

OLIGOS USED FOR 154 BP 5S FLAP-OUT AND FLAP-IN NUCLEOSOMES

Bottom Strand For Both orientations:

74-mer (upstream)

ACA AGG CTG ACT TTT CCT CCC CTT GTG CTG CCT TCT GGG GGG GGC CCA GCC GGA TCC CGG GGC GAG CTC GAA TT

80-mer (downstream)

ACT AAC CAG GCC CGA CCC TGC TTG GCT TCC GAG ATC AGA CGA TAT CGG GCA CTT TCA GGG TGG TAT GGC CGT AGG CGA GC

40-mer splicer

GGA GGA AAA GTC AGC CTT GTG CTC GCC TAC GGC CAT ACC A

Bottom Strand reversed (3' to 5') and matched with 40-mer splice. ENDS OF OLIGOS IN BOLD

**GGAGGAAAAGTCAGCCTTGTGCTCGCCTACGGCCATACCA**

TTAAGCTCGAGCGGGGCCCTAGGCCGACCCGGGGGGGTCTTCCGTCGTGTTCCCTCCTTTTCAGTCGGAAC**AC**GAGCGGATGCCGGTATGGTGGGACTTTACGGGCTATAGCAGACTAGAGCCTTCGGTTCGTCCAGCCCGACCAATCA

5S FLAP-IN Top Strand

41-MER

CCA CTA AAG TCA GCC TTG TGC TCG CCT ACG GCC ATA CCA CC

61-MER

AAT TCG AGC TCG CCC CGG GAT CCG GCT GGG CCC CCC CCA GAA GGC AGC ACA AGG GGA GGA A

57-MER (DOWNSTREAM)

CTG AAA GTG CCC GAT ATC GTC TGA TCT CGG AAG CCA AGC AGG GTC GGG CCT GGT TAG T

40-mer top splice:

ACG ATA TCG GGC ACT TTC AGG GTG GTA TGG CCG TAG GCG A

TOP OLIGOS MATCHED WITH BOTTOM STRAND: (flap in bold, dyad highlighted; splice on top):

**AGCGGATGCCGGTATGGTGGGACTTTACGGGCTATAGCA**

**CCACTAAAGTCAGCCTTGTGCTCGCCTACGGCCATACCACCCTGAAAGTGCCCGATATCGTCTGATCTCGGAAGCCAAGCAGGGTCGGGCCTGGTTAGT**

TTAAGCTCGAGCGGGGCCCTAGGCCGACCCGGGGGGGTCTTCCGTCGTGTTCCCTCCTTTTCAGTCGGAAC**AC**GAGCGGATGCCGGTATGGTGGGACTTTACGGGCTATAGCAGACTAGAGCCTTCGGTTCGTCCAGCCCGACCAATCA

**AATTCGAGCTCGCCCCGGGATCCGGTGGGCCCCCCCCAGAAGGCAGCACAAGGGGAGGAA**

TTAAGCTCGAGCGGGGCCCTAGGCCGACCCGGGGGGGTCTTCCGTCGTGTTCCCTCCTTTTCAGTCGGAAC**AC**GAGCGGATGCCGGTATGGTGGGACTTTACGGGCTATAGCAGACTAGAGCCTTCGGTTCGTCCAGCCCGACCAATCA

5S FLAP-out Top Strand

35-MER

CC **ACT** AGC CTT GTG CTC GCC TAC GGC CAT ACC ACC

66-MER

AAT TCG AGC TCG CCC CGG GAT CCG GCT GGG CCC CCC CCA GAA GGC AGC ACA AGG GGA GGA AAA GTC

57-MER (DOWNSTREAM)

CTG AAA GTG CCC GAT ATC GTC TGA TCT CGG AAG CCA AGC AGG GTC GGG CCT GGT TAG T

40-mer top splice:

ACG ATA TCG GGC ACT TTC AGG GTG GTA TGG CCG TAG GCG A

TOP OLIGOS MATCHED WITH BOTTOM STRAND: (flap in bold, dyad highlighted; splice on top):

**AGCGGATGCCGGTATGGTGGGACTTTACGGGCTATAGCA**

**CCACTAGCCTTGTGCTCGCCTACGGCCATACCACCCTGAAAGTGCCCGATATCGTCTGATCTCGGAAGCCAAGCAGGGTCGGGCCTGGTTAGT**

TTAAGCTCGAGCGGGGCCCTAGGCCGACCCGGGGGGGTCTTCCGTCGTGTTCCCTCCTTTTCAGTCGGAAC**AC**GAGCGGATGCCGGTATGGTGGGACTTTACGGGCTATAGCAGACTAGAGCCTTCGGTTCGTCCAGCCCGACCAATCA

