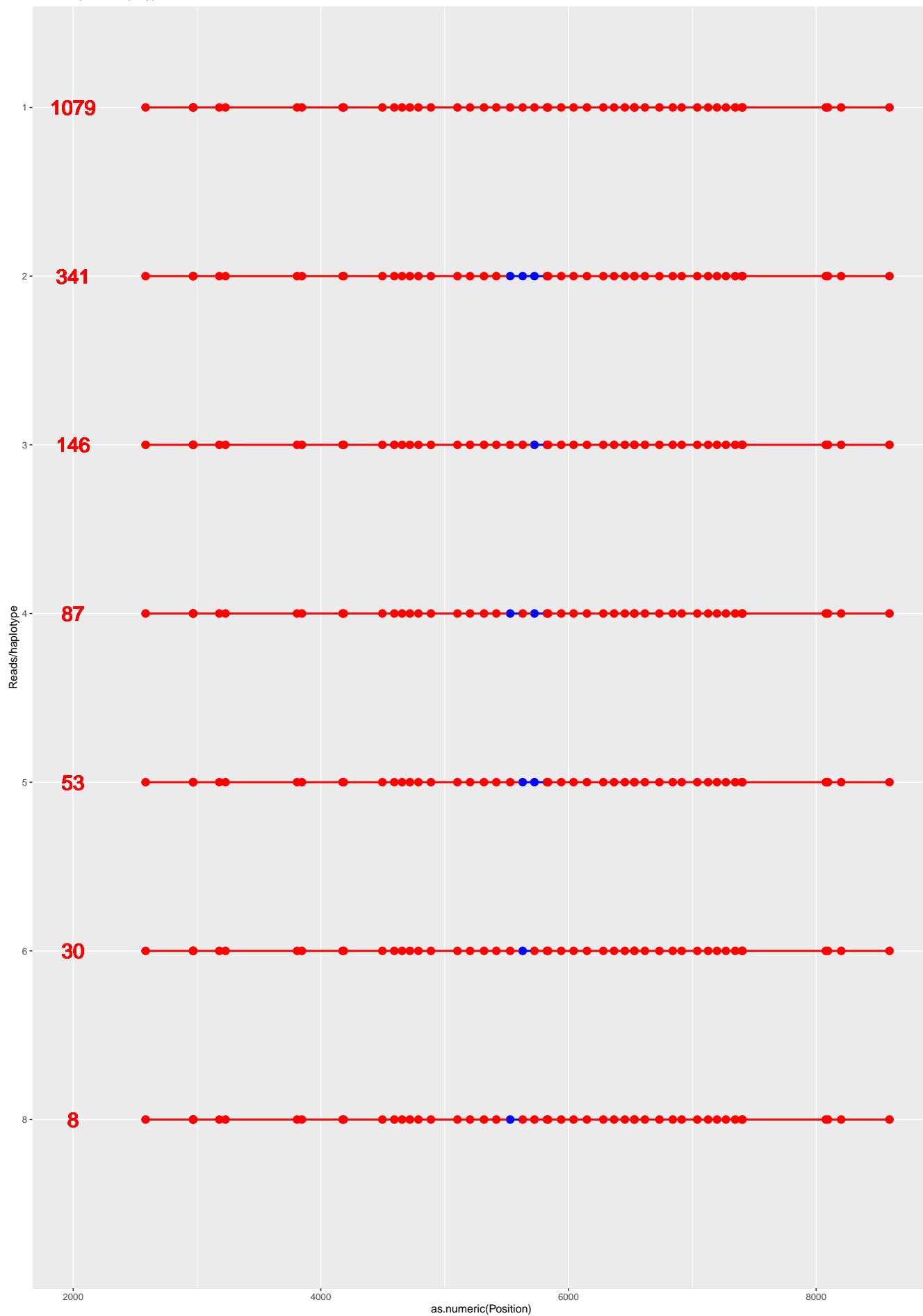


Sample = 205a tetrad = 205 spore = a

Total reads = 1838 PCR=537

haplotypes I began with n[supporting reads] = 8, 30, 53, 87, 146, 341, 1079

most frequent 7 haplotypes.

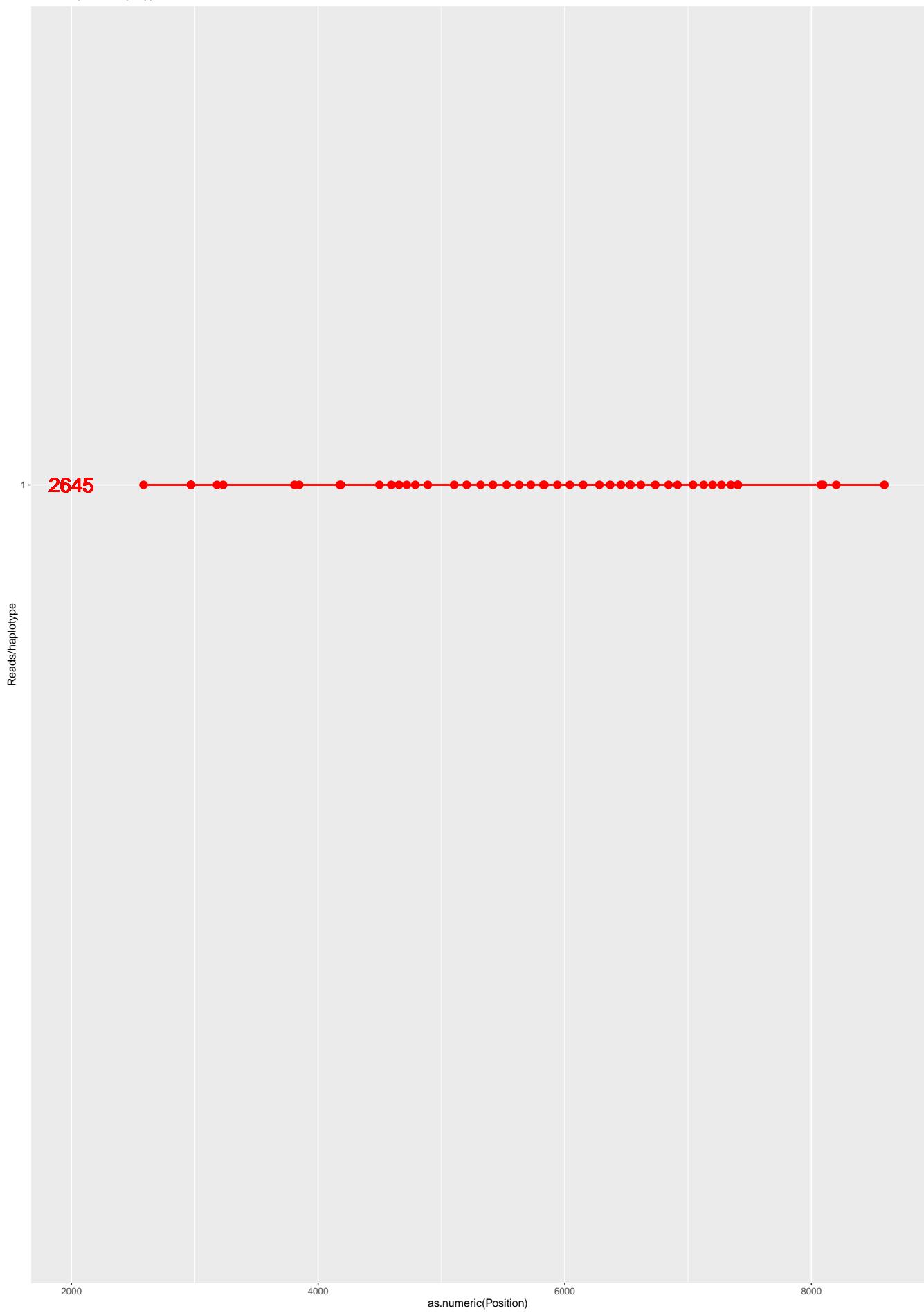


Sample = 205b tetrad = 205 spore = b

Total reads =2760 PCR=538

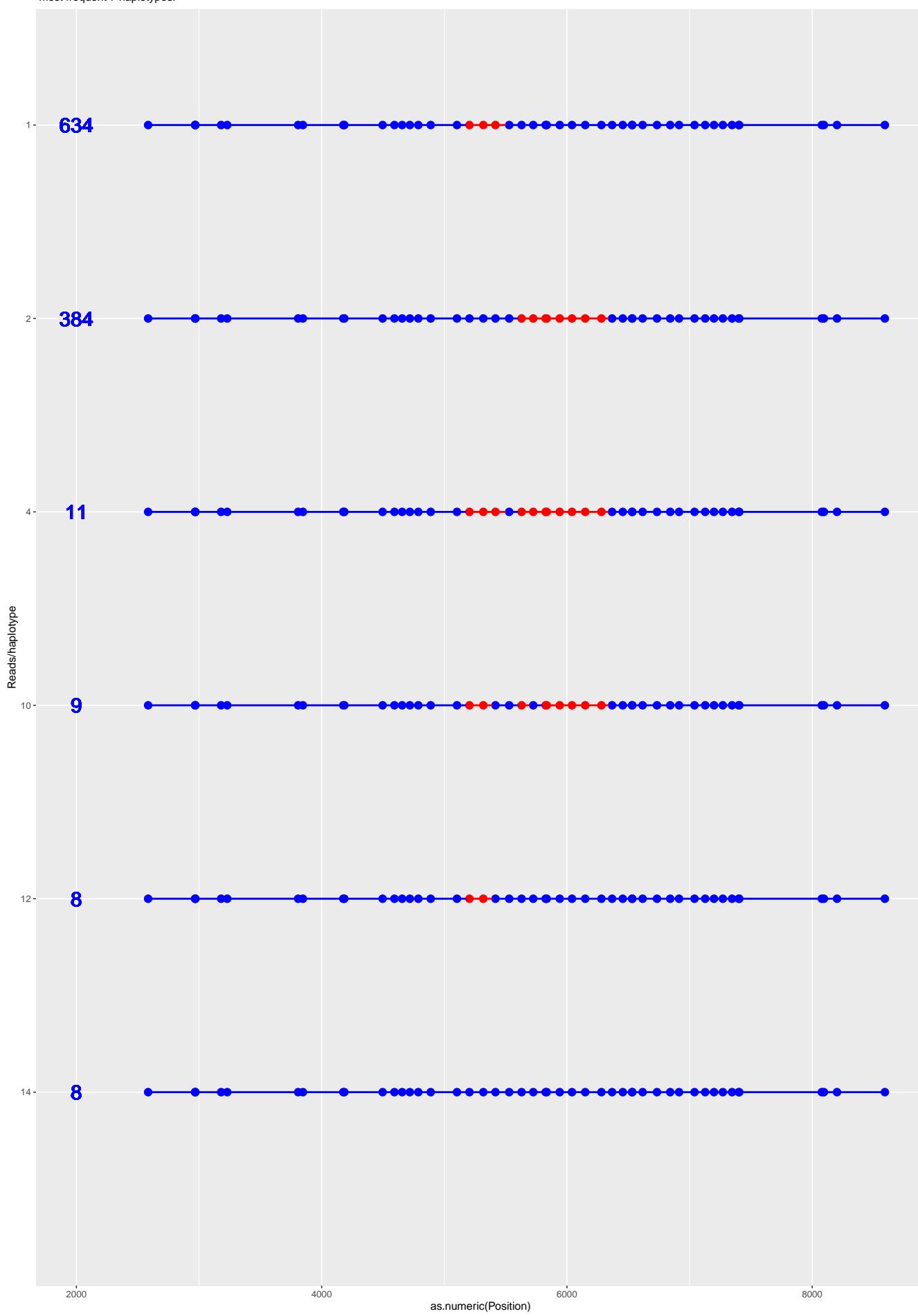
haplotypes I began with n[supporting reads] = 2645

most frequent 7 haplotypes.



barcode = GACTGAGATCATGATC & AGTATCACAGTCGCTG

Sample = 205c tetrad = 205 spore = c
Total reads = 1933 PCR=539
haplotypes I began with [n|supporting reads] = 8, 9, 11, 384, 634
most frequent 7 haplotypes.



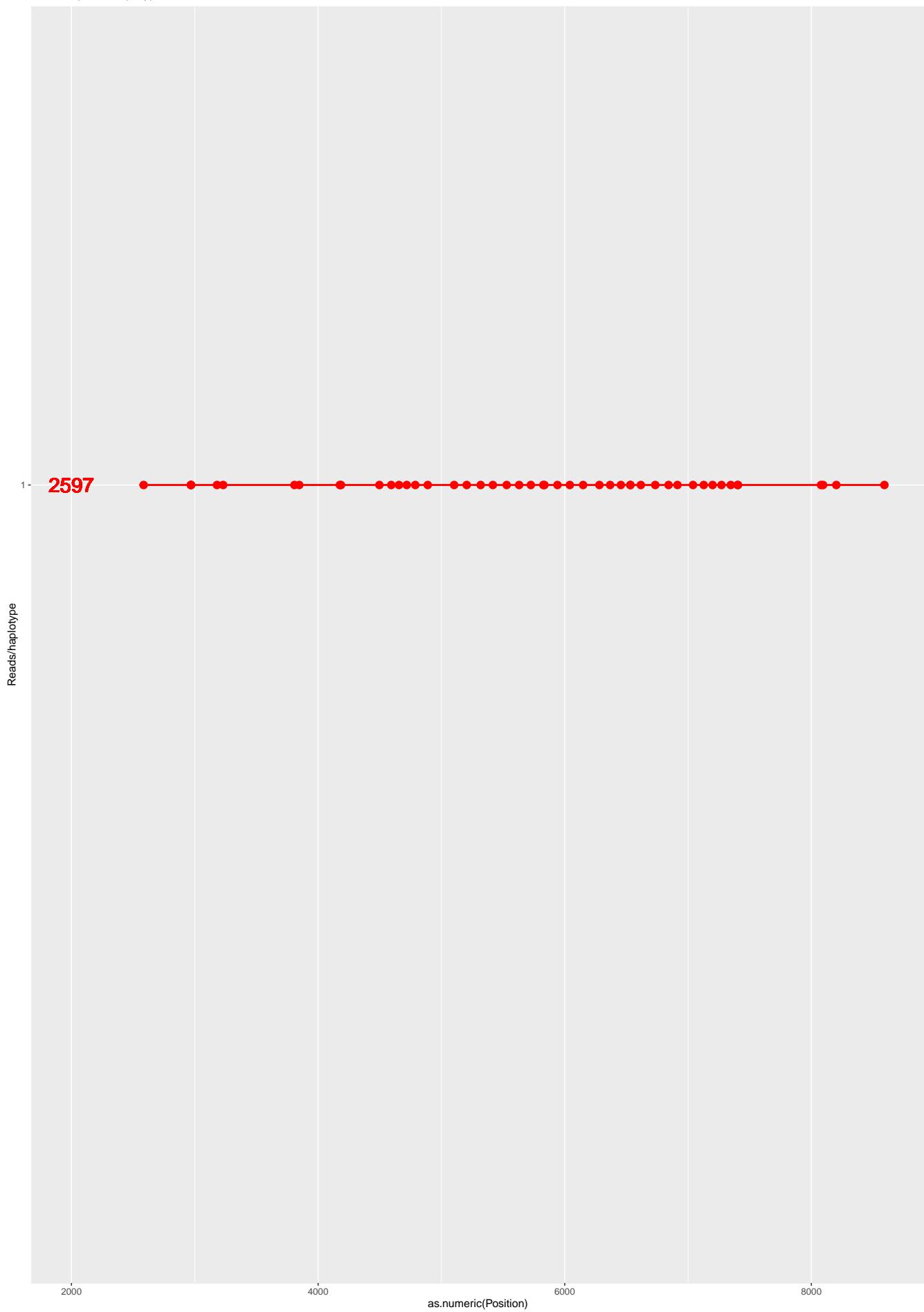
barcode = GACTGAGATCATGATC & ATCATATGATGCGACA

Sample = 205d tetrad = 205 spore = d

Total reads = 2696 PCR=540

haplotypes I began with n[supporting reads] = 2597

most frequent 7 haplotypes.



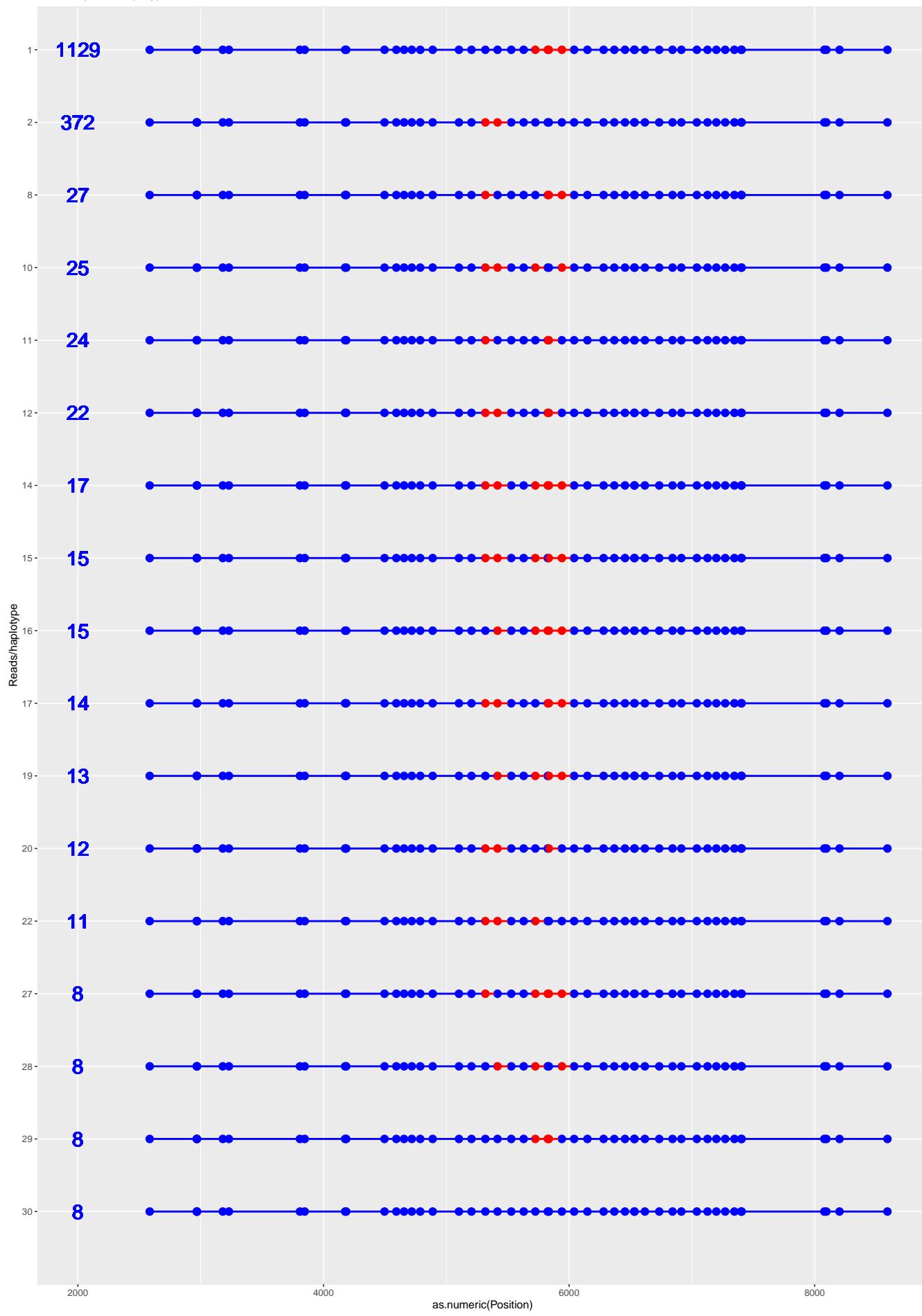
barcode = GACTGAGATCATGATC & AGACGTAGATCACAGC

Sample = 206a tetrad = 206 spore = a

Total reads =2426 PCR=541

haplotypes I began with [n(supporting reads)] = 8, 11, 12, 13, 14, 15, 17, 22, 24, 25, 27, 372, 1129

most frequent 7 haplotypes.



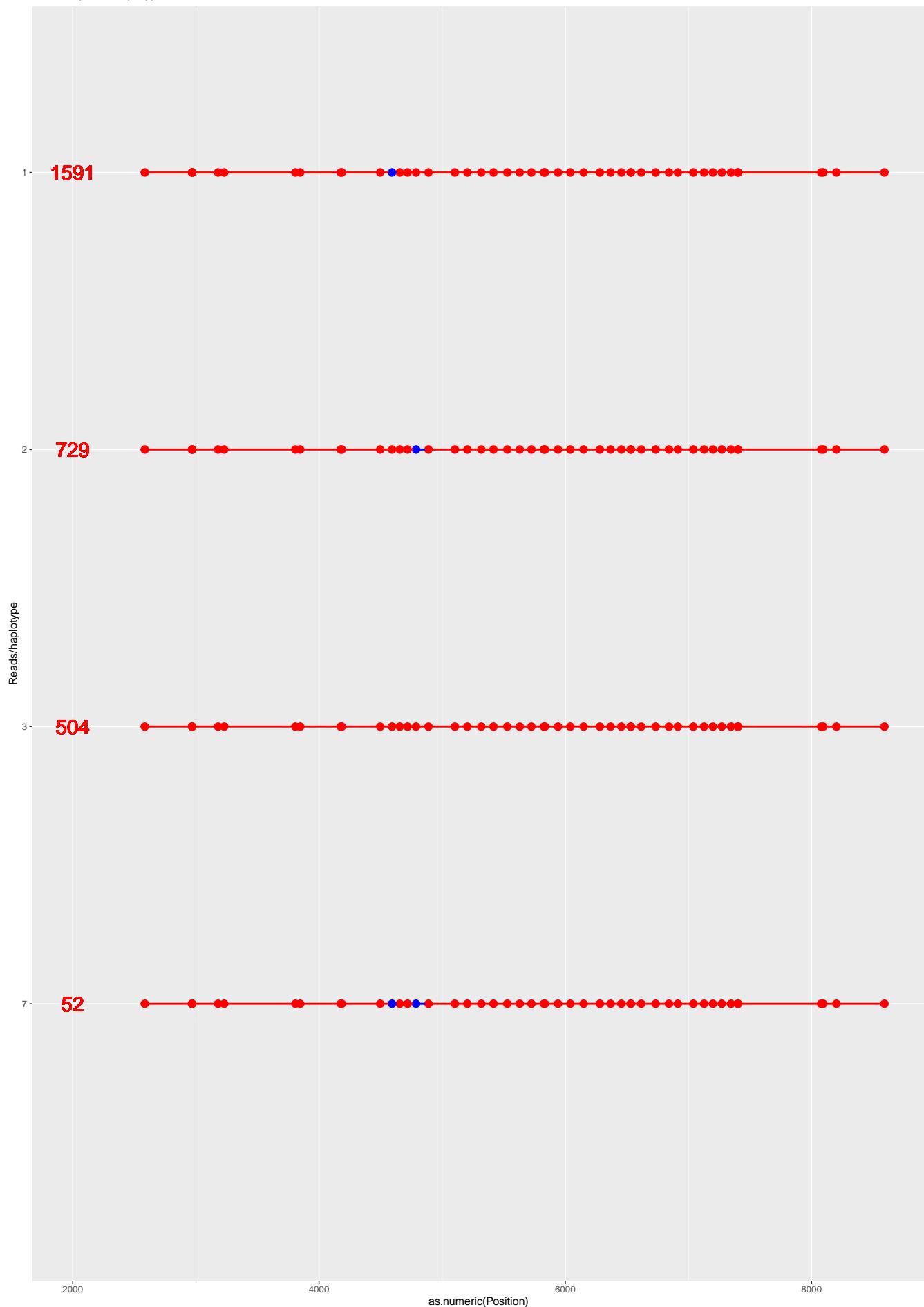
barcode = GACTGAGATCATGATC & CGTGTCACTGCTACTCA

Sample = 206b tetrad = 206 spore = b

Total reads = 3313 PCR=542

haplotypes I began with n[supporting reads] = 52, 504, 729, 1591

most frequent 7 haplotypes.

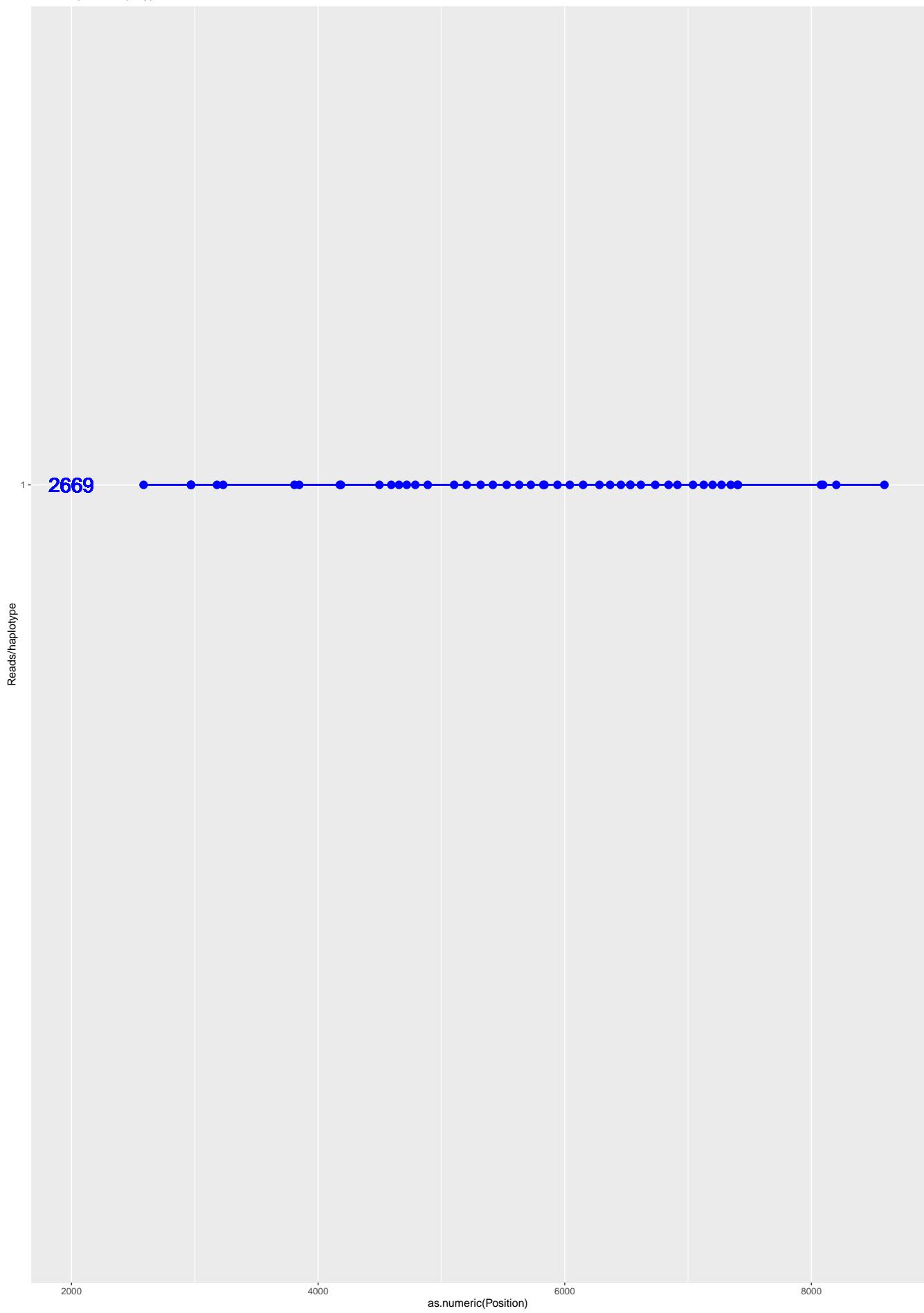


Sample = 206c tetrad = 206 spore = c

Total reads = 3102 PCR=543

haplotypes I began with n[supporting reads] = 2669

most frequent 7 haplotypes.



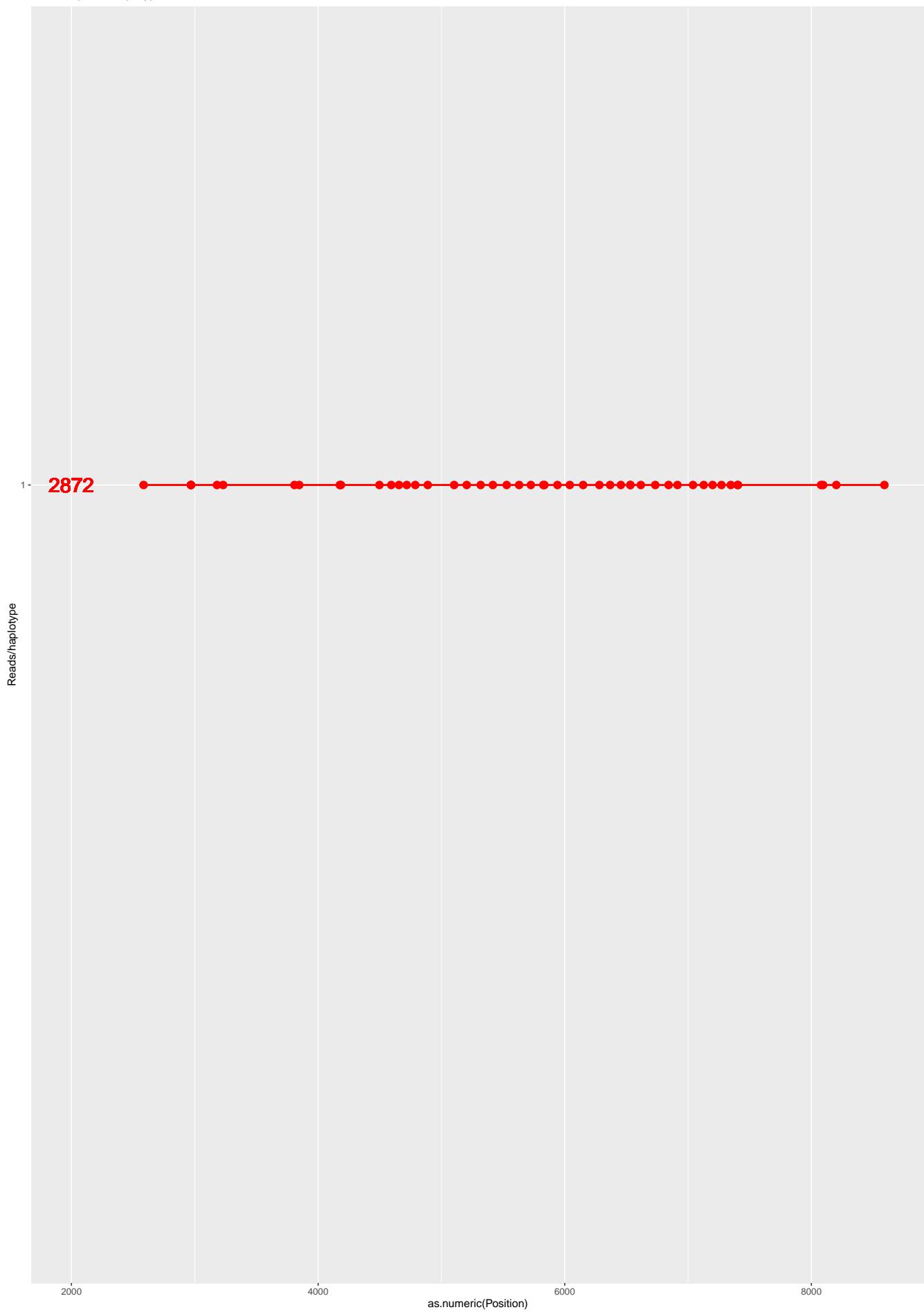
barcode = GACTGAGATCATGATC & GCTCAGTGCCTACTG

Sample = 206d tetrad = 206 spore = d

Total reads = 3002 PCR=544

haplotypes I began with n[supporting reads] = 2872

most frequent 7 haplotypes.



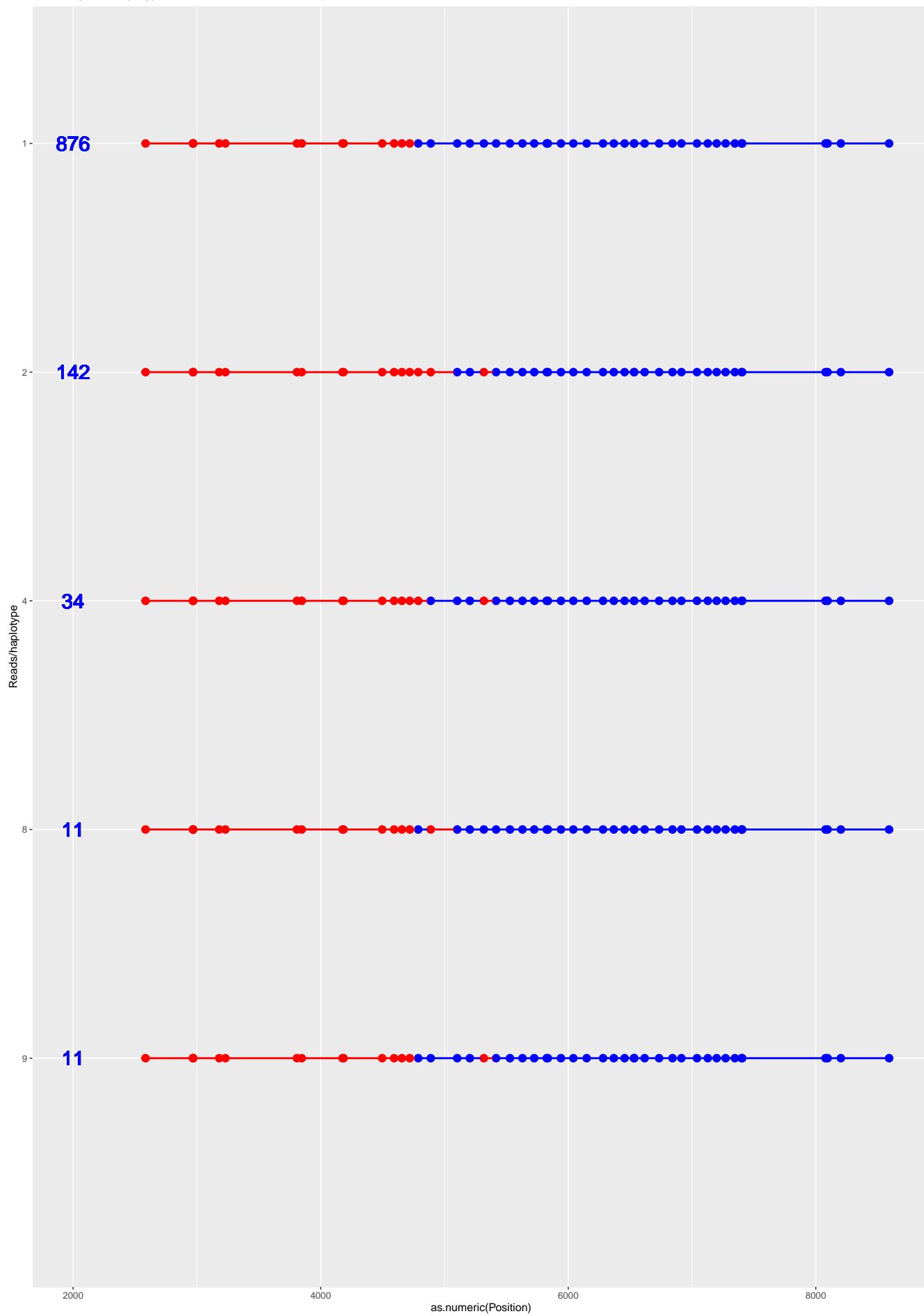
barcode = GACTGAGATCATGATC & ACTATCGCGCACGCAG

Sample = 209a tetrad = 209 spore = a

Total reads = 1350 PCR=549

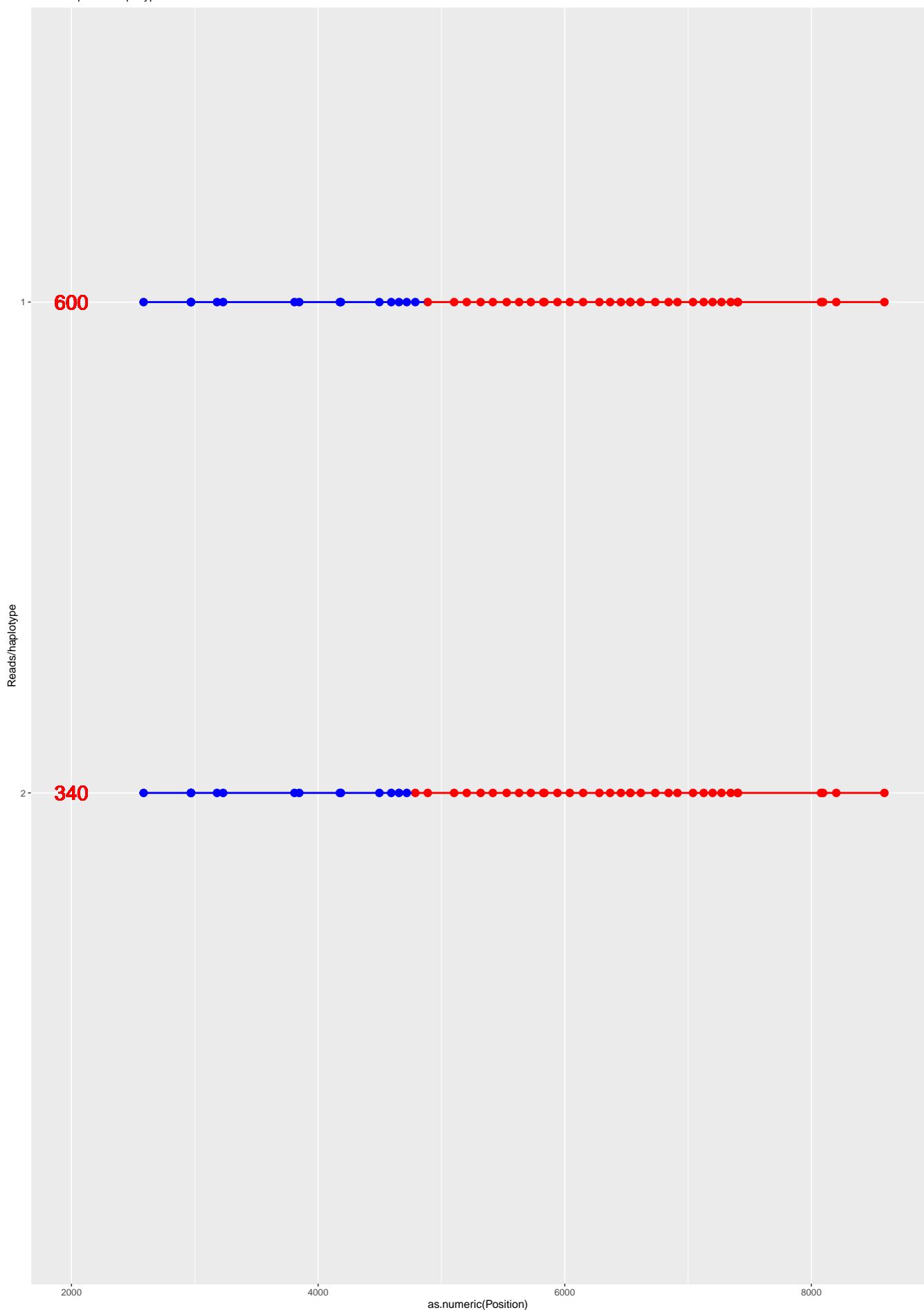
haplotypes I began with n[supporting reads] = 11, 34, 142, 876

most frequent 7 haplotypes.



barcode = ACGACATGATACTGCT & CGTGTCACTGCTACTCA

Sample = 209b tetrad = 209 spore = b
Total reads = 1066 PCR=550
haplotypes I began with n[supporting reads] = 340, 600
most frequent 7 haplotypes.



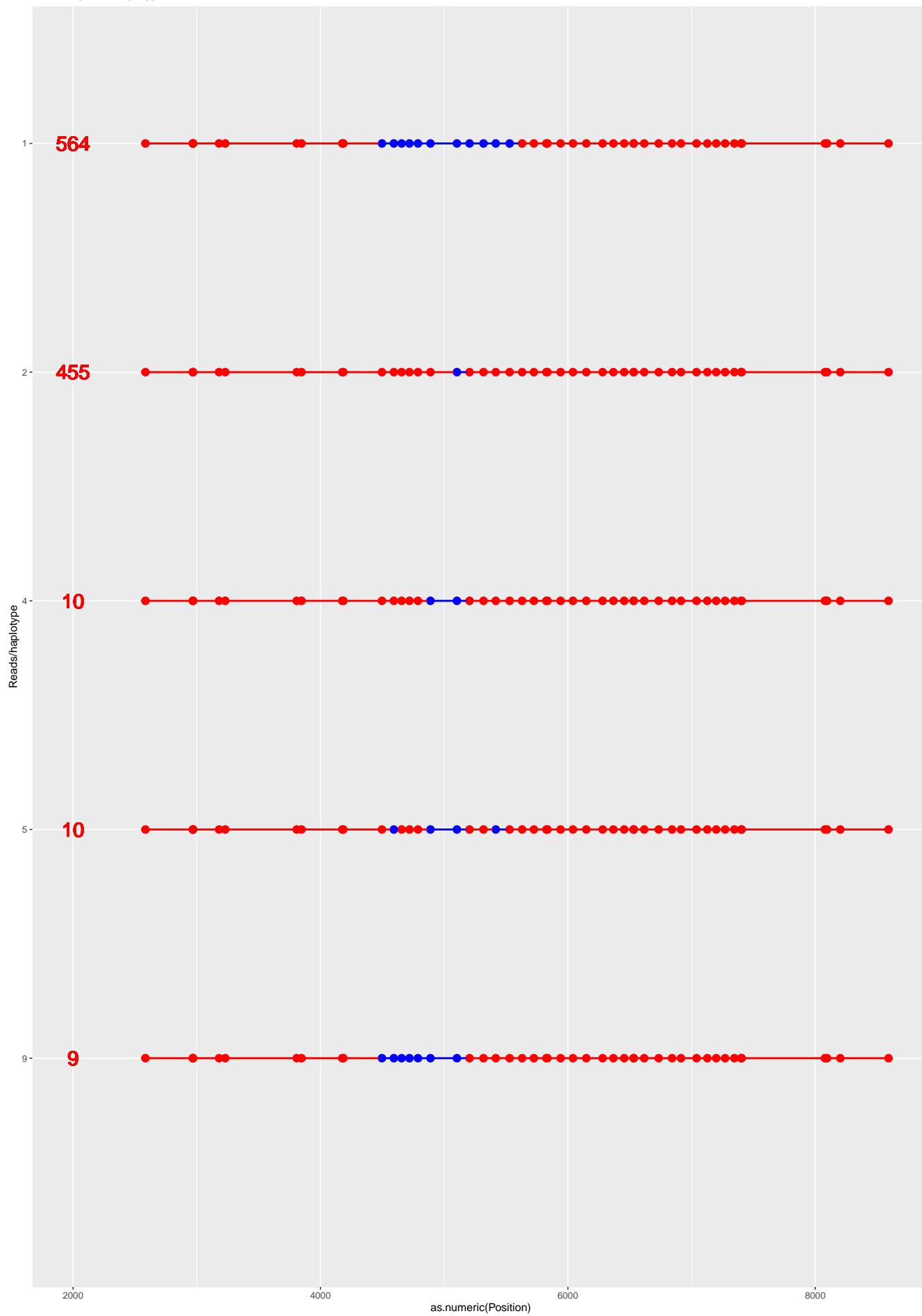
barcode = ACGACATGATACTGCT & TGTGAGACTGCATGTC

Sample = 209c tetrad = 209 spore = c

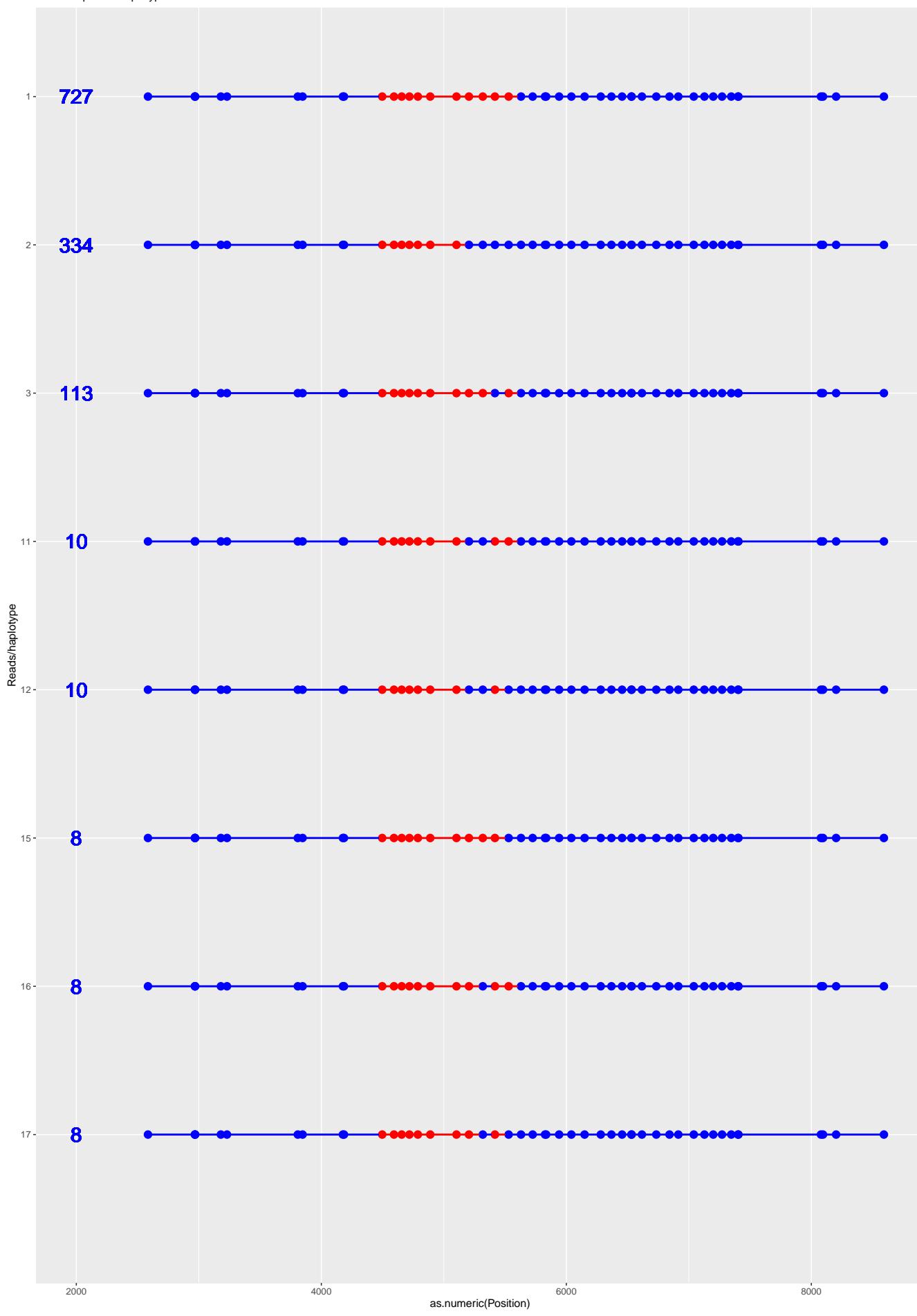
Total reads = 1669 PCR=551

haplotypes I began with n[supporting reads] = 9, 10, 455, 564

most frequent 7 haplotypes.



Sample = 209d tetrad = 209 spore = d
 Total reads = 1563 PCR=552
 haplotypes I began with [n(supporting reads)] = 8, 10, 113, 334, 727
 most frequent 7 haplotypes.

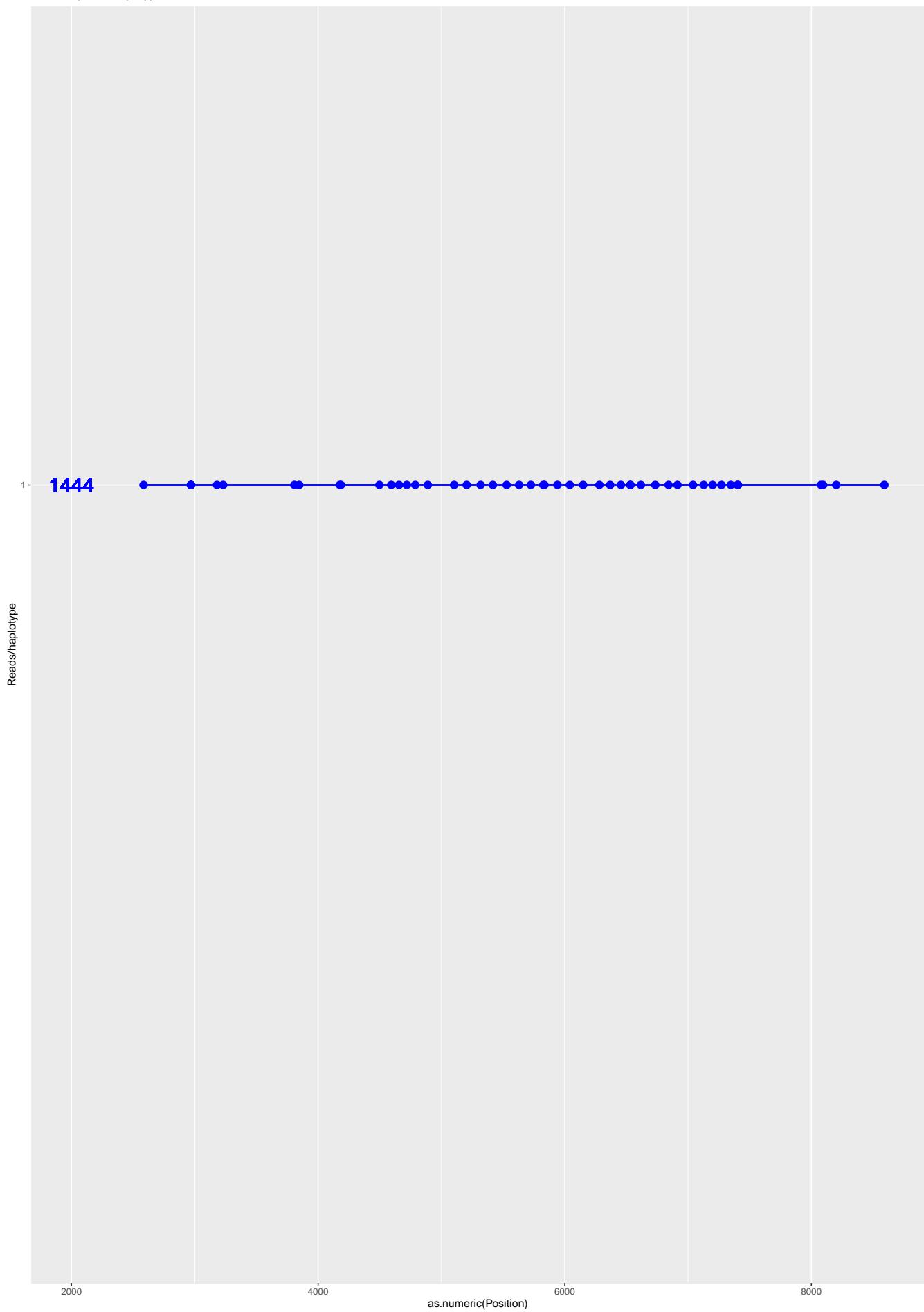


Sample = 211a tetrad = 211 spore = a

Total reads = 1694 PCR=553

haplotypes I began with n[supporting reads] = 1444

most frequent 7 haplotypes.



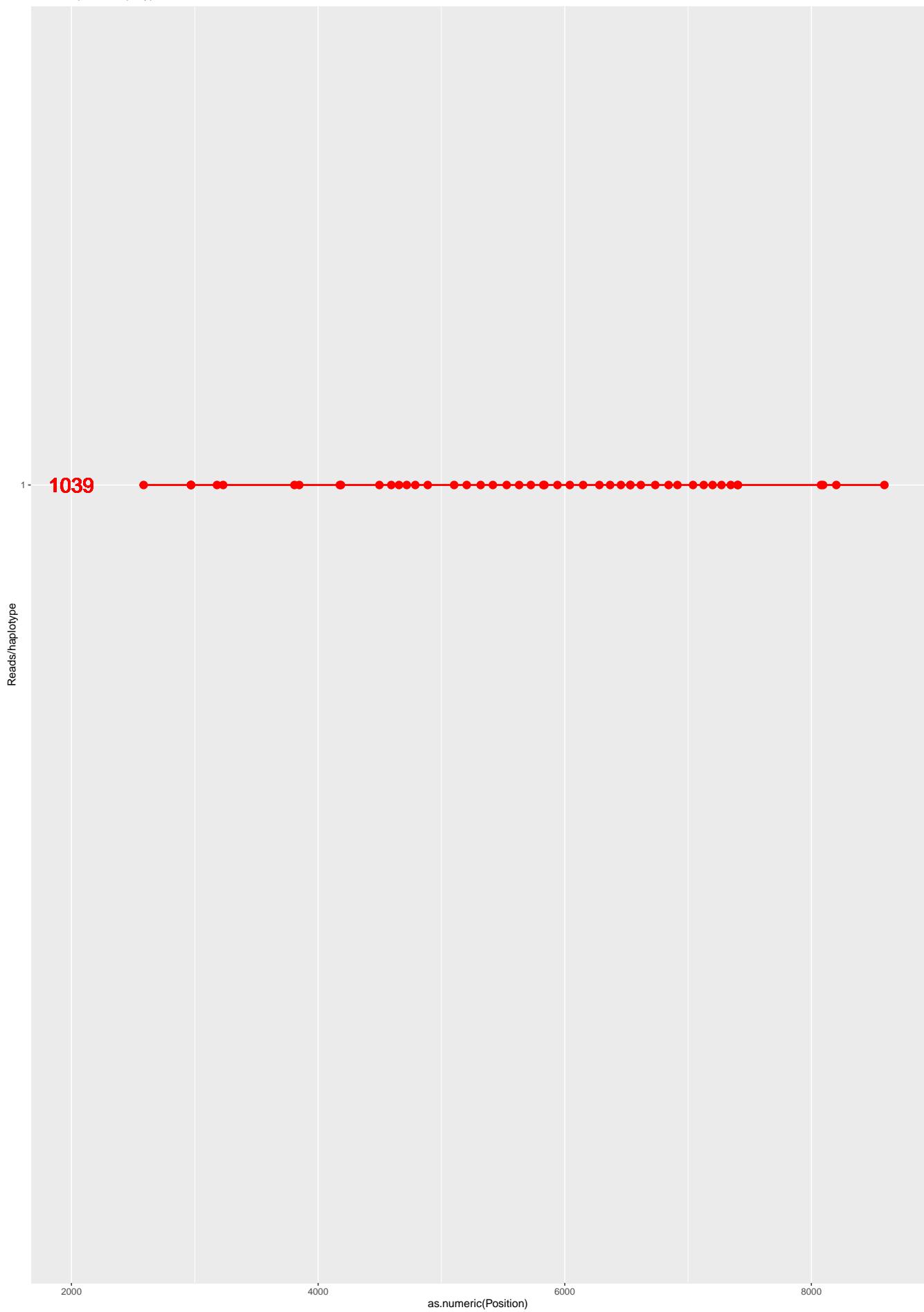
barcode = ATACAGCACAGATGTG & GCGACGAGTACTCATG

Sample = 211b tetrad = 211 spore = b

Total reads = 1091 PCR=554

haplotypes I began with n[supporting reads] = 1039

most frequent 7 haplotypes.



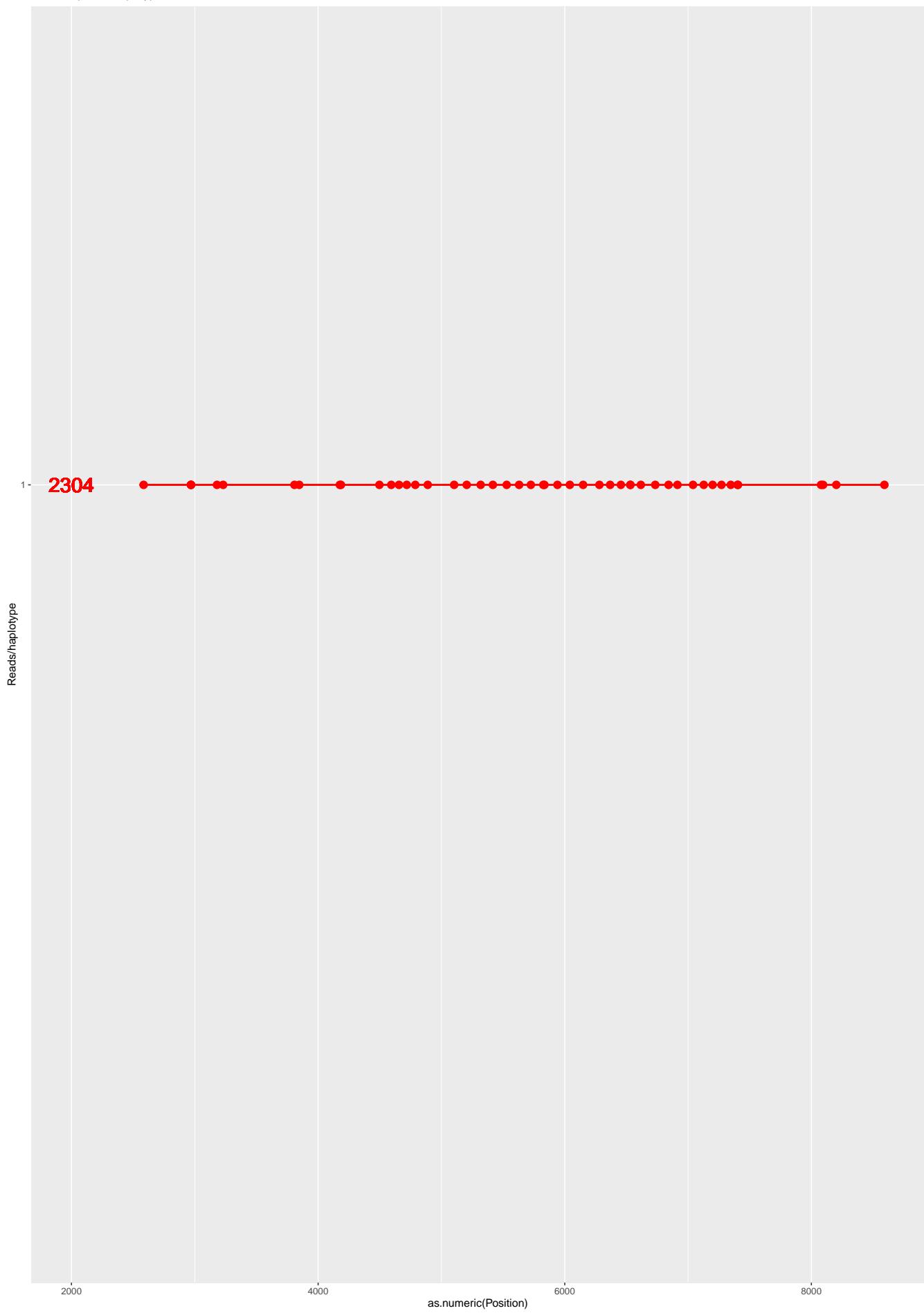
barcode = ATACAGCACAGATGTG & AGTATCACAGTCGCTG

Sample = 211c tetrad = 211 spore = c

Total reads = 2418 PCR=555

haplotypes I began with n[supporting reads] = 2304

most frequent 7 haplotypes.



barcode = ATACAGCACAGATGTG & ATCATATGATGCGACA

Sample = 211d tetrad = 211 spore = d
Total reads =2993 PCR=556
haplotypes I began with [n[supporting reads]] = 8, 9, 2543
most frequent 7 haplotypes.

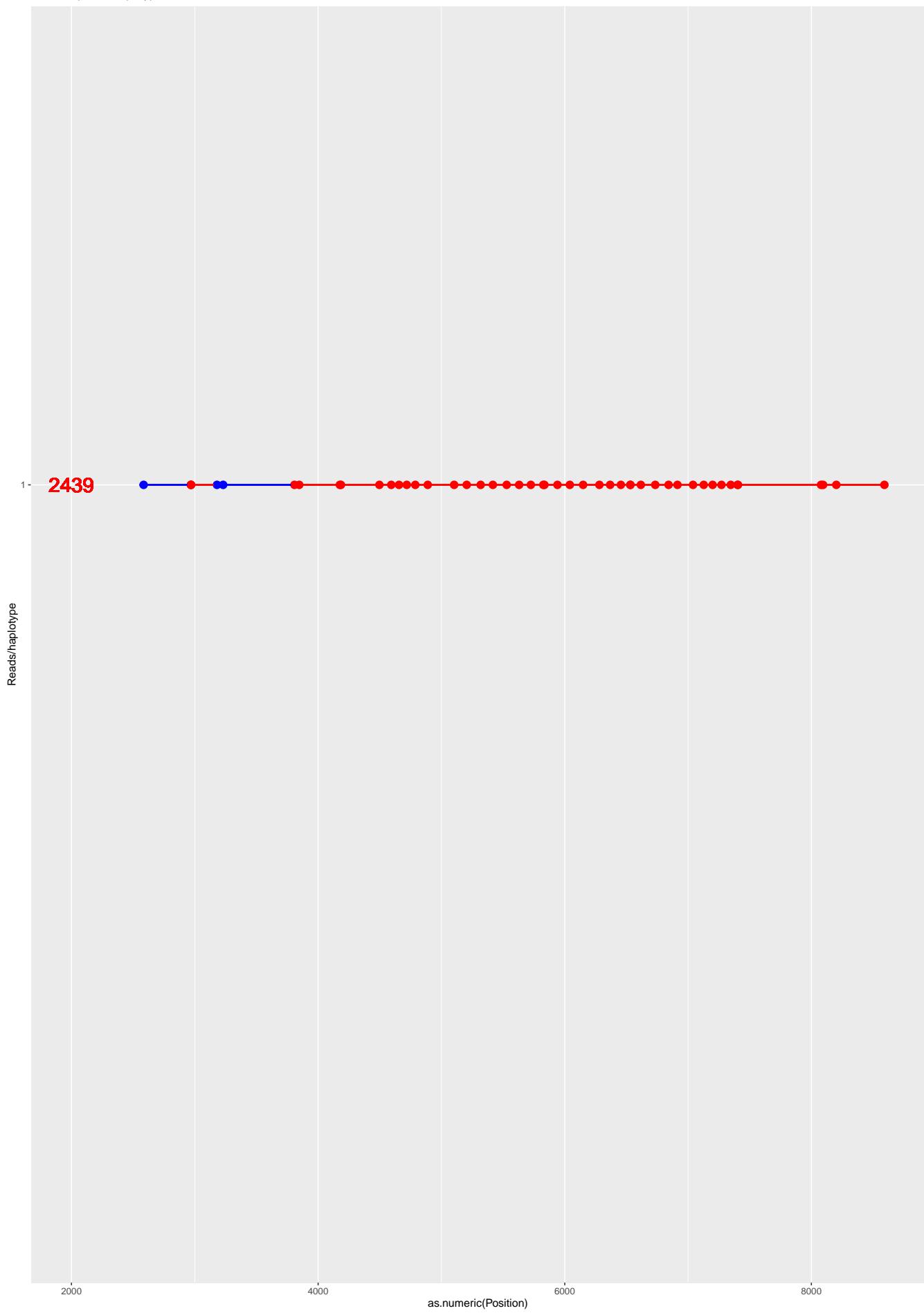


Sample = 212a tetrad = 212 spore = a

Total reads = 2565 PCR=557

haplotypes I began with n[supporting reads] = 2439

most frequent 7 haplotypes.

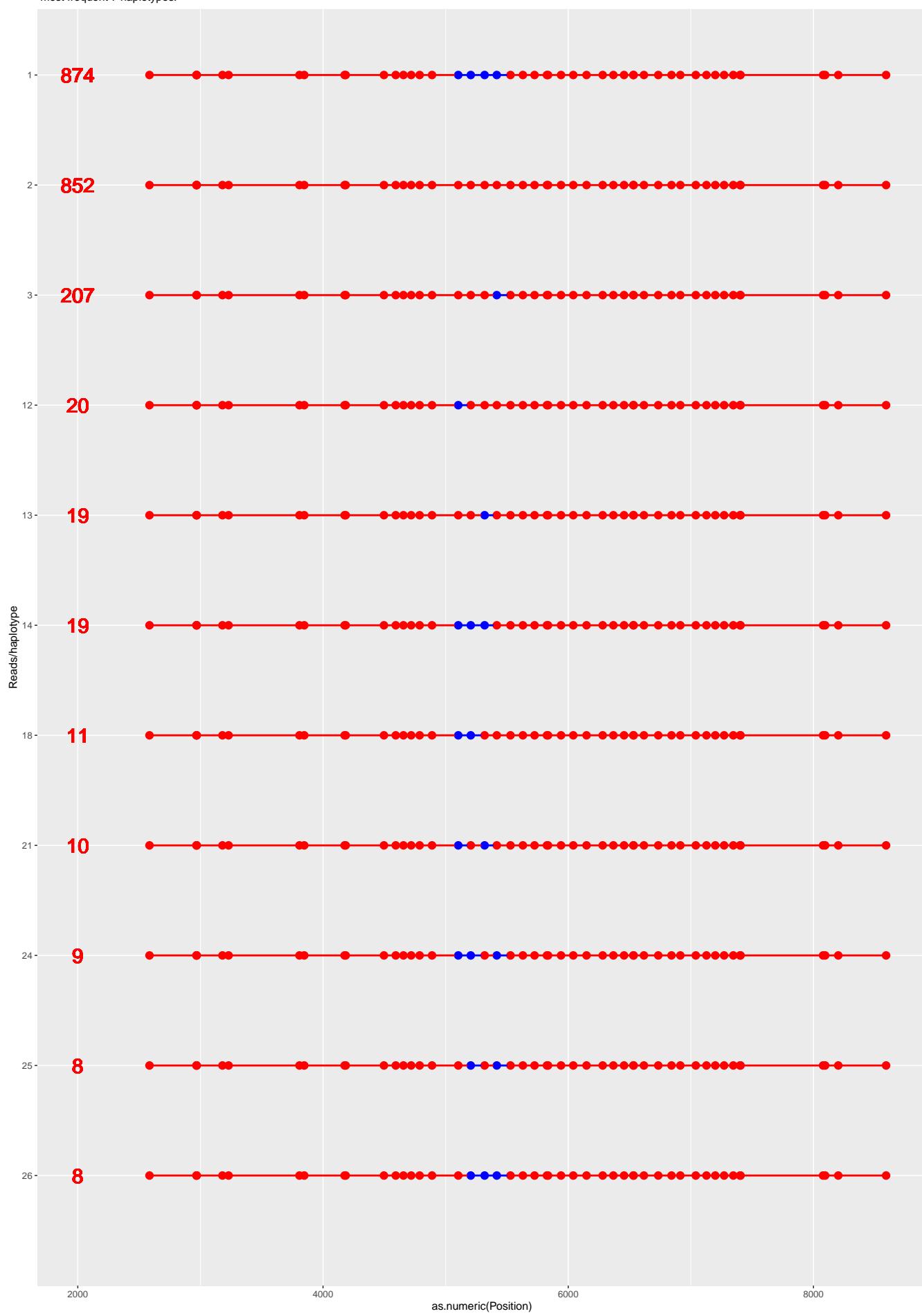


barcode = ATACAGCACAGATGTG & CGTGTCTACTCA

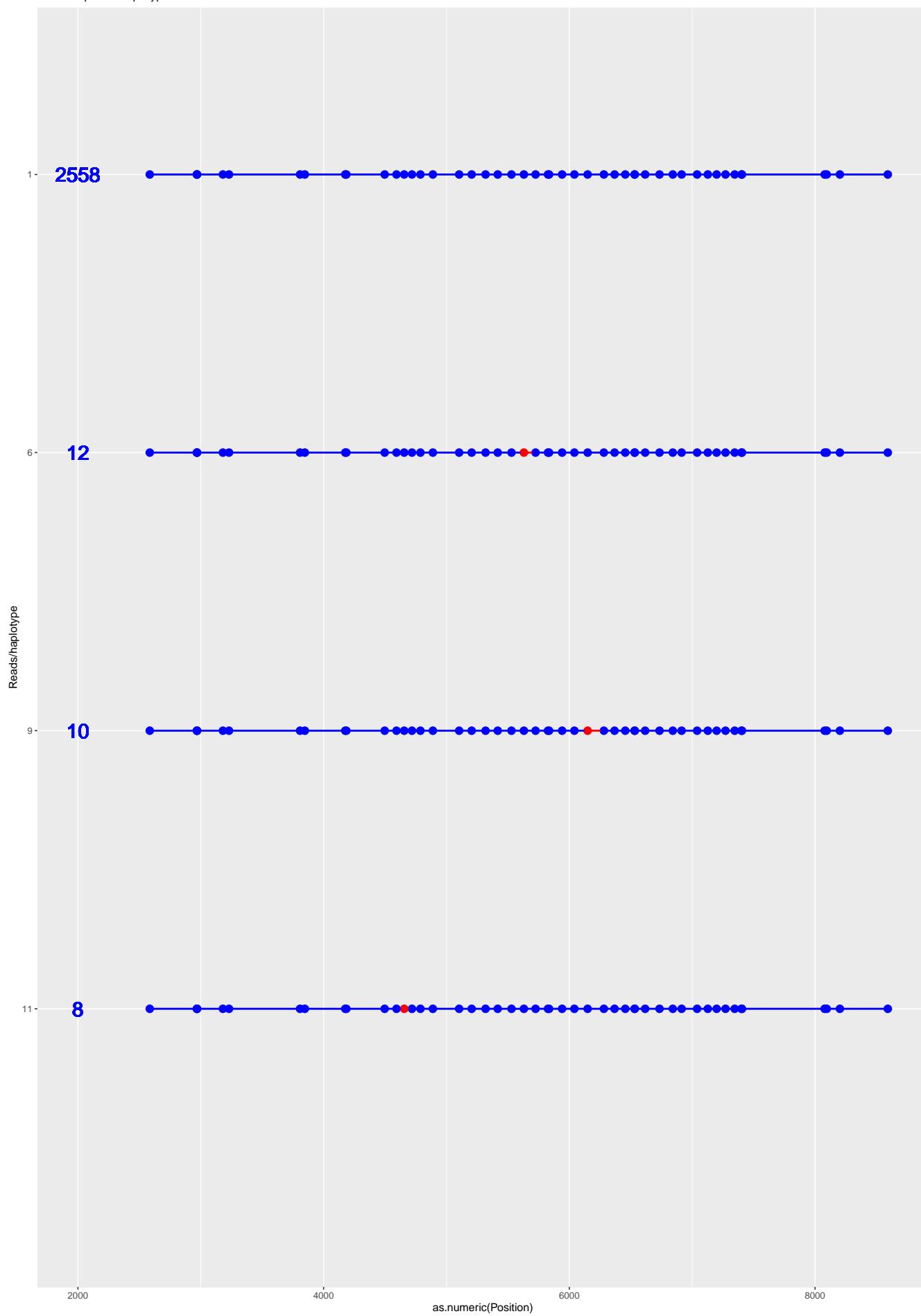
Sample = 212b tetrad = 212 spore = b

Total reads =2612 PCR=558

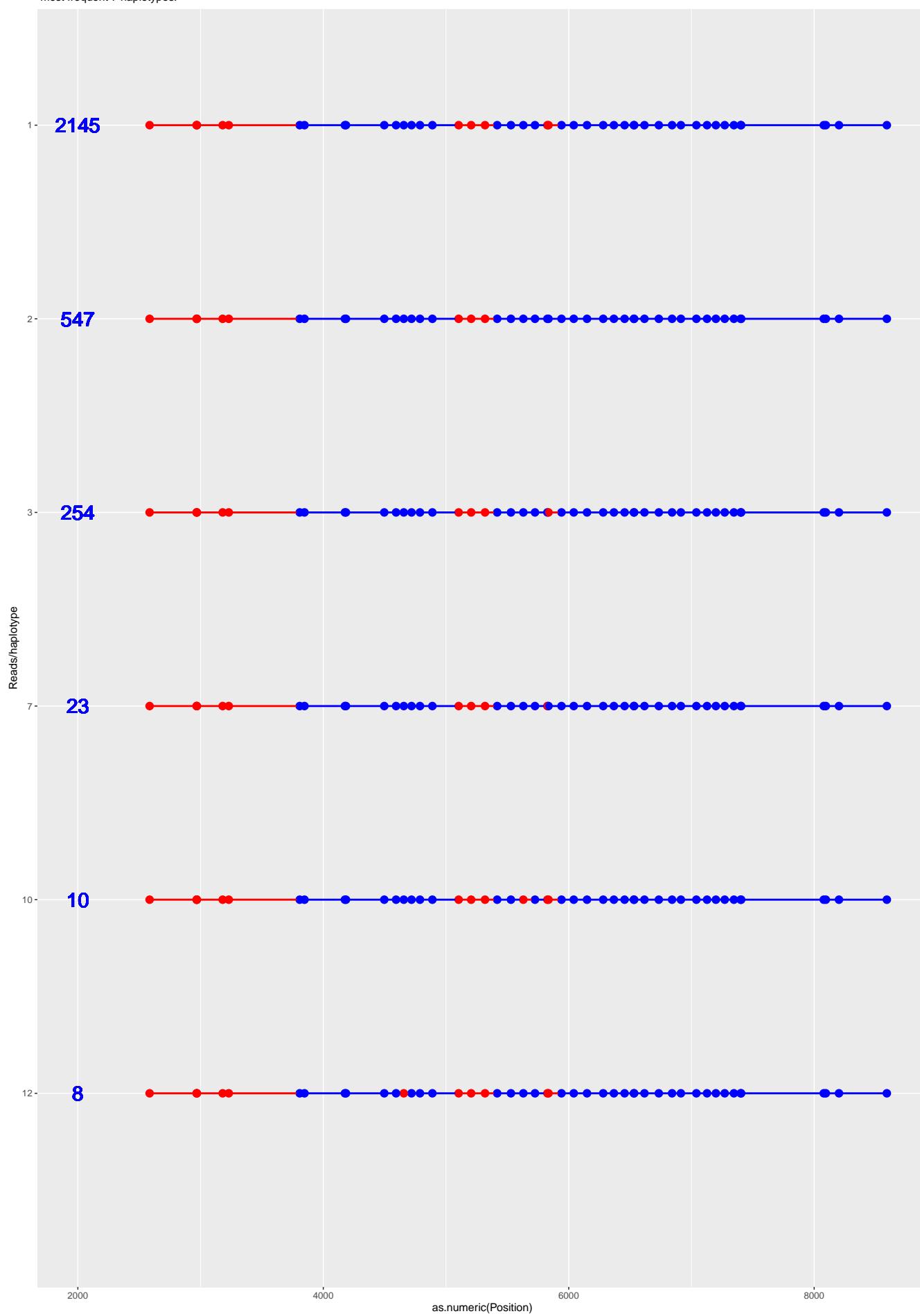
haplotypes I began with [n(supporting reads)] = 8, 9, 10, 11, 19, 20, 207, 852, 874
most frequent 7 haplotypes.



Sample = 212c tetrad = 212 spore = c
Total reads =3008 PCR=559
haplotypes I began with [n|supporting reads] = 8, 10, 12, 2558
most frequent 7 haplotypes.



Sample = 212d tetrad = 212 spore = d
Total reads = 3447 PCR=560
haplotypes I began with [n(supporting reads)] = 8, 10, 23, 254, 547, 2145
most frequent 7 haplotypes.



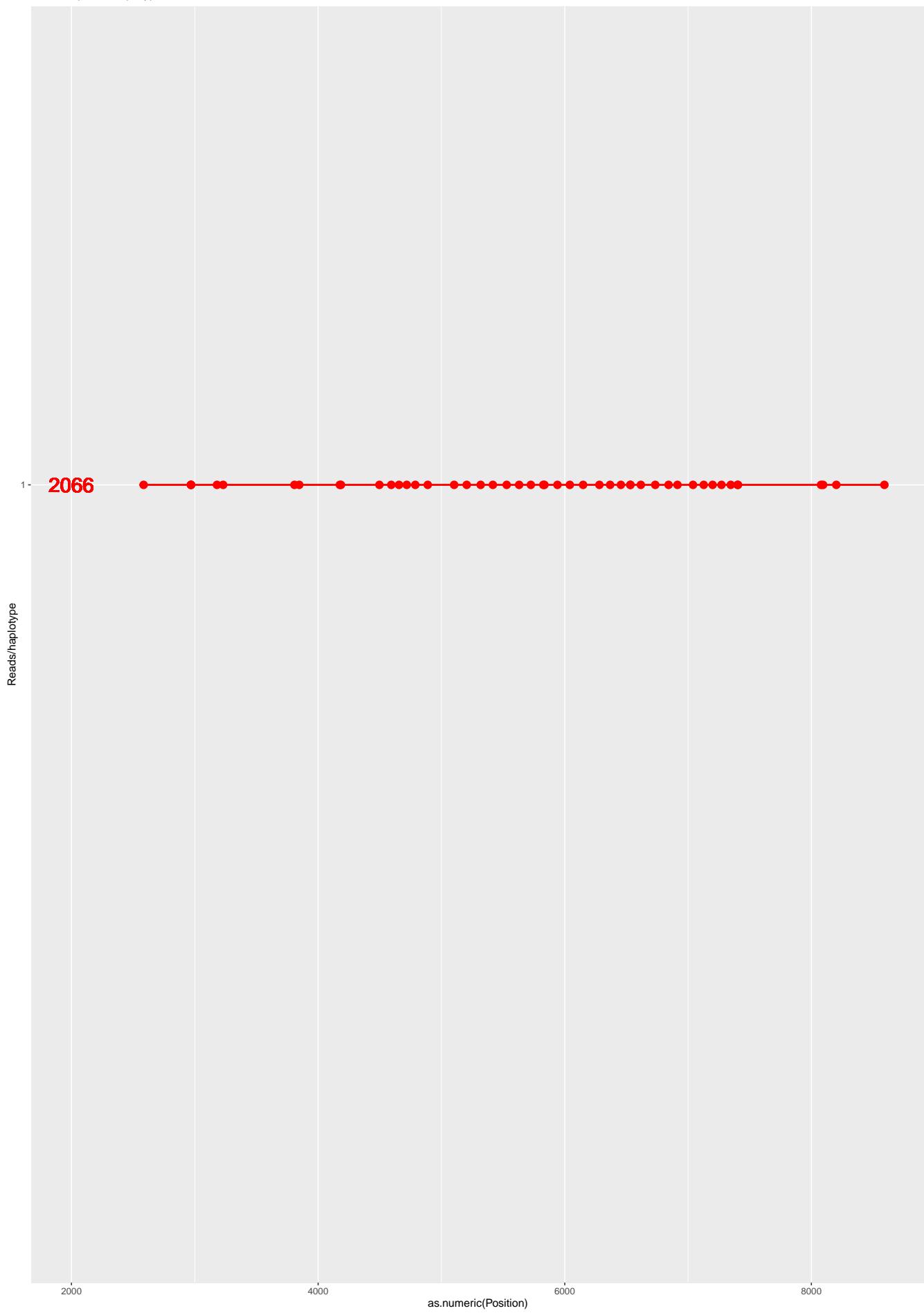
barcode = ATACAGCACAGATGTG & ACTATCGCGCACGCAG

Sample = 213a tetrad = 213 spore = a

Total reads = 2168 PCR=561

haplotypes I began with n[supporting reads] = 2066

most frequent 7 haplotypes.



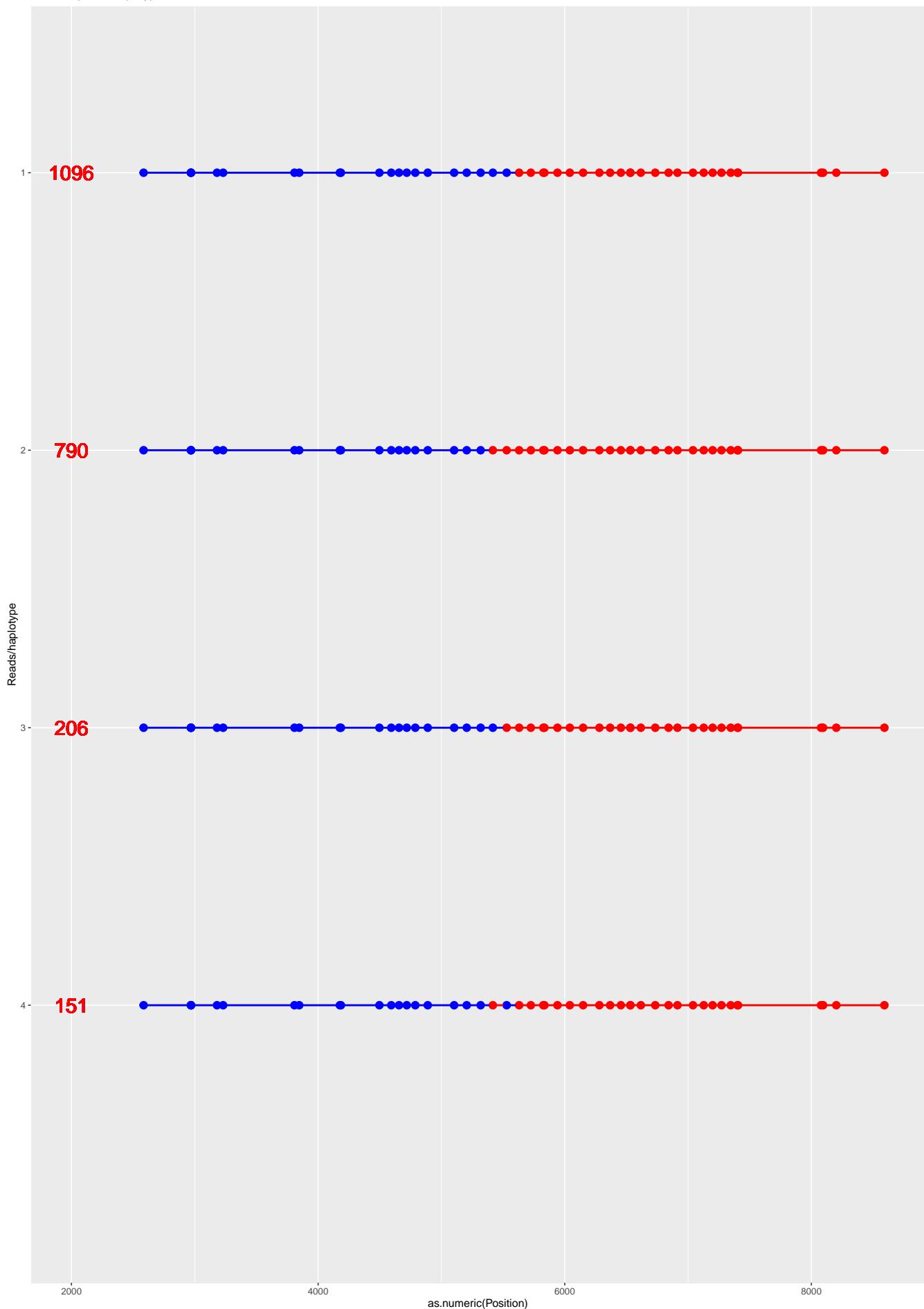
barcode = ACAGTCGATATCTCTC & GCGACGAGTACTCATG

Sample = 213b tetrad = 213 spore = b

Total reads = 2538 PCR=562

haplotypes I began with n[supporting reads] = 151, 206, 790, 1096

most frequent 7 haplotypes.



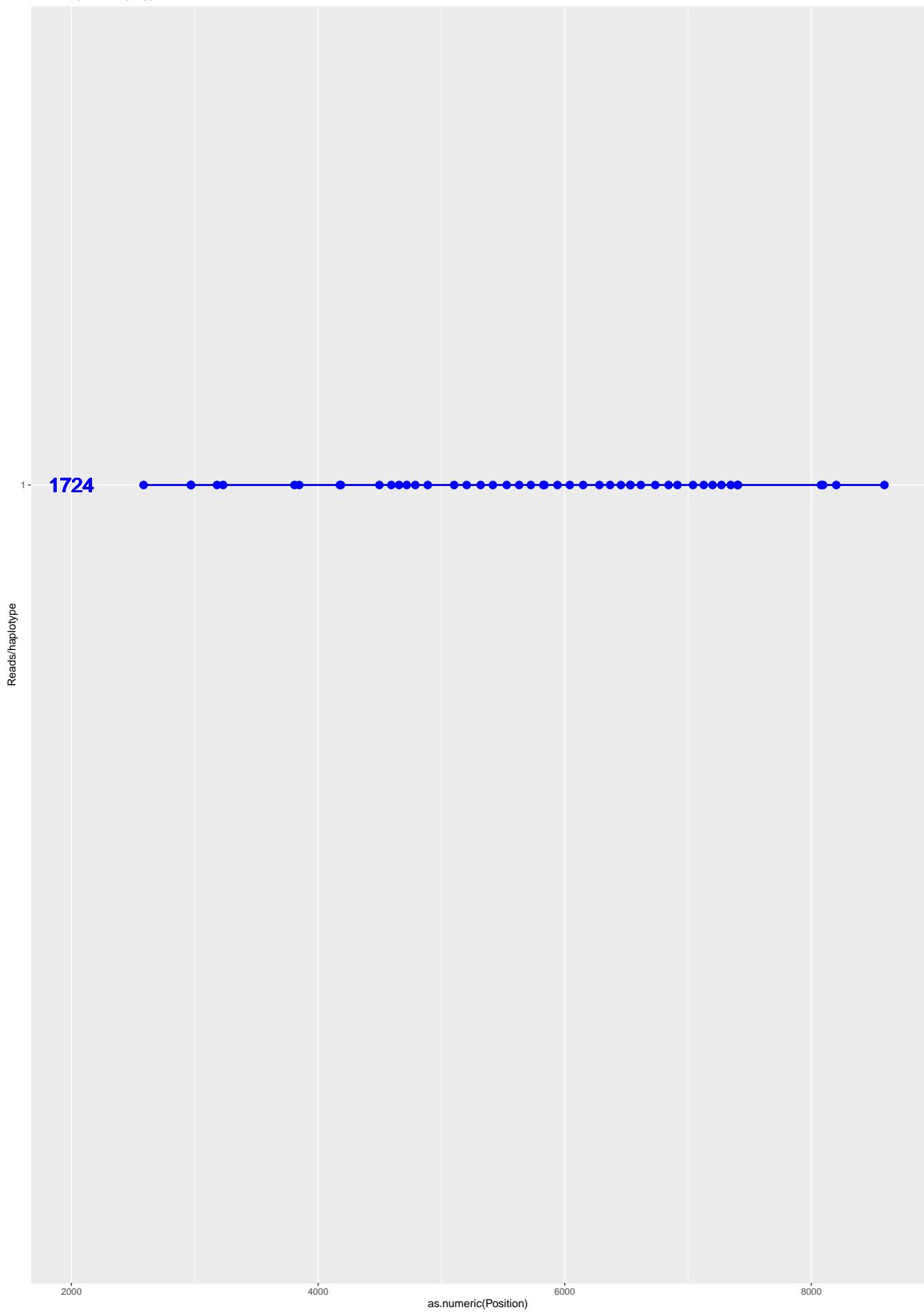
barcode = ACAGTCGATATCTCTC & AGTATCACAGTCGCTG

Sample = 213c tetrad = 213 spore = c

Total reads = 2055 PCR=563

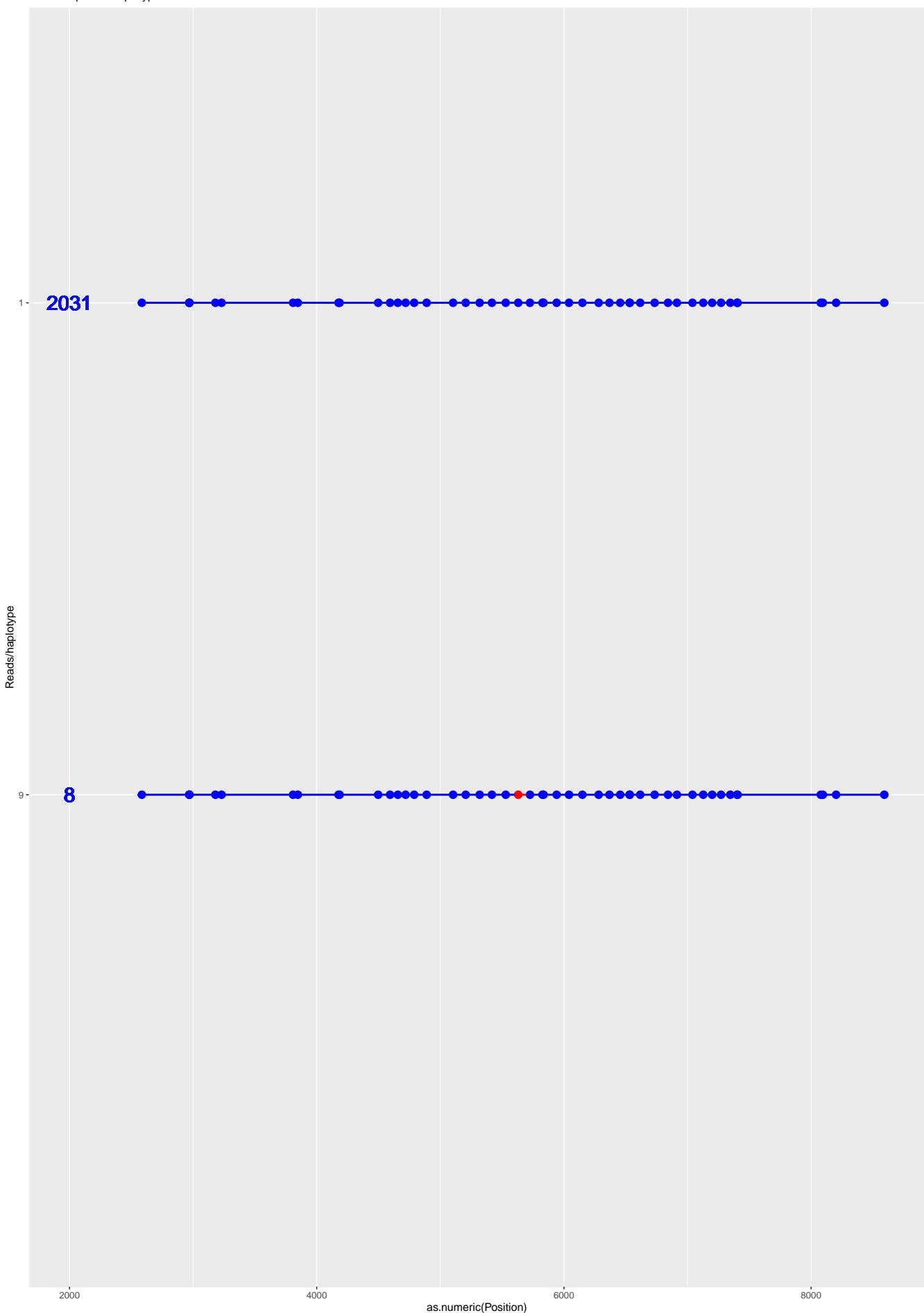
haplotypes I began with n[supporting reads] = 1724

most frequent 7 haplotypes.



barcode = ACAGTCGATATCTCTC & ATCATATGATGCGACA

Sample = 213d tetrad = 213 spore = d
Total reads = 2358 PCR=564
haplotypes I began with n[supporting reads] = 8, 2031
most frequent 7 haplotypes.

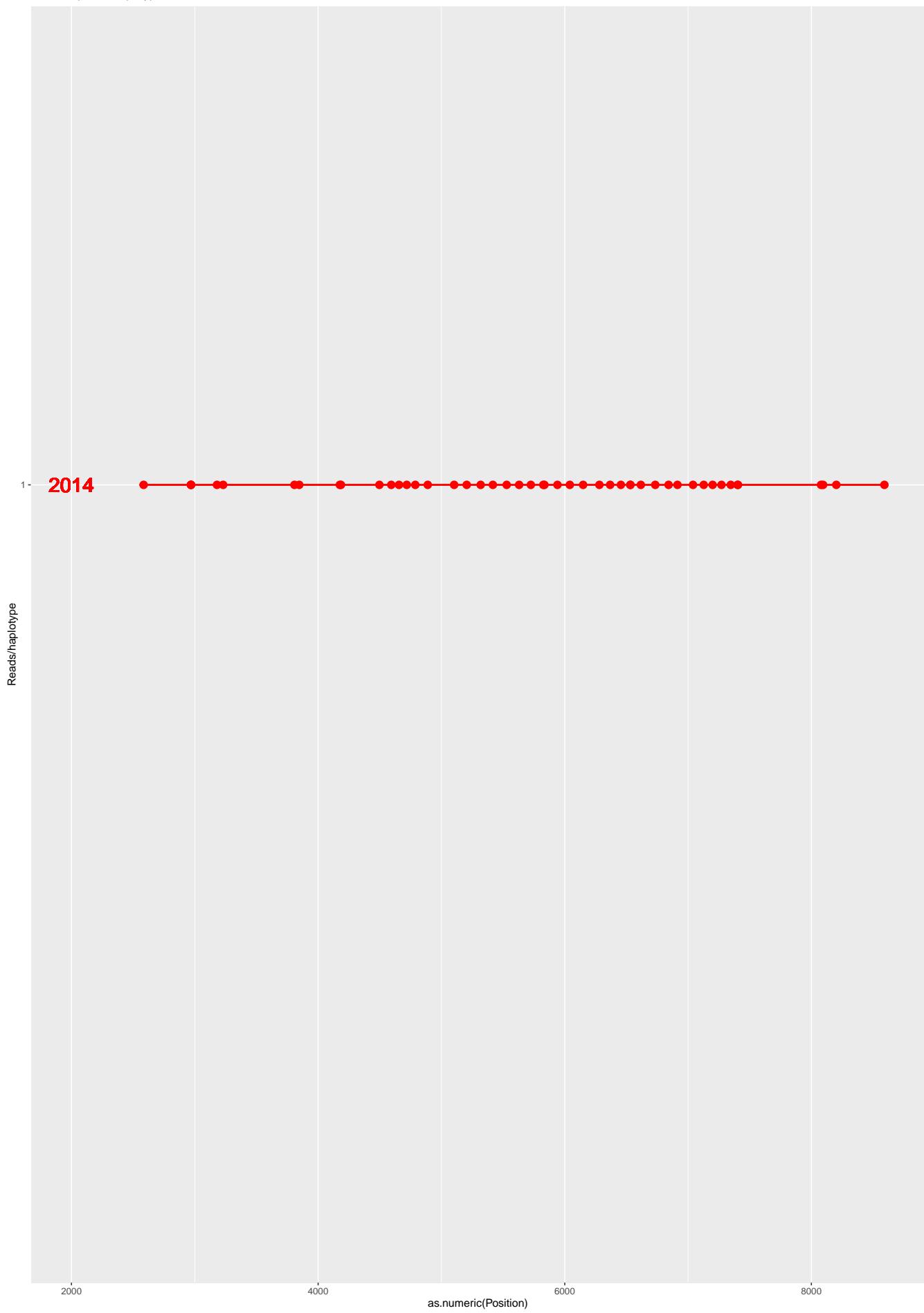


Sample = 215a tetrad = 215 spore = a

Total reads = 2101 PCR=569

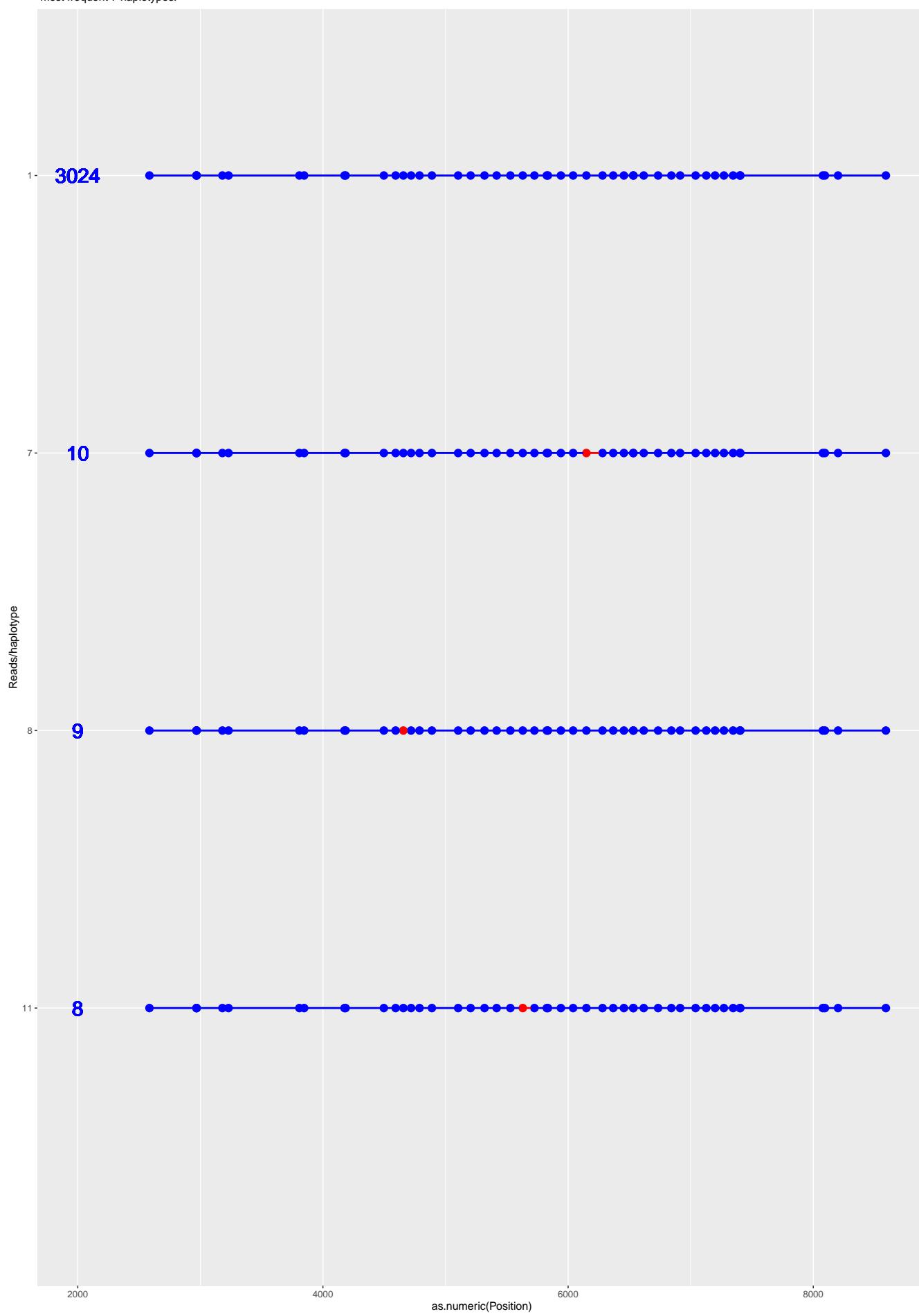
haplotypes I began with n[supporting reads] = 2014

most frequent 7 haplotypes.

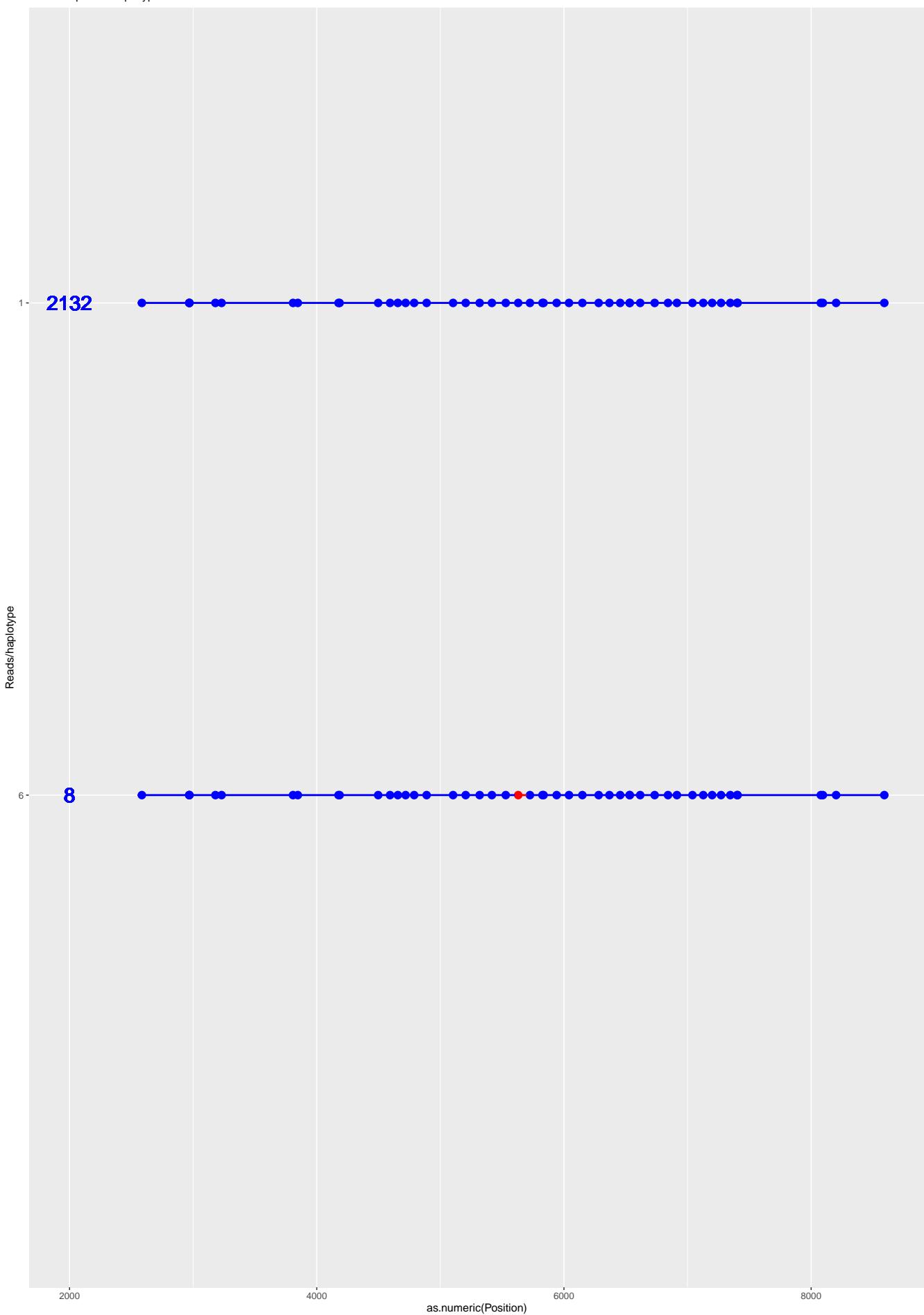


barcode = GCTCGATCACATGACG & GCGACGAGTACTCATG

Sample = 215b tetrad = 215 spore = b
Total reads = 3521 PCR=570
haplotypes I began with [n(supporting reads)] = 8, 9, 10, 3024
most frequent 7 haplotypes.



Sample = 215c tetrad = 215 spore = c
Total reads = 2488 PCR=571
haplotypes I began with n[supporting reads] = 8, 2132
most frequent 7 haplotypes.

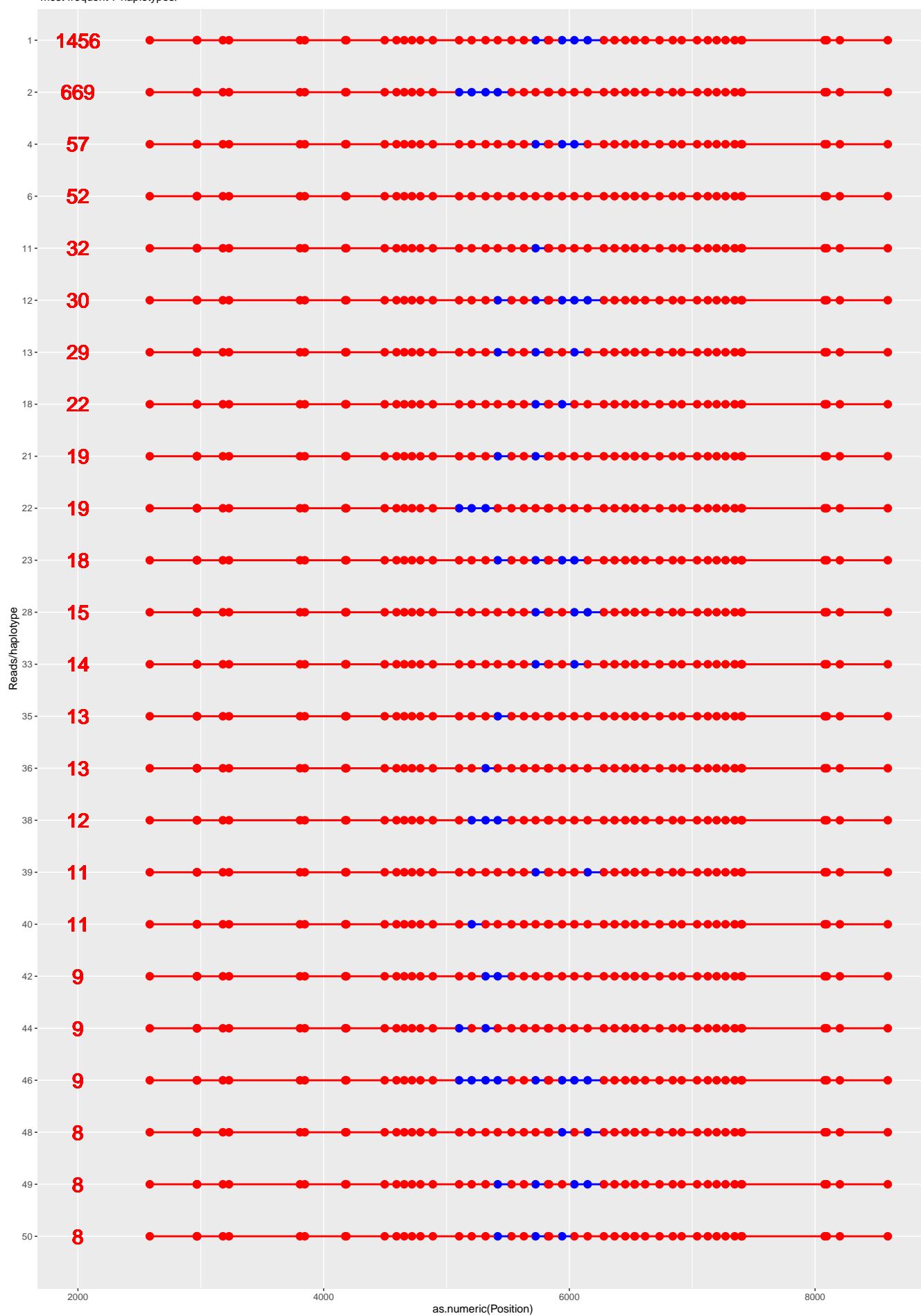


Sample = 215d tetrad = 215 spore = d

Total reads = 3846 PCR=572

haplotypes I began with [n(supporting reads)] = 8, 9, 11, 12, 13, 14, 15, 18, 19, 22, 29, 30, 32, 52, 57, 669, 1456

most frequent 7 haplotypes.

