WHAT IS CLAIMED IS:

1. Use of a nucleic acid oligomer in the manufacture of a medicament for inhibiting proliferation, survival or viability of a tumor cell, wherein the nucleic acid oligomer is characterized by:

a) a backbone comprising 2'-O-alkyl modified sugar moieties and phosphorothioate internucleoside linkages;

b) (i) a purine content of at least about 50%, or (ii) a purine content of at least about 45% with a guanosine-cytosine (GC) content of at least about 50%; and

c) a length of at least 14 nucleobases and no more than 29 nucleobases,

wherein the oligomer binds to one or both of a THO complex subunit 4 (THOC4) protein and a single-stranded DNA-binding protein 1 (SSB1).

2. The use of claim 1, wherein at least about 70% of the internucleoside linkages of the backbone comprise phosphorothioate internucleoside linkages.

3. The method of claim 1 or claim 2, wherein at least about 50% of the nucleosides of the oligomer are each a 2'-O-alkyl nucleoside.

4. The use of any one of claims 1 to 3, wherein the oligomer is further characterized in that it binds to one or both of THOC4 and SSB1 with higher affinity than a control oligomer.

5. The use of any one of claims 1 to 4, wherein the oligomer is further characterized in that has a melting temperature (Tm) of at least about 45° C.

6. The use of any one of claims 1 to 5, wherein the 2'-O-alkyl nucleoside is a 2'-O-methyl nucleoside.

7. The use of any one of claims 1 to 6, wherein the nucleobase sequence over the length of the oligomer lacks substantial complementarity to the transcriptome of the tumor cell.

8. The use of claim 7, wherein no more than about 70% of the nucleobases of the oligomer are able to engage in base-pairing with the transcriptome of the tumor cell.

9. The use of claim 8, wherein the oligomer consists of 14 to 29 nucleobases and has at least 4, 5, 6, 7, 8 or 9 non-complementary nucleobases, depending on the length of the oligomer, as calculated from TABLE 1, which are unable to base-pair with a nucleobase of a reference nucleobase sequence of the transcriptome of the tumor cell.

TABLE 1

	Percentage of nucleobases or internucleoside linkages with features										
	45%	**50%**	**55%**	**60%**	**65%**	**70%**	**75%**	**80%**	**85%**	**90%**	**95%**
Oligo Length	**Calculated number of nucleobases or internucleoside linkages with features**										
14	6	7	8	8	9	10	11	11	12	13	13
15	7	8	8	9	10	11	11	12	13	14	14
16	7	8	9	10	10	11	12	13	14	14	15
17	8	9	9	10	11	12	13	14	14	15	16
18	8	9	10	11	12	13	14	14	15	16	17
19	9	10	10	11	12	13	14	15	16	17	18

	Percentage of nucleobases or internucleoside linkages with features										
	45%	**50%**	**55%**	**60%**	**65%**	**70%**	**75%**	**80%**	**85%**	**90%**	**95%**
Oligo Length	**Calculated number of nucleobases or internucleoside linkages with features**										
20	9	10	11	12	13	14	15	16	17	18	19
21	9	11	12	13	14	15	16	17	18	19	20
22	10	11	12	13	14	15	17	18	19	20	21
23	10	12	13	14	15	16	17	18	20	21	22
24	11	12	13	14	16	17	18	19	20	22	23
25	11	13	14	15	16	18	19	20	21	23	24
26	12	13	14	16	17	18	20	21	22	23	25
27	12	14	15	16	18	19	20	22	23	24	26
28	13	14	15	17	18	20	21	22	24	25	27
29	13	15	16	17	19	20	22	23	25	26	28

10. The use of any one of claims 1 to 6, wherein the nucleobase sequence over the length of the oligomer lacks substantial complementarity to the genome of a mammal from which the tumor cell is derived.

11. The use of claim 10, wherein no more than about 70% of the nucleobases of the oligomer are able to engage in base-pairing with the genome.

12. The use of claim 11, wherein the oligomer consists of 14 to 29 nucleobases and has at least 4, 5, 6, 7, 8 or 9 non-complementary nucleobases, depending on the length of the oligomer, as calculated from TABLE 1, which are unable to base-pair with a nucleobase of a reference nucleobase sequence of the genome.

13. The use of any one of claims 1 to 12, wherein the nucleobase sequence over the length of the oligomer lacks homology to the genome of a mammal from which the tumor cell is derived.

14. The use of claim 13, wherein the nucleobase sequence over the length of the oligomer has no more than about 70% sequence identity to any equal length of contiguous nucleobases defining a reference nucleobase sequence in the genome.

15. The use of claim 14, wherein the oligomer consists of 14 to 29 nucleobases and has at least 4, 5, 6, 7, 8 or 9 nucleobases, depending on the length of the oligomer, as calculated from TABLE 1, which are not identical to, or does not have the same or equivalent nucleobase-pairing ability as, a nucleobase at a matching position of the reference nucleobase sequence.

16. The use of any one of claims 1 to 6, wherein the nucleobase sequence is selected from any one of SEQ ID NO: 1, 2, 3, 5, 14, 16, 17, 31, 34, 35, 36, 38, 39, 52, 56, 67, 68, 69, 70, 71, 79, 80, 81, 82, 83, 91, 92, 93, 100, 103, 109, 110, 111, 114, 119, 131, 133, 134, 135, 143, 153, 155, 158, 159, 161, 164, 168, 169, 171, 181, 182, 203, 253, 272, 300, 301 and 303.

17. The use of any one of claims 1 to 16, wherein the tumor cell is selected from breast, prostate, ovarian, cervical, pancreatic, colorectal, lung, hepatocellular, gastric, liver, bladder, urinary tract, thyroid, renal, carcinoma, melanoma, brain, non-small cell lung, squamous cell of the head and neck, endometrial, multiple myeloma, rectal, and esophageal tumor cells.

18. The use of any one of claims 1 to 16, wherein the tumor cell is selected from prostate, lung, pancreatic, breast, ovarian or bone tumor cells.

19. The use of any one claims 1 to 19, wherein THOC4 binds the oligomer with a K_D that is at least two fold lower than the K_D for a negative control oligomer under the same conditions.

20. The use of any one of claims 1 to 19, wherein SSB1 (*e.g.*, hSSB1) binds the oligomer with a K_D that is at least two fold lower than the K_D for a negative control oligomer under the same conditions.