

Karyotype and comparative genomic hybridization (CGH) analysis for DNA copy number alterations and karyotype.

- iPSC ND40066 clone 8 aCGH analysis performed at P9:



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 ^a	Overlap Normal CNVs? ^b
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

Total Amp/Del: 15

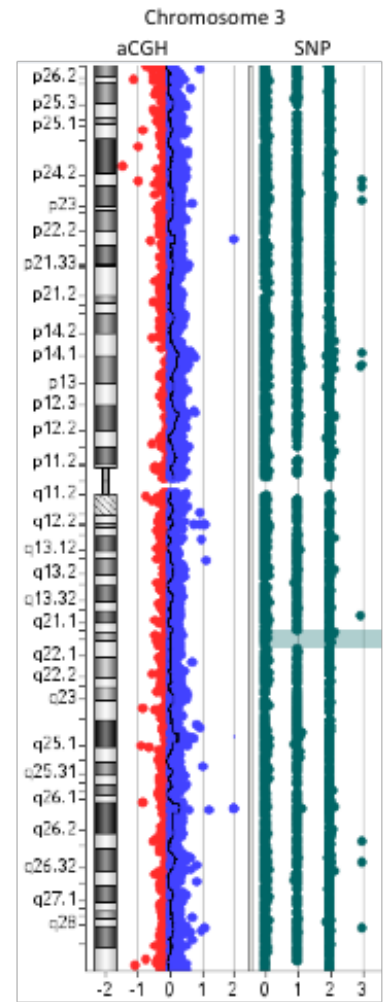
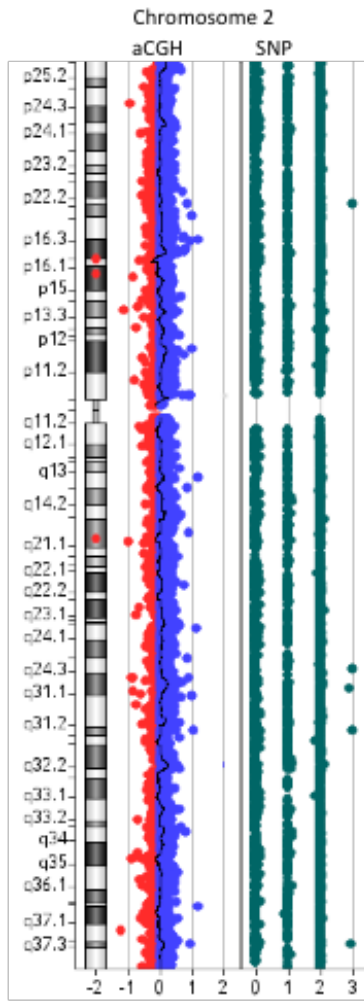
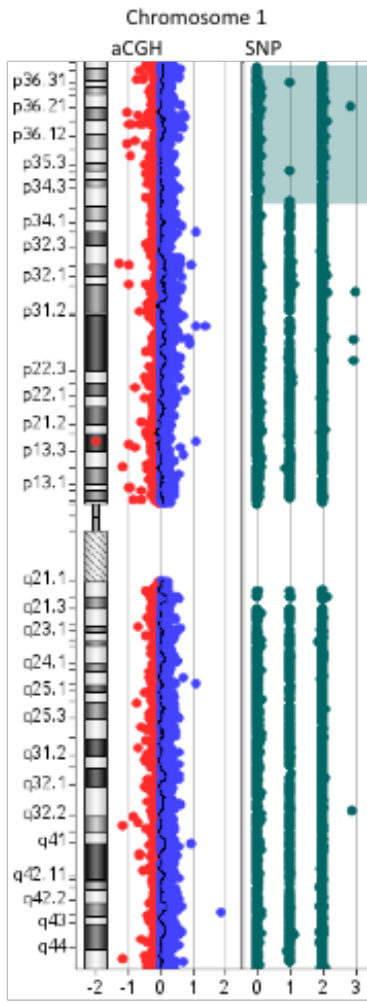
LOH Intervals Table							
Chr	Start(bp)	Stop(bp)	Size(kb)	Chr Band	# Probes	LOH Score	Genes ^a
1	1,089,699	39,243,405	38,154	p36.33 - p34.3	402	36.74485	Too Numerous to List
