J Hum Genet (1998) 43:165–168 © Jpn Soc Hum Genet and Springer-Verlag 1998

ORIGINAL ARTICLE

**Yuka Yamane-Tanaka · Keiko Kogawa**
**Toshihiro Tanaka Yusuke Nakamura · Minoru Isomura**

# Heterozygosities and allelic frequencies of 358 dinucleotide-repeat marker loci in the Japanese population

Received: March 11, 1998 / Accepted: April 11, 1998

**Abstract** We examined 64 normal Japanese chromosomes to determine the heterozygosities and allelic frequencies of 358 dinucleotide-repeat marker loci spanning the whole human genome. Comparisons of the data for each marker in the Japanese population sample with data for the same markers among Caucasian samples in the Genome Database (GDB) revealed a slightly lower average of heterozygosity in Japanese (71% vs 79%). Although the majority of the markers were as informative as in Caucasians, some in our sample were uninformative due to low heterozygosity; 38 loci revealed heterozygosities lower than 50% and 11 of these were less than 30%. Furthermore, allelic distributions at many of the marker loci were quite different in the two racial groups. Since such differences will influence statistical analyses between markers and disease loci, our data will be essential for linkage analyses, sib-ship pair analyses, and association studies involving the Japanese population. Therefore we have archived this database on a home page on the Internet (http://www.ims.u-tokyo.ac.jp/nakamura/Yamane.html).

**Key words** Microsatellite · Heterozygosity · Japanese · population

## Introduction

Because polymorphic DNA markers can distinguish the paternal or maternal origin of homologous chromosomes, they are exploited widely for forensic medicine and studies of genes associated with diseases. Among the various types of polymorphic DNA markers, microsatellites (i.e., dinucleotide-repeat loci) are the most useful because their heterozygosities in a given population tend to be much higher than 50% and because they can be analyzed in a very small amount of DNA by amplification with a polymerase chain reaction and subsequent electrophoresis. Such markers have contributed substantially to efforts to map disease loci by means of linkage analyses, sib-ship pair analyses, or association studies.

Dib et al. (1996) documented 5264 dinucleotide repeat markers in a linkage map that covers all human chromosomes. Genotypic information regarding each of these markers, such as allelic frequency and heterozygosity, is available through various databases. However, most of these data were derived from DNA analyses using Caucasian samples. Since allelic information sometimes significantly influences a statistical analysis, it is not certain that we can apply such information to studies of disease genes in other racial or ethnic groups. We previously examined the allelic frequencies of 12 dinucleotide markers on chromosome 13 in a Japanese population sample, and found significant differences between Japanese and Caucasians in the allelic distributions of two of these markers (Yamane et al. 1997).

Here we report results of an extended investigation of allelic distributions and heterozygosities at 358 dinucleotide-repeat marker loci lying an average of 10 cM apart across the whole human genome, among normal Japanese subjects. The results represent an essential database for disease studies in Japanese families.

Y. Yamane-Tanaka · T. Tanaka · Y. Nakamura (✉) · M. Isomura
Laboratory of Molecular Medicine, Human Genome Center, Institute of Medical Science, The University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Tel. +81-3-5449-5372; Fax +81-3-5449-5433
e-mail: yusuke@ims.u-tokyo.ac.jp

Y. Yamane-Tanaka · K. Kogawa · Y. Nakamura · M. Isomura
Department of Human Genome Analysis, The Cancer Chemotherapy Center, Foundation for Cancer Research, Tokyo, Japan

## Materials and methods

Genomic DNAs were extracted from 32 normal Japanese volunteers, according to a method described previously (Sato et al. 1990). The Perkin-Elmer Linkage Mapping Set (Perkin-Elmer, Norwalk, CT, USA) provided pairs of fluorescently labeled primers for genotyping, and PCR amplifications were carried out according to the

