# Matching identities of iPSCs and donors using Identifiler STR profiling kits

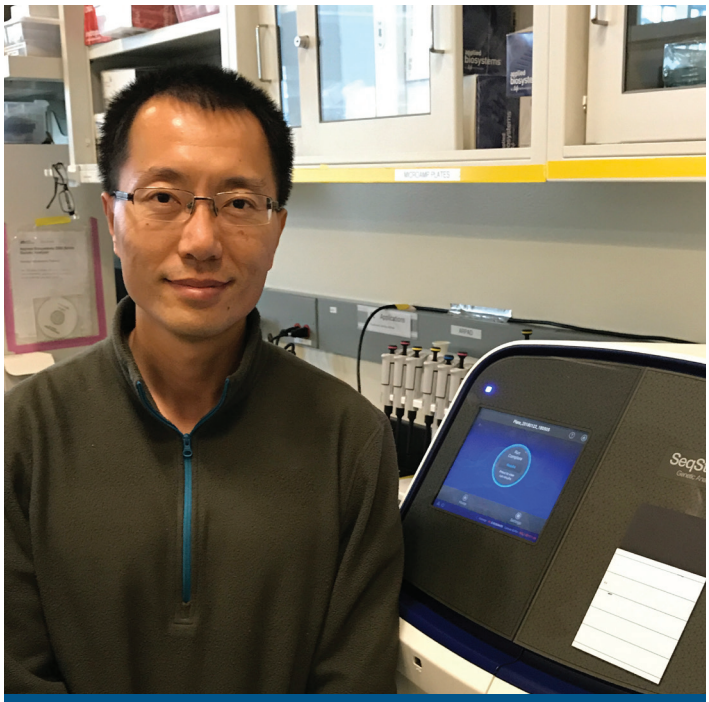
**In this report, we show:**

- Induced pluripotent stem cells (iPSCs) and donor blood draws can be matched using short tandem repeat (STR) profiling
- Applied Biosystems™ Identifiler™ Direct kits and NUCLEIC-CARD™ devices can simplify authentication by bypassing DNA purification steps
- The Applied Biosystems™ SeqStudio™ Genetic Analyzer provides a "right-throughput" option for iPSC researchers

## Introduction

Research on stem cells as potential treatments for debilitating syndromes is progressing at a rapid rate. The discovery that differentiated adult cells could be induced to become iPSCs by treating with a defined set of genes (e.g., by transforming/transducing with DNA or mRNA) [1,2] opened the door to novel opportunities for basic research, disease modeling, and drug discovery. One exciting outcome of these studies is the potential development of *ex vivo* cellular therapies for some debilitating syndromes.

An important step in developing *ex vivo* therapies is ensuring that the cells derived from the iPSCs are matched to the original donor. Matching iPSCs to the original donor ensures that the appropriate cells are utilized and potential immunological rejection is minimized. Several methods are used to authenticate the iPSC samples: one of these, single-nucleotide polymorphism (SNP) genotyping, is performed with either next-generation sequencing (NGS) or hybridization arrays. Although SNP genotyping methods provide high resolution, the workflows are often tedious and time-to-results can be long. Another method is based on the analysis of STR fragments with highly variable lengths. This method is widely used in forensic analysis since a unique molecular fingerprint of alleles at different genomic loci is generated.



**Guangwen (Gavin) Wang is Director of the Stem Cell Core in the Department of Genetics, Stanford University.** In 2012 he initiated the Stem Cell Core at Stanford University. The major focus of the facility is to collaborate with different labs for derivation, characterization, and differentiation of iPSCs. His group is now working to build an iPSC biobank from 300 donors with different types of heart disease. With the support of the Grace Science Foundation, the lab is also using iPSCs as the tool to study the mechanism underlying the ultra-rare *NGLY1* deficiency.

ThermoFisher SCIENTIFIC

An added benefit of STR genotyping is that the workflow and analysis are simple and can be performed in a matter of hours. Analysis of STRs is performed by capillary electrophoresis (CE) of fragments amplified from microsatellite loci with variable numbers of repeats. Thermo Fisher Scientific has established the gold standard for CE instrumentation, developing and offering instruments that are optimized for researchers' needs in both sensitivity and throughput. Furthermore, the Applied Biosystems™ product portfolio has several different kits for PCR-based STR fingerprinting for use on CE instruments. The Applied Biosystems™ Identifiler™ Plus PCR Amplification Kit has been optimized to analyze 16 highly variant human STRs over a wide range of purified genomic DNA (gDNA) preparations. The Applied Biosystems™ Identifiler™ Direct PCR Amplification Kit was developed to analyze the same 16 STR loci, starting from dried blood or buccal spots (for example, on NUCLEIC-CARD devices), or buccal swabs. For the NUCLEIC-CARD device, a 1.2 mm punch from the card is placed directly into a PCR tube or well, and amplified without any further purification. An illustration of the complete workflows for STR analysis is shown in Figure 1 (see also reference 3).

