

Report Date: 2024-03-18

1.Sample

SW 780 [SW-780, SW780]

2.Method and Procedure

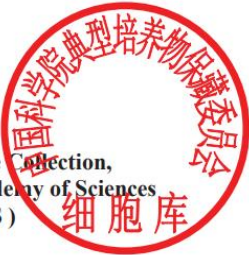
Sample DNA was extracted by Microread Genomic DNA Kit.
PCR was amplified with STR Multi-amplification Kit(MicroreaderTM21 ID System).
PCR products were assayed with ABI 3730xl DNA Analyzer(Applied Biosystems®).
Data were analyzed using GeneMapperID-X software and then compared with the ATCC and DSMZdatabases for reference matching.

3.Results

D5S818	11, 12
D13S317	11, 12
D7S820	9, 10
D16S539	9, 11
vWA	16, 19
TH01	6
Amelogenin	X
TP0X	8
CSF1PO	10, 11

The above results were consistent with the DNA profiles reported by ATCC and DSMZ, and indicated no other human cell lines contamination.

Cell Bank,
Type Culture Collection,
Chinese Academy of Sciences
(CBTCCCAS)



Certificate of STR Analysis

1. Sample

T24

2. Methods

The sample DNA was analyzed in Genesky Biotechnologies. Inc., Shanghai.

The PCR product was loaded into ABI 3730xl Genetic Analyzer and the STR profiling was generated by GeneMapper 5.0 software (Applied Biosystems®).

3. Results

Amelogenin:	X
CSF1PO:	10,12
D13S317:	12
D16S539:	9
D5S818:	10,12
D7S820:	10,11
THO1:	6
TPOX:	8,11
vWA:	17

The locations of the cell sample were consistent with the STR data of **T24** cell found in the databases of ATCC, DSMZ, JCRB and EXPASY.

There was no cross-contaminant of human source cell line.

Cell Bank/Stem Cell Bank
Center for Excellence in Molecular Cell Science
Chinese Academy of Sciences

Date: 2023/4/13



Certificate of STR Analysis

1. Sample

TCCSUP

2. Methods

The sample DNA was analyzed in Genesky Biotechnologies, Inc., Shanghai.

The PCR product was loaded into ABI 3730xl Genetic Analyzer and the STR profiling was generated by GeneMapper 5.0 software (Applied Biosystems®).

3. Results

Amelogenin:	X
CSF1PO:	10
D13S317:	11,14
D16S539:	9,11
D5S818:	12
D7S820:	8,9
TH01:	6,9.3
TPOX:	8
vWA:	14,16

The locations of the cell sample were consistent with the STR data of **TCCSUP** cell found in the databases of ATCC, DSMZ, JCRB and EXPASY.

There was no cross-contaminant of human source cell line.

Cell Bank/Stem Cell Bank
Center for Excellence in Molecular Cell Science
Chinese Academy of Sciences

Date: 2023/8/25



Cell Line Authentication Service
STR Profile Report

Sample Submitted By: Dr. Yang Li
Anhui Medical University
Email Address: liyang@ahmu.edu.cn
Sales Order: 240326L
Cell Line Designation: 5637
Date Sample Received: Mar 26th, 2024
Report Date: Mar 26th, 2024

Methodology: Twenty-one short tandem repeat (STR) loci plus the Amelogenin locus were amplified using the commercially available SiFaSTR™ 23 plex Kit. The cell line sample was processed using the ABI Prism® 3130 XL Genetic Analyzer. Data were analyzed using GeneMapper® ID v3.2 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

Data Interpretation: Cell lines were authenticated using Short Tandem Repeat (STR) analysis as described in 2021 in ANSI Standard (ASN-0002) by the ATCC Standards Development Organization (SDO) and in Jamie L. Almeida et al., Authentication of Human and Mouse Cell Lines by Short Tandem Repeat (STR) DNA Genotype Analysis. Assay Guidance Manual. PMID: 23805434. Bookshelf ID: NBK144066.

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NOTE: According to the recommendations of *J/C* on cell line authentication, the report is valid for 3 years since the issue date.

