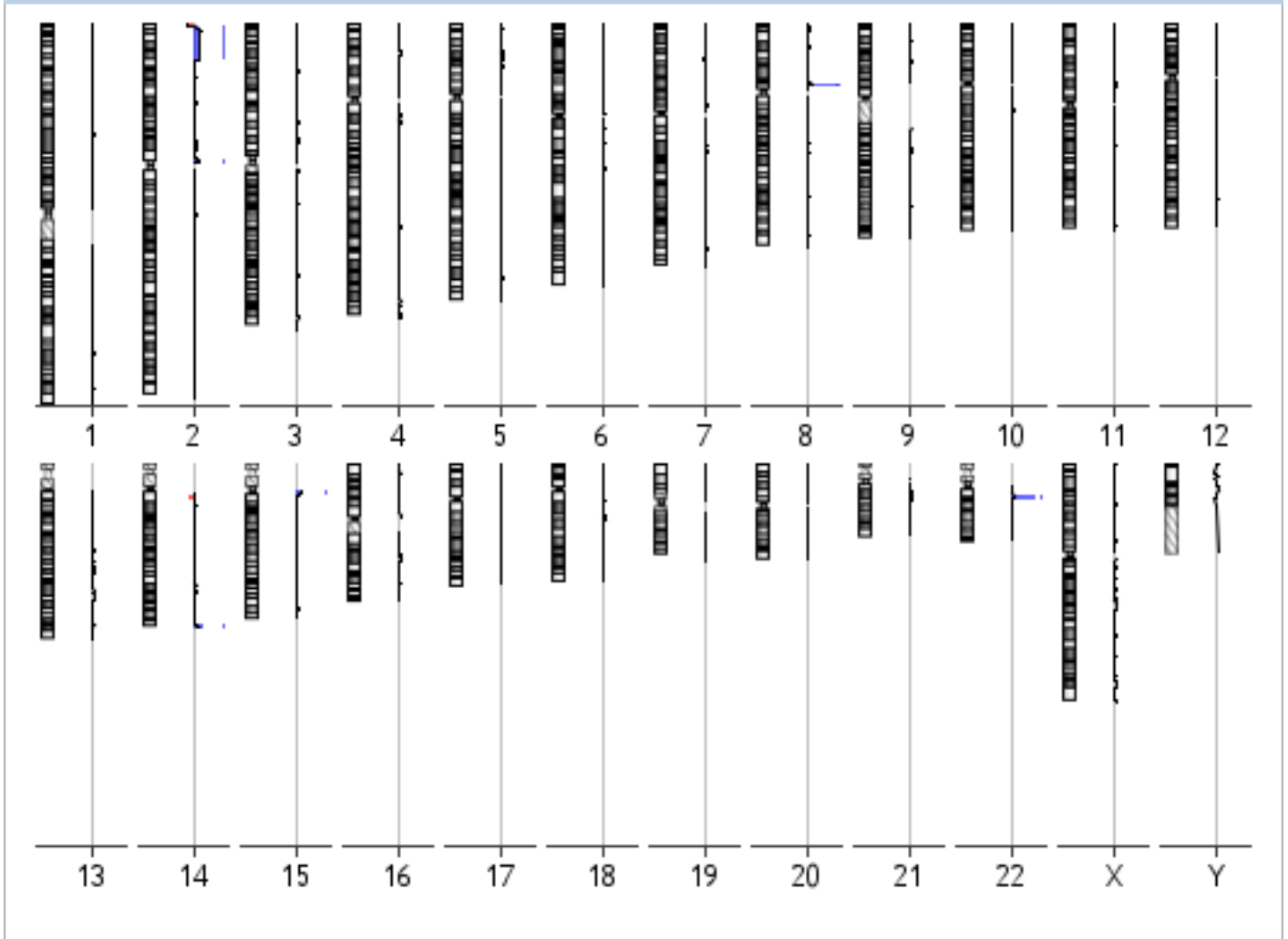


Sample Information

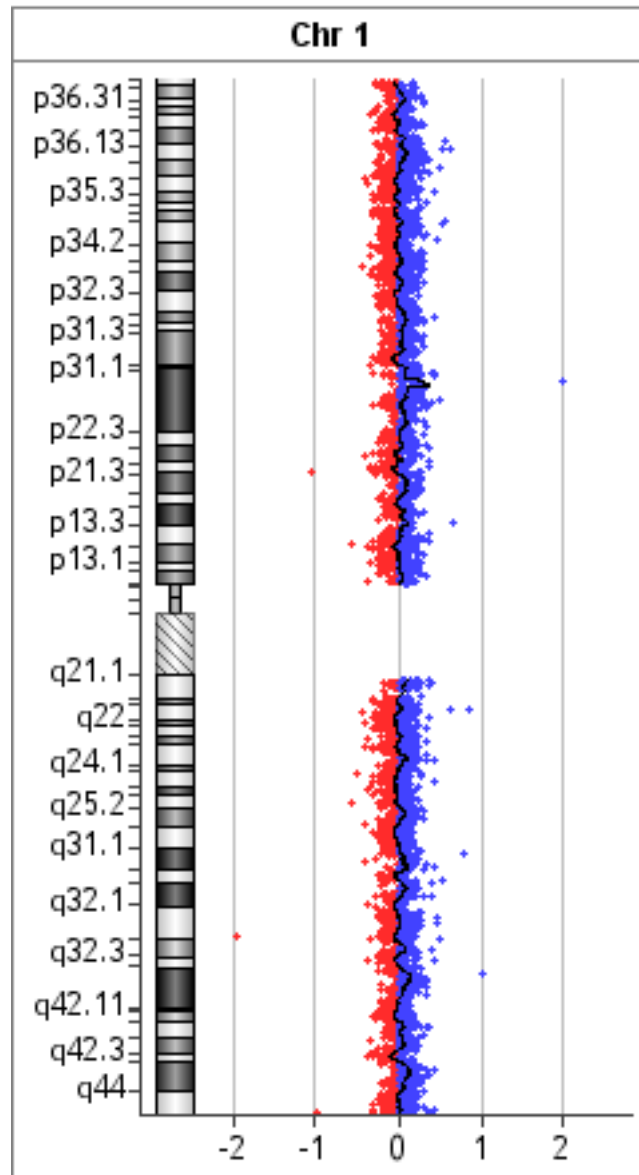
Green Sample : Agilent Euro Female
 Array ID : 252192429011_2_2
 Global Display Name : 9011_2_2_1802-3
 Polarity : 1
 Red Sample :
 DerivativeOfLogRatioSD : 0.115211
 Intermediate Report by : SKRYABIN\admin

Genome View (Amp/Del)

