Supplemental materials:

Figures

Fig. S1. Densities of polymorphic *Alu* insertions and all *Alu* insertions in human chromosomes. The data were taken from the last four columns of Table 3. The first Y-axis shows the densities of polymorphic *Alu* insertions (number of elements per 50 Mb of genomic region) and genes (number of genes per Mb), while the second Y-axis shows the densities of all *Alu* insertions (the number of elements per Mb) and *Alu*-integration sites (number of "NT-AARA" *Alu* sites per 50 Kb).

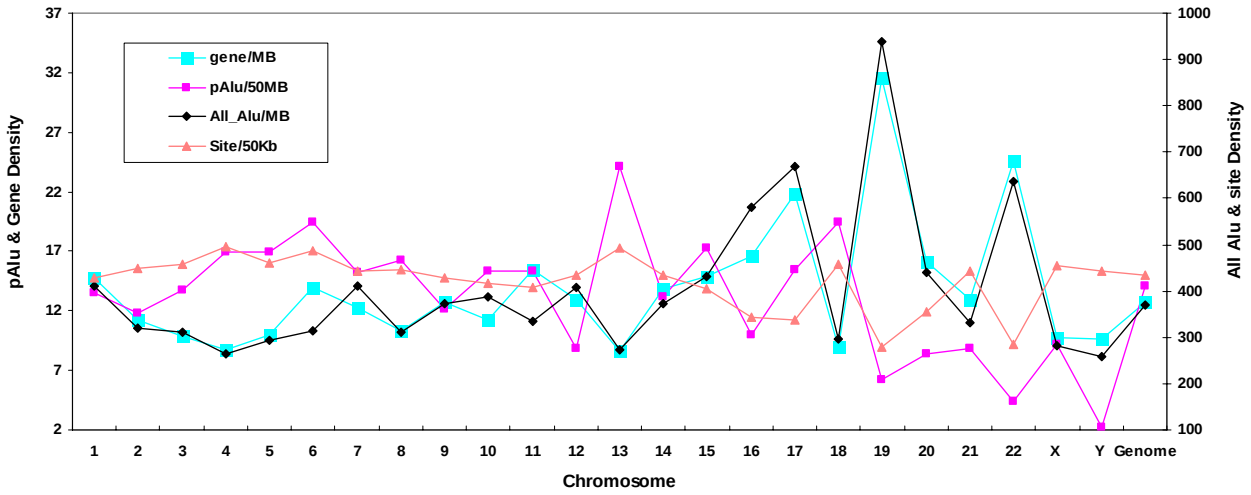

Fig. S2. Multiple sequence alignment of all AluYb11 sequences

Note: the grey columns indicate the two diagnostic mutations of Yb11 subfamily elements. Yb11chr5_3 is from CHGS, and all others are from PHGS.

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Yb11ch10_1       GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11chr4_1       GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11chr5_3       GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11ch10_2       GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11chr5_2       GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11chr7_1       GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11chr2_1       GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGACGGGTGGA
Yb11chr14_1      GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11chr7_2       GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11chr9_1       GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11chr2_2       GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11chr6_1       GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11chr6_2       GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11chr1_1       GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11chr5_1       GGCCGGGCGCGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11chr1_2       ----------------------CCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
Yb11chr11_1      AGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
                                      ****** ********************** ********

Yb11ch10_1       TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr4_1       TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr5_3       TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11ch10_2       TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr5_2       TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr7_1       TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr2_1       TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr14_1      TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr7_2       TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr9_1       TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr2_2       TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr6_1       TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr6_2       TCATGAGGTCAGGAGATCGAGACCAGCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr1_1       TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr5_1       TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr1_2       TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
Yb11chr11_1      TCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACTAA
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Yb11ch10_1      A-----AATACAAAAAAAAA----TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCACAGCTAC
Yb11chr4_1      A-----AATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
Yb11chr5_3      A-----AATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
Yb11ch10_2      A-----AATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
Yb11chr5_2      A-----AATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
Yb11chr7_1      A-----AATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
Yb11chr2_1      A-----AATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGTGCCTGTAGTCCCAGCTAC
Yb11chr14_1     AAAAAAAATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
Yb11chr7_2      A-----AATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
Yb11chr9_1      A-----AATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
Yb11chr2_2      A-----AATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
Yb11chr6_1      A-----AATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
Yb11chr6_2      A-----AATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
Yb11chr1_1      A-----AATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
Yb11chr5_1      A-----AATACAAAAAAAAAAAAATTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
Yb11chr1_2      A-----AATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
Yb11chr11_1     A-----AATACAAAAAA-------TTAGCCGGGCGCGGTGGCGGGCGCCTGTAGTCCCAGCTAC
                *     ***********       ********************** ********** *******

