Certificate of Analysis - Amended

Product Description	WA25	
Cell Line Provider	WiCell	
Parent Material	This material descended from derivation.	
Lot Number	WB0132	
Date Vialed	28-February-2012	
Passage Number	p7[1]	
Culture Platform	Feeder Independent	
	Medium: E8 plus PVA	Matrix: Recombinant Human Vitronectin

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	Pass[2]
Identity by STR	UW Molecular Diagnostics Laboratory	PowerPlex 16 HS System by Promega	Consistent with known profile	Pass
Sterility - Direct transfer method	Apptec	30744	Negative	Pass
Mycoplasma	Charles River	ID 91/0	Negative	Pass
Karyotype by G-banding	WiCell	SOP-CH-003	Normal karyotype	Pass

[1]These cells were cultured for 6 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. Footnote provided by TL on 17Sep12.

[2]Post-Thaw Viable Cell Recovery was obtained using Rho-Kinase Inhibitor (Y-27632) during thaw.

The following tests were performed on the cell line. The tests do not apply to any particular lot.
Please see the individual test reports for results of each test.

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	WiCell	SOP-CH-024
Comprehensive Human Virus Panel	Charles River	ID 91/0

Certificate of Analysis - Amended

Cells distributed by WiCell are intended for research purposes only and are not intended for use in humans.

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.

Amendment(s):

Reason for Amendment	Date
CoA updated to include copyright information.	See Signature
Amended STR test method and HLA test provider and test method.	05-October-2012
Original CoA.	16-August-2012

Date of Lot Release	Quality Assurance Approval
16-August-2012	1/3/2014 X AMC 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: 10501-STR Label on Tube: 10501-STR Sample Date: 05/11/12
Lab Received 05/11/12

Requestor: WiCell Research Institute

Test Date: 05/16/12 File Name: 120517 Report Date: 05/19/12

Sample Name: (label on tube) 10501-STR

Description: WI Cell Research Institute provided genomic DNA
252 ug/mL 260/280=1.94

Locus	Repeat #	STR Genotype
D16S539	5, 8-15	8,14
D7S820	6-14	10,11
D13S317	7-15	11,12
D5S818	7-15	11,12
CSF1PO	6-15	11,13
TPOX	6-13	8,9
Amelogenin	NA	X,X
TH01	5-11	6,6
vWA	11, 13-21	16,17

Comments: Based on the 10501-STR DNA submitted by WI Cell dated and received on 05/11/12, this sample (Label on Tube: 10501-STR) exactly matches the STR profile of the human stem cell line WA25 comprising 15 allelic polymorphisms across the 8 STR loci analyzed. No STR polymorphisms other than those corresponding to the human WA25 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 suggests that the 10501-STR DNA sample submitted corresponds to the WA25 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]

Molecular Diagnostics Laboratory

[redacted]

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

Test Facility:
[redacted]

WuXi AppTec

WiCell Research Institute
[redacted]

June 12, 2012
P.O. #: [redacted]

STERILITY TEST REPORT

Sample Information: Stem Cells

1: WA27-WB0130 10504
2: WA26-WB0131 10505
3: WA25-WB0132 10506
4: WA25-WB0127 10507
5: WA26-WB0128 10508
6: WA27-WB0138 10509
7: WA26-WB0152 10514
8: WA25-WB0151 10512
9: WA09-WB0143 10521
10: WA09-WB0139 10520
11: WA27-WB0150 10522
12: H9 hOct4-pGZ-WB0140 10518
13: MIRJT6i-mND1-4-WB0142.10519

Date Received: May 23, 2012
Date in Test: May 29, 2012
Date Completed: June 12, 2012

Test Information: Test Codes: 30744, 30744A
Immersion, USP / 21 CFR 610.12
Procedure #: BS210WCR.201

TEST PARAMETERS	PRODUCT	
Approximate Volume Tested	0.5 mL	0.5 mL
Number Tested	26	26
Type of Media	SCD	FTM
Media Volume	400 mL	400 mL
Incubation Period	14 Days	14 Days
Incubation Temperature	20 °C to 25 °C	30 °C to 35 °C
RESULTS	26 NEGATIVE	26 NEGATIVE

[redacted]
QA Reviewer **Date**

[redacted]
Technical Reviewer **Date**

Testing conducted in accordance with current Good Manufacturing Practices.