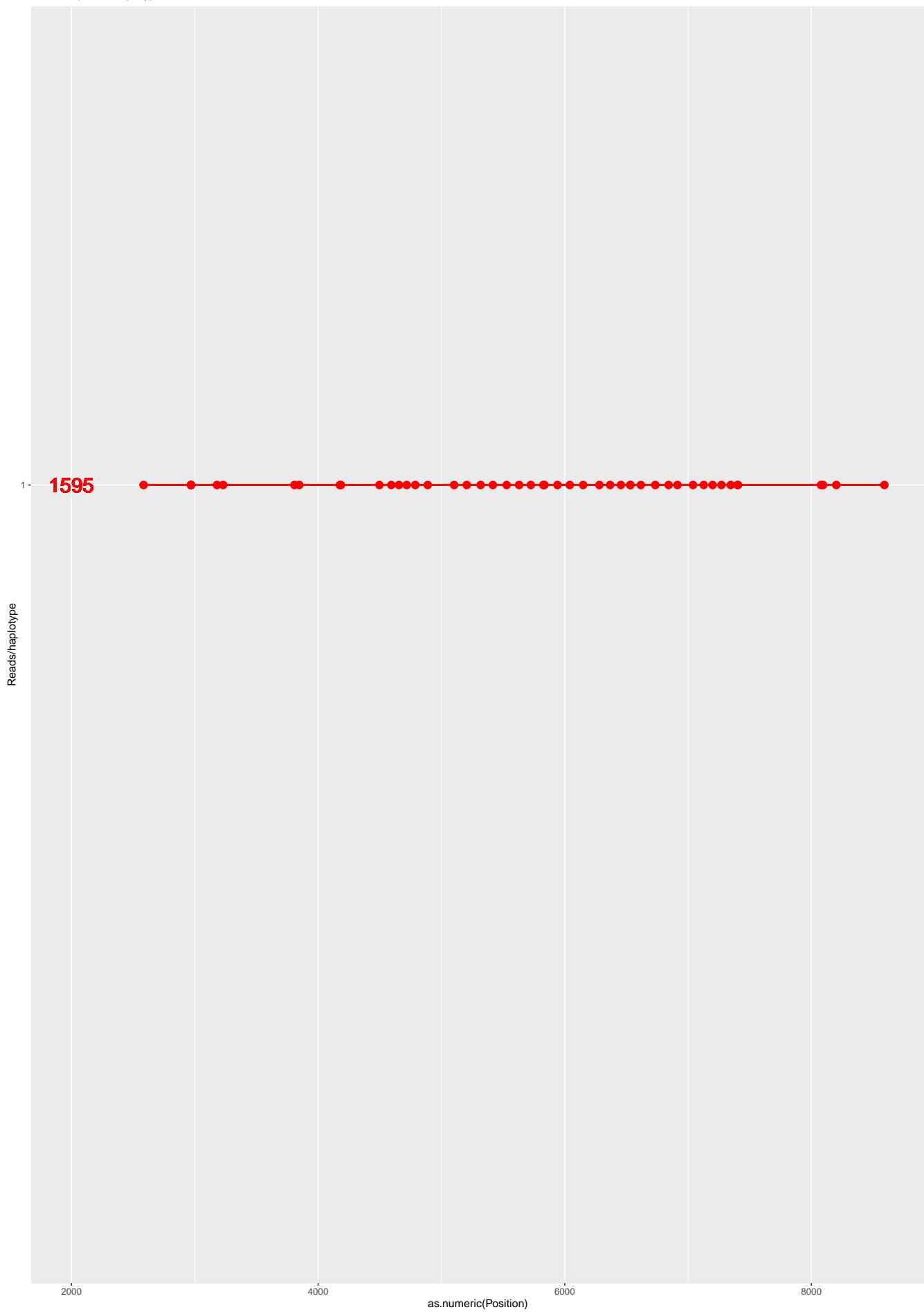


Sample = 216a tetrad = 216 spore = a

Total reads = 1660 PCR=573

haplotypes I began with n[supporting reads] = 1595

most frequent 7 haplotypes.



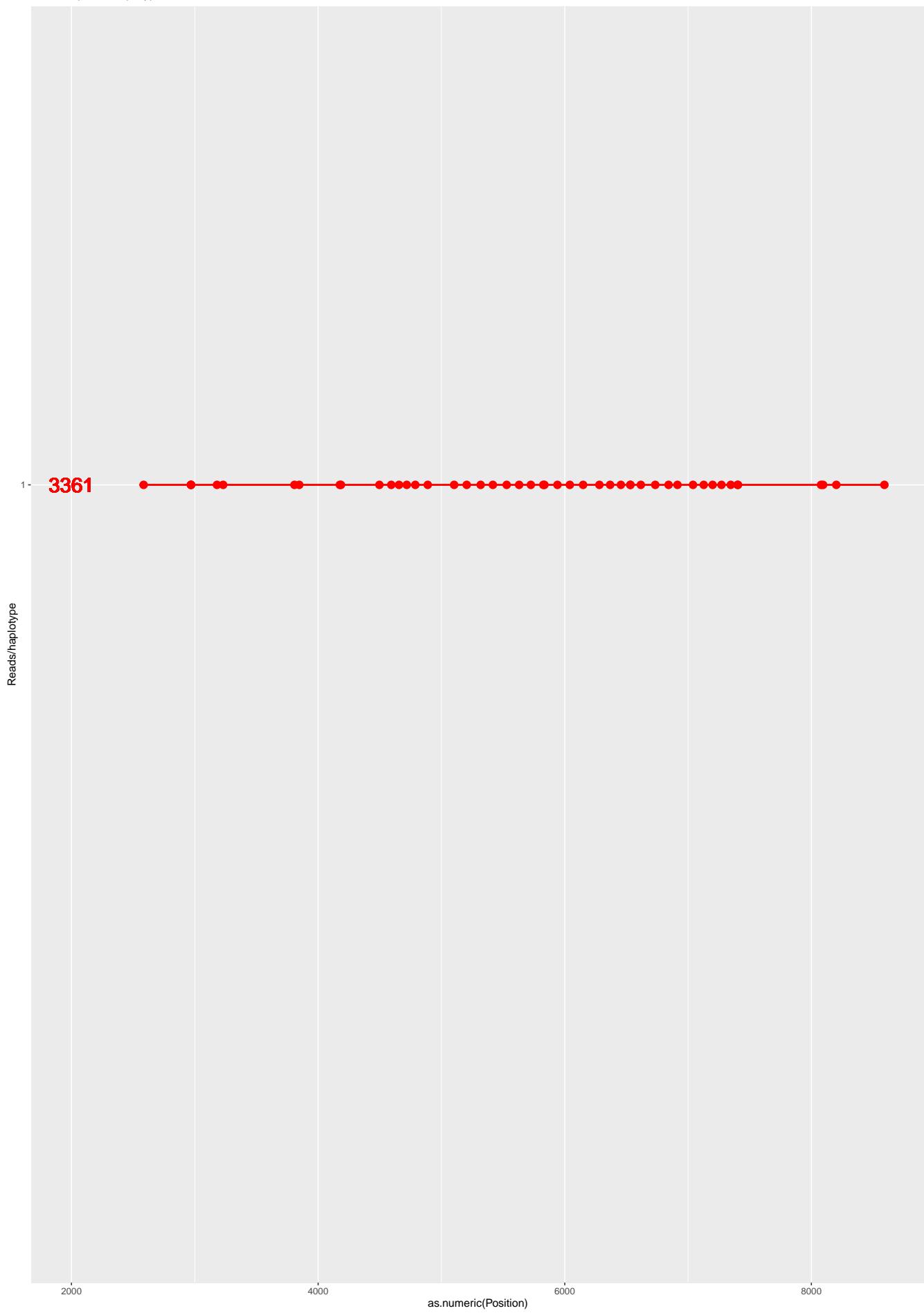
barcode = GCTCGATCACATGACG & CGTGTCACTGCTACTCA

Sample = 216b tetrad = 216 spore = b

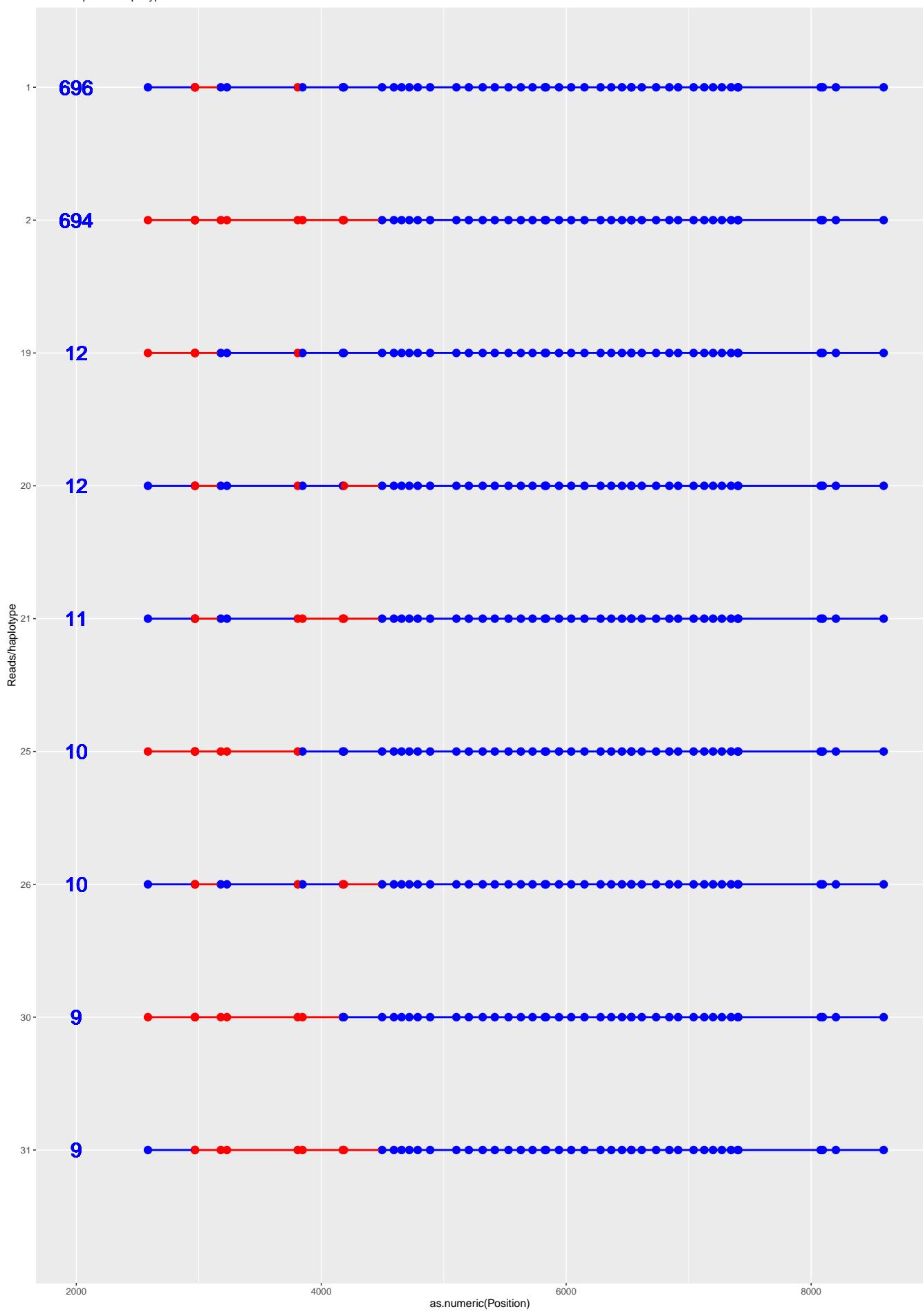
Total reads = 3503 PCR=574

haplotypes I began with n[supporting reads] = 3361

most frequent 7 haplotypes.

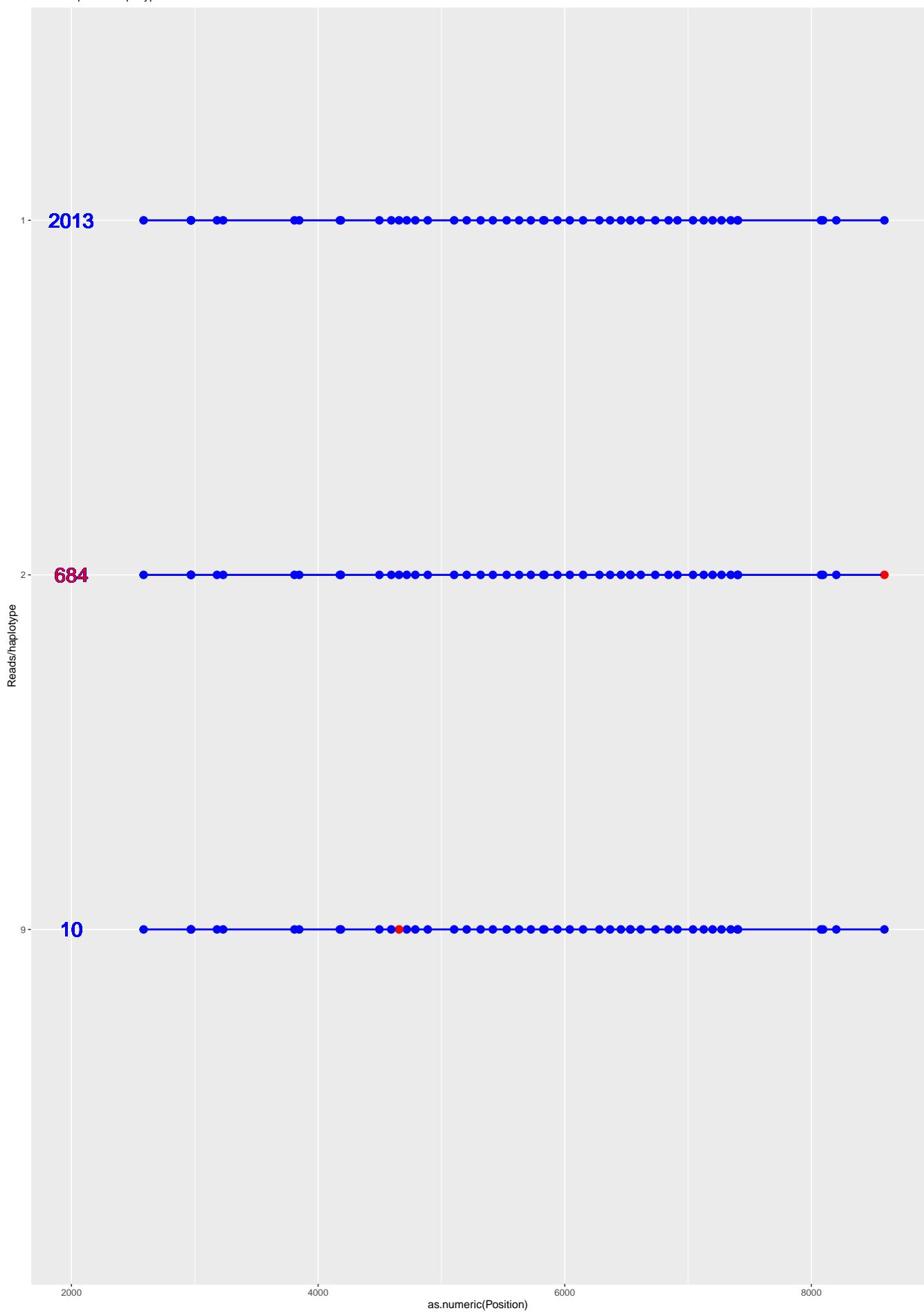


Sample = 216c tetrad = 216 spore = c
 Total reads = 2474 PCR=575
 haplotypes I began with [n|supporting reads] = 9, 10, 11, 12, 694, 696
 most frequent 7 haplotypes.



barcode = GCTCGATCACATGACG & GCTCAGTGCCTACTG

Sample = 216d tetrad = 216 spore = d
Total reads = 3160 PCR=576
haplotypes I began with n[supporting reads] = 10, 684, 2013
most frequent 7 haplotypes.



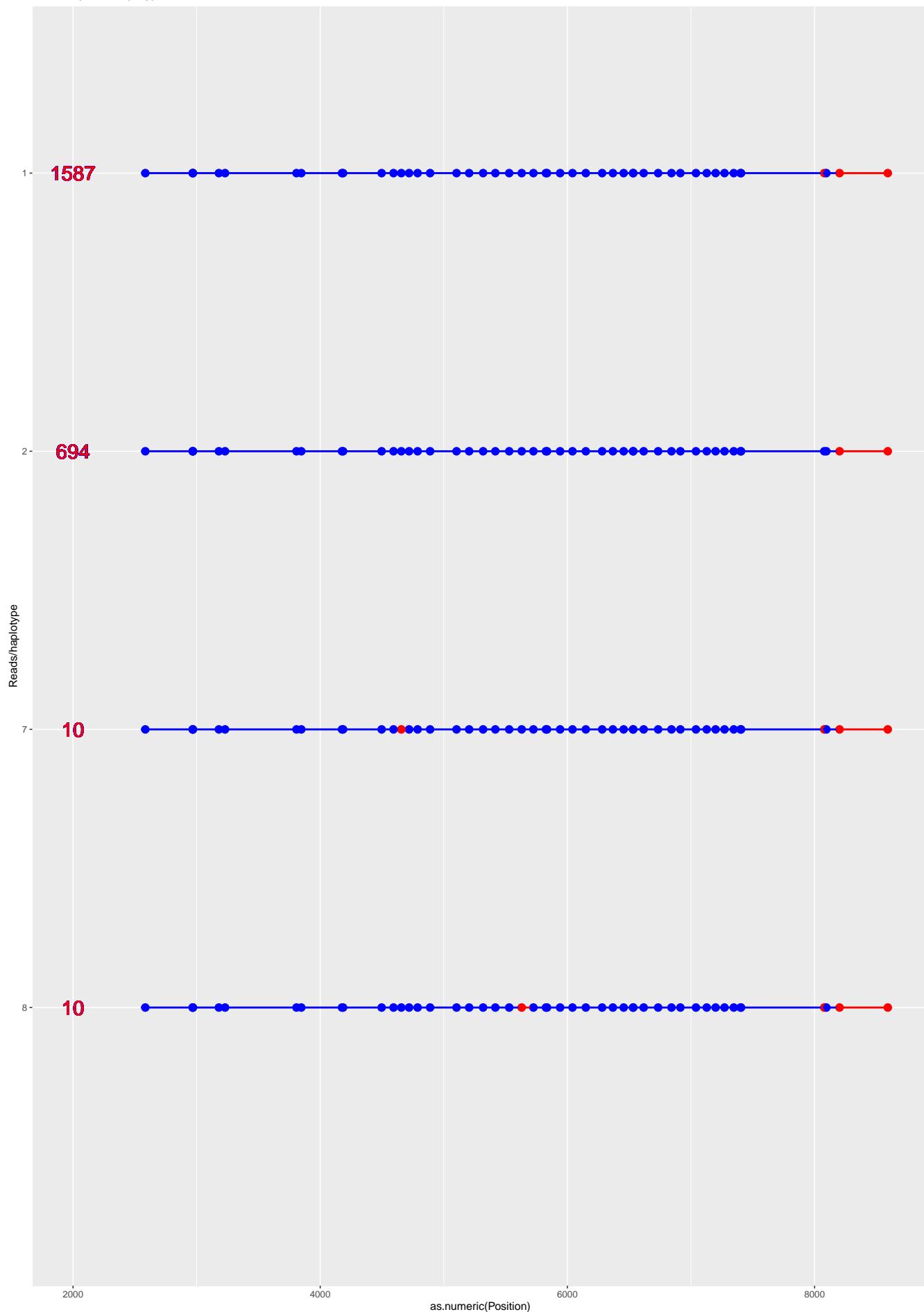
barcode = GCTCGATCACATGACG & ACTATCGCGACGCAG

Sample = 218a tetrad = 218 spore = a

Total reads = 2639 PCR=577

haplotypes I began with n[supporting reads] = 10, 694, 1587

most frequent 7 haplotypes.



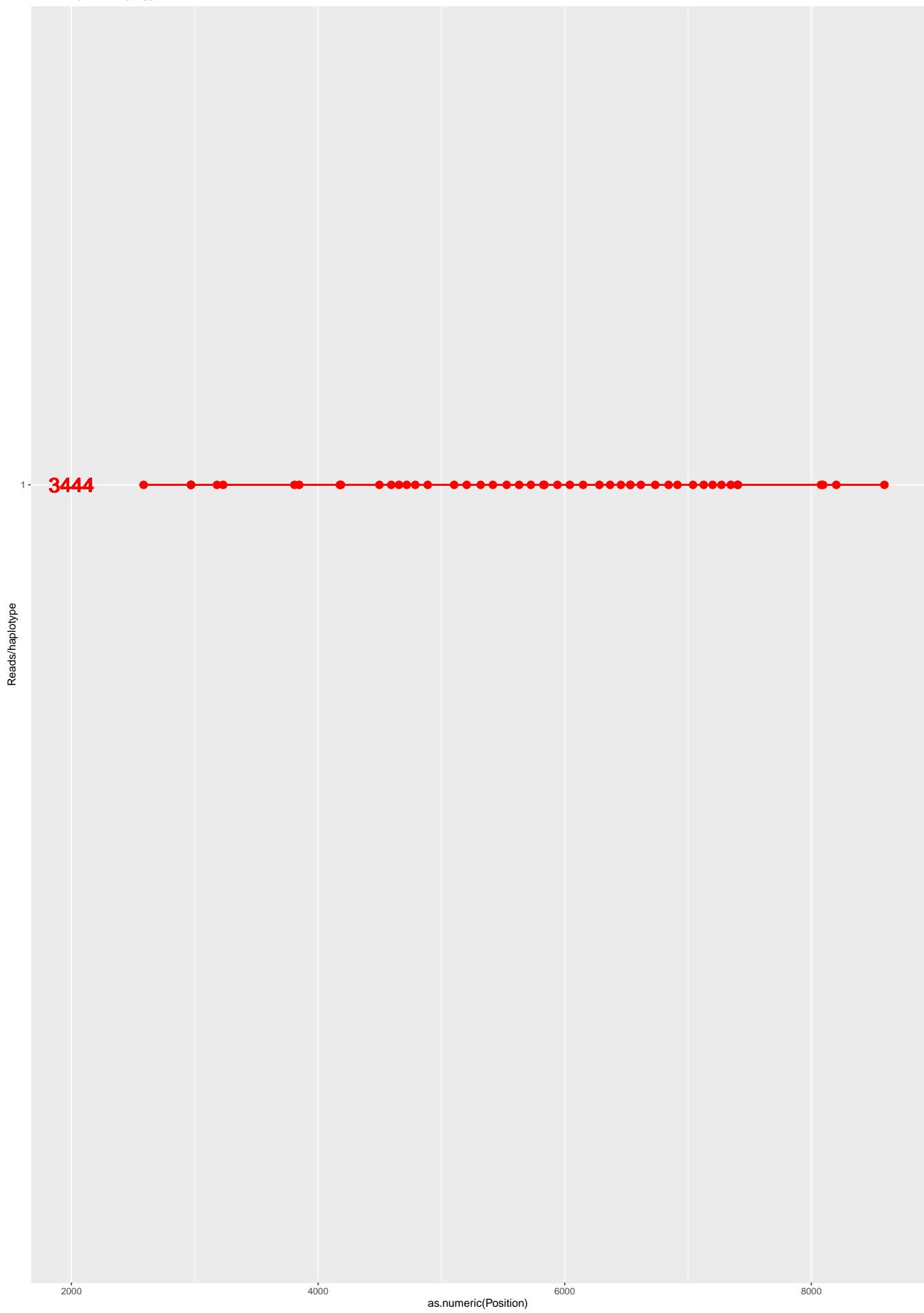
barcode = GCGCTCTGTGTCAGC & TCAGCTGACGATGTGA

Sample = 218b tetrad = 218 spore = b

Total reads =3582 PCR=578

haplotypes I began with n[supporting reads] = 3444

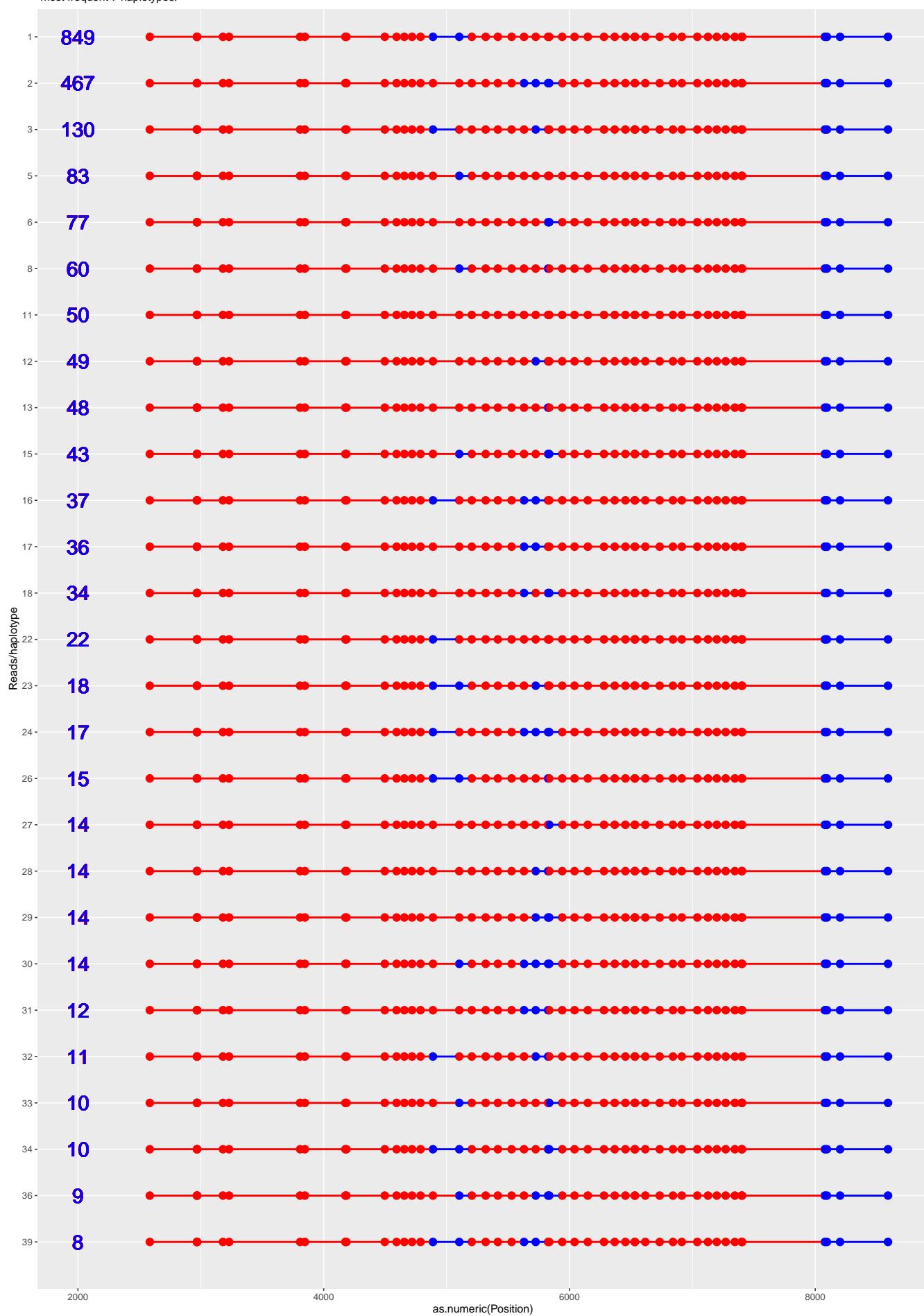
most frequent 7 haplotypes.



Sample = 218c tetrad = 218 spore = c

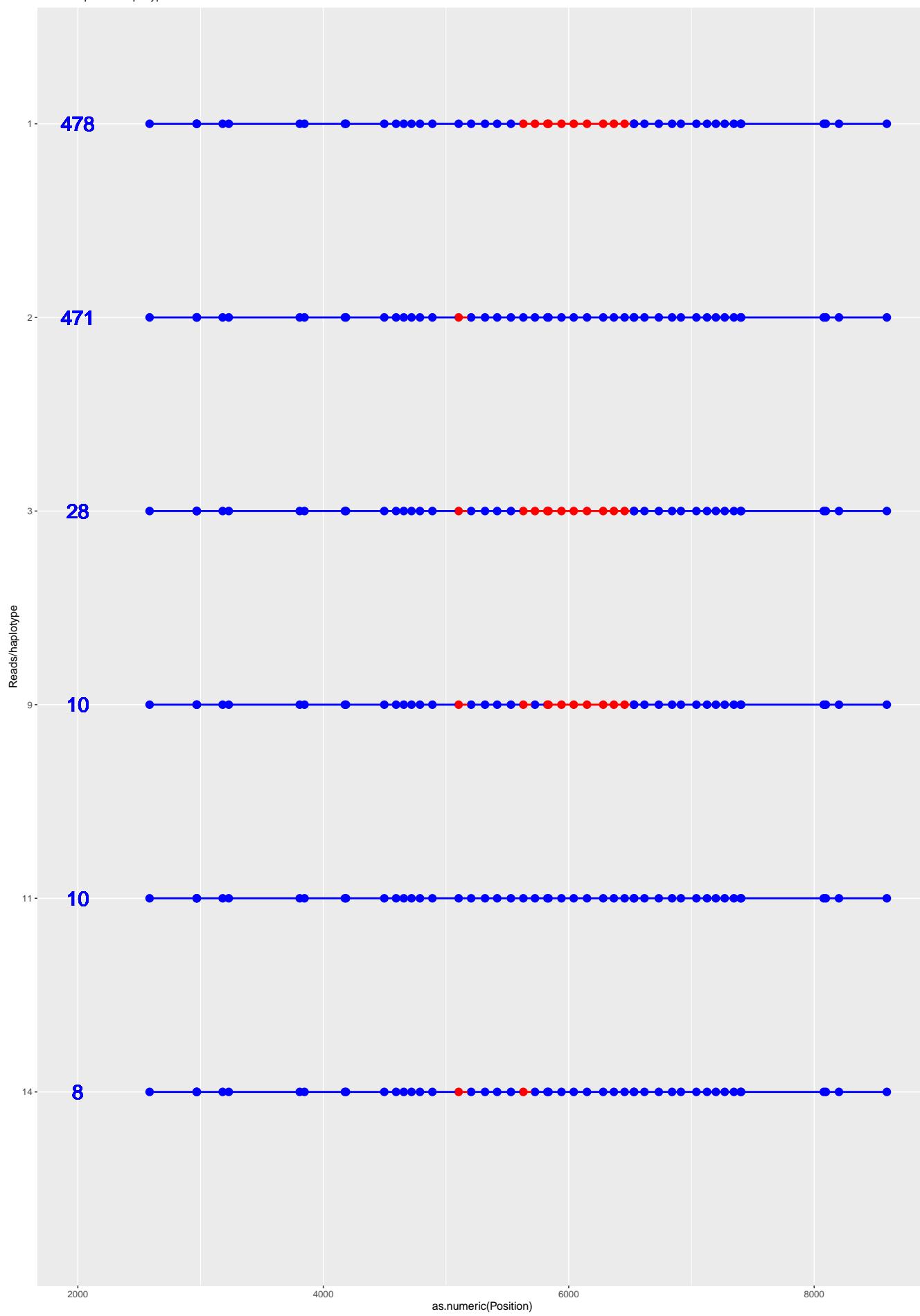
Total reads = 2912 PCR=579

haplotypes I began with [n(supporting reads)] = 8, 9, 10, 11, 12, 14, 15, 17, 18, 22, 34, 36, 37, 43, 48, 49, 50, 60, 77, 83, 130, 467, 849
most frequent 7 haplotypes.



barcode = GCGCTCTGTGTCAGC & CTACTCTCAGCAGTGA

Sample = 218d tetrad = 218 spore = d
Total reads = 2009 PCR=580
haplotypes I began with [n|supporting reads] = 8, 10, 28, 471, 478
most frequent 7 haplotypes.

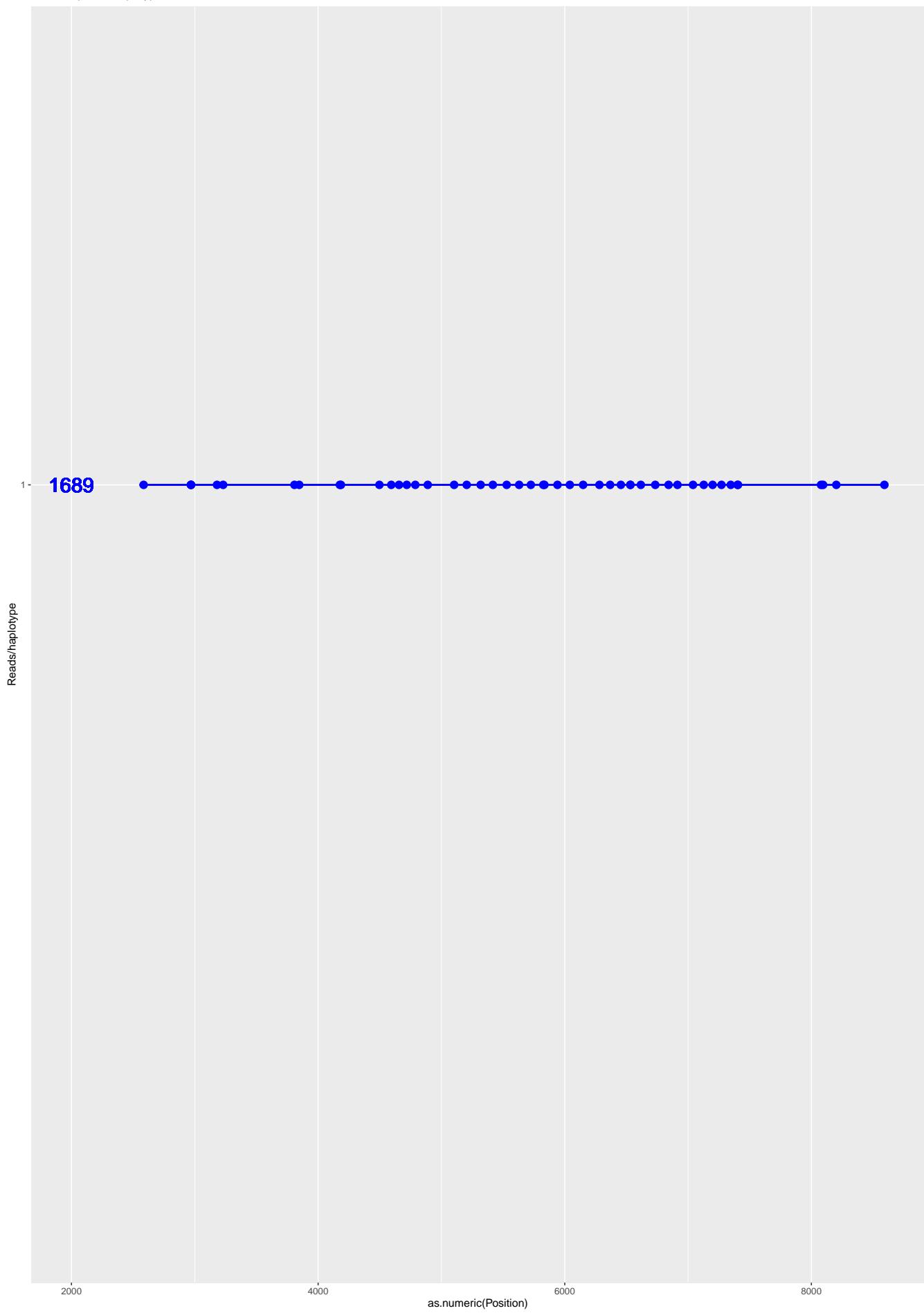


Sample = 221a tetrad = 221 spore = a

Total reads = 1966 PCR=585

haplotypes I began with n[supporting reads] = 1689

most frequent 7 haplotypes.



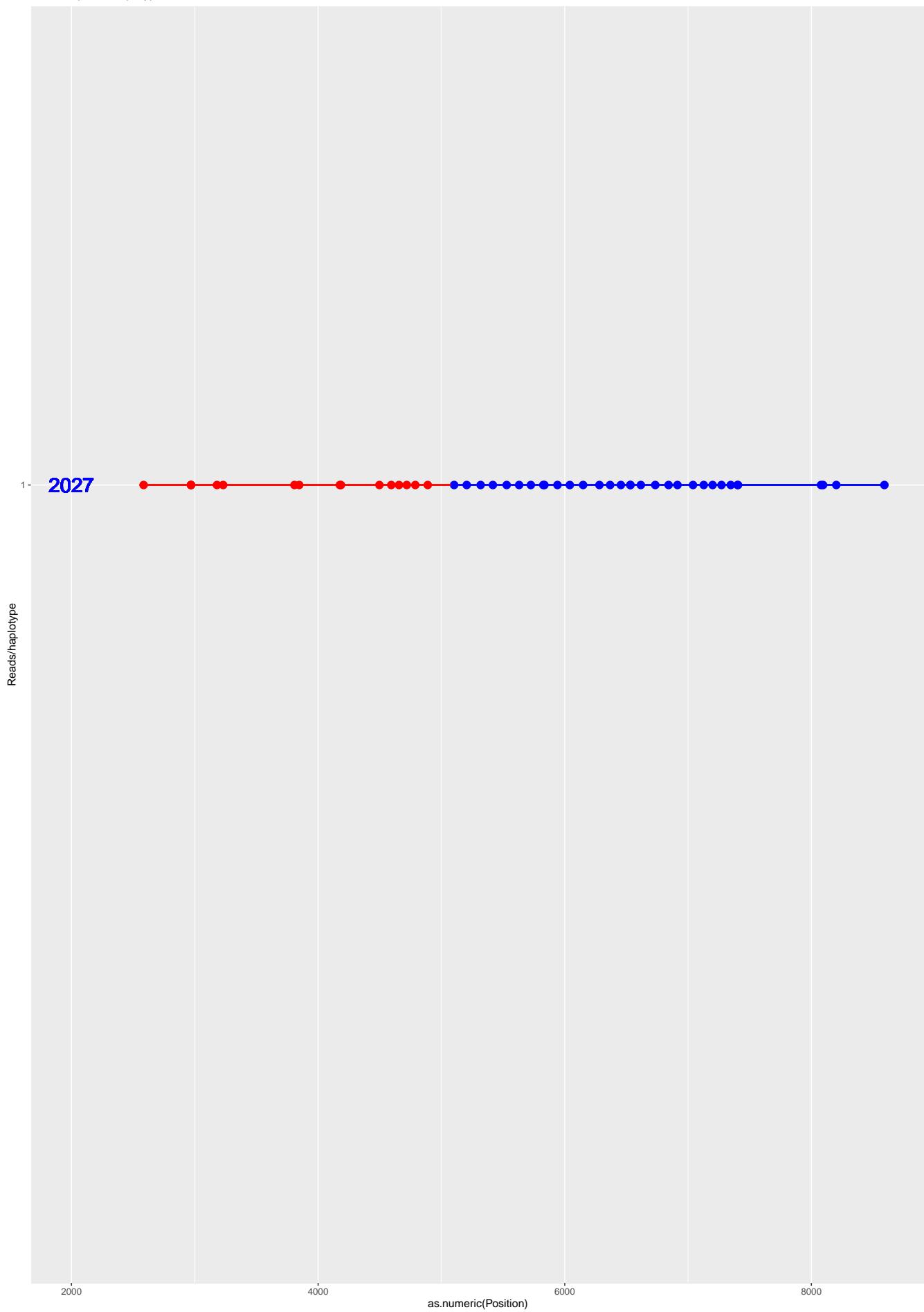
barcode = TCATGAGTCGACACTA & TCAGCTGACGATGTGA

Sample = 221b tetrad = 221 spore = b

Total reads = 2328 PCR=586

haplotypes I began with n[supporting reads] = 2027

most frequent 7 haplotypes.



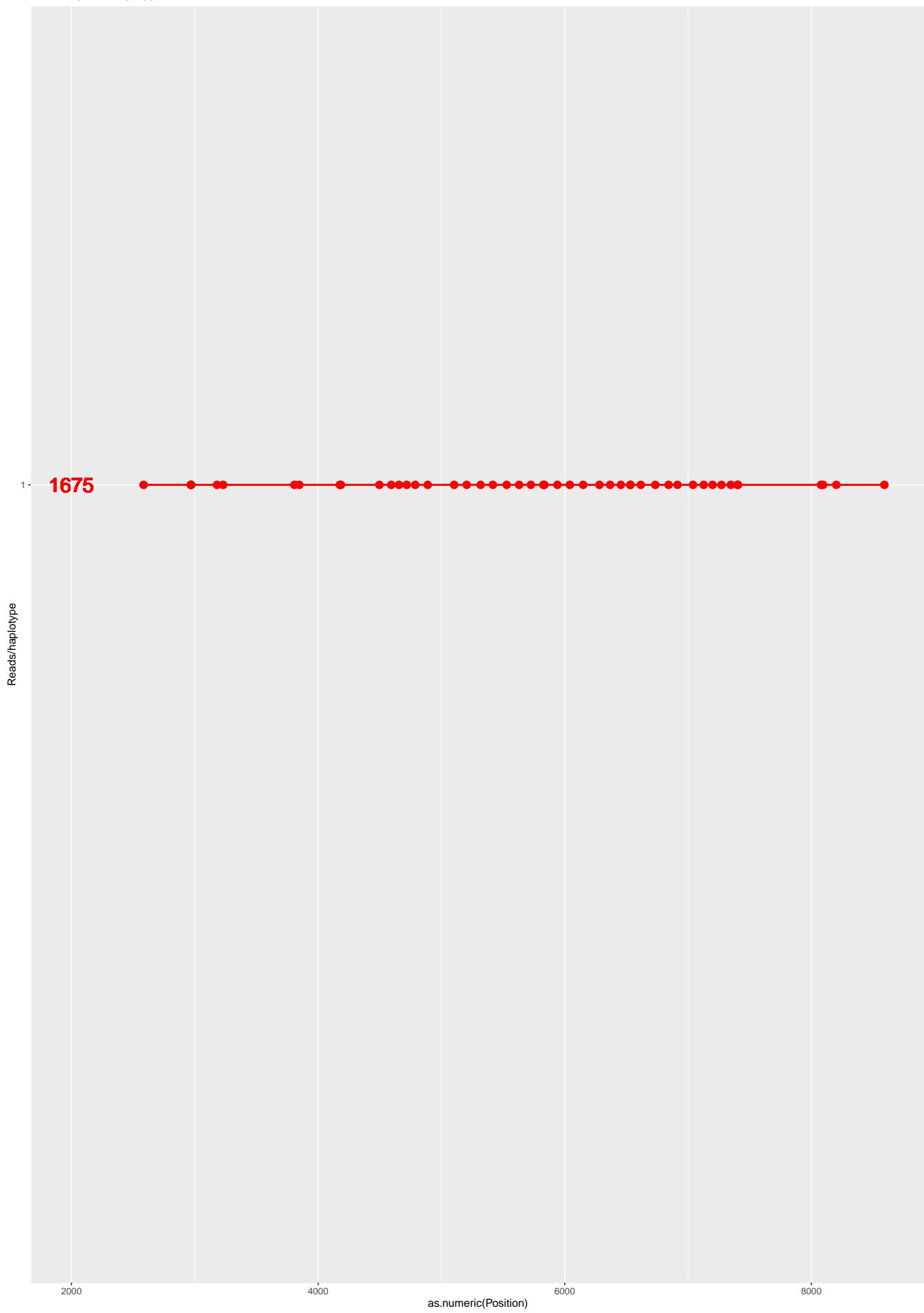
barcode = TCATGAGTCGACACTA & ACTGATGCGCACATGT

Sample = 221c tetrad = 221 spore = c

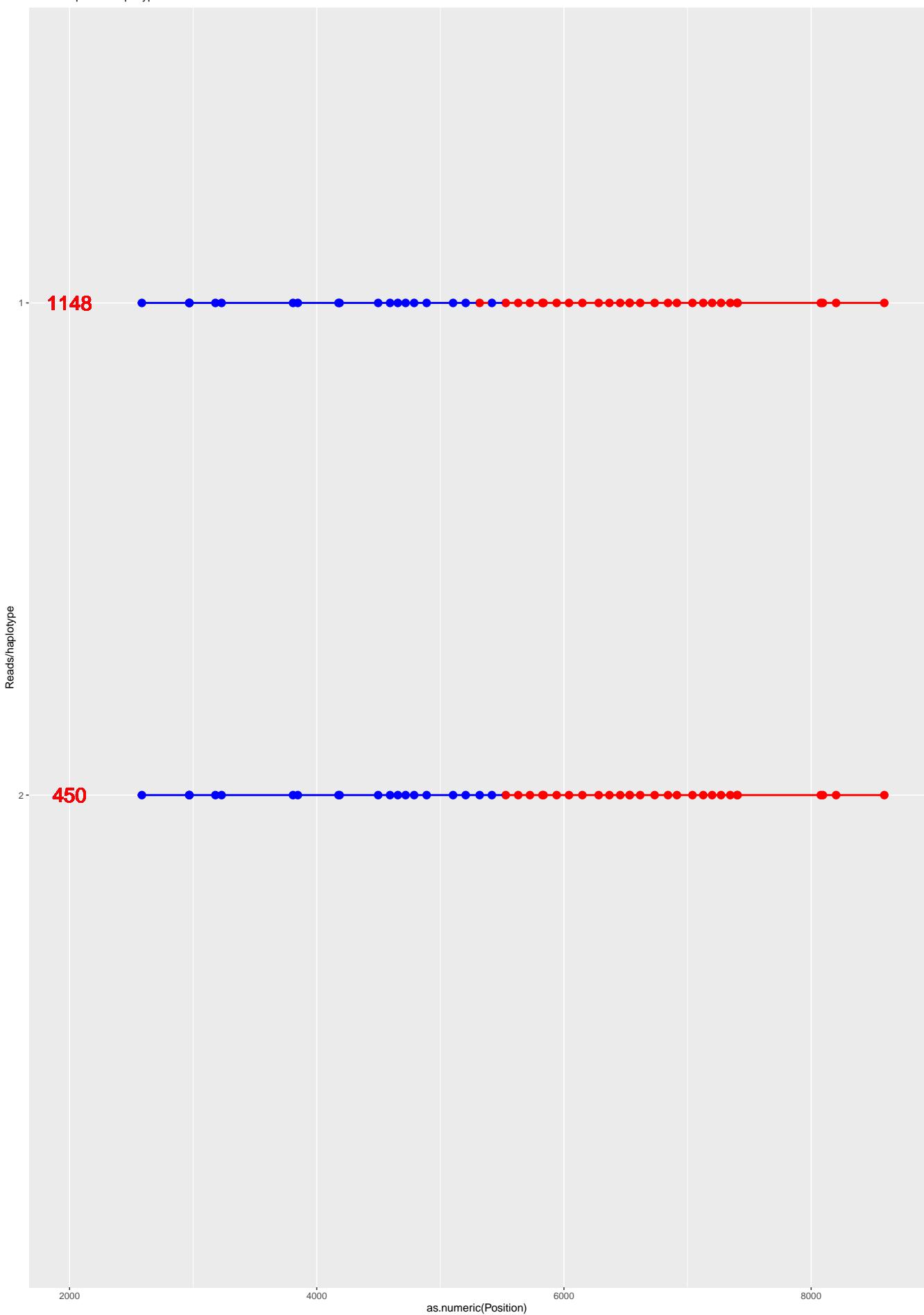
Total reads = 1743 PCR=587

haplotypes I began with n[supporting reads] = 1675

most frequent 7 haplotypes.

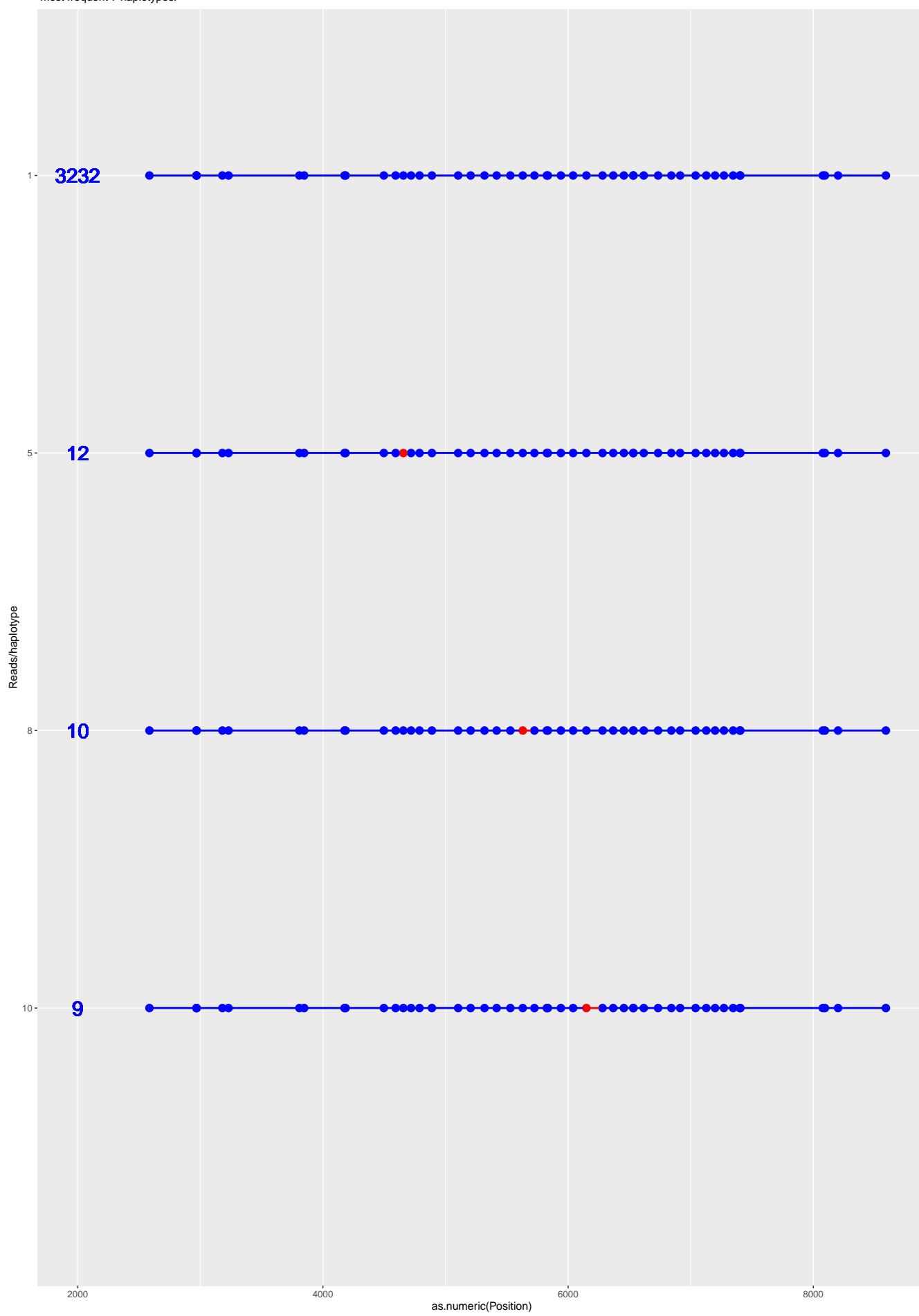


Sample = 221d tetrad = 221 spore = d
Total reads = 2131 PCR=588
haplotypes I began with n[supporting reads] = 450, 1148
most frequent 7 haplotypes.



barcode = TCATGAGTCGACACTA & ATCTACATCACGACTC

Sample = 222a tetrad = 222 spore = a
Total reads = 3724 PCR=589
haplotypes I began with [n(supporting reads)] = 9, 10, 12, 3232
most frequent 7 haplotypes.



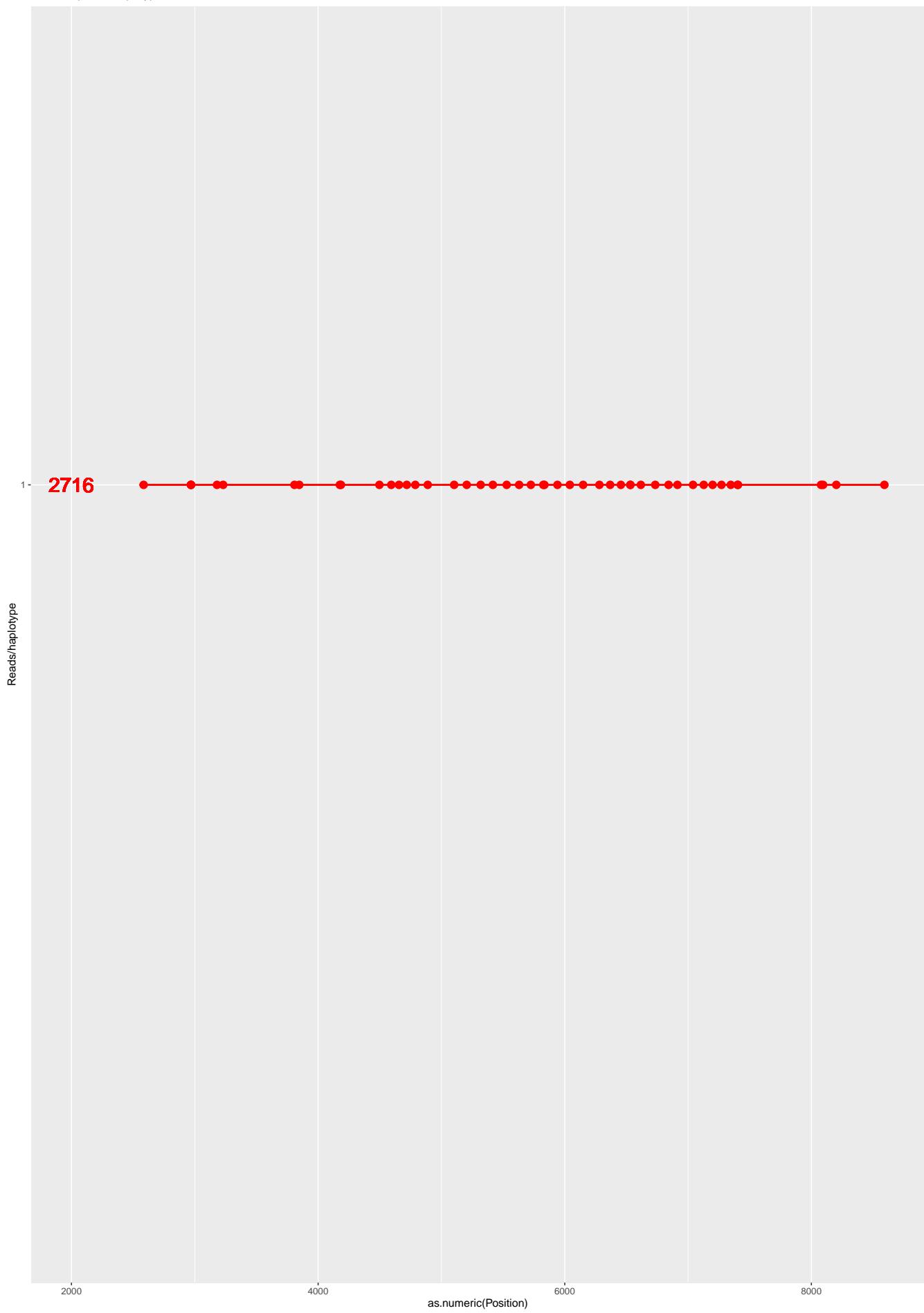
barcode = TCATGAGTCGACACTA & ATATAGTACAGCGTCT

Sample = 222b tetrad = 222 spore = b

Total reads = 2852 PCR=590

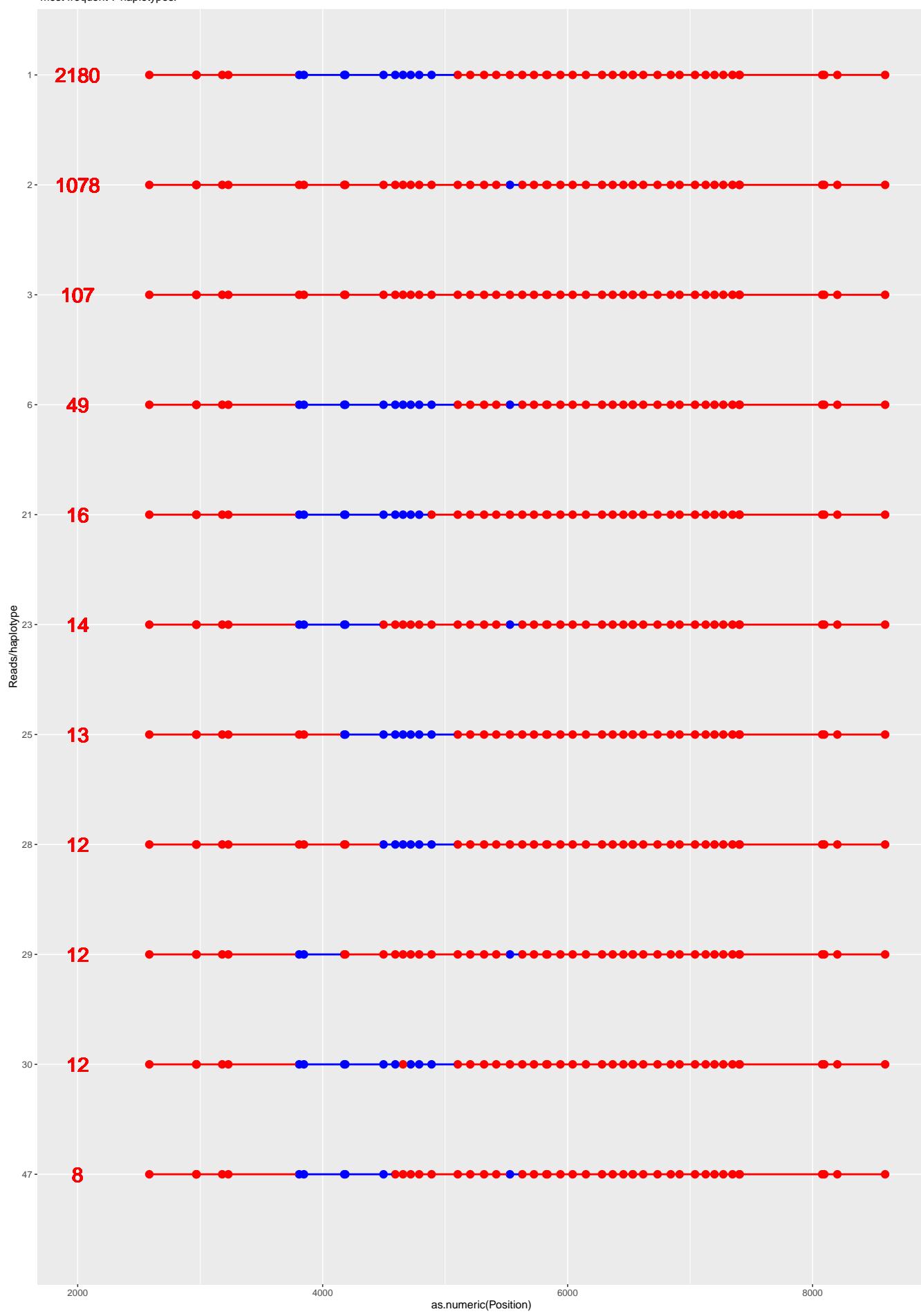
haplotypes I began with n[supporting reads] = 2716

most frequent 7 haplotypes.



barcode = TCATGAGTCGACACTA & GACACGACTAGATCGC

Sample = 222c tetrad = 222 spore = c
 Total reads = 6441 PCR=591
 haplotypes I began with [n(supporting reads)] = 8, 12, 13, 14, 16, 49, 107, 1078, 2180
 most frequent 7 haplotypes.

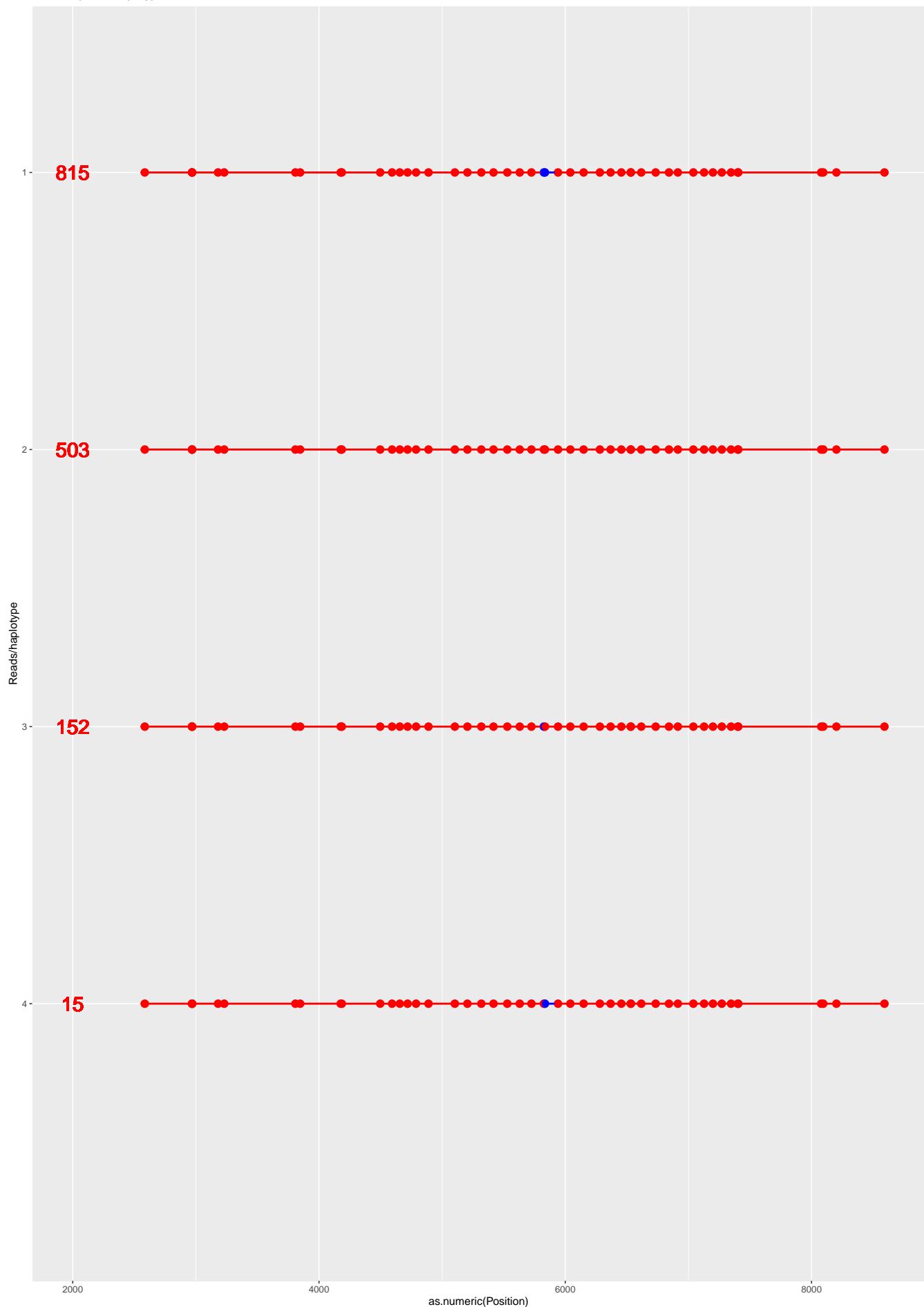


Sample = 226a tetrad = 226 spore = a

Total reads = 1568 PCR=593

haplotypes I began with n[supporting reads] = 15, 152, 503, 815

most frequent 7 haplotypes.



barcode = TATCTATCGTATAACGC & TCAGCTGACGATGTGA

Sample = 226b tetrad = 226 spore = b
Total reads = 2648 PCR=594
haplotypes I began with [n|supporting reads] = 8, 10, 2282
most frequent 7 haplotypes.

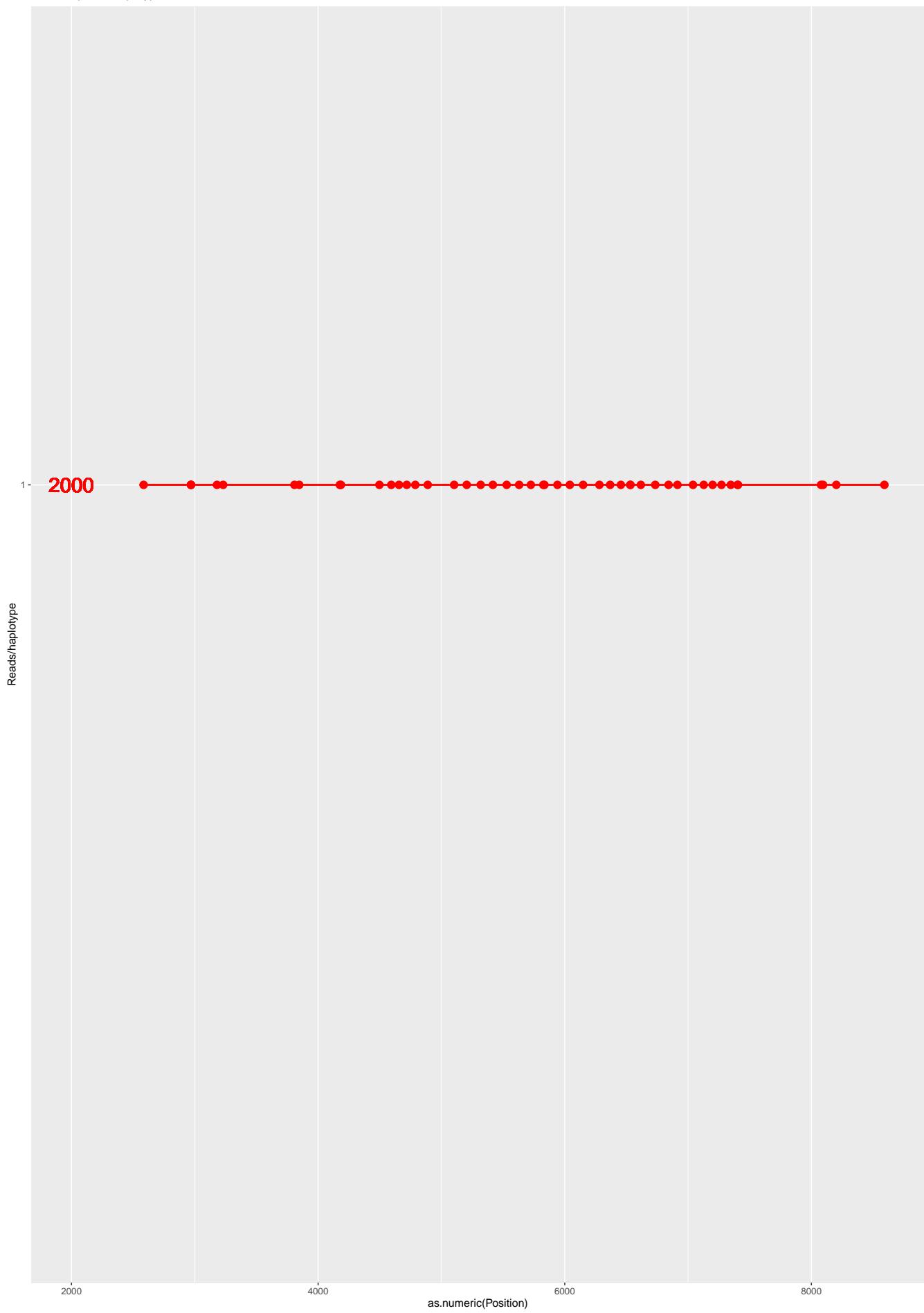


Sample = 226c tetrad = 226 spore = c

Total reads = 2104 PCR=595

haplotypes I began with n[supporting reads] = 2000

most frequent 7 haplotypes.



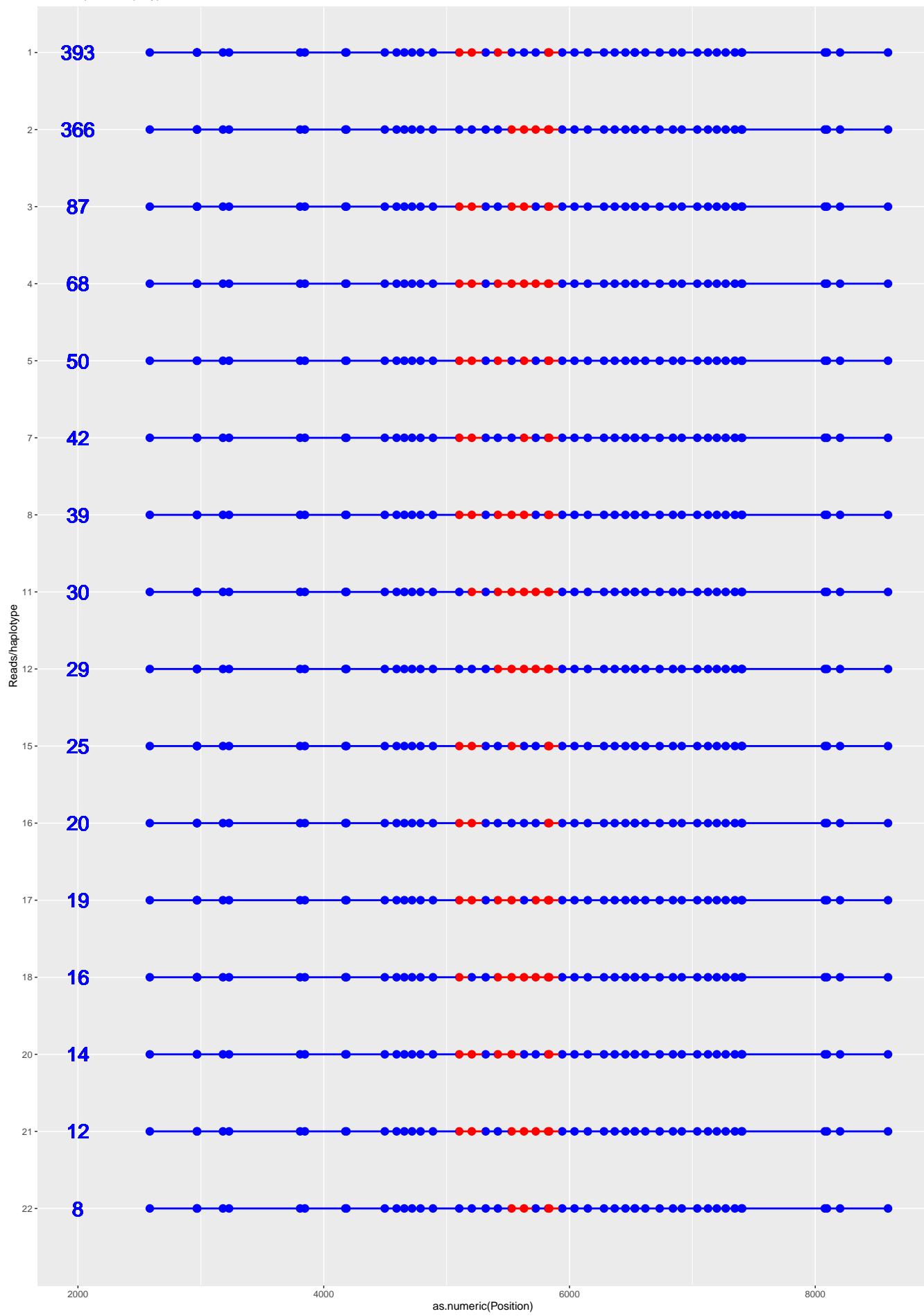
barcode = TATCTATCGTATAACGC & CTACTCTCAGCAGTG

Sample = 226d tetrad = 226 spore = d

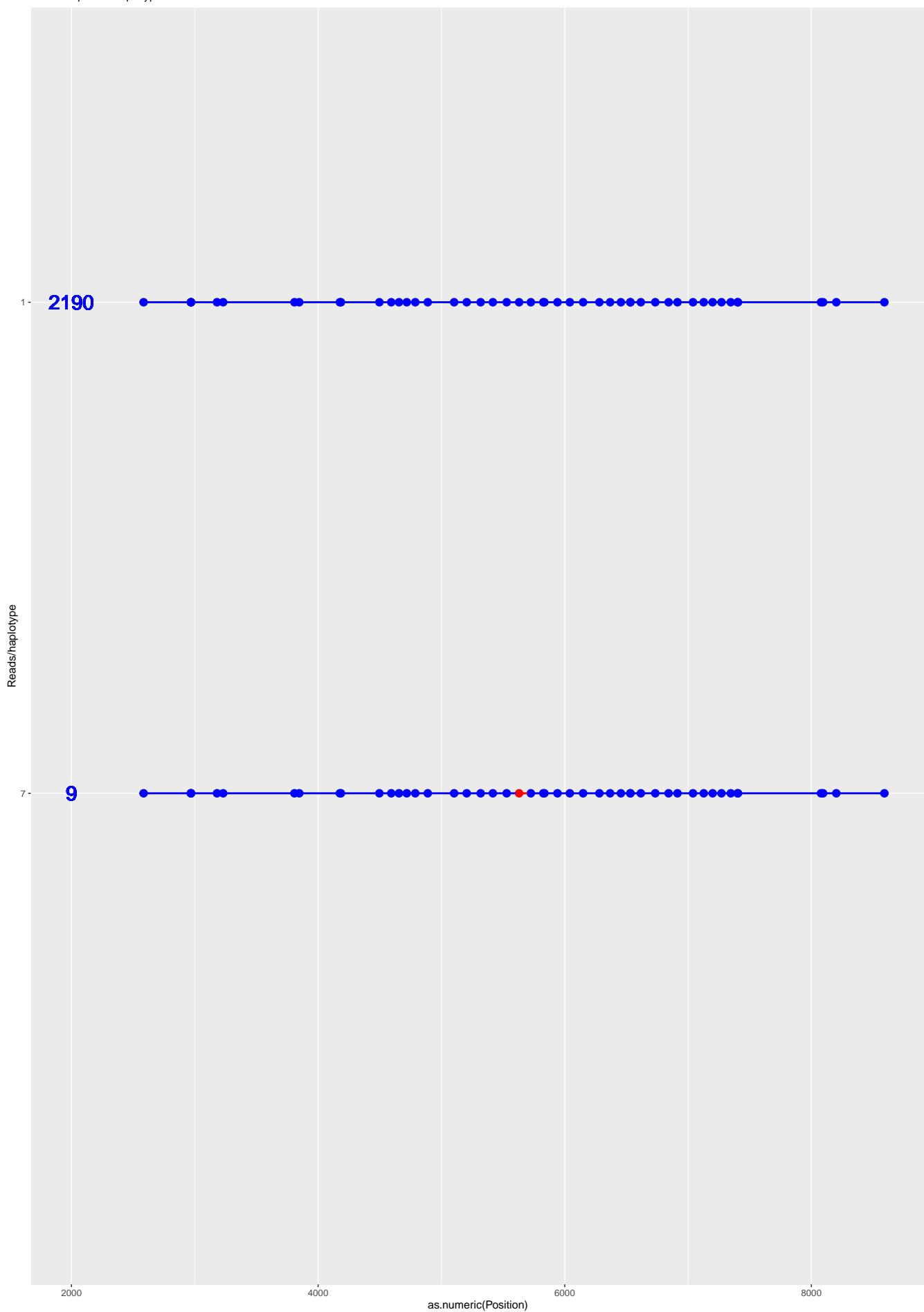
Total reads = 1672 PCR=596

haplotypes I began with [n(supporting reads)] = 8, 12, 14, 16, 19, 20, 25, 29, 30, 39, 42, 50, 68, 87, 366, 393

most frequent 7 haplotypes.

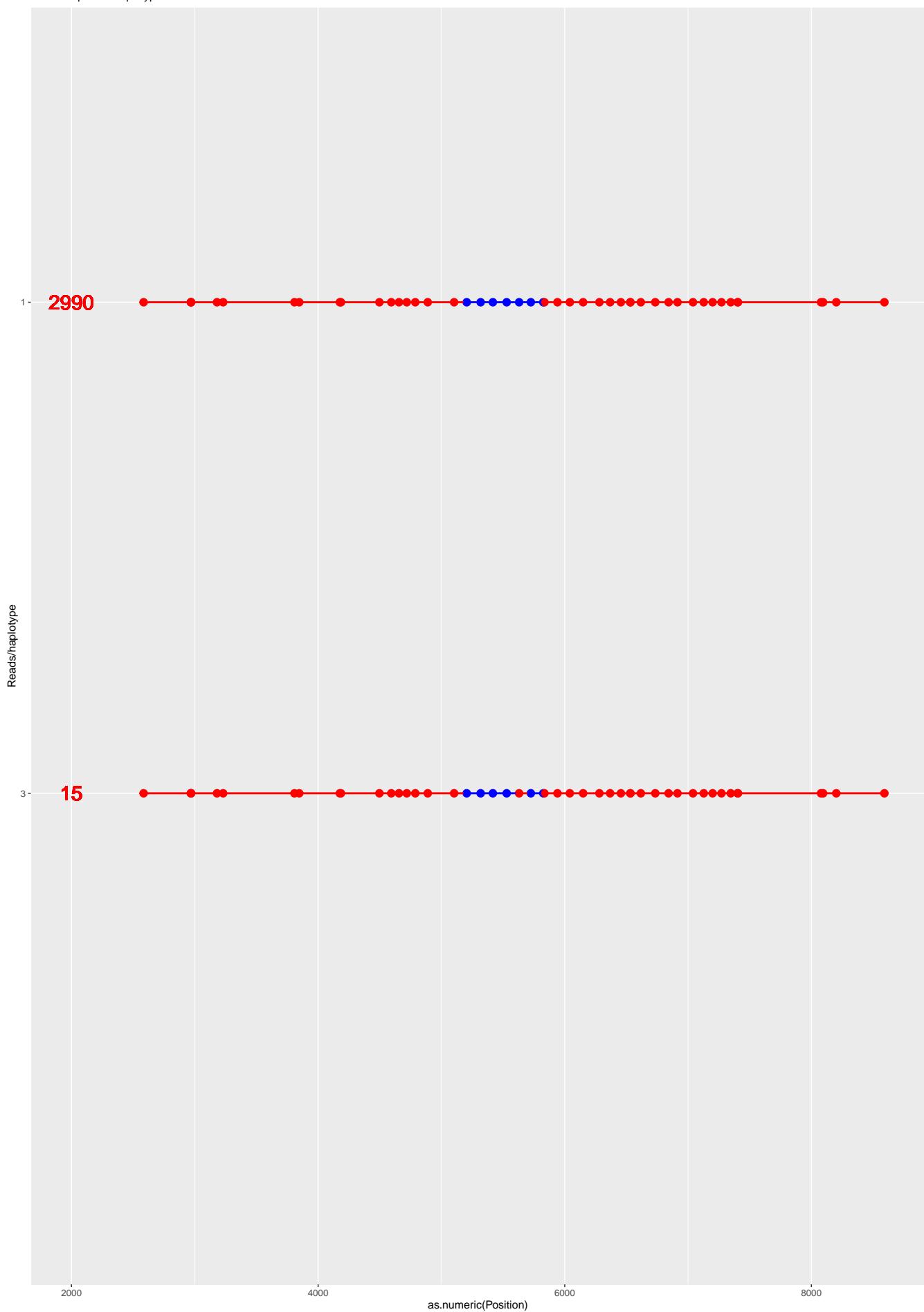


Sample = 228c tetrad = 228 spore = c
Total reads = 2545 PCR=599
haplotypes I began with n[supporting reads] = 9, 2190
most frequent 7 haplotypes.



barcode = TATCTATCGTATAACGC & TACGAGTCTGTACATAC

Sample = 229a tetrad = 229 spore = a
Total reads = 3307 PCR=601
haplotypes I began with n[supporting reads] = 15, 2990
most frequent 7 haplotypes.



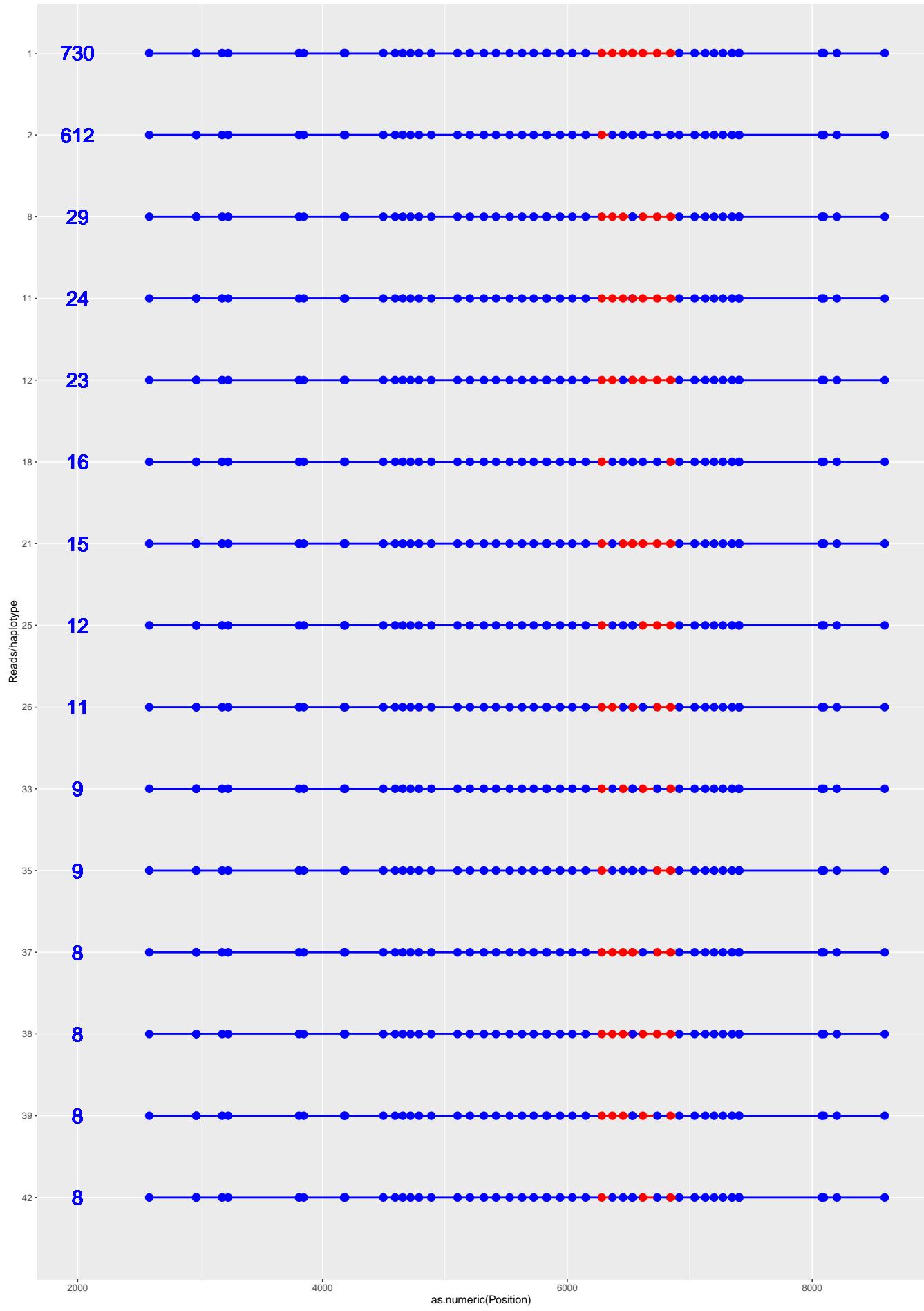
barcode = ATCACACTGCATCTGA & TCAGCTGACGATGTGA

Sample = 229b tetrad = 229 spore = b

Total reads = 3003 PCR=602

haplotypes I began with [n(supporting reads)] = 8, 9, 11, 12, 15, 16, 23, 24, 29, 612, 730

most frequent 7 haplotypes.



barcode = ATCACACTGCACTGA & ACTGATGCGCACATGT

Sample = 229c tetrad = 229 spore = c

Total reads = 3544 PCR=603

haplotypes I began with n[supporting reads] = 10, 3047

most frequent 7 haplotypes.



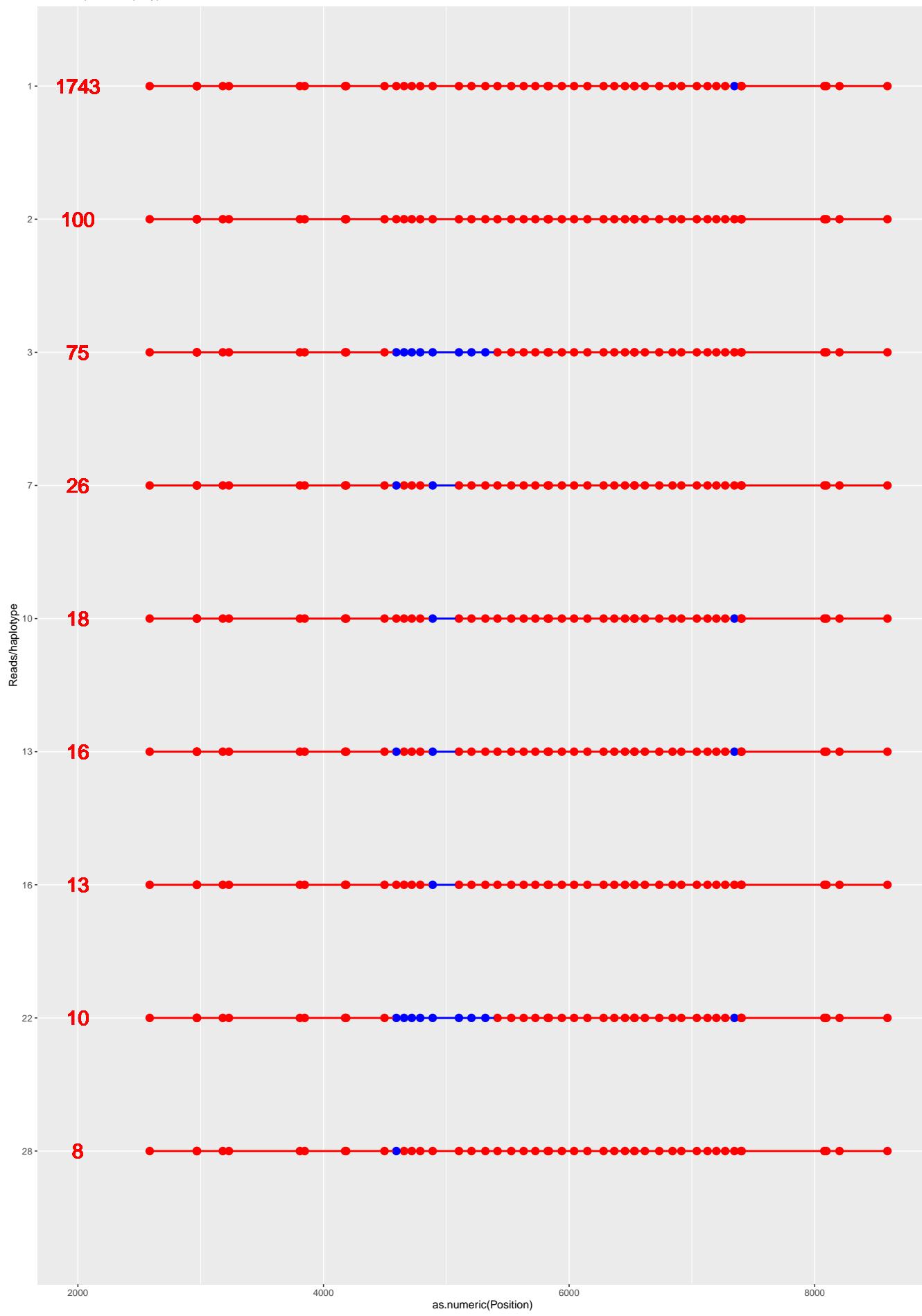
barcode = ATCACACTGCATCTGA & CTACTCTCAGCAGTGA

Sample = 229d tetrad = 229 spore = d

Total reads = 3068 PCR=604

haplotypes I began with [n(supporting reads)] = 8, 10, 13, 16, 18, 26, 75, 100, 1743

most frequent 7 haplotypes.



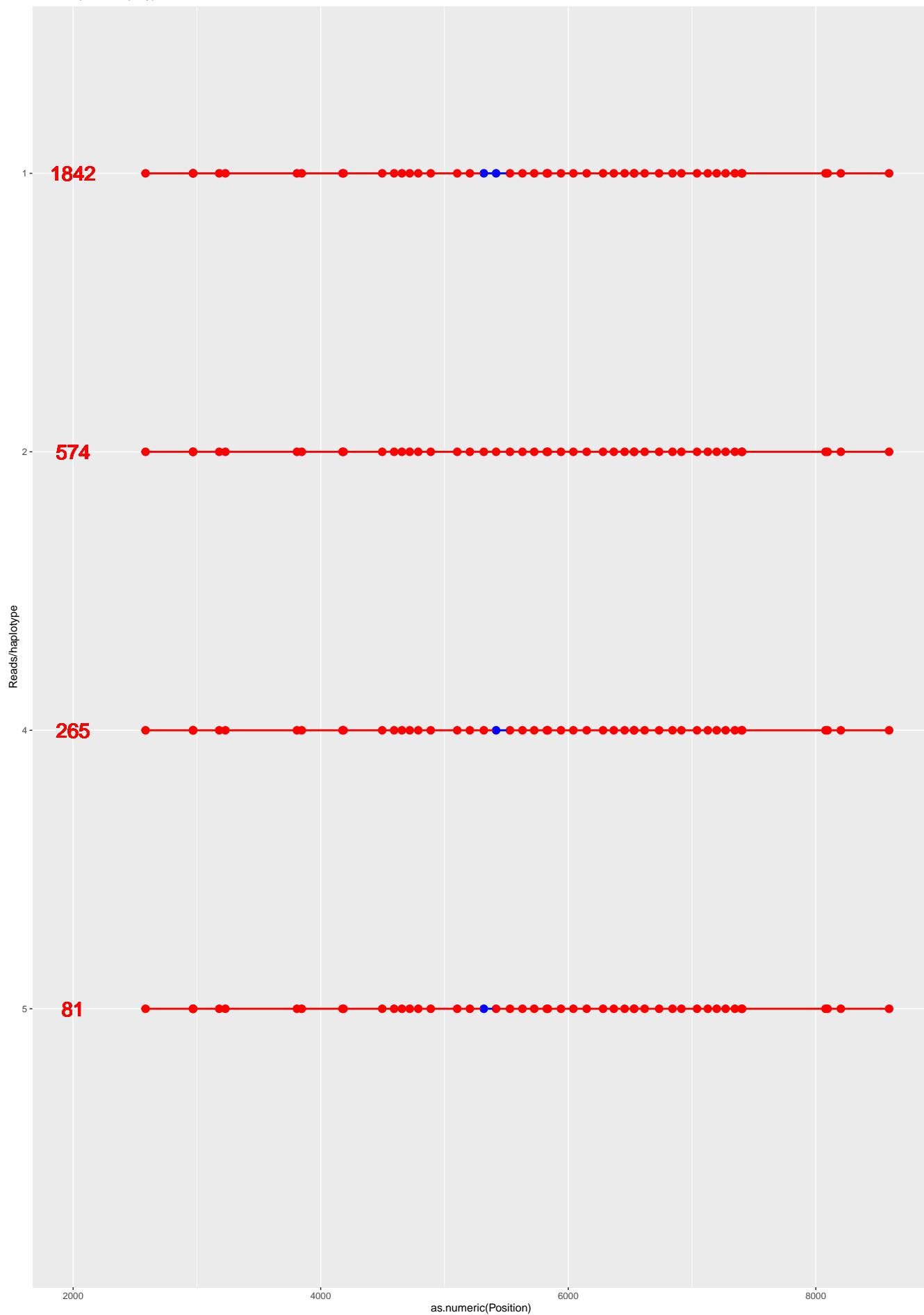
barcode = ATCACACTGCATCTGA & ATCTACATCACGACTC

Sample = 232a tetrad = 232 spore = a

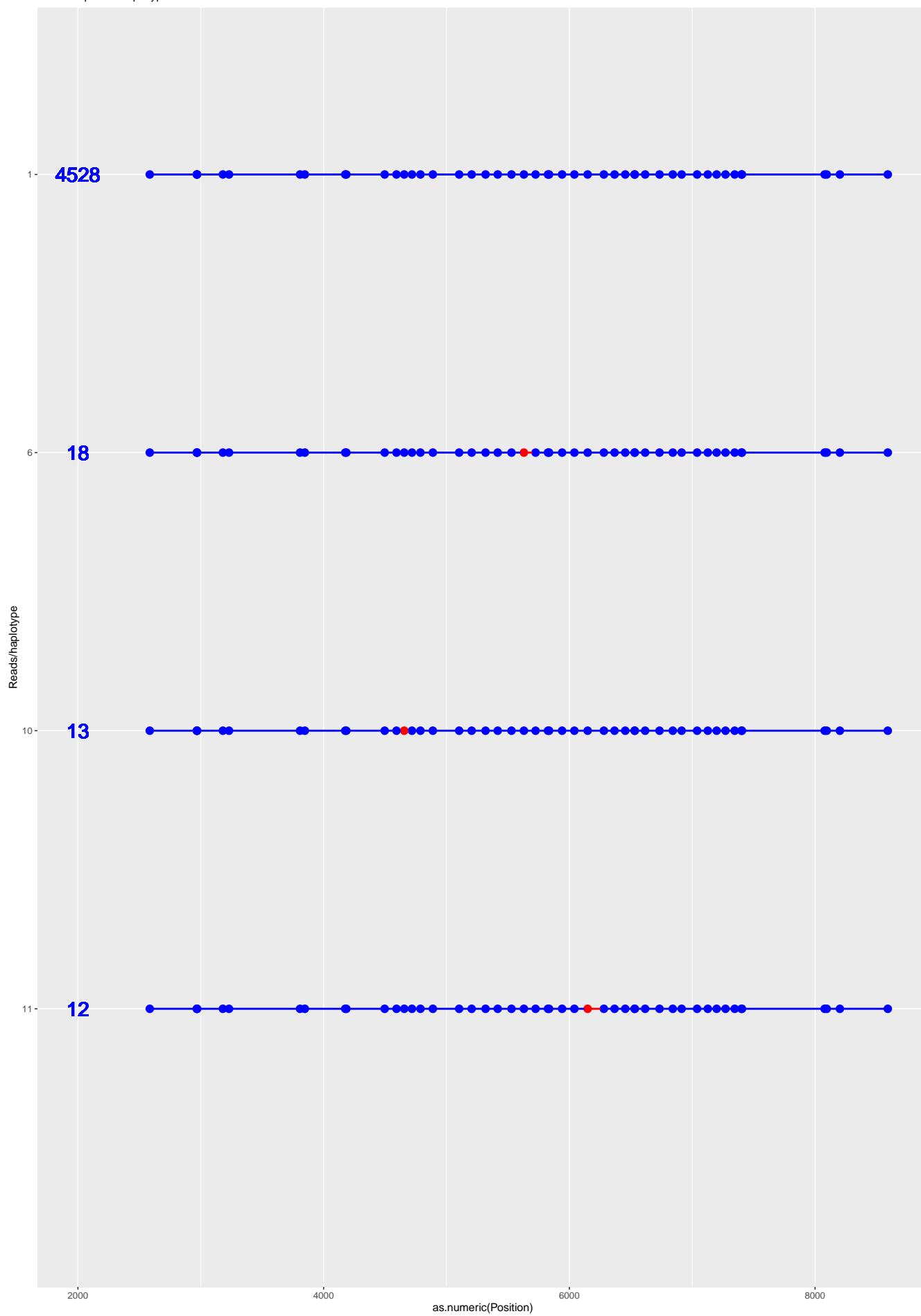
Total reads = 3290 PCR=609

haplotypes I began with n[supporting reads] = 81, 265, 574, 1842

most frequent 7 haplotypes.



Sample = 232b tetrad = 232 spore = b
Total reads =5275 PCR=610
haplotypes I began with [n|supporting reads] = 12, 13, 18, 4528
most frequent 7 haplotypes.

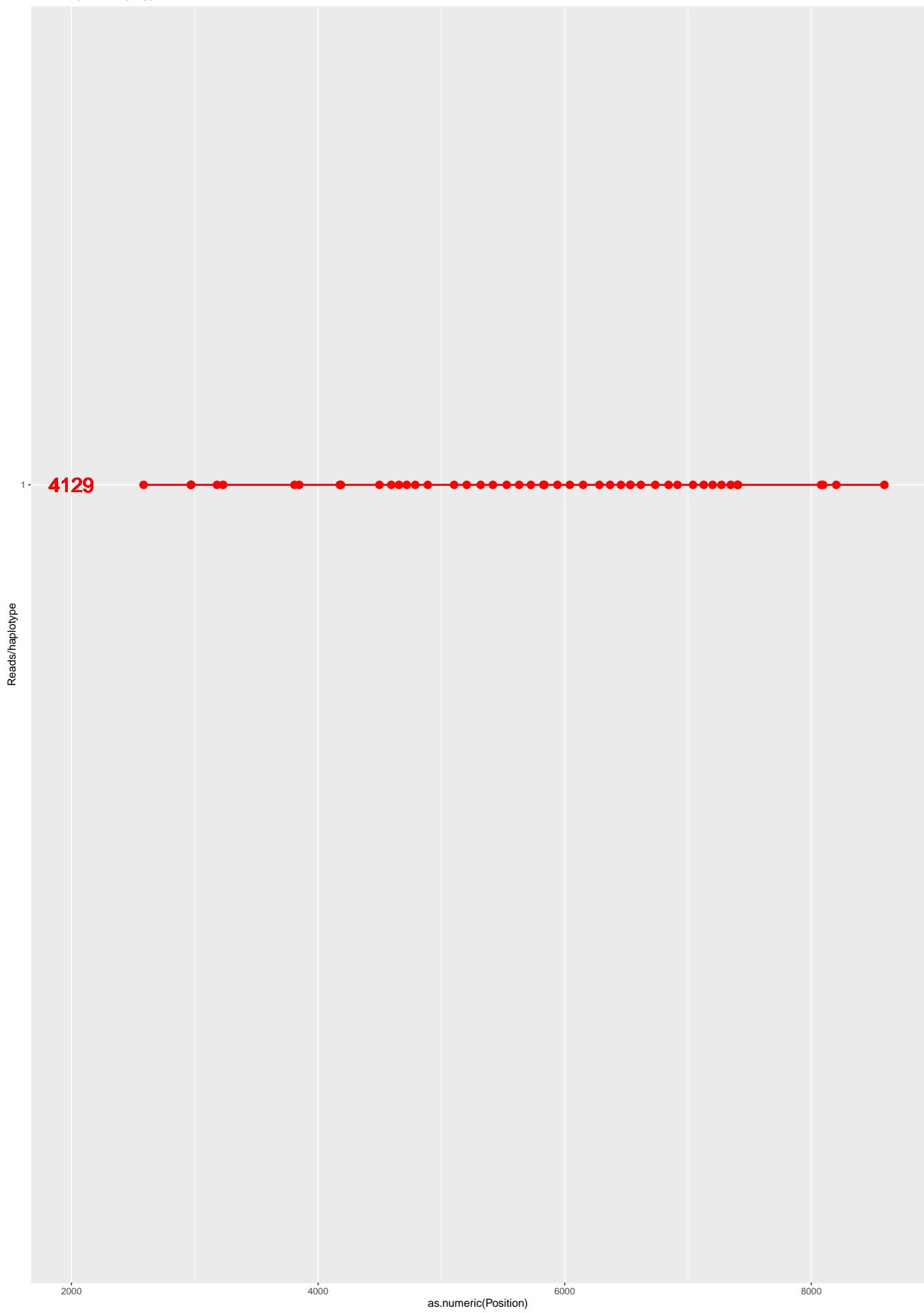


Sample = 232c tetrad = 232 spore = c

Total reads = 4301 PCR=611

haplotypes I began with n[supporting reads] = 4129

most frequent 7 haplotypes.



barcode = ACGTACGCTCGTCATA & CTACTCTCAGCAGTGA

Sample = 232d tetrad = 232 spore = d
Total reads = 2985 PCR=612
haplotypes I began with n[supporting reads] = 9, 10, 2556
most frequent 7 haplotypes.

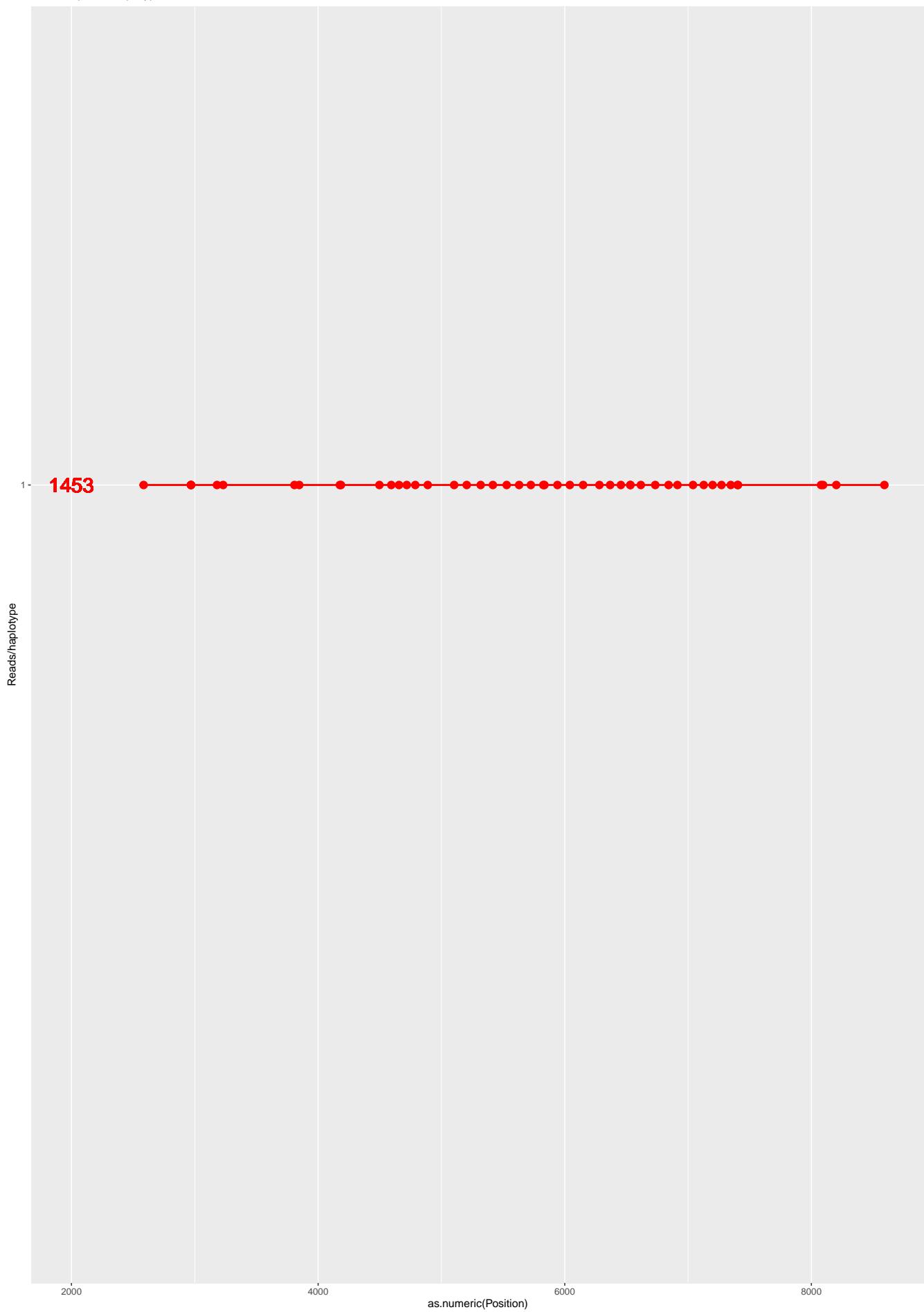


Sample = 233a tetrad = 233 spore = a

Total reads = 1514 PCR=613

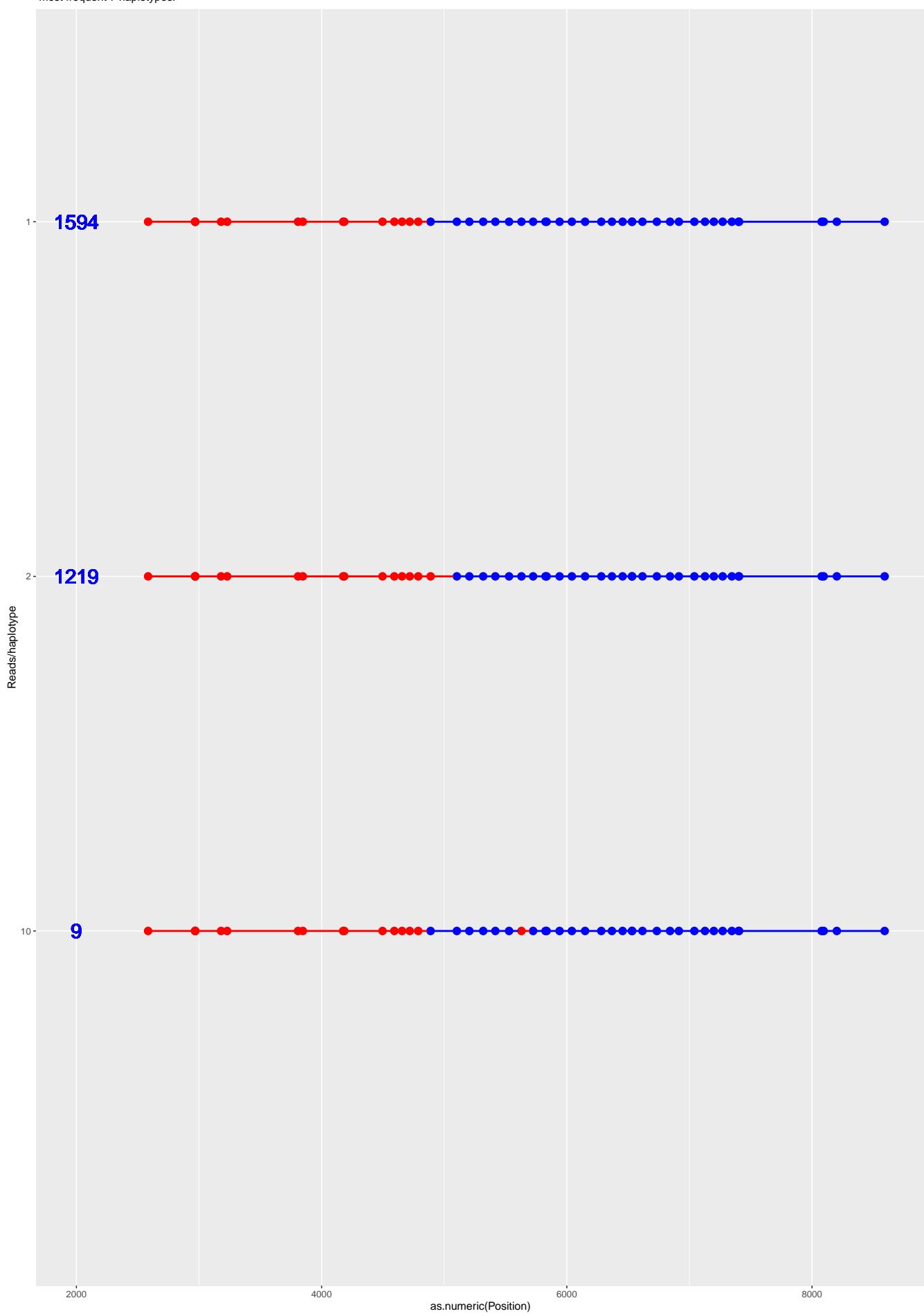
haplotypes I began with n[supporting reads] = 1453

most frequent 7 haplotypes.

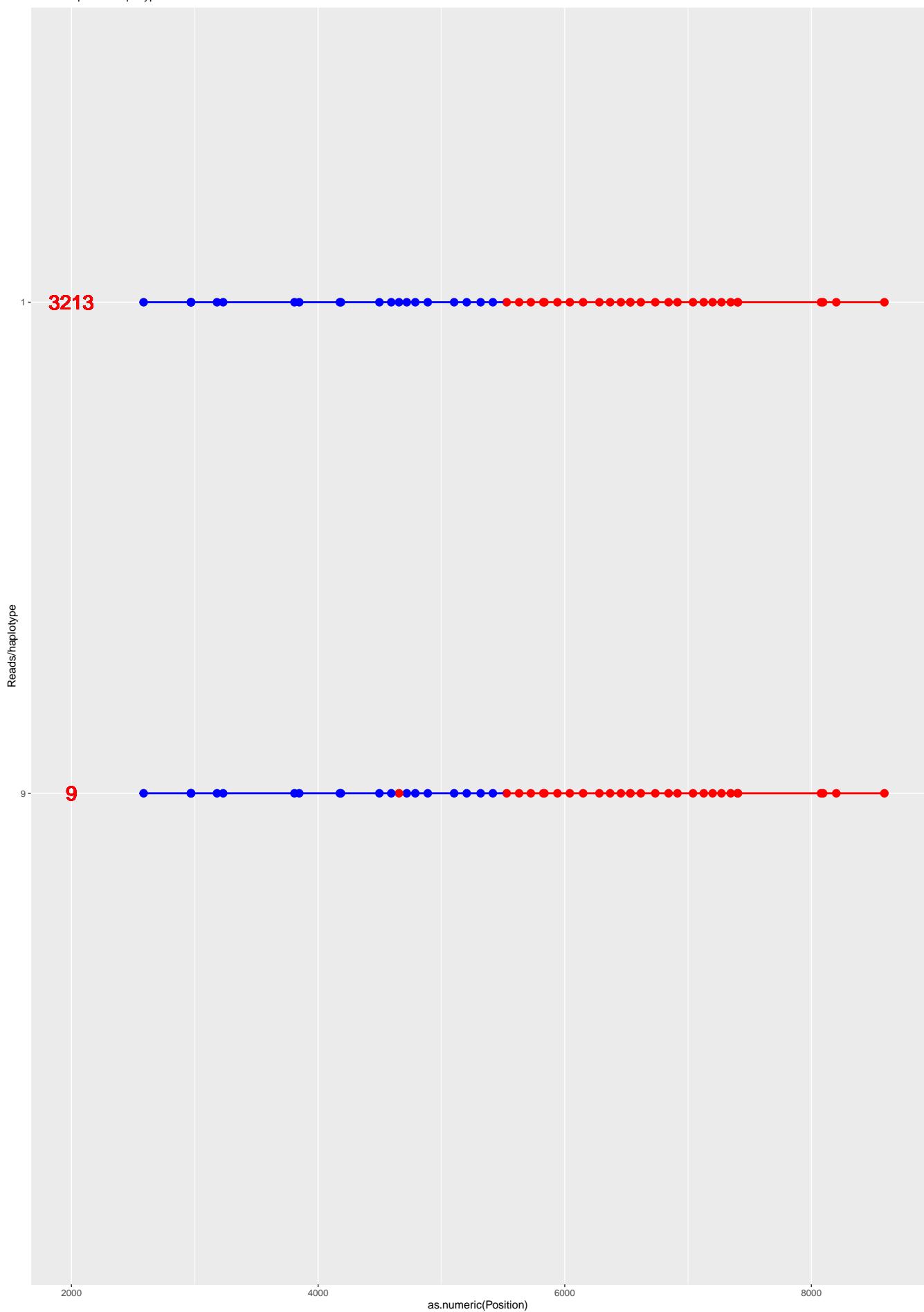


barcode = ACGTACGCTCGTCATA & ATATAGTACAGCGTCT

Sample = 233b tetrad = 233 spore = b
Total reads = 3576 PCR=614
haplotypes I began with [n|supporting reads] = 9, 1219, 1594
most frequent 7 haplotypes.



