Certificate of Analysis - Amended

Product Information

Product Name	WA26
Lot Number	WB0268
Parent Material	WA26-WB0131
Depositor	WiCell
Banked by	WiCell
Thaw Recommendation	Thaw 1 vial into 2 wells of a 6 well plate. WiCell recommends thawing using ROCK Inhibitor for best results.
Culture Platform	Feeder Independent
	Medium: E8
	Matrix: Recombinant Human Vitronectin
Protocol	WiCell Feeder Independent E8 Medium Protocol
Passage Number	p13 These cells were cultured for 12 passages prior to freeze. WiCell adds +1 to the passage number at freeze so that the number on the vial best represents the overall passage number of the cells at thaw.
Date Vialed	30-September-2013
Vial Label	WA26 WB0268 p13 30SEP13
Biosafety and Use Information	Appropriate biosafety precautions should be followed when working with these cells. The end user is responsible for ensuring that the cells are handled and stored in an appropriate manner. WiCell is not responsible for damages or injuries that may result from the use of these cells. Cells distributed by WiCell are intended for research purposes only and are not intended for use in humans.

Lot Specific Testing Performed by WiCell

The following testing specifications have been met for the specified product lot.

Test Description	Test Provider	Test Method	Test Specification	Result
Post-Thaw Viable Cell Recovery	WiCell	SOP-CH-305	≥ 15 Undifferentiated Colonies, ≤ 30% Differentiation and recoverable attachment after passage	Pass
Identity by STR	UW Molecular Diagnostics Laboratory	PowerPlex 16 HS System by Promega	Consistent with known profile	Pass
Sterility	Biotest Laboratories	ST/07	Negative	Pass
Mycoplasma	WiCell	SOP-QU-004	Negative	Pass
Karyotype by G-banding	WiCell	SOP-CH-003	Expected karyotype	Pass

Certificate of Analysis - Amended

General Cell Line Testing Performed by WiCell

The following tests were performed on the cell line. The tests do not apply to any particular lot.

Test Description	Test Provider	Test Method
Differentiation Potential by Teratoma	WiCell	SOP-CH-213 SOP-CH-214
HLA	UW Histocompatibility Laboratory	High resolution sequencing method with Celera reagents on the ABI 3100 instrument
ABO	New York Blood Center	For ABO: Olsson ML, Chester MA. A rapid and simple ABO genotype screening method using a novel B/O2 versus A/O2 discriminating nucleotide substitution at the ABO locus. Vox Sang 1995; 69(3):242-7. For RHD: Singleton BK, Green CA, Avent ND, Martin PG, Smart E, Daka A, Narter-Olaga EG, Hawthorne LM, Daniels G. The presence of an RHD pseudogene containing a 37 base pair duplication and a nonsense mutation in Africans with the Rh D-negative blood group phenotype. Blood 2000; 95(1): 12-8.
Growth Curve (Doubling Time)	WiCell	Varies by culture platform
Flow Cytometry for ESC Marker Expression	UW Flow Cytometry Laboratory	SOP-CH-101 SOP-CH-102 SOP-CH-103 SOP-CH-105
Comprehensive Human Virus Panel	Charles River	ID 91/0

Date of Lot Release	Quality Assurance Approval
22-November-2013	8/6/2015 X AMK AMC Quality Assurance Signed by: [redacted]

UW Health

University of Wisconsin
Hospital and Clinics

Histocompatibility/Molecular Diagnostics Laboratory

[redacted]

Short Tandem Repeat Analysis*

Sample Report: 10902-STR | Label on Tube: 10902-STR | Sample Date: 10/30/13
Lab Received 10/30/13

Requestor: WiCell Research Institute

Test Date: 11/06/13 | File Name: 131106 TCS | Report Date: 11/07/13

Sample Name: (label on tube) 10902-STR

Description: WI Cell Research Institute provided genomic DNA
200.6 ug/mL 260/280=1.99

Locus	Repeat #	STR Genotype
D16S539	5, 8-15	12,14
D7S820	6-14	10,10
D13S317	7-15	11,12
D5S818	7-15	12,12
CSF1PO	6-15	11,11
TPOX	6-13	8,11
Amelogenin	NA	X,X
TH01	5-11	7,10
vWA	11, 13-21	17,17

Comments: Based on the 10902-STR DNA submitted by WI Cell dated and received on 10/30/13, this sample (Label on Tube: 10902-STR) exactly matches the STR profile of the human stem cell line WA26 comprising 12 allelic polymorphisms across the 8 STR loci analyzed. No STR polymorphisms other than those corresponding to the human WA26 stem 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 suggest that the 10902-STR DNA sample submitted corresponds to the WA26 stem cell line and was not contaminated with any other human stem cells or a significant amount of mouse feeder layer cells. Sensitivity limits for detection of STR polymorphisms unique to either this or other human stem cell lines is ~5%.