[redacted]

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.*

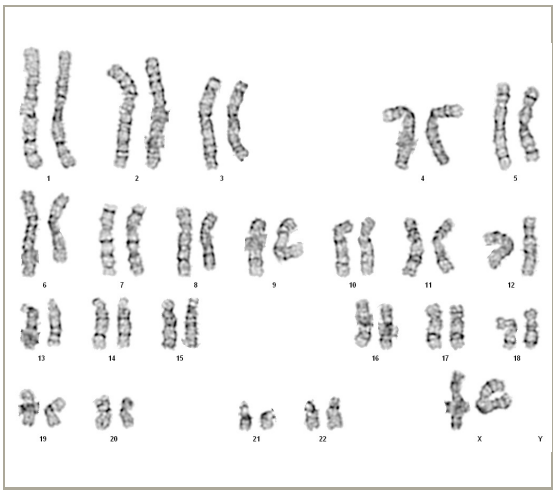
Chromosome Analysis Report: 008498

Report Date: July 06, 2012

Cell Line: WA25-WB0132 10545
Passage #: 7
Date of Sample: 6/25/2012
Date Completed: 7/6/2012

Cell Line Gender: Female
Reason for Testing: Testing directly out of thaw
Investigator: [redacted] WiCell Derivation

Specimen: hESC on rh Vitronectin
Results: 46,XX



Cell: S01-21
Slide: 3(10)KARYOTYPE
Slide Type: Karyotyping

# of Cells Counted: 20
# of Cells Karyotyped: 4
# of Cells Analyzed: 7
Band Level: 400-500

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

Completed by [redacted] **MS, CG(ASCP), on 7/6/2012**
Reviewed and interpreted by [redacted]**, PhD, FACMG, on 7/6/2012**

A signed copy of this report is available upon request.

Date:_____ **Sent To:**_____
Sent By:_____ **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".

This assay was conducted solely for listed investigator/institution. The results may not be relied upon by any other party without the prior written consent of the Director of the WiCell Cytogenetics Laboratory. The results of this assay are for research use only. If the results of this assay are to be used for any other purpose, contact the Director of the WiCell Cytogenetics Laboratory.

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**

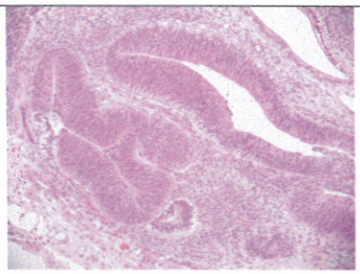
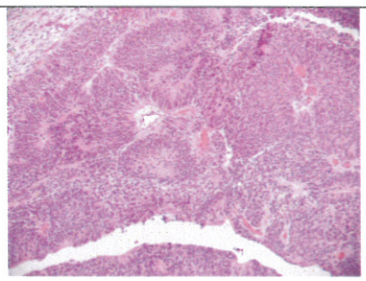
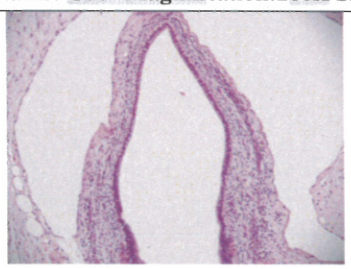
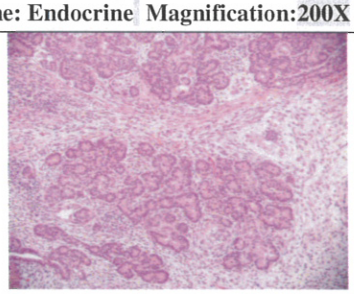
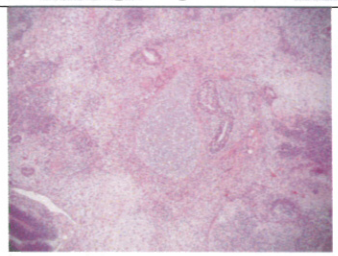
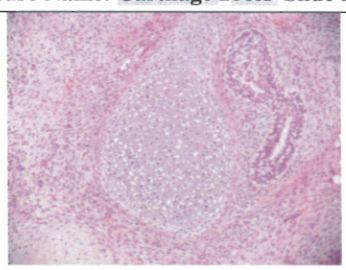
Remarks: - = Negative; I = Inhibition, +/- = Equivocal; + = Positive.

