Supplement 6 Test characteristics by type of test

Test characteristics – MPSS (whole genome)

Reference	**Blood sampling** (volume, time of sampling)	**Type and number of markers used**	**Sequencing platform**	**Multiplexing**	**Threshold**	**Denominator**	**GC correction / repeat masked**	**Human reference genome**	**Alignment algorithm / mismatches allowed**
Alberti 2015[56] France	10 ml / Before invasive testing	All fragments mapping to Chr21 (no markers)	Illumina HiSeq2000	NR (10 libraries prepared at the same time)	z-score > 3 for T21, used 23 euploid pregnancies as reference set.	Total count of unique sequences mapped in the control-sequencing run.	No / no	NR	SOAP2 / 0 mismatch
Bianchi 2012[47] USA	17 ml / Before invasive test	All fragments mapping to Chr13, Chr18 or Chr21 (no markers)	Illumina HiSeq 2000	6-plex	NCV > 4.0 aneuploid, NCV < 2.5 euploid, 2.5 ≤ NCV ≤ 4.0 unclassified; Used 110 independent unaffected samples	Normalizing chromosome denominators not specified	Normalising chr denominators / NR	hg18 (UCSC)	Bowtie short read aligner (version 0.12.5) / ≤ 2 mismatches
Bianchi 2014[19] USA	10 ml / Before or > 2 weeks after invasive test	All fragments mapping to Chr13, Chr18 or Chr21 (no markers)	Illumina HiSeq 2000	8-plex	NCV ≥ 4.0 affected, NCV ≤ 3.0 unaffected, 3.0 < NCV < 4.0: resequenced in 1-plex	Normalising chromosome denominators not specified	Normalising chr denominators / NR	hg18 (UCSC)	Bowtie short read aligner (version 0.12.5) / ≤ 2 mismatches
Chen 2011[48] Hong Kong,	5-10 ml / Before	All fragments mapping to Chr13 or	Genome Analyzer IIx	2-plex	z-score > 3 for T13 and T18;	Total GC-corrected read counts from a	GC correction (LOESS regression)	Hg18 NCBI.36	Short Oligonucleotide Alignment

Reference	Blood sampling (volume, time of sampling)	Type and number of markers used	Sequencing platform	Multiplexing	Threshold	Denominator	GC correction / repeat masked	Human reference genome	Alignment algorithm / mismatches allowed
Netherlands, UK, China	invasive test	Chr18 (no markers)	(Illumina)		103 independent male euploid samples as controls	sample	/ non-repeat masked		Programme 2 (SOAP2); no mismatch
Chiu 2011[49] Hong Kong, Netherlands, UK, China	5-10 ml / Before invasive test	All fragments mapping to Chr21 (no markers)	Genome Analyzer IIx (Illumina) for 2-plex; Genome Analyzer II (Illumina) for 8-plex	2-plex or 8-plex	z-score > 3 for T21; used 82 and 96 independent male euploid samples as controls for 2-plex and 8-plex, respectively	Total reads sequenced from a sample	no / repeat-masked	NCBI Build 36, version 48	ELAND, version 1.0 for Genome Analyzer II and version 1.4 for Genome Analyzer IIx / NR
Dan 2012[20] China, Hong Kong	5 ml / Before invasive test	All fragments mapping to chr18 and chr21 (no markers)	Illumina GAIIx or Illumina HiSeq 2000	4-plex or 12-plex	Binary hypothesis t-test and logarithmic LR between the two t-tests (NIFTY): t >2.5 and L >1: test positive, t >2.5 or L >1: test positive, t <2.5 and L <1: test negative.	Total number of unique reads. Then normalisation by average *k*-mer coverage of the 22 autosomes	GC correction (Losses regression) / NR	hg18, NCBI build 36	NR / 0 mismatch
Ehrich	10 ml /	All fragments aligned to	Genome Analyzer IIx	4-plex	z-score > 2.5 for T21;	All sequence reads excluding	no / non-repeat	UCSC hg19 human	CASAVA version 1.6 / up