[redacted] 11/8/13
Date
Molecular Diagnostics Laboratory

[redacted] 11/07/13
Date
Molecular Diagnostics Laboratory

* Testing to assess engraftment following bone marrow transplantation was accomplished by analysis of human genetic polymorphisms at STR loci. This methodology has not yet been approved by the FDA and is for investigational use only.

File: Final STR Report

Sterility Report

Biotest Laboratories, Inc.
Making life-saving products possible

WiCell Research Institute, Inc.
WiCell Quality Assurance
[redacted]

BIOTEST SAMPLE # 13100572

VALIDATION # NG

TEST PURPOSE NG

PRODUCT	Please see packing list under product name.		
PRODUCT LOT	NA		
STERILE LOT	NA	BI LOT	NA
STERILIZATION LOT	NA	BI EXPIRATION DATE	NA
STERILIZATION DATE	NA	DATE RECEIVED	2013-10-10
STERILIZATION METHOD	NA	TEST INITIATED	2013-10-10
SAMPLING BLDG / ROOM	NA	TEST COMPLETED	2013-10-24

REFERENCE: Processed according to LAB-003: Sterility Test Procedure

Ten (10) products were each divided between 40 mL TSB and 40 mL FTG. The samples were then cultured at 20-25 C and 30-35 C respectively and were monitored for a minimum of 14 days.

☒ USP
☐ BI Manufacturers Specifications
☐ Other

RESULTS	# POSITIVES	# TESTED	POSITIVE CONTROL	NEGATIVE CONTROL
Sterile	0	10	NA	2 Negatives

COMMENTS NA

REVIEWED BY [redacted] DATE 24OCT13

[redacted]

WiCell Research Institute

Packing Slip

[redacted]

Sent to:
Sterility Testing Services
Biotest Labs, Sterility Testing Services
[redacted]

Date:
09Oct13

Contents – Number of Vials	Condition
[redacted]8 WA26-WB0268 #10891 [redacted]	-80

