GEDmatch

Comparing Kit AA2746231 (*LR) [Ancestry] and Kit A148500 (*cgpittman) [Migration - F2 - A]

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: 1/33

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
2	16,251,998	25,714,916	11.8	1,423	184	110	0.24

Chr 2

Image size reduction: 1/34

Chr 3

Image size reduction: 1/28

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
4	140,643,322	155,007,625	14.1	1,574	220	132	0.23

Chr 4

Image size reduction: 1/25

Chr 5

Image size reduction: 1/26

Chr 6

Image size reduction: 1/27

Chr 7

Image size reduction: 1/23

Chr 8

Image size reduction: 1/23

Chr 9

Image size reduction: 1/20

Chr 10

Image size reduction: 1/23

Chr 11

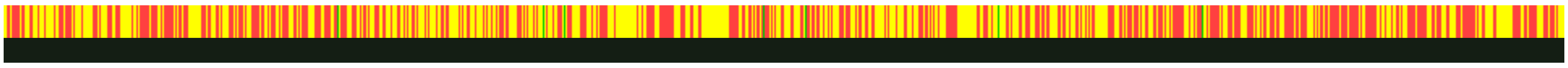

Image size reduction: 1/21

Chr 12

Image size reduction: 1/21

Chr 13

Image size reduction: 1/16

Chr 14

Image size reduction: 1/14

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
15	27,417,670	29,710,092	7.2	361	215	129	0.33

Chr 15

Image size reduction: 1/14

Chr 16

Image size reduction: 1/14

Chr 17

Image size reduction: 1/13

Chr 18

Image size reduction: 1/13

Chr 19

Image size reduction: 1/9

Chr 20

Image size reduction: 1/12

Chr 21

Image size reduction: 1/7

Chr 22

Image size reduction: 1/7

Largest segment = 14.1 cM

Total Half-Match segments (HIR) 33.1cM (0.924 Pct)
Estimated number of generations to MRCA = 4.4

3 shared segments found for this comparison.

411868 SNPs used for this comparison.

52.062 Percent of SNPs are full identical.

Comparison took 0.291.
CPU time used: 0.041.

Ver: Feb 25 2025 05 48 47