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DNA Fingerprinting of the NCI-60 Cell Line Panel

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Abstract

The National Cancer Institute's NCI-60 cell line panel, the most extensively characterized set of cells in existence and a public resource, is frequently used as a screening tool for drug discovery. Since many laboratories around the world rely on data from the NCI-60 cells, confirmation of their genetic identities represents an essential step in validating results from them. Given the consequences of cell line contamination or misidentification, quality control measures should routinely include DNA fingerprinting. We have, therefore, used standard DNA microsatellite short tandem repeats to profile the NCI-60, and the resulting DNA fingerprints are provided here as a reference. Consistent with previous reports, the fingerprints suggest that several NCI-60 lines have common origins: the melanoma lines MDA-MB-435, MDA-N, and M14; the central nervous system lines U251 and SNB-19; the ovarian lines OVCAR-8 and OVCAR-8/ADR (also called NCI/ADR); and the prostate lines DU-145, DU-145 (ATCC), and RC0.1. Those lines also demonstrate that the ability to connect two fingerprints to the same origin is not affected by stable transfection or by the development of multidrug resistance. As expected, DNA fingerprints were not able to distinguish different tissues-of-origin. The fingerprints serve principally as a barcodes.

Keywords

DNA fingerprinting; NCI-60; cell contamination

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INTRODUCTION

The first human cell line, HeLa, was established in 1951, and, by 1956, mycoplasma contamination had been detected in it (1). As other cell lines have been established, contamination with microorganisms, contamination with other cell types, and misidentification have grown in importance as hindrances to incisive research with those cells. In particular, over the past decade, inter- and intra-species cross contaminations have been reported in 18 – 36% of the lines deposited in worldwide cell banks (2, 3), and repeated occurrences of cell misidentification have underscored the necessity of regular assessment of the origin of cell line DNA. In recent years, therefore, new techniques have been developed for identifying contaminated and misidentified lines by DNA microsatellite fingerprinting (4, 5). Given the low cost, high efficiency, and high reproducibility of the assays, the scientific community is expected to move toward a model in which manuscript submission and grant application processes require researchers to provide DNA fingerprinting data for their cell lines. Toward that end, we here describe a DNA fingerprinting analysis of the NCI-60 human cancer cell line panel as a reference for research with those widely used cells.

The NCI-60 panel, originally assembled to screen for anticancer agents (6–8), has been profiled more extensively at the molecular level than any other set of cells in existence (9). That molecular characterization, a central subject of this journal's Spotlight on Molecular Profiling Series (9–18), provided motivation for the present study. The 60 lines include cancers of breast, central nervous system, colon, lung, ovary, prostate, and renal origin, plus leukemias and melanomas. Drug discovery with the panel has recently been reviewed by Shoemaker (8) and by Holbeck (7). More than 100,000 chemically defined compounds as well as a large number of natural product extracts have been screened for activity. The panel has also been molecularly profiled using array-based platforms (9) and small-molecule profiling techniques (unpublished data). Those data can be accessed through several databases: the NCI Developmental Therapeutics Program website (http://dtp.nci.nih.gov/); CellMiner (http://discover.nci.nih.gov/cellminer) (9, 17); the SKY/M-FISH/CGH Database (http://www.ncbi.nlm.nih.gov/sky/); and the Gene Expression Omnibus (http://www.ncbi.nlm.nih.gov/geo/). Those data sets have provided the foundation for many translational discoveries (e.g., (15)), but misidentification has been reported for several of the lines: OVCAR-8/ADR was initially thought to be a doxorubicin (Adriamycin)-resistant derivative of MCF7 breast cancer. However, we observed that it bore no relation in phenotype to those cells, hence it was renamed, agnostically, NCI/ADR. We later found, on the basis of spectral karyotyping and comparative genomic hybridization (12, 19, 20), that it is actually a derivative of OVCAR-8. MDA-MB-435 and its HER2/ERBB2-transfectant MDA-N were previously thought to be of breast origin. However, we found on the basis of transcript expression profiles and other characteristics that they are melanomas (21, 22). Re-sequencing (12) and genotyping (23) then showed the two to be direct relatives of the melanoma line M14. Likewise, SNB-19 was found (by re-sequencing) to be a direct relative of U251 (12).

DNA fingerprinting takes advantage of hypervariable regions within DNA (24). An inexpensive, standardized technique was developed for forensic and paternity applications

based on short tandem repeat (STR) profiling of those hypervariable DNA regions (25), and it is now commonly employed for cell line characterization (26, 27). The kit used in this study included the 13 combined DNA index system (CODIS) loci, the amelogenin gender-determining marker used in forensics, and 2 additional loci for a total of 16 loci (32 alleles). Those loci have been selected based on desirable properties: they are discrete, they behave according to known principles of population genetics, and STR profiles can be determined with very small amounts of DNA. The multiplexed assay uses PCR to amplify tetranucleotide repeat sequences for those 16 loci. The resulting data indicate the number of STRs at each locus surveyed. These data provide a reference fingerprint for the cell lines.

MATERIALS AND METHODS

Cell culture

Cell lines were maintained in RPMI-1640 (Lonza) containing 5% fetal bovine serum, 2 mM L-glutamine, and no antibiotics. All cell lines were tested for mycoplasma using the MycoAlert assay (Lonza) at the commencement of this study and found to be negative. Sources and patient donor information are described elsewhere (28), updated and expanded at http://discover.nci.nih.gov/cellminer. The abbreviation before each cell line name denotes tissue-of-origin (BR = breast, CNS = central nervous system, CO = colon, ME = melanoma, OV = ovarian, PR = prostate, RE = renal). Additional DNA samples from BT-549, MCF7, and MDA-MB-231 cell lines were kindly provided by Natasha Caplen and Kristen Gehlhaus. Michael Birrer and Laurent Ozbun provided additional OVCAR-3 and SK-OV-3 cell samples, and Christina Annunziata and Elise Kohn provided additional DNA samples of OVCAR-3, OVCAR-4, OVCAR-5, OVCAR-8, and SK-OV-3.

DNA Fingerprinting

DNA was prepared from cells using the Qiagen Blood & Cell Culture DNA Maxi Kit according to the manufacturer's protocol (Qiagen). DNA fingerprints were obtained for all cell lines using the AmpF STR Identifiler PCR Amplification Kit (Applied Biosystems) according to the manufacturer's protocol. The kit amplifies the amelogenin gender-determining marker and 15 tetranucleotide repeat loci (listed in Table 1) in a single PCR amplification using 33 primers (the extra one is a degenerate primer targeting a mutation at the D8S1179 locus). That combination of markers is consistent with worldwide database recommendations for identity testing. Each of the STRs used in this study has a tetranucleotide repeat sequence. Allele calls were made from peak plots by comparing peaks to known fragment sizes using GeneMapper 4.0 (Applied Biosystems). Intermediate-sized alleles were observed for D19S433, D21S11, D7S820, FGA, and TH01 (Table 1), and, accordingly, a decimal followed by an integer indicates additional alleles at those loci.

Comparative analysis

The STR data from all possible combinations of cell line pairs were compared using a similarity metric previously reported by Masters et al. (27). Percent similarity was computed by dividing the number of identical alleles by 32 (the total number of surveyed alleles) then multiplying by 100 (Supplementary Table S1), where "identical" means same number of STRs. Since technical repeats suggested that a difference of one STR at one site probably

does not indicate a different allele (data not shown), we computed a second set of comparisons in which the definition of "identical" was relaxed to include a difference of one STR at one site (Table 2). The algorithm used to compute those similarity metrics and instructions for using it are provided on our website (http://discover.nci.nih.gov). Both sets of calculations used 80% similarity as a cutoff for "same" (27).