Mycoplasma Report

Testing Performed by WiCell

LRT #10893 10-17-2013

FORM SOP-QU-004.01

Version B

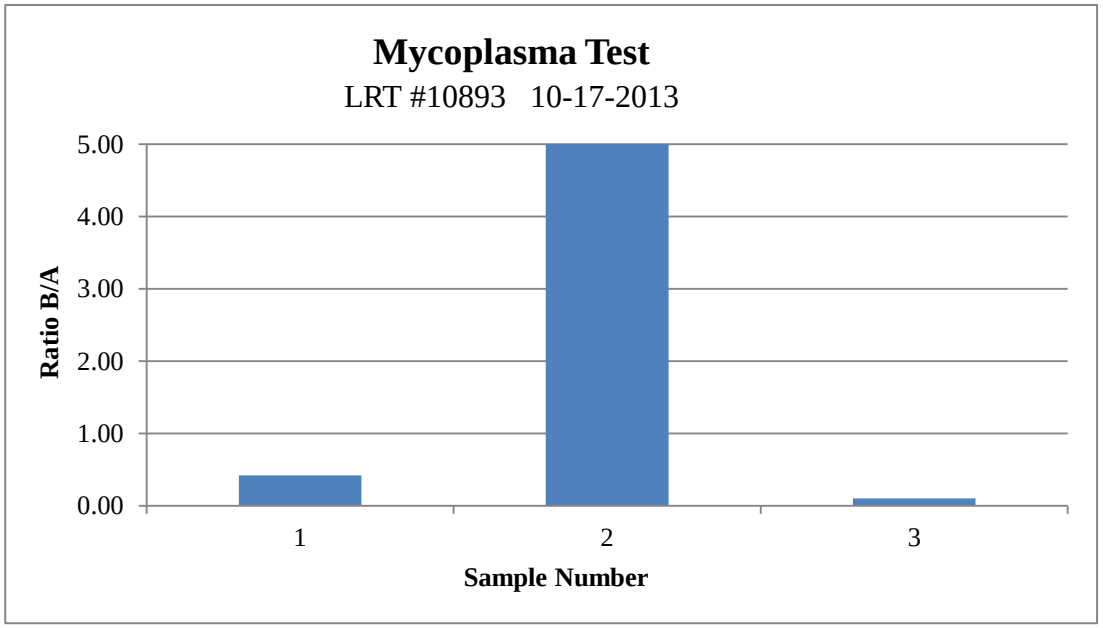
Edition 01

Assay performed and reported by: MWS

Reviewed by: JB

Equipment : Berthold 1150

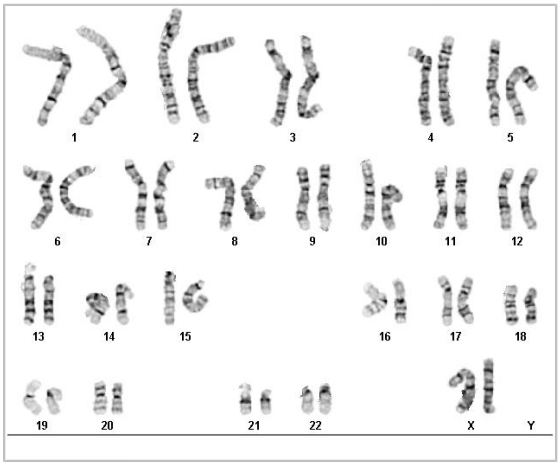
	Sample Number and ID	Reading A		A	Reading B		B	Ratio	Mycoplasma Results	Comments/Suggestions
		A1	A2	Average	B1	B2	Average	B/A		
1	WA26-WB0268 LRT 10893	209	211	210	88	88	88	0.42	Negative	
2	Positive (+) Control	319	320	319.5	23057	23015	23036	72.10	Positive	
3	Negative (-) Control	505	500	502.5	53	52	52.5	0.10	Negative	



Chromosome Analysis Report: 012354

Date Reported: Sunday, October 20, 2013
Cell Line: WA26-WB0268 10893
Passage#: 14
Date of Sample: 10/14/2013
Specimen: hESC
Results: 46,XX

Cell Line Gender: Female
Reason for Testing: Lot release testing
Investigator: [redacted] WiCell CDM



Cell: 9
Slide: 2
Slide Type: Karyotype

Total Counted: 20
Total Analyzed: 8
Total Karyotyped: 4
Band Resolution: 450 - 525

Interpretation:

This is a normal karyotype. No clonal abnormalities were detected at the stated band level of resolution.

Completed by: [redacted] CG(ASCP)
Reviewed and Interpreted by: [redacted] PhD, FACMG

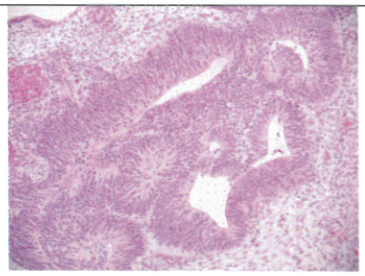
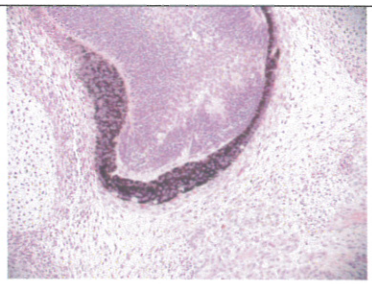
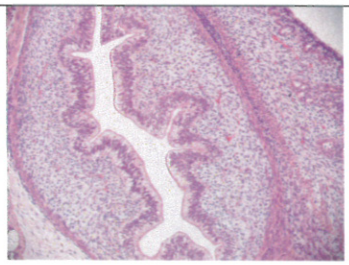
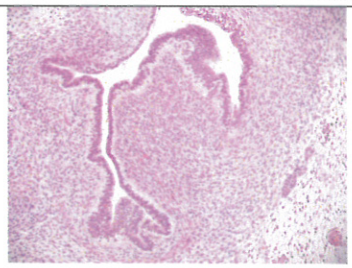
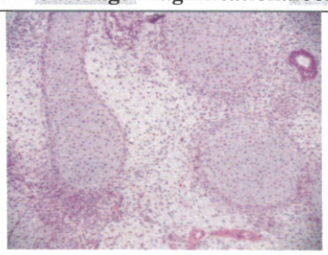
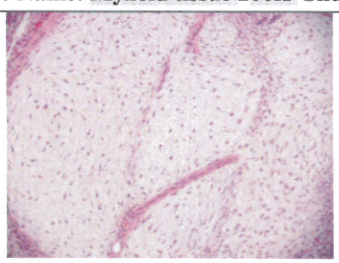
A signed copy of this report is available upon request.

