Cell Line GENETICS
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CLG Microarray Test Results

Cell Line ID: ND29369 p2 **Lab #:** CLG-22692 **Date received:** 2/18/16

Date Reported: 3/11/16 **Contact Person:** Gabriela Novak **PI:** Steven Finkbeiner

Institute: Gladstone **Test Code:** aCGH 110 **Email:** gabriela.novak@gladstone.ucsf.edu **PO #:** NA

Mailing Address: 1650 Owens Street, San Francisco, CA 94138

Sample Type: Human Fibroblast Culture **dsDNA Concentration:** 121.6 ng/µl **Total dsDNA:** 2.7 ug

Sex: Female **260/280 (1.7-1.9):** 1.8 **260/230 (≥1.90):** 1.9 **Array Type:** Agilent 180K Standard aCGH+SNP

Array ID Number: 252983032920_1_1 **Reference DNA:** Agilent Euro Female

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Quality Control

A sufficient amount of high quality genomic DNA, as determined by UV spec. (NanoVue), fluorometer (Qubit) and Agarose Gel analysis, was extracted from cell line ND29369 p2 and passed our internal quality standards for aCGH labeling.

aCGH Probes (PASS/FAIL): Pass
SNP Probes (PASS/FAIL): Pass

Experimental Deviations**:** None

Results:

Clonal Fraction: 100%

See attached sheets for Tabular and Graphical presentation of microarray results.

Variants are considered provisional until confirmed by another technique. For further confirmation of a particular variant, CLG recommends using Karyotyping (variants >5Mb), FISH (variants>200Kb).

Amp/Deletion Table									
Chr	Amp/Del	Start(bp)	Stop(bp)	Size(kb)	Chr Band	# Probes	Log2 Ratio	Genes[α]	Overlap Normal CNVs?[β]
1	DEL	149,041,013	149,232,481	191	q21.2	7	-0.55798		Yes
4	AMP	45,882	68,211	22	p16.3	7	0.642602	ZNF595, ZNF718	Yes
15	AMP	24,587,026	24,777,982	191	q11.2	8	0.78897		Yes

Total Amp/Del: 3

LOH Intervals Table							
Chr	Start(bp)	Stop(bp)	Size(kb)	Chr Band	# Probes	LOH Score	Genes[α]
13	105,388,837	108,010,176	2,621	q33.2 - q33.3	84	11.01117	DAOA, EFNB2, LOC728192, ARGLU1, FAM155A
18	65,138,642	68,441,027	3,302	q22.1 - q22.2	78	6.758874	DSEL, CD226, LOC643542, TMX3, CCDC102B, DOK6, RTTN, SOCS6

Total LOH Intervals: 2

[α] Genes amplified or deleted are cross referenced against the Online Mendelian Inheritance in Man® (OMIM®) database. Genes well documented with disorders and morbidity are Orange. Genes with some association with disease are Teal. Genes in Black have no known association with disease.

[β] Amplifications and deletions are cross referenced against the Database of Genomic Variants (DGV), which contains genomic variations observed in healthy individuals.