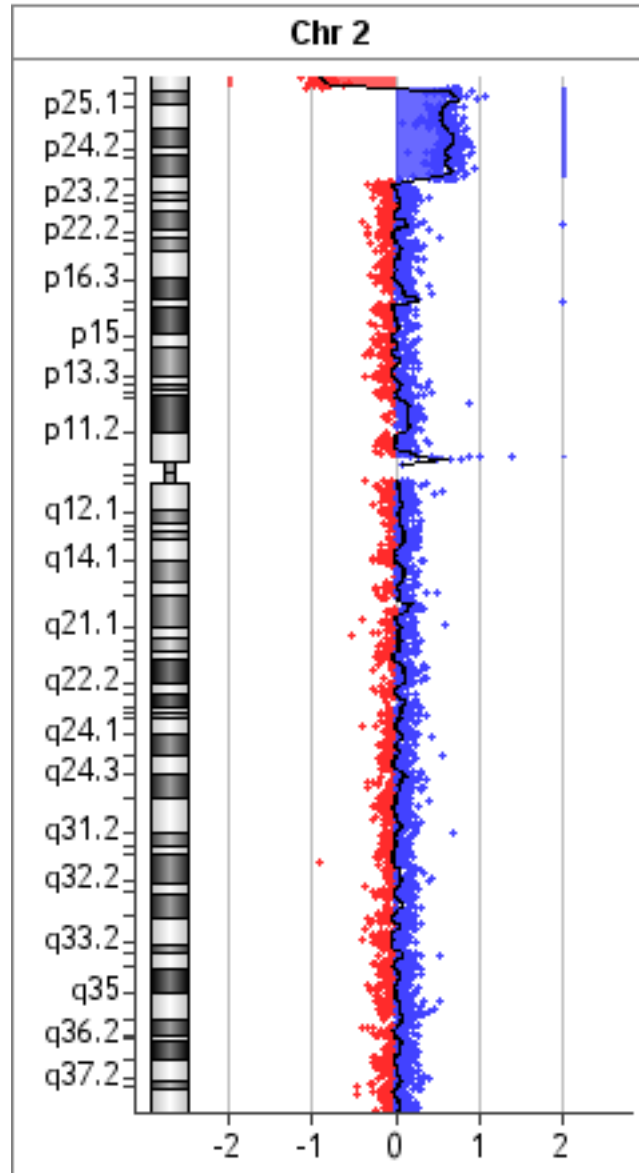


This is an intermediate report and not a final signed off report

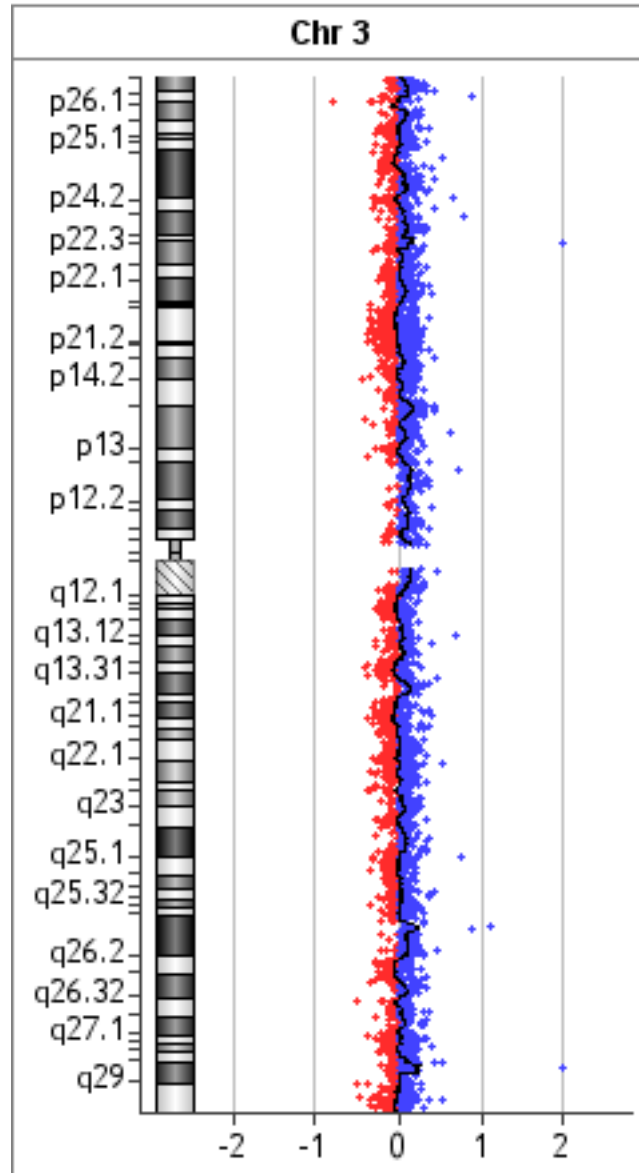
Chromosome Views (Amp/Del)



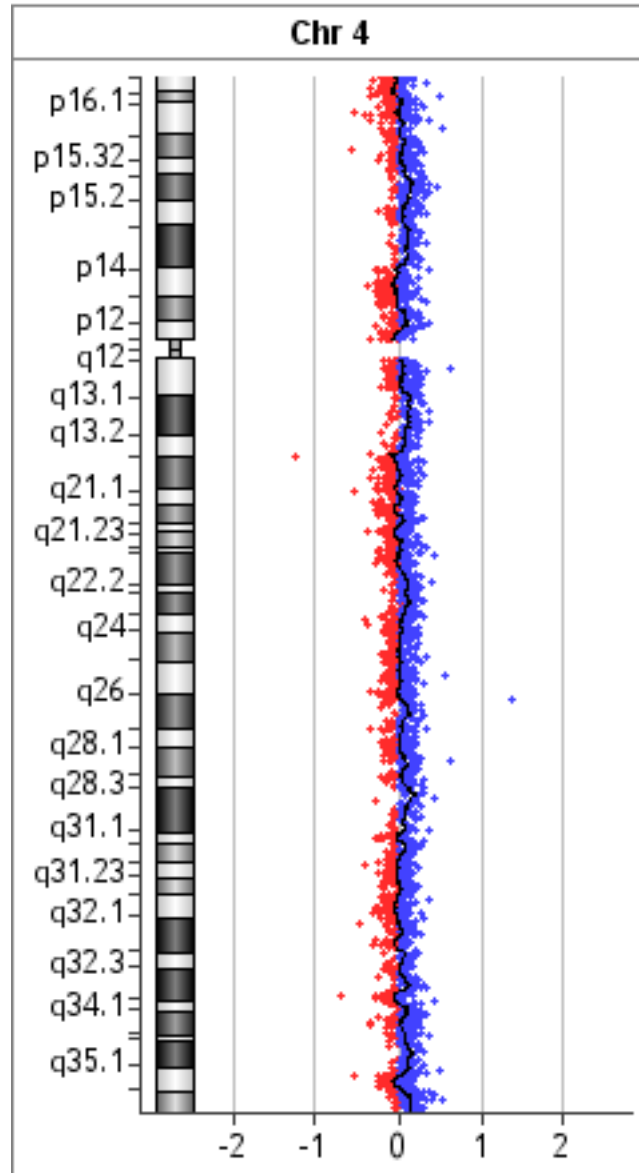
This is an intermediate report and not a final signed off report



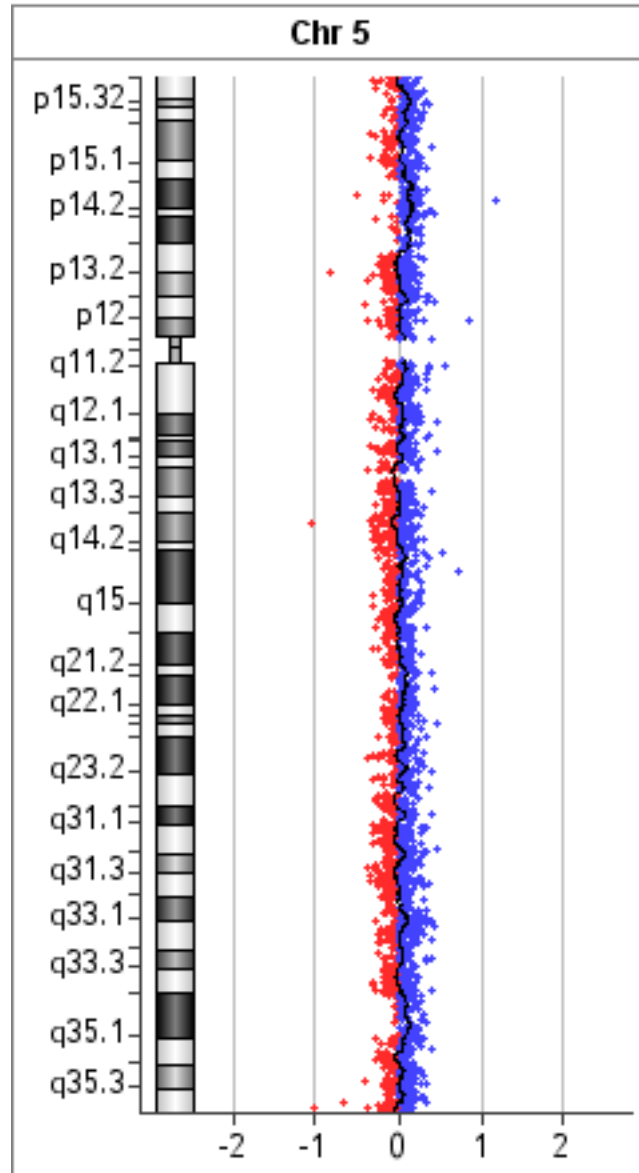
This is an intermediate report and not a final signed off report