Date:_____ **Sent By:**____ **Sent To:**_____ **QC Review By:** ____

Limitations: This assay allows for microscopic visualization of numerical and structural chromosome abnormalities. The size of structural abnormality that can be detected is >3-10Mb, dependent upon the G-band resolution obtained from this specimen. For the purposes of this report, band level is defined as the number of G-bands per haploid genome. It is documented here as "band level", i.e., the range of bands determined from the four karyograms in this assay. Detection of heterogeneity of clonal cell populations in this specimen (i.e.,mosaicism) is limited by the number of metaphase cells examined, documented here as "# of cells counted".

WiCell Research Institute	Teratoma Histology Report	FORM SOP-CH-~~014.~~01 Version B Edition 01

Cell Line: WA26 **Cell Lot Number: NA** **Sample Number: 10405-A,B,C**

ECTODERM	
Structure Name: Neural tubules Magnification:200X Slide ID: A	**Structure Name: Pigmented neuroectoderm Magnification: 200X Slide ID: B**
	
ENDODERM	
Structure Name: Gut Magnification:200X Slide ID: A	**Structure Name: Respiratory Magnification:200X Slide ID: B**
	
MESODERM	
Structure Name: Cartilage Magnification:200X Slide ID: B	**Structure Name: Myxoid tissue 200X Slide ID: B**
	

Comments: Structures identified include Ectoderm (2), Mesoderm (2) and Endoderm (2)

Sample(s) were assessed for the presence of differentiation into cell types characteristic of the three embryonic germ layers, which, if present in the sample(s) examined, are represented in the photographs above. The individual's signature below verifies that this report accurately reflects the pathology observed.

Pathologist (By/Date): 6/27/2012

[redacted]

QA Review (By/Date): [redacted] 03JUN12

QSOP ID SOP-CH-214. Error. 03JUN12 JHT

Print Date: 28-Jun-12

UW Health

University of Wisconsin
Hospital and Clinics

Name: WICELL, 10405_HLA
MRN: OS000183
DOB:
HLA#: WICELL

Hospital:
Physician: ,
Category:

Bone Marrow Case Histocompatibility Summary
301417-DT

HLA Typing Results

Patient	Relation	Hap	A*	B*	C*	DRB1*	DRB3*	DRB4*	DRB5*	DQB1*	DPB1*	Tested Date / Collect Date
WICELL, 10405_HLA			02:01	18:01:01G	07:01:01G	01:01						03/12/12
OS000183 / WICELL	Patient		02:01	51:01	07:02:01G	07:01						03/01/12

HLA typings performed by sequencing, SSO, SSP or a combination. For low-resolution testing, results are reported by Serologic Equivalents. A "+" in the HLA allele designation indicates that the typing was performed by low/mid-resolution molecular method and that additional alleles are possible. Only the most frequent allele is listed.

HLA DNA-Based Typing

Name / HLA / MR# / Received	Method / Test Date	A*	B*	C*	DRB1*	DRB3*	DRB4*	DRB5*	DQB1*
WICELL, 10405_HLA		02:01							
OS000183 / WICELL	SEQ	02:01							
03/01/2012	03/20/2012								
		HLA Allele database: IMGT 3.7.0 2012-01-12							
			18:01:01G						
	SEQ		51:01						
03/01/2012	03/20/2012								
		The reported allele group B*18:01:01G includes the following alleles, which share identical sequences in the antigen recognition site of exons 2 and 3: B*18:01 B*18:17N HLA Allele database: IMGT 3.7.0 2012-01-12							
				07:01:01G					
	SEQ			07:02:01G					
03/01/2012	03/20/2012								
		HLA Allele database: IMGT 3.7.0 2012-01-12 The reported allele group C*07:01:01G includes the following alleles, which share identical sequences in the antigen recognition site of exons 2 and 3: C*07:01 C*07:06 C*07:18 The reported allele group C*07:02:01G includes the following alleles, which share identical sequences in the antigen recognition site of exons 2 and 3: C*07:02 C*07:50							
					01:01				
	SEQ				07:01				
03/01/2012	03/20/2012								
		HLA Allele database: IMGT 3.7.0 2012-01-12 The following allele combination(s), in which both alleles are listed by the ASHI CWD review committee as rare or not well defined, cannot be excluded: DRB1*01:21,07:11							

