

Table 1. Examples of Individual Specific Recombination Active Regions in P0

Chr	Start	End	Size (kb)	P0 Events	deCODE Male (cM)/p Value ^a	HapMap Sex-ave (cM)/p Value ^a	P0 Activity by Allelic PCR (cM)	P0 Activity by 2 Loci Typing (cM)
2 Mb Sliding Window Scanning (66 Comparisons)								
20	58,753,528	59,651,027	897	12	0/< 4.7 × 10 ⁻¹⁵	3.3753/3.8 × 10 ⁻³	—	—
10	20,012,520	21,553,899	1541	6	1.175/0.049	0.7817/5.7 × 10 ⁻³	—	—
11	132,525,133	133,419,195	1393	14	3.97 ^b /9.5 × 10 ⁻⁴	2.3364/1.9 × 10 ⁻⁶	—	—
P0 Self-Overlapping Sets (324 Comparisons)								
16	7,988,699	7,990,230	1.5	2	0.12/1.00	0.0407/0.21	0.77	0.84
9	1,864,696	1,868,831	4.1	2	0.019 ^b /0.05	0.1090/1.00	—	0.81
20	58,753,528	59,651,027	897	12	<1 × 10 ⁻⁶ /< 1.5 × 10 ⁻¹²	3.3753/0.019	—	—
15	21,445,700	21,732,000	286	3	<1 × 10 ⁻⁶ /< 1.5 × 10 ⁻¹²	1.2007/1.00	—	—
Non-Hot-Spot Overlapping^c (135 Comparisons)								
3	197,249,108	197,250,198	1.1	1	0.0035 ^b /1.00	0.0027/0.33	ND ^d	—
4	18,404,324	18,406,601	2.3	1	<1 × 10 ⁻⁶ /< 1.2 × 10 ⁻⁴	0.0072/0.88	1.0	1.2

See also Figure S2.

^ap value calculated as the chance of expecting equal or more recombination events from historical data than in P0 from 91 meioses using binomial statistics; further adjusted with Bonferroni correction.

^b2002 deCODE data.

^cOnly showing those with sperm typing results.

^dRecombination activity not detected in P0.