

Supplementary Material for the article:Mishmar et al., *Human Mutation* 23: 125-133, 2004.**Mitochondrial DNA-like Sequences in the Nucleus (NUMTs): Insights into our African Origins and the Mechanism of Foreign DNA Integration**

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Supplementary Table S1: List of studied NUMTs*

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
1p36.3 (1C)	R {39%GC}	GA_x5J8B7P0VAE:1..500000 Also in GenBank: AL663100.12	402617-402926 403225-403024 403234-403437	82	<i>AluY</i> 910-1123 <i>Charlie4a(Mer1)</i>
1p36.3 (1D)	R {50%GC}	GA_x5J8B7P0VAE:4000001..4500000 Also in GenBank: AL356693.37	134519-134728	90	2466-2675
1p36.3 (1B)	R {45%GC}	GA_x5J8B7P0VAE:1000001..1500000 Also in GenBank: AL139415.10	67560-67686 67760-67922 67938-68046 68227-68065 68234-68291 68292-68600 68601-68612 68613-68738 68739-68962	89	<i>L2(np2481-2611)</i> <i>AluSx</i> <i>L2(np2725-2833)</i> 8040-8202 <i>LTR16A(np442-385)</i> <i>AluSc</i> <i>LTR16A(np385-373)</i> <i>L1PB2</i> <i>LTR16A(np374-145)</i>
1p34.3 (1D)	R {43.5% GC}	GA_x5L2HTVAVSK:8500001..9000000 Also in GenBank: AL513220.9	488658-488731	100	8934-9007
1p32 (15q26) (1A)	R (R) {38%GC}	GA_x54KRE9971S:1..3319 AL645730.10	2-358 364-751 77023-77460 77459-77868 77874-78236	78 77	4666-5022 <i>L1Pa15</i> <i>L1PA5(np5360-5801)</i> 4612-5022 <i>L1PA5(np5782-6133)</i>
1p31 (1C)	G {35% GC}	GA_x5HB7VCJ5FA:3500001..4000000 Also in GenBank: AC096951.2	467872-467706 467904-467988	89	16401-16567 <i>LIME</i>

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			58350-58558 58612-59265 59337-59470 59607-59910 59910-60877	70 69	(NC_001821.1 armadillo mtDNA) <i>AluJb</i> 9921-10579 <i>FLAM_A(Alu)</i> <i>AluJb</i> 10915-11904 (blue whale mtDNA NC_001601.1) <i>AluSx</i> (CAAAA) <i>n</i> 12032-12340 12665-12897 (NC_001602.1 mtDNA of the gray seal) <i>XM_015980.4 (Human 16.7Kd protein-removed from GenBank)</i> (CAG) <i>n</i> <i>FLAM_C(Alu)</i> (A) <i>n</i> 12586-12653 <i>AluSx</i> 12639-12875
			60882-61158 61164-61193 61190-61485 61485-61693	72 67	
			61703-62490	73	
			62052-62075 62508-62625 62639-62666 62689-62756 62757-63055 63052-63280	78 72	
1p11 (1B)	Centromere {39% GC}	AC022192.3	103004-103534 103535-103832 103833-103886 104418-103878 104487-104441 105835-104485 105846-106807 106584-106643 106810-107498	82 80 74 73	<i>SATRI(np969-492)</i> <i>AluY</i> <i>SATRI(np492-1)</i> 987-1534 15042-15087 5604-6979 9394-10319 (TA) <i>n</i> <i>SATRI(np779-1)</i>
1q12 (1B)	Grey {42% GC}	GA_x54KRE8AV33:1..500000 Also in GenBank: AC068398.3	79526-79415 14706-15623 16596-15626 15791-15850 16595-17950 18017-18555 18548-18581NNN	88 74 74 83	6870-6981 <i>SATRI(np1-1028)</i> 9386-10319 (TA) <i>n</i> 5596-6979 987-1526 <i>SATRI(np216-250)</i>
1q24 (1C)	G {40% GC}	GA_x54KRE8EL5L:6500001..7000000 Also in GenBank: AL160059.7	290898-291033 291093-291486 291598-291644 291662-291724	76	<i>MIR(np82-226)</i> 12143-12536 <i>MIR(np216-262)</i> <i>MIR3</i>

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
1q43 (1B)	G {39% GC}	GA_x5J8B7NYNCY:4000001..4500000 Also in GenBank: AL590396.13	299067-309581 42076-42201 42298-42371 48098-42476 48101-48143 48613-48705 49016-48776 53428-49033	81 78 70 72	12562-6189 <i>MER117(Mer1_type)</i> <i>MIR</i> 573-6196 <i>(TA)n</i> <i>(CGTG)n</i> 12-244 12156-16563
1q43 (1B; 1A)	G {43% GC}	GA_x5J8B7NYNCY:6500001..7000000 Also in GenBank: AL451068.13	219597-224583 241914-241006 112001-112272 112298-112442 112436-113344 113336-113344 113345-113426 113427-113469 129666-129714 129744-129801 134797-129811 134814-135001	74 71 71 74	9771-14799 14796-15722 <i>AluJo</i> <i>THE1b(LTR/MaLR)</i> 14796-15722 <i>(CATATA)n</i> <i>LIPA17</i> <i>(CATATA)n</i> <i>Alu</i> <i>AluSx(np290-233)</i> 9771-14799 <i>AluSx(np249-62)</i>
2p22 (1D)	G {34% GC}	GA_x5L2HTTHY8E:16000001..16500000 Also in GenBank: AC007317	396385-396225	88	956-1124
2p16 (1B)	G {36% GC}	GA_x5L2HTTHY8E:6500001..7000000 Also in GenBank: AC009234	100787-100839 100849-101082 101089-101816	83	<i>MIR</i> <i>AluJb</i> 6270-6998
2p12 (1D)	G {50% GC}	GA_x54KRE9UVK8:5500001..6000000 Also in GenBank: AC007400	100292-100187	90	2998-3103
2p11.2 (1D)	R {36%GC}	GA_x54KRE9UVK8:12000001..12500000 Also in GenBank: AC013262.7	193858-193617	87	7862-8103
2p11.1 Chromosome 2 centromere. (1B)	Grey {42% GC}	GA_x54KRE9YMAP:1..500000 Partly also in GenBank: AC097374.3	105901-105941 105942-106249 105250-105298 106830-106312 108276-106903 108307-109052 109055-109151 71005-71347 71348-71655 71656-71706 72236-71718 72305-72259	84 74 77 84 85	<i>SATR1(np221-188)</i> <i>AluY</i> <i>SATR1(np188-137)</i> 987-1511 5624-6973 9394-10138 <i>(TA)n</i> <i>SATR1(np761-448)</i> <i>AluY</i> <i>SATR1(np448-1)</i> 987-1511 15042-15087

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			73682-72309 73713-74458 74530-74557 74563-74670 <i>74686-75000</i>	74 77 92 86	5624-6973 9394-10138 9586-9513 hedgehog mtDNA (ND3) (NC_002080.1) 9640-9747 Pongo mtDNA (ND3)(NC_001646) and element found in several mitoch ESTs such as: BE809230 <i>SATRI(Satellite)</i>
2p11.1 (1E) [2p11.2 (1E)]	Grey {35% GC} R {36%GC}	GA_x54KRE9UVK8:1300001..1350000 Also in GenBank: AC098817.3	340061-345043 345086-345132 345209-345247 <i>345261-345345</i> 345340-345399 345425-345499 <i>345778-345919</i> 345951-346084 <i>18271-23253</i> <i>23265-23460</i> <i>23471-23555</i> 23635-23709 <i>23988-24129</i> <i>24161-24294</i>	71 87 92 92 73 85 71 64 73 85	11593-16569 15964-16011 Elephant_mtDNA (NC_000934.1) NC_001992.1 (tRNA-Thr)_Papio mtDNA <i>(CA)n</i> 15303-15361 NC_001992.1 (tRNA-Thr)_Papio mtDNA 336-404 <i>CT_Rich</i> 577-710 <i>11592-16567</i> Dloop_Hylobates (AF311721,np564-798) <i>(CA)n</i> 334-402 <i>CT_Rich</i> 575-708
2q13 (1B)	R {39% GC}	AC021029.5	<i>106001-</i> <i>106670</i> <i>107631-</i> <i>106673</i> <i>107650-</i> <i>108984</i> <i>109054-109573</i> <i>109587-109635</i> <i>109636-109939</i> <i>109940-110100</i>	74 73 85	<i>SATRI(np1-748)</i> 9394-10319 5612-6976 987-1511 <i>SATRI(np137-185)</i> <i>AluY</i> <i>SATRI(np185-345)</i>
2q13	R {36% GC; 36%	GA_x5J8B7P878N:1250001..1300000	<i>142984-143634</i>		<i>LIMda(np948-261)</i>

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
(1B; 1D)	GC}	Also in GenBank: NT_005445.2	<i>143635-143657</i> <i>143658-143821</i> <i>143848-143885</i> <i>149704-143891</i> <i>149758-149846</i> <i>150671-150541</i> <i>420047-419863</i> 1334852-1341636	81 83 85 71	<i>(TTG)n</i> <i>LIMda(np261-104)</i> <i>A_Rich</i> 596-6431 <i>(GAAA)n</i> 16434-16563 16444-60 16434-6431
2q14.1 (1E)	G {49% GC}	GA_x5J8B7P878N:9000001..9500000 Also in GenBank: NT_025657.1	<i>457963-457306</i> <i>458620-458165</i> <i>458621-458935</i> <i>460409-458940</i> <i>461968-460455</i> <i>461965-462269</i> <i>463589-462354</i>	76 74 74 74 75	13247-13907 12744-13215 <i>AluY</i> 11276-12755 9785-11318 <i>AluY</i> 8513-9755
2q14.1 (1B)	R {40% GC}	AC092107.5	<i>119501-119757</i> <i>119758-120050</i> <i>120051-120106</i> <i>120636-120118</i> <i>122041-120706</i> <i>122061-122792</i> <i>123797-123853</i> <i>123019-123300</i>	 84 75 78	<i>SATRI(np365-90)</i> <i>AluY</i> <i>SATRI(np90-38)</i> 987-1511 5613-6976 9394-10138 <i>(TA)n</i> <i>SATRI(365-49)</i>
2q14.2 (1C)	R {37% GC}	GA_x5J8B7P878N:3500001..4000000 Also in GenBank: AC097499.3	<i>369964-370282</i> <i>370761-370342</i> <i>371241-371470</i> <i>371476-371506</i> <i>371577-371548</i> <i>371779-371713</i> <i>372064-371795</i>	79 93 81 74	<i>AluY(np1-308)</i> 575-998 <i>AluY(np78-308)</i> <i>(TACG)n</i> 206-235 11-76 16295-16563
2q21 (1C)	R {46% GC}	GA_x5L2HTVCF7A:1..849 GA_x5HB7VCBQU9:1..1119 Also in GenBank: AC068137.8	<i>1-849</i> <i>9-834</i> <i>132507-132960</i> <i>144506-132985</i> <i>144530-145614</i> <i>145767-</i> <i>145637</i> <i>145920-</i> <i>145777</i> <i>145755-</i> <i>145656</i>	75 83 75 72 76 75	10005-10859 11400-12340 <i>LTR22A(LTR/ERVK)</i> 3799-15398 <i>MER11C(LTR/ERVK)</i> 3646-3781 15391-15534 3658-3762
2q21 (1E)	R {34% GC}	AC023928.3	<i>170802-166248</i> <i>164545-163578</i> <i>171679-171304</i>	76 76 78	576-5176 5175-6145 16434-239

