

**Isonucleotide Incorporation into Middle and Terminal siRNA Duplexes
Exhibits High Gene Silencing Efficacy and Nuclease Resistance**

Electronic Supplementary Information

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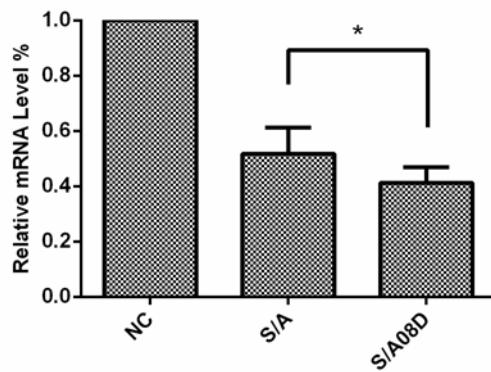


Figure S1. Quantitative PCR analysis of Braf-mu mRNA (2 nM). A375 cells were harvested for total RNA 48 h post transfection.

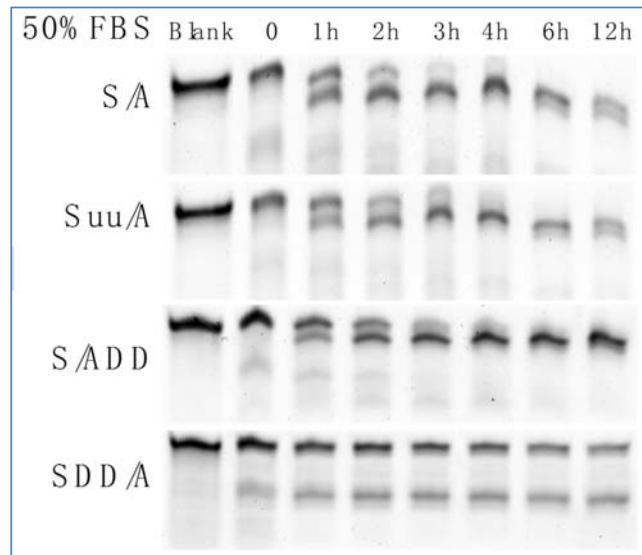


Figure S2. Serum stability of modified siRNAs at 3'-overhangs. These siRNAs were incubated in 50% fetal bovine serum at 37 °C and sampled at various time points, followed by separation on 20% PAGE gel with siRNA products visualized by SYBR Gold staining.

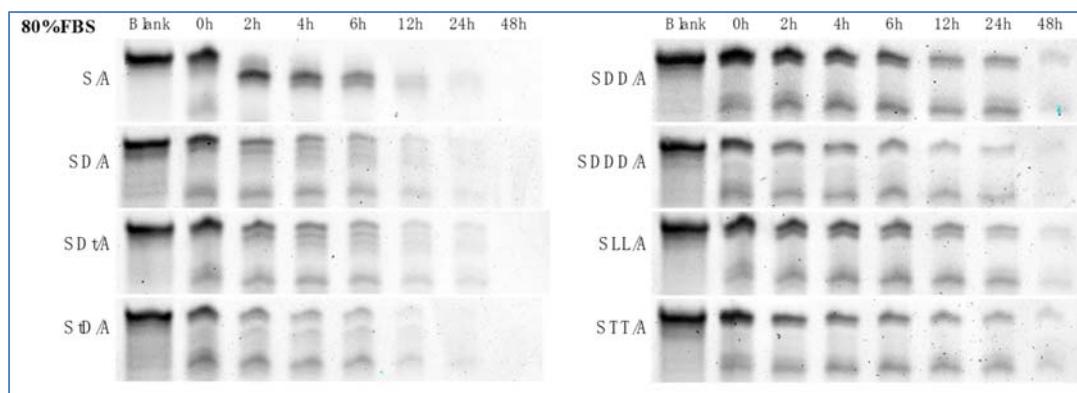


Figure S3. Serum stability of D-/L-IsoNAs modified siRNAs at 3'-overhangs of sense strand. These siRNAs were incubated in 50% fetal bovine serum at 37 °C and sampled at various time points, followed by separation on 20% PAGE gel with siRNA products visualized by SYBR Gold staining.

