ANTISENSE OLIGONUCLEOTIDES

The present invention relates to antisense oligonucleotides. In particular, the present invention relates to antisense oligonucleotides capable of inducing exon skipping of RNA.

More particular, the present application relates to the field of cancer, particularly to that of cancers overexpressing glycine decarboxylase (GLDC), such as non-small cell lung carcinoma (NSCLC) and other cancers such as lymphomas (e.g. follicular lymphoma, burkitt lymphoma, Diffuse Large B cell lymphoma), glioblastoma, breast-, prostate-, lung- and colon-cancer, etc. It is shown herein that direct and selective targeting of GLDC protein abundance (e.g. by antisense oligonucleotide (ASO)-mediated exon skipping), leads to cell cycle arrest and/or apoptosis of cancer cells. Also provided is evidence that partial depletion (e.g. by antisense oligonucleotide (ASO)-mediated exon skipping) of GLDC in normal tissue has no adverse effects.

GLDC is an enzyme belonging to the family of oxidoreductases, specifically those acting on the CH-NH_2 group of donors with a disulfide as acceptor. This enzyme participates in glycine, serine and threonine metabolism. It employs pyridoxal phosphate as a cofactor. GLDC is one of four proteins that form the glycine cleavage system in all eukaryotes which catalyzes the degradation of glycine. High levels of glycine in humans or glycine build up is known to glycine encephalopathy.

The listing or discussion of an apparently prior-published document in this specification should not necessarily be taken as an acknowledgement that the document is part of the state of the art or is common general knowledge.

Any document referred to herein is hereby incorporated by reference in its entirety.

In a first aspect of the present invention, there is provided an isolated antisense oligonucleotide for modulating the activity of GLDC.

Preferably, the term modulating refers to the activation, inhibition, delay, repression or interference of one or more of; the activity of GLDC; the RNA splicing or posttranslational processing to GLDC; the phosphorylation of GLDC; the level of expression of GLDC including both mRNA and/or pre-mRNA expression and protein expression; or the sub-cellular localisation of GLDC. Preferably, in the present invention, the oligonucleotide modulates one or more of activity; or level of pre-mRNA, matured mRNA and protein expression. In various embodiments, the oligonucleotide inhibits the expression of GLDC or modify its expression products. In particular embodiments, the oligonucleotide inhibits the expression of GLDC by inducing the skipping of an exon of a GLDC pre-mRNA or mature mRNA to induce cell cycle arrest and/or apoptosis. More particularly, the oligonucleotide inhibits the expression of GLDC in a cell that expresses GLDC.

Preferably, the oligonucleotide specifically hybridises to a target region of a GLDC pre-mRNA or mature mRNA. As used herein, "hybridisation" means an interaction between two or three strands of nucleic acids by hydrogen bonds in accordance with the rules of Watson-Crick DNA complementarity, Hoogstein binding, or other sequence specific binding known in the art. Hybridisation can be performed under different stringency conditions known in the art.

More preferably, the antisense oligonucleotide of the present invention exerts a steric hindrance effect against one or more RNA-binding splicing regulators. For example, in an embodiment, the oligonucleotide prevents translation of the mRNA by steric hindrance.

Preferably, the oligonucleotide specifically hybridises to an exon, intron or exon-intron boundary target region of a GLDC RNA, the target region is any one selected from the group comprising: exon 2, exon 3, exon 6, exon 7, exon 8, exon 9, exon 10, exon 12, exon 13, exon 15, exon 16, exon 19, exon 20, exon 21, intron 6, intron 7 and intron 8. These sequences are shown in the table below.

Table : genomic sequences of target exons and introns

Target	**Sequence (5' to 3')**
Exon 2	agcattgatgaattgatcgagaagacggtccctgccaacatccgtttgaaaagacccttgaaaatggaagaccctgttt
Exon 3	gtgaaaatgaaatccttgcaactctgcatgccatttcaagcaaaaaccagatctggagatcgtatattggcatgggctattataactgctca gtgccacagacgattttgcggaacttactggagaactcaggatg

Exon 6	atatactggagtcctcactgagctgaagttaccctgtgaaatggacttcagtggaaaagatgtcagtggagtgttgttccagtacccagac acggaggggaaggtggaagactttacggaactcgtggagagagctcatcagagtggg
Exon 7	agcctggcctgctgtgctactgacctttagctttgtgcatcttgaggccacctggagaatttggggtagacatcgccctgggcagctcccag agatttggagtgccactgggctatgggggaccccatgcagcatttttttgctgtccgagaaagcttggtgagaatgatgcctggaagaatgg tgggggtaacaag
Exon 8	agatgccactgggaaagaagtgtatcgtcttgctcttcaaaccagggagcaacacattcggagagacaaggctaccagcaacatctgtac agctcag
Exon 9	gccctcttggcgaatatggctgccatgtttgcaatctaccatggttcccatgggctggagcatattgctaggagggtacataatgccactttg attttgtcagaag
Exon 10	gtctcaagcgagcagggcatcaactccagcatgacctgttctttgataccttgaagattcagtgtggctgctcagtgaaggaggtcttgggc agggccgctcagcggcagatcaattttcggctttttgaggatggcaca
Exon 12	gaactggttgctgaaagcatgggagaggagtgcagaggtattccagggtctgtgttcaagaggaccagcccgttcctcacccatcaagtg ttcaacag
Exon 13	ctaccactctgaaacaaacattgtccggtacatgaagaaactggaaaataaagacatttcccttgttcacagcatgattccactg
Exon 15	cctatcacatggaaagaatttgcaaacatccacccctttgtgcctctggatcaagctcaaggatatcagcagcttttccgagagcttgagaa ggatttgtgtgaactcacaggttatgaccaggtctgtttccagccaaacag
Exon 16	cggagcccagggagaatatgctggactggccactatccgagcctacttaaaccagaaaggagaggggcacagaacg
Exon 19	gtgggaatctgtcgccctggagacttcgggtctgatgtctcgcacctaaatcttcacaagaccttctgcattccccacggaggaggtggtcc tggcatggggcccatcggagt
Exon 20	gaagaaacatctcgccccgtttttgcccaatcatcccgtcatttcactaaagcggaatgaggatgcctgtcctgtgggaaccgtcagtgcgg ccccatggggctccagttccatcttgcccatttcctgggcttatatcaag
Exon 21	atgatgggaggcaagggtcttaaacaagccacggaaactgcgatattaaatgccaactacatggccaagcgattagaaacacactacag aattcttttcaggggtgcaagag
Intron 6	gtaggtatacctttcttgtgggggtccgtggaggcgtatcccaacttgtatctgtctacctatctctctctctgtcttttcatgtgccttaattt ctttaccattatcacatggaatggtaaaactctccttcctgactccttgctgctactttttttctgttcccggattcctggcacatggtgggcact cagtatgtatttactgaatgaatgaatgagcaatggagttcacaggatgtgaacacactctgcccgtcttcctgtagttaagataatttccta ctctcccactactctcagggaaaggtagcaaccttgttccttttctctcacttccttttctag
Intron 7	gtaaaggggctcatgtttctctacttttattgtgattatgatttccctgatttcttctgatcacaaatgttgatttctatctgaattcaactgggc catgttgagtcagttaaggaaatgtacaacatagattcagaagaacaattctgtttgggatatgagctagtacttctcaaatactataaatt tgtaaatttttgaaaaattttgtgtataatttacaatgtatcgaagtcatgtaacgcatttgcttagattgatggacgccttgaaagactaaat attttaggcatgttttgtgtctcgacagttttcgttctcaaaagcattatgccacgtggctctgtaaagacaaatgcactgagactgcaaagt acacactgagtttgctccgcgttccttcctagaggcttccgccacgtggccatttgagtaatttccaaatttccaaatgtactttcctgactgc ttctcattggtgaaacttctcagattaaaaacgtagatgttcagaagtagtctttgttccttaaaaaaaaaagaaaagaaaagaaaaaaa gggctgggtgcggtggctcacacctgtaatcccagcattctgggaggccgagtcaggcagatcacaaggtcaggagtcccagacgagcct ggccaatatggtgaaaccctgtctttactaaaaatacaaaaattaggtgggcgtggtggtgggcgcctgtagtcccagctacttgggaggc agaggcaggagaatcacttgaaccacggaggtggaggttgcagtgagccgagatcgcgctgcctcactccagtttgggtgcagagcgag actccatctcaaaaaaaaaaaagaaaaaaaaggaaaaaaaaggagcgggggacctagatgcattccaggattattactggggaaattt

