

CLAIMS

1. A process for determining prognosis for prostate cancer comprising detecting the presence or absence of all 6 of chromosome interactions shown in Table 6.
2. A process according to claim 1 in which the chromosome interactions are typed:
 - in a sample from an individual, and/or
 - by detecting the presence or absence of a DNA loop at the site of the chromosome interactions, and/or
 - detecting the presence or absence of distal regions of a chromosome being brought together in a chromosome conformation
3. A process according to claim 1 or 2 in which chromosome interactions are typed by detecting the presence of a ligated nucleic acid which is generated during said typing and whose sequence comprises two regions each corresponding to the regions of the chromosome which come together in the chromosome interaction.
4. A process according to any one of the preceding claims wherein said prognosis is in a human.
5. A process according to any one of the preceding claims, wherein the typing or 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.
6. A process according to claim 5 wherein said probe comprises:
 - a fluorophore covalently attached to the 5' end of the probe, and/or
 - a quencher covalently attached to the 3' end of the probe.
7. A process according to claim 6 wherein:
 - said fluorophore is selected from HEX, Texas Red and FAM; and/or
 - said probe comprises a nucleic acid sequence of length 10 to 40 nucleotide bases, preferably a length of 20 to 30 nucleotide bases.
8. A process according any one of the preceding claims wherein at least one chromosome interaction from Table 25 is typed.

9. A process according to any one of the preceding claims wherein at least one of the following combinations of interactions from Table 25 is typed:

(i) ETS1, MAP3K14, SLC22A3 and CASP2, or

(ii) BMP6, ERG, MSR1, MUC1, ACAT1 and DAPK1, or

(iii) HSD3B2, VEGFC, APAF1, MUC1, ACAT1 and DAPK1.