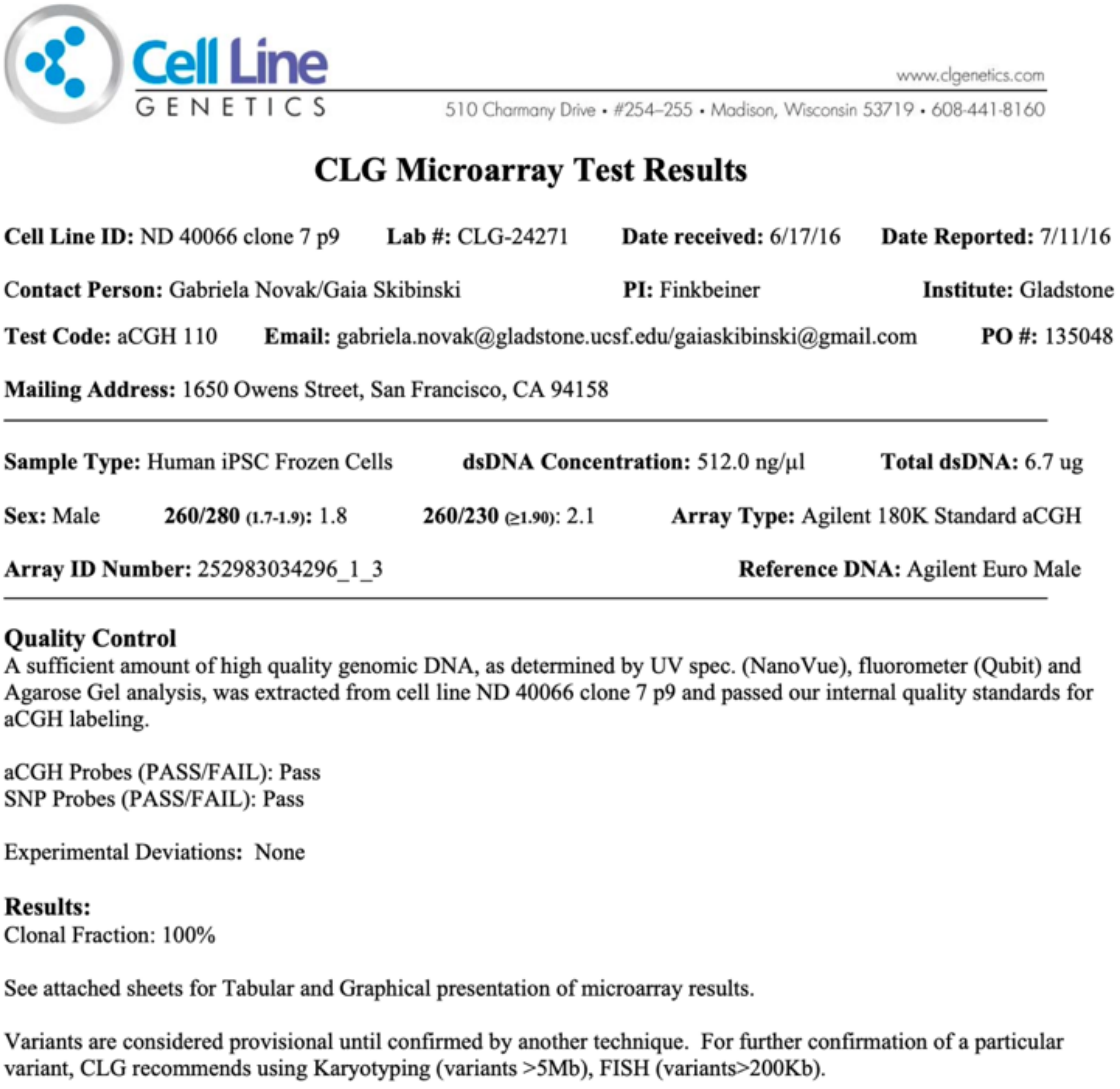
ND40066 – iPSC clone 7 – passage 9



Cell Line GENETICS
www.clgenetics.com
510 Charmany Drive • #254–255 • Madison, Wisconsin 53719 • 608-441-8160

CLG Microarray Test Results

Cell Line ID: ND 40066 clone 7 p9 **Lab #:** CLG-24271 **Date received:** 6/17/16 **Date Reported:** 7/11/16

Contact Person: Gabriela Novak/Gaia Skibinski **PI:** Finkbeiner **Institute:** Gladstone

Test Code: aCGH 110 **Email:** gabriela.novak@gladstone.ucsf.edu/gaiaskibinski@gmail.com **PO #:** 135048

Mailing Address: 1650 Owens Street, San Francisco, CA 94158

Sample Type: Human iPSC Frozen Cells **dsDNA Concentration:** 512.0 ng/µl **Total dsDNA:** 6.7 ug

Sex: Male **260/280** (1.7-1.9)**:** 1.8 **260/230** (≥1.90)**:** 2.1 **Array Type:** Agilent 180K Standard aCGH

Array ID Number: 252983034296_1_3 **Reference DNA:** Agilent Euro Male

---

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 ND 40066 clone 7 p9 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]
3	**AMP**	146,880,285	147,362,016	482	q24	74	0.286863	ZIC4, ZIC1, LOC440982	No
3	**AMP**	187,569,045	188,225,340	656	q27.3 - q28	25	0.605745	LPP-AS2, LPP, FLJ42393	No
4	**AMP**	61,647,885	63,157,938	1,510	q13.1	46	0.262564	MIR548AG1, ADGRL3, ADGRL3-AS1	No
7	**AMP**	100,980,697	101,126,393	146	q22.1	6	0.603858	COL26A1	Yes
7	**DEL**	110,564,801	110,708,070	143	q31.1	6	-0.87997	IMMP2L	Yes
7	**AMP**	121,256,234	122,628,757	1,373	q31.32	142	0.290292	PTPRZ1, AASS, FEZF1, FEZF1-AS1, CADPS2, RNF133, RNF148	No
9	**DEL**	43,590,480	43,841,603	251	p12 - p11.2	6	-0.71159	FAM74A7, SPATA31A6, CNTNAP3B, CNTNAP3P2	Yes
11	**AMP**	91,344,721	92,652,140	1,307	q14.3	43	0.266315	FAT3, LOC105369431	No
13	**AMP**	93,882,966	93,968,369	85	q31.3	12	0.82095	GPC6	Yes
14	**AMP**	19,794,577	20,421,677	627	q11.2	11	0.472473	LINC01296, DUXAP10, BMS1P22, BMS1P18, BMS1P17, POTEM, LOC100508046, OR11H2, OR4Q3, OR4M1, OR4N2, OR4K2, OR4K5, OR4K1	Yes
16	**AMP**	34,482,042	34,743,643	262	p11.2 - p11.1	11	0.395944	LINC01566, FRG2DP, TP53TG3HP	Yes
22	**AMP**	25,672,585	25,903,543	231	q11.23 - q12.1	9	0.516547	IGLL3P, LRP5L, CRYBB2P1, MIR6817	Yes