Reference	Blood sampling (volume, time of sampling)	Type and number of markers used	Sequencing platform	Multiplexing	Threshold	Denominator	GC correction / repeat masked	Human reference genome	Alignment algorithm / mismatches allowed
2011[50] USA	Before invasive test	Chr21 (no markers)	(Illumina)	(1-plex for resequencing when foetal fraction ≤ 3.9%)	used 24 independent euploid reference samples; iterative censoring to adjust for biased control group	chr X and Y	masked	reference genome	to 1 mismatch
Huang 2014[22] China, Denmark, Hong Kong	5 ml / Before invasive test	All fragments mapping to chr18 and chr21 (no markers)	Illumina GAIIx or Illumina HiSeq 2000 (from [20])	4-plex or 12-plex (from [20])	Binary hypothesis t-test and logarithmic LR between the two t-tests (NIFTY): t >2.5 and L >1: test positive, t >2.5 or L >1: test positive (or test repeated), t <2.5 and L <1: test negative.	For k-mer coverage: Total number of unique reads. Then normalisation by average *k*-mer coverage of the 22 autosomes	GC correction (Losses regression) / NR	hg18, NCBI build 36	NR / 0 mismatch
Jeon 2014[39] South Korea, China	10 ml / Before invasive testing	All fragments mapping to Chr18 or Chr21 (no markers)	Ion Proton™ System (Life Technologies, Grand Island, NY, USA)	10-plex	z-score, all 139 euploid samples from this study used as reference group. Interactive threshold.	Mapped reads without denominator used for z-score calculation	Filtered by GC contents (35%-45%) / non-repeat masked	Unmasked Human reference genome sequence (hg19)	BWA / NR
Jiang 2012[23]	5 ml /	All fragments mapping to chr13, chr18	Illumina GAIIx and Illumina	multiplex	Binary hypothesis t-test and logarithmic LR between the two t-	For k-mer coverage: total number of	GC correction (Losses regression)	hg18, NCBI build 36	NR / 0 mismatch

Reference	Blood sampling (volume, time of sampling)	Type and number of markers used	Sequencing platform	Multiplexing	Threshold	Denominator	GC correction / repeat masked	Human reference genome	Alignment algorithm / mismatches allowed
China	NR	and chr21 (no markers)	HiSeq 2000		tests (NIFTY): $\lvert t_{i;j;first} \rvert > 3$ and $\lvert t_{i;j;second} \rvert < 3$ as warning criteria. Autosomal aneuploidy if $L_{i;j} > 1$.	unique reads. Then normalisation by average k-mer coverage for the 22 autosomes	/ NR		
Lau 2012[24] Hong Kong, China, Japan	5 ml / Before invasive test	All fragments mapping to chr13, chr18 and chr21 (no markers)	Illumina HiSeq 2000	12-plex	z-score (with internal reference chr) ≥ 3 for trisomy; used 400 independent euploid samples as reference set.	Total number of unique reads	GC correction (internal reference chromosome: Chr4 for T13, Chr8 for T18, Chr14 for T21) / repeat-masked	NCBI build 36.1	ELAND / 0 mismatch
Lau 2014[25] Hong Kong, USA, China	5 ml / Before invasive test	All fragments mapping to chr13, chr18 and chr21 (no markers)	Illumina GAIIx and Illumina HiSeq 2000 (from [23])	Multiplex (from [23])	Binary hypothesis t-test and logarithmic LR between the two t-tests (NIFTY): t >2.5 and L >1: test positive, t >2.5 or L >1: test positive (or test repeated), t <2.5 and L <1: test	For k-mer coverage: total number of unique reads. Then normalisation by average k-mer coverage for the 22 autosomes (from [23])	GC correction (Losses regression) / NR	Hg18, NCBI build 36	NR / 0 mismatch

Reference	Blood sampling (volume, time of sampling)	Type and number of markers used	Sequencing platform	Multiplexing	Threshold	Denominator	GC correction / repeat masked	Human reference genome	Alignment algorithm / mismatches allowed
					negative. Threshold t-value NR				
Liang 2013[26] China	5 ml / Before invasive test	All fragments mapping to chr13, chr18 and chr21 (no markers)	Illumina HiSeq 2000	8-plex or 12-plex	z-score > 3 for T21, z-score > 5.91 for T18, z-score > 5.72 for T13; reference set of 50 independent female euploid samples	Total count of sequences uniquely mapped to all autosomal chromosomes	GC correction (slope of simple linear regression) / non-repeat masked	Unmasked human reference genome (hg19)	SOAP2 / NR
Palomaki 2012[52] USA	20-50 ml / Before invasive test	All fragments mapping to Chr13, Chr18 or Chr21 (no markers)	Illumina HiSeq 2000	4-plex	FC-robust z-scores ≥ 3 for T21, T18 and T13. Euploid pregnancies considered to be controls for each chromosome.	Counts for all 22 autosomes (from [62])	GC correction / non-repeat masked for T13 and T18, repeat-masked for T21 test and post hoc for T13 and T18 analysis	UCSC hg19 human reference genome (from [62])	CASAVA version 1.6 / 0 mismatches (from [62])
Porreco 2014[31] USA	20-30 ml / Before invasive test	All fragments mapping to chr13, chr18, chr21, X and Y (no markers)	Illumina HiSeq 2000	12-plex	FC-robust z-score ≥ 3 for T21, Flow cell-robust z-score ≥ 3.95 for T18 and T13.	Counts for all 22 autosomes (from [64])	GC correction / repeat-masked (from [64])	UCSC hg19	Bowtie version 2 / 0 mismatch (from [64])