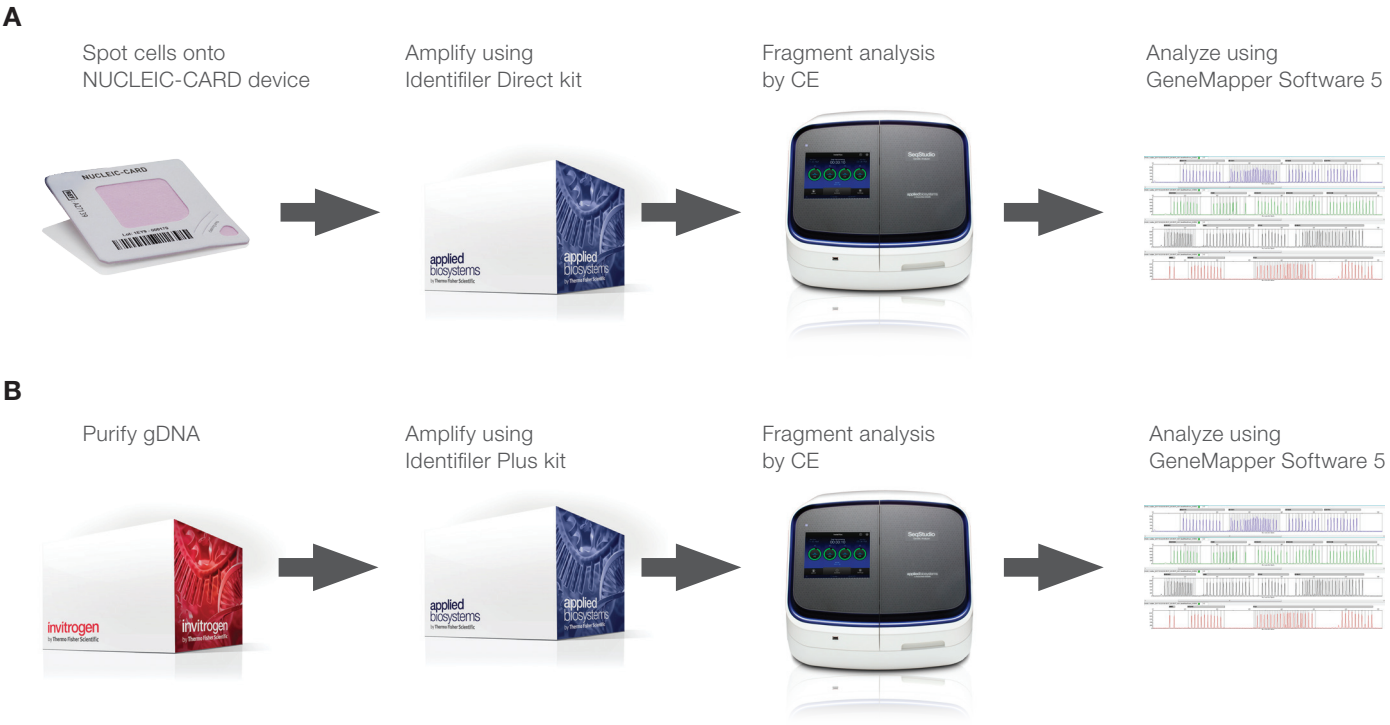



**Figure 1. Workflows for human sample authentication.** Two methods can be used to match human samples. **(A)** Samples containing intact cells can be spotted onto NUCLEIC-CARD devices, punches of the cards amplified directly using the Identifiler Direct kit, and fragments analyzed on Applied Biosystems™ CE instruments using Applied Biosystems™ GeneMapper™ Software 5. **(B)** Alternatively, gDNA can be purified from cell lines and amplified using the Identifiler Plus kit, and fragments analyzed by CE using GeneMapper Software 5.

## Background

Dr. Guangwen (Gavin) Wang is Director of the Stem Cell Core facility at Stanford University. Donor samples are sent to his laboratory, and subsequently used to generate iPSCs and their derivatives. In his laboratory Dr. Wang was using a SNP genotyping strategy for sample matching, but he found that the turnaround time was long, and data analysis was complicated. He was therefore interested in an STR-based solution.

## Materials and methods

To test how well the Identifiler kits could validate samples that came from the same individual, Dr. Wang collected blood samples from 12 donors. He generated iPSC cultures from those samples, randomized and blinded pairs, and sent purified DNA from the randomized samples to Thermo Fisher Scientific. In our laboratories, we used the Identifiler Plus kit to generate STR profiles from all of the samples, and pairs were identified by matching STR profiles.