Total Amp/Del: 12

LOH Intervals Table

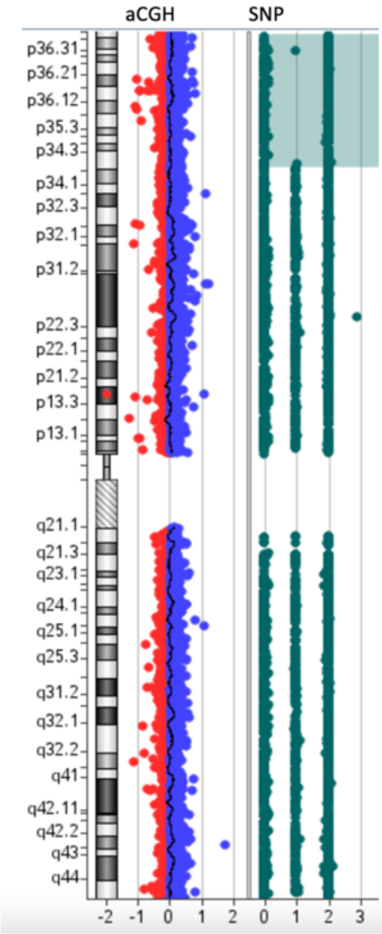
Chr	Start(bp)	Stop(bp)	Size(kb)	Chr Band	# Probes	LOH Score	Genes[α]
1	1,089,699	39,243,405	38,154	p36.33 - p34.3	395	39.25073	Too Numerous to List
6	1,696,841	18,775,310	17,078	p25.3 - p22.3	381	27.55516	Too Numerous to List
7	79,723,943	89,361,740	9,638	q21.11 - q21.13	187	14.84336	GNAI1, GNAT3, CD36, SEMA3C, HGF, PCLO, SEMA3E, SEMA3A, SEMA3D, GRM3, KIAA1324L, DMTF1, TP53TG1, CROT, ABCB4, ABCB1, SLC25A40, ADAM22, SRI, STEAP4, LOC101927269, LOC100128317, CACNA2D1,LOC101927356, LOC101927378, LINC00972, TMEM243, RUNDC3B, DBF4, LOC102723885, ZNF804B, C7orf62
16	55,121,927	84,673,276	29,551	q12.2 - q24.1	567	52.74851	Too Numerous to List
18	62,974,135	65,905,964	2,932	q22.1	74	6.889795	CDH7, CDH19, MIR5011, DSEL, LOC643542
20	39,476,952	42,671,183	3,194	q12 - q13.12	60	6.507752	TOP1, PLCG1, ZHX3, LPIN3, CHD6, PTPRT, SRSF6, L3MBTL1, SGK2, MYBL2, TOX2, LOC100128988, PLCG1-AS1, MIR6871, EMILIN3, LOC101927159, IFT52, GTSF1L, LOC105372626
22	44,261,581	48,849,346	4,588	q13.31 - q13.32	76	8.243154	To Numerous to List

Total LOH Intervals: 7

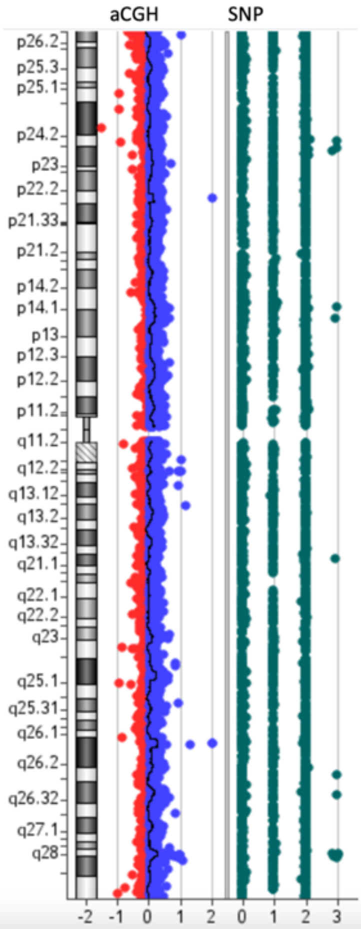
[α] Genes amplified or deleted are cross referenced against the Online Mendelian Inheritance in Man® (OMIM®) database. Genes well documented with disorders and morbidity are Orange. Genes with some association with disease are Teal. Genes in Black have no known association with disease.