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			nnn42178-41588 50073-49739nnn 50062-50424 50543-51763 56328-51773 56857-56826 57335-57076 57059-57009	78 73 76 88 73 84	5555-6145 5171-5550 <i>Tigger3(Mer2_type)</i> <i>LIPA5</i> 575-5176 212-245 16304-16562 11-60
2q21 (1C)	R {46% GC}	<u>AC073869.5</u>	42849-43304 48023-43328 48079-48175 48170-53733 53734-53825 53804-53875 57969-53893 60565-57970 60730-60587	74 73 78 75 77 78	<i>LTR22A(LTR/ERVK)</i> 10657-15398 <i>LIPA3(np2-98)</i> <i>LIPA3(np617-6176)</i> 10612-10515 6534-6461 6380-10519 3658-6262 15391-15534
2q22 (1C)	G {37% GC}	GA_x5L2HTTEENY:37500001..38000000 Also in GenBank: <u>AC013437.8</u>	142893-144860 145191-151891 152654-154239 155376-155586 62497-62987 63264-63054 63277-64402 65986-64401 66733-66483 73449-66749 73449-73742 73713-73750 75747-73780	71 73 80 76 76 80 67 73 71	7754-9764 9841-16565 577-2173 2181-2393 <i>MaLR</i> 2179-2391 <i>ERV1</i> 575-2171 11-258 9840-16563 <i>Alu</i> <i>(A)n</i> 7753-9763
2q22 (1C)	G {36% GC}	<u>AC018856.4</u>	[6016-4049] [3720-4013] [3719-3249] 96990-103198 103214-103464 103961-105546 105545-105819 105837-106347 106348-106445 106447-106670 106683-106893 106960-107450	[71 [76 73 67 80 76	[7753-9763] <i>[AluSp]</i> 9840-10310 10334-16563 11-258 575-2171 <i>LTR12c(ERV1)</i> <i>LTR12c(ERV1)</i> <i>LTR30(ERV1)</i> <i>LTR12c(ERV1)</i> 2179-2391 <i>MLTID(LTR/MaLR)</i>
2q22 (1C)	R {35% GC}	<u>AC092156.2</u>	83126-82156 89379-84826	76 76	5171-6145 575-5176

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			86615-86977 87096-88316 89908-89877 90110-90060 90386-90127 90468-90490	88 84 73	<i>Tigger3(Mer2-type)</i> <i>LIPA5</i> 212-245 11-60 16304-16562 <i>AT_Rich</i>
2q23.3 (1B; 1D)	R {41% GC; 42% GC}	AC016147.12 AC068744.2	74609-75000 74383-74442 73640-74380 73620-72285 72215-71826NNN 36373-36452	77 75 84 86	<i>SATRI(np443-1)</i> <i>(TA)n</i> 9394-10138 5613-6976 987-1394 4145-4223
2q23 (1A)	R {38% GC}	GA_x5L2HTTEENY:3300001..33500000 Also in GenBank: AC069333.8	478501-479035 479114-479031 479127-479520	90	<i>L1(np2133-2687)</i> 2771-2856 <i>L1(np2679-3074)</i>
2q23 (1D; 1C)	R {41%GC}	GA_x5L2HTTEENY:3150001..32000000 Also in GenBank: AC105402.5 AC016763.8	363905-364036 422463-422907 423085-422960 423178-423487 22517-22386 38351-38226	98 74 98 73	611-742 <i>LIMC5</i> 16444-16563 uSq 611-742 16444-16563
2q23 (1C; 1D)	R {35% GC}	AC092662.2	81362-81487 82927-81581 129202-132489	81 73	<i>GA_Rich</i> 4848-6196 11801-15087
2q32 (1D)	G {37% GC}	GA_x5L2HTTEENY:1000001..1500000 Also in GenBank: AC062033.2	60027-60472	80	823-1270
2q34 (1E; 1B)	G {38% GC; 44% GC}	GA_x54KRE9S8TU:6500001..7000000 Also in GenBank: AC007282.4 and in AC007283.3	239630-236921 21003-21509 21515-24224 24224-24271 24272-24576 24577-25020 70534-69382 70626-70955 70985-71284 71889-71287 71990-72279 74391-72288 74445-74726 74788-74953 74945-75237	75 75 69 68 67 69	10412-13131 <i>LIMA6(np4890-5391)</i> 10412-13131 <i>LIMA6(np5294-5440)</i> <i>AluSx</i> <i>LIMA6(np5440-5891)</i> 12427-13617 <i>AluSx</i> <i>AluY</i> 11705-12323 <i>AluSx</i> 9495-11610 9743-9441 (NC_001602.1 – Whale mtDNA) <i>Tigger2(Mer2type)</i> <i>Tigger2(np855-554)</i>

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			181472-181417 181533-181478 181594-181539 181655-181600 181715-181661 183055-181783 183350-183118 183412-183846	92 89 92 92 89 73 74	13048-13103 13048-13103 13048-13103 13048-13103 13049-13103 11797-13103 10087-10319 <i>MLT2A1(ERV/LTR)</i>
3p21 (2B)	R {43% GC}	AC027471.3	2480-2643 2646-3000 30697-30192 30712-30862	75 79	10152-10319 <i>SATRI(Sattelite)</i> 9485-9991 <i>AluJo</i>
3p21 (1A)	R (35% GC)	GA_x54KREA3PFF:2500001..3000000 Also in GenBank: AC092796.2	355138-355374 355374-355737 355723-355972 355974-356521 55231-54979	 79 79	<i>CT_Rich</i> <i>Tigger1(Mer2_Type,np1</i> <i>26-495)</i> 10428-10598 <i>Tigger1(Mer2_Type,np4</i> <i>83-1036)</i> 10394-10643
3p11 (1A)	Grey (46% GC)	GA_x54KREACQDQ:2500001..3000000 Also in GenBank: AC104435.2	149655-149748 149978-149750 149983-150188	82	<i>AluSx(np2-95)</i> 9137-9366 <i>AluSx(np84-297)</i>
3p11 (1D; 1C)	Grey (37% GC)	GA_x54KREACQDQ:6500001..7000000 Also in GenBank: AC096922.2	55542-55514 66559-66711 66781-67011 67012-66937 67118-67080 112868-113026 113099-113024 113205-113145 101629-101601	100 84 96 81 83 96 81 100	12612-12640 <i>MIR(SINE)</i> 3058-3217- -4354-4429 16086-16124 3058-3216 4354-4429 16086-16146 12612-12640
3q11.1 (1C)	Grey (35% GC)	GA_x54KREA92UK:500001..1000000 Also in GenBank: NT_022497.2	59565-60002 60024-63267	72	<i>MLT1C(LTR/MaLR)</i> 6027-9316
3q11.1 (1D; 1A)	Grey (36% GC; 37% GC)	GA_x54KREA9LET:2500001..3000000 Also in GenBank: AC024033.4 AC106717.2	151358-151223 299655-299511 109719-111040 77443-78220 78219-78367 78371-78423 78425-78849	97 84 94 84	(NNN)2583-2718 6535-6679 1396-2718 <i>LIM4b(np1524-694)</i> 6535-6683 <i>LIM4b(np675-623)</i> <i>LIM4</i>
3q12 rearrange? (1A)	R (37% GC)	GA_x5HB7VCG0V5:18500001..19000000 Also in GenBank: NT_005496.2	306131-306539 304408-306086	 73	<i>LIPA14(np6096-5856)</i> 10660-12340 <i>AluSx</i>

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			304074-304325 303932-304066 303826-303847 301971-303929 301623-301342 301334-299405 299128-299362 298910-297704 298509-298534 296661-297697 296615-296661	74 78 70 75 74 78	(TCTA)n AT_Rich 8620-10582 576-858 12464-14370 5975-6204 3601-4816 AT_Rich 1020-2048 LIAP14(np6152-6105)
3q13.3 (1A)	G (35% GC)	GA_x5HB7VCG0V5:4500001..5000000 Also in GenBank: AC117472.3	474481-475255 475919-475253 475870-476521	81	LIP(np3608-2836) 7161-7773 LIP(np2839-2179)
3q25 (1A)	R (38% GC)	GA_x5L2HTULD24:26500001..27000000 Also in GenBank: AC016920.14	474877-474948 474951-475165 475237-475545 475550-475615 103487-103875	90 83 85	L2(np3168-3239) 1927-2141 2007-2316 L2(np3244-3309) 1925-2314
3q26.1 (1A; 1E)	G (31% GC both)	GA_x5L2HTULD24:32000001..32500000 Also in GenBank: AC104629.10	154501-154931 155212-154938 155384-155420 157099-155265 157121-157500 221842-221747 222594-222166 222598-222760 222761-222791 222792-222901 223082-222941 223086-227507 228289-227526	70 74 78 69 72 73	LIMB8(to_np5558) 11971-12245 AT_Rich(lowcomplx) 9110-10897 LIMB8(np5591up) 1972-2067 1544-1968 AluJb (TTTA)n AluJb 1362-1503 LIPA2 612-1375
3q26.3 (mt jumped into ERVL) (1A)	G (40% GC)	GA_x5L2HTULD24:37500001..38000000 Also in GenBank: AC008134.3	13986-14218 14223-14510 14507-14729 14736-15001	86	ERVL(LTR,until np3487) MER1B 6708-6931 ERVL(LTR,np3485-up)
4p16.2 (1B; 1B)	G (41% GC; 43% GC)	AL137218.3 ; AL354697.5	92805-93072 93239-93296 93978-93299 94079-94373 127516-127816 127983-128039 128778-128043	78 78	SATRI (TA)n 9450-10138 AluJb SATRI (TA)n 9394-10138