3	123,562,478	127,688,648	4,126	q21.1 - q21.3	54	6.073903	Too Numerous to List
6	1,696,841	18,775,310	17,078	p25.3 - p22.3	385	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

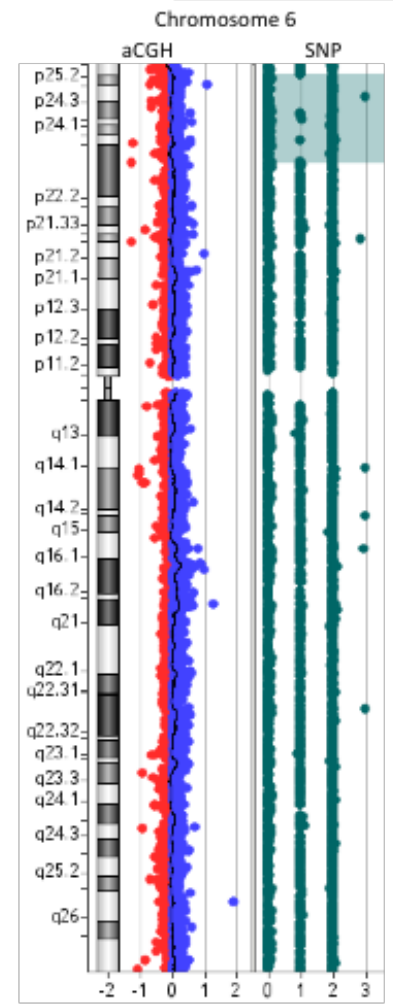
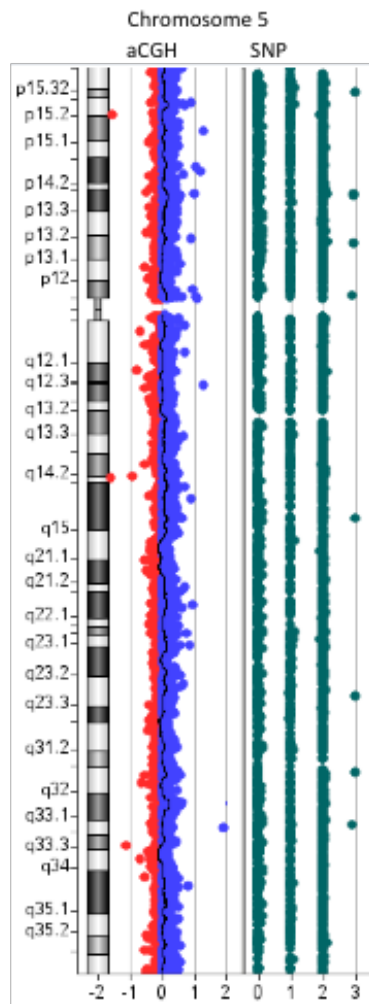
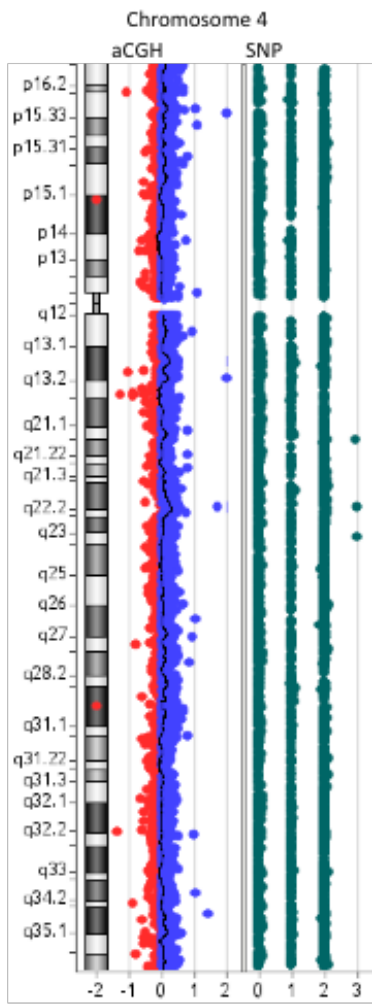
^a Genes amplified or deleted are cross referenced against the Online Mendelian Inheritance in Man® (OMIM®) database. Genes well documented with disorders and morbidity are **Orange**. Genes with some association with disease are **Teal**. Genes in Black have no known association with disease.