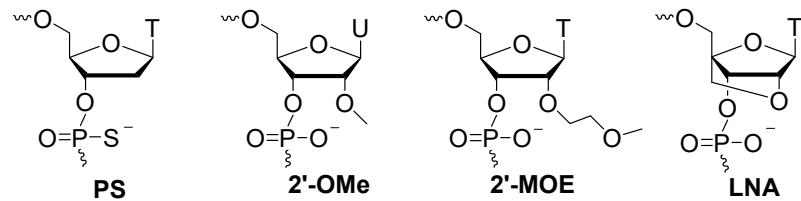


Figure S4. The selected structures of chemical modification used in siRNAs 3'-overhangs

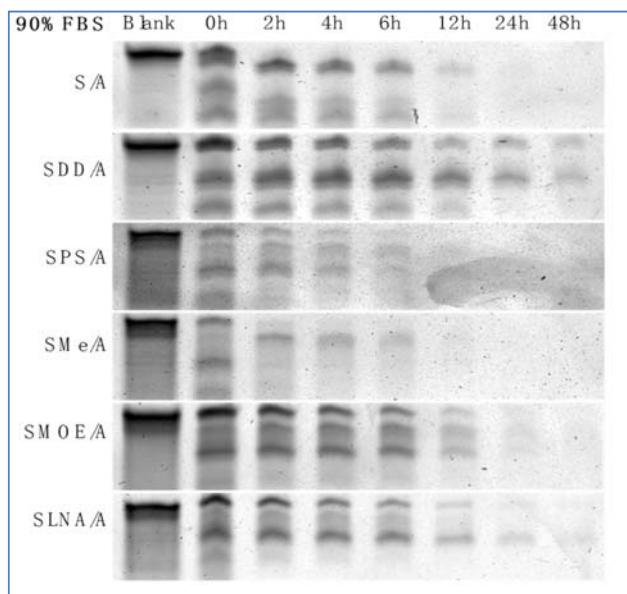


Figure S5. Serum stability of chemical modified siRNAs at 3'-overhangs of sense strand. These siRNAs were incubated in 50% fetal bovine serum at 37 °C and sampled at various time points, followed by separation on 20% PAGE gel with siRNA products visualized by SYBR Gold staining.

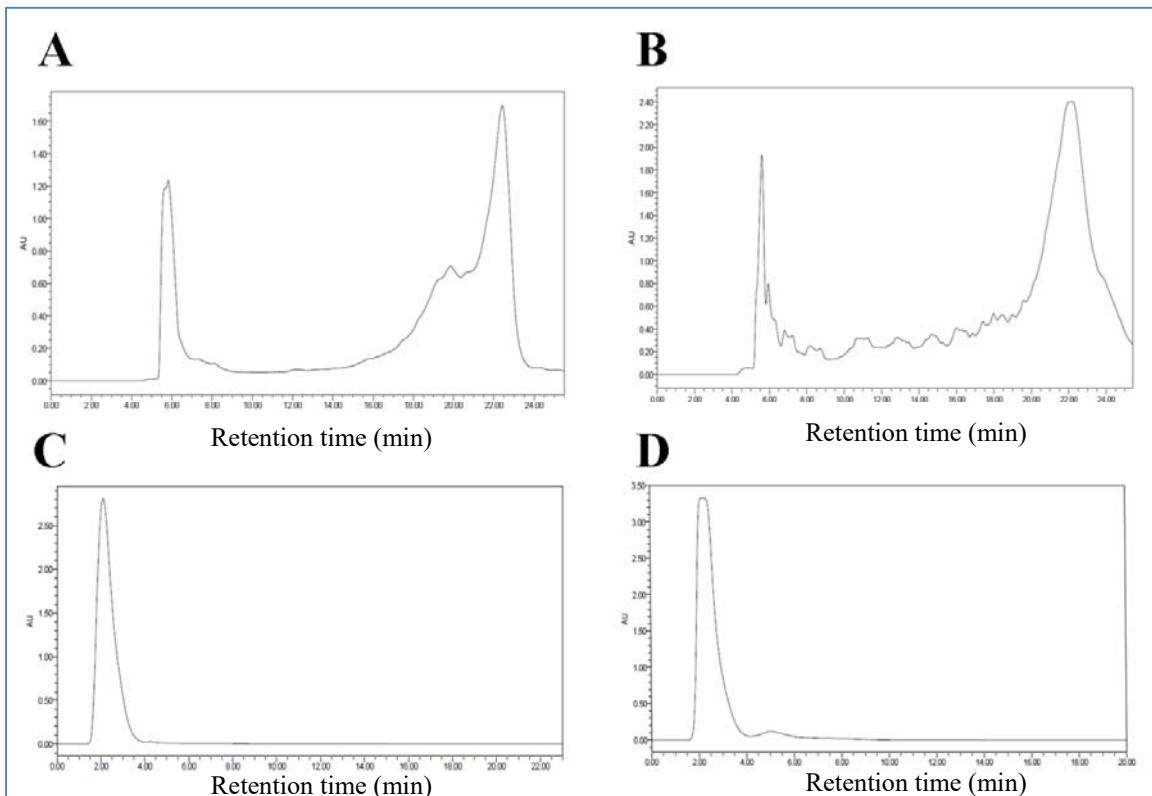


Figure S6. HPLC and desalting profiles of single oligonucleotide strand (A-B) Anion exchange HPLC of A08D and SMOE oligonucleotide strand, respectively. (C-D) Desalting images of their oligonucleotide strand, respectively.