Comments

UW Health

University of Wisconsin
Hospital and Clinics

Name: WICELL, 10405_HLA
MRN: OS000183
DOB:
HLA#: WICELL

Hospital:
Physician: ,
Category:

Bone Marrow Case Histocompatibility Summary

301417-DT

This test was developed and its performance characteristics determined by this laboratory. It has not been cleared or approved by the U.S. Food and Drug Administration. The FDA has determined that such clearance or approval is not necessary. This test is used for clinical purposes. It should not be regarded as investigational or for research. This laboratory is certified under the Clinical Laboratory Improvement Amendments of 1988 (CLIA-88) as qualified to perform high complexity clinical laboratory testing.

Electronically signed by [redacted]

Director or Delegate, HLA Laboratory

03/25/2012 12:15
Date/Time

Histocompatibility Laboratory, Room D4/231, 600 Highland Ave., Madison, WI 53792-2472
Teresa Darcy, MD, Medical Director :: Thomas M. Ellis, PhD, D(ABHI) Laboratory Director
Lab: 608.263.8815 (option 3); Fax: 608.263.9610
ASHI: 01-4-WI-03-2, CLIA: 52DO661997

New York *Blood Center*
Laboratory of Immunohematology and Genomics
45-01 Vernon Blvd., Long Island City, N.Y. 11101
718-752-4771 • Fax 718-752-4747

March 20, 2012

WiCell Research Institute
Attn: Quality Assurance
[redacted]

SAMPLE: DNA WA26 #10405 (MA#167-12)

Date Received: 03/08/12
Sample Date: 03/01/12

HISTORY: DNA from cell line.

TESTING REQUESTED: Genotype for *ABO* and common *RH*

TESTING PERFORMED: *ABO:* Polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) testing for nucleotide (nt) positions 261 (O^1), 467 (A^2), 703 (B), and 1096 (B and O^2). *RH:* Multiplex PCR-RFLP for *RHD* and *RHCE*C/c*. PCR-RFLP for RHCE Exon 5 (676C>G for E/e).

DNA MOLECULAR RESULTS: *ABO:* PCR-RFLP testing indicates the sample is homozygous for deletion of G at 261 characteristic of O^1 alleles. *RH: RHD* exons 4 and 7 are present. Negative for the inactivating *RHD* pseudogene. *RH*Cc* and *RH*ee*.

	Genotype	Predicted Phenotype
WA26 #10405:	*ABO*O^{1}O^1; RH*D, RH*Cc, RH*ee*	**Group O; RhD**+, C+E–c+e+

[redacted]
Manager, Genomics

[redacted](ASCP)SBB, PhD
Director of Immunohematology and Genomics

These *in vitro* diagnostic tests were developed and their performance characteristics established in the Molecular Analysis Laboratory. The tests have not been submitted to the Food and Drug Administration (FDA) for clearance or approval and; therefore, are not FDA-licensed tests. The Molecular Analysis Laboratory is certified under the Clinical Laboratory Improvement Amendment (CLIA) of 1988 as qualified to perform high complexity clinical testing. The New York Blood Center has been approved by the New York State Department of Health to perform these tests under its current Clinical Laboratory Permit.

These results are intended to predict a blood group antigen profile in a patient or donor, and are not intended for clinical diagnosis or as the sole means for patient management decisions. There are situations where testing DNA of a person may not reflect the red cell phenotype and not all performance characteristics have been determined. Nucleotide changes that inactivate gene expression or rare new variant alleles may not be identified in these assays. In addition, test results obtained from DNA isolated from leucocytes and other hematopoietic cells may differ from DNA isolated from other tissues in persons with a history of transplantation.