DNA fingerprinting techniques normally assume two alleles; the presence of more than two alleles in DNA from normal cells indicates genomic heterogeneity, which is typically equated with "contamination." For the cancer cells profiled here, we defined genomic heterogeneity as the presence of more than two alleles at three or more of the 16 loci. Since insertions, deletions, and translocations are a hallmark of cancer, though, one must be careful about concluding "contamination" upon the observation of genomic heterogeneity, especially if there is no evidence that the cell line has ever exhibited a clean fingerprint. In the NCI-60, only the MOLT-4 cell line was observed to exhibit genomic heterogeneity, but since numerous MOLT-4 stocks dating back as far as possible were found to exhibit the same fingerprint, we cannot apply the "contaminated" label to MOLT-4.

Heterozygosity (i.e., different alleles at a locus) was quantitated in two ways. First, overall heterozygosity was determined within each cell line over the 15 surveyed loci (amelogenin excluded) by dividing the number of loci with different alleles (i.e., at least one peak exhibiting a different number of STRs) by 15. Second, heterozygosity was determined within each of the 15 surveyed loci over the 61 successfully analyzed samples by dividing the number of loci with different alleles by 61.

RESULTS AND DISCUSSION

Molecular profiling of the NCI-60 lines at the DNA, RNA, protein, chromosomal, and pharmacological levels has been a central focus of the Spotlight on Molecular Profiling series in this journal (9–18). To minimize the chance that such profiling studies by our own and other laboratories in the future will be confounded by contamination or misidentification of lines, we undertook DNA fingerprinting of the cells. All but one (MOLT-4) of the NCI-60 cell lines were successfully analyzed. The fingerprints are shown in Table 1, which includes those of two additional cell lines—DU-145 (ATCC) and its camptothecin-resistant derivative, RC0.1. We first analyzed the fingerprints to determine whether cell lines from the same origin (i.e., same patient) could be identified. Similarly, we wondered whether cell lines from the same tissue-of-origin (not necessarily the same patient) would co-cluster. In addition we asked, "What effect does stable transfection have on DNA fingerprint?" and "What effect does the development of drug resistance have on DNA fingerprint?" As loss of heterozygosity is common in cancer, we also asked, "What degree of heterozygosity is exhibited by each cell line and by each of the loci surveyed?" Finally, we surveyed the fingerprints for cell lines that exhibit more than two alleles at a given locus, an indication of genomic contamination.

Matching Profiles

From the 61 fingerprints (MOLT-4 excluded), 1830 pairwise comparisons were made to compute all possible similarity indices (Supplementary Table S1) using a stringent definition

of “identical,” as described in Materials and Methods. By that analysis, 55 of the 61 fingerprints were unique (i.e., exhibited less than 80% similarity). Two observations, however, suggested that perfect identity was too stringent a criterion. First, a technical replicate of the OVCAR-8 cell line yielded a one-STR difference at the vWA_1 allele (changed from 16 to 17). Second, the DU-145 (ATCC)|RC0.1 and U251|SNB-19 cell line pairs yielded 78% similarity (Supplementary Table S1), despite the fact that the latter in each case is now known on the basis of other information to have been derived from the former (12, 29). Hence, a practical solution was to maintain a strict 80% cutoff but to relax the definition of “identical” to include a difference of up to one STR. That new algorithm did indeed bump the two aforementioned pairs from 78% to 81% similar (Table 2), so those similarity metrics will be considered the accepted calculations for the remainder of this discussion.

The eight cell line pairs found to be at least 80% similar were: M14|MDA-MB-435, M14|MDA-N, MDA-MB-435|MDA-N, U251|SNB-19, OVCAR-8|OVCAR-8/ADR, DU-145|DU-145 (ATCC), DU-145 (ATCC)|RC0.1, and DU-145|RC0.1. The first three of those pairs were expected based on re-sequencing (12) and genotyping (23), which showed that the MDA-MB-435 melanoma and its HER2/ERBB2-transfectant MDA-N were derived from the M14 melanoma line. Similarly, re-sequencing indicated that the SNB-19 line is derived from U251 (12). The OVCAR-8|OVCAR-8/ADR similarity was also expected since the latter was found, on the basis of spectral karyotyping and comparative genomic hybridization, to be close to identical to the former (12, 19, 20). The DU-145|DU-145 (ATCC) similarity was expected since they are the same prostate line. The absence of 100% similarity appeared to be due to deletion of the D13S317 locus in the latter (Table 1), but array-based comparative genomic hybridization data from the two DU-145 lines suggested that D13S317 was not deleted in either line (data not shown), suggesting that the marker failed to amplify in the Identifiler PCR. After 81%, the next highest similarity metric was 59% for the renal lines ACHN|CAKI-1 (Table 2). The relaxed similarity algorithm in combination with an 80% cutoff therefore identified all pairs known to be similar, and there was a large fall-off to the next highest similarity.

To determine whether DNA fingerprinting could potentially distinguish tissues of origin, we assessed whether similarity indices within each tissue-of-origin were greater than similarity indices across different tissues of origin (Table 1). Mean similarity indices (after eliminating the eight cell line pairs discussed in the previous paragraph, since they would falsely inflate the calculated indices) were 28% for breast, 28% for CNS, 27% for colon, 32% for lung, 32% for leukemia, 32% for melanoma, 29% for ovarian, 31% for prostate, and 36% for renal subsets. In comparison, the overall mean similarity index (including both same and different tissue-of-origin comparisons) was 31% (± 2 SD). It was not possible, therefore, to identify tissue of origin on the basis of the DNA fingerprints.

Interestingly, the amelogenin marker indicated only X chromosomes for the prostate line PC-3. However, amelogenin has been reported to type some males as females incorrectly due to deletion of the Y copy of amelogenin (30). Consistent with that report, cytogenetic analysis has shown that 13 NCI-60 cell lines, including PC-3 (19), have been reported to be

of male origin but exhibit Y deletions. In that regard, PC-3 does not appear to be a misidentified cell line.

To determine the effect of culture conditions on DNA fingerprinting, we analyzed a subset of NCI-60 lines from multiple users in three additional laboratories (Table 3). One sample (an OVCAR-3 culture) was only 28% similar to the DTP version. All of the other comparisons showed at least 80% similarity with the DTP counterpart. Possible explanations for that extreme observation include misidentification of an OVCAR-3 derivative selected for resistance to a particular treatment (31). Aside from that one sample, the smaller differences observed in most of the samples from different laboratories were likely due to differences in culture conditions or genetic drift due to differences in passage number. Such effects can be monoclonal or polyclonal in nature (19). For example, despite 97% similarity between the other OVCAR-3 sample and the DTP version of OVCAR-3, the two lines exhibit large differences in asparagine synthetase (ASNS) protein but not *ASNS* mRNA expression (14). In addition, the DTP version is ten-fold less sensitive to doxorubicin and expresses significantly lower levels of the transporter TRPM2 (Calcagno et al., manuscript in preparation). Hence, since differences in culture conditions can lead to different phenotypes, our laboratory has focused on using the same culture reagents (e.g., matched batches of fetal bovine serum) for every cell line and on minimizing passage crawl (our frozen stocks are believed to be at passage numbers below 30 since incorporation into the DTP screen).