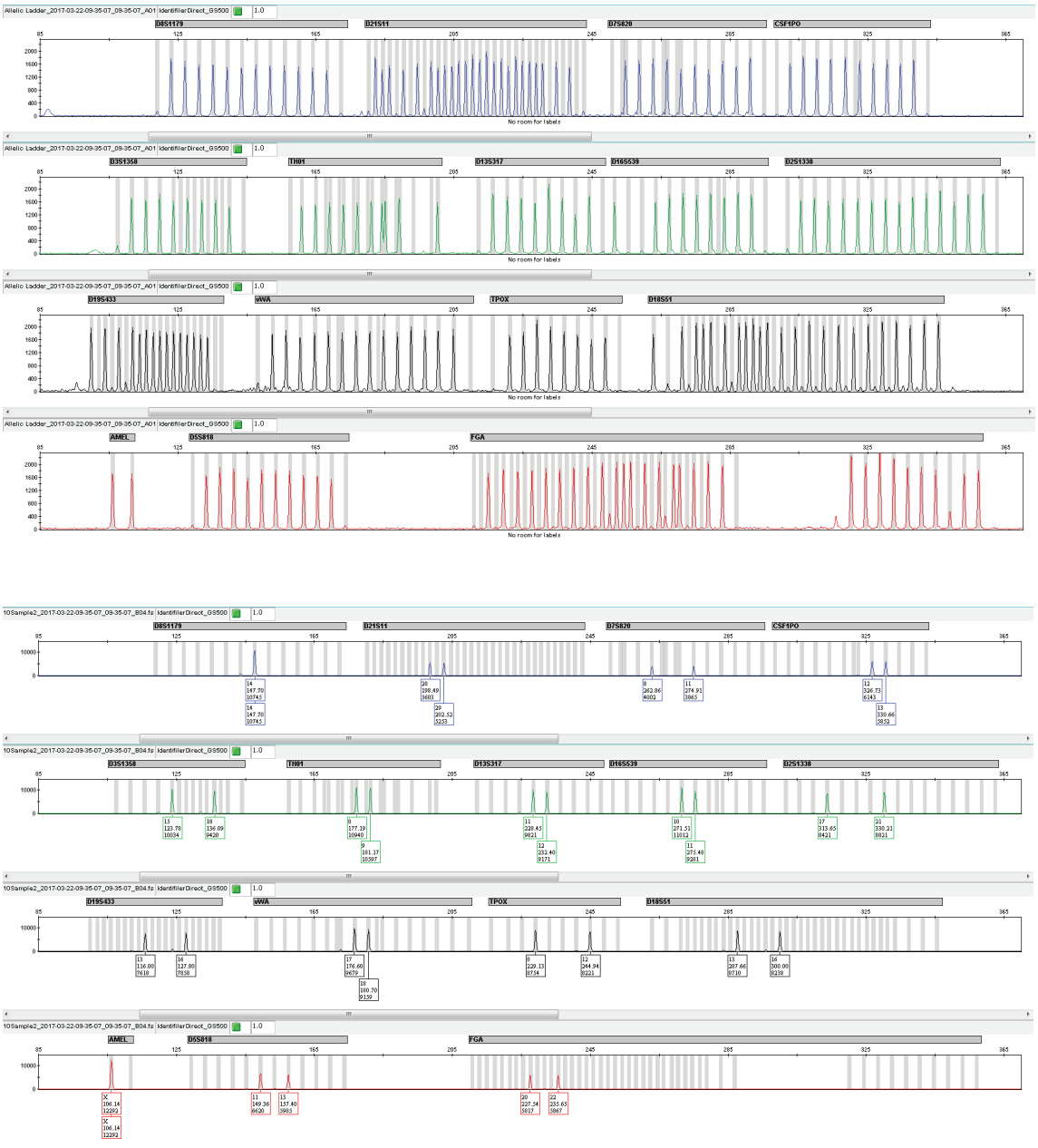



**Figure 2. Analysis of Identifiler™ Plus Allelic Ladder (top) and purified genomic DNA from an iPSC sample (bottom) by GeneMapper Software 5.** GeneMapper Software 5 uses the allelic ladder provided in the Identifiler kits to assign the alleles present in an unknown sample to known STR alleles. The boxes below the peaks show the allele number, the height of the peak, and the size of the fragment in base pairs.

## Results

Although all of the samples produced good STR results (example in Figure 2), finding matching alleles at each locus among the 24 samples proved to be tedious. To facilitate this analysis, we determined a sample allele score that was simply the sum of the allelic designations for all the autosomal STRs of a sample (Figure 3A; for details, see appendix). Finding matching scores in sample allele calls among the 24 unknown samples then became very simple, since each sample was reduced to a single representative numerical value. Of course, once putative matching pairs were identified, the results were validated by confirming that the individual allele calls at each locus were identical. Once the samples were unblinded and checked, the results were found to be 100% accurate in matching the donors to their iPSCs (Figure 3B). This procedure was repeated once with another set of blinded iPSC samples from 12 donors, and again, exact matching of donor to iPSC sample was confirmed.