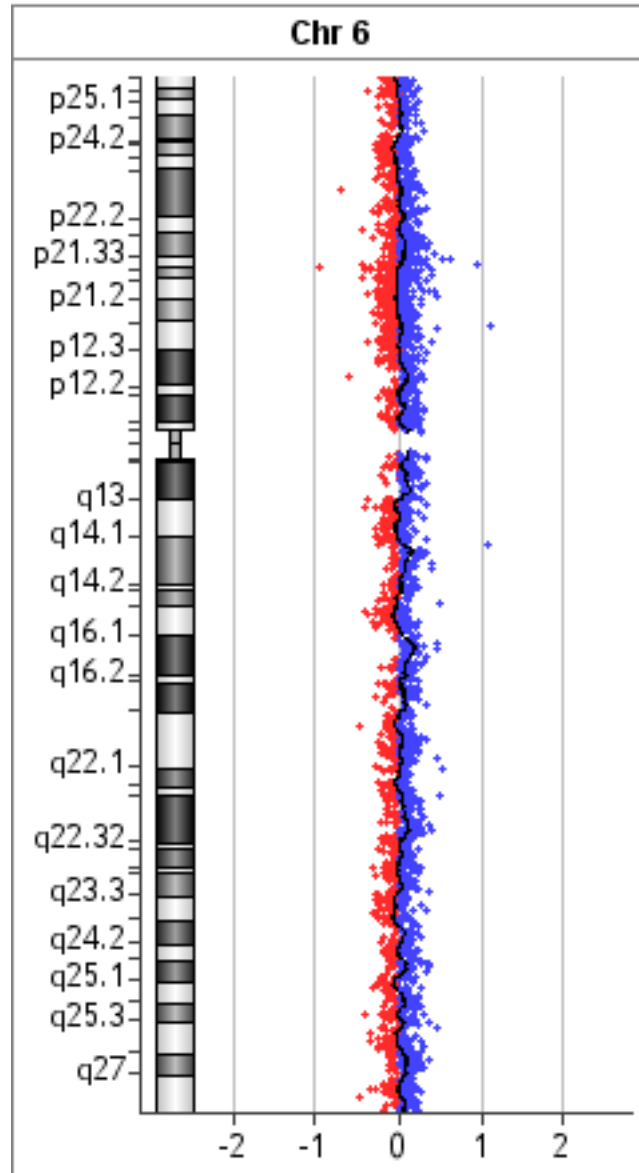
This is an intermediate report and not a final signed off report



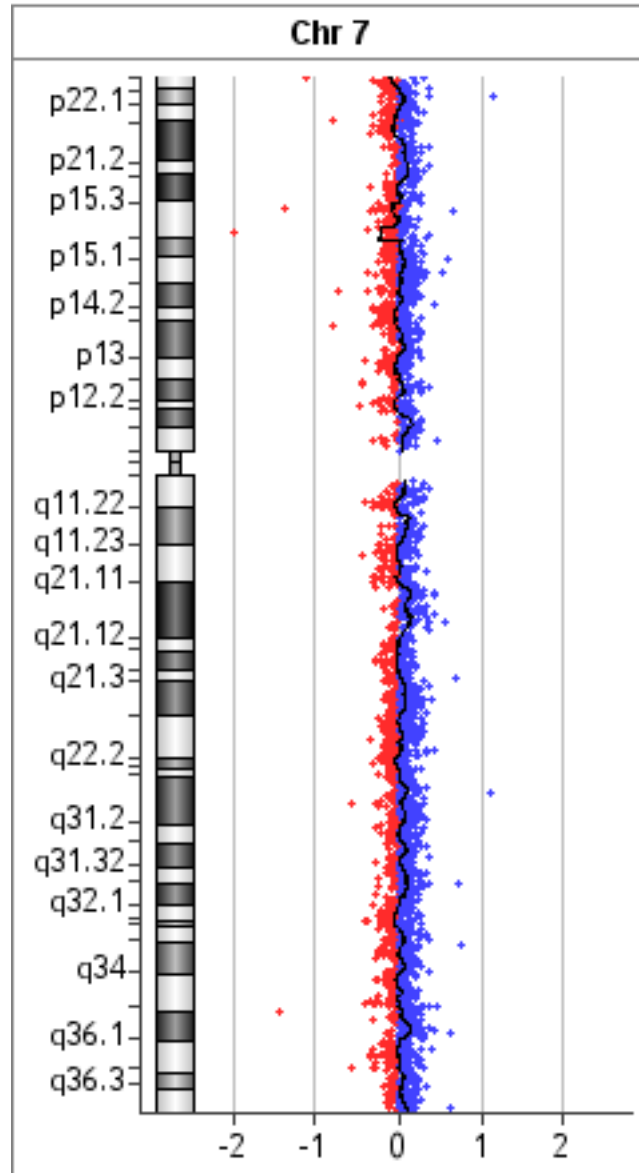
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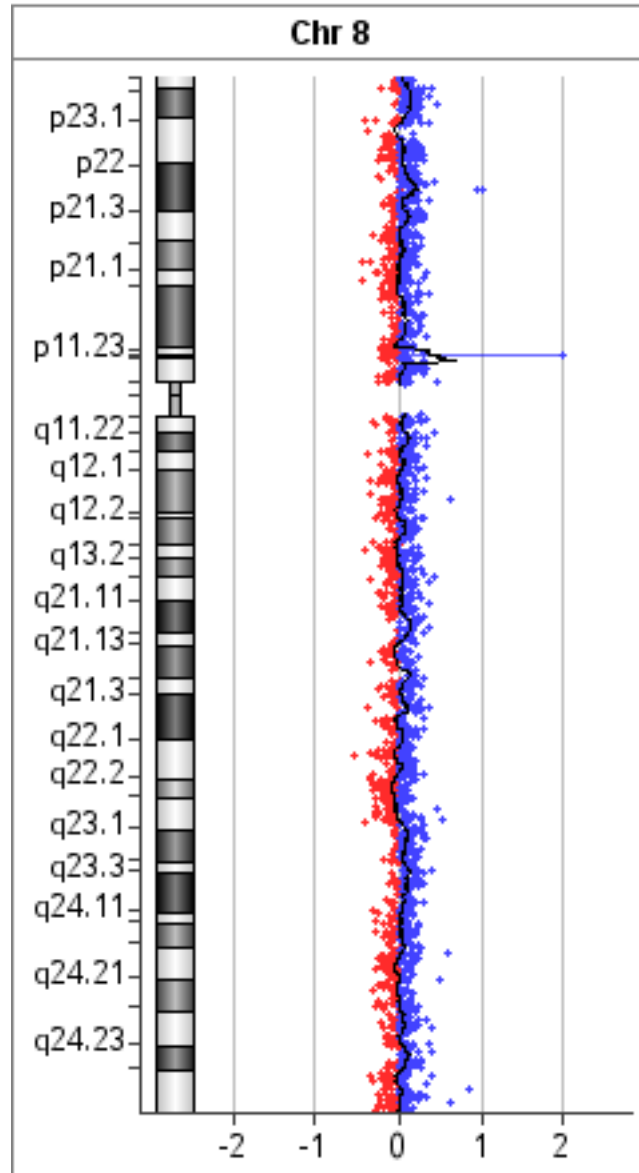
This is an intermediate report and not a final signed off report