New York BloodCenter

Immunohematology
Telephone: 718-752-4771
Genomics
Telephone: 718-752-4637

Sample: MA167-12; WA26 #10405

Test: ABO and RH - GF

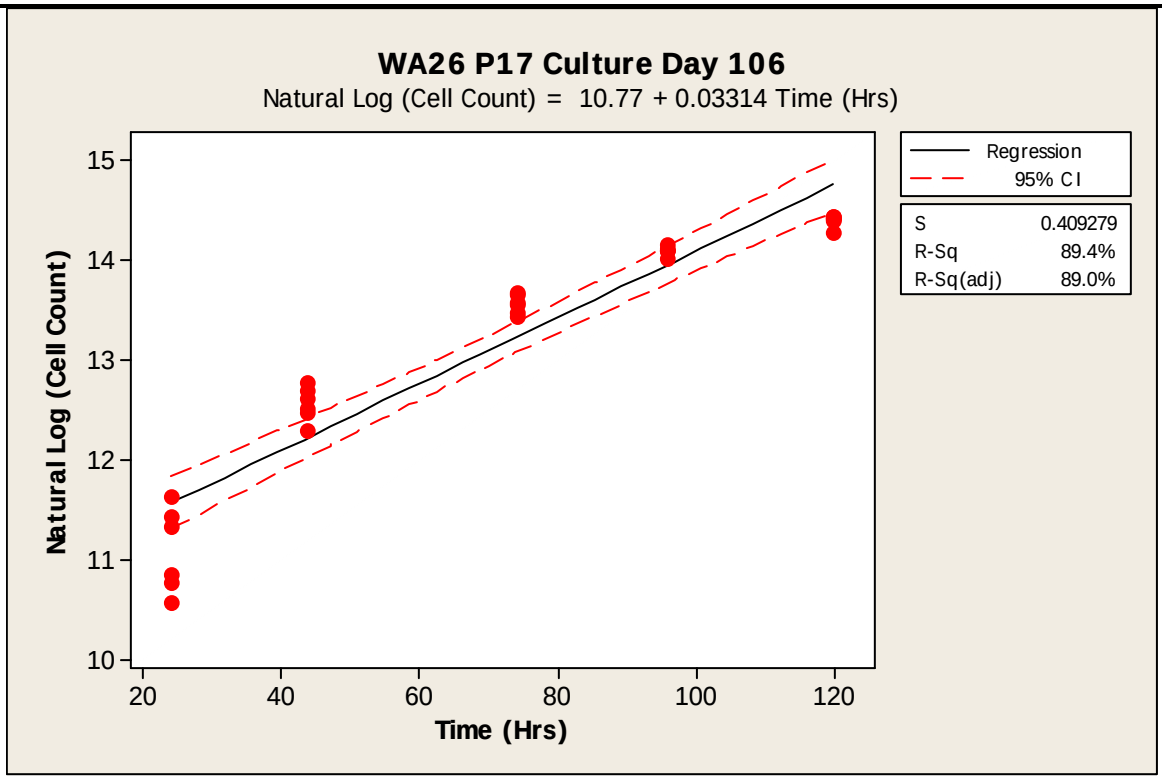
CPT CODE	Description/Molecular Testing	ABO/RH
83892	Enzymatic digestion	X2
83894	Separation by electrophoresis	x3
83898	Amplification each nucleic acid seq	x3
83912	Interpretation and report	X1

Characterization Report- Growth Characteristics

Sample ID	Cell Line	Cell lot #	Passage	Culture Day	Medium	Matrix	Passaging Additive
10449	WA26	N/A	17	106	E8 + PVA	rh-Vitronectin	Rho-kinase Inhibitor Y-27632

Documentation of Growth Assay Data	Notebook #	Page(s)	Date Initiated
	147	66-75	19APR12

Growth Assay Performed by	Report Prepared by	Date	QA Reviewed by	Date
WiCell Derivation Laboratory	LAN	14AUG12	JKT	15Aug12



Regression Analysis:
Natural Log (Cell Count) versus Time (Hrs)

The regression equation is Natural Log (Cell Count) = 10.8 + 0.0331 Time (Hrs)

