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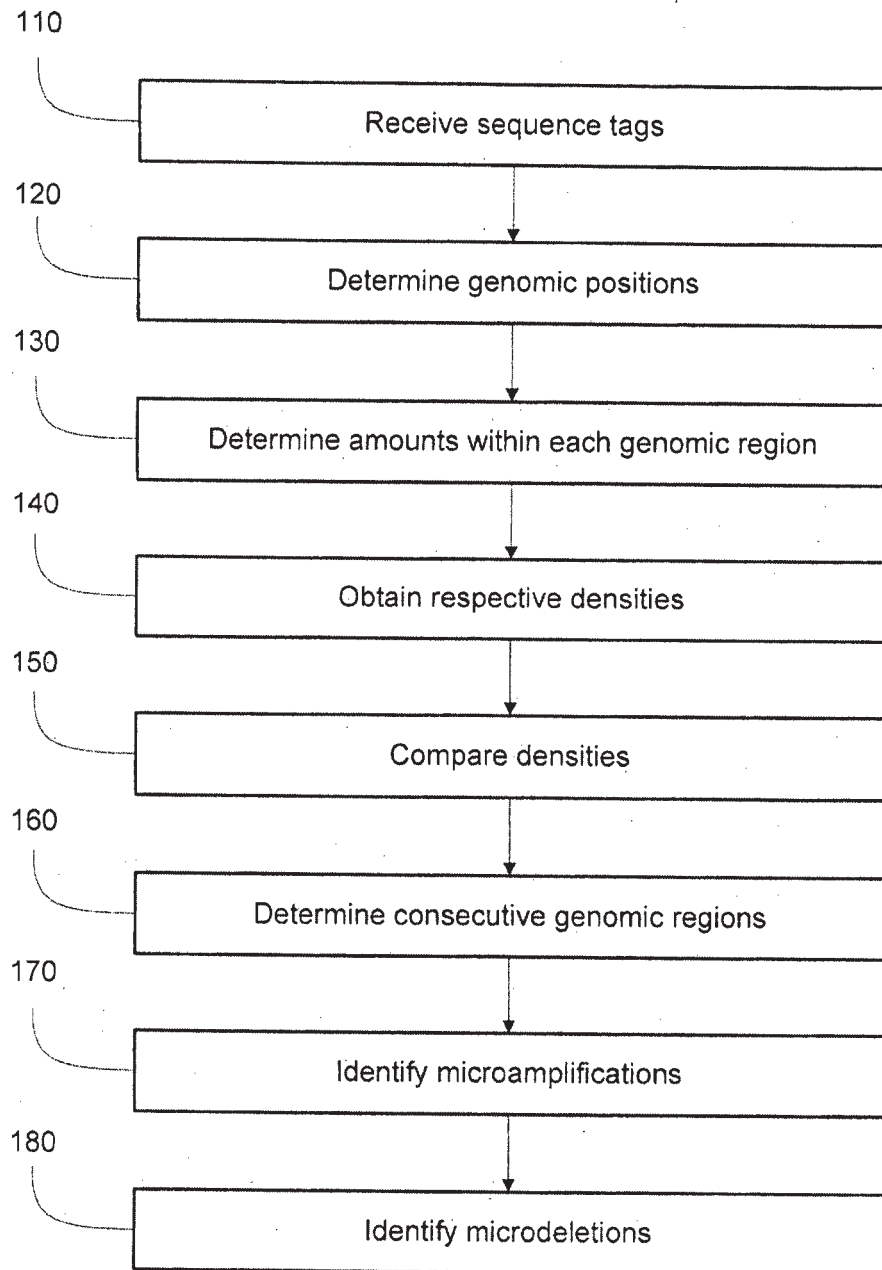