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

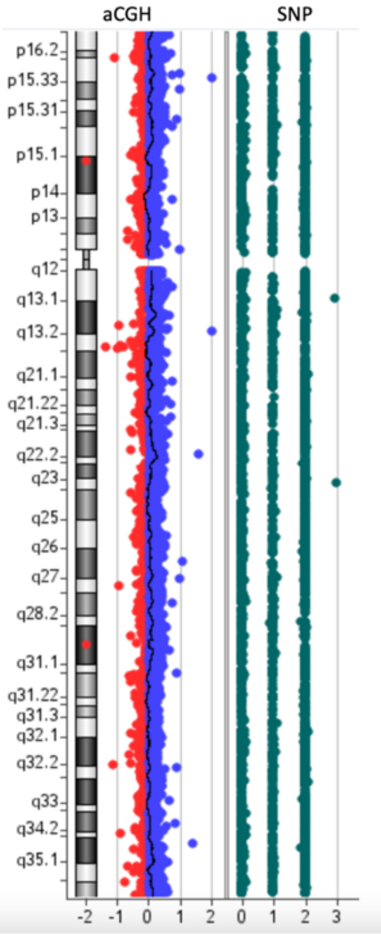
Chromosome 1



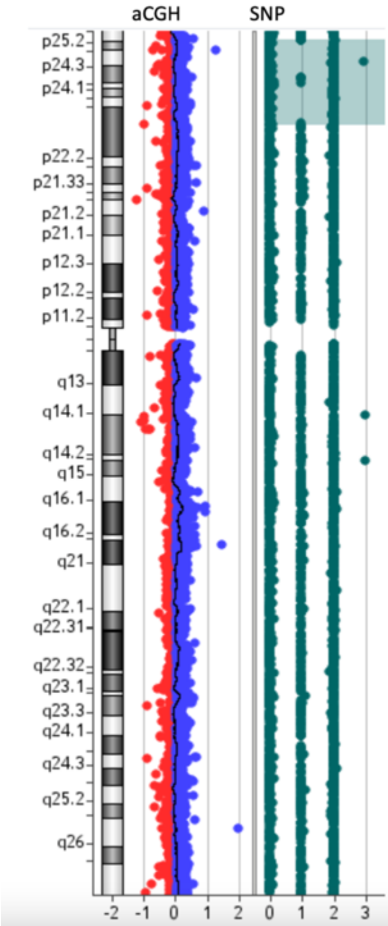
Chromosome 3



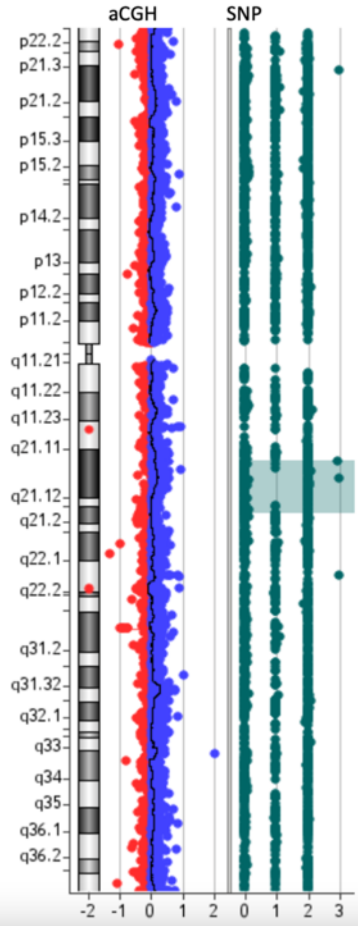
Chromosome 4



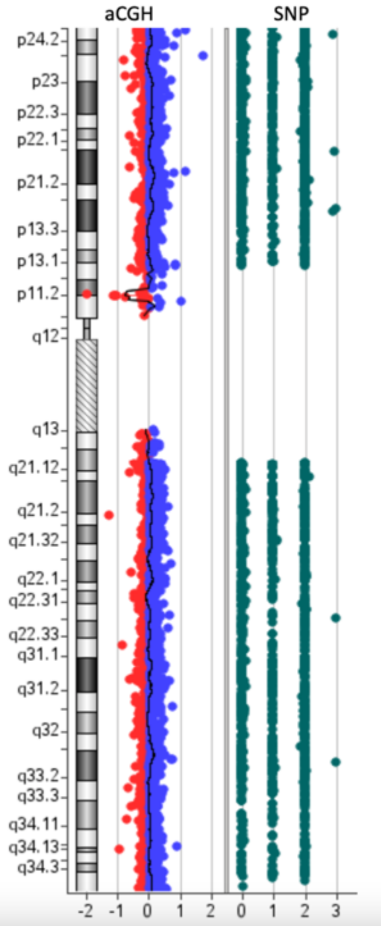
Chromosome 6

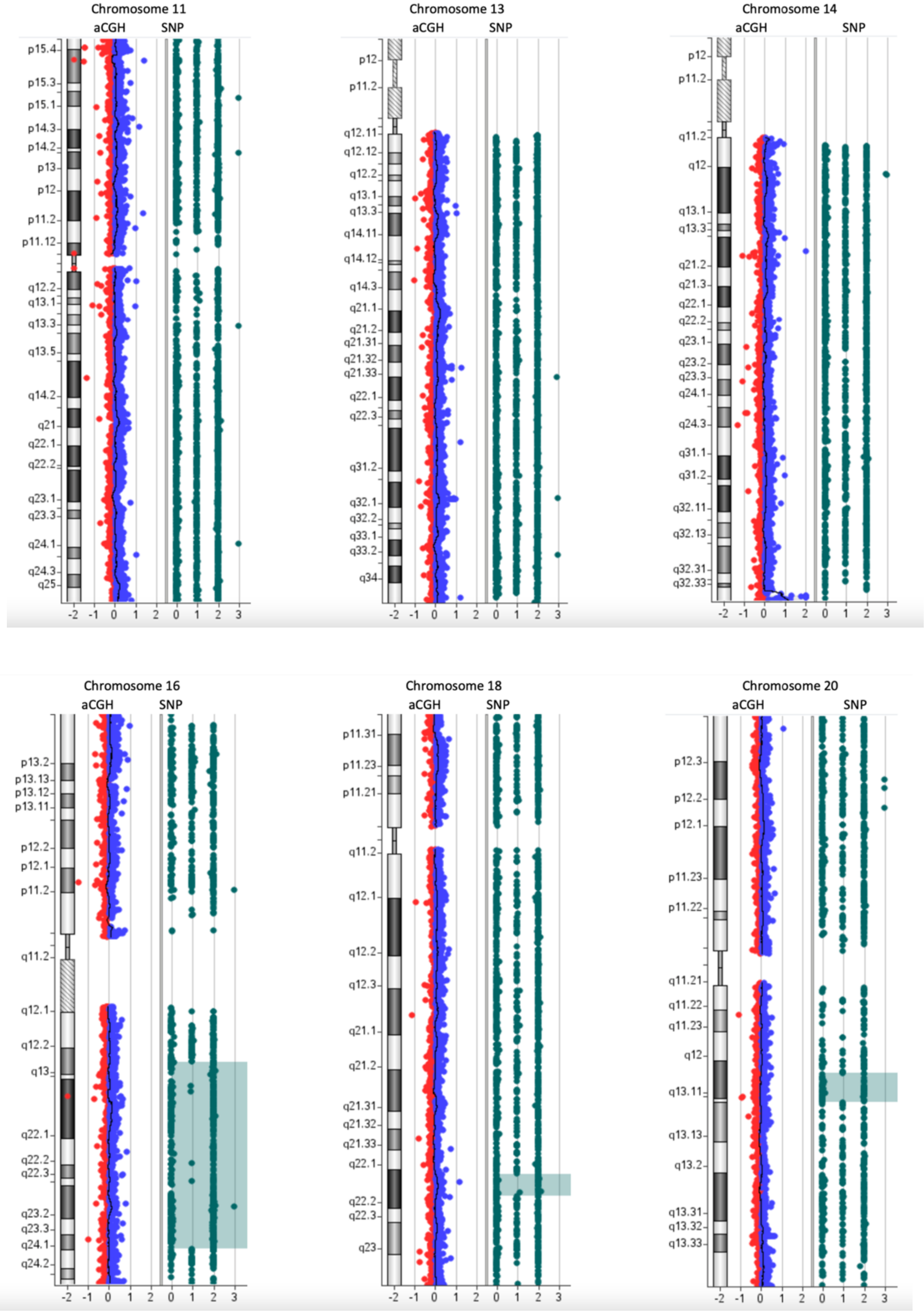


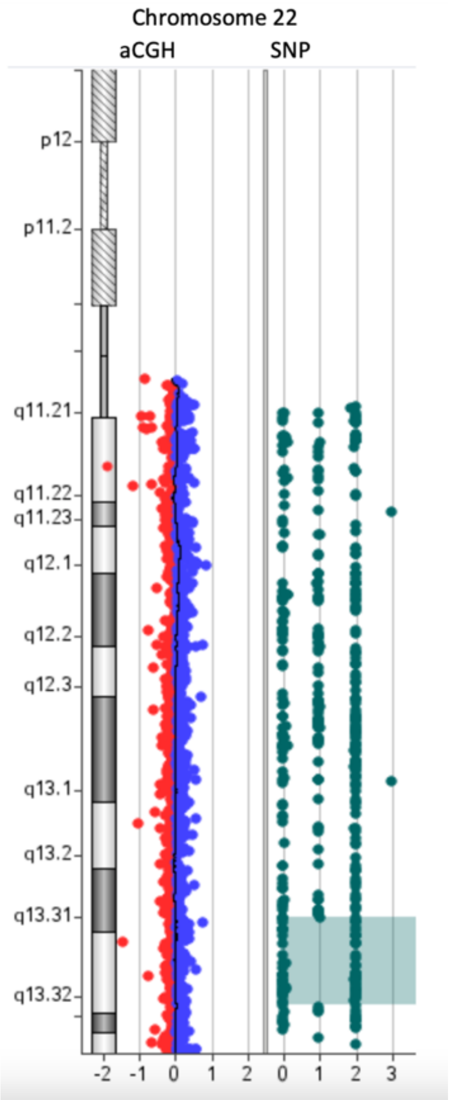
Chromosome 7



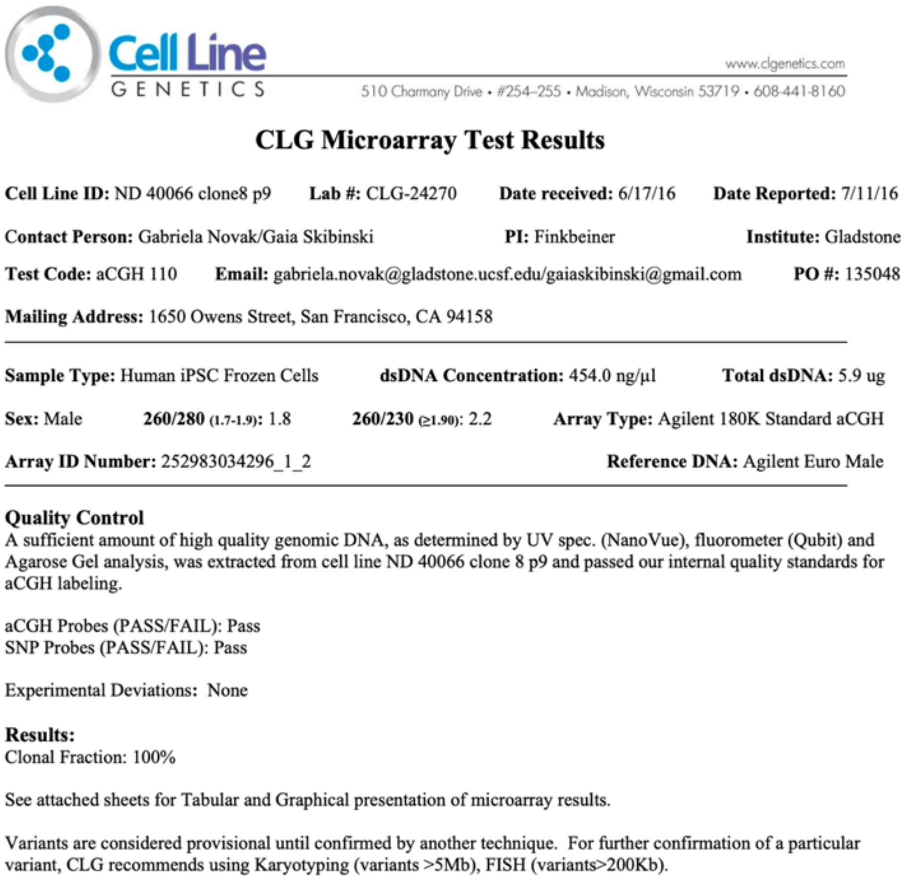
Chromosome 9




Chromosome 11
aCGH
SNP
p15.4
p15.3
p15.1
p14.3
p14.2
p13
p12
p11.2
p11.12
q12.2
q13.1
q13.3
q13.5
q14.2
q21
q22.1
q22.2
q23.1
q23.3
q24.1
q24.3
q25
-2 -1 0 1 2 0 1 2 3
Chromosome 13
aCGH
SNP
p12
p11.2
q12.11
q12.12
q12.2
q13.1
q13.3
q14.11
q14.12
q14.3
q21.1
q21.2
q21.31
q21.32
q21.33
q22.1
q22.3
q31.2
q32.1
q32.2
q33.1
q33.2
q34
-2 -1 0 1 2 0 1 2 3
Chromosome 14
aCGH
SNP
p12
p11.2
q11.2
q12
q13.1
q13.3
q21.2
q21.3
q22.1
q22.2
q23.1
q23.2
q23.3
q24.1
q24.3
q31.1
q31.2
q32.11
q32.13
q32.31
q32.33
-2 -1 0 1 2 0 1 2 3
Chromosome 16
aCGH
SNP
p13.2
p13.13
p13.12
p13.11
p12.2
p12.1
p11.2
q11.2
q12.1
q12.2
q13
q22.1
q22.2
q22.3
q23.2
q23.3
q24.1
q24.2
-2 -1 0 1 2 0 1 2 3
Chromosome 18
aCGH
SNP
p11.31
p11.23
p11.21
q11.2
q12.1
q12.2
q12.3
q21.1
q21.2
q21.31
q21.32
q21.33
q22.1
q22.2
q22.3
q23
-2 -1 0 1 2 0 1 2 3
Chromosome 20
aCGH
SNP
p12.3
p12.2
p12.1
p11.23
p11.22
q11.21
q11.22
q11.23
q12
q13.11
q13.13
q13.2
q13.31
q13.32
q13.33
-2 -1 0 1 2 0 1 2 3


Chromosome 22
aCGH
SNP
p12
p11.2
q11.21
q11.22
q11.23
q12.1
q12.2
q12.3
q13.1
q13.2
q13.31
q13.32
-2
-1
0
1
2
0
1
2
3

ND40066 – iPSC clone 8 – passage 9



Cell Line GENETICS

www.clgenetics.com
510 Charmany Drive • #254–255 • Madison, Wisconsin 53719 • 608-441-8160

CLG Microarray Test Results

Cell Line ID: ND 40066 clone8 p9 **Lab #:** CLG-24270 **Date received:** 6/17/16 **Date Reported:** 7/11/16

Contact Person: Gabriela Novak/Gaia Skibinski **PI:** Finkbeiner **Institute:** Gladstone

Test Code: aCGH 110 **Email:** gabriela.novak@gladstone.ucsf.edu/gaiaskibinski@gmail.com **PO #:** 135048

