

## University of Pittsburgh Cell Culture and Cytogenetics Facility

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--For Research Purposes Only--

Lab Number:	CCSG1550	Date of Submitted: Date of Report:	12/21/16 1/10/17
Specimen:	One DNA sample		eimin Gao, M.D., Ph.D.
Indication:	STR Profiling		ale Lewis, B.S., CG(ASCP) <sup>CM</sup>

Results and Interpretation: This DNA specimen was studied using the Promega GenePrint 10 Amplification Kit.

	GAO
Amelogenin	X,Y
CSFIPO	10,12
D13S317	11,11
D16S539	11,12
D21S11	29,29
D5S818	11,11
D7S820	8,11
TH01	8,9.3
TPOX	8,11
V WA	14,14
EV	1.0

Online verification is available using the DSMZ Online STR Analysis site

(http://www.dsmz.de/services/services-human-and-animal-cell-lines/online-str-analysis.html). The EV, the identity relationship between two cell lines or a cell line with a database entry (A and B) is calculated as the (Number of coincident peaks of STR profiles between A and B) x 2 / (Total number of peaks of STR profiles in A and B). EV values greater than 0.9 indicate that the two cell lines are derived from the same origin (Sugimoto et al. (2013) Cancer Lett 331, 115-121).

Sample "Gao" matches the expected database profile for A549 with an evaluation value (EV) of 1.0 (36/36). This confirms the identity of this cell line.

The following acknowledgement should be included when publishing these findings: These genetic studies were carried out in the University of Pittsburgh Cell Culture and Cytogenetics Facility.

Susanne M. Gollin, Ph.D., FFACMG Laboratory Director Dale W. Lewis, B.S., CG(ASCP)<sup>CM</sup> Senior Technologist



## University of Pittsburgh Cell Culture and Cytogenetics Facility

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Lab Number:	CCSG1594	Date of Submitte Date of Report:	d: 5/19/17 5/24/17
Specimen:	Two DNA samples	Submitted by:	Weimin Gao, Ph.D.
Indication:	STR Profiling	Technologist:	Dale Lewis, B.S., CG(ASCP) <sup>CM</sup>

Results and Interpretation: This DNA specimen was studied using the Promega GenePrint 10 Amplification Kit.

	Sample 1	Sample 2
Amelogenin	X,X	X,X
CSFIPO	11,11	12,12
D13S317	11,11	9,10,14
D16S539	11,12	9,12
D21S11	30,30	28,28
D5S818	11,11	11,12
D7S820	8,9	8,8
TH01	9.3,9.3	7,7
TPOX	11,11	8,11
V WA	18,18	18,18
% Match	100% with NCI-H1650	92.31% with NCI-H197

Online verification is available using the STR Analysis site (CLIMA 2.1: the Cell Line Integrated Molecular Authentication Database 2.1 Version 2.1.201505), which includes cell lines from PNAS, ATCC, JCRB, ICLC1, ICLC2, COG, and DSMZ. Percent matches of 90% or greater indicate that the two cell lines are derived from the same origin. (Romano P et al., Cell Line Data Base: structure and recent improvements towards molecular authentication of human cell lines. Nucl Acids Res 2009; 37(Database issue):D925-D932. DOI: doi:10.1093/nar/gkn730 PMID: 18927105S.)

"Sample 1" contains 100% of the expected profile alleles in the database profile for cell line NCI-H1650. This confirms the identity of this cell line.

"Sample 2" contains 92.31% of the expected profile alleles in the database profile for cell line NCI-H1975. Allele D13S317 had a noisy fragment size analysis that likely accounts for the discrepancy. The 92.31% match confirms the identity of this cell line.

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