CLAIMS

1. A method of determining prognosis for a cancer comprising detecting the presence or absence of at least one epigenetic chromosome interaction on a chromosome which relates to one or more of the following genes: FIP1L1, PDGFRA, Flt3, ABL1, FGFR1, cKIT and Bruton tyrosine kinase~~,~~;

wherein said detecting of the presence or absence of the chromosome interaction is performed by a method comprising the steps of:

- in vitro cross-linking of chromosome region which have come together in a chromosome interaction to form cross-linked nucleic acid;

- subjecting said cross-linked acid to restriction digestion cleavage with an enzyme; and

- ligating said cross-linked cleaved nucleic acid ends to form the ligated product; and

- detection of the ligated product to thereby determine the presence or absence of the chromosome interaction;

-wherein said chromosome interaction is selected from an interaction defined by:

(i) any of the following probes which amplify the ligated product made in the process of detecting the chromosome interaction:

(a) 5'-CTTATAGCCTGTCTCTCTTGCTGATCGAGGTTGCAACGAGCTGAGATTGC-3'

(b) 5'-GGGCCAAGTGTGACTCTCAGGTTTTCGACCTGCCTCAGCCTCCCAAAGT-3'

(c) 5'-TTGAGGACAAGGACCTCGAGATACTGCCGAGAAATCC-3'

(d) 5'-TCACCCAGAATAAGGCTTCTCGATTCTAAGTTCTACAAGA-3'

(e) 5'-AAACCCCAGCAGCCCCTGCCCAAGTCGAGGGAGCAGCTCCCCACCCAGCCC-3'

(f) 5'-TATGCTTGTGGGACATCGACAAAAGCAATTATGC-3'

(g) 5'-CCTCGGCGACAGAGTGAGACTCTGTCGATCTCATTCTTTGGTTTCTGAAC-3'

(h) 5'-ACTTTACTGTGTCCCCATCACGTGTCGACAGAGTCTCACTCTGTCGCCGA-3'

(i) 5'-GAGTTCAGAAACCAAAGAATGAGATCGAGTGATTGCTAGGTGATGGACCT-3'

(j) 5'-GCTGGAGGATTGCTTGAGCTTGGGAGGTCGATCTCATTCTTTGGTTTCTGAAC-3'

(k) 5'-TCAGCAAGGACCTCGAAAAGATAAAACA-3'

(l) 5'- ATTTATTCGAAAACCCTGGGACCC-3'

or

(ii) any one of the following primer pairs which amplify the ligated product made in the process of detecting the chromosome interaction:

(m) TTCCACGTGGCCTACCACAG and CAGCTGCGAGGTTTTCTTTT

(n) TGGGAGTGGGTGGAGTGAGA and ACGGACTGACATCTTTAGCTTCC

(o) GCAGCTGCGAGGTTTTCTTT and GCCATGTGGCTTGGGCATAC

(p) AGTACTTCCTCTCCCCTCCCA and GCAGCTGCGAGGTTTTCTTTT

(q) CCTCTCCCACACAAACCTGCTA and ACATGGAGCACACATACAAGCTAC

(r) AAATGATGAGGCACGGGTGAA and CATGGAGCACACATACAAGCTAC.

~~2. A method according to claim 1 wherein said typing of the chromosome interaction is performed by a method comprising the steps of:~~

~~(i) in vitro cross-linking of chromosome regions which have come together in a chromosome interaction to form cross-linked nucleic acid;~~

~~(ii) subjecting said cross-linked acid to restriction digestion cleavage with an enzyme; and~~

~~(iii) ligating said cross-linked cleaved nucleic acid ends to form the ligated product; and~~

~~(iv) detection of the ligated product~~

~~to thereby determine the presence or absence of the chromosome interaction.~~

~~3~~2. A method according to claim ~~2~~1 wherein said ligated product comprises nucleic acid sequences of length:

- 10 to 1000 nucleotide bases,
- 10 to 800 nucleotide bases,
- 10 to 500 nucleotide bases,
- 10 to 100 nucleotide bases,
- 10 to 400 nucleotide bases,
- 10 to 500 nucleotide bases,
- 200 to 600 nucleotide bases,
- 200 to 800 nucleotide bases, or
- 200 to 1000 nucleotide bases.

~~4~~3. A method according to claim ~~2~~1 or ~~2~~3 wherein said detecting comprises specific detection of the ligated product by quantitative PCR (qPCR) which uses primers capable of amplifying the ligated product and a probe which binds the ligation site during the PCR reaction, wherein said probe comprises sequence which is complementary to sequence from each of the chromosome regions that have come together in the chromosome interaction.

~~5~~4. A method according to claim ~~4~~3 wherein said probe comprises:

an oligonucleotide which specifically binds to said ligated product, ~~and/~~or

a fluorophore covalently attached to the 5' end of the oligonucleotide, ~~and/~~or

a quencher covalently attached to the 3' end of the oligonucleotide~~, and~~ .

5. A method according to claim 4 wherein~~optionally~~ said fluorophore is selected from HEX, Texas Red and FAM.

6. A method according to ~~claim 4 or 5~~ any one of claims 3 to 5, wherein said probe comprises a nucleic acid sequence of length 10 to 40 nucleotide bases~~, preferably a length of 20 to 30 nucleotide bases~~.

7. A method according to any of the preceding claims wherein the cancer is any one of the following:

(a) idiopathic hypereosinophilic syndrome (iHES)

(b) chronic and acute eosinophilic leukemias.

(c) acute myeloid leukemia (AML)

(d) PDGFRA positive non-small cell lung carcinoma

(e) glioblastoma, including glioblastoma multiforme and astrocytoma

(f) prostate cancer

(g) advanced ovarian cancer

(h) gastrointestinal stromal tumour (GIST).

~~8. A method according to claim 4 in which there is quantitative detection of the ligated product by use a probe which is detectable upon activation during the PCR reaction,~~

~~wherein said method comprises contacting the ligated sequence with the probe during a PCR reaction, and detecting the extent of activation of the probe, and~~

~~wherein said probe binds the ligation site, and~~

~~optionally:~~

~~- the probe is as defined in claim 5 or 6, and/or~~

~~- the length of the ligated product is as defined in claim 3, and/or~~

~~- the ligation site of said ligated comprises the restriction enzyme recognition sequence of the restriction enzyme used to cut the crosslinked nucleic acid, and preferably said restriction enzyme is Taq1.~~