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			128822-130132 130202-130721 130735-130785 130790-131081	74 85	5641-5976 987-1511 <i>SATRI</i> <i>AluY</i>
4p16 (1A)	R (38% GC)	GA_x54KREAGLJJ:4500001..5000000 Also in GenBank: AC093846.3	192003-192315 192922-192307 192907-193020	78	<i>LIPA15-16</i> 4613-5233 <i>LIPA15-16</i>
4p15.3 (1D)	G (41% GC)	GA_x54KREAGLJJ:7000001..7500000 Also in Genbank: AC110758.3	252506-252796	82	13098-13388
4p15.2 (1B)	R (45% GC)	AC092436.5	535091-534125 537262-535426 125342-125521 126510-125529 126510-126791 126796-126820 128672-126827	73 73 72 73	11303-12301 9446-11290 <i>MIR</i> 11288-12301 <i>AluSp</i> <i>(GAAA)n</i> 9440-11293
4p15.2 (1B)	R (36% GC)	GA_x54KREAGLJJ:17500001..18000000 Also in GenBank: AC093854.2	403112-403441 403595-403444	94	<i>THE1B(LTR/MaLR)</i> 2899-3050
4p11 (1D)	Grey (39% GC)	GA_x5J8B7PYEPE:4000001..4500000 Also in GenBank: AC104646.5	222720-222628	96	14981-15073
4q11 (1B)	Grey (35% GC)	GA_x5HB7VD3DQW:4000001..4500000 Also in GenBank: AC097648.2 (4q12-4q13 border)	416960-417229 417221-418565 418557-421763 422880-422641 422923-423040 423047-423101 423104-423241 102501-102680 102743-102885 102888-102938 102945-103062 103104-103343 103748-103426 107275-103738 108611-107267 108605-108874 108896-108999	78 77 79 79 67 77 78	<i>LIPB2</i> 9466-10836 13029-16238NNN 9169-9410 PB2 <i>(TG)n</i> <i>LIPB2</i> <i>LIP</i> <i>LIPB2</i> <i>(CA)n</i> <i>LIPB2</i> 9169-9410 110-426 13029-16569 9466-10836 <i>LIPB2</i> <i>LIP</i>
4q13 (1C;1B)	G (38% GC; 39 GC%)	GA_x5HB7VD3DJW:8500001..9000000 Also in GenBank: AC114801.4 ; AC093897.3	73577-73191 73663-73954 252640-252561 252643-252946 67450-67219 119200-119142	77 79 91 84	2090-2472 <i>AluSq</i> 15116-15197 <i>AluY</i> 2225-2456 15116-15174

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
4q21 (1B)	R (36% GC)	GA_x54KREAHVLE:6000001..6500000 Also in GenBank: AF163864	474626-475058 475104-475324 475318-475546	83	<i>MER6A(MER2type)</i> 2856-3075 <i>AluSc</i>
4q21 (1B)	R (34% GC)	GA_x54KREAHVLE:9000001..9500000 Also in GenBank: AC022317.8	426685-427500 427515-427588 427609-427880	80	2790-3590 <i>(TATAG)n</i> <i>L3</i>
4q26 (1E)	G (35% GC)	GA_x54KREAHVSH:2000001..2500000 Also in GenBank: NT_031781.1 Hs4_31952 (and in NT_022790.2)	119849-117281 119867-119907 120257-120138 119900-120138 120706-120482 120787-120723	78 64 68 76	575-3161 f_Rich 357-456 <i>Rpt(unknown)</i> 11-239 16498-16562
4q28 (1B)	G (40% GC)	GA_x54KREAK5QS:8500001..9000000 Also in GenBank: AC108045.3	123489-123788 124184-123813 124184-124444	85	<i>AluSx</i> 2008-2388 <i>AluSp</i>
4q32 Or 4q31.3 (1B)	G (37% GC)	GA_x5HB7VCDYHN:9500001..10000000 Also in GenBank: AC097526.3	236199-236325 236325-251172 242039-242062 246104-246125 247575-247622 251191-251521 57021-42198	75 77	<i>LIMC1</i> 664-15579 <i>AT_Rich</i> <i>AT_Rich</i> <i>L2</i> <i>L1</i> 664-15555
4q34 (1D)	G (35% GC)	GA_x5HB7VCDYHN:2500001..3000000 Also in GenBank: AC114770.4	291362-291529	93	12250-12417
4q35 (1D)	R (35% GC)	GA_x5L2HTUQ8NL:5000001..5500000 Also in GenBank: AC018710.4	344671-344819	84	7625-7773
5p15.3 (1C)	R (43% GC)	GA_x5J8B7Q24ES:1500001..2000000 Also in GenBank: AC091967.3	332810-333758 333838-334354 105512-106508 106540-107055 107138-107169 107170-107448	79 79 78 79	6957-7908 6597-7111 6957-7956 6957-7111 <i>(TTA)n</i> <i>AluSq</i>
5p15.3 (1D; 1D)	R (39% GC; 38% GC)	GA_x5J8B7Q2FPT:5500001..6000000 Also in GenBank: AC034217.6 ; AC002087.1	99959-97535 97525-97275 96465-95981 96513-96788 301949-301904 301950-302012 302013-302321 101106-101151 63226-62742 64286-64036 66720-64296	71 70 81 87 87 81 70 71	14164-16569 11-259 596-1087 <i>AluY</i> 15978-16024 <i>MER4A(LTR/ERV1)</i> <i>MER4A(LTR/ERV1)</i> 15978-16024 596-1087 11-259 14164-16569

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
5p13 (1B)	R (35% GC)	GA_x54KREAPDRV:1..929 Also in GenBank: AC021965.3	1-567 602-885 88096-88166 88175-88949 88950-98058	82 87	L2 6117-6408 (TA)n L2 6117-15183
5p13 (1D)	G (39% GC)	GA_x54KREAR86K:500001..1000000 Also in GenBank: AC109579.1	23239-23724	82	3822-4308
5q13 (5q14) (1C)	G (39% GC)	GA_x5J8B7Q1L5Q:11500001..12000000 correspond to GenBank: AC022223.18 (Notice –no mtDNA in Cellera and later versions in GenBank)	78463-80811 80882-81255	93	No mtDNA! 341-2697 <i>MER6(Mer2_type)</i>
5q14 (5q15) (1C)	G (38% GC)	GA_x54KREANY7M:1..500000 Also in GenBank: NT_023290.2	70104-72088 72213-72535 172278-170294	78 78	5934-7908 L2 5934-7908
5q14 (1A)	G (38% GC)	GA_x54KREANQ9F:2000001..2500000 None in GenBank.	273474-273354 273001-274014	90	12662-12782 <i>BLACKJACK</i> (DNA/AcHobo)
5q14.3 (1B; 1B; 1C)	G (38% GC; 37% GC)	GA_x54KREAQK1W:1..551 And:GA_x54KREANNNA:1..551 Also in GenBank: AC013344.4 ; AC018806.4 ; AC093311.2	1-465 1-465 11801-12232 12275-12244 12371-12300 21402-21911 NNN22005-21916 137801-138206 138204-141663NNN NNN141771-141837 137957-141419	84 84 88 84 75 86 86	15576-16041 15576-16041 <i>MER21_C(LTR/ERV1)</i> 7970-8003 (NC_001794.1 macropus mtDNA) 8413-8484 <i>BLACKJACK (np1171- 1697_DNA/AcHobo)</i> NNN16024-16124 <i>BLACKJACK(np2131- 1689)</i> 12662-16124 <i>Tigger3(MER2_type)</i> 12662-16124
5q21 (1B)	G (37% GC)	AC112203.2	108930-109009 109072-109610 109604-115175 115349-117051 117227-117324 117349-117489	67 71	<i>MIR(SINE)</i> 13799-14336 <i>LIPA4(np567-6152)</i> 14330-16033 L2 <i>MIR</i>
5q21 (1C)	G (34% GC)	GA_x5J8B7Q1NA9:1..500000 Also in GenBank: AC114285.2	155846-155672 155879-156001 12843-13148 13180-13353	90 90	14658-14829 uSq <i>AluSx</i> 14658-14829

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
5q23 (1D)	G (35% GC)	GA_x54KREAQM8V:1500001..2000000 Also in GenBank: AC008565	398062-398392	79	383-708
5q31 (1B)	R (36% GC)	GA_x54KREAQM8V:4500001..5000000 Also in GenBank: AC026409.4	120001-120310 120335-120453 120934-121898 121911-122126 122127-122430 122431-122491 122492-122520	82 84	L1 128-251 574-1537 L1 AluSp L1 (TG)n
5q32 (1C; 1C)	G (42% GC)	GA_x5HB7VCVS5L:1500001..2000000 Maybe also in GenBank: AC008670.6	112506-112798 112799-113058 113117-113417 113531-113736 113753-114001 81071-81442 81443-81702 81728-86946 87059-87264 87281-87299	90 93	L2 AluY 15186-15487 MIR AluY L2 AluY 10269-15487 MIR AluY
6p25 (or 1p36?) (1D; 1D)	R (45% GC; 42% GC)	AL451141.13 ; Harbors AF035429 and AF134583 -NOTICE MAP DISCREPANCY); AL359496.30	56249-56062 93514-87666	77 97	8505-8692 3914-9755
6p21.2 (1B)	G (40% GC)	GA_x54KREAYBCL:2300001..23392619 Also in GenBank: AL731683.11	388984-389553 389606-390395 390397-390597 390598-390663	78	HERV FH19 (LTR/ERV1) 9096-9888 AluSp AluJ/FLAM
6q16 (1B)	G (34% GC)	GA_x54KREB0N5G:3000001..3500000 Also in GenBank: AL078595.12	195017-195724 195739-196076 196076-196408 196460-197040	83 71	LIMD4 4150-4487 15478-15811 LIMDa
6q16 (1A)	G (35% GC)	GA_x54KREB0N5G:5500001..6000000 Also in GenBank: AL132766.13	417001-417395 417408-417621- -417768-> -417869-> -417874-418211 418212-418920	81 85 88 85	LIP 6532-6745-> 10622-10474-> ->5521-5622-> -8774-8437 LIP
6q23 (1A; 1B)	R (37% GC; 40% GC)	GA_x5L2HTU8439:15500001..16000000 Also in GenBank: AL356774.13 AL137783.12	75481-75801 76051-75819 76066-76251 420120-420204 420168-420284 420288-420528 26992-27224	83 77 83	LIP 15395-15628 LIP AluJ/FRAM 15167-15283 AluSq 15395-15627