Mailing Address: 1650 Owens Street, San Francisco, CA 94158

Sample Type: Human iPSC Frozen Cells **dsDNA Concentration:** 454.0 ng/µl **Total dsDNA:** 5.9 ug

Sex: Male **260/280** (1.7-1.9)**:** 1.8 **260/230** (≥1.90)**:** 2.2 **Array Type:** Agilent 180K Standard aCGH

Array ID Number: 252983034296_1_2 **Reference DNA:** Agilent Euro Male

---

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 ND 40066 clone 8 p9 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$^{\alpha}$	Overlap Normal CNVs?$^{\beta}$
2	AMP	188,058,313	189,724,370	1,666	q32.1 - q32.2	50	0.292488	CALCRL, TFPI, LINC01090, GULP1, MIR561, DIRC1	No
3	AMP	146,708,800	147,362,016	653	q24	81	0.299431	ZIC4, ZIC1, LOC440982	No
4	AMP	61,619,455	63,761,135	2,142	q13.1	66	0.255822	MIR548AG1, ADGRL3, ADGRL3-AS1	No
4	AMP	92,202,997	94,796,142	2,593	q22.1 - q22.2	87	0.293805	CCSER1, LOC101929194, GRID2, ATOH1	No
5	AMP	146,716,607	147,447,900	731	q32	44	0.313221	STK32A, DPYSL3, JAKMIP2-AS1, JAKMIP2, SPINK1, SCGB3A2, C5orf46, SPINK5	No
7	AMP	100,980,697	101,126,393	146	q22.1	6	0.609012	COL26A1	Yes
7	DEL	110,564,801	110,708,070	143	q31.1	6	-0.9213	IMMP2L	Yes
7	AMP	121,256,234	122,628,757	1,373	q31.32	142	0.328262	PTPRZ1, AASS, FEZF1, FEZF1-AS1, CADPS2, RNF133, RNF148	No
9	DEL	43,590,480	43,841,603	251	p12 - p11.2	6	-0.74614	FAM74A7, SPATA31A6, CNTNAP3B, CNTNAP3P2	Yes
11	AMP	91,344,721	92,716,856	1,372	q14.3	45	0.302978	FAT3, LOC105369431, MTNR1B	No
12	DEL	92,022,671	93,355,847	1,333	q21.33 - q22	44	-0.25259	LINC01619, BTG1, LOC101928617, CLLU1OS, CLLU1, C12orf74, PLEKHG7, EEA1	No
14	AMP	20,203,610	20,421,677	218	q11.2	8	0.511181	OR4Q3, OR4M1, OR4N2, OR4K2, OR4K5, OR4K1	Yes
16	AMP	34,452,586	34,743,643	291	p11.2 - p11.1	12	0.371214	LINC01566, FRG2DP, TP53TG3HP	Yes
22	AMP	25,672,585	25,903,543	231	q11.23 - q12.1	9	0.568746	IGLL3P, LRP5L, CRYBB2P1, MIR6817	Yes
X	AMP	112,594,478	115,303,379	2,709	q23	100	0.280264	XACT, HTR2C, MIR448, IL13RA2, LUZP4, PLS3, AGTR2, LOC101928437, SNORA35, MIR764, MIR1912, MIR1264, MIR1298, MIR1911, LRCH2, RBMXL3, PLS3-AS1, DANT2	No

