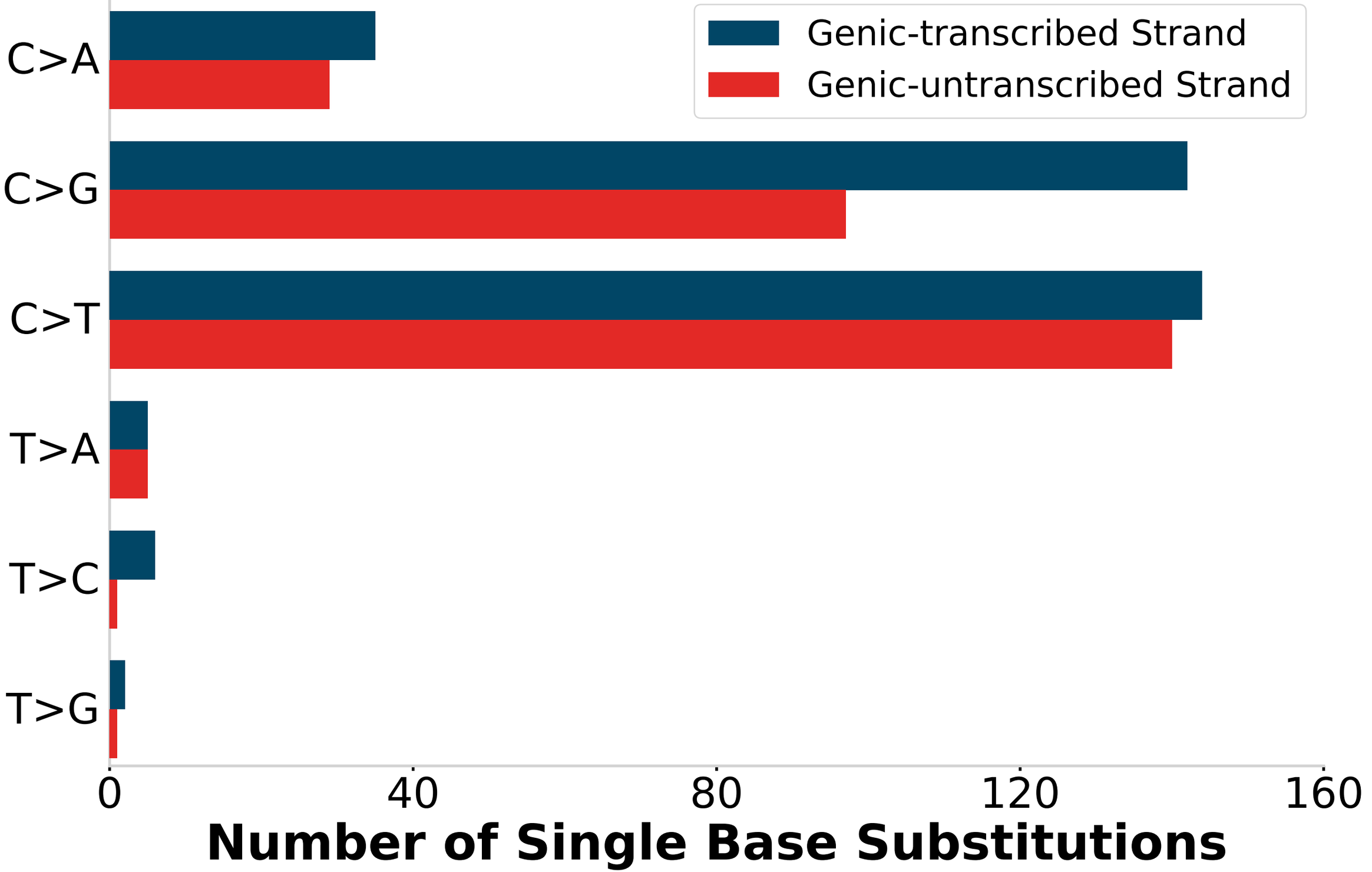
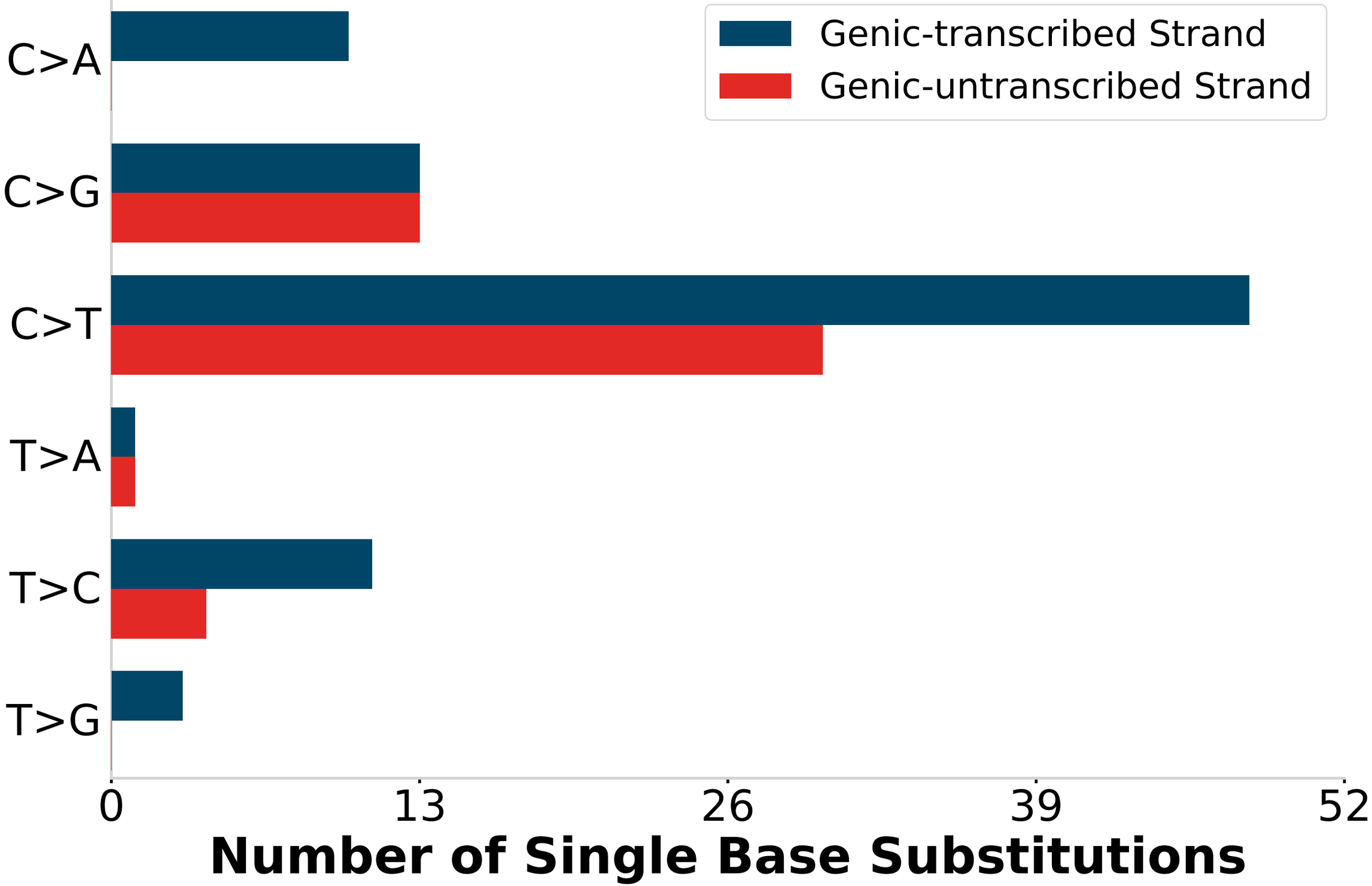
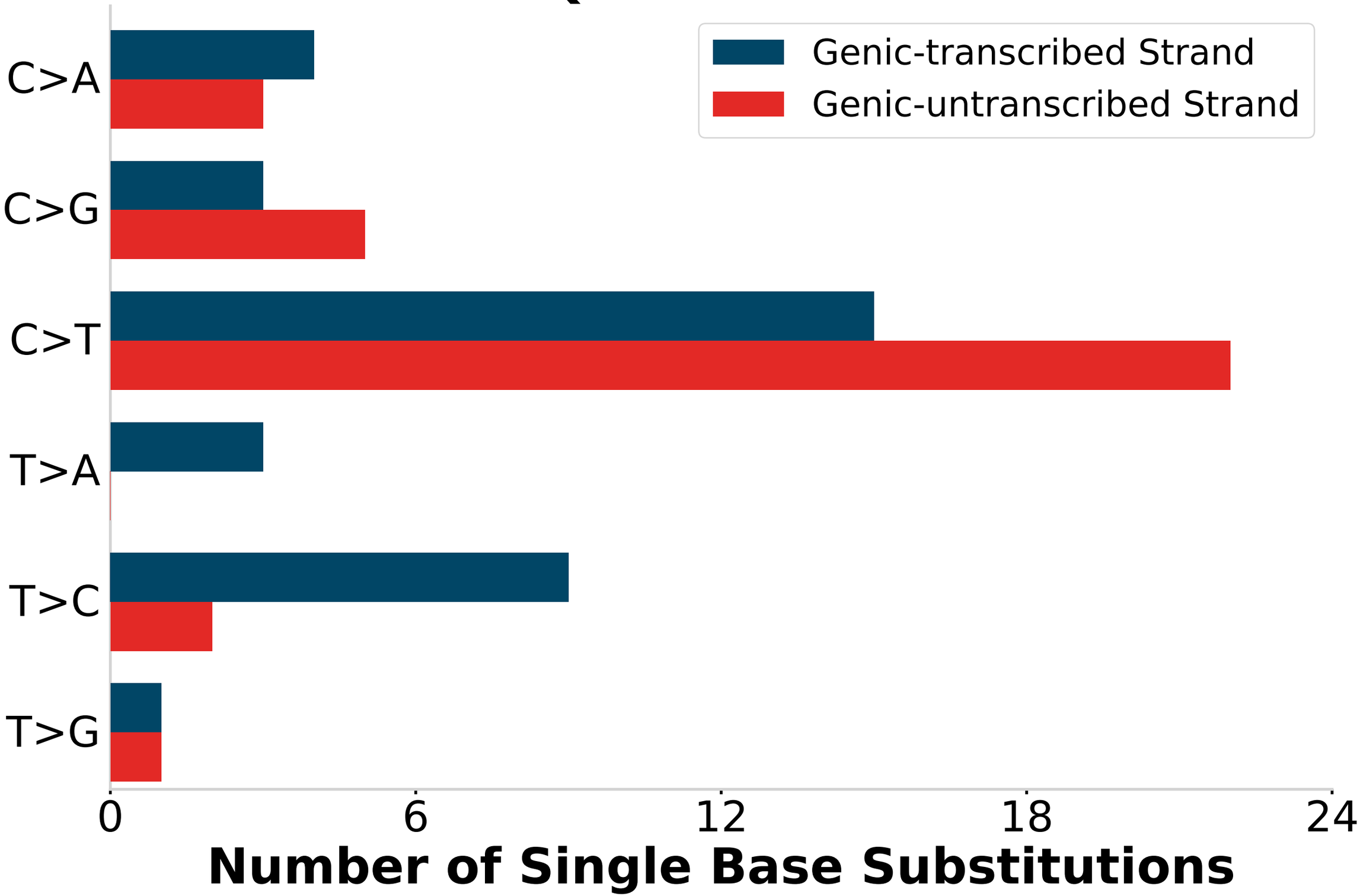
TCGA-2F-A9KO-01A-11D-A38G-08: 607 tra