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.*

Cell Line: WA25 **Cell Lot Number: NA** **Sample Number: 10404-A,B,C**

ECTODERM	
Structure Name: Neural tubules Magnification:200X Slide ID: A	**Structure Name: Brain-like tissue Magnification: 200X Slide ID: B**
	
ENDODERM	
Structure Name: Gut Magnification:200X Slide ID: C	**Structure Name: Endocrine Magnification:200X Slide ID: A**
	
MESODERM	
Structure Name: Cartilage Magnification:100X Slide ID: B	**Structure Name: Cartilage 200X Slide ID: B**
	

Comments: Structures identified include Ectoderm (2), Mesoderm (1) 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] 03JUL12

① SOP ID SOP-CH-214. Error. 03JUL12 JCT

UW Health

University of Wisconsin
Hospital and Clinics

Name: WICELL, 10404-HLA
MRN: OS000181
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, 10404-HLA			03:01	07:02:01G	07:02:01G	09:01						03/12/12
OS000181 / WICELL	Patient		11:01	51:07:01	14:02	11:01						03/02/12

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, 10404-HLA		03:01							
OS000181 / WICELL	SEQ	11:01							
03/02/2012	03/20/2012								
		HLA Allele database: IMGT 3.7.0 2012-01-12							
			07:02:01G						
	SEQ		51:07						
03/02/2012	03/20/2012								
		The reported allele group B*07:02:01G includes the following alleles, which share identical sequences in the antigen recognition site of exons 2 and 3: B*07:02 B*07:61 HLA Allele database: IMGT 3.7.0 2012-01-12							
				07:02:01G					
	SEQ			14:02					
03/02/2012	03/20/2012								
)		HLA Allele database: IMGT 3.7.0 2012-01-12 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 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:C*07:37,14:06; C*07:51,14:13; C*07:172,14:18.							
					09:01				
	SEQ				11:01				
03/02/2012	03/20/2012								
		HLA Allele database: IMGT 3.7.0 2012-01-12 Cannot rule out the rare allele DRB1*11:100, first identified in October 2010 The reported allele group DRB1*11:01:01G includes the following alleles, which share identical sequences in the antigen recognition site of exon 2 DRB1*11:01 DRB1*11:97							

Comments

UW Health

University of Wisconsin
Hospital and Clinics

Name:	WICELL, 10404-HLA	Hospital:	
MRN:	OS000181	Physician:	,
DOB:		Category:	
HLA#:	WICELL		

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]

03/25/2012 12:08
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
[redacted]

March 20, 2012

WiCell Research Institute
[redacted]

SAMPLE: DNA WA25 #10404 (MA#166-12)

Date Received: 03/08/12
Sample Date: 03/02/12

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 presence of a nt261 deleted G, characteristic of O^1 alleles, and an A background allele. *RH: RHD* exons 4 and 7 are present. Negative for the inactivating *RHD* pseudogene. *RH*Ee* and *RH*Cc*

	Genotype	Predicted Phenotype
WA25 #10404:	*ABO*AO^1; RH*D, RH*Cc, RH*Ee*	**Group A; RhD**+, C+E+c+e+

[redacted]
Manager, Genomics

[redacted]
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.