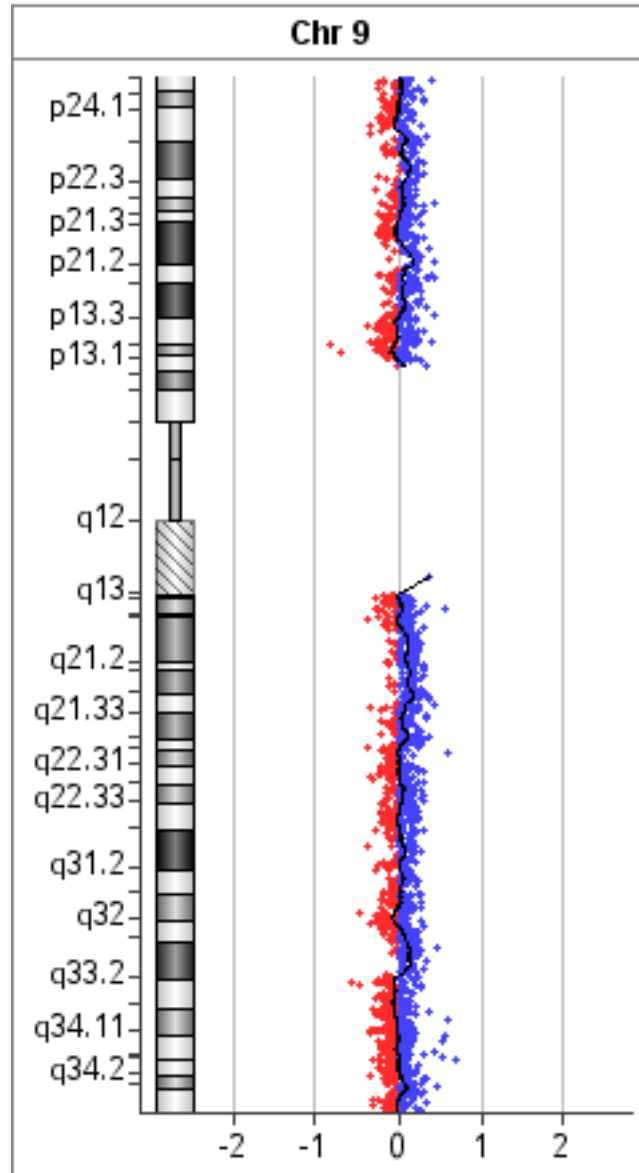
This is an intermediate report and not a final signed off report



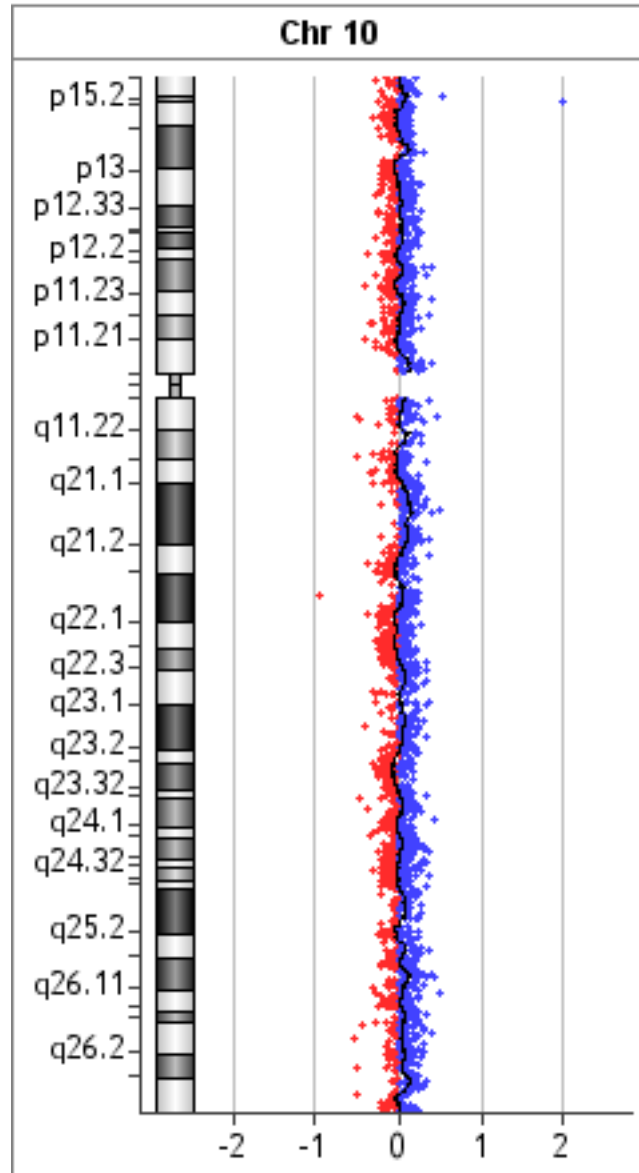
This is an intermediate report and not a final signed off report



