CLAIMS

1. A process for detecting a chromosome state which represents a 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, and wherein the subgroup relates to prognosis for autism spectrum disorder (ASD) and the chromosome interaction corresponds to any one of the chromosome interactions represented by any probe shown in Table 10.

2. A process according to claim 1, which further comprises detecting the presence or absence of any one of the chromosome interactions represented by any probe shown in any one of Tables 1 to 4.

3. A process according to claim 1 or 2 wherein the presence or absence of at least 10 chromosome interactions as represented by any probe shown in:

- Table 1, or
- Table 2, or
-Table 3, or
- Table 4;

is detected.

4. A process according to any one of the preceding claims wherein the presence or absence of at least 5, 8 or 10 chromosome interactions as represented by any probe in Table 8, 9 or 10 is detected.

5. A process according to any one of the preceding claims wherein the presence or absence of at least 5, 8, 10, 15 or 20 chromosome interactions as represented by any probe in Table 10 is detected.

6. A process according to any one of the preceding claims in which the presence or absence of the chromosome interactions is detected:

- 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, 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 a probe that has at least 70% identity to any of the specific probe sequences mentioned in any of Tables 1,

2, 3 or 4, and/or (ii) by a primer pair which has at least 70% identity to any primer pair in Table 1, 2, 3 or 4.

7. A process according to any one of the preceding claims, wherein detection of the chromosome interaction(s) is by a process comprising the steps of: -

(i) cross-linking of chromosome regions which have come together in a chromosome interaction;

(ii) subjecting said cross-linked regions to cleavage, optionally by restriction digestion cleavage with an enzyme; and

(iii) ligating said cross-linked cleaved DNA ends to form ligated DNA;

detection of the of the presence or absence of the ligated DNA.

8. A process according to any one of the preceding claims which is carried out to determine the severity or type of ASD.

9. A process according to any one of the preceding claims wherein the presence or absence of at least 1, 5, 8, 10, 15 or 20 chromosome interactions is detected which are specific for mild ASD.

10. A process according to any one of the preceding claims wherein the presence or absence of at least 1, 5, 8, 10, 15 or 20 chromosome interactions are is detected which are specific for severe ASD.

11. A process according to any one of the preceding claims, wherein the 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.

12. A process according to any one of the preceding claims wherein:

- the result of the process is provided in a report, and/or
- the result of the process is used to select a patient treatment schedule, and preferably to select a specific therapy for the individual.

13. A process according to any one of the preceding claims wherein the individual has been preselected based on a physical characteristic, risk factor or symptom, and preferably based on having a symptom of, or risk factor for; autistic disorder, childhood autism, Asperger's syndrome, PDD-NOS (Pervasive Development Disorder), childhood disintegrative disorder or addiction.