**A**

| Sample A | Panel | Locus | Dye | Allele 1 | Allele 2 | Sample B | Panel | Locus | Dye | Allele 1 | Allele 2 | Sample A allele score | Sample B allele score |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Sample 1** | Identifiler_v2 | AMEL | R | X | Y | **Sample10** | Identifiler_v2 | AMEL | R | X | Y | | |
| **Sample 1** | Identifiler_v2 | CSF1PO | B | 10 | 12 | **Sample10** | Identifiler_v2 | CSF1PO | B | 10 | 12 | | |
| **Sample 1** | Identifiler_v2 | D13S317 | G | 13 | 13 | **Sample10** | Identifiler_v2 | D13S317 | G | 13 | 13 | | |
| **Sample 1** | Identifiler_v2 | D16S539 | G | 9 | 12 | **Sample10** | Identifiler_v2 | D16S539 | G | 9 | 12 | | |
| **Sample 1** | Identifiler_v2 | D18S51 | Y | 14 | 15 | **Sample10** | Identifiler_v2 | D18S51 | Y | 14 | 15 | | |
| **Sample 1** | Identifiler_v2 | D19S433 | Y | 12 | 14 | **Sample10** | Identifiler_v2 | D19S433 | Y | 12 | 14 | | |
| **Sample 1** | Identifiler_v2 | D21S11 | B | 30.2 | 31.2 | **Sample10** | Identifiler_v2 | D21S11 | B | 30.2 | 31.2 | | |
| **Sample 1** | Identifiler_v2 | D2S1338 | G | 23 | 25 | **Sample10** | Identifiler_v2 | D2S1338 | G | 23 | 25 | | |
| **Sample 1** | Identifiler_v2 | D3S1358 | G | 16 | 18 | **Sample10** | Identifiler_v2 | D3S1358 | G | 16 | 18 | | |
| **Sample 1** | Identifiler_v2 | D5S818 | R | 11 | 12 | **Sample10** | Identifiler_v2 | D5S818 | R | 11 | 12 | | |
| **Sample 1** | Identifiler_v2 | D7S820 | B | 11 | 12 | **Sample10** | Identifiler_v2 | D7S820 | B | 11 | 12 | | |
| **Sample 1** | Identifiler_v2 | D8S1179 | B | 13 | 13 | **Sample10** | Identifiler_v2 | D8S1179 | B | 13 | 13 | | |
| **Sample 1** | Identifiler_v2 | FGA | R | 23 | 24 | **Sample10** | Identifiler_v2 | FGA | R | 23 | 24 | | |
| **Sample 1** | Identifiler_v2 | TH01 | G | 6 | 6 | **Sample10** | Identifiler_v2 | TH01 | G | 6 | 6 | | |
| **Sample 1** | Identifiler_v2 | TPOX | Y | 8 | 11 | **Sample10** | Identifiler_v2 | TPOX | Y | 8 | 11 | | |
| **Sample 1** | Identifiler_v2 | vWA | Y | 17 | 19 | **Sample10** | Identifiler_v2 | vWA | Y | 17 | 19 | 453.4 | 453.4 |
| **Sample11** | Identifiler_v2 | AMEL | R | X | Y | **Sample15** | Identifiler_v2 | AMEL | R | X | Y | | |
| **Sample11** | Identifiler_v2 | CSF1PO | B | 12 | 13 | **Sample15** | Identifiler_v2 | CSF1PO | B | 12 | 13 | | |
| **Sample11** | Identifiler_v2 | D13S317 | G | 11 | 11 | **Sample15** | Identifiler_v2 | D13S317 | G | 11 | 11 | | |
| **Sample11** | Identifiler_v2 | D16S539 | G | 10 | 15 | **Sample15** | Identifiler_v2 | D16S539 | G | 10 | 15 | | |
| **Sample11** | Identifiler_v2 | D18S51 | Y | 13 | 15 | **Sample15** | Identifiler_v2 | D18S51 | Y | 13 | 15 | | |
| **Sample11** | Identifiler_v2 | D19S433 | Y | 15 | 15.2 | **Sample15** | Identifiler_v2 | D19S433 | Y | 15 | 15.2 | | |
| **Sample11** | Identifiler_v2 | D21S11 | B | 29 | 33.2 | **Sample15** | Identifiler_v2 | D21S11 | B | 29 | 33.2 | | |
| **Sample11** | Identifiler_v2 | D2S1338 | G | 19 | 24 | **Sample15** | Identifiler_v2 | D2S1338 | G | 19 | 24 | | |
| **Sample11** | Identifiler_v2 | D3S1358 | G | 16 | 17 | **Sample15** | Identifiler_v2 | D3S1358 | G | 16 | 17 | | |
| **Sample11** | Identifiler_v2 | D5S818 | R | 10 | 12 | **Sample15** | Identifiler_v2 | D5S818 | R | 10 | 12 | | |
| **Sample11** | Identifiler_v2 | D7S820 | B | 11 | 12 | **Sample15** | Identifiler_v2 | D7S820 | B | 11 | 12 | | |
| **Sample11** | Identifiler_v2 | D8S1179 | B | 10 | 14 | **Sample15** | Identifiler_v2 | D8S1179 | B | 10 | 14 | | |
| **Sample11** | Identifiler_v2 | FGA | R | 24 | 25 | **Sample15** | Identifiler_v2 | FGA | R | 24 | 25 | | |
| **Sample11** | Identifiler_v2 | TH01 | G | 7 | 7 | **Sample15** | Identifiler_v2 | TH01 | G | 7 | 7 | | |
| **Sample11** | Identifiler_v2 | TPOX | Y | 8 | 11 | **Sample15** | Identifiler_v2 | TPOX | Y | 8 | 11 | | |
| **Sample11** | Identifiler_v2 | vWA | Y | 18 | 19 | **Sample15** | Identifiler_v2 | vWA | Y | 18 | 19 | 456.4 | =SUM(L20:M34) |

**B**

| Sample (DNA from blood or iPSC) | Well position | Allele score |
|---|---|---|
| 29 | E1 | 415.2 |
| 31 | G1 | 415.2 |
| 36 | D2 | 417.5 |
| 38 | F2 | 417.5 |
| 30 | F1 | 431.2 |
| 40 | H2 | 431.2 |
| 26 | B1 | 435.3 |
| 47 | G3 | 435.3 |

| Sample (DNA from blood or iPSC) | Well position | Allele score |
|---|---|---|
| 42 | B3 | 436.2 |
| 45 | E3 | 436.2 |
| 39 | G2 | 436.4 |
| 48 | H3 | 436.4 |
| 25 | A1 | 440.4 |
| 44 | D3 | 440.4 |
| 28 | D1 | 444.5 |
| 32 | H1 | 444.5 |

| Sample (DNA from blood or iPSC) | Well position | Allele score |
|---|---|---|
| 43 | C3 | 448.3 |
| 46 | F3 | 448.3 |
| 33 | A2 | 448.5 |
| 41 | A3 | 448.5 |
| 35 | C2 | 451.5 |
| 37 | E2 | 451.5 |
| 34 | B2 | 459.2 |
| 27 | C1 | 459.2 |

**Figure 3. Method for quickly finding matching samples among unknowns. (A)** Part of the data showing STR genotypes of four different blinded samples. A sample allelic score can be calculated by summing the numerical designation of each allele present. Matched pairs among a small set of unknown samples can then be determined quickly by finding identical allele scores. Pairing should be verified for matched samples at each allele, since there are several ways to produce an identical allele score. **(B)** Sample allelic scores were successfully used to match 12 blinded blood donor–iPSC sample pairs.