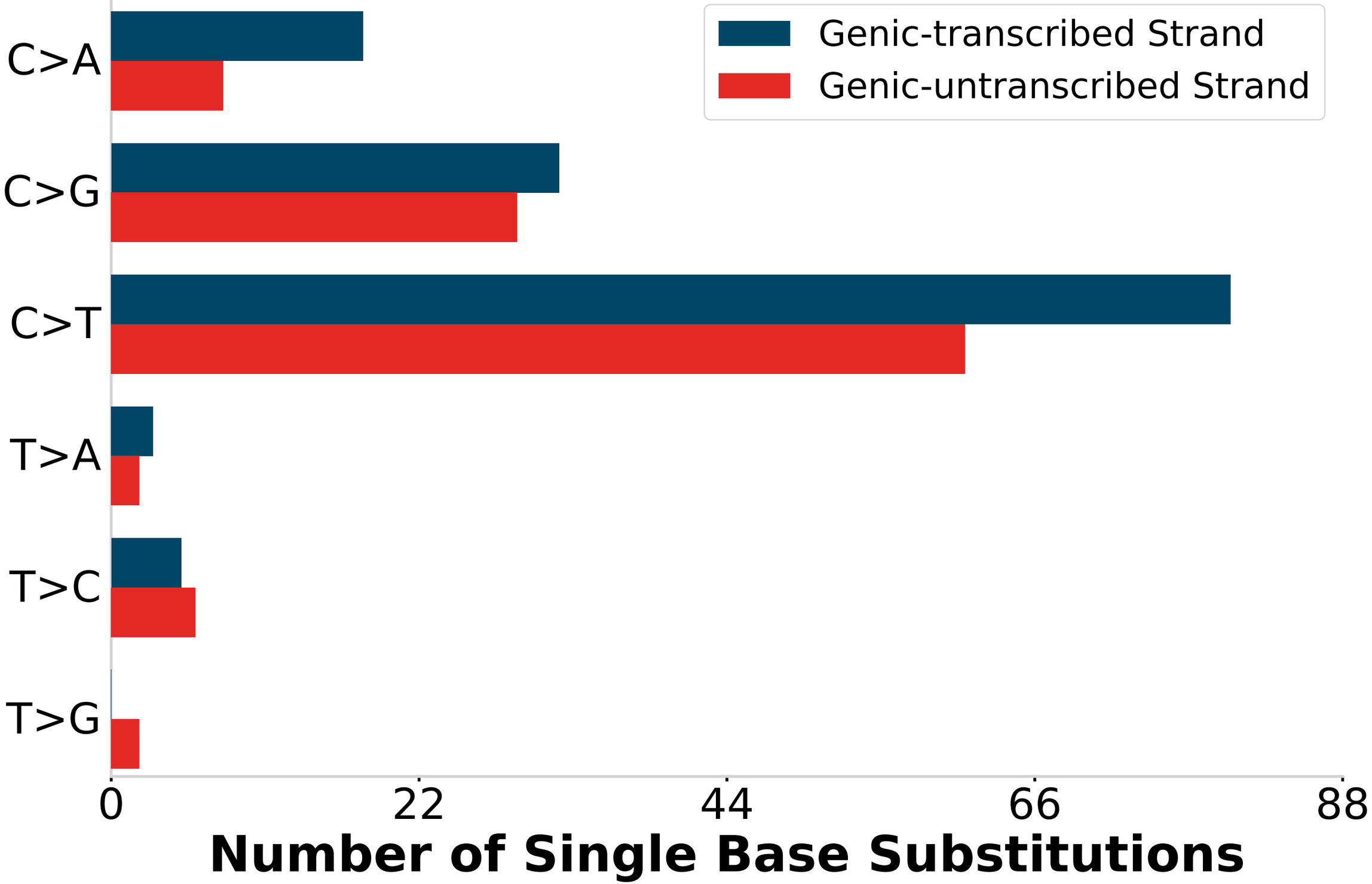
TCGA-2F-A9KP-01A-11D-A38G-08: 134 tra



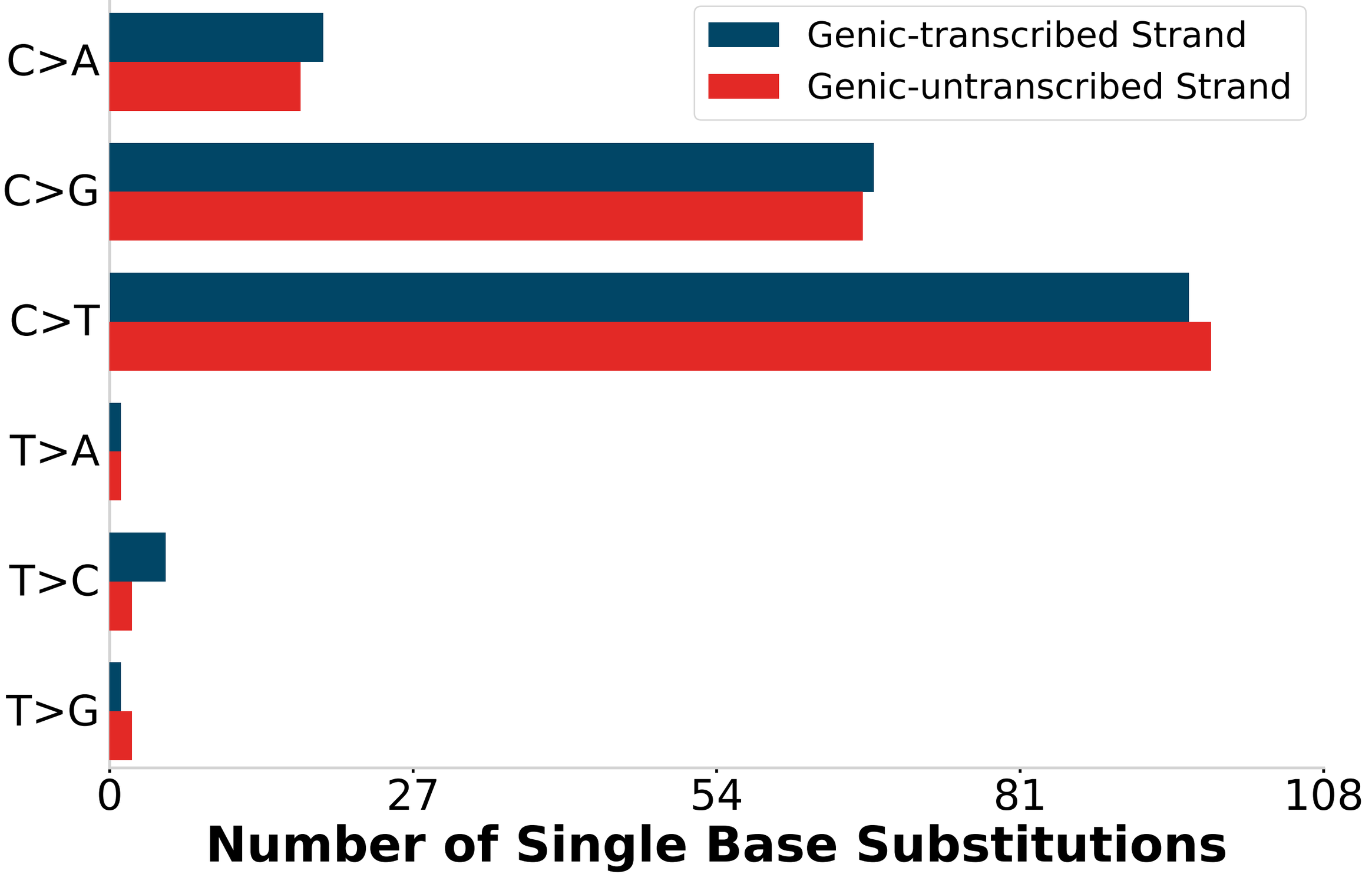
TCGA-2F-A9KQ-01A-11D-A38G-08: 68 tran



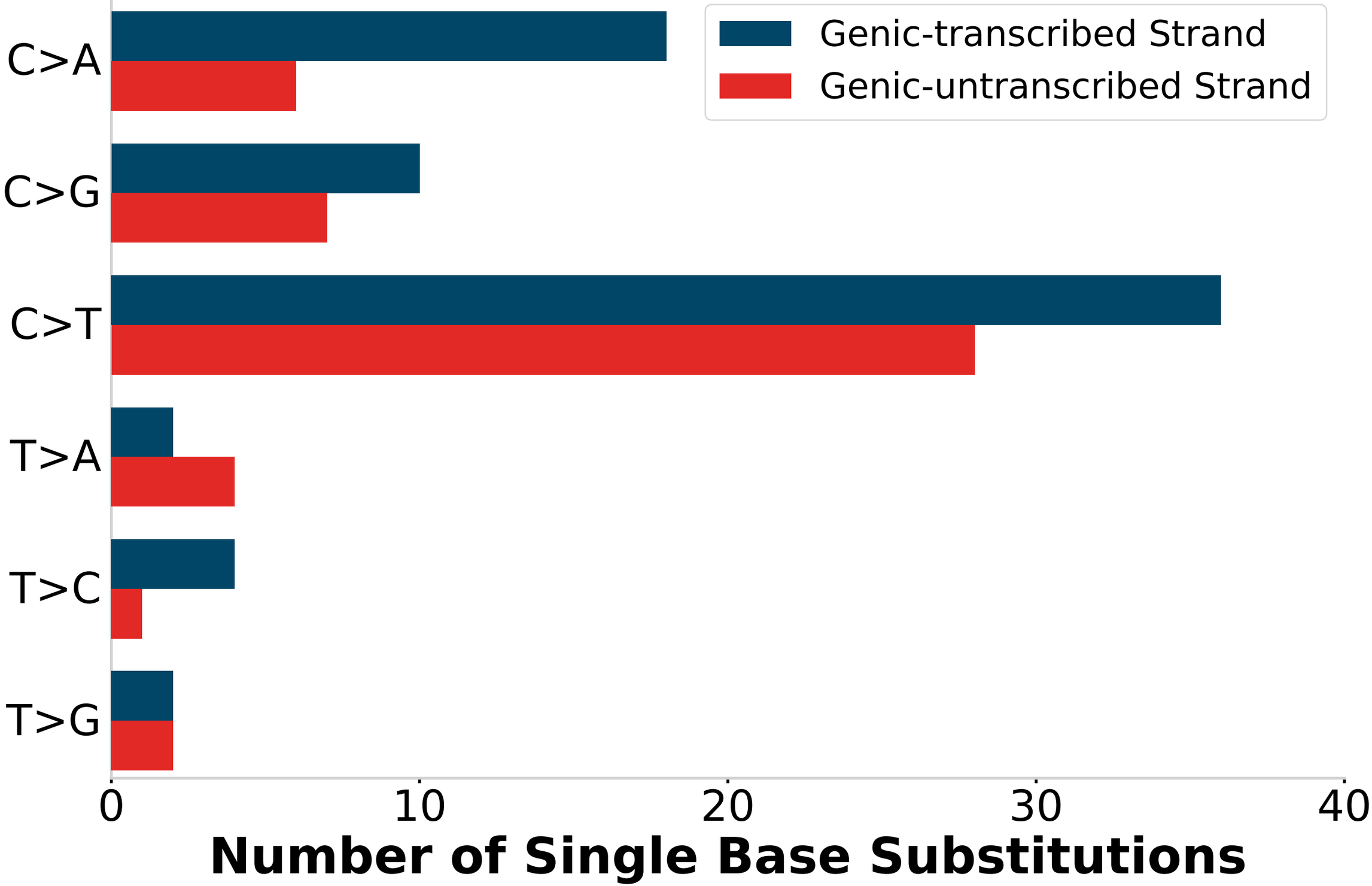
TCGA-2F-A9KR-01A-11D-A38G-08: 246 tra



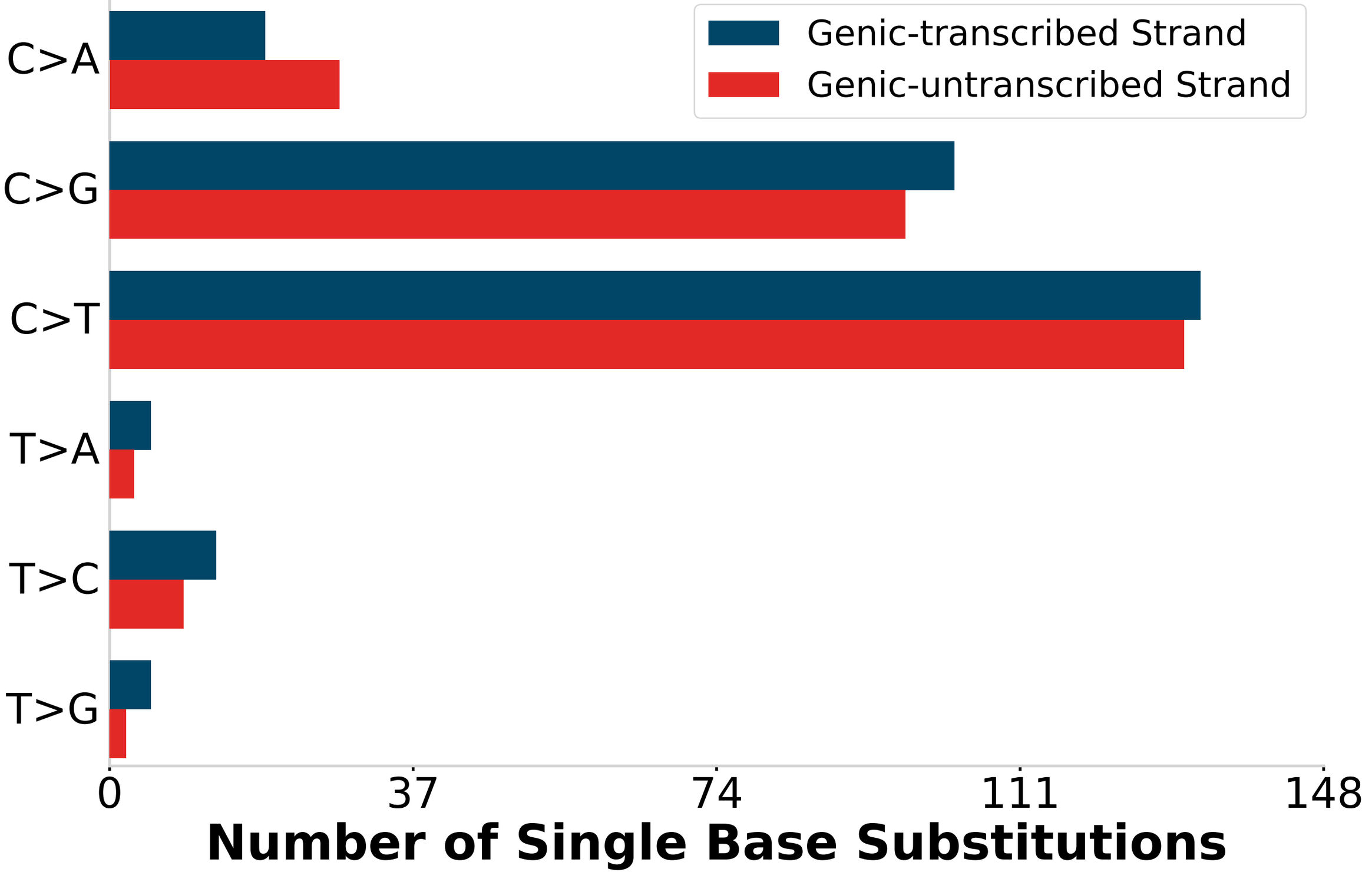
TCGA-2F-A9KT-01A-11D-A38G-08: 377 tran



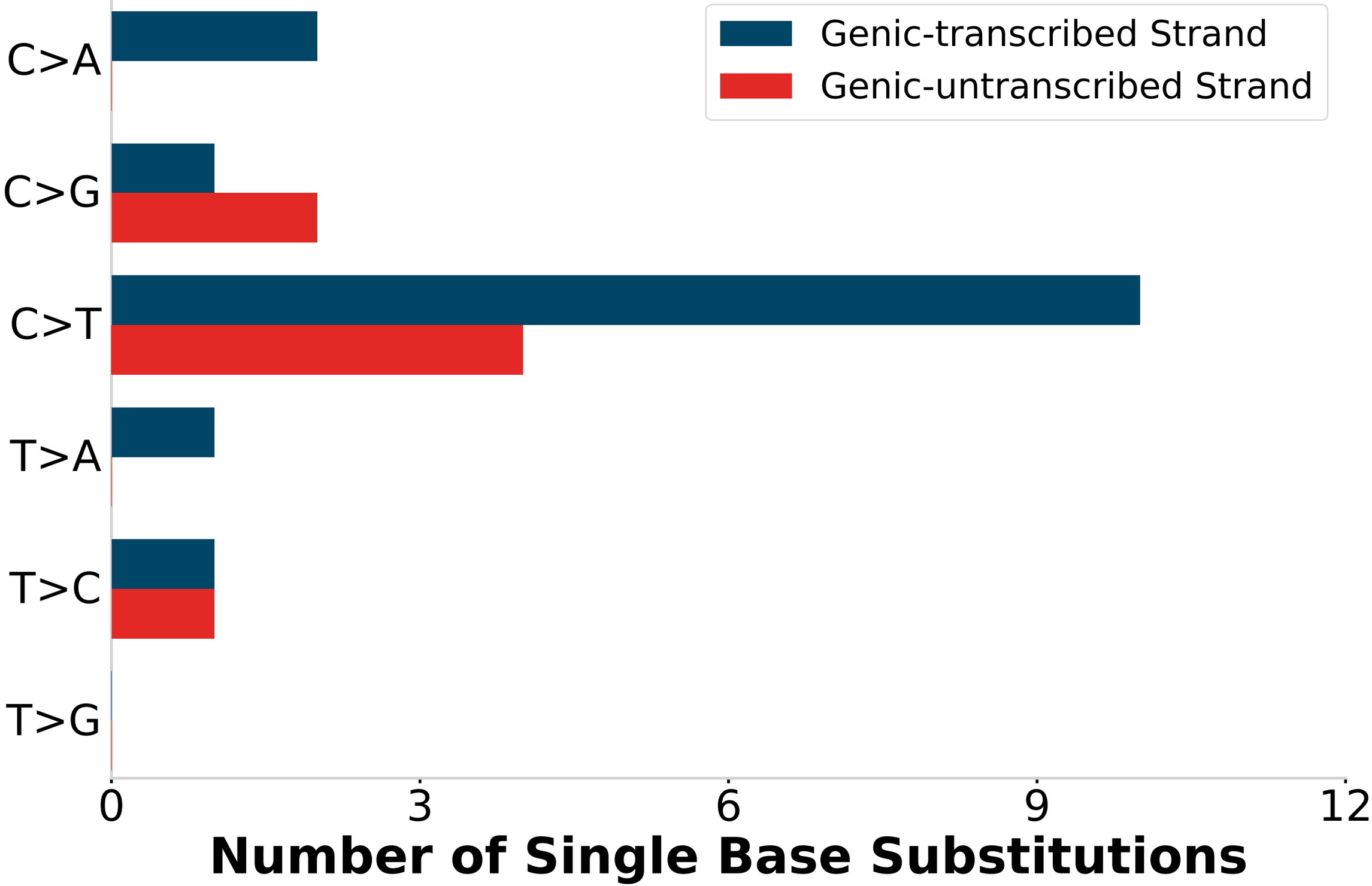
TCGA-2F-A9KW-01A-11D-A38G-08: 120 tra



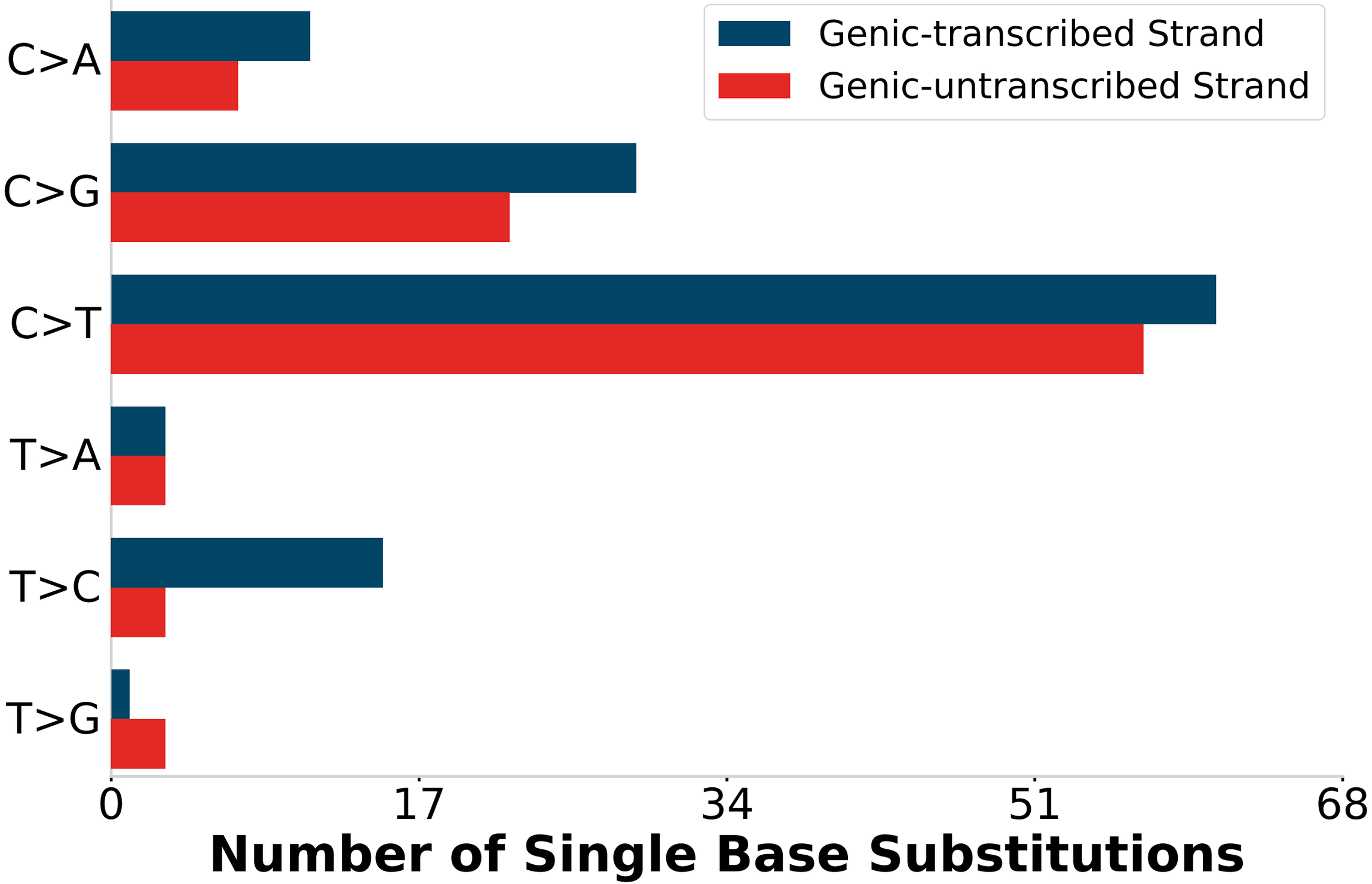
TCGA-4Z-AA7M-01A-11D-A391-08: 548 tra



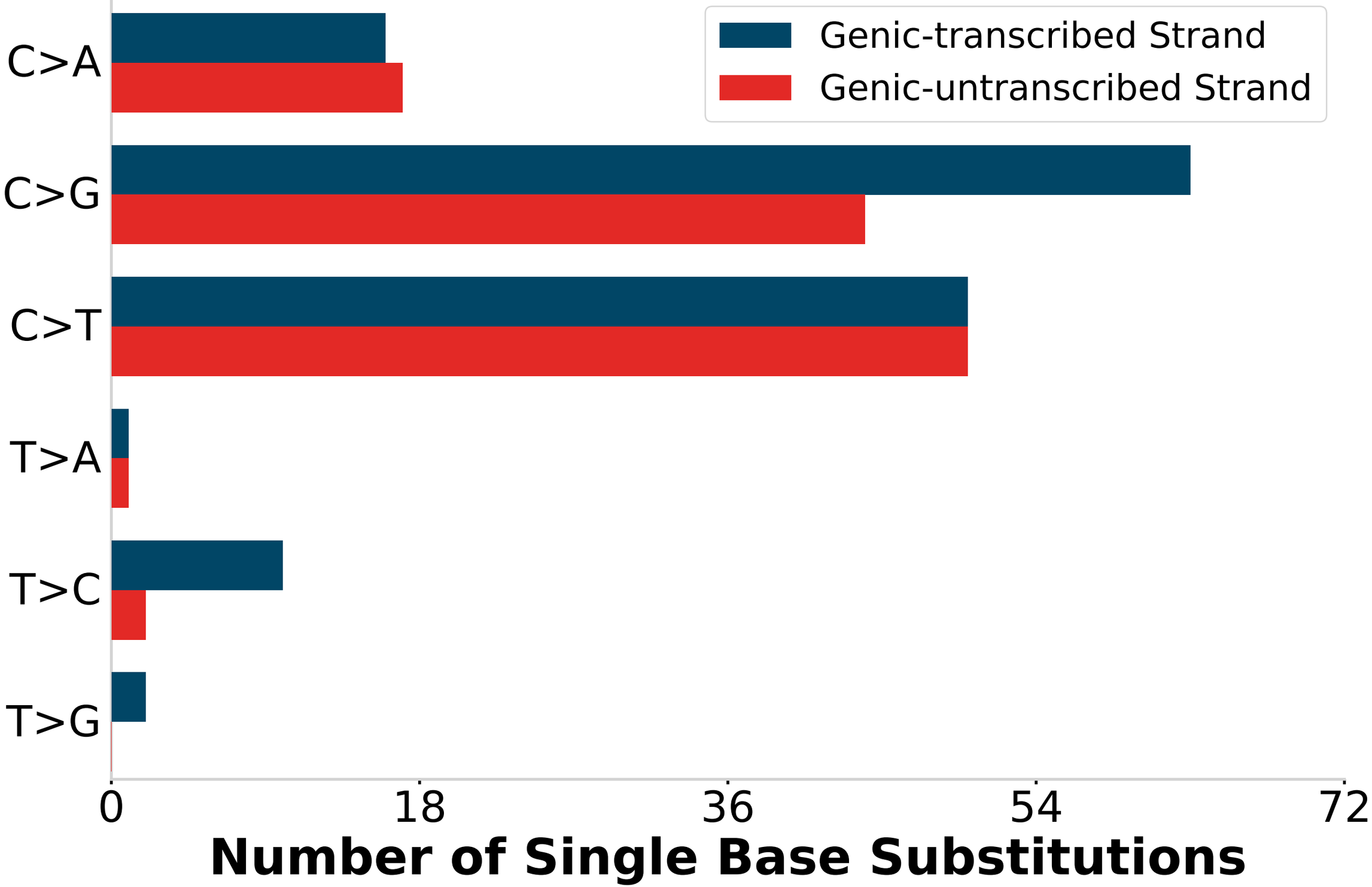
TCGA-4Z-AA7N-01A-11D-A391-08: 22 trans



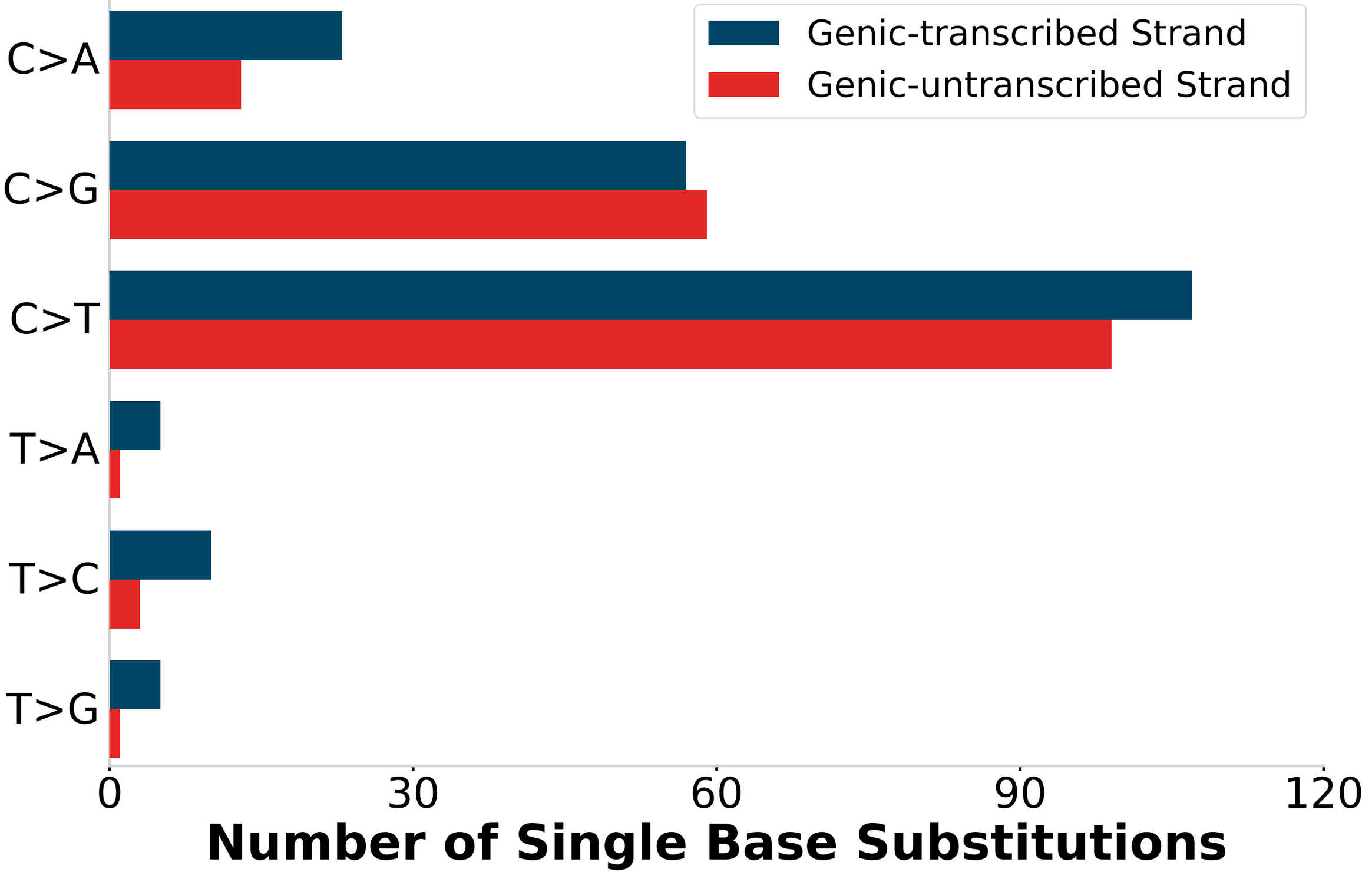
TCGA-4Z-AA7O-01A-31D-A391-08: 215 tra



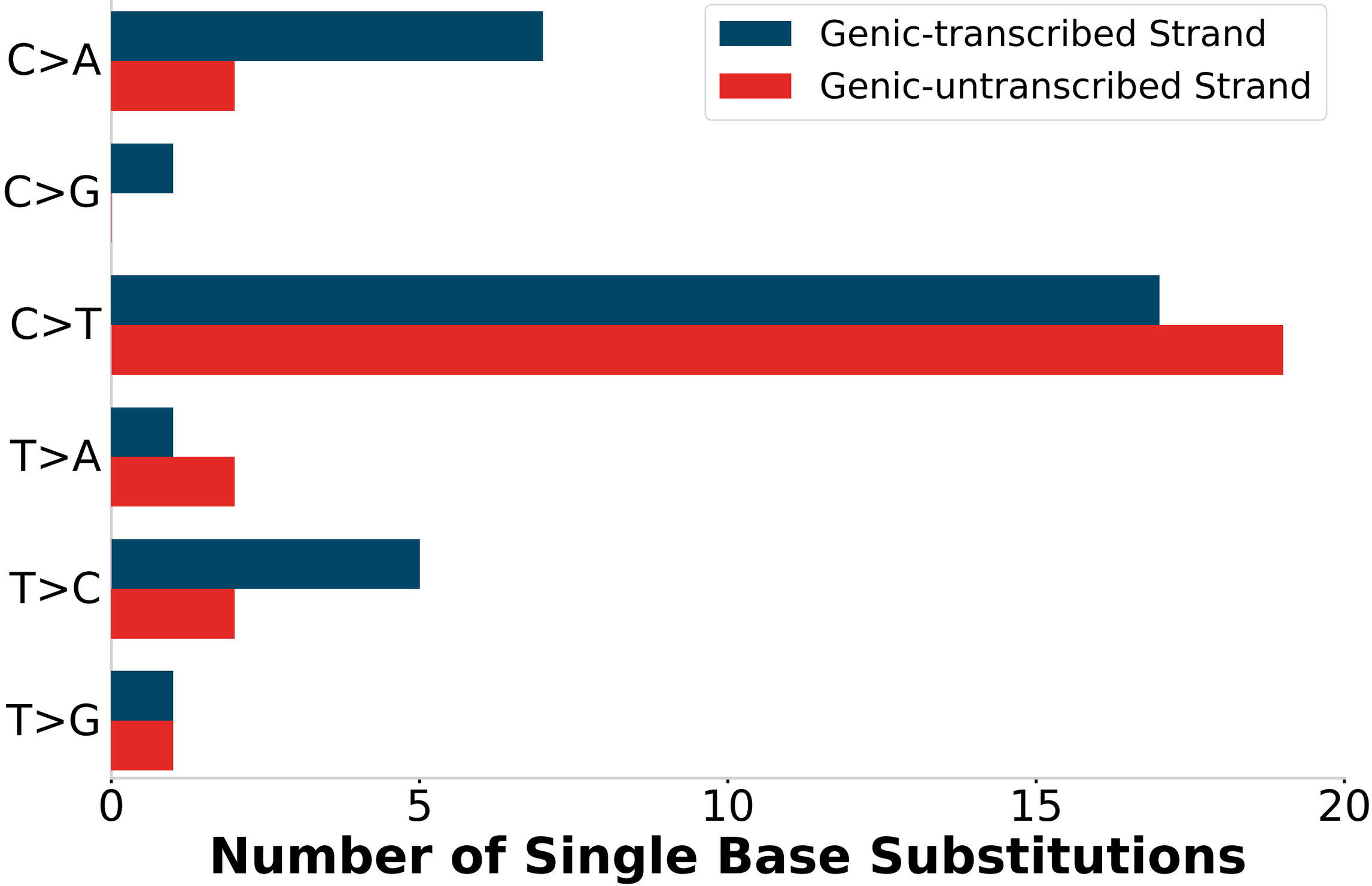
TCGA-4Z-AA7Q-01A-11D-A391-08: 256 tra



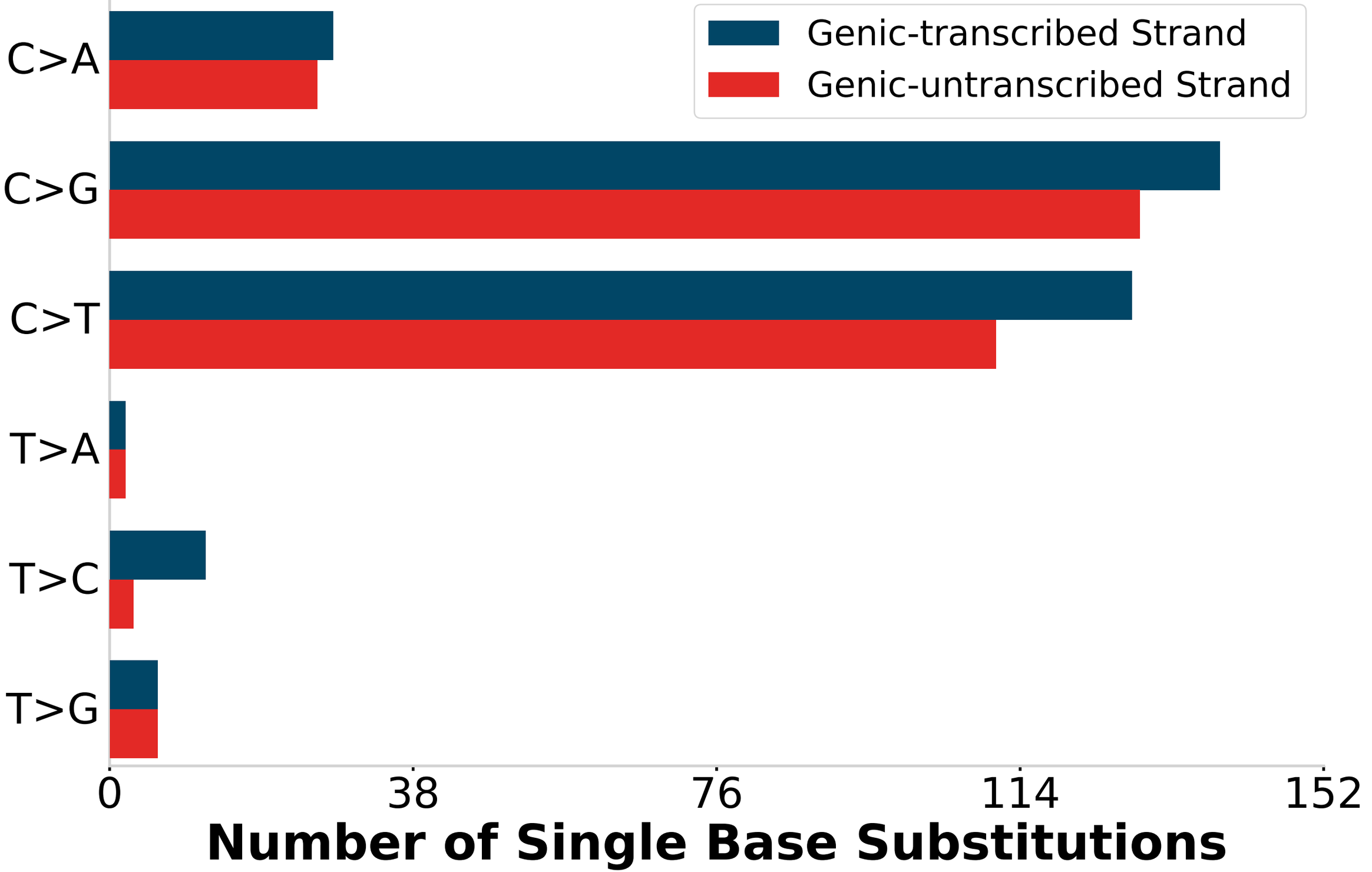
TCGA-4Z-AA7R-01A-11D-A391-08: 383 tra



