

| gRNA Target Sequence Position | | | | | | | | | | | | | | | | | | | | Oligos for generating gRNA expression plasmid | | | | | | | | | |
|-------------------------------|----|----|----|----|----|----|----|----|----|----|---|---|---|---|---|---|---|---|------------------------------|---|------------------------------|--|--|--|--|--|--|--|--|
| EGFP Target Site 1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | 5 | 4 | 3 | 2 | 1 | oligonucleotide 1 (5' to 3') | oligonucleotide 2 (5' to 3') | | | | | | | | |
| G | G | G | C | A | C | G | G | C | A | G | C | T | T | G | C | C | G | G | ACACCAGGGCACGGGAGCTTGGCGGG | AAAACCCGGCAAGCTGCCGTGCCCG | | | | | | | | | |
| G | G | G | C | A | C | G | G | C | A | G | C | T | T | G | C | C | G | c | ACACCAGGGCACGGGAGCTTGGCGCG | AAAACCGGGCAAGCTGCCGTGCCCG | | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | T | T | G | C | C | c | G | ACACCAGGGCACGGGAGCTTGGCGGG | AAAACCGGGCAAGCTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | T | T | G | C | g | G | ACACCAGGGCACGGGAGCTTGGCGGG | AAAACCCCAGCAAGCTGCCGTGCCCG | | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | T | T | G | g | C | G | ACACCAGGGCACGGGAGCTTGGCGGG | AAAACCCGCCAAGCTGCCGTGCCCG | | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | T | T | T | c | C | G | G | ACACCAGGGCACGGGAGCTTCCCGGG | AAAACCCGGGAAGCTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | T | T | T | c | C | G | G | ACACCAGGGCACGGGAGCTTCCCGGG | AAAACCCGGCATGCTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | T | a | G | C | C | G | G | ACACCAGGGCACGGGAGCTAGCCGGG | AAAACCCGGTAGCTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | a | T | G | C | C | G | G | ACACCAGGGCACGGGAGCATGCCGGG | AAAACCCGGCATGCTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | g | T | T | G | C | C | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGAACCTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | g | T | T | G | C | C | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGAAAGCTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | c | T | T | G | C | C | G | ACACCAGGGCACGGGACCTTGCCGGG | AAAACCCGGCAAGGTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | t | G | C | C | G | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCAGCCGTGCCCG | | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | g | A | G | C | T | T | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCTCCCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | c | G | A | G | C | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | c | G | A | G | C | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | c | G | A | G | C | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | t | G | C | C | G | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | g | A | G | C | T | T | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | c | T | T | G | C | C | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | t | G | C | C | G | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | g | A | G | C | T | T | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | c | T | T | G | C | C | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | t | G | C | C | G | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | g | A | G | C | T | T | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | c | T | T | G | C | C | G | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | t | G | C | C | G | g | ACACCAGGGCACGGGAGCTTGCCTGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | g | T | T | G | C | c | G | ACACCAGGGCACGGGAGCTTCCCGGG | AAAACCCGGAAAGCTGCCGTGCCCG | | | | | | | | |
