



HISTOLOGY - IHC - MOLECULAR - IMAGING

Department of Pathology and Laboratory Medicine
TRIP Laboratory (Molecular)
<http://www.pathology.wisc.edu/research/trip>

Short Tandem Repeat Analysis

1111 Highland Ave, WIMR 2062
Madison, WI 53705-8550
(608) 265-9168

Sample Report:

N25LM.6.1
Sample Name on Tube: N25LM.6.1
96.4 ng/ μ L, (A260/280=1.95)
Sample Type: Cells
Cell Count: ~1-1.5 million cells

Requestor:

Harini Desikan
Donna Peters Lab

Sample Date: N/A

Receive Date: 8/29/18
Assay Date: 09/05/18
File Name: STR 180906 wmr
Report Date: 09/07/18

STR Locus	STR Genotype Repeat #	STR Genotype
FGA	16-18,18.2,19,19.2,20,20.2,21,21.2,22, 22.2, 23, 23.2, 24, 24.2, 25, 25.2, 26-30, 31.2, 43.2, 44.2,45.2, 46.2	20,20
TPOX	6-13	8,11
D8S1179	7-18	13,14
vWA	10-22	15,19
Amelogenin	X,Y	X,Y
Penta D	2.2, 3.2, 5, 7-17	10,12
CSF1PO	6-15	12,12
D16S539	5, 8-15	11,13
D7S820	6-14	9,10
D13S317	7-15	12,14
D5S818	7-16	11,11
Penta E	5-24	5,11
D18S51	8-10, 10.2, 11-13, 13.2, 14-27	13,14
D21S11	24,24.2,25,25.2,26-28,28.2,29,29.2, 30, 30.2,31, 31.2,32,32.2,33,33.2, 34,34.2,35,35.2,36-38	27,31.2
TH01	4-9,9.3,10-11,13.3	6,9.3
D3S1358	12-20	14,15

Results: Based on the N25LM.6.1 cells submitted by Harini Desikan – Donna Peters Lab dated and received on 08/29/18, this sample (Label on Tube: N25LM.6.1) defines the STR profile of the human cell line N25LM.6.1 comprising 27 allelic polymorphisms across the 15 STR loci analyzed.

Interpretation: No STR polymorphisms other than those corresponding to the human N25LM.6.1 cell line were detected and the concentration of DNA required to achieve an acceptable STR genotype (signal/ noise) was equivalent to that required for the standard procedure (~1 ng/amplification reaction) from human genomic DNA. This result suggests that the N25LM.6.1 sample submitted corresponds to the N25LM.6.1 cell line and was not contaminated with any other human cells.

Sensitivity: Sensitivity limits for detection of STR polymorphisms unique to either this or other human cell lines is ~2-5%.

X *RMB*

Digitally Signed on 09/11/18

Rebecca M. Baus, BA
TRIP Laboratory, Molecular

X *WMR*

Digitally Signed on 09/11/18

William M. Rehrauer, PhD, Director / Co-Director
UWHC Molecular Diagnostics Laboratory / UWSMPH TRIP Laboratory



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Sample Report:

N27FL2.CS
Sample Name on Tube: N27FL2.CS
69.4 ng/ μ L, (A260/280=1.83)
Sample Type: Cells
Cell Count: ~1-1.5 million cells

Requestor:

Harini Desikan
Donna Peters Lab

Sample Date: N/A

Receive Date: 8/29/18
Assay Date: 09/05/18
File Name: STR 180906 wmr
Report Date: 09/07/18

STR Locus	STR Genotype Repeat #	STR Genotype
FGA	16-18,18.2,19,19.2,20,20.2,21,21.2,22, 22.2, 23, 23.2, 24, 24.2, 25, 25.2, 26-30, 31.2, 43.2, 44.2,45.2, 46.2	18,24
TPOX	6-13	8,8
D8S1179	7-18	13,15
vWA	10-22	18,19
Amelogenin	X,Y	X,X
Penta D	2.2, 3.2, 5, 7-17	11,12
CSF1PO	6-15	11,11
D16S539	5, 8-15	13,14
D7S820	6-14	8,9
D13S317	7-15	12,14
D5S818	7-16	11,12
Penta E	5-24	12,18
D18S51	8-10, 10.2, 11-13, 13.2, 14-27	12,14
D21S11	24,24.2,25,25.2,26-28,28.2,29,29.2, 30, 30.2,31, 31.2,32,32.2,33,33.2, 34,34.2,35,35.2,36-38	32,32.2
TH01	4-9,9.3,10-11,13.3	7,9,3
D3S1358	12-20	15,16

Results: Based on the N27FL2.CS cells submitted by Harini Desikan – Donna Peters Lab dated and received on 08/29/18, this sample (Label on Tube: N27FL2.CS) defines the STR profile of the human cell line N27FL2.CS comprising 28 allelic polymorphisms across the 15 STR loci analyzed.

Interpretation: No STR polymorphisms other than those corresponding to the human N27FL2.CS cell line were detected and the concentration of DNA required to achieve an acceptable STR genotype (signal/ noise) was equivalent to that required for the standard procedure (~1 ng/amplification reaction) from human genomic DNA. This result suggests that the N27FL2.CS sample submitted corresponds to the N27FL2.CS cell line and was not contaminated with any other human cells.

Sensitivity: Sensitivity limits for detection of STR polymorphisms unique to either this or other human cell lines is ~2-5%.