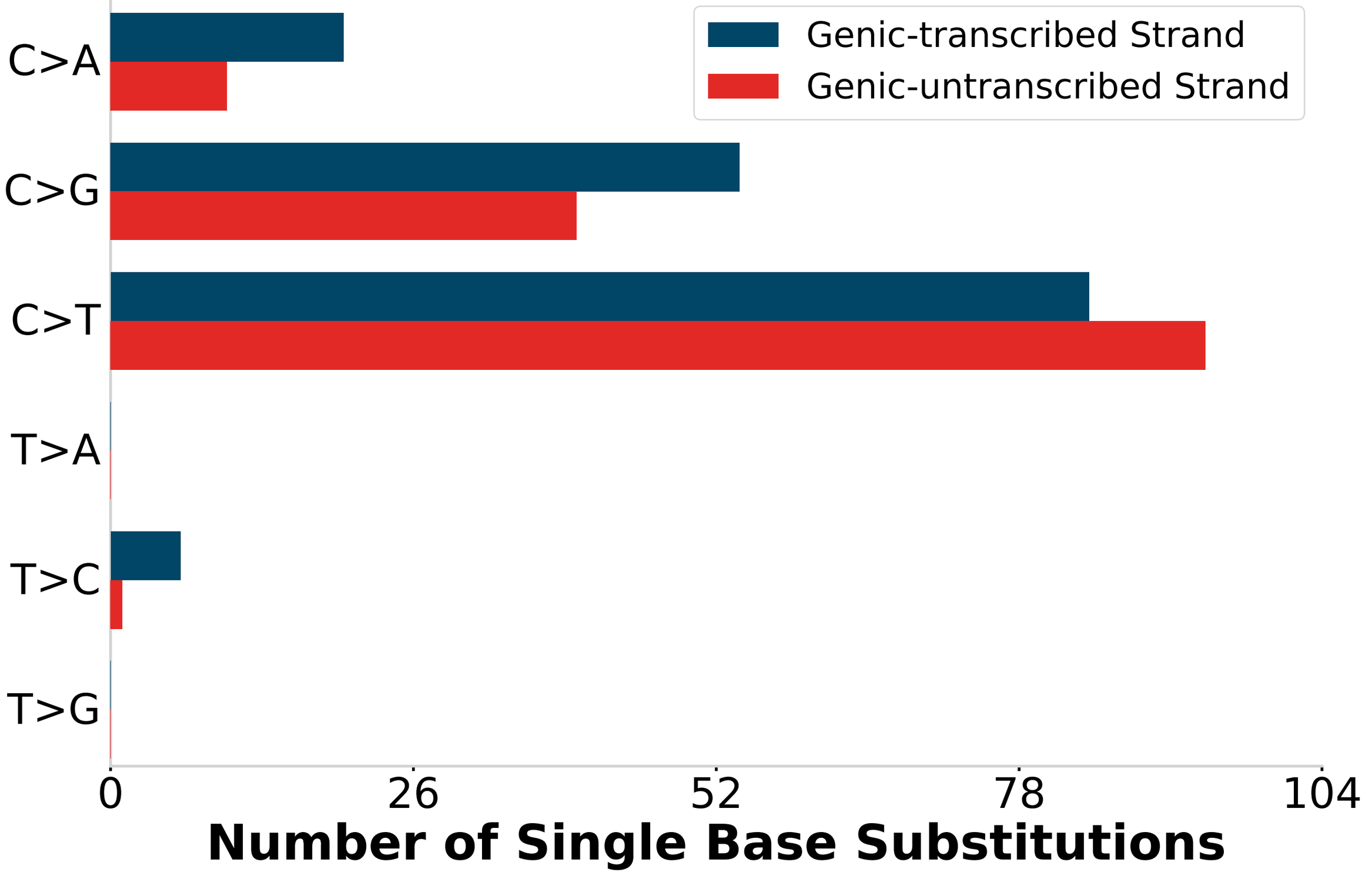
TCGA-4Z-AA7S-01A-11D-A391-08: 58 trans



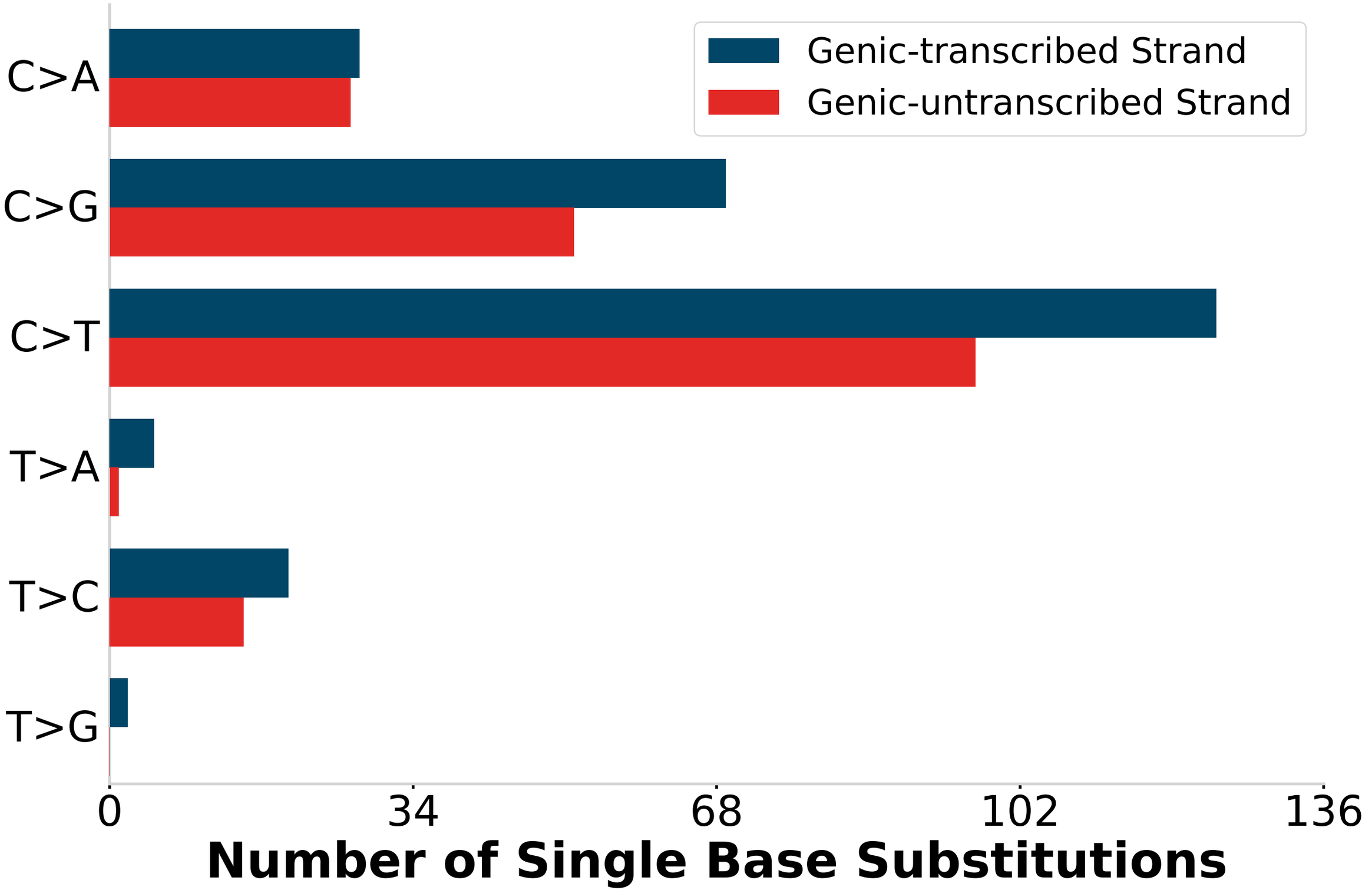
TCGA-4Z-AA7W-01A-11D-A391-08: 592 tra



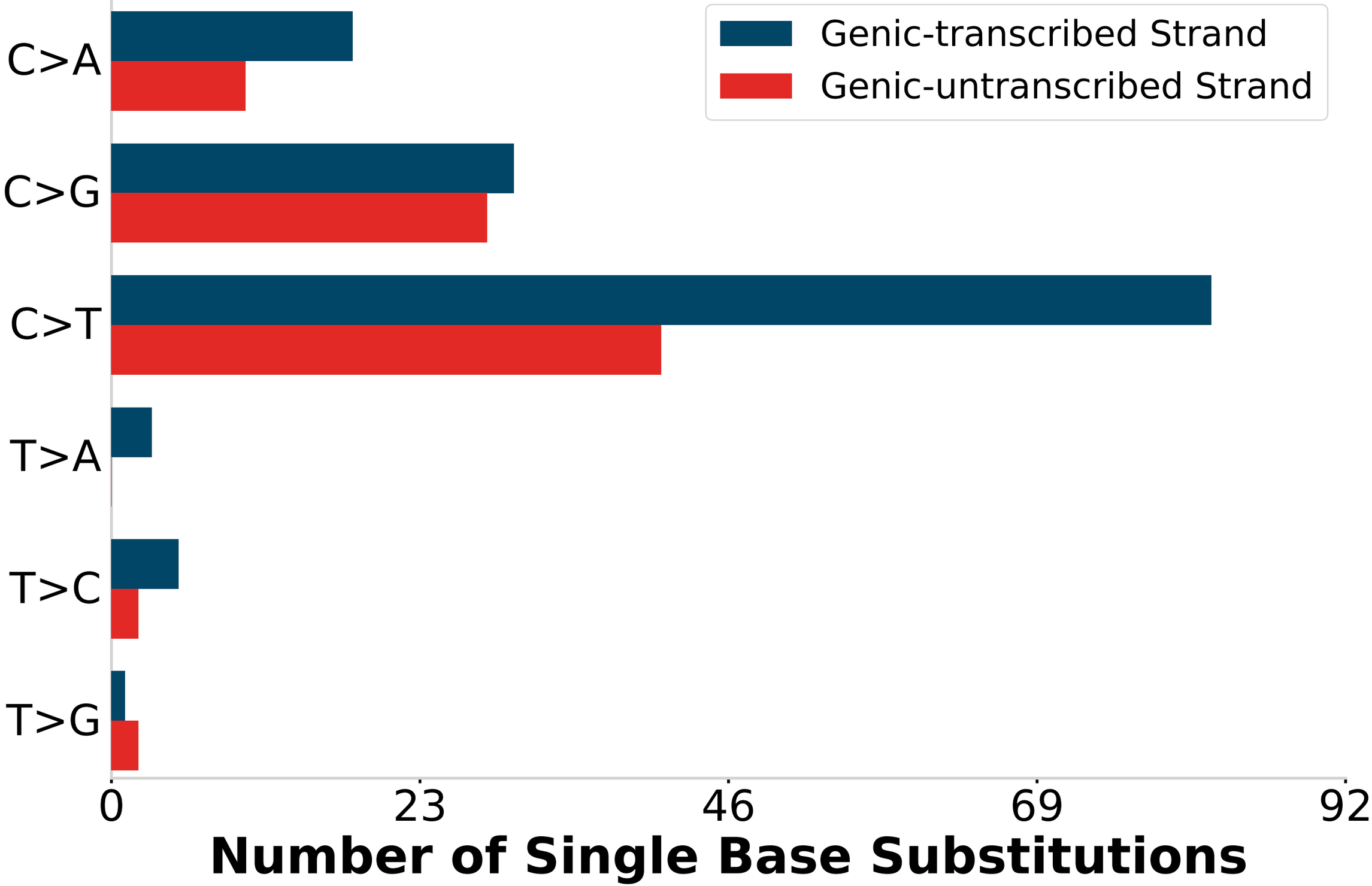
TCGA-4Z-AA7Y-01A-11D-A391-08: 309 tran



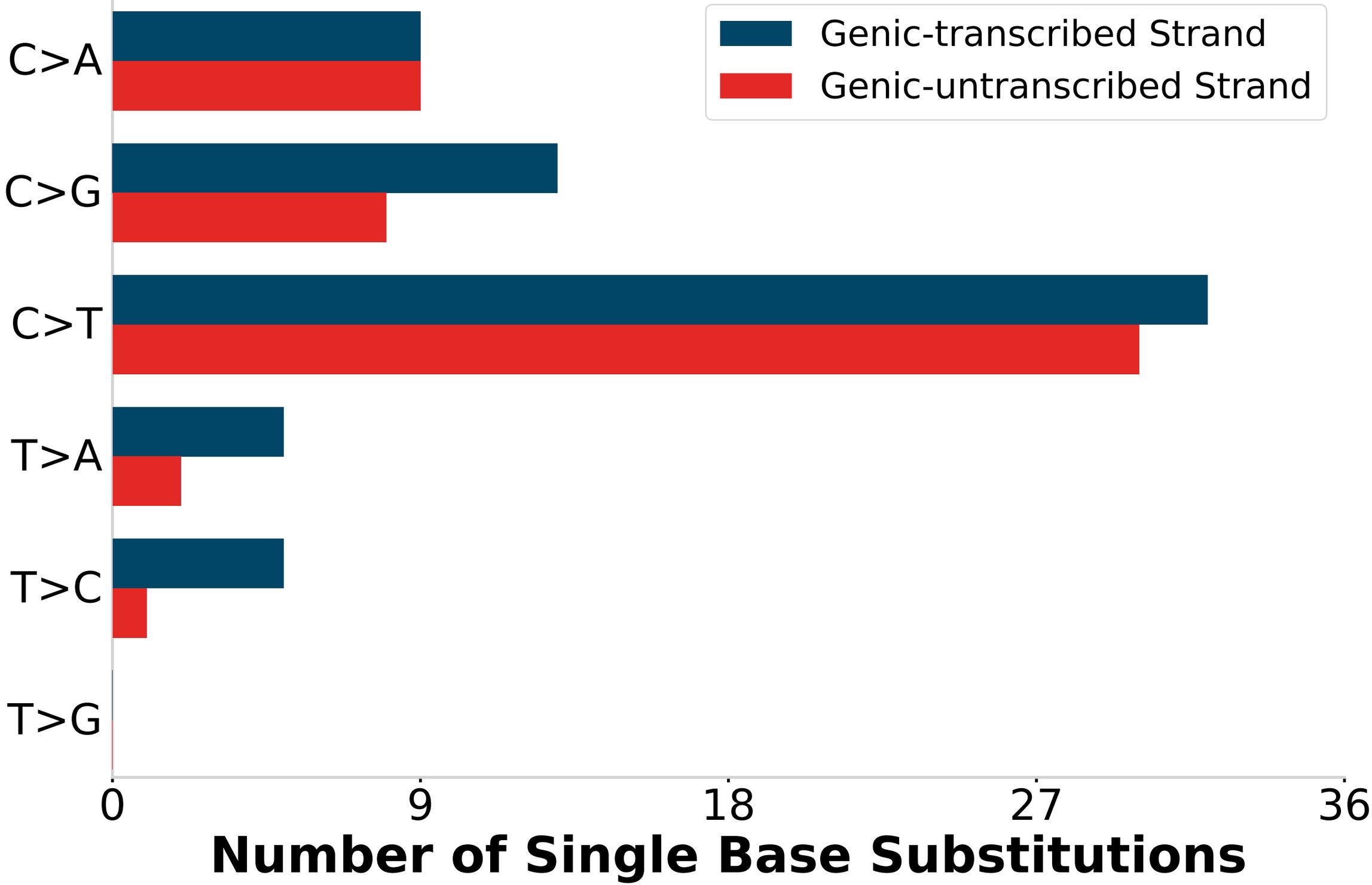
TCGA-4Z-AA80-01A-11D-A391-08: 440 tran



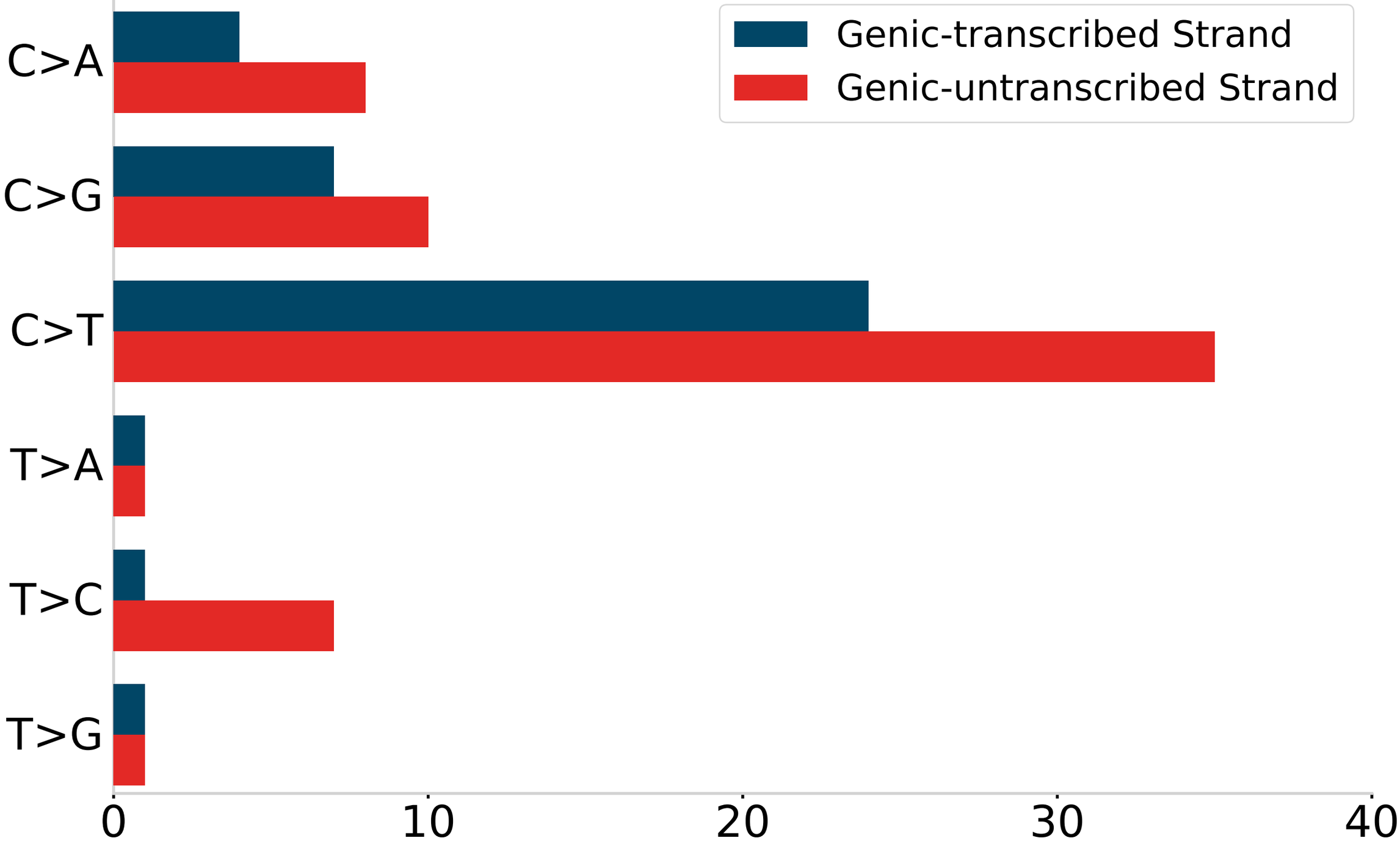
TCGA-4Z-AA81-01A-11D-A391-08: 222 tran



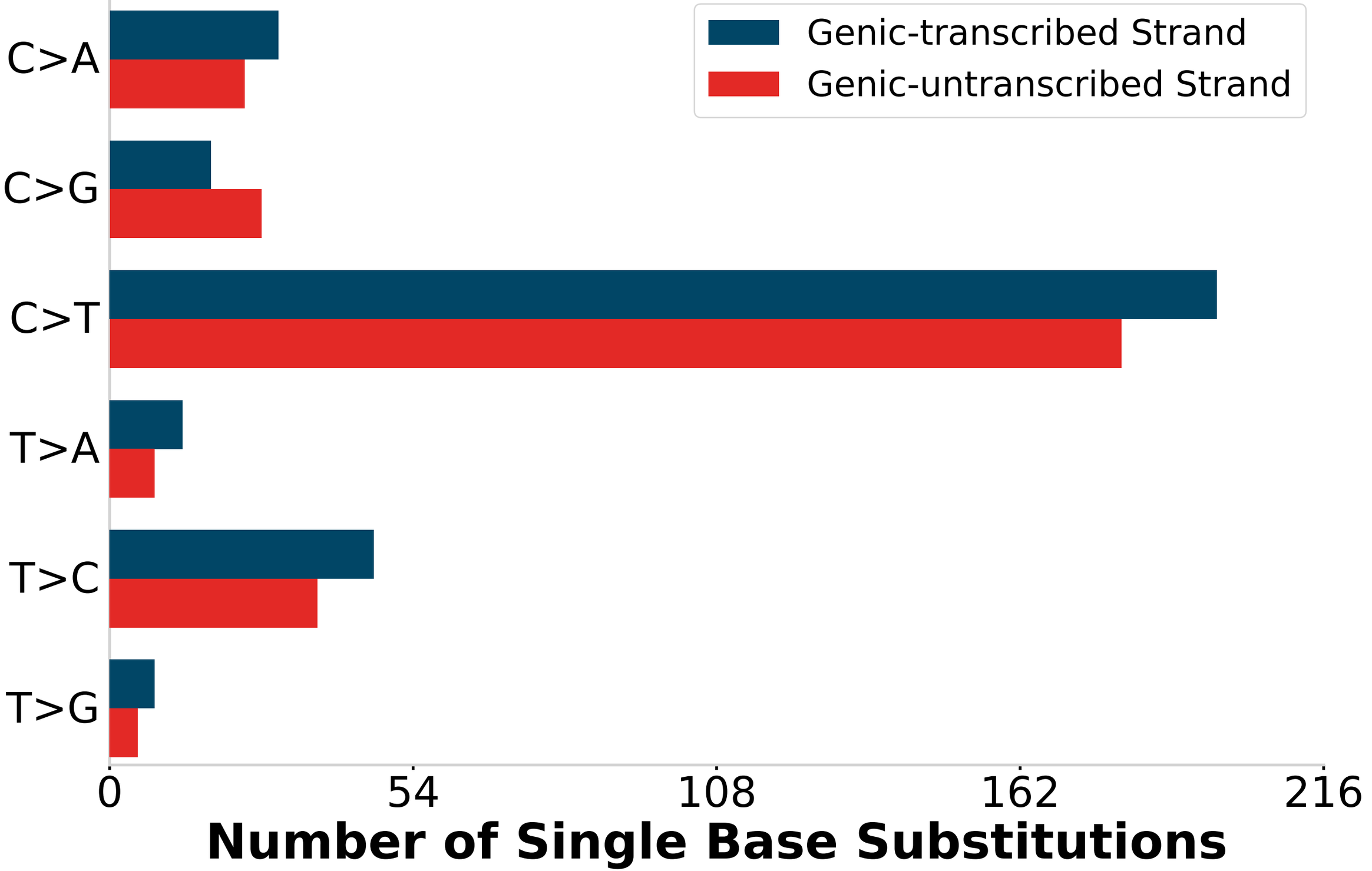
TCGA-4Z-AA82-01A-11D-A391-08: 114 tran



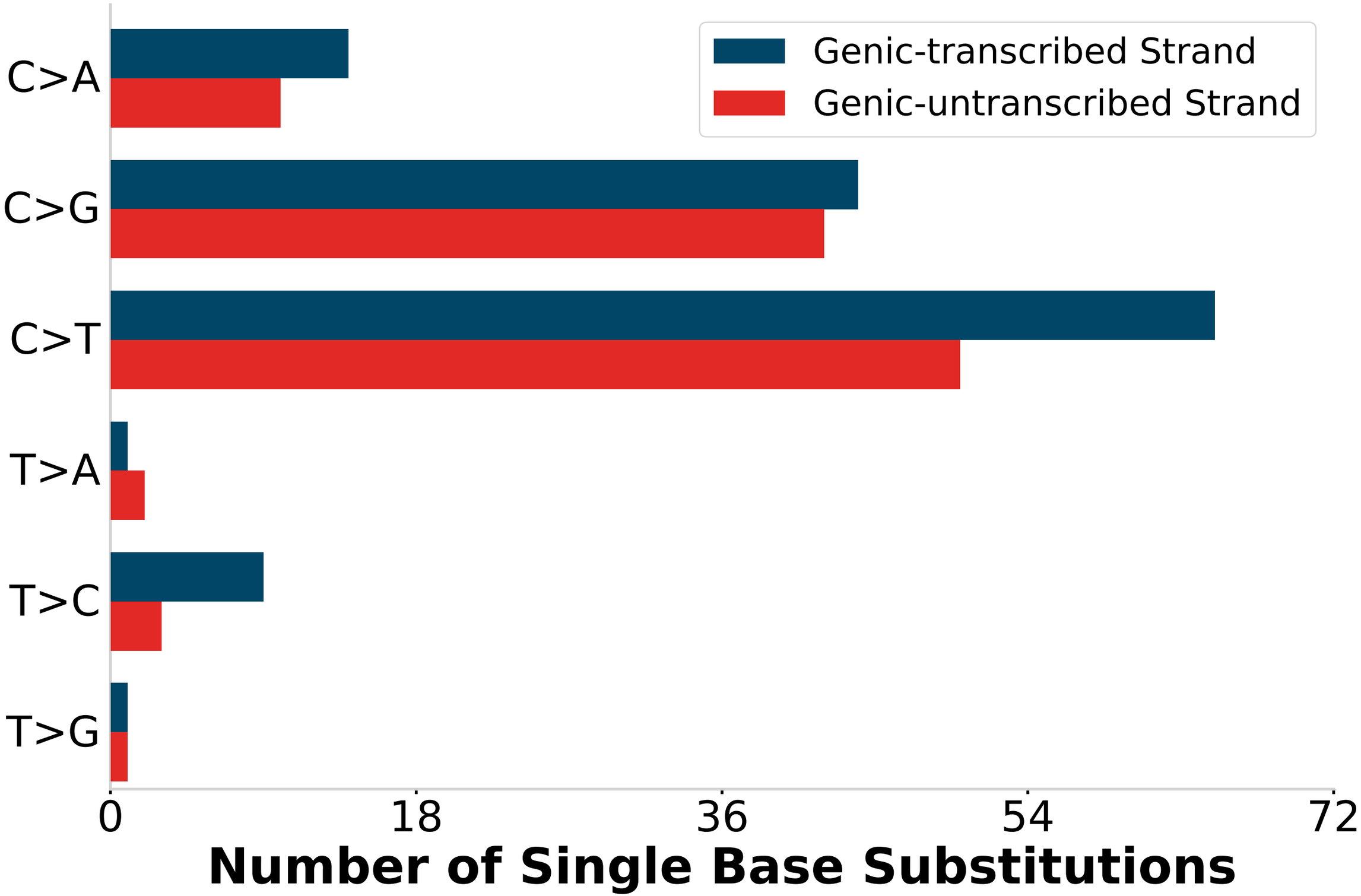
TCGA-4Z-AA83-01A-11D-A391-08: 100 tran



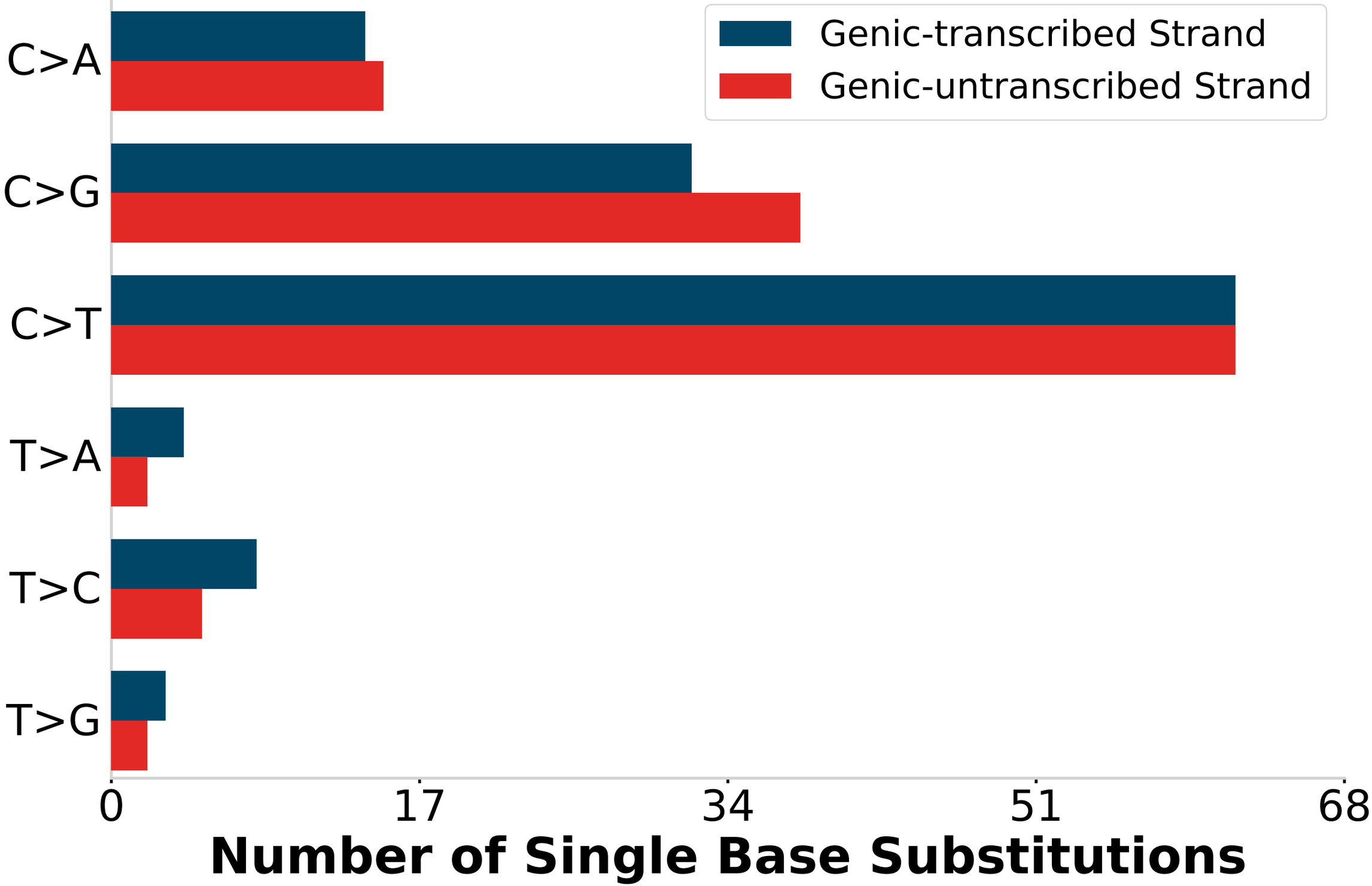
TCGA-4Z-AA84-01A-11D-A391-08: 594 tran



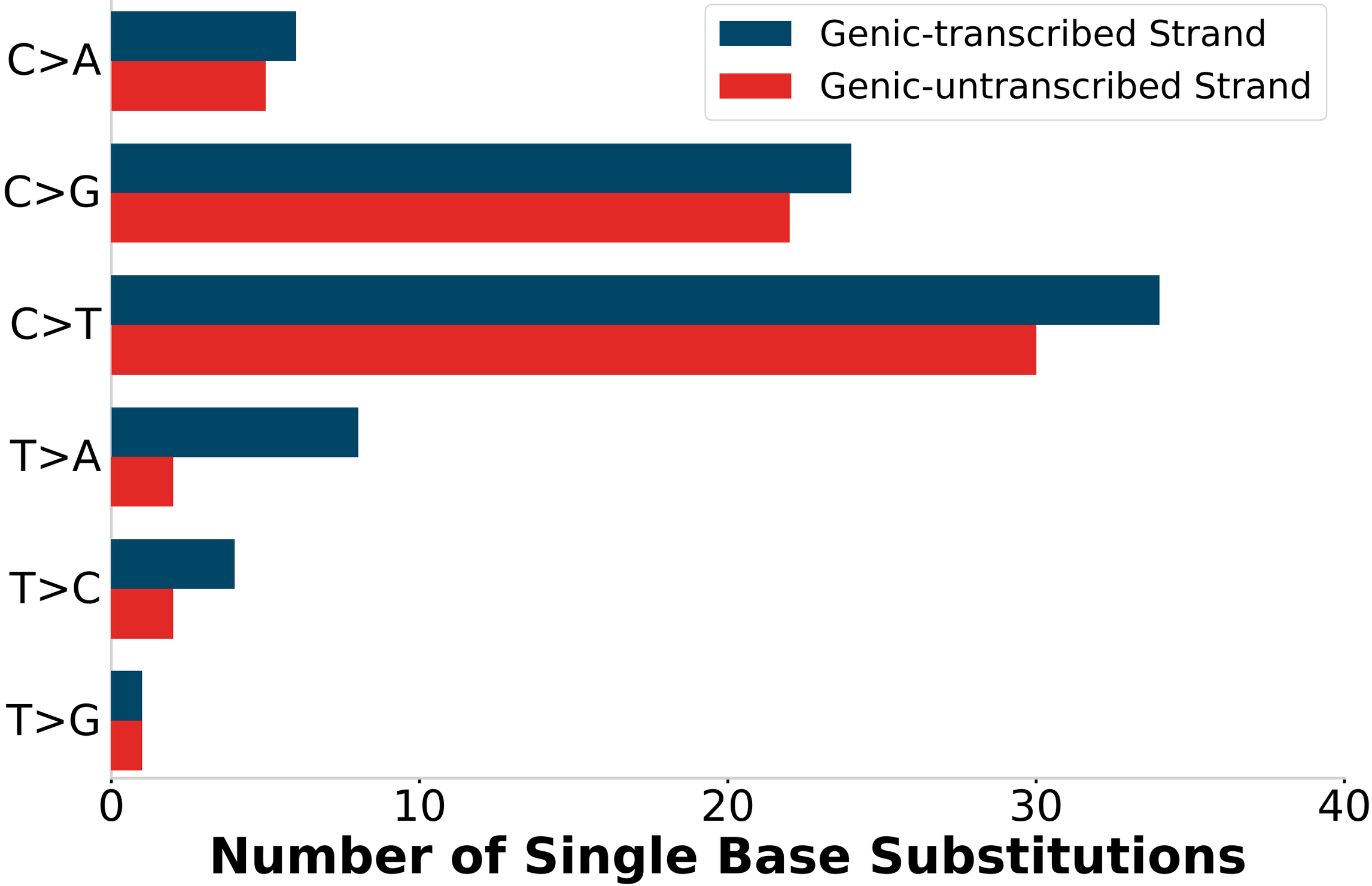
TCGA-4Z-AA86-01A-11D-A391-08: 242 tran



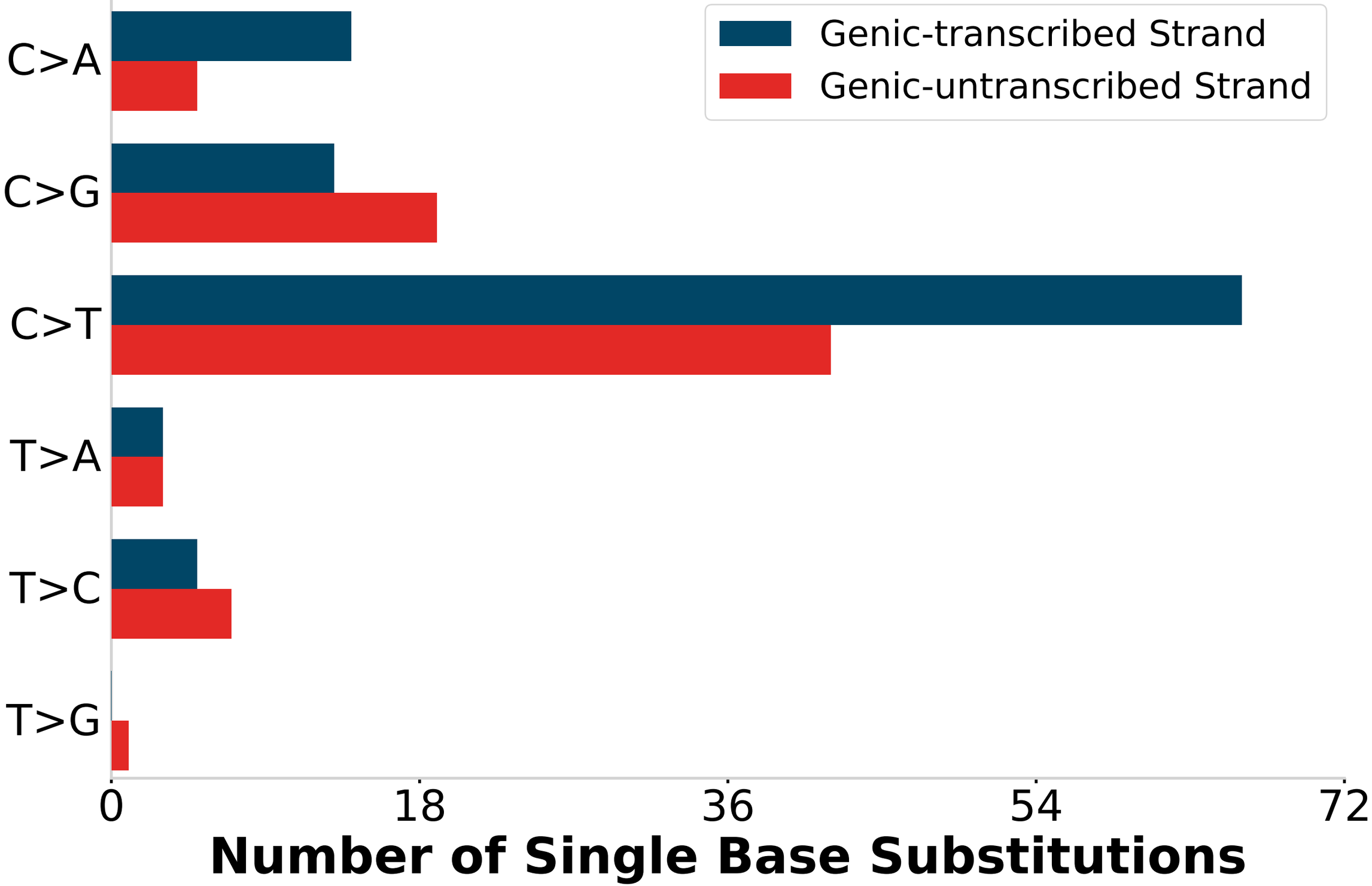
TCGA-4Z-AA87-01A-11D-A391-08: 247 tran



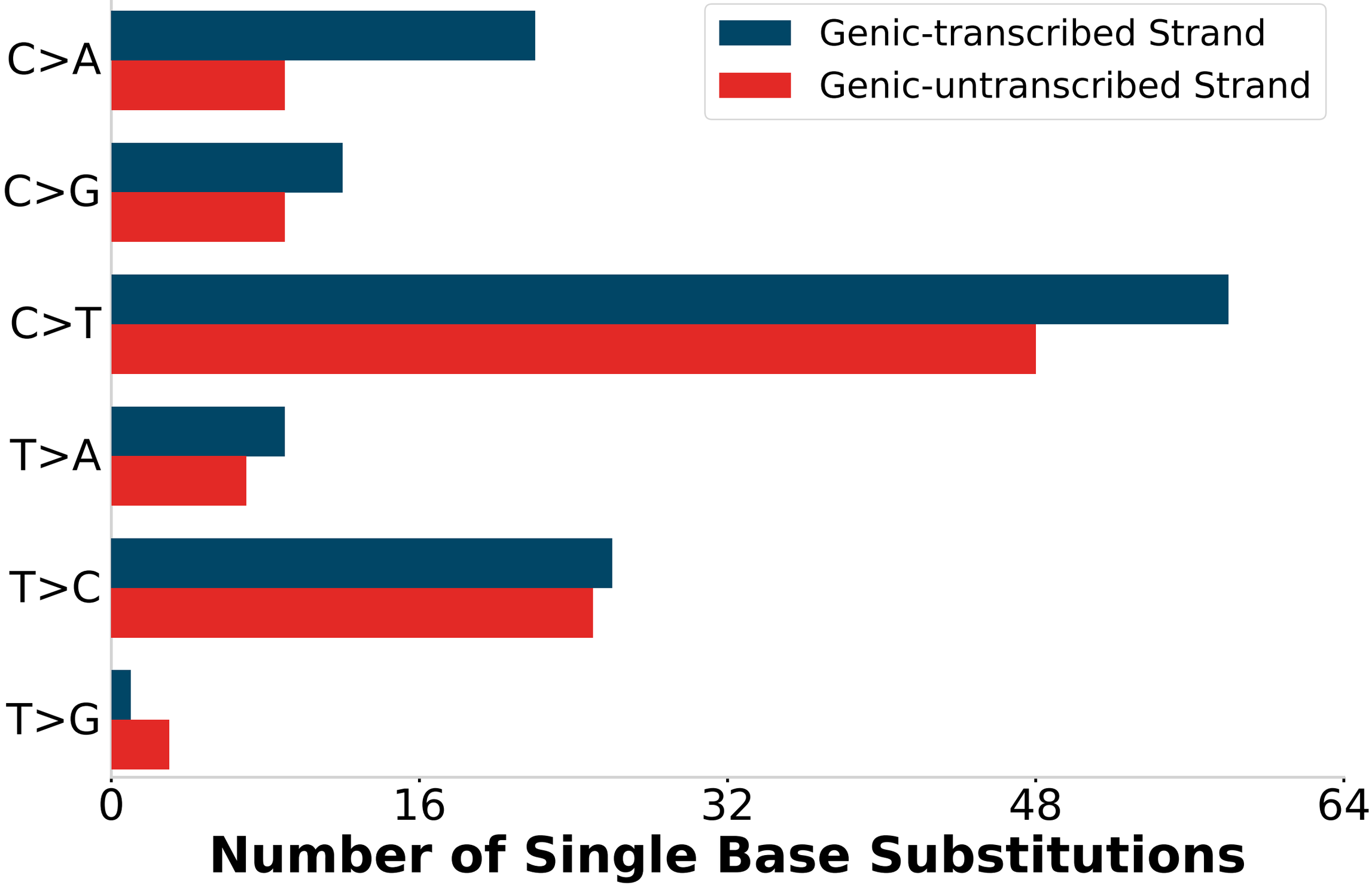