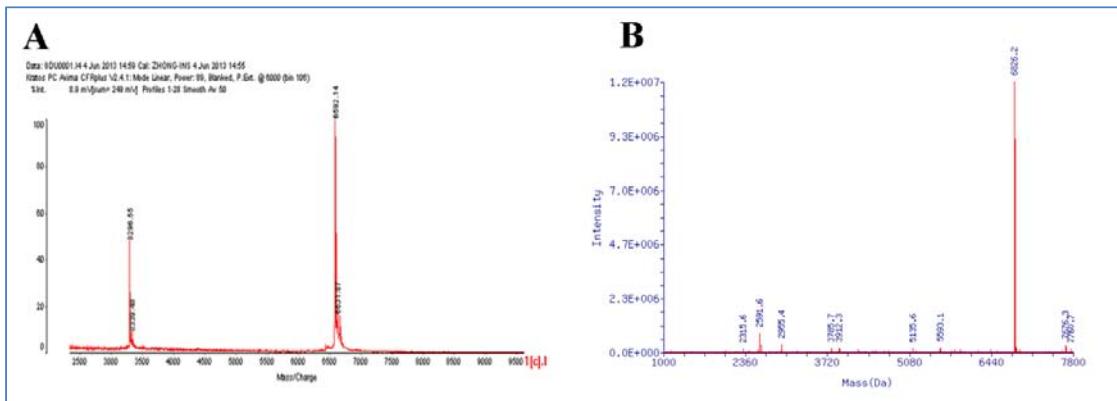


Figure S7. The MALDI-TOF-MS and ESI-MS of single oligonucleotide strand (A) The MALDI-TOF-MS of A08D strand production. (B) The ESI-MS of SMOE strand production.

Table S1. Sequence details of the synthesized oligonucleotide strands

No.	Name	Sequence	Calcd.	Found
1	MB3-SS	5'-GCUACAGAGAAAUCUCGAUtt-3'	6677.1	6678.4
2	S03D	5'-GC <u>D</u> ACAGAGAGAAAUCUCGAUtt-3'	6661.1	6661.1