Sample authentication using STR profiling was also validated using NUCLEIC-CARD devices and the Identifiler Direct kit. For these experiments, Dr. Wang again collected blood samples from the donors, but instead of purifying gDNA he spotted a fraction of the blood cells (40,000 cells) onto a NUCLEIC-CARD device and dried it at room temperature. iPSCs were obtained from the same samples, and aliquots of those cells were also spotted onto cards and dried at room temperature overnight. Once all samples were collected, the cards were sent to our laboratories for analysis. Punches (1.2 mm) were taken from the cards and analyzed using the Identifiler Direct kit without further manipulation. The PCR products were analyzed on Applied Biosystems™ SeqStudio™ and 3500 Genetic Analyzers. The profiles obtained on these two instruments were identical; in this case, the samples were not blinded, so donor–iPSC matching pairs could be validated (Figure 4). STR genotyping on the SeqStudio and 3500 Genetic Analyzers confirmed that the samples were indeed collected from the same individual; however, the 4-capillary injection throughput of the SeqStudio Genetic Analyzer means that the samples can be analyzed immediately, without having to wait for enough samples to fill larger-capacity capillary arrays.

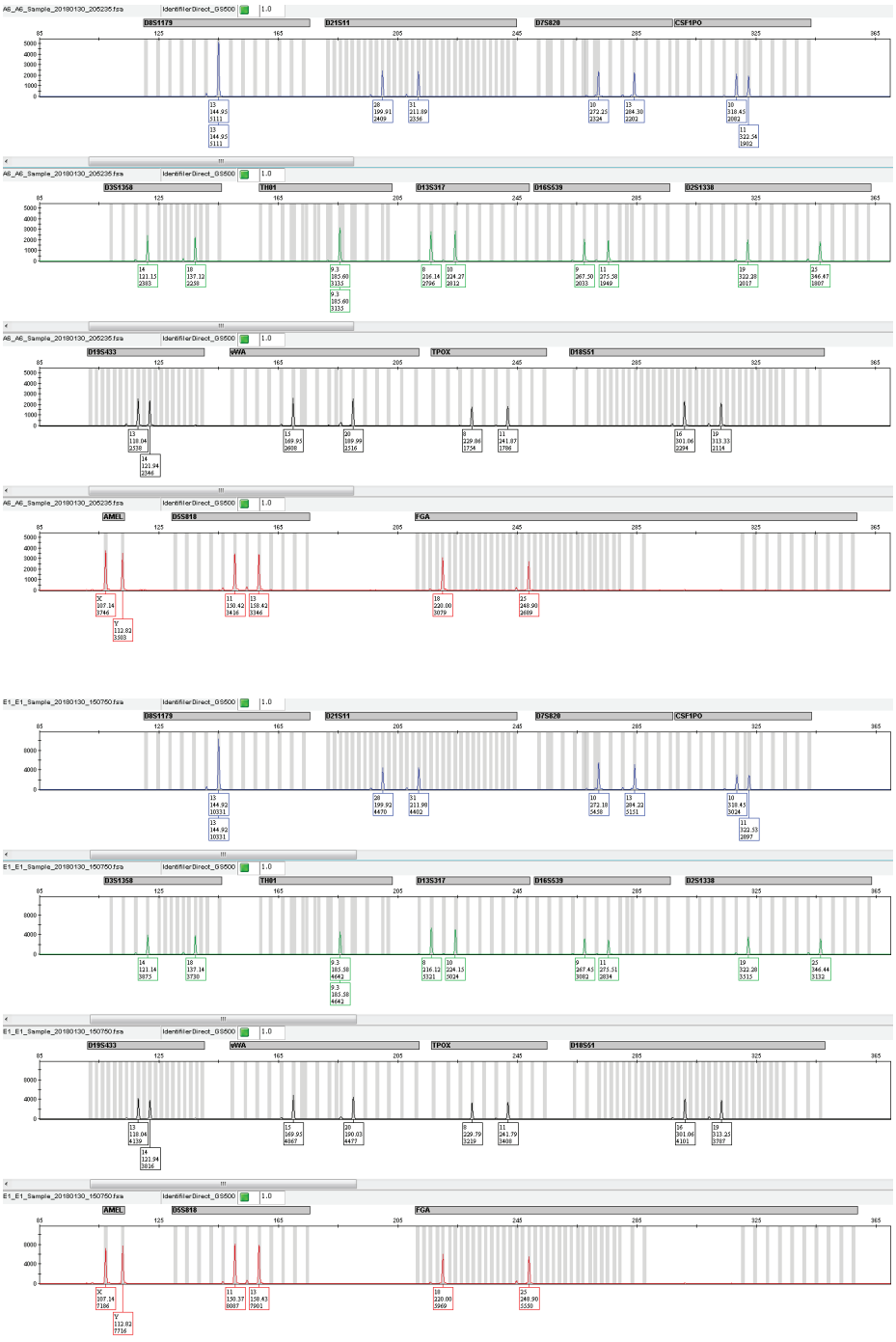




**Figure 4. Analysis of matching samples on the NUCLEIC-CARD device and SeqStudio Genetic Analyzer.** Blood (upper four sets of traces) and iPSCs (lower four sets of traces) were analyzed using the NUCLEIC-CARD device and Identifiler Direct kit. The allelic profile is identical in the two samples, verifying that the samples came from the same individual. Note that these traces were collected using the SeqStudio Genetic Analyzer, but samples run on other instruments produced data of identical quality.

## Conclusions

STR genotyping can rapidly confirm that samples of donor blood and iPSCs are from the same individual. Investigators can choose between analyzing purified gDNA or samples dried onto the NUCLEIC-CARD device, depending on the workflow that is most convenient for their lab. In addition, Thermo Fisher offers CE instruments to analyze these samples to suit the throughput of all laboratories—from the high-throughput Applied Biosystems™ 3730 DNA Analyzer and the flagship 3500 Genetic Analyzer, to the convenient and easy-to-use SeqStudio Genetic Analyzer. Together, these options provide choices that are designed to meet the needs of any stem cell research laboratory.