| locus symbol | Japanese | Caucasian |
|---|---|---|
| D1S196 | 66 | 79 |
| D1S197 | 88 | 74 |
| D1S199 | 66 | 89 |
| D1S206 | 78 | 67 |
| D1S207 | 81 | 79 |
| D1S209 | 66 | 78 |
| D1S213 | 78 | 89 |
| D1S214 | 63 | 71 |
| D1S216 | 72 | 85 |
| D1S218 | 69 | 93 |
| D1S220 | 78 | 93 |
| D1S228 | 59 | 68 |
| D1S234 | 81 | 82 |
| D1S235 | 53 | 86 |
| D1S238 | 75 | 82 |
| D1S249 | 75 | 86 |
| D1S252 | 88 | 89 |
| D1S255 | 25 | 74 |
| D1S413 | 56 | 78 |
| D1S423 | 6 | 48 |
| D1S424 | 19 | 75 |
| D1S425 | 56 | 73 |
| D1S468 | 63 | 68 |
| D1S484 | 72 | 64 |
| D1S498 | 81 | 78 |
| D1S502 | 81 | 85 |
| locus symbol | Japanese | Caucasian |
| D2S113 | 88 | 92 |
| D2S117 | 94 | 81 |
| D2S125 | 59 | 86 |
| D2S126 | 75 | 89 |
| D2S139 | 84 | 82 |
| D2S142 | 66 | 75 |
| D2S151 | 72 | 86 |
| D2S160 | 72 | 78 |
| D2S162 | 91 | 75 |
| D2S164 | 59 | 93 |
| D2S165 | 84 | 96 |
| D2S168 | 59 | 75 |
| D2S206 | 69 | 86 |
| D2S281 | 47 | 81 |
| D2S285 | 75 | 89 |
| D2S286 | 81 | 67 |
| D2S305 | 86 | 68 |
| D2S319 | 69 | 75 |
| D2S325 | 75 | 79 |
| D2S326 | 84 | 82 |
| D2S337 | 81 | 100 |
| D2S338 | 81 | 78 |
| D2S347 | 59 | 79 |

| D2S364 | 75 | 93 |
|---|---|---|
| D2S367 | 91 | 86 |
| D2S368 | 91 | 89 |
| D2S391 | 84 | 71 |
| D2S396 | 78 | 79 |
| locus symbol | Japanese | Caucasian |
| D3S1298 | 84 | 89 |
| D3S1266 | 59 | 79 |
| D3S1267 | 66 | 86 |
| D3S1289 | 72 | 79 |
| D3S1278 | 72 | 88 |
| D3S1580 | 78 | 93 |
| D3S1293 | 13 | 74 |
| D3S1566 | 94 | 93 |
| D3S1279 | 75 | 89 |
| D3S1262 | 63 | 78 |
| D3S1300 | 69 | 71 |
| D3S1304 | 78 | 86 |
| D3S1569 | 75 | 71 |
| D3S1292 | 84 | 86 |
| D3S1297 | 75 | 82 |
| D3S1311 | 69 | 89 |
| D3S1565 | 78 | 64 |
| D3S1614 | 47 | 89 |
| D3S1263 | 97 | 93 |
| D3S1285 | 69 | 57 |
| D3S1271 | 56 | 75 |
| locus symbol | Japanese | Caucasian |
| D4S1534 | 81 | 71 |
| D4S1535 | 81 | 81 |
| D4S1572 | 81 | 93 |
| D4S1575 | 31 | 48 |
| D4S1597 | 38 | 82 |
| D4S391 | 81 | 89 |
| D4S392 | 91 | 75 |
| D4S398 | 81 | 79 |
| D4S402 | 63 | 100 |
| D4S403 | 50 | 61 |
| D4S405 | 75 | 81 |
| D4S406 | 78 | 89 |
| D4S412 | 72 | 71 |
| D4S413 | 59 | 93 |
| D4S414 | 78 | 82 |
| D4S415 | 66 | 86 |
| D4S419 | 69 | 71 |
| D4S424 | 75 | 82 |
| D4S426 | 72 | 79 |
| D4S428 | 75 | 82 |
| locus symbol | Japanese | Caucasian |
| D5S393 | 88 | 82 |
| D5S400 | 91 | 82 |