**AATTCGAGCTCGCCCCGGGATCCGGTGGGCCCCCCCCAGAAGGCAGCACAAGGGGAGGAAAAGTC**

TTAAGCTCGAGCGGGGCCCTAGGCCGACCCGGGGGGGTCTTCCGTCGTGTTCCCTCCTTTTCAGTCGGAAC**AC**GAGCGGATGCCGGTATGGTGGGACTTTACGGGCTATAGCAGACTAGAGCCTTCGGTTCGTCCAGCCCGACCAATCA

OLIGOS USED FOR 151 BP 601 FLAP-OUT AND FLAP-IN NUCLEOSOMES

601 Bottom Strand

70-mer (upstream)

Ccc cgc ttt taa ccg cca agg gga tta ctc cct agt ctc cag gca cgt gtc aca tat ata cat cct atc c

81-mer (downstream)

Ccc tgg aga atc ccg gtg ccg agg ccg ctc aat tgg tcg tag aca gct cta gca ccg ctt aaa cgc acg tac gcg ctg tcc

40-mer splicer

ctt ggc ggt taa aac gcg ggg gac agc gcg tac gtg cgt t

Whole bottom strand:

Ccctggagaatcccgggtgccgaggccgctcaattggtcgtagacagctctagaccgcttaaacgcacgtacgcgctgtcccccgcttttaaccgccaaggggattactccctagctccaggcagctgtcacatatatacatcctatcc

Bottom Strand reversed (3' to 5'): (matched with 40-mer splice)

CCTATCCTACATATATACACTGTGCACGGACCTCTGATCCCTCATTAGGGGAACCGCCAATTTTCGCCC**CCTGT**CGCGCATGCACGCAAATTCGCCACGATCTCGACAGATGCTGGTAACTCGCCGGAGCCGTGGCCCTAAGAGGTCCC

601 Top Strand

39-MER

CGA CCA ATT GAG CGG CCT CGG CAC CGG GAT TCT CCA GGG

76-MER (flap out)

GGA TAG GAT GTA TAT ATG TGA CAC GTG CCT GGA GAC TAG GGA GTA ATC CCC TTG GCG GTT AAA ACG CGG GGG ACA G

42-MER (flap out)

CCT GTG CGC GTA CGT CGC TTT AAG CGG TGC TAG AGC TGT CTA

40-mer top splice:

aggccgctcaattggtcgtagacagctctagaccgctt

TOP OLIGOS MATCHED WITH BOTTOM STRAND: (flap in bold, dyad highlighted; splice on top):

FLAP-OUT:

TTCGCCACGATCTCGACAGATGCTGGTAACTCGCCGGA  
CCTATCCTACATATATACACTGTGCACGGACCTCTGATCCCTCATTAGGGGAACCGCCAATTTTCGCCC**CCTGT**CGCGCATGCACGCAAATTCGCCACGATCTCGACAGATGCTGGTAACTCGCCGGAGCCGTGGCCCTAAGAGGTCCC  
GGATAGGATGTATATATGTGACACGTGCCTGGAGACTAGGGAGTAATCCCCTTGGCGGTTAAAACGCGGGGACAG  
CCTATCCTACATATATACACTGTGCACGGACCTCTGATCCCTCATTAGGGGAACCGCCAATTTTCGCCC**CCTGT**CGCGCATGCACGCAAATTCGCCACGATCTCGACAGATGCTGGTAACTCGCCGGAGCCGTGGCCCTAAGAGGTCCC

FLAP-IN:

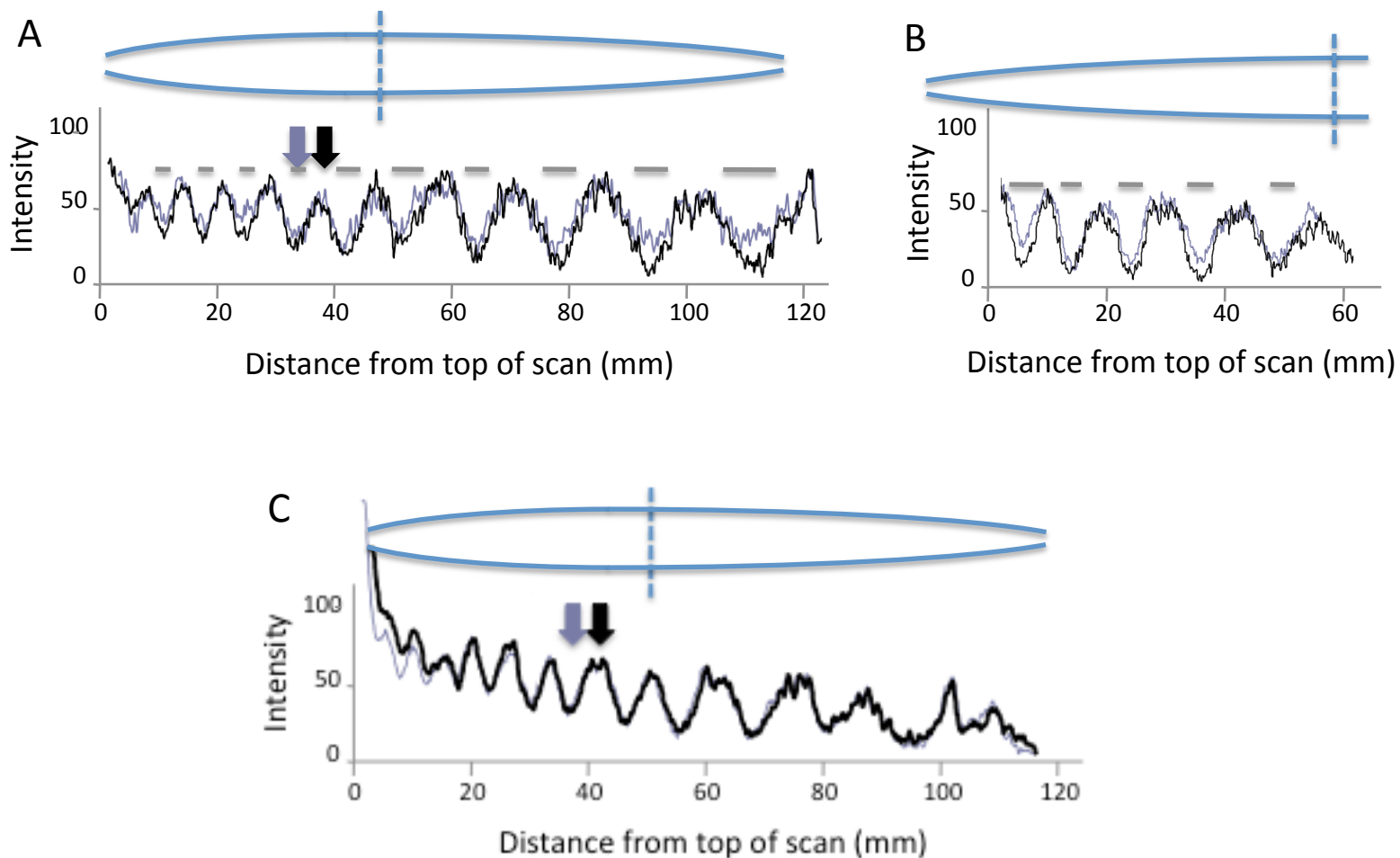
70-MER (flap-in):

GGA TAG GAT GTA TAT ATG TGA CAC GTG CCT GGA GAC TAG GGA GTA ATC CCC TTG GCG GTT AAA ACG CGG G

48-MER (flap-in):

CCT GTG GGA CAG CGC GTA CGT CGC TTT AAG CGG TGC TAG AGC TGT CTA

CCTATCCTACATATATACACTGTGCACGGACCTCTGATCCCTCATTAGGGGAACCGCCAATTTTCGCCC**CCTGT**GGGACAGCGCGTACGTTCGCTTTAAGCGGTGCTAGAGCTGTCTACGACCAATTGAGCGGCCTCGGCACCGGGATTCTCCAGGG  
GGATAGGATGTATATATGTGACACGTGCCTGGAGACTAGGGAGTAATCCCCTTGGCGGTTAAAACGCGGG  
CCTATCCTACATATATACACTGTGCACGGACCTCTGATCCCTCATTAGGGGAACCGCCAATTTTCGCCC**CCTGT**CGCGCATGCACGCAAATTCGCCACGATCTCGACAGATGCTGGTAACTCGCCGGAGCCGTGGCCCTAAGAGGTCCC



Supplemental Fig. S3. Comparison of densitometer scans of Flap-Out (black traces) and Flap-In (blue traces) from Fig. 2. A. Scans for Fig. 2A, lanes 7 and 9. The locations of the flaps in each substrate are indicated by the arrows. The nucleosome dyad is indicated by the dotted line. B. Scans for Fig. 2B, lanes 7 and 9. The regions where more •OH cleavage is observed in the Flap-out substrate are indicated by the grey horizontal lines. C. Comparison of scans from flap-out and flap-in nucleosomes. Scans are from Fig. 7C, lanes 2 and 4.