Sample = 233c tetrad = 233 spore = c
Total reads = 3633 PCR=615
haplotypes I began with n[supporting reads] = 9, 3213
most frequent 7 haplotypes.



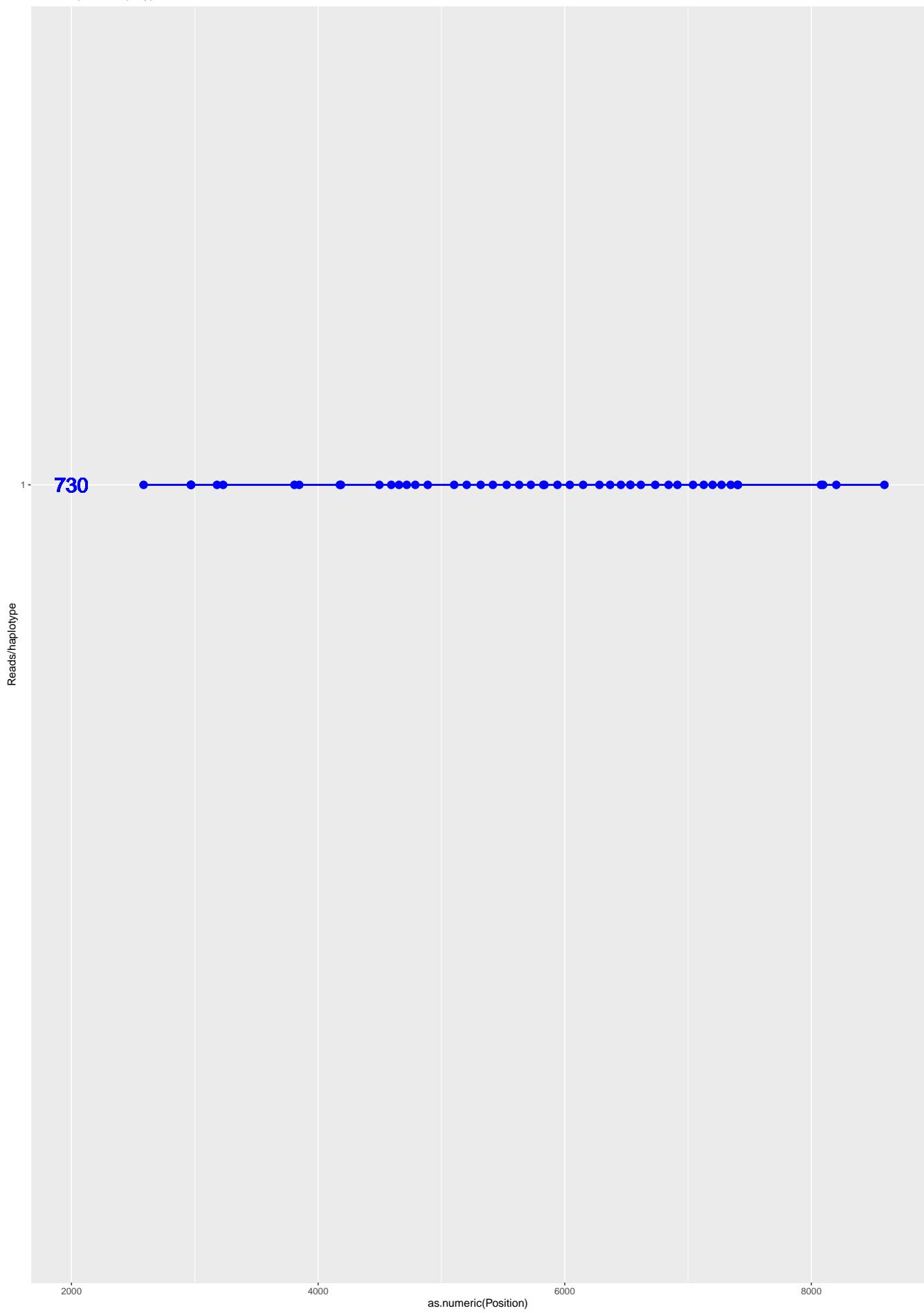
barcode = ACGTACGCTCGTCATA & TACGAGTCTGTCATAC

Sample = 233d tetrad = 233 spore = d

Total reads = 879 PCR=616

haplotypes I began with n[supporting reads] = 730

most frequent 7 haplotypes.



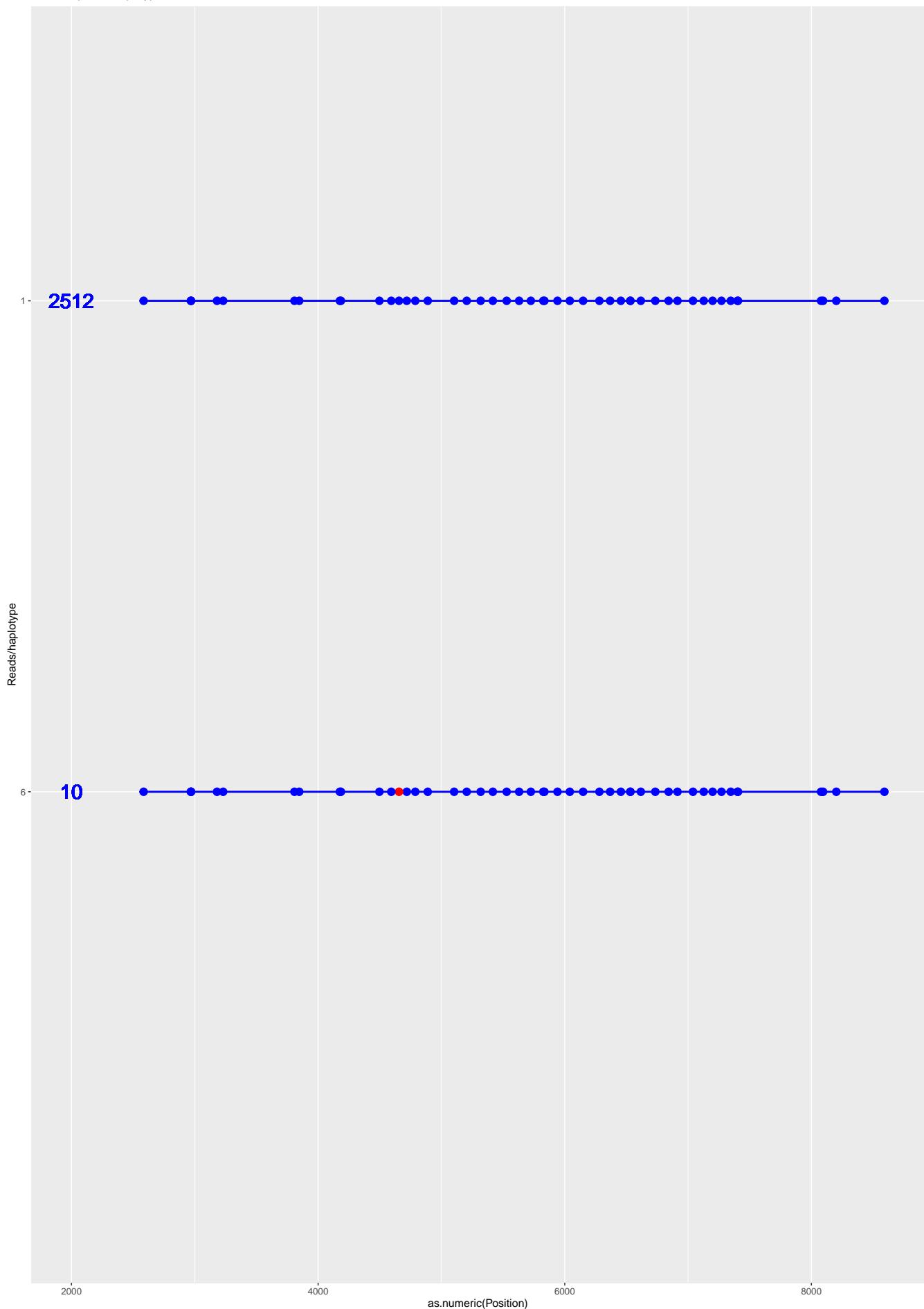
barcode = ACGTACGCTCGTCATA & ACTCAGCTACATAGTG

Sample = 234a tetrad = 234 spore = a

Total reads = 2924 PCR=617

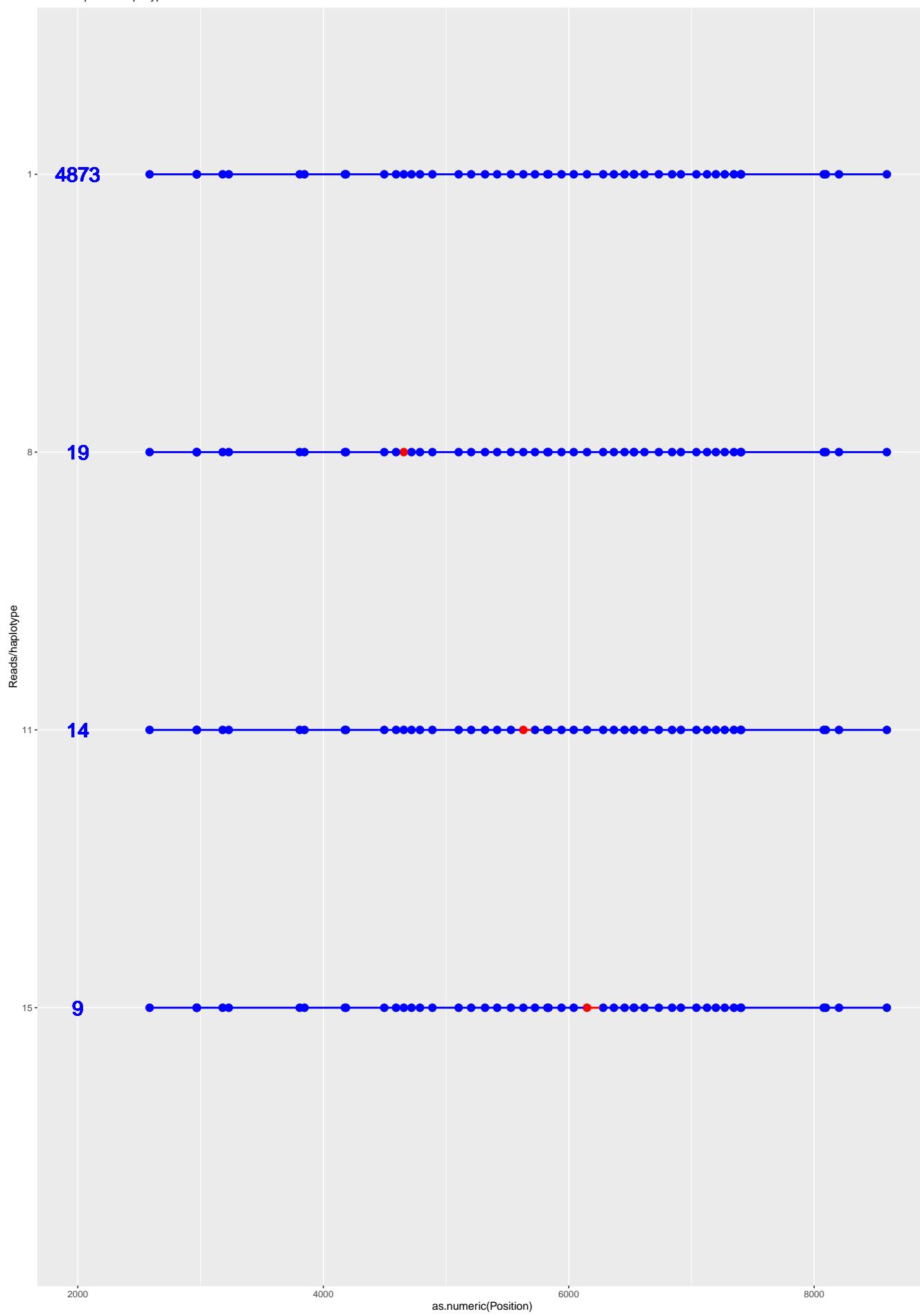
haplotypes I began with n[supporting reads] = 10, 2512

most frequent 7 haplotypes.



barcode = TGTGAGTCAGTACCGCG & TCAGCTGACGATGTGA

Sample = 234b tetrad = 234 spore = b
Total reads =5676 PCR=618
haplotypes I began with [n:supporting reads] = 9, 14, 19, 4873
most frequent 7 haplotypes.



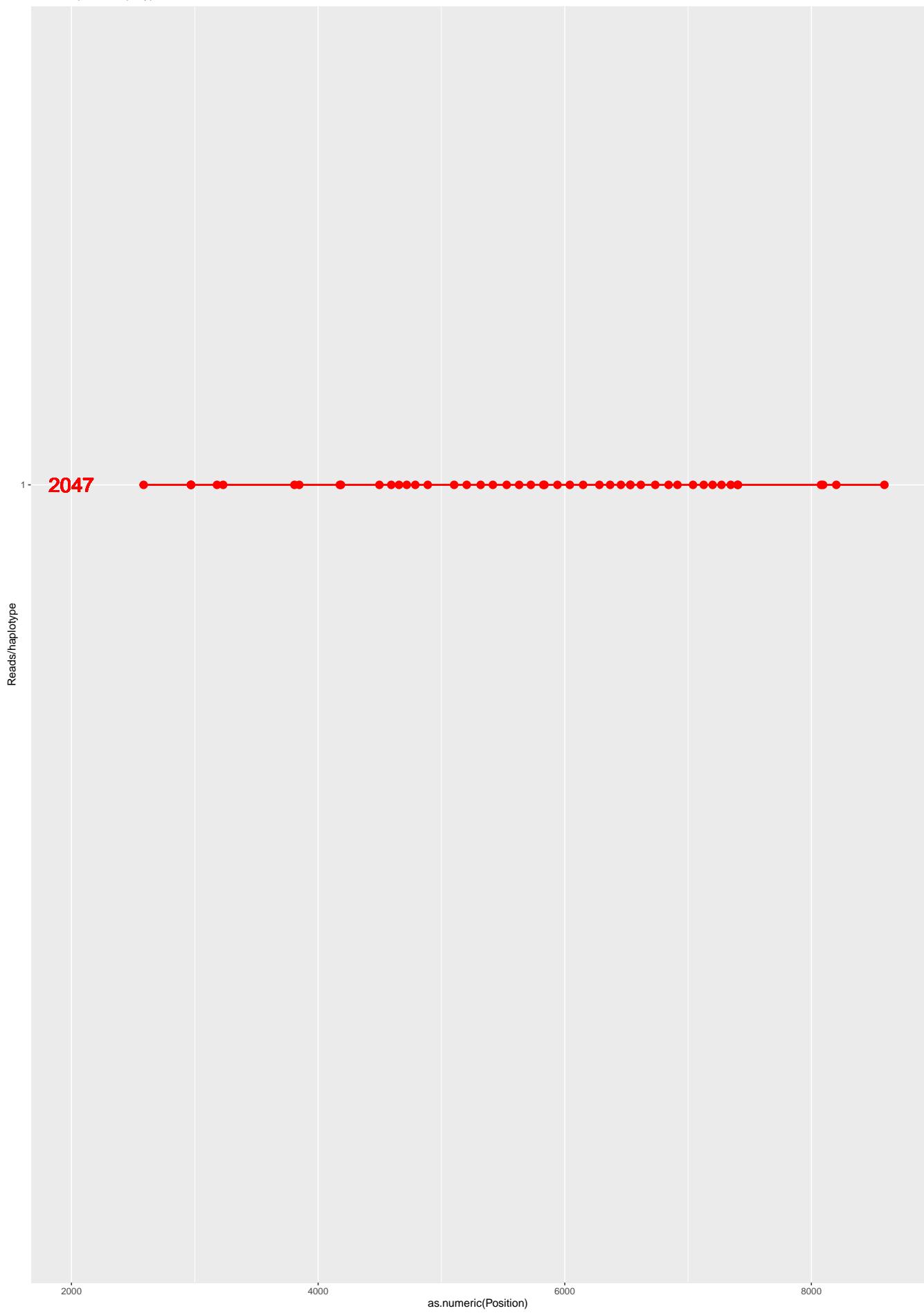
barcode = TGTGAGTCAGTACGCG & ACTGATGCGCACATGT

Sample = 234c tetrad = 234 spore = c

Total reads = 2132 PCR=619

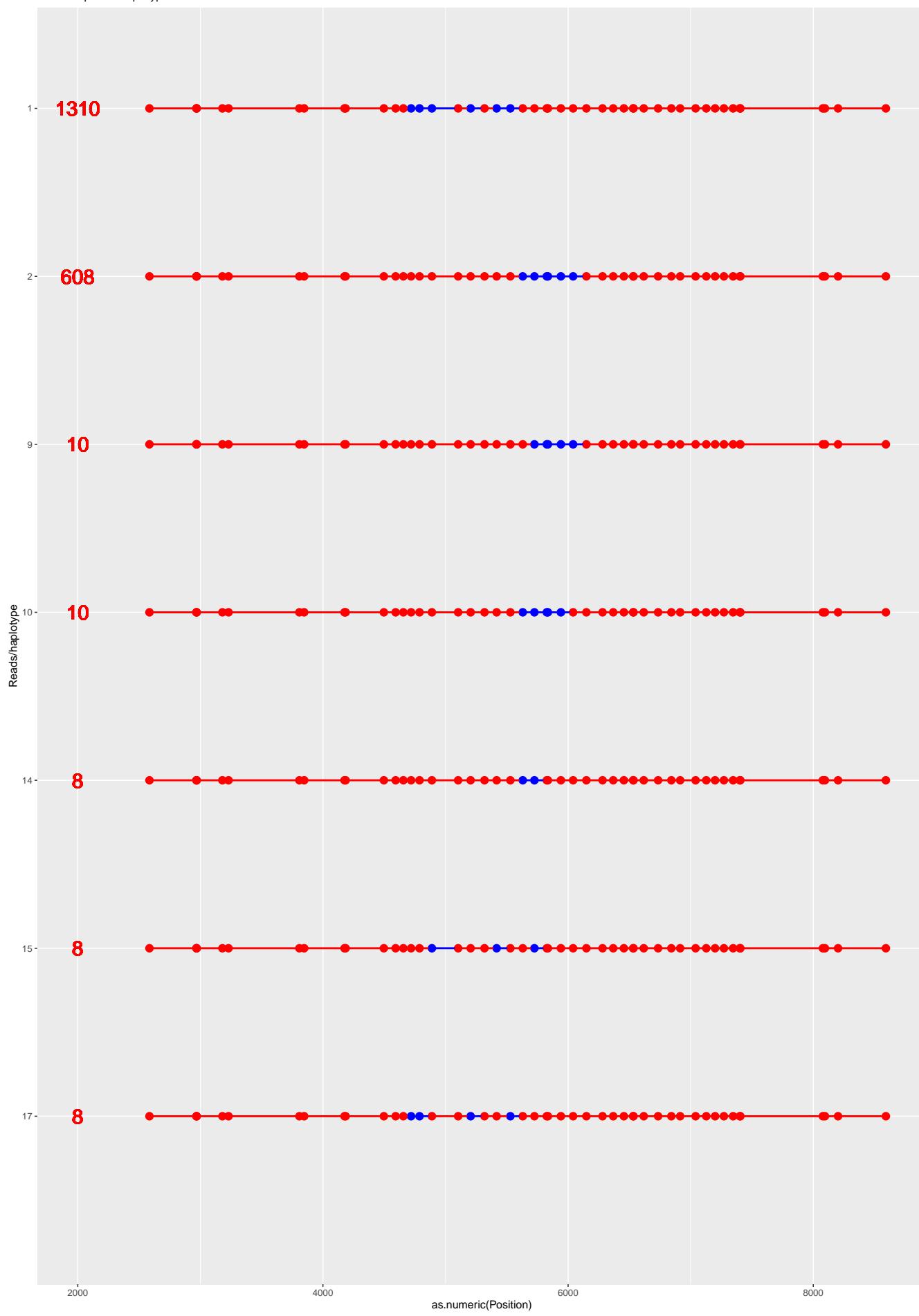
haplotypes I began with n[supporting reads] = 2047

most frequent 7 haplotypes.

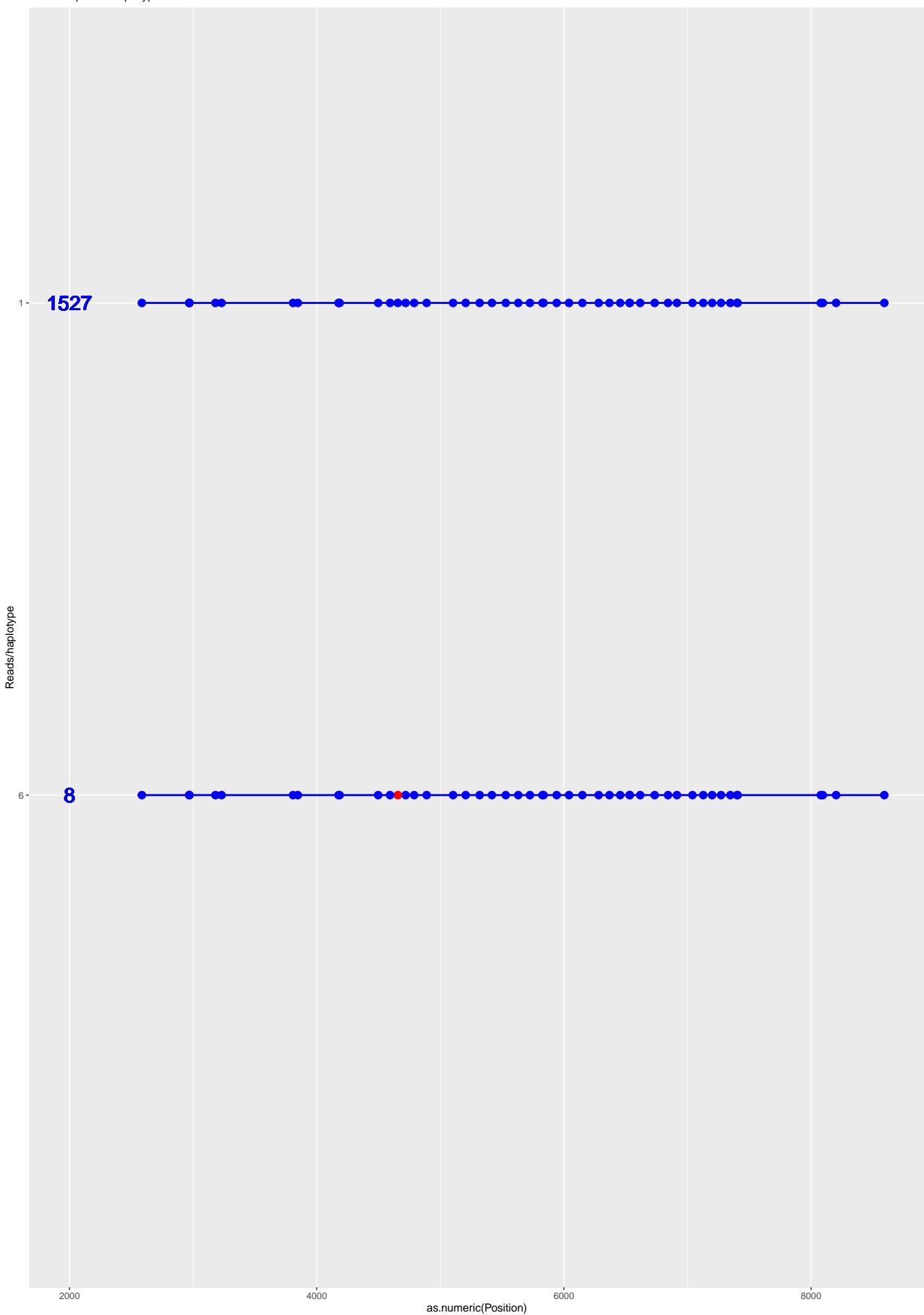


barcode = TGTGAGTCAGTACGGCG & CTACTCTCAGCAGTGA

Sample = 234d tetrad = 234 spore = d
 Total reads = 3142 PCR=620
 haplotypes I began with [n(supporting reads)] = 8, 10, 608, 1310
 most frequent 7 haplotypes.



Sample = 238a tetrad = 238 spore = a
Total reads = 1781 PCR=625
haplotypes I began with n[supporting reads] = 8, 1527
most frequent 7 haplotypes.

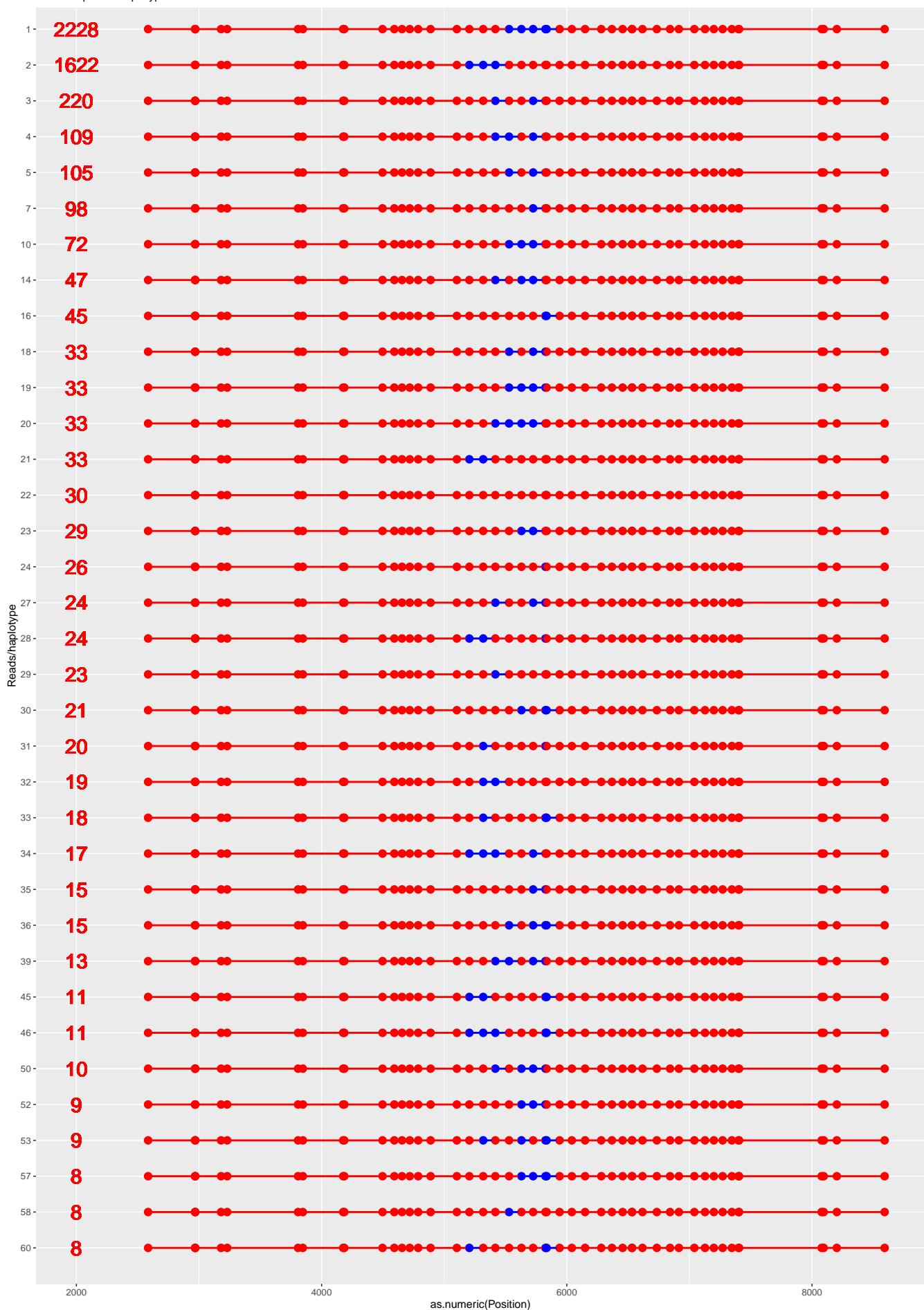


Sample = 238b tetrad = 238 spore = b

Total reads = 6483 PCR=626

haplotypes I began with [n(supporting reads)] = 8, 9, 10, 11, 13, 15, 17, 18, 19, 20, 21, 23, 24, 26, 29, 30, 33, 45, 47, 72, 98, 105, 109, 220, 1622, 2228

most frequent 7 haplotypes.



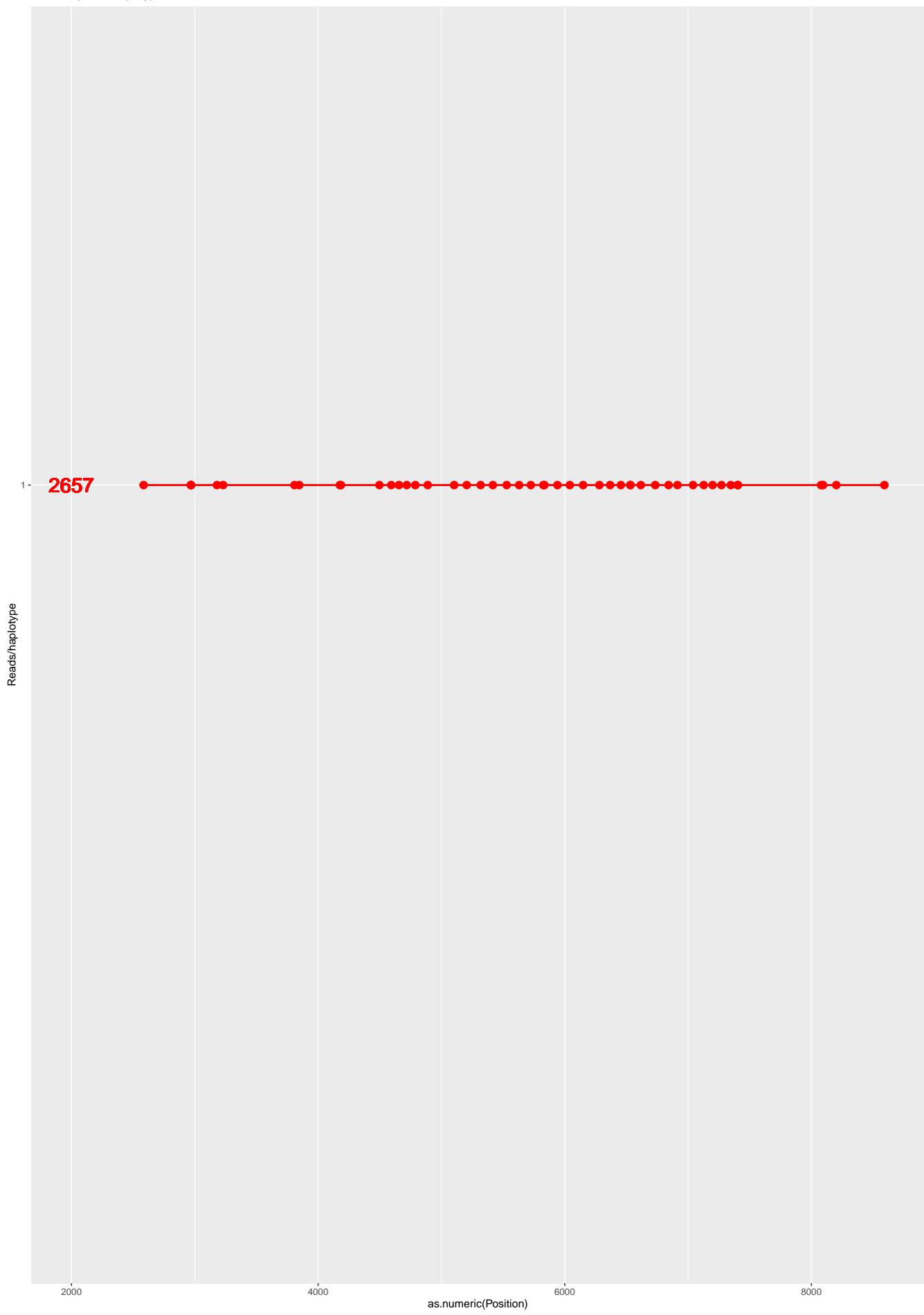
barcode = AGAGACACGATACTCA & ACTGATGCGCACATGT

Sample = 238c tetrad = 238 spore = c

Total reads = 2754 PCR=627

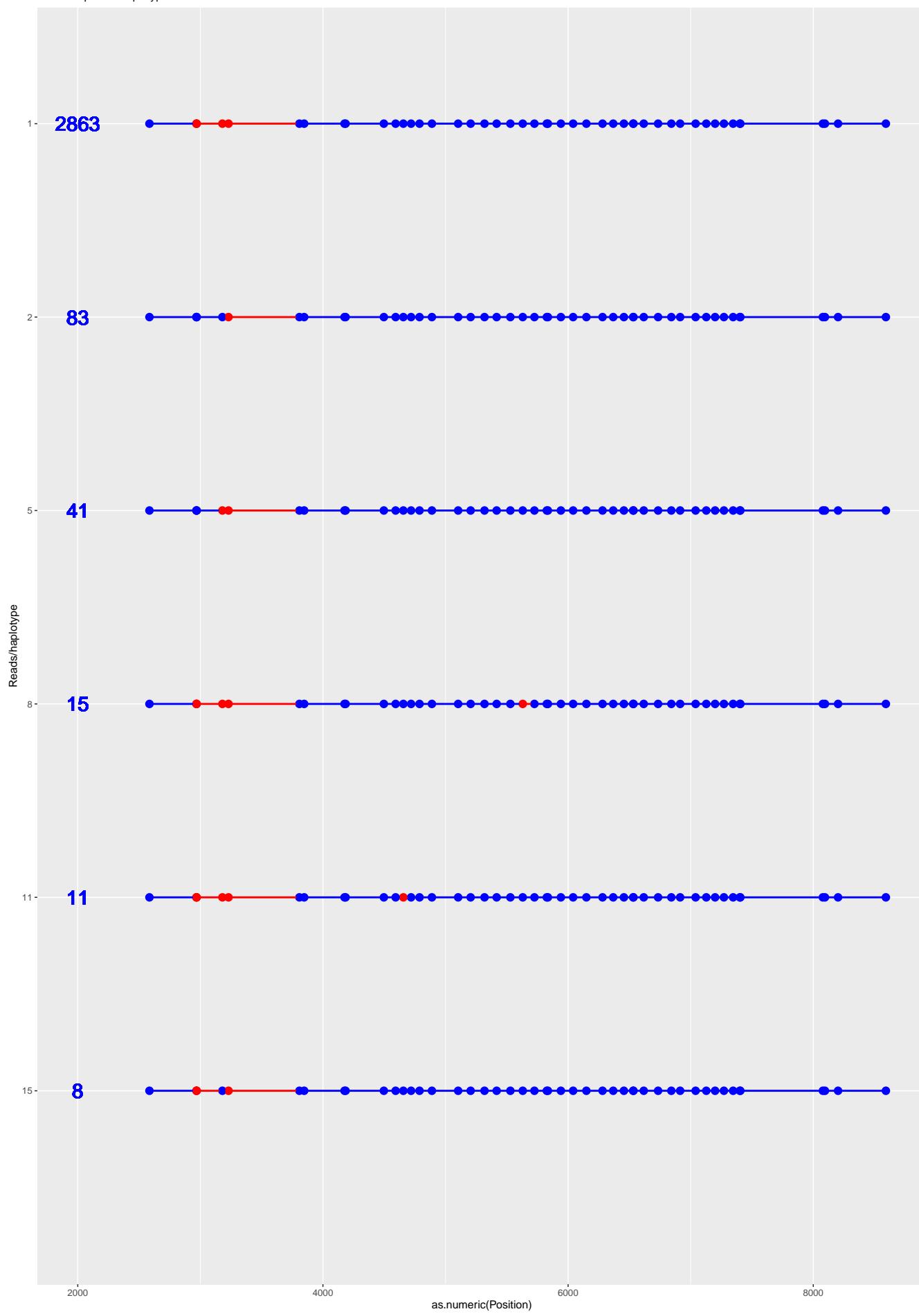
haplotypes I began with n[supporting reads] = 2657

most frequent 7 haplotypes.



barcode = AGAGACACGATACTCA & CTACTCTCAGCAGTGA

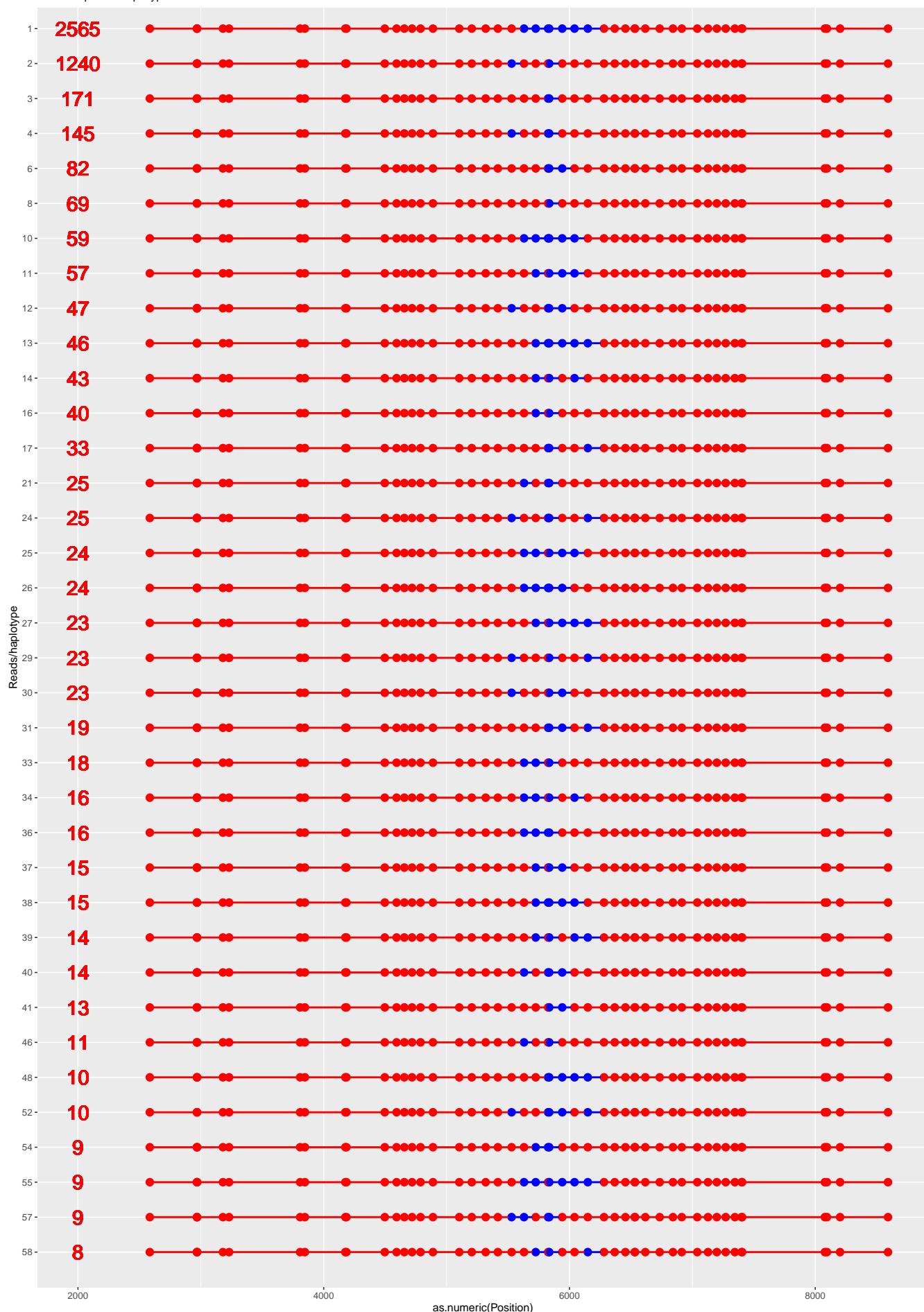
Sample = 238d tetrad = 238 spore = d
Total reads = 3588 PCR=628
haplotypes I began with [n|supporting reads] = 8, 11, 15, 41, 83, 2863
most frequent 7 haplotypes.



Sample = 239a tetrad = 239 spore = a

Total reads =6079 PCR=629

haplotypes I began with [n:supporting reads] = 8, 9, 10, 11, 13, 14, 15, 16, 18, 19, 23, 24, 25, 33, 40, 43, 46, 47, 57, 59, 69, 82, 145, 171, 1240, 2565 most frequent 7 haplotypes.

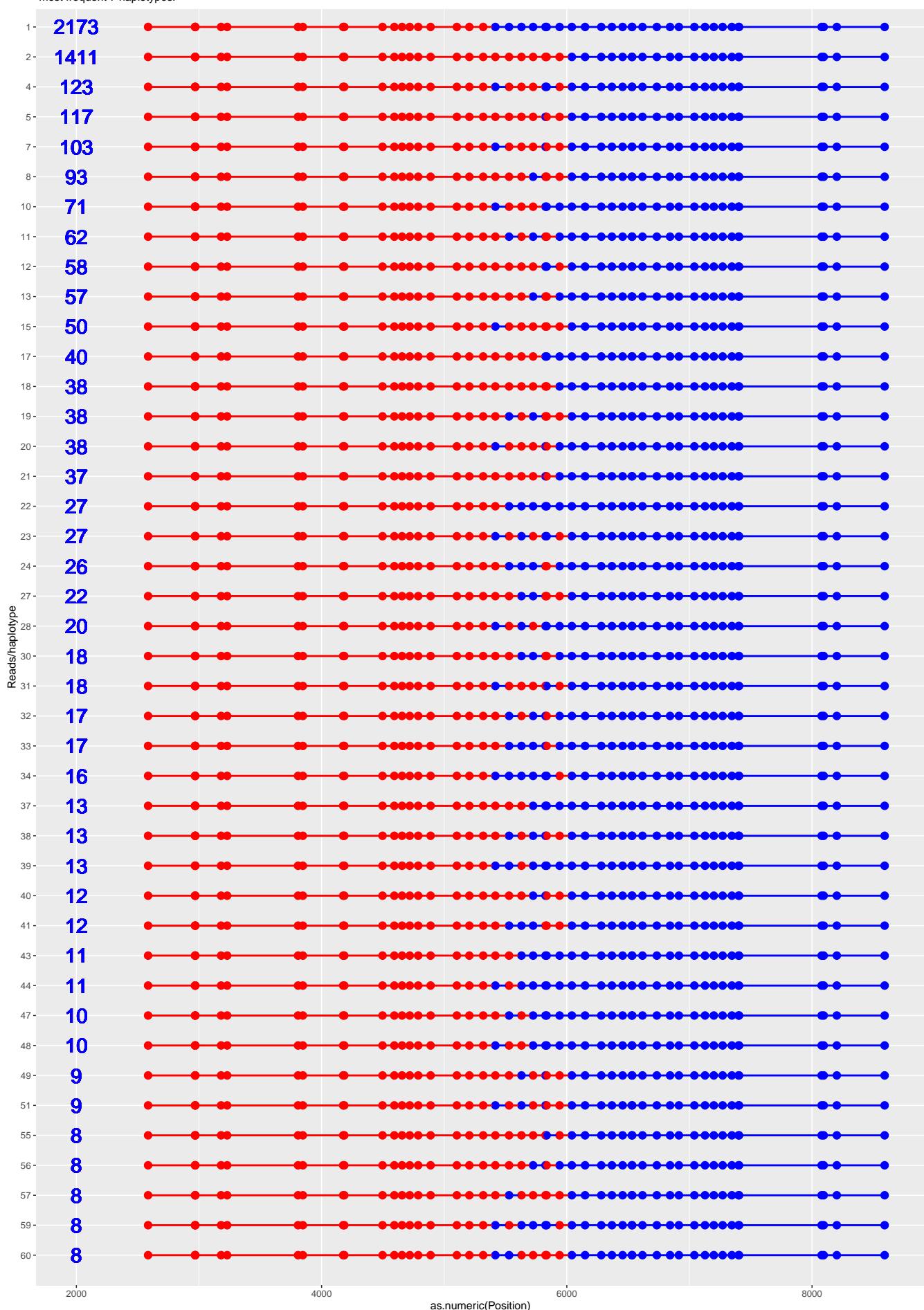


Sample = 239b tetrad = 239 spore = b

Total reads = 6164 PCR=630

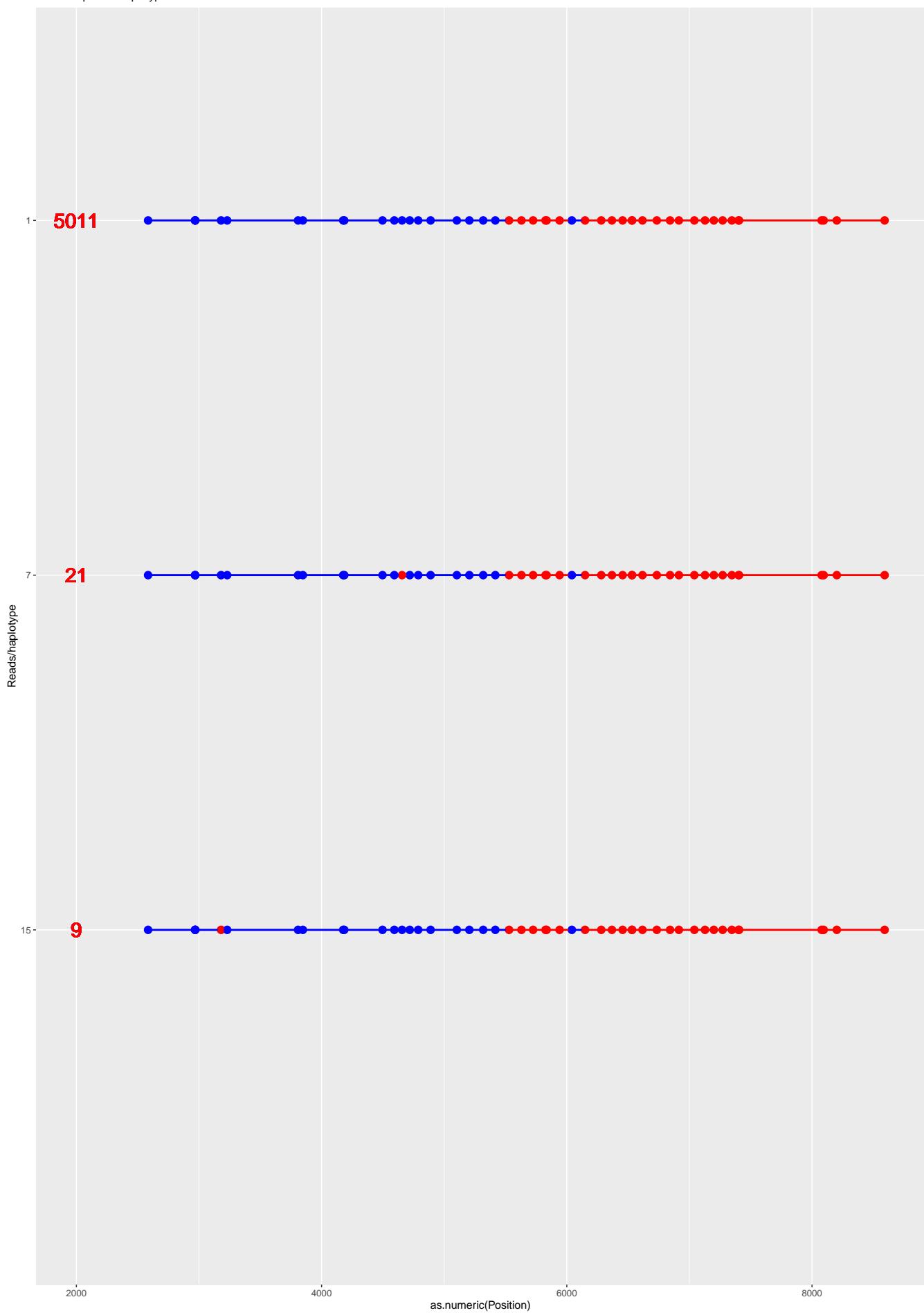
haplotypes I began with [n:supporting reads] = 8, 9, 10, 11, 12, 13, 16, 17, 18, 20, 22, 26, 27, 37, 38, 40, 50, 57, 58, 62, 71, 93, 103, 117, 123, 1411, 2173

most frequent 7 haplotypes.



barcode = AGAGACACGATACTCA & GACACGACTAGATCGC

Sample = 239c tetrad = 239 spore = c
Total reads = 5726 PCR=631
haplotypes I began with [n|supporting reads] = 9, 21, 5011
most frequent 7 haplotypes.



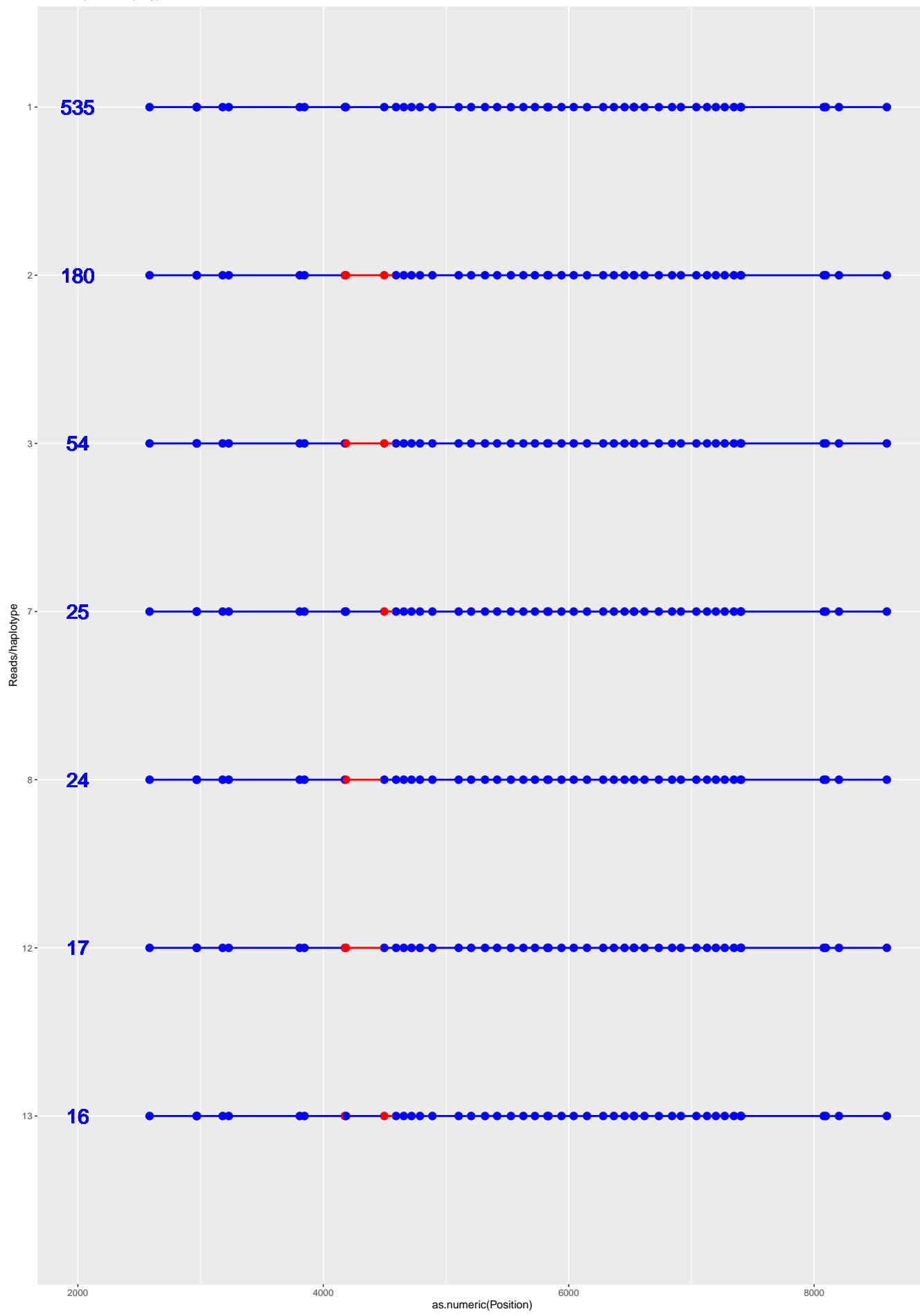
barcode = AGAGACACGATACTCA & TACGAGTCTGTCTAC

Sample = 239d tetrad = 239 spore = d

Total reads = 1193 PCR=632

haplotypes I began with [n|supporting reads] = 16, 17, 24, 25, 54, 180, 535

most frequent 7 haplotypes.



Sample = 241a tetrad = 241 spore = a
Total reads =3074 PCR=633
haplotypes I began with [n|supporting reads] = 9, 10, 2631
most frequent 7 haplotypes.



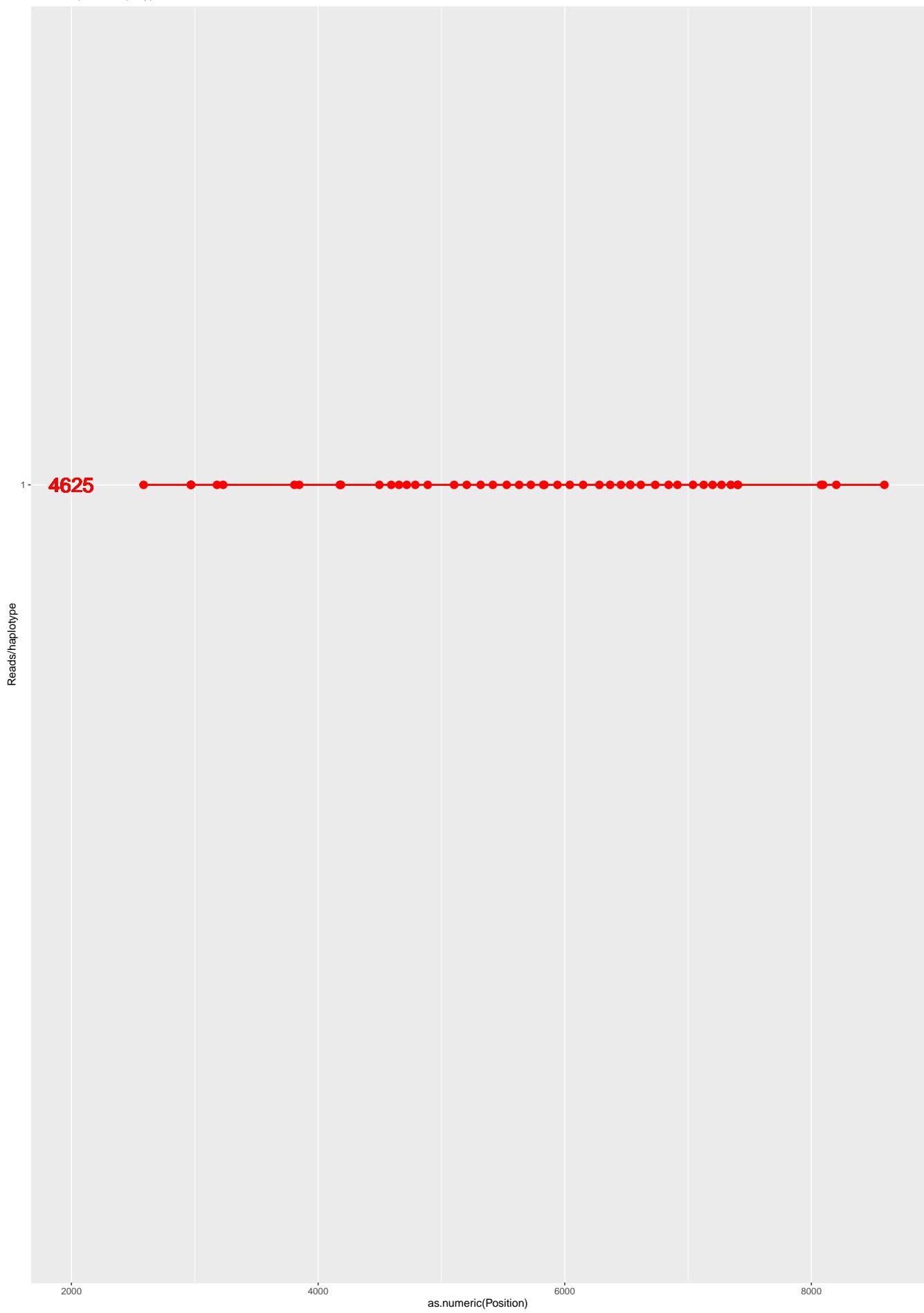
barcode = CTGCTAGAGTCTACAG & TCAGCTGACGATGTGA

Sample = 241b tetrad = 241 spore = b

Total reads = 4826 PCR=634

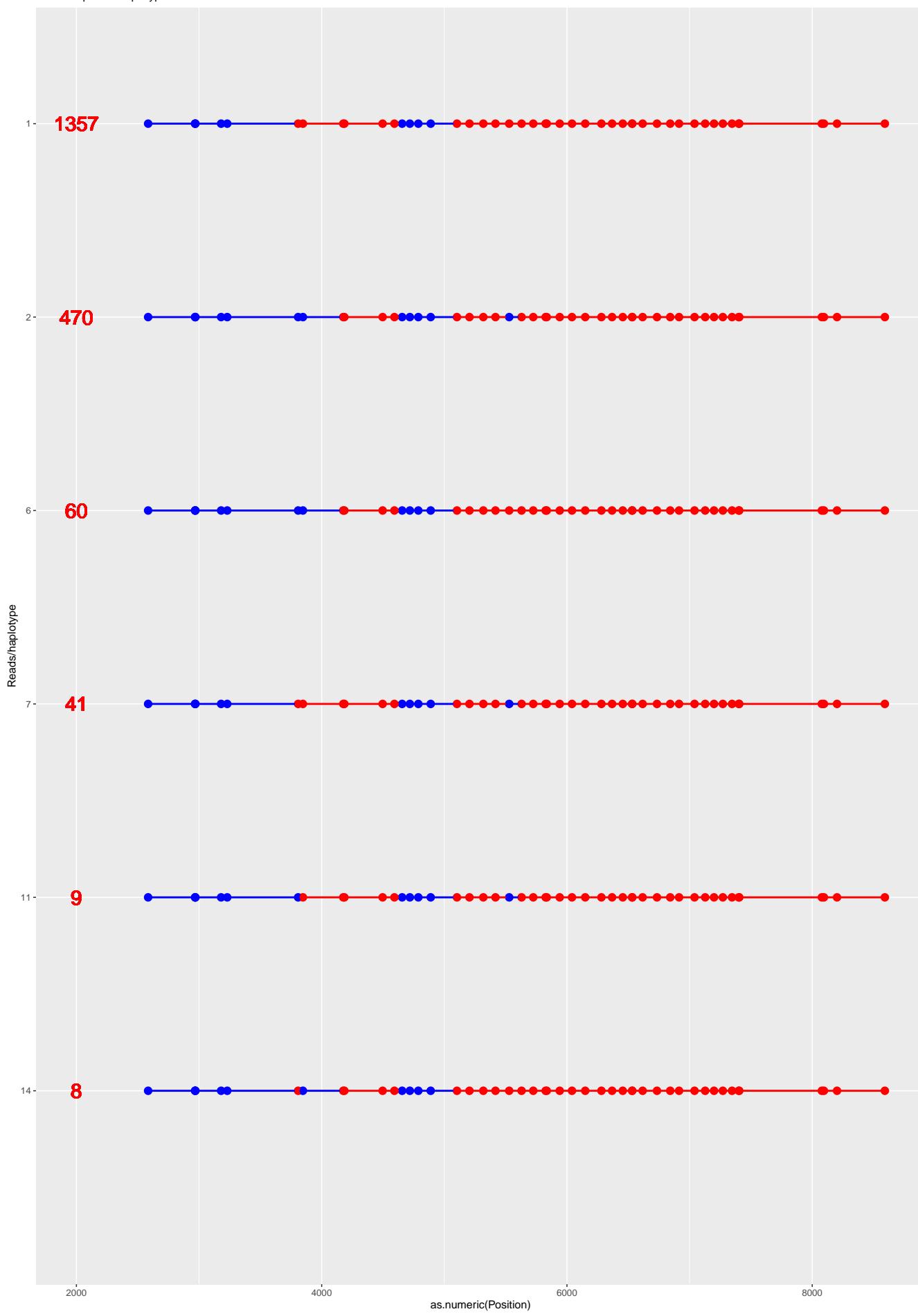
haplotypes I began with n[supporting reads] = 4625

most frequent 7 haplotypes.



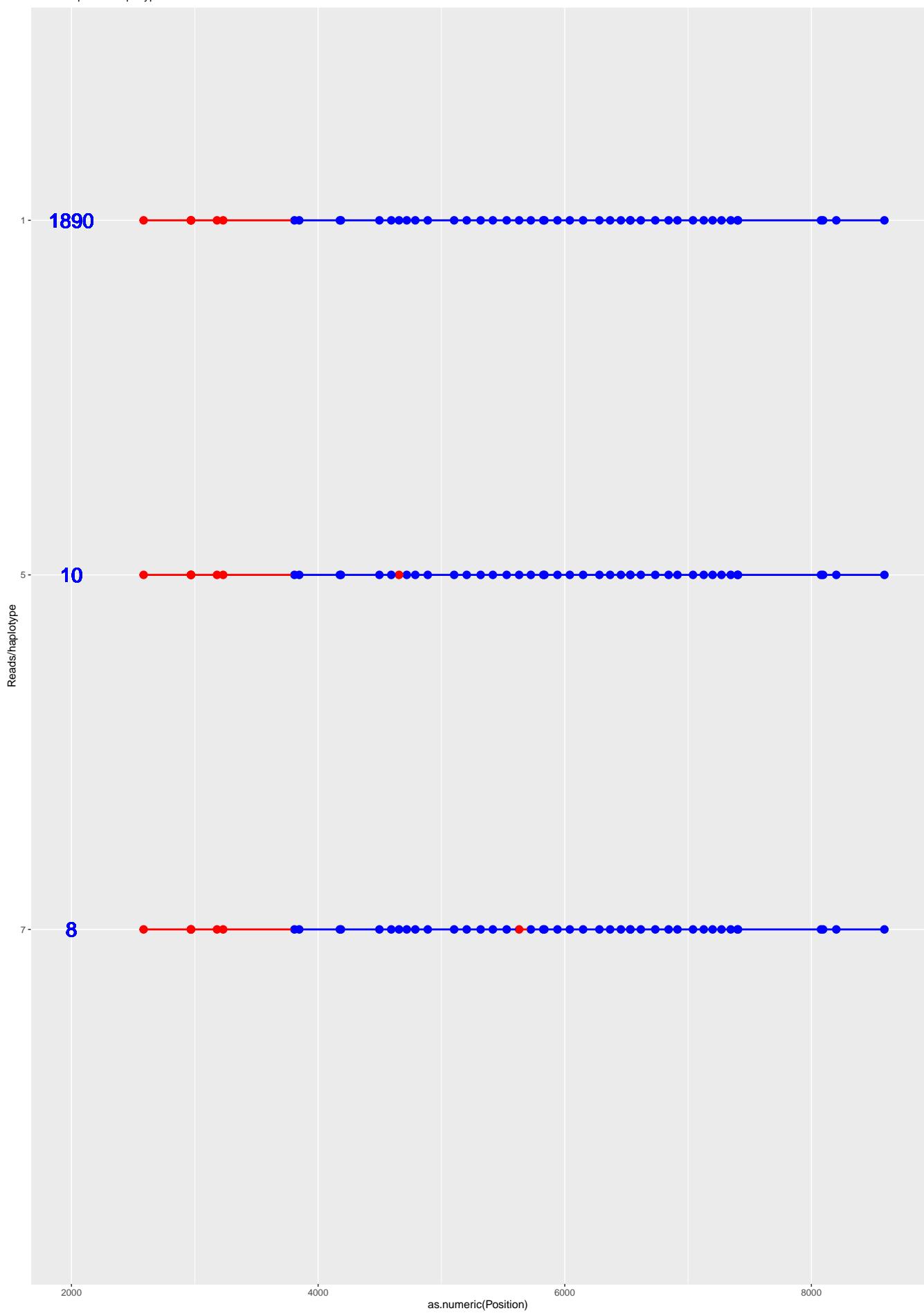
barcode = CTGCTAGAGTCTACAG & ACTGATGCGCACATGT

Sample = 241c tetrad = 241 spore = c
Total reads = 2647 PCR=635
haplotypes I began with [n(supporting reads)] = 8, 9, 41, 60, 470, 1357
most frequent 7 haplotypes.



barcode = CTGCTAGAGTCTACAG & CTACTCTCAGCAGTGA

Sample = 241d tetrad = 241 spore = d
Total reads = 2204 PCR=636
haplotypes I began with n[supporting reads] = 8, 10, 1890
most frequent 7 haplotypes.

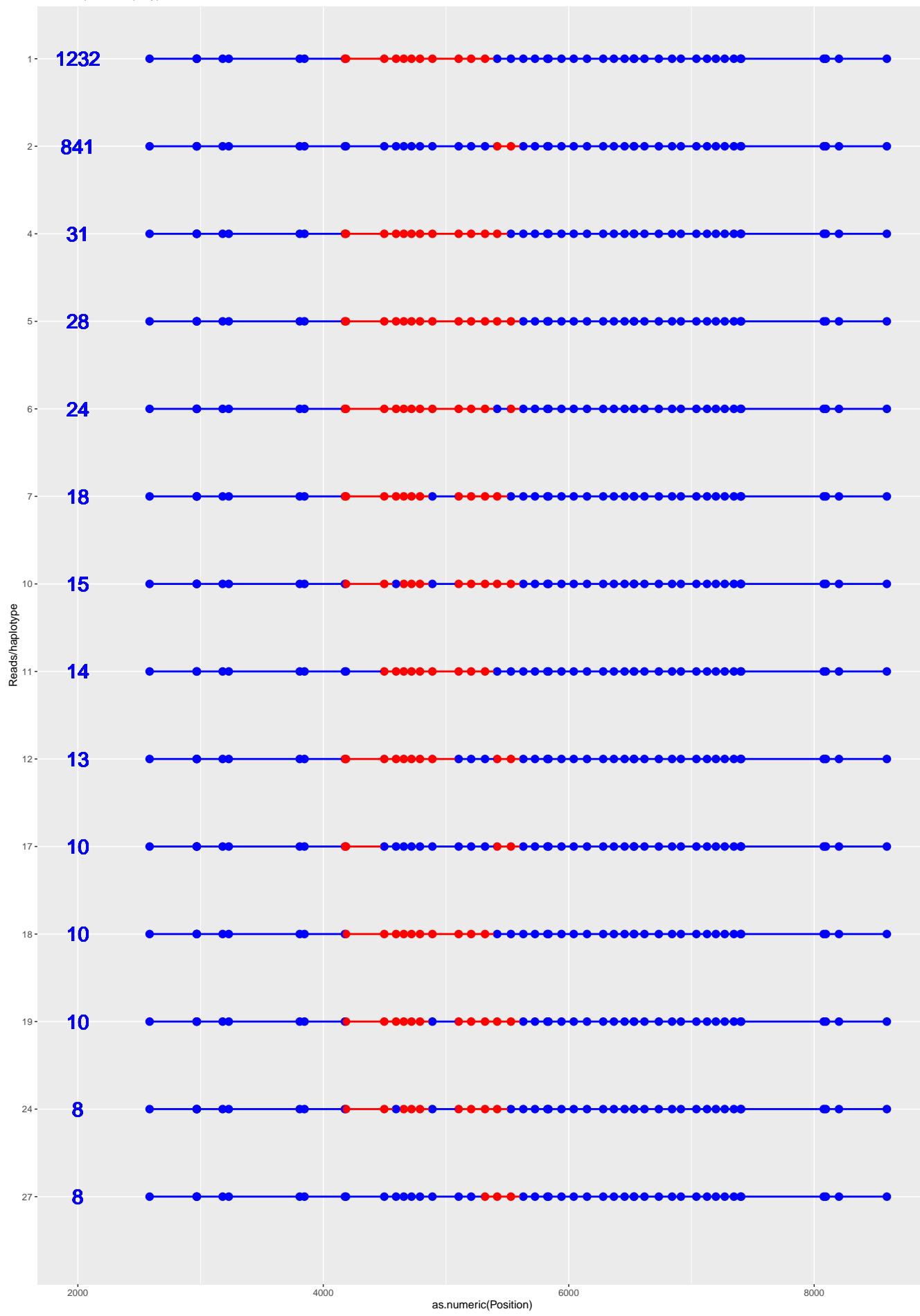


Sample = 242a tetrad = 242 spore = a

Total reads = 4236 PCR=637

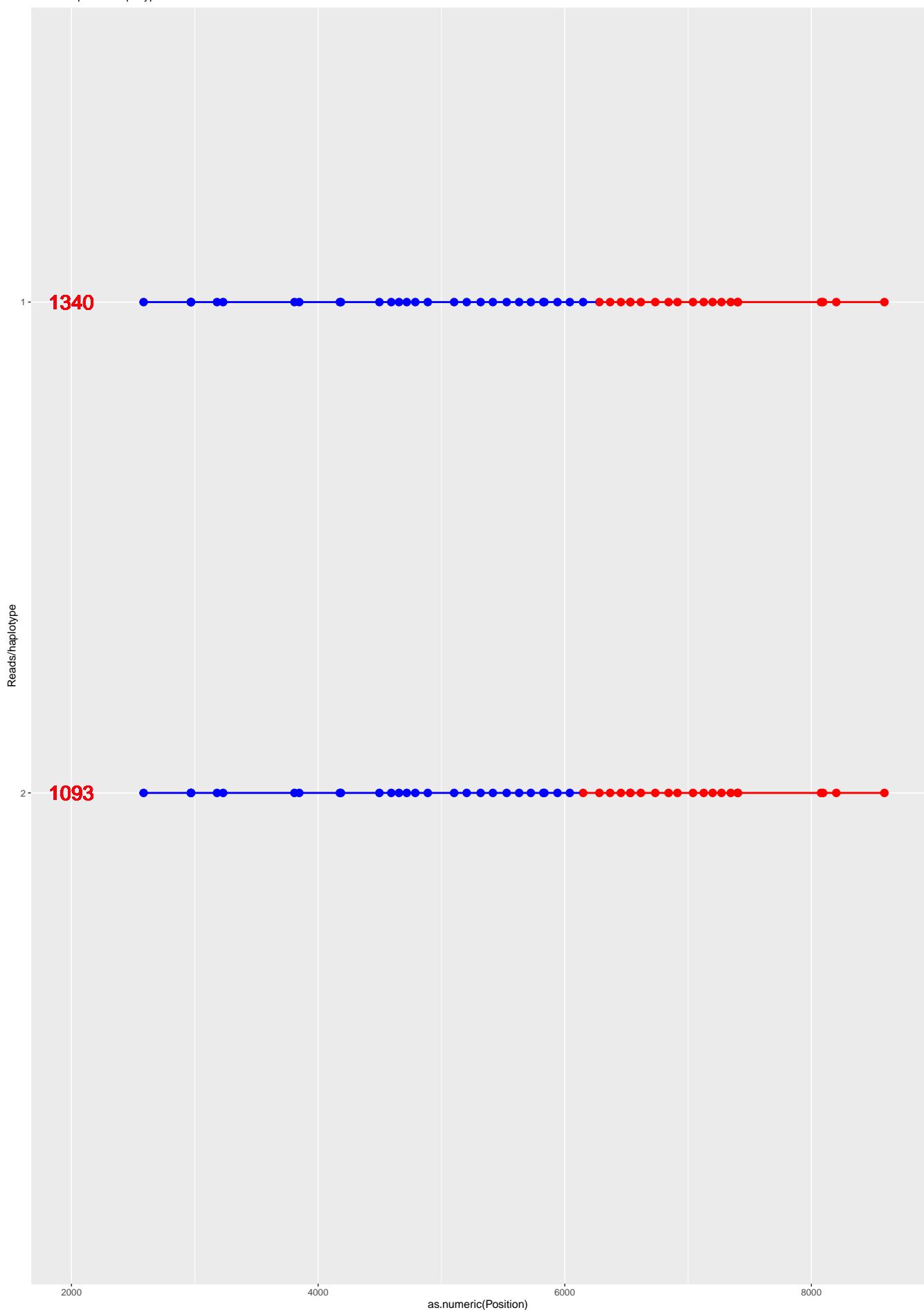
haplotypes I began with [n(supporting reads)] = 8, 10, 13, 14, 15, 18, 24, 28, 31, 841, 1232

most frequent 7 haplotypes.



barcode = CTGCTAGAGTCTACAG & ATATAGTACAGCGTCT

Sample = 242b tetrad = 242 spore = b
Total reads = 2805 PCR=638
haplotypes I began with n[supporting reads] = 1093, 1340
most frequent 7 haplotypes.



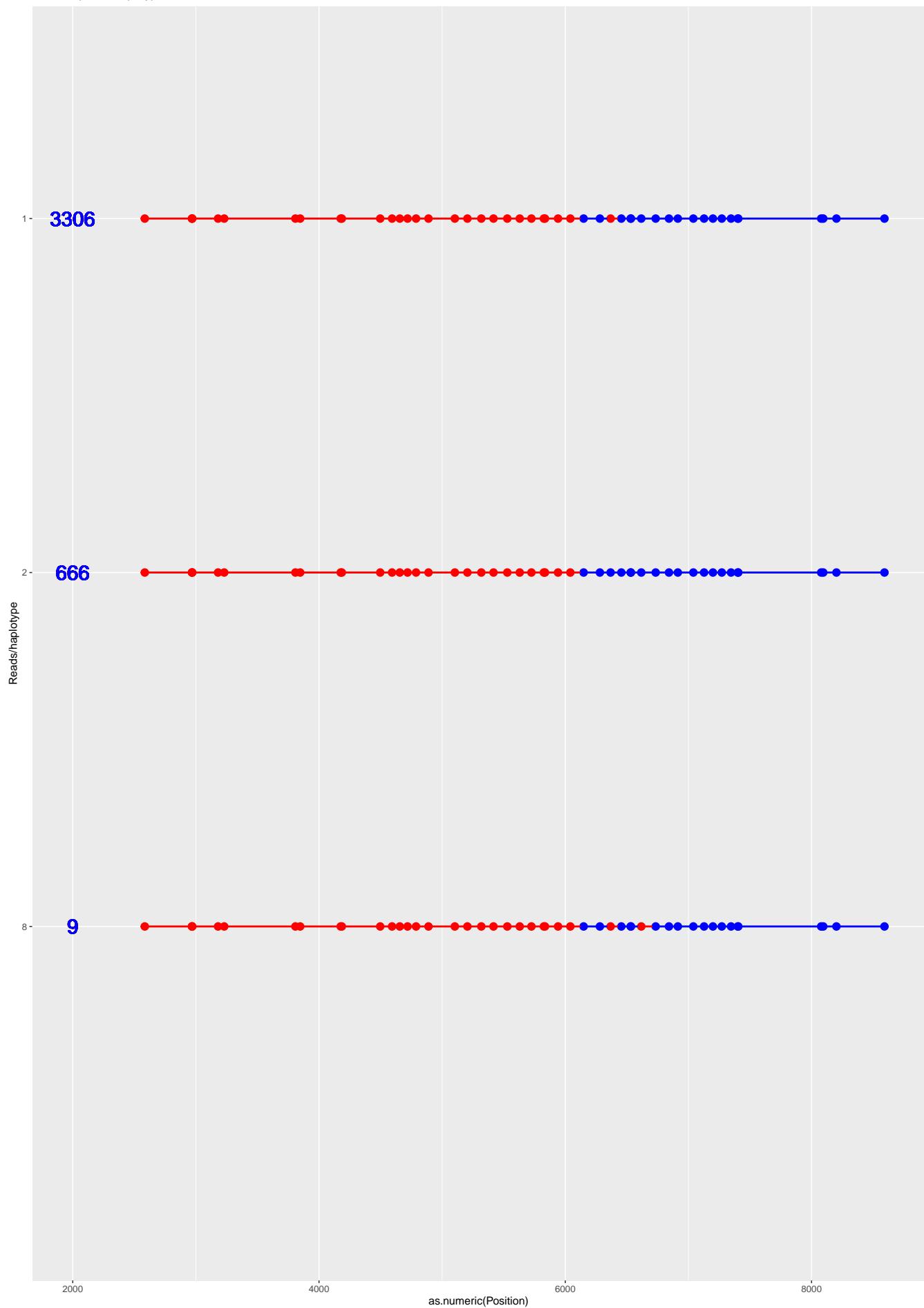
barcode = CTGCTAGAGTCTACAG & GACACGACTAGATCGC

Sample = 242c tetrad = 242 spore = c

Total reads = 4798 PCR=639

haplotypes I began with n[supporting reads] = 9, 666, 3306

most frequent 7 haplotypes.

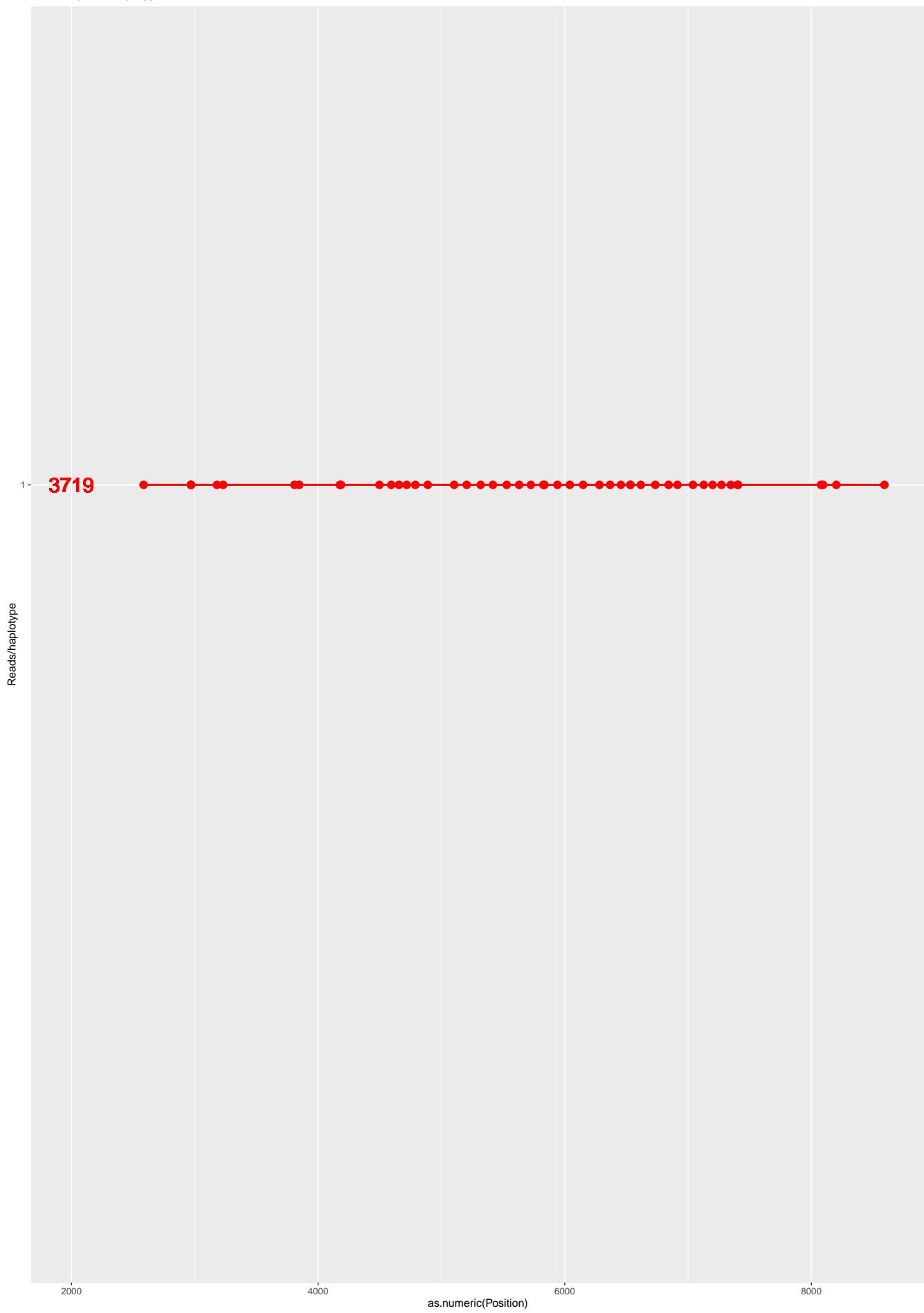


Sample = 242d tetrad = 242 spore = d

Total reads = 3847 PCR=640

haplotypes I began with n[supporting reads] = 3719

most frequent 7 haplotypes.



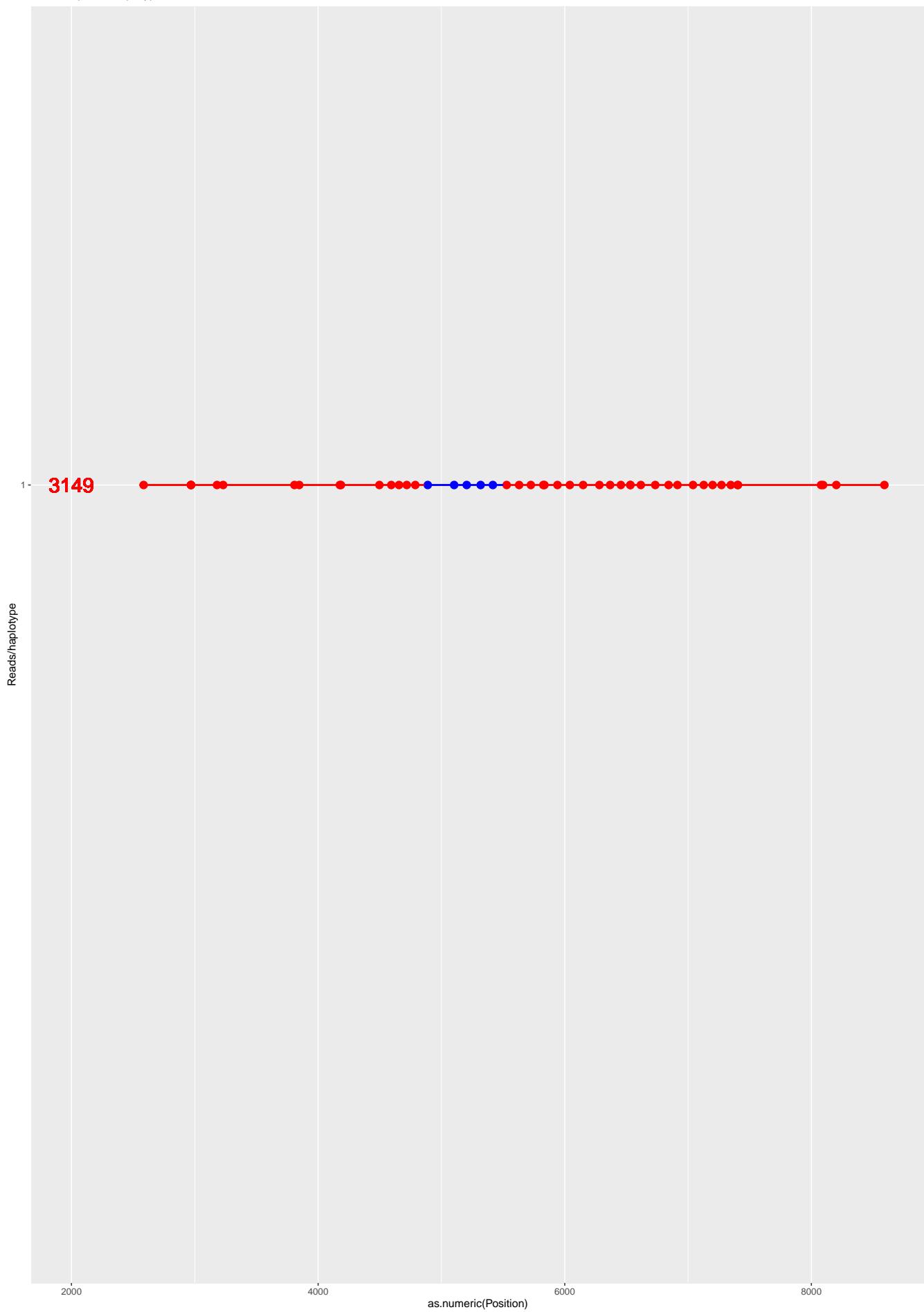
barcode = CTGCTAGAGTCTACAG & ACTCAGCTACATAGTG

Sample = 243a tetrad = 243 spore = a

Total reads =3472 PCR=641

haplotypes I began with n[supporting reads] = 3149

most frequent 7 haplotypes.



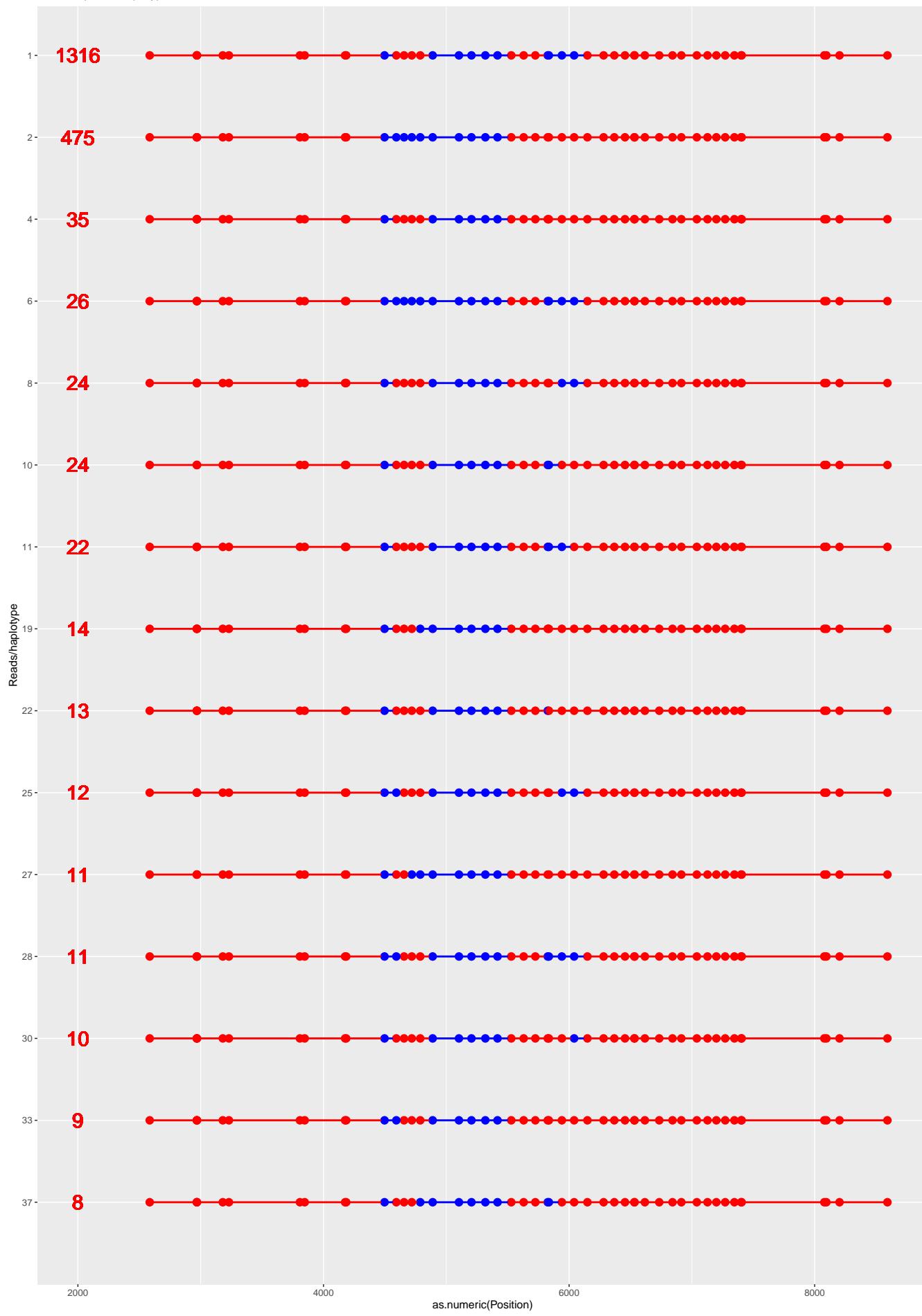
barcode = AGCACTCGCGTCAGTG & TCAGCTGACGATGTGA

Sample = 243b tetrad = 243 spore = b

Total reads = 3148 PCR=642

haplotypes I began with [n(supporting reads)] = 8, 9, 10, 11, 12, 13, 14, 22, 24, 26, 35, 475, 1316

most frequent 7 haplotypes.

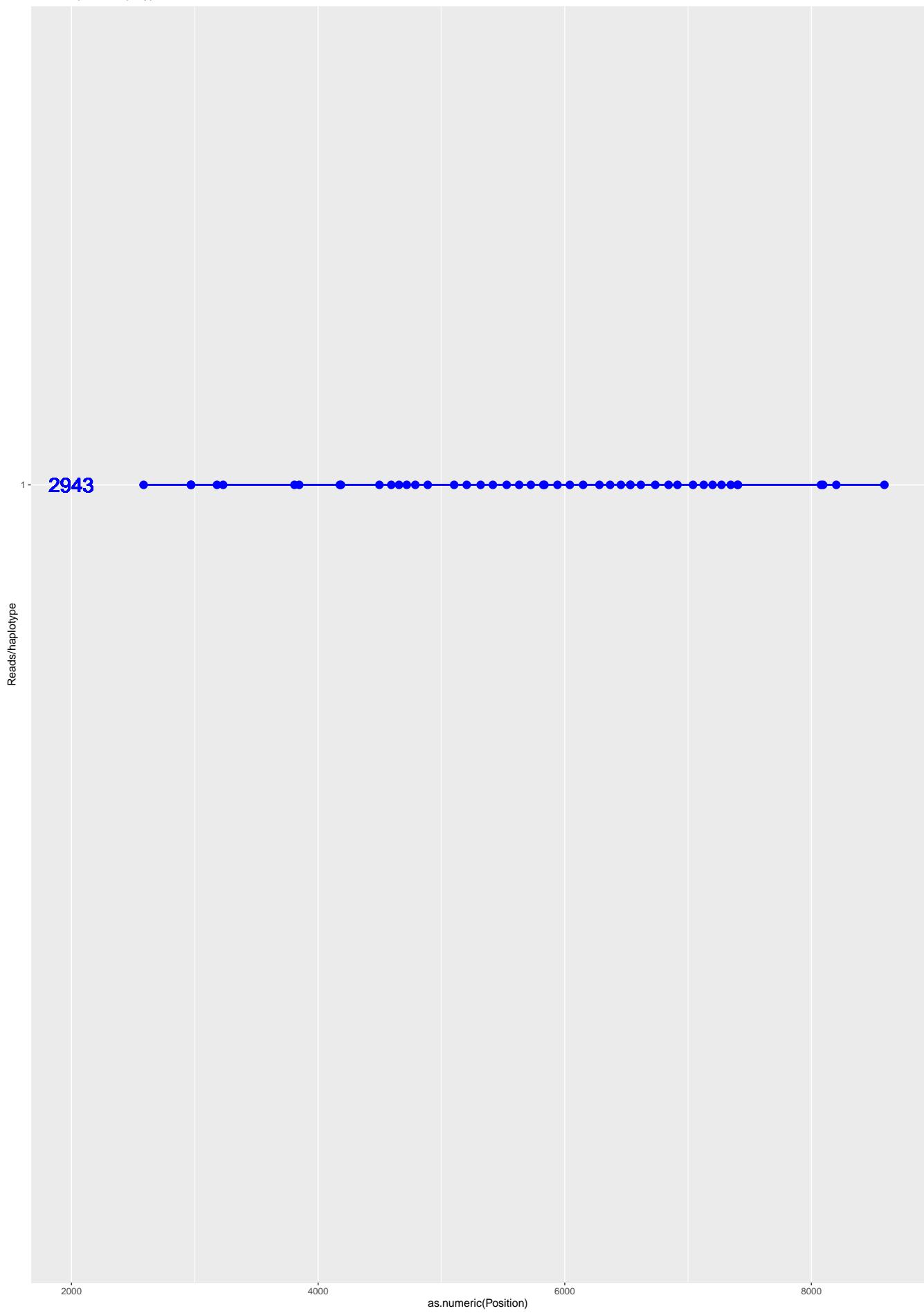


Sample = 243c tetrad = 243 spore = c

Total reads = 3402 PCR=643

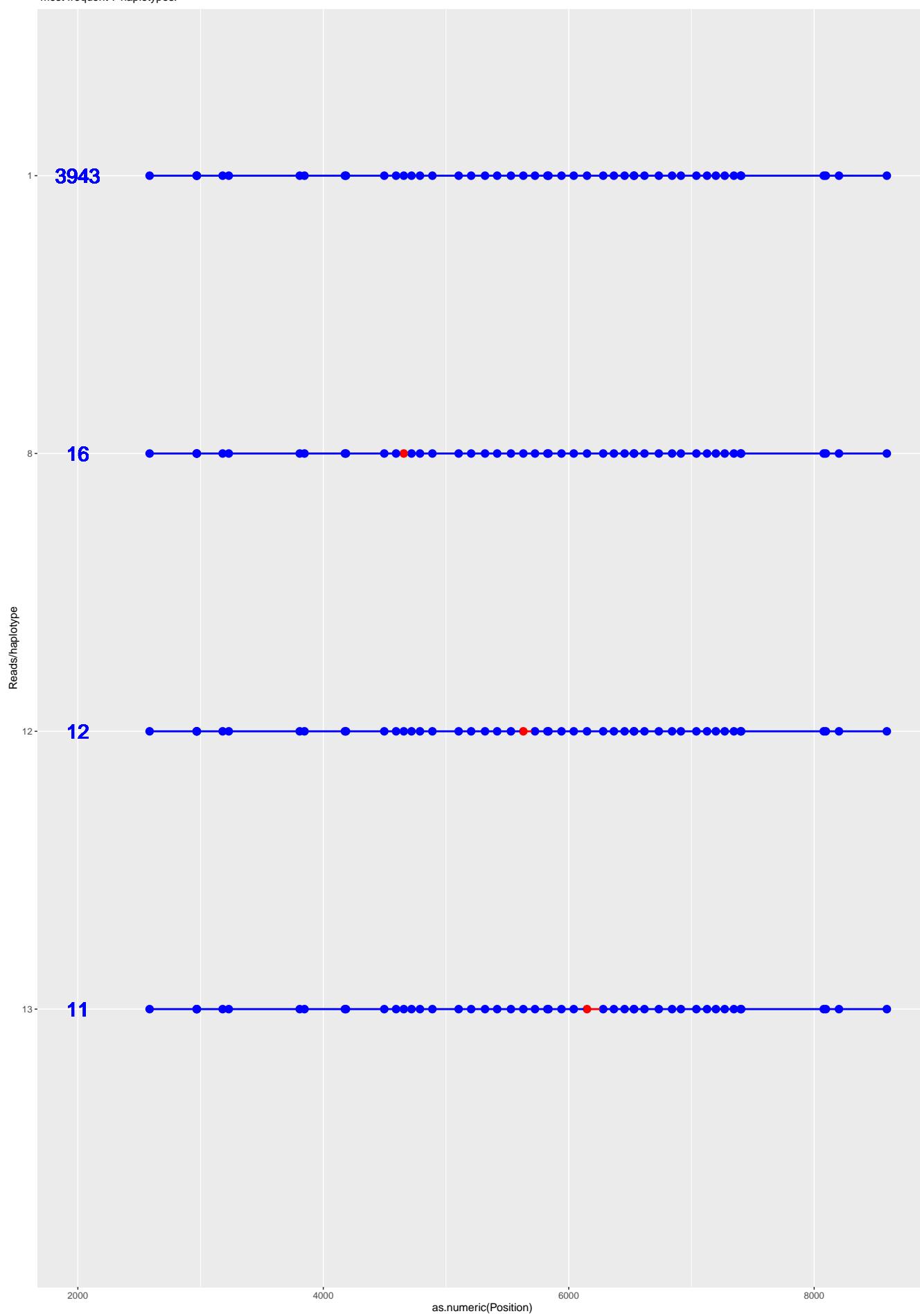
haplotypes I began with n[supporting reads] = 2943

most frequent 7 haplotypes.



barcode = AGCACTCGCGTCAGTG & CTACTCTCAGCAGTGA

Sample = 243d tetrad = 243 spore = d
Total reads = 4650 PCR=644
haplotypes I began with [n:supporting reads] = 11, 12, 16, 3943
most frequent 7 haplotypes.



Sample = 244a tetrad = 244 spore = a

Total reads = 4277 PCR=645

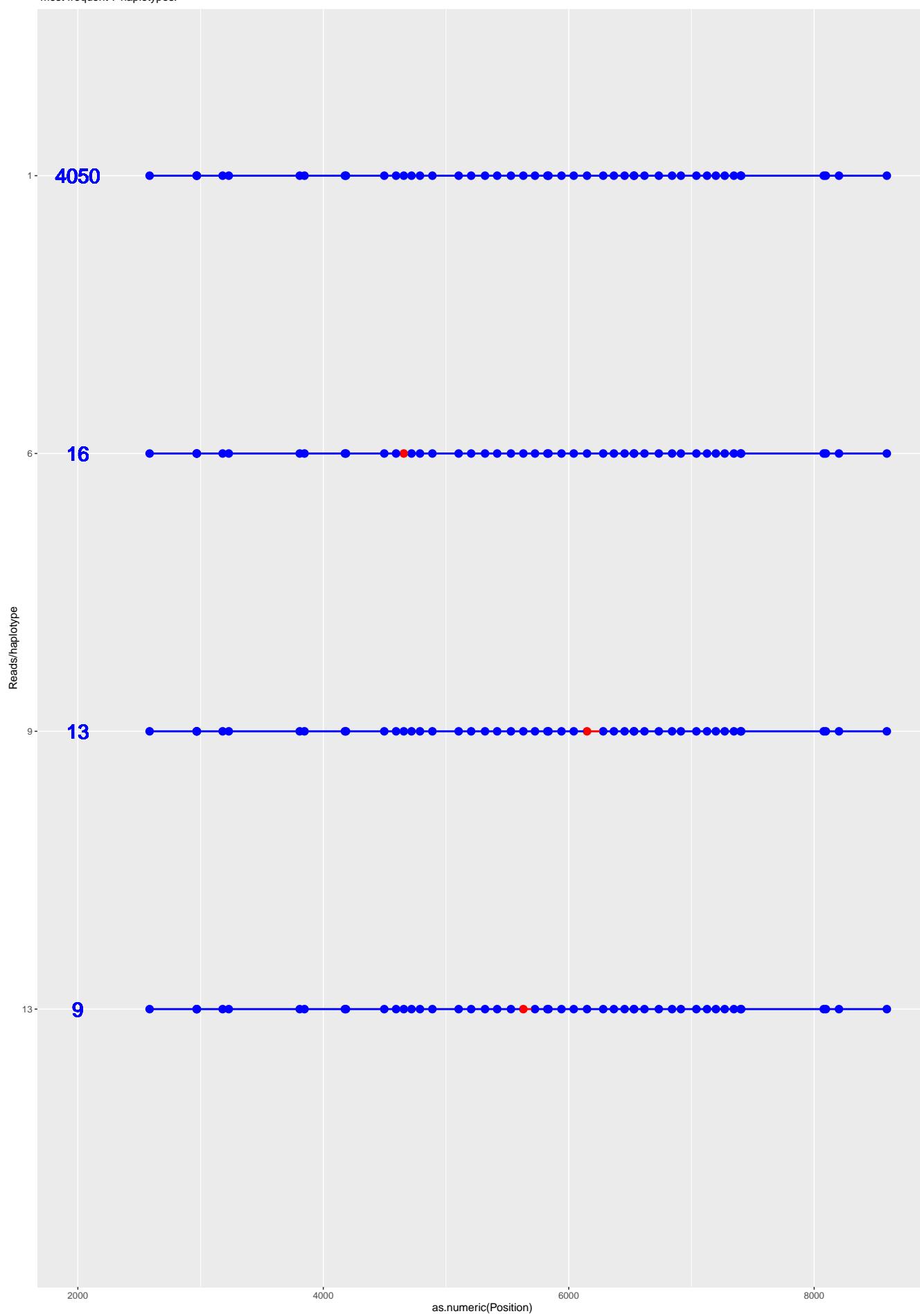
haplotypes I began with n[supporting reads] = 12, 13, 3691

most frequent 7 haplotypes.



barcode = AGCACTCGCGTCAGTG & ATATAGTACAGCGTCT

Sample = 244b tetrad = 244 spore = b
Total reads = 4738 PCR=646
haplotypes I began with [n:supporting reads] = 9, 13, 16, 4050
most frequent 7 haplotypes.

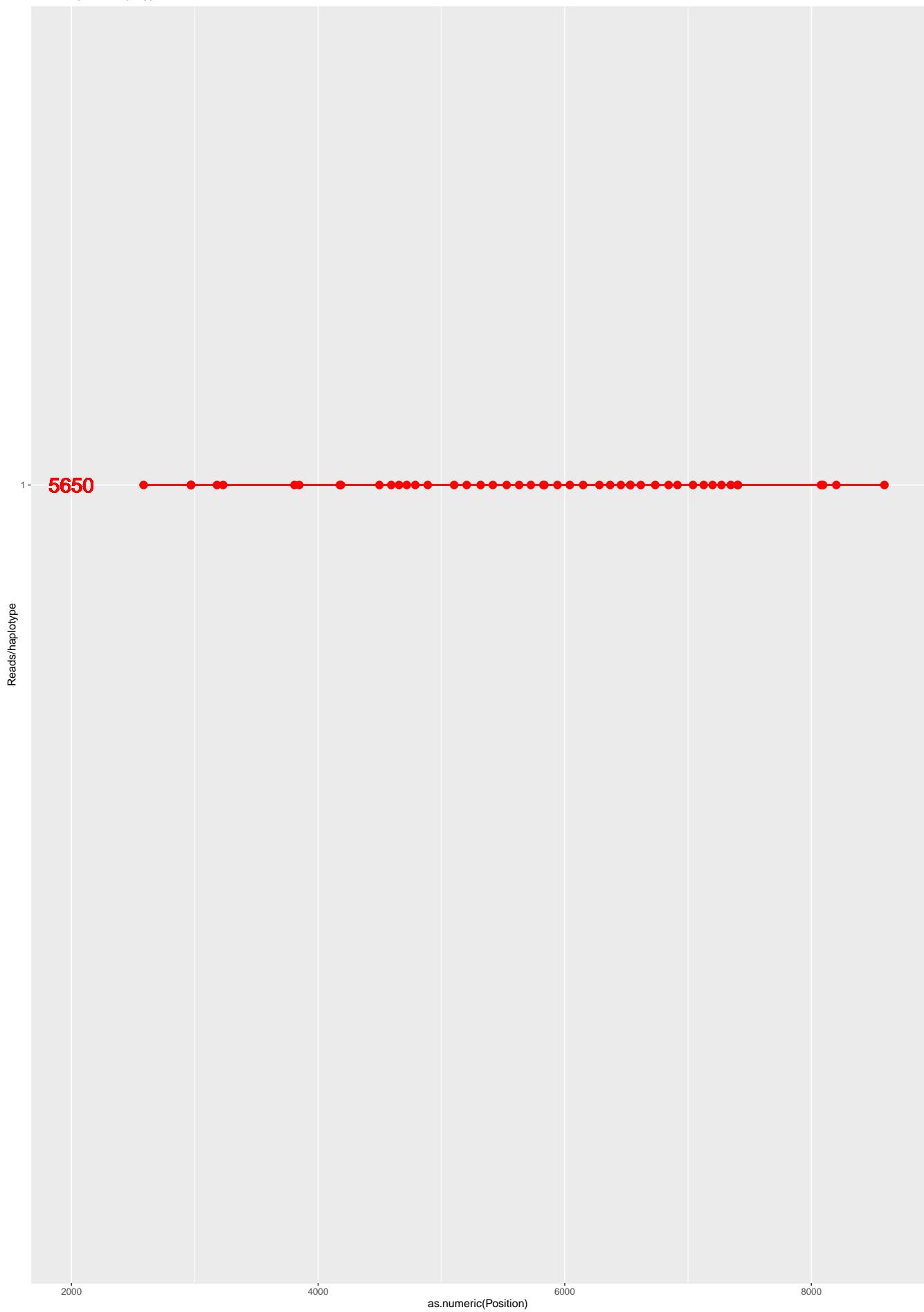


Sample = 244c tetrad = 244 spore = c

Total reads = 5887 PCR=647

haplotypes I began with n[supporting reads] = 5650

most frequent 7 haplotypes.



