more cells. One recent study found a mean value of 37 fetal lymphocytes per milliliter of blood. (Huang, *Prenatal Diagnosis* 2008 28: 892-899).

[0008] Thus, there is a need for improved methods and tools for detecting fetal alleles and fetal genetic variations.

SUMMARY

[0008A] In one aspect, there is provided an *in vitro* method of obtaining and analyzing a fetal genome from a mixture of maternal and fetal cells, comprising: enriching a sample comprising a mixture of maternal and fetal cells; dividing said enriched sample into at least about 100 subsamples; performing whole genome amplification on each at least about 100 subsamples to provide an amplified product for each subsample, wherein on average each amplified product has an amplified genome from about one maternal or fetal cell; dividing each of said amplified product into aliquots, wherein each aliquot contains at least one copy of said amplified genome from said cell; screening or genotyping an aliquot for the presence of a fetal identifier, wherein said screening or genotyping comprises: screening or genotyping said aliquot for a genotype differing from a maternal genotype at at least one target locus, wherein the presence of said genotype differing from said maternal genotype indicates the presence of an informative paternal allele in said aliquot; identifying the presence of fetal cell in at least one subsample whose aliquot contains an informative paternal allele; and analyzing another aliquot from said at least one subsample identified as containing fetal cell to detect genetic variation in said genome of said fetal cell.

[0009] Examples of the present disclosure relate to methods and genotyping panels for detecting fetal alleles and fetal genetic variations. One example of the disclosure is a method of detecting a fetal identifier, comprising: obtaining a sample comprising a mixture of maternal and fetal cells; dividing the sample into subsamples; screening or genotyping a subsample for the presence of a fetal identifier; and identifying the presence of at least one fetal identifier from a fetal cell in at least one subsample.

[0010] Examples of the disclosure can and may comprise one or more of the following: a method further comprising performing subsample amplification on at least one subsample to provide an amplified product; a method further comprising dividing the amplified product into aliquots, where screening or genotyping a subsample for the presence of at least one fetal identifier comprises

WHAT IS CLAIMED IS:

1. An *in vitro* method of obtaining and analyzing a fetal genome from a mixture of maternal and fetal cells, comprising:

enriching a sample comprising a mixture of maternal and fetal cells;

dividing said enriched sample into at least about 100 subsamples;

performing whole genome amplification on each at least about 100 subsamples to provide an amplified product for each subsample, wherein on average each amplified product has an amplified genome from about one maternal or fetal cell;

dividing each of said amplified product into aliquots, wherein each aliquot contains at least one copy of said amplified genome from said cell;

screening or genotyping an aliquot for the presence of a fetal identifier, wherein said screening or genotyping comprises:

screening or genotyping said aliquot for a genotype differing from a maternal genotype at at least one target locus, wherein the presence of said genotype differing from said maternal genotype indicates the presence of an informative paternal allele in said aliquot;

identifying the presence of fetal cell in at least one subsample whose aliquot contains an informative paternal allele; and

analyzing another aliquot from said at least one subsample identified as containing fetal cell to detect genetic variation in said genome of said fetal cell.

2. The method of Claim 1, further comprising determining whether the genetic material of said maternal cells is homozygous or heterozygous at a set of target loci to determine a maternal genotype.

3. The method of Claim 2, further comprising selecting said target loci prior to determining whether the genetic material of said maternal cells is homozygous or heterozygous.

4. The method of Claim 3, further comprising selecting a test locus from said target loci, wherein said screening or genotyping comprises screening or genotyping an aliquot or subsample for a genotype differing from said maternal genotype at said test locus.

5. The method of Claim 4, wherein said selection of said test locus comprises screening a sample of mixed maternal and fetal nucleic acids for a genotype differing from said maternal genotype at a target locus, and selecting as said test locus a target locus with a non-maternal genotype in said sample of mixed maternal and fetal nucleic acids.