

CLAIMS:

1. A method of measuring chimerism in a biological sample obtained from a subject comprising two or more genetically distinct cell populations, the method comprising:
determining the level of genomic DNA in the sample isolated from a first genetically distinct cell population based on a copy number variation (CNV) polymorphism that is an informative marker of the first genetically distinct cell population,
wherein the level of isolated genomic DNA from the first genetically distinct cell population provides the measure of chimerism in the sample.
2. The method of claim 1, further comprising determining the level of genomic DNA in the sample isolated from a second genetically distinct cell population based on a CNV polymorphism that is an informative marker of the second genetically distinct cell population, wherein the levels of isolated genomic DNA from the first and second cell populations provide the measure of chimerism in the sample.
3. The method of claims 1 or 2, wherein an informative marker of a genetically distinct cell population comprises:
 - a CNV polymorphism that is homozygous deleted in genomic DNA isolated from the first cell population and homozygous non-deleted in genomic DNA isolated from the second cell population; and,
 - a CNV polymorphism that is homozygous deleted in genomic DNA isolated from the second cell population and homozygous non-deleted in genomic DNA isolated from the first cell population.
4. The method of any one of claims 1 to 3, further comprising validating the level of DNA isolated from a genetically distinct cell population by determining the level of total isolated genomic DNA in the sample,
wherein levels of genomic DNA isolated from the genetically distinct cell populations equal to the level of total DNA indicates that the levels of isolated genomic DNA are validated.
5. The method of claim 4, wherein the measure of chimerism is expressed as a ratio of genetically distinct cells in the sample (first cell population:second cell population).

6. The method of any one of claims 1 to 5, wherein the CNV polymorphism is a copy number deletion (CND) polymorphism.
7. The method of any one of claims 1 to 6, wherein determining the level of genomic DNA isolated from a genetically distinct cell population(s) comprises subjecting the DNA to an amplification reaction with primers which target an informative CNV polymorphism(s).
8. The method of claim 7, wherein the primers target an internal region of the informative CNV polymorphism(s).
9. The method of claim 8, wherein the CNV polymorphism(s) are amplified using primers selected from Table 7.
10. The method of any one of claims 1 to 9, wherein the CND polymorphisms are selected from the CND polymorphisms listed in Table 1.
11. The method of any one of claims 1 to 10, wherein the biological sample has been processed to substantially remove circulating cell free DNA from the sample.
12. The method of any one of claims 1 to 11, wherein the biological sample is a venous blood sample, a cord blood sample, a purified population of peripheral blood mononuclear cells, a purified immune cell population or purified mixture of immune cells.
13. The method of any one of claims 1 to 12 wherein the purified immune cell population or purified mixture of immune cells comprises white blood cells, T-cells, B-cells, granulocytes or a mixture thereof.
14. The method of any one of claims 1 to 13, wherein the biological sample is purified to provide at least two immune cell populations and chimerism is measured in each immune cell population.
15. The method of claim 14, wherein the two immune cell populations comprise B-cells and granulocytes.

16. The method of any one of claims 1 to 15, wherein the genetically distinct cell populations comprise self cells (first cell population) and non-self cells (second cell population).

17. The method of any one of claims 1 to 16 for use in determining the level of engraftment in a HSCT recipient.

18. The method of any one of claims 1 to 17 for use in monitoring the reestablishment of a haematopoietic stem cell transplant (HSCT) recipient's own bone marrow post HSCT transplant.

19. The method of any one of claims 1 to 12, wherein the genetically distinct cell populations comprise foetal cells (first cell population) and maternal cells (second cell population).

20. A method of measuring maternal cell contamination in a cord blood sample comprising: determining in the cord blood sample the level of self and non-self cells based on copy number variation (CNV) polymorphisms that are informative markers of the self and non-self cells,

wherein the informative markers comprise:

- CND polymorphisms that are homozygous deleted in genomic DNA isolated from self cells and heterozygous or homozygous non-deleted in genomic DNA isolated from non-self cells; and
- CND polymorphisms that are homozygous deleted in the genomic DNA isolated from non-self cells and heterozygous or homozygous non-deleted in the genomic DNA isolated from self cells;

wherein a ratio of foetal cells:maternal cells greater than about 1:100 indicates the cord blood sample is contaminated with maternal cells and not suitable for use in a haematopoietic stem cell transplant.