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Cell Line Authentication Service
STR Profile Report

Sales Order: 240326L

Test Results for Submitted Sample		ExPASy Reference Database Profile	
Loci	Query Profile: 5637	Database Profile: 5637	
Amelogenin	X		
D3S1358	15 17	15	17
D5S818	11 12	11	12
D2S1338	25		
TPOX	8	8	2
CSF1PO	11	11	
Penta D	11		
TH01	7 9	7	9
vWA	18	18	
D7S820	10 11	10	11
D21S11	36	36	
Penta E	10 12		
D10S1248	14		
D8S1179	10 16	10	16
D1S1656	15		
D18S51	16 18	16	18
D12S391	20		
D6S1043	16 20		
D19S433	13 15		
D16S539	9	9	
D13S317	11	11	
FGA	22	22	

The allele match algorithm compares the 13 core STR loci only, even though alleles from all loci will be reported when available.
Note: Loci highlighted in grey (13 core STR loci) can be made public to verify cell identity. In order to protect the identity of the donor, please do not publish the allele calls from all the STR loci tested.
The sample match is based on the reference data available at the time of comparison.

Explanation of Test Results

Cell lines with ≥80% match are derived from the same donor. Cell lines with between a 70% to 79% match require further profiling for authentication of relatedness. Cell lines with <70% match are very unlikely to be from the same donor.

- ☐ The submitted sample profile is human, but not a match for any profile in the ExPASy STR database.
- ☐ The submitted profile is an exact match for the following human cell line(s) in the ExPASy STR database (13 core STR loci):
- ☒ The submitted profile is similar to the following ExPASy human cell line(s): 5637 (97.44% match)

e-Signature of Technician:



Digitally signed by Xuekun Chen
DN: cn=Xuekun Chen, o=Genetic Testing
Biotechnology (Suzhou), ou=DNA Typing Section,
email=order@jsdna.org, c=CN
Date: 2024.03.26 16:19:54 +08'00'
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Biotechnology (Suzhou), ou=Supervision Section,
email=service@jsdna.org, c=CN
Date: 2024.03.26 16:26:49 +08'00'

e-Signature, Reviewer:



More information

Addendum: Electropherogram for the customer's sample set 1 of 1



Cell Line Authentication Service STR Profile Report

Sample Submitted By: Dr. Yang Li
Anhui Medical University
liyong@ahmu.edu.cn
Email Address:
Sales Order: 240326N
Cell Line Designation: J82
Date Sample Received: Mar 26th, 2024
Report Date: Mar 26th, 2024

Methodology: Twenty-one short tandem repeat (STR) loci plus the Amelogenin locus were amplified using the commercially available SiFaSTR™ 23 plex Kit. The cell line sample was processed using the ABI Prism® 3130 XL Genetic Analyzer. Data were analyzed using GeneMapper® ID v3.2 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

Data Interpretation: Cell lines were authenticated using Short Tandem Repeat (STR) analysis as described in 2021 in ANSI Standard (ASN-0002) by the ATCC Standards Development Organization (SDO) and in Jamie L. Almeida et al., Authentication of Human and Mouse Cell Lines by Short Tandem Repeat (STR) DNA Genotype Analysis. Assay Guidance Manual. PMID: 23805434. Bookshelf ID: NBK144066.

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NOTE: According to the recommendations of J/C on cell line authentication, the report is valid for 3 years since the issue date.

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Ver. 3.1.2



Cell Line Authentication Service STR Profile Report

Sales Order: 240326N

Test Results for Submitted Sample			ExPASy Reference Database Profile	
Loci	Query Profile: J82		Database Profile: J82	
Amelogenin	X	Y		
D3S1358	16	18	16	18
D5S818	12	13	12	13
D2S1338	19			
TPOX	11	12	11	12
CSF1PO	10	11	10	11
Penta D	9			
TH01	9.3		9.3	
vWA	17	18	17	18
D7S820	9	11	9	11
D21S11	30		30	
Penta E	12	15		
D10S1248	13			
D8S1179	8	13	8	13
D1S1656	14			
D18S51	12	12	12	
D12S391	24			
D6S1043	19			
D19S433	12	13		
D16S539	11	12	11	12
D13S317	10	12	10	12
FGA	20	24	20	24

The allele match algorithm compares the 13 core STR loci only; even though alleles from all loci will be reported when available.