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

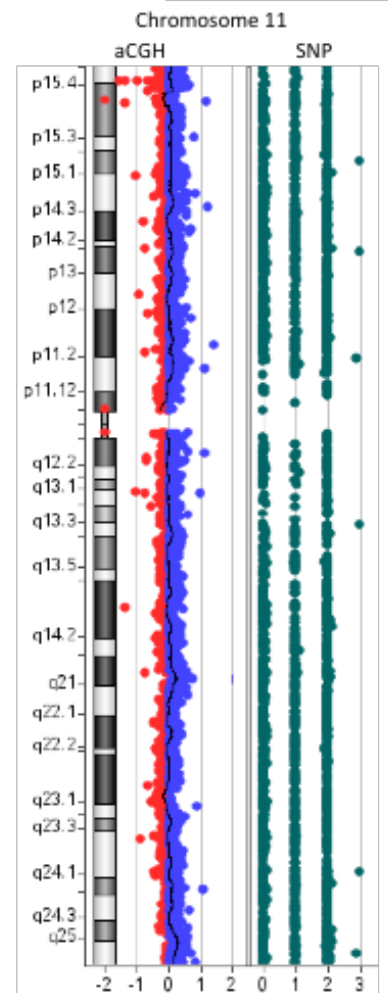
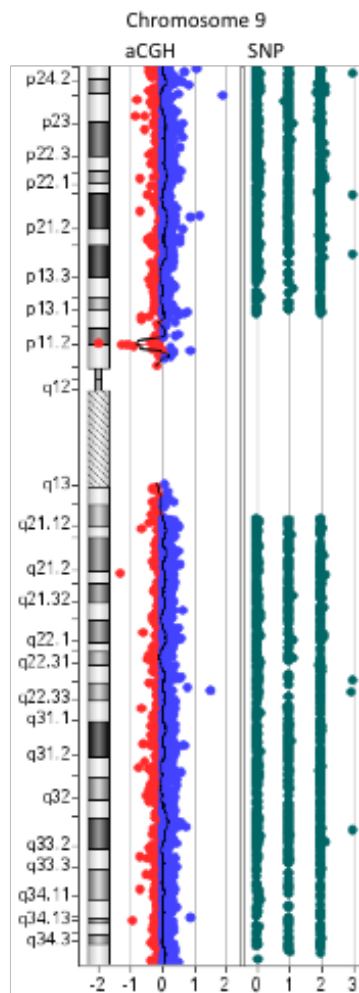
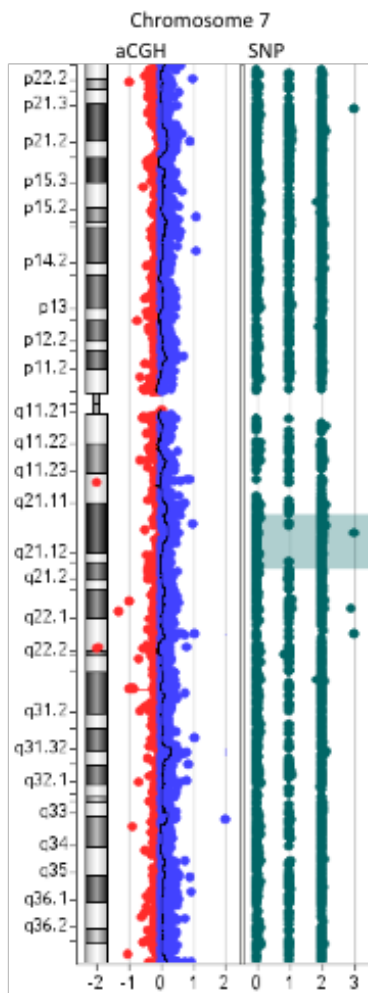