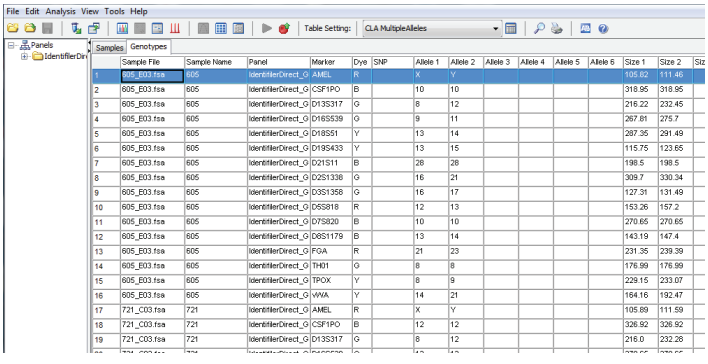
### References


1. Takahashi K, Yamanaka S (2006) Induction of pluripotent stem cells from mouse embryo and adult fibroblast cultures by defined factors. *Cell* 126:663-676.
2. Shi Y et al. (2017) Induced pluripotent stem cell technology: a decade of progress. *Nat Rev Drug Discov* 16:115-130.
3. Thermo Fisher Scientific Inc. (2017) Authenticating human cell lines using the Identifiler kits and capillary electrophoresis platforms. (Application note) Request download at thermofisher.com/us/en/home/global/forms/life-science/seqstudio-application-notes.html


## Appendix—method for determining sample allele score using Microsoft™ Excel™ format

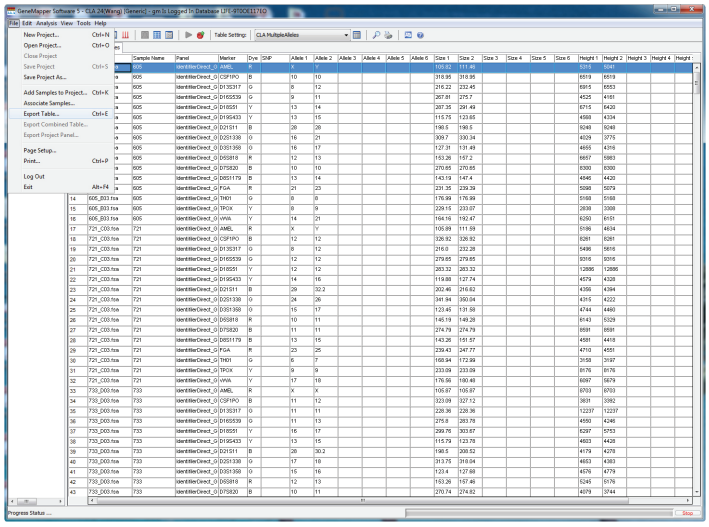
1. Using GeneMapper Software 5, process data to identify alleles present in all samples.

2. Click on the “Genotypes” tab in the results table.



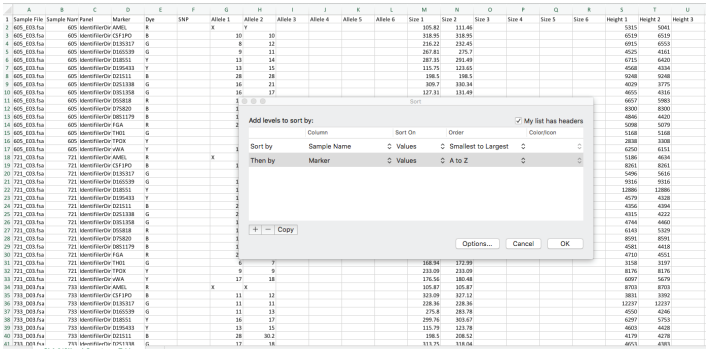
| | Sample File | Sample Name | Panel | Marker | Dye | SNP | Allele 1 | Allele 2 | Allele 3 | Allele 4 | Allele 5 | Allele 6 | Size 1 | Size 2 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 605_E03.fsa | 605 | IdentifilerDirect_G | AMEL | R | | X | Y | | | | | 105.82 | 111.46 |
| 2 | 605_E03.fsa | 605 | IdentifilerDirect_G | CSF1PO | B | | 10 | 10 | | | | | 318.95 | 318.95 |
| 3 | 605_E03.fsa | 605 | IdentifilerDirect_G | D13S317 | G | | 8 | 12 | | | | | 216.22 | 232.45 |
| 4 | 605_E03.fsa | 605 | IdentifilerDirect_G | D16S539 | G | | 9 | 11 | | | | | 267.81 | 275.7 |
| 5 | 605_E03.fsa | 605 | IdentifilerDirect_G | D18S51 | Y | | 13 | 14 | | | | | 287.35 | 291.49 |
| 6 | 605_E03.fsa | 605 | IdentifilerDirect_G | D19S433 | Y | | 13 | 15 | | | | | 115.75 | 123.65 |
| 7 | 605_E03.fsa | 605 | IdentifilerDirect_G | D21S11 | B | | 28 | 28 | | | | | 198.5 | 198.5 |
| 8 | 605_E03.fsa | 605 | IdentifilerDirect_G | D2S1338 | G | | 16 | 21 | | | | | 309.7 | 330.34 |
| 9 | 605_E03.fsa | 605 | IdentifilerDirect_G | D3S1358 | G | | 16 | 17 | | | | | 127.31 | 131.49 |
| 10 | 605_E03.fsa | 605 | IdentifilerDirect_G | D5S818 | R | | 12 | 13 | | | | | 153.26 | 157.2 |
| 11 | 605_E03.fsa | 605 | IdentifilerDirect_G | D7S820 | B | | 10 | 10 | | | | | 270.65 | 270.65 |
| 12 | 605_E03.fsa | 605 | IdentifilerDirect_G | D8S1179 | B | | 13 | 14 | | | | | 143.19 | 147.4 |
| 13 | 605_E03.fsa | 605 | IdentifilerDirect_G | FGA | R | | 21 | 23 | | | | | 231.35 | 239.39 |
| 14 | 605_E03.fsa | 605 | IdentifilerDirect_G | TH01 | G | | 8 | 8 | | | | | 176.99 | 176.99 |
| 15 | 605_E03.fsa | 605 | IdentifilerDirect_G | TPOX | Y | | 8 | 9 | | | | | 229.15 | 233.07 |
| 16 | 605_E03.fsa | 605 | IdentifilerDirect_G | vWA | Y | | 14 | 21 | | | | | 164.16 | 192.47 |
| 17 | 721_C03.fsa | 721 | IdentifilerDirect_G | AMEL | R | | X | Y | | | | | 105.89 | 111.59 |
| 18 | 721_C03.fsa | 721 | IdentifilerDirect_G | CSF1PO | B | | 12 | 12 | | | | | 326.92 | 326.92 |
| 19 | 721_C03.fsa | 721 | IdentifilerDirect_G | D13S317 | G | | 8 | 12 | | | | | 216.0 | 232.28 |