TCGA-4Z-AA89-01A-11D-A391-08: 139 tran



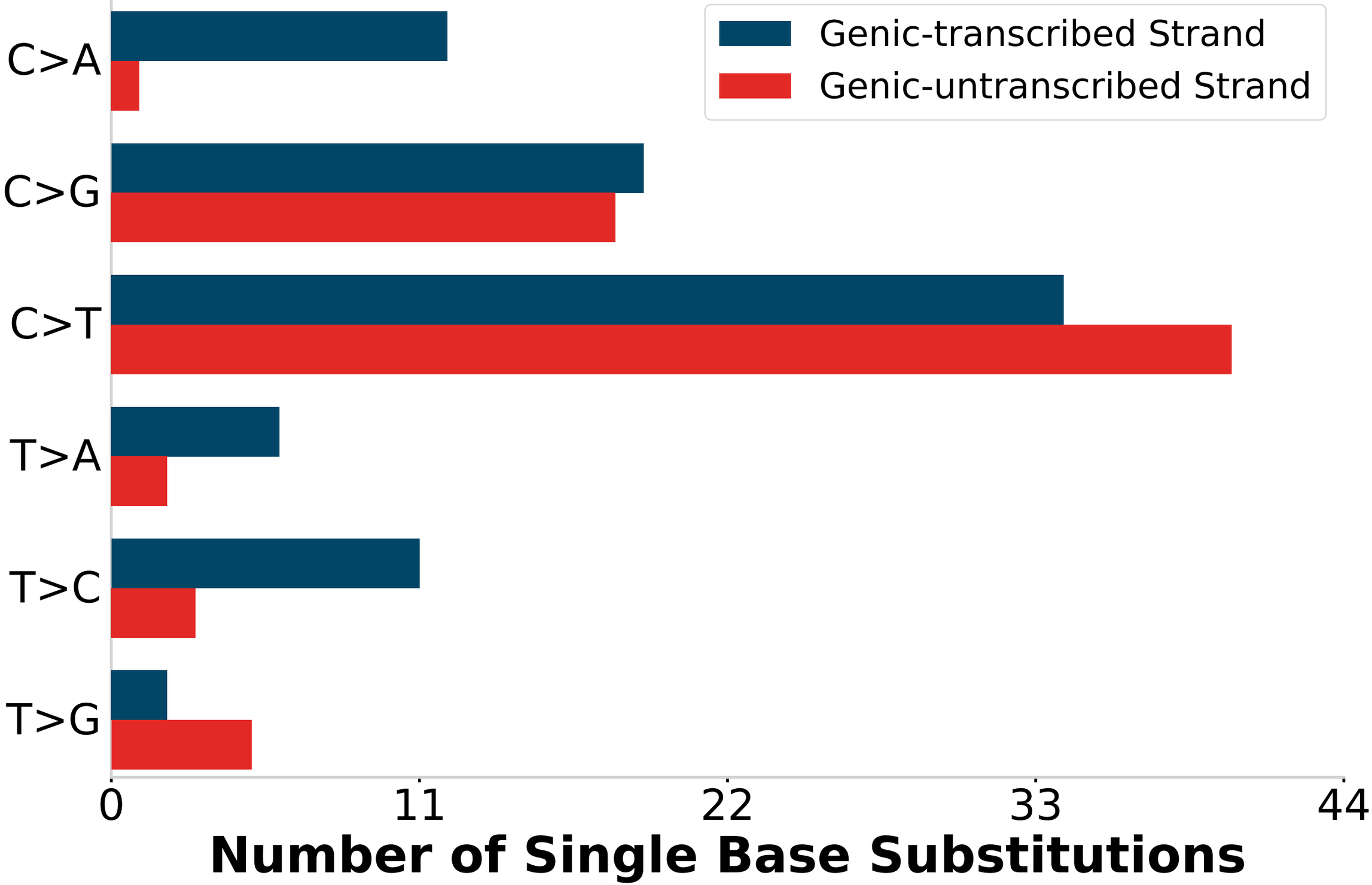
TCGA-5N-A9KI-01A-31D-A42E-08: 178 tran



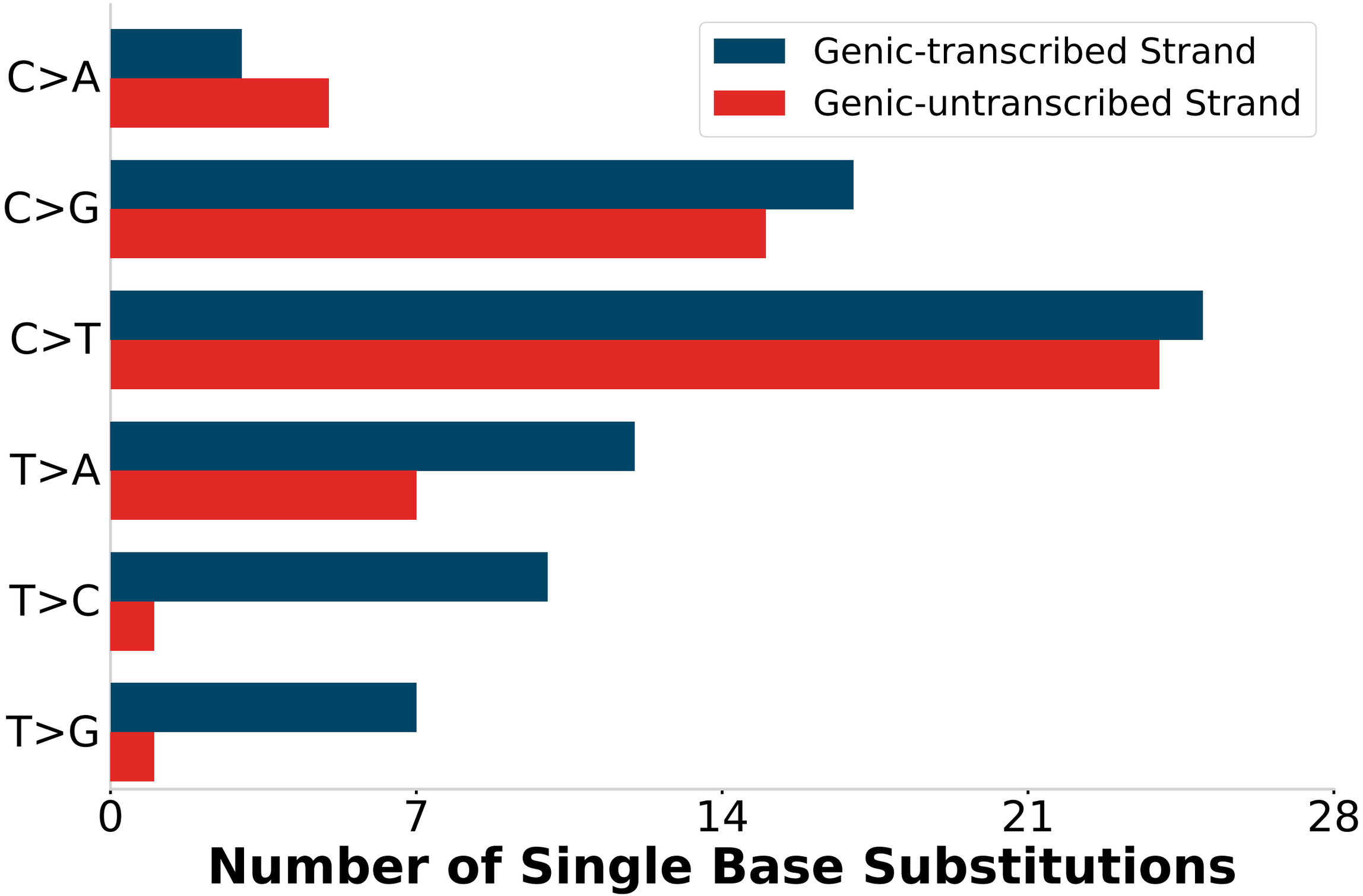
TCGA-5N-A9KM-01A-11D-A42E-08: 229 tra



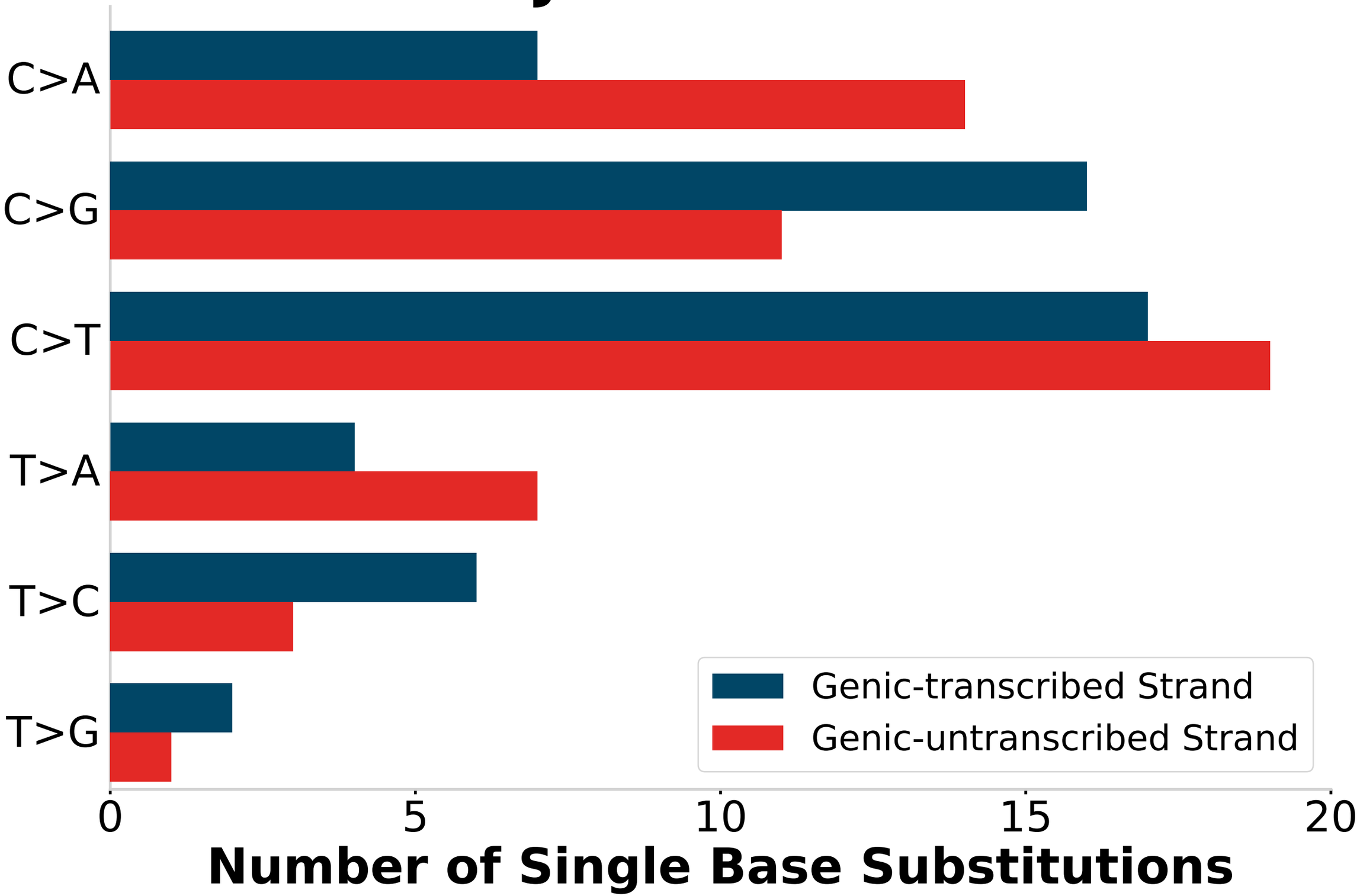
TCGA-BL-A0C8-01A-11D-A271-08: 153 tran



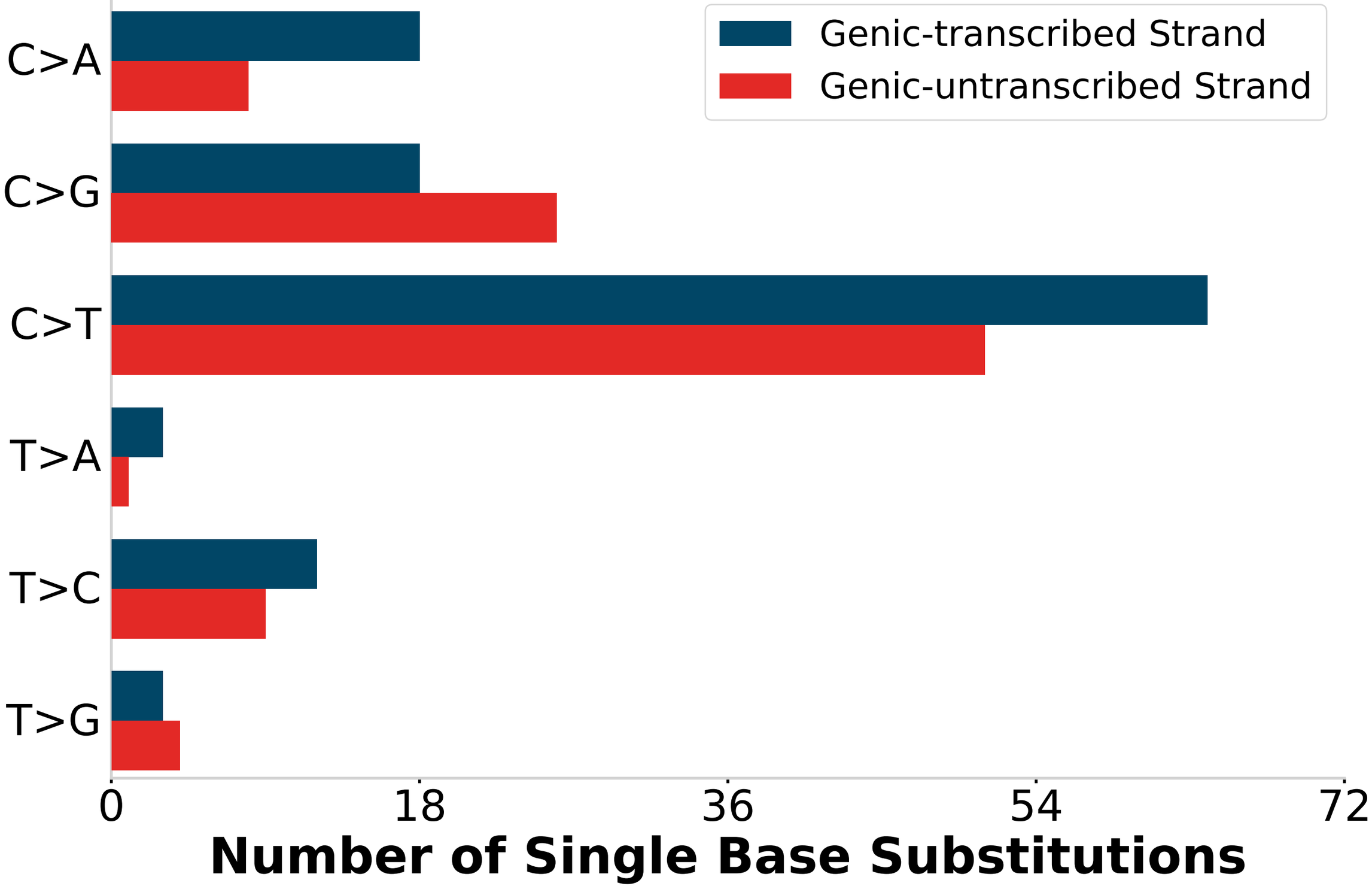
TCGA-BL-A13I-01A-11D-A271-08: 127 tran



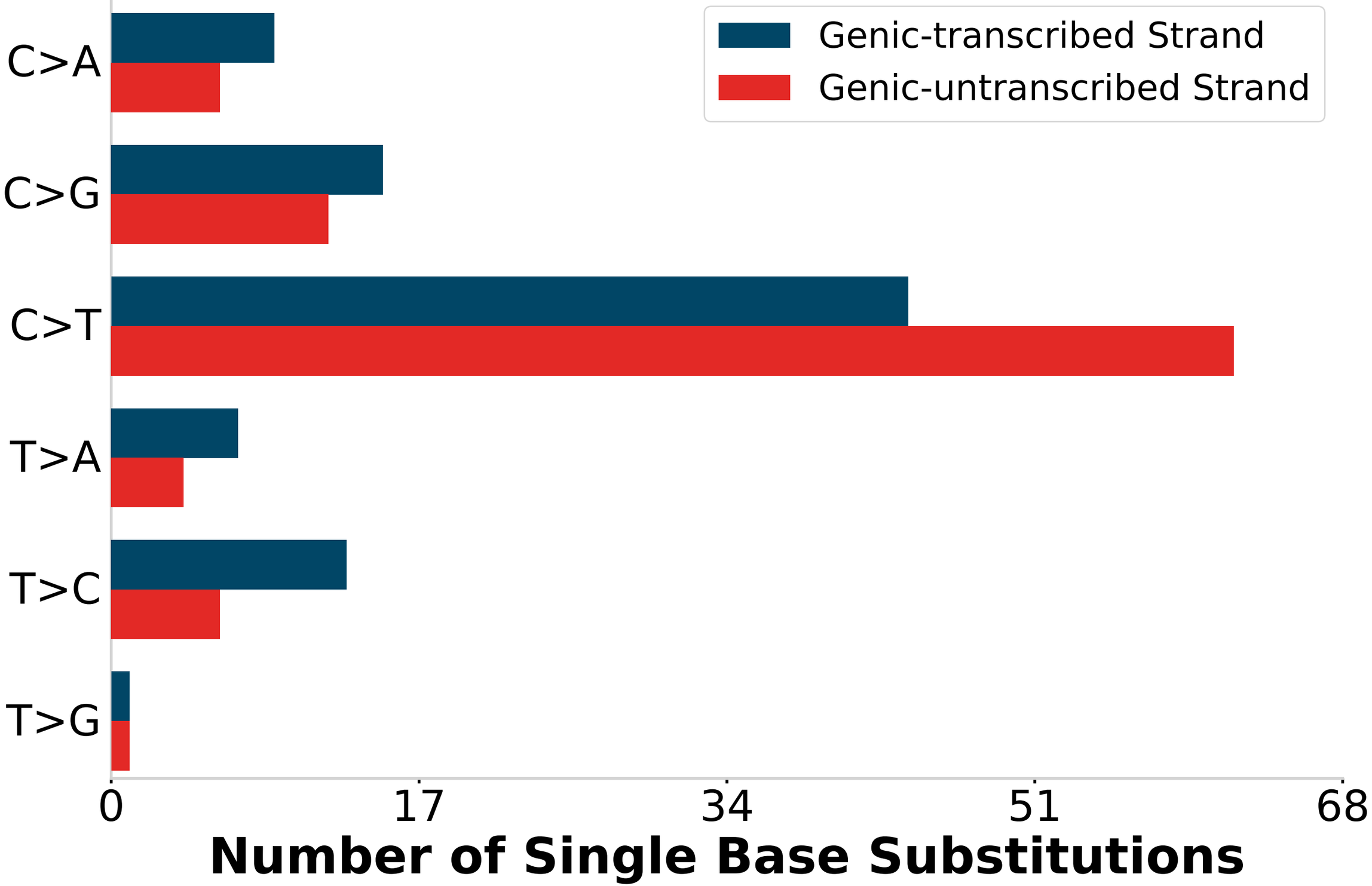
TCGA-BL-A13J-01A-11D-A271-08: 107 tran



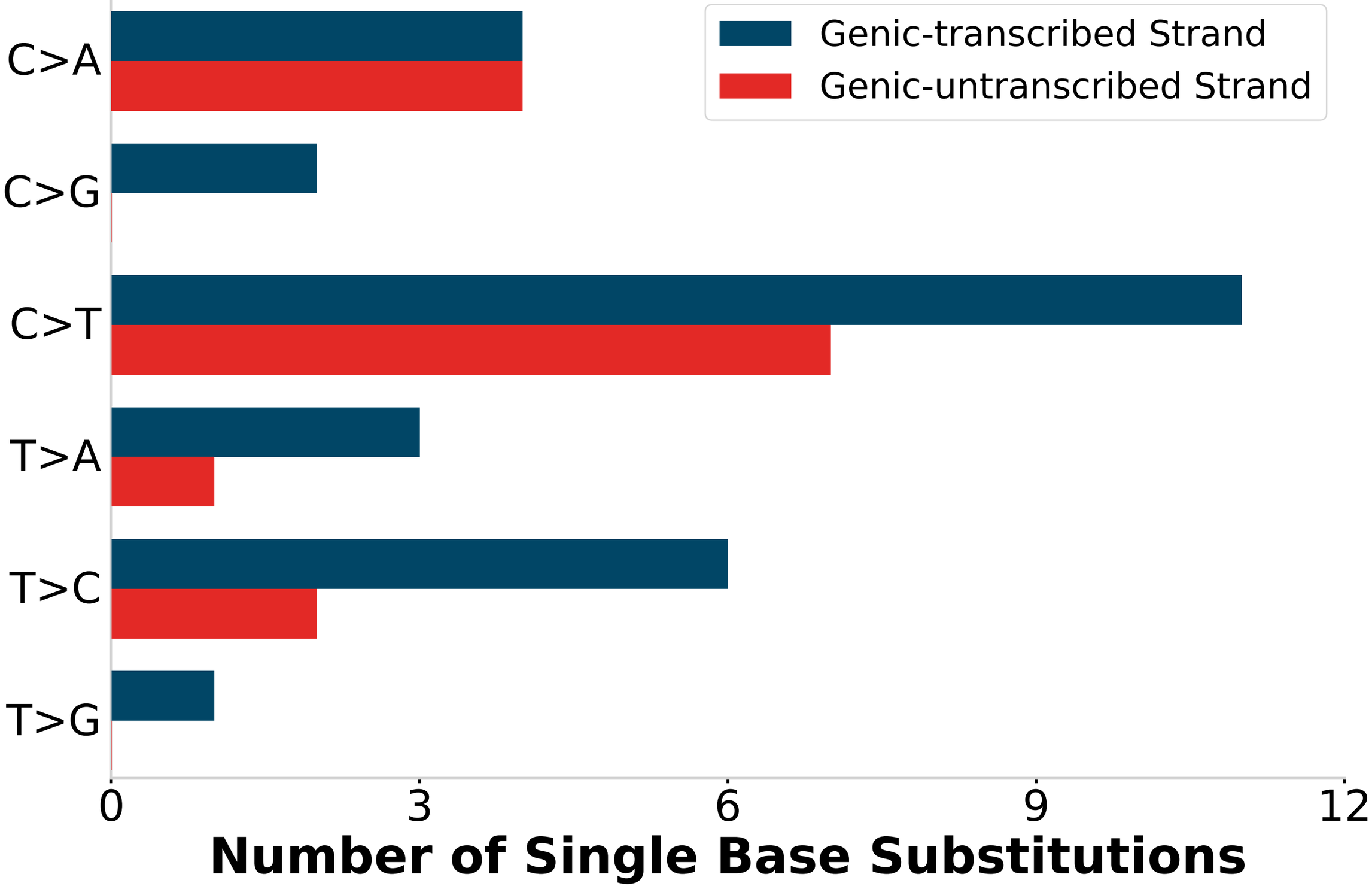
TCGA-BL-A3JM-01A-12D-A21A-08: 217 tran



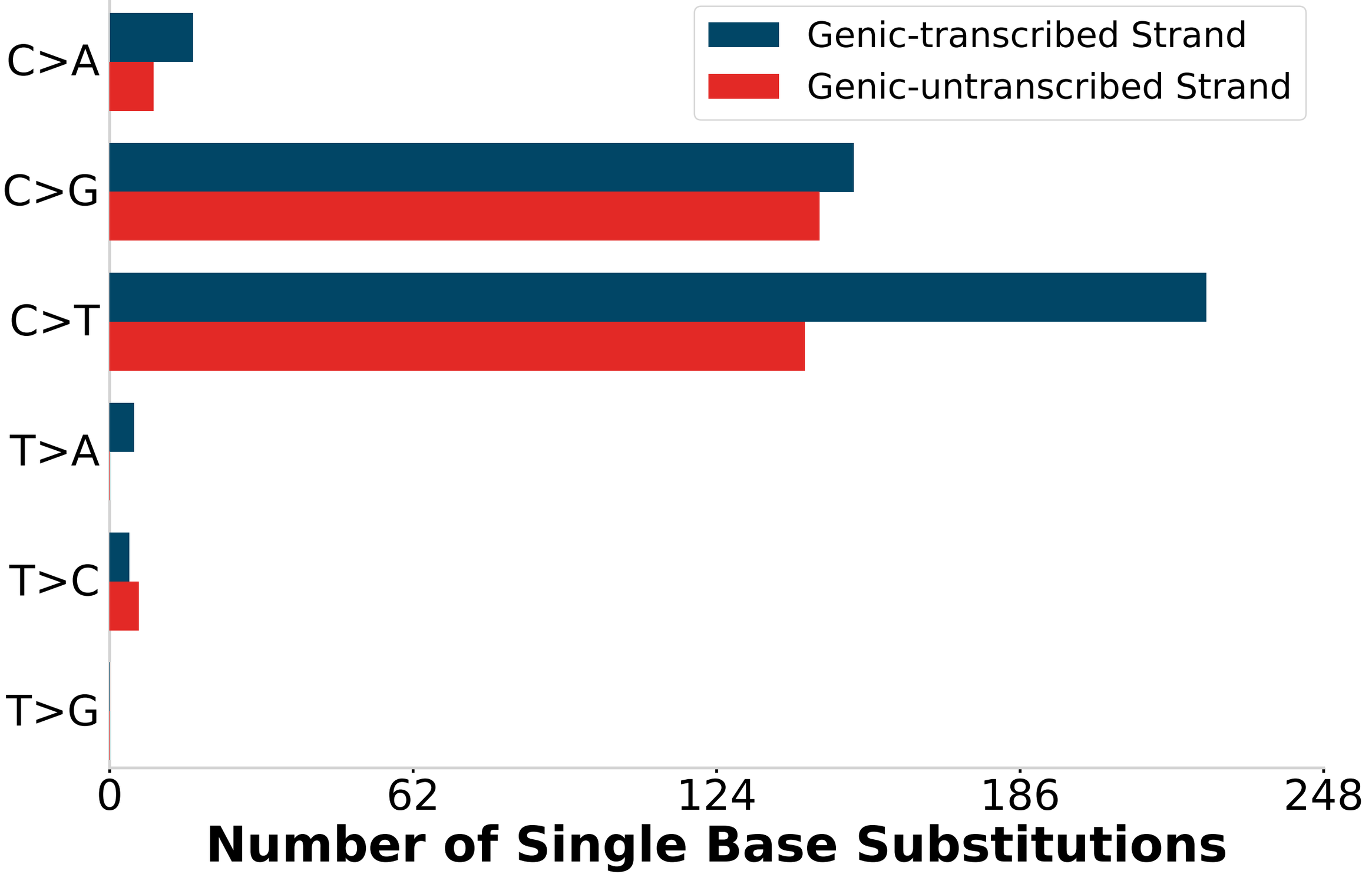
TCGA-BL-A5ZZ-01A-31D-A30E-08: 180 tran



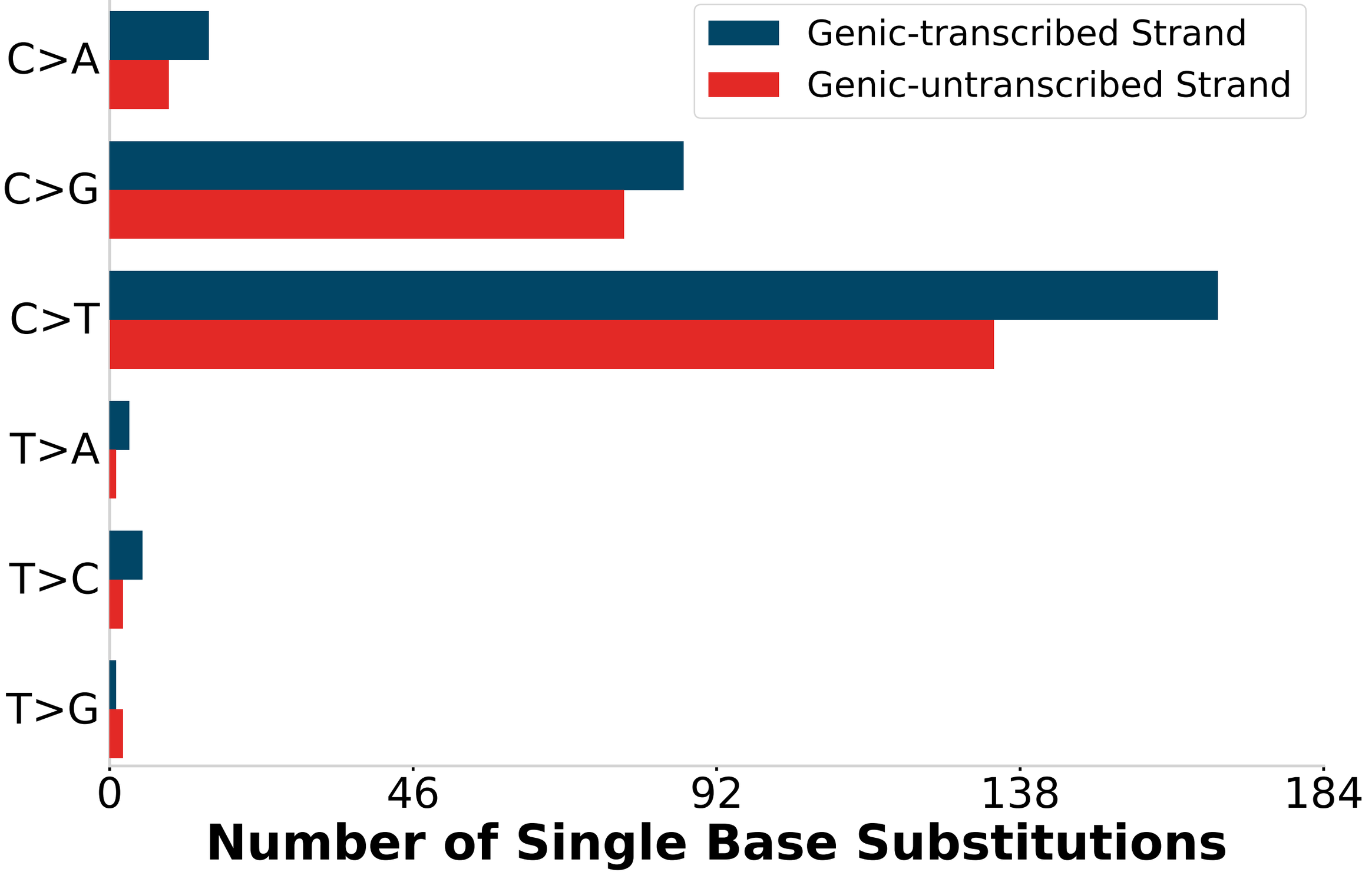
TCGA-BT-A0S7-01A-11D-A10S-08: 41 trans



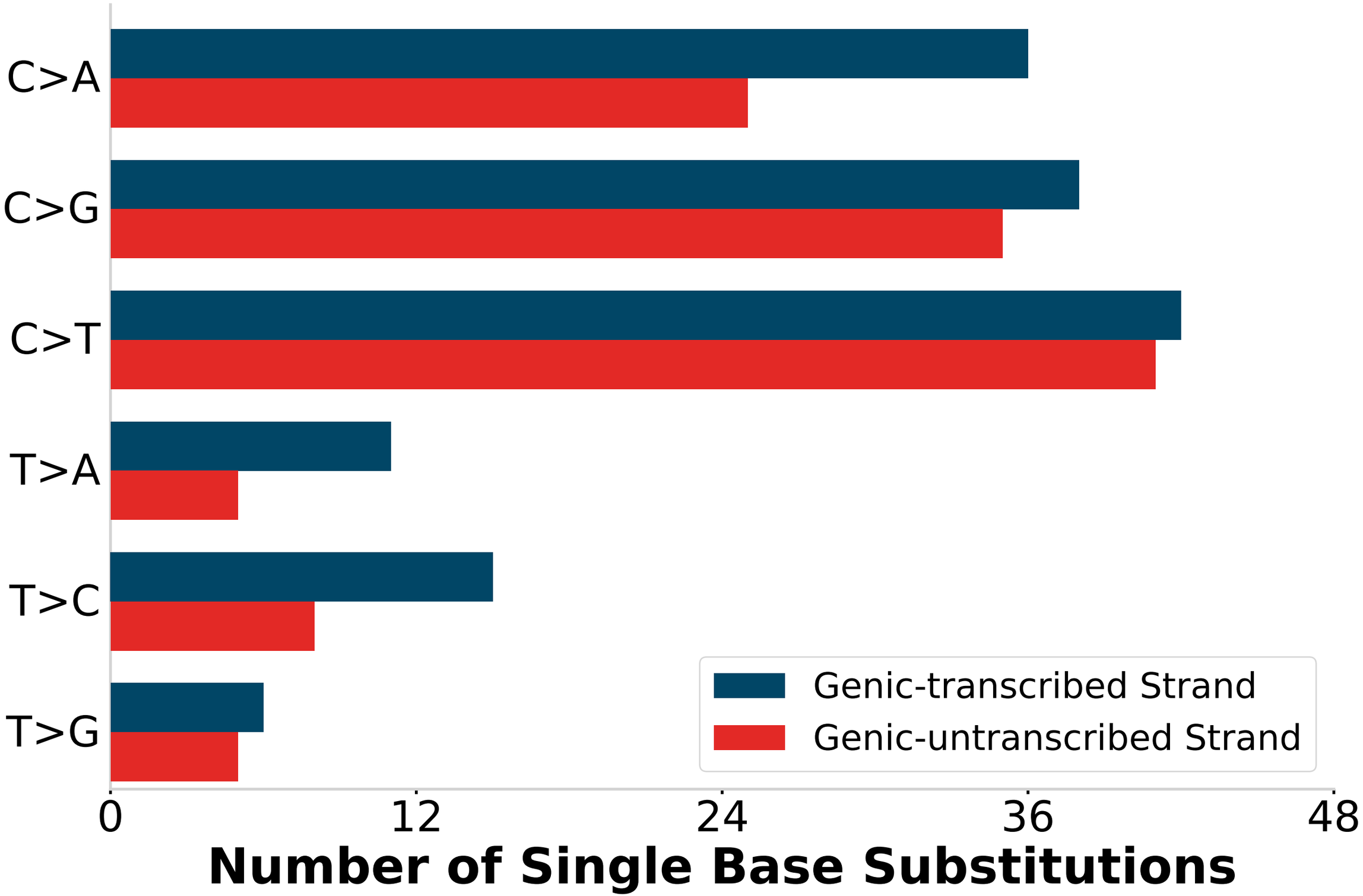
TCGA-BT-A0YX-01A-11D-A10S-08: 704 tran



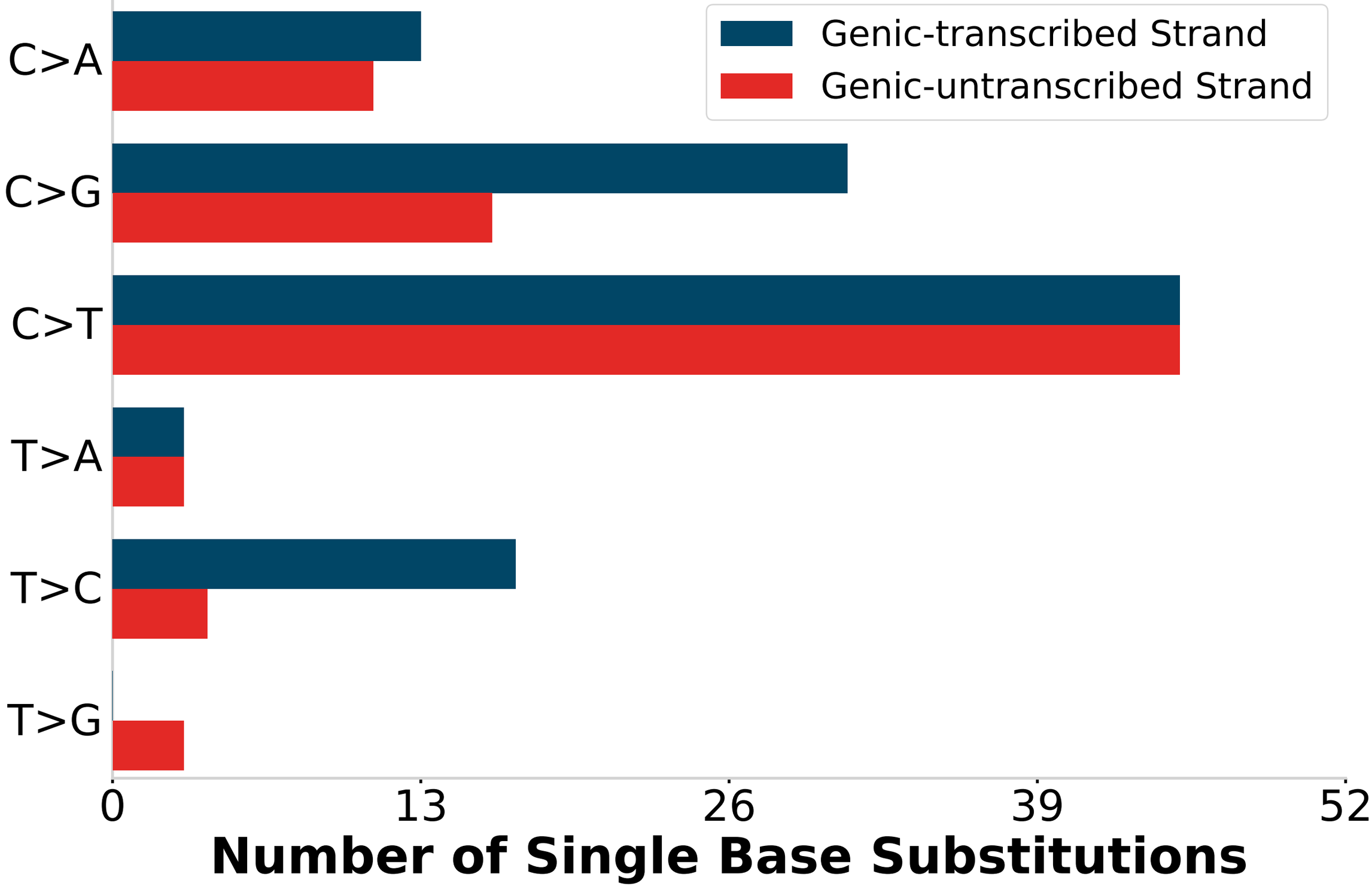