Reference	**Blood sampling** (volume, time of sampling)	**Type and number of markers used**	**Sequencing platform**	**Multiplexing**	**Threshold**	**Denominator**	**GC correction / repeat masked**	**Human reference genome**	**Alignment algorithm / mismatches allowed**
Sago 2014 [42] Japan	20 ml / Before invasive testing	NR (**MaterniT21 Plus, Sequenom:** All fragments mapping to chr13, chr18 and chr21 (no markers))	NR (Illumina HiSeq 2000[64])	NR (12-plex[64])	NR (Robust z-scores z > 3 for chromosome 21 and z > 3.95 for chromosomes 18 and 13[64]).	NR (Counts for all 22 autosomes (from [64]))	GC correction / repeat-masked (from [64])	NR (UCSC hg19 (from [64]))	NR / NR (Bowtie2 / Perfect matches within the seed sequence (from [64]))
Sehnert 2011[53] USA	20 ml / Before invasive test	All fragments mapping to chr13, chr18 and chr21 (no markers)	Genome Analyzer IIx (Illumina)	Monoplex	NCV > 4.0 aneuploid, NCV < 2.5 euploid, 2.5 ≤ NCV ≤ 4.0 unclassified; Used independent euploid samples from training set.	Chr9 for Chr21, Chr8 for Chr18, Sum of Chr(2-6) for Chr13.	Normalising chr denominators / NR	hg18 (UCSC)	Bowtie short read aligner (version 0.12.5) / ≤ 2 mismatches
Shaw 2014[32] Taiwan, China	5 ml / Before invasive test	All fragments mapping to chr13, chr18 and chr21 (no markers)	Illumina HiSeq 2000	12-plex	z-score > 3 for trisomy; Used 50 independent female euploid samples as reference set	Total count of sequences uniquely mapped to all autosomes (from [26])	GC correction (slope of simple linear regression[26]) / non-repeat masked	hg19	SOAP2 / NR

Reference	Blood sampling (volume, time of sampling)	Type and number of markers used	Sequencing platform	Multiplexing	Threshold	Denominator	GC correction / repeat masked	Human reference genome	Alignment algorithm / mismatches allowed
Song 2013[33] China	5 ml / Before invasive test	All fragments mapping to chr13, chr18 and chr21 (no markers)	Illumina HiSeq 2000	12-plex	z-score ≥ 3 for trisomy; Used 50 independent female euploid samples as reference set	Total count of sequences uniquely mapped to all autosomes (from [26])	GC correction (slope of simple linear regression[26]) / non-repeat masked	hg19	BWA / NR
Song 2015[45] China	NR / Before invasive testing	All fragments mapping to Chr13, Chr18 or Chr21 (no markers)	Illumina HiSeq 2000	12-plex (from [33])	z-score ≥ 3 for trisomy; Used 50 independent female euploid samples as reference set (from [33])	Total count of sequences uniquely mapped to all the autosomal chromosomes (from [26])	GC correction (slope of simple linear regression[26]) / non-repeat masked(from [33])	hg19	BWA / NR (from [33])
Stumm 2014[34] Germany, Switzerland	7-10 ml / Before invasive procedure	All fragments mapping to chr13, chr18 and chr21 (no markers)	Illumina HiSeq 2000	12-plex	MAD-based z-score ≥ 3 for T21, ≥ 3.9 for T13 and ≥ 3.2 for T18. 1%, 2%, 4%, 10%, 20% or 40% T21 DNA control samples in each FC.	Total counts of all autosomes, X and Y	DAP.21 for T21: no / repeat-masked (after unblinding DAP.plus for T13, T18 and T21 with GC correction (LOWESS))	DAP.21: hg18, DAP.plus: hg19	ELAND / 0 mismatch
Wax 2015[43] USA	NR / Before invasive testing	NR (Single commercial laboratory using MPSS)	NR	NR	NR	NR	NR / NR	NR	NR / NR