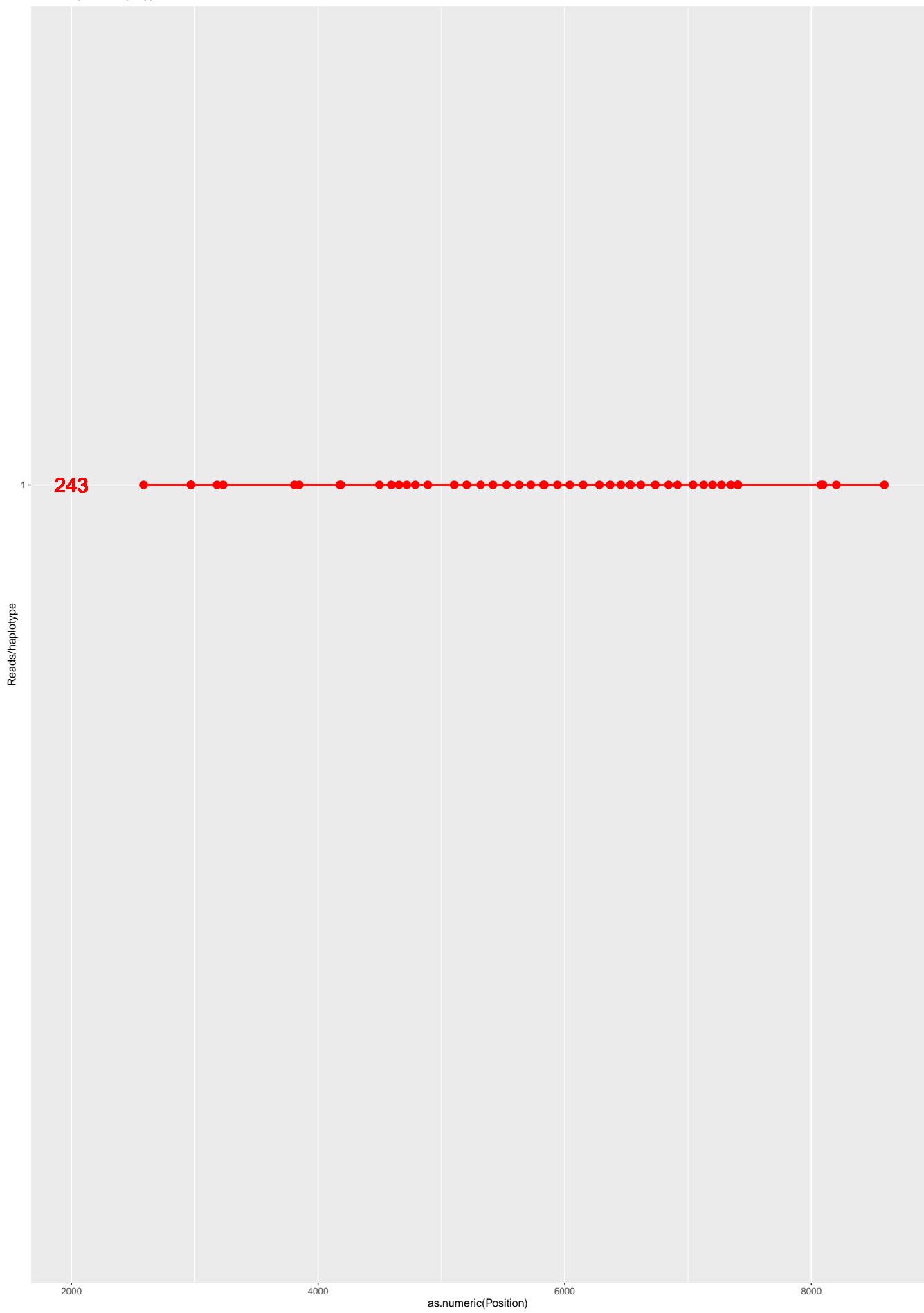
barcode = AGCACTCGCGTCAGTG & TACGAGTCTGTACATAC

Sample = 244d tetrad = 244 spore = d

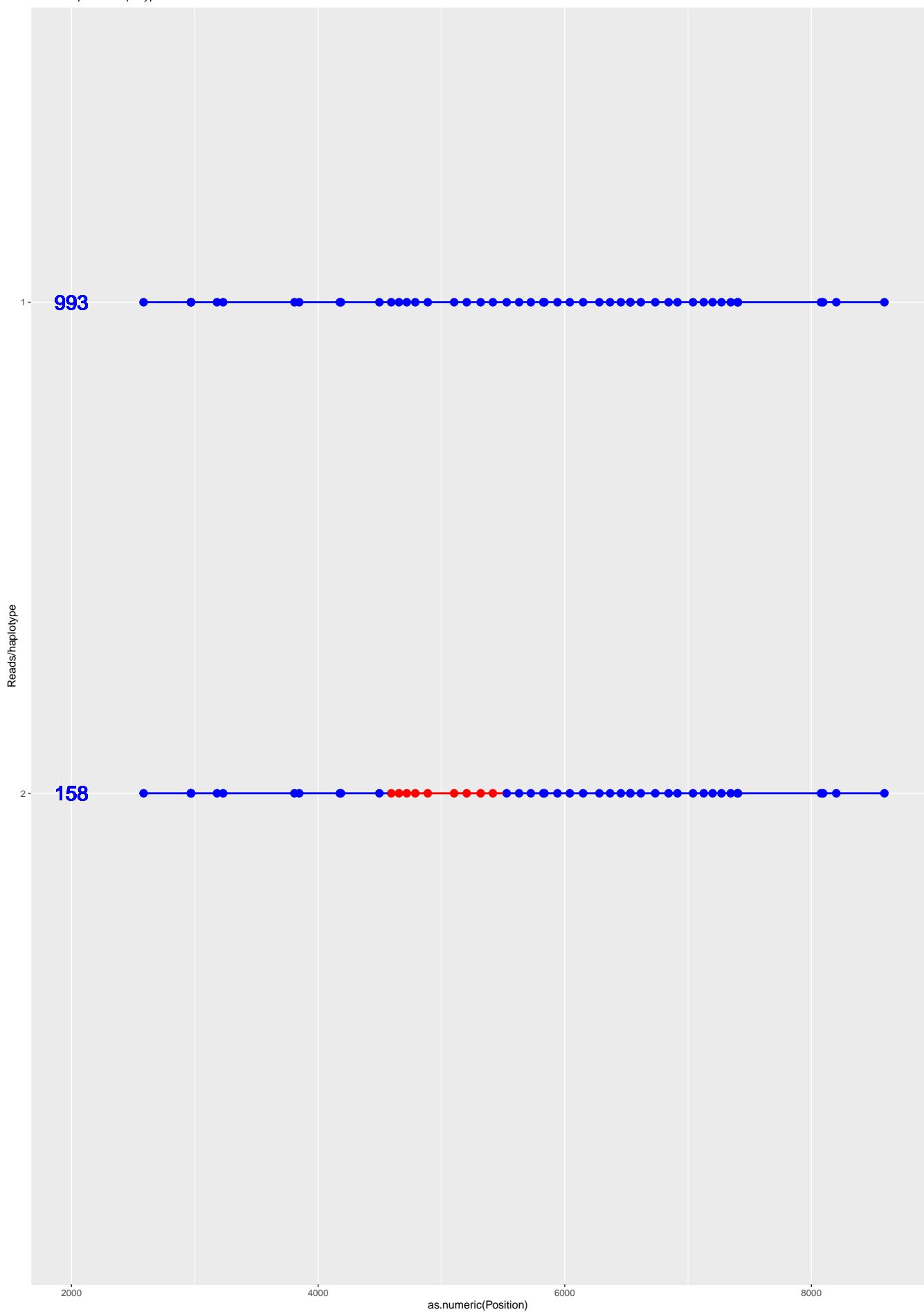
Total reads = 251 PCR=648

haplotypes I began with n[supporting reads] = 243

most frequent 7 haplotypes.

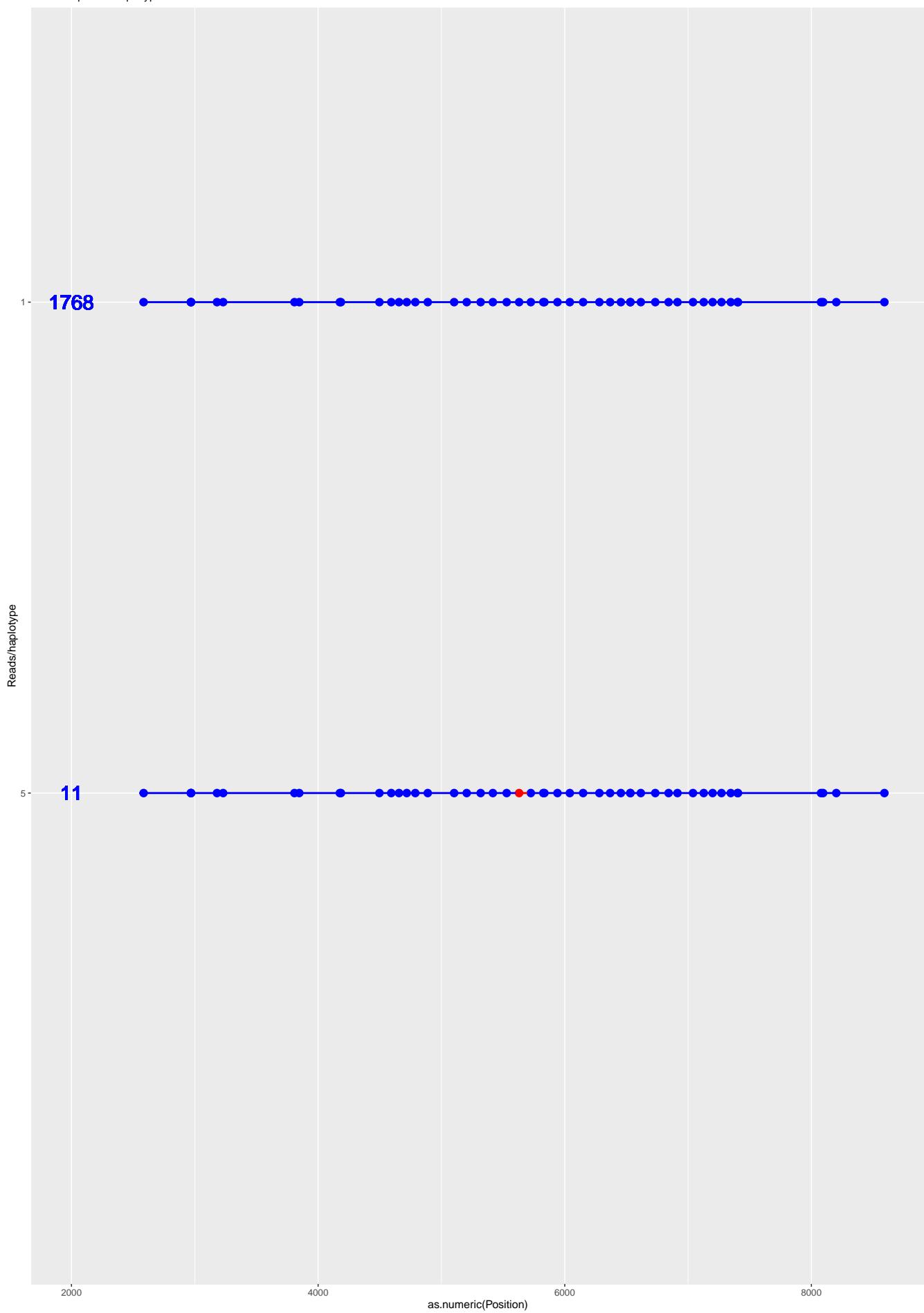


Sample = 249a tetrad = 249 spore = a
Total reads = 1604 PCR=649
haplotypes I began with n[supporting reads] = 158, 993
most frequent 7 haplotypes.



barcode = TCATGCACGTCTCGCT & TCAGCTGACGATGTGA

Sample = 249b tetrad = 249 spore = b
Total reads = 2068 PCR=650
haplotypes I began with n[supporting reads] = 11, 1768
most frequent 7 haplotypes.



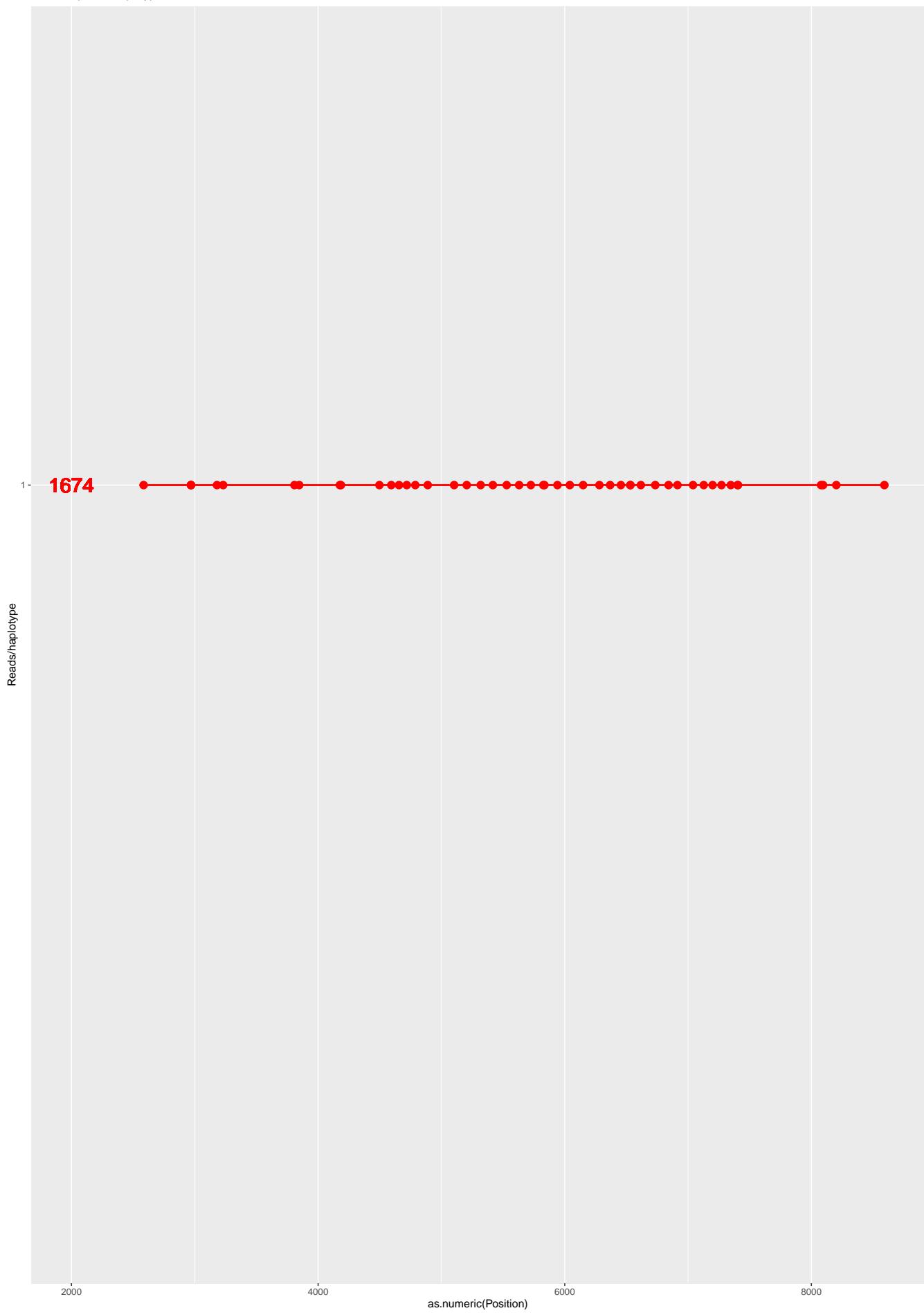
barcode = TCATGCACGTCTCGCT & ACTGATGCGCACATGT

Sample = 249c tetrad = 249 spore = c

Total reads = 1754 PCR=651

haplotypes I began with n[supporting reads] = 1674

most frequent 7 haplotypes.

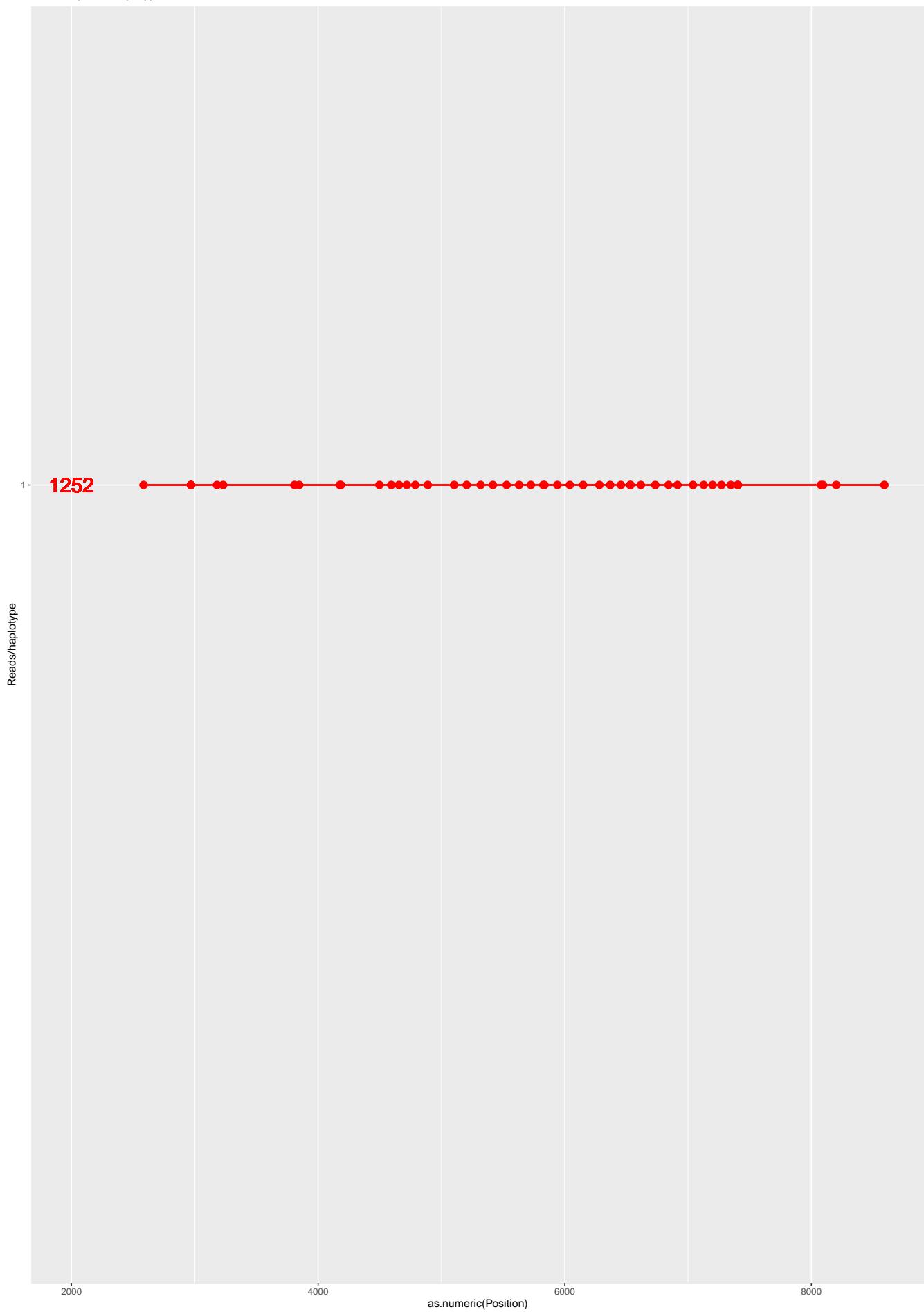


Sample = 249d tetrad = 249 spore = d

Total reads = 1299 PCR=652

haplotypes I began with n[supporting reads] = 1252

most frequent 7 haplotypes.



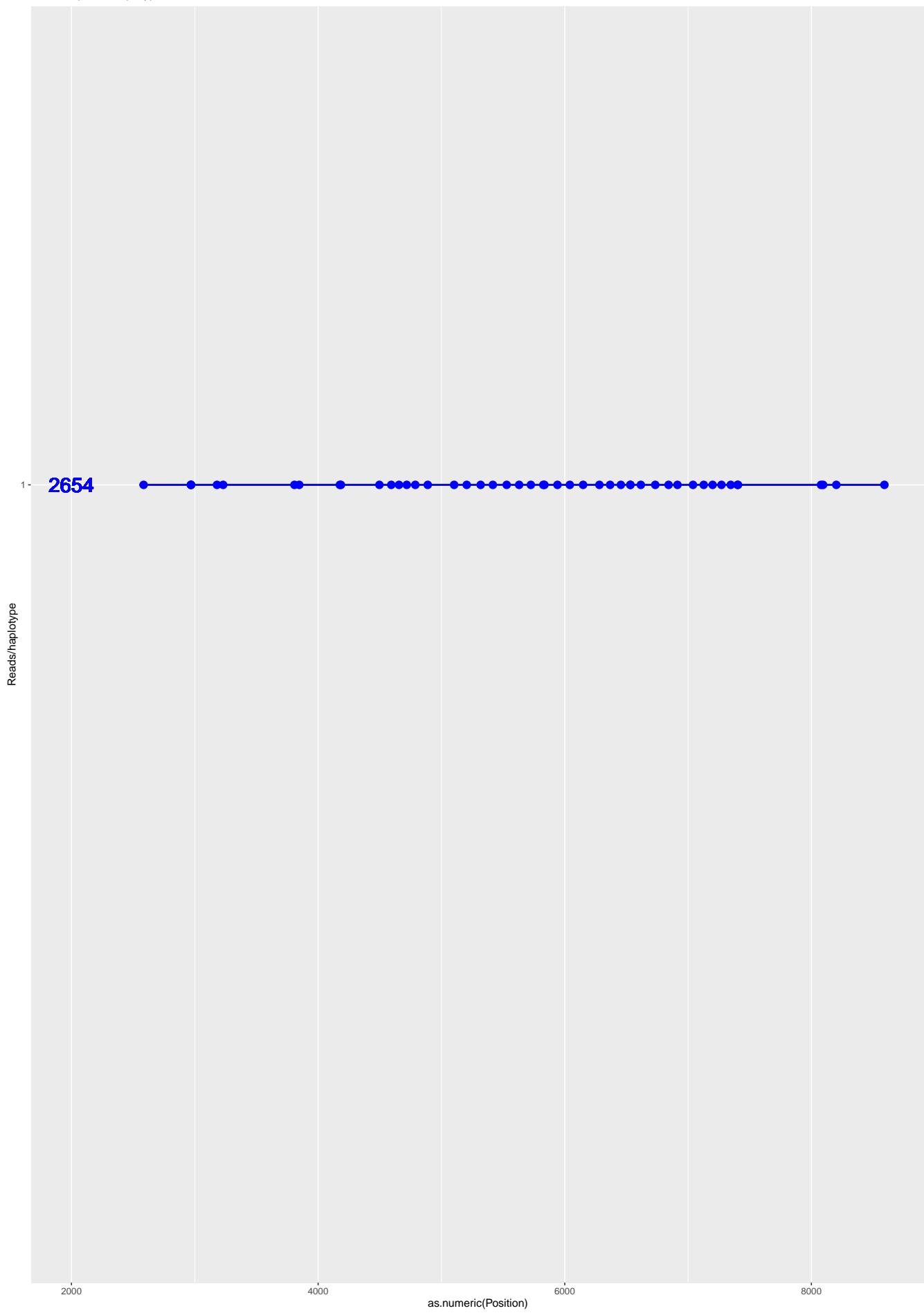
barcode = TCATGCACGTCTCGCT & ATCTACATCACGACTC

Sample = 253a tetrad = 253 spore = a

Total reads = 3096 PCR=657

haplotypes I began with n[supporting reads] = 2654

most frequent 7 haplotypes.



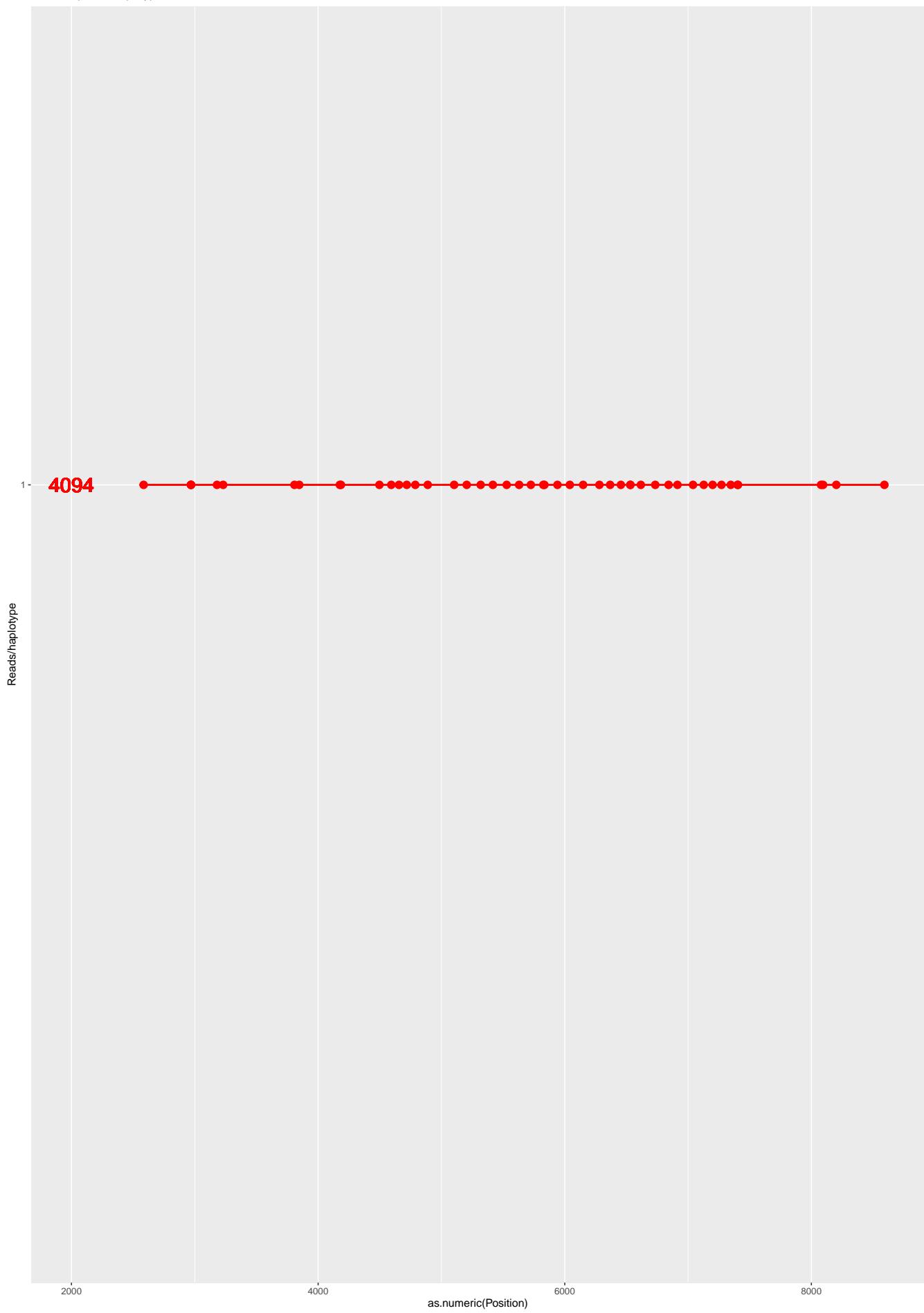
barcode = AGAGCATCTCTGTACT & TCAGCTGACGATGTGA

Sample = 253b tetrad = 253 spore = b

Total reads = 4276 PCR=658

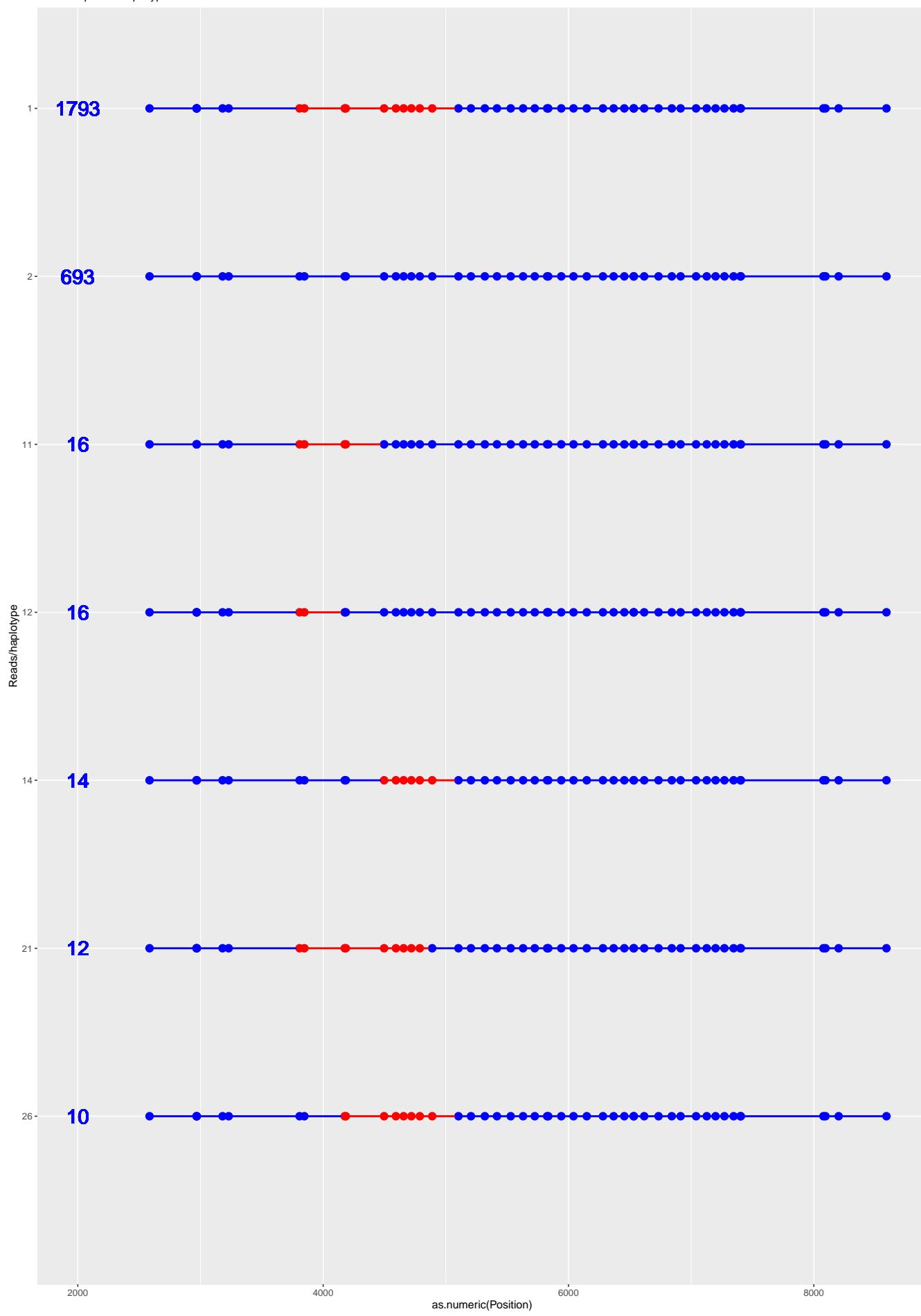
haplotypes I began with n[supporting reads] = 4094

most frequent 7 haplotypes.



barcode = AGAGCATCTCTGTACT & ACTGATGCGCACATGT

Sample = 253c tetrad = 253 spore = c
 Total reads = 4729 PCR=659
 haplotypes I began with [n(supporting reads)] = 10, 12, 14, 16, 693, 1793
 most frequent 7 haplotypes.

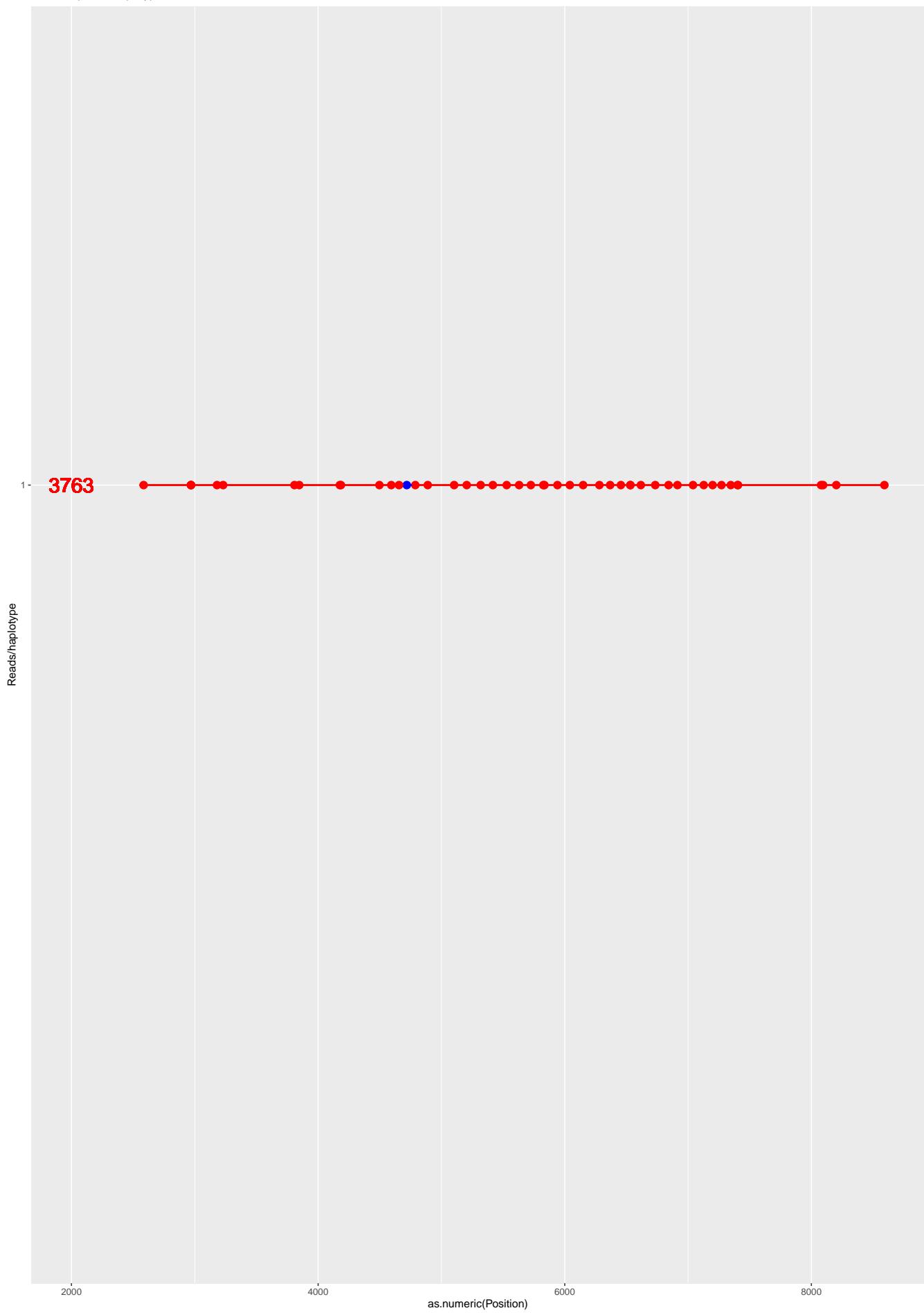


Sample = 255d tetrad = 255 spore = d

Total reads = 3911 PCR=660

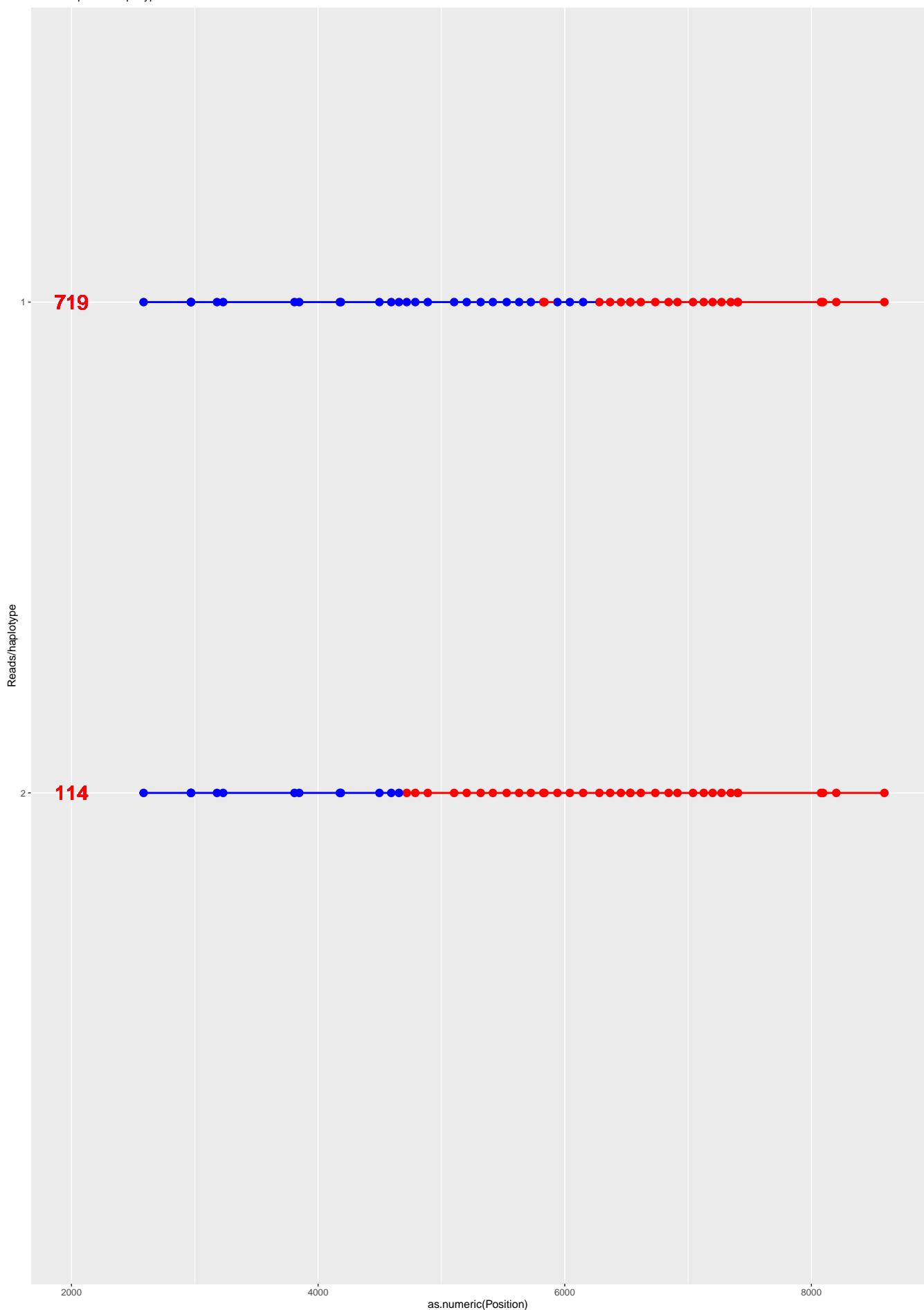
haplotypes I began with n[supporting reads] = 3763

most frequent 7 haplotypes.



barcode = AGAGCATCTCTGTACT & ATCTACATCACGACTC

Sample = 254a tetrad = 254 spore = a
Total reads = 1023 PCR=661
haplotypes I began with n[supporting reads] = 114, 719
most frequent 7 haplotypes.



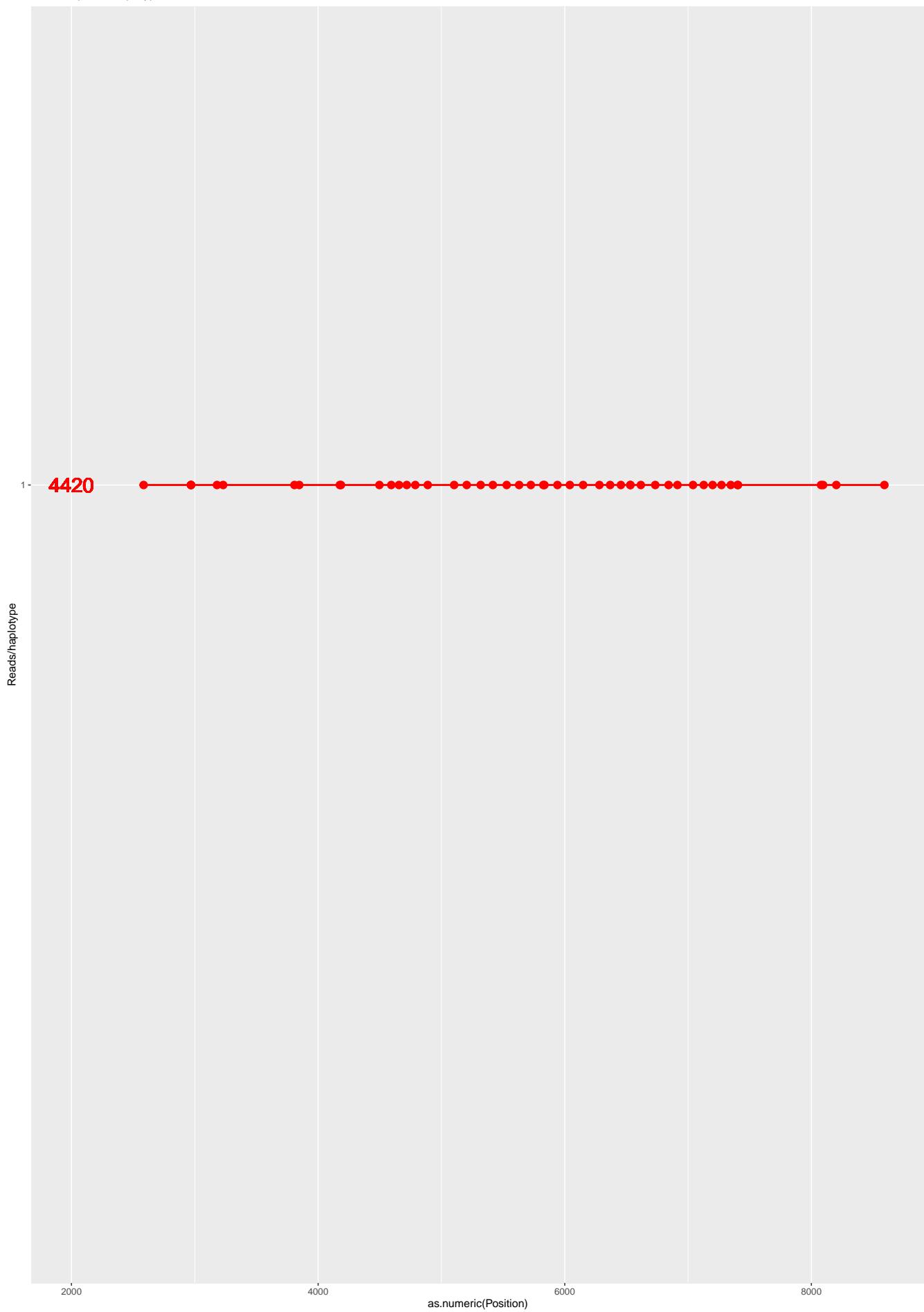
barcode = AGAGCATCTCTGTACT & ATATAGTACAGCGTCT

Sample = 254b tetrad = 254 spore = b

Total reads = 4616 PCR=662

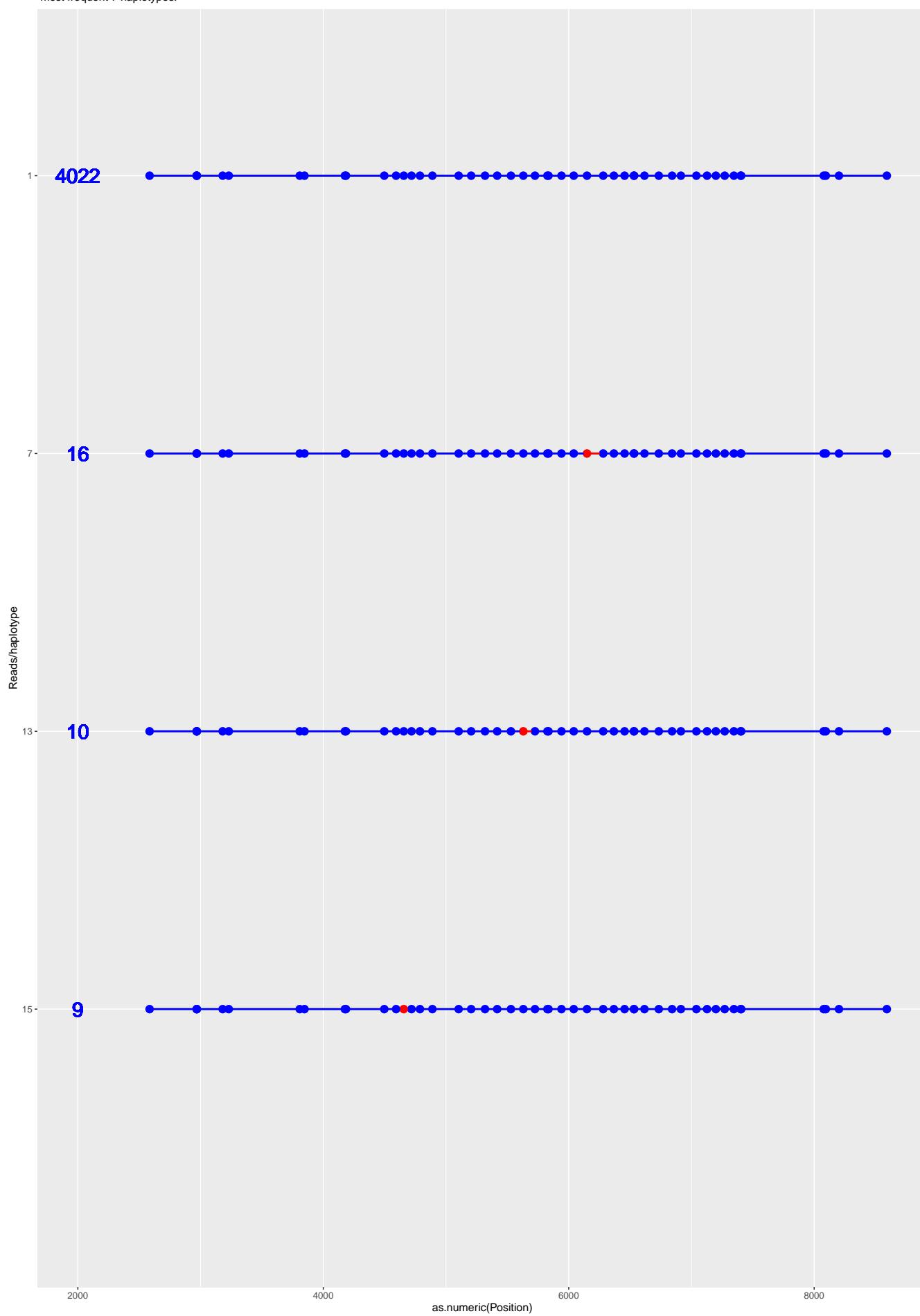
haplotypes I began with n[supporting reads] = 4420

most frequent 7 haplotypes.



barcode = AGAGCATCTCTGTACT & GACACGACTAGATCGC

Sample = 254c tetrad = 254 spore = c
Total reads = 4698 PCR=663
haplotypes I began with [n|supporting reads] = 9, 10, 16, 4022
most frequent 7 haplotypes.



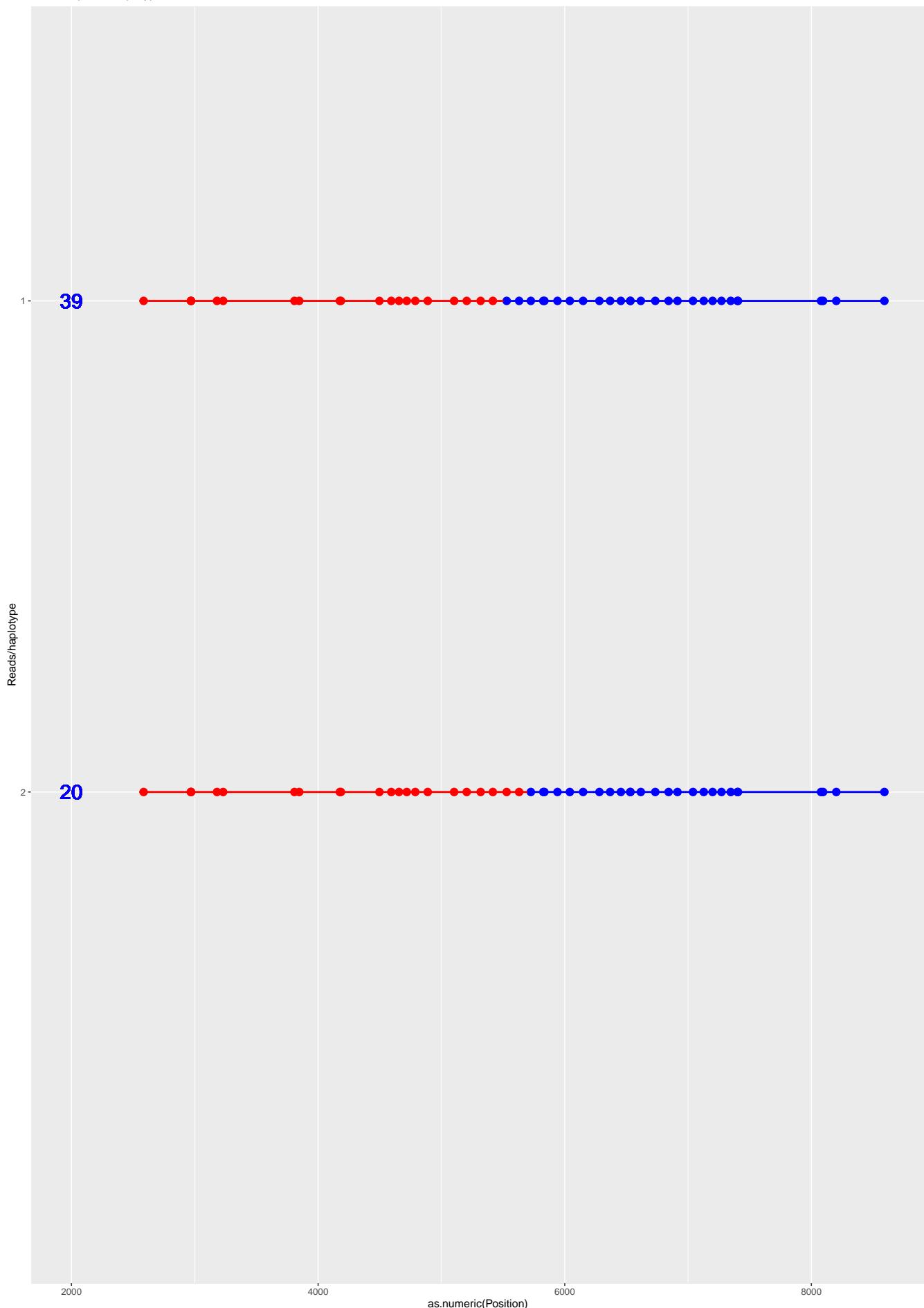
barcode = AGAGCATCTCTGTACT & TACGAGTCTGTCTAC

Sample = 254d tetrad = 254 spore = d

Total reads =78 PCR=664

haplotypes I began with n[supporting reads] = 20, 39

most frequent 7 haplotypes.



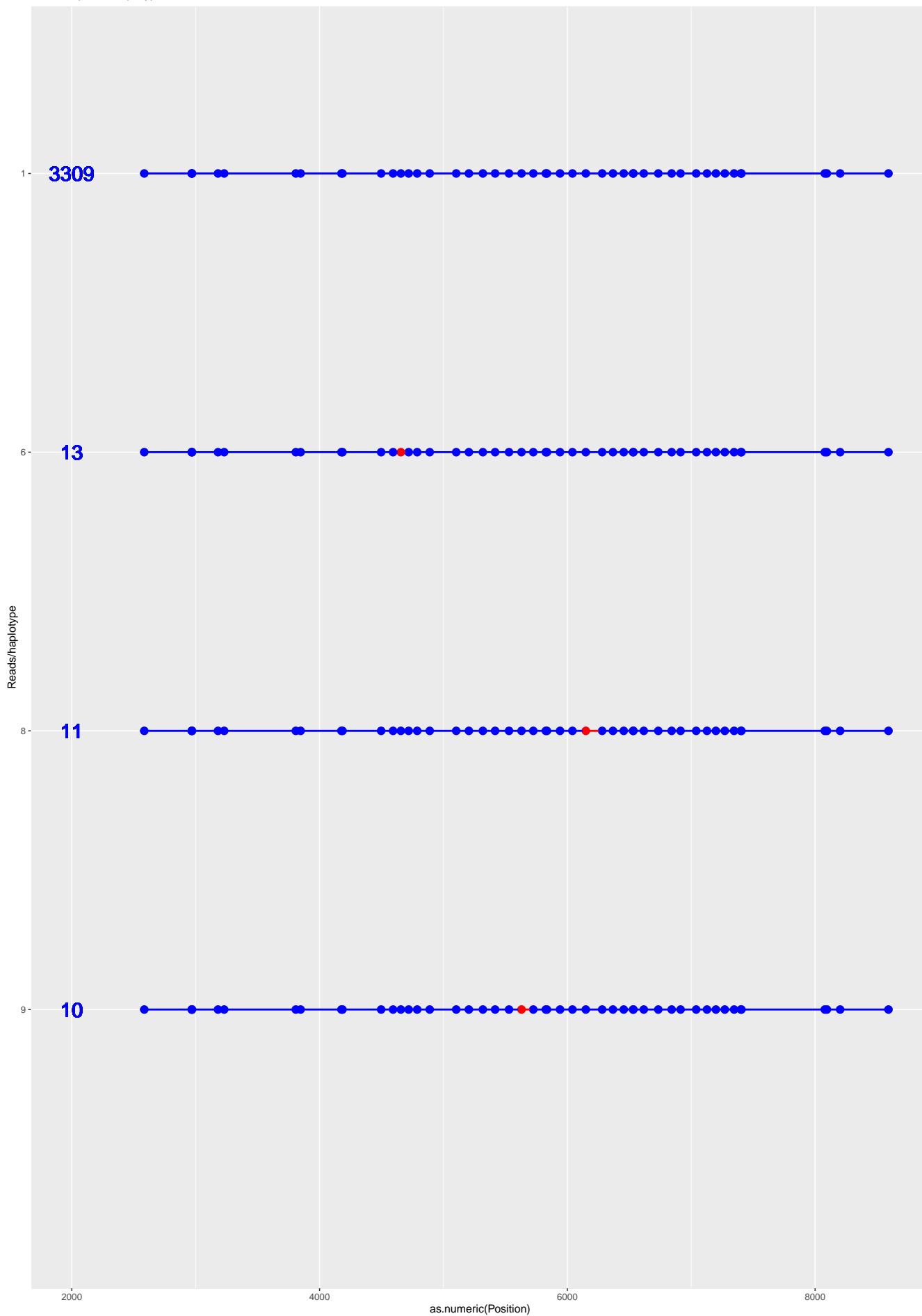
barcode = AGAGCATCTCTGTACT & ACTCAGCTACATAGTG

Sample = 255a tetrad = 255 spore = a

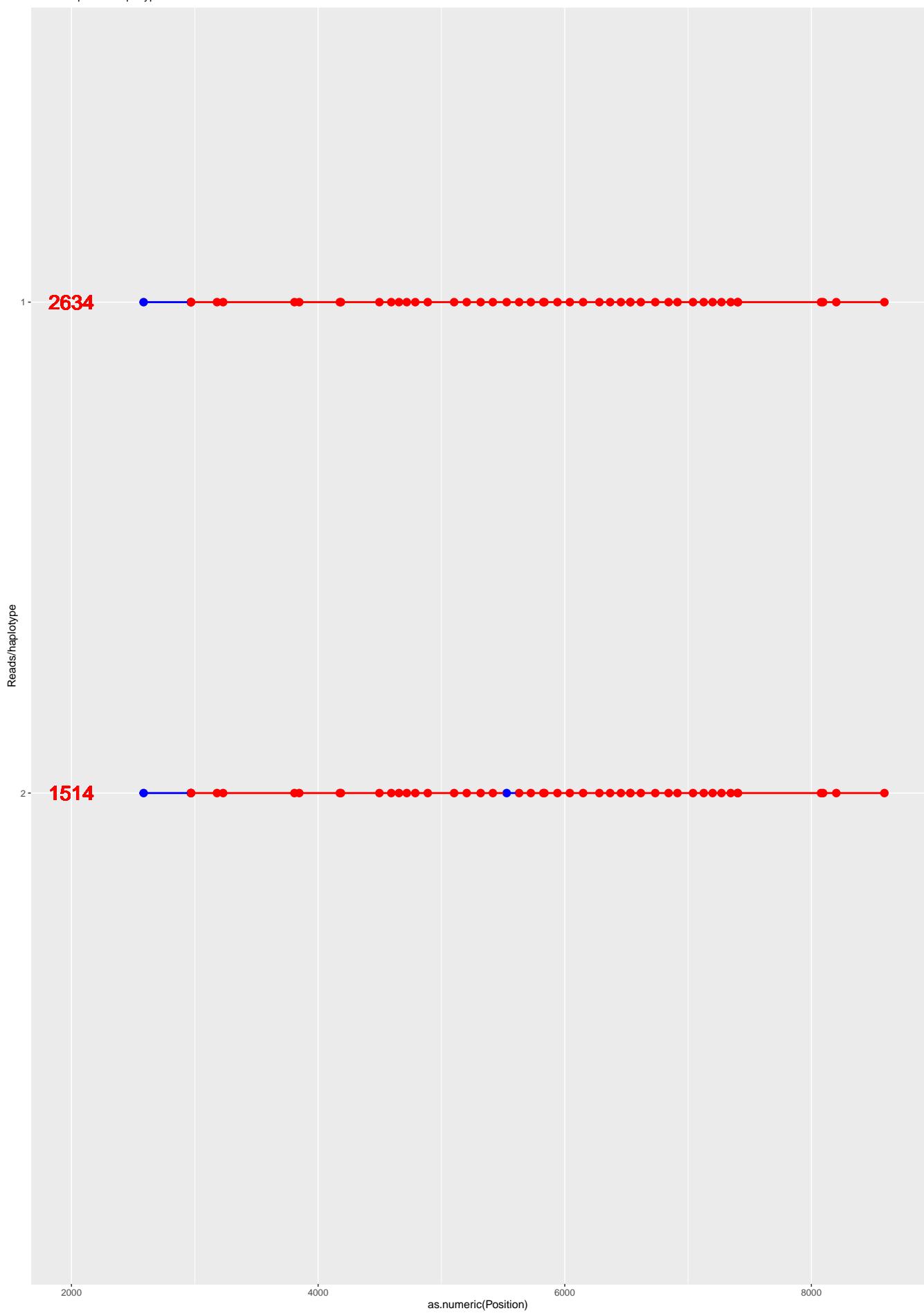
Total reads = 3837 PCR=665

haplotypes I began with n[supporting reads] = 10, 11, 13, 3309

most frequent 7 haplotypes.

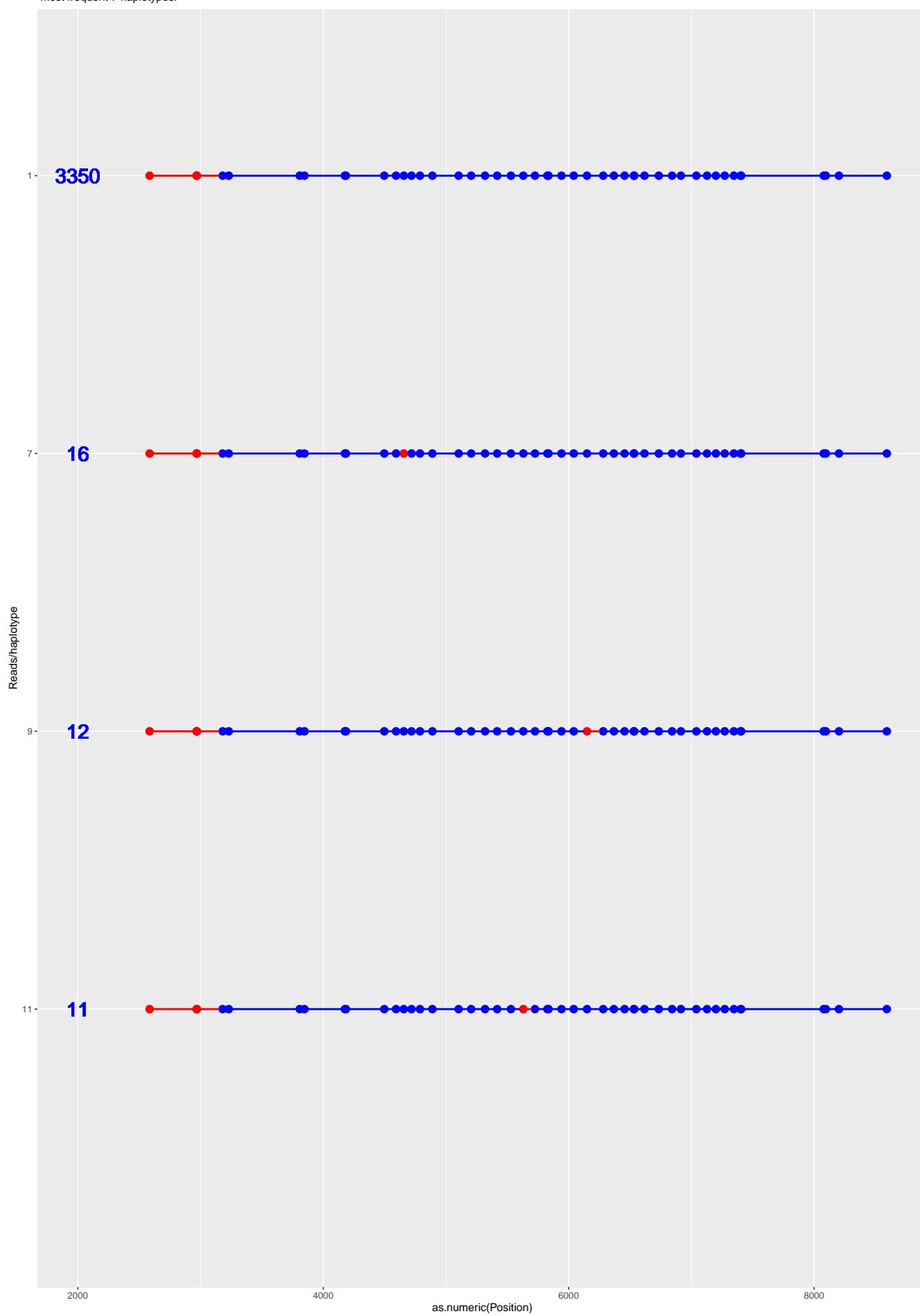


Sample = 255b tetrad = 255 spore = b
Total reads = 4370 PCR=666
haplotypes I began with n[supporting reads] = 1514, 2634
most frequent 7 haplotypes.



barcode = CGCATCGACTACGCTA & ACTGATGCGCACATGT

Sample = 255c tetrad = 255 spore = c
Total reads =3913 PCR=667
haplotypes I began with [n|supporting reads] = 11, 12, 16, 3350
most frequent 7 haplotypes.

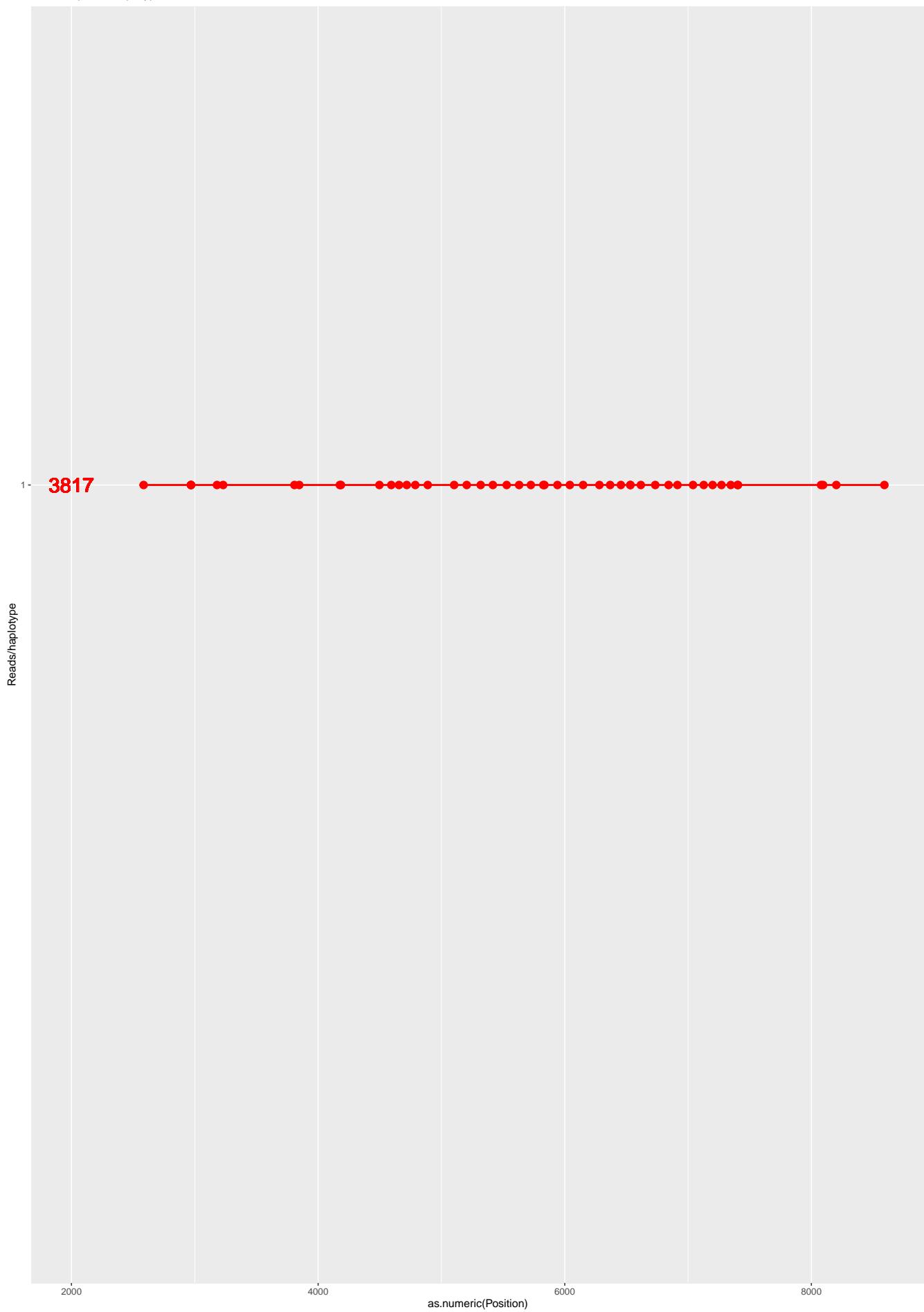


Sample = 255d tetrad = 255 spore = d

Total reads = 3999 PCR=668

haplotypes I began with n[supporting reads] = 3817

most frequent 7 haplotypes.



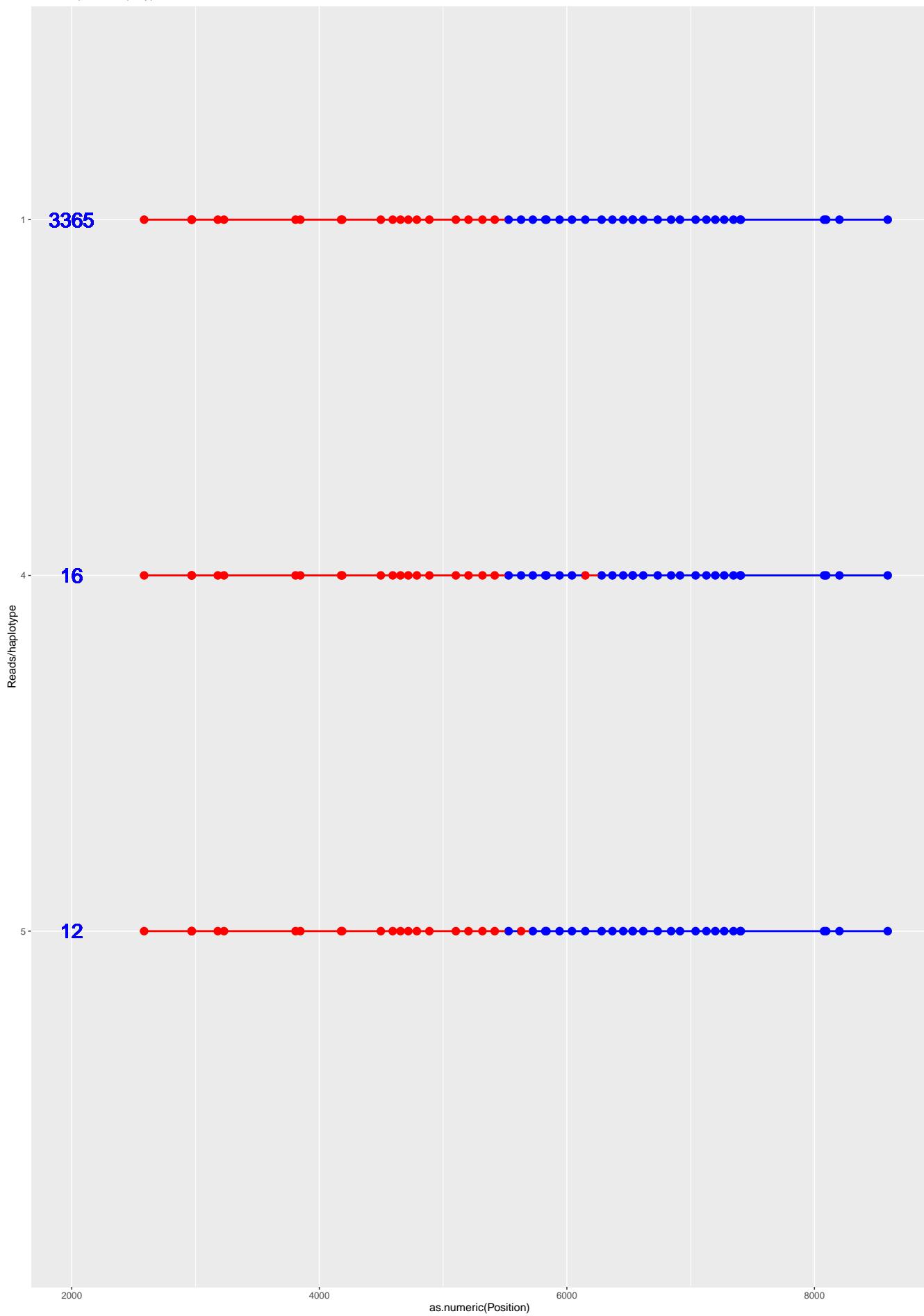
barcode = CGCATCGACTACGGCTA & ATCTACATCACGACTC

Sample = 258a tetrad = 258 spore = a

Total reads = 3635 PCR=669

haplotypes I began with n[supporting reads] = 12, 16, 3365

most frequent 7 haplotypes.



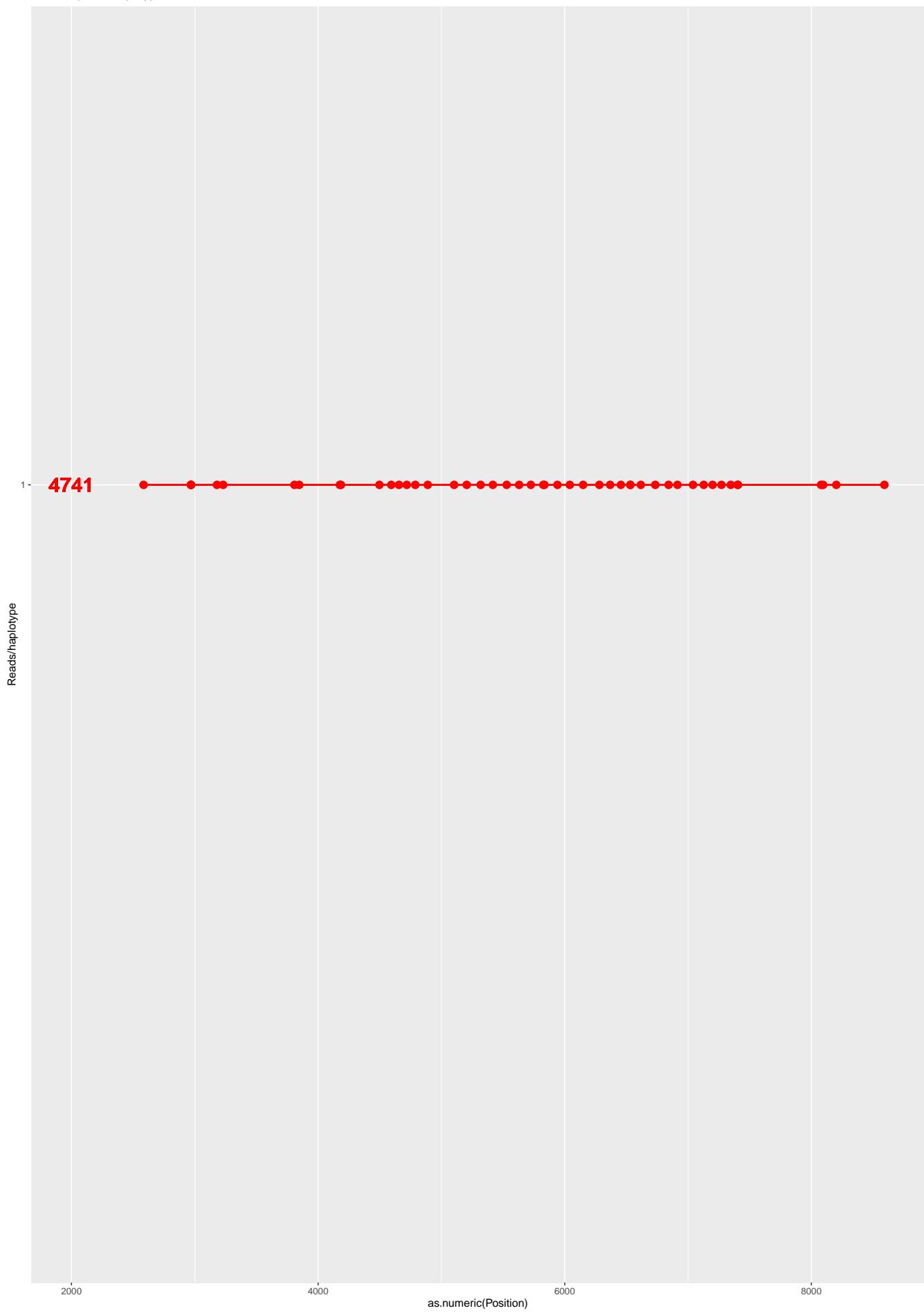
barcode = CGCATCGACTACGCTA & ATATAGTACAGCGTCT

Sample = 258b tetrad = 258 spore = b

Total reads = 4941 PCR=670

haplotypes I began with n[supporting reads] = 4741

most frequent 7 haplotypes.

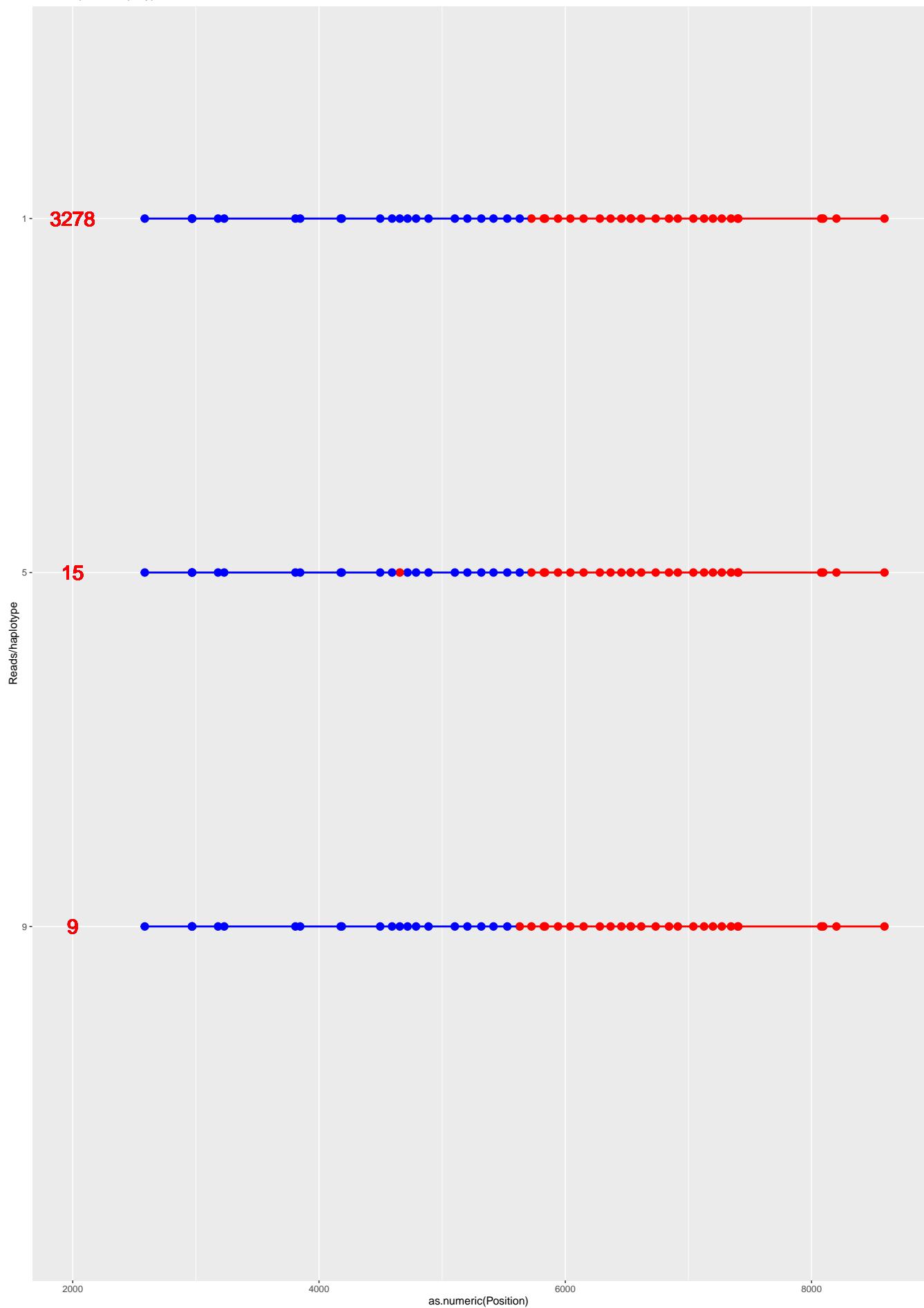


Sample = 258c tetrad = 258 spore = c

Total reads = 3741 PCR=671

haplotypes I began with n[supporting reads] = 9, 15, 3278

most frequent 7 haplotypes.

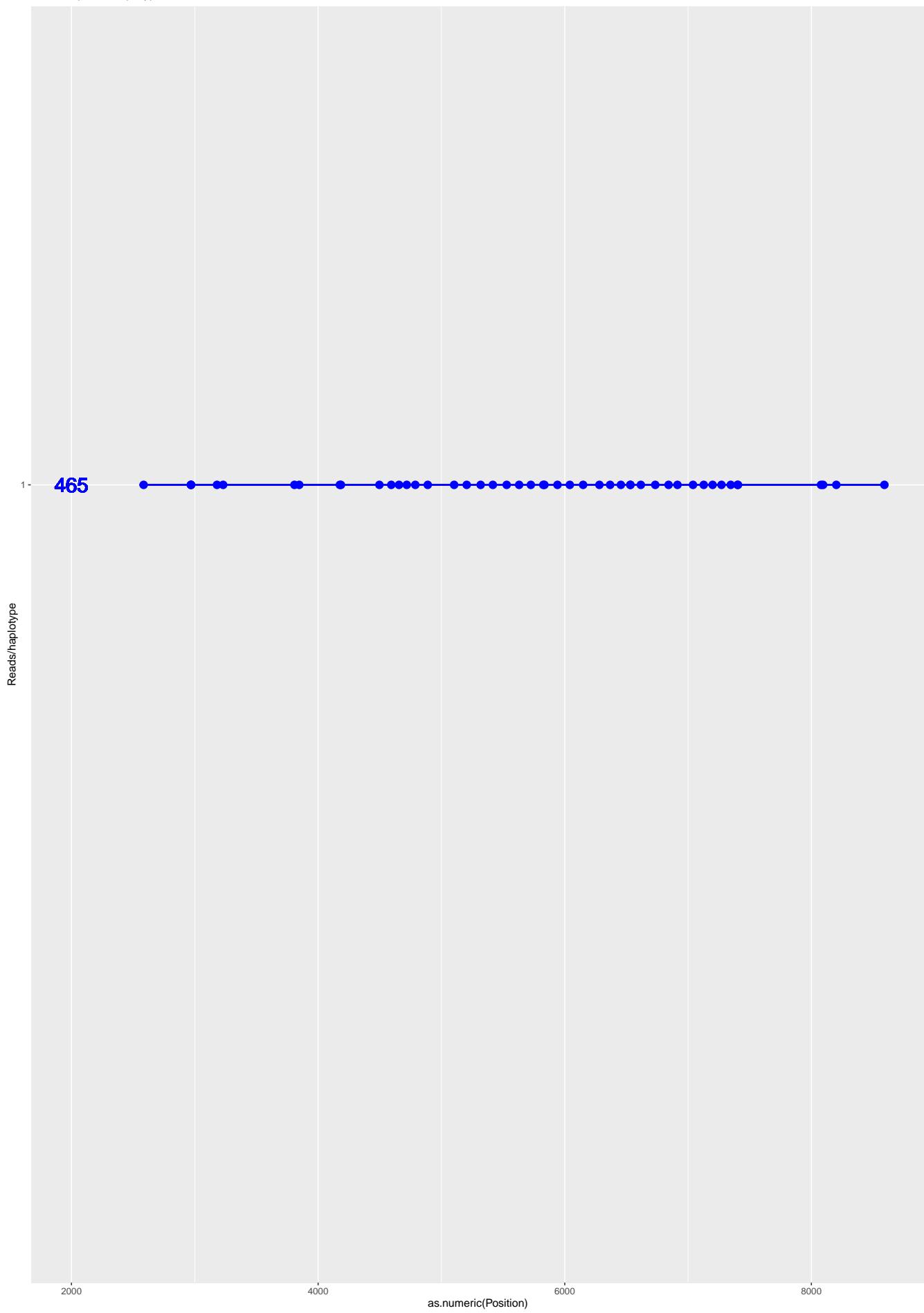


Sample = 258d tetrad = 258 spore = d

Total reads =567 PCR=672

haplotypes I began with n[supporting reads] = 465

most frequent 7 haplotypes.



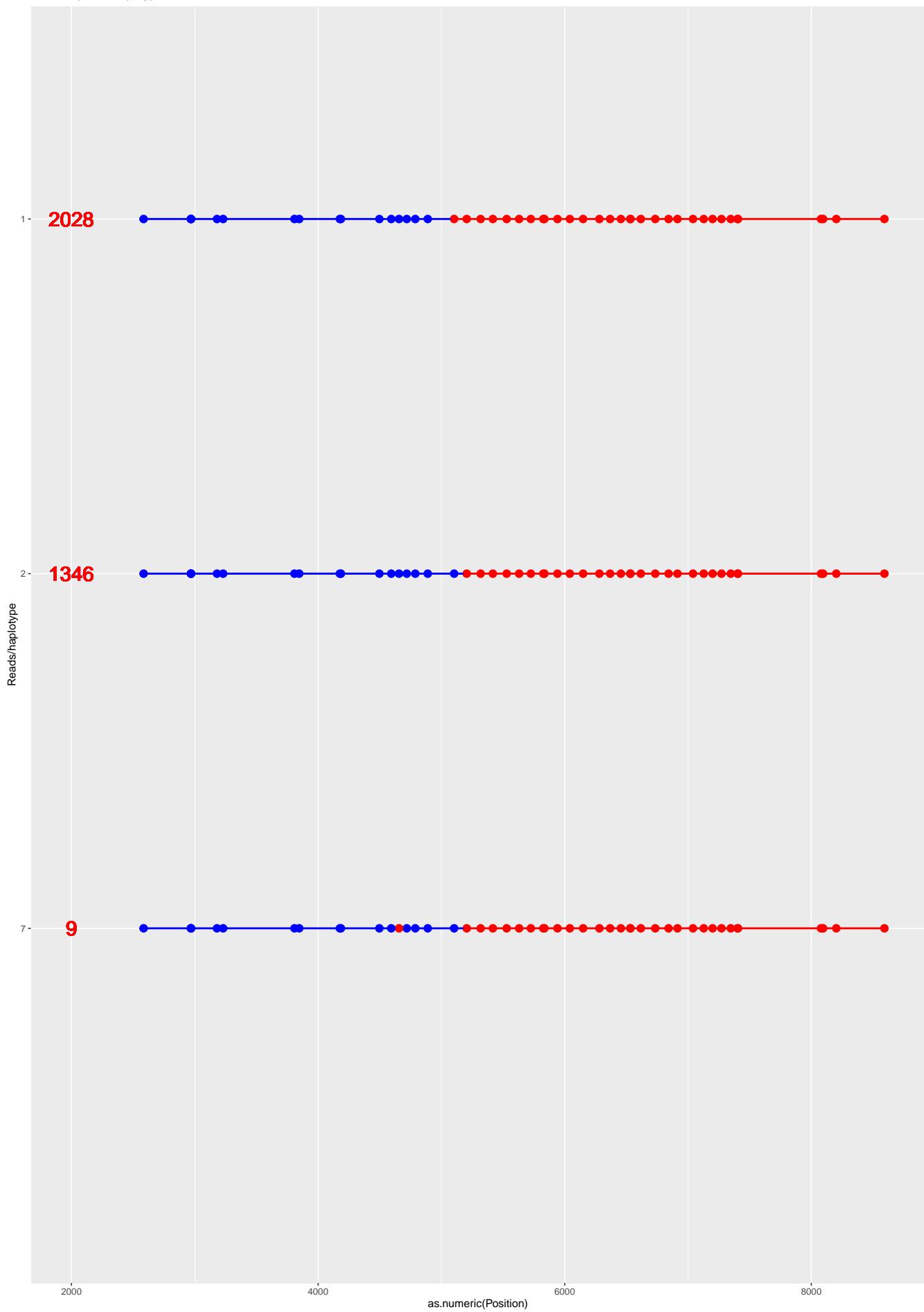
barcode = CGCATCGACTACGGCTA & ACTCAGCTACATAGTG

Sample = 259a tetrad = 259 spore = a

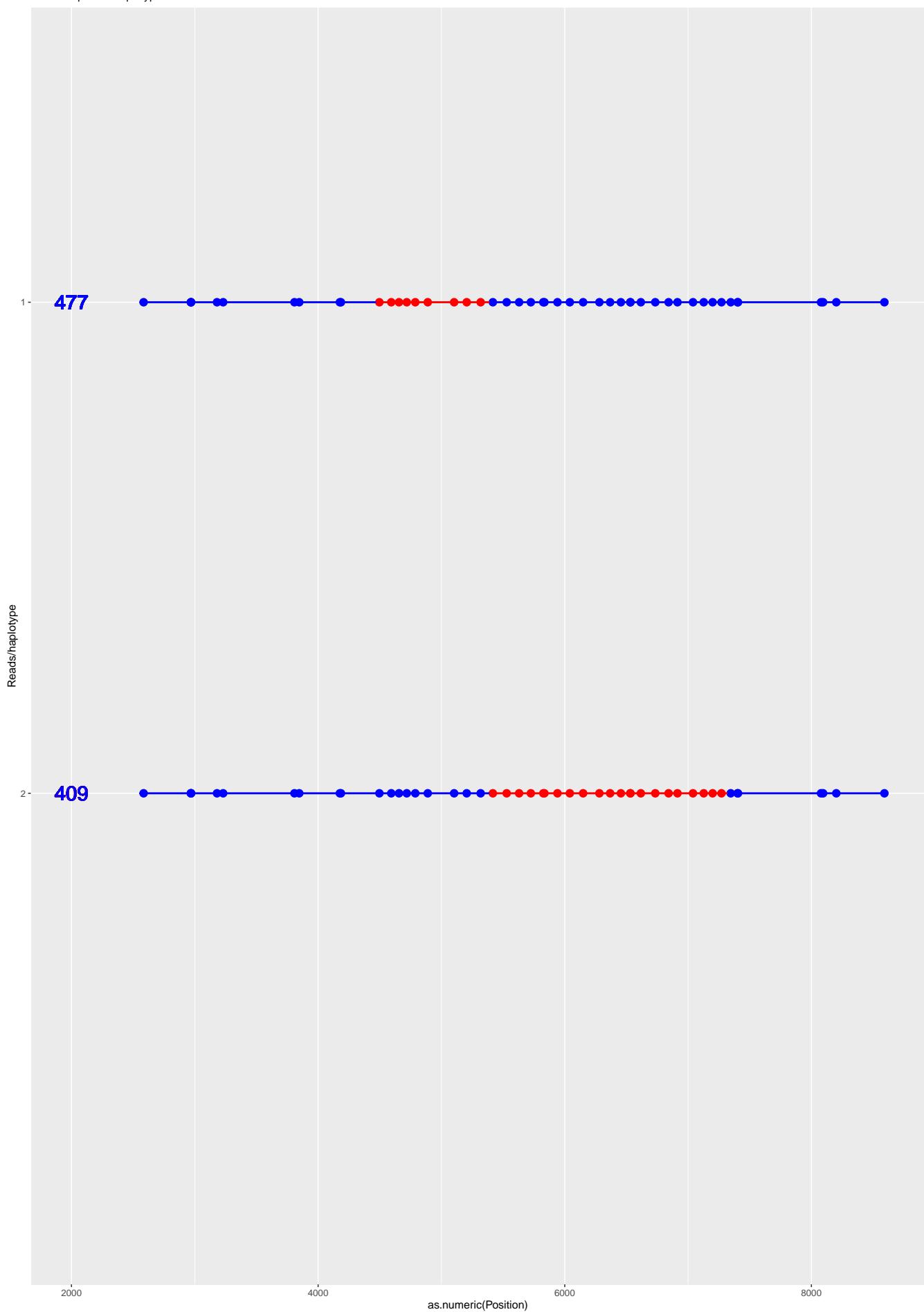
Total reads = 3842 PCR=673

haplotypes I began with n[supporting reads] = 9, 1346, 2028

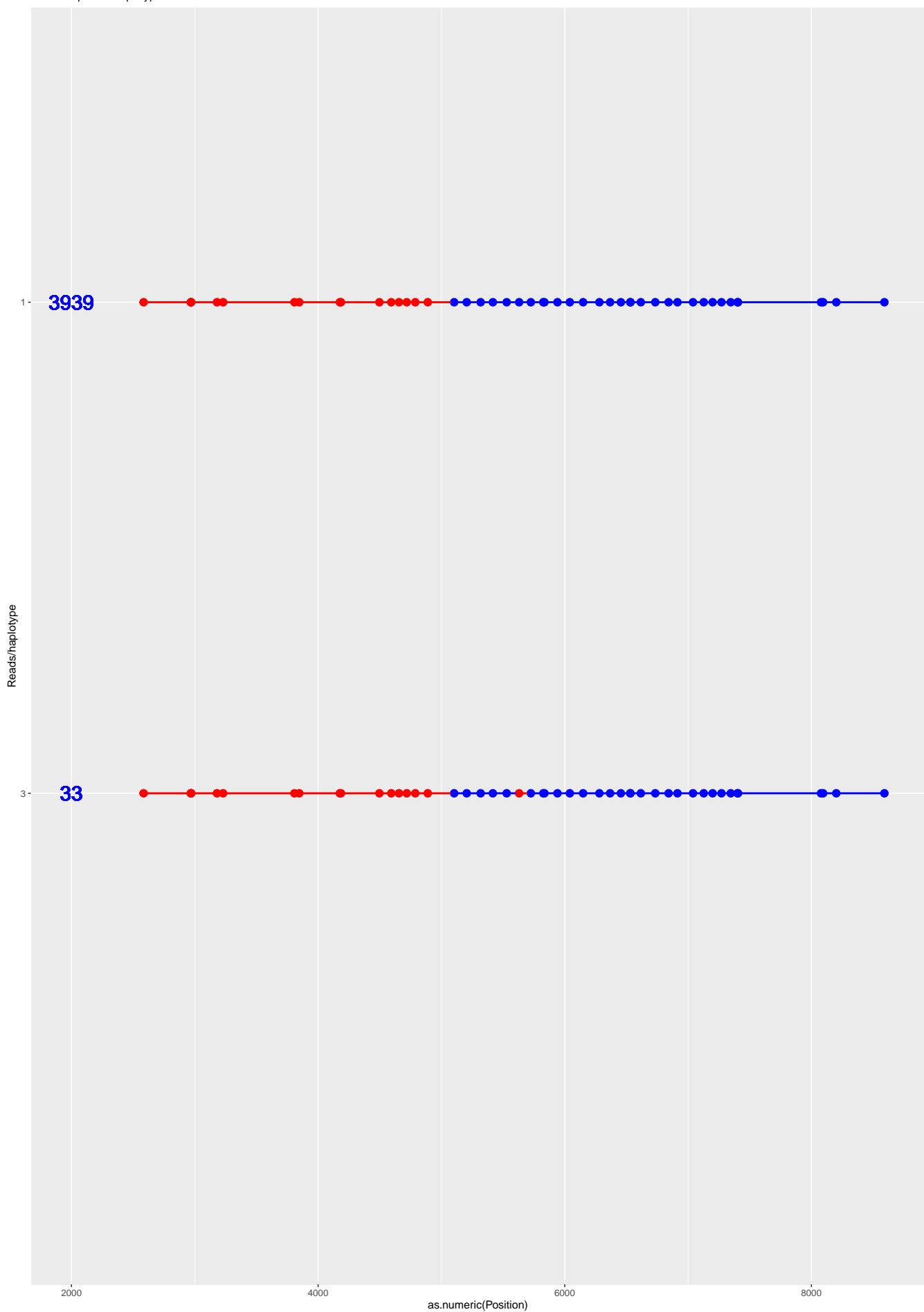
most frequent 7 haplotypes.



Sample = 259b tetrad = 259 spore = b
Total reads = 1887 PCR=674
haplotypes I began with n[supporting reads] = 409, 477
most frequent 7 haplotypes.



Sample = 259c tetrad = 259 spore = c
Total reads = 4486 PCR=675
haplotypes I began with n[supporting reads] = 33, 3939
most frequent 7 haplotypes.



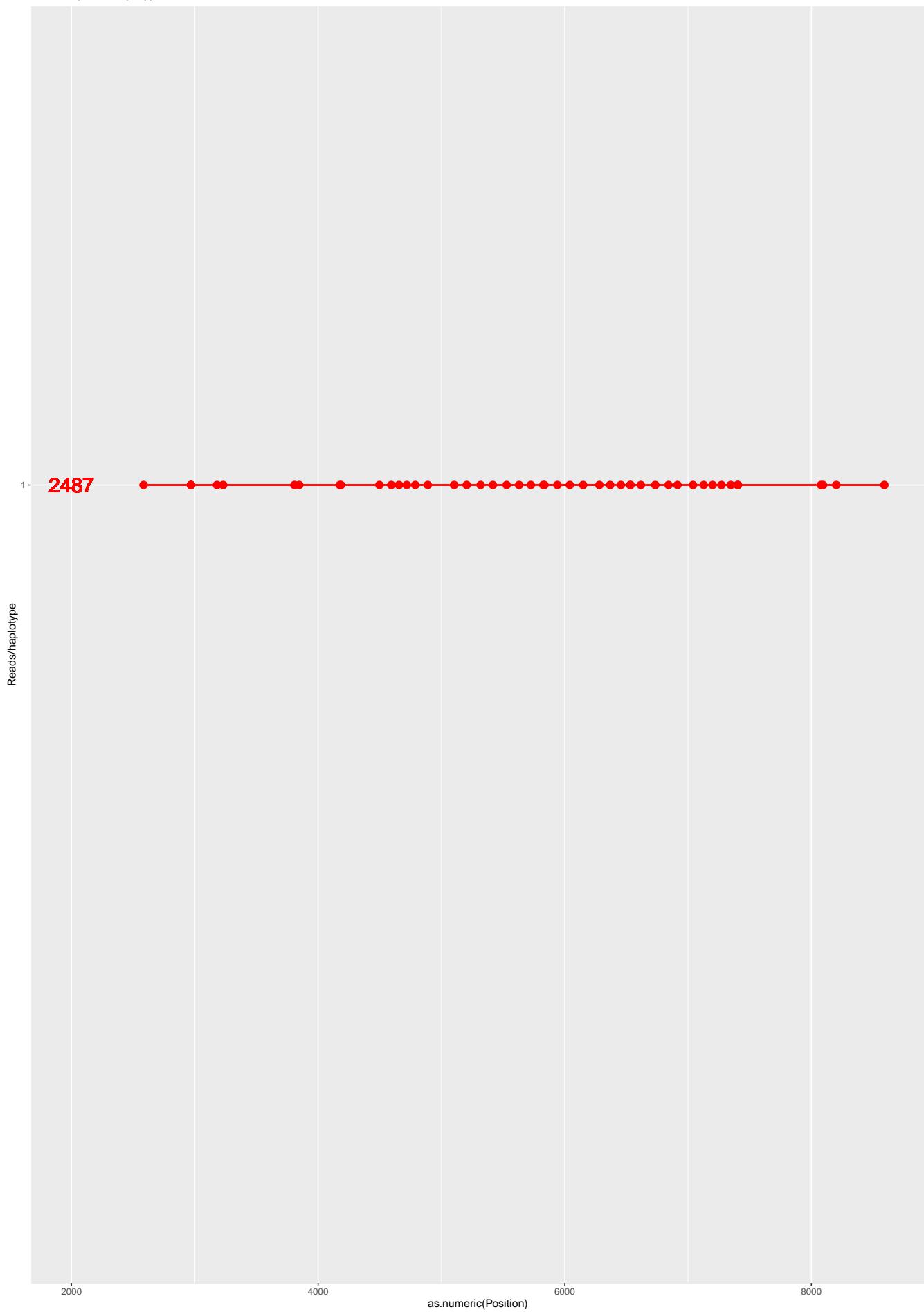
barcode = CGTAGCGTGCTATCAC & CTACTCTCAGCAGTGA

Sample = 259d tetrad = 259 spore = d

Total reads = 2589 PCR=676

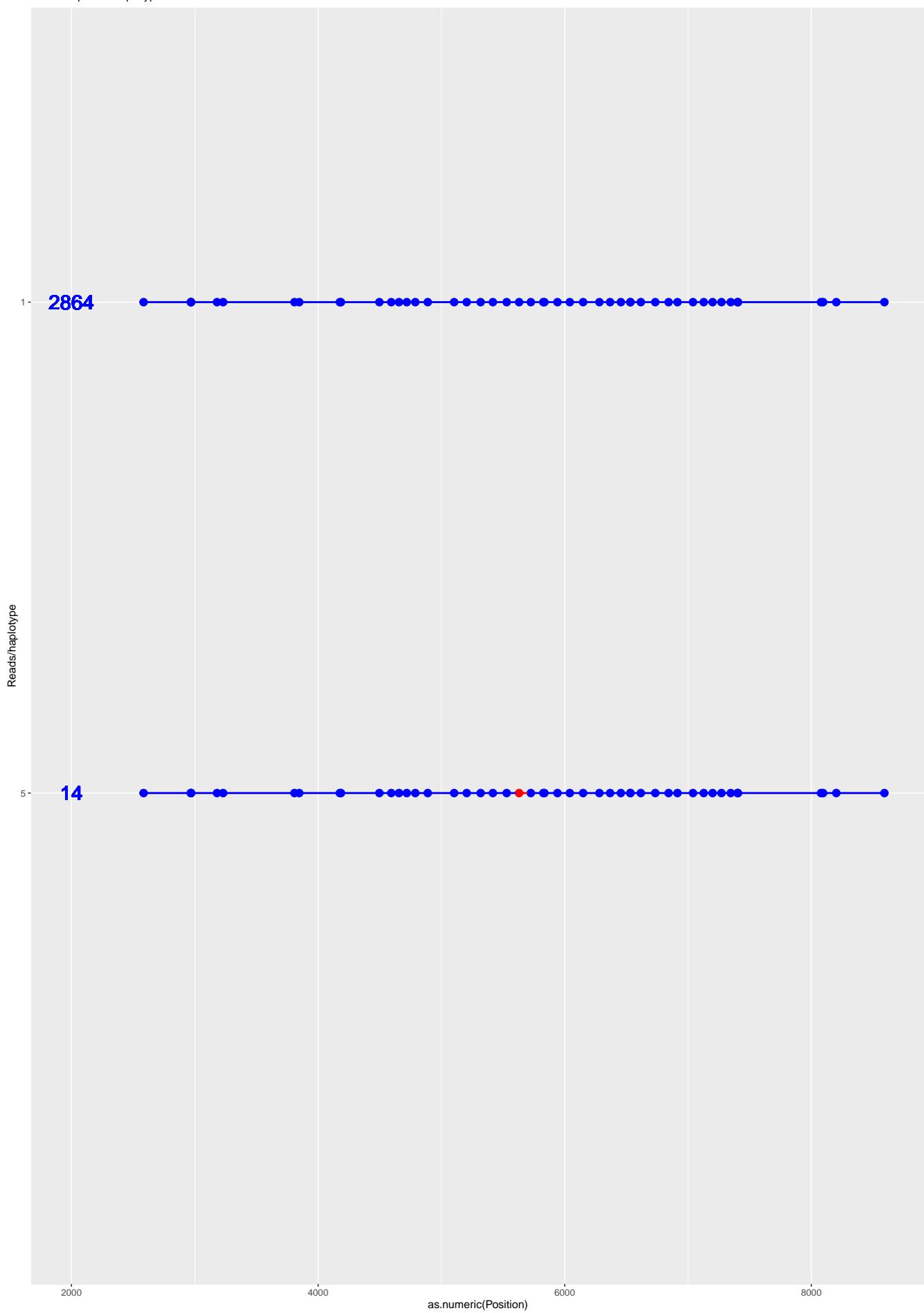
haplotypes I began with n[supporting reads] = 2487

most frequent 7 haplotypes.



barcode = CGTAGCGTGCTATCAC & ATCTACATCACGACTC

Sample = 267a tetrad = 267 spore = a
Total reads = 3374 PCR=689
haplotypes I began with n[supporting reads] = 14, 2864
most frequent 7 haplotypes.



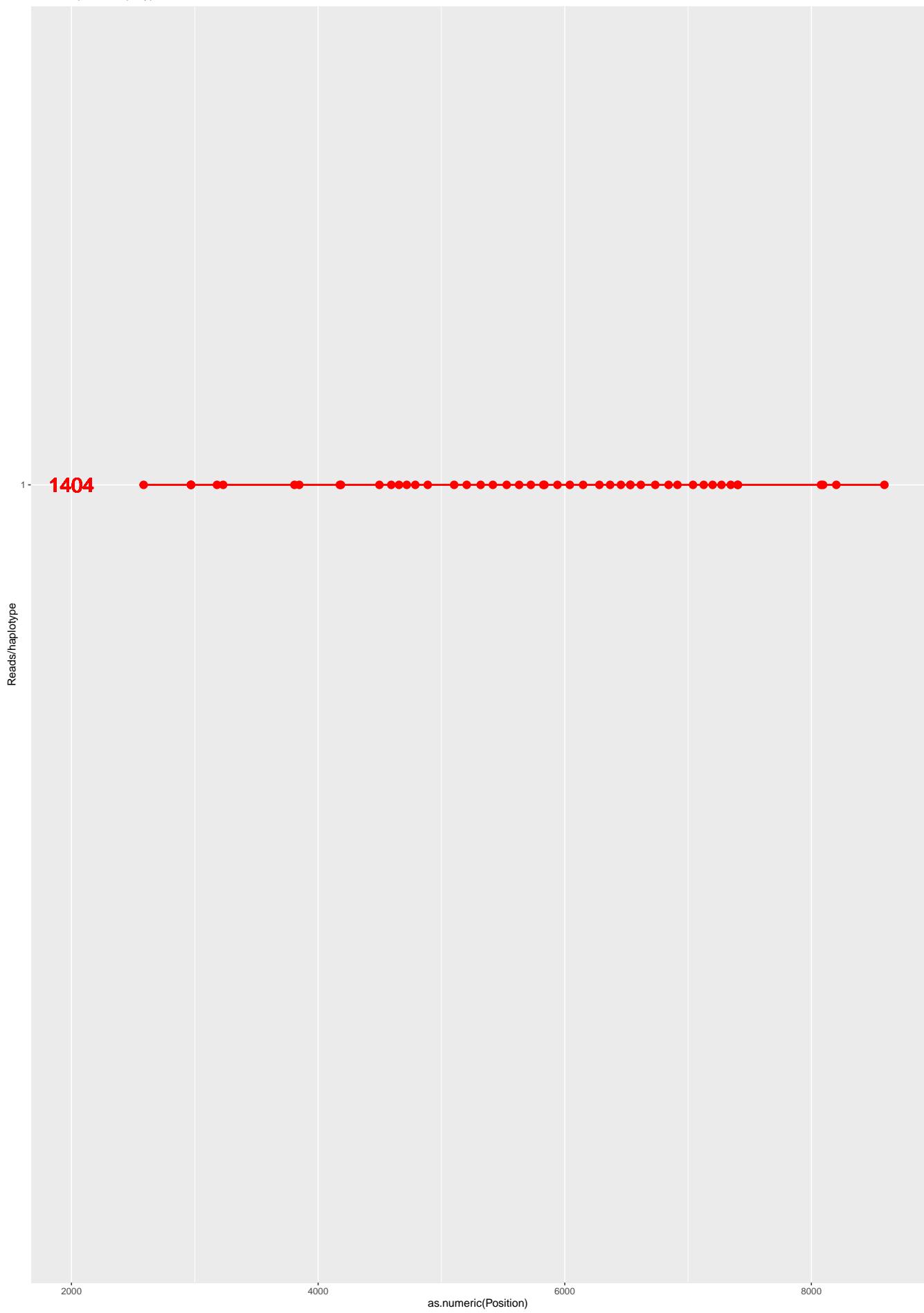
barcode = TGCCTGAGCTGTACAT & TCAGCTGACGATGTGA

Sample = 267b tetrad = 267 spore = b

Total reads = 1468 PCR=690

haplotypes I began with n[supporting reads] = 1404

most frequent 7 haplotypes.

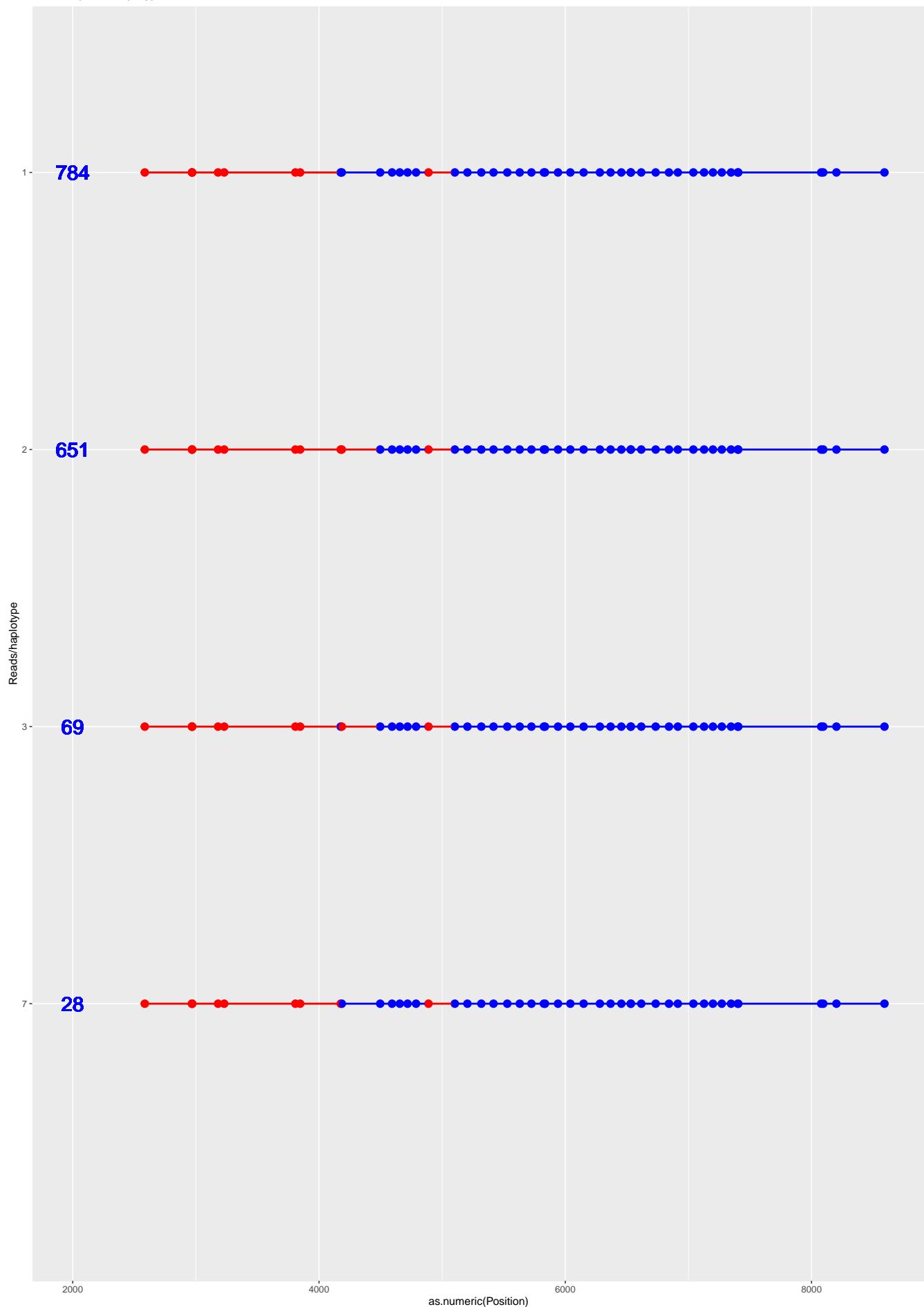


Sample = 267c tetrad = 267 spore = c

Total reads = 1899 PCR=691

haplotypes I began with n[supporting reads] = 28, 69, 651, 784

most frequent 7 haplotypes.