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			1542-1426	77	15167-15283
6q25 (1A)	R (31% GC)	GA_x54KREAVE16:6500001..7000000 Also in GenBank: AL603908.3	27053-27522 31637-27589 31624-31775	81	<i>PRIMA4_LTR(ERV1)</i> 7451-11649 <i>PRIMA4_LTR(ERV1)</i>
6q26 (1D)	G (43% GC)	GA_x54KREAVE16:3500001..4000000 Also in GenBank: AL158033.18	153511-153728	85	3163-3380
7p14 (1C)	G (28% GC)	GA_x5HB7VCTE59:1..151713 Also partly in GenBank: M11577	1237-1691 6414-1715 6470-7019	74	<i>LTR22A(LTR/ERVK)</i> 10657-15398 <i>LIP</i>
7p14 (1C; 1C)	G (43% GC; 41% GC)	GA_x5HB7VC7SEG:500001..1000000 Also in GenBank: AC069285.8 ; AC115220.1	433760-433822 433823-434034 434057-434133 434141-439261 439367-442626 441732-441752 442678-442793 157581-157646 157734-157780 65127-65343 65370-65410 65502-65576 100501-100697 100706-100794 100838-100953 100955-100985 101879-101899 104263-101004 104282-104374 109489-104369 109573-109497 109597-109808 109809-109871	83 75 76 86 90 76 75 83	(<i>CATATA</i>) <i>n</i> <i>AluSq/x</i> 3117-3191 3430-8634 8662-11973 <i>AT_Rich</i> <i>FLAM_C(SINE-alu)</i> 8758-8823 <i>ERV1</i> <i>Alu</i> 15673-15713 <i>Alu</i> <i>AluSq</i> <i>AluJ/Fram</i> <i>FLAMc/Alu</i> (<i>TAAA</i>) <i>n</i> <i>AT-Rich</i> 8662-11973 (<i>TTAA</i>) <i>n</i> 3430-8634 3117-3191 <i>AluSg/X</i> (<i>TATATG</i>) <i>n</i>
7p14 (1B; 1C)	G (44% GC)	GA_x5L2HTTW8W2:1..4474 Also in GenBank: AC099654.5 (NUMT in intron of XM_094983.1)	23-4437 39441-39717 41544-41565 39730-46937 46984-47805 47815-47865 47981-48049 48018-48320 48326-48384 58505-71204 64809-64830 68737-68759	74 74 69 88 74	9395-13830 <i>AluY</i> <i>AT_Rich</i> 8316-15614 15755-16569 11-60 <i>AluS</i> <i>AluJo</i> <i>LTR43(ERV1)</i> 3819-16563 <i>AT_Rich</i> <i>AT_Rich</i>

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			71220-71270 71386-71454 71486-71738 71740-71791	86	11-60 <i>AluS</i> <i>AluJo</i> <i>LTR43(ERV1)</i>
7p12 (1D)	G (42% GC)	GA_x5HB7VCL761:1..500000 Also in GenBank: AC004844.1	474538-474382	91	2418-2574
7q11.1 (1C; 1C; 1A)	Grey (43% GC; 43% GC; 45% GC)	GA_x5L2HTUEKN6:500001..1000000 Also in GenBank: AC006013 AC093655.4 The fragment 5385-5415 is not found in GenBank!	292891-293027 293025-293275 293277-293512 293554-293859 462330-462046 462010-461791 461198-461773 351571-351599 351457-351766 351768-352020 121403-121168 121789-121653 49026-48807 49346-49062	83 77 75 78 90 77 83 78 74	7175-7312 <i>AluY</i> 7303-7537 <i>AluY</i> 11122-11408 11307-11527 <i>LTR10A(LTR/ERV1)</i> 5385-5415 <i>AluJo (incl mt!)</i> <i>AluSx</i> 7303-7537 7175-7312 11307-11526 11122-11407
7q11.1 (1B)	Grey (40% GC)	GA_x5L2HTUEKN6:2000001..2500000 Also in GenBank: AC092100.5	27427-27449 27469-27614 27845-27613 27979-28208 29081-28224 29077-29371 30312-29373 30358-30695 31676-30696 31673-31974 32261-31976 32283-32379	70 72 78 74 74	(<i>TTG</i>) <i>n</i> <i>AluSp</i> 8510-8741 <i>MER9</i> 7515-8396 <i>AluY</i> 6594-7531 <i>AluY</i> 5513-6553 <i>AluY</i> 5239-5525 <i>AluS</i>
7q31.2 (1C)	R (40% GC)	GA_x54KREB2RL0:16000001..16500000 Also in GenBank: AC004112.2	46010-46133 49234-46300 49415-49501	73	(<i>TGGA</i>) <i>n</i> 13065-16031 <i>LIMB8</i>
7q32 (1A;1C)	R (40% GC; 43% GC)	AC004979.1 ; AC006362.2 (NUMT in intron of XM_069781)	54011-54360 54362-54743 58082-54754 58084-58390 58947-58386 58952-59108 59109-59231 59232-59500 127282-127113	75 82 81	<i>LIM4</i> <i>LI(np3416-3827)</i> 3292-6623 <i>AluY</i> 2740-3300 <i>LI(np3820-3980)</i> <i>THE1C</i> <i>THE1B</i> 12562-12731

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			<i>127331-127449</i>		<i>L2(np3151-3272)</i>
7q34 (1B)	R (38% GC)	GA_x54KREB2R4M:1..1991 Also in GenBank: AC119751.3	736-886 886-1546 <i>1549-1606</i> 1604-1689 <i>62497-61852</i> <i>61792-61626</i>	78 81 <i>79</i> <i>76</i>	<i>AluJo</i> 9471-10138 <i>(TA)n</i> 10149-10234 <i>9485-10138</i> <i>10149-10319</i>
7q36 (1A)	R (39% GC)	GA_x54KREB3J6B:1..500000 Also in GenBank: NT_007772.1	<i>237001-237096</i> <i>237097-237219</i> <i>237220-237376</i> 237381-237942 <i>237983-238244</i> 238246-241574 <i>241585-241966</i>	 82 75	<i>THE1C (LTR)</i> <i>THE1C (LTR)</i> <i>LIM4(3981-3820)</i> 2740-3300 <i>AluY</i> 3292-6623 <i>LIM4(3827-3416)</i>
7q36 (1C)	R (39% GC)	GA_x54KREB449V:1500001..2000000 Also in GenBank: NT_007914.8 Hs7_8071	<i>134579-134756</i> 134969-135064 <i>135102-135532</i>	 98	<i>AluSc</i> 1613-1708 <i>L2</i>
7q36 (1C)	R (39% GC)	GA_x54KREB44CJ:500001..1000000 Also in GenBank: U66061 , and NT_023640.7 Hs7_23796	<i>136985-137180</i> 137251-137485 137965-140485 <i>962121-962355</i> <i>962835-965355</i>	70 83 <i>71</i> <i>83</i>	<i>LIP</i> 11-243 576-3098 <i>11-243</i> <i>574-3096</i>
8q12 (1E)	G (40% GC)	AC022861.4	<i>124165-125492</i> <i>125490-128398</i> <i>125528-128398</i> <i>128401-128712</i> <i>128710-131724</i> <i>131734-131784</i> <i>132030-132064</i>	 73 73 74 71 86 88	<i>8510-9827</i> <i>11220-14157</i> <i>NC_000845.1 (Pig mtDNA)</i> <i>10659-13559</i> <i>AluSg</i> <i>13552-16569</i> 11-60 <i>334-367</i>
8p11.2 (1A)	R (39% GC)	AL355484.10 exist	<i>130019-130705</i> 130723-131257 131365-132716 <i>132735-132945</i> <i>132953-133000</i>	 75 78	<i>LIME1(np5127-5884)</i> 13931-14460 14675-16024 <i>LIME1(np5887-6096)</i> <i>Alu</i>
8p11.2 [mt]	R (38% GC; 38%	GA_x5L2HTU51L1:20000001..20500000	<i>306005-306112</i>		<i>LIME</i>

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
checked- overlap with L1!] (1B; 1A)	GC)	Also in GenBank: NT_007995.8 Hs8_8152	<i>306227-306466</i> <i>306468-306571</i> <i>306581-311714</i> <i>311786-312017</i> <i>312017-312052</i> <i>312050-312098</i> <i>312147-312361</i> <i>312363-312394</i> <i>312395-312490</i> <i>312495-313106</i> <i>313253-313494</i> <i>113009-112927</i> <i>112542-113479</i> <i>113480-113521</i>	77 70 75 87	<i>AluSx</i> <i>16469-16571</i> <i>11-5077</i> <i>MER6A</i> <i>U2 (snRNA)</i> <i>MER6A</i> <i>MER6</i> <i>(TG)n</i> <i>MER6</i> <i>5091-5721</i> <i>LIM3e</i> <i>12258-12341</i> <i>LIM4</i> <i>MLT2A2 (LTR)</i>
8p11.1 (1C)	Grey (39% GC)	GA_x5L2HTU51L1:23500001..24000000 Also in GenBank: AC124073.9	<i>87016-78068</i> <i>78069-78358</i> <i>78359-78576</i> <i>80689-78595</i> <i>80707-81000</i>	77	<i>LIME1</i> <i>AluSc</i> <i>LIME1</i> <i>13931-16024</i> <i>LIMD3</i>
8p21 (1A)	R (42% GC)	GA_x5L2HTU51L1:7500001..8000000 Also in GenBank: AC022559.12	<i>362272-362391</i> <i>362391-362601</i> <i>362565-362657</i>	84	<i>7slRNA (srpRNA)</i> <i>8666-8876</i> <i>7slRNA (srpRNA)(double checked!)</i>
8p22 (1D)	G (40% GC)	GA_x5L2HTU51L1:6000001..6500000 Also in GenBank: AC087821.5	<i>160141-160593</i>	79	<i>14793-15243</i>
8p23 (1C)	R (46% GC)	GA_x54KRE87YE8:1..347845 GA_x54KREB9DLL:1..184161 Maybe also in GenBank: NT_008292.9 Hs8_8449	<i>210763-211064</i> <i>211179-211324</i> <i>153112-152967</i> <i>153229-153530</i> <i>1333391-1333246</i>	87 87 88	<i>AluSx</i> <i>637-782</i> <i>637-782</i> <i>AluSx</i> <i>637-782</i>
8q11.1 (1C)	Grey (41% GC)	GA_x5L2HTV532K:500001..1000000 Also in GenBank: NT_023678.7 Hs8_23834	<i>346983-347305</i> <i>348237-347356</i> <i>351169-348362</i> <i>351171-351275</i> <i>351277-356125</i> <i>356249-356140</i> <i>359136-356765</i>	75 78 77 71	<i>BSR? (Satellite)</i> <i>4247-5134</i> <i>568-3480</i> <i>U6 snRNA</i> <i>LIPA4</i> <i>576-684-></i> <i>14346-239</i>
8q12 (1E)	G (39% GC)	GA_x5L2HTV532K:21500001..22000000 Also in GenBank: AC022861.4	<i>78730-77403</i> <i>77367-74498</i> <i>74185-74496</i> <i>74186-70829</i>	73 74 71	<i>8510-9827</i> <i>10659-13559</i> <i>AluSg</i> <i>13553-367</i>
8q13	R (36% GC)	GA_x5L2HTV532K:30500001..31000000	<i>122643-122999</i>		<i>LI</i>