| D5S406 | 78 | 75 |
|---|---|---|
| D5S407 | 88 | 93 |
| D5S408 | 69 | 75 |
| D5S416 | 72 | 68 |
| D5S418 | 81 | 79 |
| D5S419 | 78 | 82 |
| D5S421 | 41 | 78 |
| D5S422 | 66 | 71 |
| D5S424 | 66 | 82 |
| D5S426 | 81 | 89 |
| D5S428 | 78 | 75 |
| D5S429 | 88 | 82 |
| D5S433 | 72 | 79 |
| D5S436 | 78 | 68 |
| D5S471 | 72 | 75 |
| D5S630 | 97 | 86 |
| D5S644 | 78 | 88 |
| D5S647 | 81 | 86 |
| D5S673 | 78 | 93 |
| locus symbol | Japanese | Caucasian |
| D6S462 | 38 | 68 |
| D6S289 | 91 | 64 |
| D6S470 | 75 | 86 |
| D6S271 | 0 | 85 |
| D6S441 | 81 | 86 |
| D6S308 | 66 | 62 |
| D6S434 | 53 | 85 |
| D6S276 | 94 | 79 |
| D6S264 | 41 | 74 |
| D6S257 | 88 | 89 |
| D6S292 | 91 | 82 |
| D6S344 | 72 | 68 |
| D6S287 | 63 | 85 |
| D6S309 | 81 | 82 |
| D6S262 | 78 | 81 |
| D6S305 | 78 | 79 |
| D6S281 | 78 | 78 |
| D6S426 | 81 | 89 |
| D6S422 | 59 | 89 |
| locus symbol | Japanese | Caucasian |
| D7S484 | 81 | 78 |
| D7S486 | 63 | 80 |
| D7S493 | 78 | 100 |
| D7S507 | 81 | 93 |
| D7S510 | 69 | 86 |
| D7S513 | 81 | 84 |
| D7S515 | 78 | 83 |
| D7S516 | 78 | 79 |
| D7S517 | 94 | 93 |
| D7S519 | 63 | 86 |
| D7S530 | 69 | 79 |

| D7S531 | 78 | 70 |
|---|---|---|
| D7S550 | 78 | 89 |
| D7S636 | 88 | 93 |
| D7S640 | 88 | 85 |
| D7S657 | 69 | 78 |
| D7S669 | 88 | 79 |
| D7S684 | 78 | 82 |
| locus symbol | Japanese | Caucasian |
| D8S258 | 38 | 86 |
| D8S260 | 84 | 81 |
| D8S270 | 56 | 75 |
| D8S272 | 69 | 74 |
| D8S277 | 59 | 71 |
| D8S279 | 84 | 81 |
| D8S283 | 69 | 82 |
| D8S284 | 84 | 84 |
| D8S285 | 78 | 81 |
| D8S504 | 75 | 79 |
| D8S514 | 66 | 79 |
| D8S550 | 81 | 86 |
| D8S556 | 31 | 80 |
| locus symbol | Japanese | Caucasian |
| D9S164 | 78 | 82 |
| D9S273 | 44 | 74 |
| D9S157 | 91 | 84 |
| D9S158 | 100 | 70 |
| D9S161 | 56 | 86 |
| D9S167 | 81 | 82 |
| D9S171 | 28 | 89 |
| D9S175 | 72 | 86 |
| D9S279 | 44 | 82 |
| D9S283 | 72 | 89 |
| D9S286 | 66 | 89 |
| D9S287 | 72 | 71 |
| D9S288 | 88 | 79 |
| D9S290 | 75 | 77 |
| locus symbol | Japanese | Caucasian |
| D10S189 | 63 | 73 |
| D10S190 | 94 | 89 |
| D10S191 | 72 | 71 |
| D10S192 | 88 | 82 |
| D10S197 | 75 | 89 |
| D10S201 | 84 | 86 |
| D10S208 | 81 | 89 |
| D10S212 | 38 | 61 |
| D10S217 | 91 | 86 |
| D10S220 | 78 | 81 |
| D10S249 | 88 | 63 |
| D10S537 | 63 | 79 |
| D10S547 | 41 | 78 |
| D10S548 | 38 | 64 |

**Fig. 1** Heterozygosities among Japanese and Caucasian test populations for 358 dinucleotide-repeat marker loci. Respective heterozygosities are given in the *columns to the right of each locus symbol*. *Shaded background* indicates loci where heterozygosities deviated by more than 20% from one group to the other

manufacturer's instructions. Electrophoresis was performed with an ABI 377 DNA sequencer; the data were extracted by GeneScan Analysis software and analyzed by the Genotyper program (Perkin-Elmer). Allelic sizes for each of 358 microsatellite markers among the 64 chromosomes were determined as described previously (Yamane et al. 1997).