Stable Transfection

As expected based on previous work (12, 21–23), MDA-MB-435 was 100% similar (i.e., the same fingerprint) to its HER2/ERBB2-transfectant, MDA-N, and both of those lines were 94% similar to M14 (Table 2), from which both are believed to have originated. Hence, consistent with previous reports (27), stable transfection appears to have had little or no effect on the fingerprint results.

Drug Resistance

The ovarian line OVCAR-8/ADR is a doxorubicin (Adriamycin)-resistant derivative of OVCAR-8 (12, 19, 20). Those two lines differed at only one site, yielding a 97% similarity (Table 2). The two versions of DU-145, one from DTP and one from ATCC, were 94% similar to each other, as discussed above. The latter was only 81% similar to its camptothecin-resistant derivative RC0.1, whereas the former was 88% similar, suggesting the possibility that RC0.1 was actually derived from the DTP version of DU-145. That possibility is moot, however, in light of our observation (discussed above) that the D13S317 deletion in the ATCC version of DU-145 appears to be attributable to failure of the D13S317 primers to amplify. That is, if the D13S317 site amplified as expected, there would be no difference between the two DU-145 lines; both would exhibit 88% similarity to RC0.1.

Loss of Heterozygosity

Whereas heterozygosity among normal, non-cancerous human samples (e.g., those analyzed forensically by crime laboratories) is reported to range from 79 to 88% (27), heterozygosity

in this study ranged from 7 to 93% for a given cell line (excluding MOLT-4) over the 15 surveyed loci (excluding amelogenin) (Table 1) and from 39 to 69% for a given locus over the 61 successfully fingerprinted samples (Table 4). In the former case, the median was 53% heterozygosity, and the extremes were 7% heterozygosity in BT-549 and 93% heterozygosity in both SF-295 and IGROV1. In the latter case, the median was 56% heterozygosity, and the extremes were 39% heterozygosity at the D13S317 locus and 69% heterozygosity at the D7S820 locus.

More than Two Alleles at a Locus

MOLT-4 was the only cell line observed to have more than two alleles at multiple loci. That genomic heterogeneity (i.e., “contamination”) was repeatable in follow-up analyses (data not shown) and has been shown for MOLT-4 by other laboratories (27). In our analysis of MOLT-4, two loci (D21S11 and FGA) gave four peaks, and four loci (D7S8S0, CSF1PO, D19S433, and vWA) gave three peaks (Supplementary Table S2 and Supplementary Figure S1). Interestingly, the heterogeneity is not detected at five of those six loci by spectral karyotyping (19), suggesting that the PCR-based Identifiler assay is more sensitive than spectral karyotyping at detecting multiple alleles at a given locus.

What is the molecular basis for the heterogeneity? It could be 1) intra-cellular due to genomic instability (i.e., rapid structural rearrangement), or 2) inter-cellular due to different cell populations. The first possibility is unlikely since MOLT-4 exhibits a high degree of genomic stability (19). The second hypothesis can be addressed by single-cell subcloning, which is currently underway in our laboratory and will be the topic of a future report.

Another line, SK-OV-3, was previously reported to have three alleles at three loci (27). Contrary to that report, we found no evidence of more than two peaks at any locus for SK-OV-3, suggesting that the previously fingerprinted version of SK-OV-3 was contaminated with another culture.

Conclusion

We report reference DNA fingerprints for the NCI-60 cell line panel in expectation that many other laboratories can use the information (Table 1). We suggest that each laboratory using NCI-60 cell lines should perform the same analysis to confirm the identities of their lines. Any culture that shows a serious deviation from the reference profile should be replaced with a cryopreserved stock of the original line.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Abbreviations

DTP	Developmental Therapeutics Program
NCI	National Cancer Institute
STR	short tandem repeat

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Table 1

DNA fingerprints for NCI-60 cell lines (DTP source)

