Comparison of K-*Ras* and N-*Ras* mutagenic hot spots for UVC damage

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Supplementary Material

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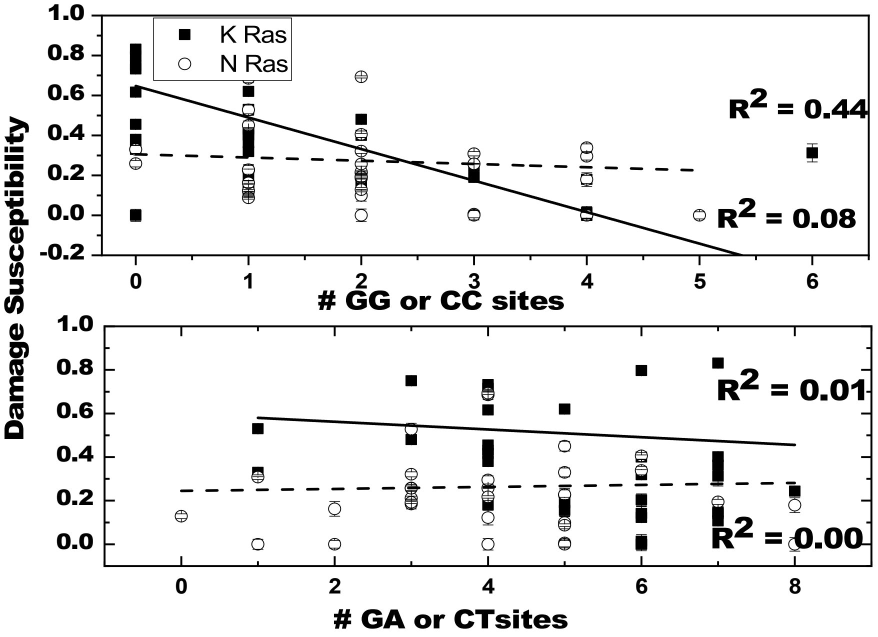

Figure S1. UVC-induced damage susceptibility (1-F) as a function of number of GG/CC and GA/CT sites. The damage susceptibility on the y-axis are 1-F, where F = F_i/F_c, F_i is the fluorescence intensity of EG-dsDNA upon UVC damage and F_c is the fluorescence intensity of the undamaged DNA-EG control sample. EG dye fluorescence intensity at 530 nm is measured in the presence of 1 µM dsDNA (10 mM Tris, 1 mM EDTA, 10 mM NaCl, pH 7.4). For all the plots, the filled squares represent the damage of K-*Ras* sequences and the open circles represent the damage of N-*Ras* sequences. The solid lines through the filled square points are linear fits for the K-*Ras* sequences with their respective R^2 values indicated in the upper portion of each plot. The dashed line through the empty circle points are linear fits for the N-*Ras* sequences with their R^2 value indicated in the lower portion of each plot.