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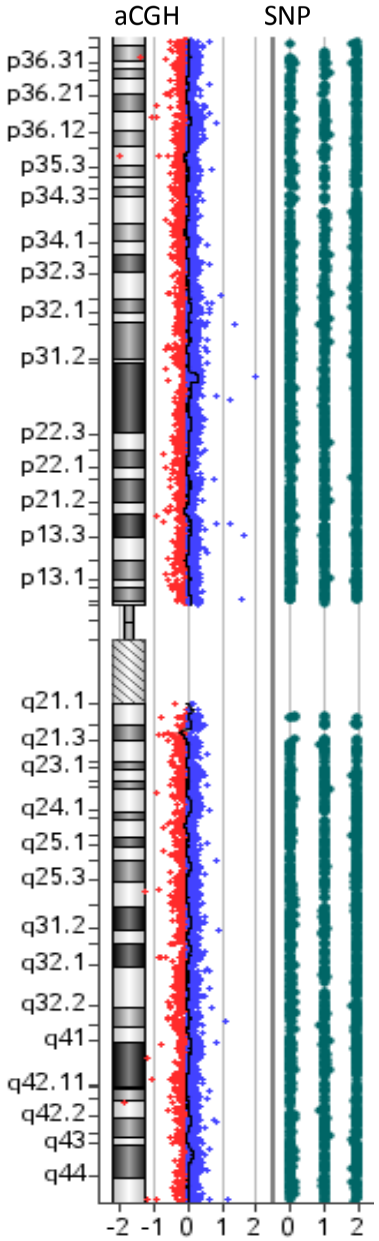
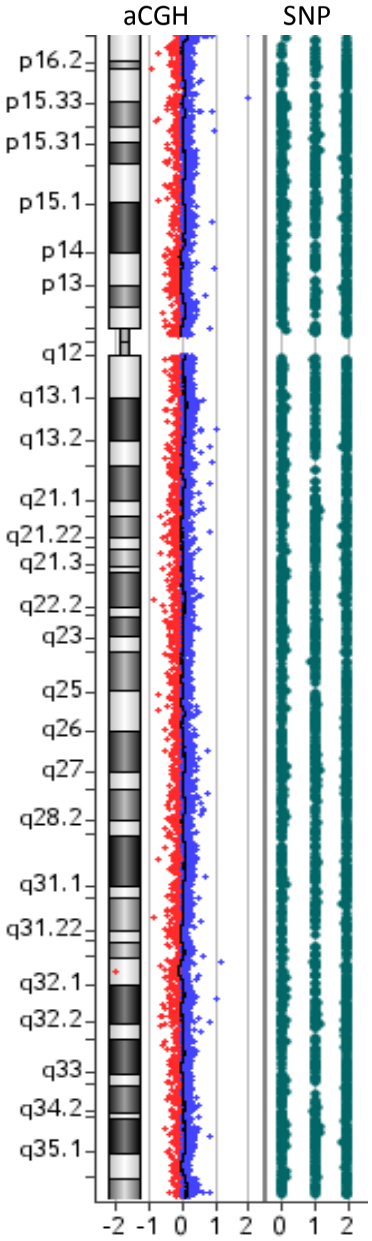
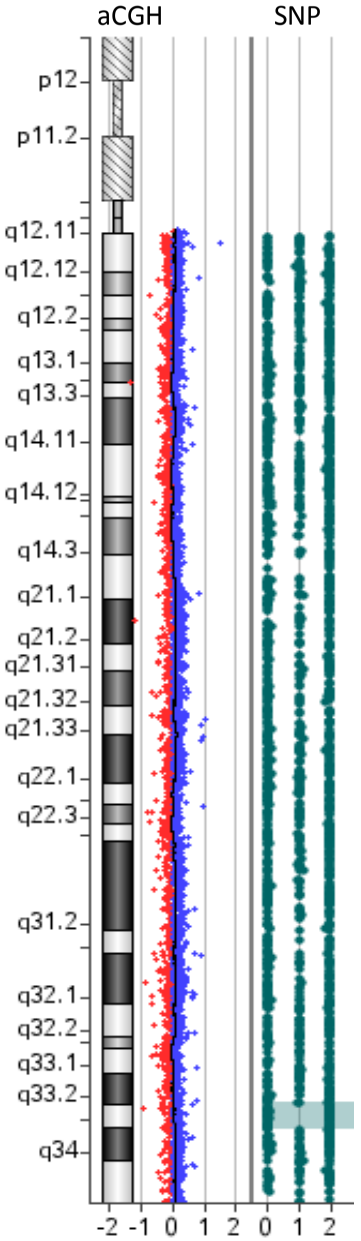
Chromosome 1



Chromosome 4



Chromosome 13



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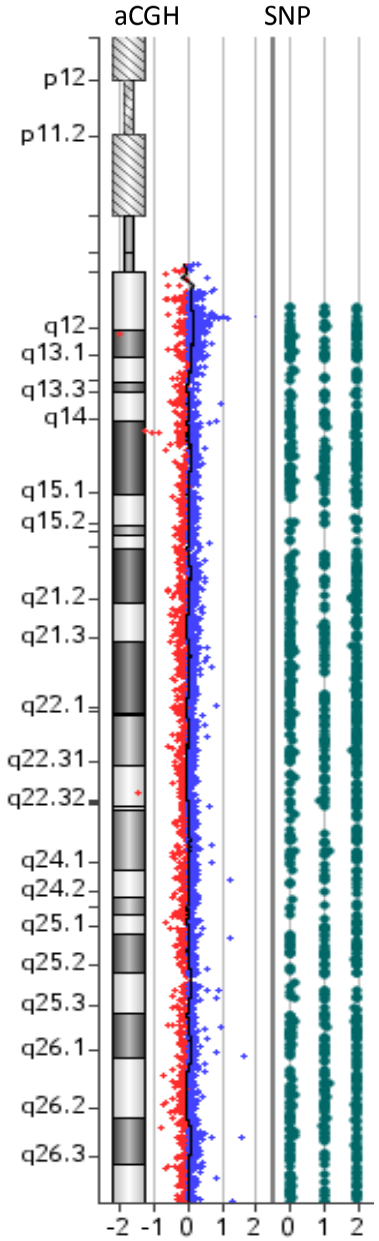
Chromosome 15



Chromosome 18