Matching identities of iPSCs and donors using Identifiler STR profiling kits

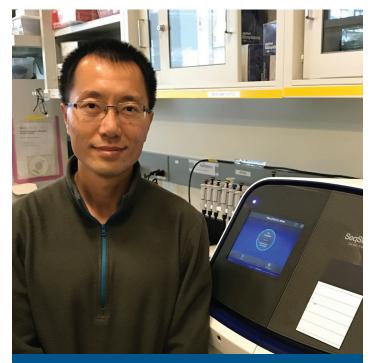
In this report, we show:

- 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.



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.

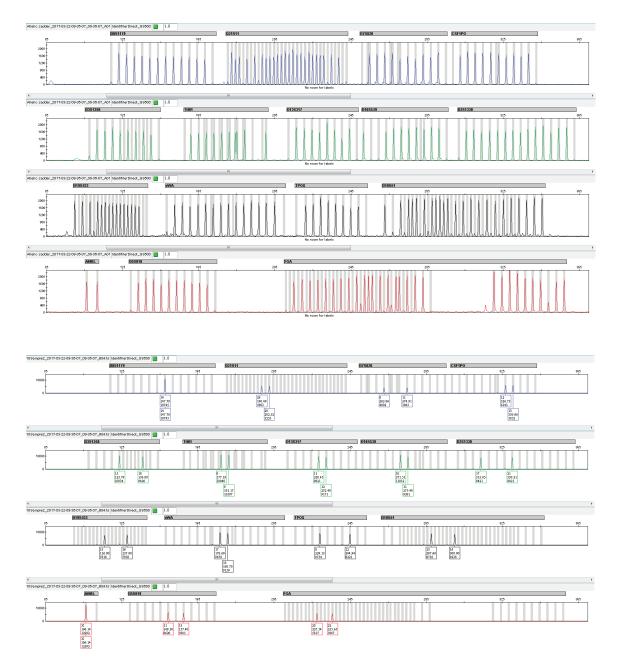


Figure 2. Analysis of Identifiler[™] Plus Allelic Ladder (top) and purified genomic DNA from an iPSC sample (bottom) by GeneMapper Software 5. GeneMapper Software 5 uses the allelic ladder provided in the Identifiler kits to assign the alleles present in an unknown sample to known STR alleles. The boxes 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.

Α												Sample A	Sample B
Sample A	Panel	Locus	Dye	Allele 1	Allele 2	Sample B	Panel	Locus	Dye	Allele 1	Allele 2	allele score	allele score
Sample 1	Identifiler_v2	AMEL	R	Х	Y	Sample10	Identifiler_v2	AMEL	R	Х	Y		
Sample 1	Identifiler_v2	CSF1PO	В	10	12	Sample10	Identifiler_v2	CSF1PO	В	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	Υ	14	15		
Sample 1	Identifiler_v2	D19S433	Υ	12	14	Sample10	Identifiler_v2	D19S433	Υ	12	14		
Sample 1	Identifiler_v2	D21S11	В	30.2	31.2	Sample10	Identifiler_v2	D21S11	В	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	В	11	12	Sample10	Identifiler_v2	D7S820	В	11	12		
Sample 1	Identifiler_v2	D8S1179	В	13	13	Sample10	Identifiler_v2	D8S1179	В	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	Х	Y	Sample15	Identifiler_v2	AMEL	R	Х	Y		
Sample11	Identifiler_v2	CSF1PO	В	12	13	Sample15	Identifiler_v2	CSF1PO	В	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	Υ	13	15	Sample15	Identifiler_v2	D18S51	Υ	13	15		
Sample11	Identifiler_v2	D19S433	Υ	15	15.2	Sample15	Identifiler_v2	D19S433	Υ	15	15.2		
Sample11	Identifiler_v2	D21S11	В	29	33.2	Sample15	Identifiler_v2	D21S11	В	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	В	11	12	Sample15	Identifiler_v2	D7S820	В	11	12		
Sample11	Identifiler_v2	D8S1179	В	10	14	Sample15	Identifiler_v2	D8S1179	В	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	Υ	8	11		
Sample11	Identifiler_v2	vWA	Υ	18	19	Sample15	Identifiler_v2	vWA	Υ	18	19	456.4	=SUM(L20:M34)