Genotypic data derived from Caucasians for each marker were obtained from the GDB (http://gdbwww.gdb.org). Data derived from a control individual (Centre d'Etudes du Polymorphisme Humain CEPH 884-15) were obtained from the CEPH database (http://www.cephb.fr)

## Results and discussion

Figure 1 summarizes heterozygosities calculated at each of the 358 marker loci for both the Japanese and Caucasian populations (the data for Caucasians were obtained from the GDB). Heterozygosities in our test population varied from 0% to 100%, with a mean value of 71% (vs 79% for Caucasians; Table 1). On the basis of heterozygosities and allelic distributions at each marker, we constructed a Japanese database that is available through our www site on the Internet (http://www.ims.u-tokyo.ac.jp/nakamura/Yamane.html). Since the primers for PCR amplification of some dinucleotide repeat loci had been redesigned by the supplier (Perkin- Elmer), we adjusted allelic sizes in the GDB to our system on the basis of data from a known individual (CEPH 884-15) in the CEPH database. The adjusted data are reflected in Table 2 and in Tables on our web site.

Among the 358 microsatellite markers we found some that showed distinctly different heterozygosities between Japanese and Caucasian samples. For example, 89% heterozygosity was reported in Caucasians at D9S171, but heterozygosity at this locus was only 28% in Japanese. None of the 32 Japanese individuals examined was heterozygotic at the locus defined by D6S271 (only a 129-bp allele was

| | | |
|---|---|---|
| D10S561 | 88 | 89 |
| D10S583 | 81 | 86 |
| D10S587 | 78 | 89 |
| D10S591 | 38 | 75 |
| D10S597 | 44 | 77 |
| locus symbol | Japanese | Caucasian |
| D11S1313 | 59 | 89 |
| D11S1314 | 78 | 78 |
| D11S1320 | 44 | 56 |
| D11S1338 | 63 | 79 |
| D11S1358 | 59 | 68 |
| D11S898 | 25 | 71 |
| D11S901 | 75 | 88 |
| D11S902 | 72 | 82 |
| D11S904 | 72 | 86 |
| D11S905 | 63 | 71 |
| D11S908 | 50 | 78 |
| D11S922 | 84 | 86 |
| D11S934 | 44 | 84 |
| D11S935 | 66 | 77 |
| D11S937 | 84 | 93 |
| D11S968 | 38 | 82 |
| D11S987 | 75 | 79 |
| D11S1345 | 56 | 74 |
| locus symbol | Japanese | Caucasian |
| D12S310 | 59 | 69 |
| D12S324 | 63 | 69 |
| D12S326 | 69 | 80 |
| D12S336 | 66 | 82 |
| D12S345 | 84 | 87 |
| D12S346 | 66 | 57 |
| D12S351 | 63 | 84 |
| D12S352 | 81 | 73 |
| D12S364 | 81 | 87 |
| D12S367 | 75 | 76 |
| D12S368 | 59 | 81 |
| D12S78 | 75 | 92 |
| D12S79 | 69 | 96 |
| D12S83 | 72 | 82 |
| D12S85 | 84 | 68 |
| D12S86 | 59 | 89 |
| D12S99 | 81 | 83 |
| locus symbol | Japanese | Caucasian |
| D13S153 | 100 | 81 |
| D13S156 | 78 | 80 |
| D13S158 | 75 | 81 |
| D13S159 | 84 | 89 |
| D13S170 | 88 | 89 |
| D13S171 | 59 | 72 |
| D13S173 | 88 | 82 |
| D13S175 | 56 | 76 |

| | | |
|---|---|---|
| D13S217 | 78 | 67 |
| D13S263 | 88 | 84 |
| D13S265 | 72 | 70 |
| D13S285 | 81 | 81 |
| locus symbol | Japanese | Caucasian |
| D14S258 | 66 | 71 |
| D14S261 | 81 | 68 |
| D14S276 | 63 | 68 |
| D14S280 | 66 | 64 |
| D14S283 | 69 | 86 |
| D14S288 | 84 | 86 |
| D14S292 | 13 | 70 |
| D14S63 | 69 | 79 |
| D14S65 | 75 | 89 |
| D14S68 | 63 | 82 |
| D14S70 | 75 | 71 |
| D14S74 | 91 | 78 |
| D14S78 | 38 | 57 |
| D14S80 | 47 | 82 |
| locus symbol | Japanese | Caucasian |
| D15S128 | 75 | 81 |
| D15S153 | 84 | 93 |
| D15S117 | 66 | 85 |
| D15S120 | 69 | 79 |
| D15S126 | 66 | 81 |
| D15S127 | 78 | 71 |
| D15S130 | 75 | 71 |
| D15S131 | 75 | 82 |
| D15S165 | 34 | 82 |
| D15S205 | 84 | 85 |
| locus symbol | Japanese | Caucasian |
| D16S401 | 63 | 70 |
| D16S405 | 72 | 73 |
| D16S407 | 91 | 92 |
| D16S411 | 66 | 79 |
| D16S415 | 66 | 64 |
| D16S420 | 34 | 79 |
| D16S423 | 81 | 71 |
| D16S503 | 63 | 75 |
| D16S511 | 91 | 88 |
| D16S515 | 72 | 89 |
| D16S516 | 72 | 73 |
| D16S520 | 81 | 86 |
| locus symbol | Japanese | Caucasian |
| D17S784 | 66 | 78 |
| D17S787 | 78 | 78 |
| D17S791 | 88 | 88 |
| D17S798 | 53 | 71 |
| D17S799 | 69 | 61 |
| D17S802 | 81 | 79 |
| D17S808 | 78 | 79 |