| G | G | G | C | A | C | G | G | G | C | A | G | C | c | T | T | G | C | g | G | ACACCAGGGCACGGGAGCTTCCCGGG | AAAACCCGGCATGCTGCCGTGCCCG | | | | | | | | |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----------------------------|-----------------------------|-----------------------------|----------------------------|
| G | G | G | C | A | C | G | G | C | A | c | C | T | T | G | C | g | G | G | ACACCAGGGCACGGGACCTTGCAGGGG | AAAACCCCGCAAGGTGCCGTGCCCG |
| G | G | G | C | A | C | G | G | g | A | G | C | T | T | G | C | g | G | G | ACACCAGGGCACGGGAGCTTGCAGGGG | AAAACCCCGCAAGCTCCCCGTGCCCG |
| G | G | G | C | A | C | G | g | C | A | G | C | T | T | G | C | g | G | G | ACACCAGGGCACGGCAGCTTGCAGGGG | AAAACCCCGCAAGCTGCCGTGCCCG |
| G | G | G | C | A | g | G | G | G | C | A | G | C | T | T | G | C | g | G | ACACCAGGGCACGGGAGCTTGCAGGGG | AAAACCCCGCAAGCTGCCGTGCCCG |
| G | G | G | g | A | C | G | G | G | C | A | G | C | T | T | G | C | g | G | ACACCAGGGCACGGGAGCTTGCAGGGG | AAAACCCCGCAAGCTGCCGTGCCCG |
| G | c | G | C | A | C | G | G | G | C | A | G | C | T | T | G | C | g | G | ACACCAGGGCACGGCAGCTTGCAGGGG | AAAACCCCGCAAGCTGCCGTGCCCG |
| G | G | G | C | A | C | G | G | g | A | G | C | T | T | G | C | C | c | ACACCAGGGCACGGGAGCTTGCAGGGG | AAAACCCGGAAAGCTCCCCGTGCCCG | |
| G | G | G | C | A | C | G | G | g | A | G | C | T | T | c | C | C | G | ACACCAGGGCACGGGAGCTTCCCAGGG | AAAACCCGGCATGCTCCCCGTGCCCG | |
| G | G | G | C | A | C | G | G | g | A | G | C | a | T | G | C | C | G | ACACCAGGGCACGGGAGCATGCCAGGG | AAAACCCGGCAAGGTCCCCGTGCCCG | |
| G | G | G | C | A | C | G | G | g | A | c | C | T | T | G | C | C | G | ACACCAGGGCACGGGAGCTTGCAGGGG | AAAACCCGGCAAGCTCCCCGTGCCCG | |
| G | G | G | C | A | C | G | c | G | A | G | C | T | T | G | C | C | G | ACACCAGGGCACGGGAGCTTGCAGGGG | AAAACCCGGCAAGCTCCCGTGCCCG | |
| G | G | G | C | A | g | G | G | g | A | G | C | T | T | G | C | C | G | ACACCAGGGCACGGGAGCTTGCAGGGG | AAAACCCGGCAAGCTCCCCGTGCCCG | |
| G | G | g | A | C | G | G | g | A | G | C | T | T | G | C | C | G | ACACCAGGGCACGGGAGCTTGCAGGGG | AAAACCCGGCAAGCTCCCCGTGCCCG | | |
| G | c | G | C | A | C | G | G | g | A | G | C | T | T | G | C | C | G | ACACCAGGGCACGGGAGCTTGCAGGGG | AAAACCCGGCAAGCTCCCCGTGCCCG | |
| G | c | G | C | A | C | G | G | C | A | G | C | T | T | G | C | c | ACACCAGGGCACGGGAGCTTGCAGGGG | AAAACCCGGCAAGCTCCCGTGCCCG | | |
| G | c | G | C | A | C | G | G | C | A | G | C | T | T | c | C | C | G | ACACCAGGGCACGGGAGCTTCCCAGGG | AAAACCCGGCAAGCTCCCCGTGCCCG | |
| G | c | G | C | A | C | G | G | C | A | G | C | T | T | G | C | C | G | ACACCAGGGCACGGGAGCATGCCAGGG | AAAACCCGGCAAGCTGCCGTGCCCG | |
| G | c | G | C | A | C | G | G | C | A | c | C | T | T | G | C | C | G | ACACCAGGGCACGGGACCTTGCAGGGG | AAAACCCGGCAAGGTCCCCGTGCCCG | |
| G | c | G | C | A | C | G | G | C | A | G | C | T | T | G | C | C | G | ACACCAGGGCACGGCAGCTTGCAGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | |
| G | c | G | C | A | g | G | G | C | A | G | C | T | T | G | C | C | G | ACACCAGGGCACGGGAGCTTGCAGGGG | AAAACCCGGCAAGCTCCCCGTGCCCG | |
| G | c | G | g | A | C | G | G | C | A | G | C | T | T | G | C | C | G | ACACCAGGGCACGGGAGCTTGCAGGGG | AAAACCCGGCAAGCTGCCGTGCCCG | |

