CLAIMS

1. A process for detecting a chromosome state which represents a disease subgroup in a population comprising determining whether a chromosome interaction relating to that chromosome state is present or absent within a defined region of the genome, wherein said disease subgroup is an amyotrophic lateral sclerosis (ALS) subgroup, and wherein at least 4 chromosome interactions are typed which are represented by any probe or primer pair shown in Table 1, 5, 10 or 11.

2. A process according to claim 1 which is carried out to diagnose ALS or to determine a prognosis for ALS.

3. A process according to claim 1 or 2 wherein a specific combination of chromosome interactions are typed

(i) comprising all of the chromosome interactions represented by the probes in Table 1 or 5; or

(ii) comprising at least 5, 6 or 7 of the chromosome interactions represented by the probes in Table 1 or 5; or

(iii) comprising all of the chromosome interactions which are represented by any probe or primer pair shown in Table 10 or 11; or

(iv) comprising at least 5, 6 or 7 of the chromosome interactions represent by the probes in Table 10.

4. A process according to any one of the preceding claims in which the chromosome interactions are typed:

- 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, and/or

- 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, wherein detection of the ligated nucleic acid is preferably by using (i) a probe that has at least 70% identity to any of the specific probe sequences mentioned in Table 1 or 5, and/or (ii) by a primer pair which has at least 70% identity to any primer pair in Table 2 or 7, and/or

- the process is carried out to select an individual for a medical treatment.

5. A process according to any one of the preceding claims wherein at least 5 to 9 different chromosome interactions are typed.

6. A process for detecting a chromosome state which represents a disease subgroup in a population comprising determining whether a chromosome interaction relating to that chromosome state is present or absent within a defined region of the genome, wherein said disease subgroup is a Huntington's disease subgroup, and, and wherein at least 4 chromosome interactions are typed which are represented by any probe shown in Table 12.

7. A process according to claim 6 which is carried out to diagnose Huntington's disease or to determine a prognosis for Huntington's disease.

8. A process according to claim 6 or 7 wherein a specific combination of chromosome interactions are typed:

(i) comprising all of the chromosome interactions represented by the probes in Table 12; or

(ii) comprising at least 5, 6 or 7 of the chromosome interactions represented by the probes in Table 12.

9. A process according to any one of claims 6 to 8 in which the chromosome interactions are typed:

- 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, and/or

- 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, wherein detection of the ligated nucleic acid is preferably by using (i) a probe that has at least 70% identity to any of the specific probe sequences mentioned in Table 12, and/or (ii) by a primer pair which has at least 70% identity to any primer pair in Table 12, and/or

- the process is carried out to select an individual for a medical treatment.

10. A process according to any one of claims 6 to 10 wherein at least 5 to 9 different chromosome interactions are typed.

11. A process according to any 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, wherein preferably 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

optionally

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.