FIG. 1

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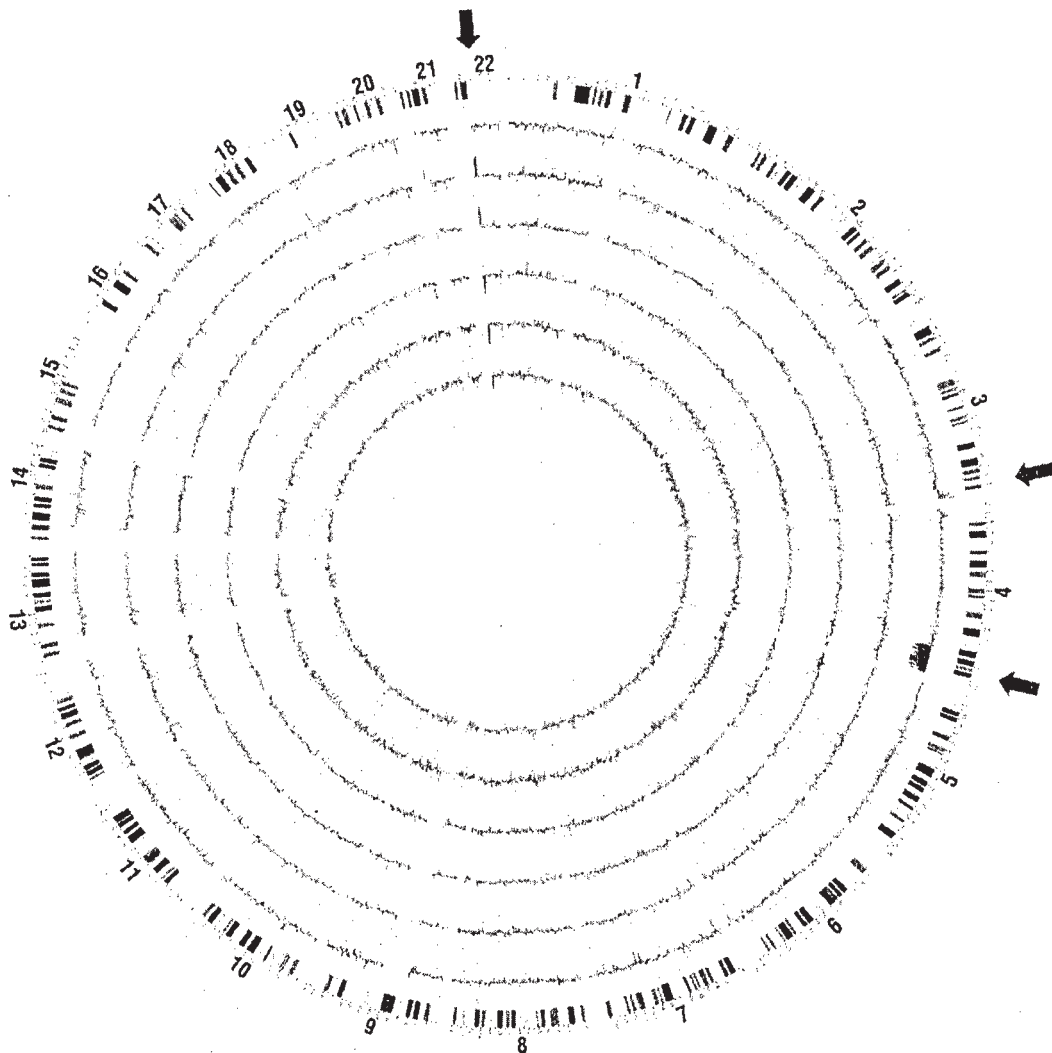
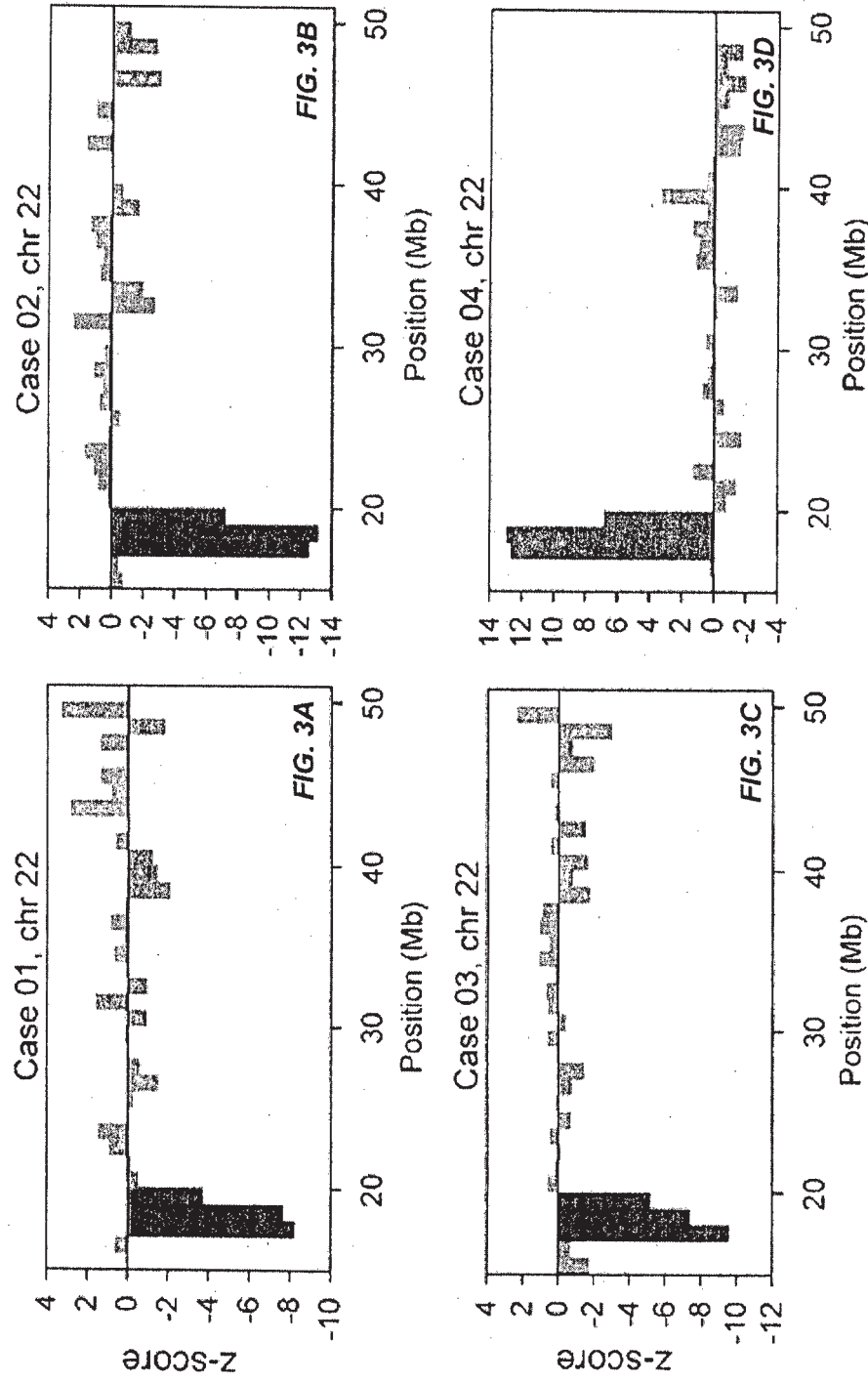