NewYork BloodCenter

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

Sample: MA166-12; WA25 #10404

Test: ABO and RH - GF

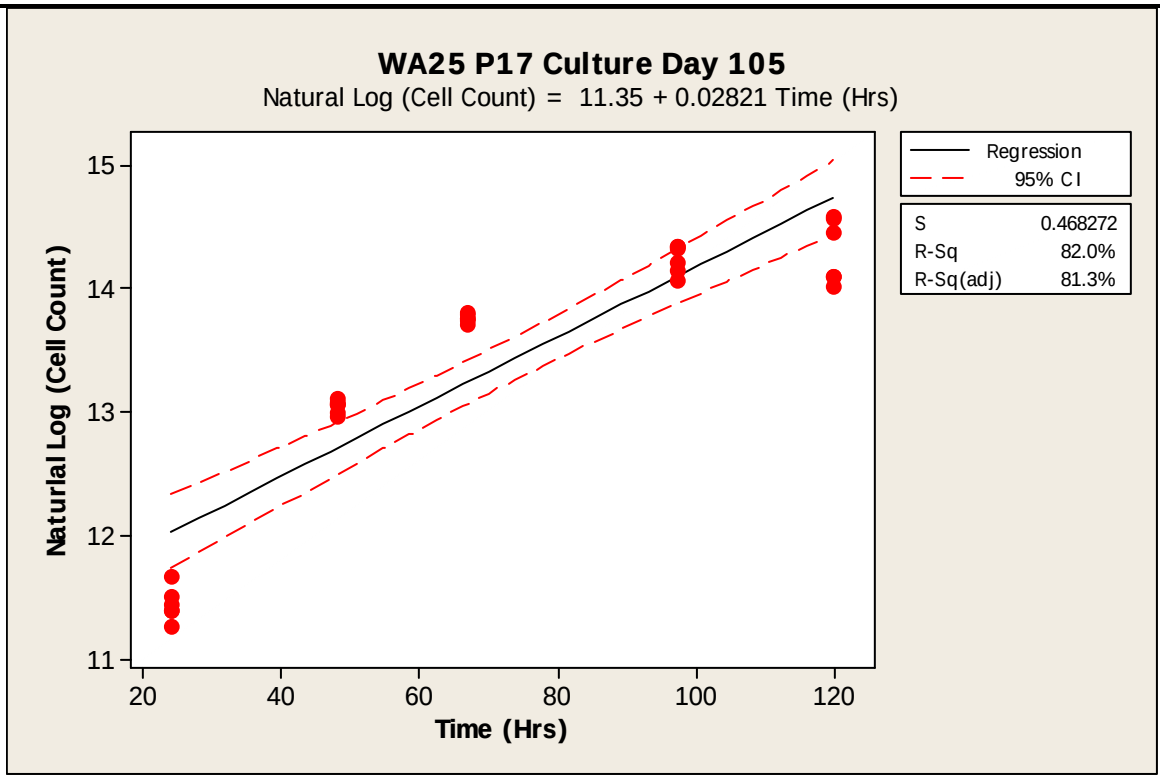
CPT CODE	Description/Molecular Testing	ABO/RH
83892	Enzymatic digestion	X2
83894	Separation by electrophoresis	x3
83898	Amplification each nucleic acid seq	x3
83912	Interpretation and report	X1

Characterization Report- Growth Characteristics

Sample ID	Cell Line	Cell lot #	Passage	Culture Day	Medium	Matrix	Passaging Additive
10448	WA25	N/A	17	105	E8 + PVA	rh-Vitronectin	Rho-kinase Inhibitor Y-27632

Documentation of Growth Curve Data	Notebook #	Page(s)	Date Growth Curve Initiated
	149	58-64	18APR12

Growth Curved performed by	Report Prepared by	Date	QA Reviewed by	Date
Derivation Laboratory	LAN	14AUG12	JKT	15Aug12



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

The regression equation is Natural Log (Cell Count) = 11.4 + 0.0282 Time (Hrs)

Predictor	*Coef*	*SE Coef*	*T*	*P*
Constant	11.3513	0.1976	57.45	0.000
Time (Hrs)	0.028206	0.002500	11.28	0.000

S = 0.468272 **R-Sq** = 82.0% **R-Sq(adj)** = 81.3%

Analysis of Variance

Source	*DF*	*SS*	*MS*	*F*	*P*
Regression	1	27.906	27.906	127.26	0.000
Residual Error	28	6.140	0.219		
Total	29	34.046			

Slope ± 95% C.I

0.0282 ± 0.0051

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

24.57 ± 2.05

Apparent Doubling Time (95% C.I.)