EGFP Target Site 2

| 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | 5 | 4 | 3 | 2 | 1 | oligonucleotide 1 (5' to 3') | oligonucleotide 2 (5' to 3') |
|----|----|----|----|----|----|----|----|----|----|----|---|---|---|---|---|---|---|---|---|-------------------------------|------------------------------|
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | G | C | T | T | G | T | ACACCAGATGCCGTTCTCTGCTTGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | G | C | T | T | G | a | ACACCAGATGCCGTTCTCTGCTTGAG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | G | C | T | T | c | T | ACACCAGATGCCGTTCTCTGCTTCTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | G | C | T | a | G | T | ACACCAGATGCCGTTCTCTGCTAGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | G | C | a | T | G | T | ACACCAGATGCCGTTCTCTGCATGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | G | C | g | T | T | G | ACACCAGATGCCGTTCTCTGCTTGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | c | C | C | T | T | G | ACACCAGATGCCGTTCTCTCCTTGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | c | C | T | T | G | T | ACACCAGATGCCGTTCTTCAGCTTGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | g | T | T | G | T | G | ACACCAGATGCCGTTCTGTGCTTGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | a | C | T | G | C | T | ACACCAGATGCCGTTCTACTGCTTGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | c | A | T | C | T | G | ACACCAGATGCCGTTCTCATCTGCTTGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | g | T | T | G | C | T | ACACCAGATGCCGTTCTGTCTGCTTGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | a | C | T | T | G | G | ACACCAGATGCCGATCTCTGCTTGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | g | T | T | G | C | T | ACACCAGATGCCGATCTCTGCTTGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | c | A | T | C | T | G | ACACCAGATGCCGATCTCTGCTTGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | G | C | C | G | T | T | C | T | T | C | T | g | T | T | G | C | T | ACACCAGATGCCGATCTCTGCTTGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | T | c | C | C | G | T | T | C | T | T | C | T | G | C | T | T | G | T | ACACCAGATGCCGATCTCTGCTTGTG | AAAACACAAGCAGAAGAACGGCATCG |
| G | A | t | G | C | C | G | T | T | C | T | T | C | T | G | C | T | T | G | T | ACACCAGATGCCGATCTCTGCTTGTG | AAAACACAAGCAGAAGAACGGCATCG |