3	S03L	5'-GCU L ACAGAGAAAUCUCGAUtt-3'	6661.1	6663.5
4	S04D	5'-GCU A D CAGAGAAAUCUCGAUtt-3'	6661.1	6662.8
5	S04L	5'-GCU A L CAGAGAAAUCUCGAUtt-3'	6661.1	6662.5
6	S10D	5'-GCUACAGAG A D AAUCUCGAUtt-3'	6661.1	6662.5
7	S10L	5'-GCUACAGAG A L AAUCUCGAUtt-3'	6661.1	6662.4
8	S11D	5'-GCUACAGAGA A D AUCUCGAUtt-3'	6661.1	6662.2
9	S11L	5'-GCUACAGAGA A L AUCUCGAUtt-3'	6661.1	6662.0
10	S12D	5'-GCUACAGAGAA A D UCUCGAUtt-3'	6661.1	6661.4
11	S12L	5'-GCUACAGAGAA A L UCUCGAUtt-3'	6661.1	6662.5
12	S13D	5'-GCUACAGAGAAA U D CUCGAUtt-3'	6661.1	6662.5
13	S13L	5'-GCUACAGAGAAA U L CUCGAUtt-3'	6661.1	6663.0
14	S18D	5'-GCUACAGAGAAAUCUCG A D Utt-3'	6661.1	6662.2
15	S18L	5'-GCUACAGAGAAAUCUCG A L Utt-3'	6661.1	6662.3
16	SDD	5'-GCUACAGAGAAAUCUCGAU U D U D -3'	6649.1	6650.1
17	Suu	5'-GCUACAGAGAAAUCUCGAUUU-3'	6681.1	6682.7
18	SDDD	5'-GCUACAGAGAAAUCUCGAU U D U D -3'	6939.3	6940.2
19	SDt	5'-GCUACAGAGAAAUCUCGAU U D t-3'	6686.1	6686.7
20	StD	5'-GCUACAGAGAAAUCUCGAU t U D -3'	6686.1	6687.8
21	SD	5'-GCUACAGAGAAAUCUCGAU U D -3'	6381.9	6384.4
22	STT	5'-GCUACAGAGAAAUCUCGAU T D T D -3'	6677.1	6678.2
23	SLL	5'-GCUACAGAGAAAUCUCGAU U L U L -3'	6649.1	6650.1
24	SPS	5'-GCUACAGAGAAAUCUCGAU t s t -3'	6693.2	6693.7
25	SMe	5'-GCUACAGAGAAAUCUCGAU U M E U M E -3'	6709.1	6709.9
26	SMOE	5'-GCUACAGAGAAAUCUCGAU T M O E T M O E -3'	6825.1	6826.2
27	SLNA	5'-GCUACAGAGAAAUCUCGAU T L N A T L N A -3'	6733.2	6734.1
28	MB3-AS	5'-AUCGAGAUUUUCUCUGUAGCtt-3'	6608.0	6608.9
29	A02D	5'-A U D CGAGAUUUUCUCUGUAGCtt-3'	6592.0	6594.3
30	A02L	5'-A U L CGAGAUUUUCUCUGUAGCtt-3'	6592.0	6592.7
31	A07D	5'-AUCGAGA D UUUCUCUGUAGCtt-3'	6592.0	6591.4
32	A07L	5'-AUCGAGA L UUUCUCUGUAGCtt-3'	6592.0	6590.4
33	A08D	5'-AUCGAGA U D UUUCUCUGUAGCtt-3'	6592.0	6592.1
34	A08L	5'-AUCGAGA U L UUUCUCUGUAGCtt-3'	6592.0	6592.5
35	A09D	5'-AUCGAGAU U D UCUCUGUAGCtt-3'	6592.0	6592.9
36	A09L	5'-AUCGAGAU U L UCUCUGUAGCtt-3'	6592.0	6592.4
37	A10D	5'-AUCGAGAU U D CUCUGUAGCtt-3'	6592.0	6593.5
38	A10L	5'-AUCGAGAU U L CUCUGUAGCtt-3'	6592.0	6592.9
39	A16D	5'-AUCGAGAUUUUCUCUG U D AGCtt-3'	6592.0	6593.3
40	A16L	5'-AUCGAGAUUUUCUCUG U L AGCtt-3'	6592.0	6592.9

41	A17D	5'-AUCGAGAUUUCUCUGU <i>A</i> <i>D</i> GCtt-3'	6592.0	6593.8
42	A17L	5'-AUCGAGAUUUCUCUGU <i>A</i> <i>L</i> GCtt-3'	6592.0	6592.0
43	ADD	5'-AUCGAGAUUUCUCUGUAGC <i>U</i> <i>D</i> <i>U</i> -3'	6580.0	6576.4
44	RNA1-SS	5'-AGAAUUGGAUCUGGAUCAUtt-3'	6695.1	6695.2
45	RNA1-AS	5'-AUGAUCCAGAUCCAAUUCUtt-3'	6575.0	6575.2
46	1A08D	5'-AUGAUCC <i>A</i> <i>D</i> GAUCCAAUUCUtt-3'	6559.0	6560.2
47	RNA2-SS	5'-AGCAUGAACCAUGAGUUGCtt-3'	6693.1	6694.0
48	RNA2-AS	5'-GCAACUCAUGGUUCAUGCtt-3'	6607.0	6608.4
49	2A08D	5'-GCAACUC <i>A</i> <i>D</i> UGGUUCAUGCtt-3'	6591.0	6592.6

Table S2. Sequences of mismatched siRNAs

	No.	Name	siRNA Sequence
Sense strand(SS)	1	siMB3-S/A	SS: 5'-GCUACAGAGAAAUCUCGAUtt-3' AS: 5'-AUCGAGAUUUCUCUGUAGCtt-3'
Antisense strand(AS)	34	S13c/A	SS: 5'-GCUACAGAGAAA <i>c</i> CUCGAUtt-3'/AS
Sense strand(SS)	35	S13a/A	SS: 5'-GCUACAGAGAAA <i>a</i> CUCGAUtt-3'/AS
Mismatched with	36	S13g/A	SS: 5'-GCUACAGAGAAA <i>g</i> CUCGAUtt-3'/AS
Antisense strand(AS)	37	S12c/A	SS: 5'-GCUACAGAGAA <i>c</i> UCUCGAUtt-3'/AS
	38	S12u/A	SS: 5'-GCUACAGAGAA <i>u</i> UCUCGAUtt-3'/AS
	39	S12g/A	SS: 5'-GCUACAGAGAA <i>g</i> UCUCGAUtt-3'/AS

Positions of **mismatch** incorporated are indicated in *Blue, italic and lowercase*