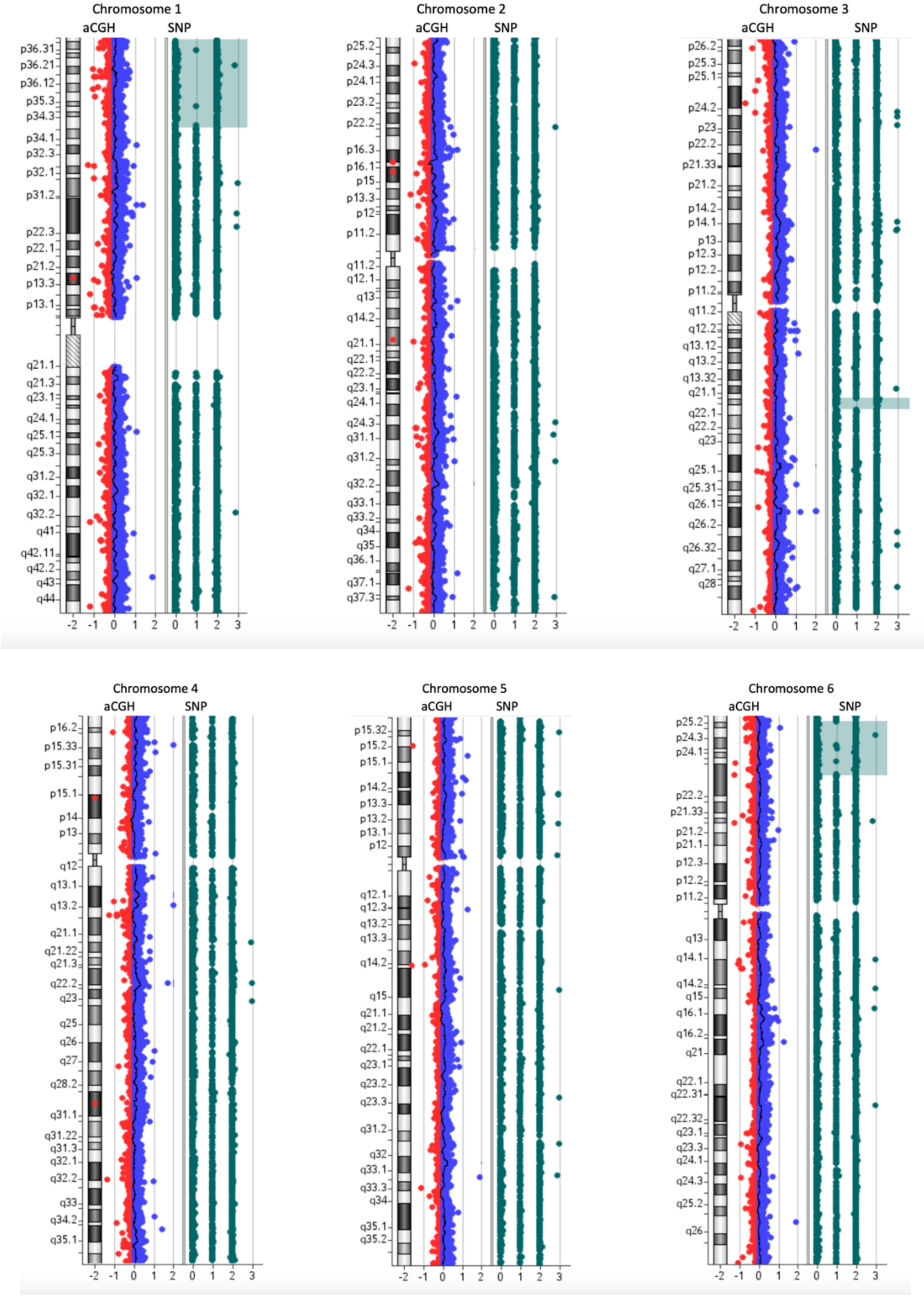
LOH Intervals Table

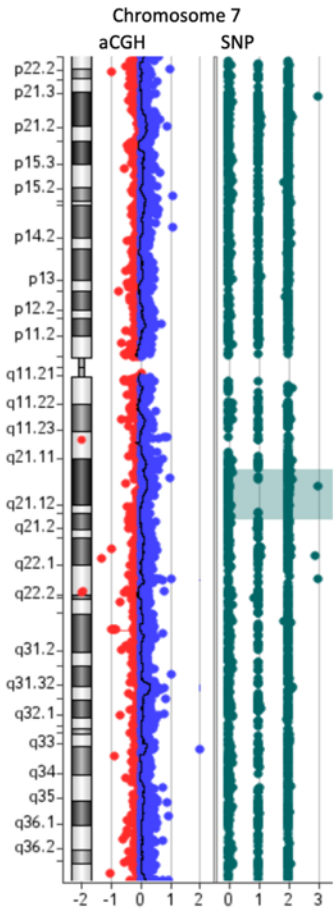
Chr	Start(bp)	Stop(bp)	Size(kb)	Chr Band	# Probes	LOH Score	Genes[α]
1	1,089,699	39,243,405	38,154	p36.33 - p34.3	402	36.74485	Too Numerous to List
3	123,562,478	127,688,648	4,126	q21.1 - q21.3	54	6.073903	Too Numerous to List
6	1,696,841	18,775,310	17,078	p25.3 - p22.3	385	28.04076	Too Numerous to List
7	79,723,943	89,361,740	9,638	q21.11 - q21.13	189	15.34061	GNAI1, GNAT3, CD36, SEMA3C, HGF, PCLO, SEMA3E, SEMA3A, SEMA3D, GRM3, KIAA1324L, DMTF1, TP53TG1, CROT, ABCB4, ABCB1, SLC25A40, ADAM22, SRI, STEAP4, LOC101927269, LOC100128317, CACNA2D1,LOC101927356, LOC101927378, LINC00972, TMEM243, RUNDC3B, DBF4, LOC102723885, ZNF804B, C7orf62
16	55,121,927	84,673,276	29,551	q12.2 - q24.1	575	55.62815	Too Numerous to List
18	62,974,135	65,905,964	2,932	q22.1	77	6.992831	CDH7, CDH19, DSEL, MIR5011, LOC643542
20	39,476,952	42,671,183	3,194	q12 - q13.12	62	6.616215	TOP1, PLCG1, ZHX3, LPIN3, CHD6, PTPRT, SRSF6, L3MBTL1, SGK2, MYBL2, TOX2, LOC100128988, PLCG1-AS1, MIR6871, EMILIN3, LOC101927159, IFT52, GTSF1L, LOC105372626
22	44,261,581	48,849,346	4,588	q13.31 - q13.32	76	6.992831	Too Numerous to List

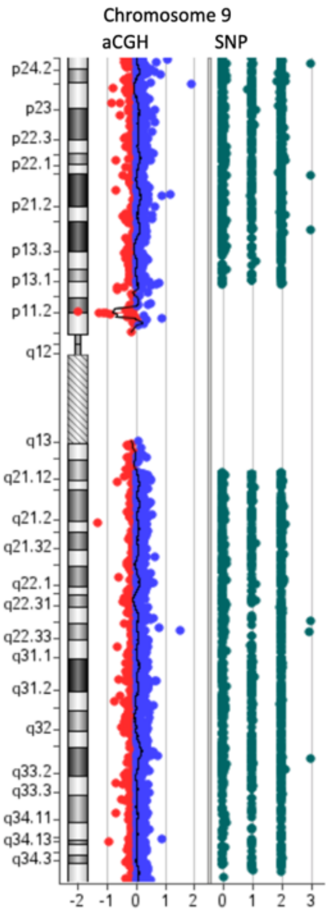
Total LOH Intervals: 8

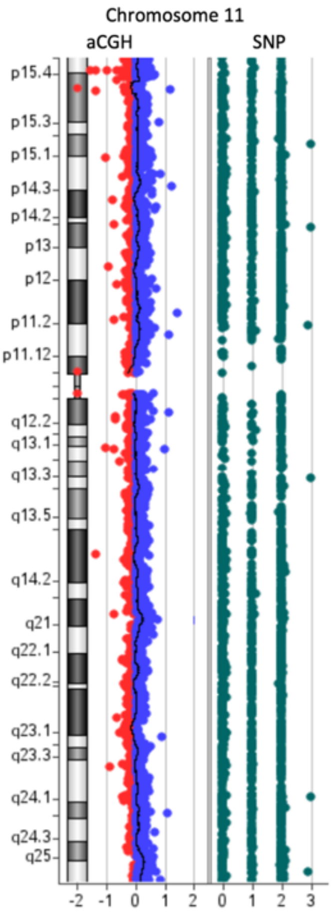
[α] Genes amplified or deleted are cross referenced against the Online Mendelian Inheritance in Man® (OMIM®) database. Genes well documented with disorders and morbidity are Orange. Genes with some association with disease are Teal. Genes in Black have no known association with disease.