G a T G C C C G T T C T T C T G C T T G T ACACCGTTGCCGTTCTTGCTTGTG
G A T G C C C G T T C T T C T G C T T G T c a ACACCGATGCCGTTCTTGCTTCAG
G A T G C C C G T T C T T C T G C T T G a a G T ACACCGATGCCGTTCTTGCAAGTG
G A T G C C C G T T C T T C T G C T T G c g T T G T ACACCGATGCCGTTCTTGCTTGTG
G A T G C C C G T T C T T C T g a G C T T G T ACACCGATGCCGTTCTTGAGCTTGTG
G A T G C C C G T T C a a C T G C T T G T ACACCGATGCCGTTCAACTGCTTGTG
G A T G C C C G T a g T T C T G C T T G T ACACCGATGCCGTAGTTCTGCTTGTG
G A T G C C C c a T C T T C T G C T T G T ACACCGATGCCCATCTTCTGCTTGTG
G A T G g g G T T C T T C T G C T T G T ACACCGATGGGTTCTTCTGCTTGTG
G A a c C C G T T C T T C T G C T T G T ACACCGAACCCGTTCTTCTGCTTGTG
G t a G C C G T T C T T C T G C T T G T ACACCGTAGCCGTTCTTCTGCTTGTG
G t a c C C G T T C T T C T G C T T G T ACACCGTACCCGTTCTTCTGCTTGTG
G t a c g C G T T C T T C T G C T T G T ACACCGTACGCGTTCTTCTGCTTGTG
G t a c g g G T T C T T C T G C T T G T ACACCGTACGGTTCTTCTGCTTGTG
G t a c g g c T T C T T C T G C T T G T ACACCGTACGGTTCTTCTGCTTGTG
G t a c g g c a T C T T C T G C T T G T ACACCGTACGGATCTTCTGCTTGTG
G t a c g g c a a C T T C T G C T T G T ACACCGTACGGCAACTTCTGCTTGTG
G t a c g g c a a g T T C T G C T T T G T ACACCGTACGGCAAGTTCTGCTTGTG
G A T G C C C G T T C T T C T G C T T a G a ACACCGATGCCGTTCTTCTGCTAGAG
G A T G C C C G T T C T T C T G g T T a a G T ACACCGATGCCGTTCTTCTGGTAGTG
G A T G C C C G T T C T T C T G C T T a a G T ACACCGATGCCGTTCTCAGCTAGTG
G A T G C C C G T T C T a C T G C C T T a a G T ACACCGATGCCGTTACTGCTAGTG
G A T G C C C G T T g T T C T G C C T T a a G T ACACCGATGCCGTTGTCTGCTAGTG
G A T G C C C G a T C T T C T G C C T T a a G T ACACCGATGCCGATCTTCTGCTAGTG
G A T G C C g G T T C T T C T G C C T T a a G T ACACCGATGCCGTTCTTCTGCTAGTG
G A T G C C C G T T C T T C T G C C T T a a G T ACACCGATGCCGTTCTTCTGCTAGTG
G A T G C C C G T T C T T C T G C C T T a a G T ACACCGATGCCGTTCTTCTGCTAGTG
G t T G C C C G T T C T T C T G C C T T a a G T ACACCGTTGCCGTTCTTCTGCTAGTG
G A T G C C C G T T g T T C T G C C T T G a ACACCGATGCCGTTGTCTGCTTGTGAG
G A T G C C C G T T g T T C T G C C T T g T T G T ACACCGATGCCGTTGTCTGGTTGTG
G A T G C C C G T T g T T C T G C a G C T T T G T ACACCGATGCCGTTGTTCTGCTTGTG
G A T G C C C G T T g T T C T G C C T T G C T T G T ACACCGATGCCGTTGTTCTGCTTGTG
G A T G C C C G a T T C T T C T G C C T T G C T T G T ACACCGATGCCGATGTTCTGCTTGTG
G A T G C C g G T T C T T g T T C T G C C T T G C T T G T ACACCGATGCCGTTGTTCTGCTTGTG
G A T c C C C G T T g T T C T G C C T T G C T T G T ACACCGATCCCCTGTTCTGCTTGTG
G t T G C C C G T T g T T C T G C C T T G C T T G T ACACCGTTGCCGTTGTTCTGCTTGTG
G t T G C C C G T T C T T C T G C C T T G g T T G T ACACCGTTGCCGTTCTTCTGGTTGTG
G t T G C C C G T T C T T C T G C a G C T T T G T ACACCGTTGCCGTTCTCAGCTTGTG
G t T G C C C G T T C T T C T G C T T G C T T T G T ACACCGTTGCCGTTACTGCTTGTG
G t T G C C C G a T C T T C T G C T T G C T T T G T ACACCGTTGCCGATCTTCTGCTTGTG
G t T G C C g G T T C T T C T G C T T G C T T T G T ACACCGTTGCCGTTGTTCTGCTTGTG
G t T G C C C G T T C T T C T G C T T G C T T T G T ACACCGTTGCCGTTCTTCTGCTTGTG