TCGA-BT-A20J-01A-11D-A14W-08: 505 tran



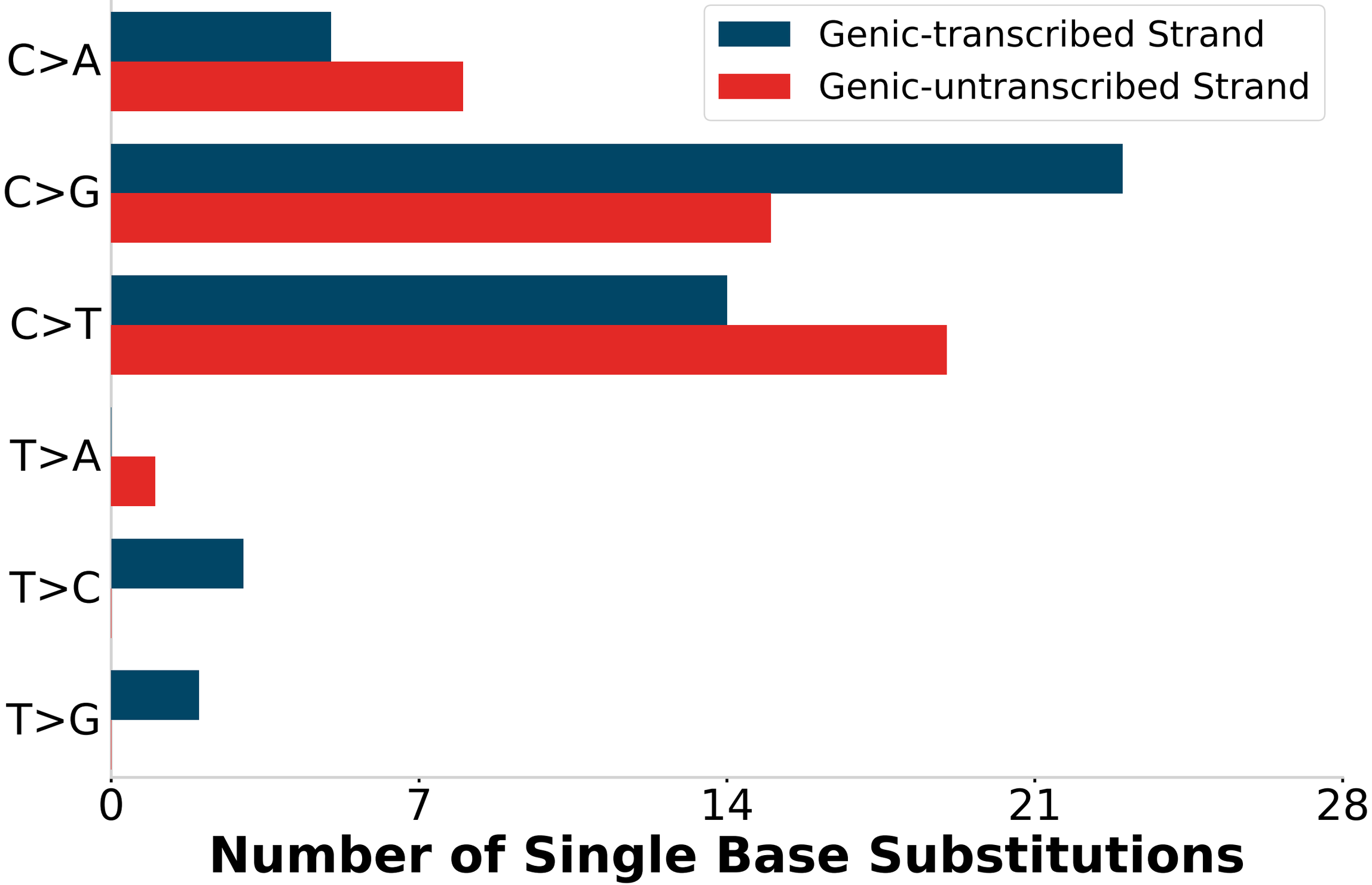
TCGA-BT-A20N-01A-11D-A14W-08: 267 tra



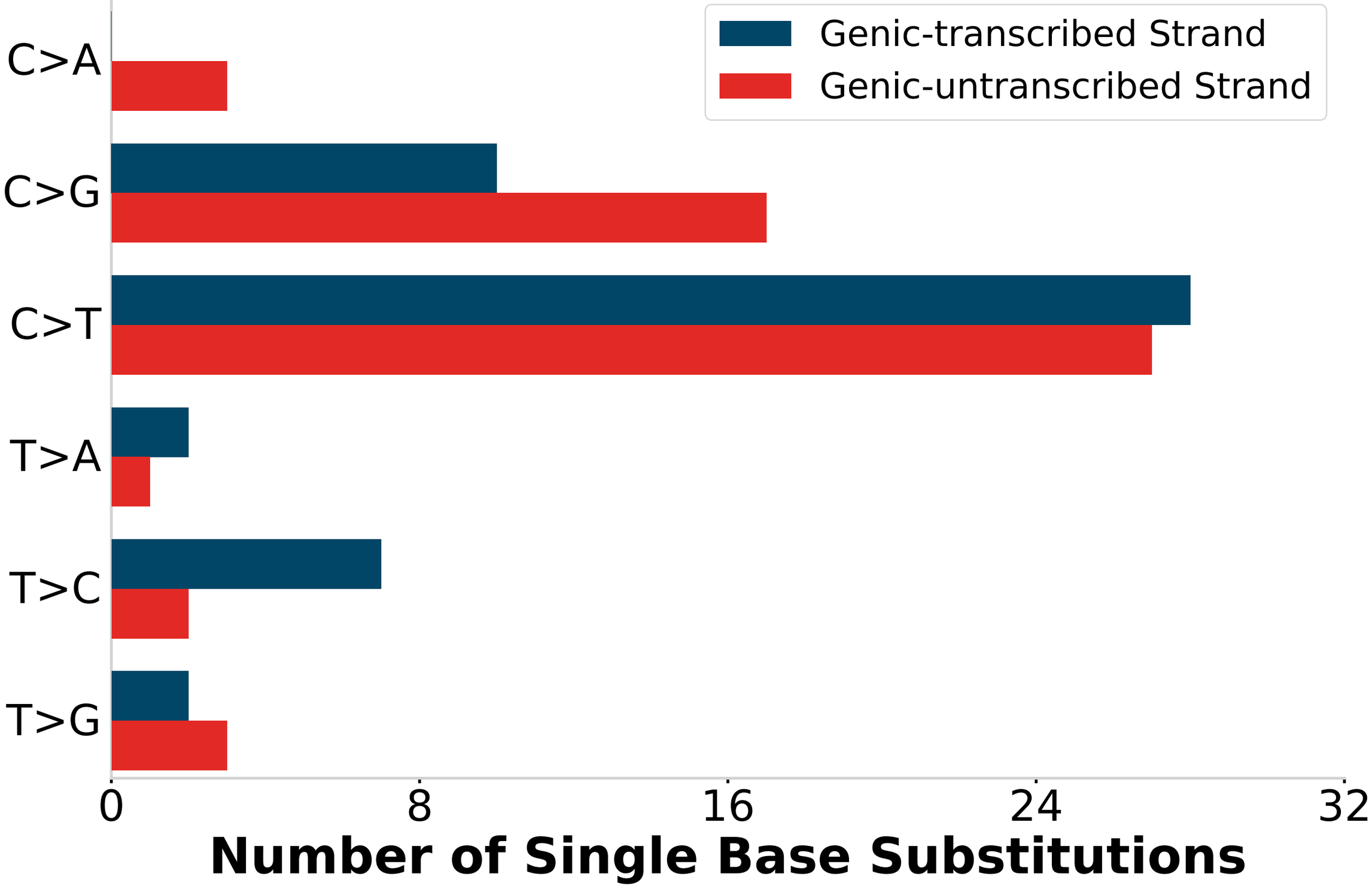
TCGA-BT-A20O-01A-21D-A14W-08: 191 tra



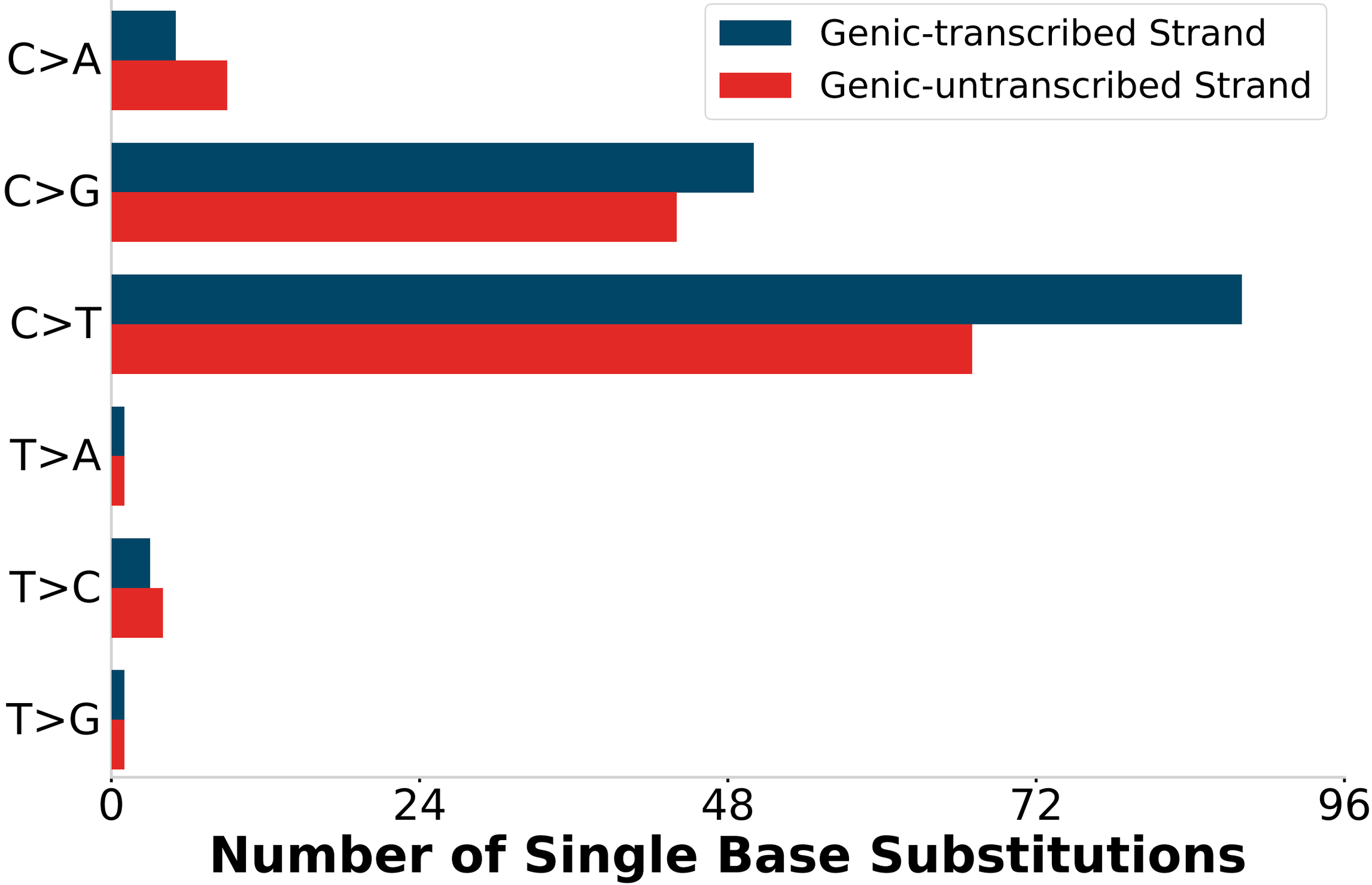
TCGA-BT-A20P-01A-11D-A14W-08: 90 trans



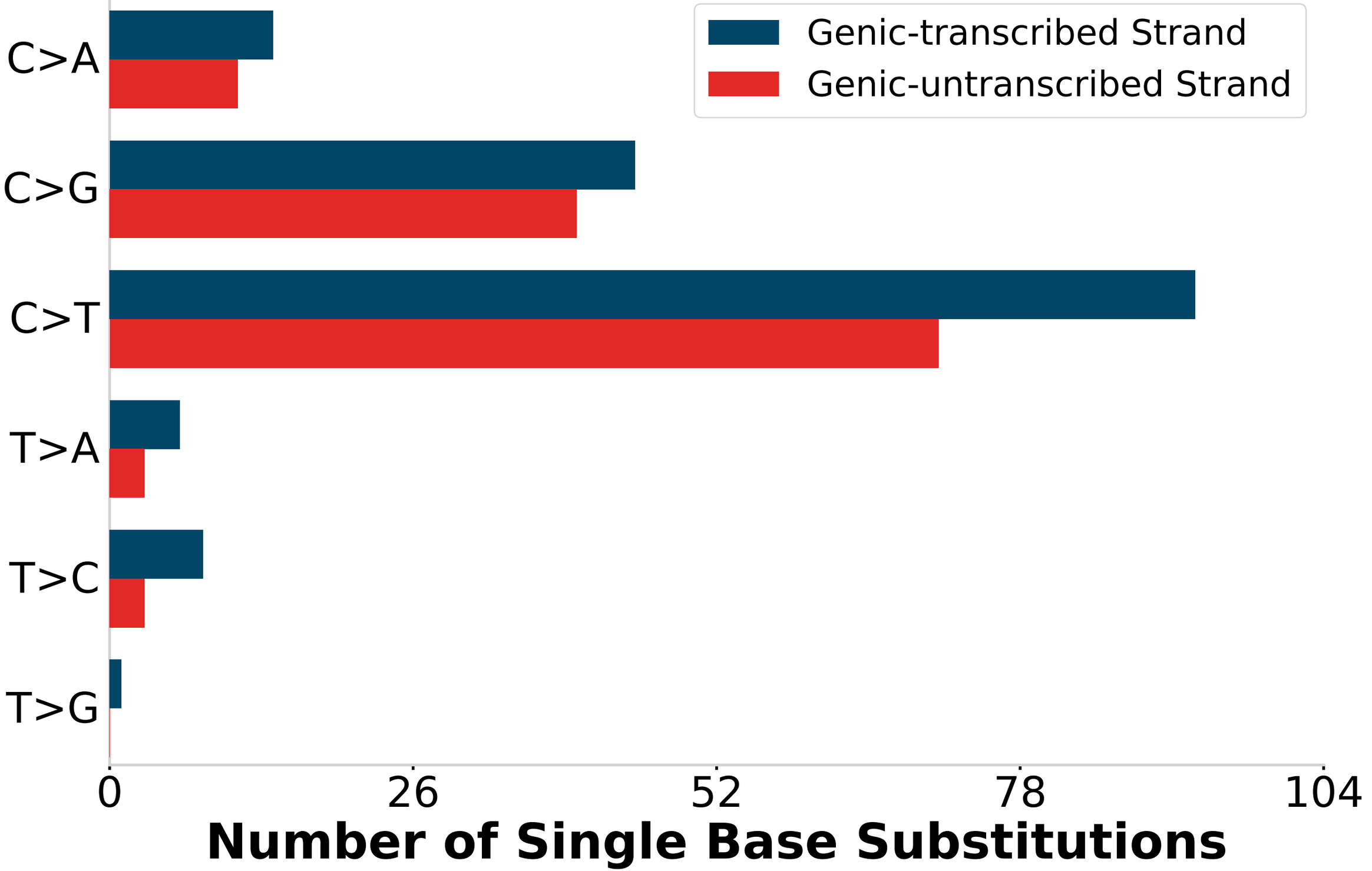
TCGA-BT-A20Q-01A-11D-A14W-08: 102 tra



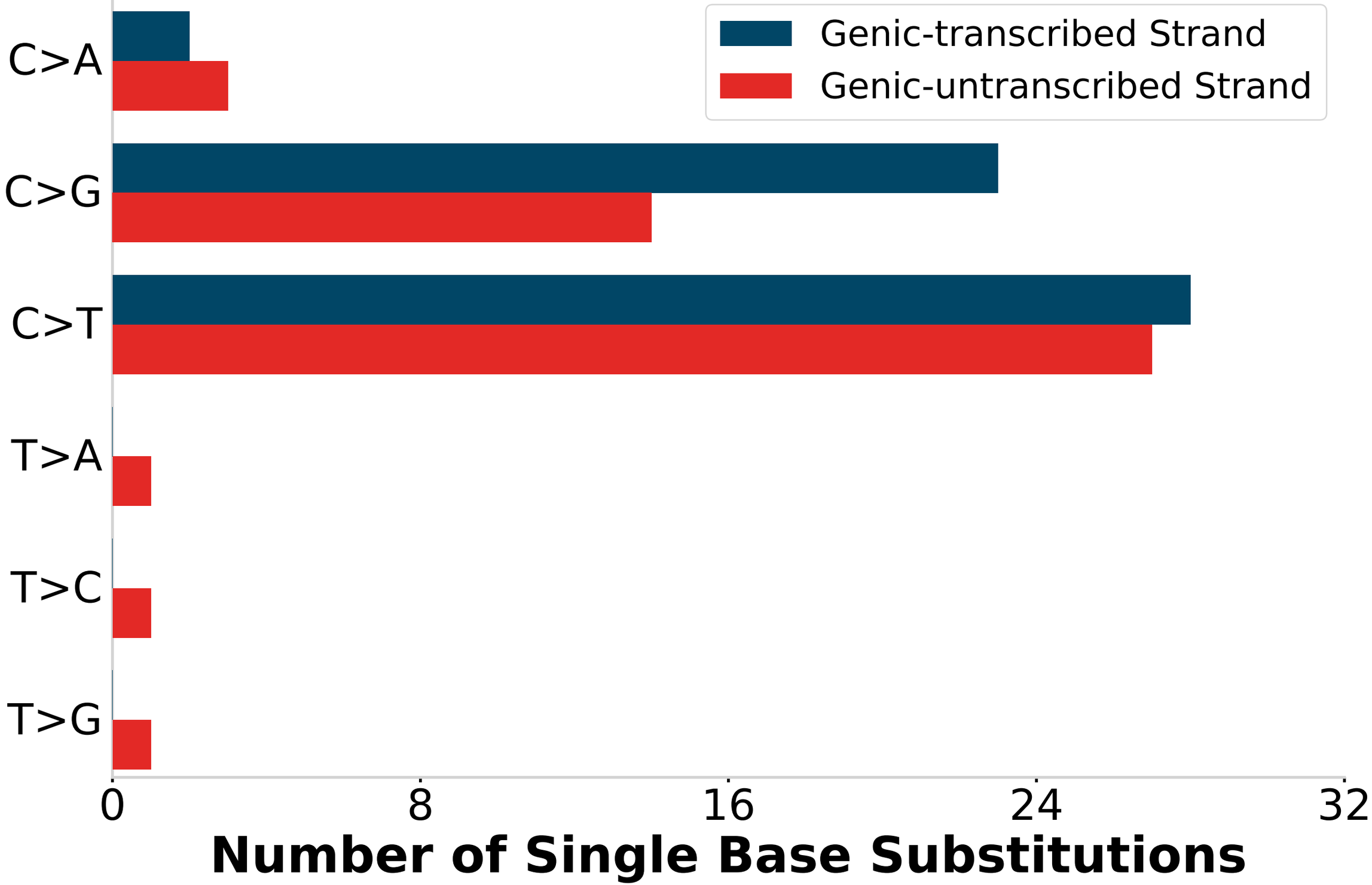
TCGA-BT-A20R-01A-12D-A16O-08: 274 tra



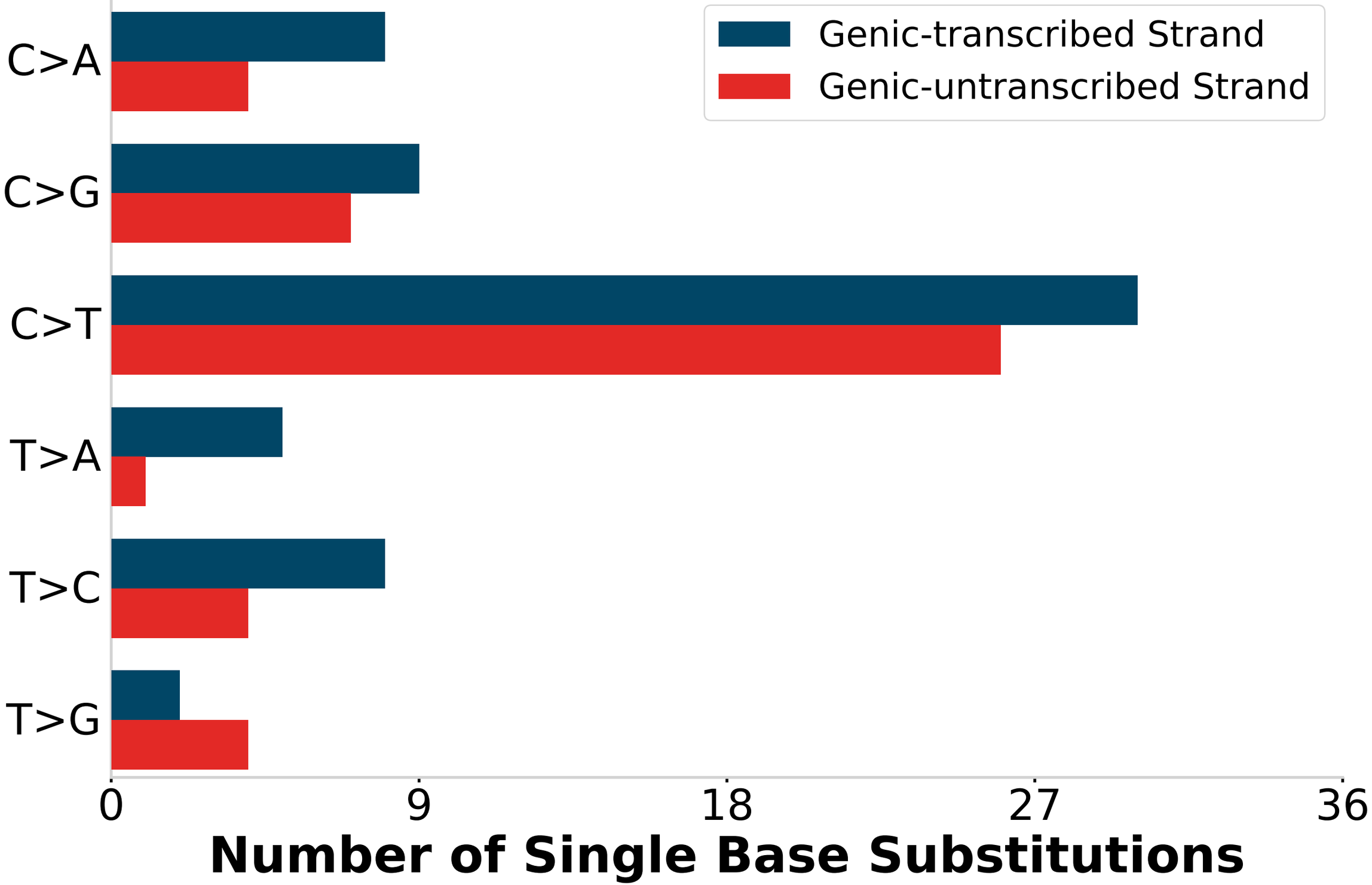
TCGA-BT-A20T-01A-11D-A14W-08: 295 tran



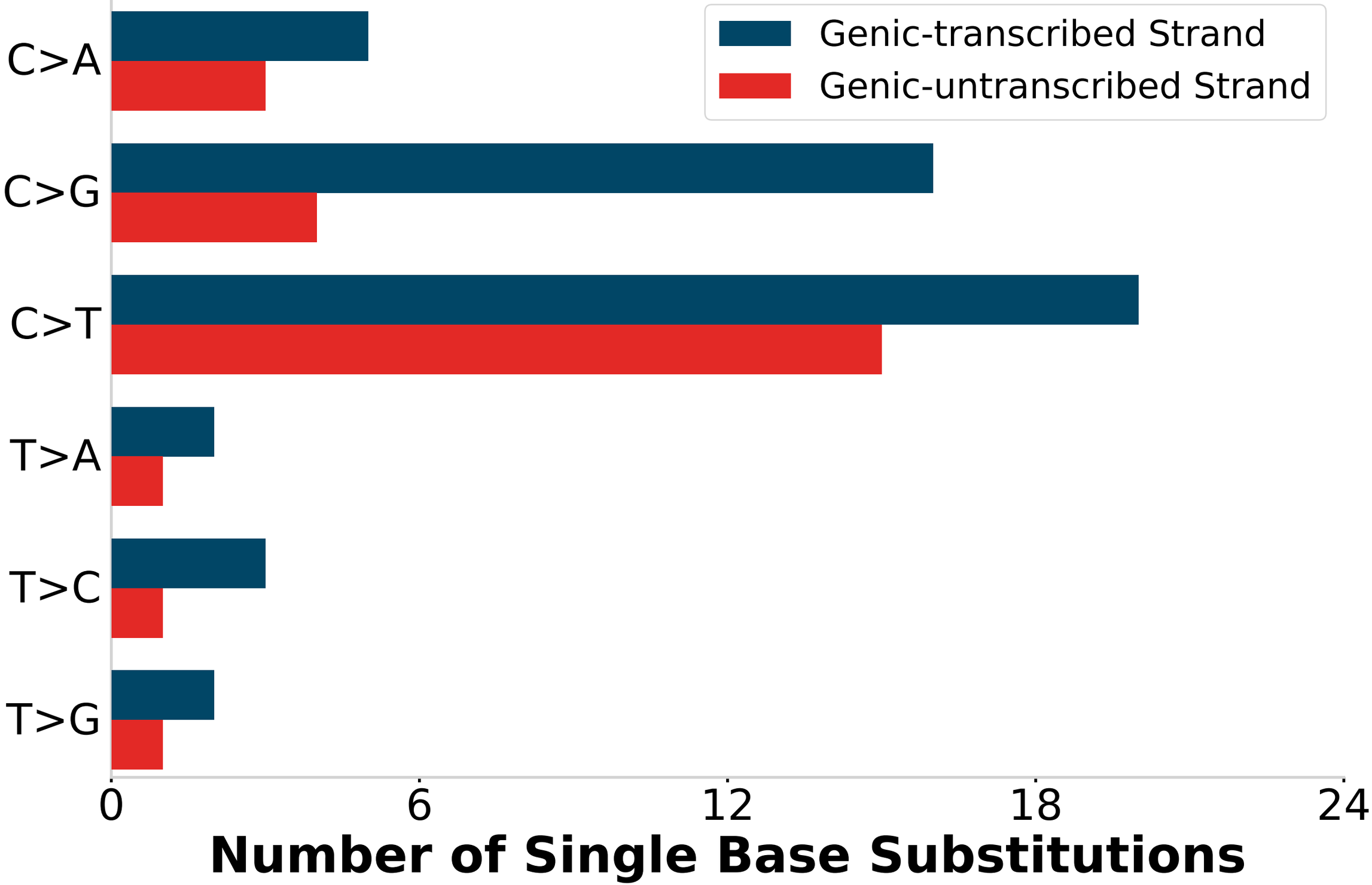
TCGA-BT-A20U-01A-11D-A14W-08: 100 tra



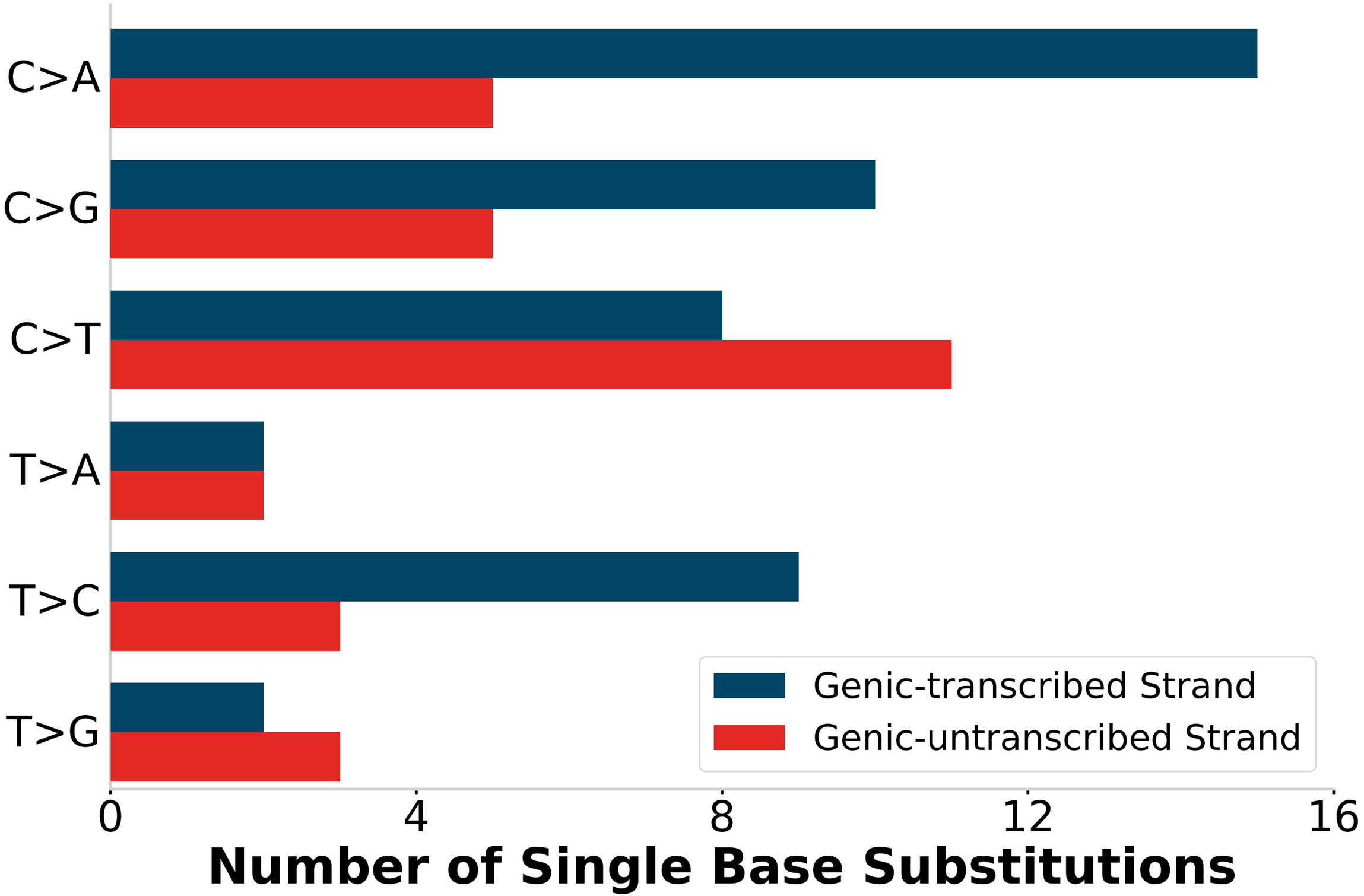
TCGA-BT-A20V-01A-11D-A14W-08: 108 tra



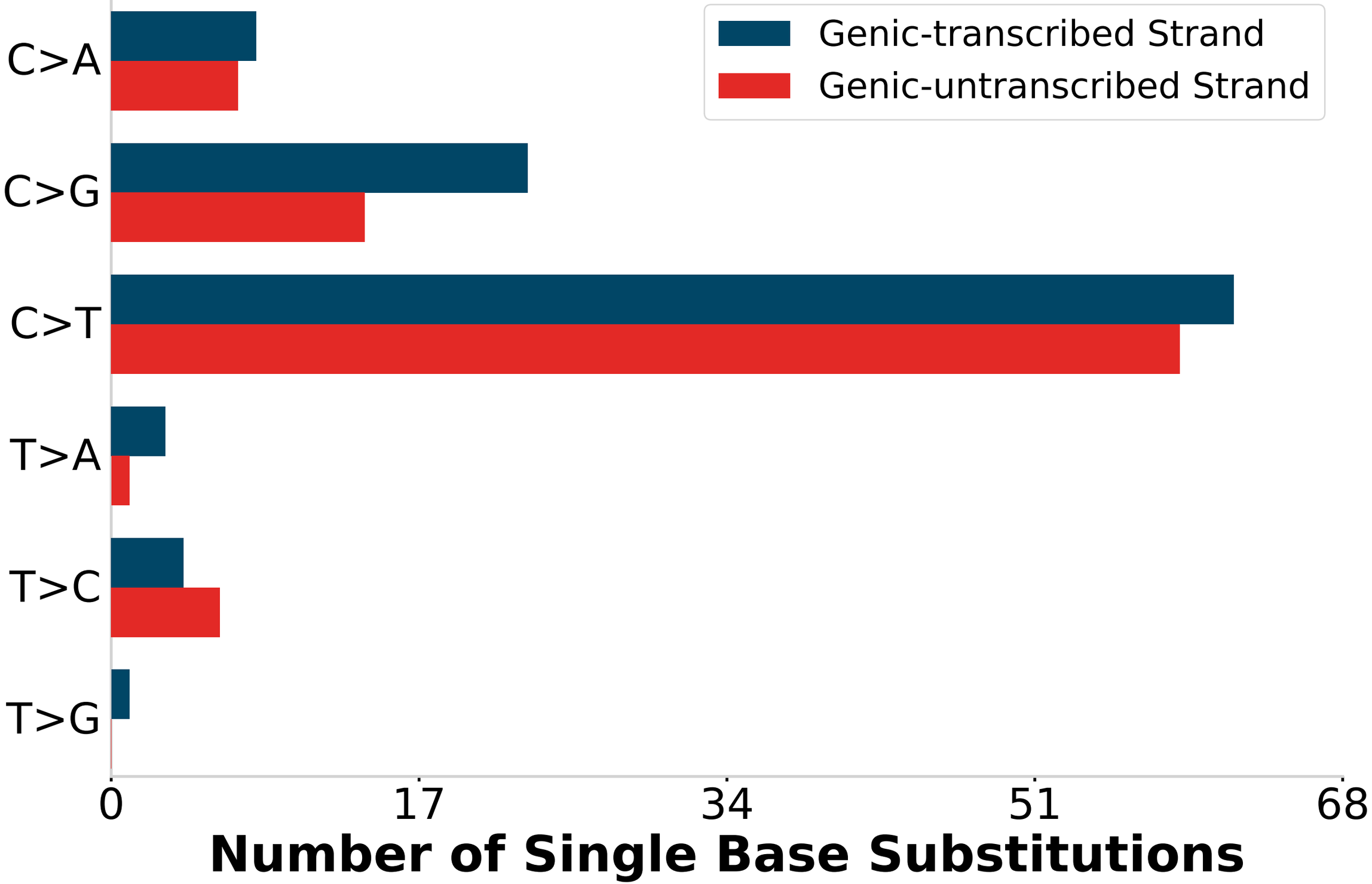
TCGA-BT-A20W-01A-21D-A14W-08: 73 tran



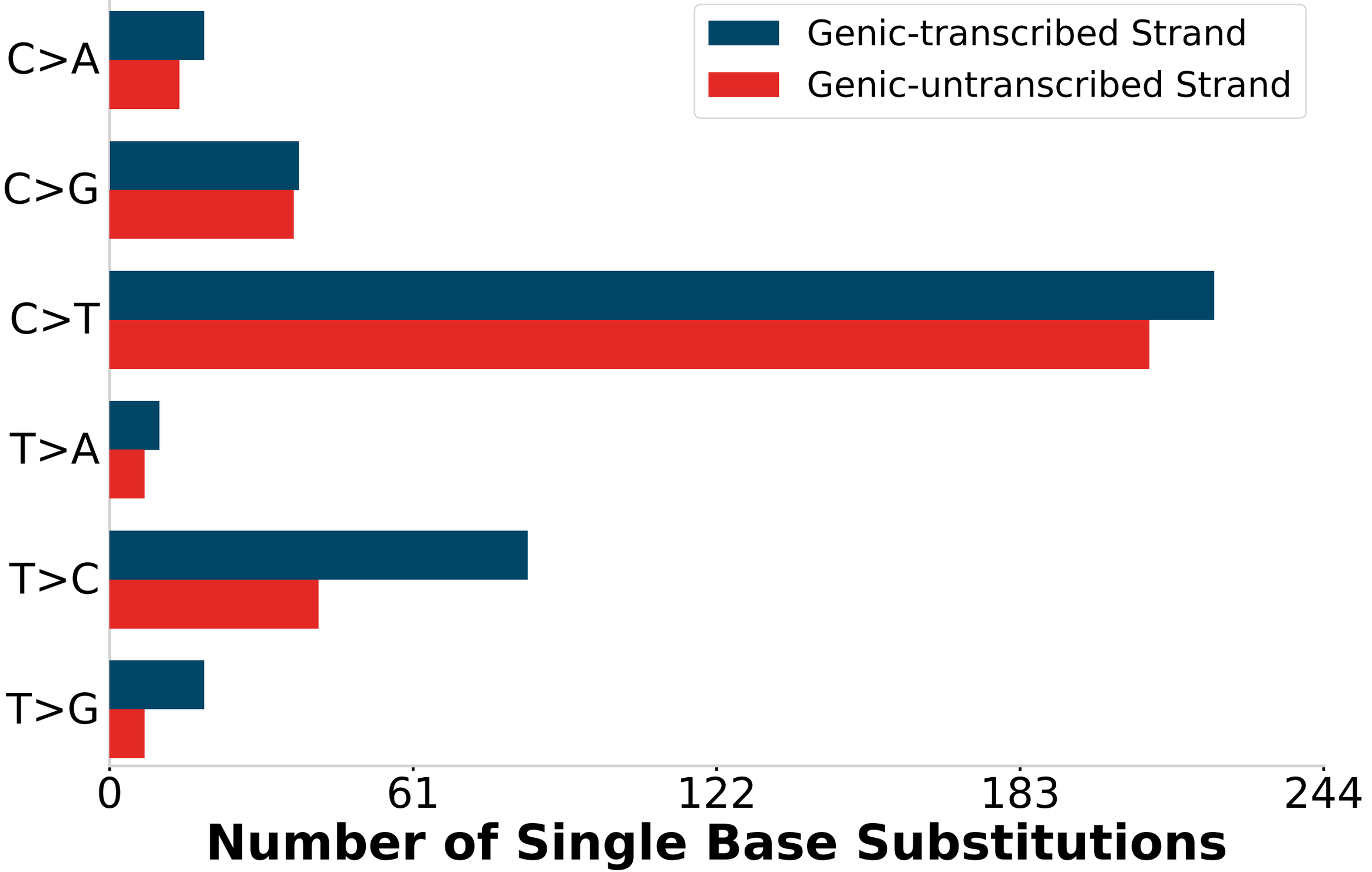