3. From the “File” menu, select “Export Table”.

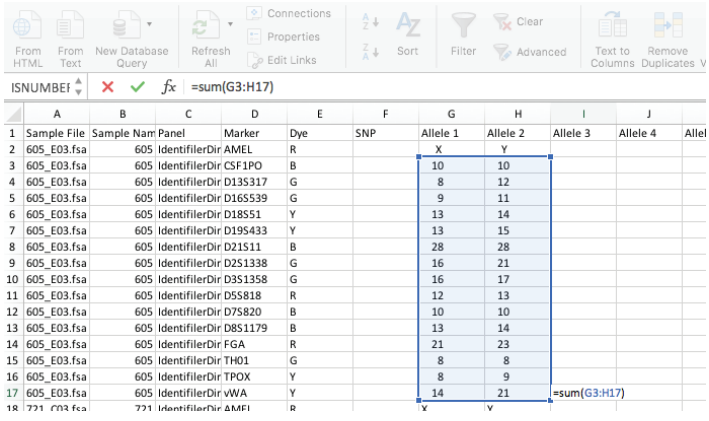


4. Find the .txt file for the table and open it in Excel software.

5. Select all rows. Sort rows by “Sample Name” and “Marker”.



6. For each sample, calculate the sum of all numerical values in the “Allele 1” and “Allele 2” columns. This sum is the sample allele score.

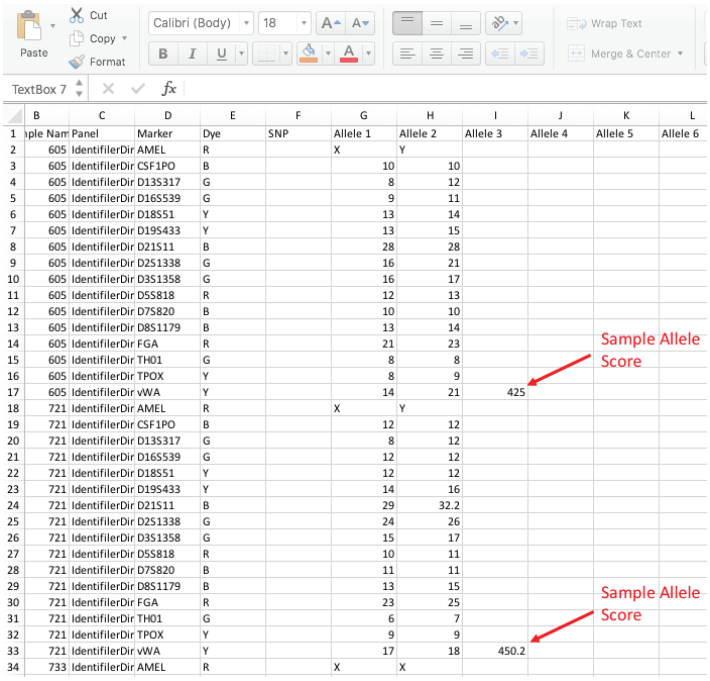


ISNUMBEI | =sum(G3:H17)

| | A | B | C | D | E | F | G | H | I | J |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Sample File | Sample Nam | Panel | Marker | Dye | SNP | Allele 1 | Allele 2 | Allele 3 | Allele 4 |
| 2 | 605_E03.fsa | 605 | IdentifilerDir | AMEL | R | | X | Y | | |
| 3 | 605_E03.fsa | 605 | IdentifilerDir | CSF1PO | B | | 10 | 10 | | |
| 4 | 605_E03.fsa | 605 | IdentifilerDir | D13S317 | G | | 8 | 12 | | |
| 5 | 605_E03.fsa | 605 | IdentifilerDir | D16S539 | G | | 9 | 11 | | |
| 6 | 605_E03.fsa | 605 | IdentifilerDir | D18S51 | Y | | 13 | 14 | | |
| 7 | 605_E03.fsa | 605 | IdentifilerDir | D19S433 | Y | | 13 | 15 | | |
| 8 | 605_E03.fsa | 605 | IdentifilerDir | D21S11 | B | | 28 | 28 | | |
| 9 | 605_E03.fsa | 605 | IdentifilerDir | D2S1338 | G | | 16 | 21 | | |
| 10 | 605_E03.fsa | 605 | IdentifilerDir | D3S1358 | G | | 16 | 17 | | |
| 11 | 605_E03.fsa | 605 | IdentifilerDir | D5S818 | R | | 12 | 13 | | |
| 12 | 605_E03.fsa | 605 | IdentifilerDir | D7S820 | B | | 10 | 10 | | |
| 13 | 605_E03.fsa | 605 | IdentifilerDir | D8S1179 | B | | 13 | 14 | | |
| 14 | 605_E03.fsa | 605 | IdentifilerDir | FGA | R | | 21 | 23 | | |
| 15 | 605_E03.fsa | 605 | IdentifilerDir | TH01 | G | | 8 | 8 | | |
| 16 | 605_E03.fsa | 605 | IdentifilerDir | TPOX | Y | | 8 | 9 | | |
| 17 | 605_E03.fsa | 605 | IdentifilerDir | vWA | Y | | 14 | 21 | =sum(G3:H17) | |
| 18 | 721_C03.fsa | 721 | IdentifilerDir | AMEL | R | | X | Y | | |