	agaaaaaaaaattatgtttttgacctttgataaaagctggactttaacataagtgagtaagctgaattagtcaatgatgtgatgataatgtg aagtgtgttttttttaaaattttatttatttatttatttatttattttgagaccaagtctcactccatcacccaggctggagtgcagtggtgtaaac gtggccactgtgtccaactaatttttttaaatttttttgtaaaaacagggtttcaccatattgctcaggctggtcttagggctcaagtgatctgcc caccccagcctcccaaaatgctcggattaccaggtgtaagccaccatgcctggcctctgtatactttaaatcatcttattaacacctaatgtt atgcaatggttgttacactgtattgtttttaaaaatttgtgtgatttgtttttttttttttattttttgagacggagtctctctctgtcacccaggct ggagtgcagtggtacgatcttggctcactgcaacctctgcctcccaggttcaagtgattcttgagcctcagcctcccaagtaactgagatta caggtgcctgtcaccatgtctggctaatttttgtatttttagtagagatggggtttcaccatgttggccaggctggtctcaaactctggacctc aggtgatccgcccaccttggccccccaaagtgctgggattatagacatgagccaccatgcgcggctcataaaatttgtgtgatttttaattg ttgtattatttttttatttttttgaatgttttcagtccgtgattggtggaatctgtggtgtagaatccacagagagccaagtcttttcaattttgtcg tatatttccacttttcctgtgtctcctaagaagttcagagtgaaacttaatcctcccagtcaccattattgtatttgtctgggaaattcctgcaa aattttctttcaaaattcctagacttattgtatatatcttggtgtctcagagtacagtctaaaaatcagtaatcctgctgggcacagtggctca tgcctgtaatcccagcactttgggaggccaaggcaggcggatcacctgaggccaggagttcaagaccagcctggccaacatggtgaaac cccatctctactaaaaatacaaaaattagctgggcgtggtgtcaggaggctgatgcagtagaatcgtttgaaaccagaaggcagaggttg cagtgagccgagatcacgccattgcactccagcctgggcgaaagagcgaaactccgtctcaaaaaaaaaaaaaaaaaatcagtaatcat gtttagatgaggaacgtttagaaattgtttctttataaatttgcacccaagtgcatttgctgaattcacttcaagctgggaaggaaagaagt aattctatttatagcatctcccagtgctgtgattatctgtgctaactggatgccttattcttggtgtag
Intron 8	gtaaatcacacgtctgacctgactactgaatgccttacgatacacagaaatgagctactcattcattcattcatttgttcatttattcaccacc tcctgagcagtgagcacaccagaaatggcaagatcttattggtgtagaaggctcattgtcttatgagaaccaaaatacagtattggctggg tacggtggctcatgcctgtaatcccagcaccttgtgaggccaaggcaggcagattgctggagcccaggagttggaaacctgcctgggcga catggcgaaacaccatctctatgaaaaataaaataaaataaattagccgtcagtggtggtatgctcctgtagtcccaggtgctagggagg ctcaggtgggaggatcaccagaatctgggaggttgaggctgcagtgagccatgattatgccactgcactccagcctgagtgacagaggga gactctgtccccaactcctgcccccacaaaaaaagttaaagaaaaagacactgtgttttactggtgttctttatatgtacaccatttgcctat gctttctcttcaccatacatgttttaatactaaaaaaaataaaaagcattatttgtttcattttacccataatcacatcttcagatcctgaaca ggcaaagcgtaagaaaggacaaaaaaggccagtcttcacttttatatacagacttaaaatatatgtaaatagaaagatggatatcagggt ctctagtattcttggcgttgggccaggtttgttatgggtggcagttgagacaccctctcttaggactgagaaggagcctctccaggaatggg ttgaggaaggcaaagcaagggcatttgtgatgactgtgcttgaggggatggtggtagtcatgaggcactcttactgggagattatgactgg cattctttttttttgttttttcgagacagagttttactctgtcgcccaggctggagtgcagtggcgcaatctcagctcactgcaacctctgctgcc cggtttcaagcaattctcctgcctcagcctcctgagtaactgggattacaggcgcctgccacagcgccaggctagtttttgcatttttagtag agacggggtttcaccatcttggccaggttggtcttgaactcctgacctcatgatccacccacctcggcctcccaaagtgttgggattacaag catgagccactgcacctggccatgtctggcattctttaaaaggatgggataaaacaggaagagcttcctgggttctgaccagggttctggg ttctgctccttgaagttgctccagggcttaggtcgaagtgtttgtgaaacccagccaaaccctaggatcagttggaggcccactcctgagca caggatccattctaagtgcatctctttttttttttcttcttctttttttttcttctttgagatagagtcctgttcctgcgtcacccaggttggaatgg ggtggcgcaatcttggctcactgcaacctctgcctcctgggttcaagtgattcttgtgcctcagcctcctaaagagctggaattacaggcca ccacacccagataatttttgtatttttagtagaggcaggtttcatcatgttggccaggctggtctcaaacgcctgacctcaagtgatggtcct gcctgggcctcccaaaattttgggattgtaggtgtgagccatggcacctggcttctttttttttttttttcttgagacagattcttgctctgttgtc cattctggagtgcagtggcatggccatagctcactgcagcctcaaccttcaacctccagggctcaaattattctccggtctcagcctcctaa gtagctgggactatgggtacattccaccacgcccagctaattttcaaaaaaatgttttgtagaggcgaggtctcactttgttgctcaggttgg tctcaaattcctgagctcaagtgatcctatcttggcctcccatagtgataggattataggcatgagccaccgtgcctggccactgtaattgca

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	gttcctccaggtttccgtctgatcataagtccatttagggcctcagttttctgcctctaggttcattttccaggtgaatttgggctgtctgcagt
	gaaccagttatgttcctgtttctttctttttttttttttttgagacggagtctttctcttgttgcccaggctggagtgcaatggcgtgatgtcggctc
	actgcaacctccgtcttccgggttcaagcgatactcctgcctcagcctcctgagtagctgggattacaggcacccacgaccatgcctggcta
	atatttttttgtatttttagtagagatggggtttcaccatgctggccaggctggtctcgaactcctgacctcaggtgatccgcccgccttggcct
	cccaaagtgctgggattacaggcatgagccattgtgcccggccttatgttcctgttgcttaatttcttccagttcatgtatagctgataatttat
	tatttaacttgggttgaaaggtctgtatcttttccagcaattgttaaaatgtttgccctggagatggccatactccagcttgtctgattttcatc
	ctcttattctgatgatcttctaactcttcactgtctatttcactgcatatgtgccttttcatagttgattgcatacaagaattactcataactcca
	gtttcactctttgtgagcatgcaagtctccctgttttgttaggagatgactggtgtcttttgagttgttccttttgtgctgtaggtctttgacccccc
	gccttctgttgtagcagctgttccacattcttctcactcttgctcttctctcttgtcactggggtgggtgggggagtccactcttagtttcgcatc
	gtggatggggcatgactctttttaatctctgaaagtgtgttaatgattctttttaaataaatttttctatagggagtctctctgagcctattct
	ggctcagcaggccccattctaaaacaaaactgaaaaaacagggtgcggtggctcacacctgtaatctcaacactttaggaggccaaggc
	aggaggattacttgagttcagcagtttaaatccatcccaggcaacatagtgagactcctgtctatataaaaaaagtacaaaaattagcca
	ggtgttgtggtacacaccagtatcccagctactcagtagactgaggtggtaggagtgcttgagctggggaggtccaggctgcagtgagctg
	caatcacaccactgcactccaacctgggtgacagaatcagaccccacctctacaaaacaaaaaggaaaagaaacaatttttttctataaat
	ttgtggcattactacagatgtctgaattttcattatgttctgttctttatattctcttatttctttttttttggagacgagtctcgctccatcgccc
	aggctggagtgcagtagcgccatctcgctcactgaagctctgcctcccgggttcacgccattctcctgcctcagcctcctgtgtagctggga
	ctacaggtgtctgctaccatgcctggctaatttattgtatttttagtagatacagggtttcaccatgttagccaggatggtctcgatctcctga
	cctcatgatccacctgcctcagcctcccaaagtgctgggattacaggcgttagccaccatgcccggccatatattctcttatttcttagcttct
	accacaatgagcagctctttcattggcttttcttatttttaatataaaaatcttttaaaatagagatgggagtcttactttgttgcccaggcta
	gtattgatctccaggcctcaagcgatcctcctgcctcagcctcccaaagtgttgggatcactggtgtgagccactgcatccagccttgttggc
	ttttctaaagtcaggtgtagtaaagaataatttacactttattagctttttttattgagatgtaactcaccgtaagtttcaccaattgcaagtat
	acagctcaatggtttttactctatttacaaggttgtgcaactatcaccagtatttaatttcagaatatttttattaccccaaaaagaaattctat
	tcctatgaagtagtcactcctcatccctctcccctttcctatagcccctggcaactactattctactttctgtctccctggatttgcctgttctgaa
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	tgtacttaattcttttctatggctgggtaatatcccattgtttggacatgctacattttgtttatccattcatcaattggtaaacatttggggtgtt
	tcaaataagcctgctgtgaacacttctgtgtaaatttttgtatggatgtaatgttttcagttcttttggttatattcctagcagtgaaattgctg
	ggtcatataactctacatttaacattttgaggaacttccagacatttttcaaagtggctgcattattttactttcctaccagcagcatatgaat
	attctaatttctccgtattttcaccaatgcttgttacttcctatcctttggttatagccatcctattggatgtcaagtgataatctcactgtggttt
	tgttttgtatttccctaataactaatgattttgagcattcattagcttttgaggcttttaagtaccttaattgtattattgttatttttatttatttatt
	ttagagatggggtcttgttatgttcttcttgctggtctttaactcctgggctaaagcaatcctcccaccttagcctcccaaagtcttgggattac

	aggcgtgagccactgattcaagccctttgtatttttaagtttgttcaatttgtgaaagaaattgtcattttcttggtctctattttaatttttttgg ttcttcttttgatattctagtgccctttgaagtttttaaaaagtggttttatacttctcatcaatttgttgttcagccgtgtgatatagcctcctga ttatggaaggaatcatctgtagattaaaaagggacatgaaccaacctctacaatattgtggtggaggctgccagggcattctgtgaatgtc aggcctgggtttctgtttccagcaacacagccatgagcatttgggcacagtgtgtcacagattctttacctcagcctcgccttttccacagct gtaaagtgctgtggagtttctgtgtttatttctgattgttgtaaggagtccataagagtgtttacactttgtctaggacttttagtacaagaatg cctacttccatgttttctgatgtctctttctcctcatttacttccttgtttgctgacttcacctttggaaactgtttcttattttgcattggctccata gagacttcctctagtagtctagcagaaaaaaagatgtacctaacaaaatggacccagtattgaacatcaactgtattttgcagagacagg gttttgtattgtcaaccgggctggagtccagtggcgcaatcataggtcactgtaacctcgaaatcctgggttcaagtgatccatctcggcttc tggagtcactgggactacagttgcacaccaccccgctcccagctgaagtgcgcattgccgtttttgccagtcctttgccacagattctccatt caactcttggttggcagaagttcagcctctagtgttttatttaagttcttaggagaattttattcctgaagttcttgaatgtttgaaaattgctt gtttctttttattcttgaagaattgcctggttgagtgtaaaattctcagatctcacttttttctccctgaggtctttattgcttcactgtcttccaac attaaacattgcttctcaatgtctgatggtagtgtgatctttgcccttaagggtgacatgattttgttgcatggaagaagcccttcgtaatggt caaatgtgaaggtttagtatagtaacaactccagggtgtcttggatgatggttcctttcaggtagtcaggcaggttatatattaattgtcccc aactatcaaagaatgtaggaaatctgatcattttgttttgtcgctgtcttcagttttgacatcccaagtcaagtaattacaccctcccactaat tgtcctccatcacgtgattctttaaatgttcttatcttttag

Preferably, the antisense oligonucleotide comprises a sequence selected from any one of SEQ ID NOs: 1 to 94. SEQ ID Nos: 1 to 12 are shown in Table 1. In addition to those sequences shown in Table 1, Table 2 shows alternative sequences of shAONs (SEQ ID Nos: 13 to 94) that are also capable of inducing exon skipping in GLDC transcripts.