| | | |
|---|---|---|
| D17S849 | 91 | 71 |
| D17S925 | 72 | 88 |
| D17S928 | 84 | 82 |
| D17S938 | 66 | 89 |
| D17S945 | 88 | 82 |
| D17S949 | 78 | 85 |
| locus symbol | Japanese | Caucasian |
| D18S452 | 81 | 82 |
| D18S462 | 59 | 75 |
| D18S464 | 56 | 70 |
| D18S469 | 47 | 57 |
| D18S474 | 75 | 82 |
| D18S478 | 59 | 57 |
| D18S52 | 69 | 59 |
| D18S53 | 78 | 75 |
| D18S57 | 78 | 89 |
| D18S59 | 75 | 61 |
| D18S61 | 88 | 78 |
| D18S64 | 81 | 88 |
| D18S68 | 75 | 89 |
| D18S70 | 84 | 86 |
| locus symbol | Japanese | Caucasian |
| D19S216 | 53 | 81 |
| D19S209 | 84 | 89 |
| D19S210 | 63 | 89 |
| D19S220 | 81 | 93 |
| D19S221 | 72 | 89 |
| D19S226 | 78 | 75 |
| D19S414 | 50 | 89 |
| D19S418 | 63 | 56 |
| D19S420 | 78 | 74 |
| locus symbol | Japanese | Caucasian |
| D20S100 | 69 | 64 |
| D20S107 | 78 | 81 |
| D20S115 | 56 | 57 |
| D20S117 | 78 | 88 |
| D20S118 | 47 | 82 |
| D20S119 | 69 | 96 |
| D20S171 | 63 | 79 |
| D20S173 | 81 | 75 |
| D20S178 | 56 | 85 |
| D20S186 | 91 | 87 |
| D20S189 | 53 | 75 |
| D20S195 | 78 | 82 |
| D20S196 | 84 | 81 |
| D20S95 | 66 | 84 |
| locus symbol | Japanese | Caucasian |
| D21S1252 | 78 | 79 |
| D21S1253 | 75 | 82 |
| D21S1256 | 69 | 75 |
| D21S263 | 72 | 75 |

| | | |
|---|---|---|
| D21S266 | 88 | 68 |
| locus symbol | Japanese | Caucasian |
| D22S274 | 88 | 82 |
| D22S280 | 84 | 89 |
| D22S283 | 75 | 85 |
| D22S315 | 81 | 96 |
| D22S420 | 63 | 70 |
| D22S423 | 75 | 79 |
| locus symbol | Japanese | Caucasian |
| DXS1001 | 75 | 83 |
| DXS1047 | 75 | 89 |
| DXS1055 | 25 | 67 |
| DXS1060 | 84 | 81 |
| DXS1068 | 69 | 59 |
| DXS1106 | 22 | 67 |
| DXS1202 | 66 | 89 |
| DXS1214 | 78 | 68 |
| DXS1226 | 72 | 78 |
| DXS1227 | 72 | 65 |
| DXS986 | 75 | 73 |
| DXS987 | 78 | 92 |
| DXS990 | 84 | 69 |
| DXS991 | 69 | 95 |
| DXS993 | 81 | 86 |