Reference	Blood sampling (volume, time of sampling)	Type and number of markers used	Sequencing platform	Multiplexing	Threshold	Denominator	GC correction / repeat masked	Human reference genome	Alignment algorithm / mismatches allowed
Zhang 2015[5] China, Hong Kong, (Denmark)	5 ml / Before invasive testing	All fragments mapping to chr13, chr18 and chr21 (no markers)	Illumina HiSeq2000	24-plex	A binary hypothesis t-test and logarithmic likelihood ratio L-score between the two t-tests (NIFTY) (from [20 23]). Threshold NR	Total number of unique reads. Then normalisation by average k-mer coverage of the 22 autosomes (from [20 23])	GC correction (Losses regression) / NR (from [20 23])	hg18, NCBI build 36	NR / 0 mismatch (from [20 23])
Zhou 2014[44] China	NR / Before invasive testing	All fragments mapping to chr13, chr18 and chr21 (no markers) (from [20])	Illumina GAIIx or Illumina HiSeq 2000 (from [20])	NR	Binary hypothesis t-test and logarithmic LR between the two t-tests (NIFTY): t >2.5 and L >1: test positive, t >2.5 or L >1: test positive, t <2.5 and L <1: test negative (from [20])	Total number of unique reads. Then normalisation by average k-mer coverage of the 22 autosomes (from [20])	GC correction (Losses regression) / NR (from [20])	hg18, NCBI build 36 (from [20])	NR / 0 mismatch (from [20])

BWA, Burrows–Wheeler Aligner; Chr, chromosome; DNA, deoxyribonucleic acid; FC, flow cell; GC, guanine cytosine; LOESS / LOWESS, locally weighted scatterplot smoothing regression; LR, likelihood ratio; MAD, median absolute deviation; MPSS, massively parallel signature sequencing; NCBI,

National Centre for Biotechnology Information; NCV, normalised chromosome value; NIFTY, Non-Invasive Fetal TrisomY test; NR, not reported; SOAP, Short Oligonucleotide Alignment Program; UCSC, University of California, Santa Cruz.

Test characteristics - DANSR (targeted sequencing)

Reference	**Blood sampling** (volume / time of sampling)	**Type and number of markers used**	**Sequencing platform**	**Multiplexing**	**Threshold**	**Denominator**	**GpC correction / repeat masked**	**Human reference genome**	**Alignment algorithm / mismatches allowed**
Ashoor 2012[46] UK	10 ml / Before invasive test	576 nonpolymorphic loci on each chr18 and chr21	Illumina HiSeq 2000	96-plex	FORTE risk score, threshold NR	Sum of mean cfDNA counts of the loci for chr18 and chr21	Median polish on log-transformed counts / NA	Expected locus sequences	NR / <3 mismatches
Bevilacqua 2015[37] Belgium, UK, Spain	20 ml / Before invasive testing	576 nonpolymorphic loci on each chr13, chr18 and chr21 (from [21 54])	Illumina HiSeq 2000 (from [21 54])	96-plex (from [21 54])	FORTE risk score (threshold NR, **Harmony™ Prenatal Test** usually uses FORTE risk score of 1% as cutoff)	Sum of mean cfDNA counts of the loci for chr13, chr18 and chr21 (from [21 54])	Median polish on log-transformed counts / NA (from [21 54])	Expected locus sequences (from [21 54])	NR / <3 mismatches (from [21 54])
Del Mar Gil 2014[21] UK	2 ml stored plasma / NR	576 nonpolymorphic loci on each chr13, chr18 and chr21	Illumina HiSeq 2000	96-plex	FORTE risk score, threshold NR	Sum of mean cfDNA counts of the loci for chr13, chr18 and chr21	Median polish on log-transformed counts /	Expected locus sequences	NR / <3 mismatches

