

Comparing Kit TF4905650 (julian land) [Ancestry] and Kit AM6017925 (Edmund.Barrow) [Ancestry]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
2	217,856,966	219,562,675	3.6	316
7	4,893,679	6,591,796	3.1	298
12	52,795,587	54,893,027	3.2	410
13	111,485,002	112,634,065	3.4	268
14	101,361,878	103,232,425	4	333
16	16,280,921	19,243,587	5.8	427
17	9,373,816	9,967,513	3.2	209
19	46,938,483	49,083,493	4.8	418

Largest segment = 5.8 cM

Total Half-Match segments (HIR) 31.2cM (0.869 Pct)

Comparing Kit TF4905650 (julian land) [Ancestry] and Kit NB5414371 (John L Griffiths) [23andMe]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
8	59,921,413	62,967,144	3.4	287

Largest segment = 3.4 cM

Total Half-Match segments (HIR) 3.4cM (0.095 Pct)

Comparing Kit AM6017925 (Edmund.Barrow) [Ancestry] and Kit NB5414371 (John L Griffiths) [23andMe]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
4	145,195,649	149,435,731	4	320
4	157,594,988	161,795,832	3.3	272
5	169,348,810	170,600,883	3.4	206
6	14,030,470	16,007,935	3.5	250
9	136,563,926	137,788,134	7	253
20	17,178,434	19,060,513	3	260
21	36,816,352	38,721,309	4.1	229

Largest segment = 7 cM

Total Half-Match segments (HIR) 28.3cM (0.789 Pct)

Comparing Kit NB5414371 (John L Griffiths) [23andMe] and Kit M920426 (E Randol Schoenberg) [Migration - V3 - M]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
9	14,538,577	16,237,822	3.4	451
12	19,872,822	21,567,793	3.1	473
13	111,360,585	112,517,079	3.4	260
20	7,953,919	9,364,463	3.2	368
21	36,677,687	37,824,911	3.1	212

Largest segment = 3.4 cM

Total Half-Match segments (HIR) 16cM (0.447 Pct)

Comparing Kit NB5414371 (John L Griffiths) [23andMe] and Kit T456608 (Ronald Schoenberg) [Migration - F2 - T]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
1	98,481,750	101,753,101	3.2	318
7	144,991,291	147,641,383	3.5	247
9	120,249,201	122,390,205	3.2	252
17	4,151,820	5,750,112	3.5	242
17	52,137,105	54,588,899	3.8	278
19	5,311,412	6,690,771	3.2	201

Largest segment = 3.8 cM

Total Half-Match segments (HIR) 20.3cM (0.566 Pct)

Comparing Kit NB5414371 (John L Griffiths) [23andMe] and Kit M015511 (Barbara Zeisl) [Migration - V3 - M]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
2	16,035,256	18,037,140	3.7	338
6	1,607,603	2,602,357	3.1	235
15	100,327,067	101,649,182	4	367

Largest segment = 4 cM

Total Half-Match segments (HIR) 10.8cM (0.302 Pct)

Comparing Kit NB5414371 (John L Griffiths) [23andMe] and Kit M896686 (Marlena Fejzo) [Migration - V4 - M]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
2	11,259,067	12,679,433	3.7	264
5	149,638,360	150,956,785	3.1	304
6	211,941	1,098,413	3.1	248
6	1,620,037	3,071,913	4.2	362
20	7,953,919	9,364,463	3.2	354

Largest segment = 4.2 cM

Total Half-Match segments (HIR) 17.2cM (0.48 Pct)

Comparing Kit TF4905650 (julian land) [Ancestry] and Kit M896686 (Marlena Fejzo) [Migration - V4 - M]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
1	76,397,972	80,416,562	3.4	432
1	115,882,541	118,909,283	3.3	309
2	220,155,834	222,105,363	3.7	228
9	37,036,247	39,184,065	3.2	233

Largest segment = 3.7 cM

Total Half-Match segments (HIR) 13.6cM (0.379 Pct)

Comparing Kit AM6017925 (Edmund.Barrow) [Ancestry] and Kit M920426 (E Randol Schoenberg) [Migration - V3 - M]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
2	238,829,613	240,739,225	6.4	389
7	137,956,892	139,486,394	3.4	269

Largest segment = 6.4 cM

Total Half-Match segments (HIR) 9.8cM (0.273 Pct)