EGFP Target Site 3

| 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | 5 | 4 | 3 | 2 | 1 | oligonucleotide 1 (5' to 3') | oligonucleotide 2 (5' to 3') | |
|----|----|----|----|----|----|----|----|----|----|----|---|---|---|---|---|---|---|----------------------------|-----------------------------|------------------------------|------------------------------|------------------------------|
| G | G | T | G | G | T | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGTGCAGATGAACCTCAG | AAAAGTGAAGTTCATCTGCACCACCG | |
| G | G | T | G | G | T | G | C | A | G | A | T | G | A | A | C | T | T | C | t | ACACCGGTGGTGCAGATGAACCTCTG | AAAACAGAAGTTCATCTGCACCACCG | |
| G | G | T | G | G | T | G | C | A | G | A | T | G | A | A | C | T | T | g | A | ACACCGGTGGTGCAGATGAACCTGAG | AAAACACTCAAGTTCATCTGCACCACCG | |
| G | G | T | G | G | T | G | C | A | G | A | T | G | A | A | C | T | a | C | A | ACACCGGTGGTGCAGATGAACCTACAG | AAAACACTGTAGTTCATCTGCACCACCG | |
| G | G | T | G | G | T | G | C | A | G | A | T | G | A | A | C | a | T | C | A | ACACCGGTGGTGCAGATGAACATCAG | AAAACACTGTAGTTCATCTGCACCACCG | |
| G | G | T | G | G | T | G | C | A | G | A | T | G | A | A | g | T | T | C | A | ACACCGGTGGTGCAGATGAAGTCAG | AAAACACTGAACCTCATCTGCACCACCG | |
| G | G | T | G | G | T | G | C | A | G | A | T | G | A | A | t | C | T | T | C | A | ACACCGGTGGTGCAGATGATCTTCAG | AAAACACTGAAGATCATCTGCACCACCG |
| G | G | T | G | G | T | G | C | A | G | A | T | G | t | A | C | T | T | C | A | ACACCGGTGGTGCAGATGTACTTCAG | AAAACACTGAAGTACATCTGCACCACCG | |
| G | G | T | G | G | T | G | C | A | G | A | T | G | c | A | A | C | T | T | C | A | ACACCGGTGGTGCAGATCAACTTCAG | AAAACACTGAAGTTGATCTGCACCACCG |
| G | G | T | G | G | T | G | C | A | G | A | T | G | a | A | C | T | T | C | A | ACACCGGTGGTGCAGAAGAACTTCAG | AAAACACTGAAGTTCTCTGCACCACCG | |
| G | G | T | G | G | T | G | C | A | G | A | T | G | t | A | C | T | T | C | A | ACACCGGTGGTGCAGTTGAACCTCAG | AAAACACTGAAGTTCAACTGCACCACCG | |
| G | G | T | G | G | T | G | C | A | c | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGTGCACATGAACCTCAG | AAAACACTGAAGTTCATGTGCACCACCG | |
| G | G | T | G | G | T | G | C | t | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGTGCCTGATGAACCTCAG | AAAACACTGAAGTTCTCTGCACCACCG | |
| G | G | T | G | G | T | G | g | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGTGGAGATGAACCTCAG | AAAACACTGAAGTTCATCTCCACCACCG | |
| G | G | T | G | G | T | c | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGTCCAGATGAACCTCAG | AAAACACTGAAGTTCATCTGGACCACCG | |
| G | G | T | G | G | a | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGAGCAGATGAACCTCAG | AAAACACTGAAGTTCATCTGCTCCACCG | |
| G | G | T | G | G | c | T | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGTGCAGATGAACCTCAG | AAAACACTGAAGTTCATCTGAGCACCG |
| G | G | T | G | G | c | T | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGTCTGAGATGAACCTCAG | AAAACACTGAAGTTCATCTGCACGACCG |