Table 1

SEQ ID NO.	shAON Label	shAON formula (5' to 3')
1	8a	UUG UCU CUC CGA AUG UGU UGC UCC CUG GUU
2	8b	UGU UGC UCC CUG GUU UGA AGA GCA AGA CG
3	8c	GGU AGC CUU GUC UCU CCG AAU GUG UUG C
4	8d	UCU CUC CGA AUG UGU UGC UCC CUG GUU UGA
5	13a	UGU GAA CAA GGG AAA UGU CUU UAU UUU C
6	13c	GUU UCU UCA UGU ACC GGA CAA UGU UUG UUU
7	13d	AUG UCU UUA UUU UCC AGU UUC UUC AUG UA
8	16b	UUU CUG GUU UAA GUA GGC UCG GAU AGU G
9	7a	AGG UGG CCU CAA GAU GCA CAA AGC UAA AAG G
10	7b	AUU CUC CAG GUG GCC UCA AGA UGC ACA AAG

11	7c	AAG CUA AAA GGU CAG UAG CAC AGC AGG CCA GG
12	7d	AAG GUC AGU AGC ACA GCA GGC CAG GCU

Table 2

SEQ ID NO.	
13	5' - GUU GGC AGG GAC CGU CUU CUC GAU CAA UUC AUC AAU - 3'
14	5' - UUC AAA CGG AUG UUG GCA GGG ACC GUC UUC - 3'
15	5' - GGC AUG CAG AGU UGC AAG GAU UUC AUU UUC A - 3'
16	5' - UUU UUG CUU GAA AUG GCA UGC AGA GUU GCA AGG AUU - 3'
17	5' - UCU GGU UUU UGC UUG AAA UGG CAU GCA GAG UU - 3'
18	5' - AUA UAC GAU CUC CAG AUC UGG UUU UUG CUU GA - 3'
19	5' - AGU UAU AAU AGC CCA UGC CAA UAU - 3'
20	5' - CUG UGG CAC UGA GCA GUU AUA AUA - 3'
21	5' - UCC ACU GAC AUC UUU UCC ACU GAA GUC CAU UUC ACA GGG - 3'
22	5' - GGG UAC UGG AAC AAC ACU CCA CUG ACA UCU UUU C - 3'
23	5' - CUC CGU GUC UGG GUA CUG GAA CAA CAC UCC ACU - 3'
24	5' - AGU UCC GUA AAG UCU UCC ACC UUC CCC UCC GUG UCU GGG - 3'
25	5' - UGA UGA GCU CUC UCC ACG AGU UCC GUA AAG - 3'
26	5' - AAA GCU AAA AGG UCA GUA GCA CAG CAG GCC AGG CU - 3'
27	5' - CAA GAU GCA CAA AGC UAA AAG GUC AGU AGC ACA GCA - 3'
28	5' - AGG UGG CCU CAA GAU GCA CAA AGC UAA AAG GUC - 3'
29	5' - AAU UCU CCA GGU GGC CUC AAG AUG CAC AAA GCU AA - 3'
30	5' - UCU ACC CCA AAU UCU CCA GGU GGC CUC AAG A - 3'
31	5' - AAA UCU CUG GGA GCU GCC CAG GGC GAU GUC U - 3'
32	5' - CCC CCA UAG CCC AGU GGC ACU CCA AAU CUC UG - 3'
33	5' - AAA AAU GCU GCA UGG GGU CCC CCA UAG CCC AGU - 3'
34	5' - CGG ACA GCA AAA AAU GCU GCA UGG GGU CCC C - 3'
35	5' - AGA CGA UAC ACU UCU UUC CCA GUG GCA UCU - 3'
36	5' - CUG GUU UGA AGA GCA AGA CGA UAC ACU UCU UUC - 3'
37	5' - GAA UGU GUU GCU CCC UGG UUU GAA GAG CAA GAC GA - 3'
38	5' - CUU GUC UCU CCG AAU GUG UUG CUC CCU GGU UUG A - 3'

39	5' - UGG UAG CCU UGU CUC UCC GAA UGU GUU GCU CCC U - 3'
40	5' - GAU GUU GCU GGU AGC CUU GUC UCU CCG AAU GUG UUG - 3'
41	5' - GUA CAG AUG UUG CUG GUA GCC UUG UCU CUC CGA AUG - 3'
42	5' - GAA CCA UGG UAG AUU GCA AAC AUG GCA GC - 3'
43	5' - CAA AAU CAA AGU GGC AUU AUG UAC CCU CCU AGC AA - 3'
44	5' - AUG CUG GAG UUG AUG CCC UGC UCG CUU GAG A - 3'
45	5' - CAA GGU AUC AAA GAA CAG GUC AUG CUG GAG UUG AU - 3'
46	5' - AAU CUU CAA GGU AUC AAA GAA CAG GUC AUG CUG G - 3'
47	5' - CCU CCU UCA CUG AGC AGC CAC ACU GAA UCU UCA AGG UA - 3'
48	5' - GAU CUG CCG CUG AGC GGC CCU GCC CAA GAC CUC CUU CA - 3'
49	5' - UCU UGA ACA CAG ACC CUG GAA UAC CUC UGC A - 3'
50	5' - UGA UGG GUG AGG AAC GGG CUG GUC CUC UU - 3'
51	5' - UCA UGU ACC GGA CAA UGU UUG UUU CAG AGU GGU AG - 3'
52	5' - AGU UUC UUC AUG UAC CGG ACA AUG UUU GUU UC - 3'
53	5' - UAU UUU CCA GUU UCU UCA UGU ACC GGA CAA UGU UUG - 3'
54	5' - AAG GGA AAU GUC UUU AUU UUC CAG UUU CUU CAU GUA - 3'
55	5' - GAA CAA GGG AAA UGU CUU UAU UUU CCA GUU UCU UCA - 3'
56	5' - UGU GAA CAA GGG AAA UGU CUU UAU UUU CCA GUU U - 3'
57	5' - CAG UGG AAU CAU GCU GUG AAC AAG GGA AAU GUC UUU A - 3'
58	5' - GGG GUG GAU GUU UGC AAA UUC UUU CCA UGU GAU AGG - 3'
59	5' - AAA GGG GUG GAU GUU UGC AAA UUC UUU CCA UG - 3'
60	5' - UCC AGA GGC ACA AAG GGG UGG AUG UUU GCA AA - 3'
61	5' - GCU GAU AUC CUU GAG CUU GAU CCA GAG GCA CAA AGG - 3'
62	5' - AAA GCU GCU GAU AUC CUU GAG CUU GAU CCA GAG GCA C - 3'
63	5' - AAA UCC UUC UCA AGC UCU CGG AAA AGC UGC UGA UA - 3'
64	5' - UUC ACA CAA AUC CUU CUC AAG CUC UCG GAA AAG - 3'
65	5' - UCA UAA CCU GUG AGU UCA CAC AAA UCC UUC - 3'
66	5' - GAU AGU GGC CAG UCC AGC AUA UUC UCC CUG GGC UCC G - 3'
67	5' - AGU AGG CUC GGA UAG UGG CCA GUC CAG CAU AUU CUC - 3'
68	5' - GUU UAA GUA GGC UCG GAU AGU GGC CAG UCC AGC AUA - 3'
69	5' - CUG GUU UAA GUA GGC UCG GAU AGU GGC CAG UCC A - 3'

70	5' - UCU CCU UUC UGG UUU AAG UAG GCU CGG AUA GUG - 3'
71	5' - GUU CUG UGC CCC UCU CCU UUC UGG UUU AAG UAG GCU - 3'
72	5' - CGA GAC AUC AGA CCC GAA GUC UCC AGG GCG ACA GAU U - 3'
73	5' - AGA UUU AGG UGC GAG ACA UCA GAC CCG AAG UC - 3'
74	5' - GAA GGU CUU GUG AAG AUU UAG GUG CGA GAC AUC AGA - 3'
75	5' - AUG CAG AAG GUC UUG UGA AGA UUU AGG UGC GAG - 3'
76	5' - CGU GGG GAA UGC AGA AGG UCU UGU GAA GAU UUA - 3'
77	5' - CUC CUC CGU GGG GAA UGC AGA AGG UCU UGU G - 3'
78	5' - CAU GCC AGG ACC ACC UCC UCC GUG GGG AAU GCA GAA G - 3'
79	5' - UGG GCC CCA UGC CAG GAC CAC CUC CUC CGU GGG - 3'
80	5' - GAU GAU UGG GCA AAA ACG GGG CGA GAU GUU U - 3'
81	5' - GCU UUA GUG AAA UGA CGG GAU GAU UGG GCA AAA - 3'
82	5' - AUU CCG CUU UAG UGA AAU GAC GGG AUG AUU - 3'
83	5' - AGG CAU CCU CAU UCC GCU UUA GUG AAA UG - 3'
84	5' - ACU GGA GCC CCA UGG GGC CGC ACU G - 3'
85	5' - CCG UGG CUU GUU UAA GAC CCU UGC CUC CCA UCA U - 3'
86	5' - AUC GCA GUU UCC GUG GCU UGU UUA AGA CCC UUG CC - 3'
87	5' - CAU UUA AUA UCG CAG UUU CCG UGG CUU GUU UAA G - 3'
88	5' - UGU AGU UGG CAU UUA AUA UCG CAG UUU CCG U - 3'
89	5' - UCG CUU GGC CAU GUA GUU GGC AUU UAA UAU CGC AGU - 3'
90	5' - UUC UAA UCG CUU GGC CAU GUA GUU GGC AUU UAA UAU - 3'
91	5' - UGU UUC UAA UCG CUU GGC CAU GUA GUU GGC AUU U - 3'
92	5' - UCU GUA GUG UGU UUC UAA UCG CUU GGC CAU GUA GUU - 3'
93	5' - AAA AGA AUU CUG UAG UGU GUU UCU AAU CGC UUG - 3'
94	5' - CCU GAA AAG AAU UCU GUA GUG UGU UUC UAA UC - 3'

In various embodiments of the present invention, each sequence set out in Table 1 or Table 2 may target one or more exon/intron.

