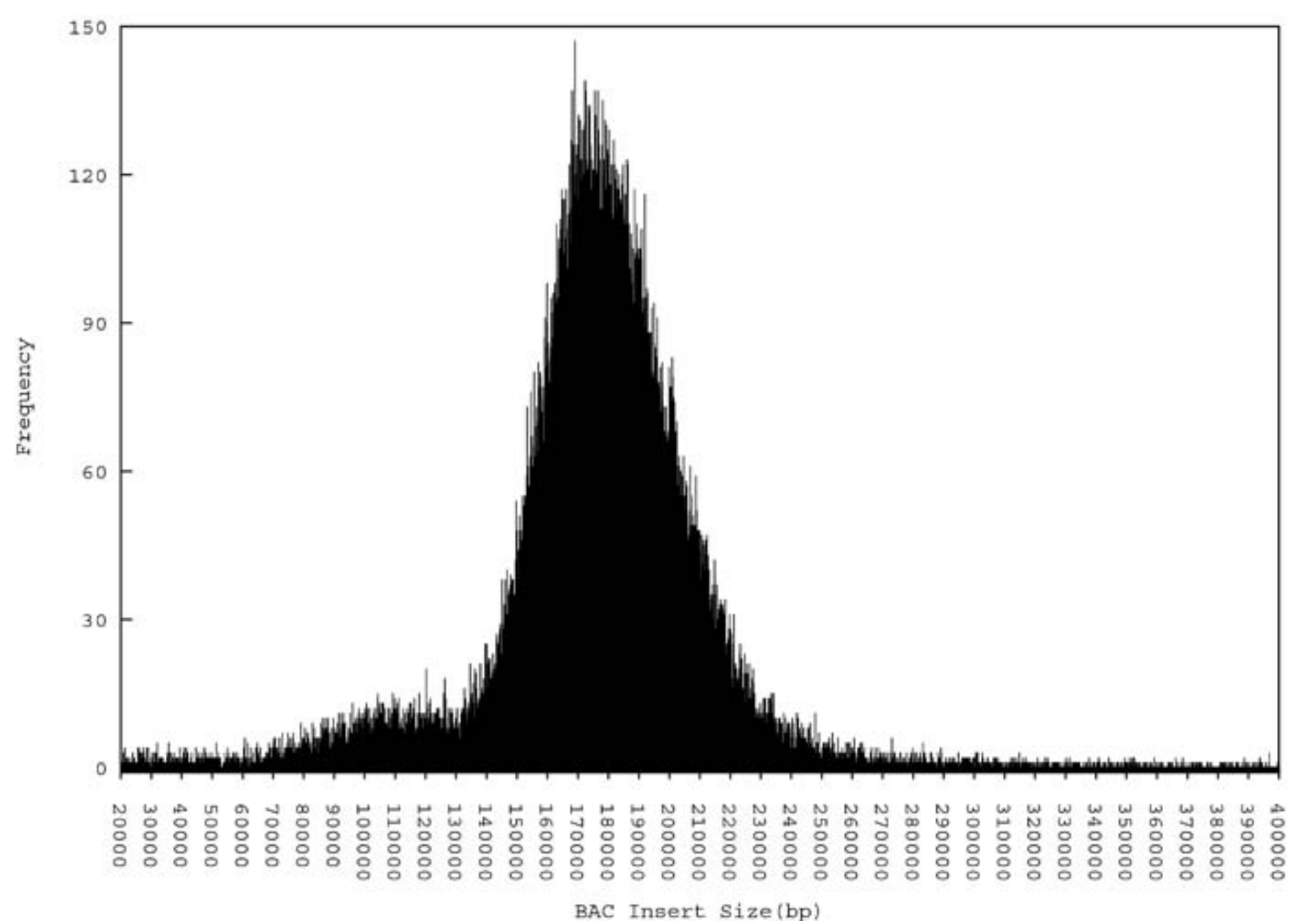
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120
90
60
30
0
Frequency
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30000
40000
50000
60000
70000
80000
90000
100000
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130000
140000
150000
160000
170000
180000
190000
200000
210000
220000
230000
240000
250000
260000
270000
280000
290000
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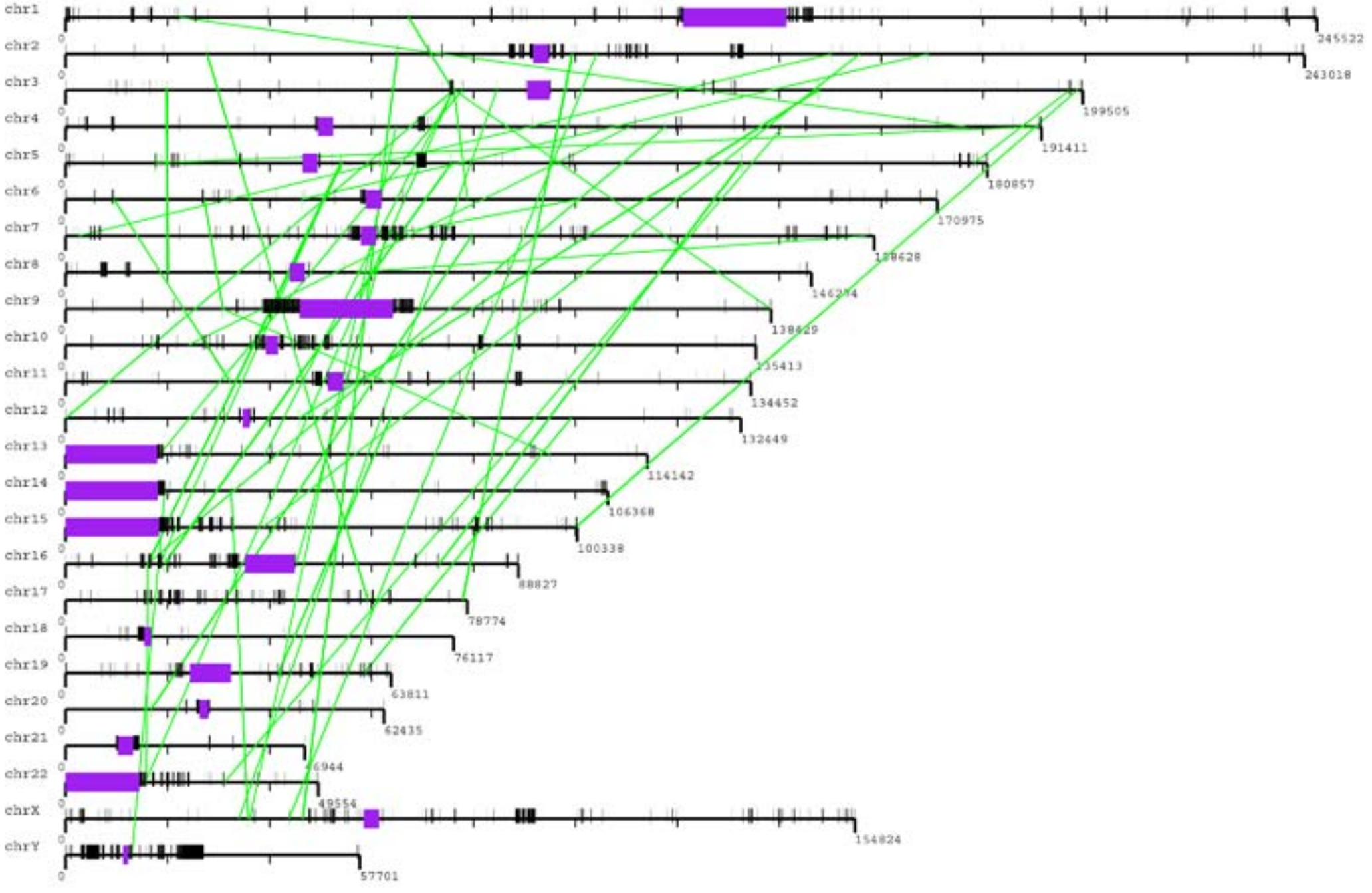