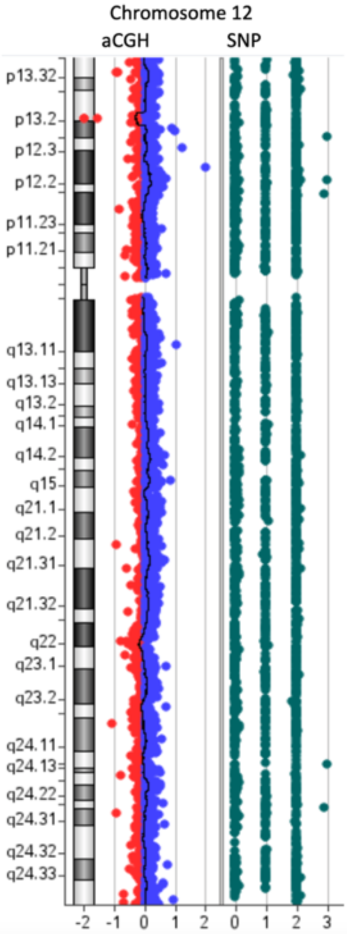
[β] Amplifications and deletions are cross referenced against the Database of Genomic Variants (DGV), which contains genomic variations observed in healthy individuals.

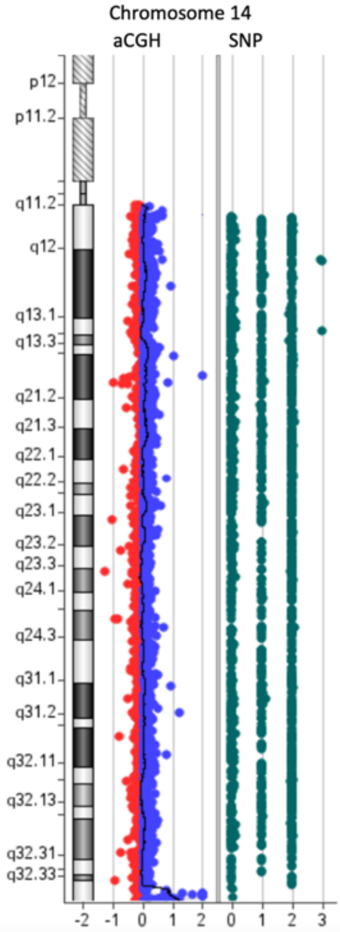

Chromosome 1
aCGH
SNP
p36.31
p36.21
p36.12
p35.3
p34.3
p34.1
p32.3
p32.1
p31.2
p22.3
p22.1
p21.2
p13.3
p13.1
q21.1
q21.3
q23.1
q24.1
q25.1
q25.3
q31.2
q32.1
q32.2
q41
q42.11
q42.2
q43
q44
-2 -1 0 1 2 0 1 2 3
Chromosome 2
aCGH
SNP
p25.2
p24.3
p24.1
p23.2
p22.2
p16.3
p16.1
p15
p13.3
p12
p11.2
q11.2
q12.1
q13
q14.2
q21.1
q22.1
q22.2
q23.1
q24.1
q24.3
q31.1
q31.2
q32.2
q33.1
q33.2
q34
q35
q36.1
q37.1
q37.3
-2 -1 0 1 2 0 1 2 3
Chromosome 3
aCGH
SNP
p26.2
p25.3
p25.1
p24.2
p23
p22.2
p21.33
p21.2
p14.2
p14.1
p13
p12.3
p12.2
p11.2
q11.2
q12.2
q13.12
q13.2
q13.32
q21.1
q22.1
q22.2
q23
q25.1
q25.31
q26.1
q26.2
q26.32
q27.1
q28
-2 -1 0 1 2 0 1 2 3
Chromosome 4
aCGH
SNP
p16.2
p15.33
p15.31
p15.1
p14
p13
q12
q13.1
q13.2
q21.1
q21.22
q21.3
q22.2
q23
q25
q26
q27
q28.2
q31.1
q31.22
q31.3
q32.1
q32.2
q33
q34.2
q35.1
-2 -1 0 1 2 0 1 2 3
Chromosome 5
aCGH
SNP
p15.32
p15.2
p15.1
p14.2
p13.3
p13.2
p13.1
p12
q12.1
q12.3
q13.2
q13.3
q14.2
q15
q21.1
q21.2
q22.1
q23.1
q23.2
q23.3
q31.2
q32
q33.1
q33.3
q34
q35.1
q35.2
-2 -1 0 1 2 0 1 2 3
Chromosome 6
aCGH
SNP
p25.2
p24.3
p24.1
p22.2
p21.33
p21.2
p21.1
p12.3
p12.2
p11.2
q13
q14.1
q14.2
q15
q16.1
q16.2
q21
q22.1
q22.31
q22.32
q23.1
q23.3
q24.1
q24.3
q25.2
q26
-2 -1 0 1 2 0 1 2 3

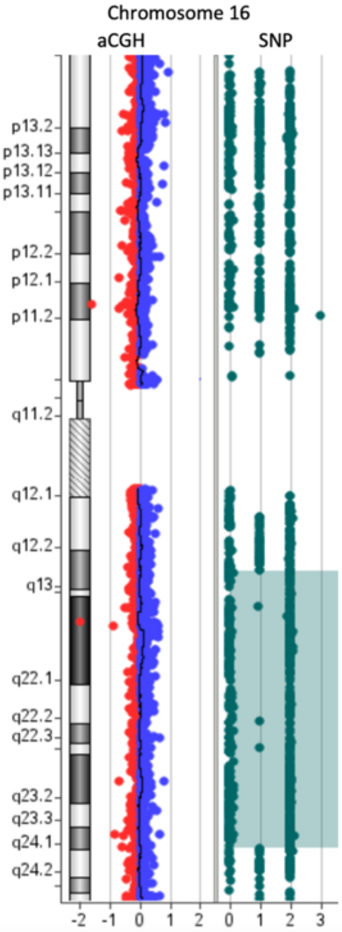

Chromosome 7
aCGH
SNP
p22.2
p21.3
p21.2
p15.3
p15.2
p14.2
p13
p12.2
p11.2
q11.21
q11.22
q11.23
q21.11
q21.12
q21.2
q22.1
q22.2
q31.2
q31.32
q32.1
q33
q34
q35
q36.1
q36.2
-2
-1
0
1
2
0
1
2
3


Chromosome 9
aCGH
SNP
p24.2
p23
p22.3
p22.1
p21.2
p13.3
p13.1
p11.2
q12
q13
q21.12
q21.2
q21.32
q22.1
q22.31
q22.33
q31.1
q31.2
q32
q33.2
q33.3
q34.11
q34.13
q34.3
-2
-1
0
1
2
0
1
2
3

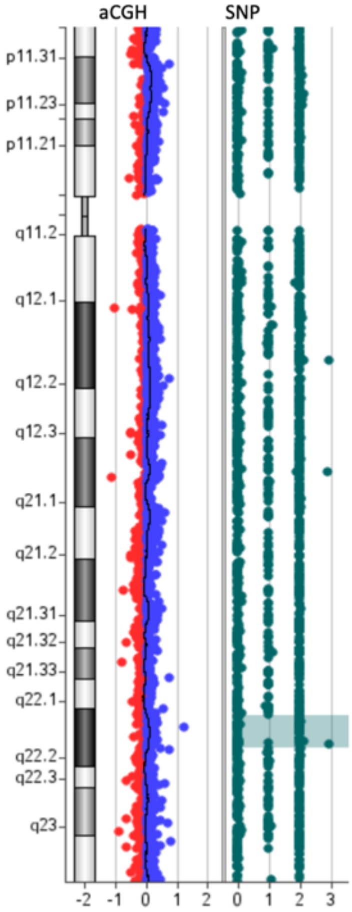

Chromosome 11
aCGH
SNP
p15.4
p15.3
p15.1
p14.3
p14.2
p13
p12
p11.2
p11.12
q12.2
q13.1
q13.3
q13.5
q14.2
q21
q22.1
q22.2
q23.1
q23.3
q24.1
q24.3
q25
-2
-1
0
1
2
0
1
2
3