By “oligonucleotide”, it is meant to refer to any polynucleotide. A "polynucleotide" is an oligomer comprised of nucleotides. A polynucleotide may be comprised of DNA, RNA

modified forms thereof, or a combination thereof. The term "nucleotide" or its plural as used herein is interchangeable with modified forms as discussed herein and otherwise known in the art. In certain instances, the art uses the term "nucleobase" which embraces naturally occurring nucleotides as well as modifications of nucleotides that can be polymerized. Thus, nucleotide or nucleobase means the naturally occurring nucleobases adenine (A), guanine (G), cytosine (C), thymine (T) and uracil (U) as well as non-naturally occurring nucleobases such as xanthine, diaminopurine, 8-oxo-N6- methyladenine, 7-deazaxanthine, 7-deazaguanine, N4,N4-ethanocytosin, N',N'-ethano-2,6- diaminopurine, 5-methylcytosine (mC), 5-(C[3]- C6)-alkynyl-cytosine, 5-fluorouracil, 5- bromouracil, pseudoisocytosine, 2-hydroxy-5-methyl-4-tr- iazolopyridin, isocytosine, isoguanine, inosine and the "non-naturally occurring" nucleobases described in Benner et ah, U. S. Pat. No. 5,432,272 and Susan M. Freier and Karl-Heinz Altmann, 1997, Nucleic Acids Research, vol. 25: pp 4429-4443. The term "nucleobase" also includes not only the known purine and pyrimidine heterocycles, but also heterocyclic analogues and tautomers thereof. Further naturally and non-naturally occurring nucleobases include those disclosed in U. S. Pat. No. 3,687,808 (Merigan, et ah), in Chapter 15 by Sanghvi, in Antisense Research and Application, Ed. S. T. Crooke and B. Lebleu, CRC Press, 1993, in Englisch et ah, 1991, Angewandte Chemie, International Edition, 30: 613-722 (see especially pages 622 and 623, and in the Concise Encyclopedia of Polymer Science and Engineering, J. I. Kroschwitz Ed., John Wiley & Sons, 1990, pages 858-859, Cook, Anti-Cancer Drug Design 1991, 6, 585-607, each of which is hereby incorporated by reference in its entirety). In various aspects, polynucleotides also include one or more "nucleosidic bases" or "base units" which include compounds such as heterocyclic compounds that can serve like nucleobases, including certain "universal bases" that are not nucleosidic bases in the most classical sense but serve as nucleosidic bases. Universal bases include 3-nitropyrrole, optionally substituted indoles {e.g., 5-nitroindole), and optionally substituted hypoxanthine. Other desirable universal bases include pyrrole, and diazole or triazole derivatives, including those universal bases known in the art.

Polynucleotides may also include modified nucleobases. A "modified base" is understood in the art to be one that can pair with a natural base {e.g., adenine, guanine, cytosine, uracil, and/or thymine) and/or can pair with a non-naturally occurring base. Exemplary modified bases are described in EP 1 072 679 and WO 97/12896, the disclosures of which are

incorporated herein by reference. Modified nucleobases include, without limitation, 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine and other alkynyl derivatives of pyrimidine bases, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8- thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5- bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7- methyladenine, 2-F-adenine, 2-amino-adenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further modified bases include tricyclic pyrimidines such as phenoxazine cytidine(lH-pyrimido[5,4-b] [l,4]benzoxazin-2(3H)- one), phenothiazine cytidine (lH-pyrimido[5,4-b] [l,4]benzothiazin-2(3H)-one), G-clamps such as a substituted phenoxazine cytidine (e.g. 9-(2-aminoethoxy)-H-pyrimido[5,4-b] [l,4]benzox- azin-2(3H)-one), carbazole cytidine (2H-pyrimido[4,5-b]indol-2-one), pyridoindole cytidine (H-pyrido[3',2':4,5]pyrrolo[2,3-d]pyrimidin-2-one). Modified bases may also include those in which the purine or pyrimidine base is replaced with other heterocycles, for example 7-deaza-adenine, 7-deazaguanosine, 2-aminopyridine and 2-pyridone. Additional nucleobases include those disclosed in U. S. Pat. No. 3,687,808, those disclosed in The Concise Encyclopedia Of Polymer Science And Engineering, pages 858-859, Kroschwitz, J. I., ed. John Wiley & Sons, 1990, those disclosed by Englisch et ah, 1991, Angewandte Chemie, International Edition, 30: 613, and those disclosed by Sanghvi, Y. S., Chapter 15, Antisense Research and Applications, pages 289- 302, Crooke, S. T. and Lebleu, B., ed., CRC Press, 1993. Certain of these bases are useful for increasing the binding affinity of the polynucleotide and include 5-substituted pyrimidines, 6- azapyrimidines and N-2, N-6 and 0-6 substituted purines, including 2-aminopropyladenine, 5- propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2.deg.C and are, in certain aspects, combined with 2'- O-methoxyethyl sugar modifications. See, U. S. Pat. Nos. 3,687,808, U. S. Pat. Nos. 4,845,205; 5,130,302; 5, 134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502, 177; 5,525,711 ; 5,552,540; 5,587,469; 5,594, 121, 5,596,091 ; 5,614,617; 5,645,985; 5,830,653; 5,763,588; 6,005,096; 5,750,692 and 5,681,941, the disclosures of which are incorporated herein by reference.

Those of skill in the art can readily design antisense polynucleotides according to the present disclosure. For example, general teachings in the art include, but are not limited to, Wee and Pramono et al, PLoS One 3:e1844 (2008); Pramono ZA et al, WO/2011/078,797; Pramono and Wee et al, Hum Gene Ther 23:781-790 (2012); Aartsma-Rus et al, Methods Mol Biol. 867: 117-29 (2012); Aartsma-Rus et al, Methods Mol Biol. 867: 97-116 (2012); van Roon-Mom et al., Methods Mol Biol. 867: 79-96 (2012), each of which is incorporated herein by reference. General guidelines also include attempting to avoid 3 consecutive G or C nucleotides, choosing lengths and sequences that do not favour formation of self-structures (hairpinning will be avoided), and avoiding those sequences likely to form primer dimers. In some embodiments, an antisense polynucleotide of the disclosure is one that is designed to specifically hybridize to an exon or an intron or an intron-exon boundary, such that the antisense polynucleotide specifically hybridises to a sequence that is completely within an exon of a PRDM15 nucleic acid, or about one nucleotide of the antisense polynucleotide spans said intron-exon boundary when the antisense polynucleotide is specifically hybridised to the PRDM15 nucleic acid. In some embodiments wherein the antisense polynucleotide specifically hybridizes to a sequence that is completely within an exon, it is contemplated that a terminus of the antisense polynucleotide is about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more nucleotides from a terminus of the exon.

In other embodiments, an antisense polynucleotide of the disclosure is one that is designed to specifically hybridize to an intron-exon boundary of a GLDC nucleic acid, such that about 2, 3, 4, 5, 6, 7, 8, 9, 10 or more nucleotides of the antisense polynucleotide span said intron-exon boundary. It is understood that a nucleotide can "span the intron-exon boundary" on either the exon side or intron side. Thus, an antisense polynucleotide that specifically and predominantly hybridises to intronic sequence and only hybridizes to one nucleotide of an adjoining exon would "span the intron-exon boundary" by one nucleotide. Similarly, an antisense polynucleotide that specifically hybridizes to exonic sequence and only hybridises to one nucleotide of an adjoining intron would "span the intron-exon boundary" by one nucleotide. In any of the aforementioned embodiments, the antisense polynucleotide is at least about 10 nucleotides and up to about 15, 20, 25, 30, 35, 40, 45, 50 or more nucleotides in length.

Preferably, the antisense oligonucleotide may comprise a modified polynucleotide backbone. The modified polynucleotide backbone may comprise a modified moiety substituted for the sugar of at least one of the polynucleotides.

Modified polynucleotides are contemplated for use wherein both one or more sugar and/or one or more internucleotide linkage of the nucleotide units in the polynucleotide is replaced with "non-naturally occurring" sugars (i.e., sugars other than ribose or deoxyribose) or internucleotide linkages, respectively. In one aspect, this embodiment contemplates a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of a polynucleotide is replaced with an amide-containing (e.g., peptide bonds between N-(2-aminoethyl)-glycine units) backbone. See, for example U. S. Patent Nos. 5,539,082; 5,714,331 ; and 5,719,262, and Nielsen et ah, Science, 1991, 254, 1497- 1500, the disclosures of which are herein incorporated by reference. Modified polynucleotides may also contain one or more substituted sugar groups. In one aspect, a modification of the sugar includes Locked Nucleic Acids (LNAs) in which the 2'- hydroxyl group is linked to the 3' or 4' carbon atom of the sugar ring, thereby forming a bicyclic sugar group. The linkage is in certain aspects a methylene (-$CH_{[2]}$-)$_{[n]}$ group bridging the 2' oxygen atom and the 4' carbon atom wherein n is 1 or 2. LNAs and preparation thereof are described in WO 98/39352 and WO 99/14226, the disclosures of which are incorporated herein by reference. In the present invention, preferably, the antisense oligonucleotide comprises a modified polynucleotide backbone. The modified polynucleotide backbone may comprise a modified moiety substituted for the sugar of at least one of the polynucleotides. The modified moiety may be selected from the group comprising of phosphorodiamidate morpholino oligomer (PMO), peptide-conjugated phosphorodiamidate morpholino oligomer (PPMO), and non-peptide dendrimeric octaguanidine moiety-tagged morpholino oligomer.

In various embodiments, the modified polynucleotide backbone comprises at least one modified internucleotide linkage. The modified internucleotide linkage comprises a modified phosphate. More preferably, the modified phosphate is any one selected from the group comprising of a non-bridging oxygen atom substituting a sulfur atom, a phosphonate, a

phosphorothioate, a phosphodiester, a phosphoromorpholidate, a phosphoropiperazidate and a phosphoroamidate.

In various embodiment of the invention, the antisense oligonucleotide comprises a backbone selected from the group comprising of ribonucleic acid, deoxyribonucleic acid, DNA phosphorothioate, RNA phosphorothioate, 2'-O-methyl-oligoribonucleotide and 2'-O-methyl-oligodeoxyribonucleotide, 2'-O-hydrocarbyl ribonucleic acid, 2´-O-hydrocarbyl DNA, 2'-O-hydrocarbyl RNA phosphorothioate, 2'-O-hydrocarbyl DNA phosphorothioate, 2'-F-phosphorothioate, 2'-F-phosphodiester, 2'-methoxyethyl phosphorothioate, 2-methoxyethyl phosphodiester, deoxy methylene(methylimino) (deoxy MMI), 2'-O-hydrocarby MMI, deoxy-methylphos-phonate, 2'-O-hydrocarbyl methylphosphonate, morpholino, 4'-thio DNA, 4'-thio RNA, peptide nucleic acid, 3'-amidate, deoxy 3'-amidate, 2'-O- hydrocarbyl 3'-amidate, locked nucleic acid, cyclohexane nucleic acid, tricycle-DNA, 2'fluoro-arabino nucleic acid, N3'-P5' phosphoroamidate, carbamate linked, phosphotriester linked, a nylon backbone modification and mixtures of the aforementioned backbones.