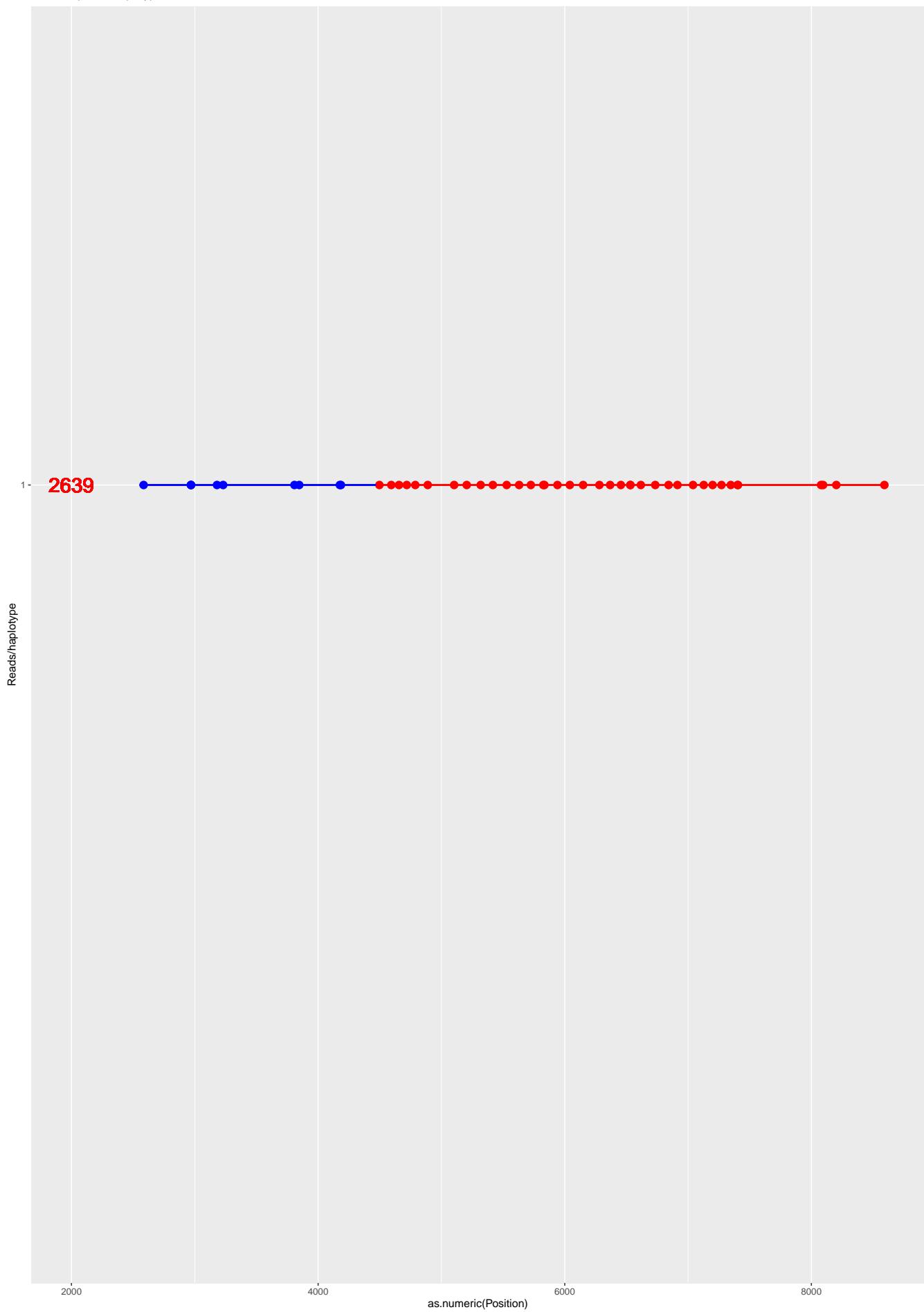


Sample = 267d tetrad = 267 spore = d

Total reads = 2830 PCR=692

haplotypes I began with n[supporting reads] = 2639

most frequent 7 haplotypes.



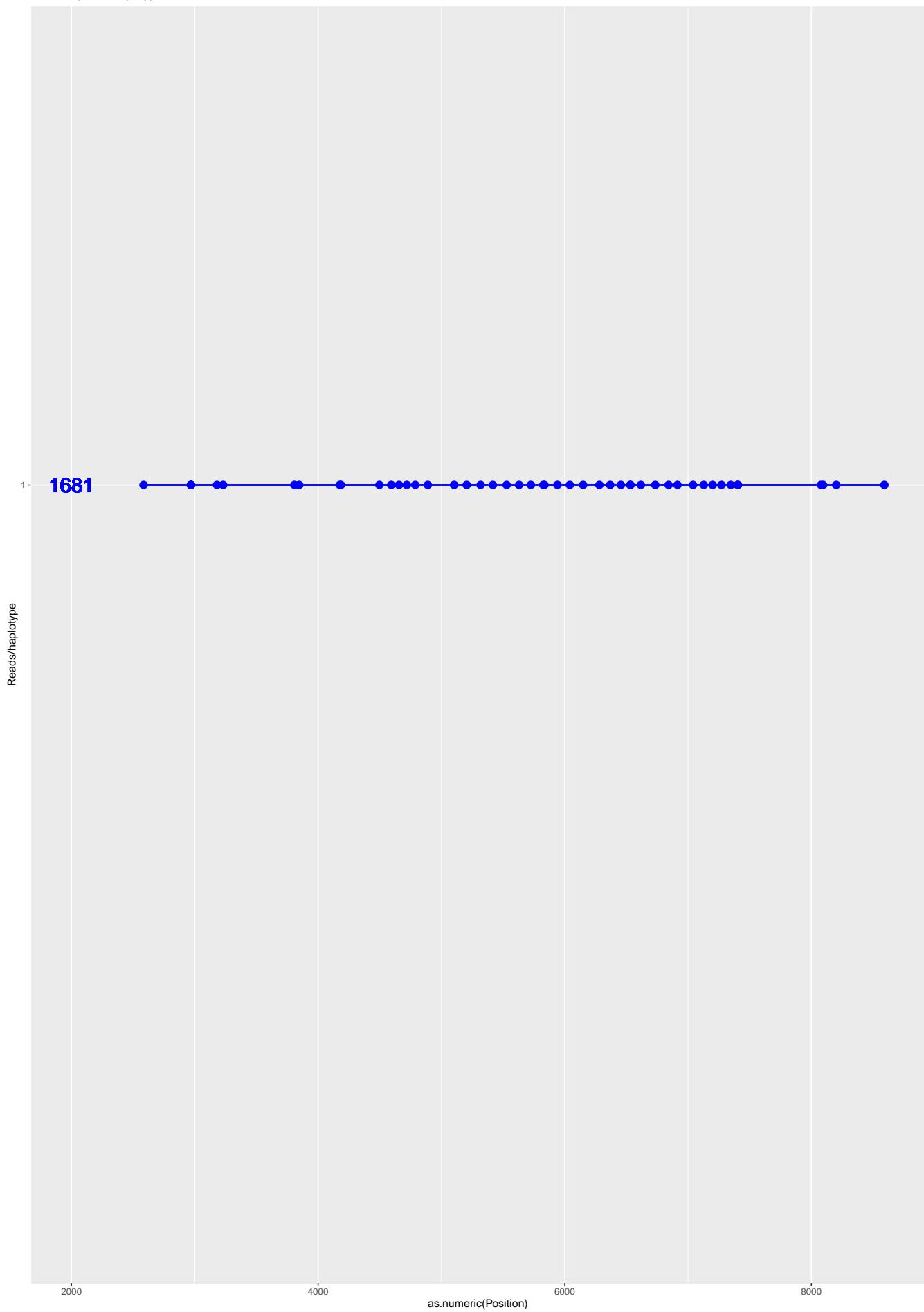
barcode = TGCGTGAGCTGTACAT & ATCTACATCACGACTC

Sample = 273a tetrad = 273 spore = a

Total reads = 1932 PCR=701

haplotypes I began with n[supporting reads] = 1681

most frequent 7 haplotypes.



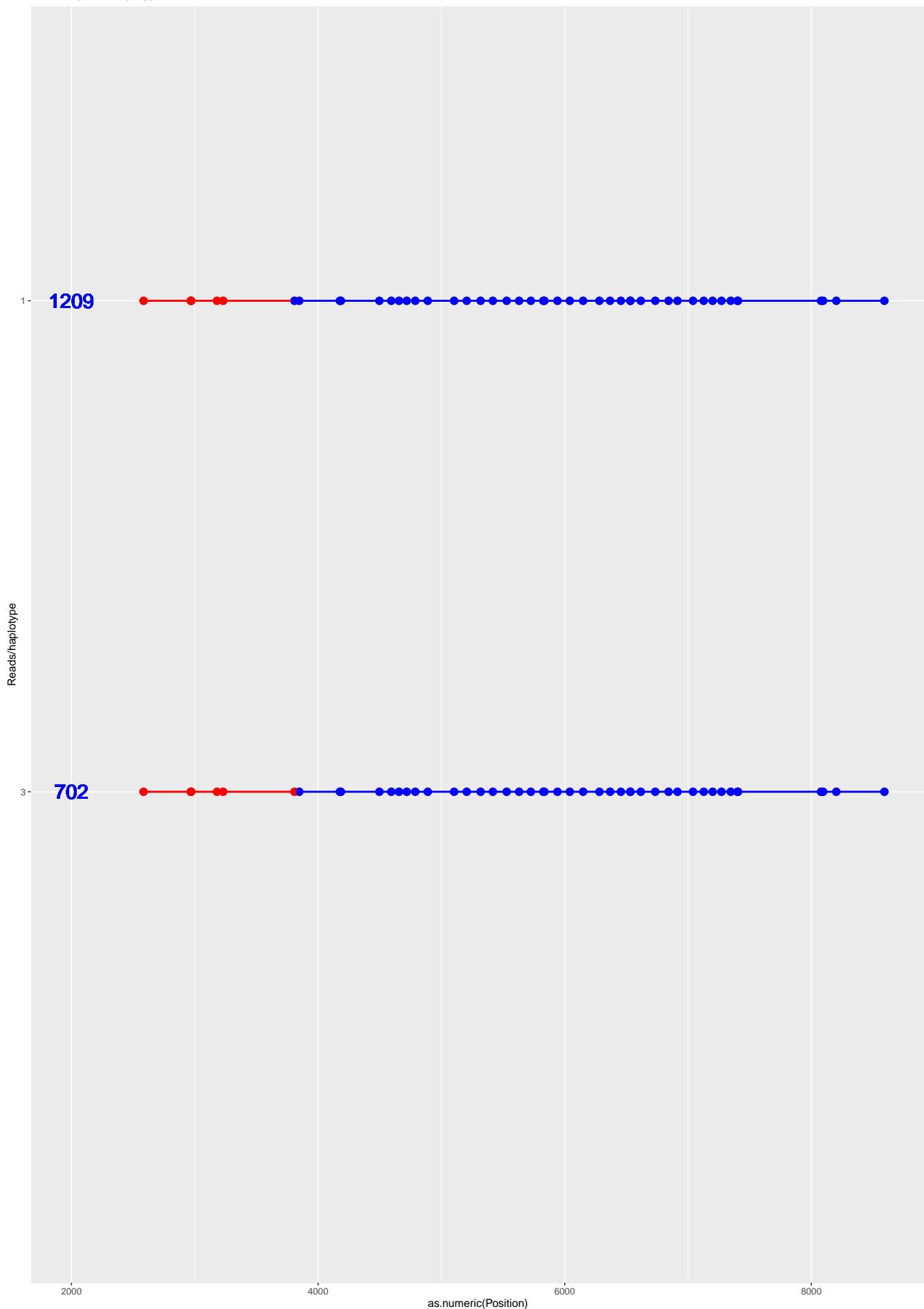
barcode = CGATCATCTATAGACA & ATATAGTACAGCGTCT

Sample = 273b tetrad = 273 spore = b

Total reads = 3306 PCR=702

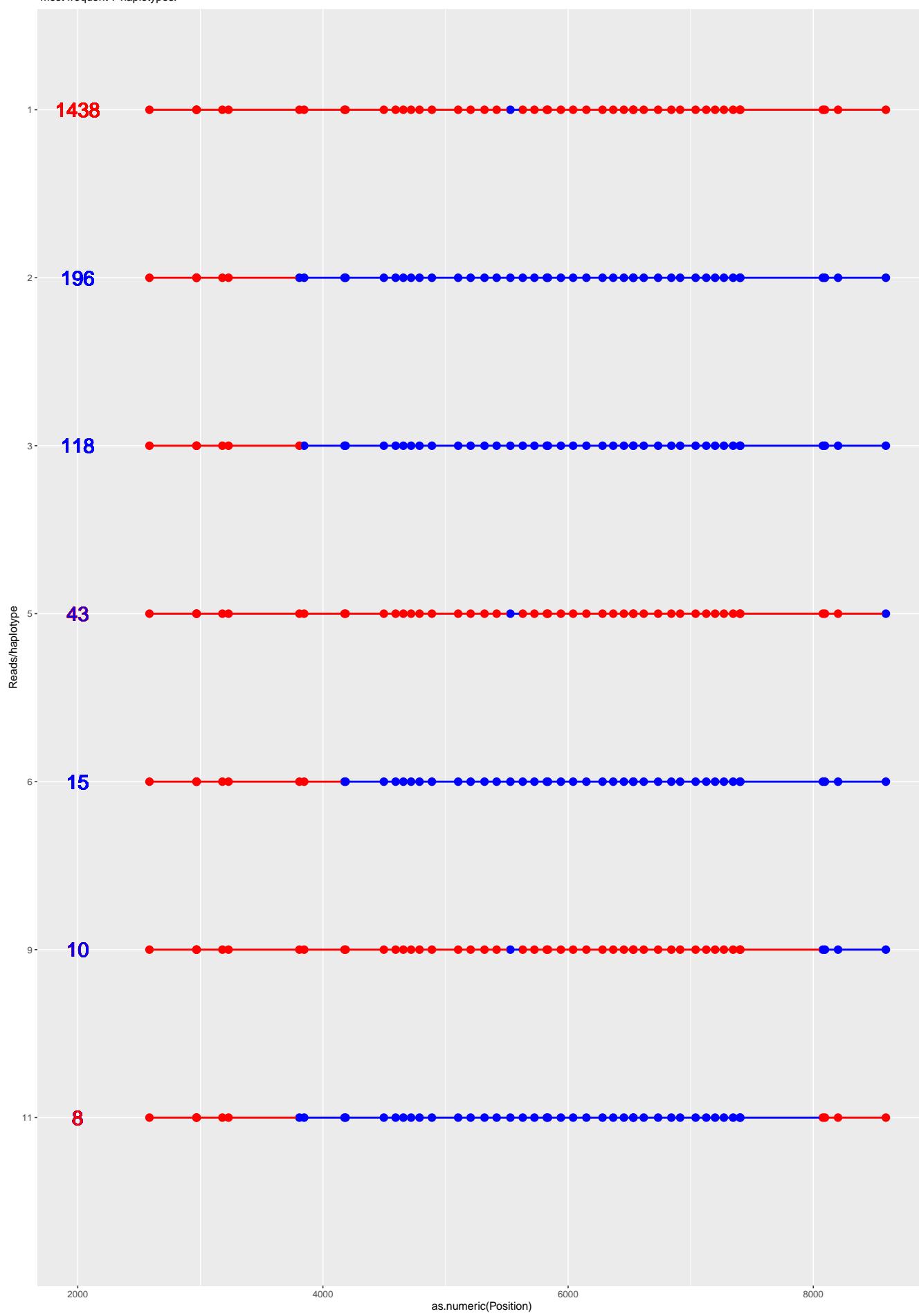
haplotypes I began with n[supporting reads] = 702, 1209

most frequent 7 haplotypes.

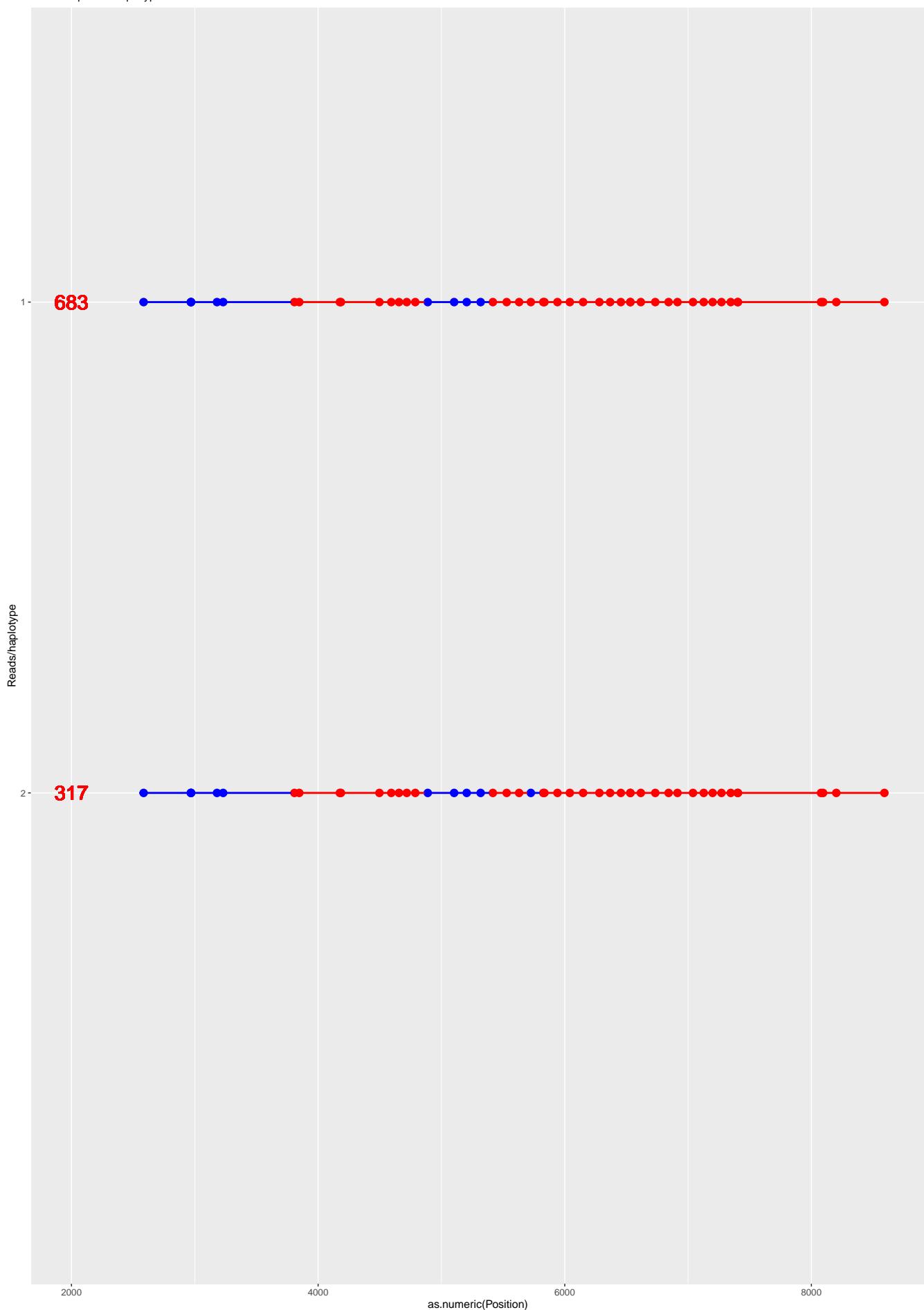


barcode = CGATCATCTATAGACA & GACACGACTAGATCGC

Sample = 273c tetrad = 273 spore = c
Total reads = 3496 PCR=703
haplotypes I began with [n(supporting reads)] = 8, 10, 15, 43, 118, 196, 1438
most frequent 7 haplotypes.

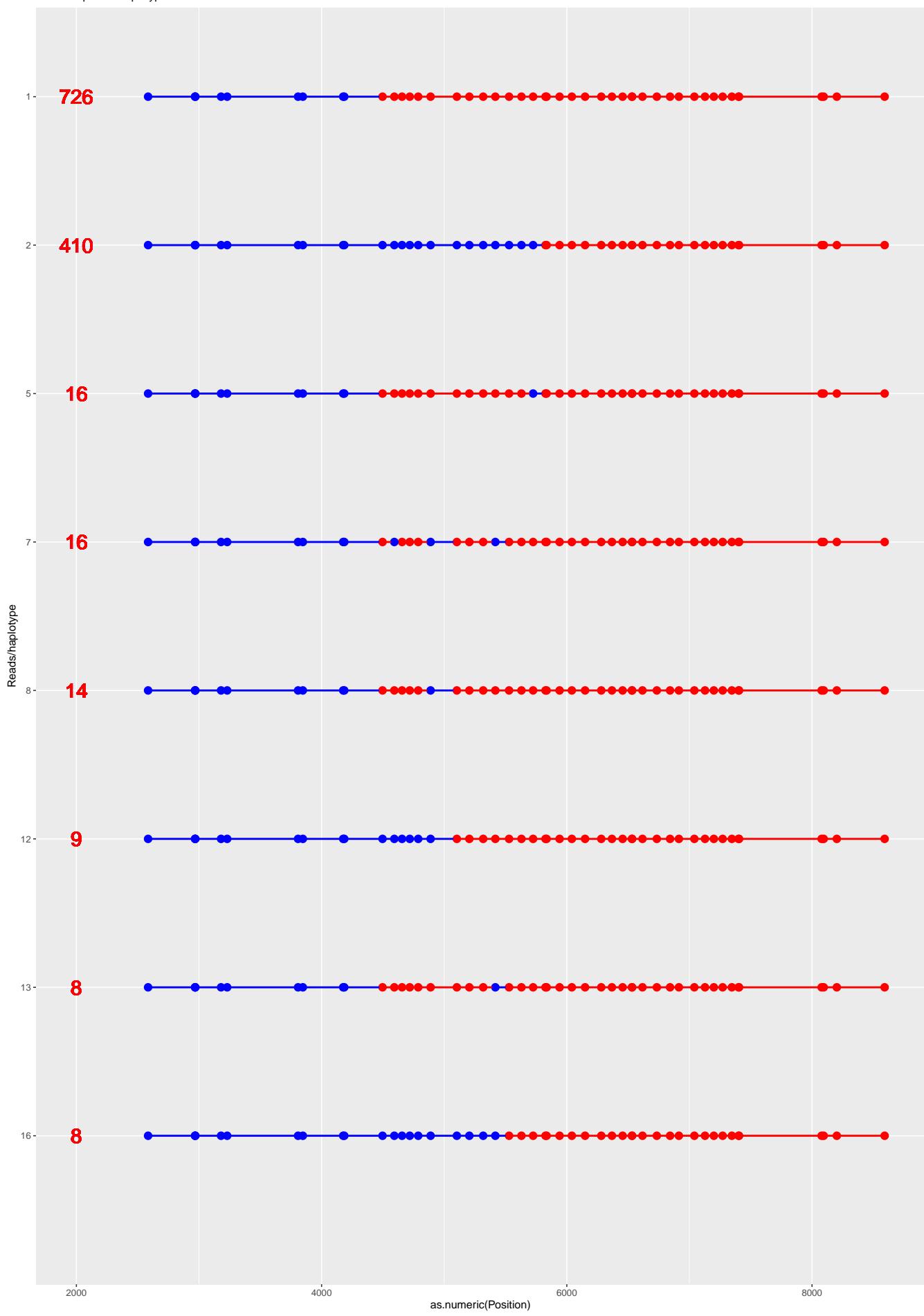


Sample = 273d tetrad = 273 spore = d
Total reads = 1048 PCR=704
haplotypes I began with n[supporting reads] = 317, 683
most frequent 7 haplotypes.



barcode = CGATCATCTATAGACA & ACTCAGCTACATAGTG

Sample = 274a tetrad = 274 spore = a
 Total reads = 2093 PCR=705
 haplotypes I began with [n(supporting reads)] = 8, 9, 14, 16, 410, 726
 most frequent 7 haplotypes.



Sample = 274b tetrad = 274 spore = b

Total reads = 4818 PCR=706

haplotypes I began with n[supporting reads] = 8, 2135, 2311

most frequent 7 haplotypes.



barcode = CGACGTATCTGACAGT & ACTGATGCGCACATGT

Sample = 274c tetrad = 274 spore = c

Total reads = 3010 PCR=707

haplotypes I began with n[supporting reads] = 10, 11, 2607

most frequent 7 haplotypes.

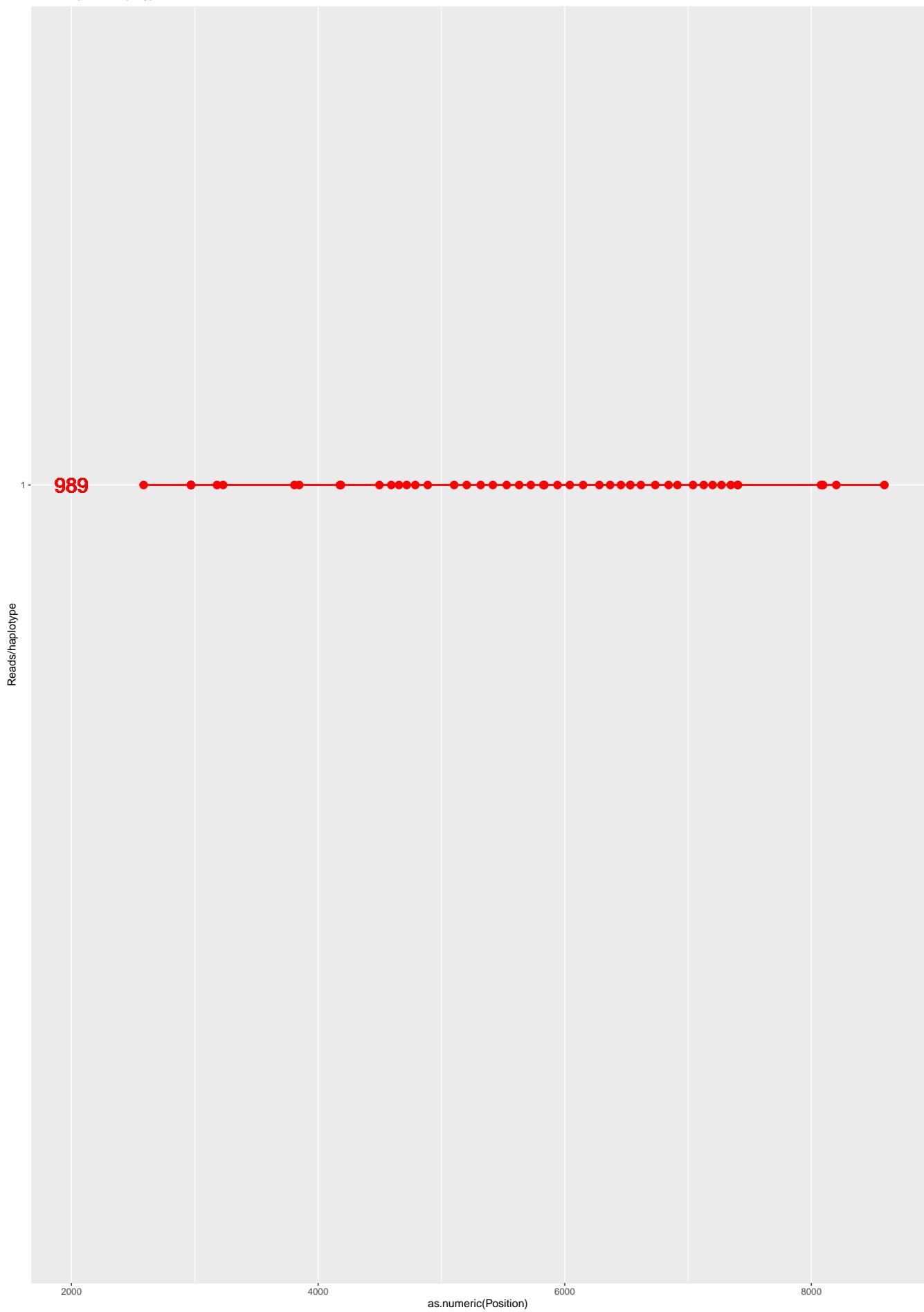


Sample = 274d tetrad = 274 spore = d

Total reads = 1030 PCR=708

haplotypes I began with n[supporting reads] = 989

most frequent 7 haplotypes.



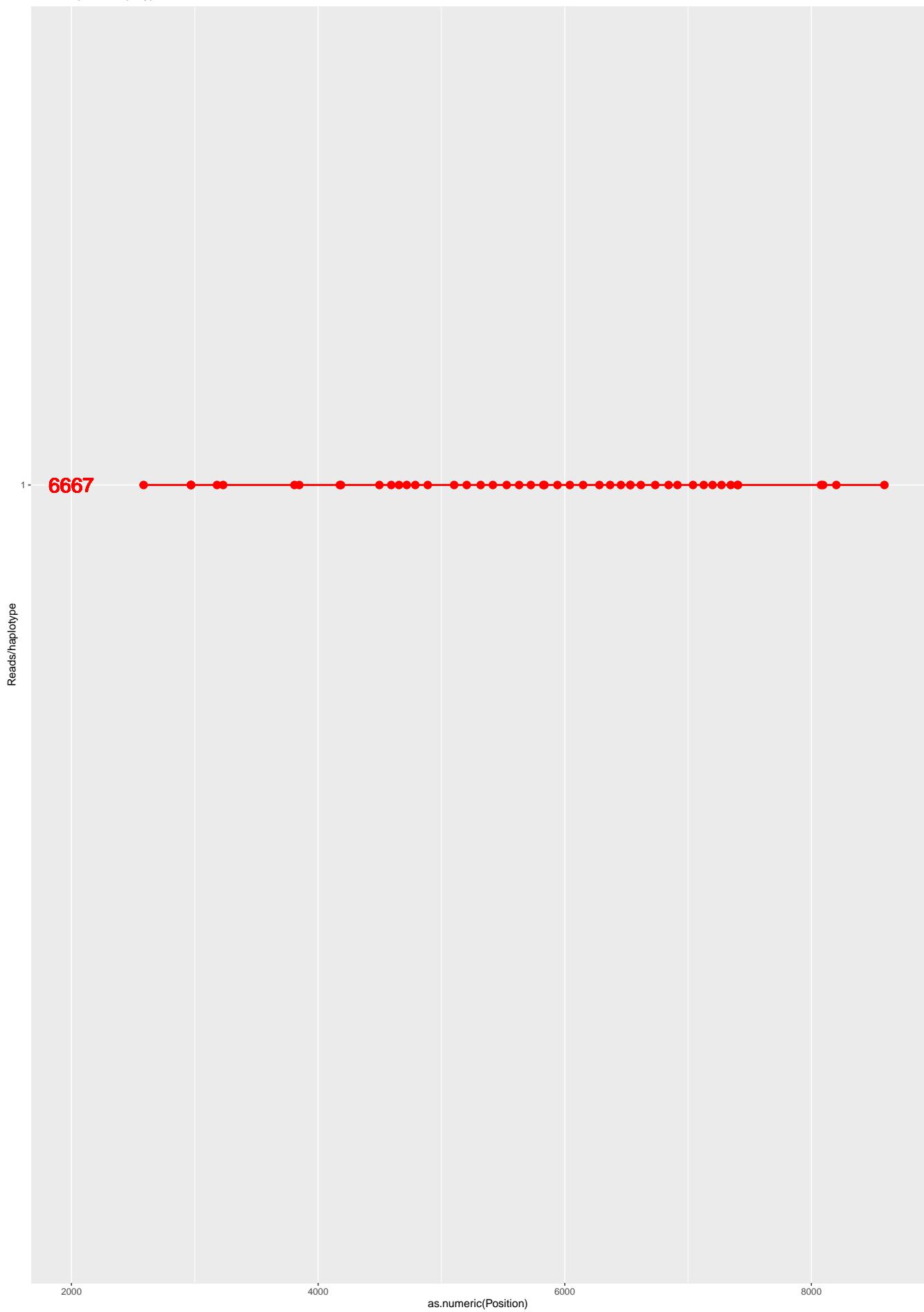
barcode = CGACGTATCTGACAGT & ATCTACATCACGACTC

Sample = 275a tetrad = 275 spore = a

Total reads = 6945 PCR=709

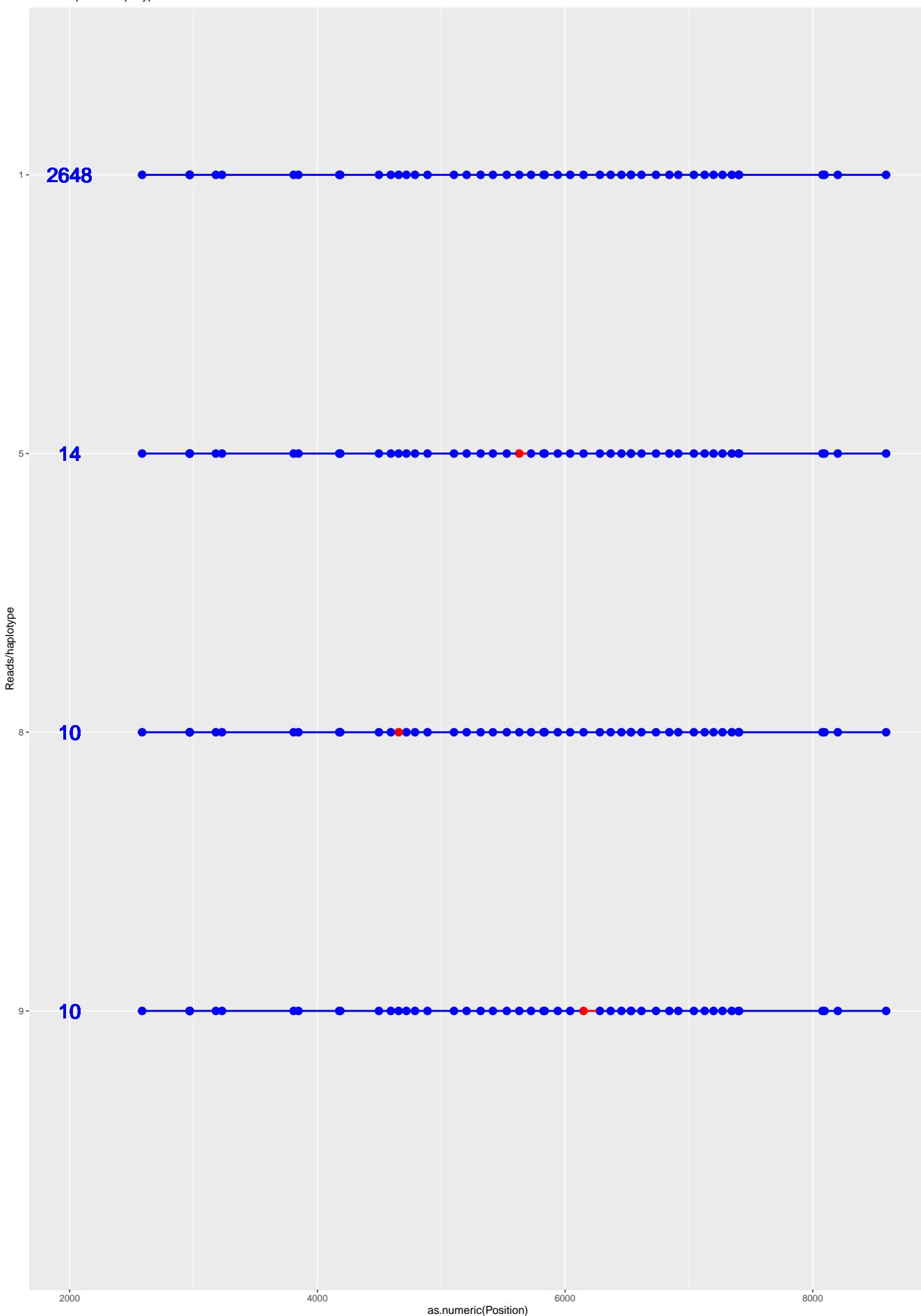
haplotypes I began with n[supporting reads] = 6667

most frequent 7 haplotypes.



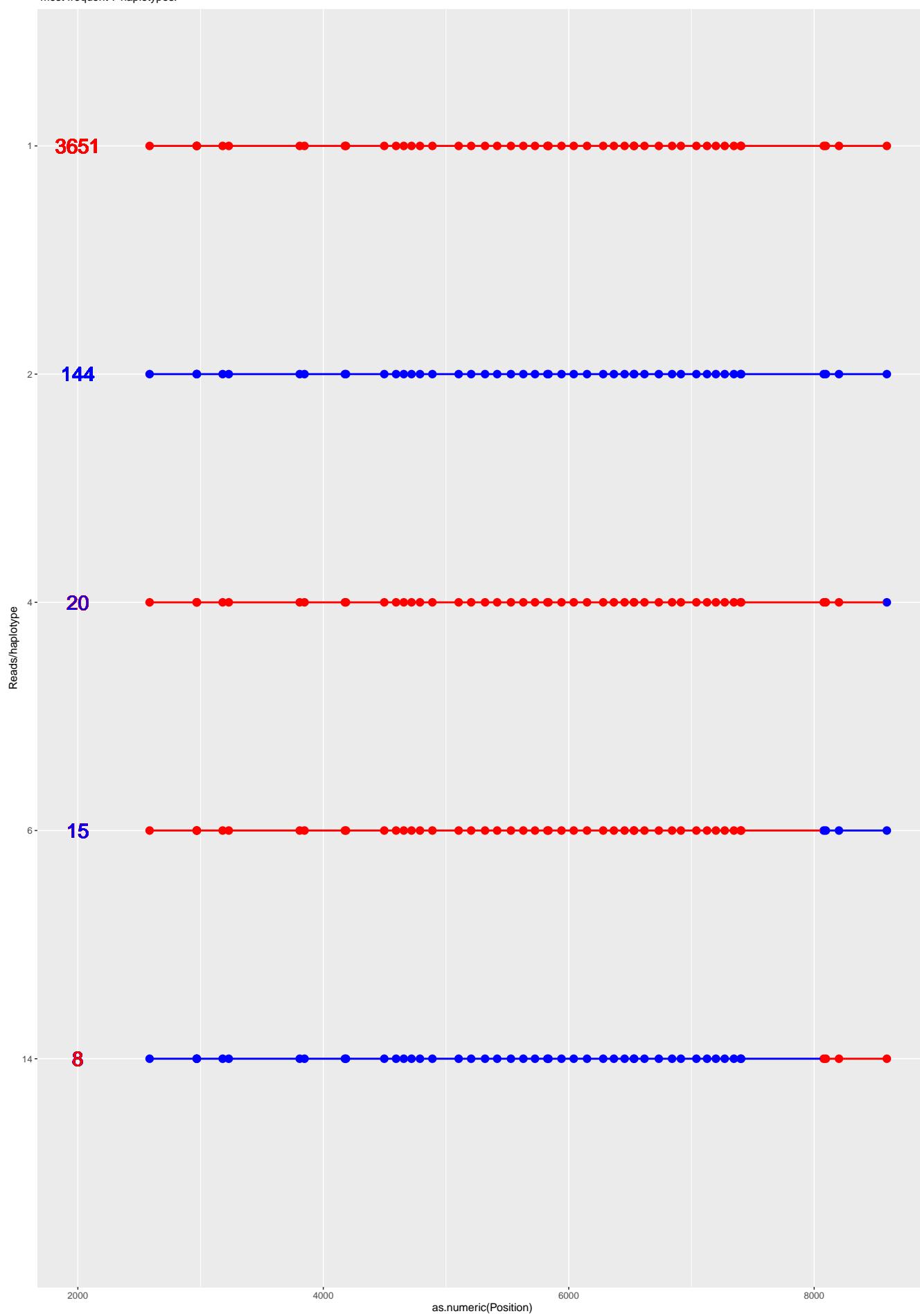
barcode = CGACGTATCTGACAGT & ATATAGTACAGCGTCT

Sample = 275b tetrad = 275 spore = b
Total reads = 3103 PCR=710
haplotypes I began with n[supporting reads] = 10, 14, 2648
most frequent 7 haplotypes.

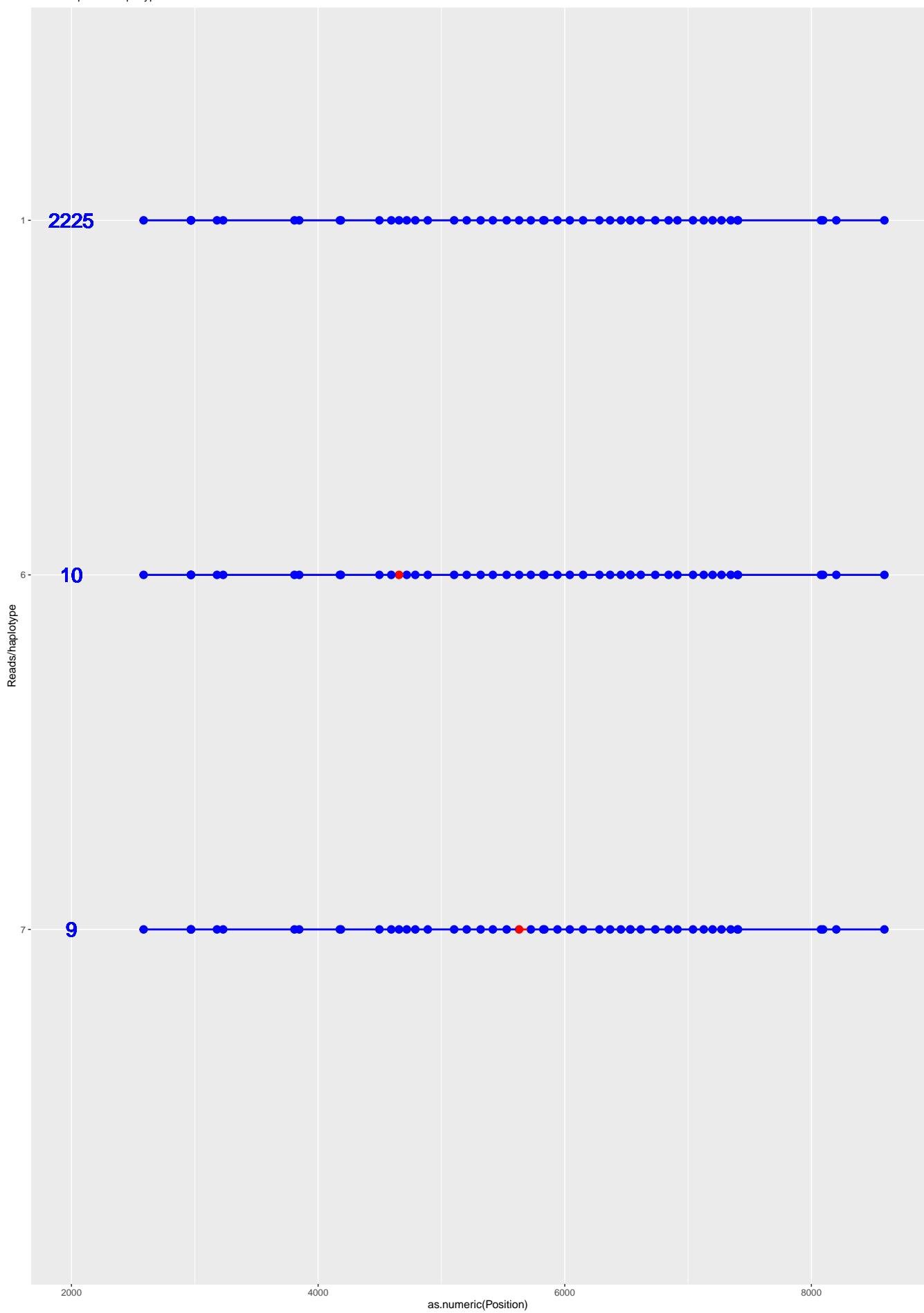


barcode = CGACGTATCTGACAGT & GACACGACTAGATCGC

Sample = 275c tetrad = 275 spore = c
Total reads = 4875 PCR=711
haplotypes I began with [n(supporting reads)] = 8, 15, 20, 144, 3651
most frequent 7 haplotypes.



Sample = 275d tetrad = 275 spore = d
Total reads = 2588 PCR=712
haplotypes I began with n[supporting reads] = 9, 10, 2225
most frequent 7 haplotypes.



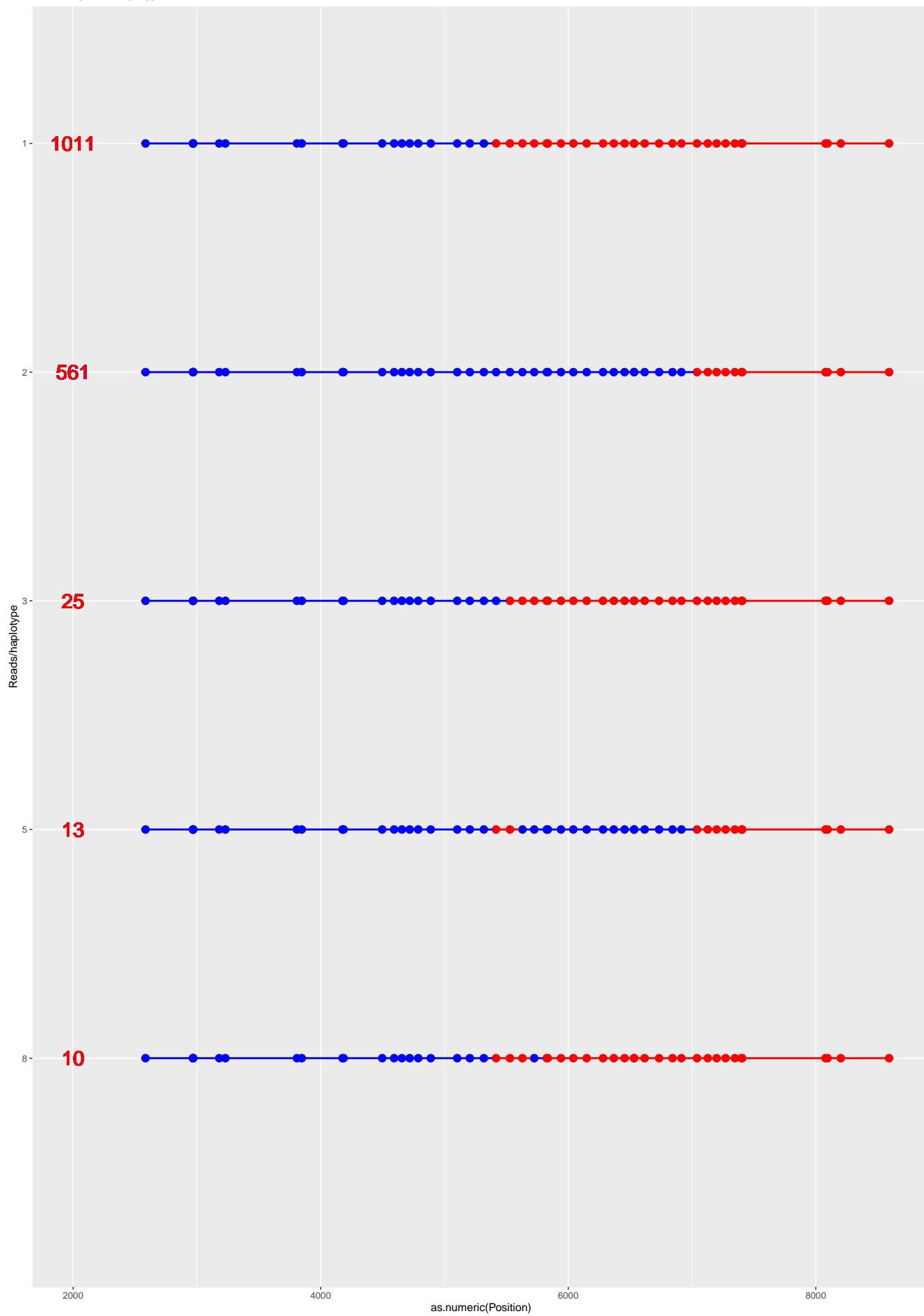
barcode = CGACGTATCTGACAGT & ACTCAGCTACATAGTG

Sample = 278a tetrad = 278 spore = a

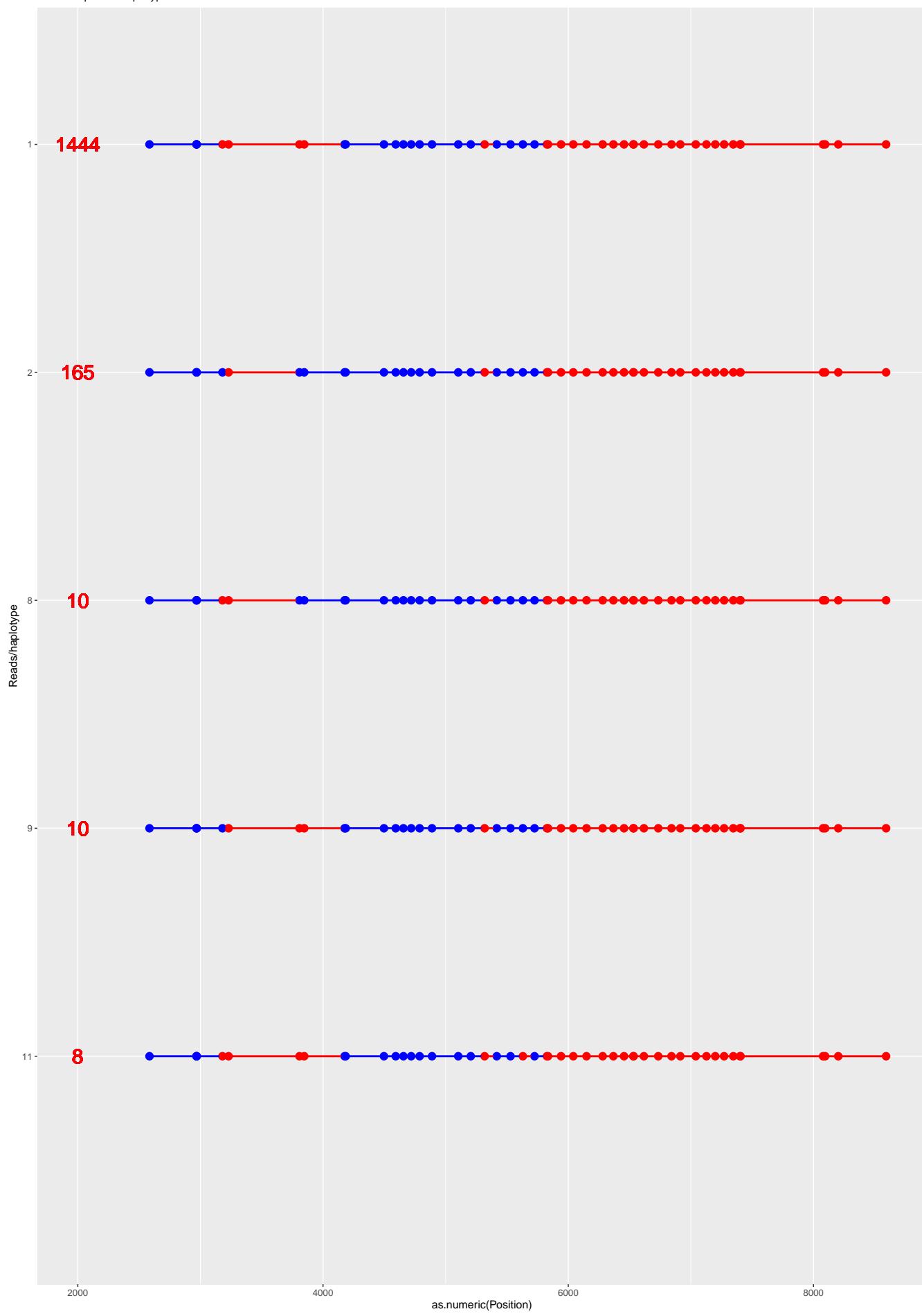
Total reads = 3210 PCR=721

haplotypes I began with n[supporting reads] = 10, 13, 25, 561, 1011

most frequent 7 haplotypes.

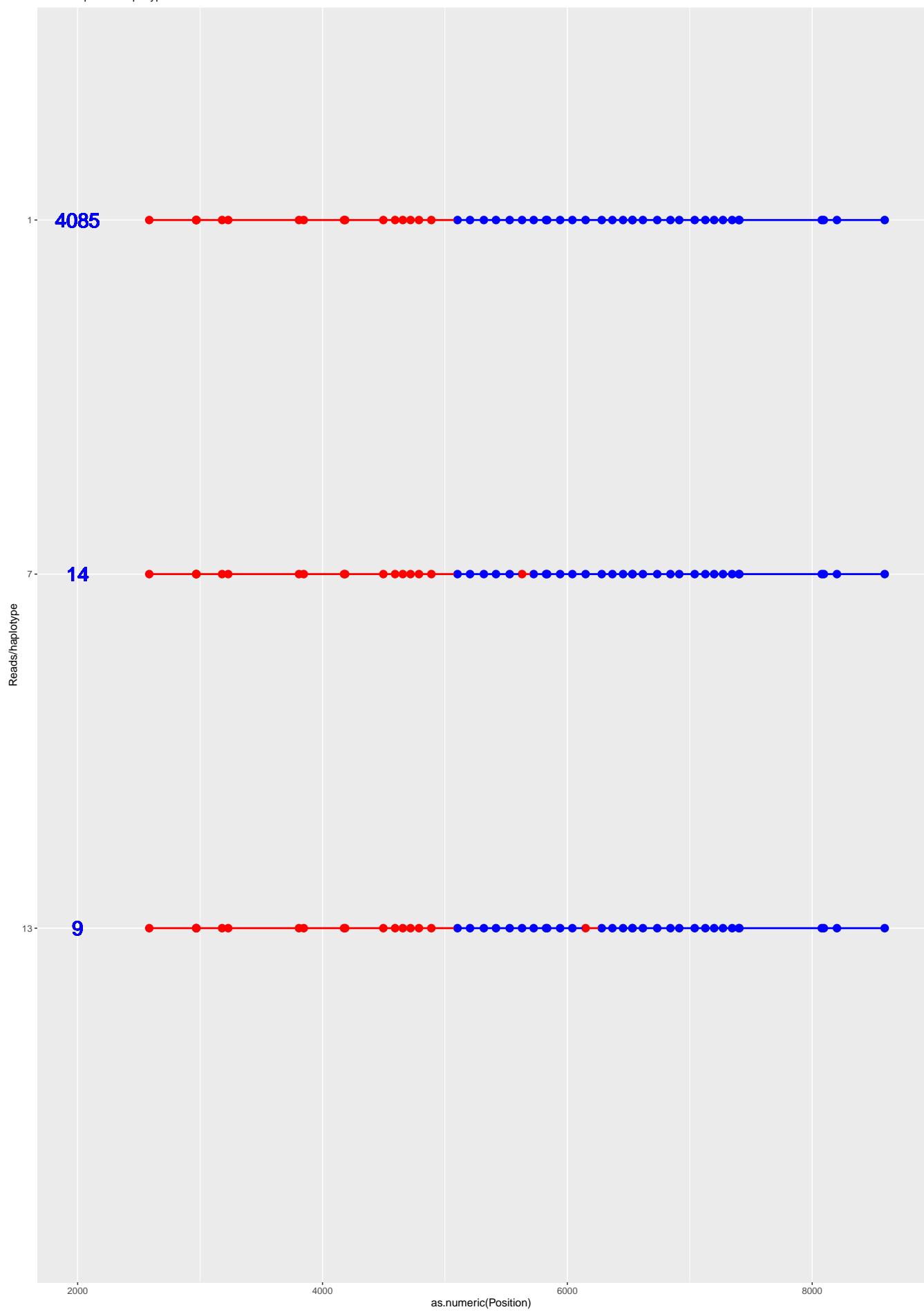


Sample = 278b tetrad = 278 spore = b
Total reads = 2016 PCR=722
haplotypes I began with [n(supporting reads)] = 8, 10, 165, 1444
most frequent 7 haplotypes.



barcode = TGTCGCAGCTACTAGT & ACTGATGCGCACATGT

Sample = 278c tetrad = 278 spore = c
Total reads = 4638 PCR=723
haplotypes I began with [n|supporting reads] = 9, 14, 4085
most frequent 7 haplotypes.

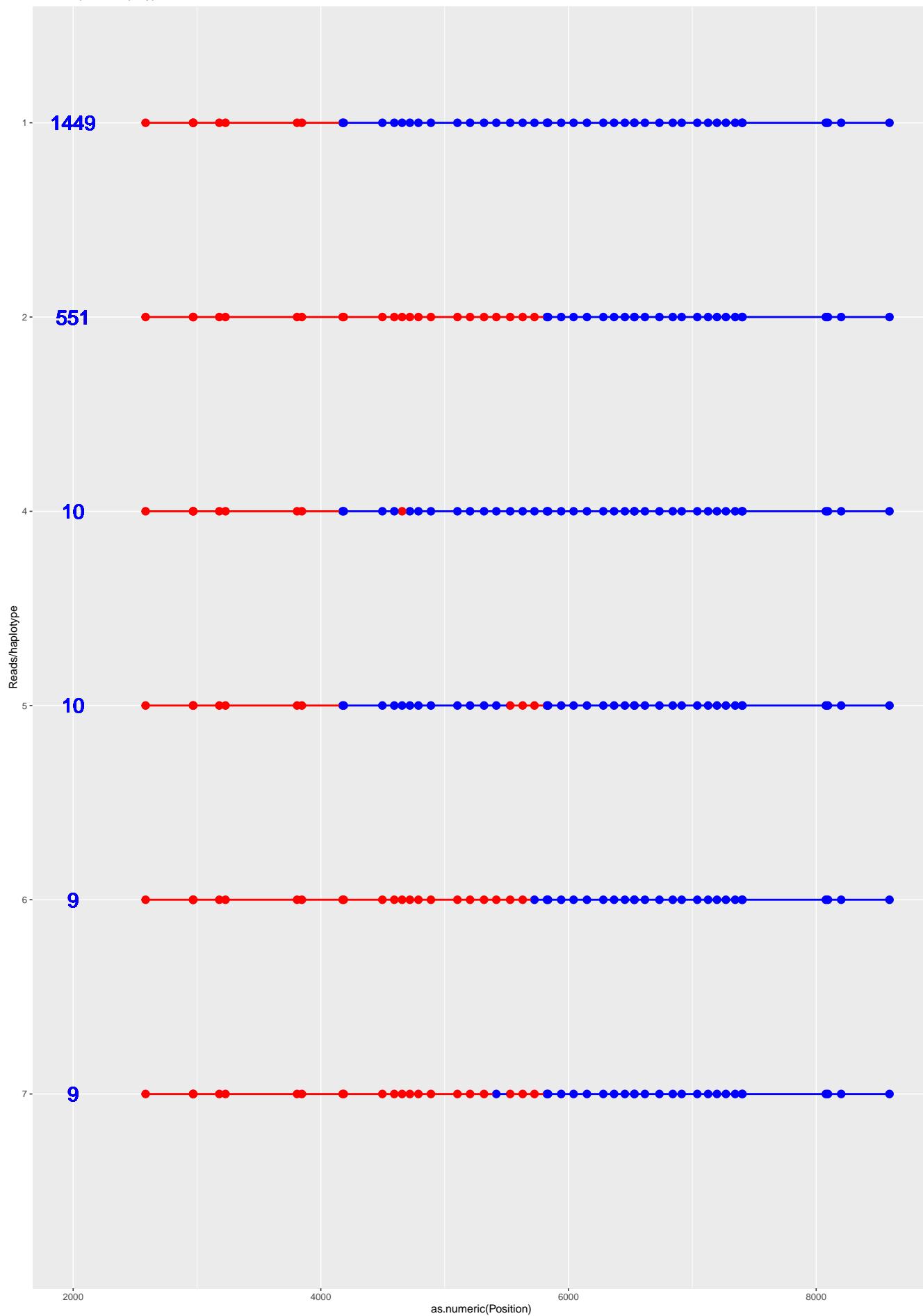


Sample = 278d tetrad = 278 spore = d

Total reads = 3304 PCR=724

haplotypes I began with n[supporting reads] = 9, 10, 551, 1449

most frequent 7 haplotypes.

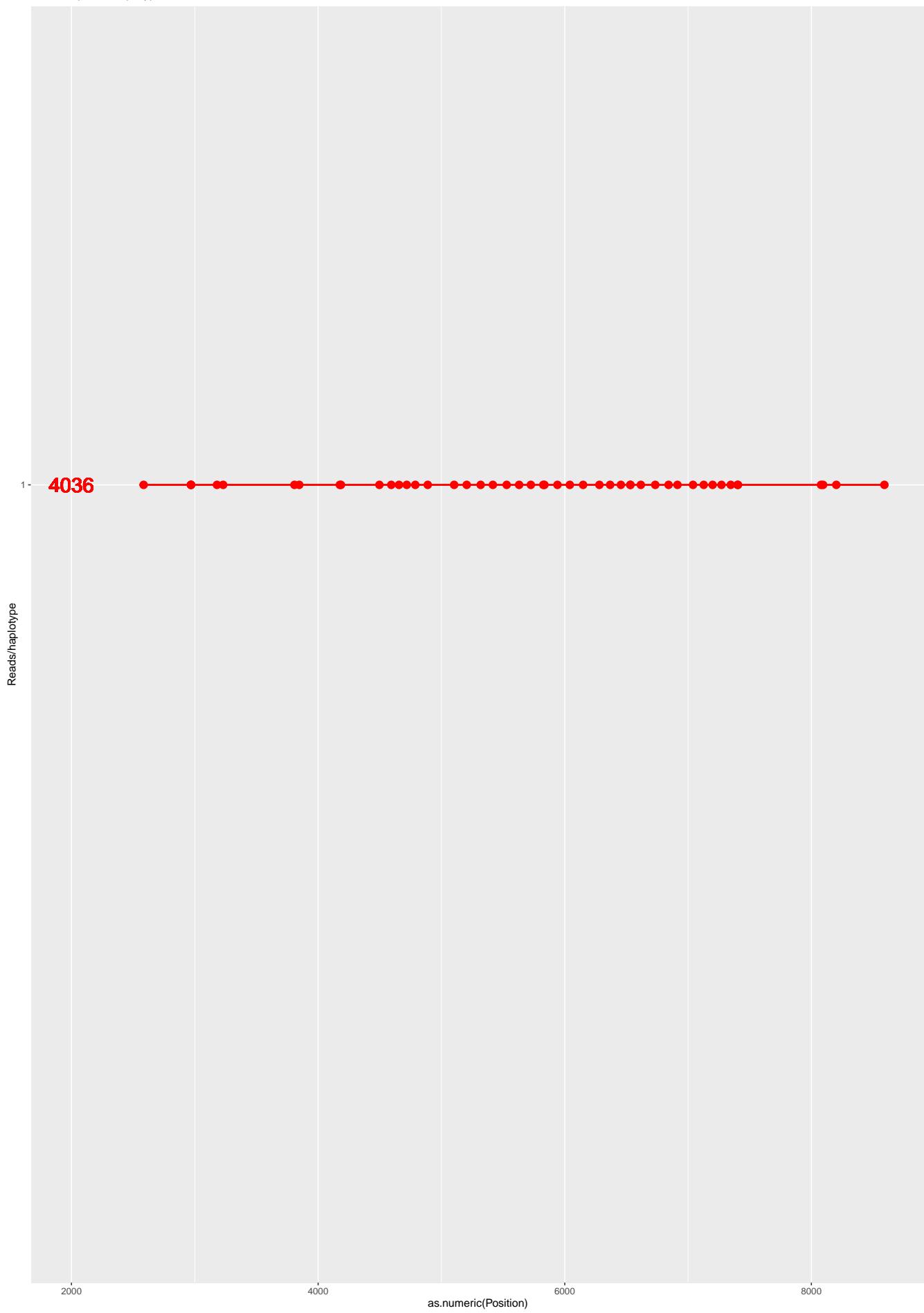


Sample = 280a tetrad = 280 spore = a

Total reads = 4212 PCR=729

haplotypes I began with n[supporting reads] = 4036

most frequent 7 haplotypes.



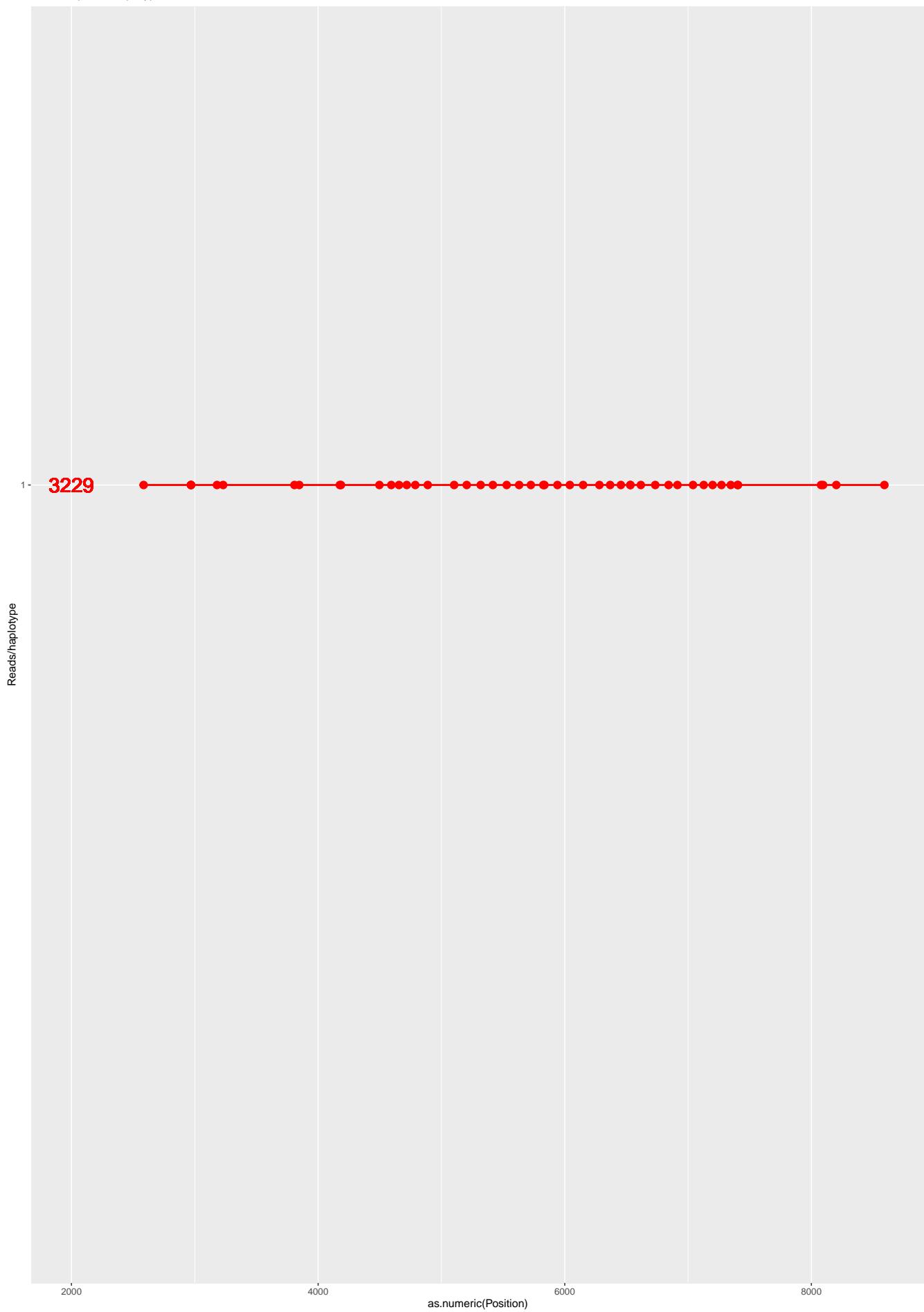
barcode = CATAACGCTGTGTAGCA & TCAGCTGACGATGTGA

Sample = 280b tetrad = 280 spore = b

Total reads =3358 PCR=730

haplotypes I began with n[supporting reads] = 3229

most frequent 7 haplotypes.



barcode = CATAACGCTGTGTAGCA & ACTGATGCGCACATGT

Sample = 280c tetrad = 280 spore = c
Total reads = 3416 PCR=731
haplotypes I began with n[supporting reads] = 9, 14, 2941
most frequent 7 haplotypes.



barcode = CATAACGCTGTGTAGCA & CTACTCTCAGCAGTGA

Sample = 280d tetrad = 280 spore = d
Total reads = 3012 PCR=732
haplotypes I began with n[supporting reads] = 8, 2591
most frequent 7 haplotypes.



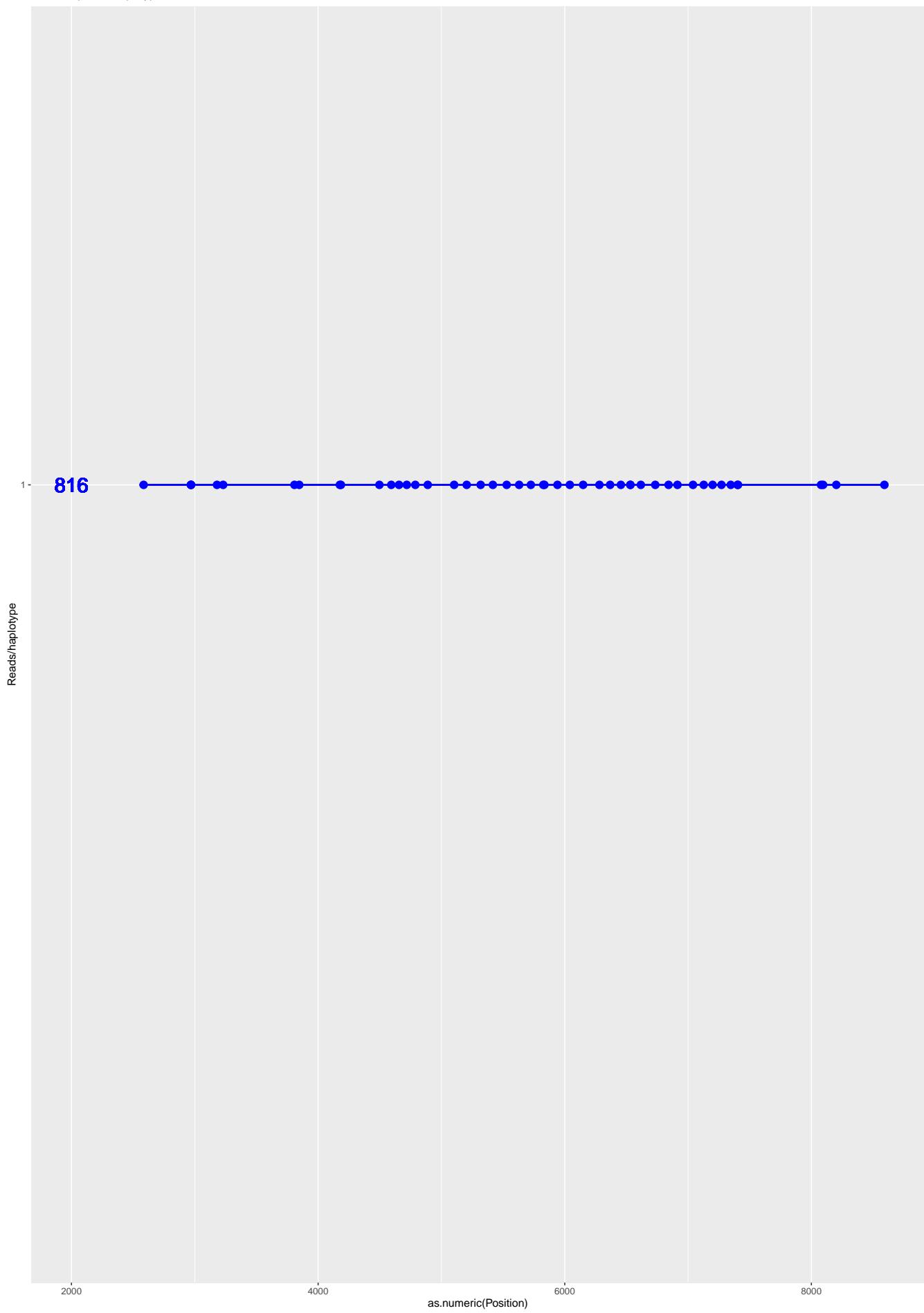
barcode = CATAACGCTGTGTAGCA & ATCTACATCACGACTC

Sample = 281a tetrad = 281 spore = a

Total reads = 939 PCR=733

haplotypes I began with n[supporting reads] = 816

most frequent 7 haplotypes.



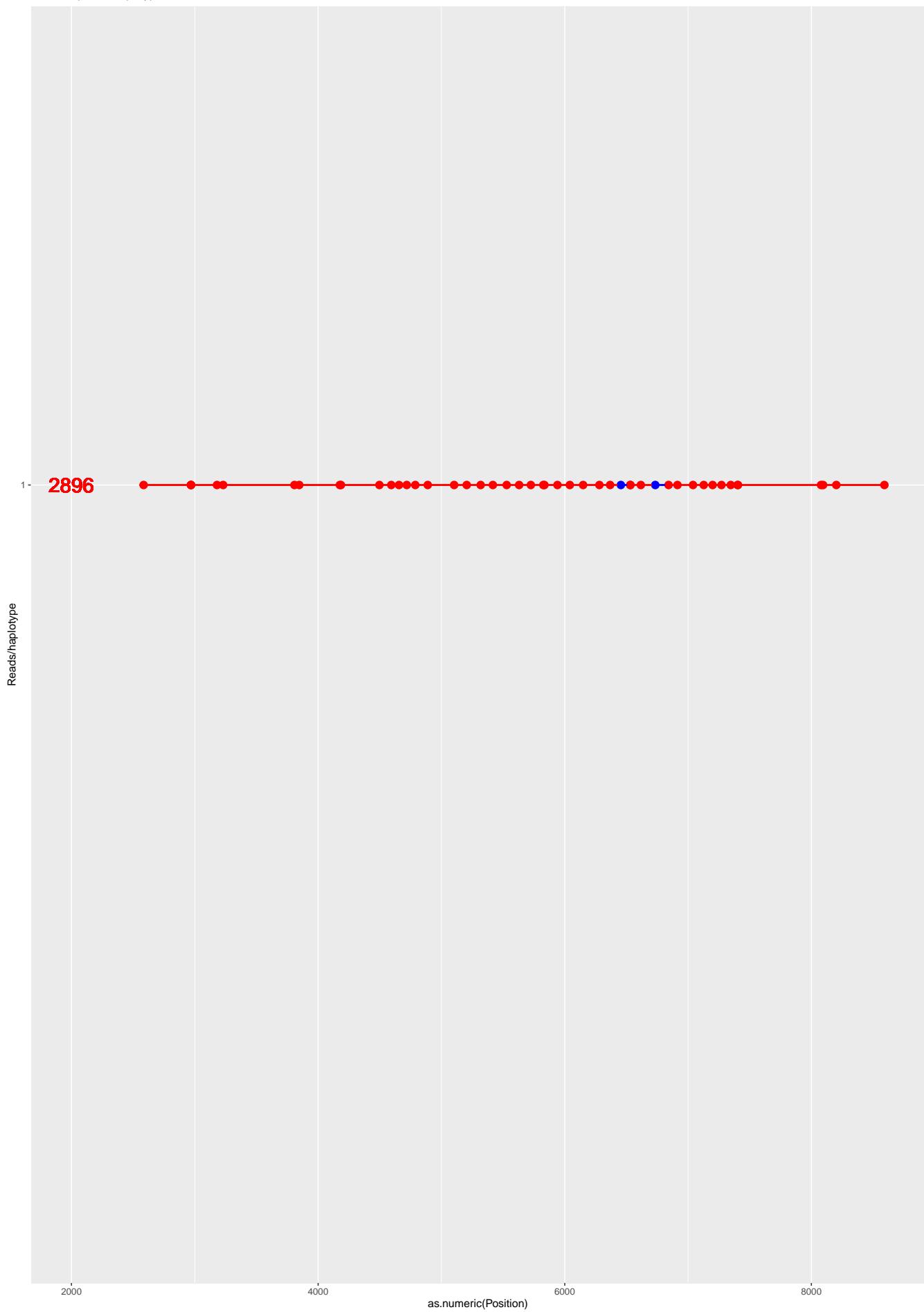
barcode = CATA CGCT GTGTAGCA & ATATAGTACAGCGTCT

Sample = 281b tetrad = 281 spore = b

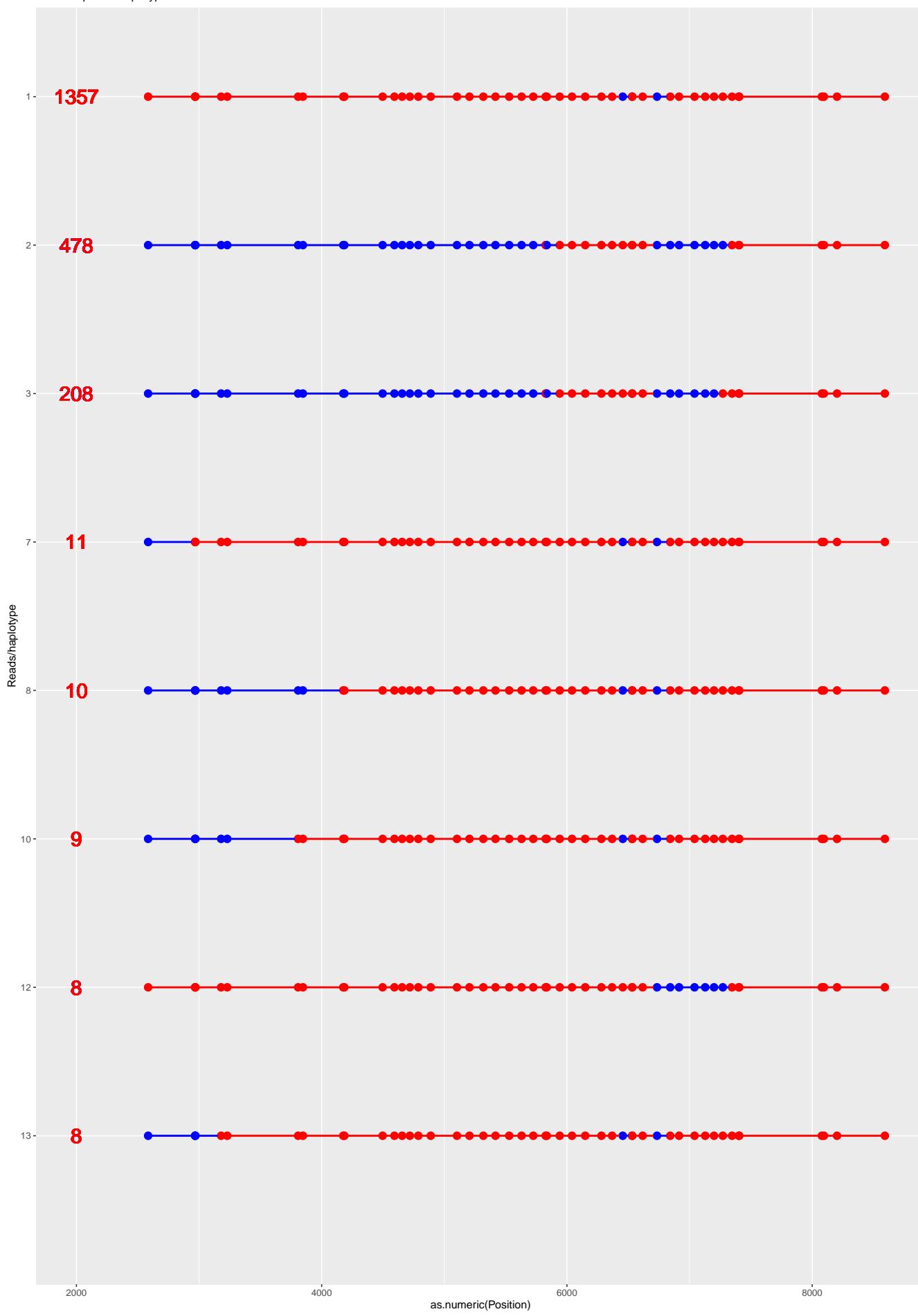
Total reads = 3094 PCR=734

haplotypes I began with n[supporting reads] = 2896

most frequent 7 haplotypes.

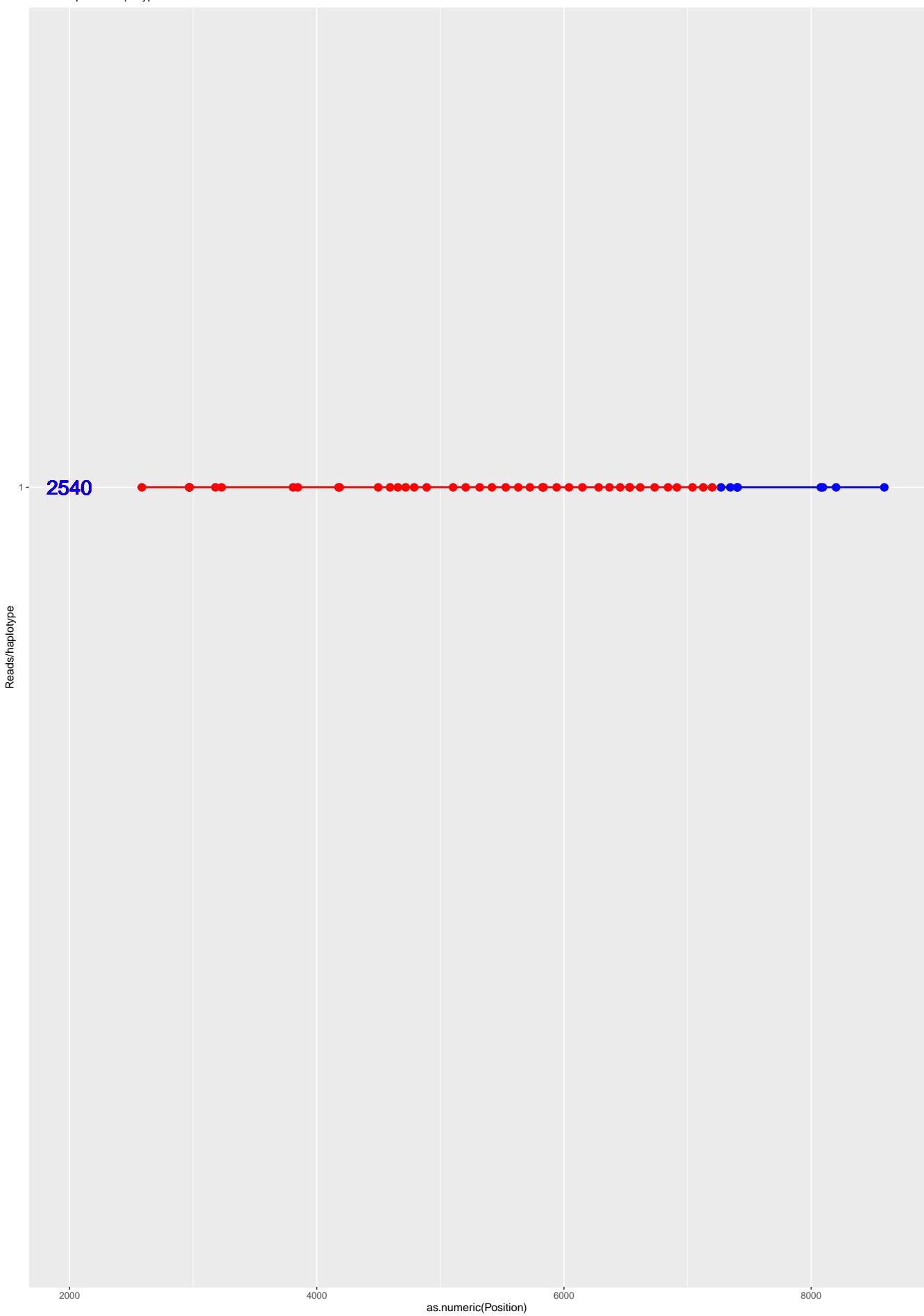


Sample = 281c tetrad = 281 spore = c
 Total reads = 3675 PCR=735
 haplotypes I began with [n(supporting reads)] = 8, 9, 10, 11, 208, 478, 1357
 most frequent 7 haplotypes.



barcode = CATA CGCT GTGTAGCA & TACG AGTCTGTCATAC

Sample = 281d tetrad = 281 spore = d
Total reads = 2671 PCR=736
haplotypes I began with n[supporting reads] = 2540
most frequent 7 haplotypes.



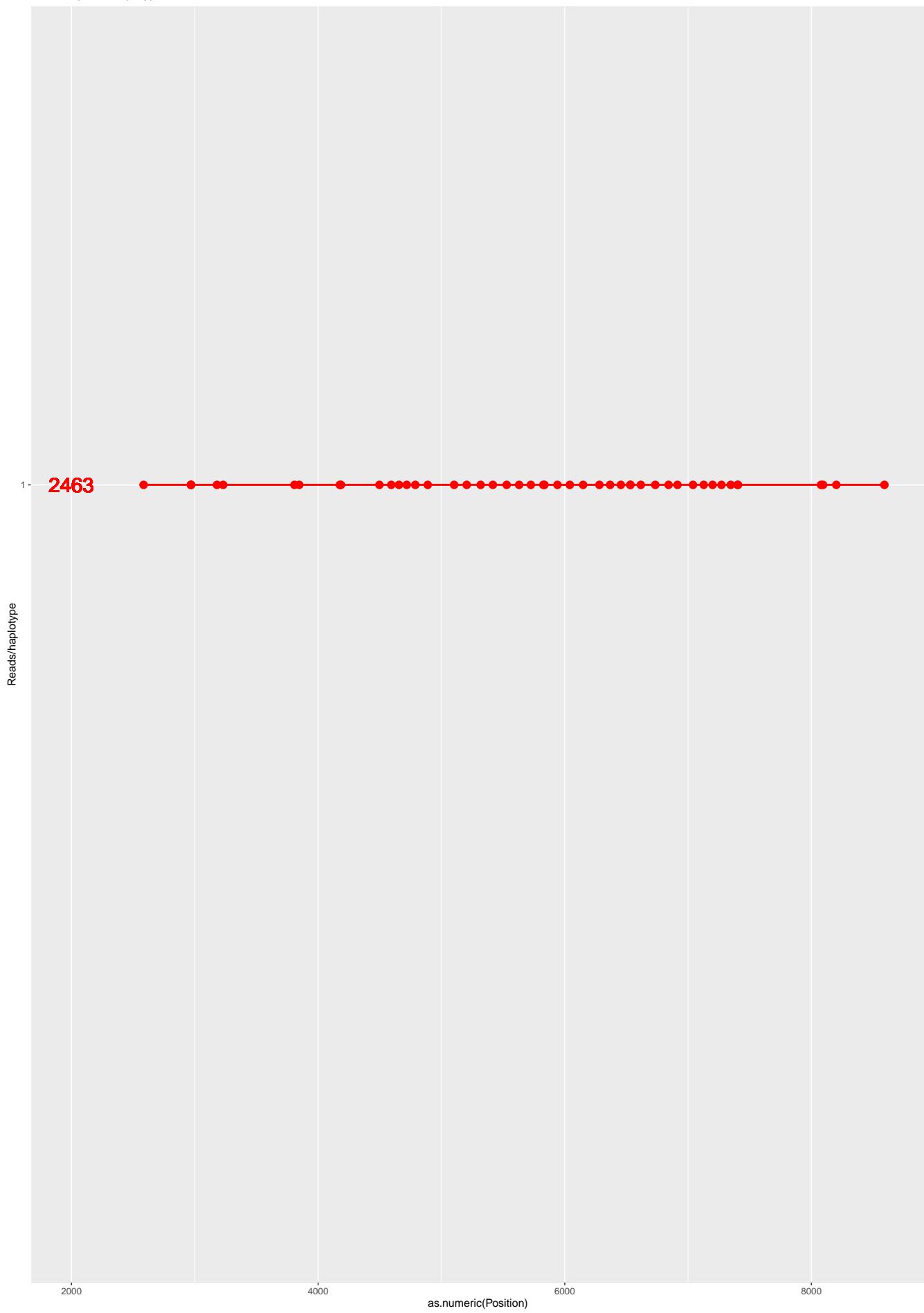
barcode = CATAACGCTGTGTAGCA & ACTCAGCTACATAGTG

Sample = 282a tetrad = 282 spore = a

Total reads = 2584 PCR=737

haplotypes I began with n[supporting reads] = 2463

most frequent 7 haplotypes.



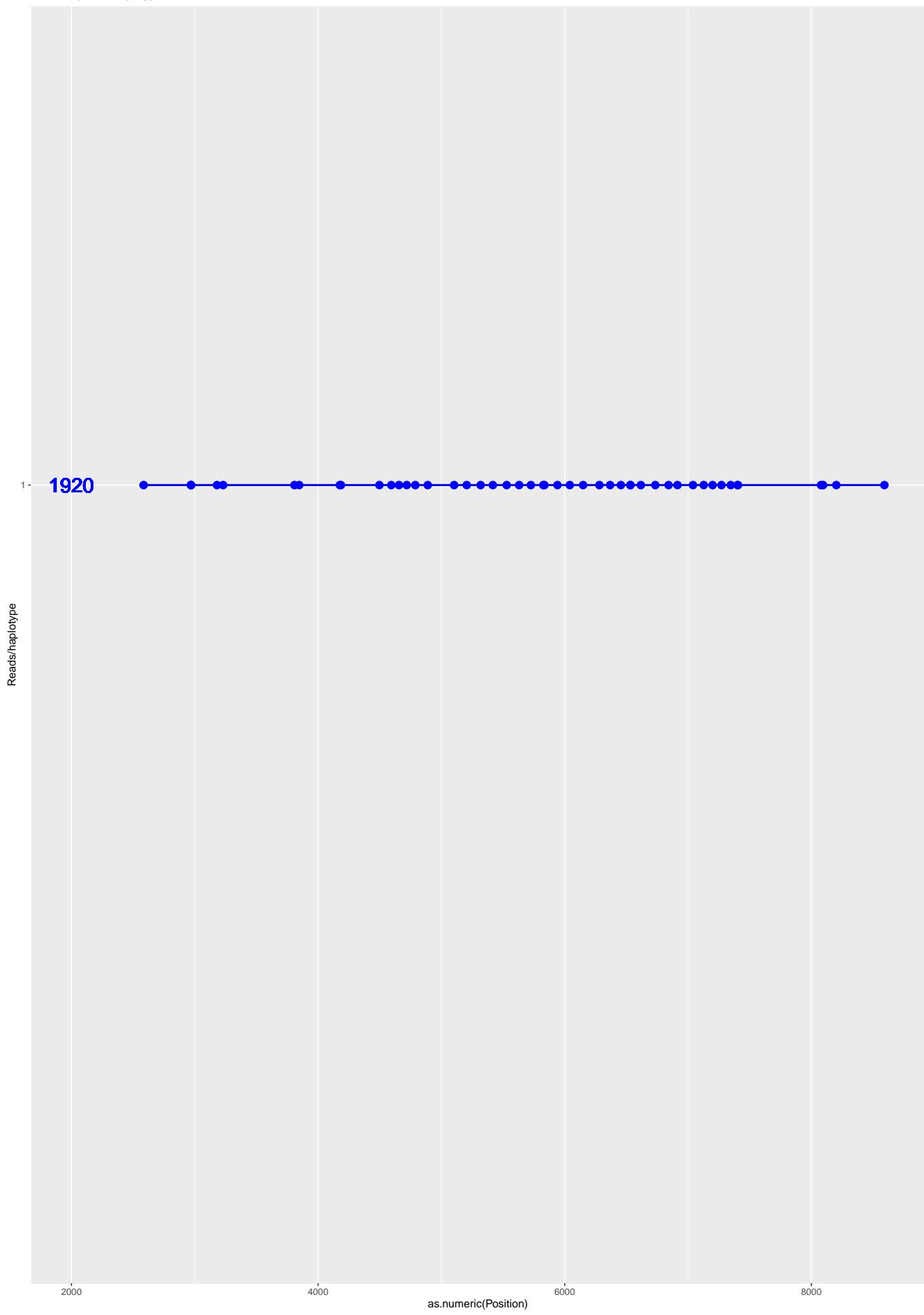
barcode = AGTCGCATGACTGTGT & TCAGCTGACGATGTGA

Sample = 282b tetrad = 282 spore = b

Total reads = 2212 PCR=738

haplotypes I began with n[supporting reads] = 1920

most frequent 7 haplotypes.



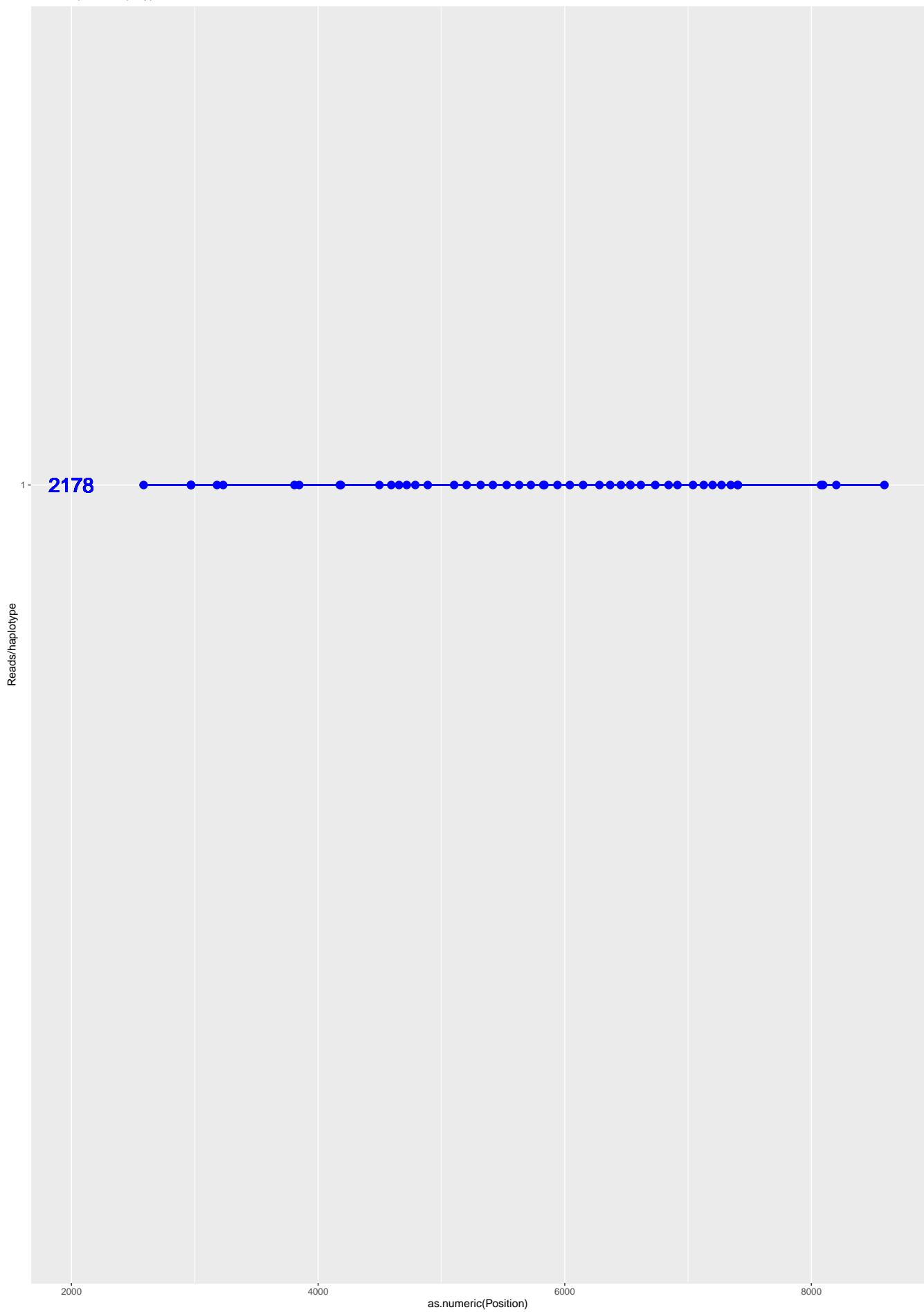
barcode = AGTCGCATGACTGTGT & ACTGATGCGCACATGT

Sample = 282c tetrad = 282 spore = c

Total reads = 2515 PCR=739

haplotypes I began with n[supporting reads] = 2178

most frequent 7 haplotypes.



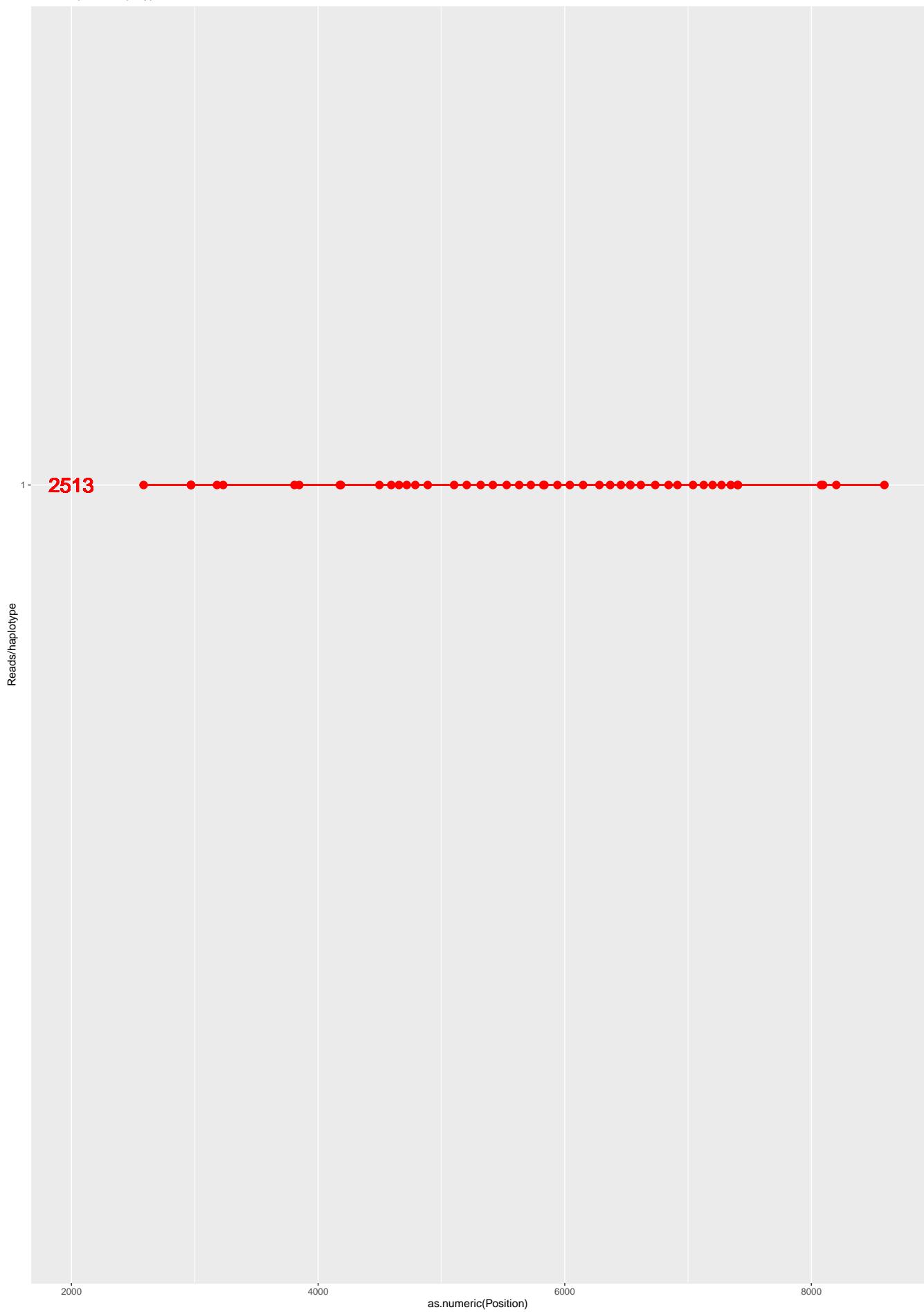
barcode = AGTCGCATGACTGTGT & CTACTCTCAGCAGTGA

Sample = 282d tetrad = 282 spore = d

Total reads = 2613 PCR=740

haplotypes I began with n[supporting reads] = 2513

most frequent 7 haplotypes.



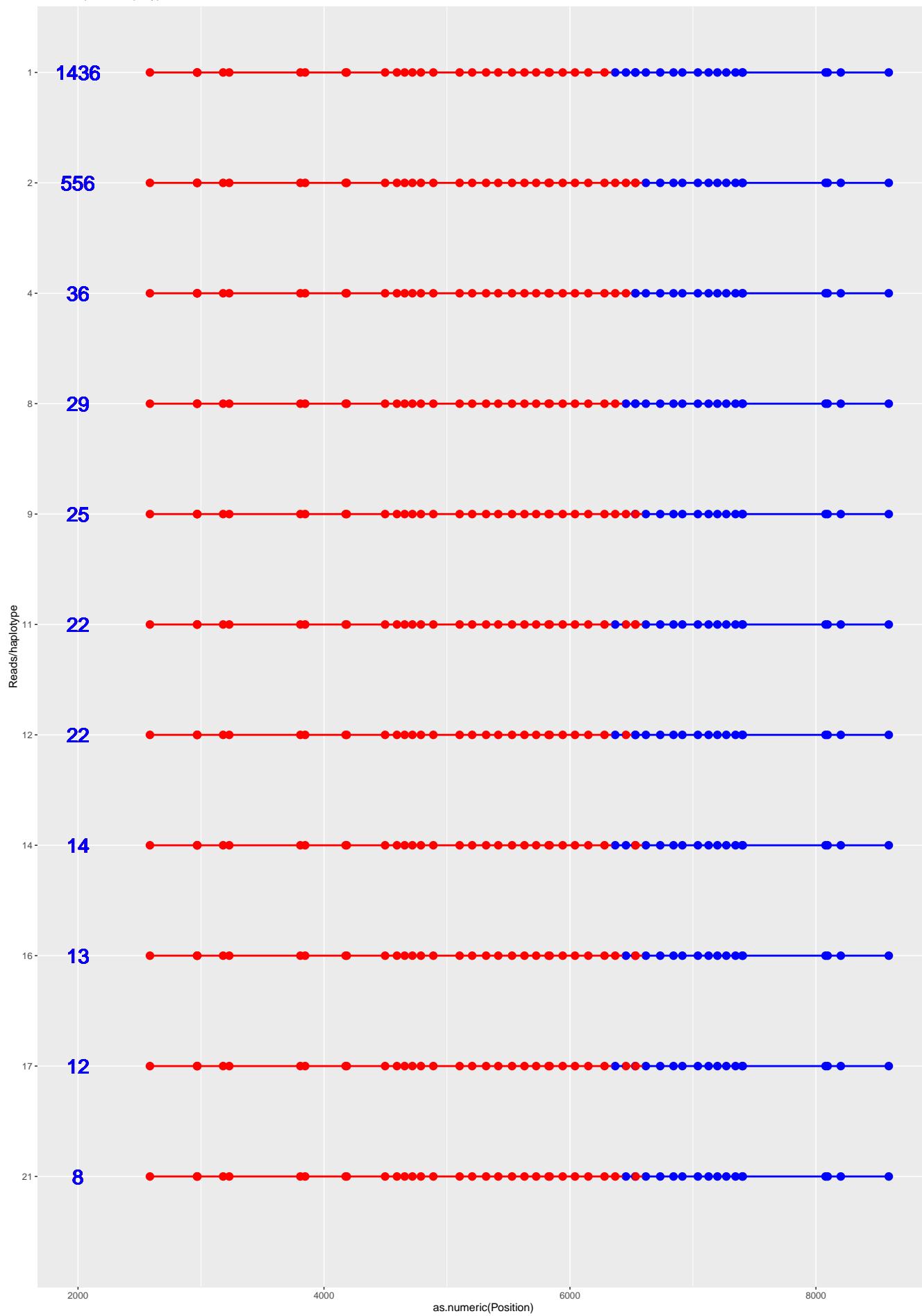
barcode = AGTCGCATGACTGTGT & ATCTACATCACGACTC

Sample = 288a tetrad = 288 spore = a

Total reads =2733 PCR=749

haplotypes I began with [n|supporting reads] = 8, 12, 13, 14, 22, 25, 29, 36, 556, 1436

most frequent 7 haplotypes.

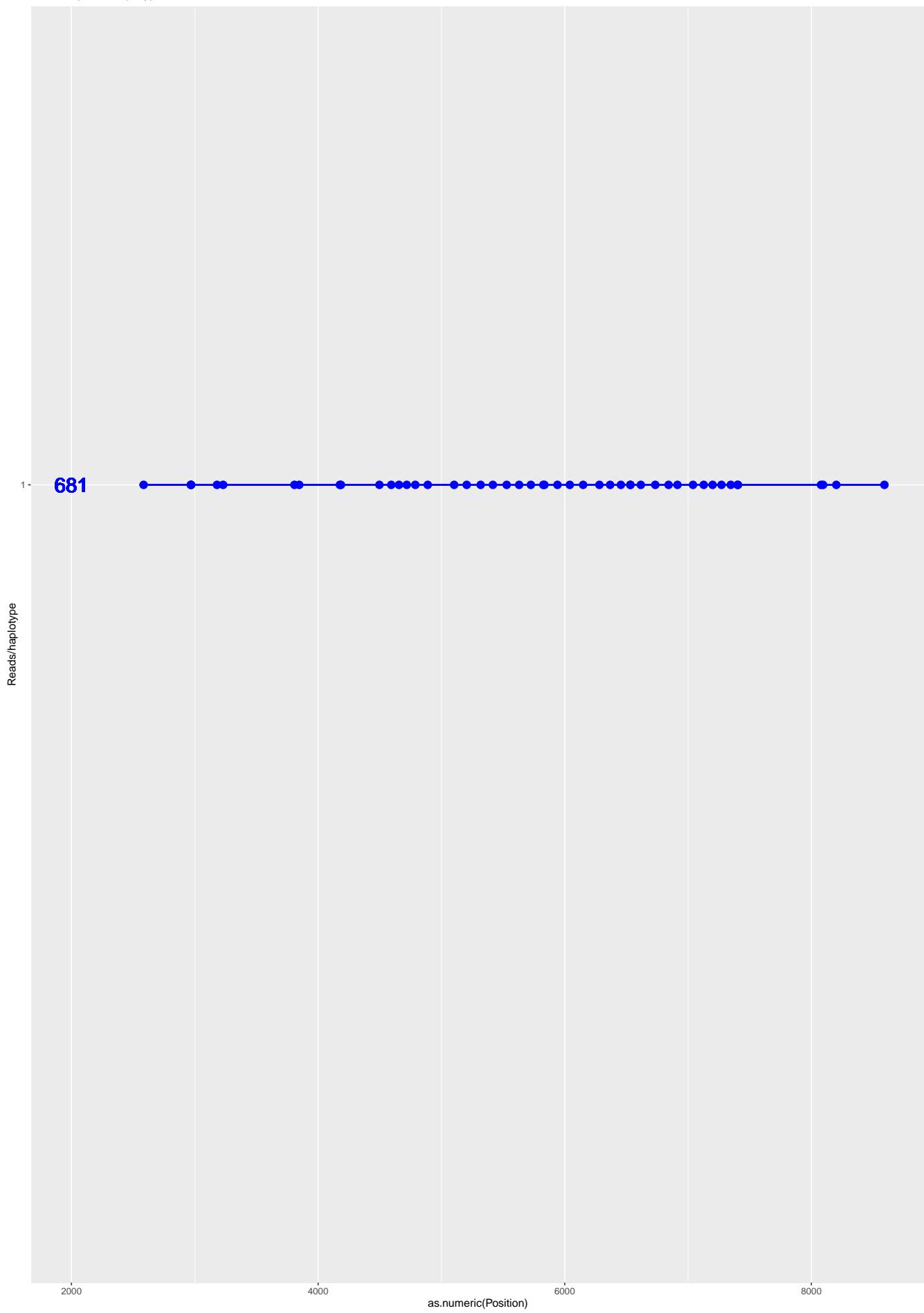


Sample = 288b tetrad = 288 spore = b

Total reads = 806 PCR=750

haplotypes I began with n[supporting reads] = 681

most frequent 7 haplotypes.