**Fig. 1** Continue

**Table 1** Comparison of heterozygosities at 358 test loci between Japanese and Caucasians

| Observed heterozygosity (%) | No. of markers in each category among Japanese tested | No. of markers in each category in GDB (Caucasian) |
|---|---|---|
| 0–20 | 5 | 0 |
| 20–30 | 6 | 0 |
| 30–40 | 11 | 0 |
| 40–50 | 16 | 2 |
| 50–60 | 32 | 10 |
| 60–70 | 70 | 42 |
| 71–80 | 108 | 114 |
| 81–90 | 87 | 161 |
| 91–100 | 23 | 29 |

GDB, Genome Database

observed) although heterozygosity at this locus is 85% among 30 Caucasians registered in the GDB. As Table 1 shows, in the Japanese sample, 38 marker loci revealed heterozygosity lower than 50% but only two markers did so in Caucasians; moreover, 11 of these markers in Japanese (vs none in Caucasians) showed heterozygosity lower than 30%. Although heterozygosity was higher overall in Caucasians, a few markers showed higher heterozygosity in Japanese; for example, at D9S158 we observed 100% heterozygosity in Japanese as opposed to the 70% reported in Caucasians. Our results should provide information for the selection of appropriate markers for disease analyses in Japanese families.

Many marker loci revealed quite different allelic distributions between the two populations; representative data are shown in Table 2. For instance, a 133-bp allele at the D16S423 locus accounted for 25% of Japanese alleles, but for only 3% of Caucasian alleles. On the other hand, the 137-bp and 149-bp alleles at this locus accounted for more than 70% of all chromosomes in Caucasians, and for just 8% in Japanese. At the locus defined by D14S292, an 80-bp allele was seen in 93% of Japanese chromosomes and in the remainder, allele sizes varied from 80 to 88 bp. However, in Caucasians, the alleles varied from 86 to 94 bp, with four alleles being most common. It is apparent that miscalculation at some loci can occur if allelic distribution information derived from Caucasians is applied to sib-ship pair analyses or association studies in the Japanese population. For

**Table 2** Allelic distributions of D16S423 and D14S292 among 64 Japanese and 60 Caucasian chromosomes

| Locus: D16S423<br>Allele (bp) | Japanese frequency | Caucasian frequency |
|---|---|---|
| 131 | 0.0156 | |
| 133 | 0.25 | 0.036 |
| 135 | 0.0469 | 0.018 |
| 137 | 0.0938 | 0.357 |
| 139 | 0.0313 | 0.018 |
| 141 | 0.0469 | 0.018 |
| 143 | 0.3125 | 0.054 |
| 145 | 0.0781 | 0.036 |
| 147 | 0.0938 | 0.054 |
| 149 | 0.0313 | 0.357 |
| 151 | | 0.054 |
| **Locus: D14S292**<br>**Allele (bp)** | **Japanese frequency** | **Caucasian frequency** |
| 80 | 0.9375 | |
| 82 | 0.0313 | |
| 84 | 0.0156 | |
| 86 | | 0.259 |
| 88 | 0.0156 | 0.278 |
| 90 | | 0.315 |
| 92 | | 0.013 |
| 94 | | 0.014 |

Frequencies are indicated to the right of each allele size. Caucasian data were obtained from the GDB.

genetic analyses of families carrying genetic diseases, for homozygosity mapping, for sib ship-pair analyses, and for association studies, one should avoid uninformative markers and, for any statistical calculations, one should consider allelic distributions in the population under study. Hence, the results reported here provide essential data for investigating genes related to diseases in Japanese families. These results may also contribute to anthropologic research, such as investigations into the origin of the Japanese people.

**Acknowledgments** This work was supported by a Grant from the Ministry of Health and Welfare of Japan.

## References

Dib C, Faure S, Fizames C, Samson D, Drouot N, Vignal A, Millasseau P, Marc S, Hazan J, Seboun E, Lathrop M, Gyapay G, Morissette J, Weissenbach J (1996) A comprehensive genetic map of the human genome based on 5264 microsatellites. Nature 380: 152–154

Sato T, Tanigami A, Yamakawa K, Akiyama F, Kasumi F, Sakamoto G, Nakamura Y (1990) Allelotype of breast cancer: Cumulative allele losses promote tumor progression in primary breast cancer. Cancer Res 50: 7184–7189

Yamane Y, Nakamura Y, Isomura M (1997) Allelic frequencies of twelve dinucleotide repeat marker loci on chromosome 13 in the normal Japanese population. Jpn J Hum Genet 42: 533–537