Tissue of Origin: Cell Line	AMEL_1	AMEL_2	CSF1PO_1	CSF1PO_2	D13S317_1	D13S317_2	D16S539_1	D16S539_2	D18S51_1	D18S51_2	D19S433_1	D19S433_2	D21S11_1	D21S11_2	D2S1338_1	D2S1338_2	D3S1358_1	D3S1358_2	D5S818_1	D5S818_2	D7S820_1	D7S820_2	D8S1179_1	D8S1179_2	FGA_1	FGA_2	TH01_1	TH01_2	TPOX_1	TPOX_2	vWA_1	vWA_2	Het (%)[2]
BR:BT-549	X	X	10	10	11	11	8	8	0	0	15.2	15.2	32.2	32.2	17	17	18	18	11	11	9	9	14	16	19	19	9.3	9.3	8	8	15	15	7
BR:HS578T	X	X	13	13	11	11	9	12	16	16	14	15	29	32.2	17	26	16	17	11	11	10	10	13	13	23	24	9	9.3	8	8	17	17	47
BR:MCF7	X	X	10	10	11	11	11	12	14	14	13	14	30	30	21	23	16	16	11	12	8	9	10	14	23	25	6	6	9	12	14	15	60
BR:MDA-MB-231	X	X	12	13	13	13	12	12	11	16	11	14	33.2	33.2	20	21	16	16	12	12	8	9	13	13	22	23	7	9.3	8	9	15	18	60
BR:T47D	X	X	11	13	12	12	10	10	17	17	14	14	28	31	24	24	15	17	12	12	11	11	13	13	23	23	6	6	11	11	14	14	20
CNS:SF-268	X	Y	12	12	11	11	9	13	16	16	13	15.2	30	32.2	19	24	14	16	11	11	10	11	14	14	21	21	6	9	8	10	17	19	60
CNS:SF-295	X	X	10	13	10	10	12	13	15	18	12	15	28	30	15	20	16	18	11	12	9	13	13	14	22	25	9.3	10	8	11	16	17	93
CNS:SF-539	X	X	11	13	12	12	11	12	20	20	14	14	29	29	17	23	15	15	14	14	11	11	15	17	20	21	7	8	9	10	16	17	53
CNS:SNB-19	X	Y	12	12	10	11	12	12	0	0	13	15	29	29	22	24	16	17	11	12	10	10	13	15	21	21	9.3	9.3	8	8	16	18	47
CNS:SNB-75	X	X	10	12	8	12	11	13	18	18	13	14	30	30	17	23	17	17	12	12	9	9	12	12	19	23	9	9	8	10	16	18	53
CNS:U251	X	Y	12	13	10	11	12	12	13	13	13	15	29	29	24	24	16	17	11	11	10	12	13	15	21	25	9.3	9.3	8	8	16	18	53
CO:HCT-116	X	X	7	10	10	12	11	13	16	17	12	13	29	30	16	16	12	19	10	11	11	12	12	14	18	23	8	9	8	8	17	17	80
CO:COLO205	X	X	11	12	10	12	12	13	18	18	13	14	30.2	30.2	17	18	16	16	10	13	9	10	9	9	21	23	8	9	11	11	15	15	60
CO:HCC-2998	X	X	11	13	11	12	9	12	12	15	12	15	29	30	18	23	17	19	12	12	10	11	11	14	25	25	7	9.3	8	11	18	19	87
CO:HCT-15	X	Y	12	12	8	11	12	13	11	17	14	16	29	32.2	17	25	17	17	13	13	10	12	15	15	22	22	7	9.3	8	11	18	19	67
CO:HT29	X	X	11	12	11	12	11	12	13	13	14	14	29	30	19	23	15	17	11	12	10	10	10	10	20	22	6	9	8	9	17	19	73
CO:KM12	X	X	10	12	12	15	11	11	13	13	11	14	27	27	0	0	14	14	10	18	8	8.3	11	13	20	22	9.3	9.3	11	12	17	19	60
CO:SW-620	X	X	13	14	12	12	9	13	13	13	13	13	30	30.2	17	24	16	16	13	13	8	9	13	13	24	24	8	8	11	11	16	16	33
LC:A549-ATCC	X	Y	10	12	11	11	11	12	14	17	13	13	29	29	24	24	16	16	11	11	8	11	13	14	23	23	8	9.3	8	11	14	14	47
LC:EKVX	X	Y	9	9	11	11	9	11	13	16	13	13	30	31	17	19	16	18	11	12	9	12	15	15	20	21	9.3	9.3	8	11	15	15	60
LC:HOP-62	X	X	11	12	12	12	11	12	14	14	13	14	30	30	19	19	14	18	11	11	10	12	13	13	22	24	8	9	8	11	15	17	60
LC:HOP-92	X	X	10	10	12	12	12	12	12	18	13	13	30	30	19	23	18	18	12	12	8	10	14	14	19	21	9	9.3	8	11	15	15	40
LC:NCI-H226	X	Y	10	11	13	14	9	12	16	16	15	15	29	32.2	25	25	16	16	11	12	8	10	14	15	20	23	8	9.3	8	8	17	17	60
LC:NCI-H23	X	X	10	10	12	12	9	11	14	16	12	14	30	30	18	23	15	15	12	13	9	10	15	15	24	24	6	6	8	9	16	17	53
LC:NCI-H322M	X	Y	12	12	12	12	11	12	17	17	14	14	28	28	19	25	15	15	11	11	11	11	12	15	22	22	7	7	8	8	17	17	20
LC:NCI-H460	X	Y	11	12	13	13	9	9	13	15	14	14	30	30	17	25	15	18	9	10	9	12	12	12	21	23	9.3	9.3	8	8	17	17	47
LC:NCI-H522	X	X	10	12	10	10	12	12	14	18	16	16	28	31.2	17	20	16	16	10	11	9	10	12	13	24	24	7	9.3	9	10	17	17	60
LE:CCRF-CEM	X	X	11	11	11	12	10	13	0	0	14	15	30	33.2	24	24	15	15	12	13	9	13	13	13	23	24	6	7	8	8	17	19	60
LE:HL-60	X	X	13	14	8	11	11	11	14	15	14	14	29	30	17	17	16	16	12	12	11	12	12	13	22	22	7	8	8	11	16	16	53
