CLAIMS

1. An oligonucleotide composition, comprising a first plurality of oligonucleotides of a particular oligonucleotide type defined by:

1) base sequence;

2) pattern of backbone linkages;

3) pattern of backbone chiral centers; and

4) pattern of backbone phosphorus modifications,

wherein at least 10% of the oligonucleotides that have the base sequence of the particular oligonucleotide type are oligonucleotides of the particular oligonucleotide type; wherein:

oligonucleotides of the particular oligonucleotide type each comprise:

1) a 5'-end region comprising 5 or more consecutive nucleoside units comprising a 2'-F modified sugar moiety and 3 or more phosphorothioate internucleotidic linkages in the *S*p configuration;

2) a 3'-end region comprising 5 or more consecutive nucleoside units comprising a 2'-F modified sugar moiety and 3 or more phosphorothioate internucleotidic linkages in the *S*p configuration; and

3) a middle region between the 5'-end region and the 3'-end region comprising 1 or more nucleotidic units comprising a phosphodiester linkage and 2 or more nucleoside units comprising a 2'-OMe modified sugar moiety; and

wherein at least 60% of phosphorothioate internucleotidic linkages of oligonucleotides of the particular oligonucleotide type are of the *S*p configuration.

2. The composition of claim 1, wherein the 5'-end region has a length of 5 or more bases and the 3'-end region has a length of 5 or more bases.

3. The composition of claim 1 or 2, wherein oligonucleotides of the particular oligonucleotide type comprise 15 or more bases.

4. The composition of any one of claims 1-3, wherein the 5'-end region comprises 5 or more phosphorothioate internucleotidic linkages in the *S*p configuration and the 3'-end region comprises 5 or more phosphorothioate internucleotidic linkages in the *S*p configuration.

5. The composition of any one of claims 1-3, wherein at least 80% of phosphorothioate internucleotidic linkages of oligonucleotides of the particular oligonucleotide type are of the *S*p configuration.

6. The composition of any one of claims 1-5, wherein oligonucleotides of the particular oligonucleotide type each further comprise one or more additional sugar modifications.

7. The composition of claim 6, wherein the additional sugar modifications comprise one or more additional modifications selected from: 2'-MOE, morpholino and bicyclic sugar moieties.

8. The composition of any one of claims 1-7, wherein the 5'-end region comprises 1 or more nucleoside units not comprising a 2'-F modified sugar moiety and/or the 3'-end region comprises 1 or more nucleoside units not comprising a 2'-F modified sugar moiety.

9. The composition of any one of claims 1-8, wherein the middle region comprises 1 or more nucleotidic units not comprising a phosphodiester linkage.

10. The composition of any one of claims 1-9, wherein 50% or more of the sugar moieties of oligonucleotides of the particular oligonucleotide type are 2’-F modified sugar moieties.

11. The composition of any one of claims 1-10, wherein each nucleotidic unit comprising a nucleoside unit of the 5 or more consecutive nucleoside units comprising a 2’-F modified sugar moiety of the 5’-end region or the 3’-end region and an internucleotidic linkage comprises a modified internucleotidic linkage, and the middle region comprises 1 or more nucleotidic units, that each independently comprises a phosphodiester linkage and a 2’−OR^1 modified sugar moiety, wherein R^1 is optionally substituted C_{1-6} alkyl.

12. The composition of any one of claims 1-11, wherein the base sequence comprises a sequence having no more than 5 mismatches from a 20 base long portion of the dystrophin gene or its complement, the length is no more than 50 bases and the oligonucleotides of the particular oligonucleotide type are capable of mediating the skipping of an exon of the dystrophin gene.

13. The composition of claim 12, wherein the oligonucleotides of the particular oligonucleotide type are capable of mediating the skipping of exon 51 of the dystrophin gene.

14. The composition of any one of claims 1-13, wherein the base sequence comprises a sequence having no more than 5 mismatches from the sequence of UCAAGGAAGAUGGCAUUUCU.

15. The composition of any one of claims 1-14, wherein the base sequence comprises the sequence of bases of UCAAGGAAGAUGGCAUUUCU.

16. The composition of any one of claims 1-15, wherein the base sequence consists of the sequence of bases of UCAAGGAAGAUGGCAUUUCU.

17. The composition of any one of claims 1-16, wherein at least 50% of the oligonucleotides that have the base sequence of the particular oligonucleotide type are oligonucleotides of the particular oligonucleotide type.

18. The composition of any one of claims 1-16, wherein at least 10% of the oligonucleotides that have the base sequence, pattern of backbone linkages, and pattern of backbone phosphorus modifications of the particular oligonucleotide type are oligonucleotides of the particular oligonucleotide type.

19. The composition of any one of claims 1-16, wherein at least 50% of the oligonucleotides that have the base sequence, pattern of backbone linkages, and pattern of backbone phosphorus modifications of the particular oligonucleotide type are oligonucleotides of the particular oligonucleotide type.

20. Use of a composition of any one of claims 1-19 for the manufacture of a medicament for the treatment of Duchenne muscular dystrophy.