Note: Loci highlighted in grey (13 core STR loci) can be made public to verify cell identity. In order to protect the identity of the donor, please do not

publish the allele calls from all the STR loci tested.

The sample match is based on the reference data available at the time of comparison.

Explanation of Test Results

Cell lines with >80% match are derived from the same donor. Cell lines with between a 70% to 79% match require further profiling for authentication of relatedness. Cell lines with <70% match are very unlikely to be from the same donor.

- ☐ The submitted sample profile is human, but not a match for any profile in the ExPASy STR database.
- ☐ The submitted profile is an exact match for the following human cell line(s) in the ExPASy STR database (13 core STR loci):
- ☒ The submitted profile is similar to the following ExPASy human cell line(s): J82 (97.87% match)

e-Signature of Technician:
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Date: 2024.03.26 16:26:21 +08'00'
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Biotechnology (Suzhou), ou=Supervision Section,
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More information

Addendum: Electropherogram for the customer's sample set 1 of 1

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Ver. 3.1.2



Cell Line Authentication Service STR Profile Report

Sample Submitted By: Dr. Yang Li
Anhui Medical University
Email Address: liyang@ahmu.edu.cn
Sales Order: 240326K
Cell Line Designation: SV-HUC-1
Date Sample Received: Mar 26th, 2024
Report Date: Mar 26th, 2024

Methodology: Twenty-one short tandem repeat (STR) loci plus the Amelogenin locus were amplified using the commercially available SiFaSTR™ 23 plex Kit. The cell line sample was processed using the ABI Prism® 3130 XL Genetic Analyzer. Data were analyzed using GeneMapper® ID v3.2 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

Data Interpretation: Cell lines were authenticated using Short Tandem Repeat (STR) analysis as described in 2012 in ANSI Standard (ASN-0002) by the ATCC Standards Development Organization (SDO) and in Capes-Davis et al., Match criteria for human cell line authentication: Where do we draw the line? Int J Cancer. 2013;132(11):2510-9.

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NOTE: According to the recommendations of I/C on cell line authentication, the report is valid for 3 years since the issue date.

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Cell Line Authentication Service STR Profile Report

Sales Order: 240326K

Test Results for Submitted Sample			ExPASy Reference Database Profile	
Loci	Query Profile: SV-HUC-1		Database Profile: SV-HUC-1	
Amelogenin	X	Y	X	Y
D3S1358	14	17		
D5S818	12	14	12	14
D2S1338	17			
TPOX	8	10	8	10
CSF1PO	10	11	10	11
Penta D	13			
TH01	9	9.3	9	9.3
vWA	14		14	
D7S820	10	11	10	11
D21S11	29	30		
Penta E	10	20		
D10S1248	13	14		
D8S1179	14	16		
D1S1656	11	15		
D18S51	15	16		
D12S391	18			
D6S1043	11			
D19S433	14			
D16S539	11		11	
D13S317	12		12	13
FGA	21	22		

The allele match algorithm compares the 8 core loci plus amelogenin only, even though alleles from all loci will be reported when available.

Note: Loci highlighted in grey (8 core STR loci plus Amelogenin) can be made public to verify cell identity. In order to protect the identity of the donor, please do not publish the allele calls from all the STR loci tested.

The sample match is based on the reference data available at the time of comparison.

Explanation of Test Results

Cell lines with ≥80% match are considered to be related; i.e., derived from a common ancestry. Cell lines with between a 55% to 80% match require further profiling for authentication of relatedness.