Comparing Kit T456608 (Ronald Schoenberg) [Migration - F2 - T] and Kit M015511 (Barbara Zeisl) [Migration - V3 - M]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
1	30,885,525	34,156,533	4.2	693
1	71,325,299	76,745,026	3.3	956
1	205,470,836	210,527,418	7.2	1,213
1	236,095,773	237,165,077	3.4	341
3	185,574,131	186,984,518	4.3	429
4	169,685,036	173,920,304	4.2	688
6	42,267,031	43,751,359	3.4	301
8	56,550,203	61,849,086	6.3	1,134
8	128,603,409	131,642,423	4.6	769
11	79,366,322	82,370,960	3.2	865
12	9,494,051	12,727,200	5.9	917
12	62,279,661	68,485,984	7.7	1,470
12	82,406,506	89,445,539	3.4	991
12	92,822,306	95,101,402	3.6	665
12	95,126,798	102,020,446	8.3	1,795
14	99,654,322	101,356,010	4.4	428
15	27,518,429	29,338,502	6	293
15	32,245,584	33,567,517	3.8	346
16	943,107	2,125,788	3.6	351
16	78,877,418	79,396,836	4.1	349
17	8,765,412	9,981,026	5.8	406
18	6,104,755	8,432,545	10.8	767
18	59,019,891	60,820,571	3	492
18	71,889,999	73,483,409	5	514
20	48,662,582	51,911,199	5.8	963
22	37,077,364	37,674,547	3.2	228

Largest segment = 10.8 cM

Total Half-Match segments (HIR) 128.4cM (3.58 Pct)

Comparing Kit TF4905650 (julian land) [Ancestry] and Kit M920426 (E Randol Schoenberg) [Migration - V3 - M]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
1	16,277,647	18,335,916	3.7	352
1	57,203,501	58,825,601	3.1	386
9	86,744,475	89,142,905	3.5	448
12	5,712,164	7,249,598	3.6	348
15	46,619,110	49,247,520	3.4	430
15	97,706,696	98,646,496	3.4	236
21	36,679,830	37,809,408	3	203
22	20,795,757	22,521,158	3.4	252

Largest segment = 3.7 cM

Total Half-Match segments (HIR) 27.1cM (0.757 Pct)

Comparing Kit TF4905650 (julian land) [Ancestry] and Kit T456608 (Ronald Schoenberg) [Migration - F2 - T]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
1	76,443,585	81,282,173	4.3	716
4	183,143,114	184,283,411	3.8	257
9	136,043,270	137,104,155	3.7	254
15	46,630,941	49,247,520	3.4	402
16	59,578,821	62,312,517	3.1	322
18	60,050,641	61,425,379	3	270
19	46,948,243	48,564,927	3.1	268

Largest segment = 4.3 cM

Total Half-Match segments (HIR) 24.3cM (0.677 Pct)

Comparing Kit TF4905650 (julian land) [Ancestry] and Kit M015511 (Barbara Zeisl) [Migration - V3 - M]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
1	25,406,674	29,181,525	3.1	346
1	57,291,520	59,330,863	4	445
2	220,337,196	222,681,528	4.4	455
17	14,282,778	14,854,669	3.2	203
22	18,520,582	19,730,592	3.2	218

Largest segment = 4.4 cM

Total Half-Match segments (HIR) 17.9cM (0.499 Pct)

Comparing Kit AM6017925 (Edmund.Barrow) [Ancestry] and Kit M015511 (Barbara Zeisl) [Migration - V3 - M]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
2	8,630,749	9,909,114	3.4	202
6	43,911,551	45,520,572	3.4	278
7	5,416,248	7,163,442	3	219
17	31,979,473	33,714,452	4.1	414
19	29,749,444	31,751,259	4	223

Largest segment = 4.1 cM

Total Half-Match segments (HIR) 17.9cM (0.498 Pct)

Comparing Kit AM6017925 (Edmund.Barrow) [Ancestry] and Kit M896686 (Marlena Fejzo) [Migration - V4 - M]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
2	72,136,328	75,138,842	4.1	214
2	236,970,210	240,957,801	9.3	572
3	128,427,739	132,642,627	3.3	330
6	40,560,797	42,123,052	3.3	251
6	158,422,080	160,687,866	3.6	306
7	137,647,262	139,473,243	4.1	223
17	31,920,154	33,516,594	4	286
22	23,623,284	25,294,369	3.5	200

Largest segment = 9.3 cM

Total Half-Match segments (HIR) 35.2cM (0.981 Pct)

Comparing Kit AM6017925 (Edmund.Barrow) [Ancestry] and Kit T456608 (Ronald Schoenberg) [Migration - F2 - T]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 3.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
2	238,829,613	240,970,422	7	411
5	2,538,080	3,581,760	3.1	378
6	39,911,241	41,371,118	3	293
8	139,781,866	141,281,899	4	400
13	104,629,909	105,619,268	3	225
17	8,792,029	9,625,559	3.7	209

Largest segment = 7 cM

Total Half-Match segments (HIR) 23.7cM (0.662 Pct)