TCGA-BT-A20X-01A-11D-A16O-08: 75 trans



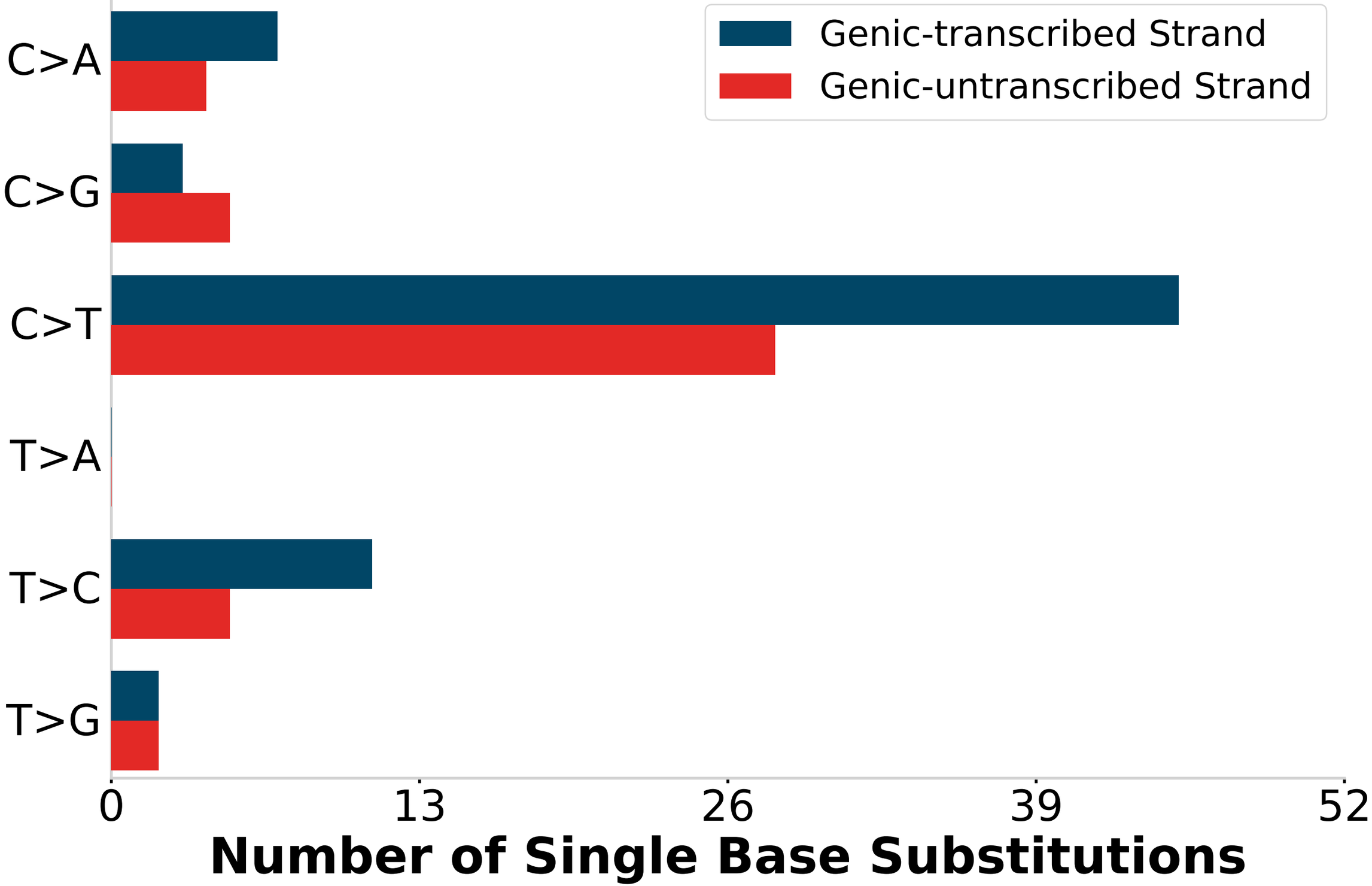
TCGA-BT-A2LA-01A-11D-A18F-08: 188 tran



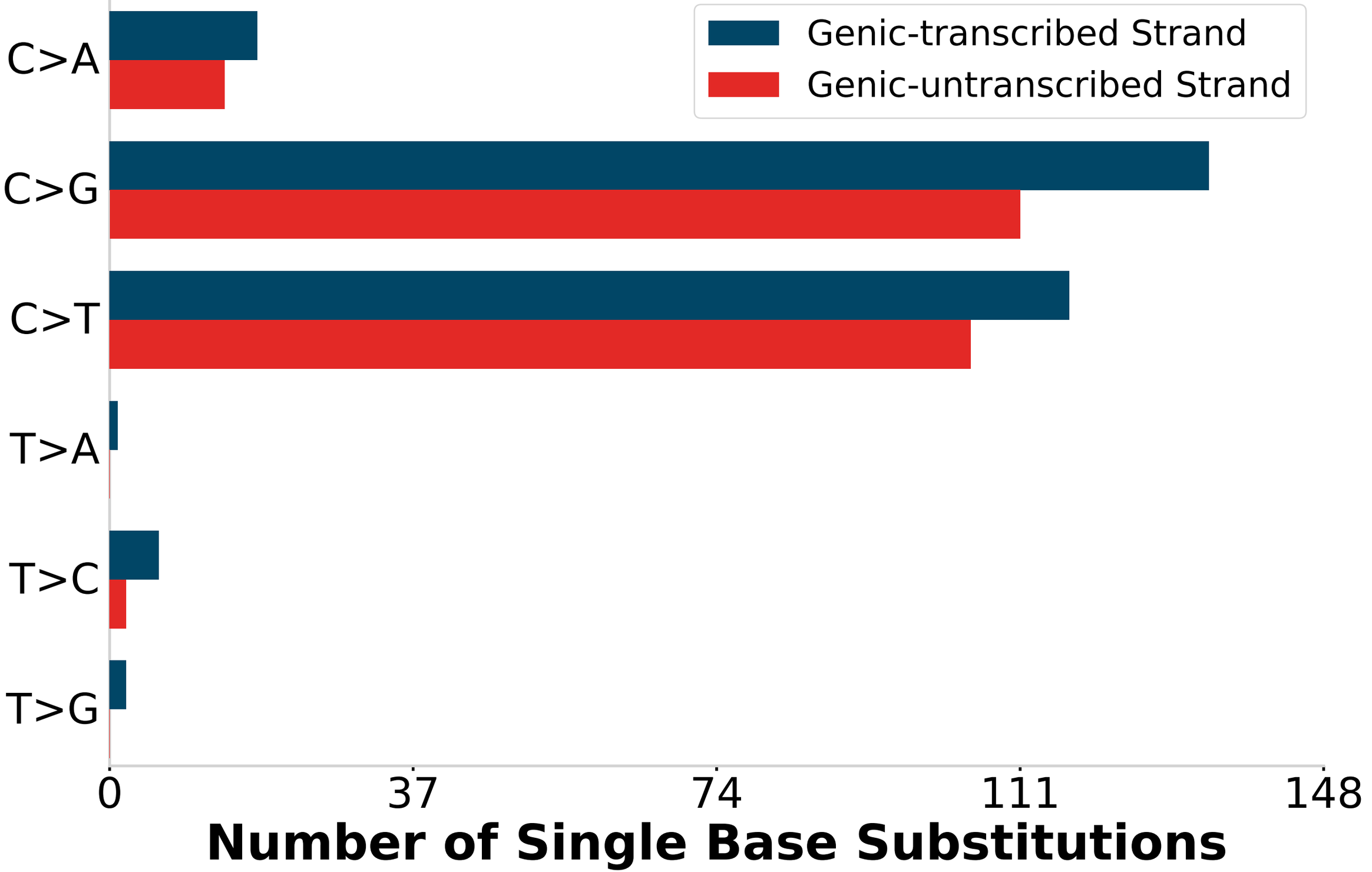
TCGA-BT-A2LB-01A-11D-A18F-08: 708 tran



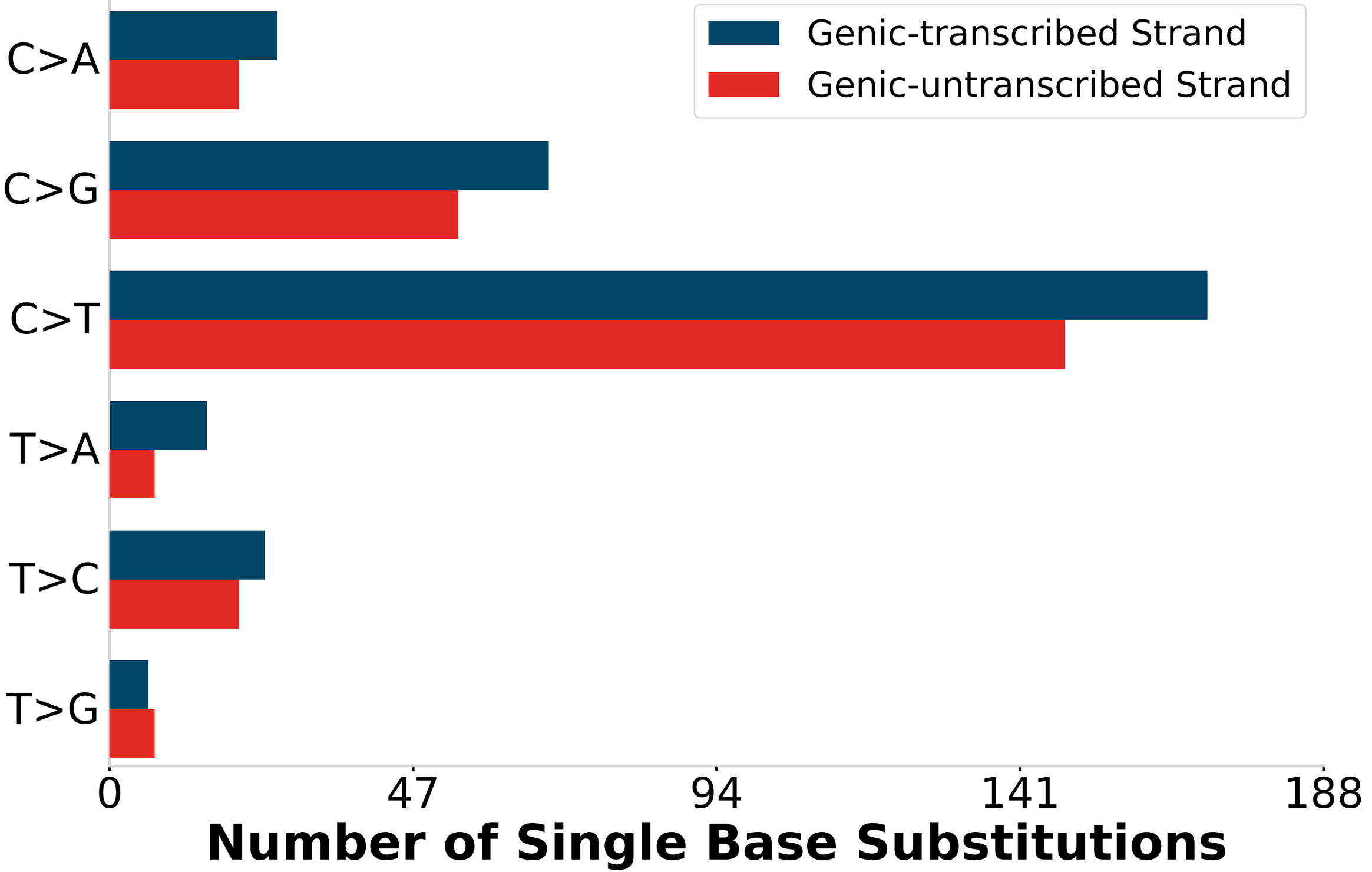
TCGA-BT-A2LD-01A-12D-A20D-08: 112 tra



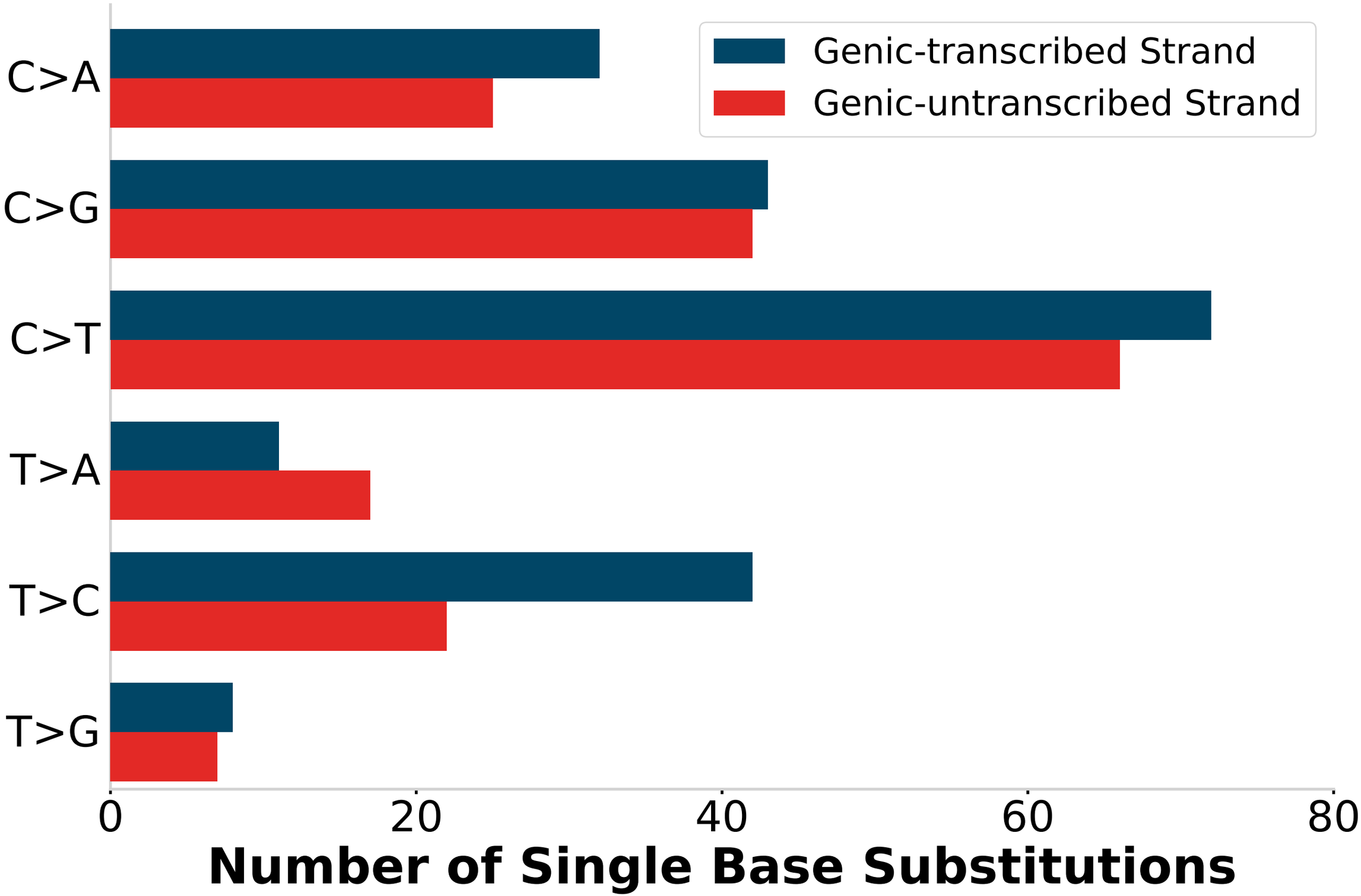
TCGA-BT-A3PH-01A-11D-A21Z-08: 510 tran



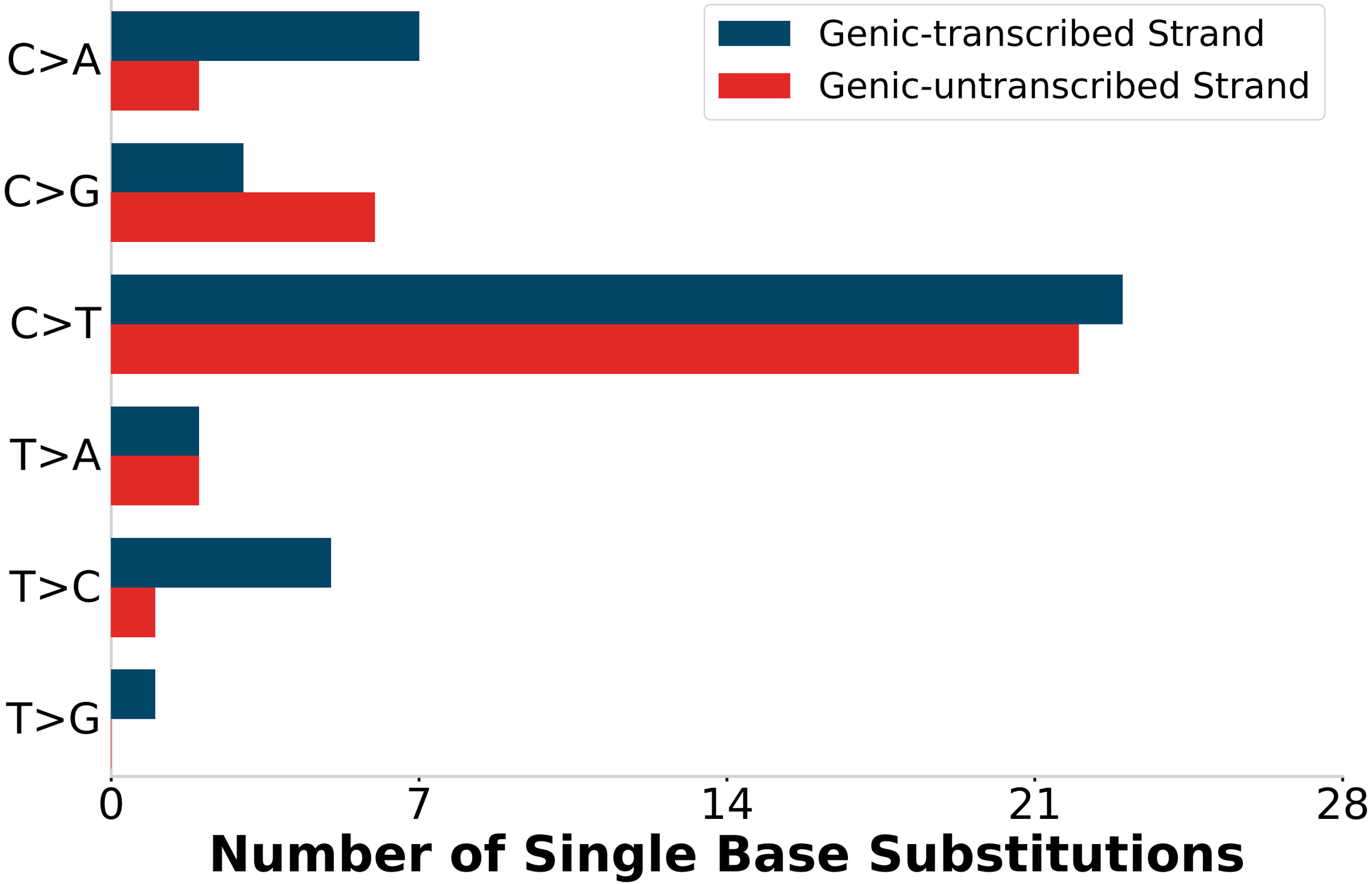
TCGA-BT-A3PJ-01A-21D-A21Z-08: 565 tran



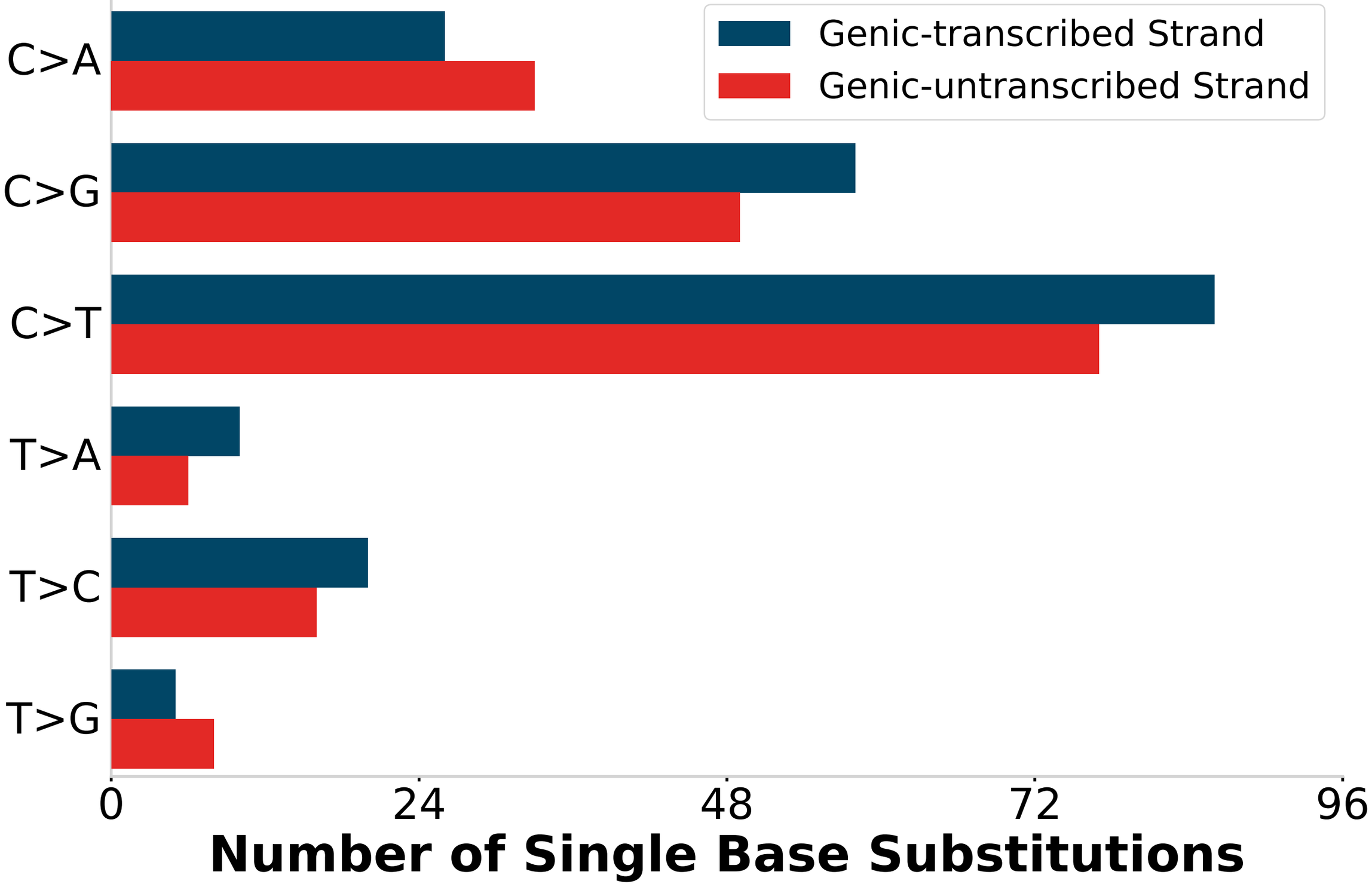
TCGA-BT-A3PK-01A-21D-A21Z-08: 387 tran



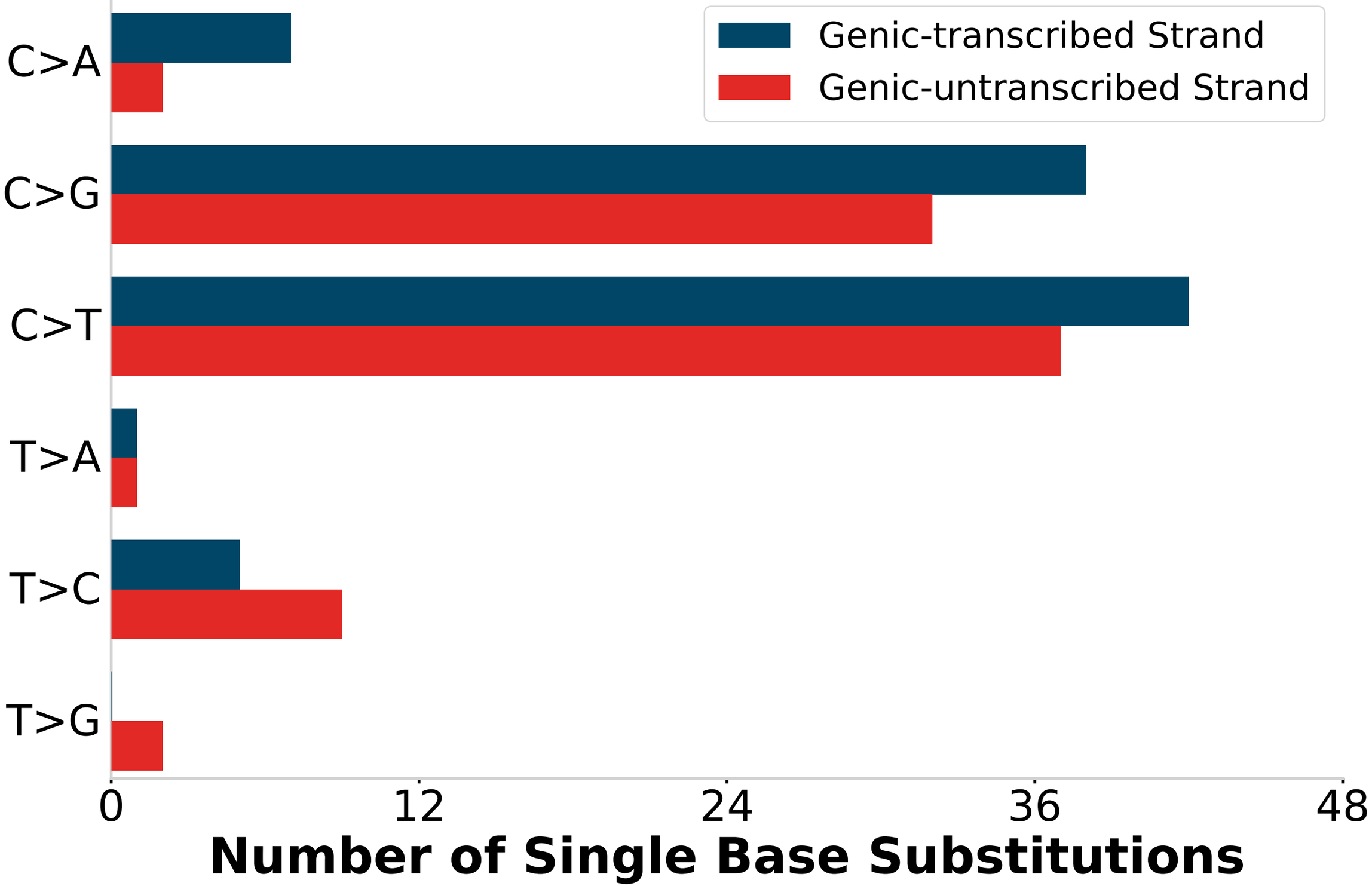
TCGA-BT-A42B-01A-32D-A23M-08: 74 trans



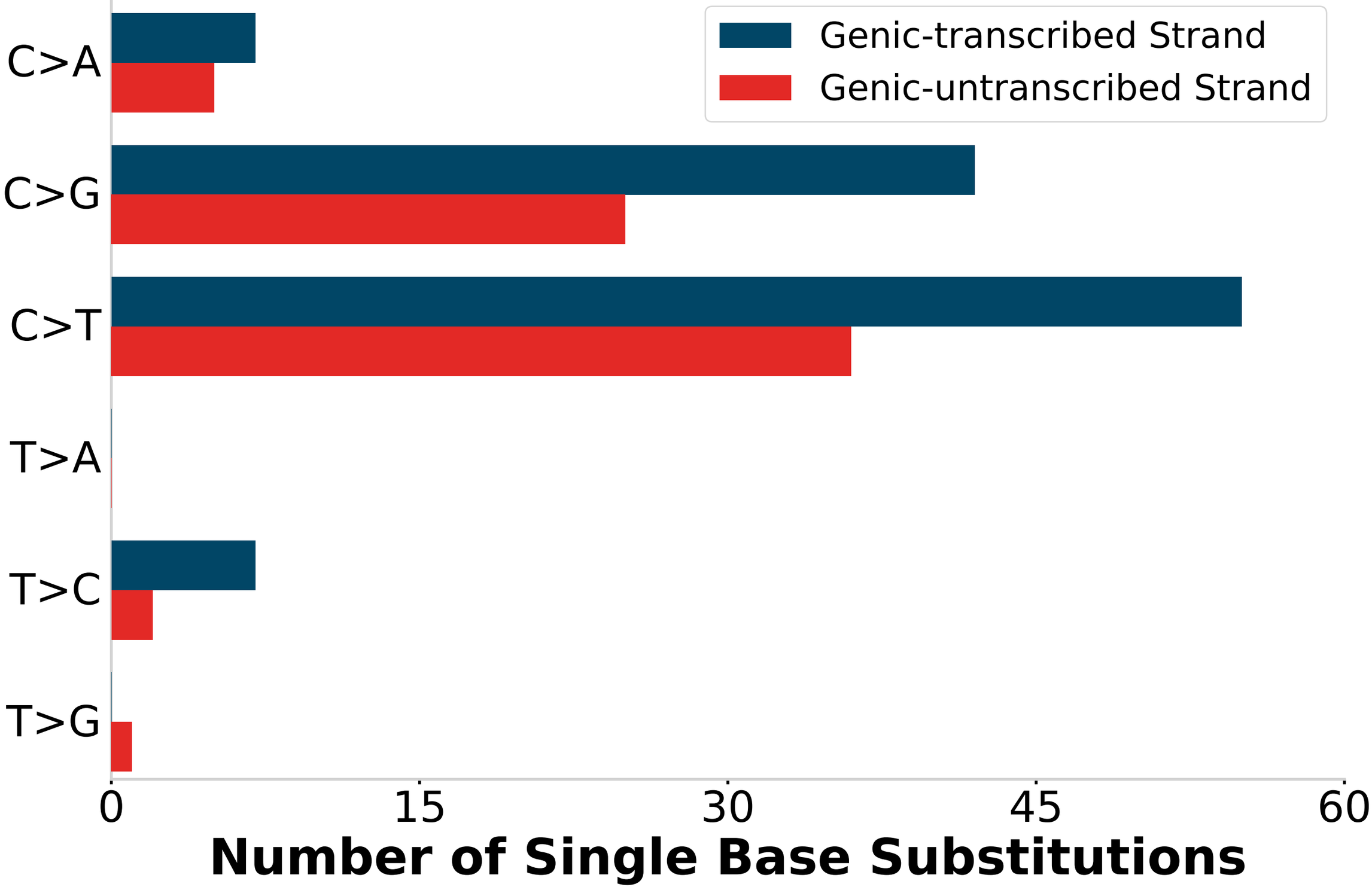
TCGA-BT-A42C-01A-11D-A23M-08: 394 tra



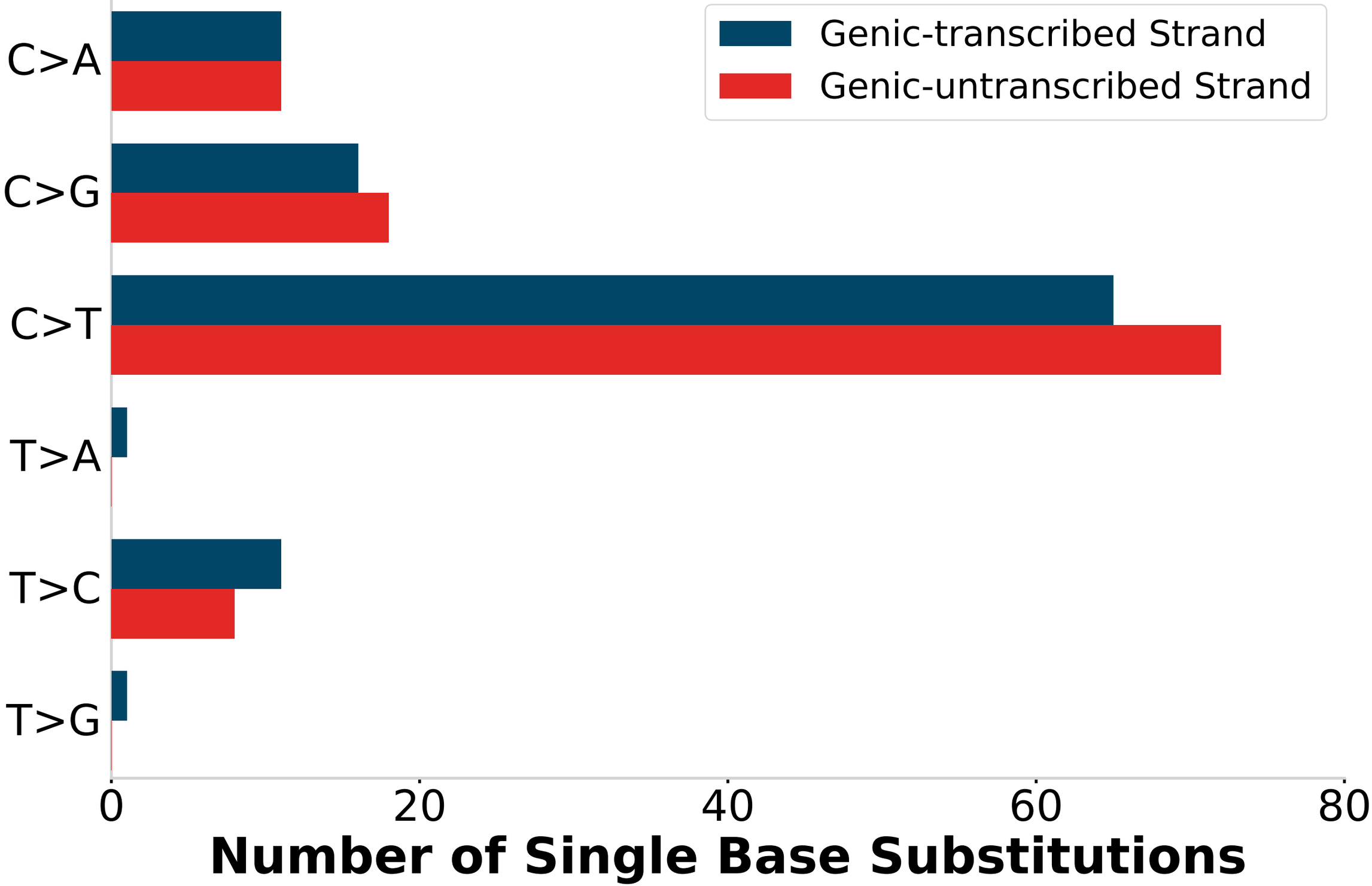
TCGA-BT-A42E-01A-11D-A23U-08: 176 tran



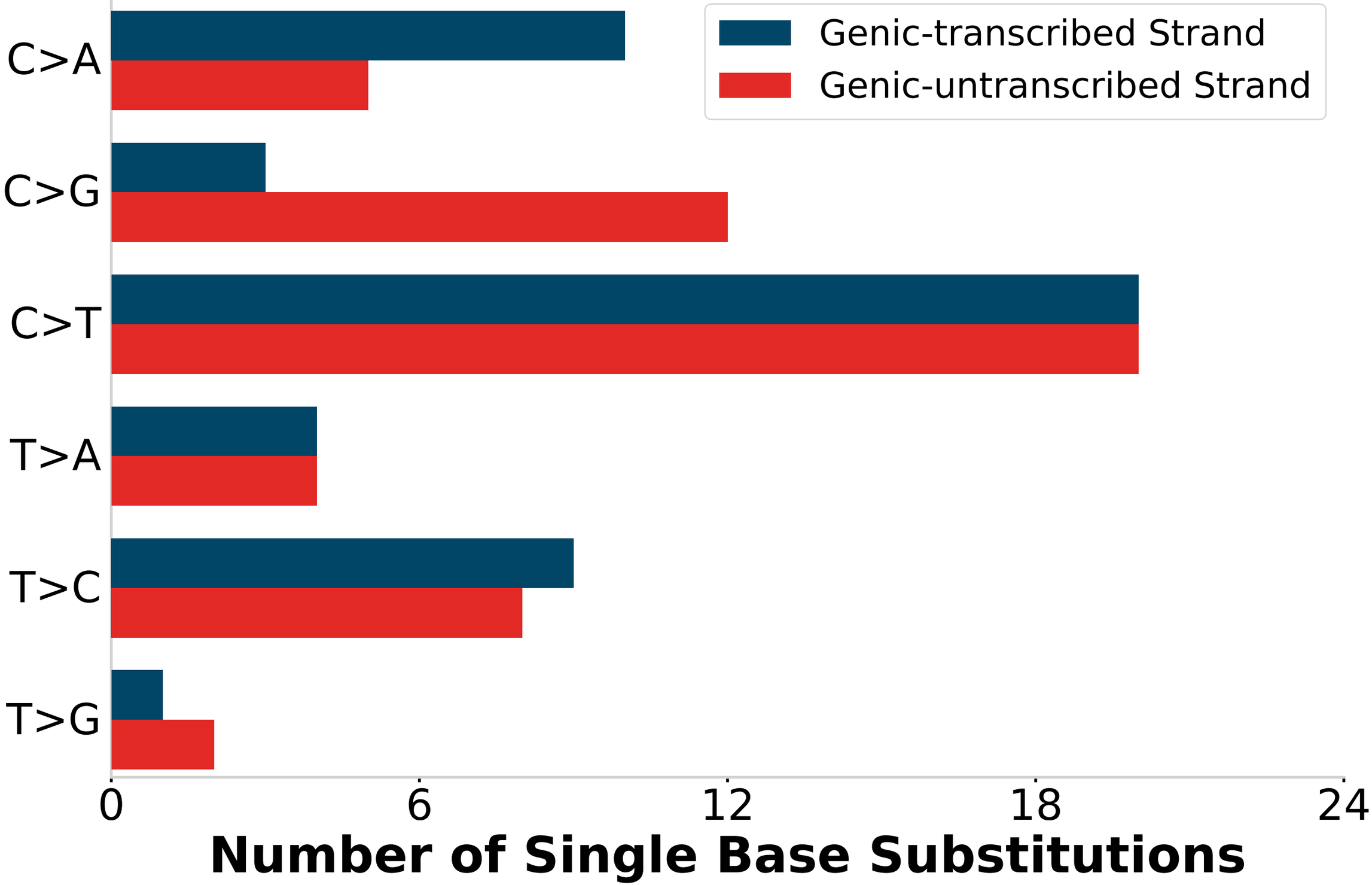