Yb11ch10_1      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr4_1      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr5_3      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11ch10_2      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr5_2      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr7_1      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr2_1      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr14_1     TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr7_2      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr9_1      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr2_2      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr6_1      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr6_2      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr1_1      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr5_1      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr1_2      TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCGGAGCTTGCAGTGAGCCG
Yb11chr11_1     TGGGGAGGCTGAGGCAGGAGAATGGCGTTGAACCCGGGAAGCAGAGCTTGCAGTGAGCCG
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Yb11ch10_1      AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr4_1      AGATTGTGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr5_3      AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11ch10_2      AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr5_2      AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr7_1      AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr2_1      AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr14_1     AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr7_2      AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr9_1      AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr2_2      AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr6_1      AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr6_2      AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr1_1      AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr5_1      AGGTTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr1_2      AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
Yb11chr11_1     AGATTGCGCCACTGCAGTCCGCAGTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAA
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Yb11ch10_1       AAAAAAAAAAAAAAAAAAAAACAAAA
Yb11chr4_1       AAAAAAAAAAAAAA-------------
Yb11chr5_3       AAAAAAAAAAAAAA-------------
Yb11ch10_2       AAAAAAAAAAAAAAAAAA---------
Yb11chr5_2       AAAAAAAAAAAAAAAAAA---------
Yb11chr7_1       AAAAAAAAAAAAAAAAAA---------
Yb11chr2_1       AAAAAAAAAAAAAAAAAAAA------
Yb11chr14_1      AAAAAAAAAAAAAAAAAAAAAAAAAAA
Yb11chr7_2       AAAAAAAAAAAAAAAAAAAAAAA---
Yb11chr9_1       AAAAAAAAAAAAAAAAAAAAAAA---
Yb11chr2_2       AAAAAAAAAAAAAAAAAAAAAAAA-
Yb11chr6_1       AAAAAAAAAAAAAAAAAAAAAAAAA
Yb11chr6_2       AAAAAAAAAAAAAAAAAAAAAAAAA
Yb11chr1_1       AAAAAAAAAAAAAAAAAAAAAAAAA
Yb11chr5_1       AAAAAAAAAAAAAAAAAAAAAAAAA
Yb11chr1_2       AAAAAAAAAAAAAAAAAA---------
Yb11chr11_1      AAAAAAAAAAAAAAAAAAAAAAA---
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Table S1*. PCR primers used for genotyping*

Alu locus	Forward primer (5'-3')	Reverse primer (5'-3')	Product size (bp) (*Alu*+/-)
pAlu6-4040151-Ya4	AGCCTGTTGTTCCAGTACATATGAC	CAGTAATGTTGTACGAGCCAGAG	596/291
pAlu6-11965898-Ya5	TTATTGGGTCTGACCTCCAACTCAG	AAGCCTGCAACTCCTACCCAGAATG	553/255
pAlu6-17534722-Ya5	TACCTCGATAGTCTCACTTC	GTGTTGGTAGTGAAGAGAGCCAAC	400/102
pAlu6-24040896-Yb7	CTCTGTGAACCAAGTCCAGGGCATG	ACAATTGCGAGAACATGCAGGCAGG	678/371
pAlu6-43896890-Ya5	GAGTTCACCTTAGACTAAGAGAAGG	AACCCAACTGCTGGCTATATGACC	521/217
pAlu6-44614813-Ya5	GCTTAACACAACCCATAAATGGCTG	AAATCCTCGTGAGCTGACTGTTTCC	508/206
pAlu6-51518660-Ya5	ATATTTGGCCTTATCTAGCC	TCTCAAAGCTACTAAGCCGAGTTCC	444/129
pAlu6-104772799-Ya5	TATCATCCTACGCCAATGAAAGATC	GAAACATGTTCATTATCCGC	637/333
pAlu6-105567882-Ya5	TAGGACTGATGTTCCTTCGTTGTGC	TGACCTCAGTCAGCACTCTAACTAC	726/403
pAlu6-108266151-Ya5	TCATTGTATCATCTGCTGTACCTGT	GTTTATGTCAGTAGGAGTTTTCTCGTGTAG	433/139
pAlu6-119352555-Yb7	TAACGTGGTACTGCTTTGAAAGGAG	TTTATCCAGAGTGCTATCACTCCC	472/161
pAlu6-120503383-Yb7	GAAGCCACTTAGGCCATTATC	ATGATATTGGCCATACCATC	614/311
pAlu6-131110606-Yb7	CTCAAACTTCGTTTCTCAAG	TTGGTGACACTCTAAGCGTTACCAG	857/553
pAlu6-154401955-Ya5	CCTCTTGGACAGTGAAATCACAACC	ACTTACGCTCTTTCGCTTCAAATGC	675/362
pAlu6-163023807-Yb7	GGACAGACTAAACTTGTAATCTGC	AGCTAAGGTAAAGATCGCTGCTCAC	853/547
pAlu6-170176227-Yc1	TGCCAGTGACAATGGGACGTTTGAC	GTTGTAATTCTAACGCCTCTC	491/169