20.80 hours – 30.03 hours

WiCell Research Institute

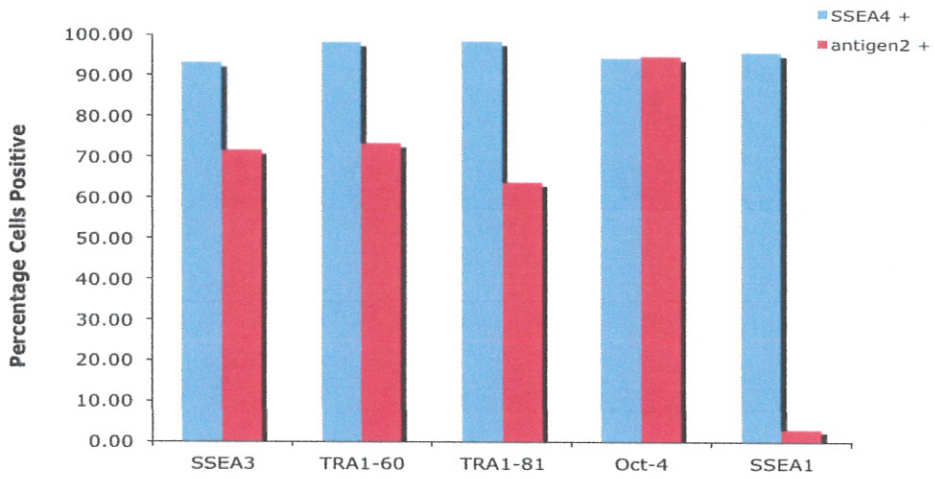
Procedure performed: **Cell line: WA25**
Passage 8
Sample ID: 10412

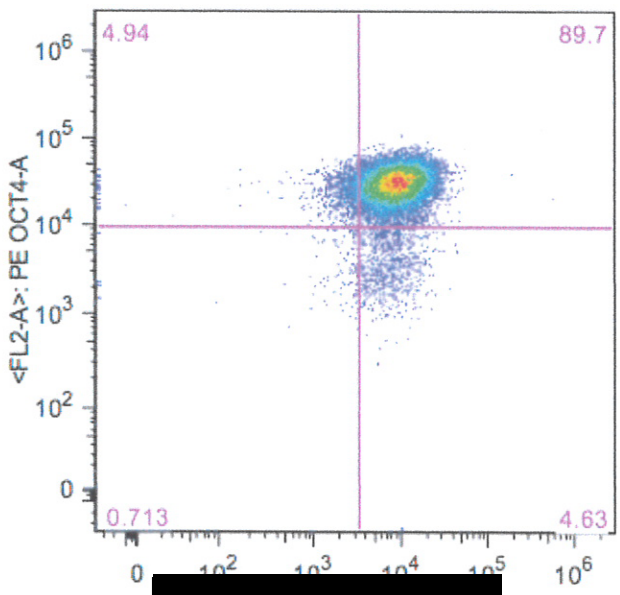
Date of: *(03/06/12)*
acquisition:
file creation:
file submission:

PERCENTS

antigen2:	SSEA4 - antigen2 +	SSEA4 + antigen2 +	SSEA4 + antigen2 -	SSEA4 - antigen2 -	ALL SSEA4 +	ALL antigen2 +
SSEA3	0.88	70.70	22.30	6.08	93.00	71.58
TRA1-60	1.55	71.80	26.30	0.31	98.10	73.35
TRA1-81	1.25	62.50	35.80	0.45	98.30	63.75
Oct-4	4.94	89.70	4.63	0.71	94.33	94.64
SSEA1	0.19	2.93	92.80	4.05	95.73	3.12

Percent analyzable events: 27
#wells submitted: 6
Total # cells analyzed: 12.8 X 10^6





prepared by [redacted]
10412 *(signature)*