LE:K-562	X	X	9	10	8	8	11	12	15	16	14	14.2	0	0	17	17	16	16	11	12	9	11	12	12	21	24	9.3	9.3	8	9	16	16	53
LE:MOLT-4[1]	X	Y	11,12	13	12	13	11	14	13	17	14,15	16	28,29	30,31	23	24	14	16	0	12	8,10	11	9	14	22,23	24,25	6	8	0	8	17	18,19	100
LE:RPMI-8226	X	X	12	12	11	11	9	9	15	19	13.2	14	28	29	20	20	16	17	11	13	9	10	13	13	19	19	8	8	8	11	16	18	53
LE:SR	X	Y	14	15	11	11	11	13	13	14	12	14	28	30	24	24	14	16	11	11	9	12	13	13	20	22	6	7	8	11	17	18	73
ME:LOXIMVI	X	X	10	12	11	11	10	12	15	18	14.2	14.2	28	31	18	24	14	15	11	13	9	11	11	13	22	22	7	9.3	9	11	14	17	80
ME:M14	X	X	11	11	12	12	9	13	13	17	14	15	30	30	19	24	14	16	11	12	8	10	13	13	21	21	6	7	8	11	16	18	67
ME:MALME-3M	X	Y	12	12	8	13	9	12	14	14	13	14	30.2	32.2	24	24	14	18	11	11	9	12	13	13	21	22	8	8	8	9	15	16	60
ME:MDA-MB-435	X	X	11	11	12	12	13	13	13	17	14	14	30	30	19	24	14	14	11	12	8	10	13	13	21	21	6	7	8	11	16	18	47
ME:MDA-N	X	X	11	11	12	12	13	13	13	17	14	14	30	30	19	24	14	14	11	12	8	10	13	13	21	21	6	7	8	11	16	18	47
ME:SK-MEL-2	X	Y	10	12	11	11	8	9	15	16	12	15	29	30	0	0	14	16	12	13	11	12	12	13	0	0	9	9	8	9	17	17	67
ME:SK-MEL-28	X	Y	10	10	11	12	9	12	12	16	14	14	28	29	18	18	16	18	13	13	10	10	13	13	19	19	7	7	12	12	19	19	33
ME:SK-MEL-5	X	X	10	13	10	12	10	12	15	16	14	15	29	29	17	25	16	17	11	13	9	12	12	15	20.2	22	6	9	11	11	14	14	80
ME:UACC-257	X	X	11	13	8	13	9	11	15	15	12	15	30	31.2	17	25	17	17	12	13	11	12	13	15	22	22	8	8	9	12	16	17	73
ME:UACC-62	X	X	10	11	12	12	9	12	15	15	15	15	28	31	18	20	15	15	10	12	8	11	10	13	23	23	6	9	8	11	16	17	67
OV:IGROV1	X	X	11	13	8	10	11	12	15	16	13	14	26	30.2	17	25	13	15	12	13	0	0	14	16	21	26	7	9.3	8	11	17	21	93
OV:OVCAR-3	X	X	11	12	12	12	12	12	13	13	16.2	16.2	29	31.2	17	21	17	18	11	12	10	10	10	15	21	21	9	9	8	8	17	17	40
OV:OVCAR-4	X	X	10	10	9	9	11	11	15	15	13	15	28	31	23	23	15	15	13	13	10	11	13	13	21	21	9	9	8	8	14	18	27
OV:OVCAR-5	X	X	10	10	10	13	11	11	12	12	13	14	31	31	17	23	15	16	11	13	10	10	13	14	23	23	7	9.3	8	11	16	16	53
OV:OVCAR-8	X	X	11	11	12	12	13	13	14	14	14	16	28	28	19	23	16	18	12	12	12	12	10	10	20	20	7	7	8	8	16	17	27
OV:OVCAR-8/ADR	X	X	11	11	12	12	13	13	14	14	14	16	28	28	19	23	18	18	12	12	12	12	10	10	20	20	7	7	8	8	16	17	20
OV:SK-OV-3	X	X	11	11	8	11	12	12	16	17	14	14.2	30	31.2	18	23	13	14	11	11	13	14	14	15	0	0	9	9.3	8	11	18	18	67
PR:DU-145 (ATCC)	X	Y	10	11	0	0	11	13	12	12	13	13	30	33	16	16	16	16	10	13	0	0	13	14	22	22	7	7	11	11	17	18	40
PR:DU-145	X	Y	10	11	12	14	11	13	12	12	13	13	30	33	16	16	16	16	10	13	0	0	13	14	22	22	7	7	11	11	17	18	47
PR:PC-3	X	X	11	11	11	11	11	14	15	14	14	29	31.2	18	20	16	16	13	13	8	11	13	13	24	24	6	7	8	9	17	17	40
PR:RC0.1	X	Y	10	11	12	14	0	0	12	12	13	13	30	33	16	17	16	16	10	13	7	11	13	14	22	22	7	7	11	11	17	18	53
RE:786-0	X	Y	10	10	8	8	12	12	13	14	14	15	29	30	17	18	16	16	9	9	11	12	13	13	24	24	6	9.3	8	11	15	17	53
RE:A498	X	X	11	12	12	12	12	12	17	17	12	12	28	32	26	26	15	15	11	13	10	11	13	15	18	20	6	9.3	8	11	18	18	53
RE:ACHN	X	X	11	11	12	12	12	13	16	16	14	14	30	30	17	17	17	17	12	12	9	11	12	12	22	22	8	8	8	11	16	17	27
RE:CAKI-1	X	X	10	11	11	12	12	12	14	14	14	14	28	30	17	17	17	17	11	12	12	12	12	14	26	26	6	8	8	11	17	17	47
RE:RXF-393	X	X	10	12	9	12	11	11	16	18	13	14	28	33.2	18	18	15	15	12	13	11	12	13	13	24	27	7	8	8	11	16	17	73
RE:SN12C	X	X	9	10	9	9	11	11	12	12	14	14	29	30	17	25	15	15	11	11	9	9	12	12	21	22	6	8	8	11	15	15	40
RE:TK-10	X	X	12	12	9	9	12	12	16	16	14	15	29	29	17	17	15	17	11	12	10	11	15	16	18	22	8	8	11	11	18	19	47
RE:UO-31	X	X	10	12	9	11	11	13	14	16	13	16.2	32.2	32.2	23	23	15	17	11	12	10	10	13	13	21	25	7	7	11	11	16	20	60