Table S2. Genotyping results of 16 *Alu* loci among the 95 individuals representing 10 ethnic groups

Alu Locus[1]	N_Europe +/+:+/-:-/- (f*Alu*/Het)[2]	Russian +/+:+/-:-/- (f*Alu*/Het)	Chinese +/+:+/-:-/- (f*Alu*/Het)	Japanese +/+:+/-:-/- (f*Alu*/Het)	SE_Asian +/+:+/-:-/- (f*Alu*/Het)	Mex_Ind +/+:+/-:-/- (f*Alu*/Het)	Mayan +/+:+/-:-/- (f*Alu*/Het)	M. East +/+:+/-:-/- (f*Alu*/Het)	Baka_Pygmy +/+:+/-:-/- (f*Alu*/Het)	Burunge +/+:+/-:-/- (f*Alu*/Het)	Average +/+:+/-:-/- (f*Alu*/Het)
pAlu6-4040151-Ya4	0:1:9 (0.05/0.1)	0:1:9 (0.05/0.1)	1:3:5 (0.27/0.44)	1:4:4 (0.33/0.49)	2:5:3 (0.45/0.54)	1:2:2 (0.4/0.6)	0:0:4 (0/0)	0:1:8 (0.05/0.1)	0:3:10 (0.11/0.21)	0:0:12 (0/0)	5:20:66 (0.16/0.27)
pAlu6-24040896-Yb7	5:4:1 (0.7/0.46)	3:5:2 (0.55/0.55)	0:5:5 (0.25/0.41)	0:5:5 (0.25/0.41)	0:4:6 (0.2/0.35)	1:2:2 (0.4/0.6)	1:2:1 (0.5/0.66)	4:4:1 (0.66/0.5)	5:5:1 (0.68/0.47)	1:1:2 (0.37/0.62)	20:37:26 (0.46/0.5)
pAlu6-43896890-Ya5	7:0:1 (0.87/0.25)	6:3:0 (0.83/0.31)	7:1:0 (0.93/0.14)	7:2:1 (0.8/0.35)	8:1:1 (0.85/0.28)	3:2:0 (0.8/0.39)	3:1:0 (0.87/0.3)	6:3:1 (0.75/0.41)	0:4:8 (0.16/0.29)	6:3:0 (0.83/0.31)	53:20:12 (0.74/0.38)
pAlu6-44614813-Ya5	7:2:1 (0.8/0.35)	8:2:0 (0.9/0.19)	10:0:0 (1/0)	10:0:0 (1/0)	10:0:0 (1/0)	2:3:0 (0.7/0.52)	4:0:0 (1/0)	5:4:1 (0.7/0.46)	8:5:0 (0.8/0.34)	5:5:2 (0.62/0.51)	69:21:4 (0.84/0.27)
pAlu6-105567882-Ya5	0:0:10 (0/0)	0:0:10 (0/0)	2:0:8 (0.2/0.35)	0:0:10 (0/0)	0:0:10 (0/0)	0:0:5 (0/0)	0:0:4 (0/0)	0:1:9 (0.05/0.1)	0:0:11 (0/0)	0:0:4 (0/0)	2:1:81 (0.02/0.03)
pAlu6-120503383-Yb7	10:0:0 (1/0)	10:0:0 (1/0)	9:0:0 (1/0)	10:0:0 (1/0)	10:0:0 (1/0)	5:0:0 (1/0)	3:0:1 (0.75/0.5)	10:0:0 (1/0)	10:2:0 (0.91/0.17)	10:1:2 (0.8/0.34)	87:3:3 (0.95/0.09)
pAlu6-170176227-Yc1	0:9:1 (0.45/0.54)	1:7:2 (0.45/0.54)	2:7:0 (0.61/0.53)	3:5:2 (0.55/0.55)	3:5:2 (0.55/0.55)	2:3:0 (0.7/0.52)	1:3:0 (0.62/0.62)	1:7:3 (0.4/0.52)	2:7:4 (0.42/0.52)	0:6:7 (0.23/0.38)	15:59:21 (0.46/0.5)
pAlu6-17534722-Ya5	4:1:1 (0.75/0.45)	4:4:1 (0.66/0.5)	0:2:8 (0.1/0.19)	0:0:10 (0/0)	0:1:9 (0.05/0.1)	0:2:3 (0.2/0.39)	0:3:1 (0.37/0.62)	0:5:5 (0.25/0.41)	0:3:9 (0.12/0.23)	1:6:6 (0.3/0.45)	9:27:53 (0.25/0.37)