Reference	Blood sampling (volume / time of sampling)	Type and number of markers used	Sequencing platform	Multiplexing	Threshold	Denominator	GpC correction / repeat masked	Human reference genome	Alignment algorithm / mismatches allowed
							NA		
Nicolaides 2012[27] UK	2 ml stored plasma / Before invasive test	576 nonpolymorphic loci on each chr18 and chr21	HiSeq 2000	96-plex	FORTE risk score > 1%: High risk for T18 or T21	Sum of mean cfDNA counts of the loci for chr18 and chr21	Median polish on log-transformed counts / NA	Expected locus sequences	NR / <3 mismatches
Norton 2012[29] USA, Sweden, Netherlands	20 ml / Before invasive test	576 nonpolymorphic loci on each chr18 and chr21	Illumina HiSeq 2000	96-plex	FORTE risk score > 1%: High risk for T18 or T21	Sum of mean cfDNA counts of the loci for chr18 and chr21	Median polish on log-transformed counts / NA	Expected locus sequences	NR / <3 mismatches
Norton 2015[6] USA, Sweden	NR / Before invasive testing	**Harmony™ Prenatal test:** 576 nonpolymorphic loci on each chr13, chr18 and chr21 for chromosome proportion.	Illumina HiSeq 2000 (from [54])	96-plex (from [54])	FORTE risk score > 1%: High risk for T13, T18 or T21, respectively.	Sum of mean cfDNA counts of the loci for chr13, chr18 and chr21 (from [54])	Median polish on log-transformed counts / NA (from [54])	Genome Reference Consortium human build 37	NR / <3 mismatches (from [54])
Quezada 2015[41] UK	20 ml / Before invasive testing	**Harmony™ Prenatal test**: 576 nonpolymorphic loci on each	Illumina HiSeq 2000 (from [46 54])	96-plex (from [46 54])	FORTE risk score (threshold NR, usually 1% cutoff).	Sum of mean cfDNA counts of the loci for chr13, chr18 and chr21 (from [46 54])	Median polish on log-transformed counts / NA (from [46	Expected locus sequences (from [46 54])	NR / <3 mismatches (from [46 54])

Reference	Blood sampling (volume / time of sampling)	Type and number of markers used	Sequencing platform	Multiplexing	Threshold	Denominator	GpC correction / repeat masked	Human reference genome	Alignment algorithm / mismatches allowed
		chr13, chr18 and chr21 for chromosome proportion.					54])		
Sparks 2012[54] USA	8 ml / NR	576 nonpolymorphic loci on each chr18 and chr21	Illumina HiSeq 2000	96-plex	Training set: Standard Z-test of proportions; iterative censoring on each lane of 96 samples; z-score > 3. Validation set: FORTE risk score, threshold 1:100-1:300	Sum of mean cfDNA counts of the loci for chr18 and chr21	Median polish on log-transformed counts / NA	Expected locus sequences	NR / <3 mismatches
Verweij 2013[35] Netherlands, Sweden, USA	20 ml / Before invasive test	576 nonpolymorphic loci on each chr18 and chr21	Illumina HiSeq 2000	96-plex	FORTE risk score > 1%: High risk	Sum of mean cfDNA counts of the loci for chr18 and chr21	Median polish on log-transformed counts / NA	Expected locus sequence	NR / <3 mismatches

cfDNA, cell-free deoxyribonucleic acid; Chr, chromosome; DANSR, digital analysis of selected regions; FORTE, Fetal-fraction Optimized Risk of Trisomy Evaluation; NA, not applicable; NR, not reported.

Test characteristics – Single-nucleotide polymorphism-based NIPT (with PS or NATUS algorithm)

Reference	**Blood sampling** (volume / time of sampling)	**Type and number of markers used**	**Sequencing platform**	**Multiplexing**	**Threshold**	**Paternal genetic sample**	**GpC correction / repeat masked**	**Human reference genome**	**Alignment algorithm / mismatches allowed**
Hall 2014[51] USA	NR / NR	11,000 or 19,488 SNPs on chromosomes 21, 18, 13, X, and Y	Illumina GAIIx or HiSeq sequencer	11,000-plex or 19,488-plex targeted PCR	NATUS: calls foetal genotype and foetal fraction with maximum likelihood, calculates copy number call accuracy, threshold NR	yes	NA / NR	NR	Proprietary algorithm adapted from Novoalign (Novocraft, Selangor, Malaysia) / NR (from [55])
Korostelev 2014[40] Russia	NR / Before invasive testing	>19,000 polymorphic loci covering chromosomes 21, 13, 18, X, and Y.	NR (Illumina GAIIx or HiSeq sequencer (from [55]))	NR (19,488-plex targeted PCR (from [30])	Maximum likelihood estimate generated by the NATUS algorithm combined with maternal and gestational age prior risks. Threshold NR.	NR	NA / NR	NR	NR / NR (Proprietary algorithm adapted from Novoalign (Novocraft, Selangor, Malaysia) / NR (from [55]))
Nicolaides, 2013[28] UK	20 ml / Before invasive test	19,488 SNPs on chromosomes 21, 13, 18, X, and Y	Illumina GAIIx or HiSeq sequencer (from [55])	19,488-plex targeted PCR	NATUS: calls foetal genotype and foetal fraction with maximum likelihood, calculates copy number call accuracy, threshold NR	no	NA / NR	NR	Proprietary algorithm adapted from Novoalign (Novocraft, Selangor, Malaysia) / NR (from [55])
Pergament 2014[30]	NR / 93% before invasive test,	19,488 SNPs on chromosomes 21, 13, 18, X,	Illumina GAIIx or HiSeq sequencer	19,488-plex targeted PCR	NATUS: calls foetal genotype and foetal fraction with maximum likelihood,	yes for 48.1% of samples	NA / NR	NR	Proprietary algorithm adapted from Novoalign (Novocraft,