Preferably, the oligonucleotide is chemically linked to one or more conjugates that enhance the activity, cellular distribution, or cellular uptake of the antisense oligonucleotide.

The compounds of the disclosure also can be used as a prophylactic or therapeutic, which may be utilized for the purpose of treatment of a genetic disease. In an embodiment, the antisense oligonucleotide may be used in treating a GLDC-expressing cancer patient. The patient may be administered a further anti-cancer agent or treatment. The cancer is any one selected from the group comprising: non-small cell lung carcinoma (NSCLC), breast cancer, ovarian cancer, haematological malignancies, lung cancer, prostate cancer, stomach cancer, testis cancer, larynx cancer, liver cancer, uterus cancer, colorectal cancer, melanoma, glioblastoma, sarcomas, retinoblastoma, thyroid cancer, and glioma, carcinoid and phyllode tumours. The haematological malignancies is either lymphoma or leukaemia. In particular, the lymphoma is a B-cell lymphoma. More particularly, the B-cell lymphoma is a follicular lymphoma or a diffuse large B-cell lymphoma.

In another aspect of the present invention, there is provided a pharmaceutical composition comprising the antisense oligonucleotide according to the first aspect of the invention and a pharmaceutically acceptable carrier. The composition is suitable for parenteral administration either naked or complexed with a delivery agent to a patient. The carrier is selected from the group consisting of a nanoparticle, such as a polymeric nanoparticle; a liposome, such as pH-sensitive liposome, an antibody conjugated liposome; a viral vector, a cationic lipid, a polymer, a UsnRNA, such as U7 snRNA and a cell penetrating peptide. The antisense oligonucleotide is administered orally, or rectal, or transmucosal, or intestinal, or intramuscular, or subcutaneous, or intramedullary, or intrathecal, or direct intraventricular, or intravenous, or intravitreal, or intraperitoneal, or intranasal, or intraocular.

A pharmaceutically acceptable carrier refers, generally, to materials that are suitable for administration to a subject wherein the carrier is not biologically harmful, or otherwise, causes undesirable effects. Such carriers are typically inert ingredients of a medicament. Typically a carrier is administered to a subject along with an active ingredient without causing any undesirable biological effects or interacting in a deleterious manner with any of the other components of a pharmaceutical composition in which it is contained. Suitable pharmaceutical carriers are described in Martin, Remington's Pharmaceutical Sciences, 18th Ed., Mack Publishing Co., Easton, Pa., (1990), incorporated by reference herein in its entirety.

In a more specific form of the disclosure there are provided pharmaceutical compositions comprising therapeutically effective amounts of an antisense polynucleotide together with pharmaceutically acceptable diluents, preservatives, solubilizers, emulsifiers, adjuvants and/or carriers. Such compositions include diluents of various buffer content (e.g., phosphate, Tris-HCl, acetate), pH and ionic strength and additives such as detergents and solubilizing agents (e.g., Tween 80, Polysorbate 80), anti-oxidants (e.g., ascorbic acid, sodium metabisulfite), preservatives (e.g., Thimersol, benzyl alcohol) and bulking substances (e.g., lactose, mannitol). The material may be incorporated into particulate preparations of polymeric compounds such as, for example and without limitation, polylactic acid or polyglycolic acid, or into liposomes. Hylauronic acid may also be used. Such compositions may influence the physical state, stability, rate of in vivo release, and rate of in vivo clearance of

the disclosed compositions. The compositions may be prepared in liquid form, or may be in dried powder, such as lyophilized form.

It will be appreciated that pharmaceutical compositions provided according to the disclosure may be administered by any means known in the art. Preferably, the pharmaceutical compositions for administration are administered by injection, orally, or by the pulmonary, or nasal route. The antisense polynucleotides are, in various embodiments, delivered by intravenous, intra-arterial, intraperitoneal, intramuscular, or subcutaneous routes of administration.

The antisense molecules of the invention encompass any pharmaceutically acceptable salts, esters, or salts of such esters, or any other compound which, upon administration to an animal including a human, is capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. Accordingly, for example, the disclosure is also drawn to prodrugs and pharmaceutically acceptable salts of the compounds of the invention, pharmaceutically acceptable salts of such pro-drugs, and other bioequivalents.

The term "pharmaceutically acceptable salts" refers to physiologically and pharmaceutically acceptable salts of the compounds of the invention: i.e., salts that retain the desired biological activity of the parent compound and do not impart undesired toxicological effects thereto.

For polynucleotides, preferred examples of pharmaceutically acceptable salts include, but are not limited to, (a) salts formed with cations such as sodium, potassium, ammonium, magnesium, calcium, polyamines such as spermine and spermidine; (b) acid addition salts formed with inorganic acids, for example hydrochloric acid, hydrobromic acid, sulfuric acid, phosphoric acid, nitric acid; (c) salts formed with organic acids such as, for example, acetic acid, oxalic acid, tartaric acid, succinic acid, maleic acid, fumaric acid, gluconic acid, citric acid, malic acid, ascorbic acid, benzoic acid, tannic acid, palmitic acid, alginic acid, polyglutamic acid, naphthalenesulfonic acid, methanesulfonic acid, p-toluenesulfonic acid, naphthalenedisulfonic acid, polygalacturonic acid; and (d) salts formed from elemental anions such as chlorine, bromine, and iodine. The pharmaceutical compositions of the disclosure may be administered in a number of ways depending upon whether local or systemic treatment is

desired and upon the area to be treated. Administration may be topical (including ophthalmic and to mucous membranes including rectal delivery), pulmonary, e.g., by inhalation of powders or aerosols, (including by nebulizer, intratracheal, intranasal, epidermal and transdermal), oral or parenteral. Parenteral administration includes intravenous, intra-arterial, subcutaneous, intraperitoneal or intramuscular injection or infusion; or intracranial, e.g., intrathecal or intraventricular, administration. Polynucleotides with at least one 2'-0-methoxyethyl modification are believed to be particularly useful for oral administration.

The pharmaceutical formulations of the disclosure, which may conveniently be presented in unit dosage form, may be prepared according to conventional techniques well known in the pharmaceutical industry. Such techniques include the step of bringing into association the active ingredients with the pharmaceutical carrier(s) or excipient(s). In general the formulations are prepared by uniformly bringing into association the active ingredients with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

Combination therapy with an additional therapeutic agent is also contemplated by the disclosure. Examples of therapeutic agents that may be delivered concomitantly with a composition of the disclosure include, without limitation, a glucocorticoid steroid (for example and without limitation, prednisone and deflazacort), an angiotensin converting enzyme inhibitor, a beta adrenergic receptor blocker, an anti-fibrotic agent and a combination thereof.

In some embodiments, the present invention may be used in gene therapy such, e.g. using a vector (e.g., an expression vector) comprising a polynucleotide of the invention to direct expression of the polynucleotide in a suitable host cell. Such vectors are useful, e.g., for amplifying the polynucleotides in host cells to create useful quantities thereof, and for expressing proteins using recombinant techniques. In some embodiments, the vector is an expression vector wherein a polynucleotide of the invention is operatively linked to a polynucleotide comprising an expression control sequence.

As such, yet another aspect of the present invention provides for a method of treating cancer in a patient, the method comprising administering an antisense oligonucleotide according to the first aspect of the invention, or a pharmaceutically effective amount of a composition comprising the antisense oligonucleotide. The carrier is selected from the group consisting of a nanoparticle, such as a polymeric nanoparticle; a liposome, such as pH-sensitive liposome, an antibody conjugated liposome; a viral vector, a cationic lipid, a polymer, a UsnRNA, such as U7 snRNA and a cell penetrating peptide.

The antisense oligonucleotide or composition may be administered orally, or rectal, or transmucosal, or intestinal, or intramuscular, or subcutaneous, or intramedullary, or intrathecal, or direct intraventricular, or intravenous, or intravitreal, or intraperitoneal, or intranasal, or intraocular. Having said that, proven systemic administration options include intravenous, intraperitoneal, intranasal and intrathecal. Complexing of ASOs with delivery carriers such as nanoparticles, polymer- or liposome-based vehicles can further augment the delivery efficiency of ASOs to specific tissues.

The cancer may be any one selected from the group comprising: haematological malignancies, lung cancer, breast cancer, prostate cancer, stomach cancer, testis cancer, larynx cancer, liver cancer, uterus cancer, colorectal cancer, melanoma, glioblastoma, sarcomas, and retinoblastoma.

In an embodiment, the cancer is non-small cell lung carcinoma (NSCLC).

In yet another aspect of the present invention, there is provided the use of an antisense oligonucleotide that modulates the activity of GLDC in the manufacture of a medicament for treating cancer. The oligonucleotide modulates one or more of activity; or level of pre-mRNA, matured mRNA and protein expression. In an embodiment, the cancer is non-small cell lung carcinoma (NSCLC).

In another aspect of the present invention, there is provided a method for aiding in categorising or determining prognosis in a patient with cancer, or in selecting a therapeutic strategy for a patient with cancer, the method comprising assessing the level of GLDC nucleic

acid, protein or activity in a sample. The method comprises the step of selecting a treatment regime making use of the information on the level of GLDC nucleic acid, protein or activity in the sample. In various embodiments, the sample is obtained from the patient and the sample is a tissue sample in which cancer is suspected or in which cancer has been found, or contains cells from said tissue. If the level of GLDC nucleic acid, protein or activity in the sample is an elevated level, then the selected treatment regime comprises treating the patient with an inhibitor of GLDC activity or modulator of GLDC's pre-mRNA, mRNA and protein expression levels. In various embodiments, the inhibitor or modulator comprises an antisense oligonucleotide according to the first aspect of the present invention.

In another aspect of the present invention, there is provided a method of inducing exon-skipping of a GLDC pre-mRNA, the method comprising delivering to a cell the antisense polynucleotide according to the first aspect of the present invention, or the pharmaceutical composition comprising the antisense oligonucleotide, thereby inducing exon-skipping of the GLDC pre-mRNA.

Preferably, any one of exon 2, exon 3, exon 6, exon 7, exon 8, exon 9, exon 10, exon 12, exon 13, exon 15, exon 16, exon 19, exon 20, or exon 21 is skipped.

In various embodiments, the cell may be a human cell. The human cell is a cancer cell, the cancer is any one selected from the group comprising: NSCLC, haematological malignancies, lung cancer, breast cancer, prostate cancer, stomach cancer, testis cancer, larynx cancer, liver cancer, uterus cancer, colorectal cancer, melanoma, glioblastoma, sarcomas, and retinoblastoma.