pAlu6-163023807-Yb7	10:0:0 (1/0)	6:4:0 (0.8/0.35)	2:7:1 (0.55/0.55)	4:5:1 (0.65/0.5)	5:4:1 (0.7/0.46)	0:3:2 (0.3/0.52)	3:0:1 (0.75/0.5)	5:5:0 (0.75/0.41)	5:6:2 (0.61/0.51)	3:5:5 (0.42/0.52)	43:39:13 (0.65/0.45)
pAlu6-11965898-Ya5	0:2:8 (0.1/0.19)	0:3:7 (0.15/0.28)	1:6:3 (0.4/0.53)	1:7:3 (0.4/0.52)	2:7:1 (0.55/0.55)	1:2:2 (0.4/0.6)	0:3:1 (0.37/0.62)	0:0:10 (0/0)	0:4:9 (0.15/0.27)	0:0:12 (0/0)	5:34:56 (0.23/0.35)
pAlu6-131110606-Yb7	0:2:8 (0.1/0.19)	0:7:3 (0.35/0.5)	0:1:8 (0.05/0.1)	0:1:9 (0.05/0.1)	0:1:9 (0.05/0.1)	0:0:5 (0/0)	0:0:4 (0/0)	0:5:5 (0.25/0.41)	0:0:13 (0/0)	0:0:11 (0/0)	0:17:75 (0.09/0.16)
pAlu6-24040896-Yb7	0:0:10 (0/0)	0:1:9 (0.05/0.1)	0:0:10 (0/0)	0:0:10 (0/0)	0:0:10 (0/0)	0:0:4 (0/0)	0:0:4 (0/0)	0:0:10 (0/0)	0:1:11 (0.04/0.08)	0:0:9 (0/0)	0:2:87 (0.01/0.02)
pAlu6-51518660-Ya5	0:1:8 (0.05/0.1)	1:3:5 (0.27/0.44)	0:0:10 (0/0)	0:0:10 (0/0)	0:0:10 (0/0)	0:0:5 (0/0)	0:1:3 (0.12/0.28)	0:0:10 (0/0)	0:1:12 (0.03/0.06)	0:0:13 (0/0)	1:6:86 (0.04/0.07)
pAlu6-105567882-Ya5	0:0:10 (0/0)	0:0:10 (0/0)	2:0:8 (0.2/0.35)	0:0:10 (0/0)	0:0:10 (0/0)	0:0:5 (0/0)	0:0:4 (0/0)	0:1:9 (0.05/0.1)	0:0:11 (0/0)	0:0:4 (0/0)	2:1:81 (0.02/0.03)
pAlu6-154401955-Ya5	0:0:10 (0/0)	0:1:9 (0.05/0.1)	0:0:10 (0/0)	0:0:10 (0/0)	0:0:10 (0/0)	0:0:5 (0/0)	0:0:4 (0/0)	0:0:10 (0/0)	2:3:8 (0.26/0.41)	0:0:11 (0/0)	2:4:87 (0.04/0.07)
pAlu6-108266151-Ya5 (NBC54)	1:2:7 (0.2/0.35)	0:0:10 (0/0)	0:0:10 (0/0)	0:3:7 (0.15/0.28)	0:0:10 (0/0)	0:0:5 (0/0)	0:1:3 (0.12/0.28)	0:0:10 (0/0)	0:0:13 (0/0)	0:0:13 (0/0)	1:6:88 (0.04/0.07)

[1]The *Alu* loci are arranged in order of their chromosome locations (indicated by the number in the middle section of the IDs) in the UCSC hg15 sequence. The last locus is identical to a known polymorphic *Alu*, NCB54; [2]The three numbers indicate the number of genotypes that are *Alu+/Alu+* homozygous, Alu+/Alu- heterozygous, and Alu-/Alu- homozygous, respectively, within each ethnic group. The samples that failed to generate products were excluded from the allele frequency calculation. The numbers in parentheses indicate the *Alu* allele frequency and the estimated heterozygosity values.