| G | G | T | G | G | a | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGAGGTGCAGATGAACCTCAG | AAAACACTGAAGTTCATCTGCACCTCCG | |
| G | c | T | G | G | T | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGCTGGTGCAGATGAACCTCAG | AAAACACTGAAGTTCATCTGCACCAGCG | |
| G | G | T | G | G | T | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGTGCAGATGAACCTCAG | AAAACACTGAAGTTCATCTGCTCCACCG | |
| G | G | T | c | G | T | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGTCTGAGATGAACCTCAG | AAAACACTGAAGTTCATCTGCACGACCG | |
| G | G | T | G | G | a | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTCGTGCAGATGAACCTCAG | AAAACACTGAAGTTCATCTGCACGACCG | |
| G | G | T | G | G | T | G | C | A | G | A | T | G | a | A | C | T | a | C | A | ACACCGGTGGTGCAGATGAACACAG | AAAACACTGAAGTTCATCTGCACCTCCG | |
| G | G | T | G | G | T | G | C | A | G | A | T | G | t | g | T | T | C | A | ACACCGGTGGTGCAGATGATGTTTAG | AAAACACTGAACATCATCTGCACCACCG | | |
| G | G | T | G | G | T | G | C | A | G | A | T | G | a | A | C | T | T | g | t | ACACCGGTGGTGCAGATGAACCTGTG | AAAACACAAGTTCATCTGCACCACCG | |
| G | G | T | G | G | T | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGAGGTGCAGATGAACCTCAG | AAAACACTGAAGTTCATCTGCACCTCCG | |
| G | c | T | G | G | T | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGCTGGTGCAGATGAACCTCAG | AAAACACTGAAGTTCATCTGCACCAGCG | |
| G | G | T | G | G | c | T | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGTGCAGATGAACCTCAG | AAAACACTGAAGTTCATCTGCACGTCG |
| G | G | T | G | G | c | T | g | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGTGCAGATGAACCTCAG | AAAACACTGAAGTTCATCTGCACGTCG | |
| G | G | T | G | G | c | t | G | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGTGCAGATGAACCTCAG | AAAACACTGAAGTTCATCTGCACGTCG | |
| G | G | T | G | G | c | t | a | G | A | A | C | T | G | A | A | C | T | C | A | ACACCGGTGGTGCAGTGAACACTCAG | AAAACACTGAAGTTCATCTGCACGTCG | |
| G | G | T | G | G | c | t | c | A | T | G | A | A | C | T | T | C | A | C | A | ACACCGGTGGTGCCTCATGAACCTCAG | AAAACACTGAAGTTCATCTGCACGTCG | |
| G | G | T | G | G | c | t | g | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGTGCAGATGAACCTCAG | AAAACACTGAAGTTCATCTGCACGTCG | |
| G | G | T | G | G | c | t | g | t | A | G | A | T | G | A | A | C | T | T | C | A | ACACCGGTGGTGCAGATGAACCTCAG | AAAACACTGAAGTTCATCTGCACGTCG |
| G | G | T | G | G | c | t | g | t | c | A | T | G | A | A | C | T | a | C | t | ACACCGGTGGTGCAGATGAACACTTG | AAAACAGTAGTTCATCTGCACCACCG | |
| G | G | T | G | G | c | t | g | t | a | G | A | T | G | A | A | g | T | a | C | ACACCGGTGGTGCAGATGAAGTACAG | AAAACACTGTACTTCATCTGCACCACCG | |
| G | G | T | G | G | c | t | g | t | a | C | A | T | G | A | A | C | T | a | C | ACACCGGTGGTGCAGATGTACTACAG | AAAACACTGTAGTACATCTGCACCACCG | |
| G | G | T | G | G | c | t | g | t | a | G | A | A | C | T | a | C | A | ACACCGGTGGTGCAGAAGAACTACAG | AAAACACTGTAGTTCTCTGCACCACCG | | | |