Chromosome 12
aCGH
SNP
p13.32
p13.2
p12.3
p12.2
p11.23
p11.21
q13.11
q13.13
q13.2
q14.1
q14.2
q15
q21.1
q21.2
q21.31
q21.32
q22
q23.1
q23.2
q24.11
q24.13
q24.22
q24.31
q24.32
q24.33
-2
-1
0
1
2
0
1
2
3

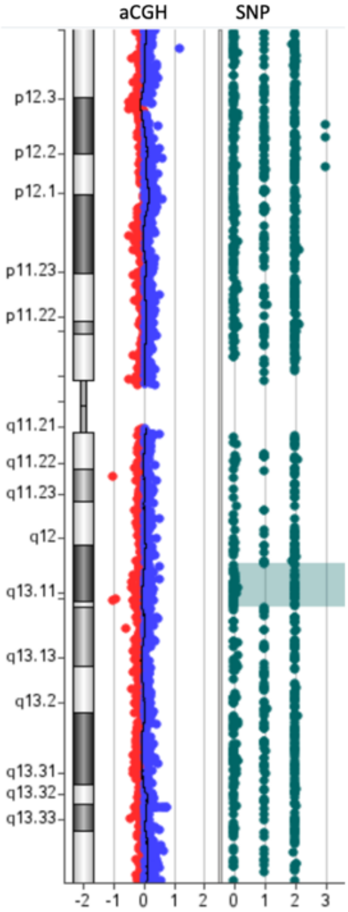

Chromosome 14
aCGH
SNP
p12
p11.2
q11.2
q12
q13.1
q13.3
q21.2
q21.3
q22.1
q22.2
q23.1
q23.2
q23.3
q24.1
q24.3
q31.1
q31.2
q32.11
q32.13
q32.31
q32.33
-2
-1
0
1
2
0
1
2
3


Chromosome 16
aCGH
SNP
p13.2
p13.13
p13.12
p13.11
p12.2
p12.1
p11.2
q11.2
q12.1
q12.2
q13
q22.1
q22.2
q22.3
q23.2
q23.3
q24.1
q24.2
-2
-1
0
1
2
0
1
2
3

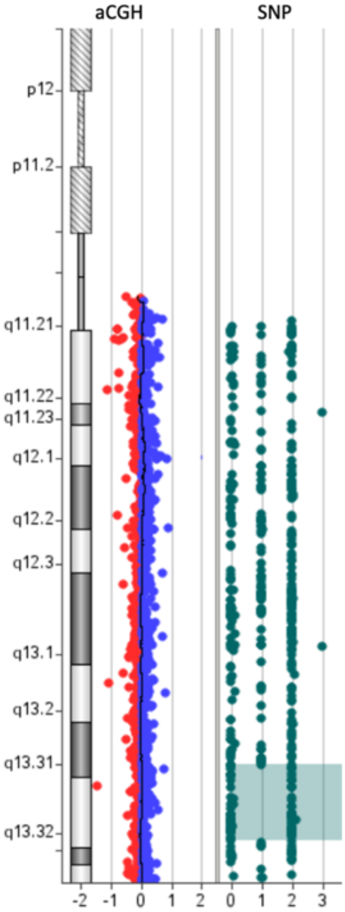
Chromosome 18



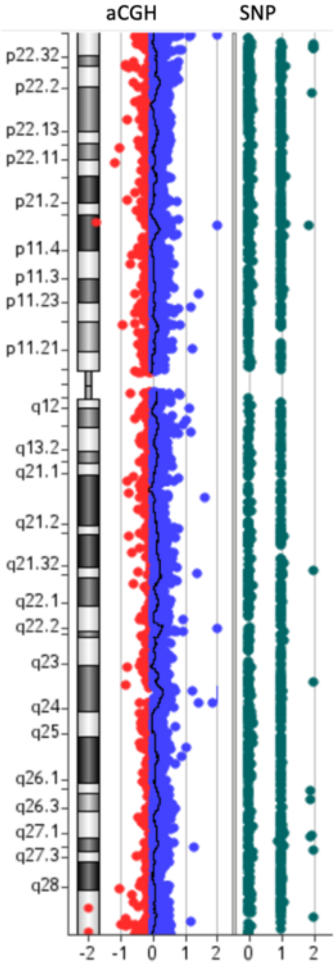
Chromosome 20



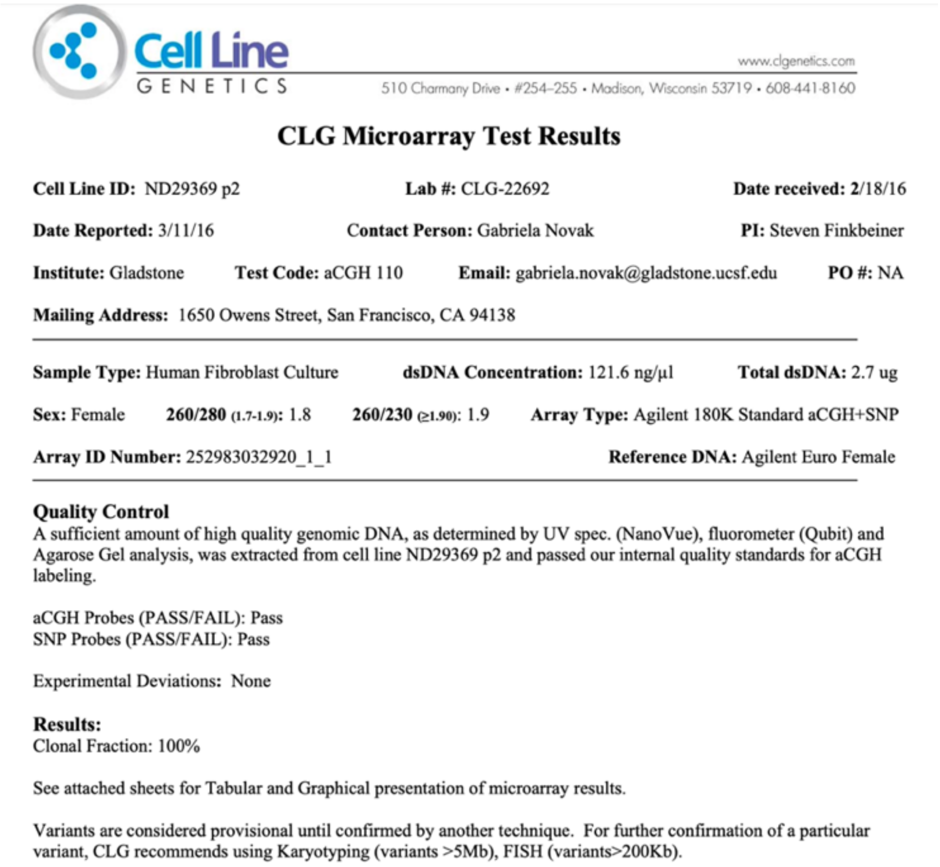
Chromosome 22



Chromosome X



ND29369 – fibroblasts, passage 2 - Karyotype / aCGH analysis



Cell Line GENETICS

www.clgenetics.com
510 Charmany Drive • #254–255 • Madison, Wisconsin 53719 • 608-441-8160

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

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.