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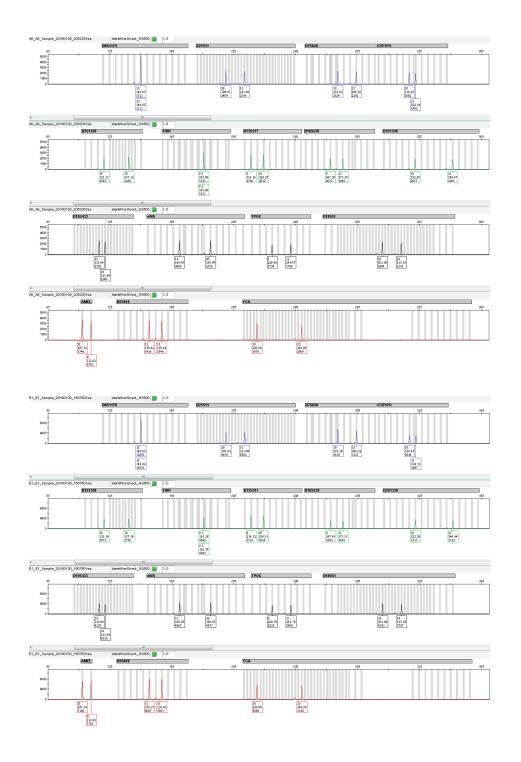
Sample (DNA from blood or iPSC)	Well position	Allele score	Sample (DNA from blood or iPSC)	Well position	Allele score	Sample (DNA from blood or iPSC)	Well position	Allele score
29	E1	415.2	42	B3	436.2	43	C3	448.3
31	G1	415.2	45	E3	436.2	46	F3	448.3
36	D2	417.5	39	G2	436.4	33	A2	448.5
38	F2	417.5	48	H3	436.4	41	A3	448.5
30	F1	431.2	25	A1	440.4	35	C2	451.5
40	H2	431.2	44	D3	440.4	37	E2	451.5
26	B1	435.3	28	D1	444.5	34	B2	459.2
47	G3	435.3	32	H1	444.5	27	C1	459.2

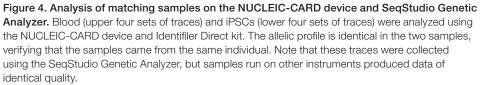
Figure 3. Method for quickly finding matching samples among unknowns. (A) Part of the data showing STR genotypes of four different blinded samples. A sample allelic score can be calculated by summing the numerical designation of each allele present. Matched pairs among a small set of unknown samples 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.









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

- 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.
- 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.

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- 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".

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605_E03.fta	605	IdentifilerDir	TH01	G					Column		So	rt On	Order		c	olor/licon		5168	5168	
605_E03.fta	605	IdentifilerDir	TPOK	Y														2836		
605_E03.fsa	605	IdentifilerDir	WWA .	Y			Sort	by .	Sample M	lame	0 Vi	lues	C Smaller	st to Large	ist 0			6250	6151	
721_003.fsa		IdentifilerDir		R		x	Then	hu	Marker		0 Vi	duna	CAtoZ		0		0	5186		
721_003.fsa	721	IdentiFilerDir	CSF1PO	8			(69	Privat Mart		0 11	1003	O HIGH		~		0	8261	8261	
721_003.fsa	721	MentiFilerDir	D135317	6														5496		
721_003.fsa		MentiFilerDir		6			i.											9316		
721_003.fsa	721	IdentifilerDir	D18551	Y			i.											12896	12886	
721_003.fsa	721	IdentifilerDir	D195433	Y			i.											4575		
721_003.fsa	721	IdentifilerDir	D21511	8			ŧ.											4356	4394	
721_C03.fsa	721	IdentifilerDir	0251338	G			ŧ.											4315	4222	
721_C03.fsa	721	IdentifilerDir	D351358	G														4764	4460	
721 C03.fsa	721	IdentiFilerDir	D55818	8			+	 Copy 										6143	5329	
721 003.fsa	721	MentiFilerDir	075820	8														8591	8591	
721 003.fsa	721	MentiFilerDir	D8S1179	8			i i						Op	tions	Cancel	I) (0	ĸ	4581	4418	
721 C03.fsa	721	MentiFilerDir	FGA	8			i i											4710	4551	
721 C03.fsa	721	MentifilerDir	TH01	6			6	7				168.94	172.9	1				3158	3197	
721_C03.fsa	721	IdentifilerDir	TPOK	Y			9	9				233.09	233.00					8170	8176	
721_003.fsa	721	IdentifilerDir	WA	Y			17	18				176.56	180.48					6097	5679	
733_D03.fsa	733	IdentifilerDir	AMEL	R		х	x					105.87	105.83					8703	8703	
733_D03.fsa	733	IdentifilerDir	CSF1PO	8			11	12				323.09	327.12					3831	3392	
733 D03 fsa	733	IdentifilerDir	D135317	6			11	11				228.36	228.3					12237	12237	
733 D03 fsa	733	MentiFilerDir	D165539	6			11	13				275.8						4550		
733 D03.fsa		klenti filerDir		Ŷ			16	17				299.76						6297		
733 D03/5a		MentifilerDir		Ŷ			13	15				115.79						4603		
733 D03/5a		IdentifilerDir		8				0.2				198.5	208.52					4175		
733 D01 fsa		MentifilerDir		6			17	18				313.25						4653		