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
(1B; 1C)		Also in GenBank: NT_008055.8 Hs8_8212	122642-122433 160794-160753 <i>160584-160672</i> <i>627858-628067</i>	86 83 86	1524-1734 8422-8459 <i>GA_Rich</i> 1524-1734
8q13 (1D)	R (34% GC)	GA_x5L2HTV532K:3000001..30500000 Also in GenBank: NT_008055.8 Hs8_8212	179380-179756	81	2288-2663
8q13 (1C)	R (41% GC)	GA_x5L2HTV532K:2650001..27000000 Also in GenBank: AC022893.6	<i>465481-465576</i> <i>465577-465888</i> <i>465991-466148</i>	86	<i>AluSg/x</i> <i>AluSg</i> 625-782
8q22 (1C)	R (34% GC)	GA_x5HB7VCY1B9:13500001..14000000 Also in GenBank: AC026827.6	<i>143041-143475</i> 143660-143577	98	<i>LIMEd</i> 14861-14944
8q23 (1C) 8q22	G (40% GC)	GA_x5HB7VCY1B9:17000001..17500000 Also in GenBank: NT_008136.2	227973-228083 228686-230354 <i>230450-230721</i> 230784-232697 <i>232702-232998</i> 233002-233119 <i>234101-234310</i> 234414-234850 <i>234956-235278</i> 235421-236623 <i>236789-237096</i> <i>237097-237130</i> 237116-237405 237508-237606 <i>237607-237902</i> <i>237903-238021</i>	71 69 69 81 75 70 71	16457-16565 583-2342 <i>AluJo</i> 2467-4370 <i>AluSx</i> 4366-4481 <i>AluJb</i> 5517-5960 <i>AluSx</i> 6095-7325 <i>AluSq</i> <i>(GAAA)n</i> 7449-7736 <i>Tigger1 (MER2 type)</i> <i>AluYa5</i> <i>Tigger1</i>
8q23 (1D)	G (31% GC)	GA_x5L2HTU3MBV:1..500000 Also in GenBank: AP002980.2	72337-72121 72851-72515	82 74	15008-15225 16297-60
8q24.3 (1D/1B)	R (43% GC)	GA_x54KREBBWRK:11500001..12000000 Also in GenBank: AC090821.13	NNN91476-92179 <i>35233-35309</i> <i>35310-35377</i> <i>35422-37239</i> <i>37252-37435</i>	83 76	5511-6214 <i>Alusp/q</i> <i>MLT1C</i> <i>4859-6678</i> <i>MIR</i>
9p24 (1E)	R (37% GC)	GA_x5L2HTUGAQ2:24500001..25000000 Also in GenBank: NT_008413.8 Hs9_8570	240790-241709 240689-234078 <i>233782-234079</i> <i>233270-233298</i> 233741-231859 <i>225743-231861</i> 225731-222065 222223-222191	69 76 73 74 88	13724-14701 1288-7947 <i>AluY</i> <i>AT_Rich</i> 7972-9891 <i>LIPA6</i> 9882-13588 15281-15315

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
9p24.3 (1A; 1C)	R (37% GC; 39% GC)	AL591968.4; AL512605.13	3011-3456 3658-3463 3658-3729 3742-3948 3947-4018 55474-55617 55778-55644	100 79	LIMB1(np5651-6101) 6225-6420 LIMB1(np6099-6168) Tigger3(np3004-2801) Tigger3(np97-2) (TA) _n 3757-3891
9p12 (1C; 1C; 1C)	G (44% GC; 41% GC; 43% GC)	GA_x5L2HTTPM0J:1..500000 [And GA_x54KRE8WC29:1..123045 and GA_x5L2HTUTQDW:1.191478 and GA_x5HB7VD8UY6:4500001..4887684 and GA_x5HB7VD8UY6:3000001..3500000] Also in GenBank: AL355377.25; AL356489.14; AL139113.21	270961-271056 271060-271561 271634-271856 272342-274865 123568-123870 124173-123902 1-264 268-773 843-1065 1551-4074 119364-119642 119783-120044	71 83 77 71 84 73	HSMAR1 (Meriner) P 11-235 574-3096 AluSx 16193-16479 HSMAR1 (Meriner) LIP 11-235 574-3096 AluSg 15515-15774
9q21 (1C)	G (37% GC)	GA_x5L2HTVCTL9:3000001..3500000 Also in GenBank: AL390788.15	406038-406108 405984-406406 24686-24616 24319-24741	76 77	7506-7573 LIME 7505-7572 LIM4
9q21 (1C; 1E, 1B) [1C]	G (36% GC; 38% GC; 40% GC)	GA_x5L2HTVCTL9:5000001..5500000 Also in GenBank: AL160267.17(NUMT in intron of XM_095995.3); AL592047.10	61066-62873 60798-61065 60376-60797 59310-59657 54239-54410 54567-54703 57137-54768 65086-63279 65088-65355 65776-65355 66842-66555 66545-66495 132676-133138 133240-133133	76 81 73 76 76 81 73 90 80	4397-6215 AluSg 583-1010 16306-60 MER3(Mer1_type) GA_Rich 4613-6990 4396-6214 AluSg 581-1008 16304-16569 11-60 MER115(AcHobo) 3811-3920
9q21 1B	G (39% GC)	GA_x5L2HTVCTL9:5500001..6000000 May correspond in GenBank to: AL160278.24	339481-340017 340530-340040 340547-341005 100443-100901 100917-101407 101431-101999	74 75	LIME(5710-5137) 13856-14352 LIME(3035-2570) LIME(np2570-3055) 13856-14352 LIME(np5137-5743)

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
9q22 (1C; 1E)	R (42% GC; 44% GC)	GA_x5L2HTTPLFK:2500001..3000000 Also in GenBank: AL157827.17 ; AL354751.7 {mtDNA insertion comprises most of the 2 nd intron of the gene XM_011798.1}	352194-352255 352049-351448 59881-59280 60025-60086 47875-48647 48648-48942 48943-50727	79 79 76 73	<i>LIME</i> 5443-6016 [contain a (G) _n /a X 5 insert] 5443-6016 <i>LIME</i> 9109-9888 <i>AluSp</i> 9880-11699
10p15 (1C)	R (39% GC)	GA_x54KRE8JUR1:2000001..2500000 Also in GenBank: AL354747.12	132826-132903 133078-133256 133285-133324	80	<i>MADE1</i> (<i>Mariner</i>) 13002-13184 (<i>TA</i>) _n
10p13 (1B)	R (37% GC)	AL353147.10	12067-12095 12125-12365 12523-12553 12565-13105 13451-13168 13448-14585 13583-14973	78 76 74	(<i>TA</i>) _n <i>LIME3A</i> <i>LIME1</i> 2305-2844 3226-3515 4179-5306 <i>LIMB7</i>
10p12 (1C)	G (41% GC)	GA_x5L2HTTFEJ9:6000001..6500000 Also in GenBank: AL139404.9	19074-19087 19088-19393 19394-19534 19673-19529 19698-20008	88	<i>AluSg/X</i> <i>AluSx</i> <i>AluSg/X</i> 2515-2659 <i>AluY</i>
10p12 (1B)	G (38% GC)	GA_x5L2HTTFEJ9:13000001..13500000 Also in GenBank: AL353147.10	129481-129808 129808-130031 131165-130028 131162-131445 132048-131508	74 76 78	<i>LIMA9</i> <i>LIMB7</i> 4179-5306 3226-3515 2305-2844
10p11.1 (1A; 1C)	Grey (37% GC;; 39% GC)	GA_x54KRE8L8BD:1..500000 Also in GenBank: AC018684.3 ; AL121927.24	403510-403657 403654-404041 406227-404070 101027-101378 101403-101458 101464-101568 101683-101567 101674-101817 86001-86073 86070-86457 88643-86486 88783-88997 60-820	77 80 77 82	<i>L1</i> <i>LIPA15-16</i> 1721-3875 <i>LIM4</i> (<i>TAA</i>) _n <i>MIR</i> (<i>np256-148</i>) 1345-1459 <i>MIR</i> (<i>np152-2</i>) <i>L1</i> (<i>np4028-3955</i>) <i>LIPA15-16</i> (<i>3146-2757</i>) 1721-3875 <i>LIPA15</i> (<i>np5669-5881</i>) 12818-13577
10p11.1 (1B)	Grey (38% GC)	GA_x54KRE8L8DP:3500001..4000000 Also in GenBank: AL590730.6	106476-104607 2001-2096	75	NNN12074-13949 <i>AluY</i>