Number of STRs at each of the sixteen surveyed loci (two alleles, designated by _1 and _2, per locus). Numbers following a decimal indicate the number of bases in an incomplete final STR.

[1] A genomic mixture; values shown for reference purposes only. A comma separates allele calls for multiple peaks.

[2] Overall heterozygosity calculated within each cell line over 15 surveyed loci (AMEL excluded).

Table 2

Percent similarity of each pair of cell lines (allowing a difference of one STR at one locus)

Tissue of Origin: Cell Line	BR:BT-549	BR:HS578T	BR:MCF7	BR:MDA-MB-231	BR:T47D	CNS:SF-268	CNS:SF-295	CNS:SF-539	CNS:SNB-19	CNS:SNB-75	CNS:U251	CO:CO-HCT-116	CO:COLO205	CO:HCC-2998	CO:HCT-15	CO:HT29	CO:KM12	CO:SW-620	LC:A549-ATCC	LC:EKVX	LC:HOP-62	LC:HOP-92	LC:NCI-H226	LC:NCI-H23	LC:NCI-H322M	LC:NCI-H460	LC:NCI-H522	LE:CCRF-CEM	LE:HL-60	LE:K-562	LE:RPMI-8226	LE:SR
BR:BT-549	100	38	31	22	9	31	28	13	31	28	28	22	22	19	22	19	19	16	28	41	25	41	28	22	19	28	25	28	22	34	31	25
BR:HS578T	38	100	28	34	28	41	31	28	47	22	50	31	19	38	34	41	19	31	41	34	38	25	53	28	31	31	41	41	34	38	41	31
BR:MCF7	31	28	100	31	28	31	31	25	25	38	25	22	25	31	9	41	25	28	50	31	38	44	28	38	19	16	28	22	34	31	25	34
BR:MDA-MB-231	22	34	31	100	31	19	31	22	34	31	34	16	28	31	28	25	25	28	31	25	31	34	38	25	25	25	31	25	38	34	34	25
BR:T47D	9	28	28	31	100	16	25	38	19	28	22	22	28	31	19	34	22	31	38	16	31	25	13	31	38	22	16	47	31	19	28	31
CNS:SF-268	31	41	31	19	16	100	19	16	41	28	38	28	25	28	34	38	19	25	44	38	38	28	38	22	34	28	22	31	16	25	28	44
CNS:SF-295	28	31	31	31	25	19	100	19	38	34	41	31	31	38	22	22	16	25	28	31	34	38	28	31	22	25	41	28	31	34	41	34
CNS:SF-539	13	28	25	22	38	16	19	100	22	31	22	25	22	34	22	41	22	25	22	19	31	25	19	38	44	25	28	25	38	28	22	16
CNS:SNB-19	31	47	25	34	19	41	38	22	100	28	81	19	28	28	41	34	16	22	47	41	28	31	44	19	31	28	28	28	25	34	44	28
CNS:SNB-75	28	22	38	31	28	28	34	31	28	100	22	34	44	31	28	41	22	31	25	25	38	47	19	41	25	38	31	28	41	38	34	28
CNS:U251	28	50	25	34	22	38	41	22	81	22	100	25	22	31	41	31	19	28	50	41	31	22	38	16	31	31	25	25	25	31	38	41
CO:CO-HCT-116	22	31	22	16	22	28	31	25	19	34	25	100	31	31	22	31	19	22	34	16	38	28	31	28	38	31	28	25	31	22	16	31
CO:COLO205	22	19	25	28	28	25	31	22	28	44	22	31	100	19	25	28	22	44	28	28	38	34	22	25	16	28	41	25	25	25	34	22
CO:HCC-2998	19	38	31	31	31	28	38	34	28	31	31	31	19	100	34	44	19	19	31	25	31	44	28	34	22	25	19	31	34	25	22	22
CO:HCT-15	22	34	9	28	19	34	22	22	41	28	41	22	25	34	100	31	19	22	31	34	25	19	28	19	41	31	25	22	41	22	28	28
CO:HT29	19	41	41	25	34	38	22	41	34	41	31	31	28	44	31	100	38	19	28	25	47	34	31	38	44	34	22	38	34	31	31	41
CO:KM12	19	19	25	25	22	19	16	22	16	22	19	19	22	19	19	38	100	28	22	22	28	22	22	22	25	25	28	19	25	19	19	31
CO:SW-620	16	31	28	28	31	25	25	25	22	31	28	22	44	19	22	19	28	100	34	31	38	31	22	34	13	19	28	34	41	28	38	28
LC:A549-ATCC	28	41	50	31	38	44	28	22	47	25	50	34	28	31	31	28	22	34	100	38	41	34	44	16	34	22	31	25	31	31	38	44
LC:EKVX	41	34	31	25	16	38	31	19	41	25	41	16	28	25	34	25	22	31	38	100	34	41	38	31	19	41	19	19	31	38	31	38
LC:HOP-62	25	38	38	31	31	38	34	31	28	38	31	38	38	31	25	47	28	38	41	34	100	44	22	38	44	34	31	31	38	25	34	44
LC:HOP-92	41	25	44	34	25	28	38	25	31	47	22	28	34	44	19	34	22	31	34	41	44	100	31	41	22	22	28	22	25	25	22	16
LC:NCI-H226	28	53	28	38	13	38	28	19	44	19	38	31	22	28	28	31	22	22	44	38	22	31	100	28	34	38	31	22	22	31	25	25
LC:NCI-H23	22	28	38	25	31	22	31	38	19	41	16	28	25	34	19	38	22	34	16	31	38	41	28	100	31	31	31	41	31	31	31	25
LC:NCI-H322M	19	31	19	25	38	34	22	44	31	25	31	38	16	22	41	44	25	13	34	19	44	22	34	31	100	41	31	31	34	28	25	38
LC:NCI-H460	28	31	16	25	22	28	25	25	28	38	31	31	28	25	31	34	25	19	22	41	34	22	38	31	41	100	28	31	31	34	25	31
LC:NCI-H522	25	41	28	31	16	22	41	28	28	31	25	28	41	19	25	22	28	28	31	19	31	28	31	31	31	28	100	22	31	34	31	25
LE:CCRF-CEM	28	41	22	25	47	31	28	25	28	28	25	25	25	31	22	38	19	34	25	19	31	22	22	41	31	31	22	100	22	22	28	41
LE:HL-60	22	34	34	38	31	16	31	38	25	41	25	31	25	34	41	34	25	41	31	31	38	25	22	31	34	31	31	22	100	47	34	38
LE:K-562	34	38	31	34	19	25	34	28	34	38	31	22	25	25	22	31	19	28	31	38	25	25	31	31	28	34	34	22	47	100	28	22
LE:RPMI-8226	31	41	25	34	28	28	41	22	44	34	38	16	34	22	28	31	19	38	38	31	34	22	25	31	25	25	31	28	34	28	100	41
LE:SR	25	31	34	25	31	44	34	16	28	28	41	31	22	22	28	41	31	28	44	38	44	16	25	25	38	31	25	41	38	22	41	100
ME:LOXIMVI	28	31	31	25	34	28	38	28	25	22	22	13	25	34	31	25	31	22	41	28	34	25	22	28	38	19	44	31	28	31	41	38
ME:M14	16	34	31	31	44	44	38	28	41	34	34	25	31	34	22	44	25	50	31	31	47	44	34	38	31	31	19	50	34	31	38	50
ME:MALME-3M	28	31	25	34	22	44	22	16	38	25	44	19	31	16	31	28	22	31	44	34	56	22	28	25	34	38	25	25	34	31	41	50
ME:MDA-MB-435	16	28	31	31	47	38	34	31	38	38	31	25	31	28	22	47	31	44	28	28	50	44	25	38	34	31	16	47	34	28	38	50
ME:MDA-N	16	28	31	31	47	38	34	31	38	38	31	25	31	28	22	47	31	44	28	28	50	44	25	38	34	31	16	47	34	28	38	50
ME:SK-MEL-2	22	38	22	25	16	38	28	16	25	31	25	38	19	28	28	31	28	16	31	25	31	22	34	34	28	34	28	28	38	25	31	41
ME:SK-MEL-28	25	38	28	28	25	25	22	25	28	19	25	13	25	34	28	31	22	28	28	25	28	31	28	34	31	22	28	31	22	22	44	28
ME:SK-MEL-5	22	41	28	22	41	19	38	31	34	31	41	28	38	28	38	38	19	28	34	31	28	22	34	31	31	25	31	31	34	38	34	25
ME:UACC-257	13	31	19	25	28	13	34	34	22	31	28	25	22	34	38	19	19	34	13	25	31	16	25	38	25	34	22	28	44	22	34	19
ME:UACC-62	16	31	31	28	47	22	41	34	22	31	19	28	25	41	13	34	25	31	31	22	34	34	41	44	34	25	31	38	28	28	34	22
OV:IGROV1	25	31	22	34	25	25	25	34	22	31	25	19	34	34	31	28	22	25	25	25	31	31	28	28	31	31	28	28	34	38	25	22
OV:OVCAR-3	25	44	22	25	22	31	28	34	47	34	41	31	34	34	31	56	25	25	22	31	44	41	38	28	38	38	34	25	22	28	22	19
OV:OVCAR-4	22	31	28	22	31	28	28	28	34	34	31	25	22	28	19	28	22	25	28	22	31	31	19	34	28	22	19	34	25	28	31	25
OV:OVCAR-5	28	34	41	34	31	25	34	31	34	38	31	28	38	34	28	34	25	34	44	31	34	41	28	41	25	28	31	25	41	38	34	28
OV:OVCAR-8	19	25	28	25	31	16	34	38	22	31	22	28	22	31	25	41	16	25	16	25	41	34	28	34	41	28	28	38	38	25	22	28
OV:OVCAR-8/ADR	22	22	25	22	31	16	31	38	19	31	19	28	19	31	25	41	16	22	13	22	41	38	25	34	41	28	25	38	34	22	19	28
OV:SK-OV-3	28	38	25	25	22	28	22	22	31	28	34	22	19	34	38	28	16	16	31	28	31	38	31	25	28	22	25	25	25	31	25	25
PR:DU-145 (ATCC)	9	16	28	25	16	28	28	13	22	25	22	31	31	19	28	16	25	38	38	25	25	28	25	16	28	16	25	28	28	16	22	38
PR:DU-145	9	16	28	25	19	28	28	16	22	25	22	31	31	19	28	16	28	41	38	25	28	31	28	19	31	16	25	28	28	16	22	38
PR:PC-3	19	44	38	34	31	28	25	31	22	19	22	25	25	31	25	41	28	38	41	22	38	16	31	44	31	28	41	47	47	34	38	41
PR:RC0.1	13	16	25	25	22	28	25	16	22	19	22	22	28	22	25	13	25	38	38	25	25	31	28	19	31	16	25	25	28	19	22	31
RE:786-0	25	44	31	34	25	19	34	25	34	22	41	28	28	28	38	28	19	34	38	34	41	34	38	31	25	38	41	28	44	41	22	41
RE:A498	19	31	19	28	44	25	31	31	38	22	34	25	28	41	38	38	19	25	34	22	41	31	22	38	47	22	25	34	16	25	34	31
RE:ACHN	22	31	22	31	41	25	41	41	22	56	19	34	38	38	38	38	19	38	19	28	44	38	28	44	38	41	25	38	53	44	34	28
RE:CAKI-1	28	38	44	25	34	25	41	31	25	41	25	34	25	38	31	47	19	22	31	28	44	38	31	34	38	34	38	31	47	34	34	41
RE:RXF-393	16	25	22	31	38	19	34	41	22	41	22	31	34	28	25	28	28	38	28	22	44	31	19	50	41	25	34	38	47	19	41	31
RE:SN12C	38	28	34	22	25	22	25	34	19	38	22	31	31	25	28	41	22	22	25	34	34	31	19	38	41	41	22	28	47	44	28	38
RE:TK-10	22	41	19	25	31	31	25	38	41	22	34	22	28	38	47	44	22	25	31	25	28	22	31	19	31	19	22	22	34	34	34	16
RE:UO-31	25	38	38	25	31	34	34	25	41	38	34	16	31	28	31	38	25	31	34	25	38	28	25	31	25	16	28	25	34	28	38	31