- ☐ The submitted sample profile is human, but not a match for any profile in the ExPASy STR database.
- ☐ The submitted profile is an exact match for the following human cell line(s) in the ExPASy STR database (8 core loci plus Amelogenin):
- ☒ The submitted profile is similar to the following ExPASy human cell line(s): SV-HUC-1 (96.77% match)

e-Signature Technician:



e-Signature Supervisor:

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More information

Addendum: Electropherogram for the customer's sample set 1 of 1



GENETIC TESTING BIOTECHNOLOGY

Cell Line Authentication Service STR Profile Report

Sample Submitted By: Dr. Yang Li
Anhui Medical University
Email Address: liyang@ahmu.edu.cn
Sales Order: 240326M
Cell Line Designation: UM-UC-3
Date Sample Received: Mar 26th, 2024
Report Date: Mar 26th, 2024

Methodology: Twenty-one short tandem repeat (STR) loci plus the Amelogenin were amplified using the commercially available SiFaSTR™ 2: Kit. The cell line sample was processed using the ABI Prism® 31 Genetic Analyzer. Data were analyzed using GeneMapper® II software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

Data Interpretation: Cell lines were authenticated using Short Tandem Repeat analysis as described in 2021 in ANSI Standard (ASN-0002) by ATCC Standards Development Organization (SDO) and in Jar Almeida et al., Authentication of Human and Mouse Cell Line Short Tandem Repeat (STR) DNA Genotype Analysis. Assay Guide Manual. PMID: 23805434. Bookshelf ID: NBK144066.

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NOTE: According to the recommendations of I/C on cell line authentication, the report is valid for 3 years since the issue date.

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Ver



GENETIC TESTING BIOTECHNOLOGY

Cell Line Authentication Service STR Profile Report

Sales Order: 240326M

Test Results for Submitted Sample		ExPASy Reference Database Profile	
Loci	Query Profile: UM-UC-3	Database Profile: UM-UC-3	
Amelogenin	X		
D3S1358	17 18	17	18
D5S818	12	12	
D2S1338	23		
TPOX	10	10	
CSF1PO	10 11	10	11
Penta D	13		
TH01	6 9	6	9
vWA	17	17	
D7S820	8 9	8	9
D21S11	31	31	
Penta E	12		
D10S1248	14 15		
D8S1179	13	13	
D1S1656	15 17.3		
D18S51	14	14	
D12S391	22		
D6S1043	11 13		
D19S433	14 15		
D16S539	8 9	8	9
D13S317	8	8	
FGA	20 21	20	21

The allele match algorithm compares the 13 core STR loci only, even though alleles from all loci will be reported when available.
Note: Loci highlighted in grey (13 core STR loci) can be made public to verify cell identity. In order to protect the identity of the donor, please do not publish the allele calls from all the STR loci tested.
The sample match is based on the reference data available at the time of comparison.

Explanation of Test Results

Cell lines with ≥80% match are derived from the same donor. Cell lines with between a 70% to 79% match require further profiling for authentication of relatedness. Cell lines with <70% match are very unlikely to be from the same donor.

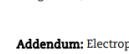
- ☐ The submitted sample profile is human, but not a match for any profile in the ExPASy STR database.
- ☒ The submitted profile is an exact match for the following human cell line(s) in the ExPASy STR database (13 core STR loci): UM-UC-3
- ☐ The submitted profile is similar to the following ExPASy human cell line(s):

e-Signature, Investigator:



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Date: 2024.03.26 16:23:25 +08'00'

e-Signature, Reviewer:



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Addendum: Electropherogram for the customer's sample set 1 of 1

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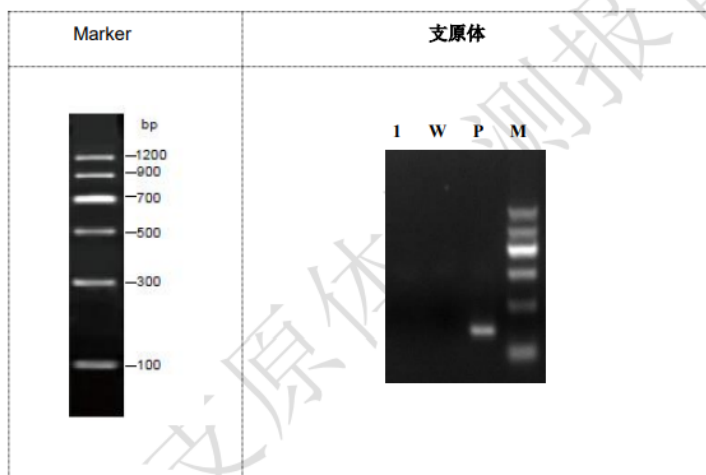