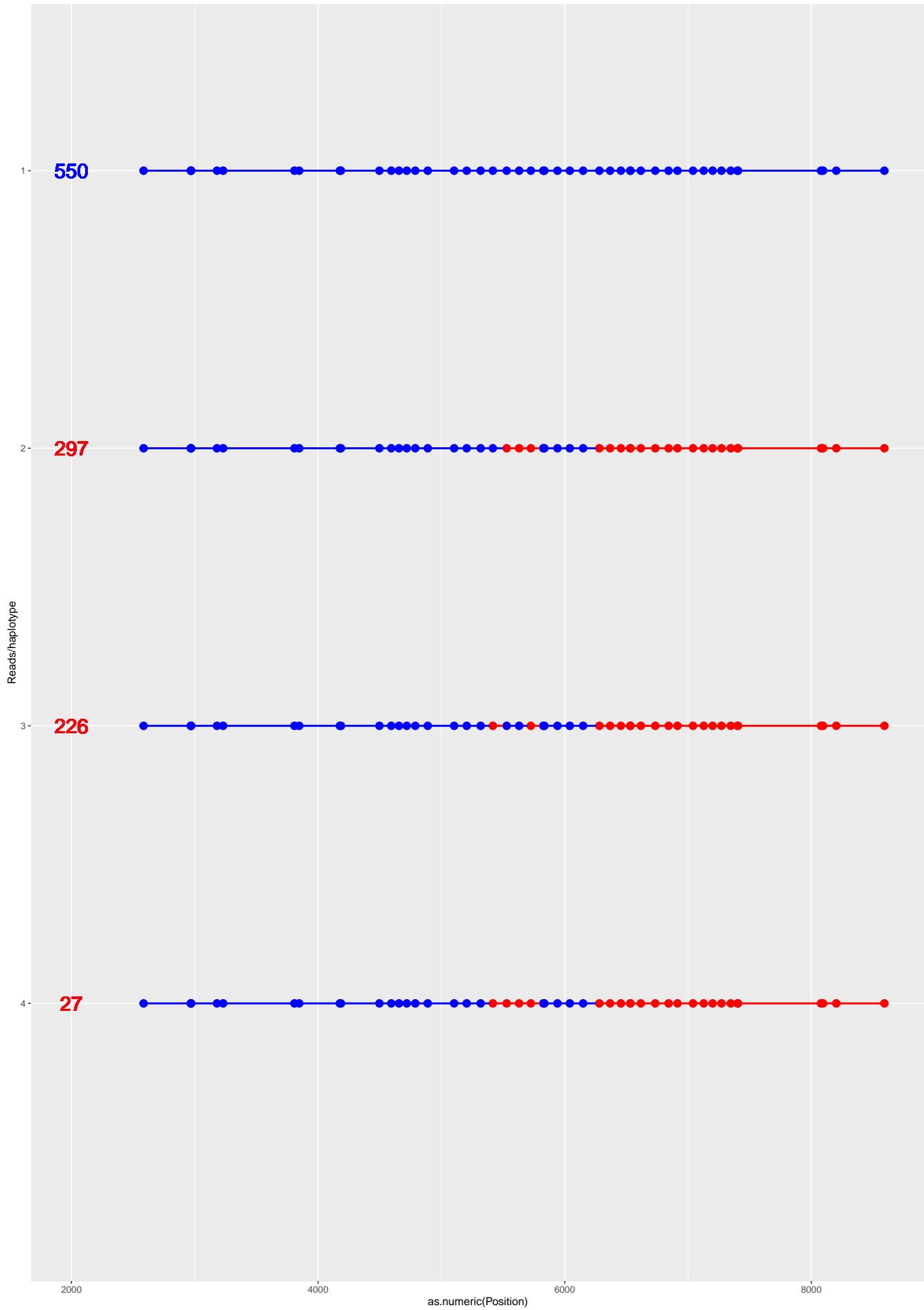
barcode = CAGTACTGCACGATCG & GACACGACTAGATCGC

Sample = 288c tetrad = 288 spore = c

Total reads = 1508 PCR=751

haplotypes I began with n[supporting reads] = 27, 226, 297, 550

most frequent 7 haplotypes.



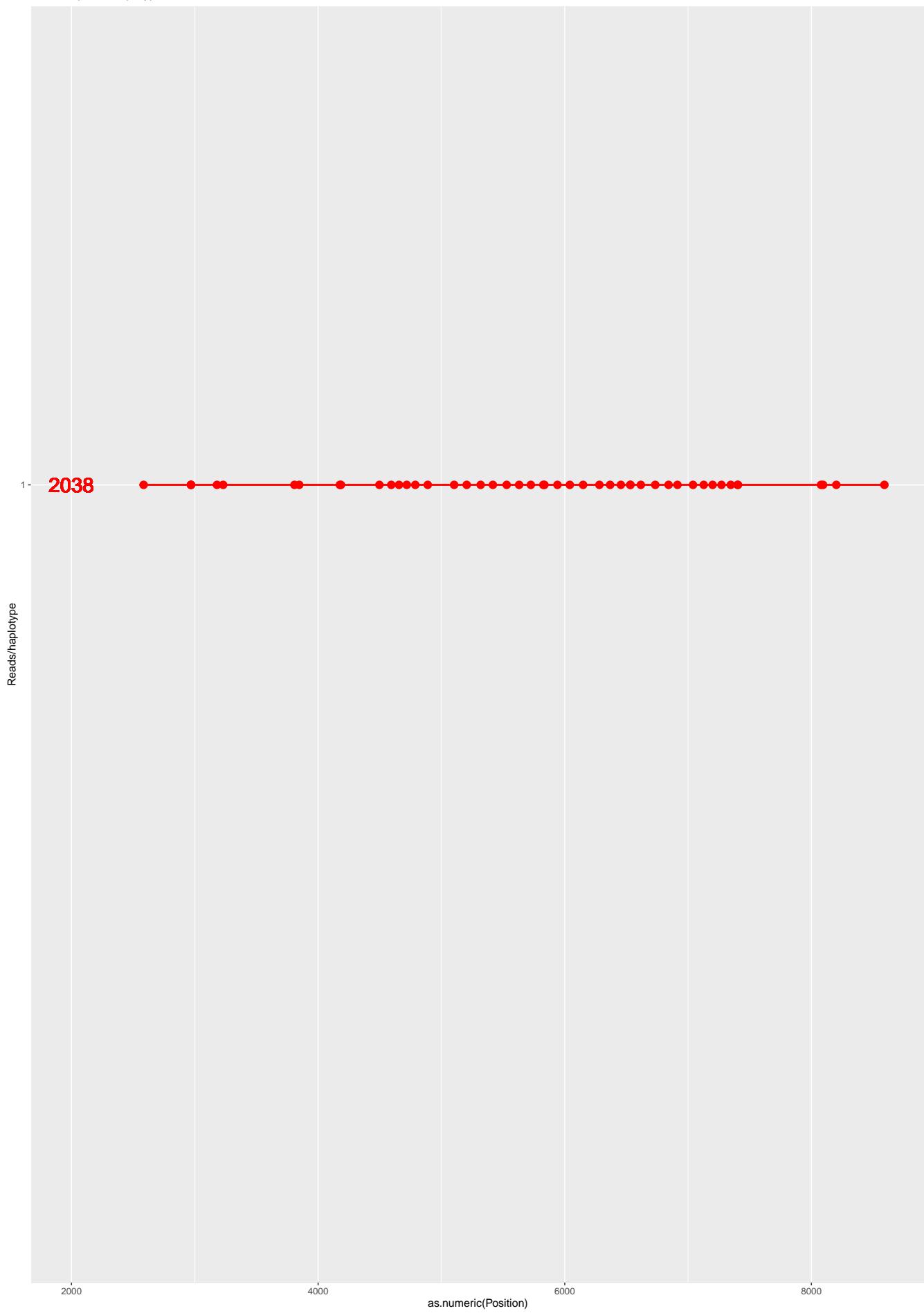
barcode = CAGTACTGCACTATCG & TACGAGTCTGTAC

Sample = 288d tetrad = 288 spore = d

Total reads = 2118 PCR=752

haplotypes I began with n[supporting reads] = 2038

most frequent 7 haplotypes.



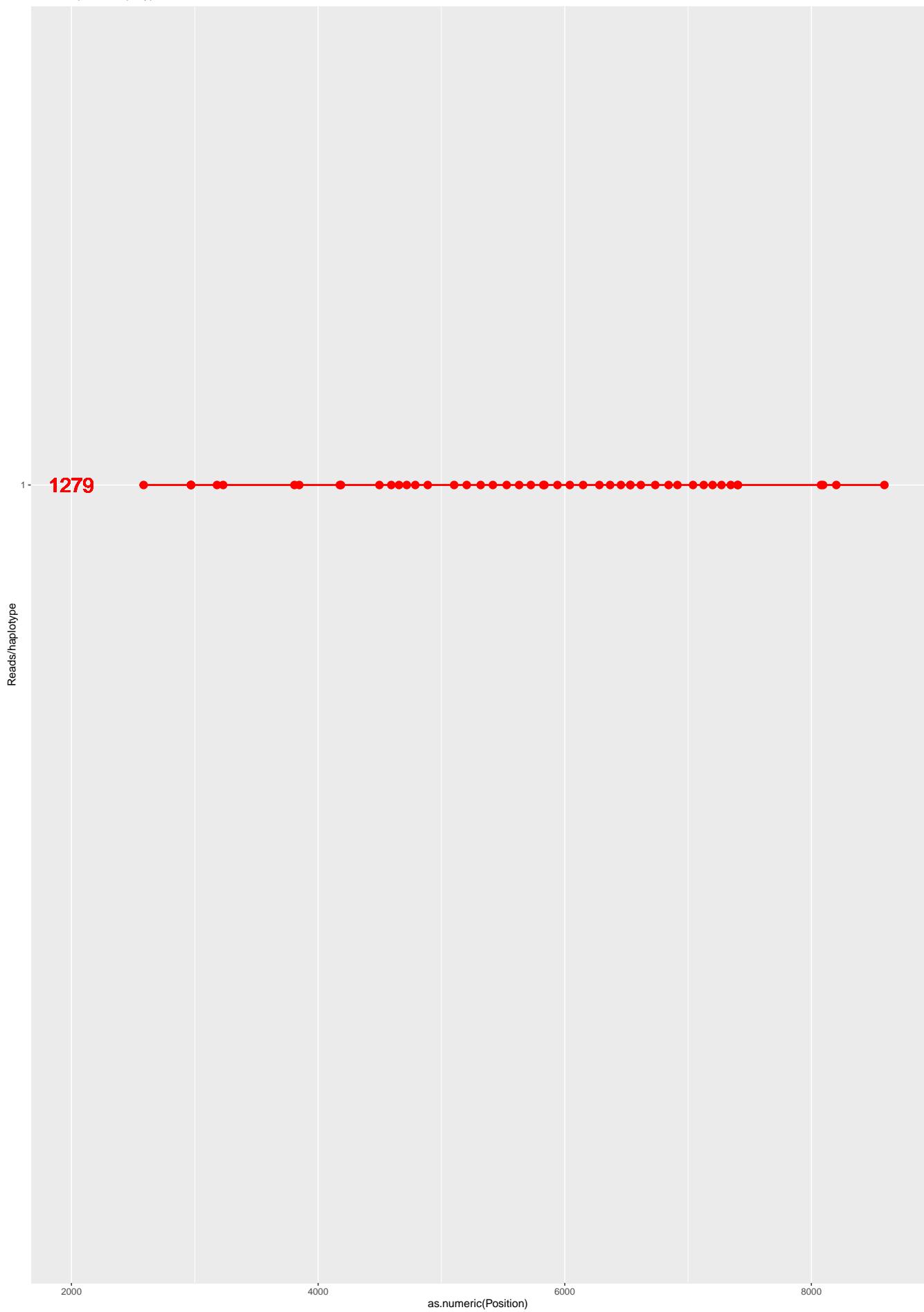
barcode = CAGTACTGCACGATCG & ACTCAGCTACATAGTG

Sample = 289a tetrad = 289 spore = a

Total reads = 1330 PCR=753

haplotypes I began with n[supporting reads] = 1279

most frequent 7 haplotypes.



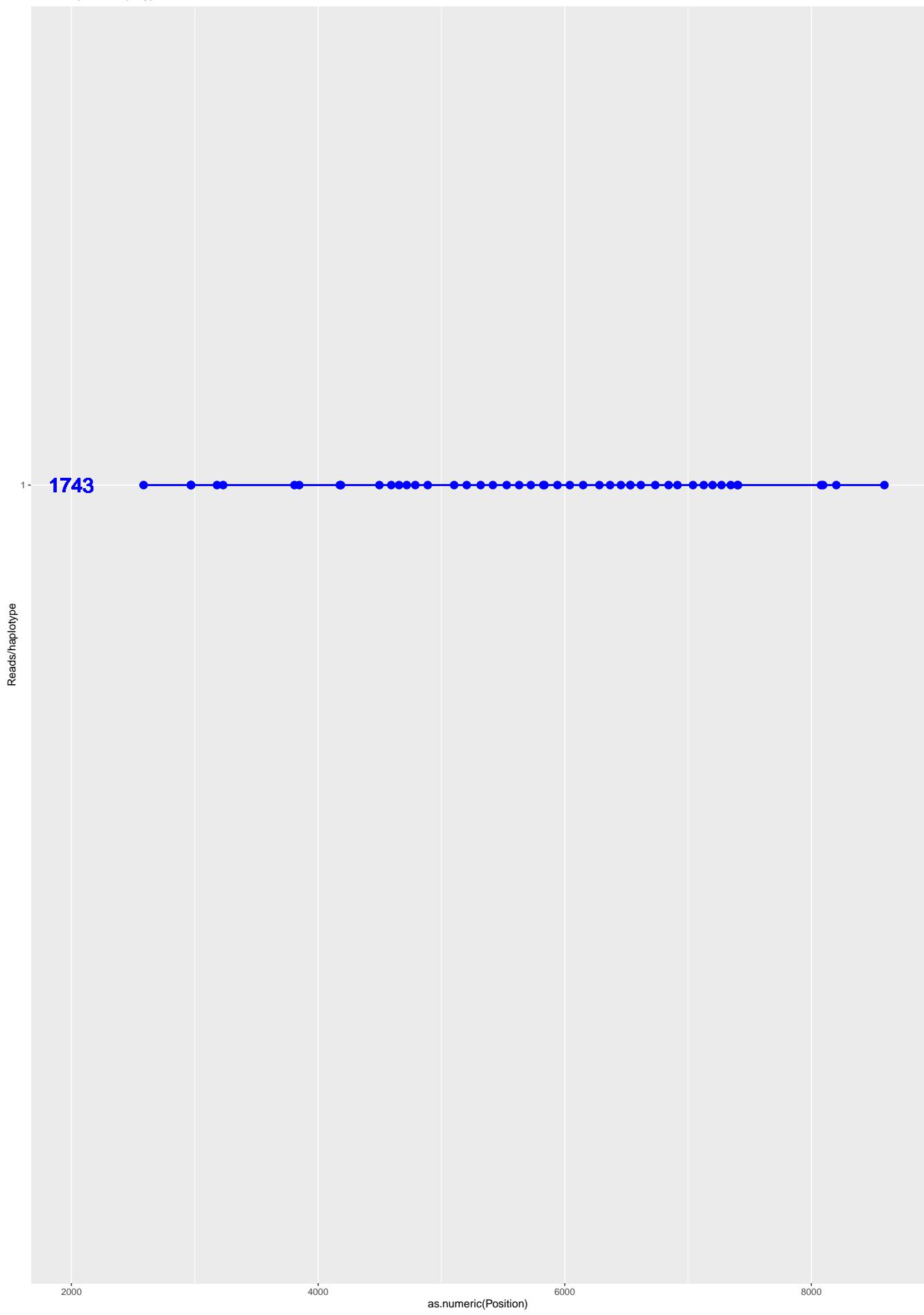
barcode = GTGCTGAGCATCAGAC & TCAGCTGACGATGTGA

Sample = 289b tetrad = 289 spore = b

Total reads = 2040 PCR=754

haplotypes I began with n[supporting reads] = 1743

most frequent 7 haplotypes.



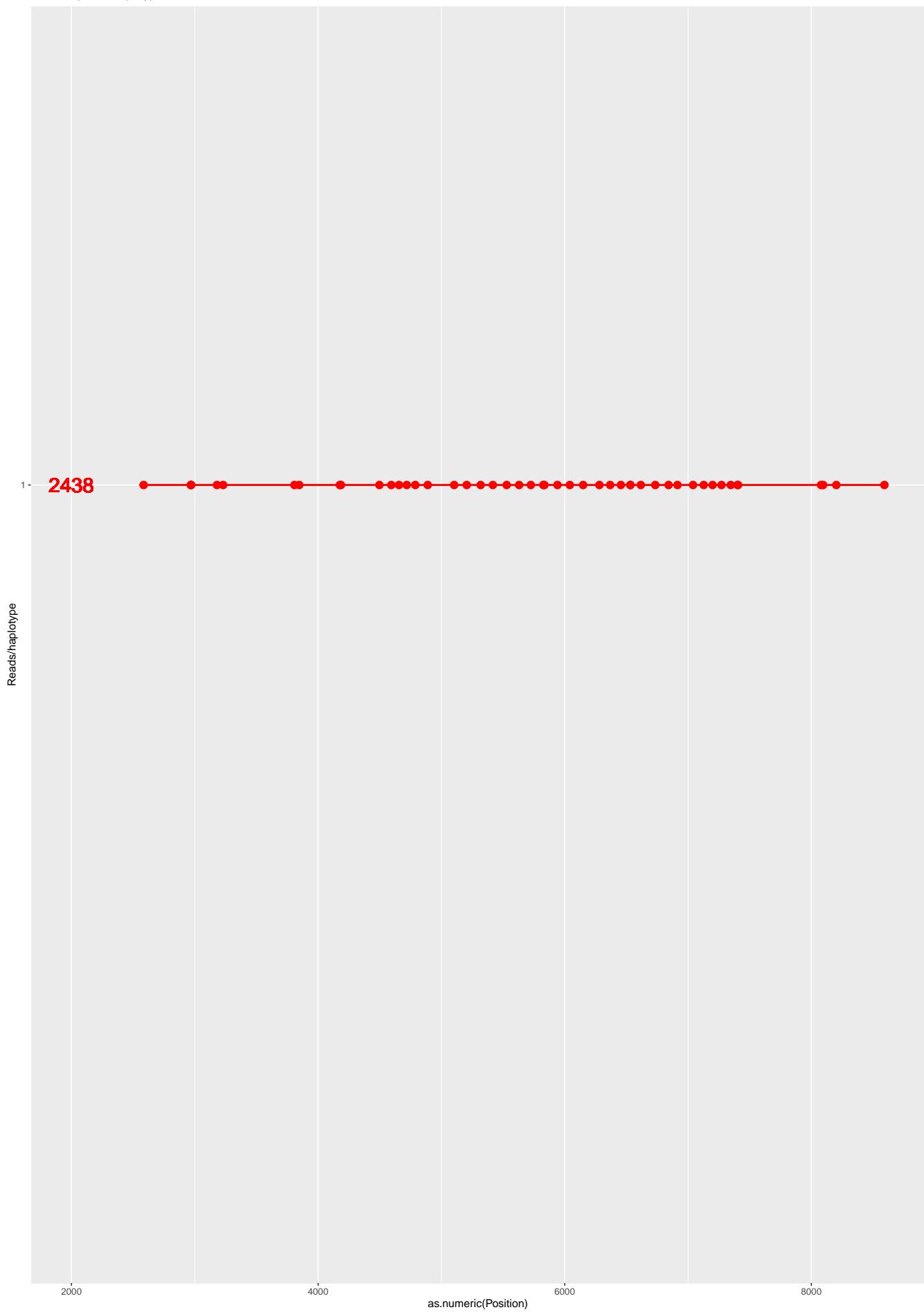
barcode = GTGCTGAGCATCAGAC & ACTGATGCGCACATGT

Sample = 289c tetrad = 289 spore = c

Total reads = 2535 PCR=755

haplotypes I began with n[supporting reads] = 2438

most frequent 7 haplotypes.



Sample = 289d tetrad = 289 spore = d
Total reads = 2607 PCR=756
haplotypes I began with n[supporting reads] = 13, 2277
most frequent 7 haplotypes.



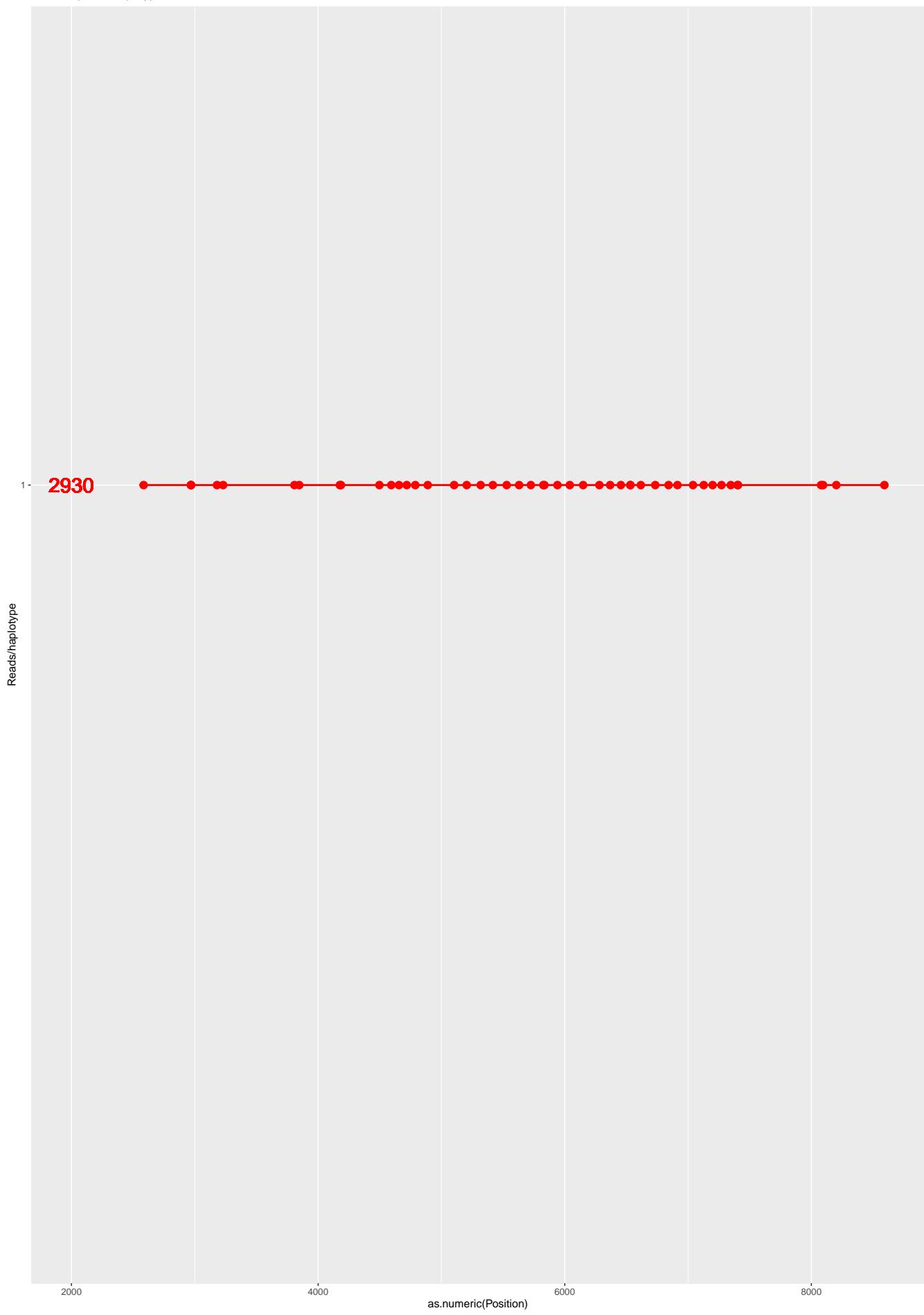
barcode = GTGCTGAGCATCAGAC & ATCTACATCACGACTC

Sample = 290a tetrad = 290 spore = a

Total reads = 3036 PCR=757

haplotypes I began with n[supporting reads] = 2930

most frequent 7 haplotypes.



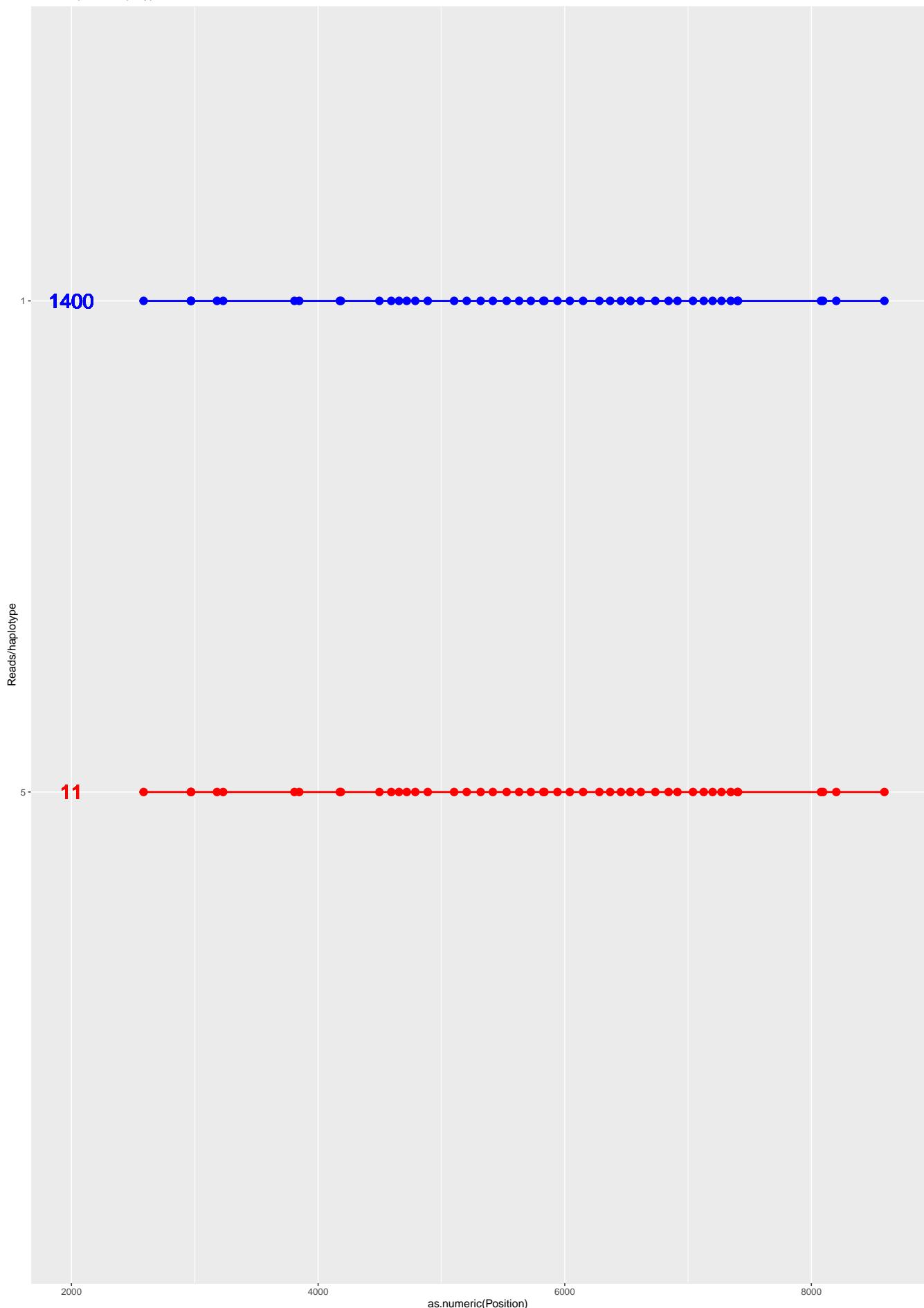
barcode = GTGCTGAGCATCAGAC & ATATAGTACAGCGTCT

Sample = 290b tetrad = 290 spore = b

Total reads = 1663 PCR=758

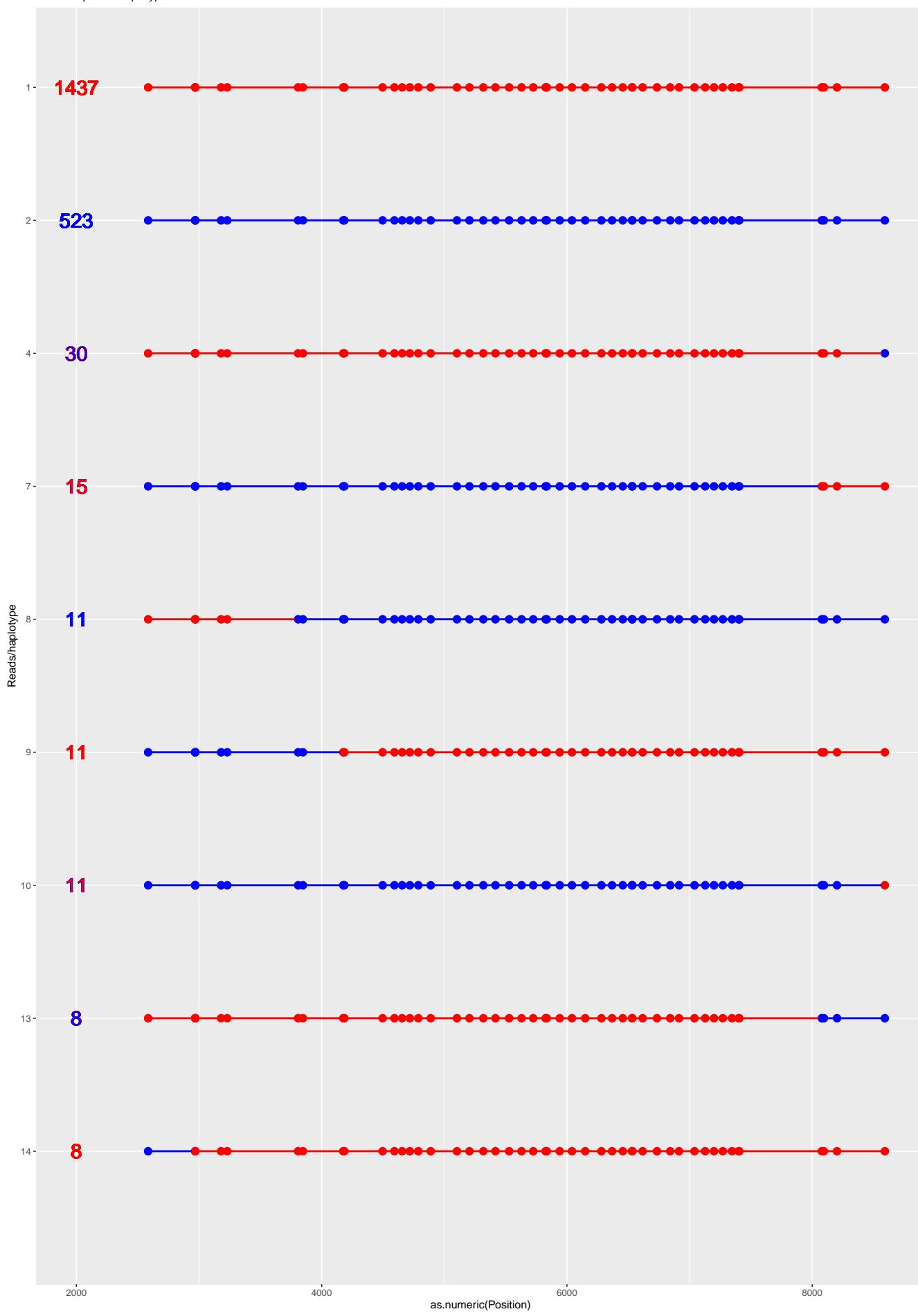
haplotypes I began with n[supporting reads] = 11, 1400

most frequent 7 haplotypes.



barcode = GTGCTGAGCATCAGAC & GACACGACTAGATCGC

Sample = 290c tetrad = 290 spore = c
 Total reads = 3613 PCR=759
 haplotypes I began with [n(supporting reads)] = 8, 11, 15, 30, 523, 1437
 most frequent 7 haplotypes.



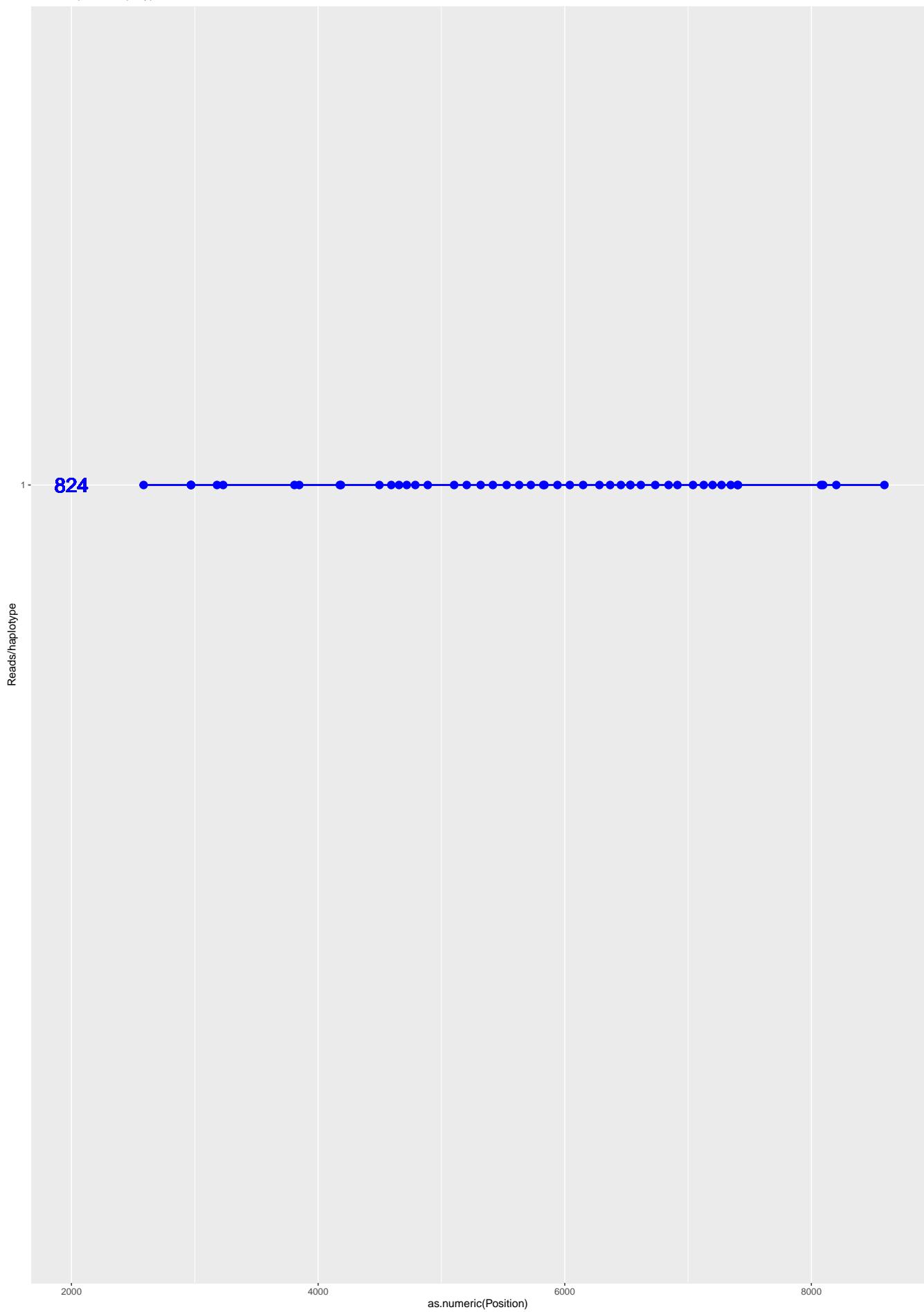
barcode = GTGCTGAGCATCAGAC & TACGAGTCTGTACATAC

Sample = 290d tetrad = 290 spore = d

Total reads = 949 PCR=760

haplotypes I began with n[supporting reads] = 824

most frequent 7 haplotypes.



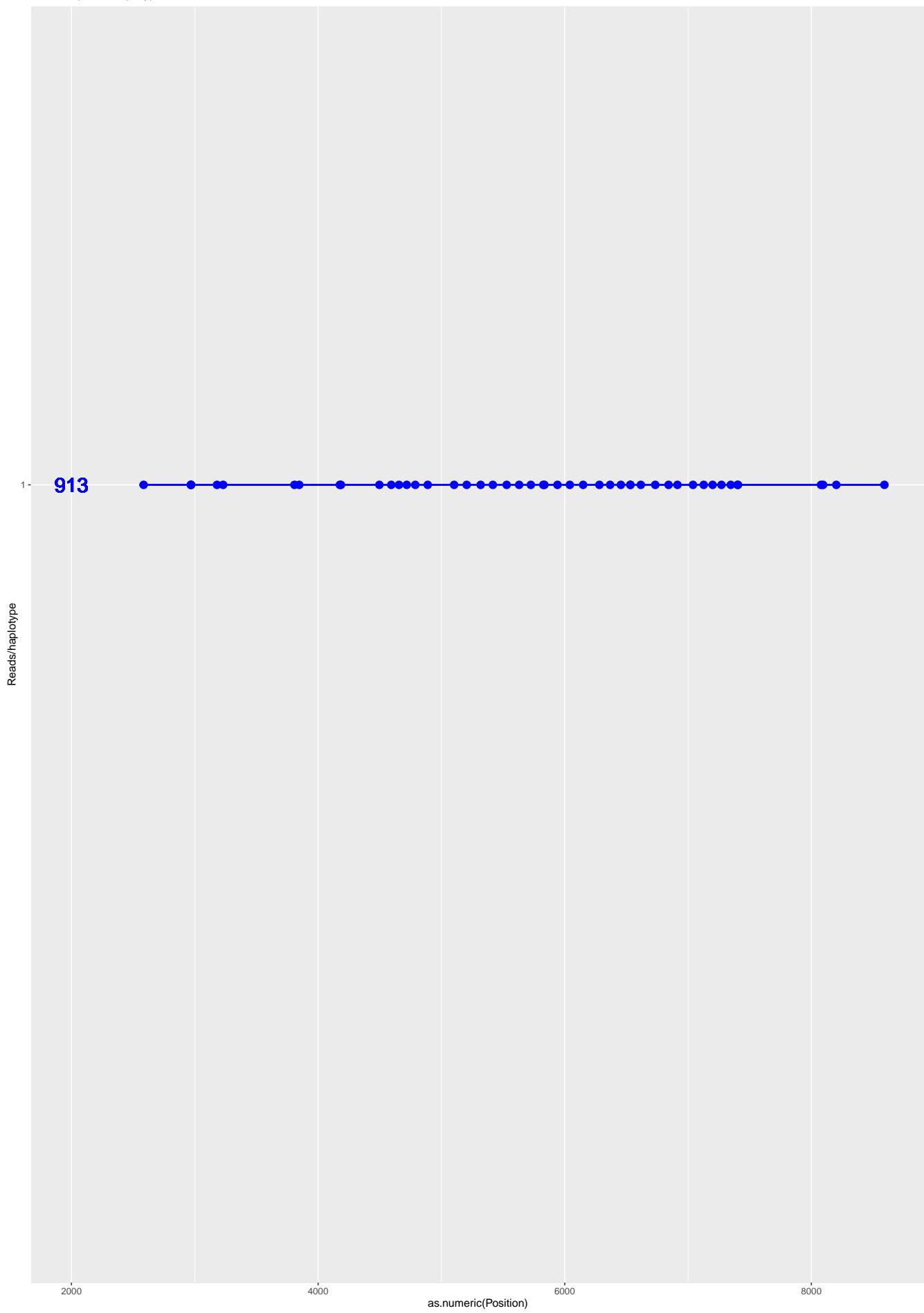
barcode = GTGCTGAGCAGCATCAGAC & ACTCAGCTACATAGTG

Sample = 294a tetrad = 294 spore = a

Total reads = 1079 PCR=765

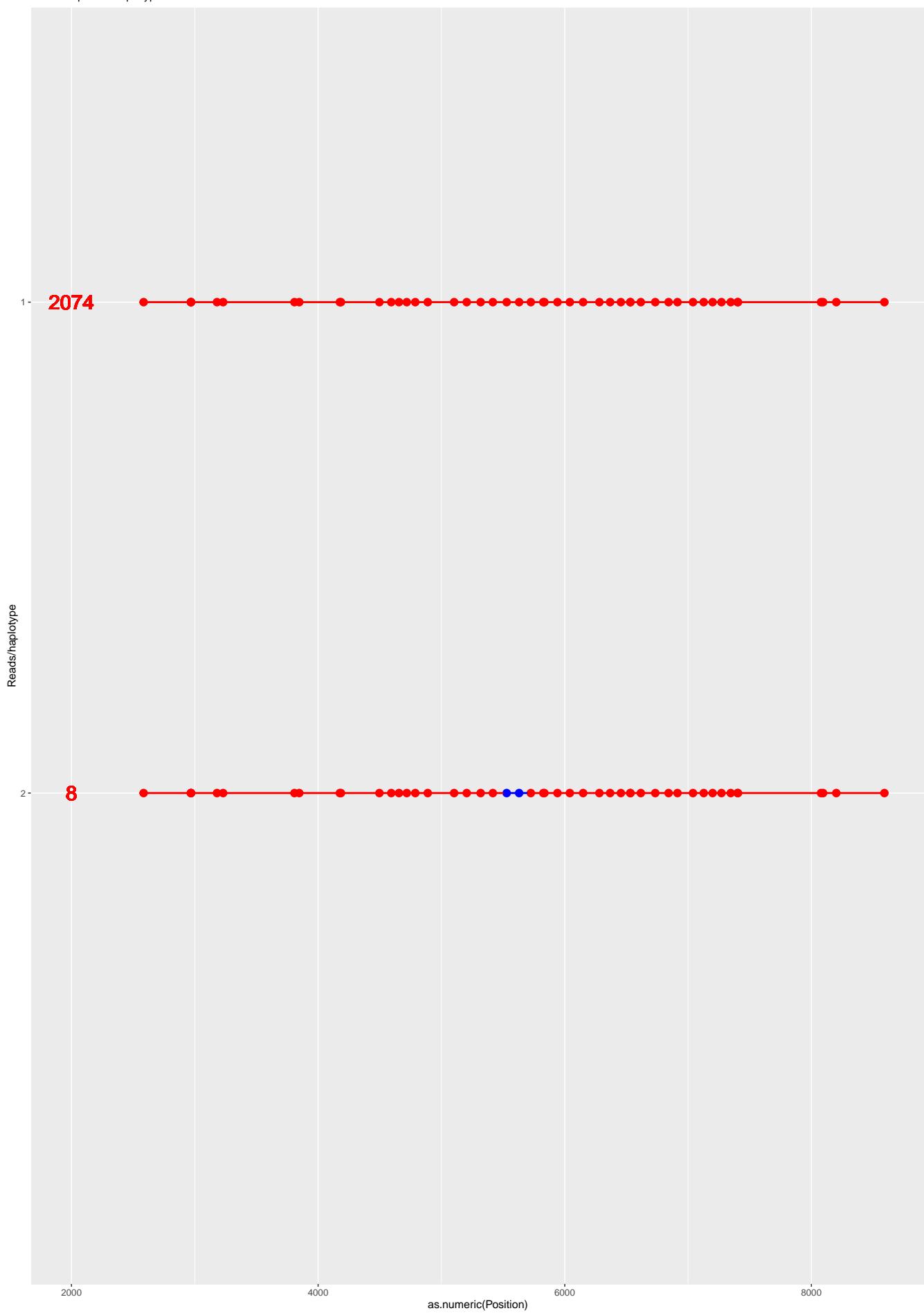
haplotypes I began with n[supporting reads] = 913

most frequent 7 haplotypes.



barcode = CACTGATCGATATGCA & ATATAGTACAGCGTCT

Sample = 294b tetrad = 294 spore = b
Total reads = 2160 PCR=766
haplotypes I began with n[supporting reads] = 8, 2074
most frequent 7 haplotypes.

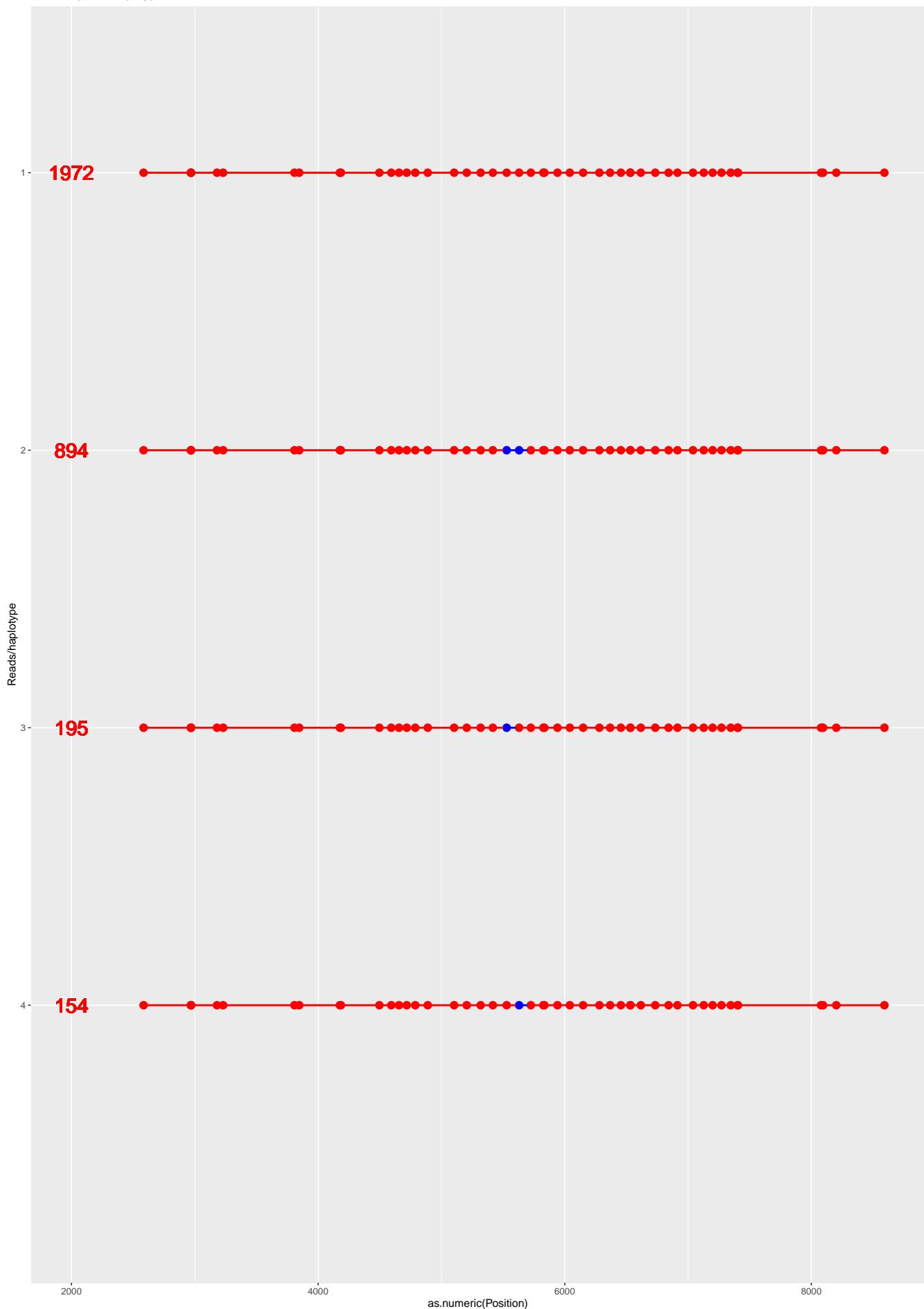


Sample = 294c tetrad = 294 spore = c

Total reads = 3366 PCR=767

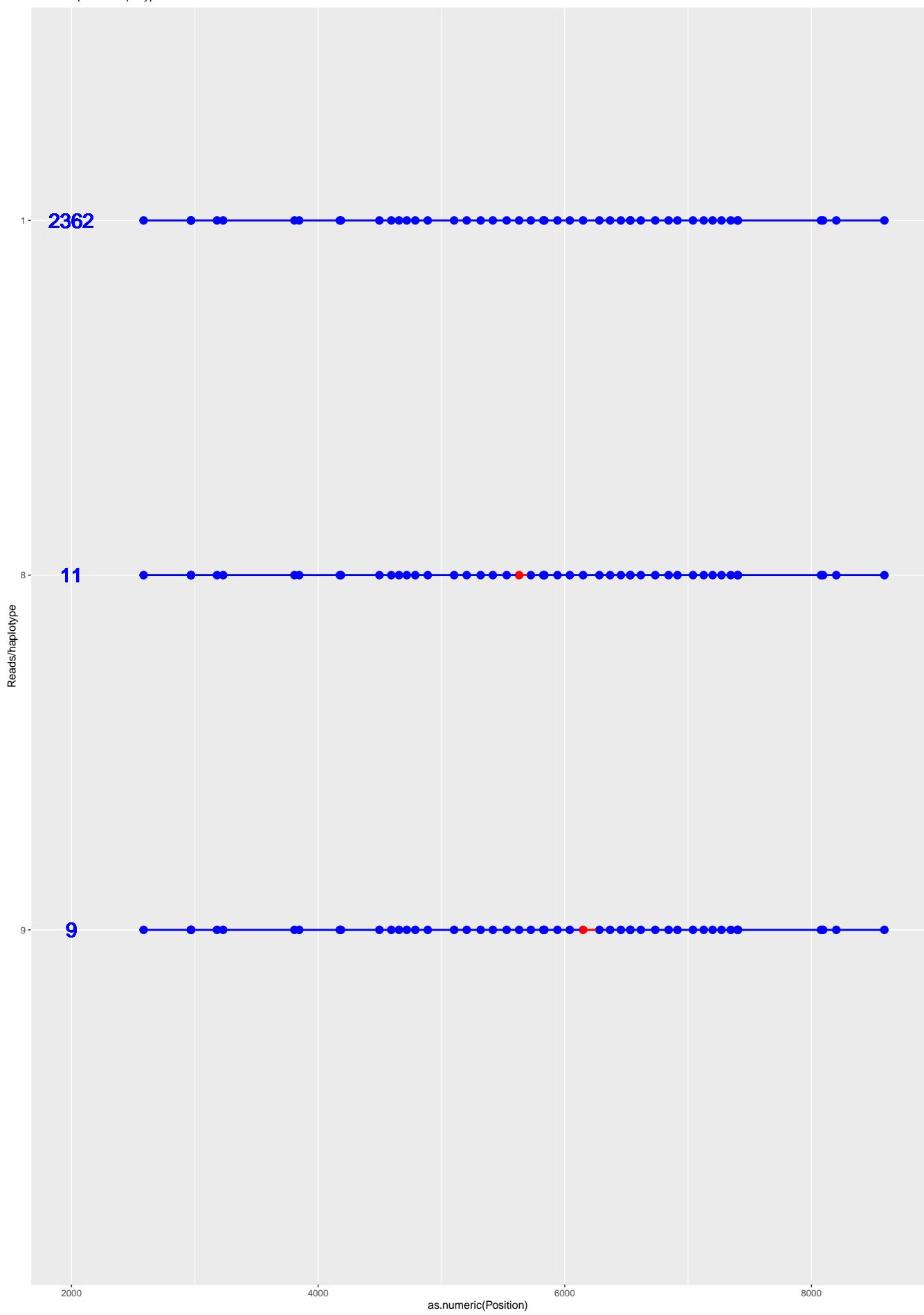
haplotypes I began with n[supporting reads] = 154, 195, 894, 1972

most frequent 7 haplotypes.

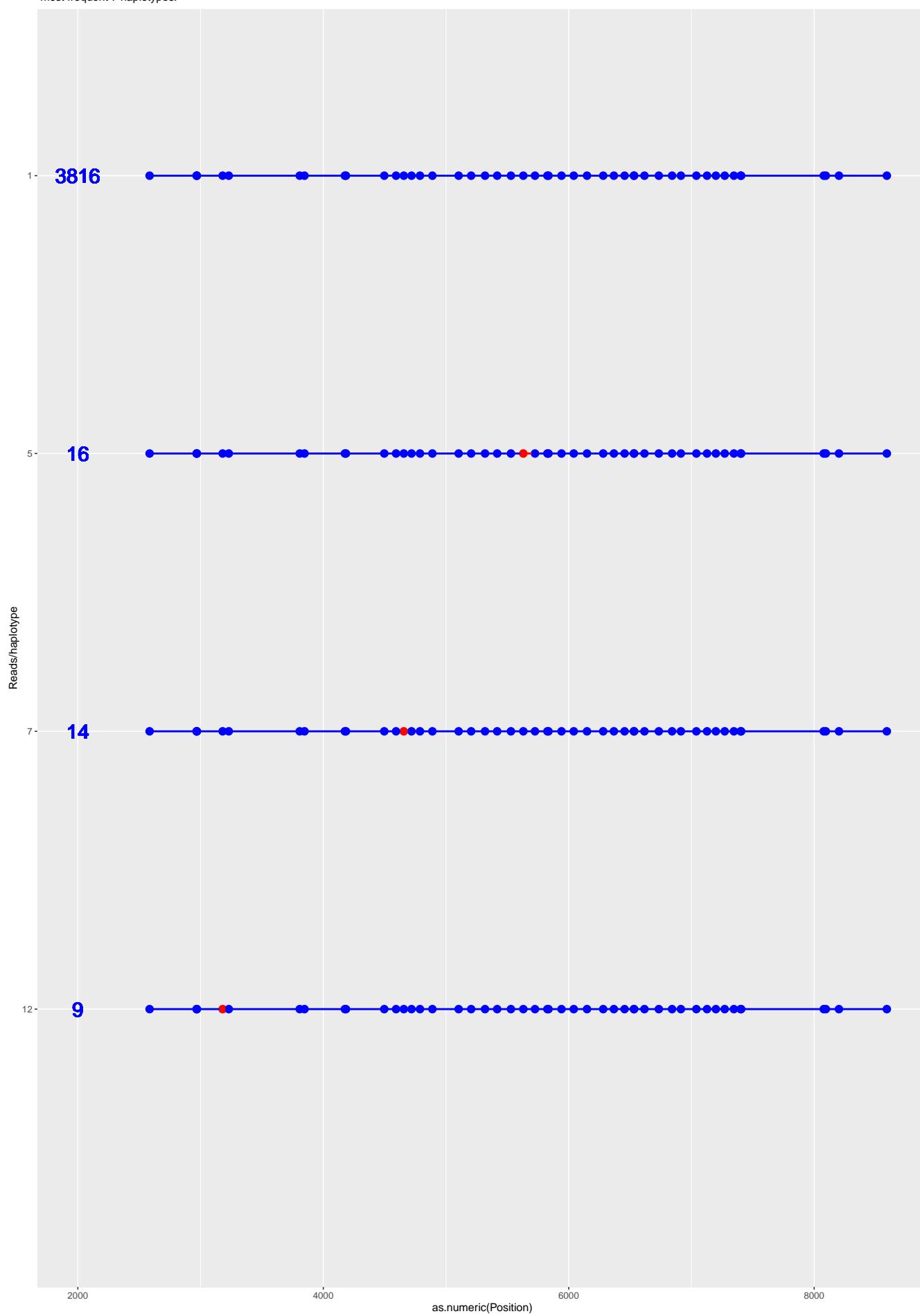


barcode = CACTGATCGATATGCA & TACGAGTCTGTAC

Sample = 294d tetrad = 294 spore = d
Total reads = 2780 PCR=768
haplotypes I began with n[supporting reads] = 9, 11, 2362
most frequent 7 haplotypes.



Sample = 296a tetrad = 296 spore = a
Total reads = 4455 PCR=769
haplotypes I began with [n(supporting reads)] = 9, 14, 16, 3816
most frequent 7 haplotypes.

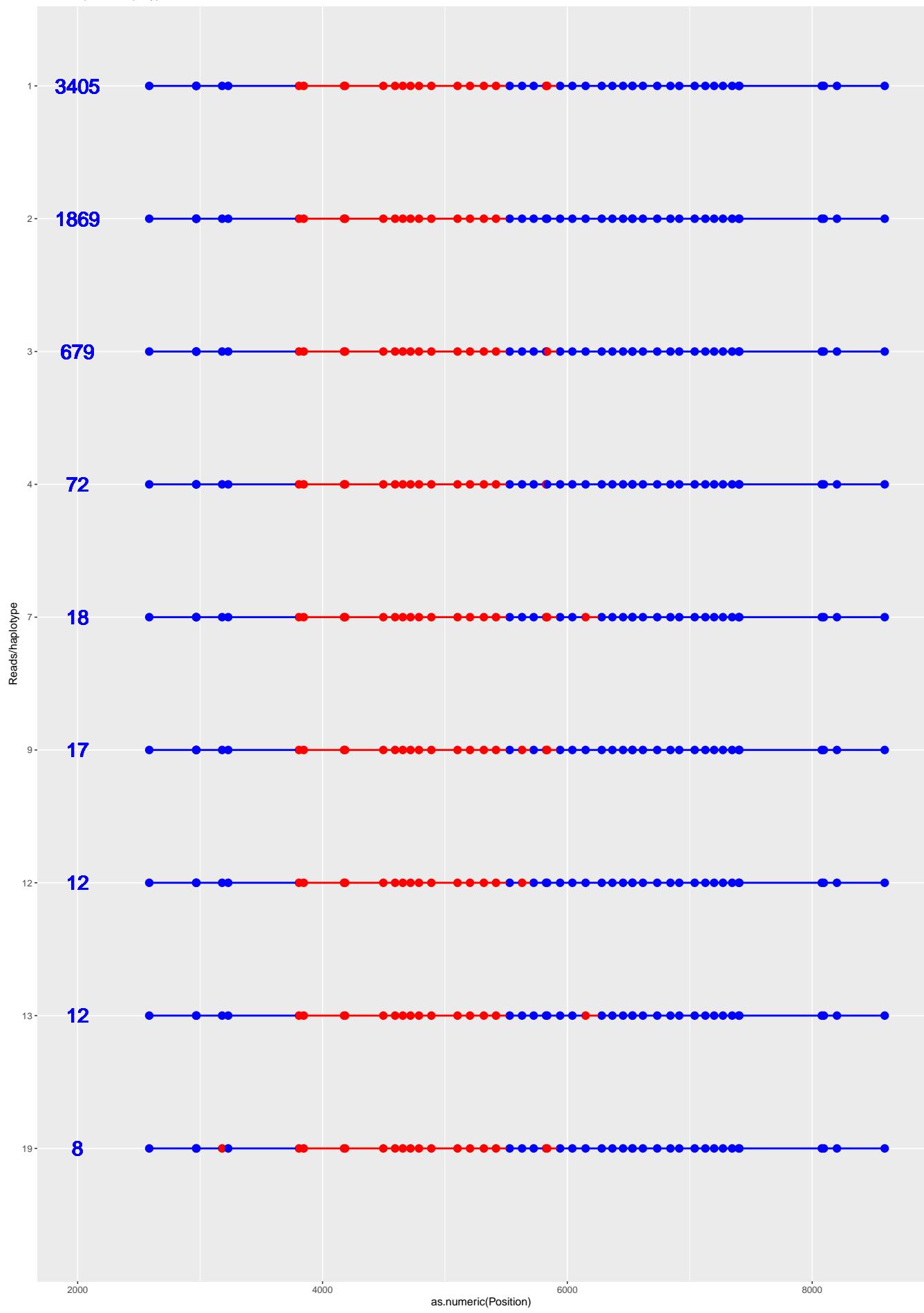


Sample = 296b tetrad = 296 spore = b

Total reads =6672 PCR=770

haplotypes I began with [n(supporting reads)] = 8, 12, 17, 18, 72, 679, 1869, 3405

most frequent 7 haplotypes.



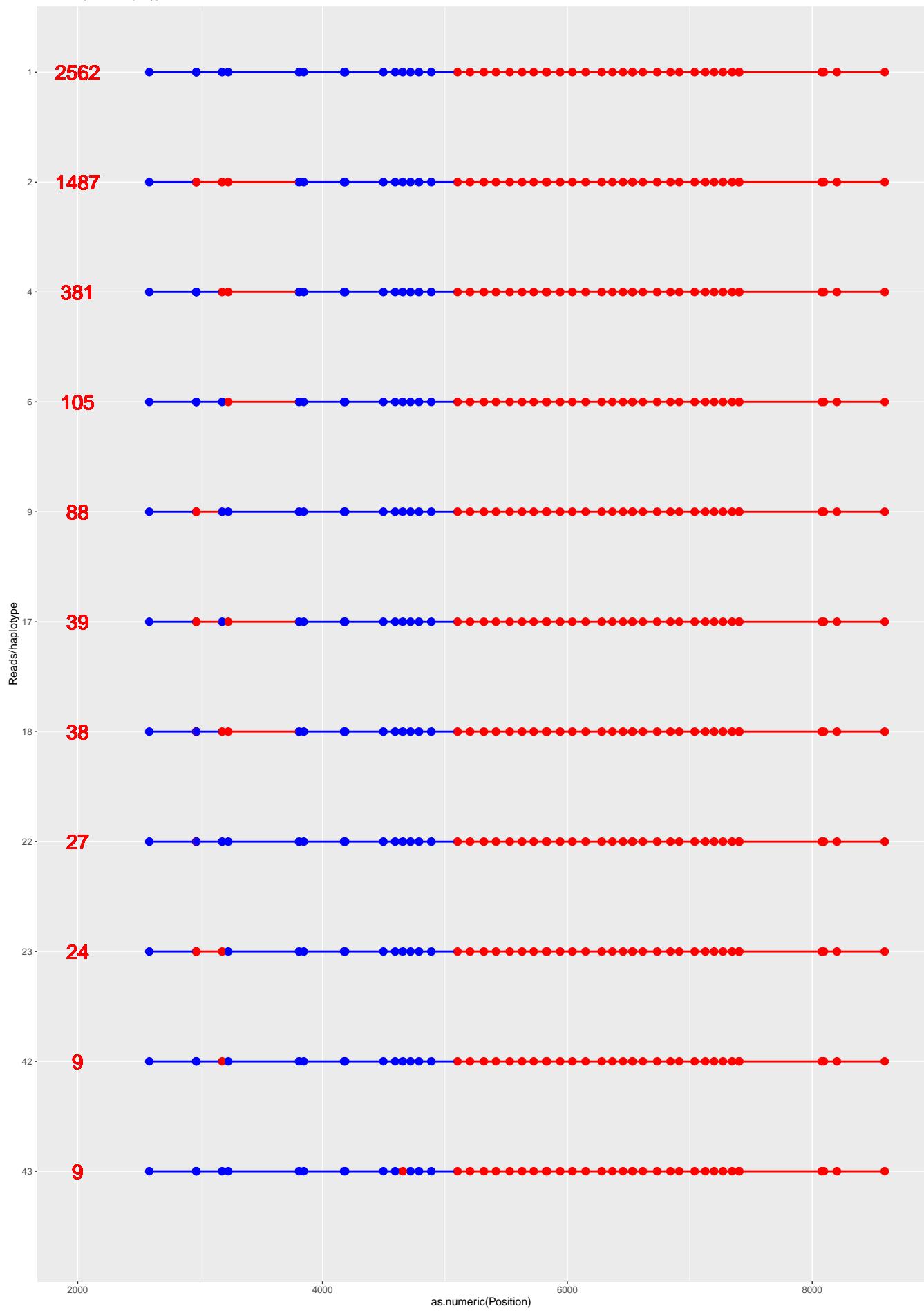
barcode = TACAGTGTCTGCTGCG & ACTGATGCGCACATGT

Sample = 296c tetrad = 296 spore = c

Total reads = 6869 PCR=771

haplotypes I began with [n(supporting reads)] = 9, 24, 27, 38, 39, 88, 105, 381, 1487, 2562

most frequent 7 haplotypes.



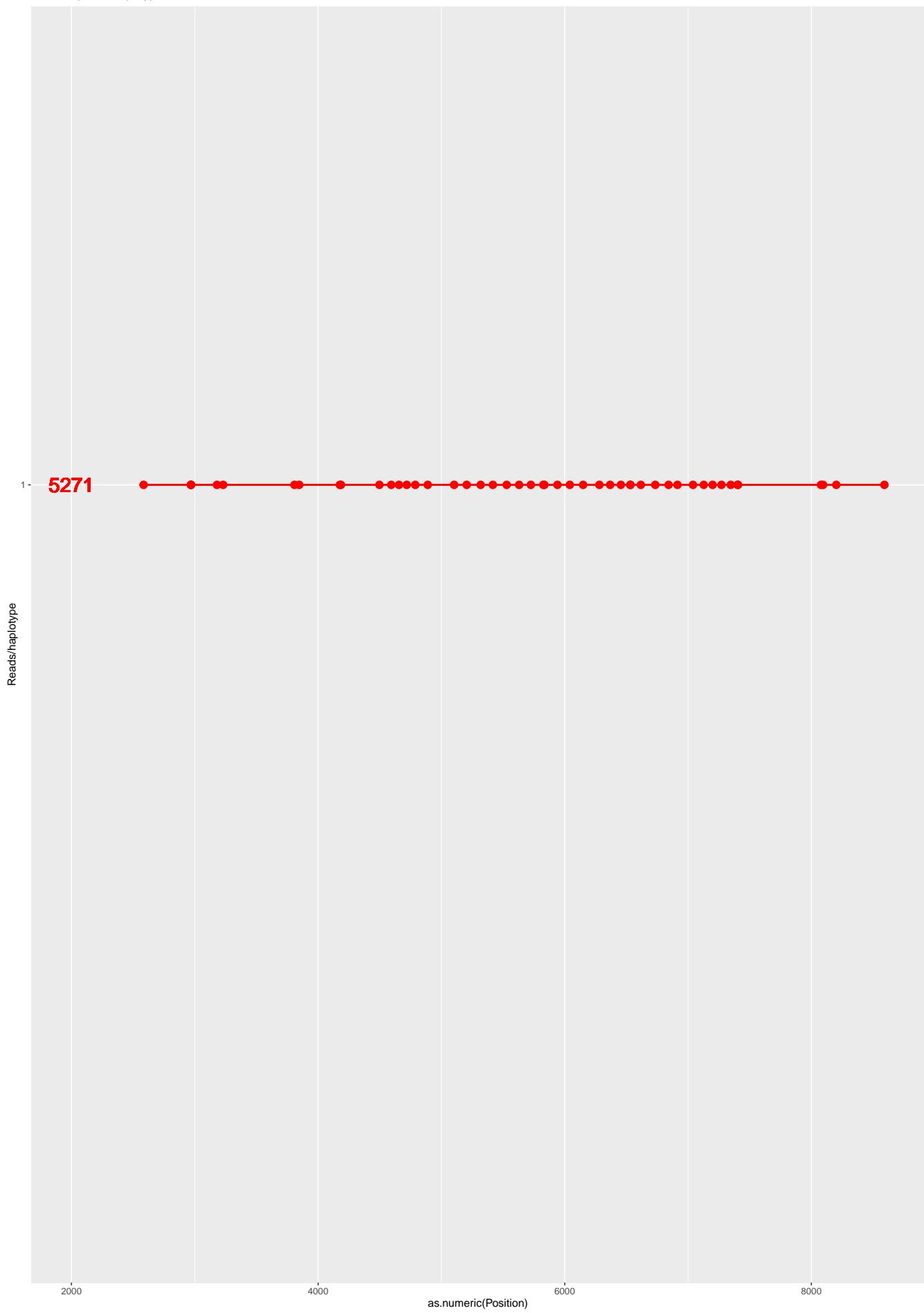
barcode = TACAGTGTCTGCTGCG & CTACTCTCAGCAGTGA

Sample = 296d tetrad = 296 spore = d

Total reads = 5524 PCR=772

haplotypes I began with n[supporting reads] = 5271

most frequent 7 haplotypes.



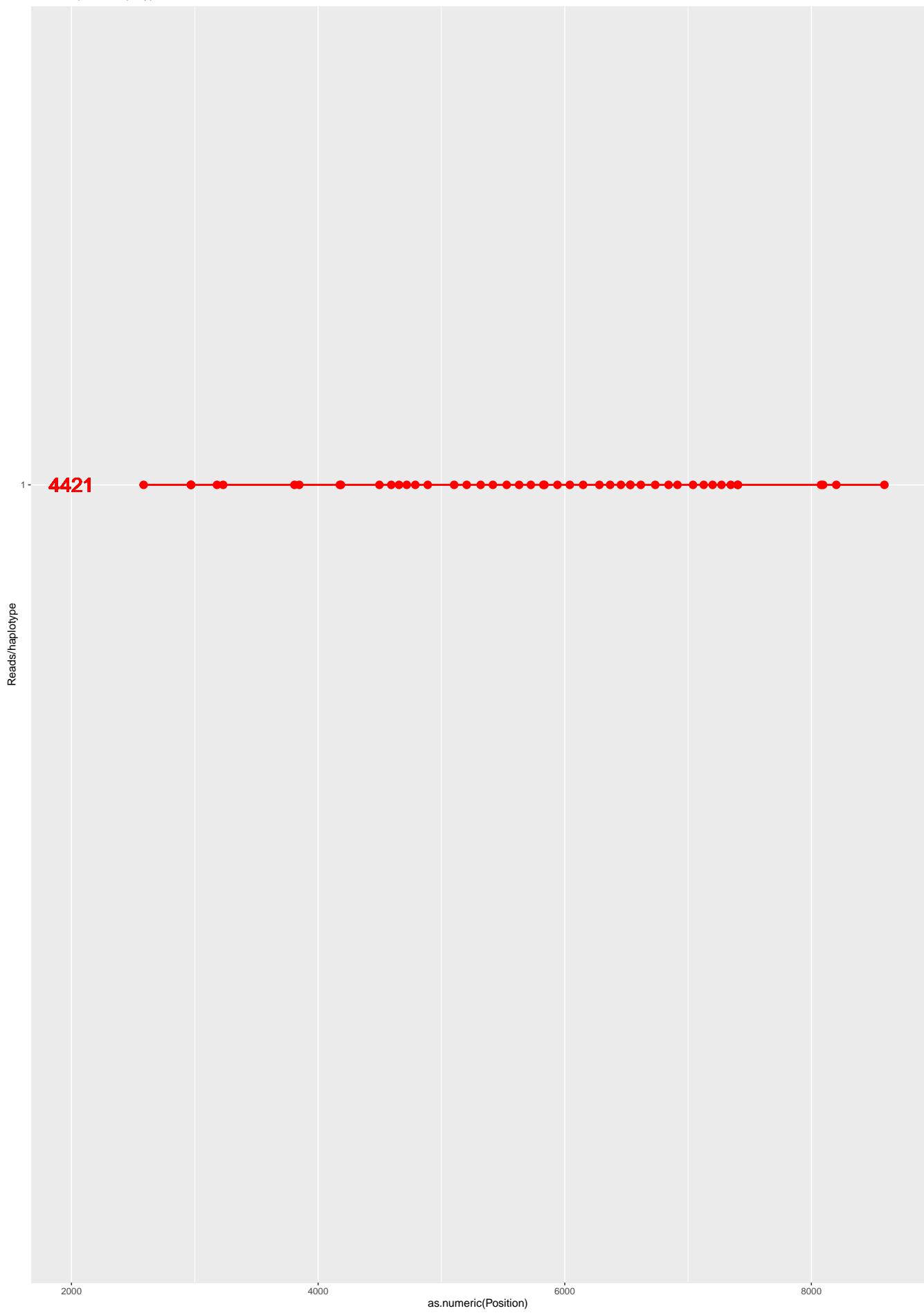
barcode = TACAGTGTCTGCTGCG & ATCTACATCACGACTC

Sample = 300a tetrad = 300 spore = a

Total reads = 4621 PCR=777

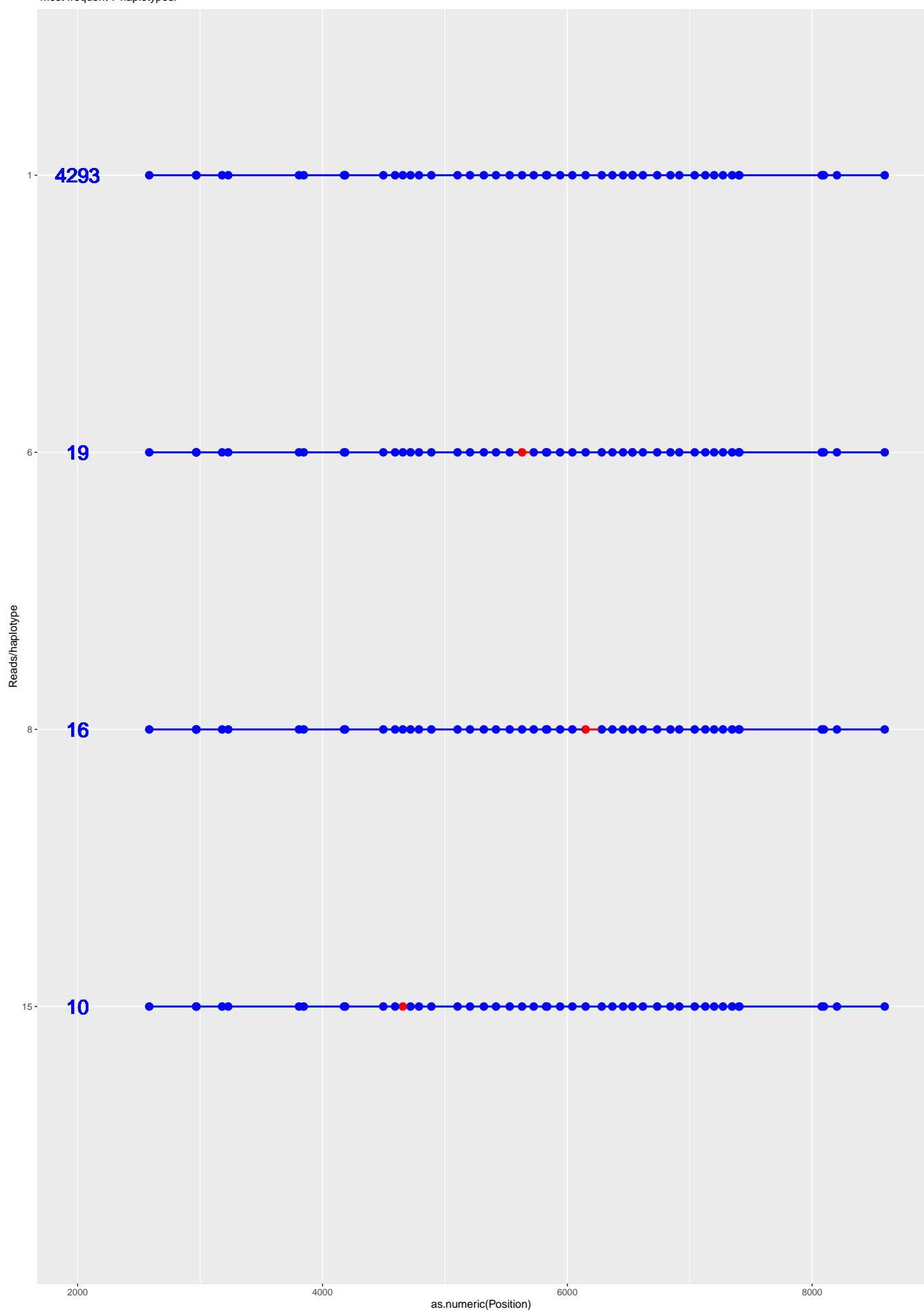
haplotypes I began with n[supporting reads] = 4421

most frequent 7 haplotypes.



barcode = TACAGATAGTGTAGCG & TCAGCTGACGATGTGA

Sample = 300b tetrad = 300 spore = b
Total reads = 5020 PCR=778
haplotypes I began with [n|supporting reads] = 10, 16, 19, 4293
most frequent 7 haplotypes.

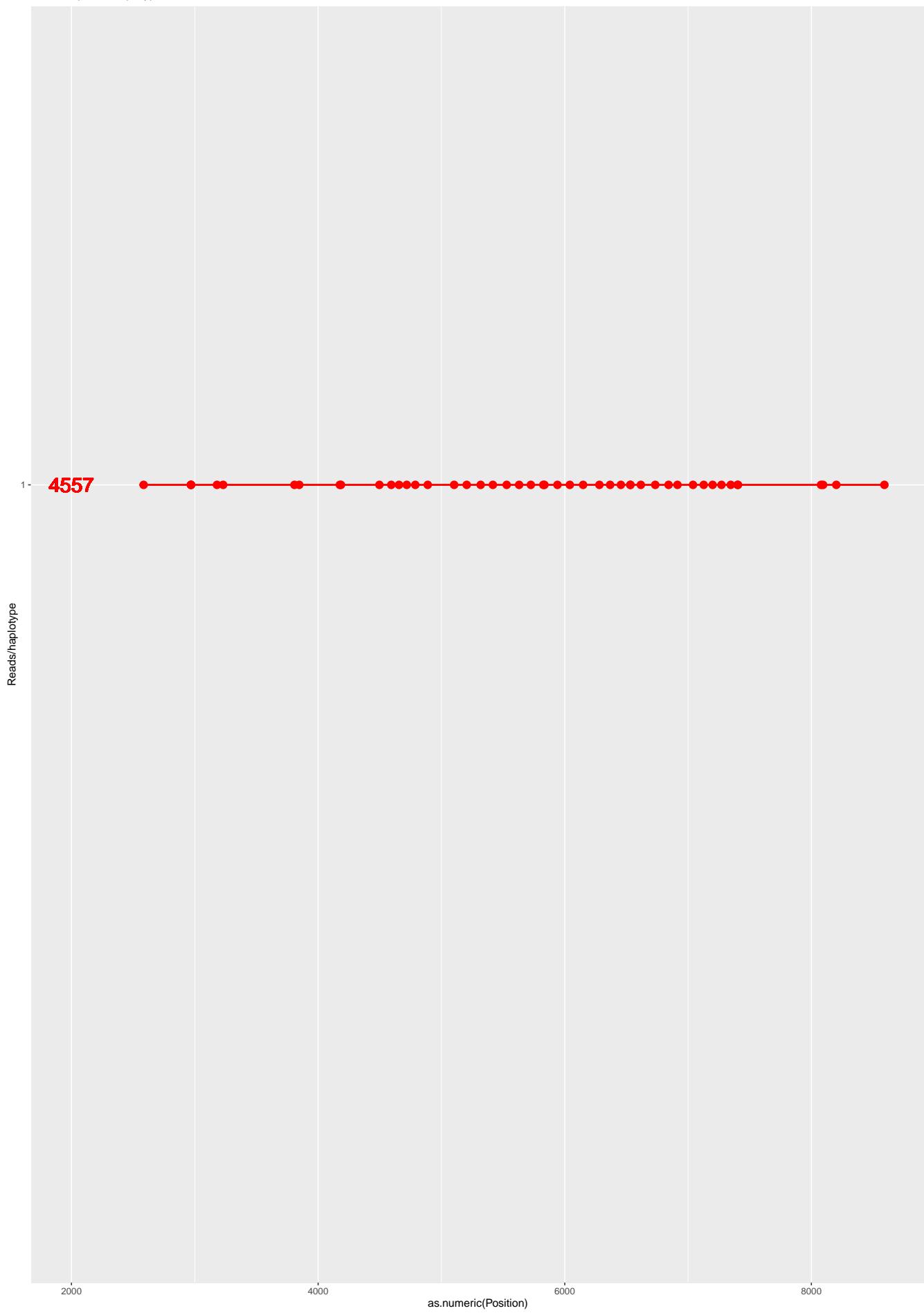


Sample = 300c tetrad = 300 spore = c

Total reads = 4787 PCR=779

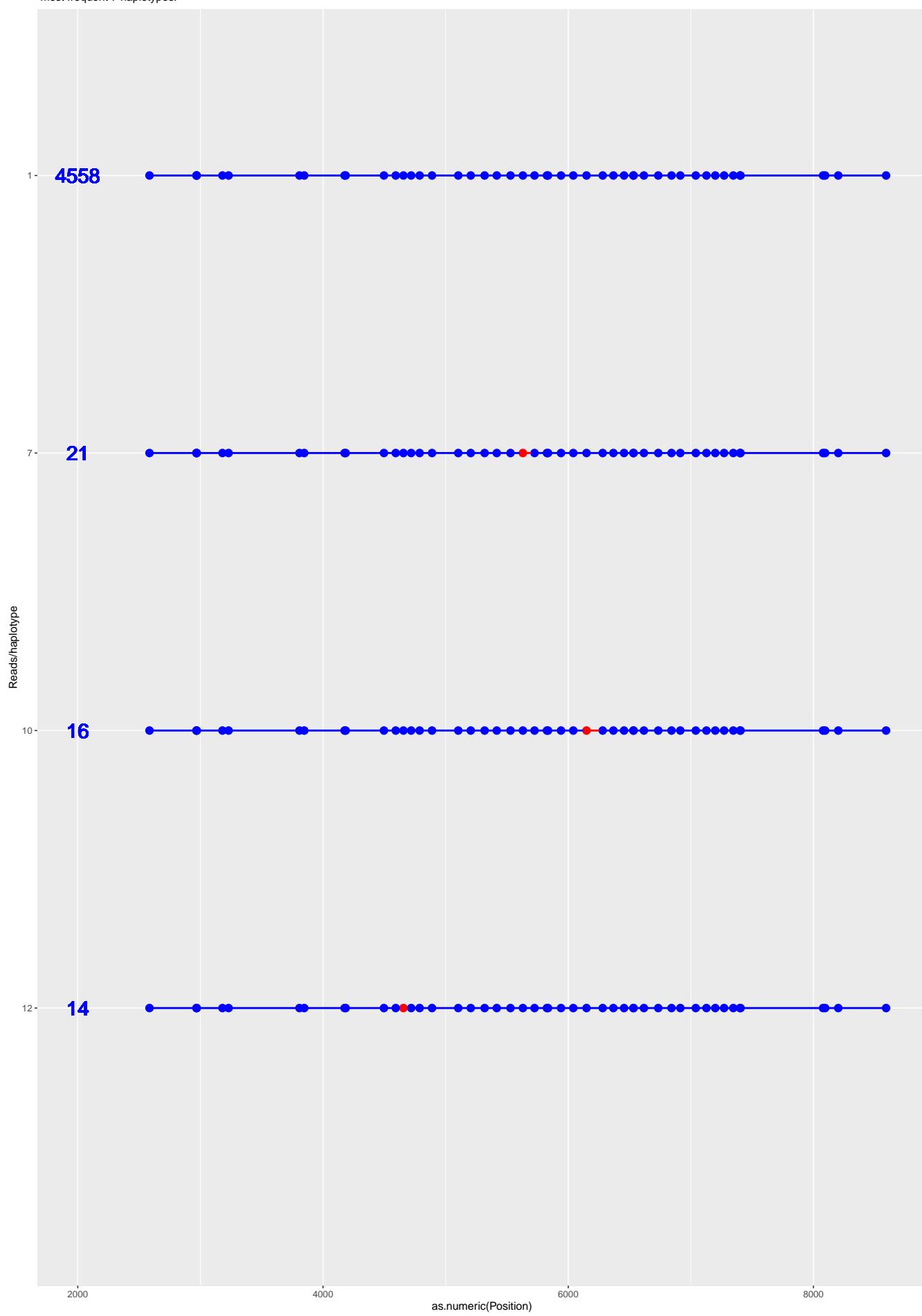
haplotypes I began with n[supporting reads] = 4557

most frequent 7 haplotypes.



barcode = TACAGATACTGTAGCG & CTACTCTCAGCAGTGA

Sample = 300d tetrad = 300 spore = d
Total reads =5346 PCR=780
haplotypes I began with [n(supporting reads)] = 14, 16, 21, 4558
most frequent 7 haplotypes.

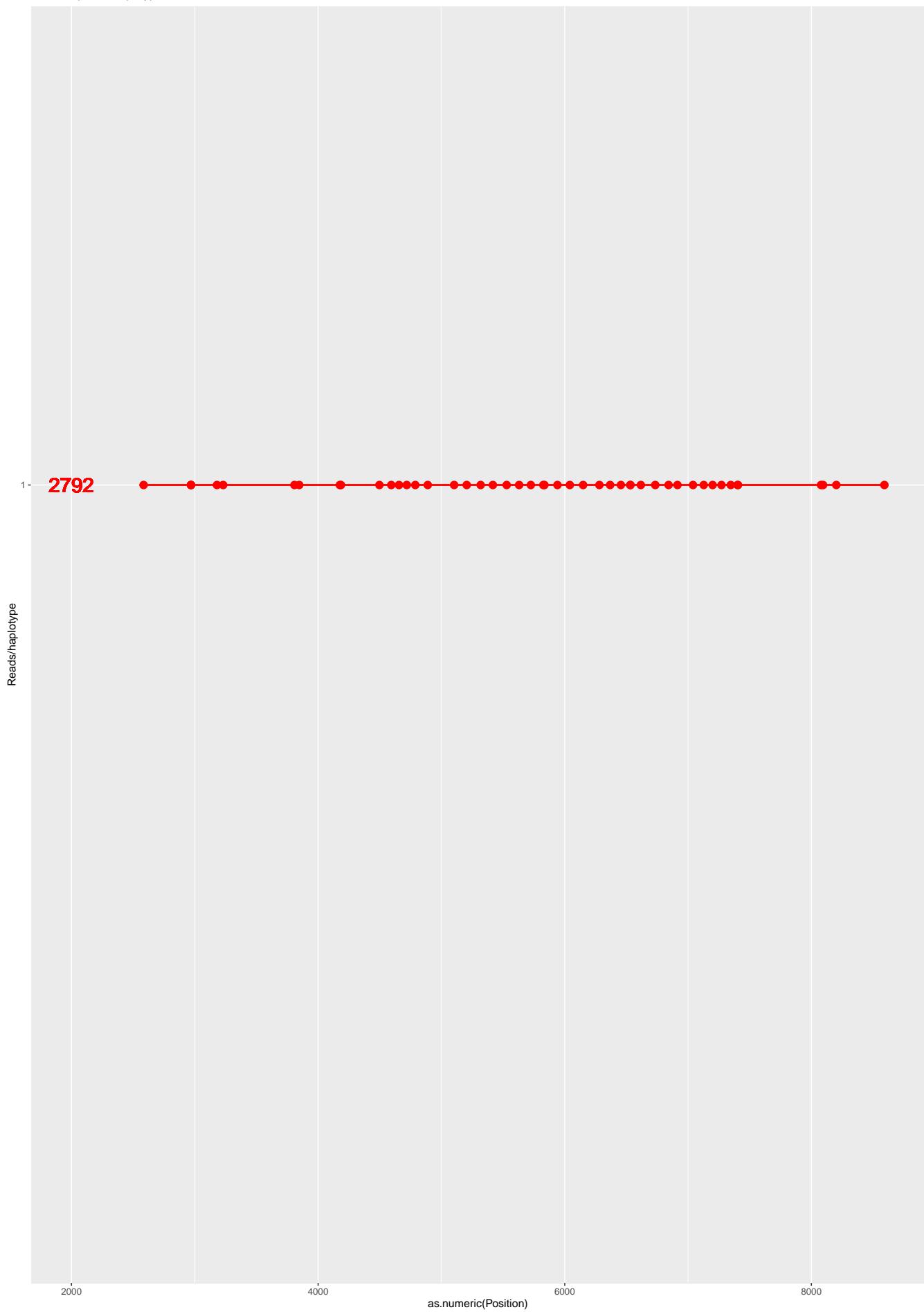


Sample = 302a tetrad = 302 spore = a

Total reads = 2904 PCR=785

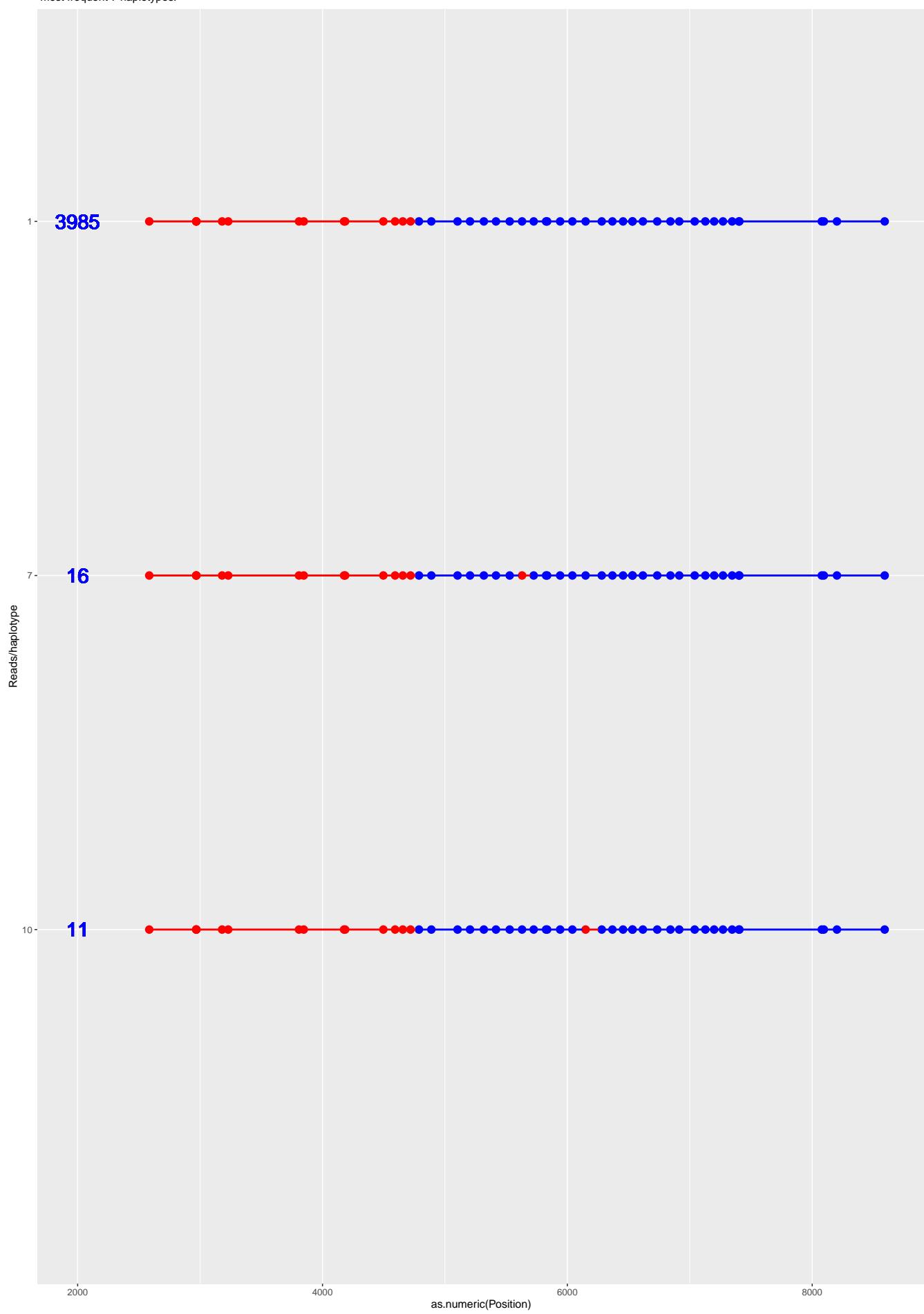
haplotypes I began with n[supporting reads] = 2792

most frequent 7 haplotypes.



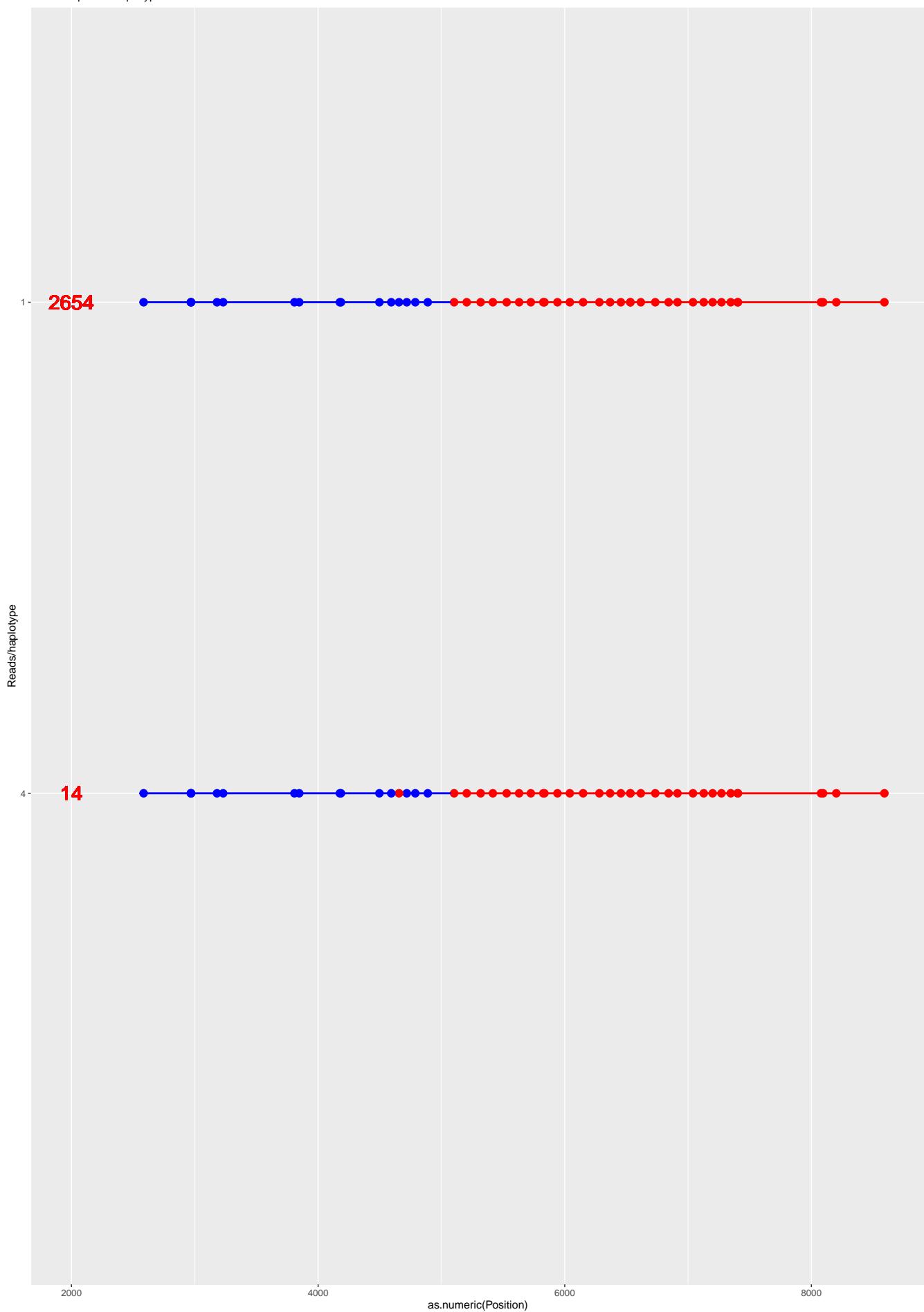
barcode = TCGTAGAGCTCGAGAC & TCAGCTGACGATGTGA

Sample = 302b tetrad = 302 spore = b
Total reads = 4581 PCR=786
haplotypes I began with [n:supporting reads] = 11, 16, 3985
most frequent 7 haplotypes.



barcode = TCGTAGAGCTCGAGAC & ACTGATGCGCACATGT

Sample = 302c tetrad = 302 spore = c
Total reads = 2878 PCR=787
haplotypes I began with n[supporting reads] = 14, 2654
most frequent 7 haplotypes.



barcode = TCGTAGAGCTGAGAC & CTACTCTCAGCAGTGA

Sample = 302d tetrad = 302 spore = d
Total reads =3321 PCR=788
haplotypes I began with [n|supporting reads] = 8, 19, 2822
most frequent 7 haplotypes.

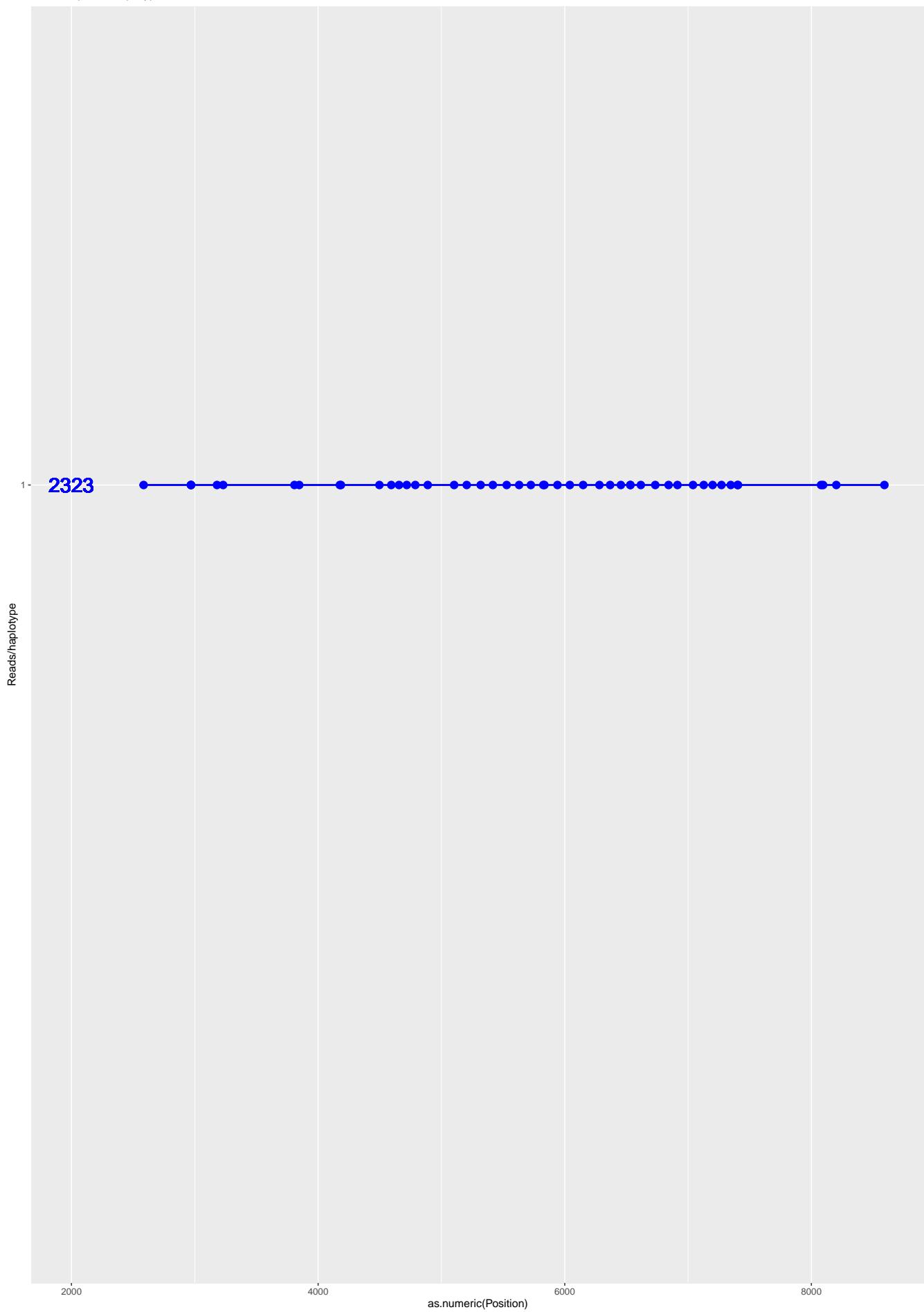


Sample = 303a tetrad = 303 spore = a

Total reads =2699 PCR=789

haplotypes I began with n[supporting reads] = 2323

most frequent 7 haplotypes.



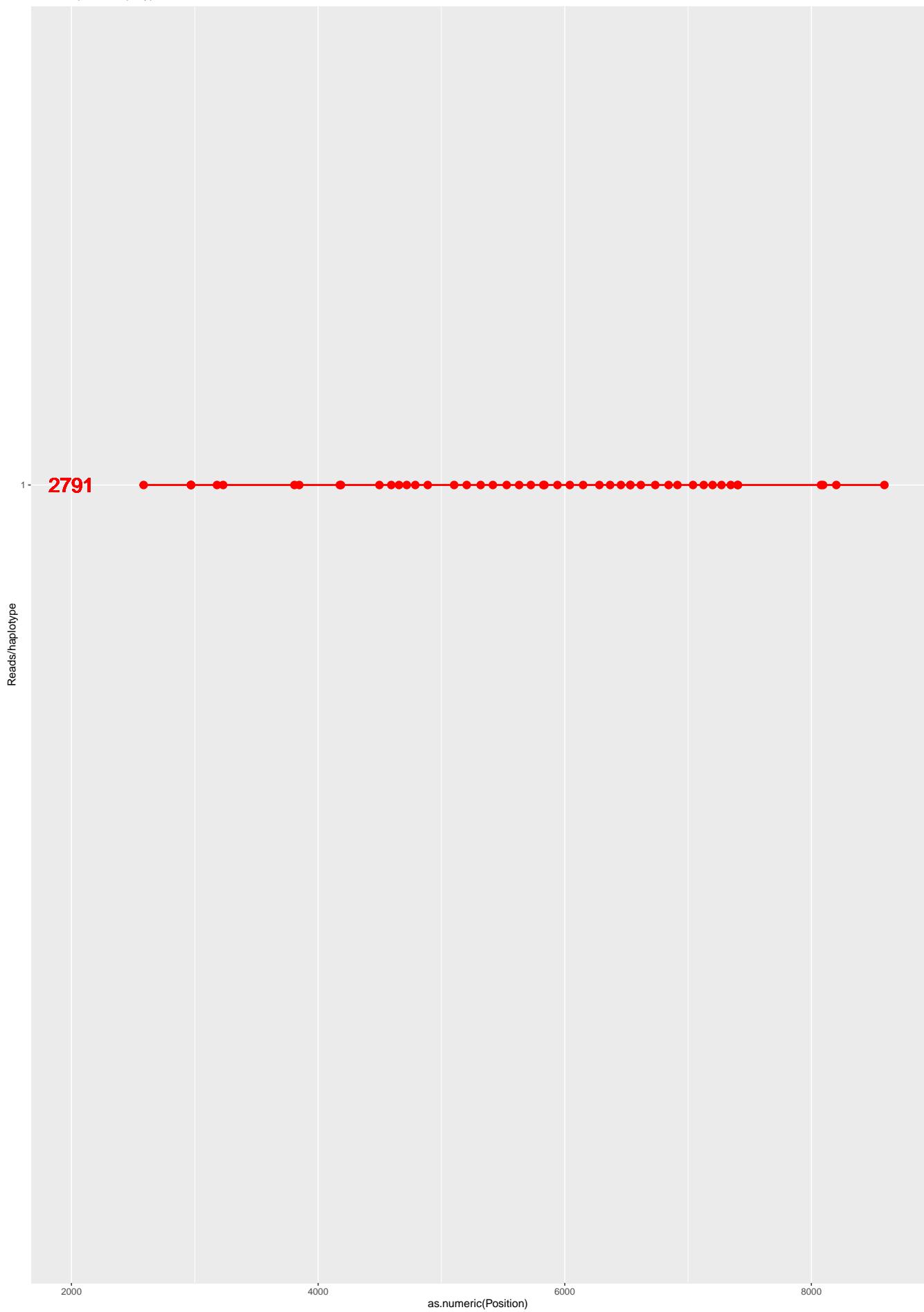
barcode = TCGTAGAGCTCGAGAC & ATATAGTACAGCGTCT

Sample = 303b tetrad = 303 spore = b

Total reads = 2920 PCR=790

haplotypes I began with n[supporting reads] = 2791

most frequent 7 haplotypes.



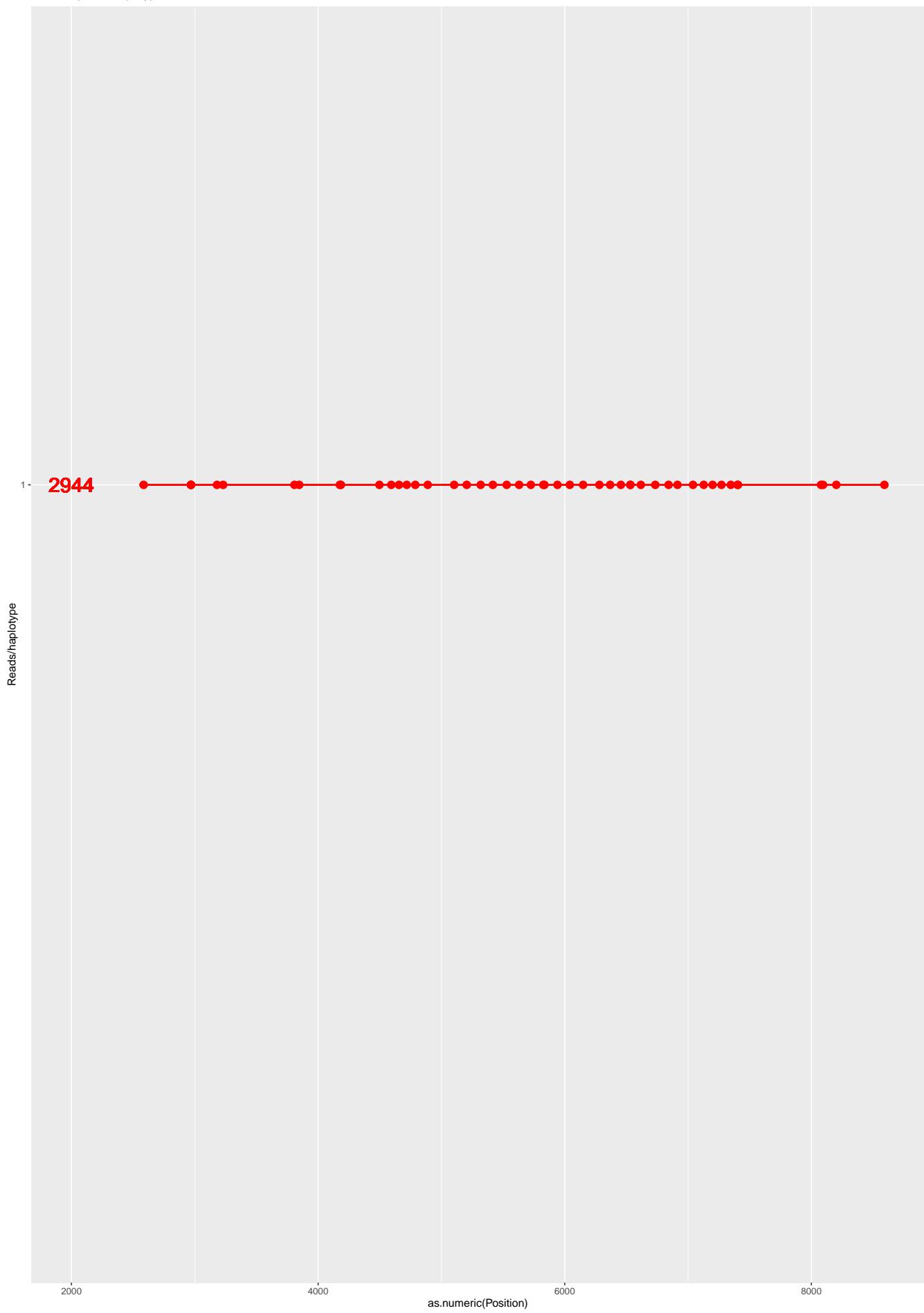
barcode = TCGTAGAGCTCGAGAC & GACACGACTAGATCGC

Sample = 303c tetrad = 303 spore = c

Total reads = 3079 PCR=791

haplotypes I began with n[supporting reads] = 2944

most frequent 7 haplotypes.