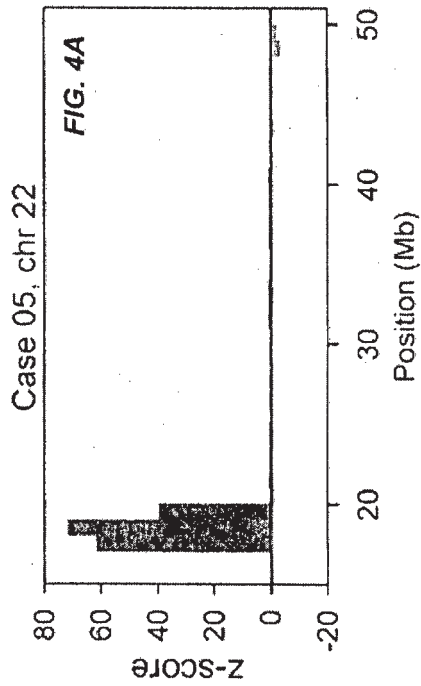
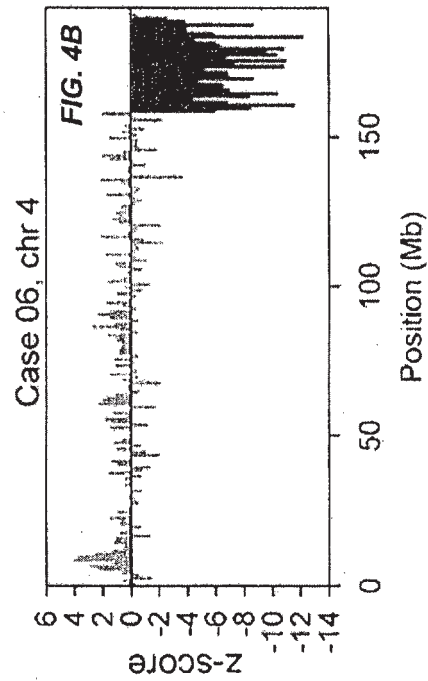
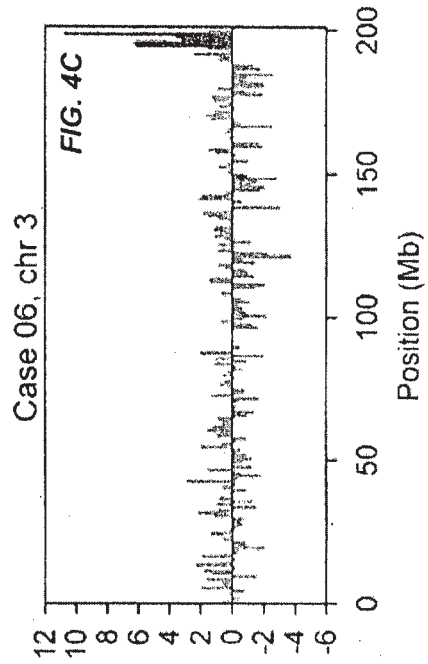