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			2101-2480 2481-2530 2531-2745 5042-2768 5073-5366 5395-5500	74	<i>LIMec(np2493-2189)</i> (<i>TG</i>) <i>n</i> <i>LIMec(np2189-1980)</i> 11669-13949 <i>AluSg</i> <i>LIMec(np1898-1792)</i>
10q11.1 (1B)	Grey (44% GC)	GA_x39G1FFS6TE:1..1218 Also in GenBank: AC024235.3	636-4 651-801 103700-103850 103865-104510 104513-104572 104739-104995	80 79	9485-10125 uJ0 <i>AluJo</i> 9485-10138 (<i>TA</i>) <i>n</i> <i>SATRI</i>
10q23 (1C)	G (34% GC)	GA_x5J8B7Q1L3K:1..133998 Also in GenBank: AF227907.1	548-568 16-7046 7291-7040 75-377 483-2691 7315-7335 2692-13807 14052-13798 14217-14274	81 85 80 82 85	<i>AT_Rich</i> 4064-11117 14328-14580 <i>AluJo</i> 14360-16569 <i>AT_Rich</i> 1-11116 14327-14582 <i>AT_Rich</i>
10q22 (1C)	R (46% GC)	GA_x5L2HTUSATD:2500001..3000000 Also in GenBank: NT_025827.1	277354-277573 277649-278841 278863-279160 279286-280031 280091-280390 280413-280698 280778-284220	75 70 72	<i>LTR33A</i> 3294-4489 <i>AluSX</i> 4624-5373 <i>AluSX</i> <i>AluSq</i> 5512-9035
10q25 (1C)	G (43% GC)	GA_x5HB7VCTE6R:12500001..13000000 Also in GenBank: AL441886.18	54315-54382 54689-54709 54896-54382 54912-54997	84	<i>LIMA5A</i> <i>AT_Rich</i> 8295-8809 <i>LIMA5A</i>
10q26 or 10q11.23 (1B)	R (34% GC)	GA_x5L2HTVF5SB:1..25969 And GA_x5L2HTVEPJC:1..2306 Also in GenBank: AC074322.4	1-1035 1-139 154-204 359-430 935-1631 1633-1692 438-635 1219-1915 74701-74859 74862-74912 75067-75138	74 84 78 76 78 84	1450-2482 <i>LI</i> 11-60 (<i>CACG</i>) <i>n</i> 575-1281 (<i>TA</i>) <i>n</i> 11-245 577-1283 <i>LI</i> 11-60 (<i>CACG</i>) <i>n</i>

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			76340-76394 75642-77907 77909-78203 78199-78559	76 80	(TA) _n 575-2817 AluY 2801-3165
11 (1B)	? (44% GC)	AC000382.1)	84001-84229 84230-84280 84810-84291 86220-84880 86233-86976 87012-87047	83 74 78	AluY SATRI(Satellite) 987-1511 5613-6976 9386-10138 (TA) _n
11p15 (1D)	R (43% GC)	GA_x5L2HTTV9VQ:5000001..5500000 Also in GenBank: AC021914.7	320780-320576- -318824-318677 43146-45595	94 90 93	523-728-NNN- -2828-2974 521-2972
11p12 (1B)	G (38% GC)	GA_x5L2HTTV9VQ:34500001..35000000 Also in GenBank: AC027806.8	80162-80985 81064-81335	77	6919-7745 LIPBa
11p11.1 (1D)	Grey (50% GC)	GA_x54KRE8RWR0:1000001..1500000 Also in GenBank: AC018410.24	24440-24243	86	13225-13452
11q13 (1C; 1C; 1A; 1B)	R (44% GC; 43% GC; 42% GC; 36% GC)	GA_x54KRE8TKVU:1500001..2000000 Also in GenBank: AP001104.4;AP000763.4; AP002789.3; AP000676.5	108844-108921 108923-108978 108983-109061 109112-109274 37503-37361 37530-37681 131874-131951 131953-132008 132013-132091 132143-132305 79750-79840 79847-79922 79923-80128 80129-80342 43382-43439 44011-43452 44636-44024 46604-46630 44628-44936 46378-44949	92 76 92 84 82 66 74	MIR MADE1(Mariner) MIR3 (SINE) 6642-6804 15892-16031 AluJb MIR(np20-101) MADE1 MIR3(np105-196) 6642-6804 AluSx(np2-92) 10822-10897 AluSx(np91-294) (TA) _n (CA) _n 596-1163 15864-16475 (GA) _n AluY 14414-15867
11q13 (1C)	R (35% GC)	GA_x54KRE8TL24:4000001..4500000 Also in GenBank: AP002783.3	304981-35719 305720-305760 305781-311528 306550-306588 311636-311999 42501-43028 43029-43065	73	LIPB4 (CA) _n 9820-15567 AT_Rich LIPB4 LIP5 (CA) _n

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			43087-48831 43855-43889	73	9820-15567 <i>AT_Rich</i>
11q22 (1E)	G (36% GC)	GA_x54KRE8WCAA:13500001..14000000 Also in GenBank: AP003461.2	91634-91655 87621-96696 17651-8576	75 75	<i>AT_Rich</i> 575-9745 575-9745
11q23 (1D)	R (40% GC)	GA_x54KRE8WCAA:6000001..6500000 Also in GenBank: NT_009151.8 Hs11_9308	137196-137332 13209296-13209137	89 86	15475-15611 15453-15612
11q25 (1D, 1B)	R (42% GC; 45% GC)	GA_x54KRE8WCJ9:3500001..4000000 Also in GenBank: AP003040.2 AP000926.5	246993-246922 383853-383411 383072-383411 58891-58810 118239-117797	94 72 94 72	14660-14741 15391-15833 <i>AluSg</i> 14660-14741 15391-15833
12 (1B)	? (41% GC)	AC078877.9	189401-190380 190548-190383 190546-190605 190714-190608	76 74	<i>SATRI(Satellite)</i> 10149-10319 (<i>TA</i>) _n 10031-10138
12p12 (1A)	G (38% GC)	GA_x54KRE902N0:15000001..15500000 Also in GenBank: AC092862.12	237961-238135 238137-238377 238378-238482 238493-238556 238557-238823 238827-239101	90	<i>L1</i> <i>AluSX</i> 1722-1826 <i>AluSX</i> <i>L1</i> <i>AluSX</i>
12q11 (1D, 1C)	Grey (36% GC; 38% GC)	GA_x54KRE91FD8:8500001..9000000 Also in GenBank: AC018698 AC073607.19	78029-79473 79574-79822 79832-80041 414631-414719 179750-178306 21185-21273	73 100 73 98	3605-5069 <i>HSMAR2(Mariner)</i> <i>HSMAR2(Mariner)</i> 3791-3879 3605-5069 3791-3879
12q12 (1A)	G (49% GC)	GA_x54KRE91FD8:1..500000 Also in GenBank: AC131157.4	472501-472742 472746-473073 473260-473087 473242-473576	84	<i>AluSX</i> <i>L1</i> 4251-4423 <i>L1</i>
12q24.3 (1C)	R (43% GC)	GA_x5L2HTV8TDQ:1500001..2000000 Also in GenBank: NT_009482.8 Hs12_9639	350475-350677 350702-350785	84	12142-12344 <i>THE1B</i>
13 (1B)	? (42% GC)	GA_x5L2HTU7TGA:1..2170 May also be in GenBank: AC024975.2	1-1056 1057-1355 1356-1405 1915-1426 113001-113178 113179-113479 113480-113535 114067-113547	84 84	<i>SATRI(np1544-44)</i> <i>AluY</i> <i>SATRI(np44-1)</i> 1019-1507 <i>SATRI(np521-340)</i> <i>AluY</i> <i>SATRI(np340-1)</i> 987-1511

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			115476-114137 115496-116233 116256-116294 116261-116936	74 78	5613-6976 9394-10138 <i>AT_Rich</i> <i>SATRI(np523-1)</i>
13q12 (1D)	R (38% GC)	GA_x5HB7VCN3FD:1600001..16500000 Also in GenBank: AL157694.7	121366-121161	85	4210-4415
13q14 (1A; 1C)	R (34% GC; 35% GC)	GA_x5HB7VCN3DA:7000001..7500000 Also in GenBank: AC006442.1 ; AL353657.26	7945-8170 8365-8192 8365-8518 52708-52928 52941-53166 53362-53189 53361-53514 25909-26088 26157-26349 26338-26678	90 89 71 68	L2 2898-3071 L2 <i>LIMI</i> <i>L2(np1957-1706)</i> 2898-3071 <i>L2(np1687-1527)</i> L2 7250-7446 (NC_001941.1 sheep mtDNA) 8002-8369
13q14 (1D)	R (34% GC)	GA_x5HB7VCN3DA:7500001..8000000 Also in GenBank: AL138997.18	224461-224782 224785-224911 225081-225203 13230-13108 13401-13527 13530-13700	91 91	<i>MSTA(LTR)</i> <i>LIPA16</i> 5108-5230 5108-5230 <i>LIPA16</i> <i>MSTA</i>
13q21 (1D)	G (35% GC)	GA_x5HB7VCN3DA:9500001..10000000 Also in GenBank: AL390722.10	300410-300246 40373-40537	81 81	13012-13177 13012-13177
13q21 (1B)	G (38% GC)	GA_x5HB7VCN3QP:10500001..11000000 Also in GenBank: AL137244.28	115210-115261 115272-115437 102552-102387 102564-102615	85 84 100	(<i>TA</i>) ₂₆ 9874-10039 9874-10039 (<i>TA</i>) ₂₆
13q31 (1E)	G (35% GC)	AL445195.4	117771-115992 115608-114100 103970-102462 103975-104354 106133-104354	70 70 70 70	11042-12783 12787-14300 12787-14300 <i>LTR46(LTR/ERV1)</i> 11042-12783
13q32 (1A)	R (40% GC)	GA_x54KRE96ECP:9000001..9500000 Also in GenBank: AL138955.14	438388-438415 438418-438791 438808-439092 439092-439383 439389-442780 440865-440893 442804-443024 48531-48629 48641-49005	78 71	(<i>GGGAGA</i>) _n <i>LI</i> 13051-13337 LUY 13327-60 f-Rich <i>LI</i>