In another aspect of the present invention, there is provided a kit comprising the antisense oligonucleotide according to the first aspect of the present, optionally in a container, and a package insert, package label, instructions or other labelling.

Advantageously, the present invention provides for an antisense oligonucleotide that induces exon skipping of GLDC mRNA, and the use of said antisense oligonucleotide for the treatment of GLDC-expressing cancers.

Those of ordinary skill in the art will appreciate that applications of the above method has wide application for identifying antisense molecules suitable for use in the treatment of many other diseases.

In order that the present invention may be fully understood and readily put into practical effect, there shall now be described by way of non-limitative examples only preferred embodiments of the present invention, the description being with reference to the accompanying illustrative figures.

In the Figures:

Figure 1 Selection of shAONs leading to efficient and specific skipping of GLDC target exon. 100 nM of shAONs targeting GLDC were transfected into A549 cells using Lipofectamin 2000. Cells were harvested 16-24 h after transfection and total RNA was extracted and reverse transcribed to cDNA. shAON efficiency in inducing the skipping of the specific target exon was determined by PCR amplification of the region covering the target exon, followed by densitometry analysis of the PCR products. shAON efficiency is presented as a percentage of the amplicons with exon skipping relative to total amplicons. 100 μg/ml of cycloheximide was added into the culturing medium 5 h after transfection to prevent protein synthesis and RNA degradation. a) Images of agarose gel electrophoresis of the PCR products demonstrating specific exon skipping. b) the calculated exon skipping efficiency induced by each shAON. c) DNA sequencing of the bands corresponds to the skipped transcript excised from agarose gel [as indicated in (a)] to confirm skipping of the specific target exon. d) The extent to which the skipped transcripts were degraded by NMD was estimated by shAON transfection under the same conditions as above but in the absence of cycloheximide. Comparison between the skipping efficiency in the two experimental conditions indicate that cycloheximide protects the skipped transcript from NMD, as there is higher proportion of skipped transcript in cycloheximide treated samples.

Figure 2 The 3 selected shAONs induce target exon skipping and inhibit GLDC protein expression at low dose. a) Dose response curves. b) Time course experiment showing the skipping efficiency at different time points up to 144 hours. c) Western blotting of GLDC protein with β-actin as loading control.

Figure 3 shAONs inhibit A549 cell growth/proliferation and tumorigenesis. a) Growth curve of A549 cells after shAON transfection at 10 nM; NC – scrambled shAON, lipo only – Lipofectamin 2000 only. b) Effect of various concentrations of shAONs on A549 cell viability at 120 h after transfection. c) Comparison of cell viability between A549, MRC5 and HLF cells at 120 hours after transfected with shAONs 7C, 7D or 8D at 10 nM. d) Soft agar assay of A549 cells transfected with shAON. The number of colonies was counted 7 days after transfection and was normalized with respect to the NC. '*' indicates that the results are significantly different ($p<0.01$, student's t test) from the scrambled AON control.

Figure 4 shAONs induced GLDC knockdown in lung tumor sphere cells inhibited cell growth/proliferation and tumorigenesis. a) Dose response curves of shAON-induced exon skipping efficiency in tumour sphere cells (measured by densitometry analysis). Cells were harvested 24 hours post-transfection. 100 μg/ml cycloheximide was added 5 h after shAON transfection to inhibit the skipped transcripts from undergoing NMD. b) Western blotting of GLDC protein (200 nM) in tumor sphere cells (72 h after transfection) with β-actin as loading control. c) shAON dose response measured using cell viability assay at 72 h after transfection. d) Growth curve of tumour spheres cells transfected with 150 nM of shAONs. e) Soft agar assay for tumor sphere cells transfected with shAON. The number of colonies was counted 7 days after transfection and was normalized with respect to NC samples. '*' indicates that the results are significantly different ($p<0.01$, student's t test) from the scrambled AON control.

Figure 5 GLDC shAONs may be effective in inducing GLDC down-regulation in other types of cancers. a) Real time PCR measurement of GLDC expression in different cell lines. b) GLDC shAONs (100 nM) induced exon skipping efficiency in MLL cell lines (with 25 μg/ml cycloheximide added 5 h after shAON transfection).

Figure 6 GLDC shAON induced exon skipping and inhibited tumour growth in human tumor xenografts grown subcutaneously in immune deficient mice. a) Dot plot comparing tumour mass from mice treated with either shAON 7D or NC (Scrambled) (7-8 mice/treatment group). Medians with error bars showing the 25th and 75th percentiles are indicated. The median mass of tumors from 7D treated mice is 60% smaller than from NC treated mice; P-values = 0.000676 (unpaired t-sample test) and 0.00391 (unpaired Wilcoxon rank sum test). b) Gel electrophoresis analysis showing exon 7 skipping induced by shAON 7D compared with NC in 20 tumour samples (12 from scrambled control group, 8 from shAON 7D group) extracted from mice. Samples with no detectable PCR products due to RNA degradation are not included in the gel photo.

Figure 7 shAON 7D was able to induce exon skipping, GLDC down regulation and TS32 cell growth inhibition in the absence of transfection agent (Lipofectamin). Comparison of shAON 7D (100 nM) induced specific exon skipping (a) and GLDC transcript down-regulation (b) with or without lipofectamin at 24 h after transfection. (c) Effect of shAON 7D on TS32 cell growth in the absence of lipofectamin at 72 hours post-transfection. In the absence of transfection agent (Lipofectamin), 100 nM concentration of shAON 7D was able to induce exon 7 skipping, GLDC downregulation, and TS32 cell growth inhibition at efficiencies of 55%, 37% and 18%, respectively. The cell growth inhibition increased to 32% when shAON 7D concentration increased to 200 nM.

The present invention relates to the steric hindrance of antisense oligonucleotides (shAONs) targeting glycine decarboxylase (GLDC) expression. In particular, such shAONs may be used as drug candidates for non-small cell lung carcinoma (NSCLC) and other cancers. The application of shAON to induce nonsense-mediated decay of GLDC mRNA has not been illustrated in previous work. Hence, the present invention may be used to develop novel chemical formulas for a group of highly efficacious (IC50 < 10 nM) drug candidates against GLDC for NSCLC and other cancers.

Example 1

Here, we have identified 12 novel shAONs (steric hindrance antisense oligonucleotides) that each degrades GLDC (glycine decarboxylase) mRNA as a therapeutic strategy for NSCLC (non-small cell lung carcinoma), Figure 1 of the attached write-up. GLDC is highly expressed in tumor initiating cells from NSCLC and promotes cellular transformation and tumorigenesis (Zhang et al. Cell 2012; Jain et al. Science 2012); catalytically inactive GLDC is unable to promote cellular transformation. The shAON is a synthetic single-stranded chemically-modified RNA molecule in which every base is modified with 2'-O-methyl linked by phosphorothioate backbones. Each shAON is designed to bind nascent GLDC mRNA complementarily at specific sites and exerts steric hindrance effects against RNA-binding splicing regulators, which are critical for exon recognition and its splicing. Mechanistically, when a shAON induces the exclusion of a specific out-of-frame exon that generates numerous downstream premature termination codons in the mature RNA, the resultant mRNA is targeted for degradation via the nonsense-mediated decay process.

We select the three most efficient shAONs for further in vitro validation on human cancer cell line and patient's primary cancer cells. In cancer cell lines, each of the shAONs induces specific exon skipping in GLDC mRNA and subsequent suppression of GLDC protein expression with IC50 < 10 nM (Figure 2), and inhibits >70% of cancer cell growth (Figure 3). In primary cancer cells, the shAONs inhibit cell growth/proliferation and tumorigenesis of lung tumor sphere cells (Figure 4). In addition, the shAONs are efficacious in downregulating GLDC in acute leukemia cell lines (Figure 5). We further select one shAON for in vivo studies in mice engrafted with lung tumor sphere cells from a NSCLC patient. When shAON is administered systematically via intraperitoneal injection to the engrafted mice, it inhibited 60% of human tumor growth (Figure 6).

The invention is described in greater detail below.

MATERIAL AND METHODS

Cell line culture

Human lung adenocarcinoma epithelial cell line A549 was maintained in DMEM media supplemented with 10% FBS, 2 mML-glutamine, and 1% penicillin-streptomycin. Normal human fetal lung fibroblast MRC-5 cells and human adult lung fibroblasts HLF cells were maintained in DMEM media supplemented with 10% FBS and 1% penicillin-streptomycin.

Tumour Sphere Culture

Tumour sphere TS32 cells were prepared as previously described (Zhang, WC; et al., 2012) and maintained in DMEM/F12 containing ITS (Sigma) and supplemented with 0.4% BSA(Sigma), 20 ng/ml EGF, 4 ng/ml basic fibroblast growth factor (bFGF) (Invitrogen), 1% Penicillin-Streptomycin (Gibco) in non- treated petri dish. Fresh medium was replenished every 3 days. Cells were split with Accutase (EMD-Millipore) to obtain single cell suspensions.

shAON design and synthesis

shAON was designed using our patented computational method and synthesized by Sigma-Aldrich Pte Ltd (Singapore) modified with 2'-O-methyl of phosphorothioate backbone (2OMePS). shAON with scrambled sequence was included in all experiments.

Cell transfection with shAONs

Growth medium without antibiotics (i.e. penicillin-streptomycin) was used as transfection medium during cell transfection for all cells/cell lines.

A549 cells were seeded at 1.0-1.5$\times 10^5$ cells/wellin 6-well plates containing 1 mL of transfection mediumand incubated for overnight.Cells reached around 40% confluence and the culture medium was reduced to 900 μLbefore transfection. 10×Transfection mixture with a fixed ratio of 1:2 of shAON (in 100 pmol) : lipofectamin 2000 (in μL) at various concentration

was prepared in Opti-MEM medium(Invitrogen) to a total volume of 100 μL, incubated for 20 minutes at room temperature, and added into the cell culture.

TS32 cells were seeded at a density of 1.0-1.5×10^5 cells/ml in 24-well plates containing 900 μL of transfection medium. 10× Transfection mixture with various amounts of shAON and a fixed amount of lipofectamin 2000 (5μL) was prepared in Opti-MEM medium to a total volume of 100μL, incubated for 20 minutes at room temperature, and added into the cell culture.To ensure reproducibility, transfection was usually done in duplicate or triplicate.

