GEDmatch

Hard Breaks Checked for cM (2.0) if GAP is greater than 500000 Basis Pairs.

Segment threshold size will be adjusted dynamically with an average of 208 SNPs. About 2/3 will occur between 191 and 225.
Mismatch-bunching Limit will be adjusted to 60 percent of the segment threshold size for any given segment.

Chr 1

Image size reduction: 1/24

Chr 2

Image size reduction: 1/24

Chr 3

Image size reduction: 1/20

Chr 4

Image size reduction: 1/17

Chr 5

Image size reduction: 1/18

Chr 6

Image size reduction: 1/20

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
7	135,013,131	152,318,718	27.8	1,809	198	119	0.19

Chr 7

Image size reduction: 1/16

Chr 8

Image size reduction: 1/17

Chr 9

Image size reduction: 1/15

Chr 10

Image size reduction: 1/16

Chr 11

Image size reduction: 1/15

Chr 12

Image size reduction: 1/15

Chr 13

Image size reduction: 1/11

Chr 14

Image size reduction: 1/10

Chr 15

Image size reduction: 1/10

Chr 16

Image size reduction: 1/10

Chr 17

Image size reduction: 1/9

Chr 18

Image size reduction: 1/9

Chr 19

Image size reduction: 1/6

Chr 20

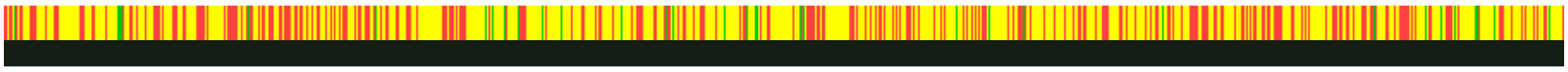

Image size reduction: 1/9

Chr 21

Image size reduction: 1/5

Chr 22

Image size reduction: 1/5

Largest segment = 27.8 cM

Total Half-Match segments (HIR) 27.8cM (0.775 Pct)
Estimated number of generations to MRCA = 4.5

1 shared segments found for this comparison.

289347 SNPs used for this comparison.

52.396 Percent of SNPs are full identical.

Comparison took 0.296.
CPU time used: 0.042.

Ver: Feb 25 2025 05 48 47