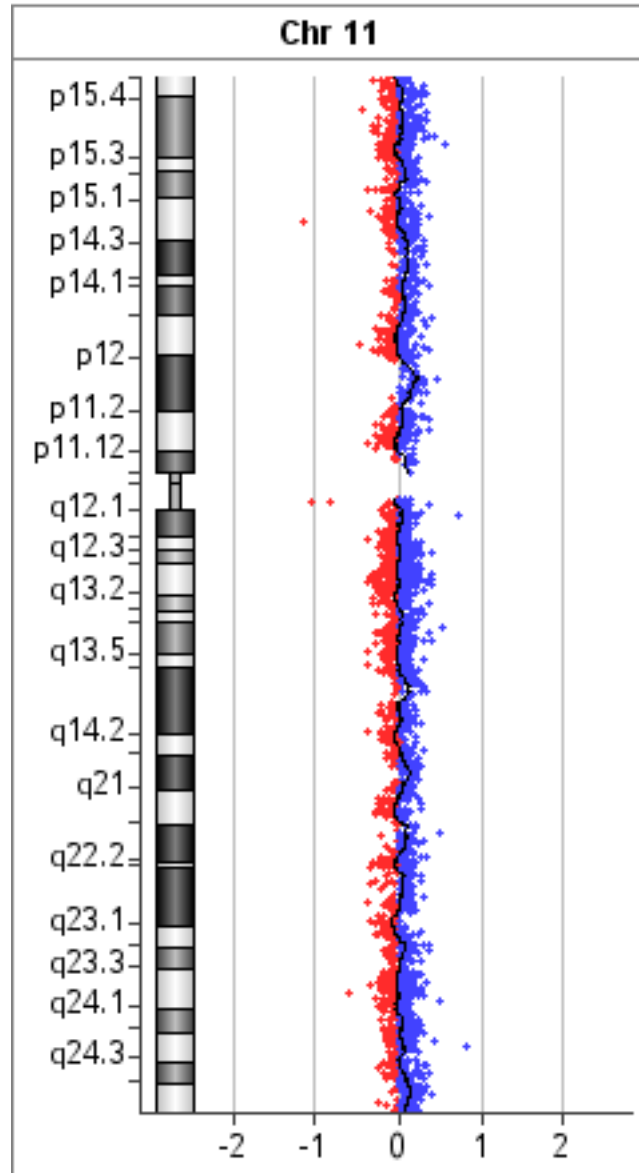
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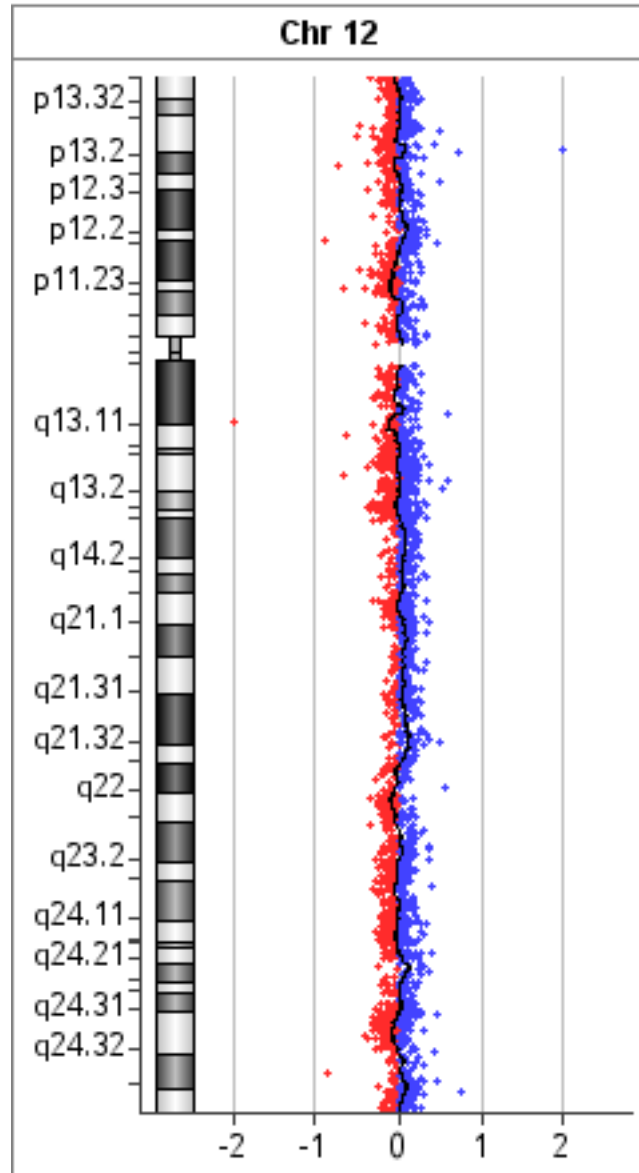
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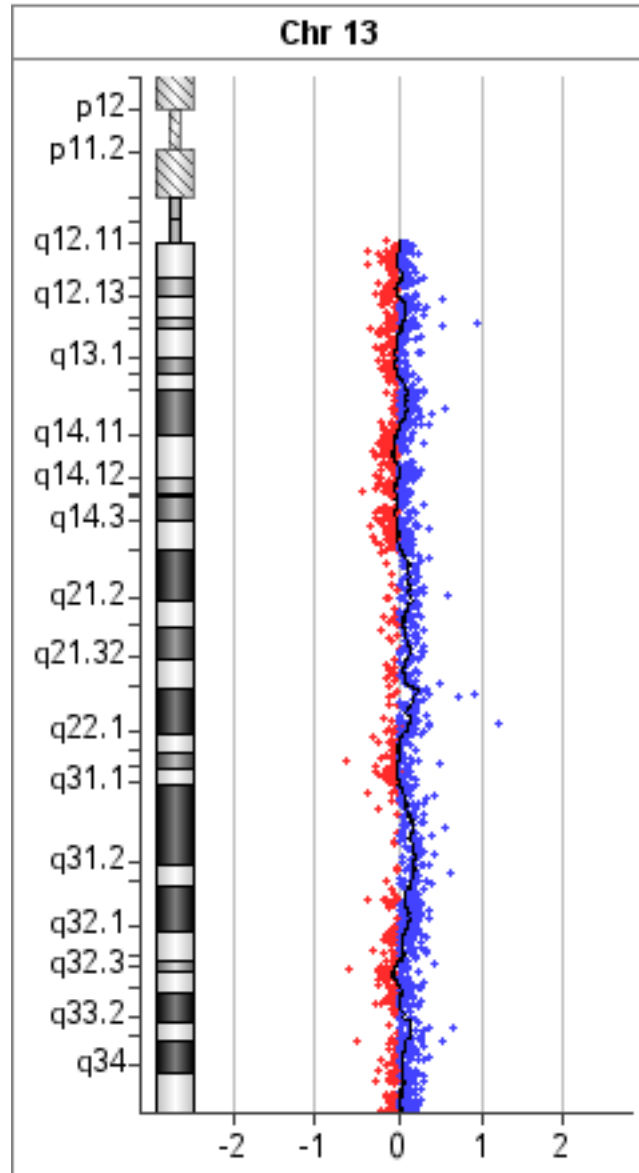
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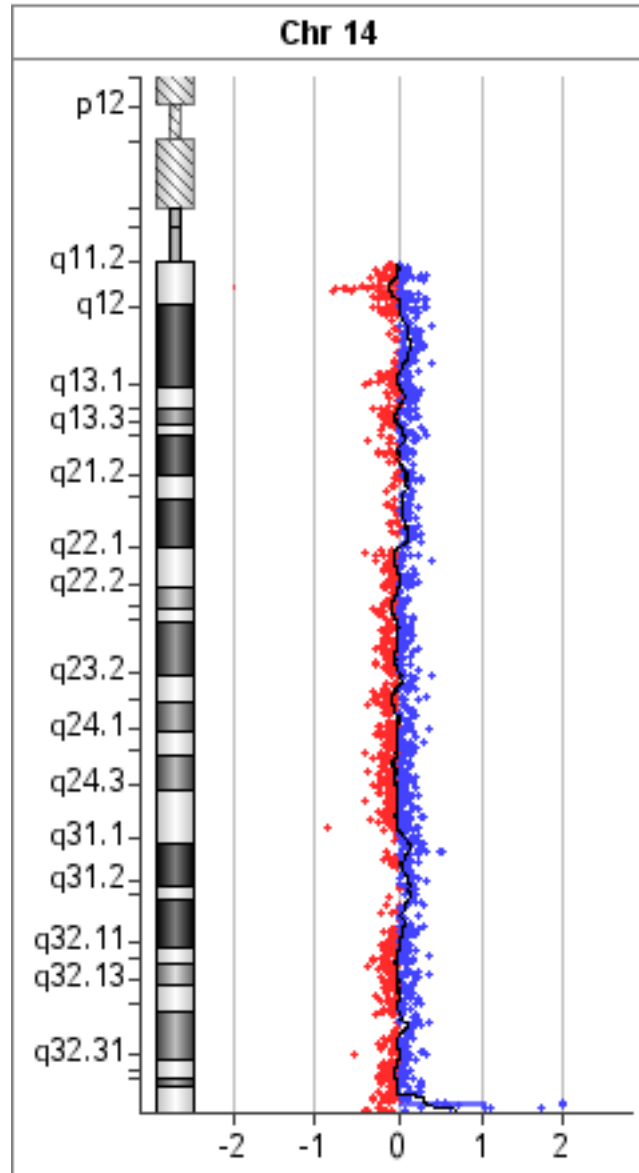
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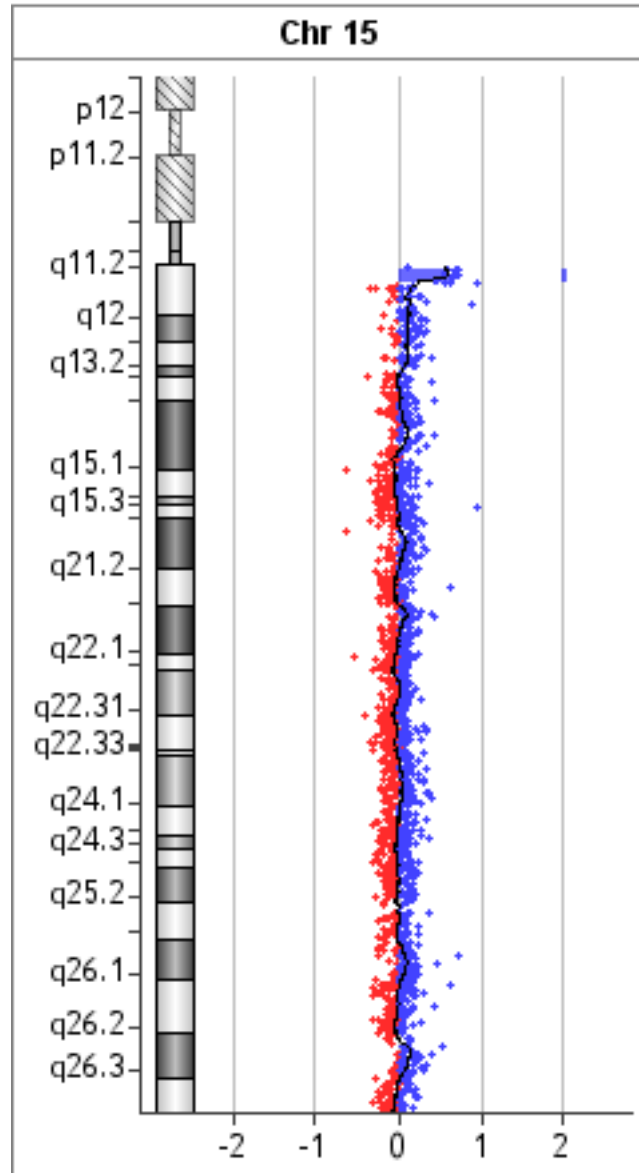
