WHAT IS CLAIMED IS:

1. A method for screening a plurality of L-nucleic acid aptamers for an L-nucleic acid aptamer having a binding affinity to a target molecule, comprising:

(a) contacting said plurality of L-nucleic acid aptamers with the target molecule under conditions that selectively capture target-bound L-nucleic acid aptamers from said plurality of L-nucleic acid aptamers;

(b) amplifying L-nucleic acid aptamers of said target-bound L-nucleic acid aptamers to generate amplified, double-stranded L-nucleic acid oligonucleotides; and

(c) isolating amplified double stranded L-nucleic acid oligonucleotides using an electrophoresis based method, thereby screening the plurality of L-nucleic acid aptamers.

2. The method of claim 1, further comprising converting amplified double-stranded L-nucleic oligonucleotides to single stranded oligonucleotides following step (b) and prior to step (c).

3. The method of claim 2, wherein steps (a) and (b) and said step of converting are repeated at least three times prior to said isolating in order to enrich for said target-bound L-nucleic acid aptamers.

4. The method of claim 3, further comprising monitoring enrichment of said target-bound L-nucleic acid aptamers.

5. The method of claim 4, wherein said monitoring is effected by an electrophoretic mobility shift assay (EMSA).

6. The method of any one of claims 1-4, wherein said electrophoresis based method comprises DGGE.

7. The method of any one of claims 1-6, wherein said target molecule is comprised in a cell or a tissue.

8. The method of any one of claims 1-7, wherein said amplifying utilizes a D-amino acid polymerase.

9. The method of claim 8, wherein said D-amino acid polymerase is selected from the group consisting of D-ASFV pol X, D-Taq polymerase, D-Pfu polymerase, *Sulfolobus* and *solfataricus* P2 DNA polymerase IV (DPO4), a fusion protein comprising said DPO4and a polymerase having an amino acid sequence at least 80 % identical to said DPO4.

10. The method of any one of claims 1-9, further comprising sequencing said isolated members following step (c) so as to obtain the sequence of the L-nucleic acid aptamer having a binding affinity to said target molecule.

11. The method of claim 10, wherein said sequencing is L-DNA phosphorothioate sequencing.

12. The method of claim 11, further comprising contacting said amplified double stranded L-nucleic acid oligonucleotides with a phosphatase prior to said sequencing.

13. The method of claim 10, further comprising constructing an additional aptamer library, wherein each member of said library has an identical 5’ and 3’ nucleic acid sequence and is up to 60 % randomized compared to the sequence of the isolated L-nucleic acid aptamer.

14. The method of any one of claims 1-12, further comprising synthesizing said plurality of L-nucleic acid aptamers prior to step (a).

15. The method of claim 14, wherein said synthesizing comprises error-prone PCR.

16. A kit for identifying L-nucleic acid aptamers comprising:

(i) calf intestinal phosphatase (CIP);

(ii) L-deoxyribonucleotide triphosphates (L-dNTPs) or modified L-dNTPs; and/or

(iii) a polymerase which is capable of adding one or more L-nucleotides to the 3' end of a first L-nucleic acid.

17. The kit of claim 16, wherein said polymerase comprises *Sulfolobus solfataricus* P2 DNA polymerase IV (DPO4) or a polymerase having an amino acid sequence at least 80 % identical to said DPO4.

18. A method of sequencing purified L-DNA molecules comprising:

(a) treating a sample comprising said purified L-DNA molecules with a phosphatase under conditions that remove 3'-monophosphates from said L-DNA molecules: and

(b) subjecting said sample to phosphorothioate sequencing, thereby sequencing purified L-DNA molecules.

19. An isolated thrombin-binding L-DNA aptamer comprising a sequence as set forth in SEQ ID NOs: 10, 12, 14, 16, 27 or 28 or a sequence at least 80 % identical to said SEQ ID Nos: 10, 12, 14, 16, 27 or 28.

20. The isolated thrombin-binding L-DNA aptamer comprising a sequence as set forth in SEQ ID Nos: 10, 14 or 28 or a sequence at least 80 % identical to said SEQ ID Nos: 10, 12, 14, 16, 27 or 28.