USA	7% at least 4 days after	and Y	(from [55])		calculates copy number call accuracy, threshold NR				Selangor, Malaysia) / NR (from [55])
Zimmermann 2012[55] USA	20-40 ml / Putative euploid samples before, most aneuploidy samples after invasive test	11,000 SNPs on chromosomes 21, 18, 13, X, and Y	Illumina GAIIx or HiSeq sequencer	11,000-plex targeted PCR	PS: calls foetal genotype and foetal fraction with maximum likelihood, calculates copy number call accuracy, threshold NR	yes	NA / NR	NR	Proprietary algorithm adapted from Novoalign (Novocraft, Selangor, Malaysia) / NR

NA, not applicable; NATUS, Next-generation Aneuploidy Test Using SNPs; NIPT, non-invasive prenatal testing; NR, not reported; PCR, polymerase chain reaction; PS, Parental Support™ algorithm; SNP, single-nucleotide polymorphism.

Test characteristics – other approaches

Reference	**Blood sampling** (volume / time of sampling)	**Type and number of markers used**	**Sequencing platform**	**Multiplexing**	**Threshold**	**Paternal genetic sample**	**Denominator (reference chromosome)**	**Human reference genome**	**Alignment algorithm / mismatches allowed**
Dhallan 2007[57] USA	25-50 ml / NR	549 SNPs on chr 13; 570 SNPs on chr 21	NA (Allelic SNP ratio: PCR followed by quantification of bands on sequencing gels)	NA	Mean log ratio of foetal DNA between chr 13 and chr 21 significantly different (two-tailed Student's t-test allowing for unequal variances, significance level <0.05)	yes	Chr 13	NA	NA / NA

Chr, chromosome; DNA, deoxyribonucleic acid; NA, not applicable; NR, not reported; PCR, polymerase chain reaction; SNP, single-nucleotide polymorphism.

Test characteristics – more than one approach

Reference	**Blood sampling** (volume, time of sampling)	**Type and number of markers used**	**Sequencing platform**	**Multiplexing**	**Threshold**	**Denominator**	**GC correction / repeat masked**	**Human reference genome**	**Alignment algorithm / mismatches allowed**
Beamon 2014[36] USA	NR / Before invasive testing	NR (**Verinata** and **Sequenom** commercial tests: All fragments mapping to Chr13, Chr18 or Chr21 (no markers))	NR	NR	**Verinata**: Normalised chromosome value (NCV) >4.0 for autosomal aneuploidy and <2.5 for unaffected foetuses. NCV between 2.5 and 4.0 as "unclassified". **Sequenom:** NR (Robust z-scores, cutoff NR)	NR	NR / NR	NR	NR / NR
Comas 2014[38] Spain	≤ 20 ml / Before invasive testing **Panorama:** Paternal genetic	NR **(Harmony test:** 576 nonpolymorphic loci on each chr13, chr18 and chr21. **Panorama test:** 19,488 polymorphic loci covering chromosomes 21, 13, 18, X,	NR	NR	NR **(Harmony:** FORTE risk score (usually 1% cutoff). **Panorama:** Maximum likelihood estimate generated by the NATUS algorithm combined with maternal and gestational age prior risks.	NR (**Harmony:** Sum of mean cfDNA counts of the loci for chr13, chr18 and chr21 (from [46 54]) **Panorama:** NA)	NR / NR	NR	NR / NR

Reference	Blood sampling (volume, time of sampling)	Type and number of markers used	Sequencing platform	Multiplexing	Threshold	Denominator	GC correction / repeat masked	Human reference genome	Alignment algorithm / mismatches allowed
	sample in 51% of samples.	and Y.)			Threshold NR.)				

cfDNA, cell-free deoxyribonucleic acid; Chr, chromosome; NA, not applicable; NCV, normalised chromosome value; NR, not reported.