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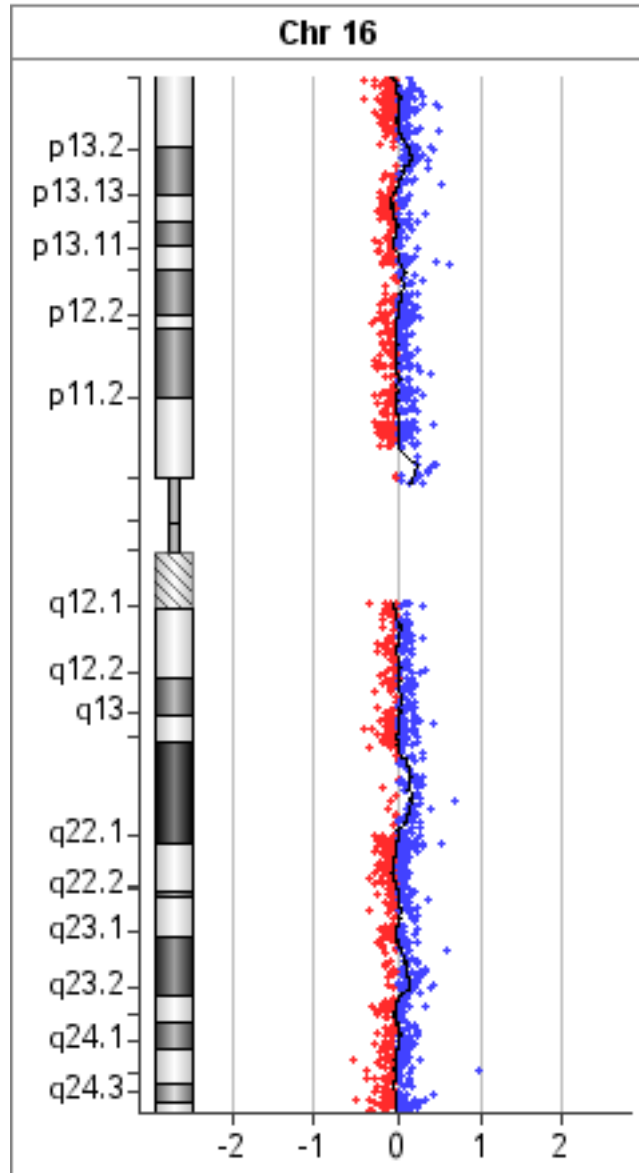
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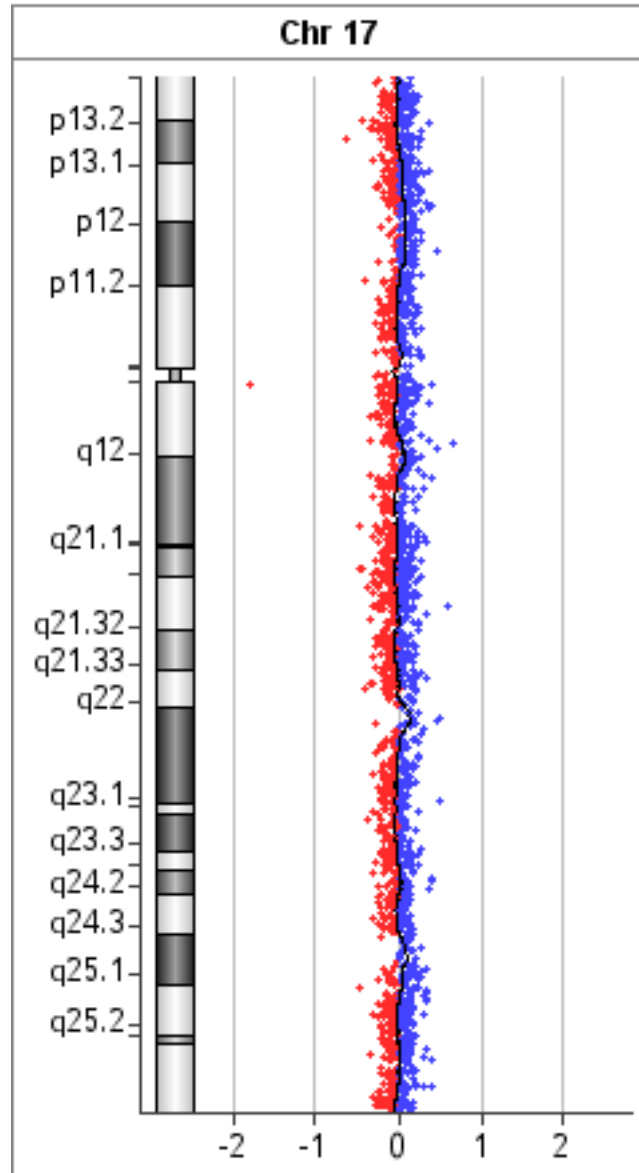
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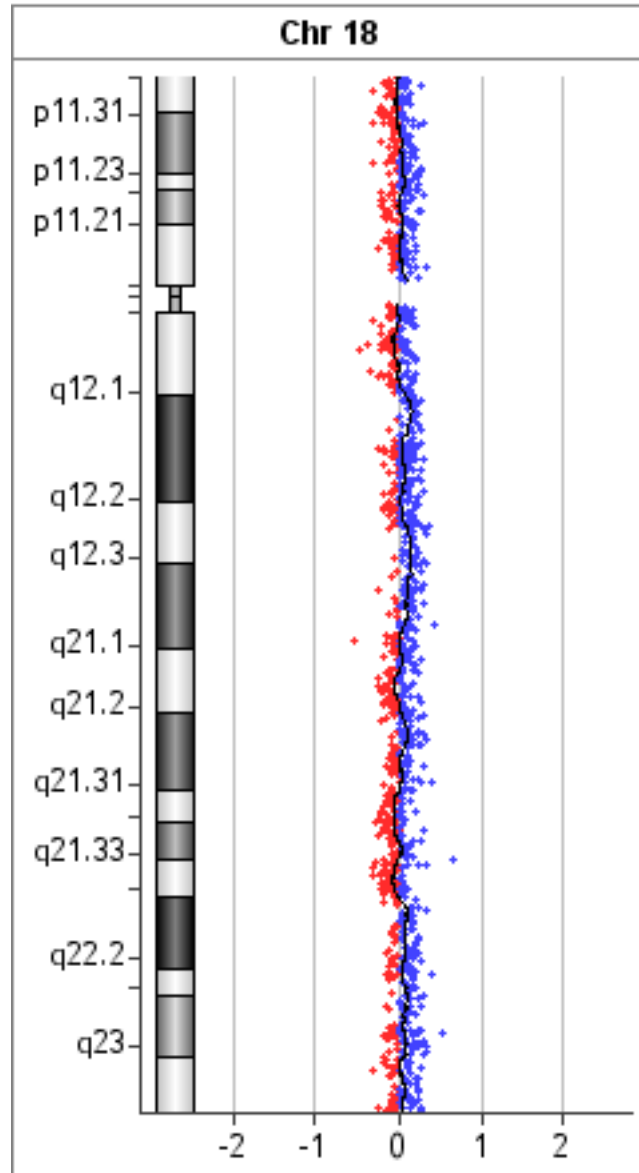
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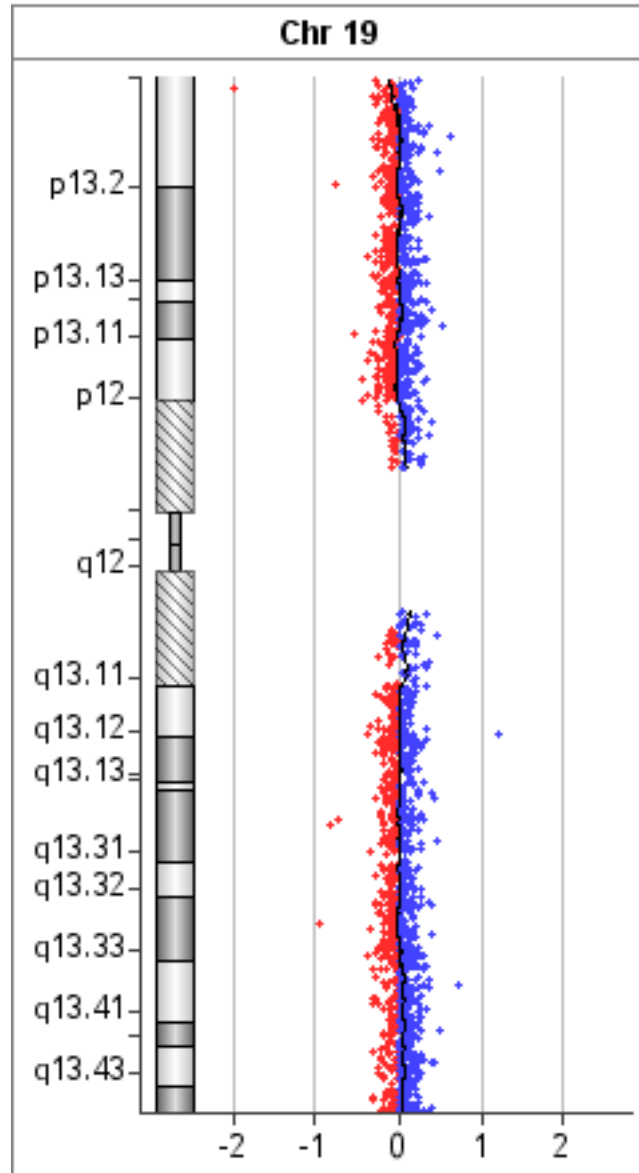
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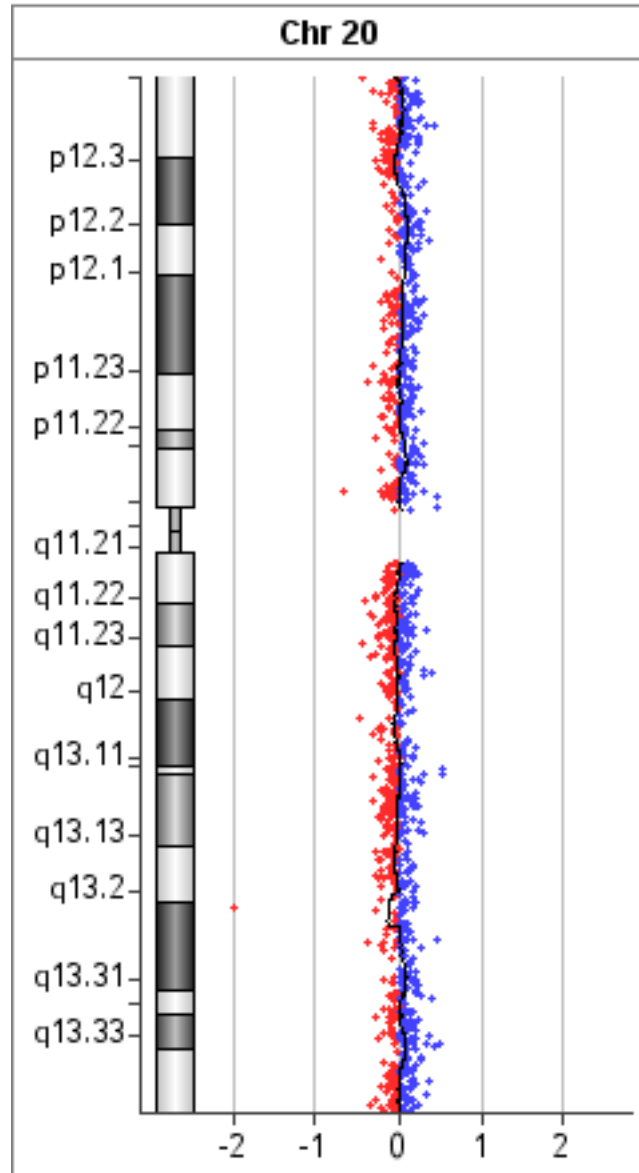