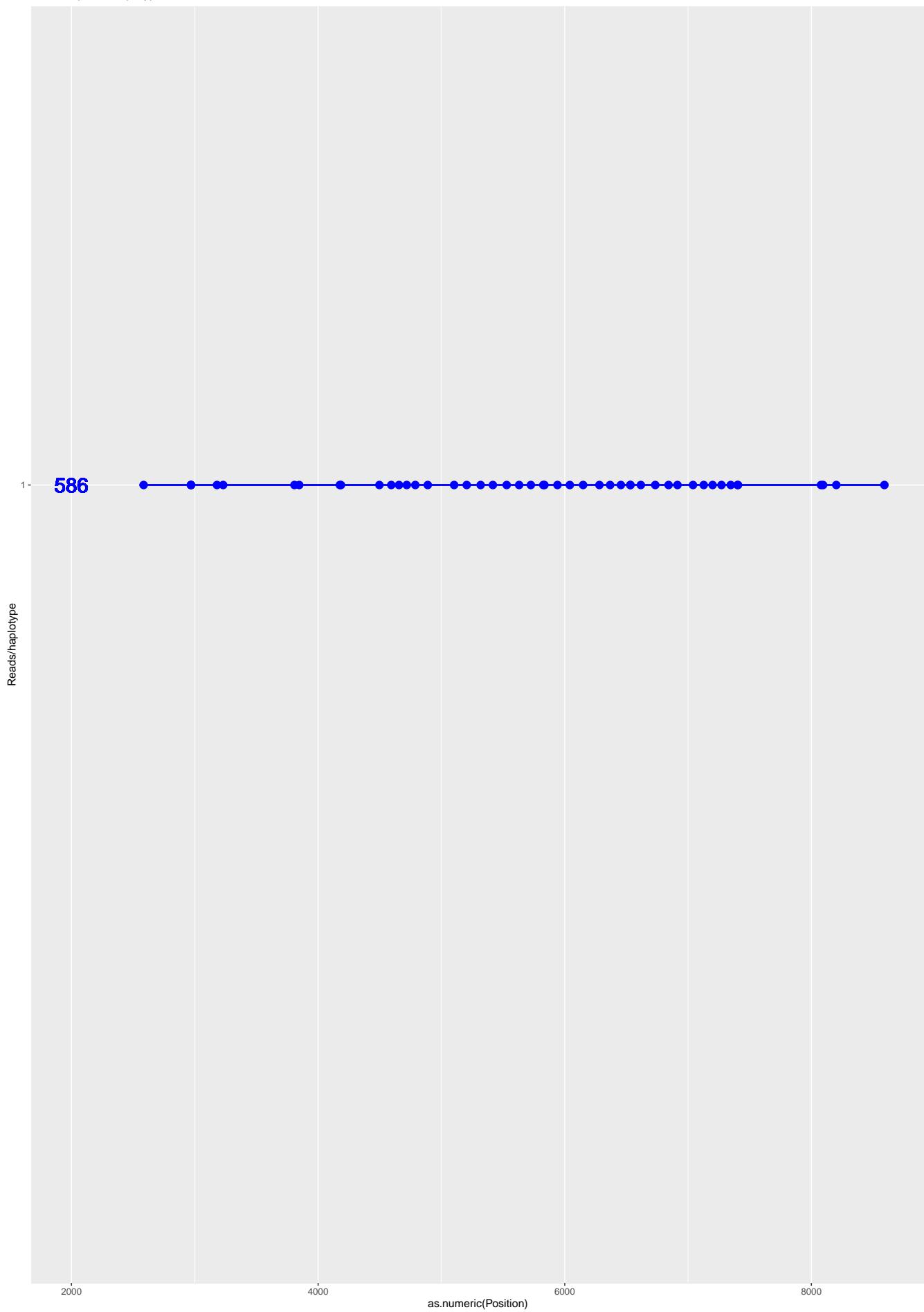


Sample = 303d tetrad = 303 spore = d

Total reads = 687 PCR=792

haplotypes I began with n[supporting reads] = 586

most frequent 7 haplotypes.



barcode = TCGTAGAGCTGAGAC & ACTCAGCTACATAGTG

Sample = 304a tetrad = 304 spore = a

Total reads = 3249 PCR=793

haplotypes I began with n[supporting reads] = 11, 16, 2839

most frequent 7 haplotypes.



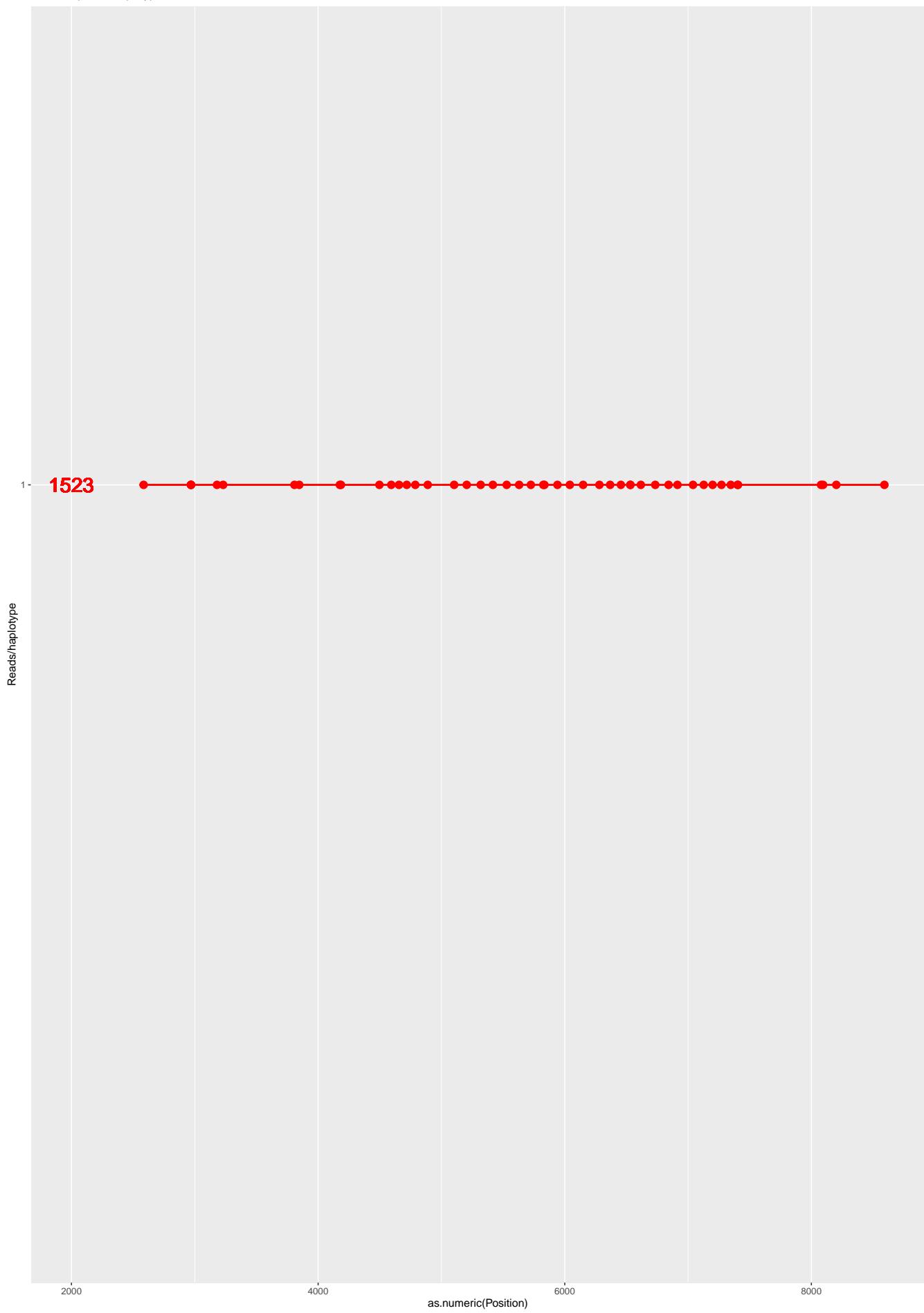
barcode = GAGCTGCGCACTCGAT & TCAGCTGACGATGTGA

Sample = 304b tetrad = 304 spore = b

Total reads = 1573 PCR=794

haplotypes I began with n[supporting reads] = 1523

most frequent 7 haplotypes.

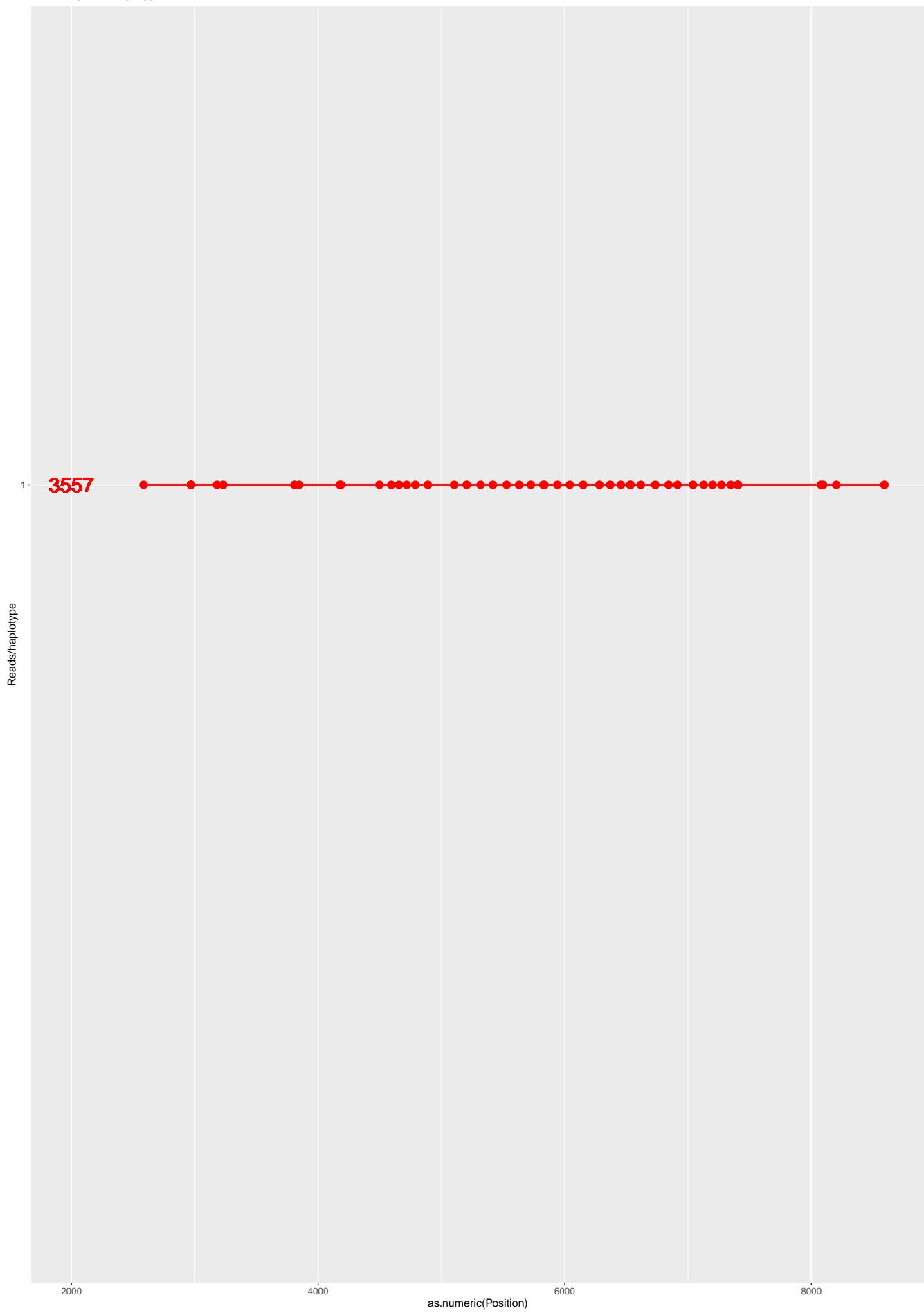


Sample = 304c tetrad = 304 spore = c

Total reads = 3696 PCR=795

haplotypes I began with n[supporting reads] = 3557

most frequent 7 haplotypes.



Sample = 304d tetrad = 304 spore = d
Total reads = 3133 PCR=796
haplotypes I began with [n|supporting reads] = 8, 12, 2685
most frequent 7 haplotypes.

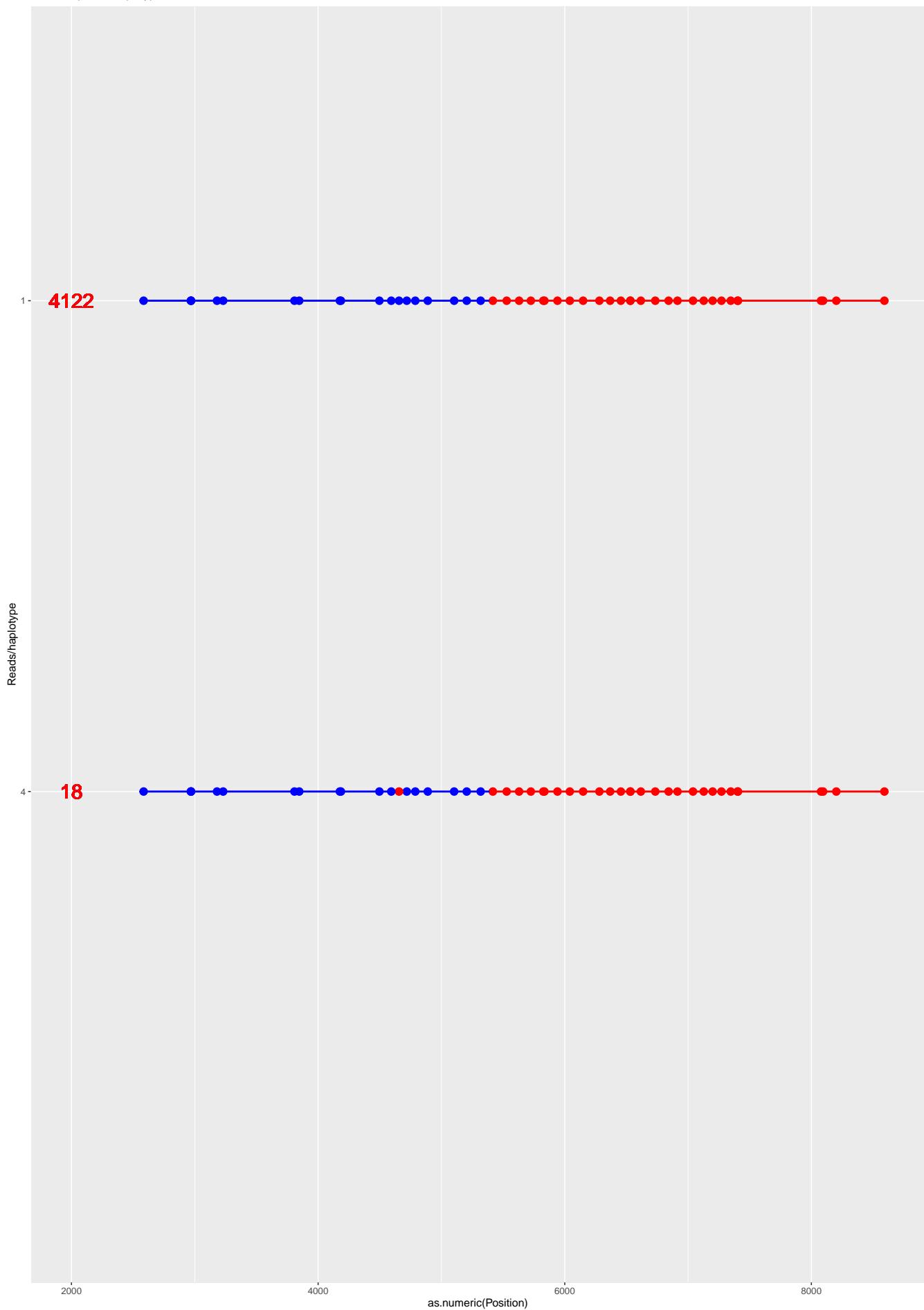


Sample = 307a tetrad = 307 spore = a

Total reads = 4473 PCR=801

haplotypes I began with n[supporting reads] = 18, 4122

most frequent 7 haplotypes.



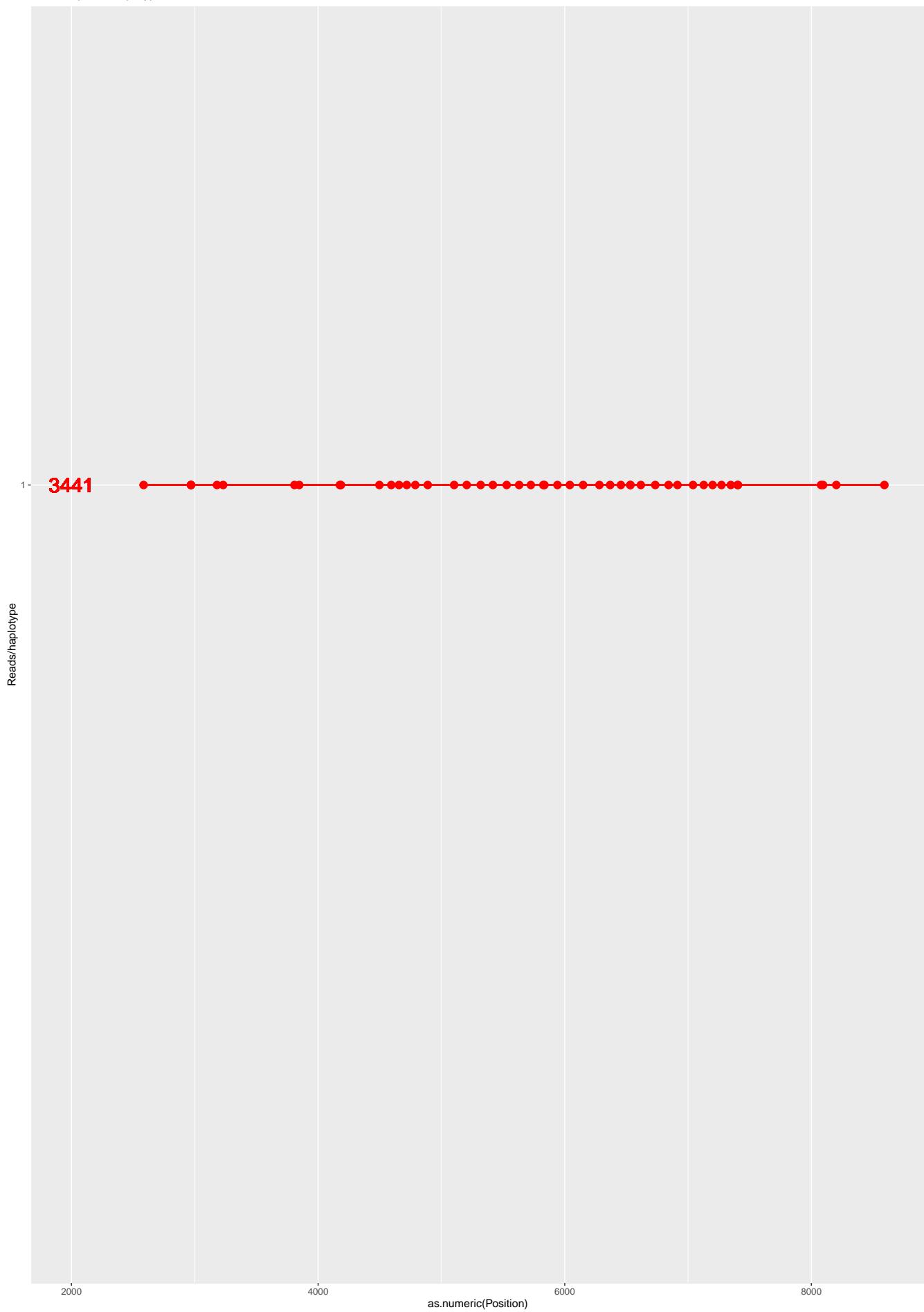
barcode = GCGATGTCGCTATGTG & TCAGCTGACGATGTGA

Sample = 307b tetrad = 307 spore = b

Total reads = 3585 PCR=802

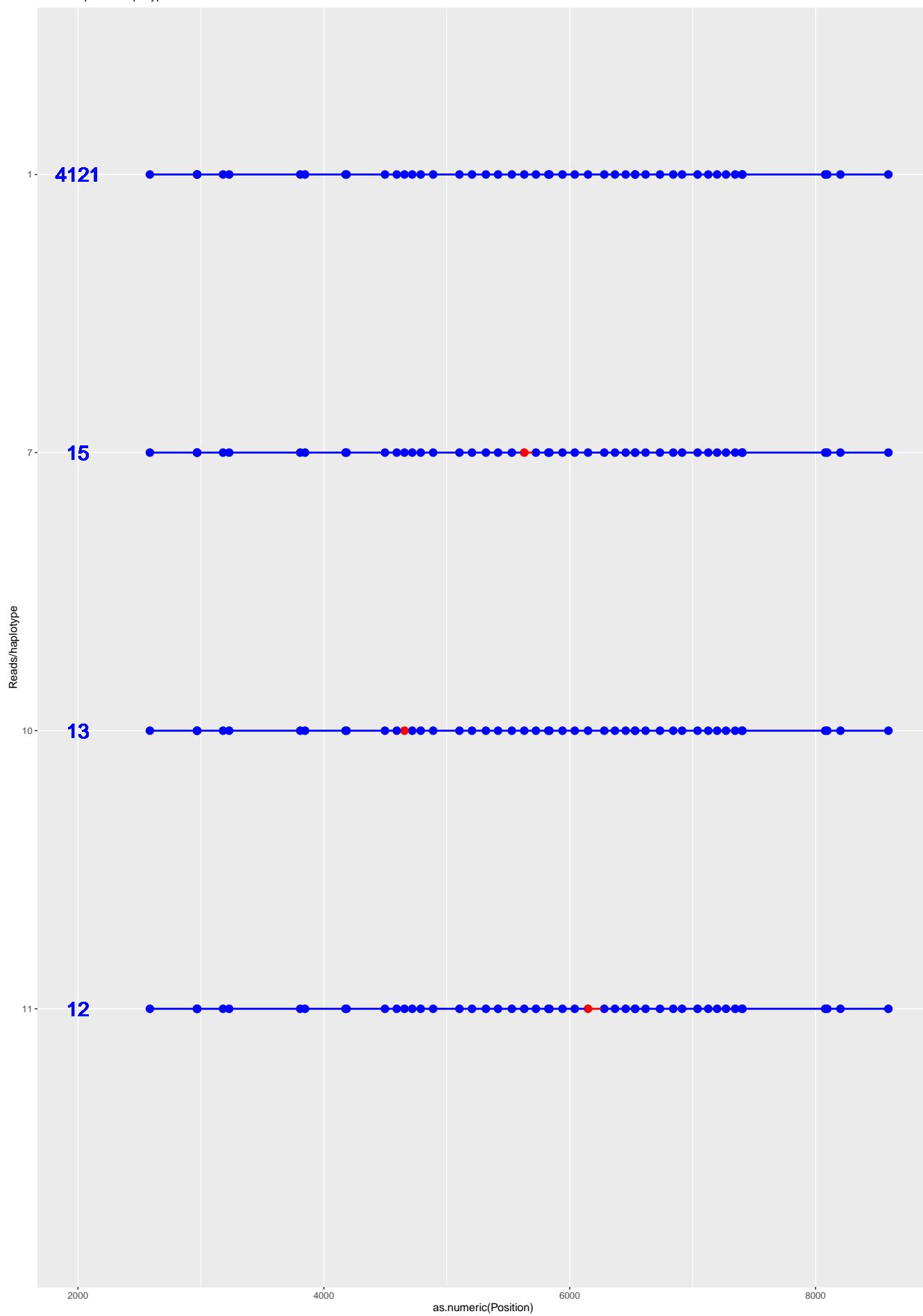
haplotypes I began with n[supporting reads] = 3441

most frequent 7 haplotypes.

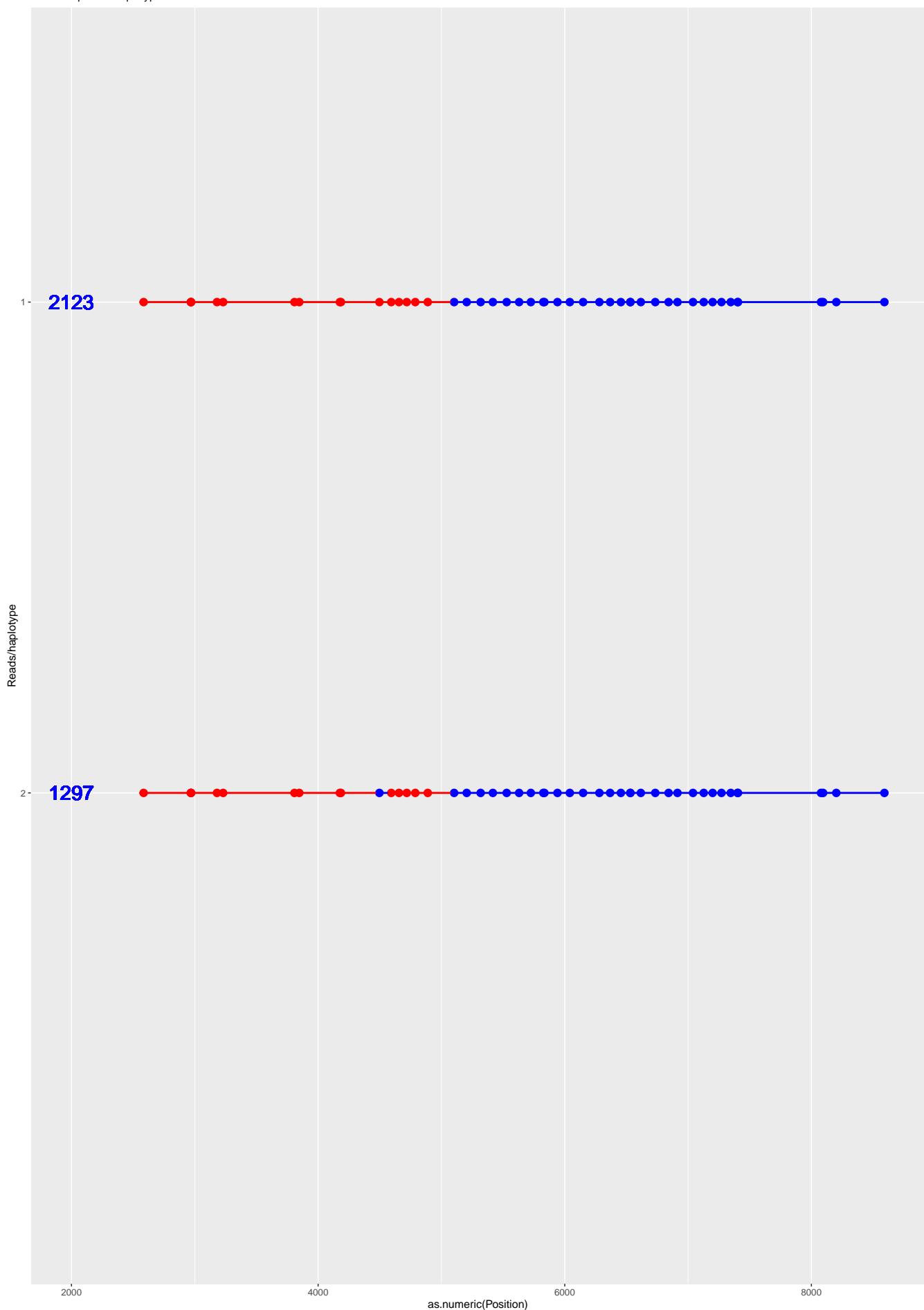


barcode = GCGATGTCGCTATGTG & ACTGATGCGCACATGT

Sample = 307c tetrad = 307 spore = c
Total reads = 4796 PCR=803
haplotypes I began with [n(supporting reads)] = 12, 13, 15, 4121
most frequent 7 haplotypes.



Sample = 307d tetrad = 307 spore = d
Total reads = 4363 PCR=804
haplotypes I began with n[supporting reads] = 1297, 2123
most frequent 7 haplotypes.



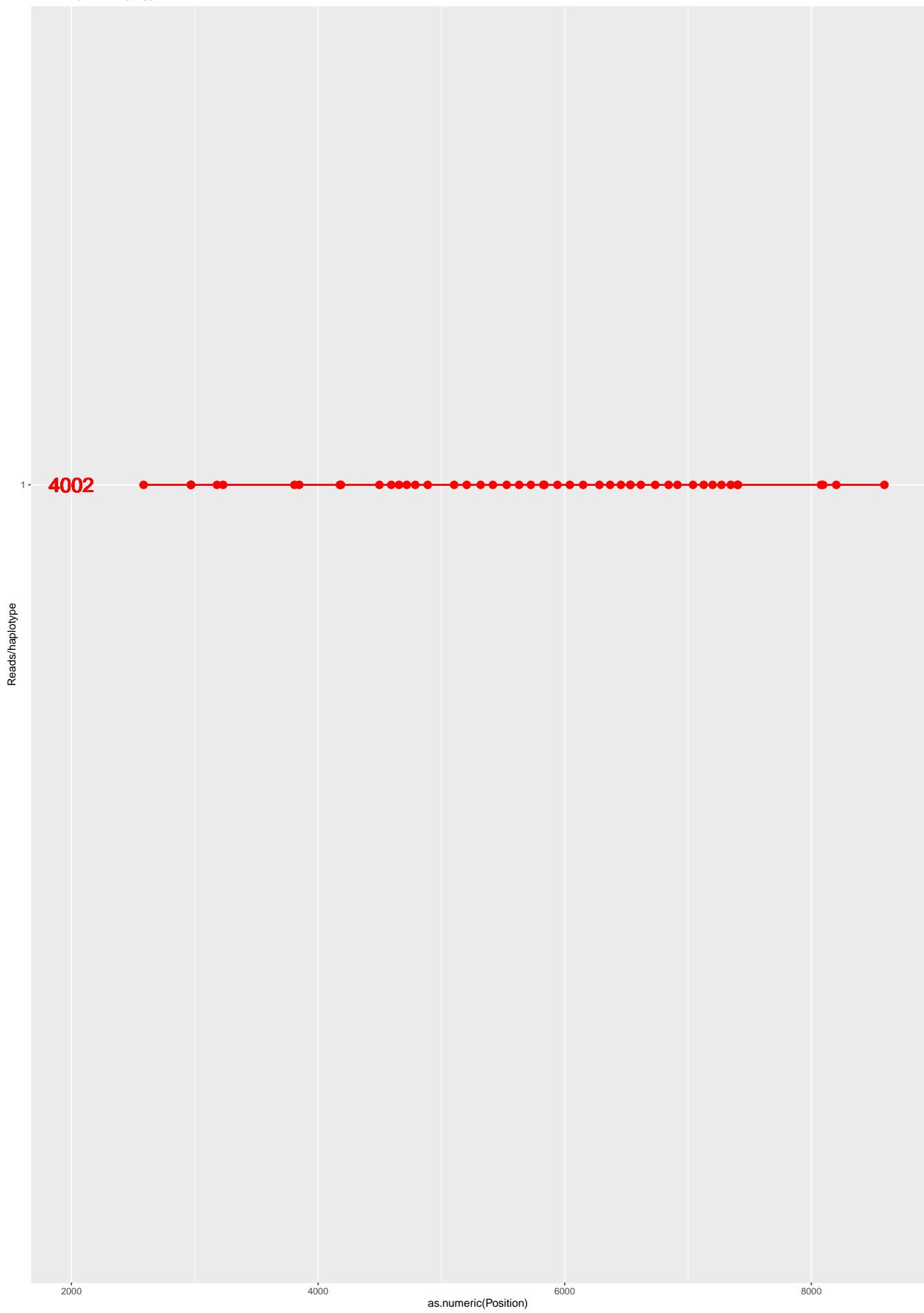
barcode = GCGATGTCGCTATGTG & ATCTACATCACGACTC

Sample = 310a tetrad = 310 spore = a

Total reads = 4160 PCR=805

haplotypes I began with n[supporting reads] = 4002

most frequent 7 haplotypes.



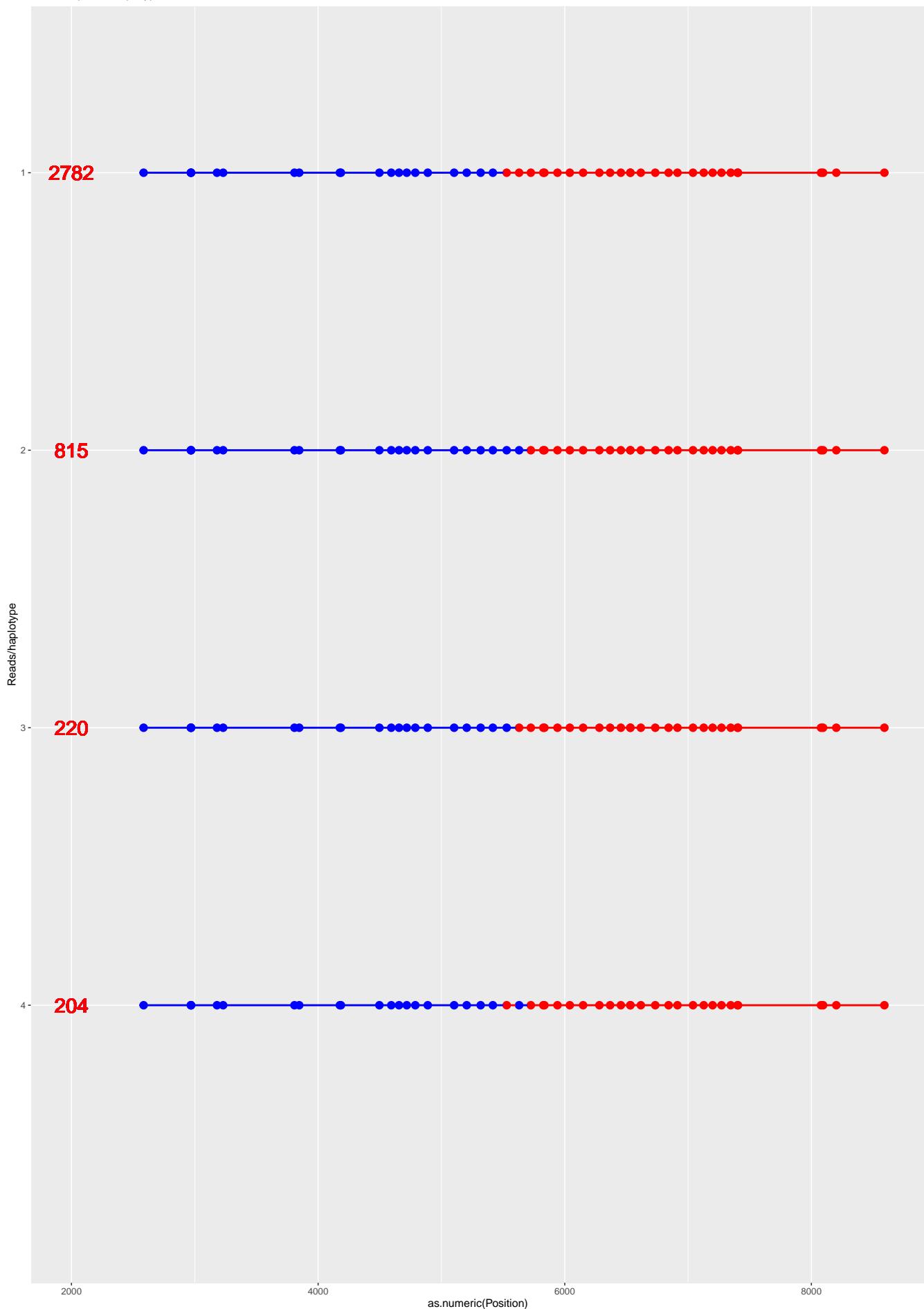
barcode = GCGATGTCGCTATGTG & ATATAGTACAGCGTCT

Sample = 310b tetrad = 310 spore = b

Total reads = 4589 PCR=806

haplotypes I began with n[supporting reads] = 204, 220, 815, 2782

most frequent 7 haplotypes.



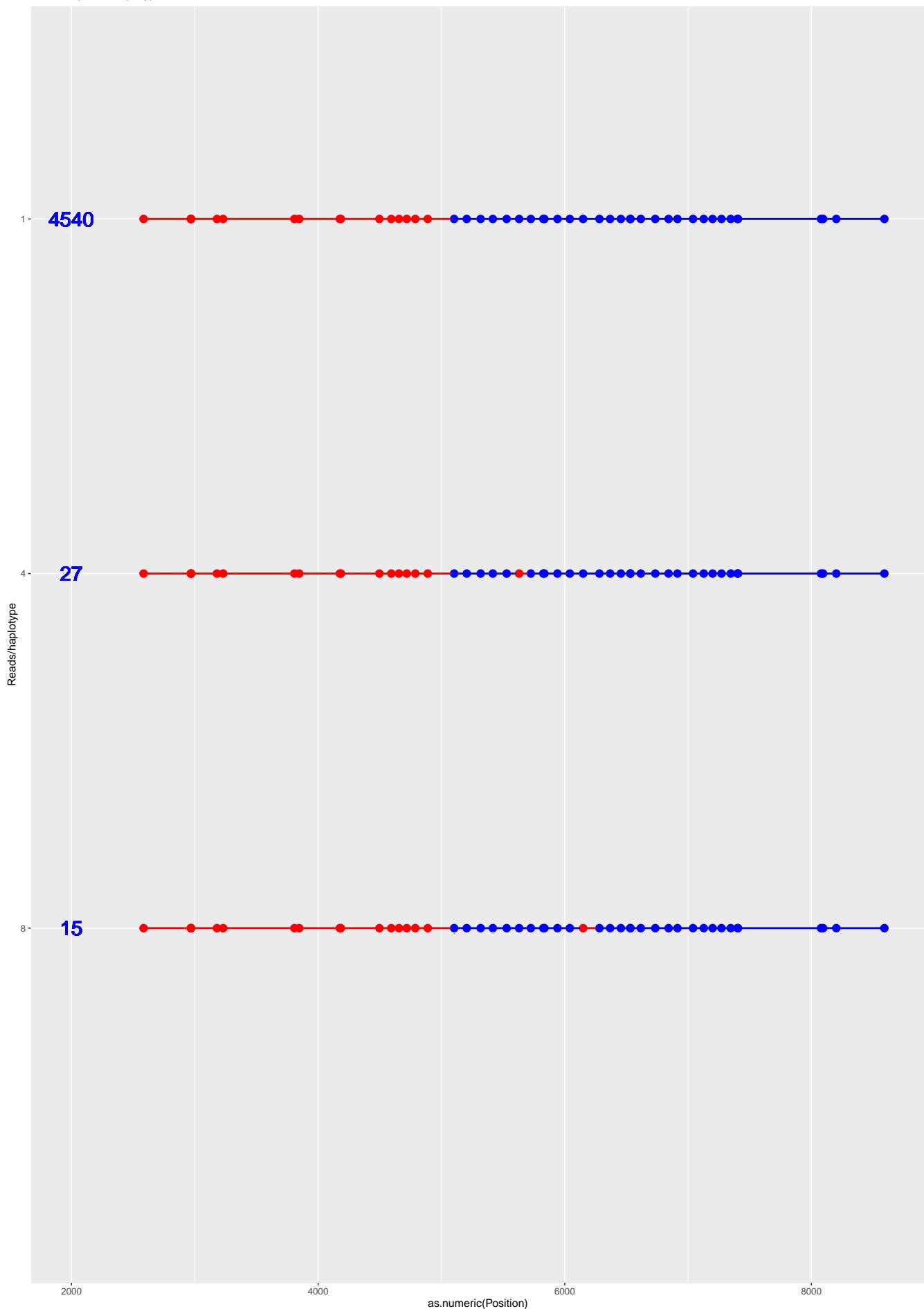
barcode = GCGATGTCGCTATGTG & GACACGACTAGATCGC

Sample = 310c tetrad = 310 spore = c

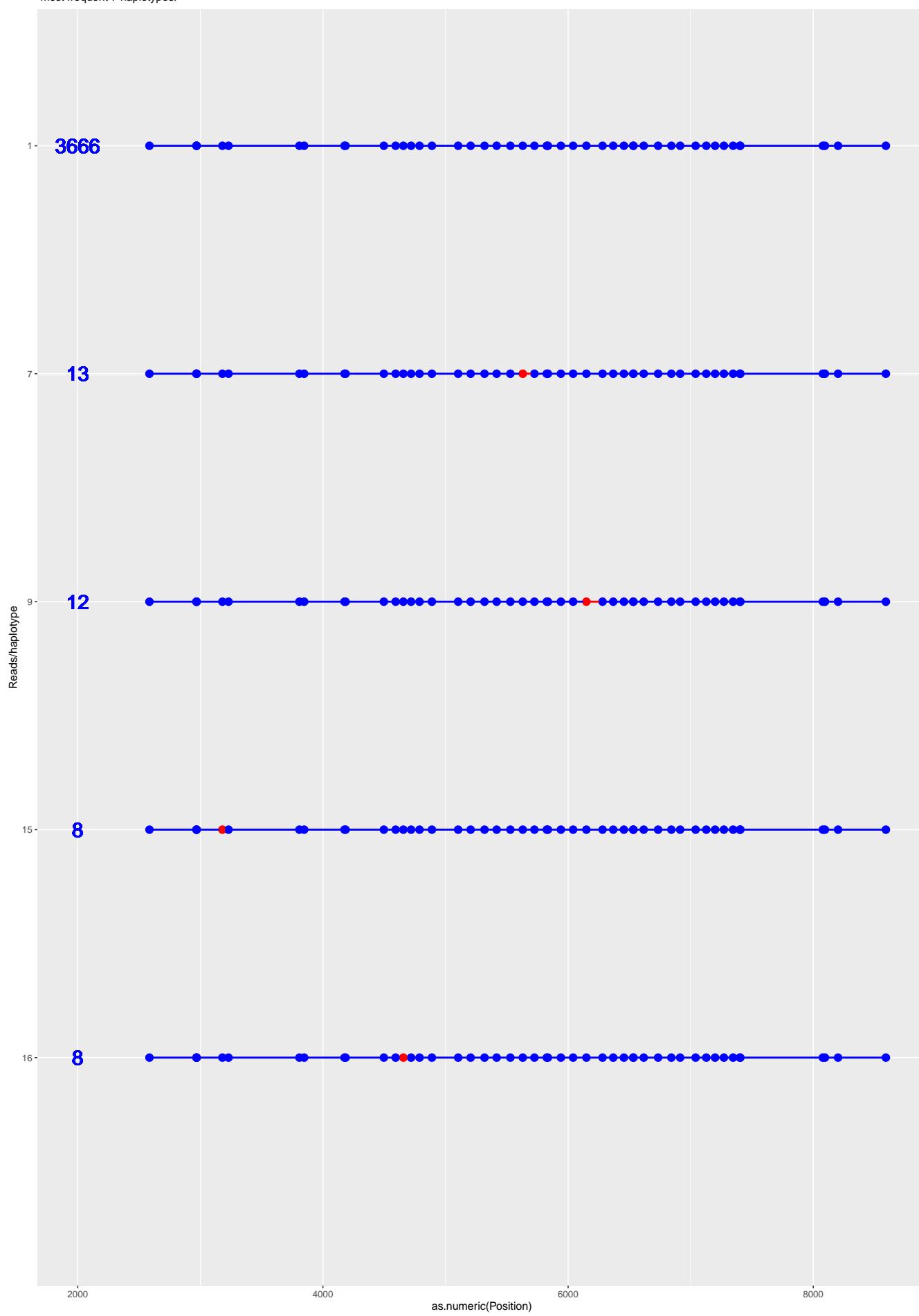
Total reads = 5210 PCR=807

haplotypes I began with n[supporting reads] = 15, 27, 4540

most frequent 7 haplotypes.



Sample = 310d tetrad = 310 spore = d
Total reads = 4312 PCR=808
haplotypes I began with [n|supporting reads] = 8, 12, 13, 3666
most frequent 7 haplotypes.

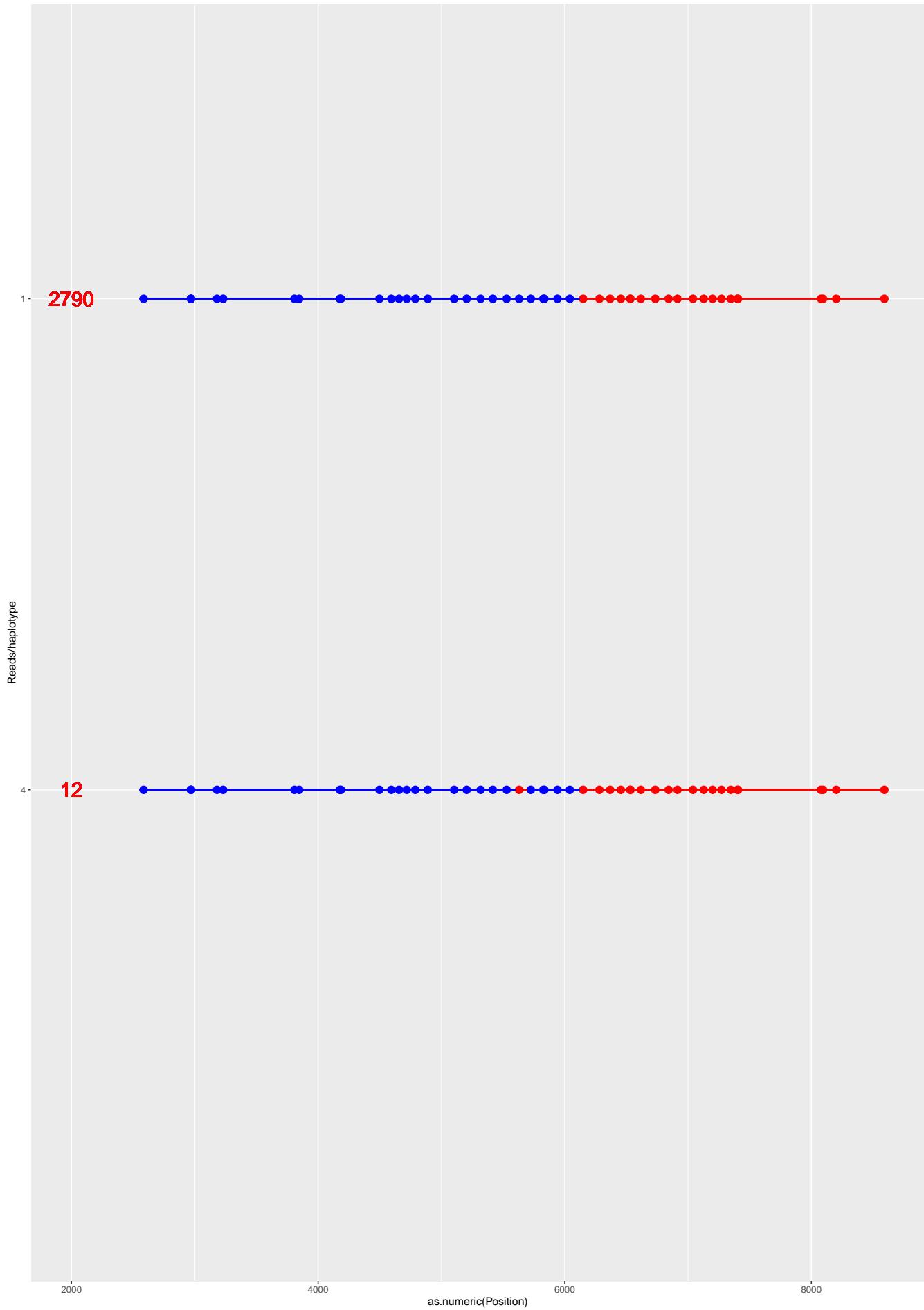


Sample = 311a tetrad = 311 spore = a

Total reads = 3176 PCR=809

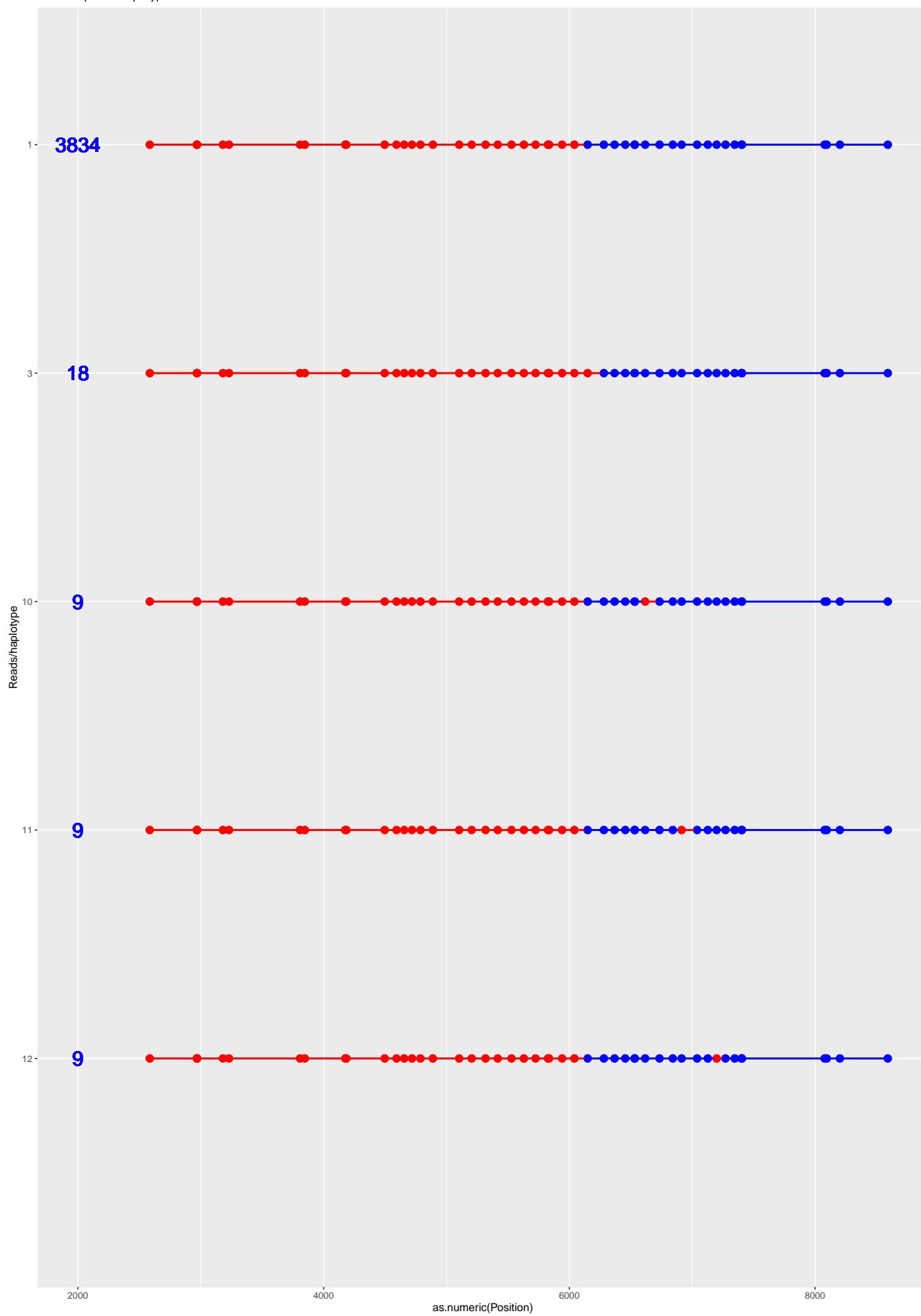
haplotypes I began with n[supporting reads] = 12, 2790

most frequent 7 haplotypes.



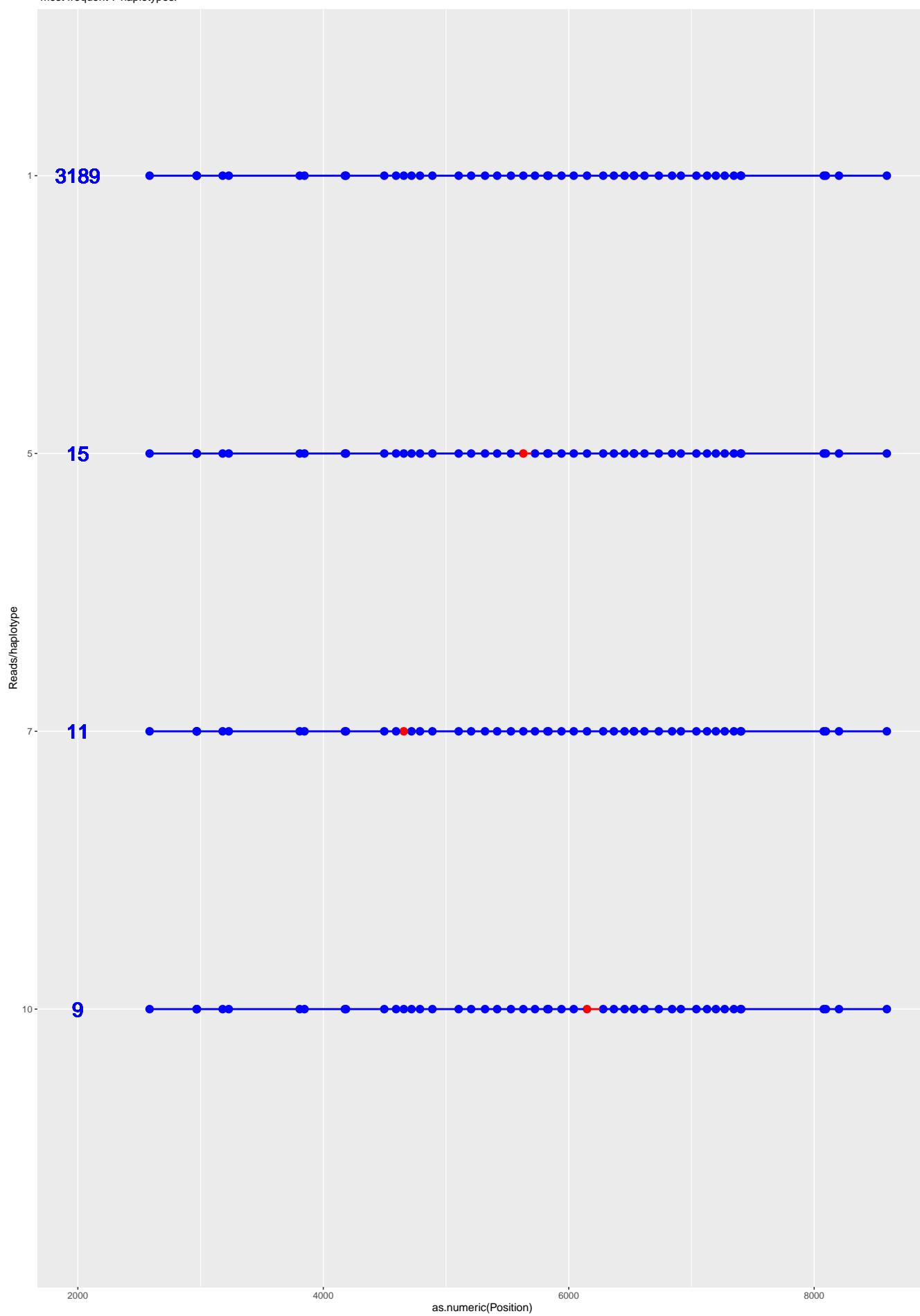
barcode = CGAGAGTCAGCGCATA & TCAGCTGACGATGTGA

Sample = 311b tetrad = 311 spore = b
Total reads = 4125 PCR=810
haplotypes I began with [n(supporting reads)] = 9, 18, 3834
most frequent 7 haplotypes.



barcode = CGAGAGTCAGCGCATA & ACTGATGCGCACATGT

Sample = 311c tetrad = 311 spore = c
Total reads =3703 PCR=811
haplotypes I began with [n|supporting reads] = 9, 11, 15, 3189
most frequent 7 haplotypes.



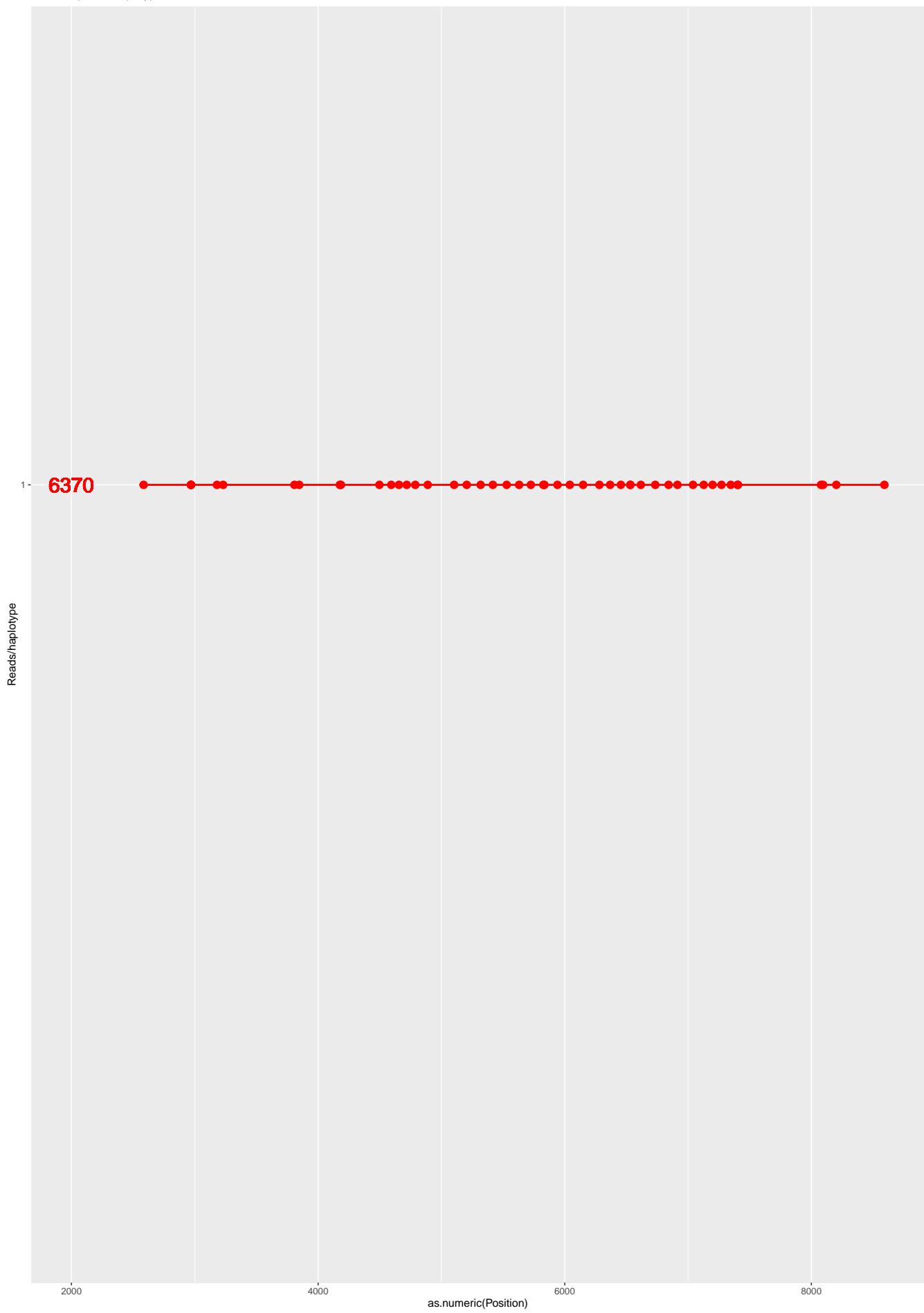
barcode = CGAGAGTCAGCGCATA & CTACTCTCAGCAGTGA

Sample = 311d tetrad = 311 spore = d

Total reads = 6649 PCR=812

haplotypes I began with n[supporting reads] = 6370

most frequent 7 haplotypes.



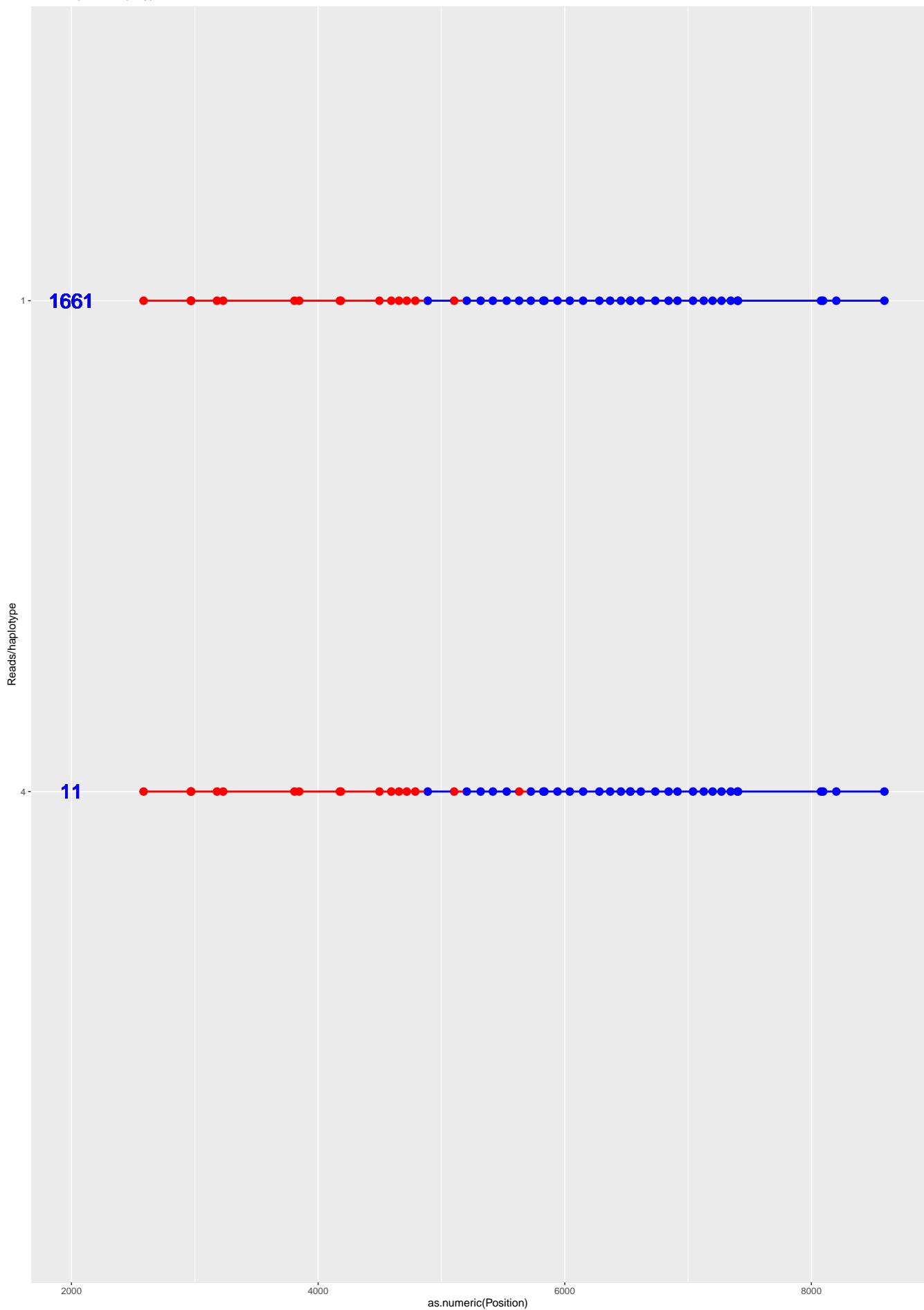
barcode = CGAGAGTCAGGCCATA & ATCTACATCACGACTC

Sample = 315a tetrad = 315 spore = a

Total reads = 1876 PCR=817

haplotypes I began with n[supporting reads] = 11, 1661

most frequent 7 haplotypes.



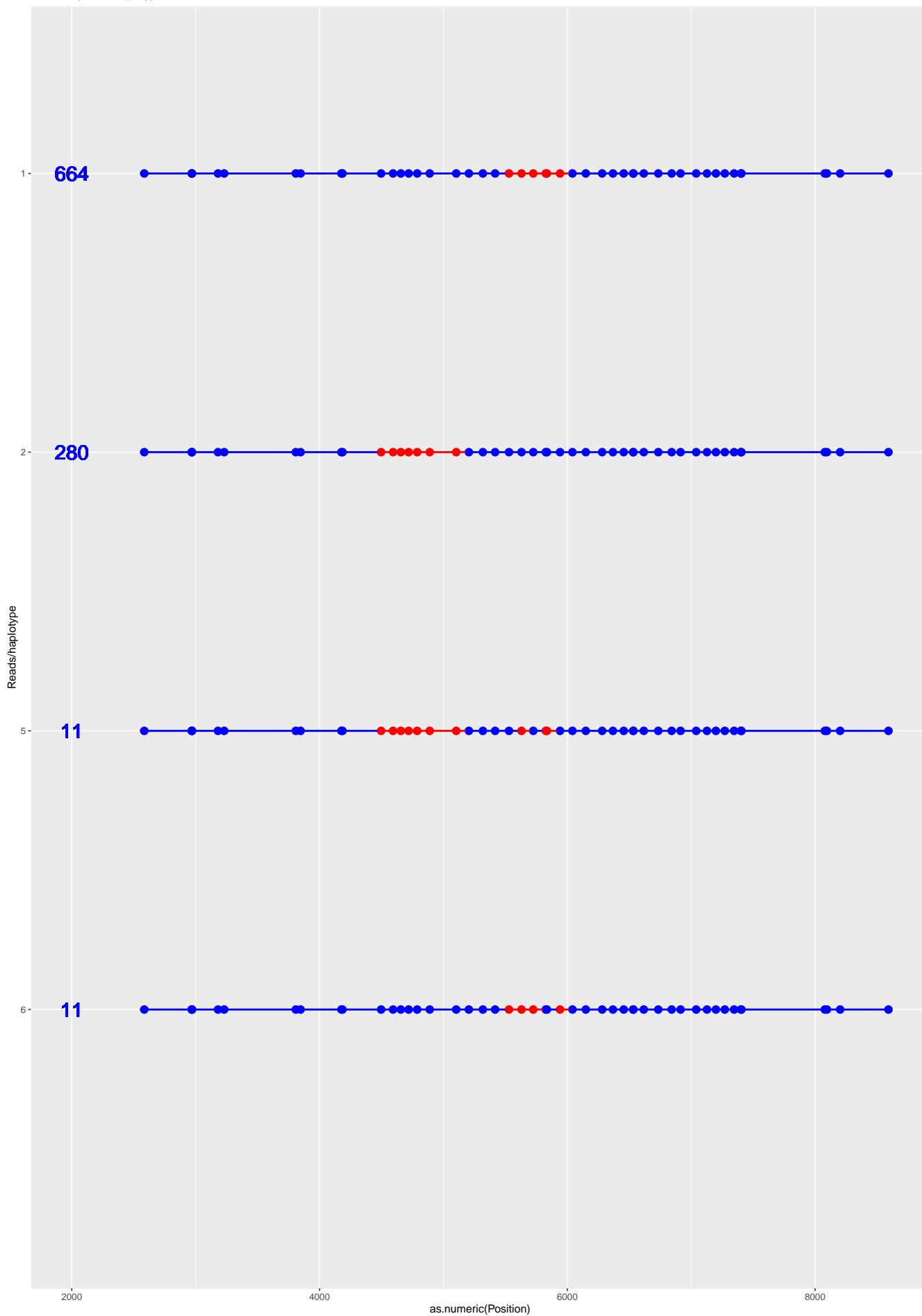
barcode = TCACGATGAGCACGTA & TCAGCTGACGATGTGA

Sample = 315b tetrad = 315 spore = b

Total reads = 2421 PCR=818

haplotypes I began with n[supporting reads] = 11, 280, 664

most frequent 7 haplotypes.



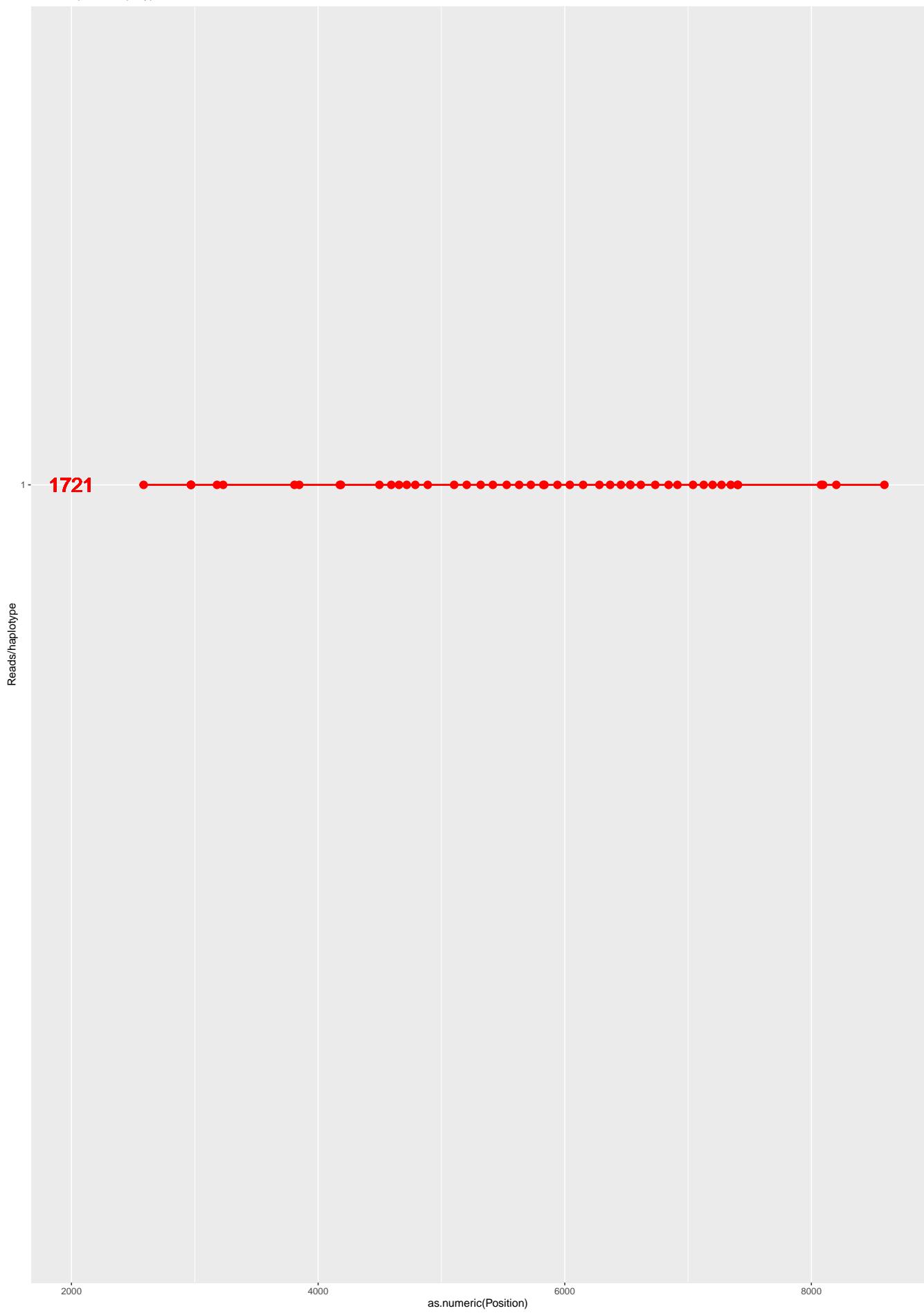
barcode = TCACGATGAGCACGTA & ACTGATGCGCACATGT

Sample = 315c tetrad = 315 spore = c

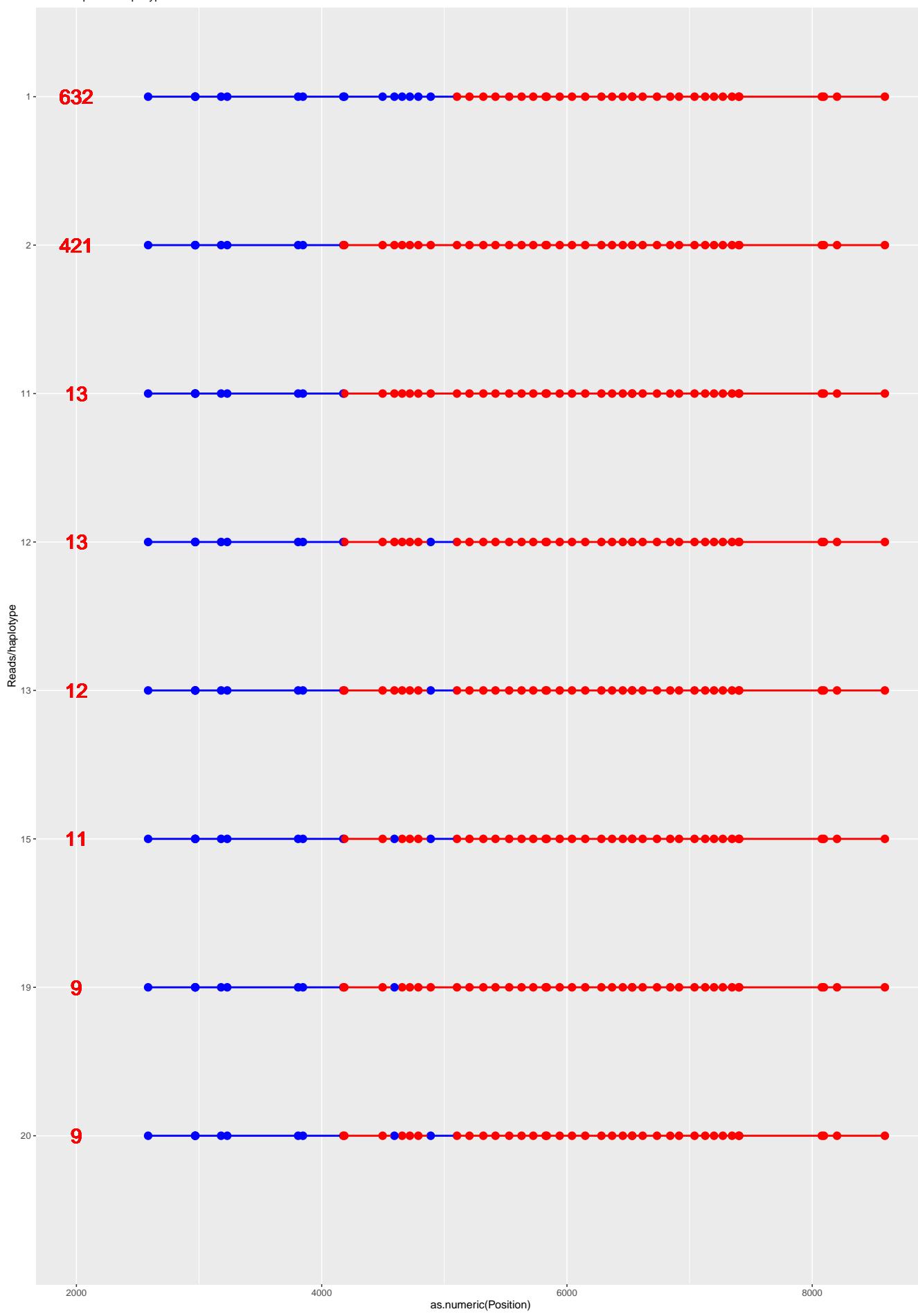
Total reads = 1800 PCR=819

haplotypes I began with n[supporting reads] = 1721

most frequent 7 haplotypes.



Sample = 315d tetrad = 315 spore = d
 Total reads = 2185 PCR=820
 haplotypes I began with [n(supporting reads)] = 9, 11, 12, 13, 421, 632
 most frequent 7 haplotypes.

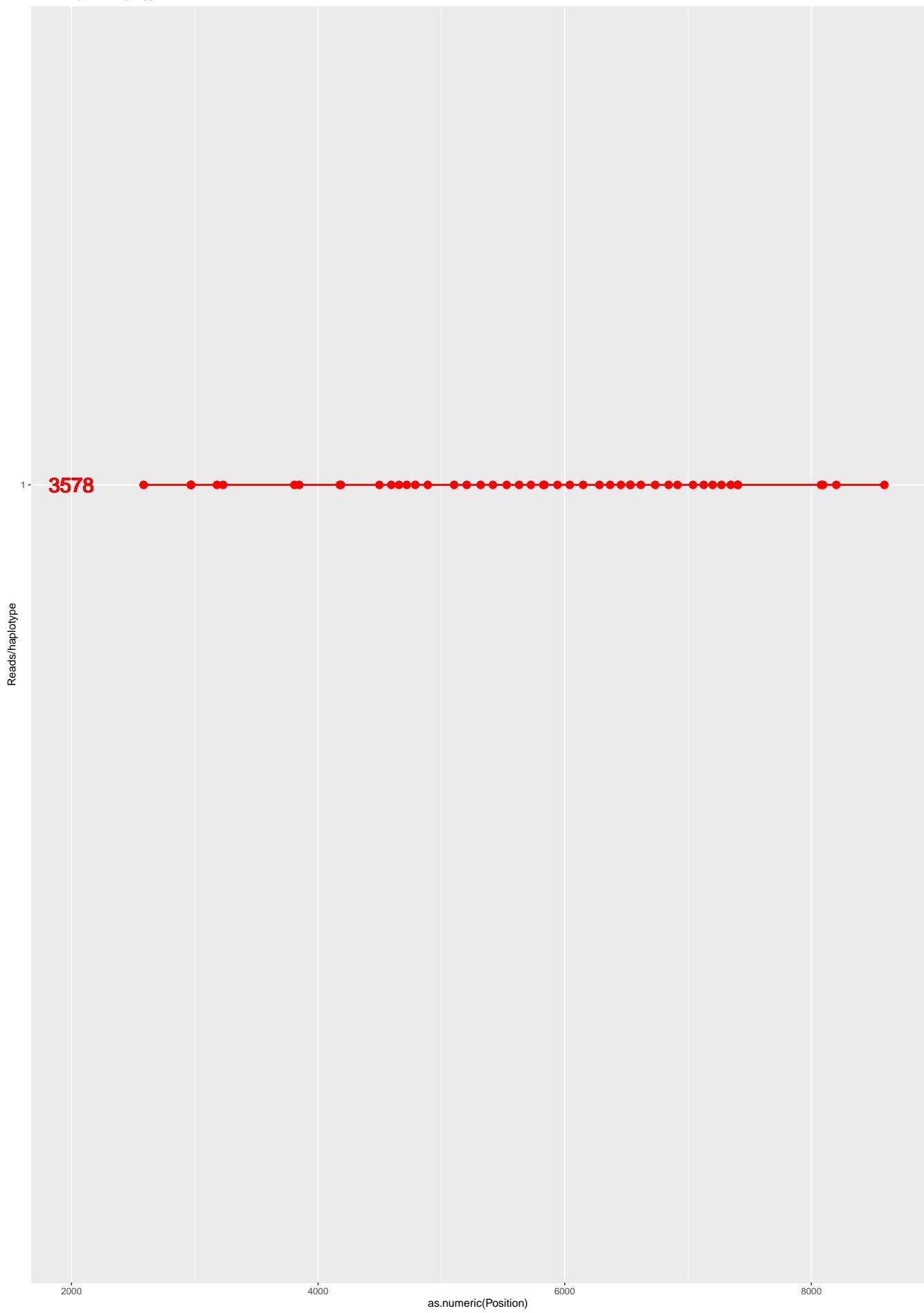


Sample = 323a tetrad = 323 spore = a

Total reads =3736 PCR=825

haplotypes I began with n[supporting reads] = 3578

most frequent 7 haplotypes.



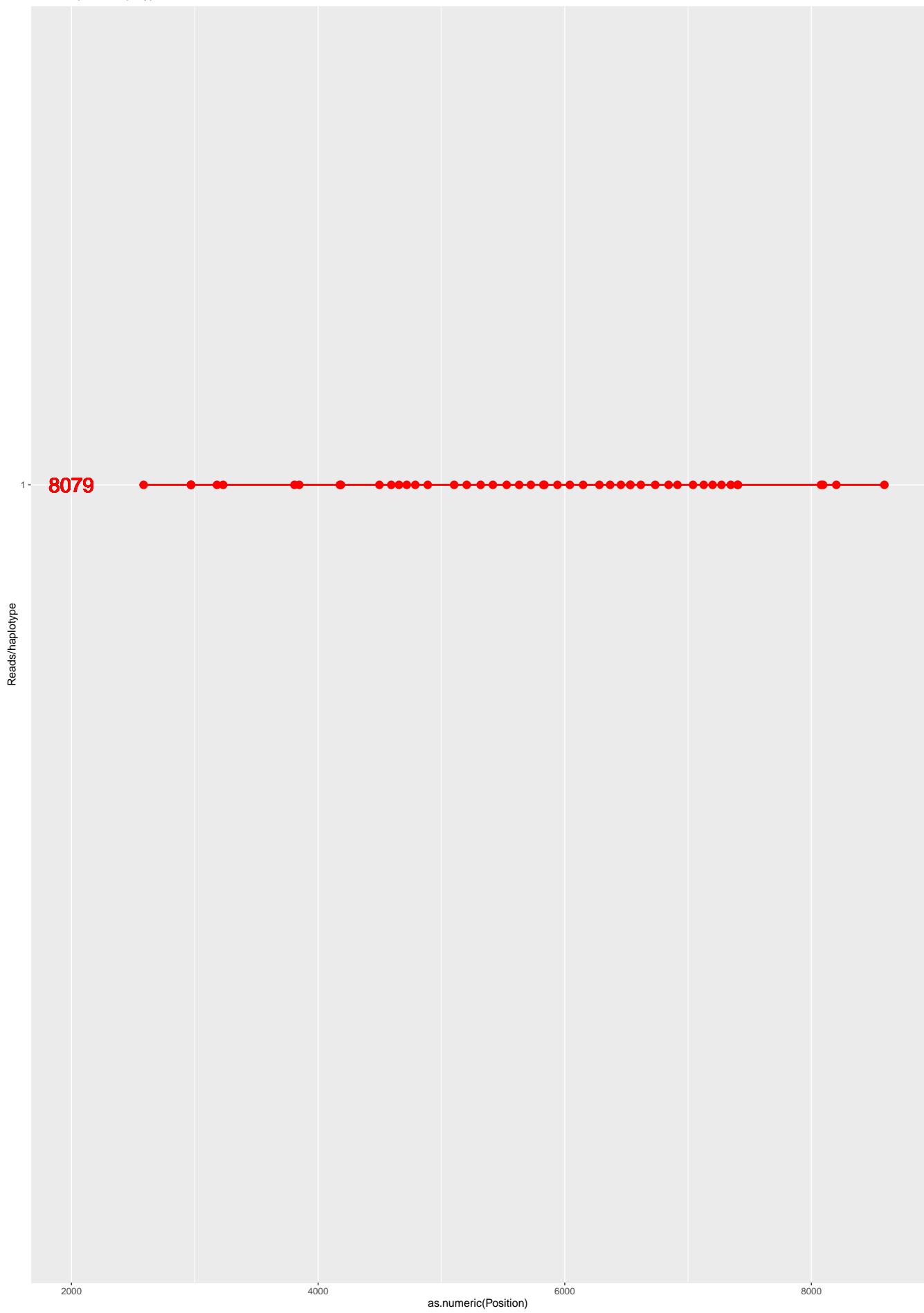
barcode = GACTGAGATCATGATC & TCAGCTGACGATGTGA

Sample = 323b tetrad = 323 spore = b

Total reads = 8423 PCR=826

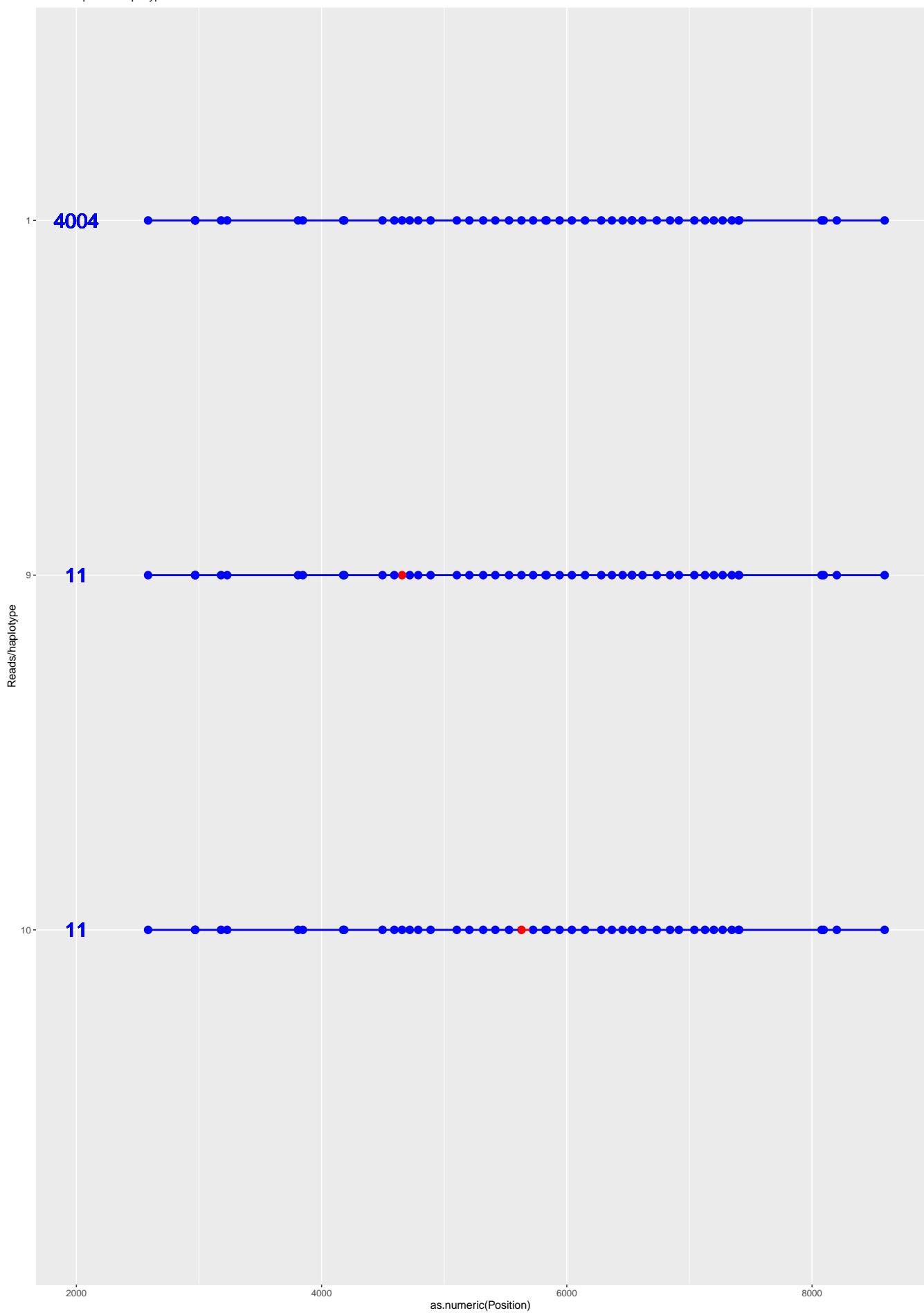
haplotypes I began with n[supporting reads] = 8079

most frequent 7 haplotypes.



barcode = GACTGAGATCATGATC & ACTGATGCGCACATGT

Sample = 323c tetrad = 323 spore = c
Total reads = 4633 PCR=827
haplotypes I began with [n|supporting reads] = 11, 4004
most frequent 7 haplotypes.



barcode = GACTGAGATCATGATC & CTACTCTCAGCAGTGA

Sample = 323d tetrad = 323 spore = d

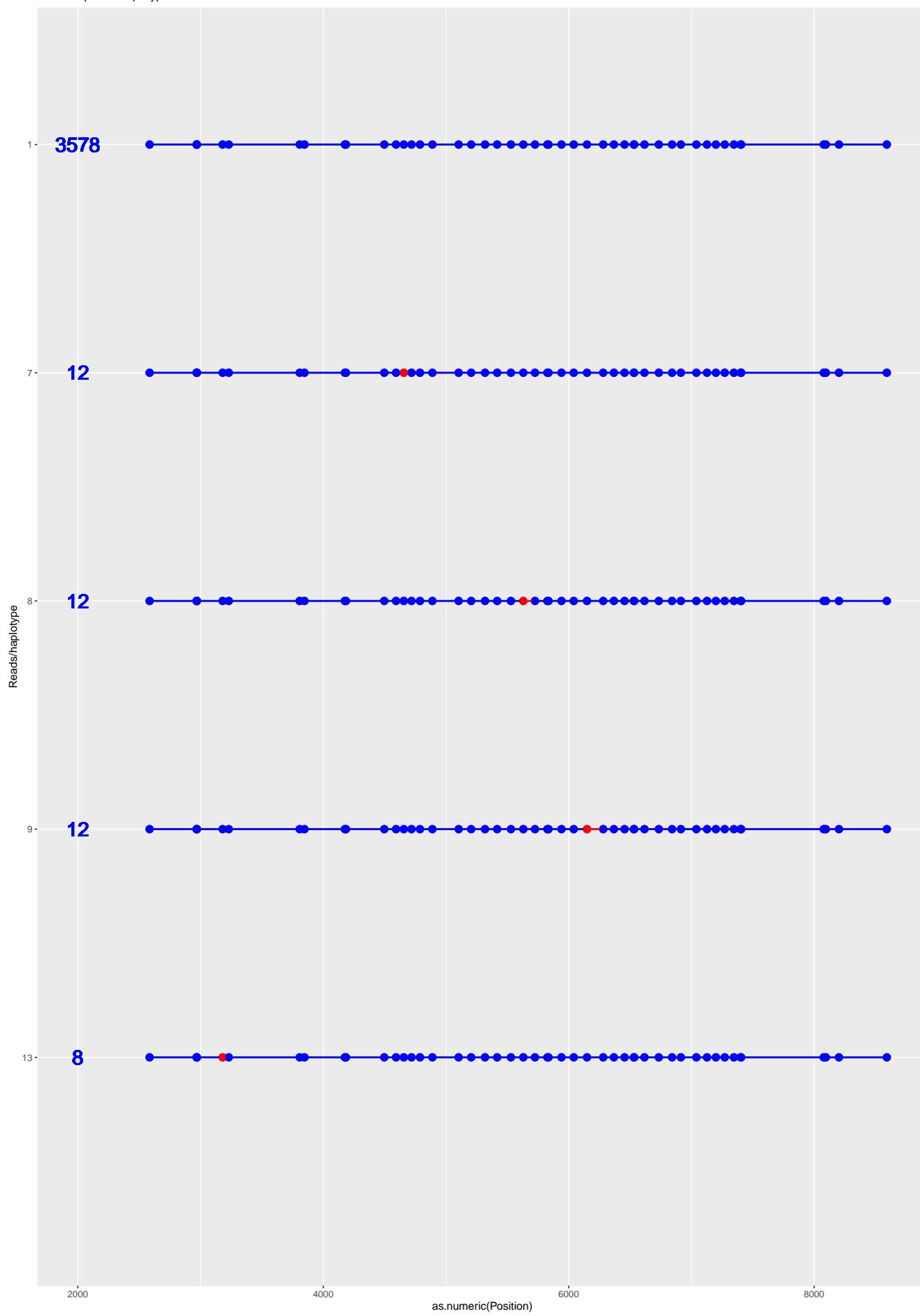
Total reads = 3352 PCR=828

haplotypes I began with n[supporting reads] = 10, 11, 2842

most frequent 7 haplotypes.



Sample = 324a tetrad = 324 spore = a
Total reads = 4150 PCR=829
haplotypes I began with [n|supporting reads] = 8, 12, 3578
most frequent 7 haplotypes.



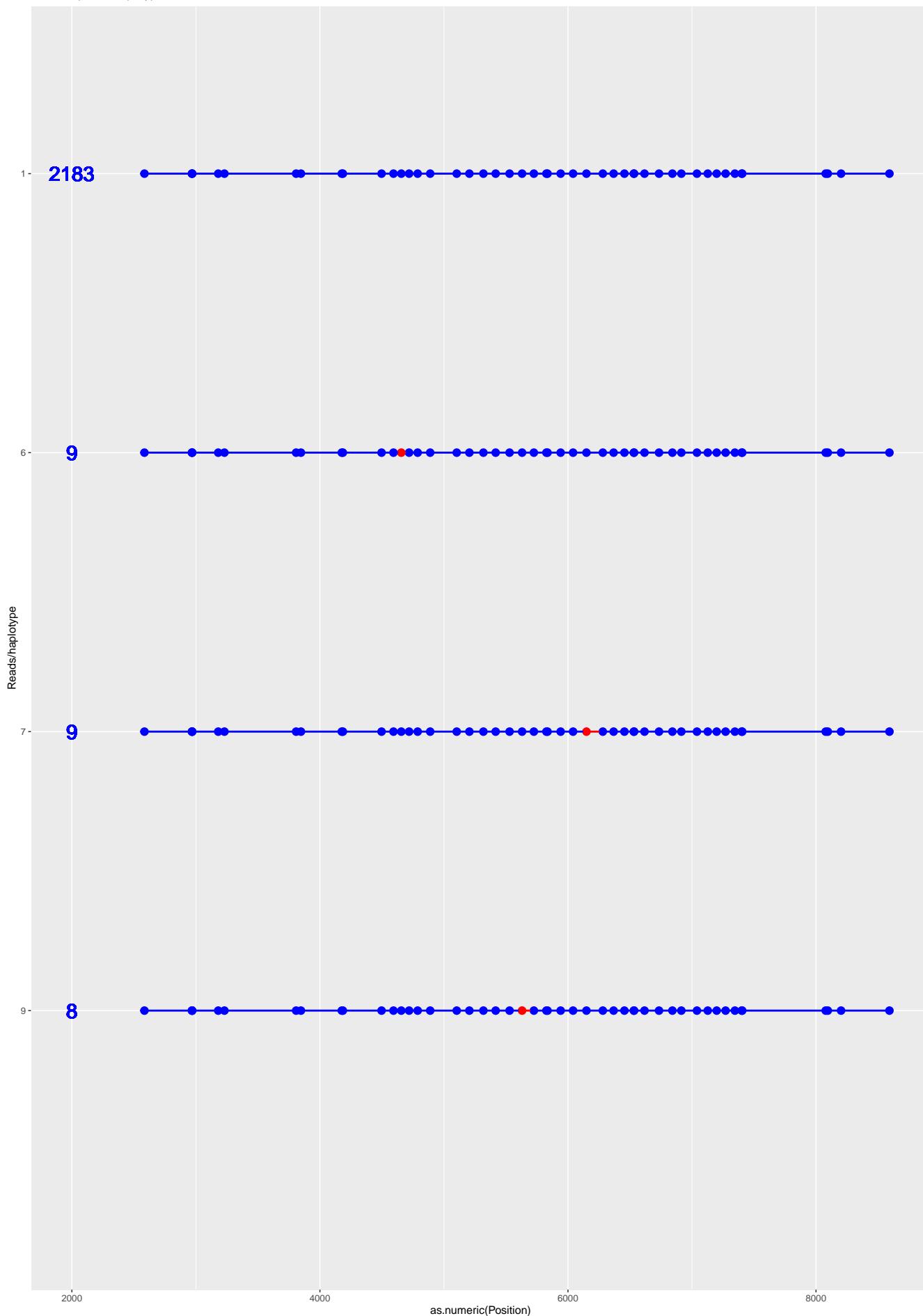
barcode = GACTGAGATCATGATC & ATATAGTACAGCGTCT

Sample = 324b tetrad = 324 spore = b

Total reads = 2528 PCR=830

haplotypes I began with n[supporting reads] = 8, 9, 2183

most frequent 7 haplotypes.



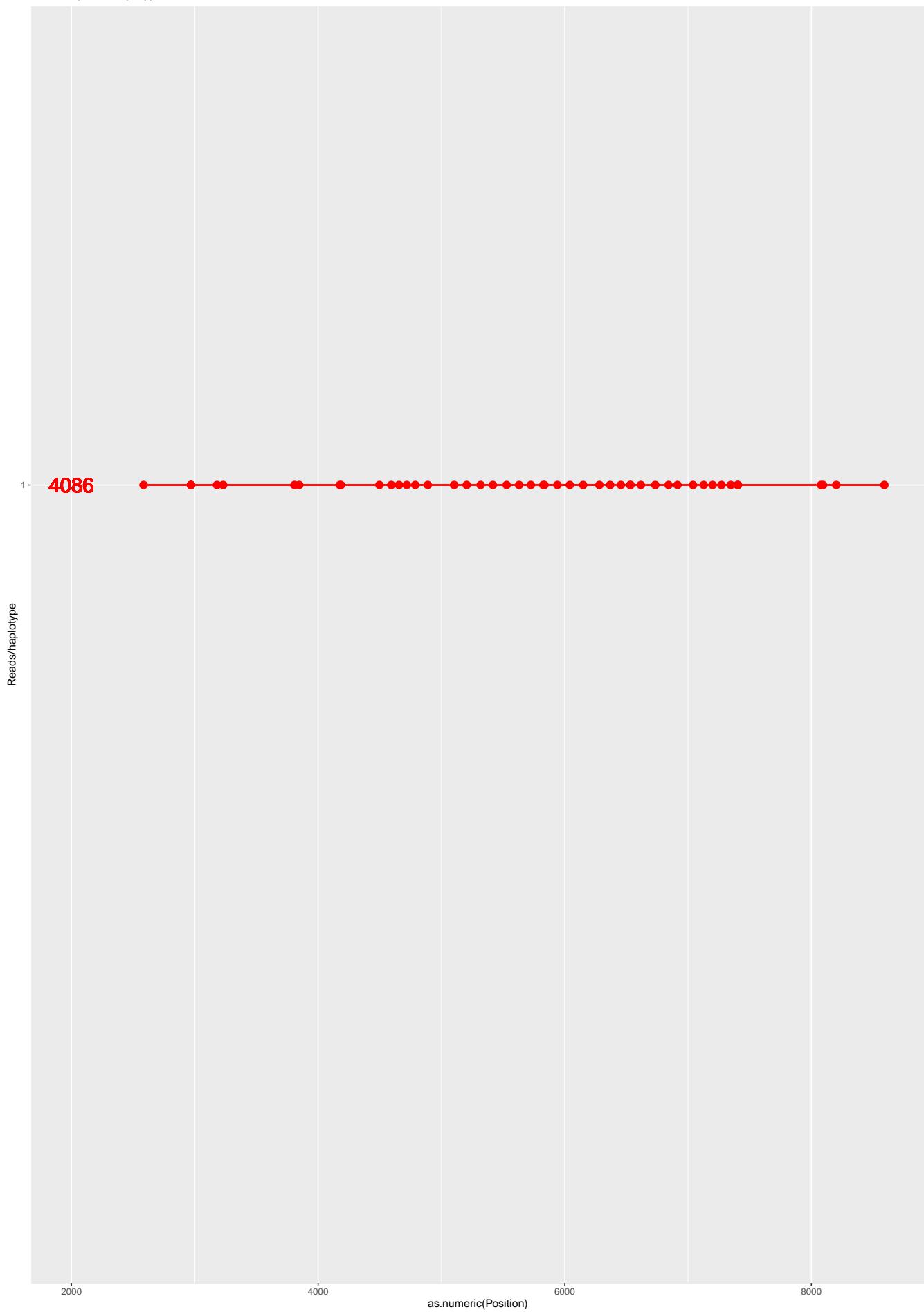
barcode = GACTGAGATCATGATC & GACACGACTAGATCGC

Sample = 324c tetrad = 324 spore = c

Total reads = 4262 PCR=831

haplotypes I began with n[supporting reads] = 4086

most frequent 7 haplotypes.



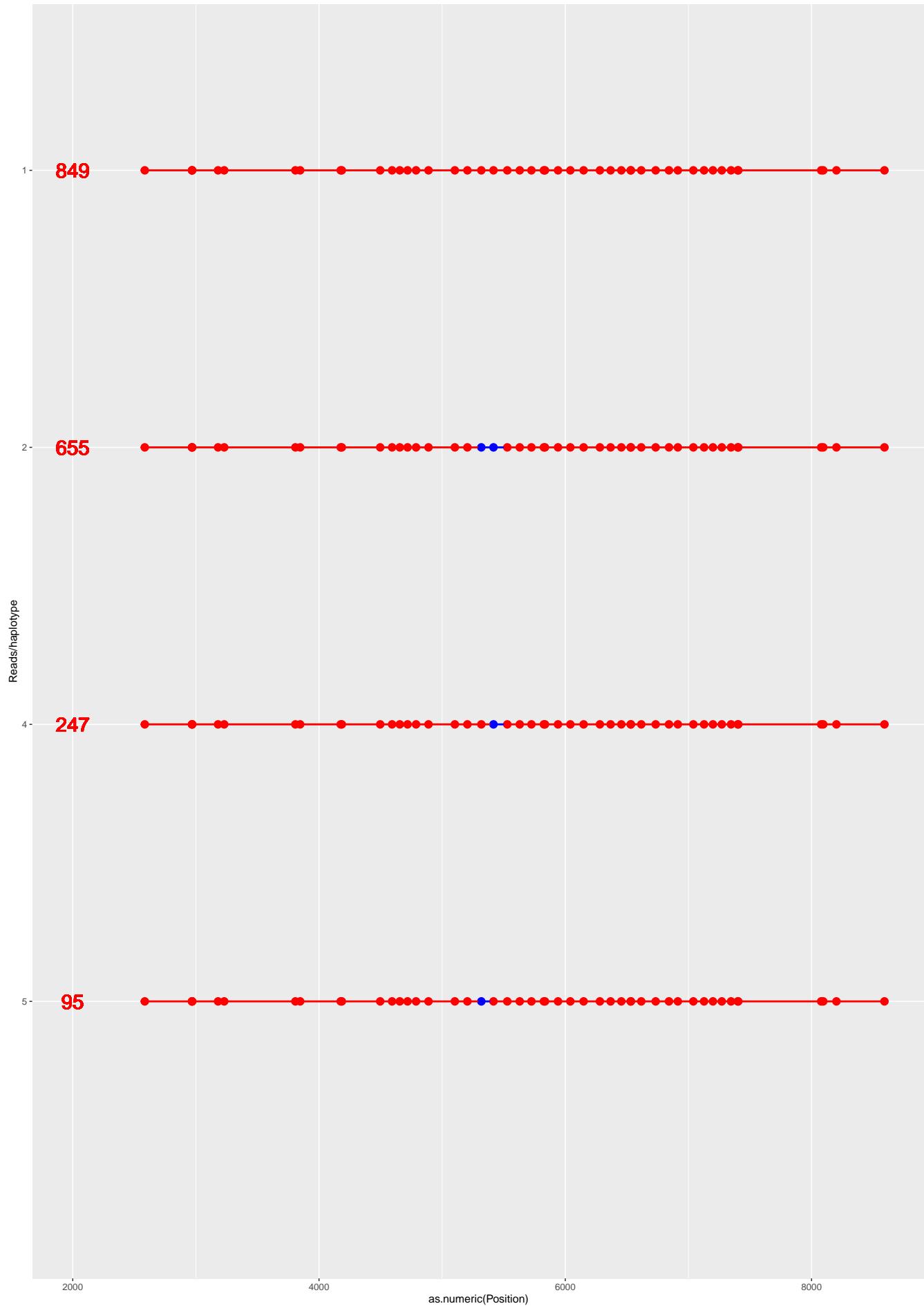
barcode = GACTGAGATCATGATC & TACGAGTCTGTACATAC

Sample = 324d tetrad = 324 spore = d

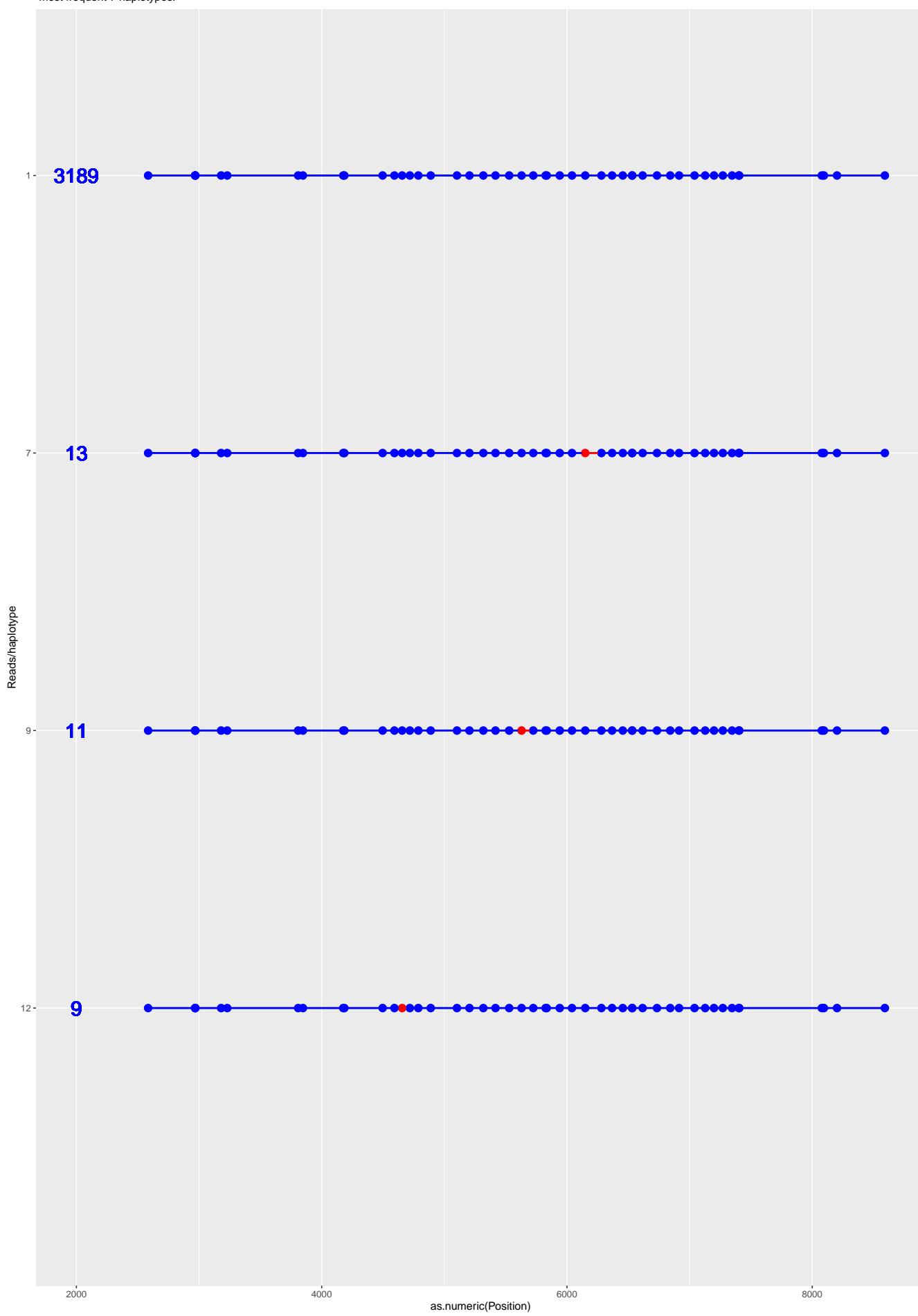
Total reads = 2275 PCR=832

haplotypes I began with n[supporting reads] = 95, 247, 655, 849

most frequent 7 haplotypes.



Sample = 325a tetrad = 325 spore = a
Total reads =3722 PCR=833
haplotypes I began with [n|supporting reads] = 9, 11, 13, 3189
most frequent 7 haplotypes.