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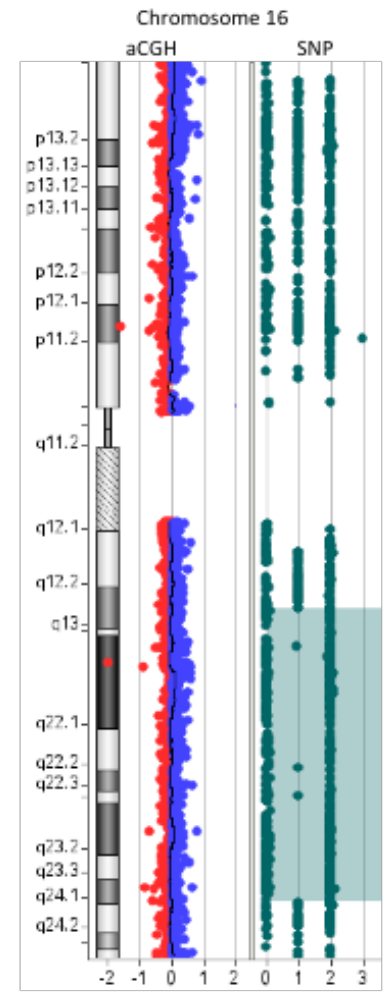
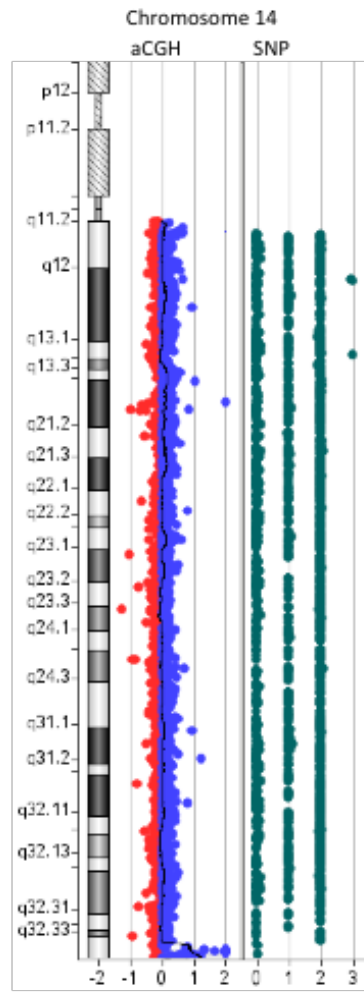
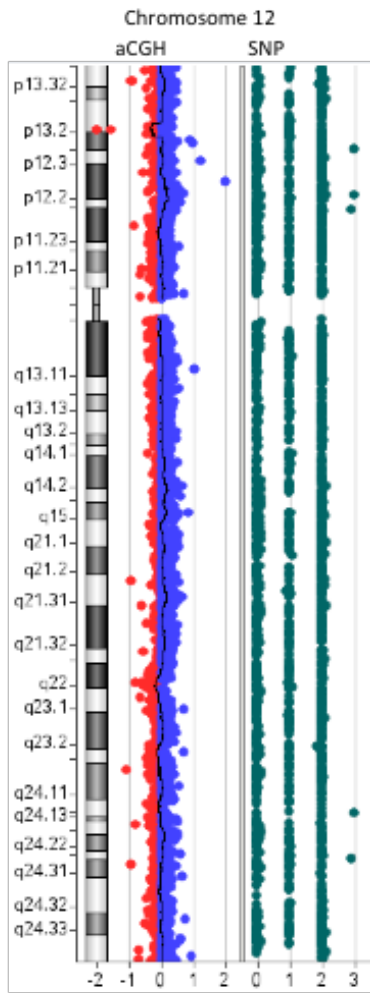
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