Predictor	*Coef*	*SE Coef*	*T*	*P*
Constant	10.7714	0.1716	62.75	0.000
Time (Hrs)	0.033143	0.002160	15.35	0.000

S = 0.409279 **R-Sq** = 89.4% **R-Sq(adj)** = 89.0%

Analysis of Variance

Source	*DF*	*SS*	*MS*	*F*	*P*
Regression	1	39.452	39.452	235.52	0.000
Residual Error	28	4.690	0.168		
Total	29	44.143			

Unusual Observations

Obs	*Time (Hrs)*	*Natural Log (Cell Count)*	*Fit*	*SE Fit*	*Residual*	*St Resid*
1	24	10.5672	11.5668	0.1270	-0.9996	-2.57R
5	24	10.7769	11.5668	0.1270	-0.7899	-2.03R

**R denotes an observation with a large standardized residual*.*

Slope ± 95% C.I

0.0331 ± 0.0044

Apparent Doubling Time (hours) ± 95% C.I.

20.91 ± 2.05

Apparent Doubling Time (95% C.I.)

18.45 hours – 24.14 hours

WiCell Research Institute

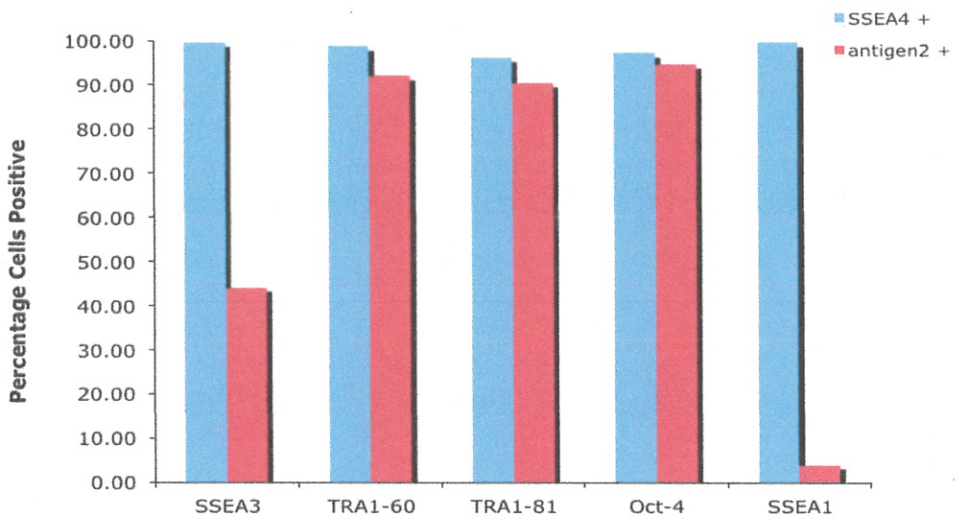
Procedure performed: **Cell line: WA26**
Passage 9
Sample ID: 10413

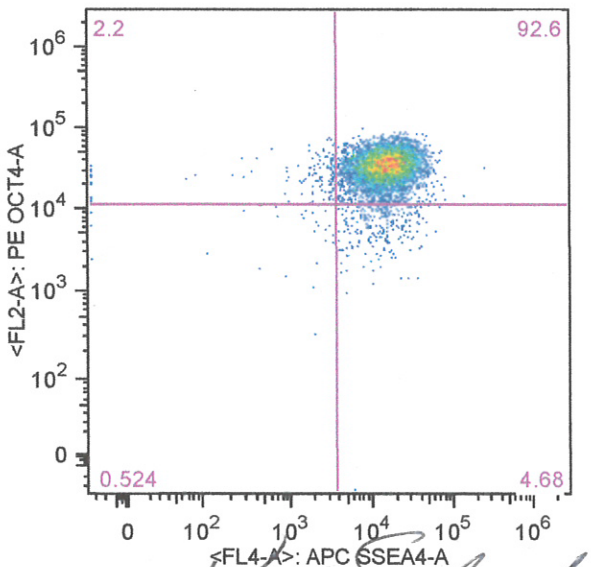
Date of: *(03/05/12)*
acquisition:
file creation:
file submission:

