Additional file 6 – Table. Definition of the best hotspot sequences for siRNA using the I-Score Designer software

Hotspot position within the gene according to I-Score Designer*	Hotspot sequence	Number of appearances of the hotspot according to I-Score Designer*	Match of hotspots inside tiling regions
151	GGTTTTGGTCGGAAGAAAA	2	tile 1
157	GGTCGGAAGAAAAAGAAAA	1	tile 1
162	GAAGAAAAAGAAAAAAGAA	1	tile 1
429	CGTAGCTATTTATATTTTA	1	tile 1, tile 2
457	CTGTTTTCATTTTTTATAA	1	tile 1, tile 2
566	CGTTCGAATCAGCTGTAAA	2	tile 2
810	CAGAGATGTGATAATTTTA	2	tile 2, tile 3
1069	GGTTATGGAGATAATCCAA	3	tile 3
1240	GGTTCGTTCTACCTTGTAA	1	tile 4
1463	GCTACGAGCTGTTCGTGAA	1	tile 4,tile 5
1619	GCGCGTTTACGATACGTAA	1	tile 5
2001	GCGAGACTTTGATATGTCA	1	tile 6
2477	CGATAGAAGCAACGATGAA	1	tile 7, tile 8
2631	GCTTCGAGTGTTCAAGCTA	1	tile 8
2636	GAGTGTTCAAGCTAGCGAA	1	tile 8
3134	CGCTCAAGTTCGTGAAAAA	2	-
3329	GGATGGAGTTCACGATACA	1	-
3483	CGATGATACTGCCAGTATA	1	-
3962	CGGTGATATTTTTTCTAGA	1	-
4006	GGTTTTCGAGTTTACTTTA	1	-
5267	GGCTGGACGATGTGTACAA	1	-
6135	GGCTAACTTAGGTATAGTA	1	-

*Hotspot definition using I-Score Designer software according to prediction scores of Best i-Scores, Best s-Biopredsi and Best DSIR

Reference I-Score Designer:

Ichihara M, Murakumo Y, Masuda A, Matsuura T, Asai N, Jijiwa M, Ishida M, Shinmi J, Yatsuya H, Qiao S, Takahashi M, Ohno K. Thermodynamic instability of siRNA duplex is a prerequisite for dependable prediction of siRNA activities. Nucleic Acids Res 35:e123, 2007