

NO1 TTGGGGGCGACACTCCACCATAGATCACTCCCCCTGTGAGGTACTACTGTCTTCACGCAGA 60  
NO5 TTGGGGGCGACACTCCACCATAGATCACTCCCCCTGTGAGGAACTACTGTCTTCACGCAGA 60  
4a TTGGGGGCGACACTCCACCATAGATCACTCCCCCTGTGAGGAACTACTGTCTTCACGCAGA 60  
\*\*\*\*\*

NO1 AAGCGTCTAGCCATGGCAGTTAGTATAGAGTGTTCGTACAGCCTCCAGGACCCCCCTCCC  
120  
NO5 AAGCGTCTAGCCATGGCAGTTAGTATAGAGTGTTCGTACAGCCTCCAGGACCCCCCTCCC  
120  
4a AAGCGTCTAGCCATGGC-GTTAGTAT-GAGTGTGTGTCAGCCTCCAGGACCCCCCTCCC  
118  
\*\*\*\*\*

NO1 GGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATCGCCAGGACGACCGGG  
180  
NO5 GGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATCGCCAGGACGACCGGG  
180  
4a GGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATCGCCAGGACGACCGGG  
178  
\*\*\*\*\*

NO1 TCCTTTCTTGGATAAACCCGCTCCATGCCTGGAAATTTGGGCGTGCCCCGCAAGACTGC  
240  
NO5 TCCTTTCTTGGATAAACCCGCTCCATGCCTGGAAATTTGGGCGTGCCCCGCAAGACTGC  
240  
4a TCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCGCGAGACTGC  
238  
\*\*\*\*\*

NO1 TAAGCGAGTAGTGTTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAAGGTGCTTGCGA  
300  
NO5 TAGCCGAGTAGTGTTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGTGCGA  
300  
4a TAGCCGAGTAGTGTTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGTGCGA  
298  
\*\* \*\*\*\*\*  
**S-ODN2**

NO1 GTCGCCGGGGAGGTACTCGTAGACCTGTGCACCATGAGCACAATTCCTAAACCTCAAAG  
360  
NO5 GTGCCCCNGGAGGTA-TCGTAGACC-GTGCACCATGAGCACAATTCCTAAACCTCAAAG  
358  
4a GTGCCCCGGGAGGTC-TCGTAGACC-GTGCATCATGAGCACAAT-CCTAAACCTCAAAG  
355  
\*\* \*\* \*\*\*\*\*  
**S-ODN1**