PERCENTS

antigen2:	SSEA4 - antigen2 +	SSEA4 + antigen2 +	SSEA4 + antigen2 -	SSEA4 - antigen2 -	ALL SSEA4 +	ALL antigen2 +
SSEA3	0.01	44.10	55.50	0.32	99.60	44.11
TRA1-60	1.05	91.00	7.69	0.23	98.69	92.05
TRA1-81	2.96	87.50	8.69	0.85	96.19	90.46
Oct-4	2.18	92.60	4.66	0.52	97.26	94.78
SSEA1	0.02	3.98	95.70	0.33	99.68	4.00

Percent analyzable events: 12.7
#wells submitted: 6
Total # cells analyzed: 2.26 X 10^6





prepared by [redacted]
10413 *(signature)*

Charles River Research Animal Diagnostic Services

[redacted]

Sponsor: WiCell Research Institute **Accession #: 2012-015912**

Diagnostic Summary Report

[redacted]

Received: 20 Mar 2012
Approved: 27 Mar 2012, 13:11

Bill Method: [redacted]
Test Specimen: Human

Sample Set	Service (# Tested)	Profile	Assay	Tested	+	+/-	?	PDG
#1	Infectious Disease PCR (3)	All Results Negative						

+ = Positive, +/- = Equivocal, ? = Indeterminate, PDG = Pending

Service Approvals

Service	Approved By*	Date
Infectious Disease PCR	[redacted]	27 Mar 2012, 13:11

To assure the SPF status of your research animal colonies, it is essential that you understand the sources, pathobiology, diagnosis and control of pathogens and other adventitious infectious agents that may cause research interference. We have summarized this important information in infectious agent **Technical Sheets**, which you can view by visiting http://www.criver.com/info/disease_sheets.

**This report has been electronically signed by laboratory personnel. The name of the individual who approved these results appears in the header of this service report. All services are performed in accordance with and subject to General Terms and Conditions of Sale found in the Charles River Laboratories-Research Models and Services catalogue and on the back of invoices.*

Charles River Research Animal Diagnostic Services
[redacted]

Sponsor: WiCell Research Institute **Accession #: 2012-015912**

Product: Not Indicated **Test Specimen:** Human **Received:** 20 Mar 2012

Molecular Diagnostics Infectious Disease PCR Results Report

Department Review: Approved by [redacted] 27 Mar 2012, 13:11*

Human Comprehensive Virus Panel

Sample #: / Code :	1 WA25-WB0132 10429	2 WA26-WB0131 10430	3 WA27-WB0130 10431
John Cunningham virus	-	-	-
BK virus	-	-	-
Herpesvirus type 6	-	-	-
Herpesvirus type 7	-	-	-
Herpesvirus type 8	-	-	-
Parvovirus B19	-	-	-
Epstein-Barr Virus	-	-	-
Hepatitis A virus	-	-	-
Hepatitis B virus	-	-	-
Hepatitis C virus	-	-	-
HPV-16	-	-	-
HPV-18	-	-	-
Human T-lymphotropic virus	-	-	-
Human cytomegalovirus	-	-	-
HIV-1	-	-	-
HIV-2	-	-	-
Adeno-associated virus	-	-	-
Human Foamy Virus	-	-	-
LCMV PCR	-	-	-
Hantavirus Hantaan PCR	-	-	-
Hantavirus Seoul PCR	-	-	-
Mycoplasma Genus PCR	-	-	-
DNA Spike	**PASS**	**PASS**	**PASS**
RNA Spike	**PASS**	**PASS**	**PASS**
NRC	**PASS**	**PASS**	**PASS**

Remarks: - = Negative; I = Inhibition, +/- = Equivocal; + = Positive.

Sample Suitability/Detection of PCR Inhibition:
Sample DNA or RNA is spiked with a low-copy number of a exogenous DNA or RNA template respectively. A spike template-specific PCR assay is used to test for the spike template for the purpose of determining the presence of PCR inhibitors. The RNA spike control is also used to evaluate the reverse-transcription of RNA. Amplification of spike template indicates that there is no detectable inhibition and the assay is valid.

NRC:
The nucleic acid recovery control (NRC) is used to evaluate the recovery of DNA/RNA from the nucleic acid isolation process. The test article is spiked with a low-copy number of DNA/RNA template prior to nucleic acid isolation. A template-specific PCR assay is used to detect the DNA/RNA spike.

**This report has been electronically signed by laboratory personnel. The name of the individual who approved these results appears in the header of this service report.*