

## GENEWIZ, Inc. Beijing

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www.genewiz.com.cn



Customer: JiangLin

Institution: Xin Hua Hospital Affiliated to ShangHai Jiao Tong University School of

Medicine

Quotation Number: HJ1601121

Completion Date: 02/04/2016

## 1. Sample ID: NOZ

## 2. Original Material: Cell pellets

### 3. Methods:

1).Genomic DNA was extracted from the cell pellets provided by the customer.

2).Samples, together with positive and negative control were amplified using GenePrint 10

System(Promega).

3). Amplified products were processed using the ABI3730xl Genetic Analyzer.

4).Data were analyzed using GeneMapper4.0 software and then compared with the ATCC,

DSMZ or JCRB databases for reference matching.

### 4. Results:

1) 10 Loci STR Profile:

Genetic Site	ATCC		Customer sample			
(Locus)	NOZ		NOZ			
Amelogenin	Х		Х			
CSF1PO	11	13	11	13		
D13S317	8	12	8	12		
D16S539	9	11	9	11		
D5S818	11	13	11	13		
D7S820	10	11	10	11		
THO1	7	9	7	9		
ТРОХ	8	11	8	11		
vWA	19		19			
D21S11			30	31		
Percent match between the sample and the database						



profile: 100%

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Summary:

 Your cell line is considered to be "identical" to the reference cell line in the ATCC STR database, as the STR profile yields a 100% match.

Notes:

1. P=100% x (2xM)/N; M=16, N=32 P=100% x (2x16)/32=100%

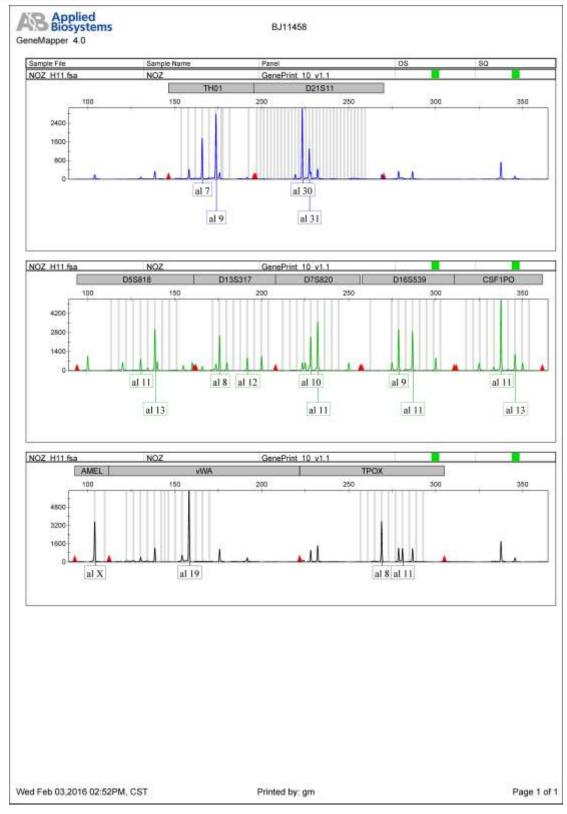
M: number of the matching peaks; N: number of all peaks

2. Based on the ANSI Standard, cell lines with  $\geq$ 80% match are considered to be related; i.e., derived from a common ancestry. Cell lines with between a 55% to 80% match require futher profiling for authentication of relatedness.

3. The short tandem repeat (STR) profile generated by GENEWIZ Inc. is indicative only of the sample sent to GENEWIZ Inc. at the time it was sent. This data and analysis are for research use only.

### 2) Electrophoretogram





Note: Raw data in appendix



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Customer: JiangLin

Institution: Xin Hua Hospital Affiliated to Shanghai Jiao Tong University School of

Medicine

Quotation Number: GWBJYJ15121801

Completion Date: 12/30/2015

## 1. Sample ID: OCUG-1

## 2. Original Material: Cell pellets

### 3. Methods:

1).Genomic DNA was extracted from the cell pellets provided by the customer.

2).Samples, together with positive and negative control were amplified using GenePrint 10

System(Promega).

3). Amplified products were processed using the ABI3730xl Genetic Analyzer.

4).Data were analyzed using GeneMapper4.0 software and then compared with the ATCC,

DSMZ or JCRB databases for reference matching.

## 4. Results:

1) 10 Loci STR Profile:

Genetic Site	JCRB			Customer sample			
(Locus)	OCUG-1			OCUG-1			
Amelogenin	Х			Х			
CSF1PO	10		12	10	12		
D13S317	8		11	8	11		
D16S539	9		13	9	13		
D5S818	10		12	10	12		
D7S820	10		11	10	11		
THO1	7		?	7	9.3		
ТРОХ	8		11	8	11		
vWA	?	15	16	16			
D21S11				28	29		
Percent match between the sample and the database							



profile: 88.2%

### Summary:

1) Your cell line is considered "related" to the reference cell line in the ATCC STR database, as the STR profile yields matches that are  $\geq 80\%$  but less than 100%.

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Notes:

1. P=100% x (2xM)/N; M=15, N=34 P=100% x (2x15)/34=88.2%

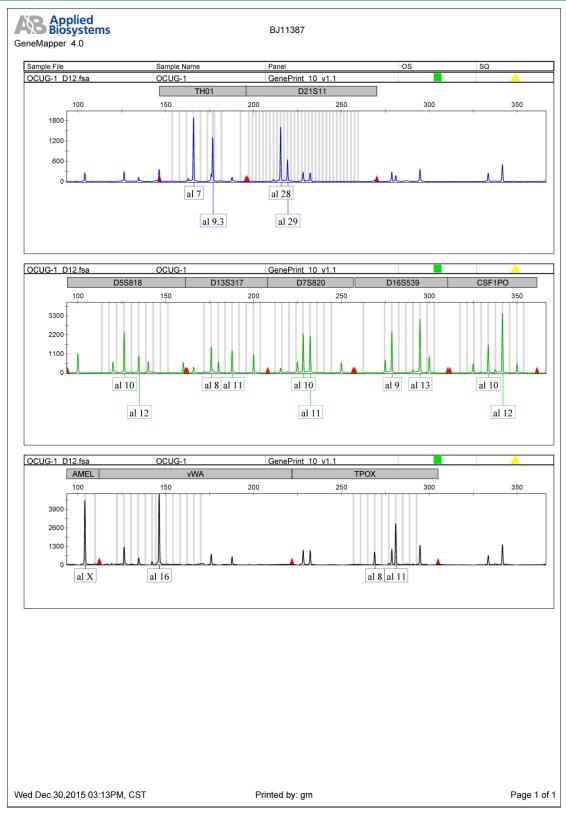
M: number of the matching peaks; N: number of all peaks

2. Based on the ANSI Standard, cell lines with  $\geq$ 80% match are considered to be related; i.e., derived from a common ancestry. Cell lines with between a 55% to 80% match require futher profiling for authentication of relatedness.

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## 2) Electrophoretogram





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