Tissue of Origin: Cell Line	BR:BT-549	BR:HS578T	BR:MCF7	BR:MDA-MB-231	BR:T47D	CNS:SF-268	CNS:SF-295	CNS:SF-539	CNS:SNB-19	CNS:SNB-75	CNS:U251	CO:CO-HCT-116	CO:COLO205	CO:HCC-2998	CO:HCT-15	CO:HT29	CO:KM12	CO:SW-620	LC:A549-ATCC	LC:EKVX	LC:HOP-62	LC:HOP-92	LC:NCI-H226	LC:NCI-H23	LC:NCI-H322M	LC:NCI-H460	LC:NCI-H522	LE:CCRF-CEM	LE:HL-60	LE:K-562	LE:RPMI-8226	LE:SR
BR:BT-549	28	16	28	16	16	22	25	22	13	16	25	25	22	28	19	22	28	9	9	19	13	25	19	22	28	16	38	22	25
BR:HS578T	31	34	31	28	28	38	38	41	31	31	31	44	31	34	25	22	38	16	16	44	16	44	31	31	38	25	28	41	38
BR:MCF7	31	31	25	31	31	22	28	28	19	31	22	22	28	41	28	25	25	28	28	38	25	31	19	22	44	22	34	19	38
BR:MDA-MB-231	25	31	34	31	31	25	28	22	25	28	34	25	22	34	25	22	25	25	25	34	25	34	28	31	25	31	22	25	25
BR:T47D	34	44	22	47	47	16	25	41	28	47	25	22	31	31	31	31	22	16	19	31	22	25	44	41	34	38	25	31	31
CNS:SF-268	28	44	44	38	38	38	25	19	13	22	25	31	28	25	16	16	28	28	28	28	28	19	25	25	25	19	22	31	34
CNS:SF-295	38	38	22	34	34	28	22	38	34	41	25	28	28	34	34	31	22	28	28	25	25	34	31	41	41	34	25	25	34
CNS:SF-539	28	28	16	31	31	16	25	31	34	34	34	34	28	31	38	38	22	13	16	31	16	25	31	41	31	41	34	38	25
CNS:SNB-19	25	41	38	38	38	25	28	34	22	22	22	47	34	34	22	19	31	22	22	22	22	34	38	22	25	22	19	41	41
CNS:SNB-75	22	34	25	38	38	31	19	31	31	31	31	34	34	38	31	31	28	25	25	19	19	22	22	56	41	41	38	22	38
CNS:U251	22	34	44	31	31	25	25	41	28	19	25	41	31	31	22	19	34	22	22	22	22	41	34	19	25	22	22	34	34
CO:CO-HCT-116	13	25	19	25	25	38	13	28	25	28	19	31	25	28	28	28	22	31	31	25	22	28	25	34	34	31	31	22	16
CO:COLO205	25	31	31	31	31	19	25	38	22	25	34	34	22	38	22	19	19	31	31	25	28	28	28	38	25	34	31	28	31
CO:HCC-2998	34	34	16	28	28	28	34	28	34	41	34	34	28	34	31	31	34	19	19	31	22	28	41	38	38	28	25	38	28
CO:HCT-15	31	22	31	22	22	28	28	38	38	13	31	31	19	28	25	25	38	28	28	25	25	38	38	38	31	25	28	47	31
CO:HT29	25	44	28	47	47	31	31	38	19	34	28	56	28	34	41	41	28	16	16	41	13	28	38	38	47	28	41	44	38
CO:KM12	31	25	22	31	31	28	22	19	19	25	22	25	22	25	16	16	16	25	28	28	25	19	19	19	19	28	22	22	25
CO:SW-620	22	50	31	44	44	16	28	28	34	31	25	25	25	34	25	22	16	38	41	38	38	34	25	38	22	38	22	25	31
LC:A549-ATCC	41	31	44	28	28	31	28	34	13	31	25	22	28	44	16	13	31	38	38	41	38	38	34	19	31	28	25	31	34
LC:EKVX	28	31	34	28	28	25	25	31	25	22	25	31	22	31	25	22	28	25	25	22	25	34	22	28	28	22	34	25	25
LC:HOP-62	34	47	56	50	50	31	28	28	31	34	31	44	31	34	41	41	31	25	28	38	25	41	41	44	44	44	34	28	38
LC:HOP-92	25	44	22	44	44	22	31	22	16	34	31	41	31	41	34	38	38	28	31	16	31	34	31	38	38	31	31	22	28
LC:NCI-H226	22	34	28	25	25	34	28	34	25	41	28	38	19	28	28	25	31	25	28	31	28	38	22	28	31	19	19	31	25
LC:NCI-H23	28	38	25	38	38	34	34	31	38	44	28	28	34	41	34	34	25	16	19	44	19	31	38	44	34	50	38	19	31
LC:NCI-H322M	38	31	34	34	34	28	31	31	25	34	31	38	28	25	41	41	28	28	31	31	31	25	47	38	38	41	41	31	25
LC:NCI-H460	19	31	38	31	31	34	22	25	34	25	31	38	22	28	28	28	22	16	16	28	16	38	22	41	34	25	41	19	16
LC:NCI-H522	44	19	25	16	16	28	28	31	22	31	28	34	19	31	28	25	25	25	25	41	25	41	25	25	38	34	22	22	28
LE:CCRF-CEM	31	50	25	47	47	28	31	31	28	38	28	25	34	25	38	38	25	28	28	47	25	28	34	38	31	38	28	22	25
LE:HL-60	28	34	34	34	34	38	22	34	44	28	34	22	25	41	38	34	25	28	28	47	28	44	16	53	47	47	47	34	34
LE:K-562	31	31	31	28	28	25	22	38	22	28	38	28	28	38	25	22	31	16	16	34	19	41	25	44	34	19	44	34	28
LE:RPMI-8226	41	38	41	38	38	31	44	34	34	34	25	22	31	34	22	19	25	22	22	38	22	22	34	34	34	41	28	34	38
LE:SR	38	50	50	50	50	41	28	25	19	22	22	19	25	28	28	28	25	38	38	41	31	41	31	28	41	31	38	16	31
ME:LOXIMVI	100	25	31	25	25	34	31	41	28	44	31	22	38	31	19	19	31	25	25	31	28	25	38	28	31	44	25	28	31
ME:M14	25	100	31	94	94	25	28	28	28	47	22	41	31	31	44	44	38	31	34	41	31	38	41	47	38	28	31	25	41
ME:MALME-3M	31	31	100	31	31	28	28	22	31	19	25	25	22	28	22	22	22	19	19	25	19	34	22	25	31	31	34	28	31
ME:MDA-MB-435	25	94	31	100	100	19	28	25	22	41	25	41	28	31	47	47	41	28	31	41	28	31	41	50	41	31	34	22	41
ME:MDA-N	25	94	31	100	100	19	28	25	22	41	25	41	28	31	47	47	41	28	31	41	28	31	41	50	41	31	34	22	41
ME:SK-MEL-2	34	25	28	19	19	100	25	34	31	28	25	28	31	19	19	19	22	22	22	38	22	41	19	25	31	34	19	19	22
ME:SK-MEL-28	31	28	28	28	28	25	100	31	19	28	22	22	31	34	28	25	16	31	31	38	31	34	25	19	28	38	19	25	31
ME:SK-MEL-5	41	28	22	25	25	34	31	100	41	34	34	31	28	28	22	19	25	25	25	25	25	38	31	38	44	25	41	47	28
ME:UACC-257	28	28	31	22	22	31	19	41	100	28	34	28	28	28	25	25	25	22	22	31	22	28	25	47	28	38	25	28	19
ME:UACC-62	44	47	19	41	41	28	28	34	28	100	25	34	47	34	38	38	25	19	22	41	25	31	41	38	41	44	25	28	28
OV:IGROV1	31	22	25	25	25	25	22	34	34	25	100	28	31	38	22	22	34	31	31	28	22	25	31	31	31	38	34	25	28
OV:OVCAR-3	22	41	25	41	41	28	22	31	28	34	28	100	31	25	38	38	34	9	13	28	13	28	41	38	41	22	25	34	31
OV:OVCAR-4	38	31	22	28	28	31	31	28	28	47	31	31	100	47	22	22	22	25	25	38	25	25	38	16	19	47	38	28	44
OV:OVCAR-5	31	31	28	31	31	19	34	28	28	34	38	25	47	100	22	22	25	41	41	31	38	31	34	25	31	47	44	25	47
OV:OVCAR-8	19	44	22	47	47	19	28	22	25	38	22	38	22	22	100	97	25	22	25	34	22	25	28	44	44	34	16	16	31
OV:OVCAR-8/ADR	19	44	22	47	47	19	25	19	25	38	22	38	22	22	97	100	25	19	22	31	19	22	28	44	44	34	16	16	31
OV:SK-OV-3	31	38	22	41	41	22	16	25	25	25	34	34	22	25	25	25	100	19	19	31	19	28	44	34	31	22	25	31	22
PR:DU-145 (ATCC)	25	31	19	28	28	22	31	25	22	19	31	9	25	41	22	19	19	100	94	31	81	25	19	25	22	28	22	16	34
PR:DU-145	25	34	19	31	31	22	31	25	22	22	31	13	25	41	25	22	19	94	100	31	88	25	22	28	22	28	22	16	34
PR:PC-3	31	41	25	41	41	38	38	25	31	41	28	28	38	31	34	31	31	31	31	100	31	41	28	31	38	41	31	19	28
PR:RC0.1	28	31	19	28	28	22	31	25	22	25	22	13	25	38	22	19	19	81	88	31	100	25	25	31	25	25	19	22	28
RE:786-0	25	38	34	31	31	41	34	38	28	31	25	28	25	31	25	22	28	25	25	41	25	100	28	28	44	38	34	28	19
RE:A498	38	41	22	41	41	19	25	31	25	41	31	41	38	34	28	28	44	19	22	28	25	28	100	31	34	38	28	41	28
RE:ACHN	28	47	25	50	50	25	19	38	47	38	31	38	16	25	44	44	34	25	28	31	31	28	31	100	59	38	44	50	28
RE:CAKI-1	31	38	31	41	41	31	28	44	28	41	31	41	19	31	44	44	31	22	22	38	25	44	34	59	100	38	41	41	28
RE:RXF-393	44	28	31	31	31	34	38	25	38	44	38	22	47	47	34	34	22	28	28	41	25	38	38	38	38	100	38	28	44
RE:SN12C	25	31	34	34	34	19	19	41	25	25	34	25	38	44	16	16	25	22	22	31	19	34	28	44	41	38	100	41	28
RE:TK-10	28	25	28	22	22	19	25	47	28	28	25	34	28	25	16	16	31	16	16	19	22	28	41	50	41	28	41	100	41
RE:UO-31	31	41	31	41	41	22	31	28	19	28	28	31	44	47	31	31	22	34	34	28	28	19	28	28	28	44	28	41	100