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			49023-49307 49306-49597 51079-51107 49604-52926 52945-52995 53029-53233 53234-53439 53440-54948	78 71 88	<i>GA_Rich</i> <i>LI(np2766-2398)</i> 13051-13337 <i>AluY</i> <i>AT_Rich</i> 13327-16560 11-60, within intron of XM_012277 <i>LI(np2408-2216)</i> <i>AluY</i> <i>LIPA15(np2216-565)</i>
13q34 (1C; 1C; 1C)	R (38% GC; 39% GC; 41% GC)	GA_x54KRE96ECP:23000001..23500000 Also in GenBank: <i>AL138816.12</i> ; <i>AL160158.10</i> ; <i>AL160031.9</i>	<i>171002-171325</i> 171534-171412 <i>3873-4221</i> 4280-4424 <i>10478-10521</i> 10547-10506 <i>10573-10665</i> <i>10722-11000</i> <i>65001-65367</i> 65710-65455 <i>65855-65998</i>	99 82 92 99	<i>LIMB7</i> 1115-1237 <i>HAL1(LI)</i> 7472-7617, within intron of XM_063885 <i>AT_Rich</i> 11077-11118, in intron of XM_101396.1 <i>HAL1b(LI)</i> <i>THE1c(LTR/MaLR)</i> <i>LIMB7</i> 982-1237, in intron of XM_062793.1 <i>MIR</i>
14q11.1 (1C)	Grey (53% GC)	<i>AJ238393.1</i>	11555-11624 <i>11658-11778</i>	87	2011-2079 <i>MIR3</i>
14q22 (1D)	R (40% GC)	GA_x5L2HTU0SRS:53000001..53500000 Also in GenBank: <i>AL122125.4</i>	149216-149563	83	574-920
14q31 (1E)	G (35% GC)	<i>AC021835.3</i>	69248-69738 85685-85309 85695-85995 87891-86028 88870-87895 90381-88854	76 69 74 75 79	14922-15411 14333-14715 <i>AluY</i> 12427-14298 11352-12333 1796-3314
14q32 (1D)	R (35% GC;	GA_x5L2HTU0SRS:21000001..21500000 Also in GenBank: <i>AL355887.4</i>	144973-146761 <i>68635-66864</i>	77 77	577-2364 <i>575-2350</i>
15q13 (1C)	R (45% GC)	GA_x5L2HTUCKNG:5500001..6000000 Also in GenBank: <i>AC025429.6</i>	46925-45484 <i>45410-45467</i> <i>45006-45393</i>	75	11687-13134 <i>SATR1 (Satellite)</i> <i>SATR1 (Satellite)</i>
15q15 (1C; 1D)	R (39% GC; 38% GC)	GA_x5L2HTUCKTJ:2500001..3000000 Also in GenBank: <i>AC022467.7</i> and <i>AC091074.3</i>	98514-98718 <i>24026-24058</i> <i>24187-24210</i> 24372-24285	80 76	12980-13184 <i>(ATG)n</i> <i>AT_Rich</i> 13205-13292

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			24405-24444 47504-47708	80	(TCTA) <i>n</i> 12980-13184
15q21 (1D; 1B)	G (42% GC; 41% GC)	GA_x5L2HTUCKTJ:14000001..14500000 Also in GenBank: AC025916.5 and AC066616.6	383169-383285 383292-384650 384685-385687 384740-384761 389273-385810 22425-22373 404902-404946 404914-404952 68203-68151 8659-8802 8810-10168 10257-10278 10203-11205 11328-14791	73 75 73 87 85 86 73 75 73	<i>MER102b</i> 9615-11019 11231-12237 <i>AT_rich</i> 12465-16016 11366-11418 (<i>CAT</i>) <i>n</i> 5297-5334 11366-11418 <i>MIR</i> 9614-11019 <i>AT_Rich</i> 11231-12237 12465-16016
16p13.3 (1D)	R (45% GC)	GA_x5L2HTVF6CQ:8000001..8500000 Also in GenBank: NT_010530.8 Hs16_10687	164576-159392 159279-157749 1654725-1647930	74 75 74	8514-13708 14492-16030 8514-16030
16p13.3 (1E)	R (44% GC)	GA_x5L2HTVF6CQ:500001..1000000 Also in GenBank: NT_010577.2	319808-317997 319809-320106 321896-320129 321919-322226 322843-322227 322839-323149 323248-323148 -alu-382263-380452 -384351-382584- -385298-384682- <i>alu</i> - 385703-385603- <i>alu</i> - 502726-502234	76 76 78 83 77 76 78 83 77	5856-7684 <i>AluSc</i> 2828-4596 <i>AluSc</i> 2197-2819 <i>AluSp</i> 2112-2211 -5855-7683 -2826-4595- <i>alu</i> - -2195-2817- <i>alu</i> - 2110-2209- <i>alu</i> - <i>alu</i> -2195-2685
16p13.3 (1C; 1D)	R (41% GC)	AC024953	777-707 633-664 52460-52402	100 84	1272-1342 <i>AT-rich</i> 3011-3069
16p13.1 (1D)	R (42% GC)	GA_x5L2HTV7HJN:500001..742907 Also in GenBank: NT_031896.1 Hs16_32067	125140-126493	75	12221-13575
16p12 (1C)	G (47% GC)	AC007595.7	47068-47212 47491-52675 52788-54318 54385-54506 54597-54871 54629-54990	74 75 71	<i>LIPA10</i> 8513-13707 14491-16029 15508-15618 NC_001992.1 (Papio mtDNA <i>SATR2</i> <i>SATR1</i>

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
16p11.1 (1C)	Grey (47% GC)	GA_x54KRE99UHB:500001..1000000 Also in GenBank: AC026474.6	84209-84481 84710-84530 84730-84829 84831-84886	80	<i>Tigger3-Mer2</i> (2 copies) 12197-12370 <i>Tigger3-Mer2</i> (CATATA) <i>n</i>
16q22 (1C) 16q23 (1C)	R (41% GC) G (41% GC)	GA_x54KRE9B9GJ:5500001..6000000 Also in GenBank: AC009140.6	233542-235702 233603-233623 48842-49098 49256-49206 51933-49273 51353-51373 51956-52265	79 86 72	14435-16562 <i>Atrich</i> <i>LIMI</i> 11-60 13930-16562 <i>AT_Rich</i> <i>AluY</i>
17 (1B)	Centromere? (44% GC)	AC091085.2	44001-44543 44710-44769 45514-44772 45527-46866 46936-47455 47469-47517 47518-47816 47817-48000	79 74 83	<i>SATRI(np1-601)</i> (TA) <i>n</i> 9386-10138 5613-6976 987-1511 <i>SATRI(np137-185)</i> <i>AluY</i> <i>SATRI(np185-368)</i>
17p11.2/ 17p13.1 (2C)	R (42% GC)	GA_x5HB7VCTDR9:1..17488 GA_x9V1A74:1..1215 [<i>and</i> <i>GA_x5L2HTVDDBJD:1..932;</i> <i>GA_x5J8B7Q1AL2:1..932;</i> <i>GA_x5HB7VCSLWB:1..932, 99% sim to Hs17_25018]</i> Also in GenBank: (12-1225) Also in GenBank: NT_024862.8 (374947-391795, sim ends at np 16851, 99% sim) especially in: AC107940.6 [contains a Np 3510-3673 correspond to Ac# L27599.1, published mtDNA by Hu and Thilly, 1995] Another GenBank hit: NT_033222.1 Hs10_33398 (106277-89144, sim str from np 349, 99% sim)	16680-17483 4-1037 8-754 81-718 81-718 1-4596 4841-4587 391624-391795 45696-45753 45918-46172 46163-57283 52640-52660 57284-57935NNN 162387-162689 162795-164098	85 74 78 83 85 81 85 83 85 82 76 82	14360-15163 16019-480 16304-480 16376-447 16376-447 6518-11116 14327-14582 14360-14528 <i>AT_Rich</i> 14327-14582 11116-1 <i>AT_Rich</i> 16569-15920NNN <i>AluJo</i> 14360-15662
17p11.1 (1C)	Grey (47% GC)	GA_x54KRE9GCSG:500001..1000000 Also in GenBank: AC025627.13	214491-214642 214719-216166 216177-216472 216525-216783 216794-217105 217123-218438 218440-218622 219754-220692	77 78 78 81	uJb 6392-4942 usq 4887-4626 uY

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			220011-220321 220324-222578- -222828 74226-74323 <i>126179-126427</i> <i>126491-126530</i> <i>126585-126629</i> 126740-126974 126990-127229 127728-129243 <i>129247-129556</i> 129554-130129 <i>130128-130431</i> 130433-131053 <i>131050-131382</i> 131383-132698 <i>132717-133028</i> 133038-133296 <i>133350-133645</i> 133655-135102 <i>135180-135331</i> <i>135340-135600</i>	73 75 78 68 81 79 82 77 78 77	4595-3261 uY 2340-2084 uY 2097-11 -16331 11797-11897 <i>L2</i> <i>(TTTGT)n</i> <i>(CA)n</i> 16331-16563 11-245 575-2097 <i>AluY</i> 2084-2665 <i>AluY</i> 2656-3274 <i>AluY</i> 3261-4595 <i>AluY</i> 4626-4887 <i>AluSq</i> 4942-6392 <i>AluJb</i> <i>AluSx</i>
17p11.1 (1C)	Grey (46% GC)	AC005722.1	88383-88525 88556-88596 88636-88733 88765-89027	75	<i>(CA)n</i> <i>CT_Rich</i> 11797-11897 <i>AluSq</i>
17p11.1 (1C)	Grey (53% GC)	AC003957.1	46876-47014 47073-47250 47305-47468 49922-50009 50082-50184	76 80	<i>MIR3</i> 8672-8858 <i>MIR</i> 8790-8876 <i>MIR</i>
17q11.2 (1C)	R (44% GC)	GA_x9V1AYL:1..500000 also in: GA_x5L2HTTED7M:1..456335 Also in GenBank: AC004134	495961-496267 496307-496640 496684-496782 <i>243382-243480</i> <i>243855-243522</i> <i>243882-244018</i>	79 79	<i>LIME3</i> 2265-2601 <i>LIM4</i> <i>LIM4</i> 2267-2603 <i>LIME3</i>
17q21 (1A)	R (49% GC)	GA_x9V1AR7:500001..1000000 Also in GenBank: NT_010755.8 Hs17_10912	173450-174016 173805-173872	97	<i>L2</i> 10143-10210