For measurement of shAON induced exon skipping efficiency, cycloheximide (Sigma) was added in the cell medium (100 μg/ml) 5 h after transfection to stop protein synthesis and RNA degradation.

Quantification of shAONs induced exon skippingefficiency and mRNA down-regulation

24 h after transfection with shAONs, cells were harvested and total RNA was extracted using Qiagen RNeasy Mini Kit, treated with DNase (AmbionTurbo DNA-Free kit) to remove contaminating DNA, and transcribed into cDNA using SuperScript™ IIIReverse Transcriptase(Invitrogen) with random hexamer according to manufacturers' instruction.

For measurement of shAON induced exon skipping efficiency, PCR reactions were performed with primers amplifying the region covering the target exon and at least 1 neighbouring exon on both sides. The PCR products were then verified by agarose gel electrophoresis and DNA sequencing to confirm skipping of the specific target exon. Exon skipping efficiency was estimated by densitometry analysis of the gel images by calculating the amount of the targeted exon skip product relative to the total products. Densitometry analysis was performed using ImageJ software (Rasband, WS, ImageJ, U.S. National Institutes of Health, Bethesda, MD, USA).

Quantitative real time-PCR (qPCR) was performed with primers in the targeted exon and outside the targeted exon to measure the amount of full length GLDC transcript using GADPH

as endogenous reference in the corresponding samples, and relative to the cells transfected with the same concentration of shAON with scrambled sequence for calculation of skipping efficiency.

Cell viability assay

Measurement of cell viability and proliferation was performed in 96 well plate (3.5×10^3cells in 100 μL medium per well) using the Thiazolyl Blue Tetrazolium Bromide (MTT) assay (Sigma) or CellTiter-Blue cell viability assay (Promega). Cells were transfected in the 96 well plate with a mixture of shAON andlipofectamin 2000. For MTT assay (used for adherent cells), medium was replaced by DMEM media (100 μL/well) with MTT (0.5 mg/ml) and incubated for 4 hours at 37°C, and then changed to 100 μL of isopropanol. Absorbance was measured using a microplate reader (Molecular Devices) at a wavelength of 570 nm with background subtraction at 630 nm, and converted to the number of live cells using a calibration curve for absorbance against live cell number. For CellTiter-Blue cell viability assay (for suspension cells), Cell-Titer Blue reagent was added (11 μL/well) and incubated for 4 hours at 37 °C.Fluorescence was measured using a microplate reader (Molecular Devices) with an excitation of 570 nm and an emission of 600 nm. To ensure reproducibility, assay was performed at least twice and transfection was done in triplicate wells in each experiment.

Soft agar assay

24 hours following shAON transfection, cells were harvested, resuspended with 0.4 % of noble agar in DMEM medium, and plated onto 96 well plate (5×10^3 cells/well) containing a solidified bottom layer (0.6 % noble agar in DMEM medium). Each well was covered with 100 μL of growth medium, and incubated under standard culture conditions for 1 week. Cells were stained with CellTiter Blue and colony counting was performed using a fluorescence microplate reader.

Western-blotting (need to double check concentration and company)

Proteins were extracted from cells using M-PER lysis buffer containing Halt protease inhibitor cocktail with gentle shaking for 10 min at 4 degree. Cell debris was removed by centrifugation at highest speed (12,000 g?) for 20 min at 4 degree and protein concentration of the supernatant was measured using BioRad protein assay according to manufacturer's instruction. 16 μg of protein from each sample was loaded in a 8% Bis-Tris SDS-PAGE gel (Bio-rad) which was prepared according manufacturer's instructions, and then transferred to a Bio-rad nitrocellulose membrane. After blocking with 5% milk in PBST for 1 hour, the membrane was incubated with polyclonal rabbit anti-human GLDC antibody (1:2000) in 3% milk/PBST at 4 degree for overnight, followed by incubation with horseradish peroxidase-conjugated anti-rabbit IgG (1:4000) in 3% milk/PBST for 3 h at room temperature. Beta-actin was used as loading control for western blotting and mouse anti-human beta-actin antibody (1:1000) and horseradish peroxidase-conjugated anti-mouse IgG (1:4000) were used as 1st and 2nd antibodies, respectively. Visualization was achieved by the ECL system using the Supersignal West Pico chemiluminescent substrate (Thermo Scientific).

Mouse xenograph experiment

NOD.Cg-Prkdcscid Il2rgtm1Wjl/SzJ mice at 4–6 weeks old were subcutaneously transplanted (500,000 cells/mouse) with single-cell suspensions of tumor spheres in serum-free medium and Matrigel (BD) (1:1). 50 mg/kg dose of shAON was injected intraperitoneally 3 times/week. Mice were sacrificed after 6 weeks of injection and tumors were extracted and weighed. After cell disruption using 0.5 mm glass beads (Sigma-Aldrich) in Micro Smash MS-100 (3 x 45 s at 4500 rpm), total RNA and proteins were extracted from tumor samples using Qiagen RNeasy Mini Kit and M-PER lysis buffer, respectively.

Results

Selection of shAONs leading to efficient and specific skipping of GLDC target exon

Out of the twenty-five exons in GLDC transcript, we selected five out-of-frame exons (exon 7, 8, 13, 15 and 16) as our target for designing shAONs. When each of them is skipped

individually, the resultant transcript will have a shifted reading frame downstream of the targeted exon and generate multiple PTCs in the skipped transcript. As a result, the target gene will be either down-regulated via a combination of nonsense-mediated degradation (NMD) pathway wherein the transcript is actively degraded or leading to the translation of a truncated and non-functional gene product. We designed twenty shAONs (4 shAONs / exon) using the computational method which we previously developed and validated. One shAON with a scrambled sequence was included in every experiment as negative control. These shAONs were synthesized with phosphorothioate backbones and 2'-O-methyl ribose modifications (2OMePS) for increased stability and sequence-specificity.

We tested the ability of the designed shAONs to induce specific exon skipping of the GLDC transcript by transfecting A549 human lung adenocarcinoma epithelial cells (Figure 1) and selected the best shAONs based on the calculated skipping efficiency in inducing GLDC target exon skipping in A549 cells 24 hour post transfection using 100 nM of shAONs. 12 out of the 20 designed shAONs were able to induce skipping of the target exon; Table 1 tabulates the formula of the 12 efficacious shAONs. Overall, shAONs targeting exon 7 and 8 were more efficient in inducing target exon skipping. Three shAONs (7D, 7C, and 8D) were selected as they were able to induce skipping of the target exon in more than 80% of the GLDC transcript.

Table 1

S/No.	shAON Label	shAON formula (5' to 3')
1	8a	UUG UCU CUC CGA AUG UGU UGC UCC CUG GUU
2	8b	UGU UGC UCC CUG GUU UGA AGA GCA AGA CG
3	8c	GGU AGC CUU GUC UCU CCG AAU GUG UUG C
4	8d	UCU CUC CGA AUG UGU UGC UCC CUG GUU UGA
5	13a	UGU GAA CAA GGG AAA UGU CUU UAU UUU C
6	13c	GUU UCU UCA UGU ACC GGA CAA UGU UUG UUU
7	13d	AUG UCU UUA UUU UCC AGU UUC UUC AUG UA
8	16b	UUU CUG GUU UAA GUA GGC UCG GAU AGU G
9	7a	AGG UGG CCU CAA GAU GCA CAA AGC UAA AAG G
10	7b	AUU CUC CAG GUG GCC UCA AGA UGC ACA AAG

11	7c	AAG CUA AAA GGU CAG UAG CAC AGC AGG CCA GG
12	7d	AAG GUC AGU AGC ACA GCA GGC CAG GCU

GLDC shAONs induced target exon skipping and inhibit GLDC protein expression at low dose

The time and dose response effect of the 3 selected shAON on inducing specific exon skipping in A549 cells was assessed by PCR followed by densitometry analysis. As shown in Figure 2a, all of the 3 shAONs could induce specific exon skipping at low dose, with IC_{50} ranging from 3.5 to 7 nM. Based on the time course experiment with 10 nM of shAONs (Figure 2b), their effect on inducing exon skipping decreased with time, but could still induce skipping in >40% of GLDC transcript at 72 hour after transfection.

We performed quantitative real-time PCR (qPCR) to measure the effect of the 3 selected shAON in down-regulating GLDC mRNA transcript in A549 cells. Compared with the cells transfected with the scrambled shAON, the qPCR analysis showed >70% down-regulation of GLDC full length transcript 24 h after transfection with 10 nM of GLDC shAONs. 72 h after transfection, each of the 3 shAONs could still induce >40% down-regulation, consistent with the result from densitometry.

Western blotting analysis was performed to examine the effect of the selected shAONs on GLDC expression at protein level (Figure 2c). Reduction of protein levels to almost complete depletion was present 72 hours after transfection with 10 or 20 nM of the selected shAONs.

GLDC shAONs inhibit A549 cell growth/proliferation and tumoregenesis

Lung cancer cells have been found to be addicted to high level of GLDC (Zhang WC, et al, ***Cell***. 2012 Jan 20;148(1-2):259-72). As the shAONs can induce effective knockdown of GLDC when transfected into cells, we therefore tested their effect on cancer cell growth and proliferation. A549 cell viability was measured using MTT assay at 0, 24, 48, 72 and 120 h after transfection with various concentrations of the selected shAONs, and compared with several negative controls including untreated cells, cells transfected with lipofectamin 2000 or the scrambled shAON. The shAON induced GLDC knockdown appeared to inhibit cell proliferation for up to

120 hours after transfection (Figure 3a and 3b). Inhibition of cell growth increased from 35% inhibition with 5 nM of shAONs to almost 100% inhibition with 30 nM of shAONs. As shown in Figure 3c, when transfected with 10 nM of shAONs, growth of two non-cancer cells, HLF and MRC-5 didn't seem to be inhibited while ~70% of cells growth was inhibited in A549 cells.

The shAON transfected A549 cells were then examined for their abilities to form colonies in soft agar, a measure of anchorage-independent growth that typically correlates with tumorigenicity. 7 days after transfection, cells treated with the three GLDC shAONs originated 70-92% less colonies in soft agar compared with cells treated with scrambled shAON, indicating shAON induced GLDC knockdown greatly inhibited cancer cell tumorigenicity.

shAONs induced GLDC knockdown in lung tumour sphere cells inhibited cell growth/proliferation and tumoregenesis

The cancer stem cells (CSCs) or tumor-initiating cells (TICs), possesses the ability to drive and sustain tumour growth and can be isolated and enriched by sphere formation when grown in *in vitro* culture. We therefore tested the effect of the GLDC shAONs in affecting growth of tumour sphere cells which are highly enriched for tumour initiating cells. As shown in Figure 4a, the GLDC shAONs can effectively induce skipping of the specific target exon in GLDC transcripts, with skipping efficiency ranging from 51 - 93%, and IC_{50} ranging from 65 nM to 220 nM (Figure 4a). At protein level as measured using western blotting, GLDC protein expression was also effectively inhibited (Figure 4b). Higher amount of shAONs were required to induce effective exon skipping and GLDC knockdown in tumour sphere cells than in A549 cells.