TCGA-BT-A42F-01A-11D-A23U-08: 180 tran



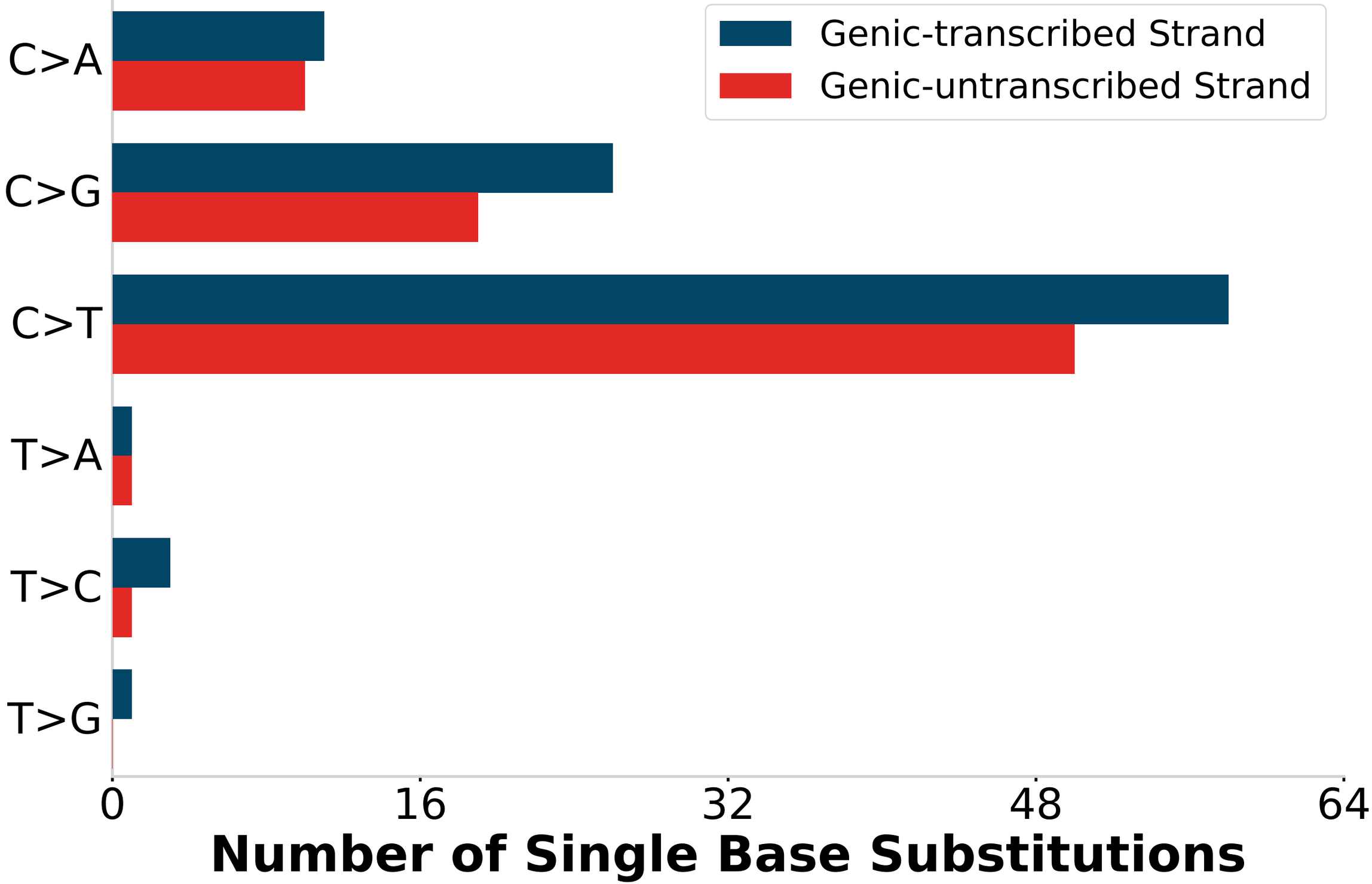
TCGA-C4-A0EZ-01A-21D-A10S-08: 214 tran



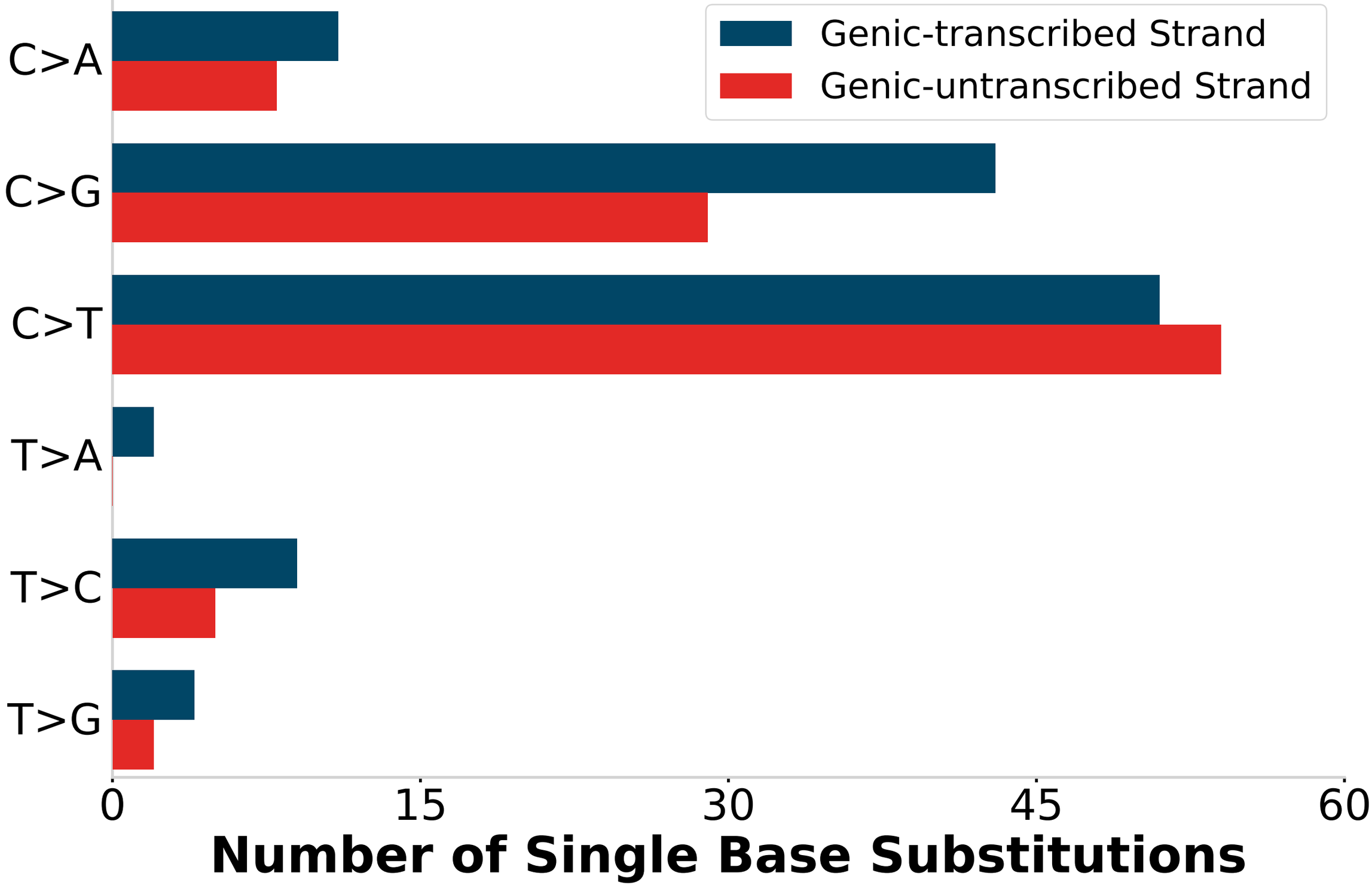
TCGA-C4-A0F0-01A-12D-A10S-08: 98 trans



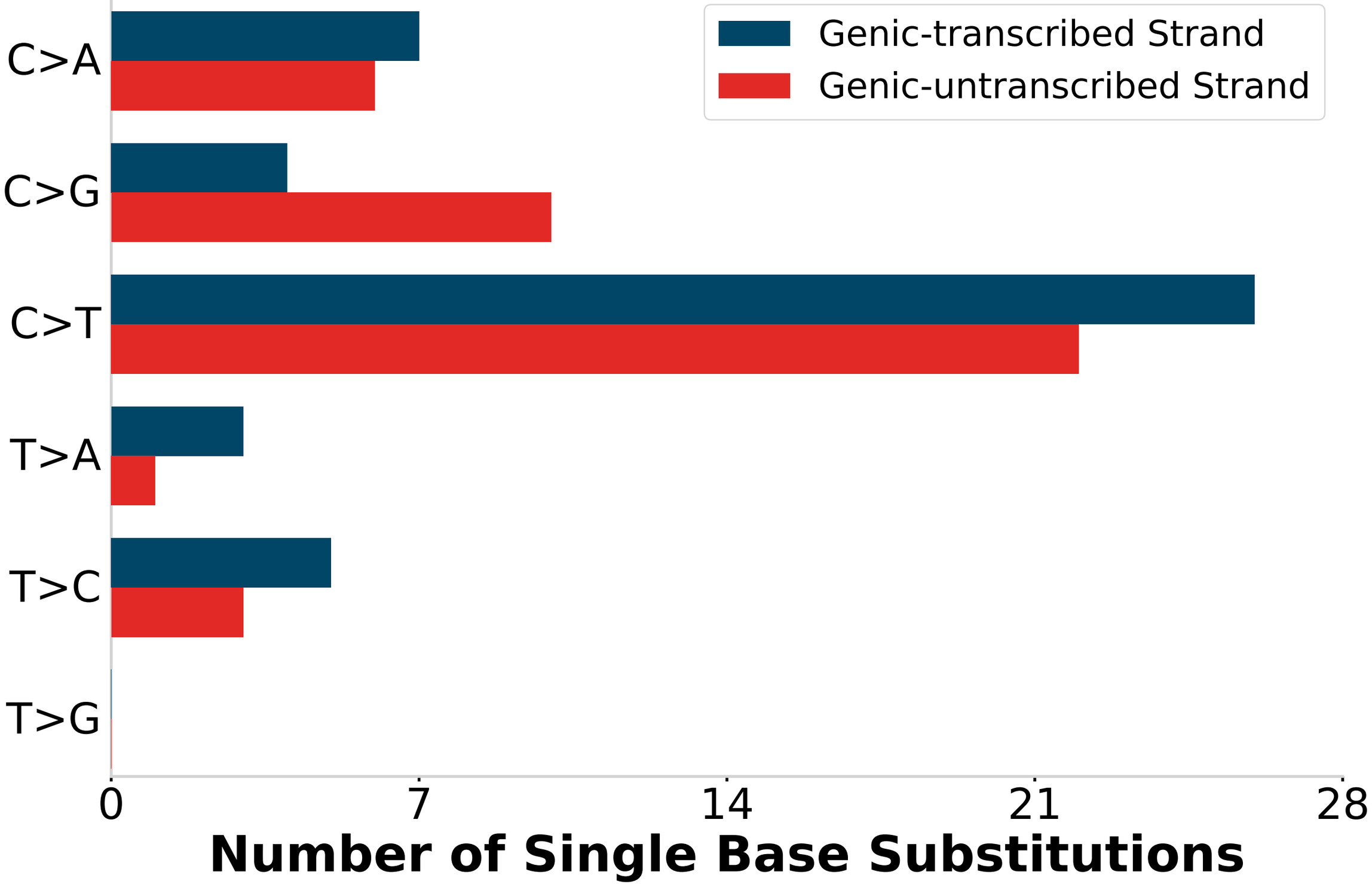
TCGA-C4-A0F1-01A-11D-A10S-08: 181 tran



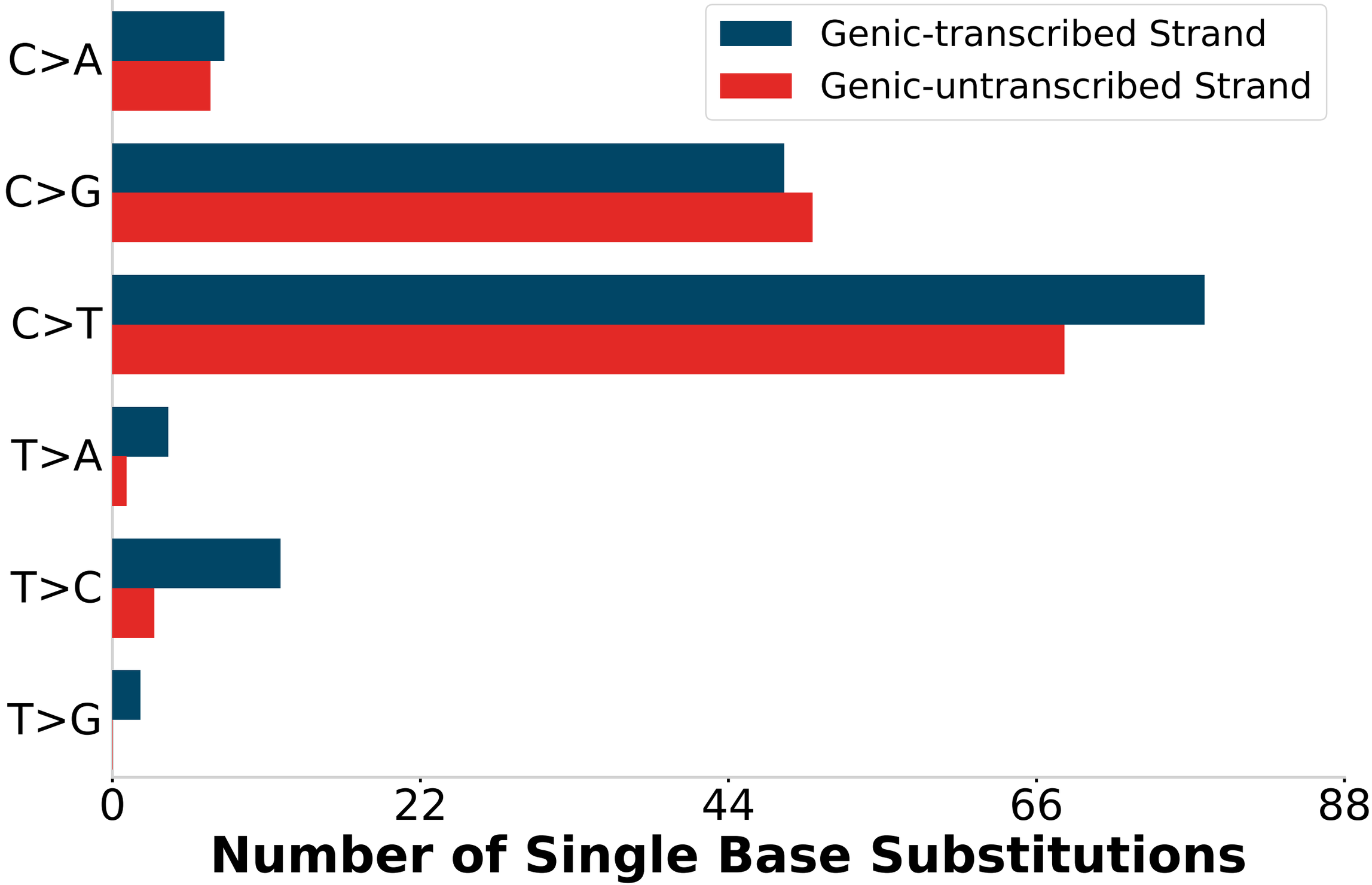
TCGA-C4-A0F6-01A-11D-A10S-08: 218 tran



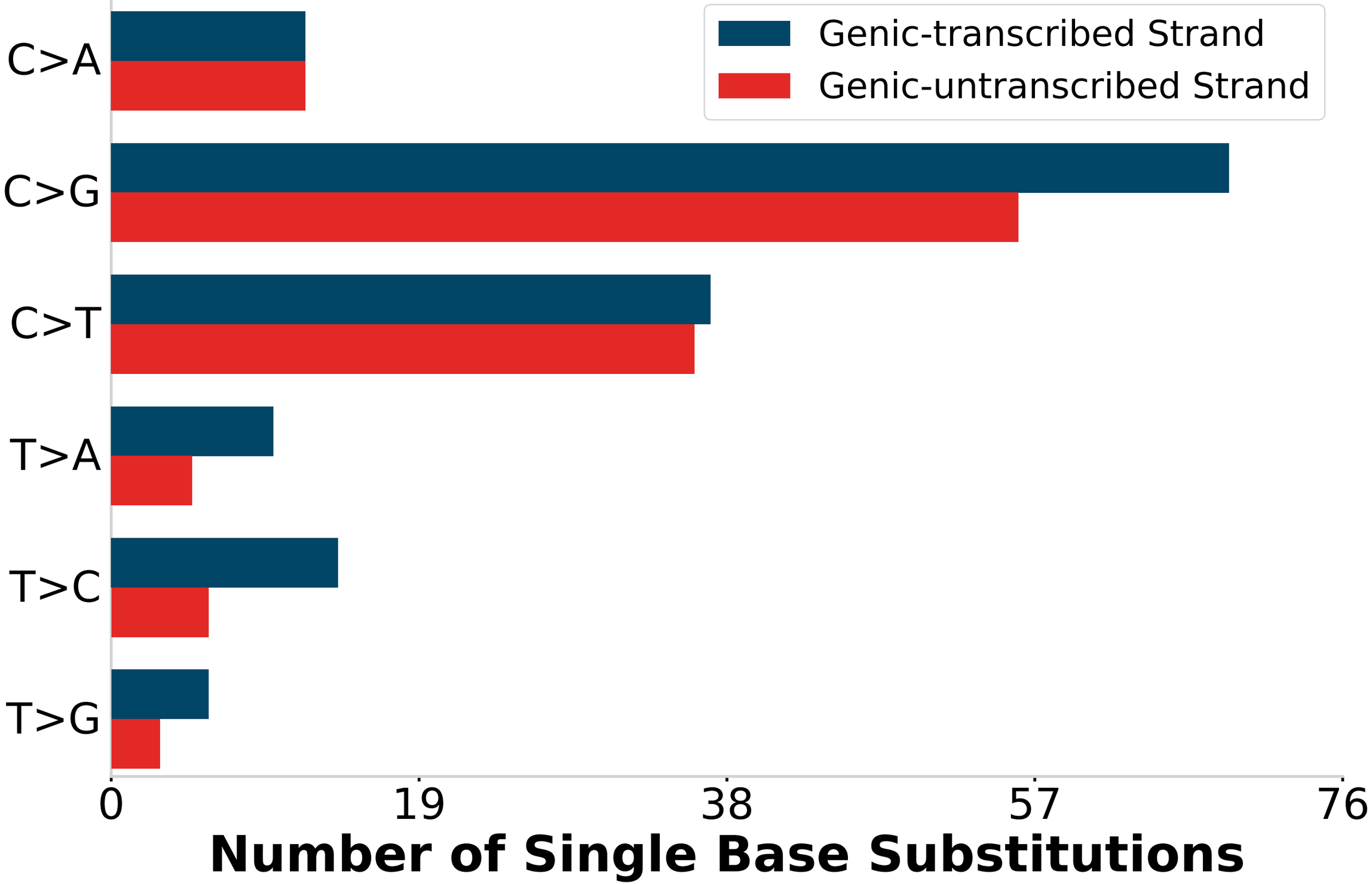
TCGA-C4-A0F7-01A-11D-A10S-08: 87 trans



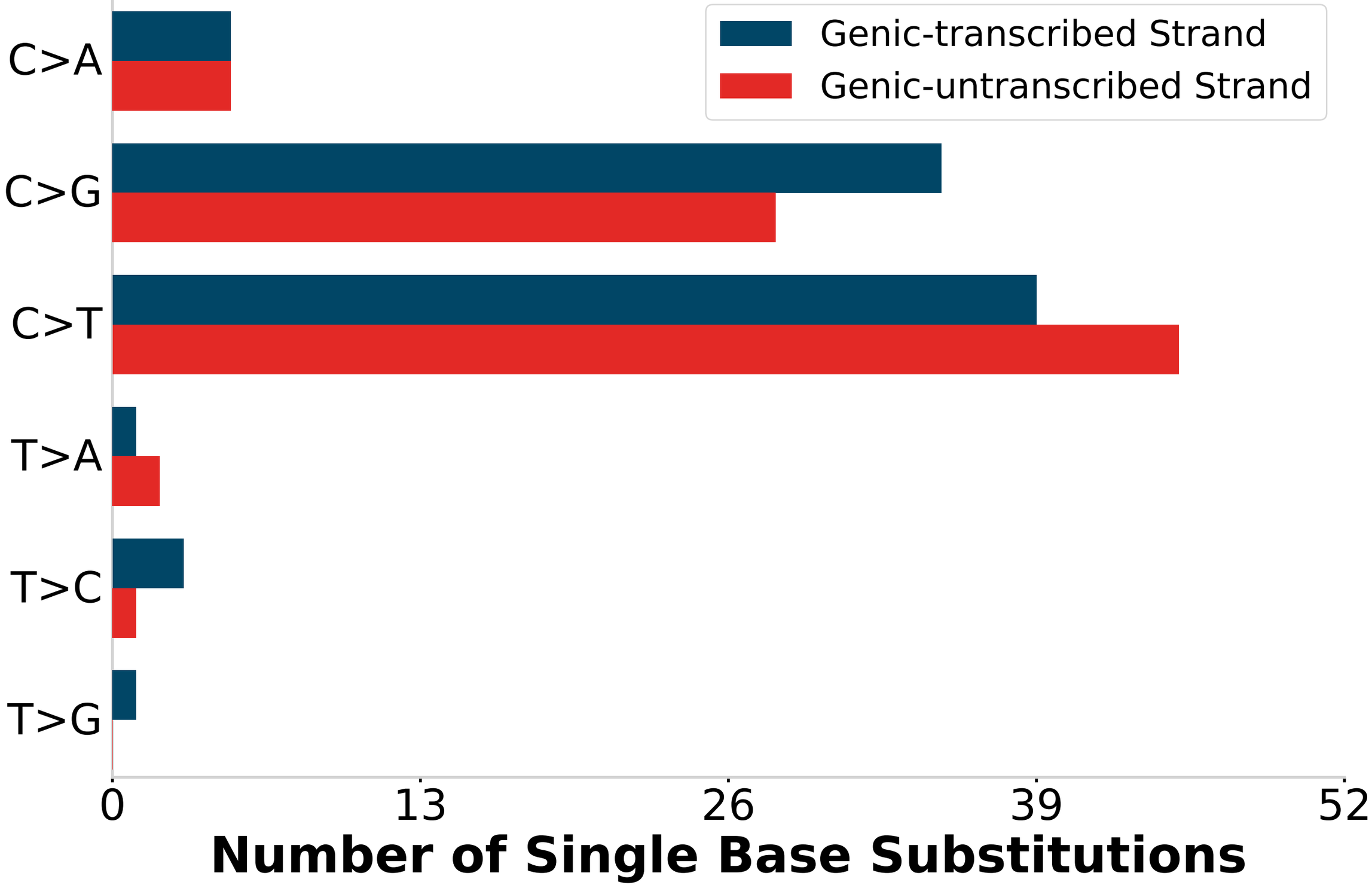
TCGA-CF-A1HR-01A-11D-A13W-08: 281 tra



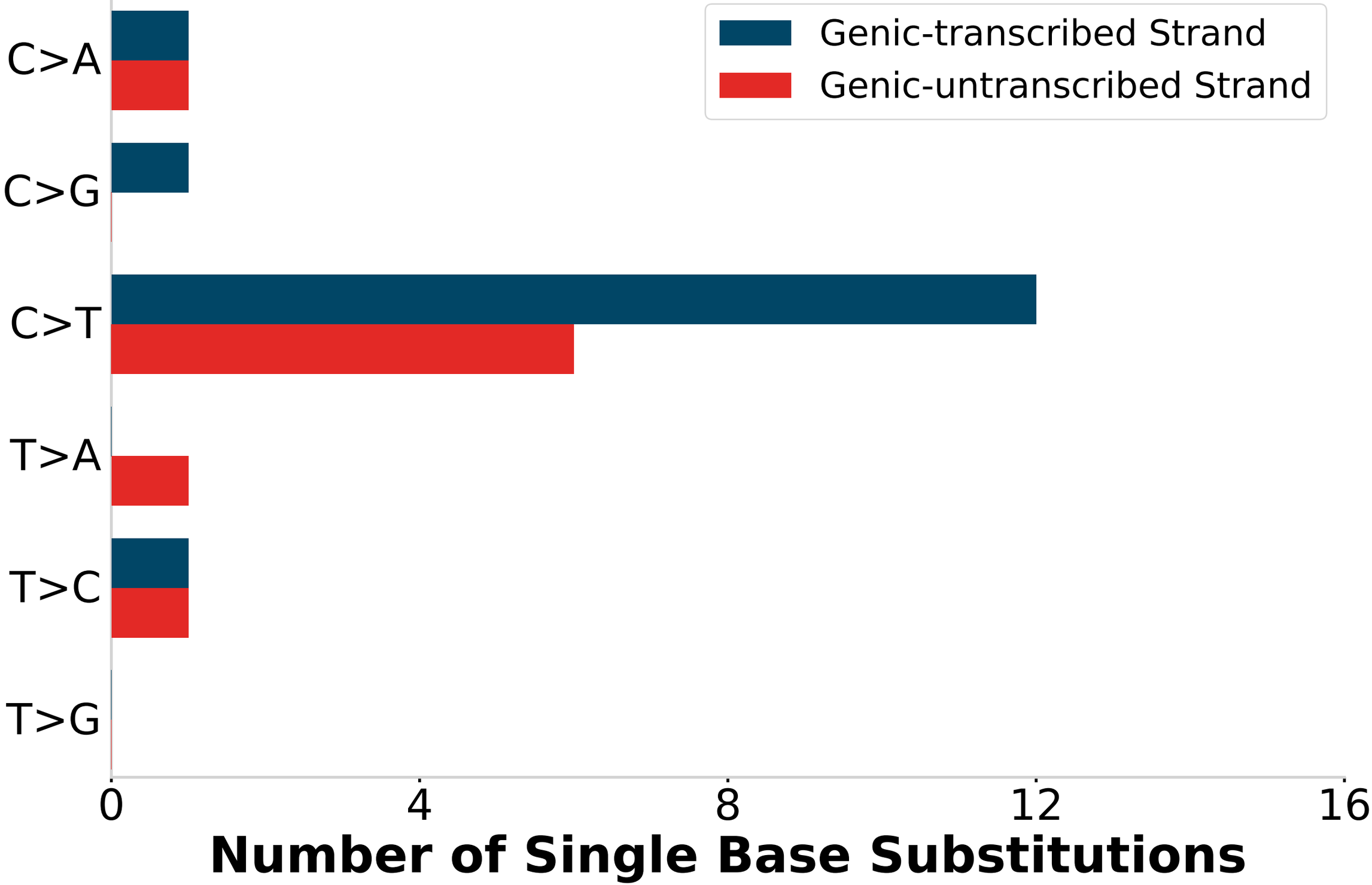
TCGA-CF-A1HS-01A-11D-A13W-08: 266 tra



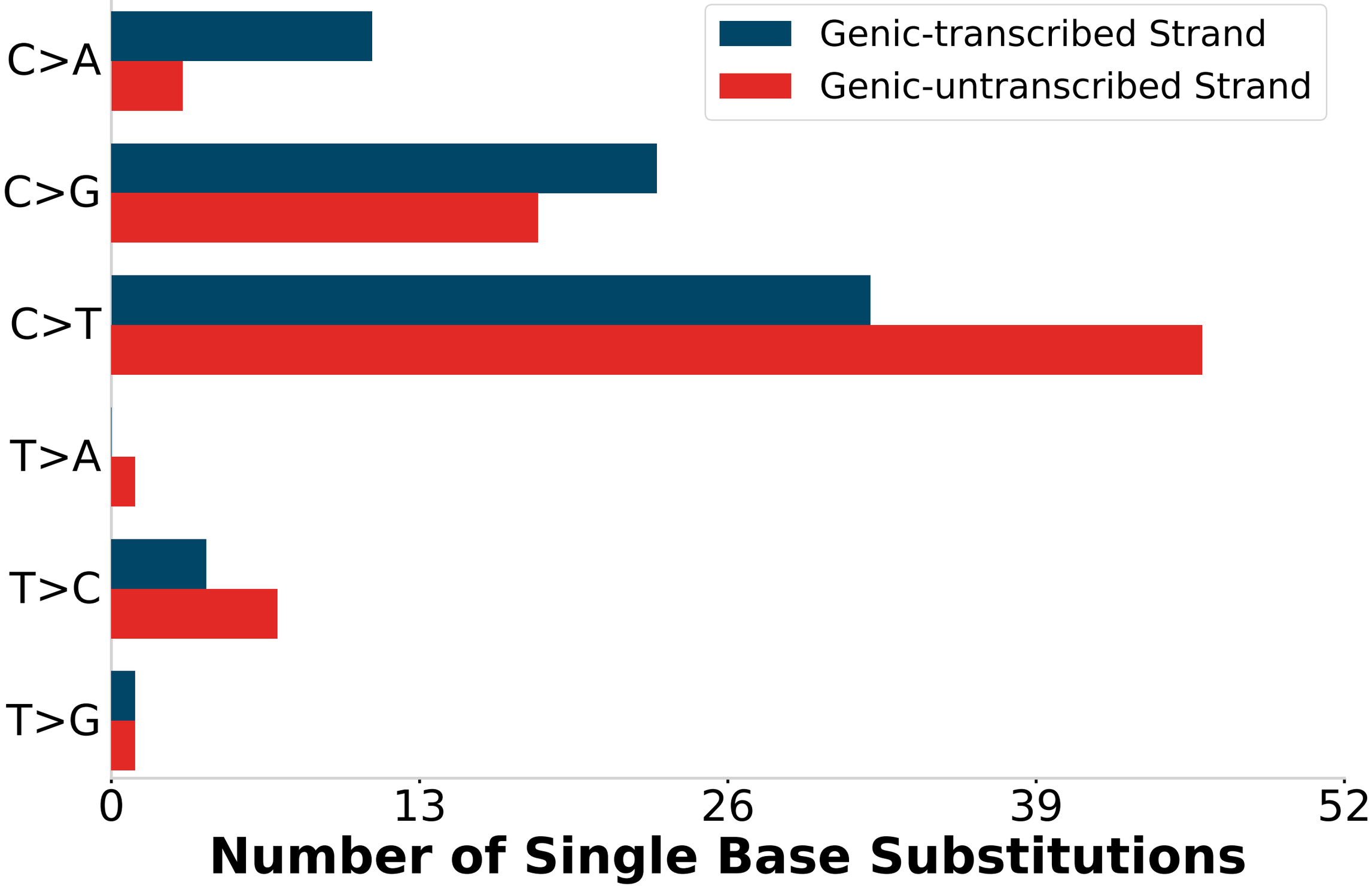
TCGA-CF-A27C-01A-11D-A16O-08: 165 tra



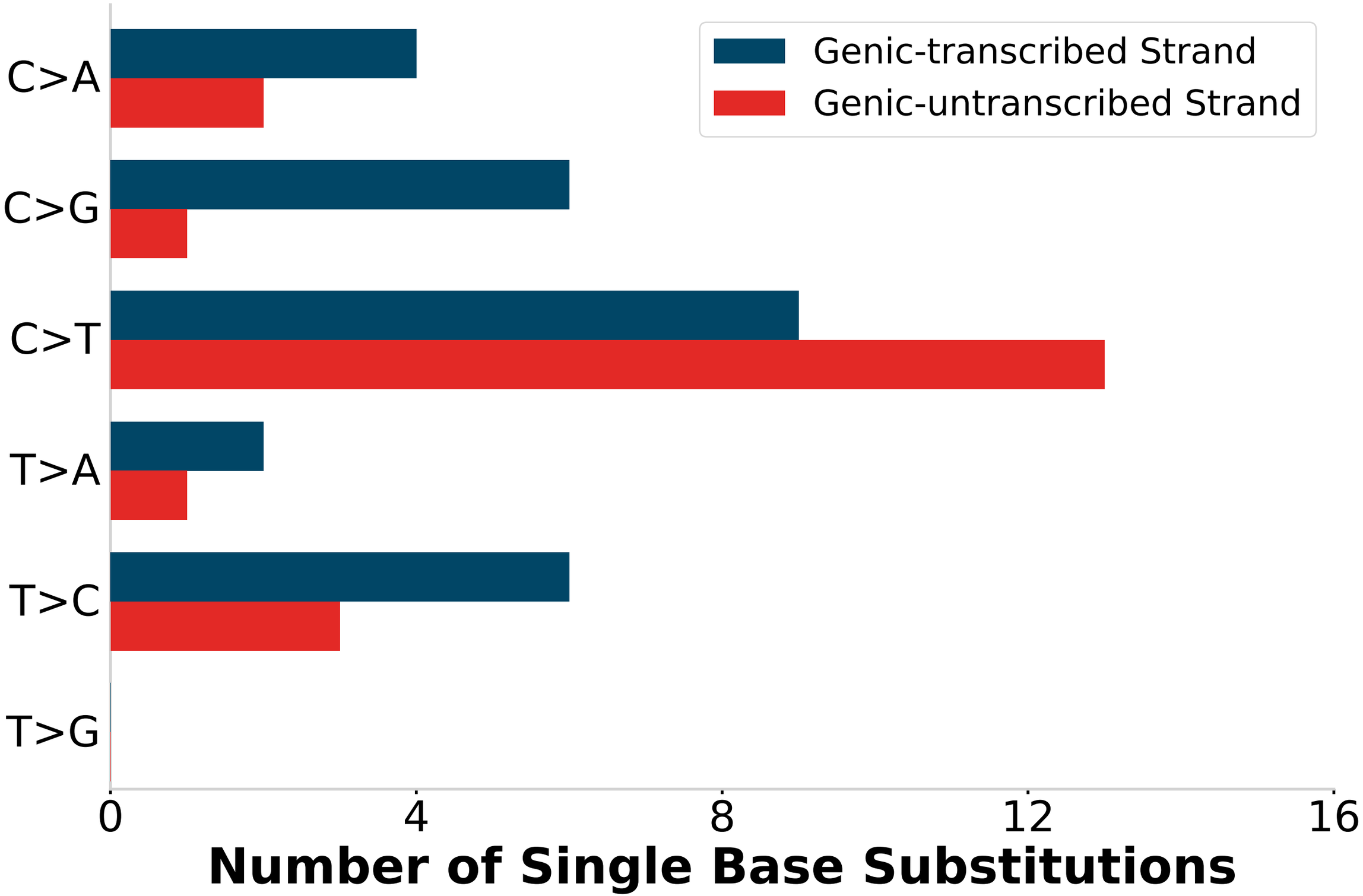
TCGA-CF-A3MF-01A-12D-A21A-08: 24 tran



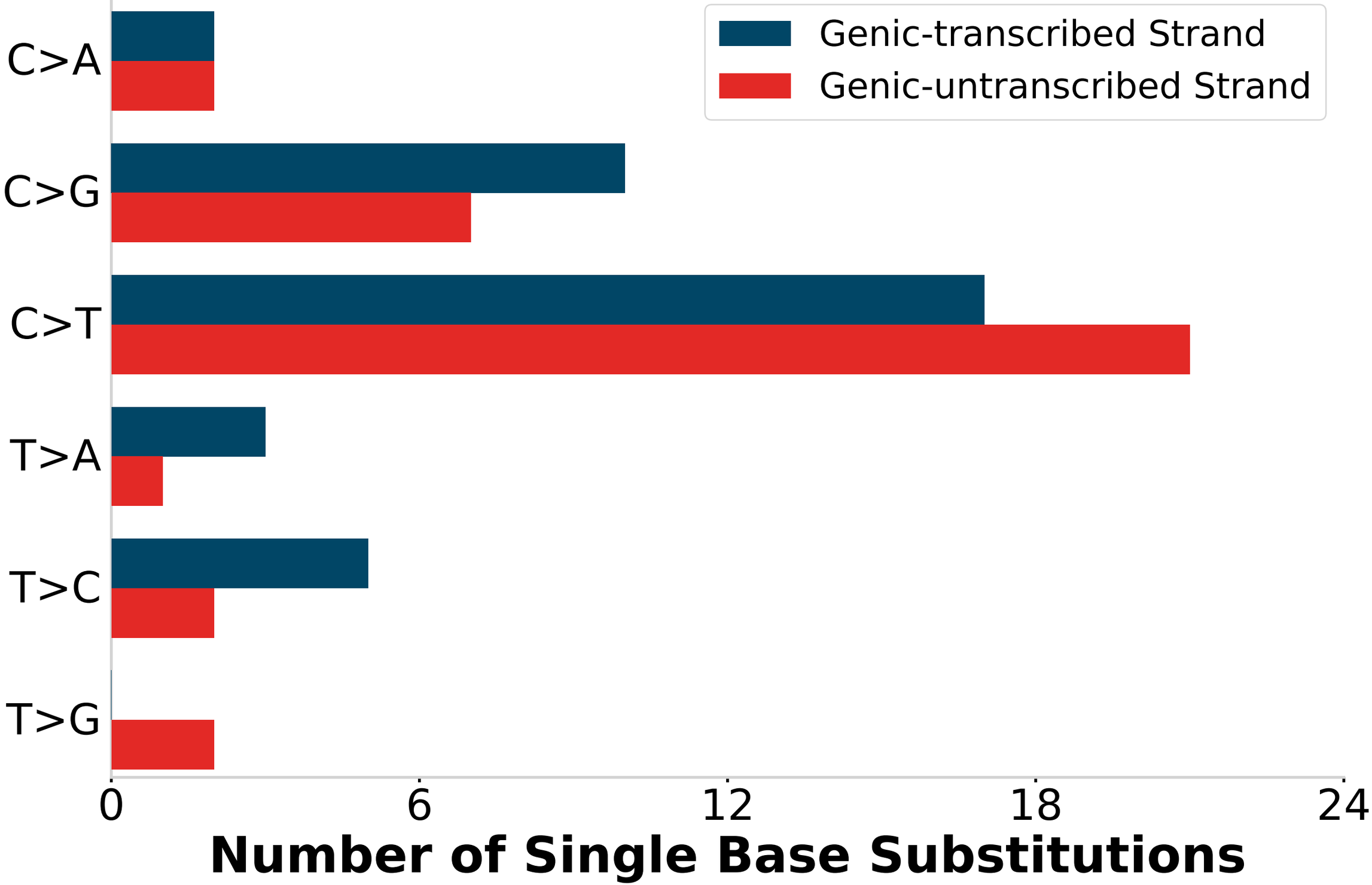
TCGA-CF-A3MG-01A-11D-A20D-08: 147 tra



