

A

Full 2'-O-MOE

5' GCCCCTA G C G C GCGACTC 3'

Probe pairs

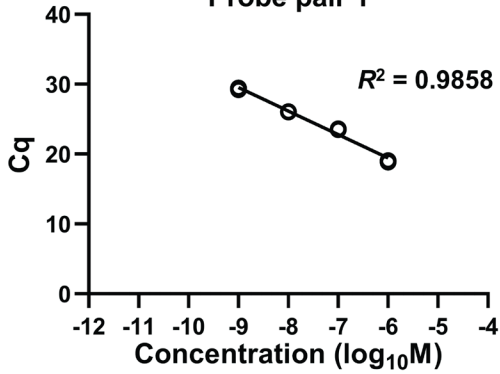
3' AATTCGGGACGCACAGAGGCTGAGTCGCCGGGGATpC	G C G	CGCTGAGGACAGCACTGACGGGTATCTCTCCAGCTC	5'	1
3' AATTCGGGACGCACAGAGGCTGAGTCGCCGGGGAT CpG	C G	CGCTGAGGACAGCACTGACGGGTATCTCTCCAGCTC	5'	2
3' AATTCGGGACGCACAGAGGCTGAGTCGCCGGGGAT C GpC	G G	CGCTGAGGACAGCACTGACGGGTATCTCTCCAGCTC	5'	3
3' AATTCGGGACGCACAGAGGCTGAGTCGCCGGGGAT C G CpG	C G	CGCTGAGGACAGCACTGACGGGTATCTCTCCAGCTC	5'	4
3' AATTCGGGACGCACAGAGGCTGAGTCGCCGGGGAT C G C GpC	G C G	CGCTGAGGACAGCACTGACGGGTATCTCTCCAGCTC	5'	5

Probe B

Probe A

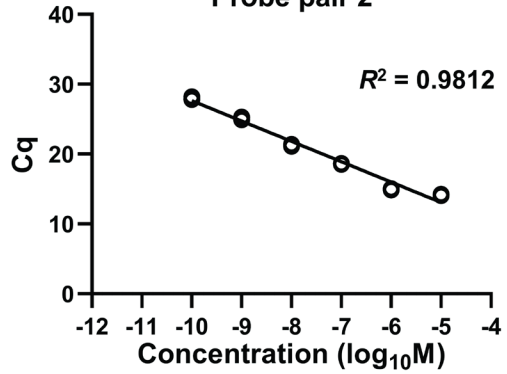
B

Probe pair 1



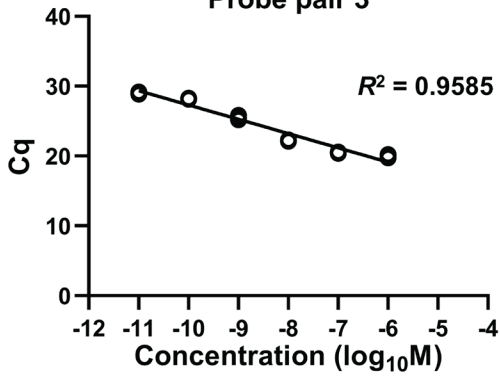
C

Probe pair 2



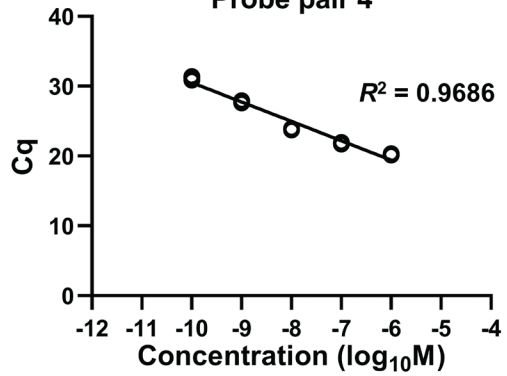
D

Probe pair 3



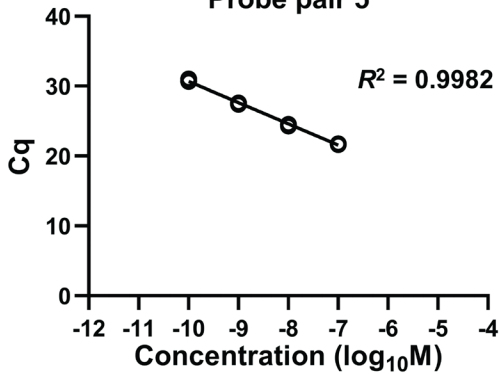
E

Probe pair 4



F

Probe pair 5



Supplementary Figure S3. Optimization of ligation probe sequences for fully modified 2'-*O*-MOE ASO. **(A)** Details of the pairs of ligation probe A (in blue) and probe B (in red) with different complementary sequences are presented along with the target ASO sequence (in black). **(B-F)** Standard curve for fully modified 2'-*O*-MOE ASO diluted in water using 25 U/reaction of SplintR ligase by different ligation probe pair. The qPCR for each standard point was performed in technical triplicate.