Compared with tumour sphere cells treated with scrambled shAON, growth/proliferation of GLDC shAON treated cells was inhibited by 57-75%, as measured using CellTiter Blue assay. Soft agar assay also showed that the numbers of colonies formed by GLDC shAONs treated cells were reduced by 61-73% of the colony number formed by scrambled shAON treated cells.

GLDC shAONs may be effective in inducing GLDC down-regulation in other types of cancers

Overexpression of GLDC was not only found in non-small cell lung cancers, but also reported in other types of cancer (Zhang WC, 2012). We evaluated GLDC expression in two MLL leukemia cell lines using qPCR, and confirmed that GLDC was overexpressed in both of them, while the non-cancer cell expressed ~600 times less GLDC (Figure 5a). We therefore tested if the GLDC shAONs can be effective in these two MLL cell lines. As shown in Figure 5b, the GLDC shAONs induced skipping of the specific exon in more than 50% of the GLDC transcript in both MLL cell lines, indicating that our designed shAONs may be also effective for other types of cancers.

GLDC shAON inhibited growth of transplanted tumour

In order to test the effect of shAON 7D in *in vivo* experiment, we transplanted the tumour sphere cells in immune deficient mice, followed by intraperitoneal injection of shAON 7D. As indicated in Figure 6, the tumours from 7D and NC treated mice weighted with medians of 0.325g and 0.820g, respectively i.e. 60% inhibition of tumor growth (P-value = 0.000676 from unpaired t-sample test or 0.00391 from unpaired Wilcoxon rank sum test). RNA analysis of 20 tumour samples (12 and eight from control and shAON 7D groups, respectively) showed that 7D treatment caused GLDC exon 7 or exons 7 and 8 (minor) skipping in all treated tumour samples, whereas almost no GLDC exon skipping was observed in NC treated tumour samples.

Whilst there has been described in the foregoing description preferred embodiments of the present invention, it will be understood by those skilled in the technology concerned that many variations or modifications in details of design or construction may be made without departing from the present invention.

Claims

1. An isolated antisense oligonucleotide for inhibiting the activity of GLDC, wherein the oligonucleotide inhibits the expression of GLDC by inducing the skipping of an exon of a GLDC pre-mRNA or mature mRNA to induce cell cycle arrest or apoptosis, the antisense oligonucleotide comprises a sequence selected from any one of SEQ ID NOs: 1 to 94.

2. The antisense oligonucleotide according to claim 1, wherein the oligonucleotide inhibits the expression of GLDC or modify its expression products.

3. The antisense oligonucleotide according to any one of the preceding claims, wherein the oligonucleotide specifically hybridises to a target region of a GLDC pre-mRNA or mature mRNA, and the antisense oligonucleotide exerts a steric hindrance effect against one or more RNA-binding splicing regulators.

4. The antisense oligonucleotide according to claim 2, wherein the oligonucleotide prevents translation of the mRNA by steric hindrance.

5. The antisense oligonucleotide according to any one of the preceding claims, wherein the oligonucleotide specifically hybridises to an exon, intron or exon-intron boundary target region of a GLDC RNA, the target region is any one selected from the group comprising: exon 2, exon 3, exon 6, exon 7, exon 8, exon 9, exon 10, exon 12, exon 13, exon 15, exon 16, exon 19, exon 20, exon 21, intron 6, intron 7 and intron 8.

6. The antisense oligonucleotide according to any one of the preceding claims, wherein the antisense oligonucleotide comprising a modified polynucleotide backbone.

7. The antisense oligonucleotide according to claim 6, wherein the modified polynucleotide backbone comprises a modified moiety substituted for the sugar of at least one of the polynucleotides.

8. The antisense oligonucleotide according to claim 7, wherein the modified moiety selected from the group consisting of phosphorodiamidate morpholino oligomer (PMO), peptide-conjugated phosphorodiamidate morpholino oligomer (PPMO), and non-peptide dendrimeric octaguanidine moiety-tagged morpholino oligomer.

9. The antisense oligonucleotide according to any one of claims 6 to 8, wherein the modified polynucleotide backbone comprises at least one modified internucleotide linkage.

10. The antisense oligonucleotide according to claim 9, wherein the modified internucleotide linkage comprises a modified phosphate.

11. The antisense oligonucleotide according to claim 10, wherein the modified phosphate is selected from the group comprising of a non-bridging oxygen atom substituting a sulfur atom, a phosphonate, a phosphorothioate, a phosphodiester, a phosphoromorpholidate, a phosphoropiperazidate and a phosphoroamidate.

12. The antisense oligonucleotide according to any one of the preceding claims, wherein the antisense oligonucleotide comprises a backbone which is selected from the group comprising of ribonucleic acid, deoxyribonucleic acid, DNA phosphorothioate, RNA phosphorothioate, 2’-O-methyl-oligoribonucleotide and 2’-O-methyl-oligodeoxyribonucleotide, 2'-O-hydrocarbyl ribonucleic acid, 2´-O-hydrocarbyl DNA, 2'-O-hydrocarbyl RNA phosphorothioate, 2'-O-hydrocarbyl DNA phosphorothioate, 2'-F-phosphorothioate, 2'-F-phosphodiester, 2'-methoxyethyl phosphorothioate, 2-methoxyethyl phosphodiester, deoxy methylene(methylimino) (deoxy MMI), 2'-O-hydrocarby MMI, deoxy-methylphos-phonate, 2'-O-hydrocarbyl methylphosphonate, morpholino, 4'-thio DNA, 4'-thio RNA, peptide nucleic acid, 3'-amidate, deoxy 3'-amidate, 2'-O- hydrocarbyl 3'-amidate, locked nucleic acid, cyclohexane nucleic acid, tricycle-DNA, 2’fluoro-arabino nucleic acid, N3’-P5’ phosphoroamidate, carbamate linked, phosphotriester linked, a nylon backbone modification and mixtures of the aforementioned backbones.

13. The antisense oligonucleotide according to any one of the preceding claims, wherein the oligonucleotide is chemically linked to one or more conjugates that enhance the activity, cellular distribution, or cellular uptake of the antisense oligonucleotide.

14. The antisense oligonucleotide according to any one of the preceding claims, wherein the oligonucleotide modulates one or more of activity; or level of pre-mRNA, matured mRNA and protein expression.

15. The antisense oligonucleotide according to any one of claims 1 to 14 for use in treating a GLDC-expressing cancer patient.

16. The antisense oligonucleotide according to claim 15, wherein the patient is administered a further anti-cancer agent or treatment.

17. The antisense oligonucleotide according to any one of claims 15 or 16 wherein the cancer is any one selected from the group comprising: non-small cell lung carcinoma (NSCLC), breast cancer, ovarian cancer, colon cancer, melanoma, testis cancer, thyroid cancer, and glioma, carcinoid and phyllode tumours.

18. A pharmaceutical composition comprising the antisense oligonucleotide according to any one of claims 1 to 17 and a pharmaceutically acceptable carrier.

19. The composition according to claim 18, wherein the composition is suitable for parenteral administration either naked or complexed with a delivery agent to a patient.

20. The composition according to claim 19, wherein the carrier is selected from the group comprising of a nanoparticle, such as a polymeric nanoparticle; a liposome, such as pH-sensitive liposome, an antibody conjugated liposome; a viral vector, a cationic lipid, a polymer, a UsnRNA, such as U7 snRNA and a cell penetrating peptide.

21. The composition according to any one of claims 18 to 20, wherein the antisense oligonucleotide is administered orally, or rectal, or transmucosal, or intestinal, or

intramuscular, or subcutaneous, or intramedullary, or intrathecal, or direct intraventricular, or intravenous, or intravitreal, or intraperitoneal, or intranasal, or intraocular.

22. Use of an antisense oligonucleotide according to any one of claims 1 to 14 in the manufacture of a medicament for treating cancer.

23. The use according to claim 22, wherein the oligonucleotide modulates one or more of activity; or level of pre-mRNA, matured mRNA and protein expression.

24. The use according to claim 23, wherein the oligonucleotide inhibits the expression of GLDC or modify its expression products.

25. The use according to any one of claims 22 to 24, wherein the cancer is non-small cell lung carcinoma (NSCLC).

26. A method for selecting a therapeutic strategy for a patient with cancer, the method comprising assessing the level of GLDC nucleic acid, protein or activity in a sample, wherein if the level of GLDC nucleic acid, protein or activity in the sample is an elevated level, then the therapeutic strategy comprises treating the patient with an inhibitor of GLDC activity, the inhibitor comprises an antisense oligonucleotide according to any one of claims 1 to 14.

27. The method according to claim 26, further comprising the step of selecting a treatment regime making use of the information on the level of GLDC nucleic acid, protein or activity in the sample.

28. The method according to any one of claims 26 or 27, wherein the sample is obtained from the patient and the sample is a tissue sample in which cancer is suspected or in which cancer has been found, or contains cells from said tissue.

29. A method of inducing exon-skipping of a GLDC pre-mRNA, the method comprising delivering to a cell the antisense oligonucleotide according to any one of claims 1 to 17, or

the composition according to any one of claim 18 to 21, thereby inducing exon-skipping of the GLDC pre-mRNA.

30. The method according to claim 29, wherein any one of exon 2, exon 3, exon 6, exon 7, exon 8, exon 9, exon 10, exon 12, exon 13, exon 15, exon 16, exon 19, exon 20, or exon 21 is skipped.

31. The method according to any one of claims 29 or 30, wherein the cell is a human cell.

32. The method according to claim 31, wherein the human cell is a cancer cell, the cancer is any one selected from the group comprising: haematological malignancies, lung cancer, breast cancer, prostate cancer, stomach cancer, testis cancer, larynx cancer, liver cancer, uterus cancer, colorectal cancer, melanoma, glioblastoma, sarcomas, and retinoblastoma.

33. A kit comprising the antisense oligonucleotide of any one of claims 1 to 17, optionally in a container, and a package insert, package label, instructions or other labelling.