**CLAIMS**

1. A process for determining prognosis for autism spectrum disorder (ASD) in an individual comprising detecting in a sample from the individual the presence or absence of 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:
- 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 or absence of a ligated DNA which is formed from the two regions of the chromosome which come together in the chromosome interaction, wherein detection of the ligated DNA 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 detecting the presence or absence 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 the cross-linked regions to cleavage, optionally by restriction digestion cleavage with an enzyme;

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

detecting the presence or absence of the ligated DNA which corresponds to the chromosome interaction(s).

8. 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.

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 are detected which are specific for severe ASD.

10. A process according to claim 6 or 7, wherein detecting the presence or absence of the chromosome interaction(s) comprises specific detection of the ligated DNA by quantitative PCR (qPCR) which uses primers capable of amplifying the ligated DNA 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.

11. 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.

12. 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.