More information

Ver. 3.1.2

支原体检测报告

编号	名称	支原体 PCR 结果	支原体测序结果	结论
1	T24 LOT20210531 P+3	阴性	/	合格
W	Negative (Water)	阴性	/	成立
P	Positive	阳性	/	成立



检测人：龙慧玲	审核人：龙慧玲
---------	---------

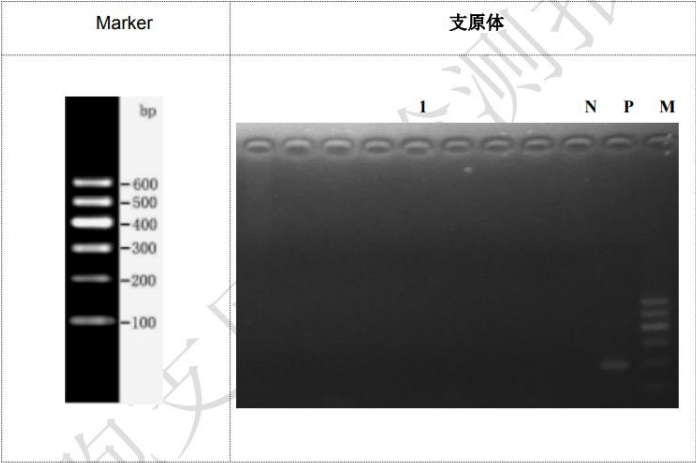
国家模式与特色实验细胞资源库

2021年05月31日



支原体检测报告

检测时间	编号	名称	批次	支原体 PCR 结果	结论
2018/09/13	1	TCCSUP	20180907	阴性	合格
	N	Negative		阴性	成立
	P	Positive		阳性	成立



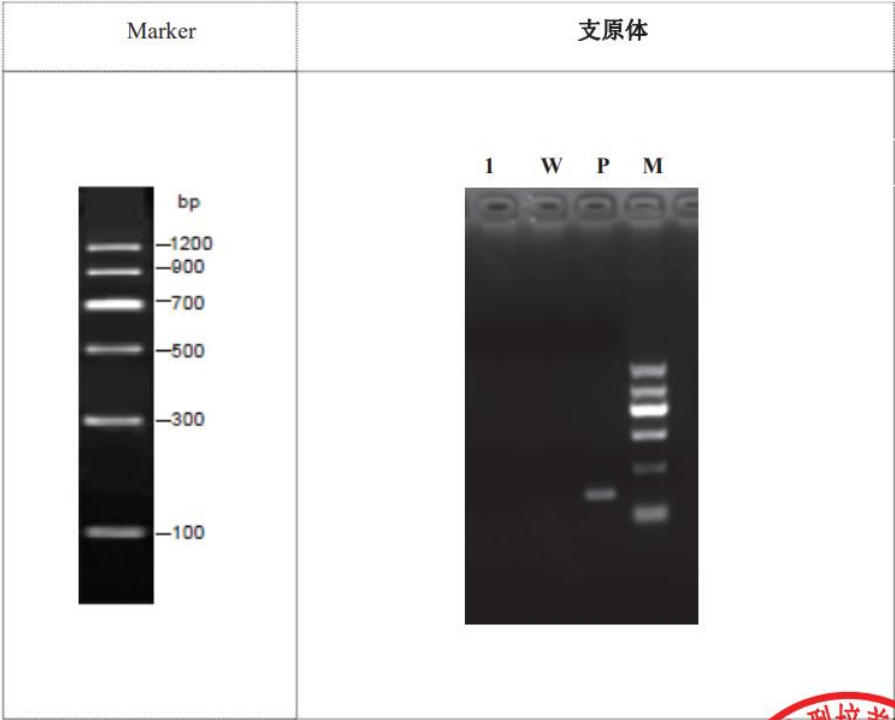
检测人	刘毅
-----	----

国家模式与特色实验细胞资源库



支原体检测报告

编号	名称	支原体 PCR 结果	支原体测序结果	结论
I	SW780	阴性	/	合格
W	Negative (Water)	阴性	/	成立
P	Positive	阳性	/	成立