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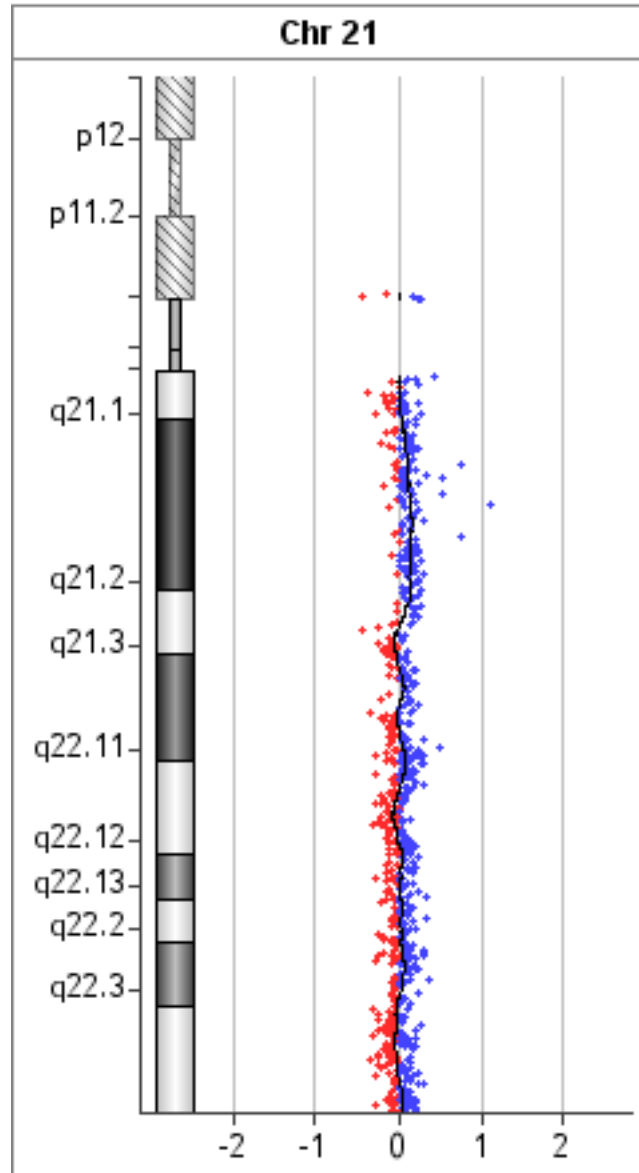
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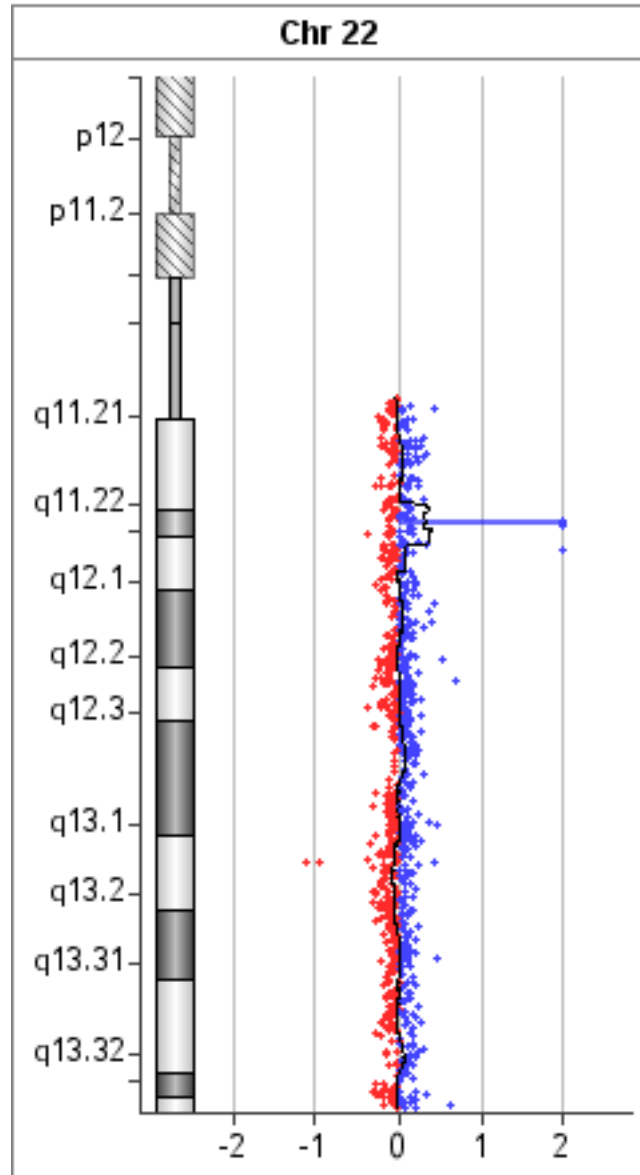
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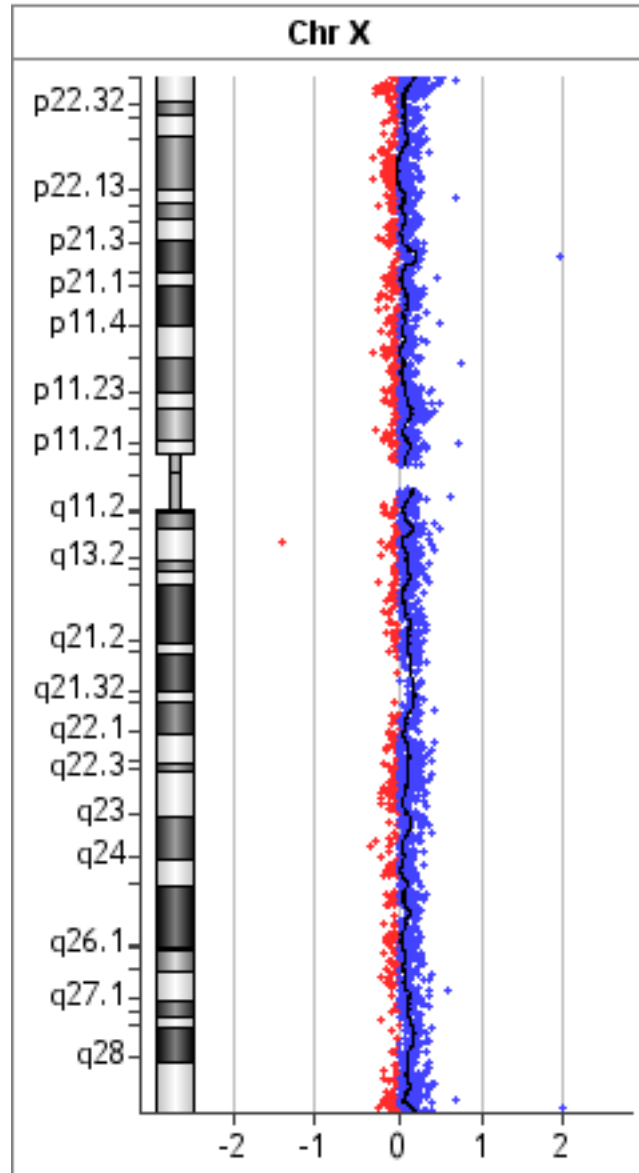
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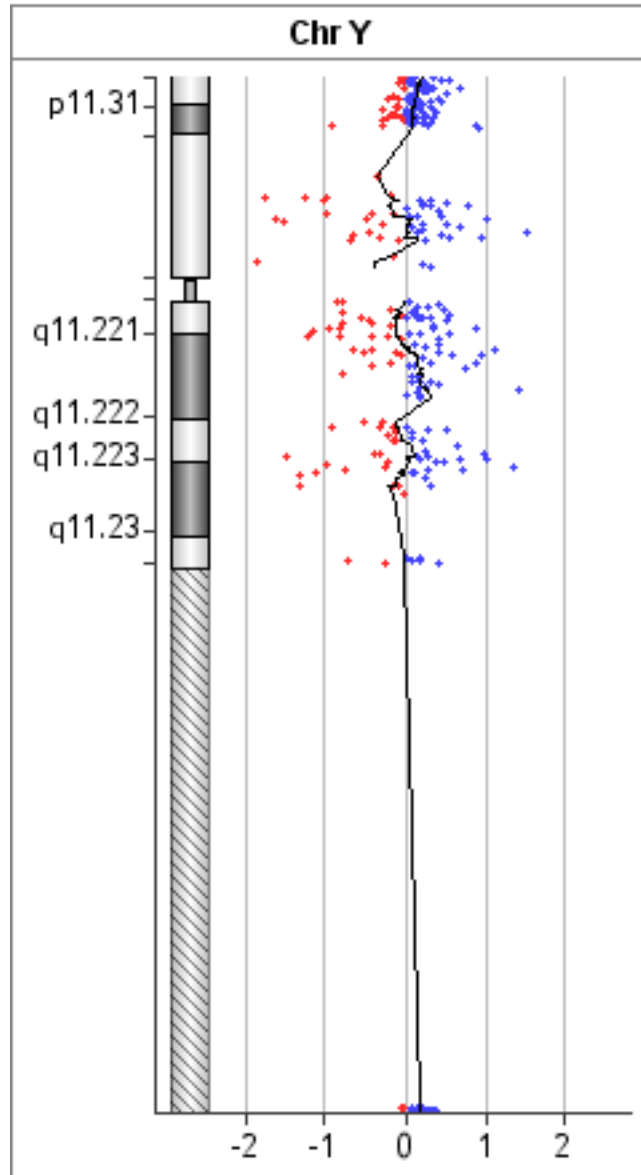
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Amp/Gain/Loss/Del Intervals Table