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|------------------------------|---------------------------------|
| G | G | T | G | G | T | G | C | A | c | A | T | G | A | A | C | T | a | C | A | ACACCGGTGGTGCACATGAACATACAG | AAAACGTAGTTCATGTGCACCAACCG |
| G | G | T | G | G | T | G | g | A | G | A | T | G | A | A | C | T | a | C | A | ACACCGGTGGTGGAGATGAACATACAG | AAAACGTAGTTCATCTCCACCAACCG |
| G | G | T | G | G | a | G | C | A | G | A | T | G | A | A | C | T | a | C | A | ACACCGGTGGAGCAGATGAACATACAG | AAAACGTAGTTCATCTGCTCCACCAACCG |
| G | G | T | c | G | T | G | C | A | G | A | T | G | A | A | C | T | a | C | A | ACACCGGTCGTGCAGATGAACATACAG | AAAACGTAGTTCATCTGCACGACCG |
| G | c | T | G | G | T | G | C | A | G | A | T | G | A | A | C | T | a | C | A | ACACCCTGGTGCAGATGAACATACAG | AAAACGTAGTTCATCTGCACCAACCG |
| G | G | T | G | G | T | G | C | A | c | A | T | G | A | A | C | T | t | C | t | ACACCCTGGTGCACATGAACATTCTG | AAAACAGAAGTTCATGTGCACCAACCG |
| G | G | T | G | G | T | G | C | A | c | A | T | G | A | A | g | T | T | C | A | ACACCCTGGTGCACATGAAGTTCA | AAAACACTGAACCTCATGTGCACCAACCG |
| G | G | T | G | G | T | G | C | A | c | A | T | G | t | A | C | T | T | C | A | ACACCCTGGTGCACATGTACTTCAG | AAAACGTAAAGTACATGTGCACCAACCG |
| G | G | T | G | G | T | G | C | A | c | A | T | G | A | A | C | T | T | C | A | ACACCCTGGTGCACAAGAACCTCAG | AAAACGTAAAGTTCTTGTGCACCAACCG |
| G | G | T | G | G | T | G | g | A | c | A | T | G | A | A | C | T | T | C | A | ACACCCTGGTGGACATGAACATTCA | AAAACGTAAAGTTCATGTCCACCAACCG |
| G | G | T | G | G | a | G | C | A | c | A | T | G | A | A | C | T | T | C | A | ACACCCTGGAGCACATGAACATTCA | AAAACGTAAAGTTCATGTGCTCCACCAACCG |
| G | G | T | c | G | T | G | C | A | c | A | T | G | A | A | C | T | T | C | A | ACACCCTGGTCGTGCACATGAACATTCA | AAAACGTAAAGTTCATGTGCACGACCG |
| G | c | T | G | G | T | G | C | A | c | A | T | G | A | A | C | T | T | C | A | ACACCCTGGTGCACATGAACATTCA | AAAACGTAAAGTTCATGTGCACCAACCG |
| G | c | T | G | G | T | G | C | A | G | A | T | G | A | A | C | T | t | C | t | ACACCCTGGTGCAGATGAACATTCTG | AAAACAGAAGTTCATCTGCACCAACCG |
| G | c | T | G | G | T | G | C | A | G | A | T | G | A | A | g | T | T | C | A | ACACCCTGGTGCAGATGAAGTTCA | AAAACGTAAACTCATCTGCACCAACCG |
| G | c | T | G | G | T | G | C | A | G | A | T | G | t | A | C | T | T | C | A | ACACCCTGGTGCAGATGTACTTCAG | AAAACGTAAAGTACATCTGCACCAACCG |
| G | c | T | G | G | T | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCCTGGTGCAGAAGAACCTCAG | AAAACGTAAAGTTCTTCTGCACCAACCG |
| G | c | T | G | G | T | G | g | A | G | A | T | G | A | A | C | T | T | C | A | ACACCCTGGTGGAGATGAACATTCA | AAAACGTAAAGTTCATCTCCACCAACCG |
| G | c | T | G | G | a | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCCTGGAGCAGATGAACATTCA | AAAACGTAAAGTTCATCTGCTCCACCAACCG |
| G | c | T | c | G | T | G | C | A | G | A | T | G | A | A | C | T | T | C | A | ACACCCTGGTCGTGCAGATGAACATTCA | AAAACGTAAAGTTCATCTGCACGAGCG |