中国科学院典型培养物保藏委员会细胞库

2024/3/18

细胞库

备注:

使用 TAKARA PCR Mycoplasma Detection Set(货号 6601) 支原体检测试剂盒检测，检测结果仅对送检样品有效。



中乔新舟

Web:WWW.zqxzbio.com

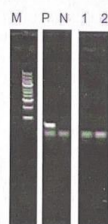
支原体检测报告

支原体检测反应体系:

Myco-PCR-Mix	18ul
待检测细胞上清液	2ul

按照以上反应比例,在PCR管中将待检测样品上清液2ul加入到18ul Myco-PCR-Mix中,每次检测请用Positive control 模版作为阳性对照,用Negative control 模版作为阴性对照。PCR反应程序为:95°C 5min, (95°C 30s, 55°C 45s, 72°C 45s) 36个循环,72°C 5min, 10°C 保存。PCR产物跑1.5%琼脂胶,用DNA Marker 显示片段大小。待检测样品中如果出现与阳性对照大小一致(250 bp)的条带,说明样品被支原体感染,若无对应条带则说明无支原体污染。

跑胶结果如下图所示:



M 孔道为 DNA Marker

N 孔道为 Negative control

P 孔道为 Positive control



中乔新舟

Web:WWW.zqxzbio.com

- 1 号孔道为待测 **J82** 细胞样品
- 2 号孔道为待测 **J82** 细胞样品复孔
- 3 细胞结论:由电泳图可知检测的 **J82** 细胞样品**没有**支原体污染。

(注:图谱中样品点样孔最下方的条带是引物二聚体,是PCR检测时的常规现象,其亮暗程度通常是与阳性条带的亮度成反比的。PCR的检测方法非常灵敏,一般极弱的阳性也可以看到有区别于二聚体的条带产生,结果可靠。)



2022.03.10

检测人签名:金竹

5637 (human bladder cancer cell line) Mycoplasma Detection Report

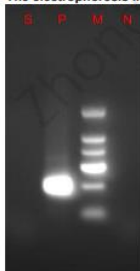
1. Reaction System

Myco-PCR-Mix 9 μ l
Cell culture supernatant to be tested 1 μ l

2. Test Procedure

According to the above reaction system, add 1 μ l of the supernatant of the sample to be tested to 9 μ l Myco-PCR-Mix in a PCR tube, use the Positive control template as the positive control, and use the Negative control template as the negative control. The PCR reaction program is: 95 $^{\circ}$ C 5min, (95 $^{\circ}$ C 15s, 56 $^{\circ}$ C 15s, 72 $^{\circ}$ C 5s), 35 cycles, 72 $^{\circ}$ C 5min; and store at 4 $^{\circ}$ C. The PCR product is subjected to 1% agarose gel electrophoresis, and the molecular weight of the band is displayed with a DNA Marker. If a band with the same molecular weight as the positive control (about 500bp) appears in the sample to be tested, it means that the sample is contaminated with mycoplasma. If there is no corresponding band, it means that the sample is not contaminated with mycoplasma.

The electrophoresis image are shown in the figure below:



Lane S is 5637 (human bladder cancer cell line)
Lane P is Positive Control
Lane M is DNAMarker
Lane N is Negative Control

(Note: The band at the bottom of the sample loading wells in the gel image is the primer dimer, which is a common phenomenon in PCR detection. Its intensity is usually inversely proportional to the brightness of the positive band. The PCR detection method is very sensitive, and even a very weak positivity can be distinguished from the dimer, making the results reliable.)

3. Test result

Sample Name	Test Result	Test Criteria	Test Interpretation
5637 (human bladder cancer cell line)	-	Compare the positive control to see if there is characteristic band	Negative, no mycoplasma contamination

Shanghai Zhong Qiao Xin Biotechnology Co., Ltd.