310000
320000
330000
340000
350000
360000
370000
380000
390000
400000
BAC Insert Size(bp)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245522
chr2
0
243018
chr3
0
199505
chr4
0
191411
chr5
0
180857
chr6
0
170975
chr7
0
159628
chr8
0
146274
chr9
0
138629
chr10
0
135413
chr11
0
134452
chr12
0
132649
chr13
0
114142
chr14
0
106368
chr15
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100338
chr16
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88827
chr17
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78774
chr18
0
76117
chr19
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chr20
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chr21
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46944
chr22
0
49554
chrX
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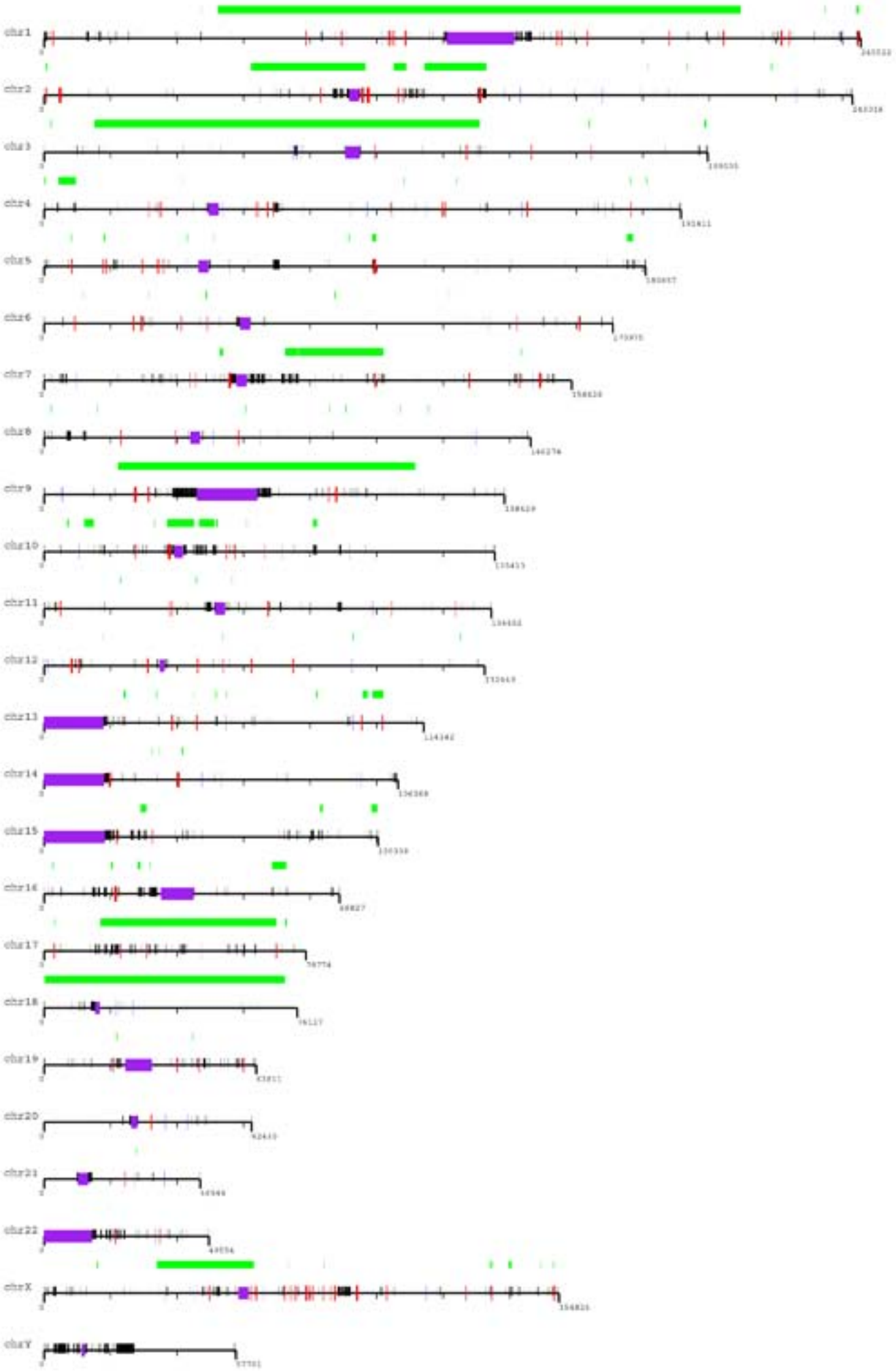
154824
chrY
0
57701


chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX
chrY

Supplemental Figure 1: Gibbon insert size distribution. *Nomascus Leucogenys* BES were optimally mapped against the human genome. For each pair of end sequences, an *in silico* insert size was calculated as the distance between (and including) end sequence positions on the human reference genome. To quantify the distribution of the BAC library insert sizes, we calculated a mean of 176.6 kb +/-33.45 kb from the set of 66,206 BAC clones within finished human genome (Figure 1a). These BAC clones had unequivocal placements (single alignments for each end) and proper end orientation within the human genome. Based on this distribution we chose a concordant insert size range of 76.45-277.18 kb (within 3 standard deviations of the mean), making it unlikely that size discordant clones deviating outside of this range would represent chance occurrences rather than true rearrangements.

Supplemental Figure 2:
Putative interchromosomal (2a) and intrachromosomal (2b) rearrangements.

Supplemental Table 1
Summary of Paired End Sequence Analysis. All regions showing two or more discordant gibbon BACs either by orientation, length or chromosome are indicated. The type of discordancy is indicated as follows: Trans =interchromosomal, B (insert too large), S (insert too small) (based on length thresholds of 76.4-277.2 kb); Orientation discordancies are indicated – or ++ based on the placement of the ends against the human genome. Experimental FISH results for an index BAC are included only for the largest events (>1 Mb).

Supplemental Table 2: human/gibbon homology synteny blocks organization in humans
The Table lists all the human BACs used in the study, arranged according to their position on the USCS May 2004 release. The first column shows the homologous syntenic block to which they belong (according to Muller et al. (2003). Yellow rows separate two contiguous homologous syntenic blocks, and, if identified, includes the splitting BAC. The “Break interval” column of the yellow rows reports the breakpoint interval. This interval usually corresponds to the extension of the splitting BAC. If more than one splitting BAC was tested and confirmed, the interval was defined as the intersection of the two . Intervals were further refined if BACs flanking the splitting one are overlapping with the latter. If no splitting BAC was identified, the homologous syntenic block break interval was derived from the closest clones. In cases in which information from non-splitting BACs were used, the extension of the BAC was conservatively adjusted 20 kb because of the limits of the FISH technique. Figures in red delimiting the interval indicate that it was restricted

taking into account the BES position of the splitting gibbon BAC clone reported in the Supplemental Table 3.The presence of segmental duplications prevented further refinement of some breakpoints. Rows or cells in pink indicate that the BAC identified two (only the cell in pink) or more (entire row in pink) FISH signals. m.s. stands for multiple signals; n.s. for no signal. The (H) or (N) on the “NLE map” column indicate if the splitting occurred in lineages leading to human (H) or gibbon (N). Few clones yielded one signal much stronger that the other. This information was also utilized to narrow the break interval that was assumed to have occurred on the side facing the homologous syntenic block with the weaker signal. Intervals refined in this way are shown in green in this Table and in Supplemental Table 3.

Supplemental Table 3: homology synteny blocks organization in gibbon

The Table lists all human BACs giving FISH signals on gibbon, ordered according to their inferred position on the gibbon chromosomes. The second column reports the orientation of each segment (+ or -) with respect to the orientation of the human sequence. The gibbon BACs are in blue rows. Their position at homologous syntenic block breaks was derived from both BES analysis and FISH data. If the gibbon clone spanning the reciprocal homologous syntenic block break of the same rearrangement was available, it was reported in the “reciprocals” column. The "Interval" column reports, for the splitting human BACs, the homologous syntenic block break interval (see Supplemental Table 2). The last column reports other biological annotation.