

GEDmatch

Individual marker indications:

Base Pairs with Full Match
Base Pairs with Half Match
Match with Phased data
Base Pairs with No Match

Validity of segments:

SNP Density 0 to 0.5. Darker blue means higher density.
Large gap between adjacent SNPs
No Match

Comparing Kit AA2746231 (*LR) [Ancestry] and Kit M296042 () [Migration - V4 - M]

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	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	

Largest segment = 27.8 cM

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

1 shared segments found for this comparison.

289347 SNPs used for this comparison.

To get full identical SNP percentage, please run this tool with graphics.

Comparison took 0.037.
CPU time used: 0.024.

Ver: Feb 10 2025 11 24 20