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			<i>174017-174325</i>		<i>ALUSX</i>
17q21 (1B; 1C)	R (35% GC; 40% GC)	GA_x9V1B0T:6500001..7000000 Also in GenBank: AC073480 ; AC025505.11	351089-350998 <i>17434-17346</i> 17346-17998 72620-72547 <i>72655-72767</i>	97 96 82	6818-6909 <i>MIR</i> 6818-7470 12265-12339 <i>MIR(SINE)</i>
18p11.3 (1B)	G (43% GC)	GA_x5HB7VCPGRD:2500001..3000000 Also in GenBank: AP000919.5	337312-337609 337307-337153	90	uJb 14381-14536
18q21/18q12 (close to border with 18q21) (1A)	R/G (38% GC)	GA_x54KRE9MHP4:500001..1000000 Also in GenBank: AP001386.3	322294-322490 322682-322489 322683-322790 <i>80610-80806</i> 80997-80806 <i>80997-81104</i>	96 97	u 7975-8166 u <i>AluSg(np1-197)</i> 7975-8166 <i>AluSg(np193-300)</i>
18q22 (1D)	G (42% GC)	GA_x54KRE9MHP4:14500001..15000000 Also in GenBank: AC105183.8	360210-359896 <i>94963-94649</i>	83 83	963-1281 <i>963-1281</i>
19p13.2 (1B;1C 1C)	G (44% GC; 43% GC; 45% GC)	AC008758.7 ; AC012618.7 ; AC022415.5	<i>209884-210206</i> 210205-210370 <i>210372-210667</i> 210672-211299 <i>211303-211555</i> 212576-212855 <i>212857-212877</i> <i>212881-213168</i> 213186-213257 213262-213710 <i>213833-214120</i> <i>214203-214497</i> <i>214609-214918</i> <i>214930-215084</i> 215084-215633 <i>18687-18881</i> 19083-18990 <i>19105-19438</i> <i>19441-19739</i> 19756-19874 <i>19906-20217</i>	70 68 87 66 72 75 80	<i>LTR51-int(LTR/ERVL)</i> 4640-4808 <i>AluSx</i> 4796-5427 <i>AluJo</i> <i>AluSx</i> <i>(CAA)n</i> <i>AluY</i> 7243-7414 NC_001821 (<i>Dasypus novemcinctus</i> mtDNA) 7971-8454 <i>AluSq</i> <i>AluSg</i> <i>AluSg</i> <i>AluJb</i> 8722-9277 <i>LTR52-int</i> 4243-4332 <i>AluSx</i> <i>AluSx</i> 3535-3653 NC_002080.1 (<i>hedgehog</i> mtDNA) <i>AluSx</i>

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			20603-20249 20622-20708 88578-88474	70 77	3660-4041 <i>AluSg/X</i> 4285-4389 NC_001779.1 (Rhinoceros mtDNA) 4215-4811 <i>AluY</i> <i>LTR10C(np347-150)</i> <i>Mer9</i> <i>HERVK9(np5916-3711)</i> <i>HERVK9(np2786-763)</i> <i>Mer5B</i> <i>HERVK9(np763-1)</i> <i>Mer9</i> <i>LTR10C(np155-1)</i> <i>AluSp</i> 2703-2899 NC_000884.1 (guinea pig mtDNA) 2363-2883 <i>AluSq</i>
			89181-88586 90669-90980 90981-91172 91173-91688 91689-93847 93848-95796 95797-95857 95858-96623 96624-97139 97140-97291 97292-97490 97689-97497	70 72	
			98201-97691 98245-98557	69	
19q13.4 (1D)	G (45% GC)	GA_x54KRE9RQ87:1500001..2000000 Also in GenBank: AC044792.6	127882-128076 45586-46169	83 71	12143-12337 11917-12500
20q13.3 (1C; 1A)	R (48% GC; 48% GC)	GA_x5L2HTTW9JV:5000001..5500000 Also in GenBank: AL109955.37 AL117380.28	117096-117435 117508-117558 118155-118183 118213-121863 121899-122137 415041-415114 415181-415107 415186-415265 2071-3 2776-2726 175495-175569	83 77 90 78 88 90	<i>MER1B</i> 11-60 (<i>TTC</i>) <i>n</i> 573-4281 <i>LIME1</i> ER53 12962-13038 ER53 573-2682 11-60 12962-13038
21 (1B)	? (42% GC)	AC027762.2	54505-54605 54670-55539 55318-55375 55542-55994	74	<i>AluJo</i> 9585-10319 (<i>TA</i>) <i>n</i> <i>SATRI</i>
21q22 (1D)	R (57% GC)	GA_x5J8B7P9YMR:3500001..4000000 Also in GenBank: AL163302.2	3421-3227 75155-74962	87 88	5995-6188 5995-6188
22q13 (1D)	R (50% GC)	GA_x39G1F6QCNE:1..500000 Also in GenBank: AL022327.17	108406-108634 98874-99102	80 80	667-898 667-898

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
Xp22.3 (1B) (1E)	R (36% GC)	GA_x5HB7VC1UUL:1000001..1500000 Maybe also in GenBank: AC119041.6	303225-301582 303594-303904 72664-74596 74593-74894 74893-74935	80 76 86	14074-15713 <i>ALUJ0</i> 14074-16005 <i>AluY</i> 15990-16030
Xp22.3 (1B)	R (41% GC)	GA_x5J8B7PLWN9:1000001..1500000 Also in GenBank: AC112497.4	42006-42613 42803-42625 42774-43598 41739-41549	83 83	<i>LIPA5 (LINE)</i> 6501-6679 <i>LINE1</i> 6501-6691
Xp22.33 (1E)	R (37% GC)	AC021859.4	137727-139665 139665-139963 139962-140004	75 86	14074-16005 <i>AluY</i> 15990-16030
Xp11.2 (1D)	R (41% GC)	AL020991.1	12115-12102	87	2613-2707
Xp11.1 (1C; 1D)	Grey(41% GC; 39% GC; 40% GC)	GA_x5J8B7PE4U0:1..500000 Also in GenBank: Z83821.1 ; AL158819.14 ; AL590240.5	174139-179931 304616-304531 <i>10001-10313</i> <i>10316-10378</i> <i>10380-10433</i> <i>10430-10520</i> <i>10613-10520</i> <i>5057-13</i> <i>130005-129170</i>	80 88 100 87 78 77	576-6407 2615-2701 <i>Mer65c(LTR/ERV1)</i> <i>L2</i> <i>AT_Rich</i> AF068624(8kb 5' to ALAS2_gene) 2613-2707 576-6407 5576-6406, part of the above one]
Xq11 (1B)	Grey (44% GC)	GA_x5L2HTUDTEL:500001..1000000 Also in: NT_019696.7 HsX_19852 (and in NT_025259.2)	<i>109033-109097</i> <i>109098-109537</i> <i>109541-109752</i> <i>109753-109910</i> <i>109936-110746</i> <i>110759-110898</i> <i>110900-111723</i> <i>111735-112047</i> <i>112049-113014</i> <i>113019-113331</i> <i>113323-113466</i> <i>113515-113797</i> <i>113859-114411</i> <i>114445-114947</i> <i>114948-116440</i> <i>116442-116465</i> <i>116474-116787</i> <i>116837-116869</i> <i>116873-117353</i>	76 70 71 71 68 90	IR TR48 <i>LTR26</i> 11613-11767 TR28 ER52A 11798-12645 <i>Alu</i> 12655-13678 <i>Alu</i> 13667-13809 <i>Alu</i> 14074-14634 <i>LTR19A</i> SVA

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			117353-119271 119425-119810 119811-119978	70	(GGGAGA) _n Alu 14695-14727 MLT2A1 (LTR) 14725-60 TR26 ER34
Xq26 (1A; 1C)	R (36% GC; 36% GC)	GA_x39G1FU7W5T:1..260539 Also in GenBank: AL359973.11 ; AL391375.11	136249-138384 138920-139050 99901-100039 100057-100407 100407-101155 101435-101170 101434-101987 101986-102159 102162-102488 38502-38372 38984-39035 39279-39038 41173-39289 41314-41695	70 87 92 96 92 87 67 73	14685-245-(CACG) ₁₂ 574-703 <i>LIM1(np1211-1353)</i> <i>LIM1(np1420-1770)</i> 6553-7302 687-953 10606-11159 <i>LIM1(np1770-1944)</i> <i>AluJb</i> 574-703 (CGTG) _n 11-245 14685-16569 <i>L1</i>
Xq28 (1E; 1B)	R (37 GC; 40% GC)	GA_x5J8B7PR68J:1500001..2000000 Also in GenBank: NT_011574.1	326710-328304 328366-328422 328462-328869 328887-329189 329208-330886 330887-331250 331251-331873 439992-440461 440466-440613 440670-440626 440682-440816 440822-440870 440871-441001	74 75 71 67 95	598-2216- ADE1 repeat 2289-2699 u-C(A)_nx3- 2714-4423 HE1B 4422-5045 NEIP u 11075-11119 u <i>L1P</i> <i>MSTA(LTR)</i>
Yp11.2 (1C; 1C)	R (36% GC; 39% GC)	GA_x5L2HTV86JQ:1..970 Also in GenBank: AC010905.3 and AC025731.12	561-491 108346-108377 108491-108421	100 100	1272-1342 <i>AT_Rich</i> 1272-1342

Map	Band Type	Celera Scaffold and GenBank accession numbers	Position in the Contig	% of sim to mtDNA	Region of similarity to Cambridge sequence
			12001-12181 12236-12617 12660-14519 12818-14957 15012-15739 15740-16308 16309-17808 17809-18635 18632-20925 20956-21826 21844-22000	70 69 78 75 72	<i>BSR_beta(Satellite)</i> <i>BSR_beta(Satellite)</i> 14260-16127 14422-16562 <i>LI(np3370...3672)</i> 596-1172 <i>LIPA4(np5305-3807)</i> <i>LIPA4(np5325-6153)</i> 1159-3458 4063-4959 <i>BSR_beta(Satellite)</i>
Yp11.1 (1B)	Grey (39% GC)	GA_x54KREA69CA:500001..1000000 Also in GenBank: AC025731	166462-165592 168786-166493 171678-171110 174592-172461 174750-172899	72 75 78 69 70	4063-4959- <i>BSR_beta</i> <i>repeat</i> -1159-3458 596-1172- <i>LIPA4</i> - 14422-16562 14260-16127- <i>BSR_beta</i> <i>repeat</i>
Yp11.1 (1A)	Grey (39% GC)	GA_x5L2HTTS0UA:1..1112 and GA_x54KREA67C8:1..810 Also in GenBank: AC009952.4	735-670 735-670 8730-8775 8760-8836 8898-8956 8963-9187 9178-9243 9244-9445	100 100 100	6499-6564 6499-6564 <i>(TG)n</i> <i>(TA)n</i> <i>LTR25(LTR/ERV1)</i> <i>HUERS-P3(LTR/ERV1,</i> <i>np 2691-2466)</i> 6499-6564 <i>ERV1</i>

*Celera Scaffold and GenBank accession numbers are indicated for each NUMT-containing contig. Nucleotide positions of NUMTs in contigs are color-coded according to the analyzed contig. To avoid redundancy, when both Celera and GenBank contigs are available for a given NUMT, repeat information is provided for one of the contig types. (1A): 1 NUMT within a repeated element in the corresponding contig; (1B): 1 NUMT within 1-15bp of a repetitive element in the corresponding contig; (1C): 1 NUMT 15-150bp away from a repetitive element in the corresponding contig; (1D): 1 NUMT more than 150bp away from a repetitive element; (1E): 1 NUMT solely truncated by repeats in the corresponding contig. {39% GC} – average GC content in 100 KB region encompassing the NUMT or NUMTs.