FIG. 2



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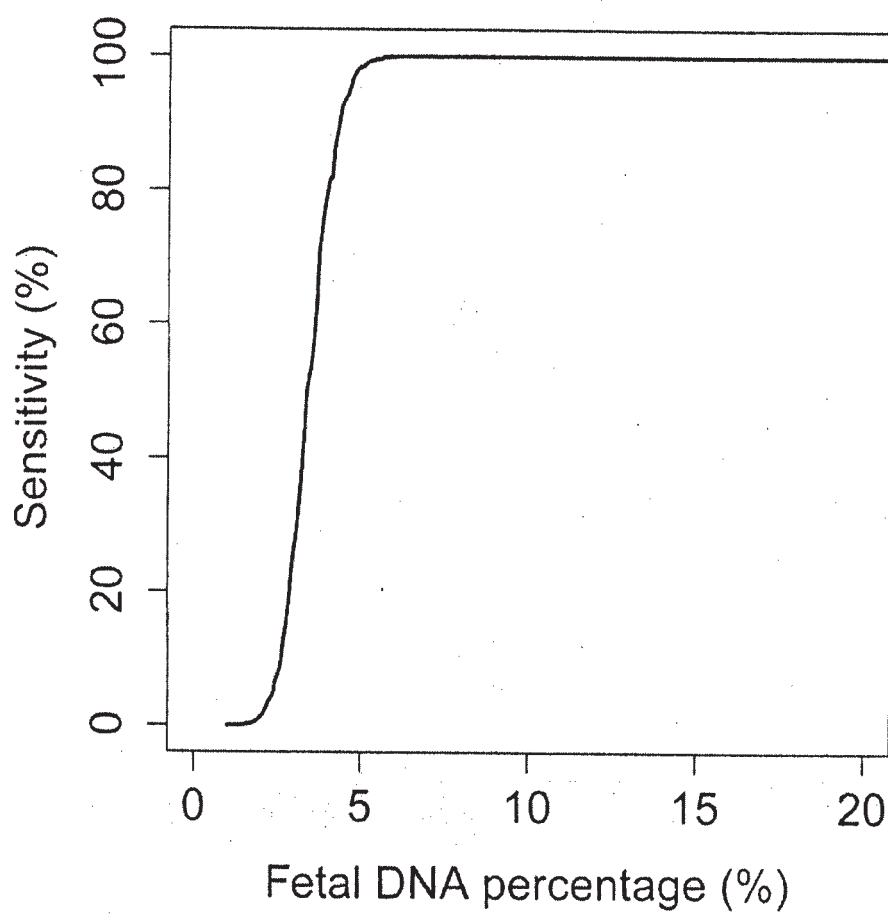


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Case	Fetal sex	Fetal DNA percentage	
		By genomic representation of the affected chromosomal region(s)	By chr Y approach ^a
01	F	10.5%	—
02	M	17.4%	21.5%
03	M	9.2%	13.7%
04	M	17.8%	20.3%
05 ^b	F	—	—
06	F	10.9 % / 13.4% ^c	—

FIG. 5

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**FIG. 6**

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Diagnostic sensitivity		Diagnostic resolution		
		3 Mb	2 Mb	1 Mb
95%	No. of molecules required in each bin	42,000	42,000	42,000
	Total no. of bins for the whole genome	3,000	4,500	9,000
	Total no. of molecules required for the whole genome	125 million	192 million	380 million
99%	No. of molecules required in each bin	53,000	53,000	53,000
	Total no. of bins for the whole genome	3,000	4,500	9,000
	Total no. of molecules required for the whole genome	160 million	240 million	480 million