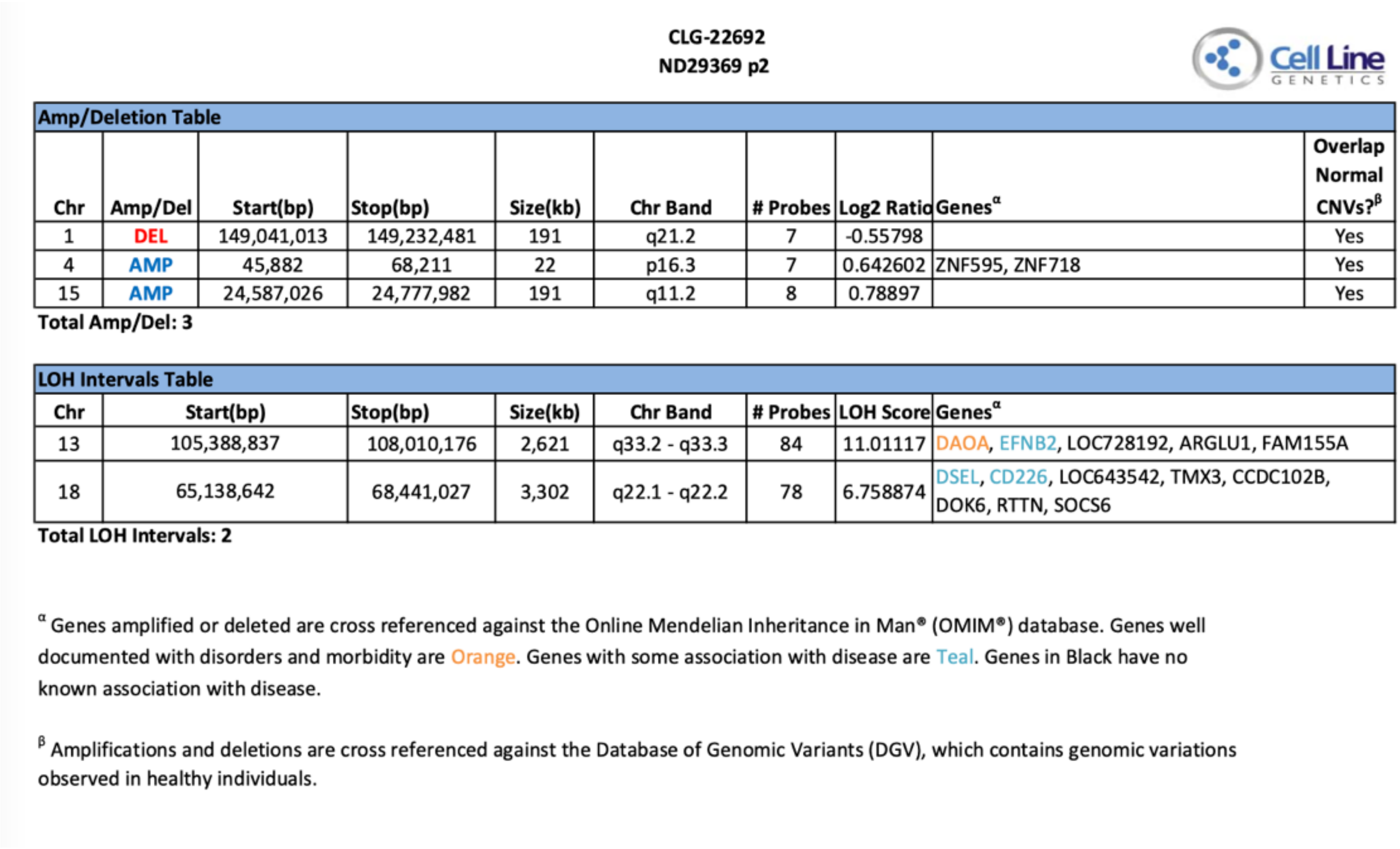
aCGH Probes (PASS/FAIL): Pass
SNP Probes (PASS/FAIL): Pass

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).



CLG-22692
ND29369 p2

Cell Line GENETICS

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

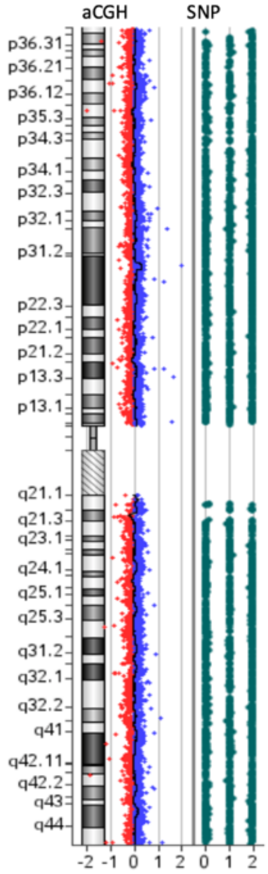
Chr	Start(bp)	Stop(bp)	Size(kb)	Chr Band	# Probes	LOH Score	Genes[α]
13	105,388,837	108,010,176	2,621	q33.2 - q33.3	84	11.01117	DAOA, EFNB2, LOC728192, ARGLU1, FAM155A
18	65,138,642	68,441,027	3,302	q22.1 - q22.2	78	6.758874	DSEL, CD226, LOC643542, TMX3, CCDC102B, DOK6, RTTN, SOCS6

Total LOH Intervals: 2

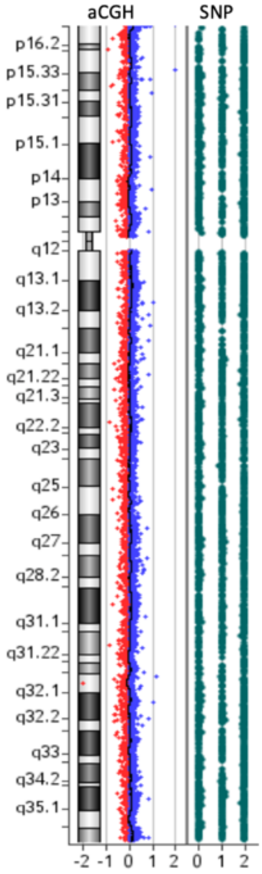
[α] Genes amplified or deleted are cross referenced against the Online Mendelian Inheritance in Man® (OMIM®) database. Genes well documented with disorders and morbidity are Orange. Genes with some association with disease are Teal. Genes in Black have no known association with disease.

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

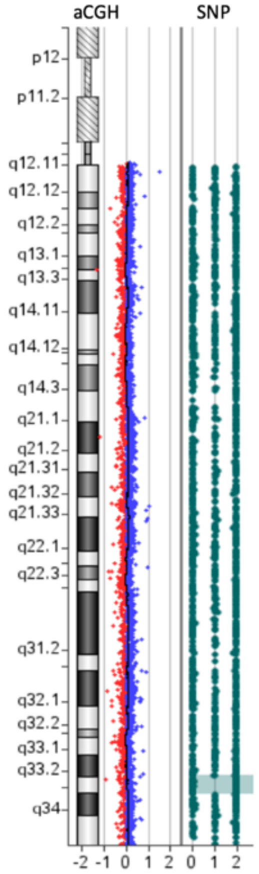
Chromosome 1



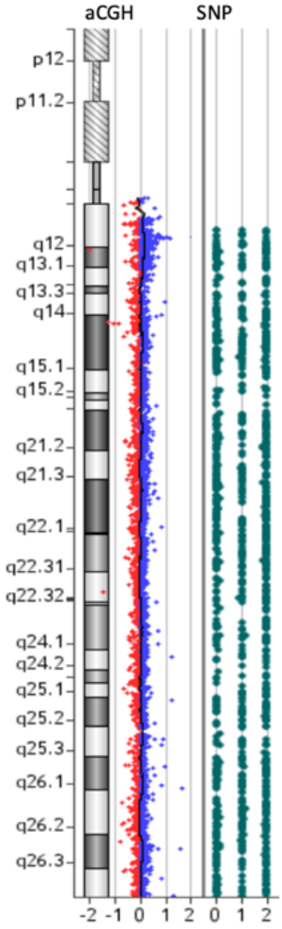
Chromosome 4



Chromosome 13



Chromosome 15



Chromosome 18