Table 3

DNA fingerprints for NCI-60 cell lines (other sources)

Tissue of Origin: Cell Line	AMEL_1	AMEL_2	CSF1PO_1	CSF1PO_2	D13S317_1	D13S317_2	D16S539_1	D16S539_2	D18S51_1	D18S51_2	D19S433_1	D19S433_2	D21S11_1	D21S11_2	D2S1338_1	D2S1338_2	D3S1358_1	D3S1358_2	D5S818_1	D5S818_2	D7S820_1	D7S820_2	D8S1179_1	D8S1179_2	FGA_1	FGA_2	TH01_1	TH01_2	TPOX_1	TPOX_2	vWA_1	vWA_2	% Sim[1]
BR:BT-549	X	X	10	12	11	11	8	8	15	15	15.2	15.2	32.2	32.2	17	17	18	18	11	11	9	9	14	16	19	19	9.3	9.3	8	8	15	15	91
BR:MCF7	X	X	10	10	11	11	11	12	14	14	13	14	30	30	0	0	16	16	11	12	9	9	10	10	23	23	6	6	12	12	14	14	84
BR:MDA-MB-231	X	X	12	13	13	13	12	12	11	16	11	14	33.2	33.2	20	21	16	16	12	12	8	8	13	13	22	23	7	9.3	8	9	15	15	97
BR:MDA-MB-231	X	X	12	13	13	13	12	12	11	16	11	14	33.2	33.2	20	21	16	16	12	12	8	8	13	13	22	23	7	9.3	8	9	15	15	97
BR:MDA-MB-231	X	X	13	13	13	13	12	12	11	16	11	14	33.2	33.2	20	21	16	16	12	12	8	9	13	13	22	23	7	9.3	8	9	15	18	100
BR:MDA-MB-231	X	X	12	13	13	13	12	12	11	16	11	14	33.2	33.2	20	21	16	16	12	12	8	9	13	13	22	23	7	9.3	8	9	15	18	100
BR:MDA-MB-231	X	X	13	13	13	13	12	12	11	11	11	14	33.2	33.2	20	21	16	16	12	12	8	8	0	0	22	22	7	9.3	8	9	15	15	81
BR:MDA-MB-231	X	X	13	13	13	13	12	12	11	16	11	14	33.2	33.2	20	21	16	16	12	12	8	8	0	0	22	22	7	9.3	8	9	15	18	88
OV:OVCAR-3	X	X	10	13	12	12	9	9	18	18	14	17	30	30	16	17	16	16	12	12	10	10	9	14	24	24	7	7	8	10	16	18	97
OV:OVCAR-3	X	X	11	12	12	12	12	12	13	13	16.2	16.2	29	31.2	17	21	17	18	11	12	10	10	15	15	21	21	9	9.3	8	8	17	17	28
OV:OVCAR-4	X	X	10	10	9	9	11	11	15	15	13	15	28	31	23	23	15	15	13	13	10	11	13	13	21	21	9	9	8	8	14	18	100
OV:OVCAR-5	X	X	10	10	10	13	11	11	12	12	13	14	31	31	17	23	15	16	11	13	10	10	14	14	23	23	7	9.3	8	11	16	16	100
OV:OVCAR-8	X	X	11	11	12	12	13	13	14	14	14	16	28	28	19	23	18	18	12	12	12	12	10	10	20	20	7	7	8	8	16	17	97
OV:SK-OV-3	X	X	11	11	8	11	12	12	16	17	14	14.2	30	31.2	18	23	14	14	11	11	13	14	14	15	24	25	9	9.3	11	11	18	18	91
OV:SK-OV-3	X	X	11	11	0	0	12	12	16	17	14	14.2	30	31.2	18	23	14	14	11	11	9	14	14	15	24	24	9	9.3	8	11	18	18	84

Number of STRs at each of the sixteen surveyed loci (two alleles, designated by _1 and _2, per locus). Numbers following a decimal indicate the number of bases in an incomplete final STR.

[1] Percent similarity comparison with corresponding DTP line in Table 1. Calculated by same method used for Table 2.

Table 4

Heterozygosity within each surveyed locus across the NCI-60

Locus	Heterozygosity (%) [1]
CSF1PO	57
D13S317	39
D16S539	56
D18S51	46
D19S433	56
D21S11	57
D2S1338	59
D3S1358	46
D5S818	57
D7S820	69
D8S1179	48
FGA	44
TH01	54
TPOX	62
vWA	59

[1] Calculated within each locus over the 61 samples from Table 1