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.

	rom From TML Text	New Databa Query	ase Refre	Pr	onnections operties lit Links	2.↓ A Z↓ So		📡 Clea			nove cates V
IS	NUMBEF 💂	× 🗸	$f_x = sum$	(G3:H17)							
	A	В	с	D	E	F	G	н	1	J	
1	Sample File	Sample Nam	Panel	Marker	Dye	SNP	Allele 1	Allele 2	Allele 3	Allele 4	Allel
2	605_E03.fsa	605	IdentifilerDir	AMEL	R		х	Y			
3	605_E03.fsa	605	IdentifilerDi	CSF1PO	В		10	10	Ī		
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	В		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	В		10	10			
13	605_E03.fsa	605	IdentifilerDir	D8S1179	В		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:H1	7)	
18	721 CO3 fsa	721	IdentifilerDir	AMEL	R		¥	v	1		

applied biosystems

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

	• •	🔏 Cut	Calibri	(Body) *	18 *	A∸ A▼	= =	- * *	=>	Wrap Text	
F	Paste	S Format	в	IU		· A ·	= = :	= • •		Merge & Cer	iter 🔻
Te	xtBox 7	$\frac{1}{2}$ ×	√ fx								
	В	с	D	E	F	G	н	1	J	к	L
1	ple Nam	Panel	Marker	Dye	SNP	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele
2	605	IdentifilerDir	AMEL	R		х	Y				
3	605	IdentifilerDir	CSF1PO	В		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	В		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	В		10	10				
13	605	IdentifilerDir	D8S1179	В		13	14				
14	605	IdentifilerDir	FGA	R		21	23			Sample	Allel
15	605	IdentifilerDir	TH01	G		8	8		/	Score	
16	605	IdentifilerDir	TPOX	Y		8	9			Score	
17	605	IdentifilerDir	vWA	Y		14	21	425	_		
18	721	IdentifilerDir	AMEL	R		х	Y				
19	721	IdentifilerDir	CSF1PO	В		12	12				
20	721	IdentifilerDir	D135317	G		8					
21		IdentifilerDir		G		12					
22		IdentifilerDir		Y		12					
23		IdentifilerDir		Y		14					
24		IdentifilerDir		B		29					
25		IdentifilerDir		G		24					
26		IdentifilerDir		G		15					
27		IdentifilerDir		R		10					
28		IdentifilerDir		В		11					
29		IdentifilerDir		B		13				c 1	
30		IdentifilerDir		R		23				Sample	Allel
31		IdentifilerDir		G		6			/	Score	
32		IdentifilerDir		Y		9					
33		IdentifilerDir		Y		17		450.2	-		
33 34		IdentifilerDir		R		X 1/	X	430.2			

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