Endogenous Target 1 (VEGFA Site 1):

| | | | | | | | | | | | | | | | | | | | | | |
|----|----|----|----|----|----|----|----|----|----|----|---|---|---|---|---|---|---|---|---|------------------------------|------------------------------|
| 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | 5 | 4 | 3 | 2 | 1 | oligonucleotide 1 (5' to 3') | oligonucleotide 2 (5' to 3') |
| G | G | G | T | G | G | G | G | G | A | G | T | T | T | T | G | C | T | C | C | ACACCGGTGGGGGGAGTTGCTCCG | AAAACGGAGCAAACCCCCCACCCG |

Endogenous Target 2 (VEGFA Site 2):

| | | | | | | | | | | | | | | | | | | | | | |
|----|----|----|----|----|----|----|----|----|----|----|---|---|---|---|---|---|---|---|---|------------------------------|------------------------------|
| 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | 5 | 4 | 3 | 2 | 1 | oligonucleotide 1 (5' to 3') | oligonucleotide 2 (5' to 3') |
| G | A | C | C | C | C | C | T | C | C | A | C | C | C | C | G | C | C | T | C | ACACCGACCCCCTCCACCCCGCTCG | AAAACGAGGCGGGGTGGAGGGGGTCG |

Endogenous Target 3 (VEGFA Site 3):

| | | | | | | | | | | | | | | | | | | | | | |
|----|----|----|----|----|----|----|----|----|----|----|---|---|---|---|---|---|---|---|---|------------------------------|------------------------------|
| 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | 5 | 4 | 3 | 2 | 1 | oligonucleotide 1 (5' to 3') | oligonucleotide 2 (5' to 3') |
| G | G | T | G | A | G | T | G | A | G | T | G | T | G | T | G | C | G | T | G | ACACCCTGGAGTGAGTGAGTGTGCGTGG | AAAACCACGCACACACTCACTCACCG |

Endogenous Target 4 (EMX1):

| | | | | | | | | | | | | | | | | | | | | | |
|----|----|----|----|----|----|----|----|----|----|----|---|---|---|---|---|---|---|---|---|------------------------------|------------------------------|
| 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | 5 | 4 | 3 | 2 | 1 | oligonucleotide 1 (5' to 3') | oligonucleotide 2 (5' to 3') |
| G | A | G | T | C | C | G | A | G | C | A | G | A | A | G | A | A | G | A | A | ACACCGAGTCCGAGCAGAAGAAGAAG | AAAACCTCTTCTGCTCGGACTCG |

Endogenous Target 5 (RNF2):

| | | | | | | | | | | | | | | | | | | | | | |
|----|----|----|----|----|----|----|----|----|----|----|---|---|---|---|---|---|---|---|---|------------------------------|------------------------------|
| 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | 5 | 4 | 3 | 2 | 1 | oligonucleotide 1 (5' to 3') | oligonucleotide 2 (5' to 3') |
| G | T | C | A | T | C | T | T | A | G | T | C | A | T | T | A | C | C | T | G | ACACCGTCATCTTAGTCATTACCTGG | AAAACCAGGTAATGACTAAGATGACG |

Endogenous Target 6 (FANCF):

20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1 oligonucleotide 1 (5' to 3') oligonucleotide 2 (5' to 3')
G G A A T C C T C T G C A G C A C C ACACCGGAATCCCTTCTGCAGCACCG AAAACGGTGCTGCAGAAGGGATTCCG