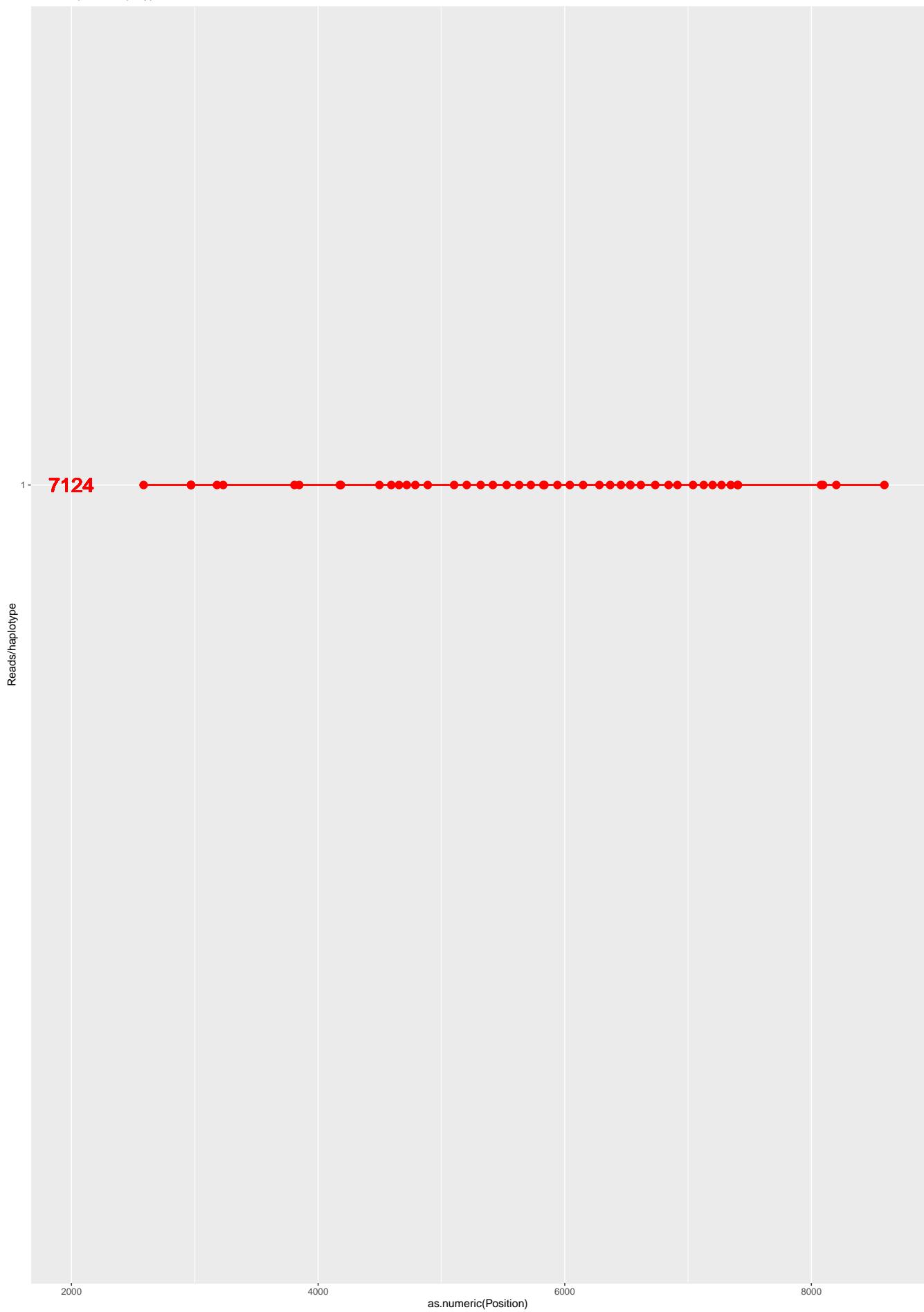


Sample = 325b tetrad = 325 spore = b

Total reads = 7430 PCR=834

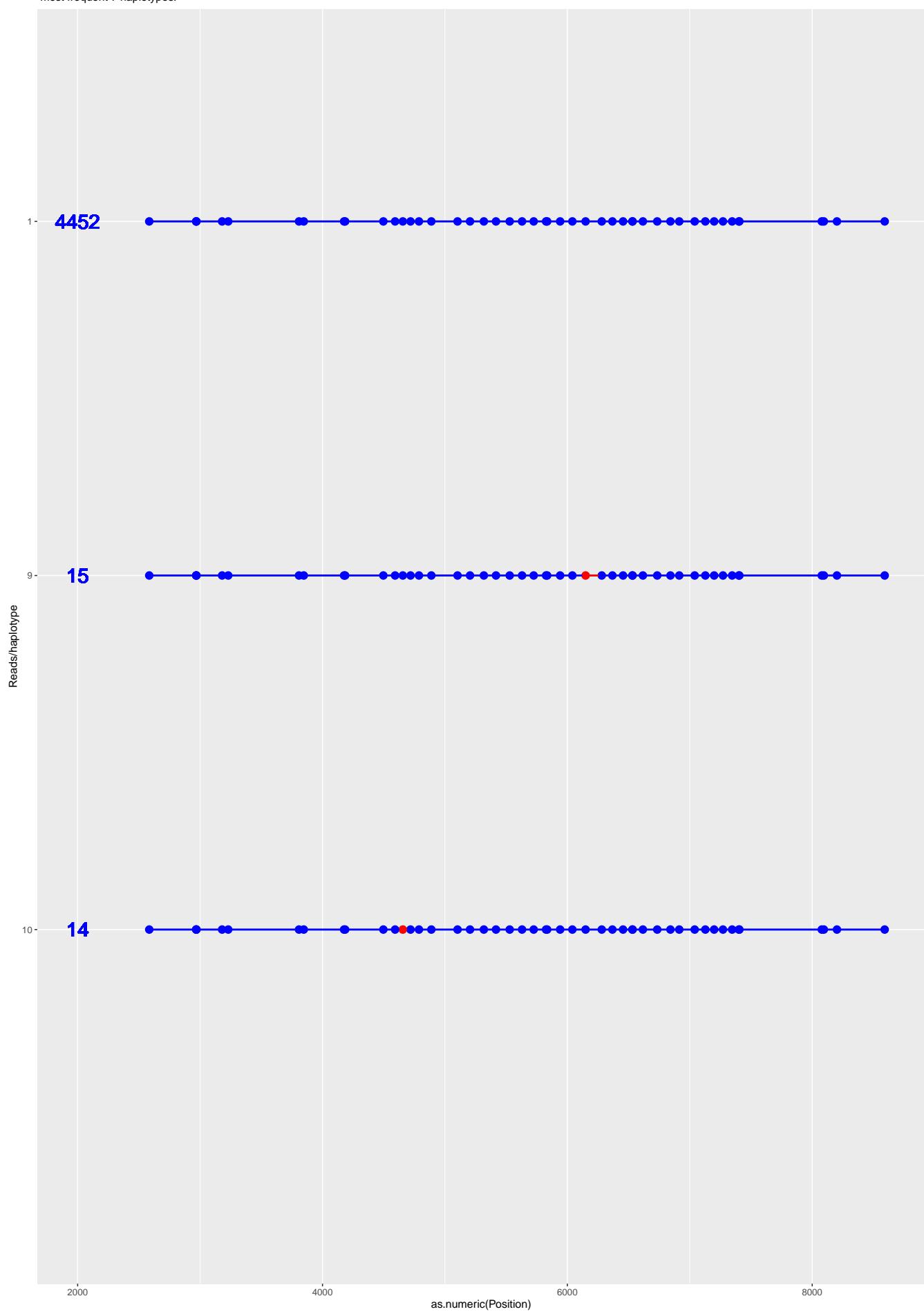
haplotypes I began with n[supporting reads] = 7124

most frequent 7 haplotypes.

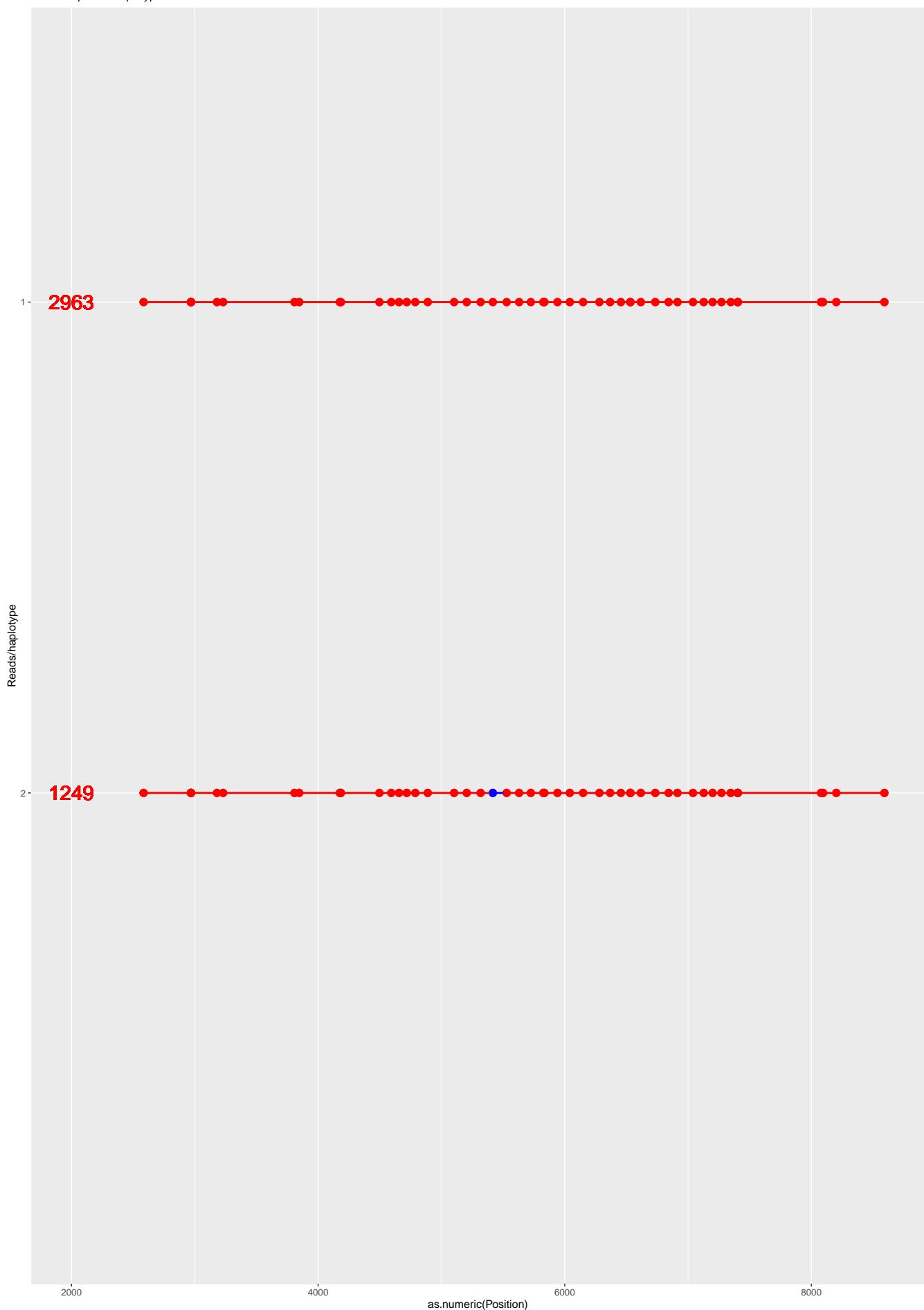


barcode = ACGACATGATACTGCT & ACTGATGCGCACATGT

Sample = 325c tetrad = 325 spore = c
Total reads = 5170 PCR=835
haplotypes I began with [n:supporting reads] = 14, 15, 4452
most frequent 7 haplotypes.



Sample = 325d tetrad = 325 spore = d
Total reads = 4463 PCR=836
haplotypes I began with n[supporting reads] = 1249, 2963
most frequent 7 haplotypes.



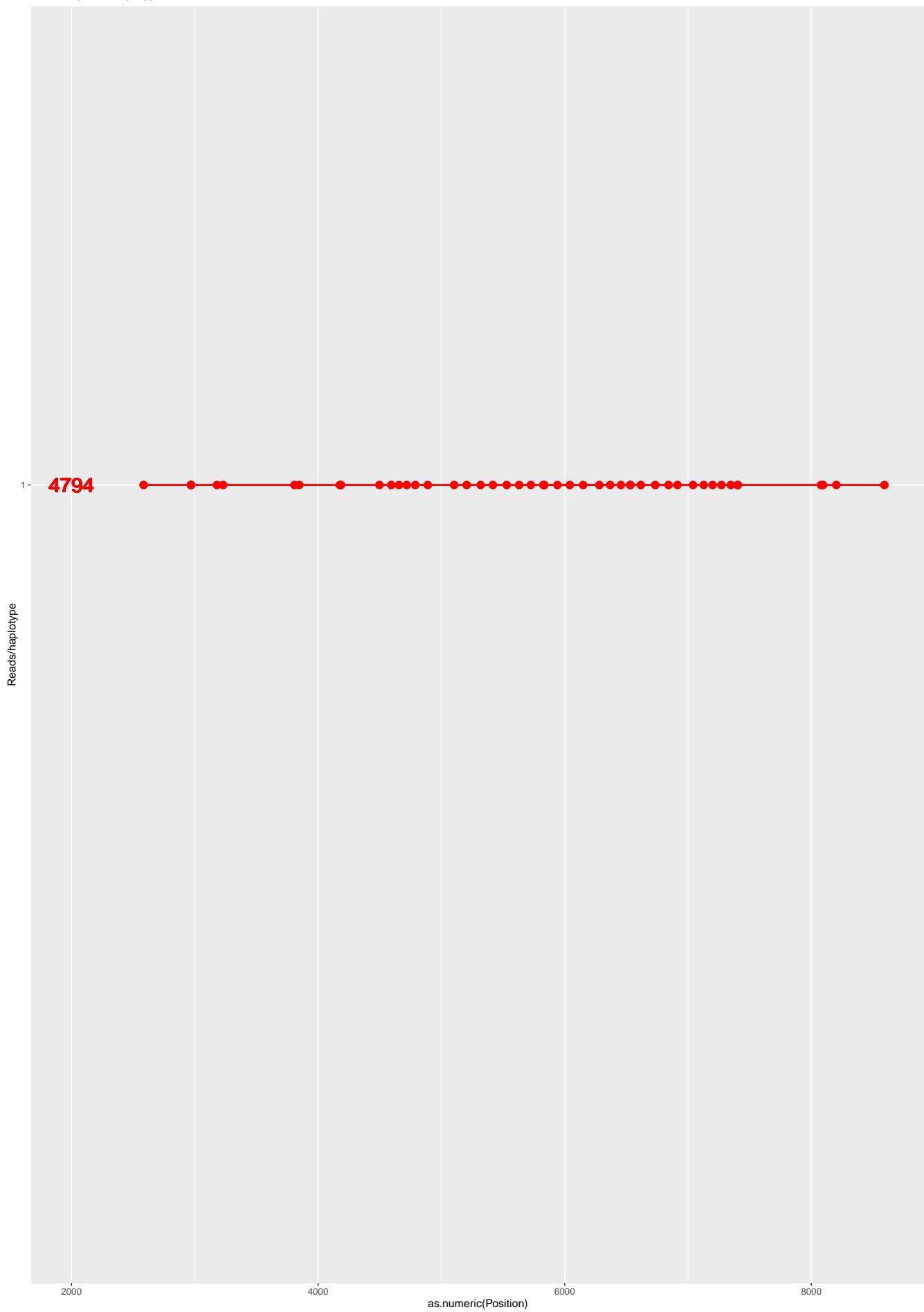
barcode = ACGACATGATACTGCT & ATCTACATCACGACTC

Sample = 326a tetrad = 326 spore = a

Total reads = 5006 PCR=837

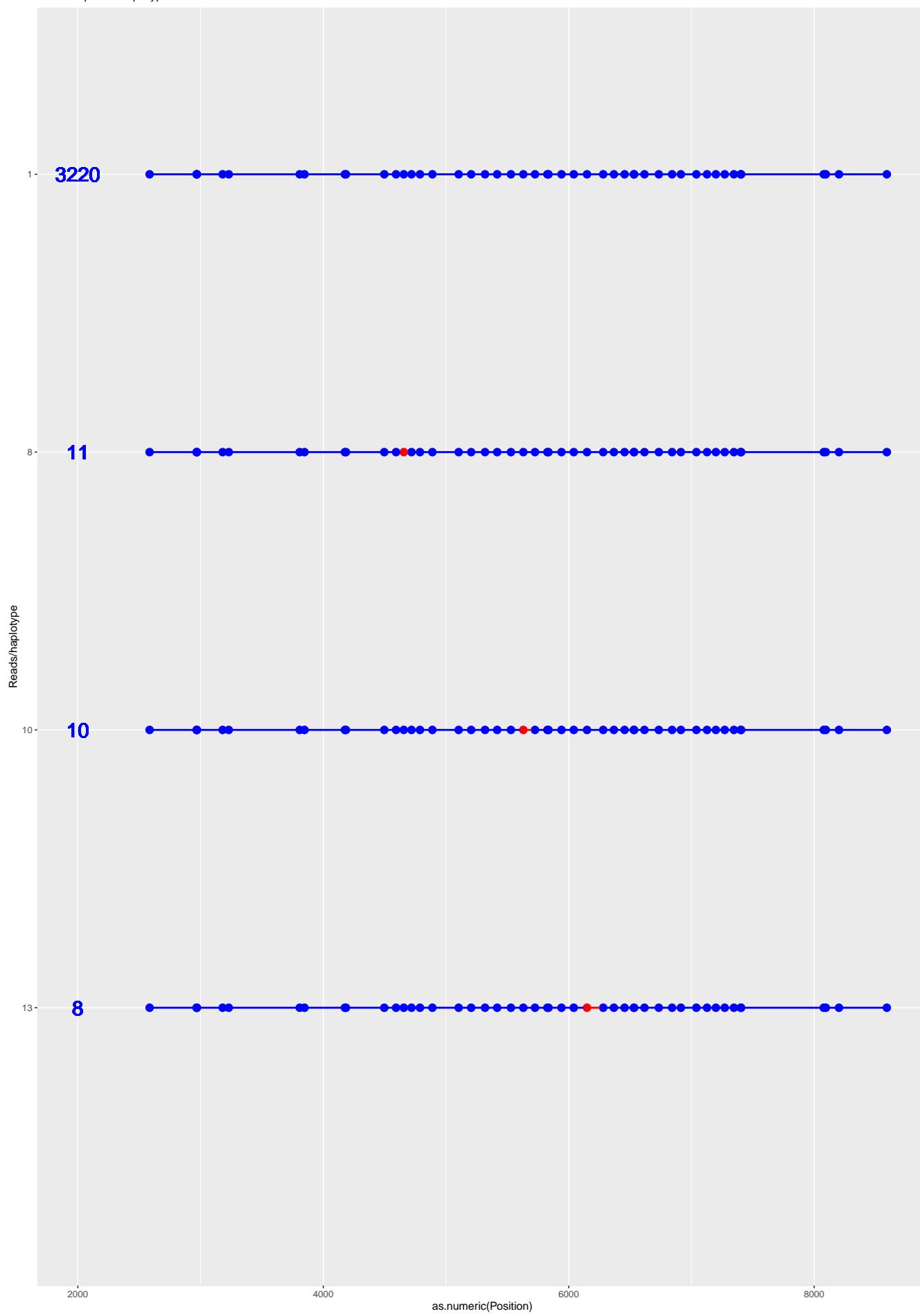
haplotypes I began with n[supporting reads] = 4794

most frequent 7 haplotypes.



barcode = ACGACATGATACTGCT & ATATAGTACAGCGTCT

Sample = 326b tetrad = 326 spore = b
Total reads = 3751 PCR=838
haplotypes I began with [n|supporting reads] = 8, 10, 11, 3220
most frequent 7 haplotypes.

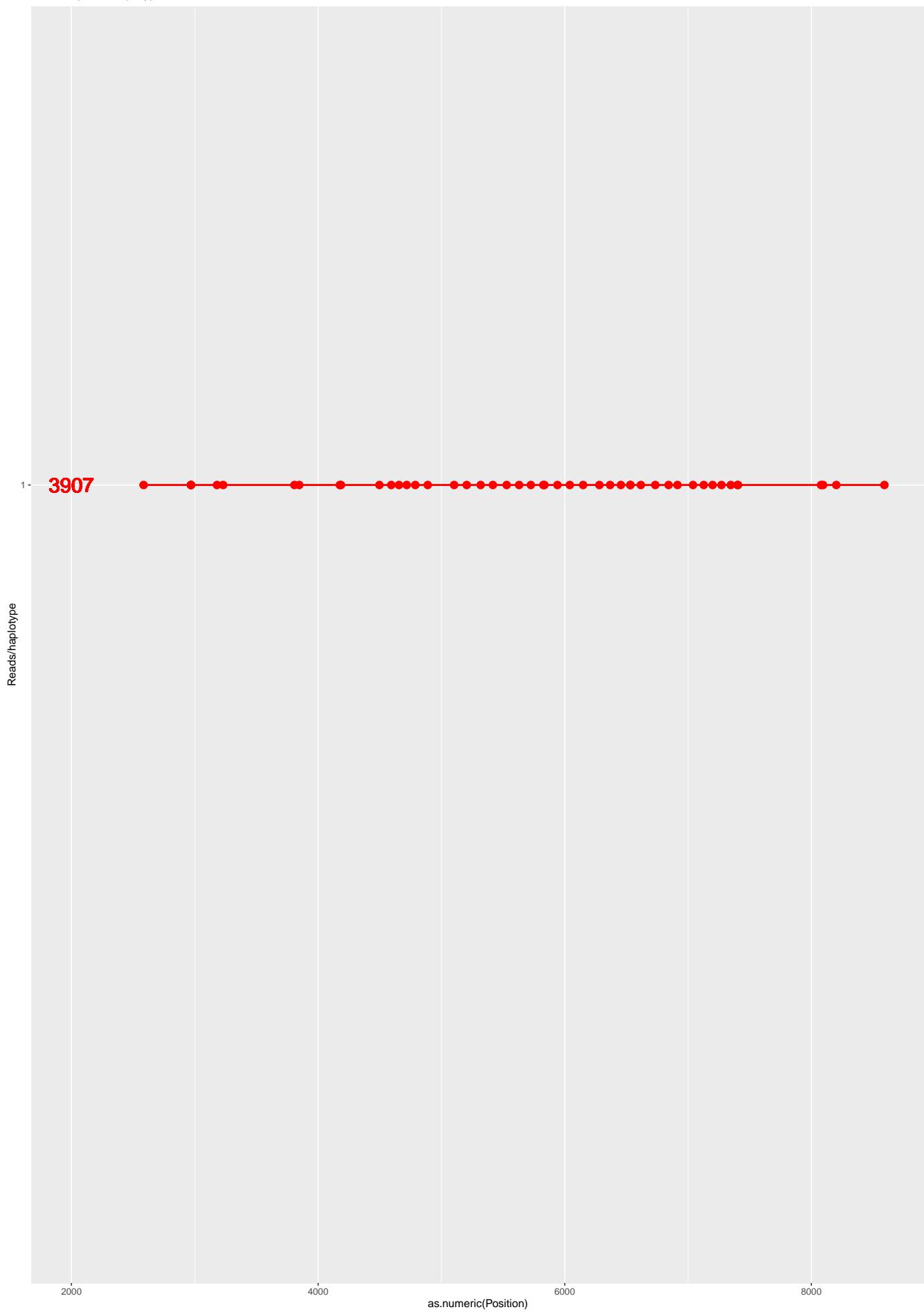


Sample = 326c tetrad = 326 spore = c

Total reads = 4081 PCR=839

haplotypes I began with n[supporting reads] = 3907

most frequent 7 haplotypes.



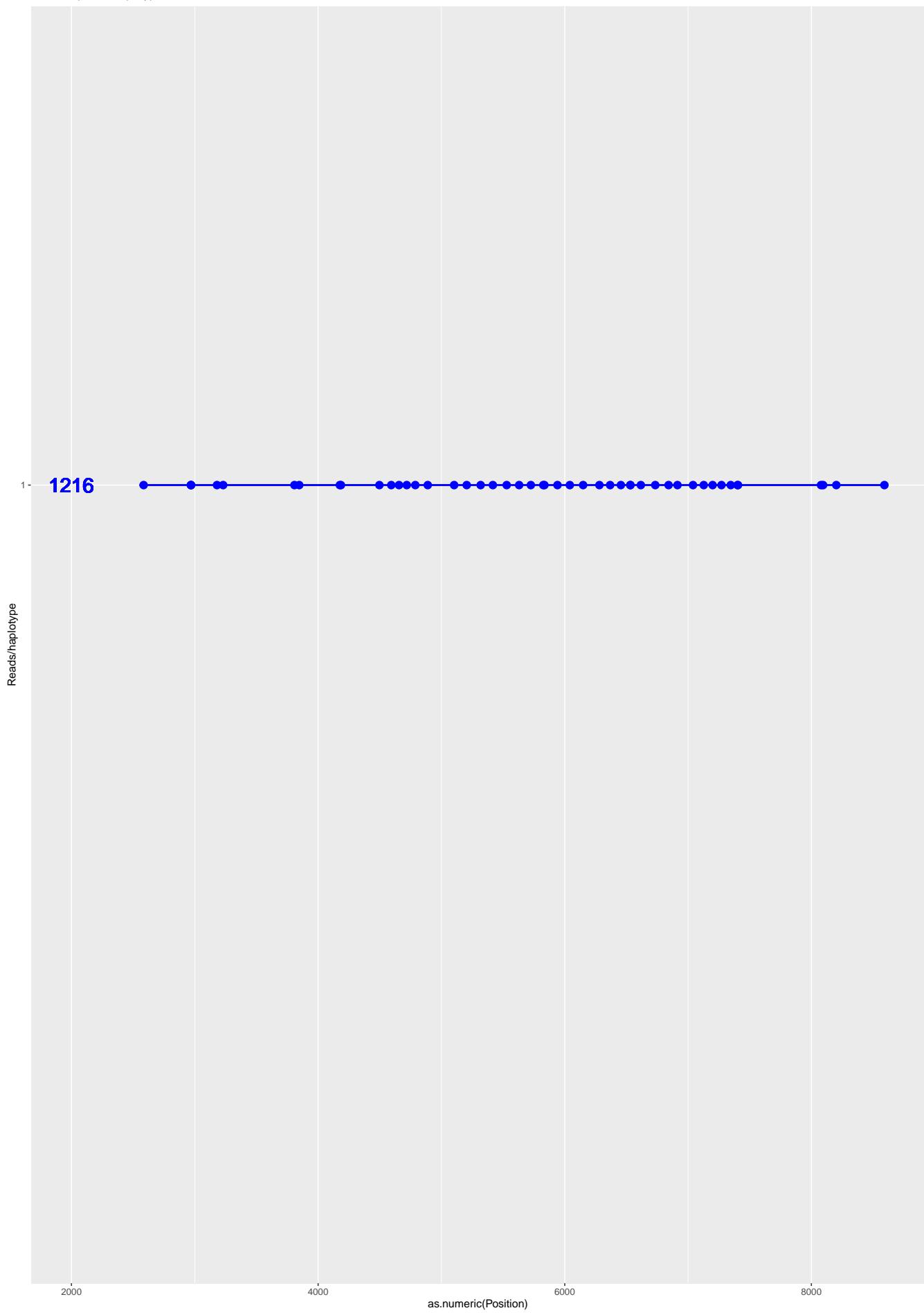
barcode = ACGACATGATACTGCT & TACGAGTCTGTAC

Sample = 326d tetrad = 326 spore = d

Total reads = 1426 PCR=840

haplotypes I began with n[supporting reads] = 1216

most frequent 7 haplotypes.



barcode = ACGACATGATACTGCT & ACTCAGCTACATAGTG

Sample = 328a tetrad = 328 spore = a

Total reads = 3146 PCR=841

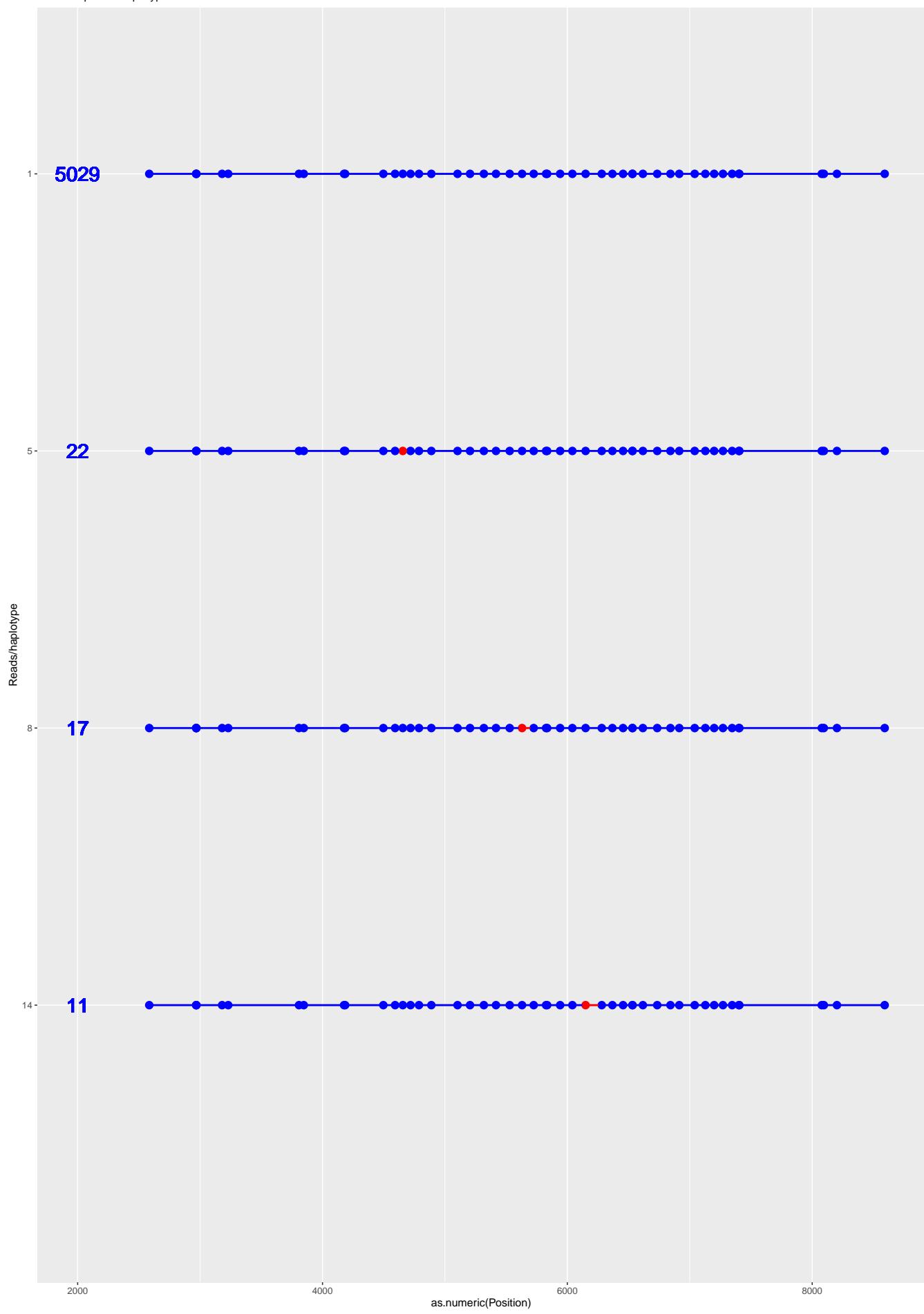
haplotypes I began with n[supporting reads] = 10, 13, 2715

most frequent 7 haplotypes.



barcode = ATACAGCACAGATGTG & TCAGCTGACGATGTGA

Sample = 328b tetrad = 328 spore = b
Total reads =5838 PCR=842
haplotypes I began with [n|supporting reads] = 11, 17, 22, 5029
most frequent 7 haplotypes.

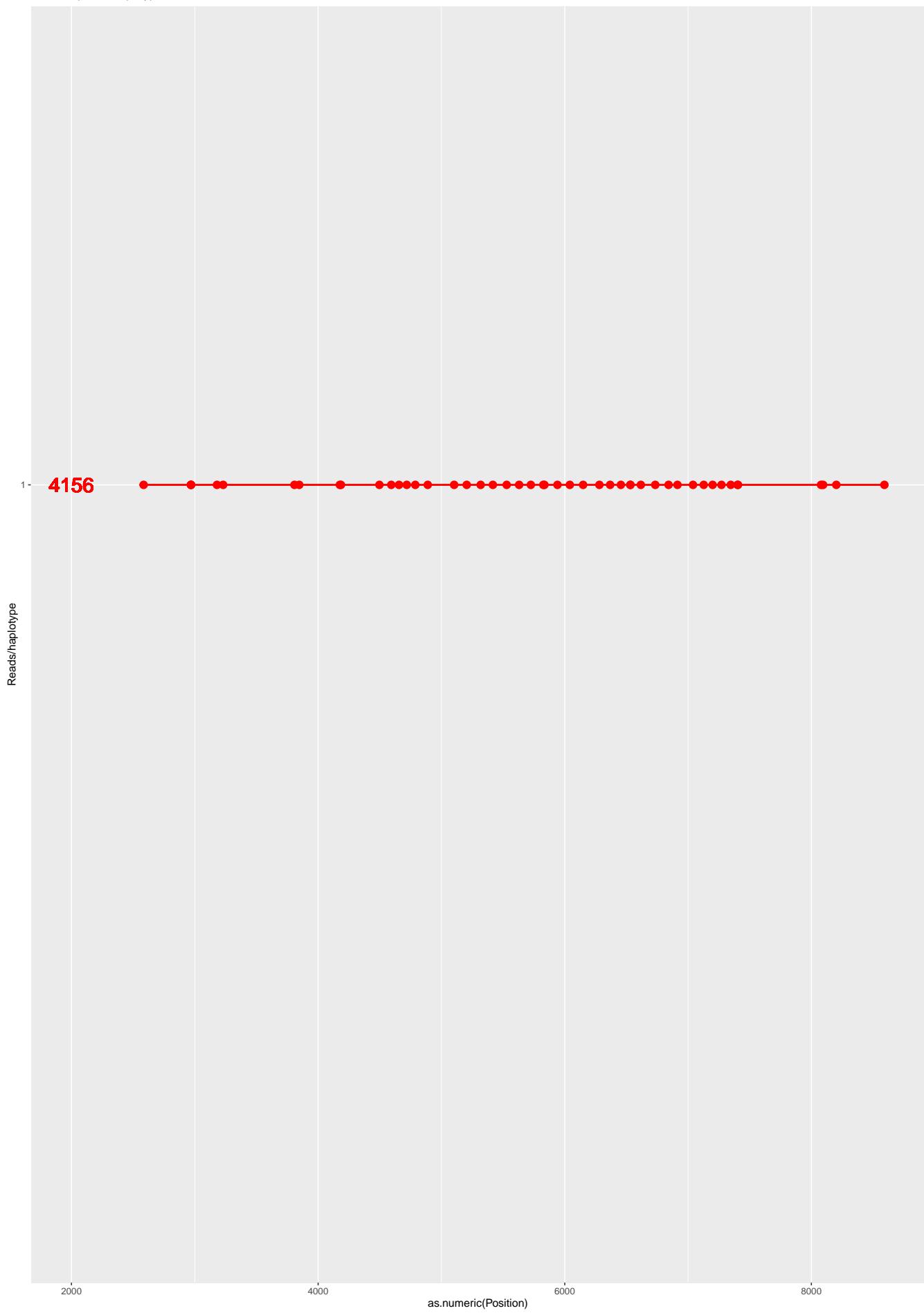


Sample = 328c tetrad = 328 spore = c

Total reads = 4355 PCR=843

haplotypes I began with n[supporting reads] = 4156

most frequent 7 haplotypes.



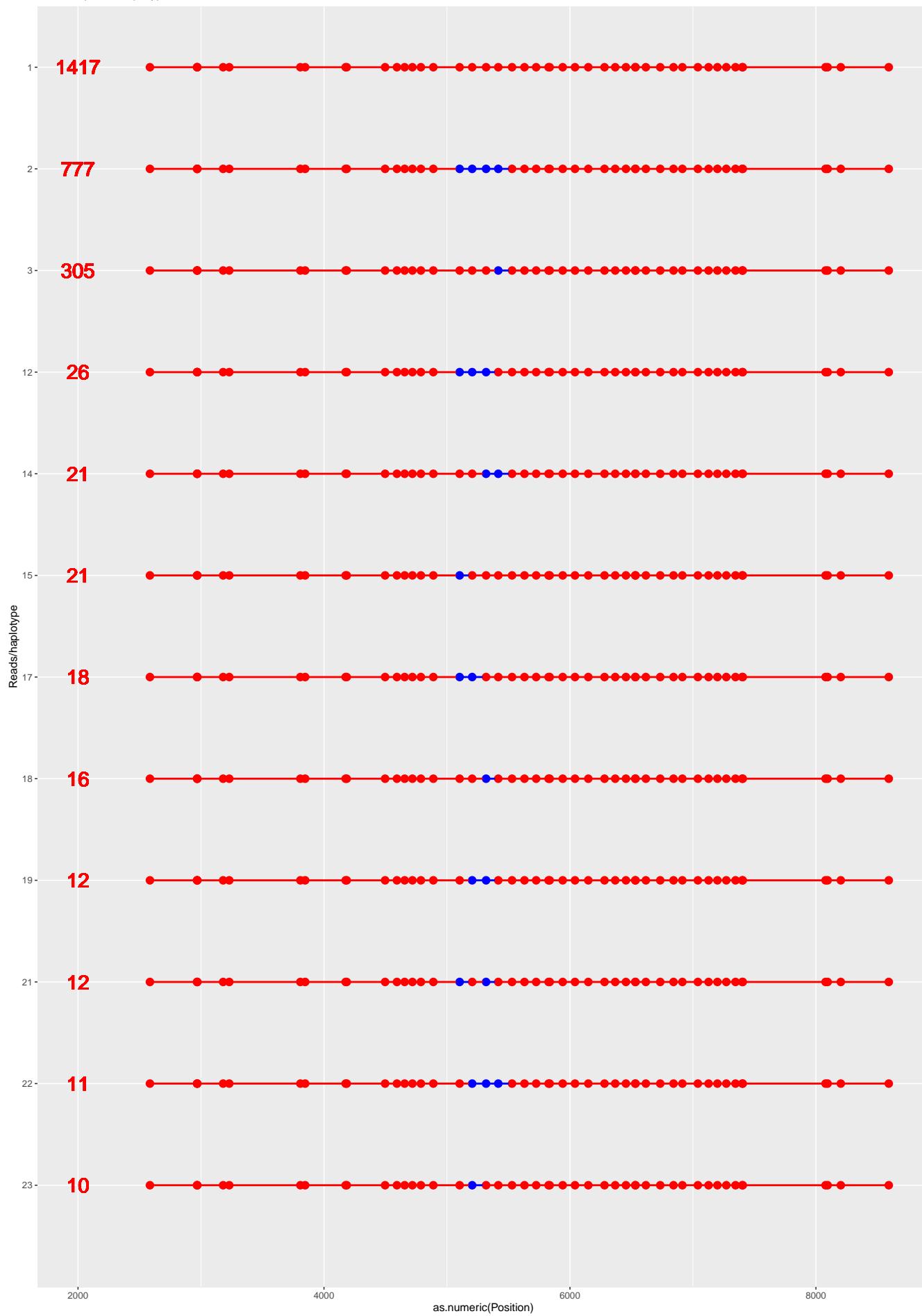
barcode = ATACAGCACAGATGTG & CTACTCTCAGCAGTGA

Sample = 328d tetrad = 328 spore = d

Total reads = 3305 PCR=844

haplotypes I began with [n(supporting reads)] = 10, 11, 12, 16, 18, 21, 26, 305, 777, 1417

most frequent 7 haplotypes.

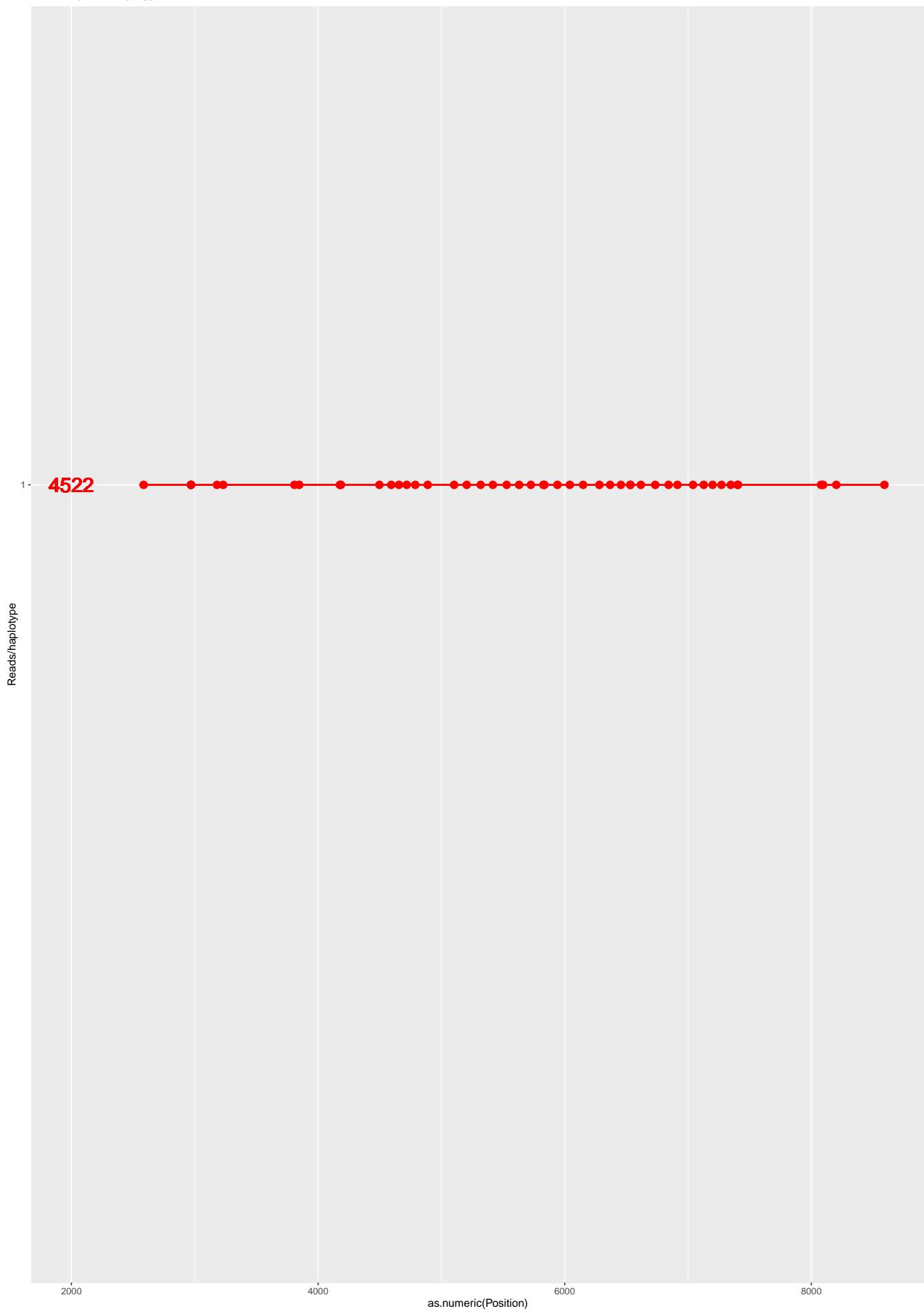


Sample = 331a tetrad = 331 spore = a

Total reads = 4720 PCR=845

haplotypes I began with n[supporting reads] = 4522

most frequent 7 haplotypes.



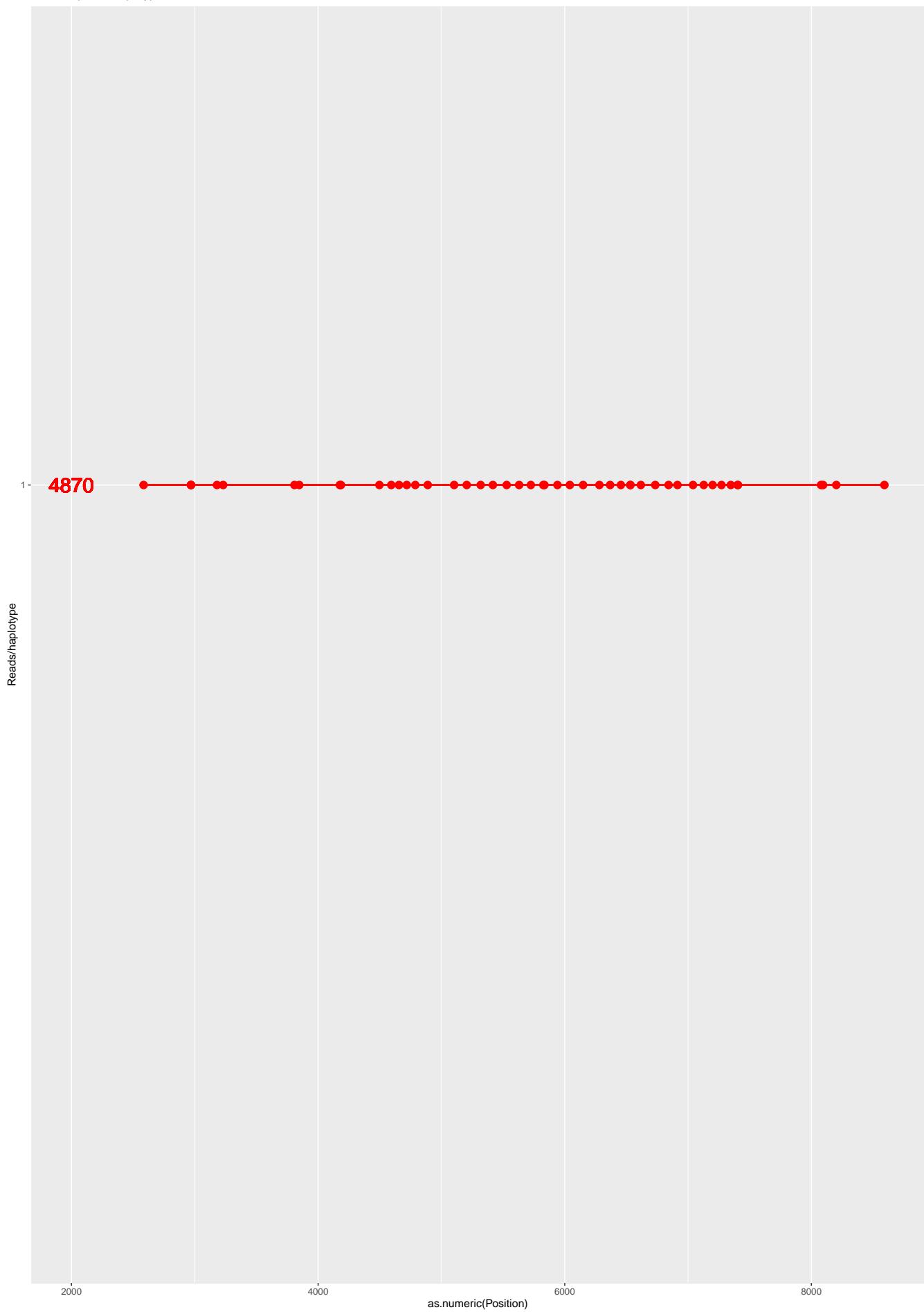
barcode = ATACAGCACAGATGTG & ATATAGTACAGCGTCT

Sample = 331b tetrad = 331 spore = b

Total reads = 5079 PCR=846

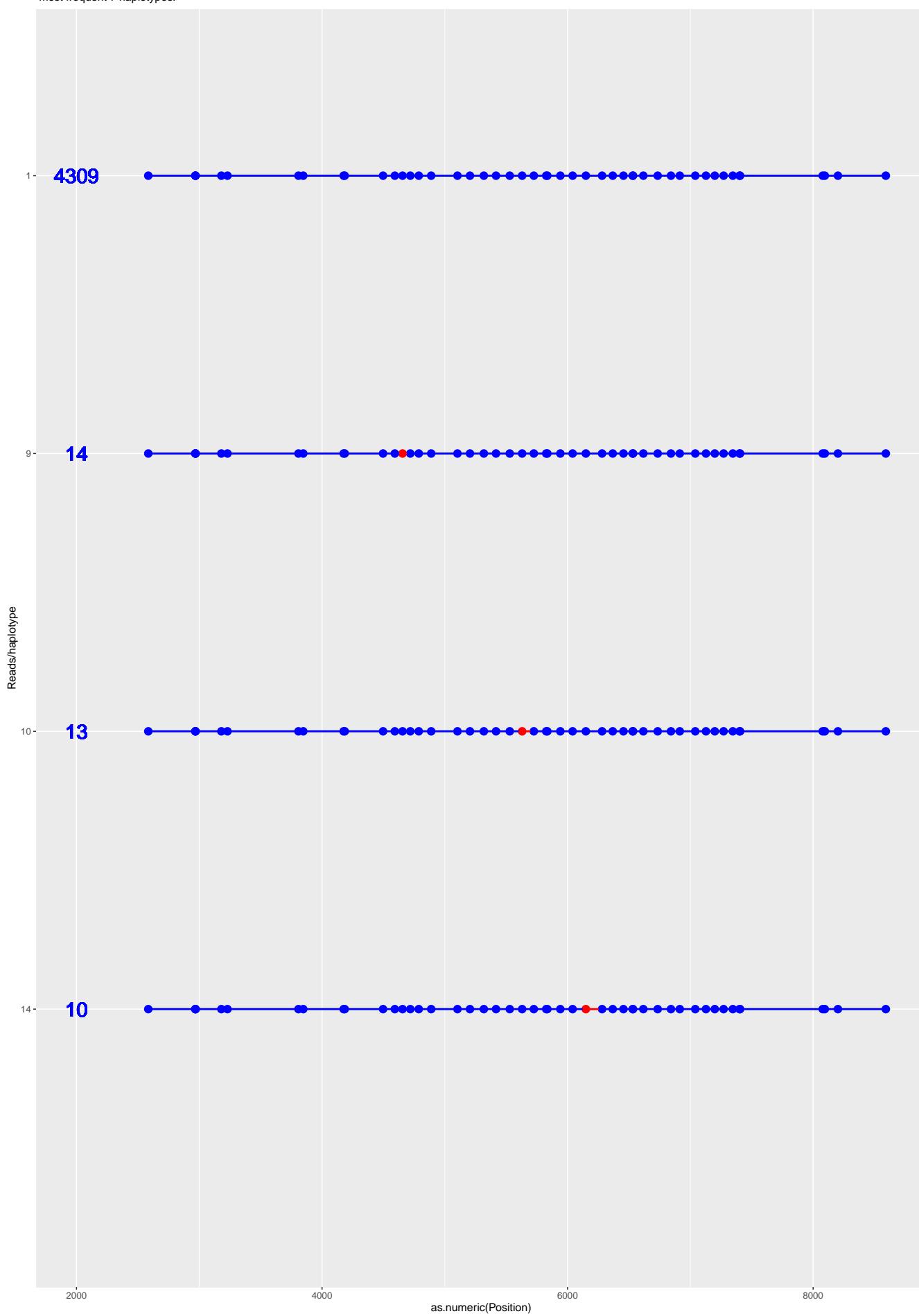
haplotypes I began with n[supporting reads] = 4870

most frequent 7 haplotypes.



barcode = ATACAGCACAGATGTG & GACACGACTAGATCGC

Sample = 331c tetrad = 331 spore = c
Total reads = 5020 PCR=847
haplotypes I began with [n|supporting reads] = 10, 13, 14, 4309
most frequent 7 haplotypes.



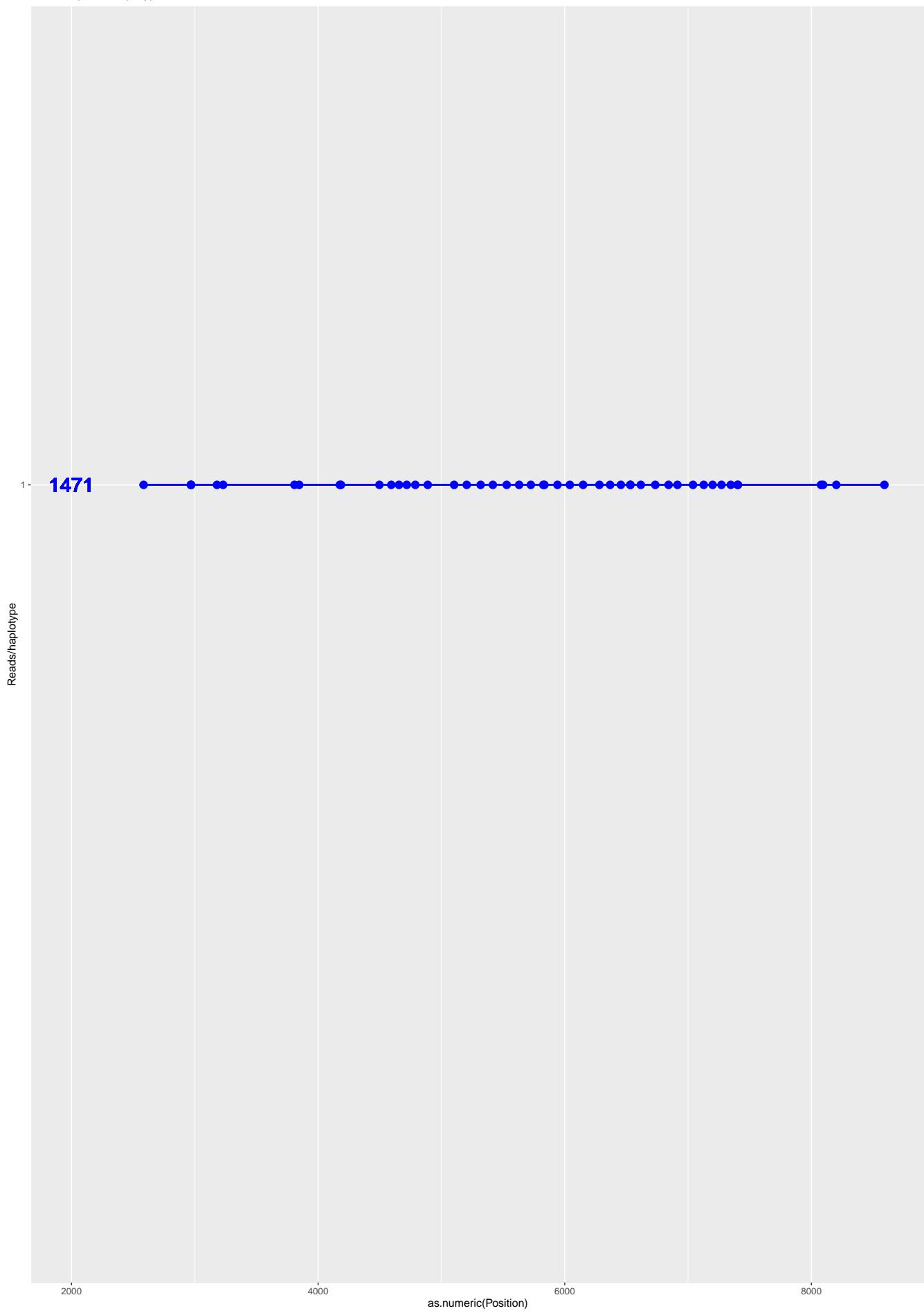
barcode = ATACAGCACAGATGTG & TACGAGTCTGTACATAC

Sample = 331d tetrad = 331 spore = d

Total reads = 1707 PCR=848

haplotypes I began with n[supporting reads] = 1471

most frequent 7 haplotypes.



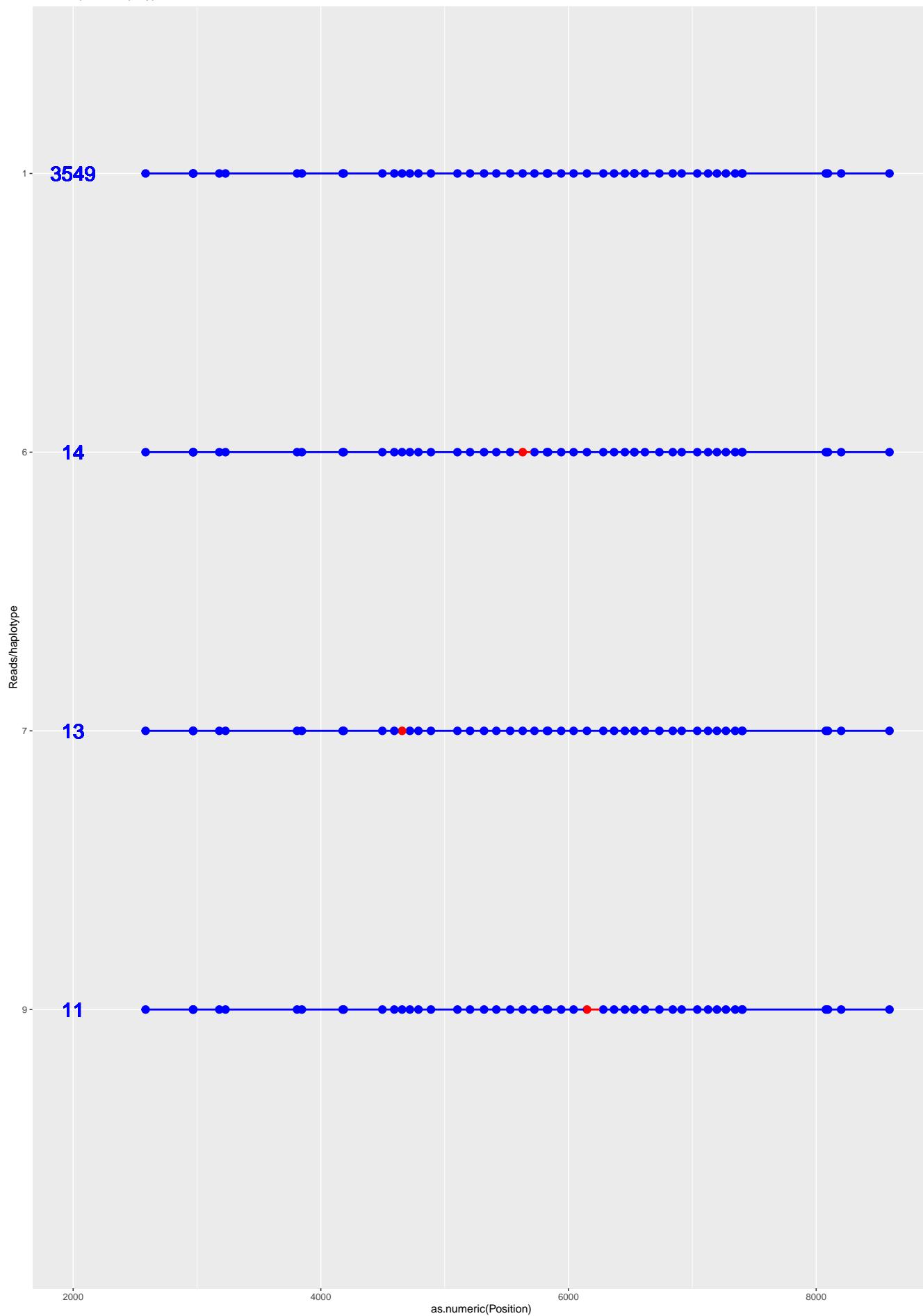
barcode = ATACAGCACAGATGTG & ACTCAGCTACATAGTG

Sample = 332a tetrad = 332 spore = a

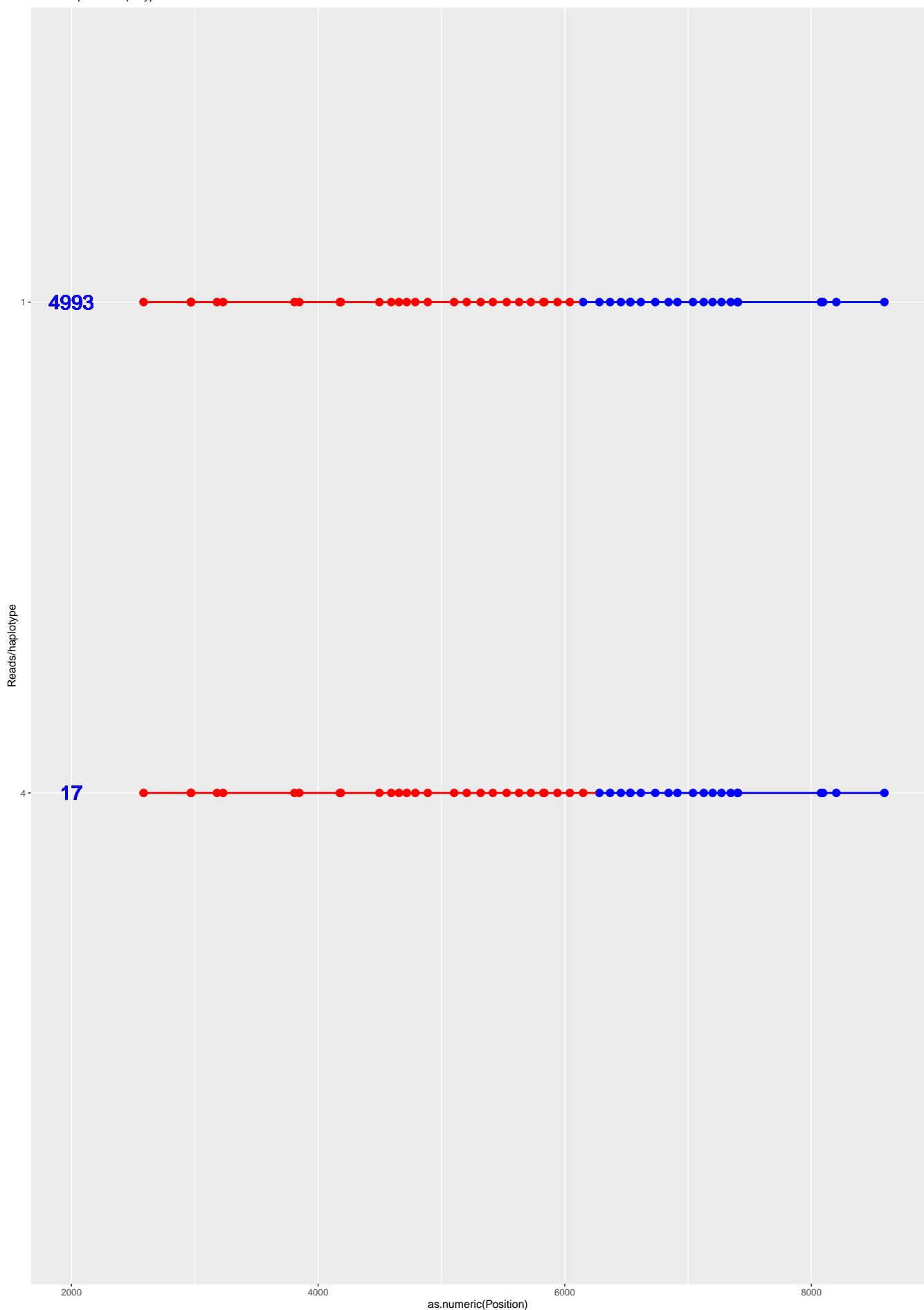
Total reads = 4115 PCR=849

haplotypes I began with n[supporting reads] = 11, 13, 14, 3549

most frequent 7 haplotypes.



Sample = 332b tetrad = 332 spore = b
Total reads = 5375 PCR=850
haplotypes I began with n[supporting reads] = 17, 4993
most frequent 7 haplotypes.



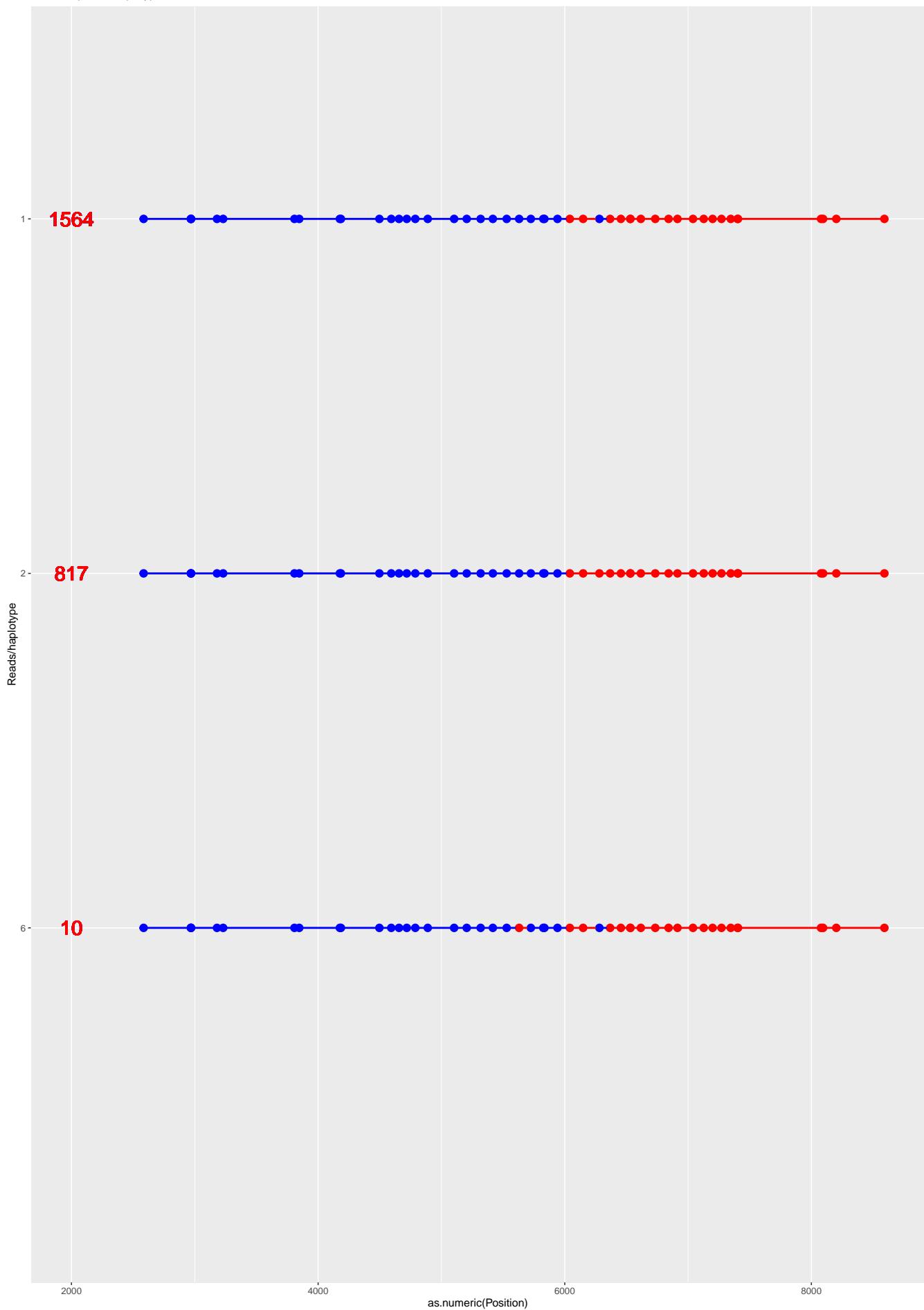
barcode = ACAGTCGATATCTCTC & ACTGATGCGCACATGT

Sample = 332c tetrad = 332 spore = c

Total reads = 2694 PCR=851

haplotypes I began with n[supporting reads] = 10, 817, 1564

most frequent 7 haplotypes.

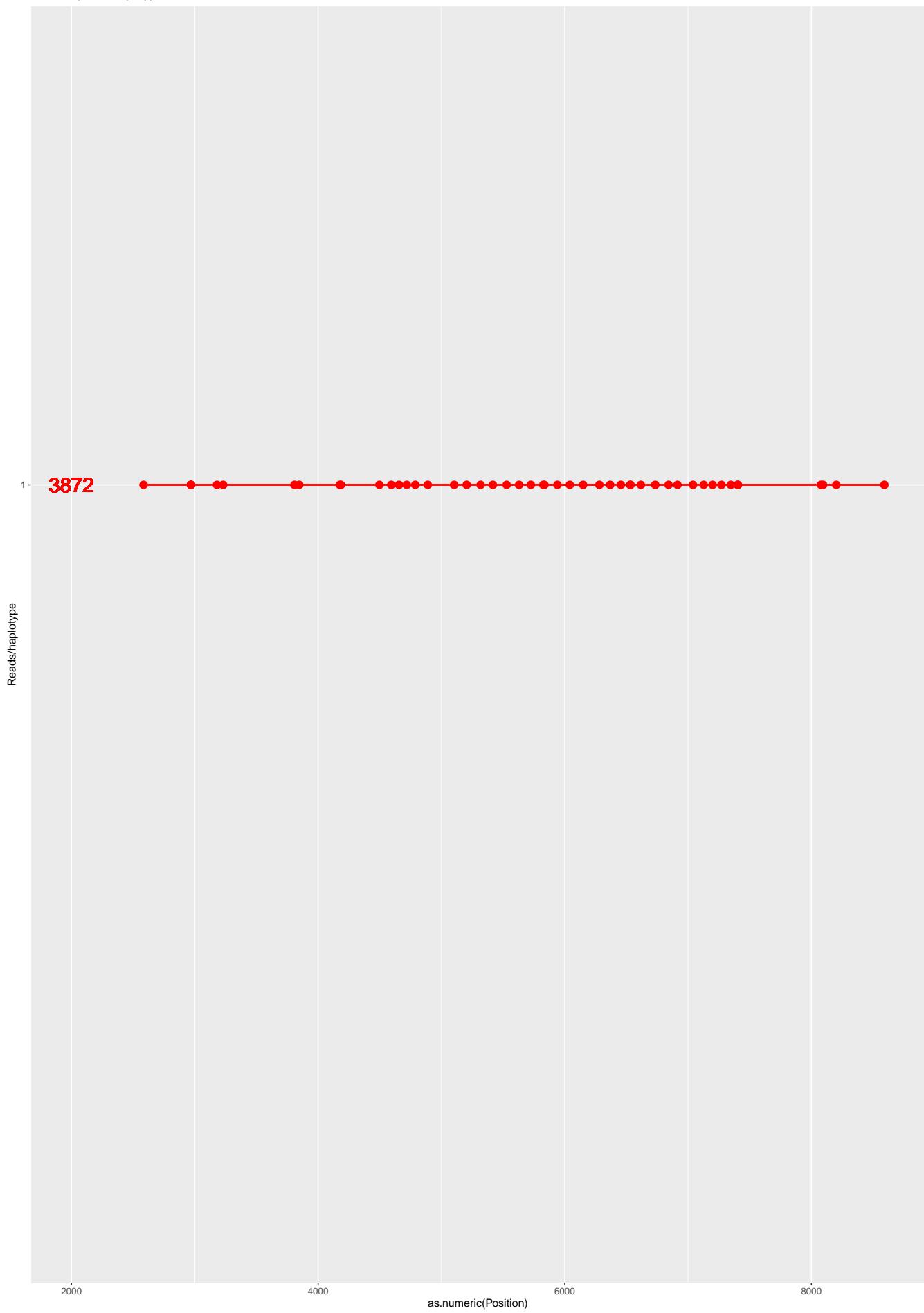


Sample = 332d tetrad = 332 spore = d

Total reads = 4033 PCR=852

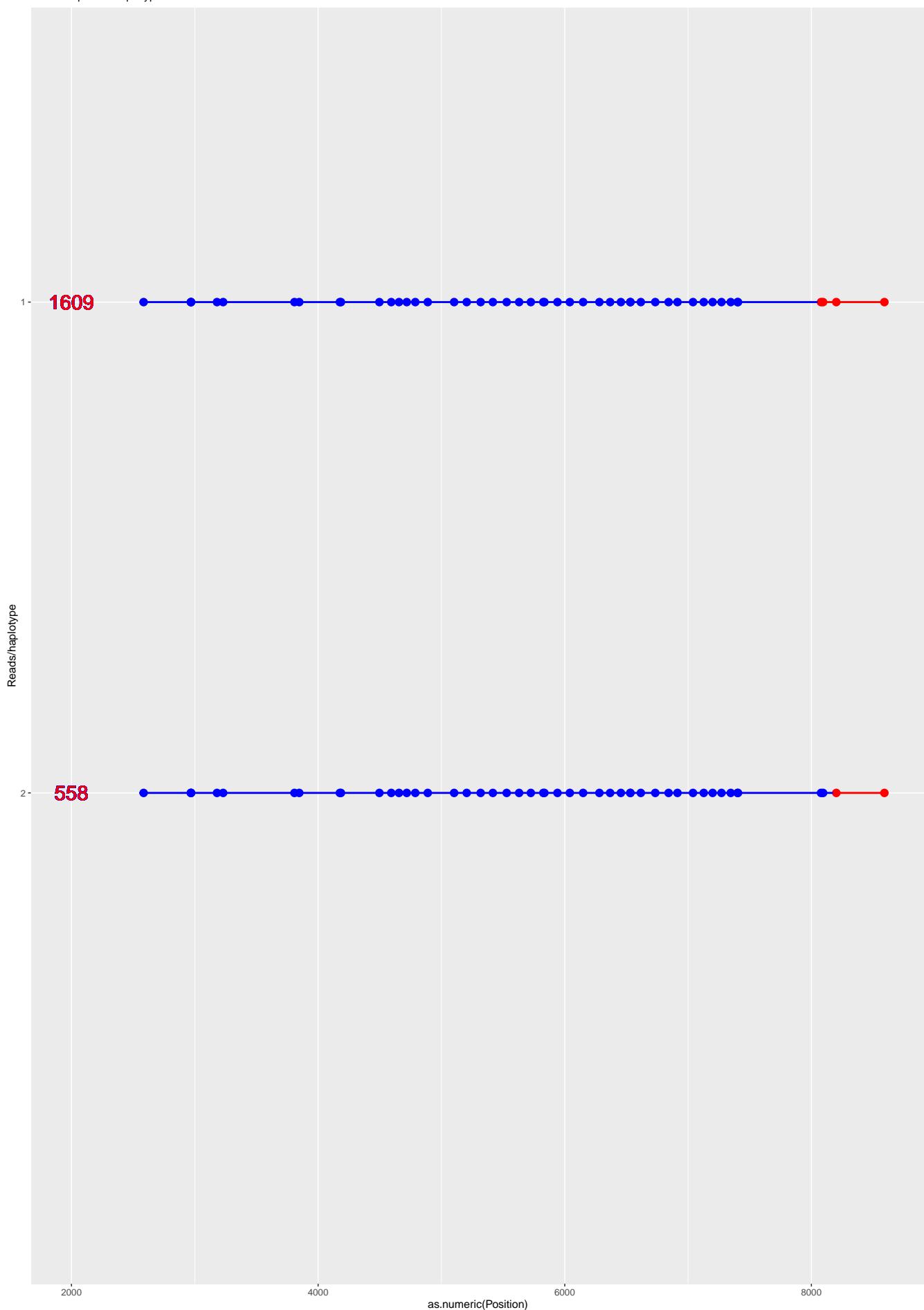
haplotypes I began with n[supporting reads] = 3872

most frequent 7 haplotypes.



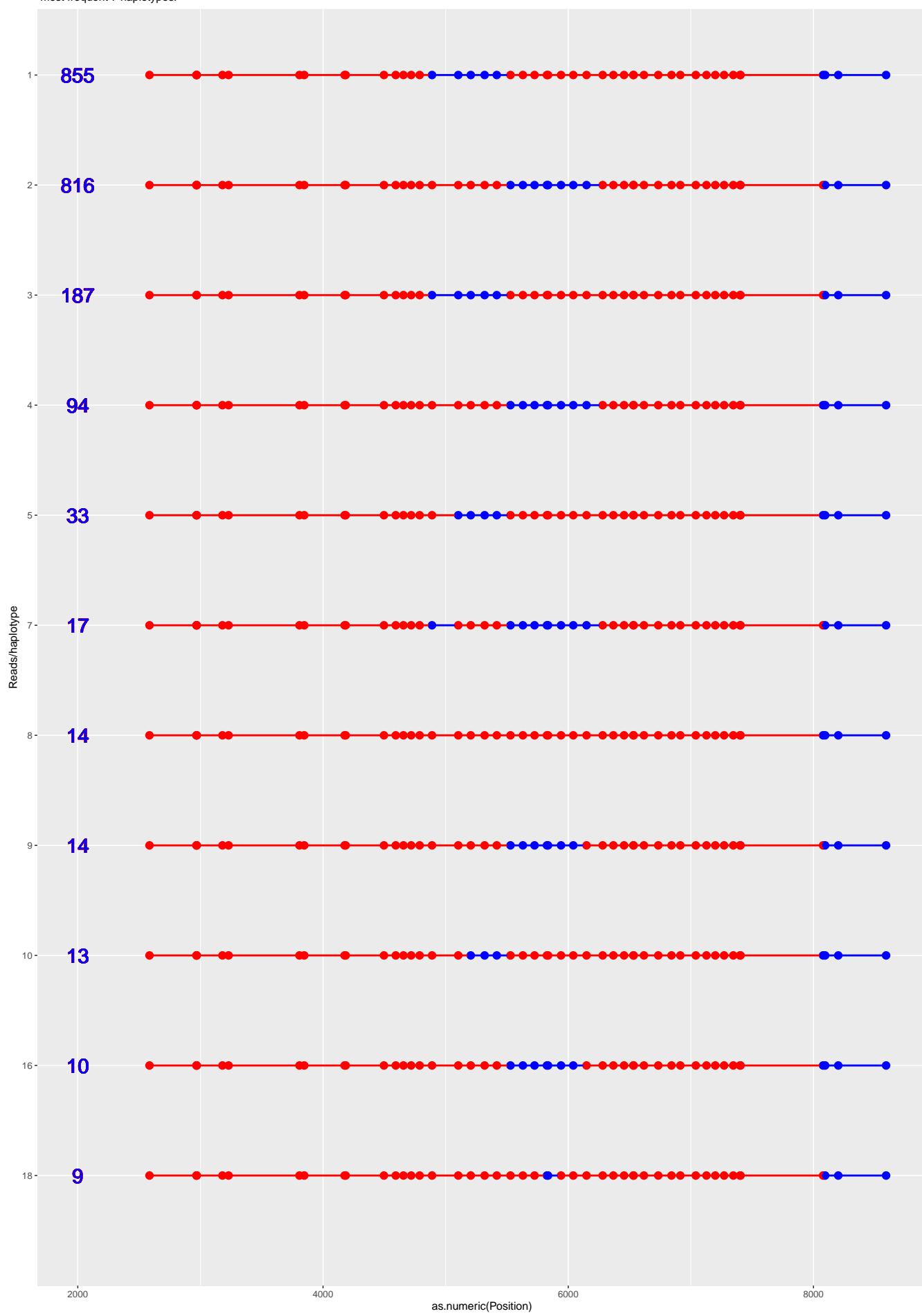
barcode = ACAGTCGATATCTCT & ATCTACATCACGACTC

Sample = 334a tetrad = 334 spore = a
Total reads = 3356 PCR=853
haplotypes I began with n[supporting reads] = 558, 1609
most frequent 7 haplotypes.



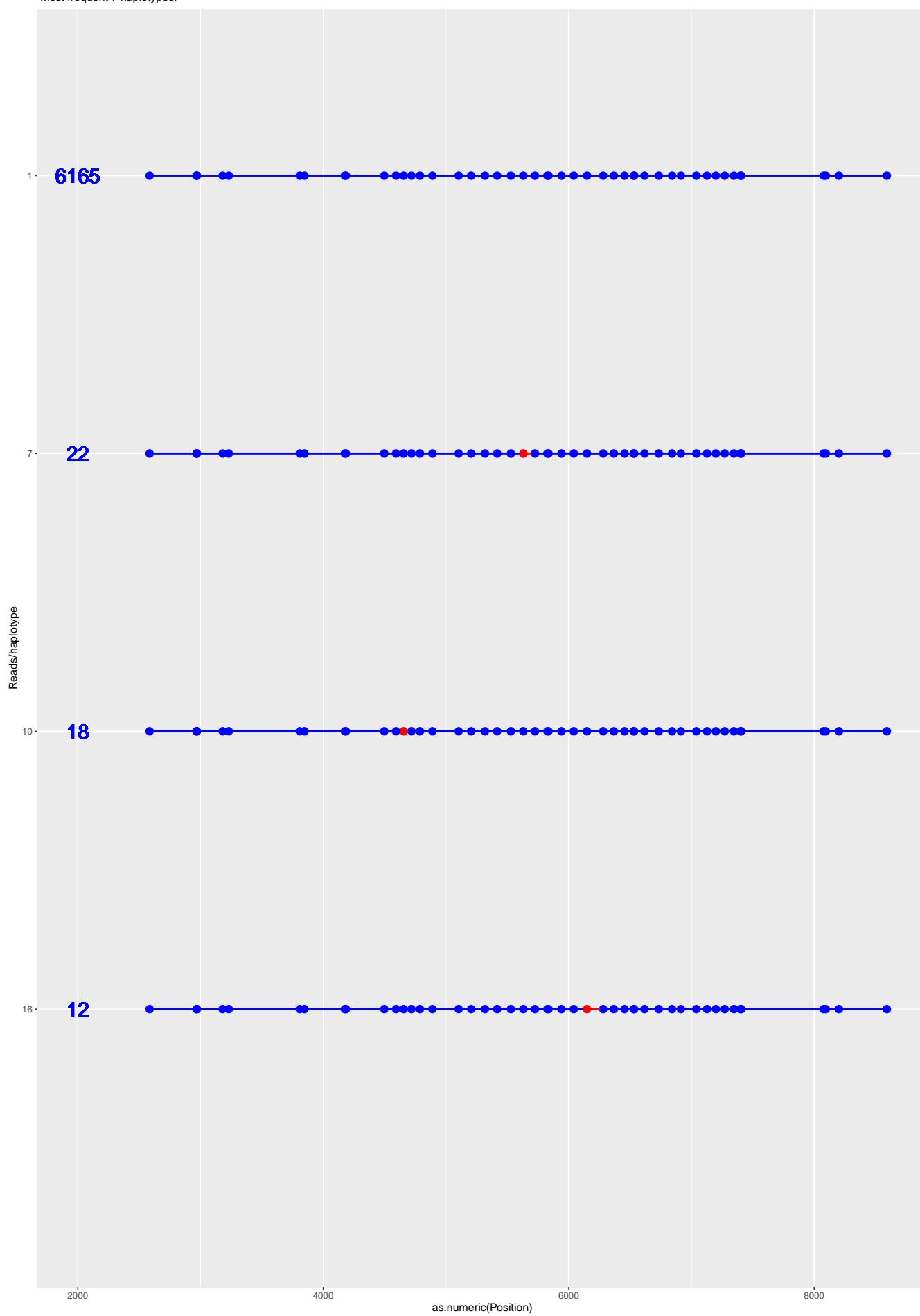
barcode = ACAGTCGATATCTCTC & ATATAGTACAGCGTCT

Sample = 334b tetrad = 334 spore = b
 Total reads = 4273 PCR=854
 haplotypes I began with [n(supporting reads)] = 9, 10, 13, 14, 17, 33, 94, 187, 816, 855
 most frequent 7 haplotypes.



barcode = ACAGTCGATATCTCTC & GACACGACTAGATCGC

Sample = 334c tetrad = 334 spore = c
Total reads = 7168 PCR=855
haplotypes I began with [n(supporting reads)] = 12, 18, 22, 6165
most frequent 7 haplotypes.



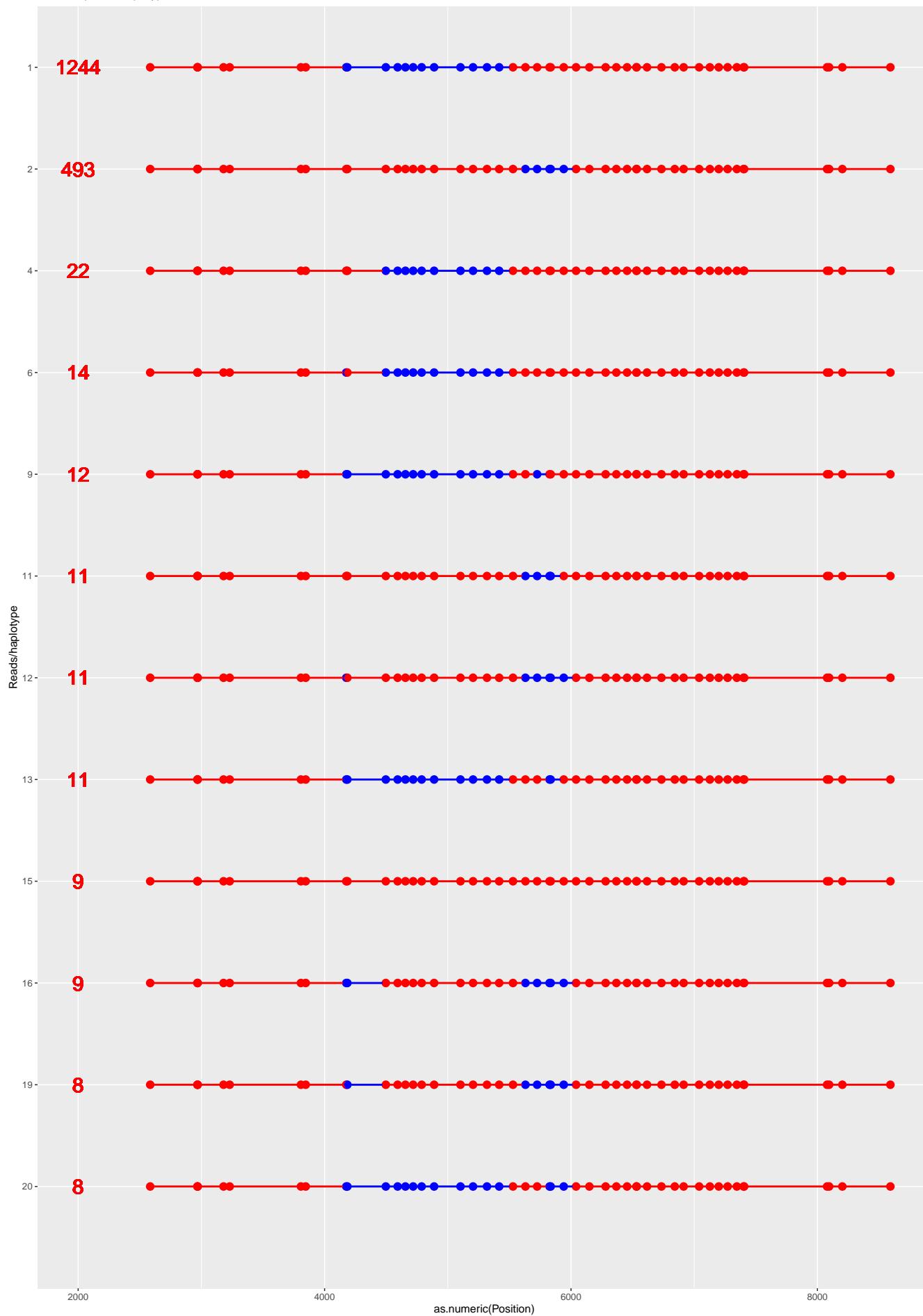
barcode = ACAGTCGATATCTCT & TACGAGTCTGTAC

Sample = 334d tetrad = 334 spore = d

Total reads = 4383 PCR=856

haplotypes I began with [n(supporting reads)] = 8, 9, 11, 12, 14, 22, 493, 1244

most frequent 7 haplotypes.



Sample = 336a tetrad = 336 spore = a

Total reads = 3248 PCR=857

haplotypes I began with n[supporting reads] = 10, 12, 2760

most frequent 7 haplotypes.

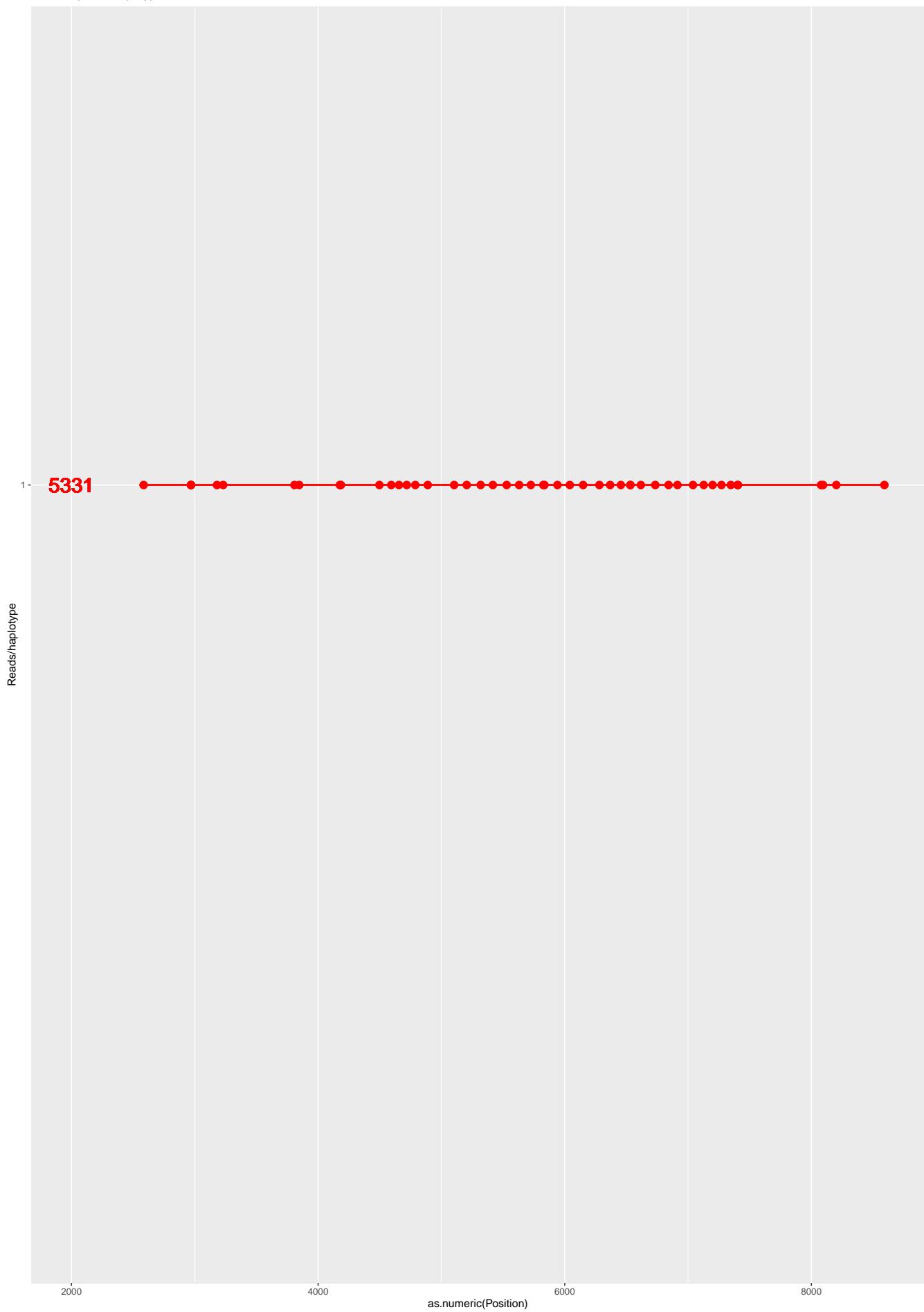


Sample = 336b tetrad = 336 spore = b

Total reads =5603 PCR=858

haplotypes I began with n[supporting reads] = 5331

most frequent 7 haplotypes.



barcode = GCTCGATCACATGACG & ACTGATGCGCACATGT

Sample = 336c tetrad = 336 spore = c
Total reads = 4138 PCR=859
haplotypes I began with [n|supporting reads] = 13, 15, 3524
most frequent 7 haplotypes.



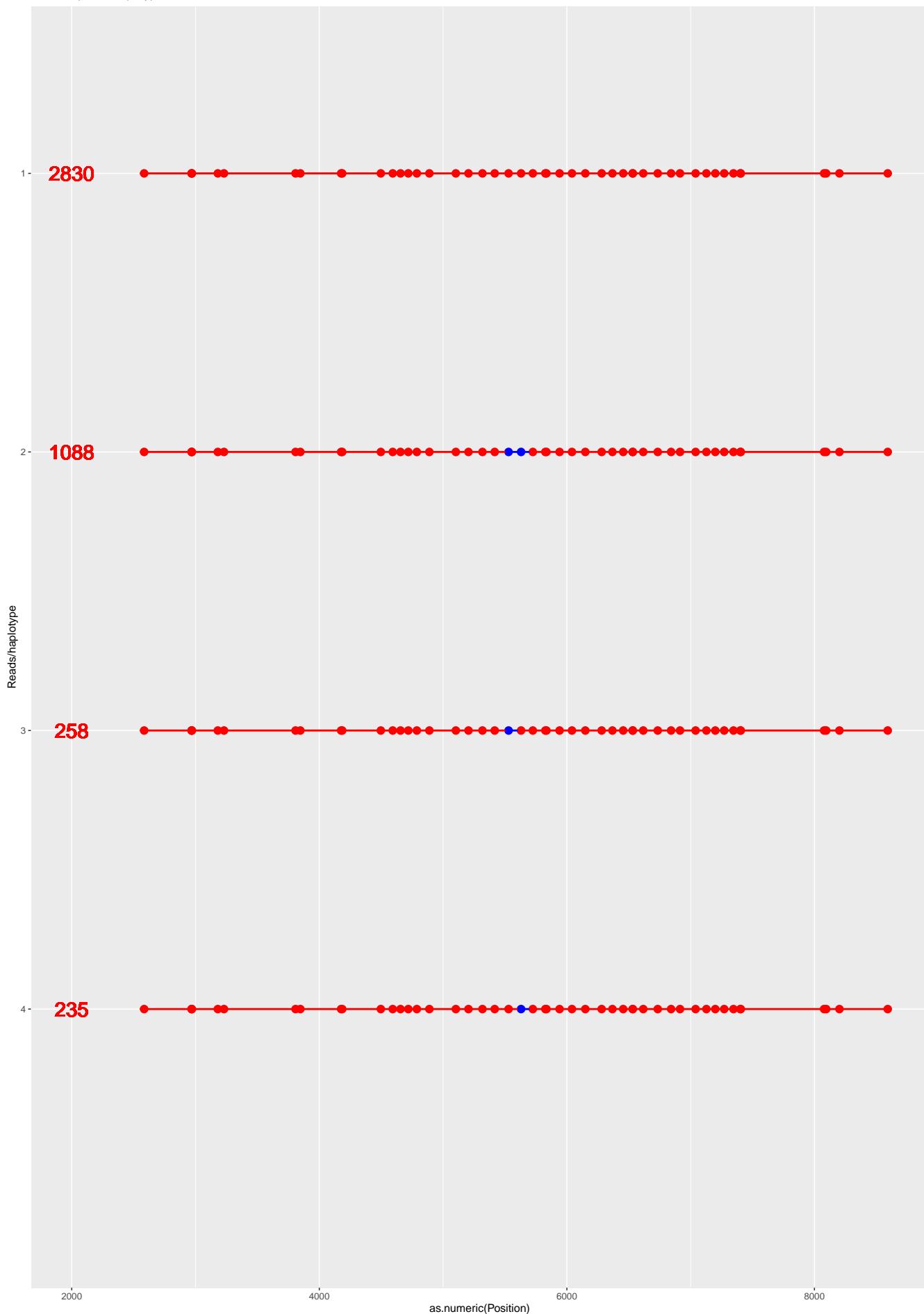
barcode = GCTCGATCACATGACG & CTACTCTCAGCAGTGA

Sample = 336d tetrad = 336 spore = d

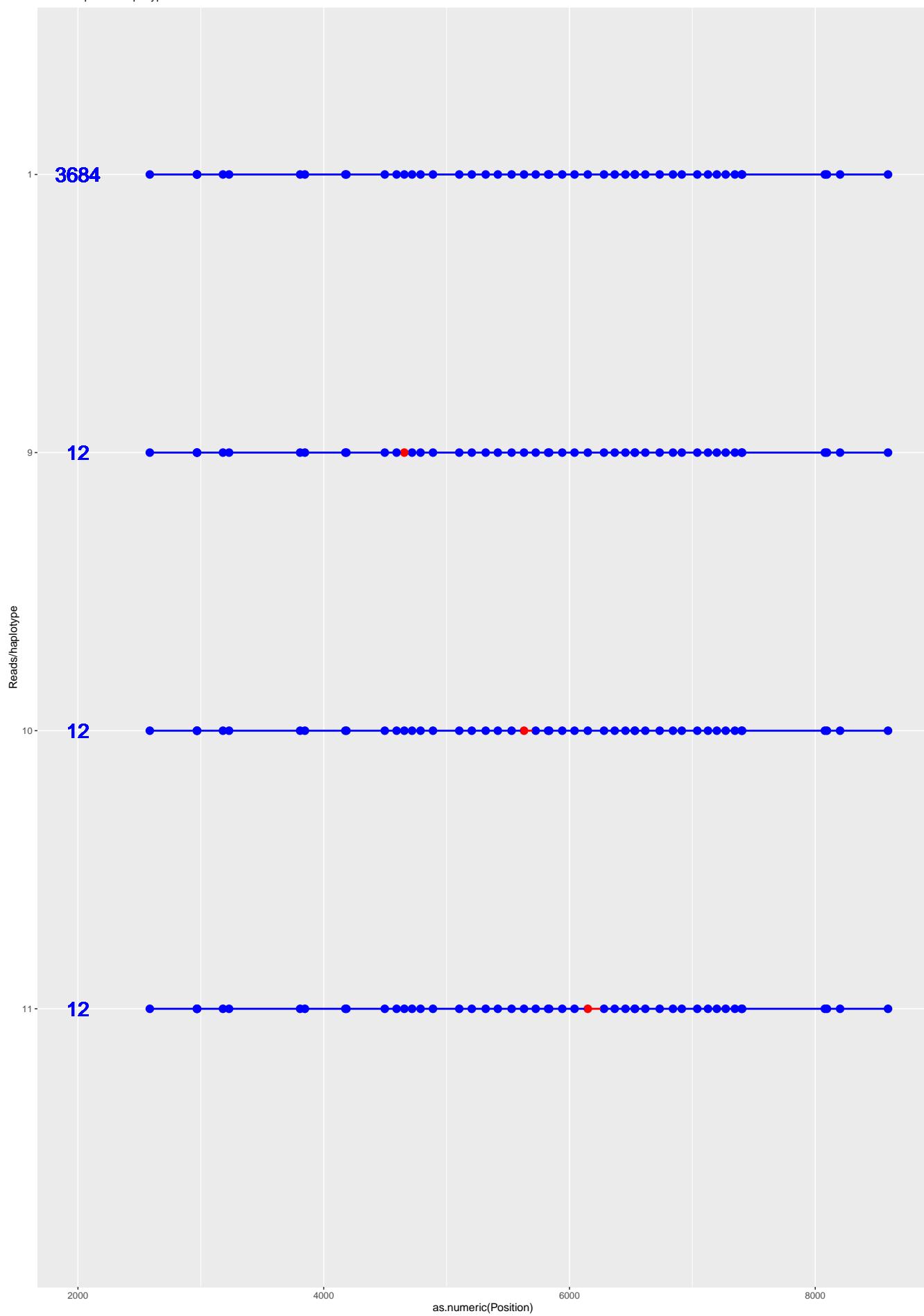
Total reads = 4635 PCR=860

haplotypes I began with n[supporting reads] = 235, 258, 1088, 2830

most frequent 7 haplotypes.

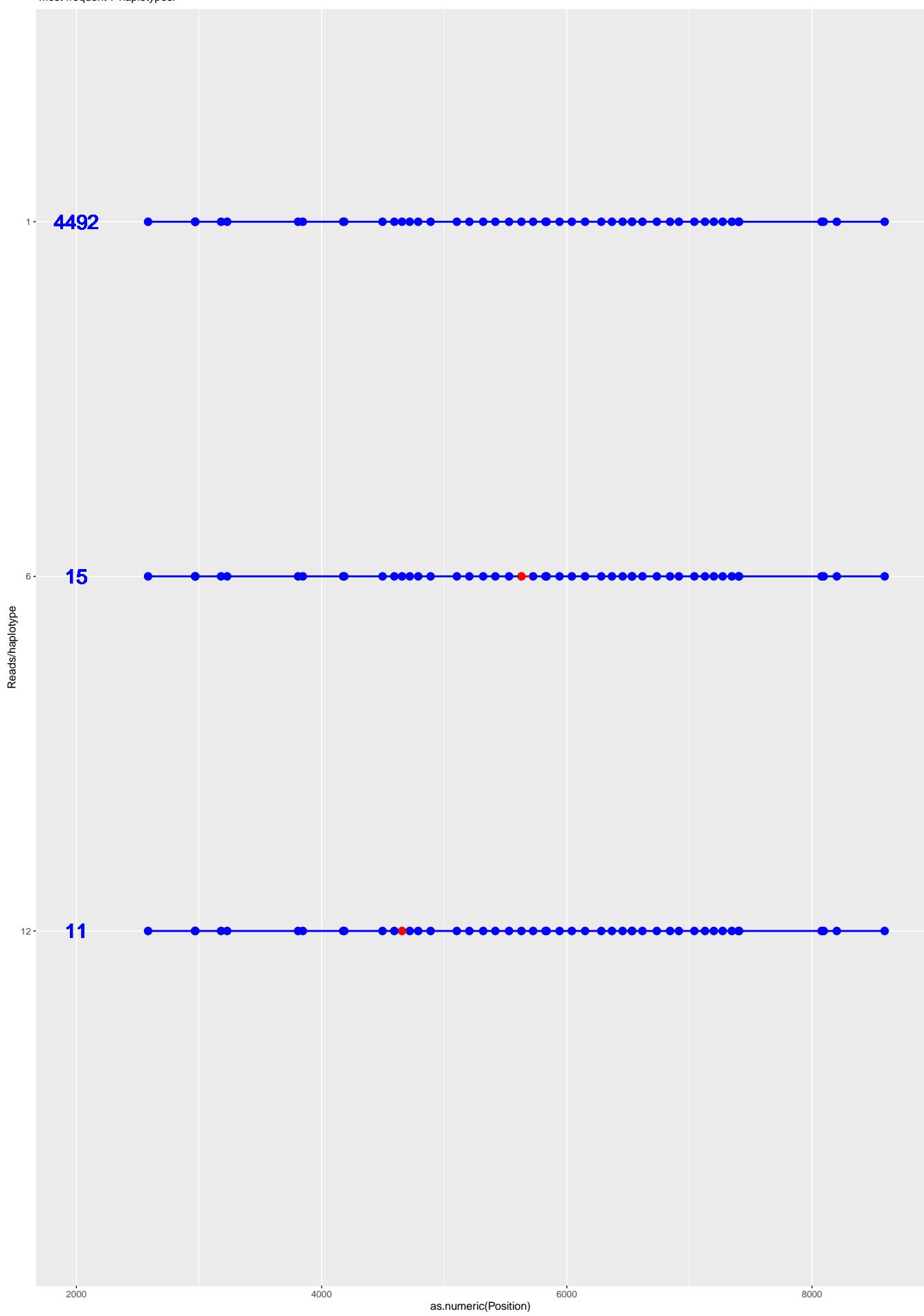


Sample = 337a tetrad = 337 spore = a
Total reads = 4307 PCR=861
haplotypes I began with [n(supporting reads)] = 12, 3684
most frequent 7 haplotypes.



barcode = GCTCGATCACATGACG & ATATAGTACAGCGTCT

Sample = 337b tetrad = 337 spore = b
Total reads = 5212 PCR=862
haplotypes I began with [n|supporting reads] = 11, 15, 4492
most frequent 7 haplotypes.

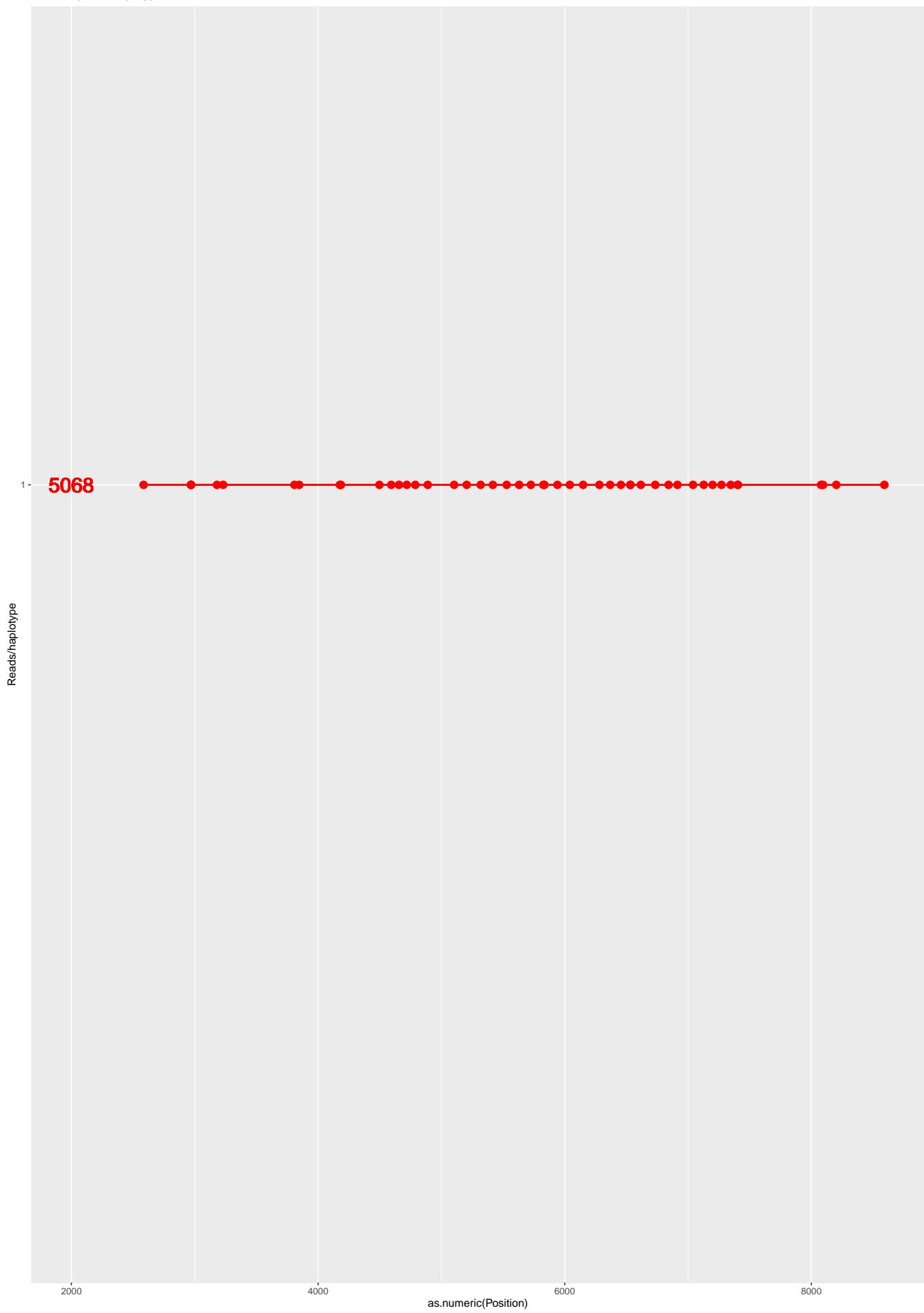


Sample = 337c tetrad = 337 spore = c

Total reads = 5280 PCR=863

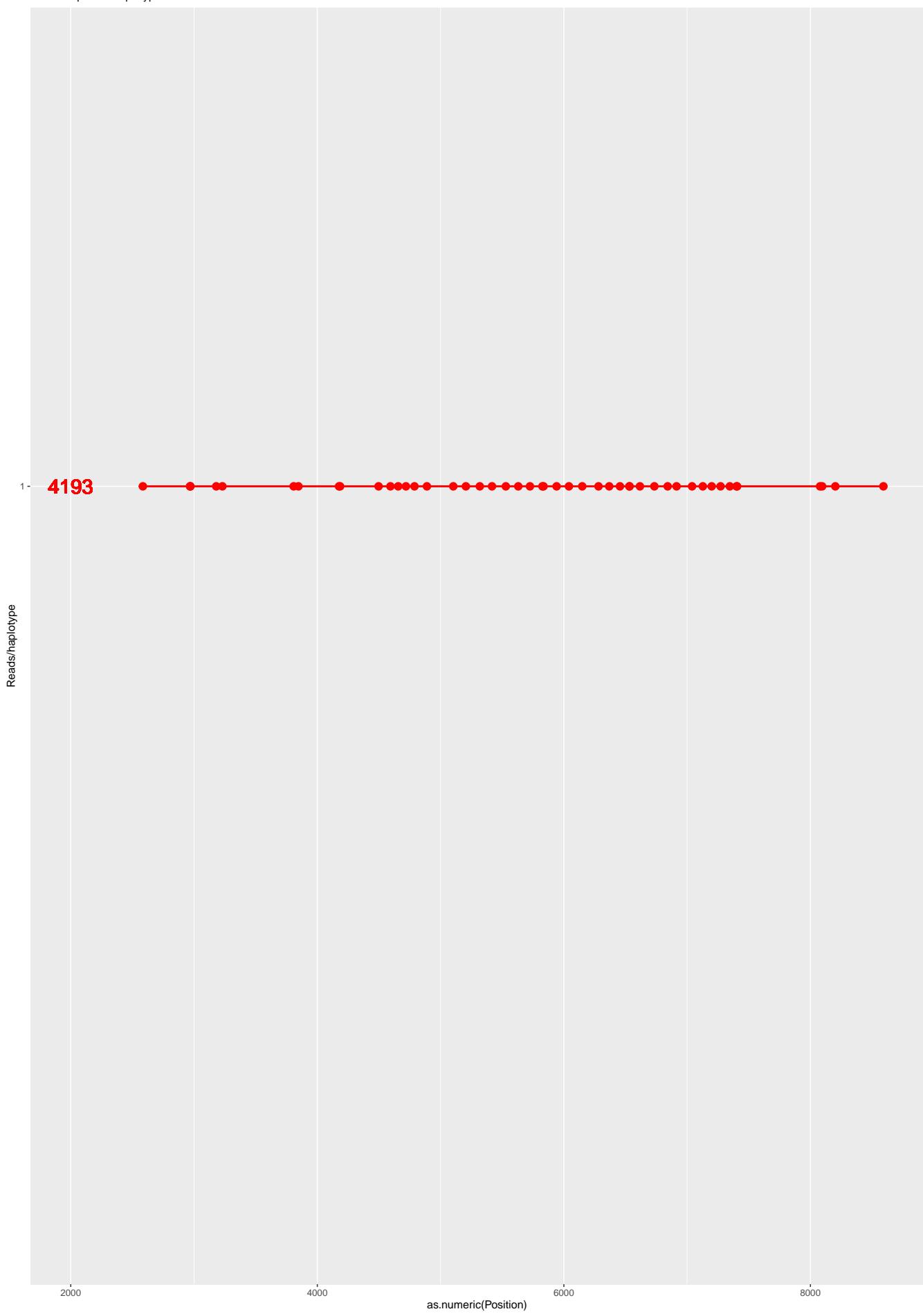
haplotypes I began with n[supporting reads] = 5068

most frequent 7 haplotypes.



barcode = GCTCGATCACATGACG & TACGAGTCTGTACATAC

Sample = 337d tetrad = 337 spore = d
Total reads = 4385 PCR=864
haplotypes I began with n[supporting reads] = 4193
most frequent 7 haplotypes.



barcode = GCTCGATCACATGACG & ACTCAGCTACATAGTG