Reporter: Ke Li

Date: 2024-05-29

质检专用章

UM-UC-3

Mycoplasma Detection Report

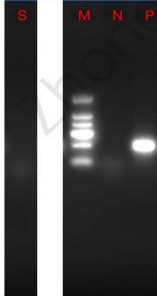
1. Reaction System

Mycos-PCR-Mix 9 μ l
Cell culture supernatant to be tested 1 μ l

2. Test Procedure

According to the above reaction system, add 1 μ l of the supernatant of the sample to be tested to 9 μ l Mycos-PCR-Mix in a PCR tube, use the Positive control template as the positive control, and use the Negative control template as the negative control. The PCR reaction program is: 95 $^{\circ}$ C 5min, (95 $^{\circ}$ C 15s, 56 $^{\circ}$ C 15s, 72 $^{\circ}$ C 5s), 35 cycles, 72 $^{\circ}$ C 5min, and store at 4 $^{\circ}$ C. The PCR product is subjected to 1% agarose gel electrophoresis, and the molecular weight of the band is displayed with a DNA Marker. If a band with the same molecular weight as the positive control (about 500bp) appears in the sample to be tested, it means that the sample is contaminated with mycoplasma. If there is no corresponding band, it means that the sample is not contaminated with mycoplasma.

The electrophoresis image are shown in the figure below:



Lane S is UM-UC-3
Lane P is Positive Control
Lane M is DNAMarker
Lane N is Negative Control

(Note: The band at the bottom of the sample loading wells in the gel image is the primer dimer, which is a common phenomenon in PCR detection. Its intensity is usually inversely proportional to the brightness of the positive band. The PCR detection method is very sensitive, and even a very weak positivity can be distinguished from the dimer, making the results reliable.)

3. Test result

Sample Name	Test Result	Test Criteria	Test Interpretation
UM-UC-3	-	Compare the positive control to see if there is characteristic band	Negative, no mycoplasma contamination

Shanghai Zhong Qiao Xin Zhou Biotechnology Co., Ltd.
Reporter: Ke Li
Date: 2024-06-03

质检专用章



SV-HUC-1 Mycoplasma Detection Report

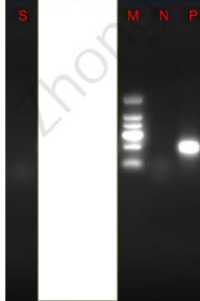
1. Reaction System

Myco-PCR-Mix 9 μ l
Cell culture supernatant to be tested 1 μ l

2. Test Procedure

According to the above reaction system, add 1 μ l of the supernatant of the sample to be tested to 9 μ l Myco-PCR-Mix in a PCR tube, use the Positive control template as the positive control, and use the Negative control template as the negative control. The PCR reaction program is: 95 $^{\circ}$ C 5min, (95 $^{\circ}$ C 15s, 56 $^{\circ}$ C 15s, 72 $^{\circ}$ C 5s), 35 cycles, 72 $^{\circ}$ C 5min, and store at 4 $^{\circ}$ C. The PCR product is subjected to 1% agarose gel electrophoresis, and the molecular weight of the band is displayed with a DNA Marker. If a band with the same molecular weight as the positive control (about 500bp) appears in the sample to be tested, it means that the sample is contaminated with mycoplasma. If there is no corresponding band, it means that the sample is not contaminated with mycoplasma.

The electrophoresis image are shown in the figure below:



Lane S is SV-HUC-1
Lane M is DNA Marker
Lane N is Negative Control
Lane P is Positive Control

(Note: The band at the bottom of the sample loading wells in the gel image is the primer dimer, which is a common phenomenon in PCR detection. Its intensity is usually inversely proportional to the brightness of the positive band. The PCR detection method is very sensitive, and even a very weak positivity can be distinguished from the dimer, making the results reliable.)

3. Test result

Sample Name	Test Result	Test Criteria	Test Interpretation
SV-HUC-1	-	Compare the positive control to see if there is characteristic band	Negative, no mycoplasma contamination

Shanghai Zhong Qiao Xin Zhou Biotechnology Co.,Ltd.
Reporter: Ke Li
Date: 2024-06-03

质检专用章