applied
biosystems

7. Finding the identical sample allele score can identify samples from the same individual.




| | B | C | D | E | F | G | H | I | J | K | L |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | ple Nam | Panel | Marker | Dye | SNP | Allele 1 | Allele 2 | Allele 3 | Allele 4 | Allele 5 | Allele 6 |
| 2 | 605 | IdentifilerDir | AMEL | R | | X | Y | | | | |
| 3 | 605 | IdentifilerDir | CSF1PO | B | | 10 | 10 | | | | |
| 4 | 605 | IdentifilerDir | D13S317 | G | | 8 | 12 | | | | |
| 5 | 605 | IdentifilerDir | D16S539 | G | | 9 | 11 | | | | |
| 6 | 605 | IdentifilerDir | D18S51 | Y | | 13 | 14 | | | | |
| 7 | 605 | IdentifilerDir | D19S433 | Y | | 13 | 15 | | | | |
| 8 | 605 | IdentifilerDir | D21S11 | B | | 28 | 28 | | | | |
| 9 | 605 | IdentifilerDir | D2S1338 | G | | 16 | 21 | | | | |
| 10 | 605 | IdentifilerDir | D3S1358 | G | | 16 | 17 | | | | |
| 11 | 605 | IdentifilerDir | D5S818 | R | | 12 | 13 | | | | |
| 12 | 605 | IdentifilerDir | D7S820 | B | | 10 | 10 | | | | |
| 13 | 605 | IdentifilerDir | D8S1179 | B | | 13 | 14 | | | | |
| 14 | 605 | IdentifilerDir | FGA | R | | 21 | 23 | | | | |
| 15 | 605 | IdentifilerDir | TH01 | G | | 8 | 8 | | | | |
| 16 | 605 | IdentifilerDir | TPOX | Y | | 8 | 9 | | | | |
| 17 | 605 | IdentifilerDir | vWA | Y | | 14 | 21 | 425 | | | |
| 18 | 721 | IdentifilerDir | AMEL | R | | X | Y | | | | |
| 19 | 721 | IdentifilerDir | CSF1PO | B | | 12 | 12 | | | | |
| 20 | 721 | IdentifilerDir | D13S317 | G | | 8 | 12 | | | | |
| 21 | 721 | IdentifilerDir | D16S539 | G | | 12 | 12 | | | | |
| 22 | 721 | IdentifilerDir | D18S51 | Y | | 12 | 12 | | | | |
| 23 | 721 | IdentifilerDir | D19S433 | Y | | 14 | 16 | | | | |
| 24 | 721 | IdentifilerDir | D21S11 | B | | 29 | 32.2 | | | | |
| 25 | 721 | IdentifilerDir | D2S1338 | G | | 24 | 26 | | | | |
| 26 | 721 | IdentifilerDir | D3S1358 | G | | 15 | 17 | | | | |
| 27 | 721 | IdentifilerDir | D5S818 | R | | 10 | 11 | | | | |
| 28 | 721 | IdentifilerDir | D7S820 | B | | 11 | 11 | | | | |
| 29 | 721 | IdentifilerDir | D8S1179 | B | | 13 | 15 | | | | |
| 30 | 721 | IdentifilerDir | FGA | R | | 23 | 25 | | | | |
| 31 | 721 | IdentifilerDir | TH01 | G | | 6 | 7 | | | | |
| 32 | 721 | IdentifilerDir | TPOX | Y | | 9 | 9 | | | | |
| 33 | 721 | IdentifilerDir | vWA | Y | | 17 | 18 | 450.2 | | | |
| 34 | 733 | IdentifilerDir | AMEL | R | | X | X | | | | |

8. Verify that the samples are identical by confirming genotypes of all alleles at all loci.

**Ordering information**

| Product | Quantity | Cat. No. |
|---|---|---|
| SeqStudio Genetic Analyzer | 1 instrument | A34274 |
| SeqStudio Analysis Software | 1 | 44443764 |
| SeqStudio Cartridge | 500 reactions | A33671 |
| SeqStudio Starter Kit | 1 kit | A35000 |
| SeqStudio Full-Day SmartStart Training | 1 | A34684 |
| 3500 Genetic Analyzer | 1 system | 4440466 |
| 3500xL Genetic Analyzer | 1 system | 4440467 |
| Identifiler Plus PCR Amplification Kit | 100 reactions | A26364 |
| Identifiler Direct PCR Amplification Kit | 200 reactions | 4467831 |
| NUCLEIC-CARD matrix, 1 spot | 100 cards | 4473973 |
| NUCLEIC-CARD COLOR matrix, 4 spots | 50 cards | 4473978 |
| RecoverAll Total Nucleic Acid Isolation Kit for FFPE | 40 reactions | AM1975 |
| GeneMapper Software 5 | 1 license | 4475074 |

Find out more at
**thermofisher.com/seqstudioapplications**

ThermoFisher SCIENTIFIC