X RMB

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TRIP Laboratory, Molecular

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Sample Report:

N27RF7.1 HTM

Sample Name on Tube: N27-2RF7.1 HTM

69.4 ng/μL, (A260/280=1.83)

Sample Type: Cells

Cell Count: ~1-1.5 million cells

Requestor:

Harini Desikan

Donna Peters Lab

Sample Date: N/A

Receive Date: 8/29/18

Assay Date: 09/05/18

File Name: STR 180906 wmr

Report Date: 09/07/18

STR Locus	STR Genotype Repeat #	STR Genotype
FGA	16-18,18.2,19,19.2,20,20.2,21,21.2,22, 22.2, 23, 23.2, 24, 24.2, 25, 25.2, 26-30, 31.2, 43.2, 44.2,45.2, 46.2	22,24
TPOX	6-13	6,9
D8S1179	7-18	13,15
vWA	10-22	16,18
Amelogenin	X,Y	X,X
Penta D	2.2, 3.2, 5, 7-17	2.2,9
CSF1PO	6-15	10,13
D16S539	5, 8-15	11,13
D7S820	6-14	8,9
D13S317	7-15	12,12
D5S818	7-16	12,13
Penta E	5-24	8,10
D18S51	8-10, 10.2, 11-13, 13.2, 14-27	16,18
D21S11	24,24.2,25,25.2,26-28,28.2,29,29.2, 30, 30.2,31, 31.2,32,32.2,33,33.2, 34,34.2,35,35.2,36-38	28,30
TH01	4-9,9.3,10-11,13.3	7,9
D3S1358	12-20	16,18

Results: Based on the N27RF7.1 HTM cells submitted by Harini Desikan – Donna Peters Lab dated and received on 08/29/18, this sample (Label on Tube: N27-2RF7.1 HTM) defines the STR profile of the human cell line N27RF7.1 HTM comprising 29 allelic polymorphisms across the 15 STR loci analyzed.

Interpretation: No STR polymorphisms other than those corresponding to the human N27RF7.1 HTM cell line were detected and the concentration of DNA required to achieve an acceptable STR genotype (signal/ noise) was equivalent to that required for the standard procedure (~1 ng/amplification reaction) from human genomic DNA. This result suggests that the N27RF7.1 HTM sample submitted corresponds to the N27RF7.1 HTM cell line and was not contaminated with any other human cells.

Sensitivity: Sensitivity limits for detection of STR polymorphisms unique to either this or other human cell lines is ~2-5%.

X RMB

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Short Tandem Repeat Analysis

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Sample Report:

TM-1
Sample Name on Tube: TM-1
193.1 ng/ μ L, (A260/280=1.96)
Sample Type: Cells
Cell Count: ~2 million cells

Requestor:

Harini Desikan
Donna Peters Lab

Sample Date: N/A

Receive Date: 8/29/18
Assay Date: 09/05/18
File Name: STR 180906 wmr
Report Date: 09/07/18

STR Locus	STR Genotype Repeat #	STR Genotype
FGA	16-18,18.2,19,19.2,20,20.2,21,21.2,22, 22.2, 23, 23.2, 24, 24.2, 25, 25.2, 26-30, 31.2, 43.2, 44.2,45.2, 46.2	20,20
TPOX	6-13	8,9
D8S1179	7-18	11,12,14**
vWA	10-22	15,15
Amelogenin	X,Y	X,X
Penta D	2.2, 3.2, 5, 7-17	14,14
CSF1PO	6-15	11,11
D16S539	5, 8-15	11,11
D7S820	6-14	12,12
D13S317	7-15	10,14**
D5S818	7-16	11,11
Penta E	5-24	10,11**
D18S51	8-10, 10.2, 11-13, 13.2, 14-27	14,22
D21S11	24,24.2,25,25.2,26-28,28.2,29,29.2, 30, 30.2,31, 31.2,32,32.2,33,33.2, 34,34.2,35,35.2,36-38	29,30
TH01	4-9,9.3,10-11,13.3	7,7
D3S1358	12-20	17,17

Results: Based on the TM-1 cells submitted by Harini Desikan – Donna Peters Lab dated and received on 08/29/18, this sample (Label on Tube: TM-1) defines the STR profile of the human cell line TM-1 comprising 22 allelic polymorphisms across the 15 STR loci analyzed.

Interpretation: No STR polymorphisms other than those corresponding to the human TM-1 cell line were detected, including a triploid genotype at the D8S1179 loci. Additionally, allelic imbalance (denoted by ** in the table above) was observed at the D8S1179, D13S317, and Penta_E loci. At the Penta_E loci the signal strength of allele 11 is much less evident relative to allele 10. Similarly, at the D8S1179 loci the signal strength of allele 11 is much less evident than alleles 12 and 14. These observations could be the result of chromosomal gains, losses and/or amplifications in this cell line. The concentration of DNA required to achieve an acceptable STR genotype (signal/ noise) was equivalent to that required for the standard procedure (~1 ng/amplification reaction) from human genomic DNA. This result suggests that the TM-1 sample submitted corresponds to the TM-1 cell line and was not contaminated with any other human cells.

Sensitivity: Sensitivity limits for detection of STR polymorphisms unique to either this or other human cell lines is ~2-5%.

X RMB

Digitally Signed on 09/10/18

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