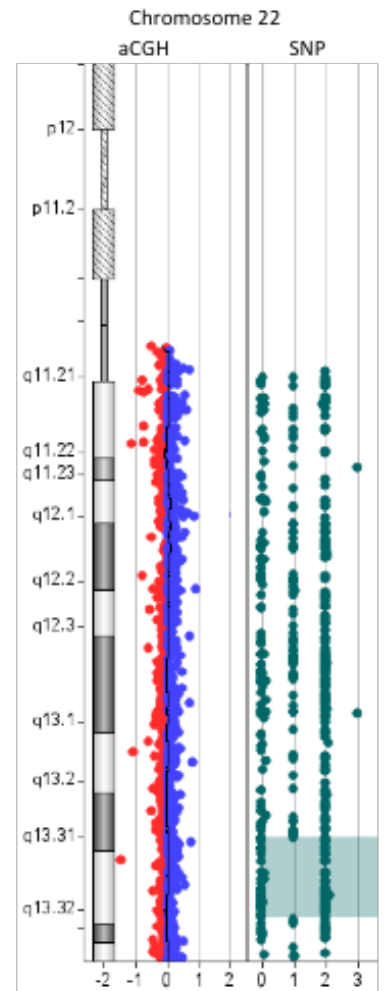
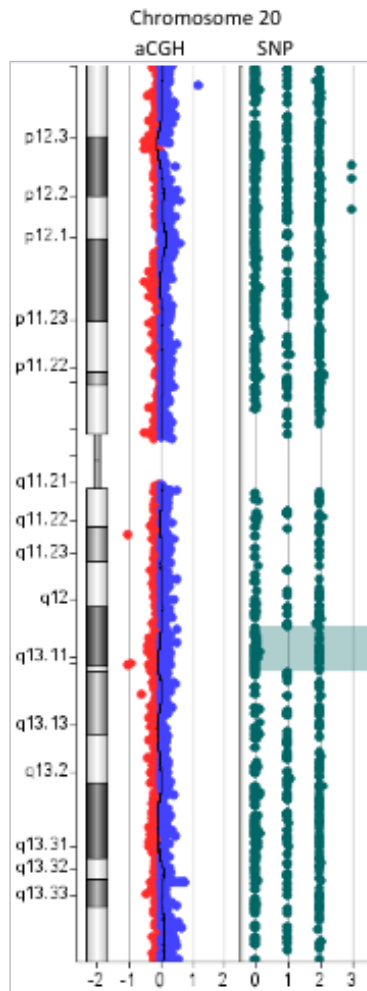
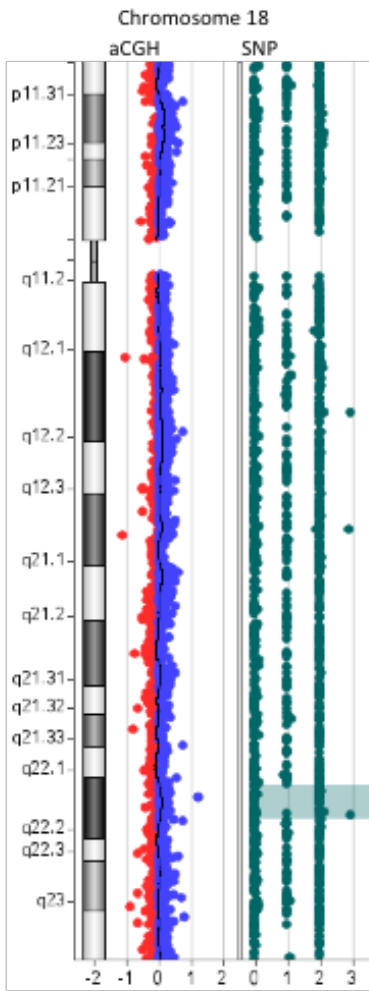
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