Chr	Start-Stop(bp)	Size(kb)	Cytoband	#Probes	Amp/Gain/ Loss/Del	P-value	Annotations
chr2	32444-2667650	2,635	p25.3	47	-0,872448	2,328e-161	FAM110C, SH3YL1, ACP1...
chr2	2754133-24334429	21,580	p25.3 - p23.3	292	0,587937	4,900e-324	TSSC1, TTC15, ADI1...
chr2	88924973-89871328	946	p11.2	11	0,570505	3,570e-19	
chr8	39378051-39505315	127	p11.23 - p11.22	4	5,395991	2,479e-83	ADAM5P, ADAM3A
chr14	21393719-21958703	565	q11.2	12	-0,475282	3,144e-15	
chr14	105432521-105947052	515	q32.33	11	1,048985	3,657e-43	KIAA0125, ADAM6, NCRNA00226
chr15	18741716-20010618	1,269	q11.2	13	0,616011	4,518e-26	GOLGA6L6, GOLGA8C, BCL8...
chr22	21386562-21520273	134	q11.22	5	2,820358	4,049e-76	MIR650

Amp=Amplification Del=Deletion

Total Amp/Gain/Loss/Del Intervals: 8

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Analysis Settings

Design	: 021924_20110331	Sample Name	: 9011_2_2_1802-3
Genome	: hg18	Aberration Algorithm	: ADM-2
Threshold	: 6.0	Fuzzy Zero	: OFF
GC Correction	: ON	Window Size	: 2Kb
Centralization (legacy)	: OFF	Diploid Peak Centralization	: ON
SNP Copy Number	: OFF	LOH	: OFF
Combine Replicates (Intra Array)	: ON	Array Level Filter	: NONE
Metric Set Filter	: NONE	Aberration Filter	: Minimum Number of Probes for Amplification \geq 3 AND Nesting Level \leq 100 AND Minimum Avg. Absolute Log Ratio for Amplification \geq 0.25 AND Minimum Size (Kb) of Region for Amplification \geq 0.0 AND Minimum Size (Kb) of Region for Deletion \geq 0.0 AND Minimum Number of Probes for Deletion \geq 3 AND Minimum Avg. Absolute Log Ratio for Deletion \geq 0.25 AND Minimum Number of Probes for Gain \geq 3 AND Minimum Number of Probes for Loss \geq 3 AND Minimum Avg. Absolute Log Ratio for Gain \geq 0.25 AND Minimum Avg. Absolute Log Ratio for Loss \geq 0.25 AND Minimum Size (Kb) of Region for Gain \geq 0.0 AND Minimum Size (Kb) of Region for Loss \geq 0.0
Feature Level Filter	: gIsSaturated = true OR rlsSaturated = true OR gIsFeatNonUnifOL = true OR rlsFeatNonUnifOL = true OR LogRatio = 0; Include matching values=false	Design Level Filter	: Homology = 0 OR IsPseudoautosomal = 1
LOH Filter	: NONE	Genomic Boundary	: OFF
Show Flat Intervals	: false	Template Name	: Default Cyto Report Template - CGH

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Notes

Sample Notes

No notes available.

Amp/Gain/Loss/Del Interval Notes

No notes available.

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