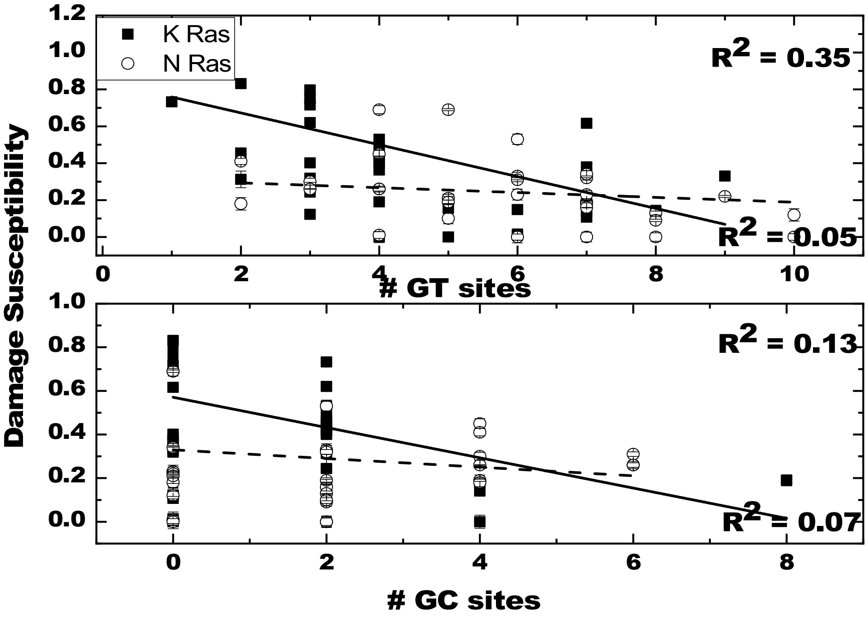

Figure S2. UVC-induced damage susceptibility (1-F) as a function of number of GT and GC sites. The damage susceptibility on the y-axis are 1-F, where $F = F_i/F_c$, F_i is the fluorescence intensity of EG-dsDNA upon UVC damage and F_c is the fluorescence intensity of the undamaged DNA-EG control sample. EG dye fluorescence intensity at 530 nm is measured in the presence of 1 µM dsDNA (10 mM Tris, 1 mM EDTA, 10 mM NaCl, pH 7.4). For all the plots, the filled squares represent the damage of K-*Ras* sequences and the open circles represent the damage of N-*Ras* sequences. The solid lines through the filled square points are linear fits for the K-*Ras* sequences with their respective R^2 values indicated in the upper portion of each plot. The dashed line through the empty circle points are linear fits for the N-*Ras* sequences with their R^2 value indicated in the lower portion of each plot.

Table S1. K-*Ras* gene sequence.

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 ATG ACT GAA TAT AAA CTT GTG GTA GTT GGA GCT GGT GGC GTA GGC AAG AGT GCC TTG ACG ATA CAG CTA 10 20 30 40 50 60
24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 ATT CAG AAT CAT TTT GTG GAC GAA TAT GAT CCA ACA ATA GAG GAT TCC TAC AGG AAG CAA GTA GTA ATT 70 80 90 100 110 120 130
47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 GAT GGA GAA ACC TGT CTC TTG GAT ATT CTC GAC ACA GCA GGT CAA GAG GAG TAC AGT GCA ATG AGG GAC 140 150 160 170 180 190 200
70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93CAG TAC ATG AGG ACT GGG GAG GGC TTT CTT TGT GTA TTT GCC ATA AAT AAT ACT AAA TCA TTT GAA GAT ATT 210 220 230 240 250 260 270
94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 CAC CAT TAT AGA GAA CAA ATT AAA AGA GTT AAG GAC TCT GAA GAT GTA CCT ATG GTC CTA GTA GGA AAT 280 290 300 310 320 330 340
117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 AAA TGT GAT TTG CCT TCT AGA ACA GTA GAC ACA AAA CAG GCT CAG GAC TTA GCA AGA AGT TAT GGA ATT 350 360 370 380 390 400 410
140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 CCT TTT ATT GAA ACA TCA GCA AAG ACA AGA CAG GGT GTT GAT GAT GCC TTC TAT ACA TTA GTT CGA GAA 420 430 440 450 460 470 480
163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 ATT CGA AAA CAT AAA GAA AAG ATG AGC AAA GAT GGT AAA AAG AAG AAA AAG AAG TCA AAG ACA AAGTGT 490 500 510 520 530 540 550
186 187 188 189 GTA ATT ATG TAA 560 567

The codon number and nucleobase number are represented above and below the sequence line, respectively.

Table S2 N-*Ras* gene sequence.

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23
ATG ACT GAG TAC AAA CTG GTG GTG GTT GGAGCA GGTGGT GTT GGG AAA AGC GCA CTG ACAATC CAG CTA
10 20 30 40 50 60

24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47
ATC CAG AAC CAC TTT GTA GAT GAA TAT GAT CCC ACC ATA GAG GAT TCT TACAGA AAA CAA GTG GTT ATA GAT
70 80 90 100 110 120 130 140

48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71
GGT GAA ACCTGT TTG TTG GAC ATA CTG GAT ACA GCT GGACAA GAA GAG TAC AGT GCC ATG AGA GAC CAA TAC
150 160 170 180 190 200 210

72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95
ATG AGG ACA GGC GAA GGC TTC CTC TGTGTA TTT GCC ATC AAT AAT AGC AAG TCA TTT GCG GAT ATT AAC CTC
220 230 240 250 260 270 280

96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119
TAC AGG GAG CAG ATTAAG CGA GTA AAA GAC TCG GAT GAT GTA CCTATG GTG CTA GTG GGA AAC AAG TGT GAT
290 300 310 320 330 340 350

120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143
TTGCCA ACA AGG ACA GTT GAT ACA AAA CAA GCCCAC GAA CTG GCC AAG AGT TAC GGG ATT CCATTC ATT GAA
360 370 380 390 400 410 420

144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167
ACC TCA GCC AAG ACC AGA CAGGGT GTT GAA GAT GCT TTT TAC ACA CTG GTAAGA GAA ATA CGC CAG TAC CGA
430 440 450 460 470 480 490 500

168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190
ATG AAA AAACTC AAC AGC AGT GAT GAT GGG ACT CAG GGT TGT ATG GGA TTG CCA TGT GTG GTG ATG TAA
510 520 530 540 550 560 570

The codon number and nucleobase number are represented above and below the sequence line, respectively