FIG. 7

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Case no.	Gestational age at plasma collection (weeks)	Plasma sampling relative to invasive procedure	Invasive procedure	Chromosomal aberration	Methods used to confirm karyotype
01	24 1/7	Post-invasive	Cordocentesis	22q11.2 microdeletion	FISH
02	28 4/7	Post-invasive	Cordocentesis	22q11.2 microdeletion	FISH
03	22 5/7	Post-invasive	Aminocentesis	22q11.2 microdeletion	QF-PCR and FISH
04	12 3/7	Pre-invasive	Chorionic villus sampling	22q11.2 microduplication (2.4Mb)	Array CGH
05	20 2/7	Pre-invasive	Amniocentesis	22q11.2 microduplication (2.4Mb)	Array CGH
06	21 4/7	Pre-invasive	Aminocentesis	3q29 microduplication (5.1Mb); 4q32.1-q35.2 microdeletion (32.9Mb)	Array CGH

FIG. 8

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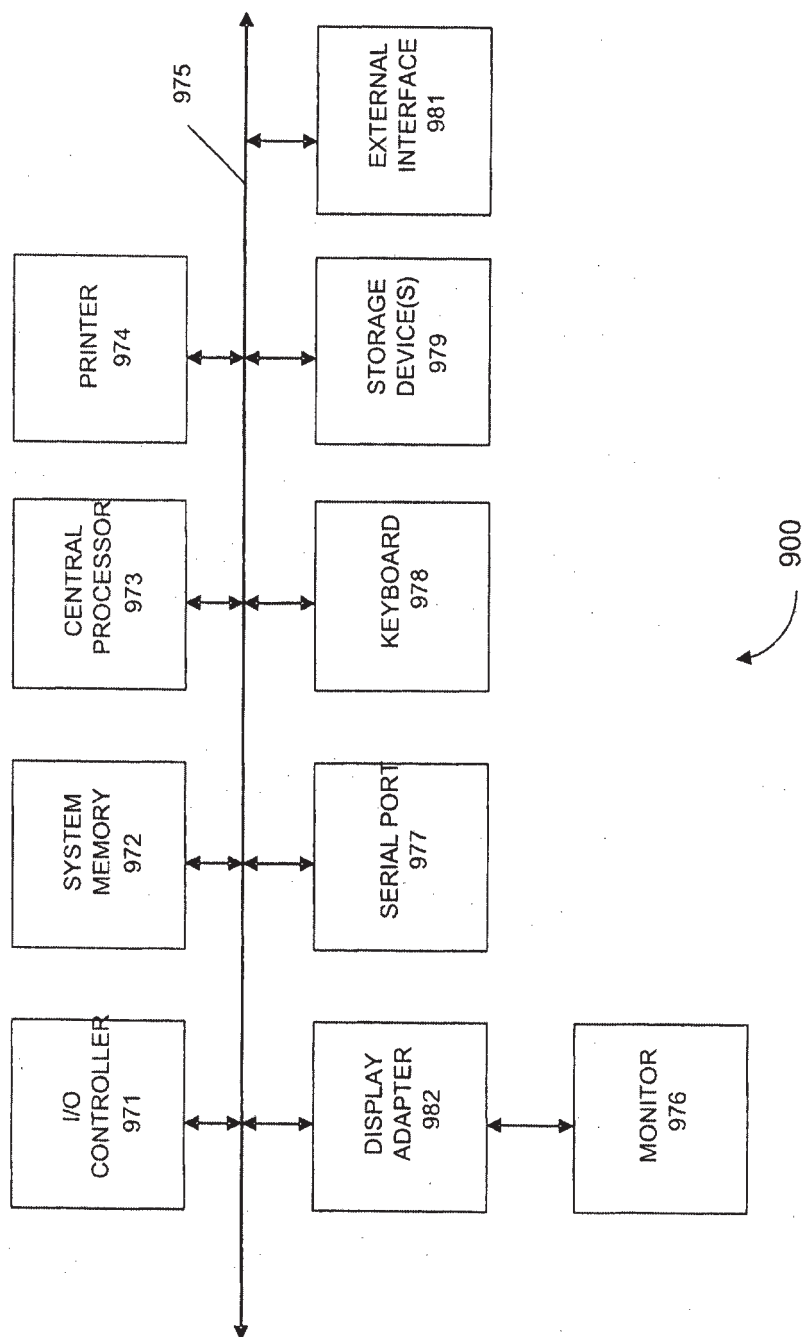


FIG. 9