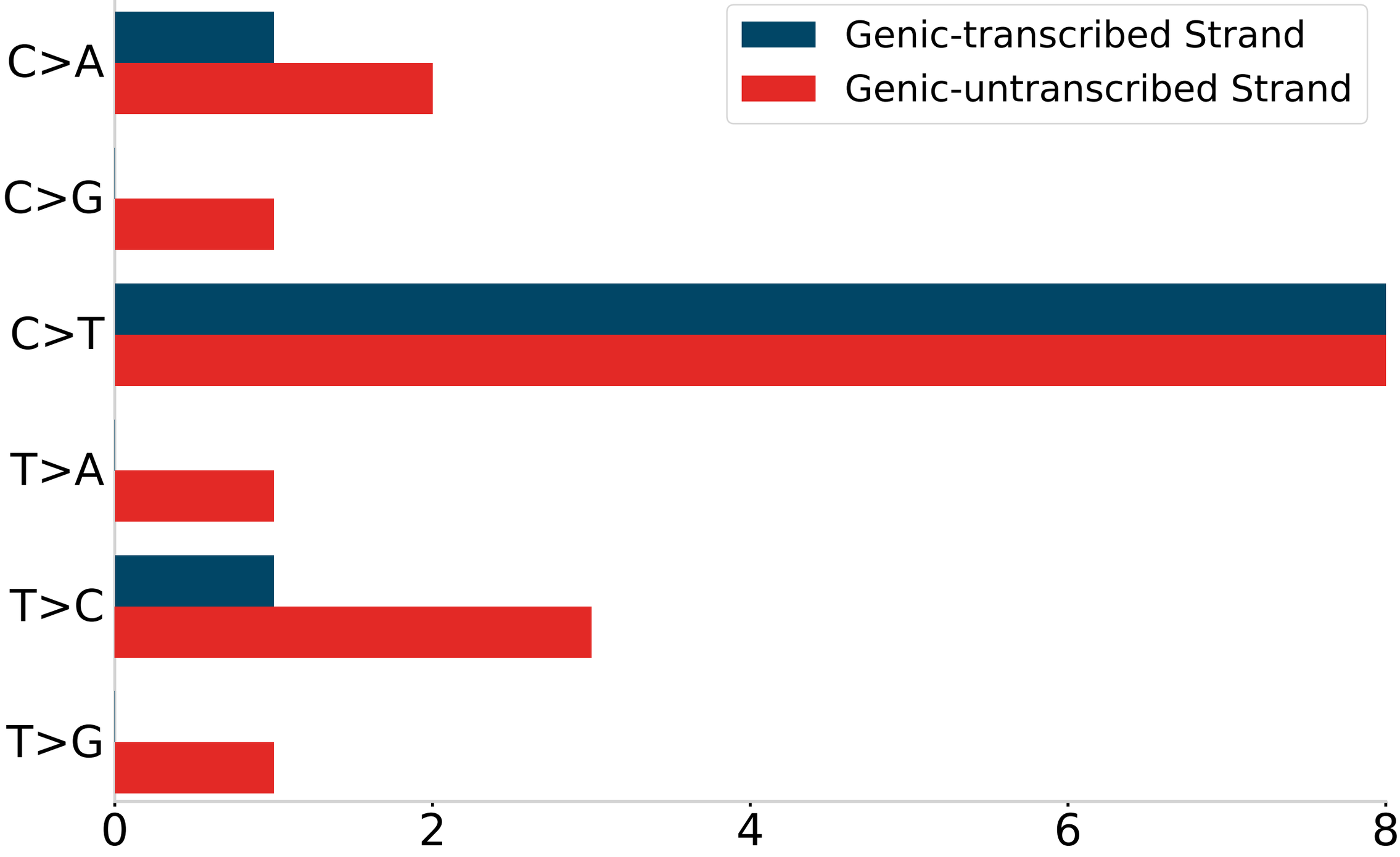
TCGA-CF-A3MH-01A-11D-A20D-08: 47 tran



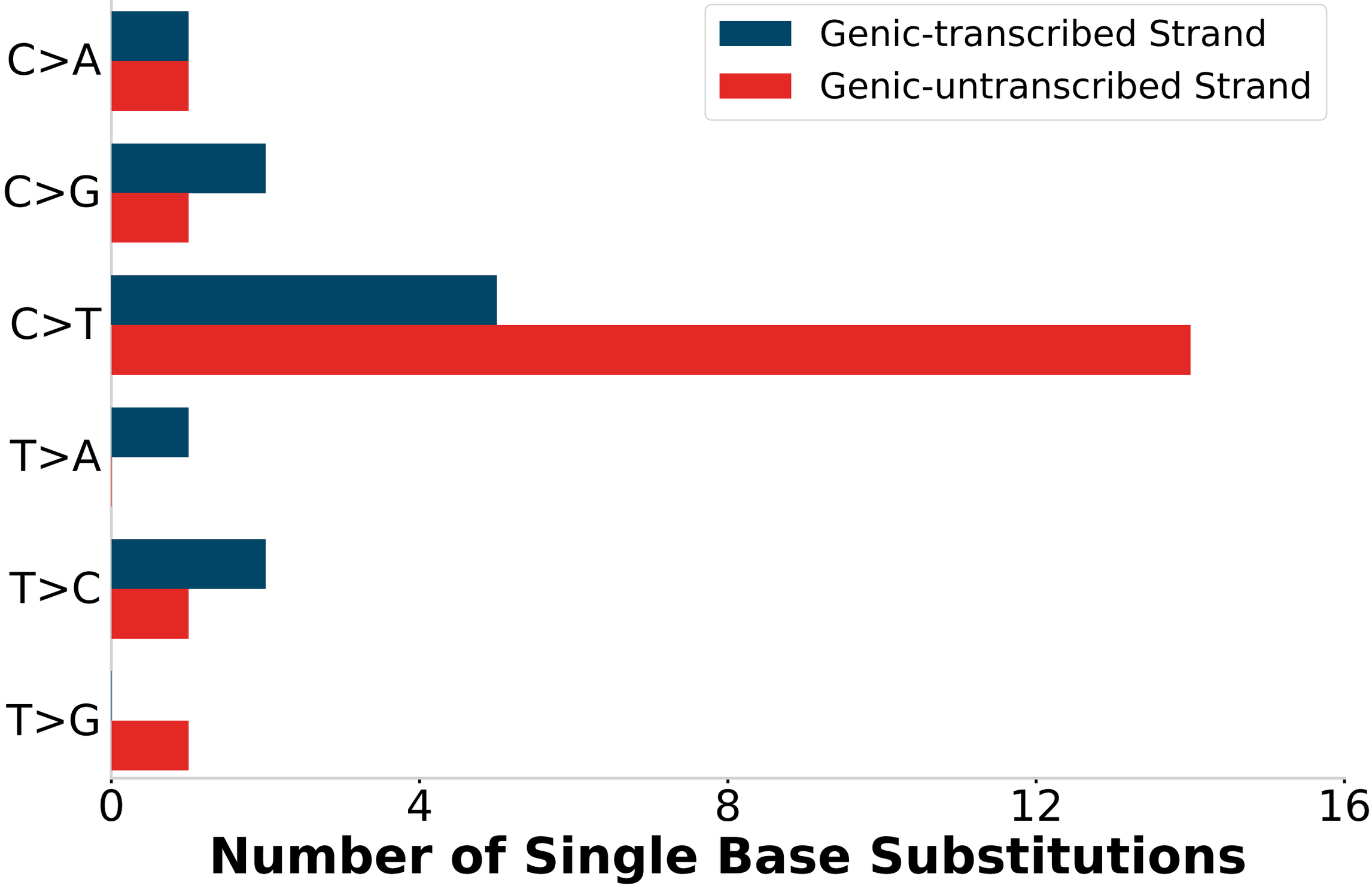
TCGA-CF-A3MI-01A-11D-A20D-08: 72 trans



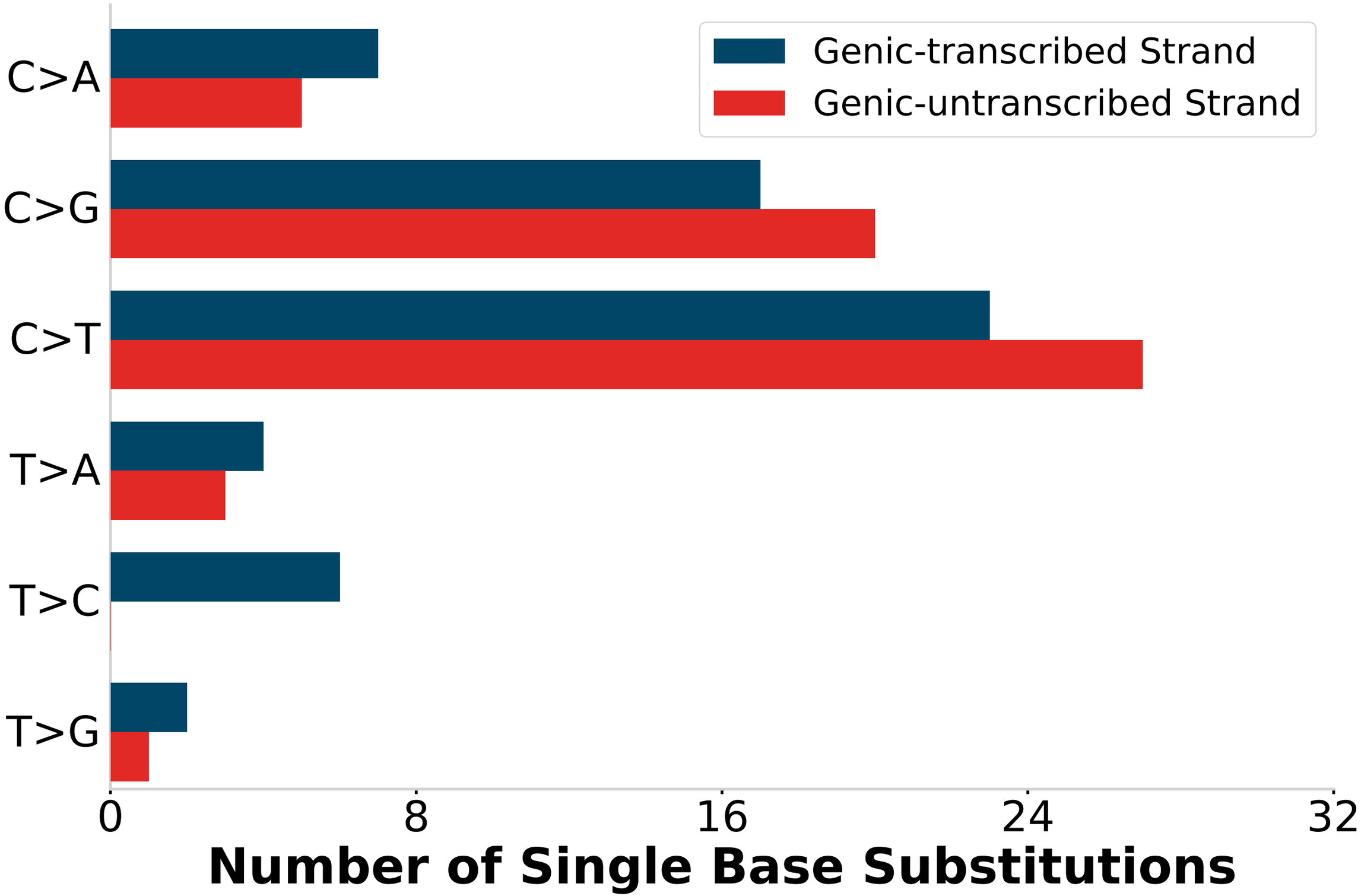
TCGA-CF-A47S-01A-11D-A23U-08: 26 trans



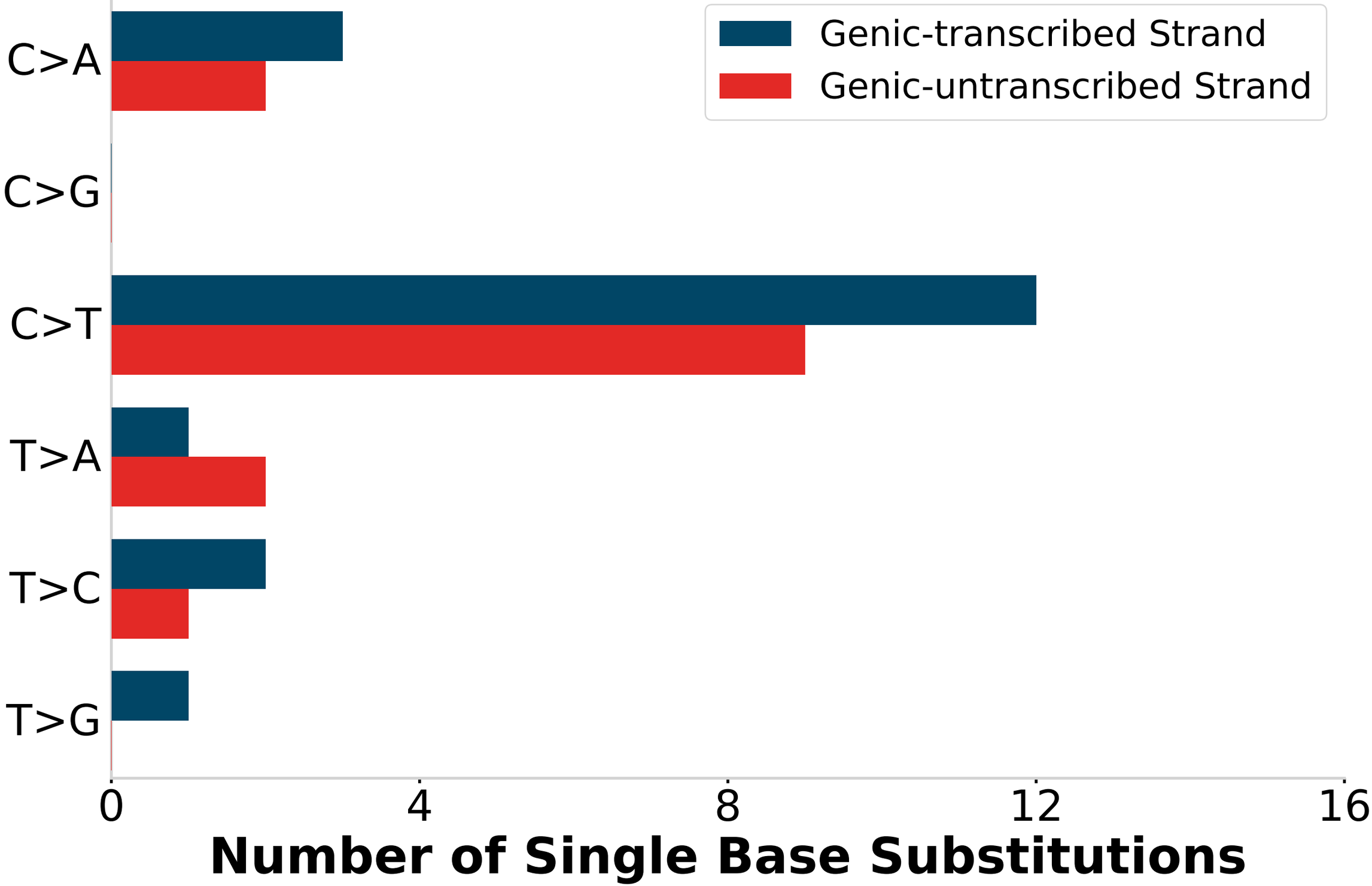
TCGA-CF-A47T-01A-11D-A23U-08: 29 trans



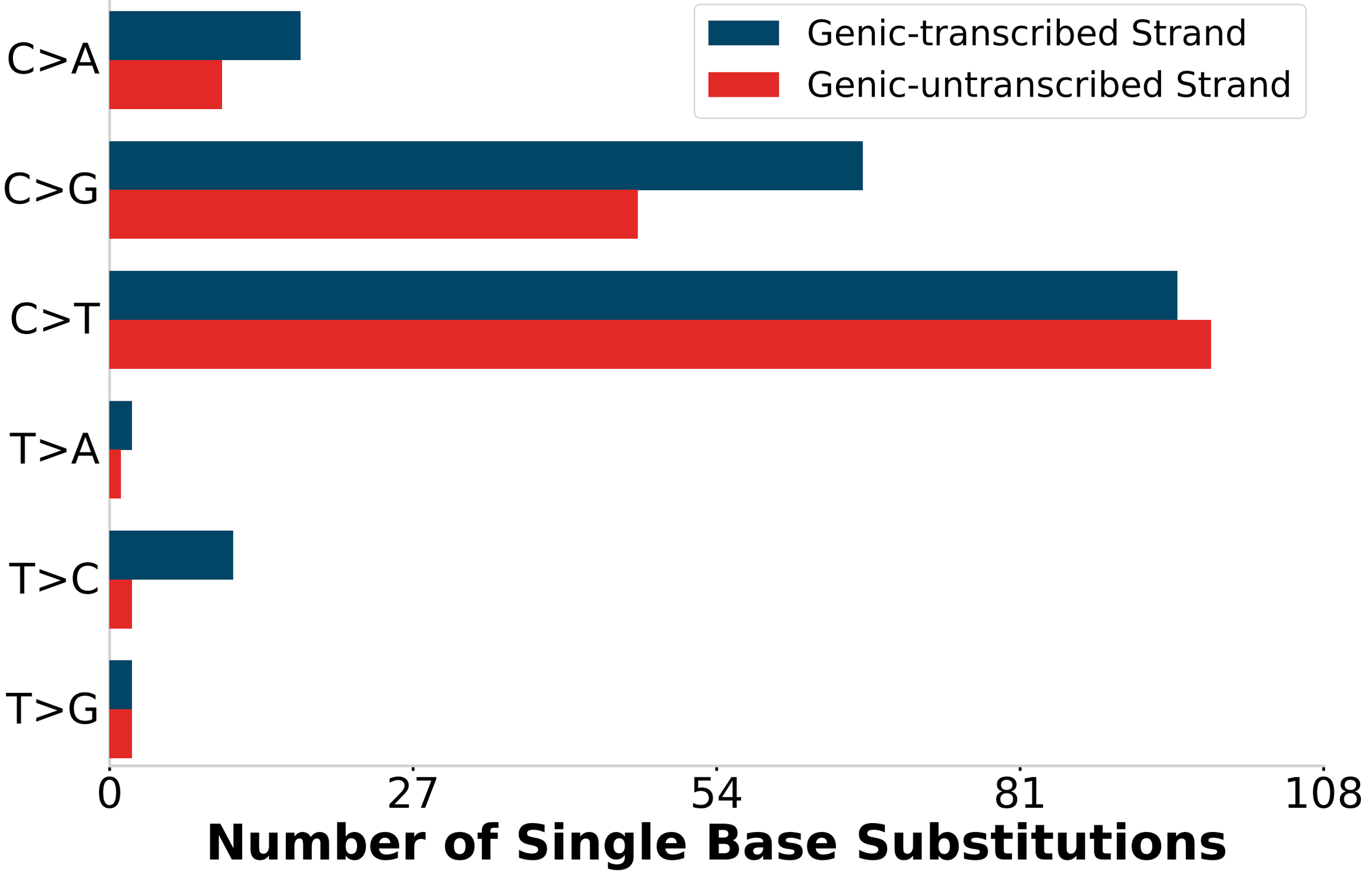
TCGA-CF-A47V-01A-11D-A23U-08: 115 tran



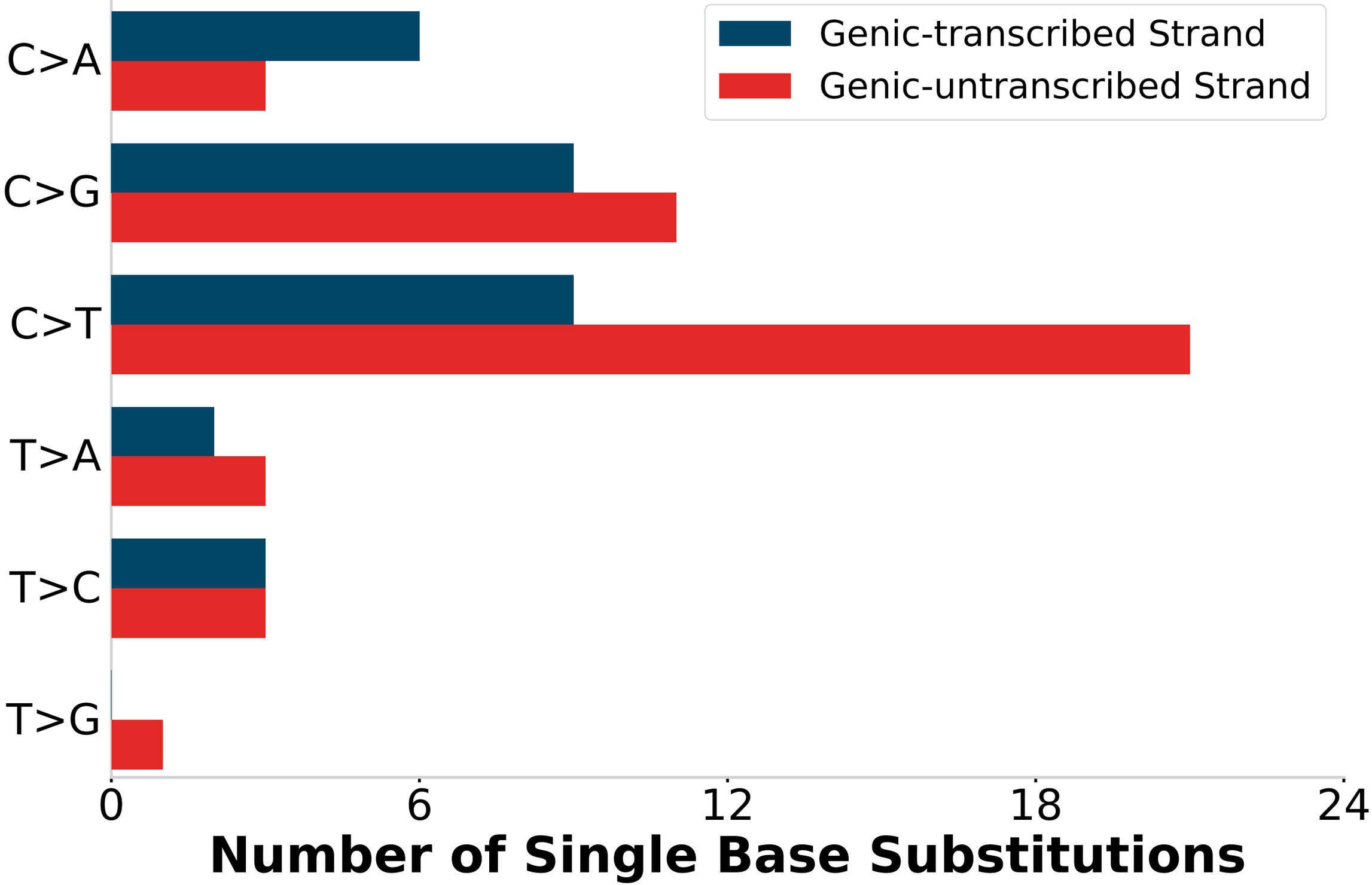
TCGA-CF-A47W-01A-11D-A23U-08: 33 tran



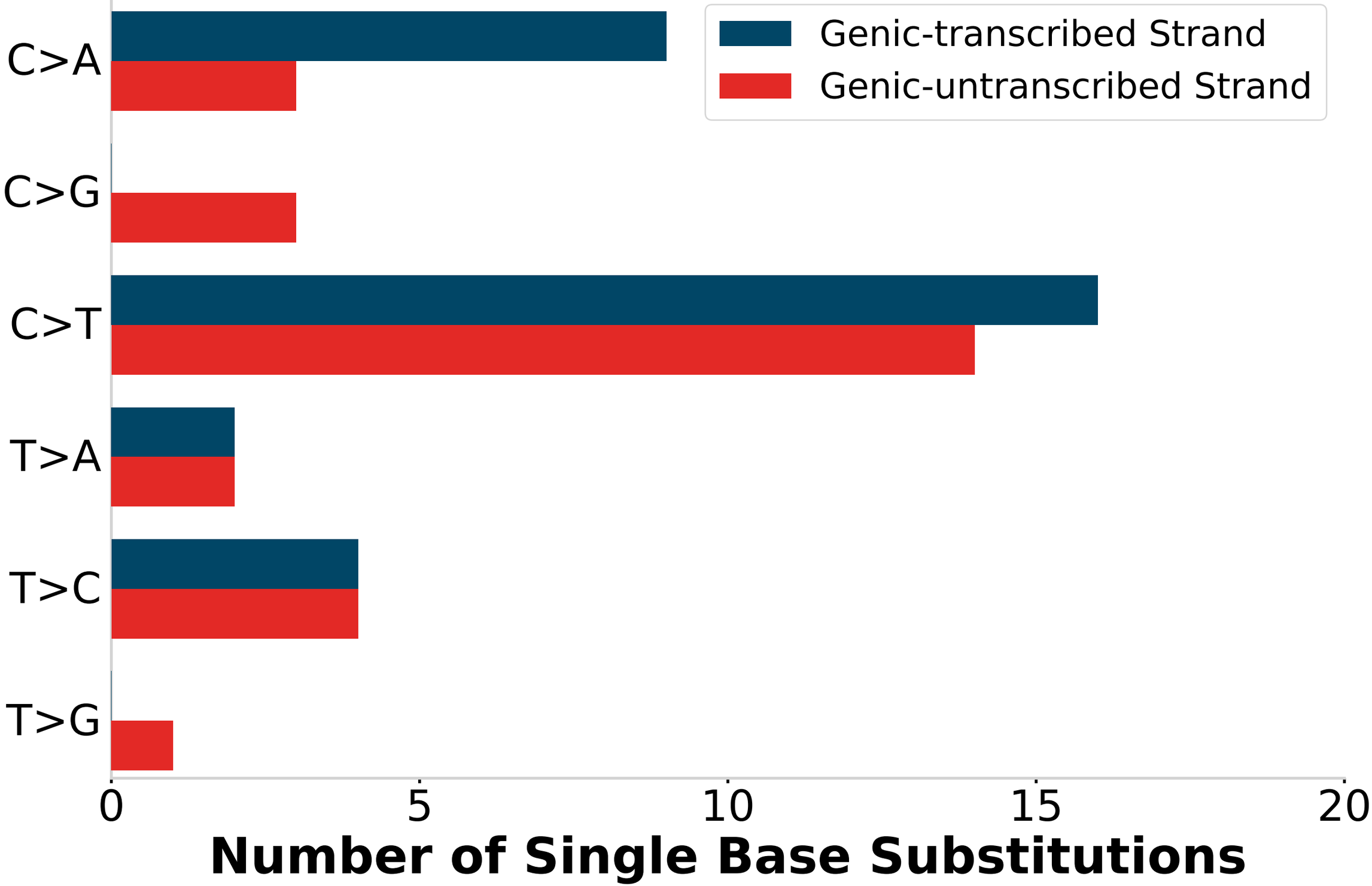
TCGA-CF-A47X-01A-31D-A23U-08: 354 tran



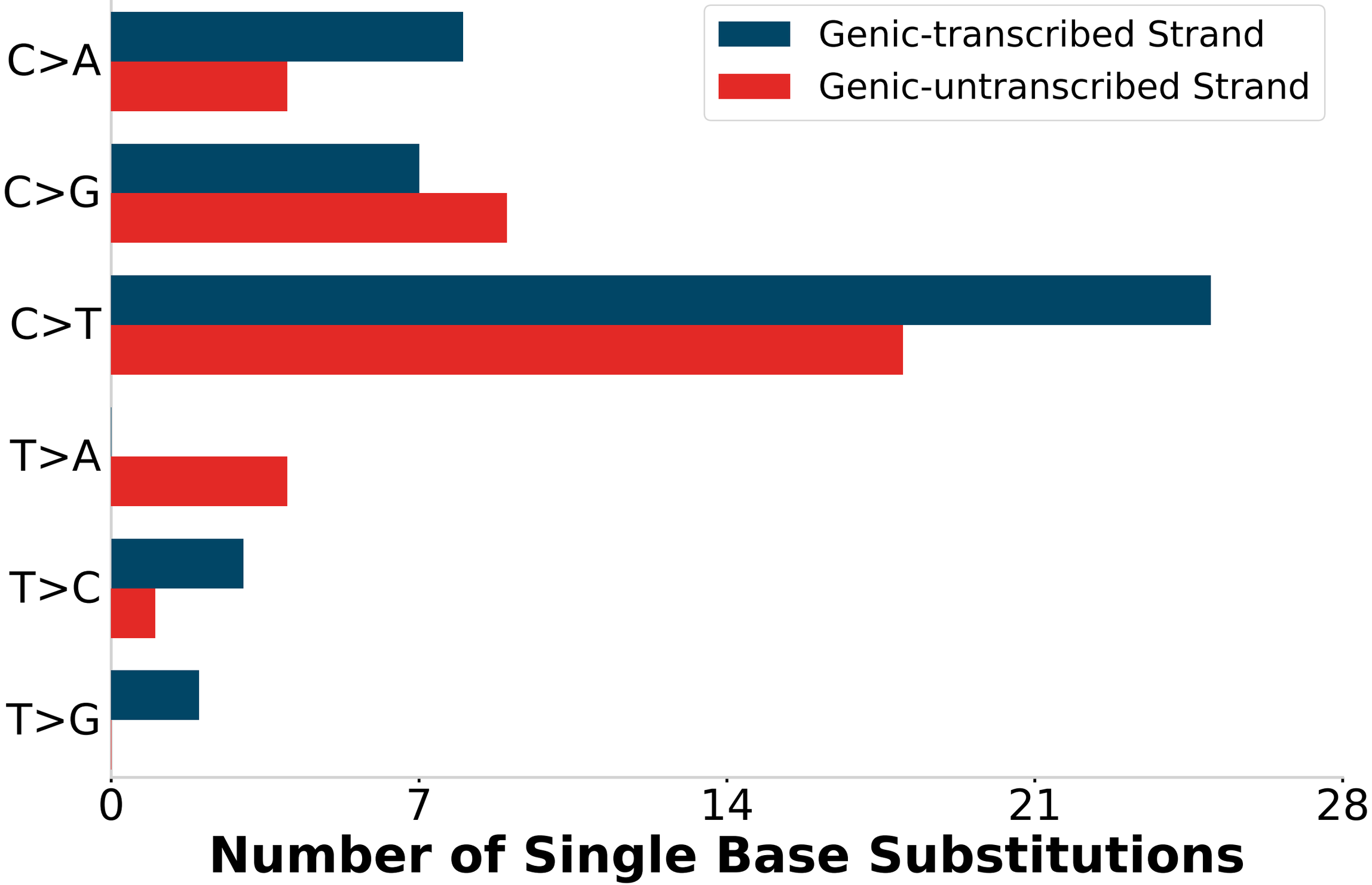
TCGA-CF-A47Y-01A-11D-A23U-08: 71 trans



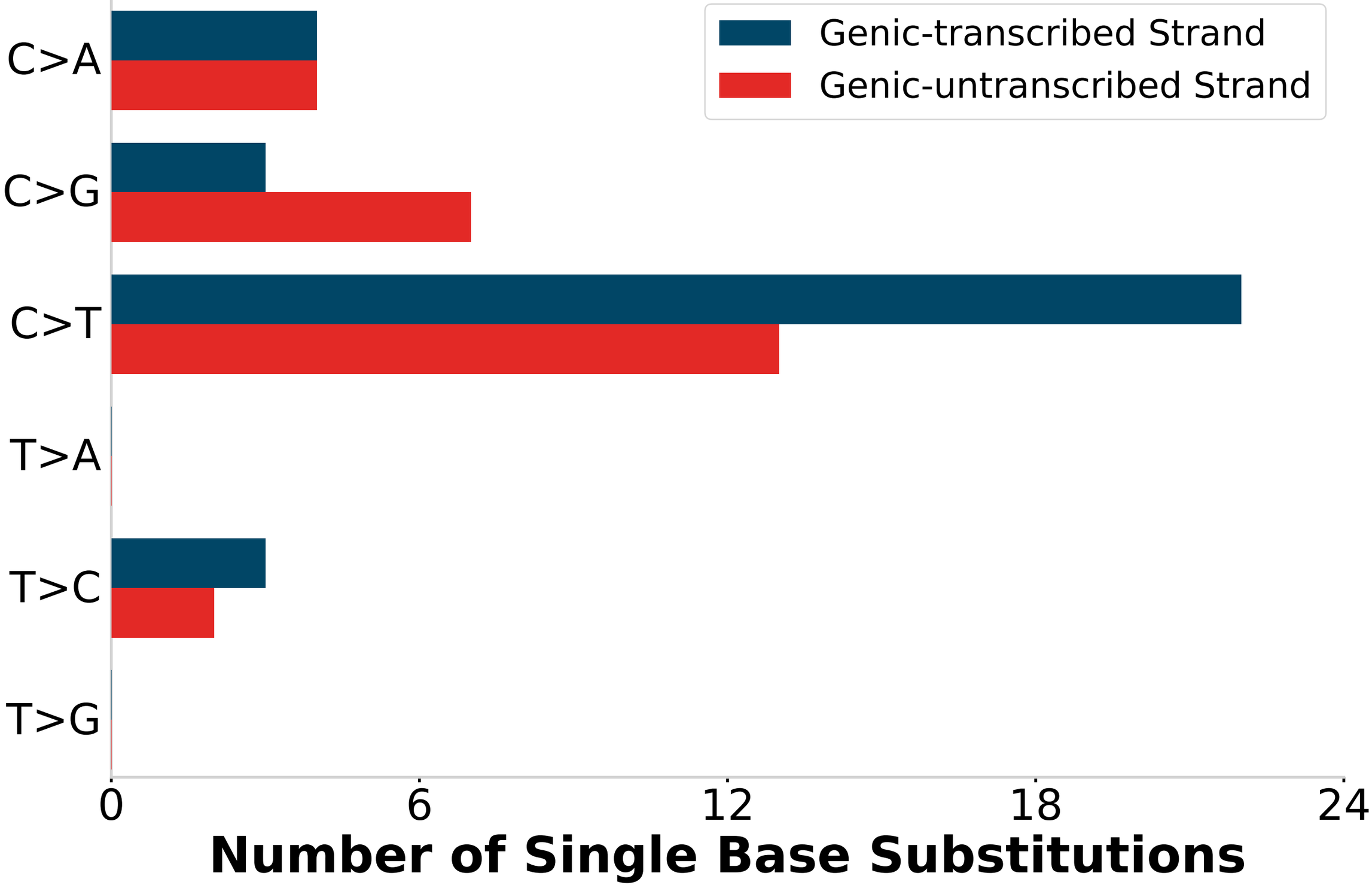
TCGA-CF-A5U8-01A-11D-A289-08: 58 trans



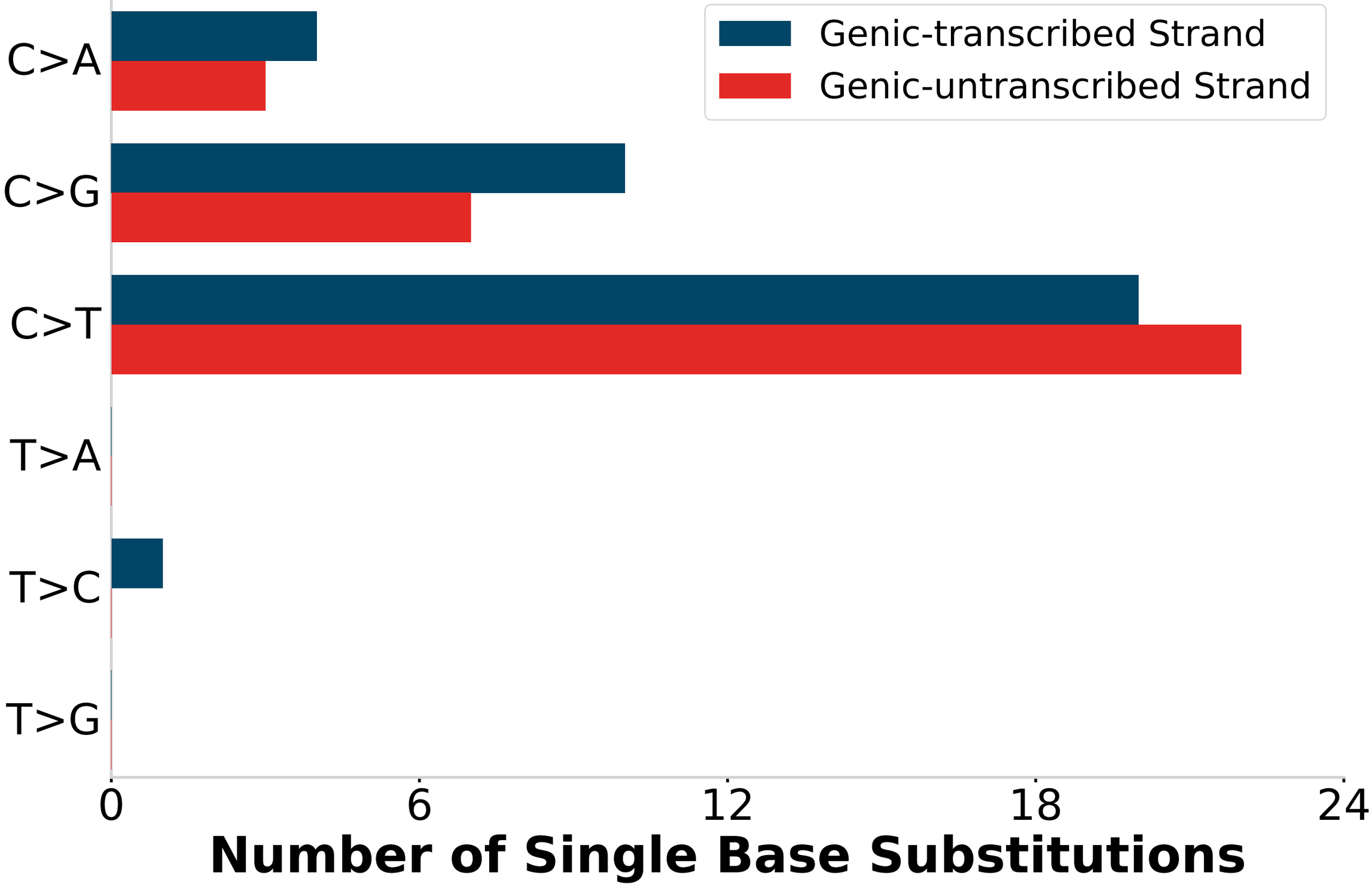
TCGA-CF-A5UA-01A-11D-A289-08: 81 trans



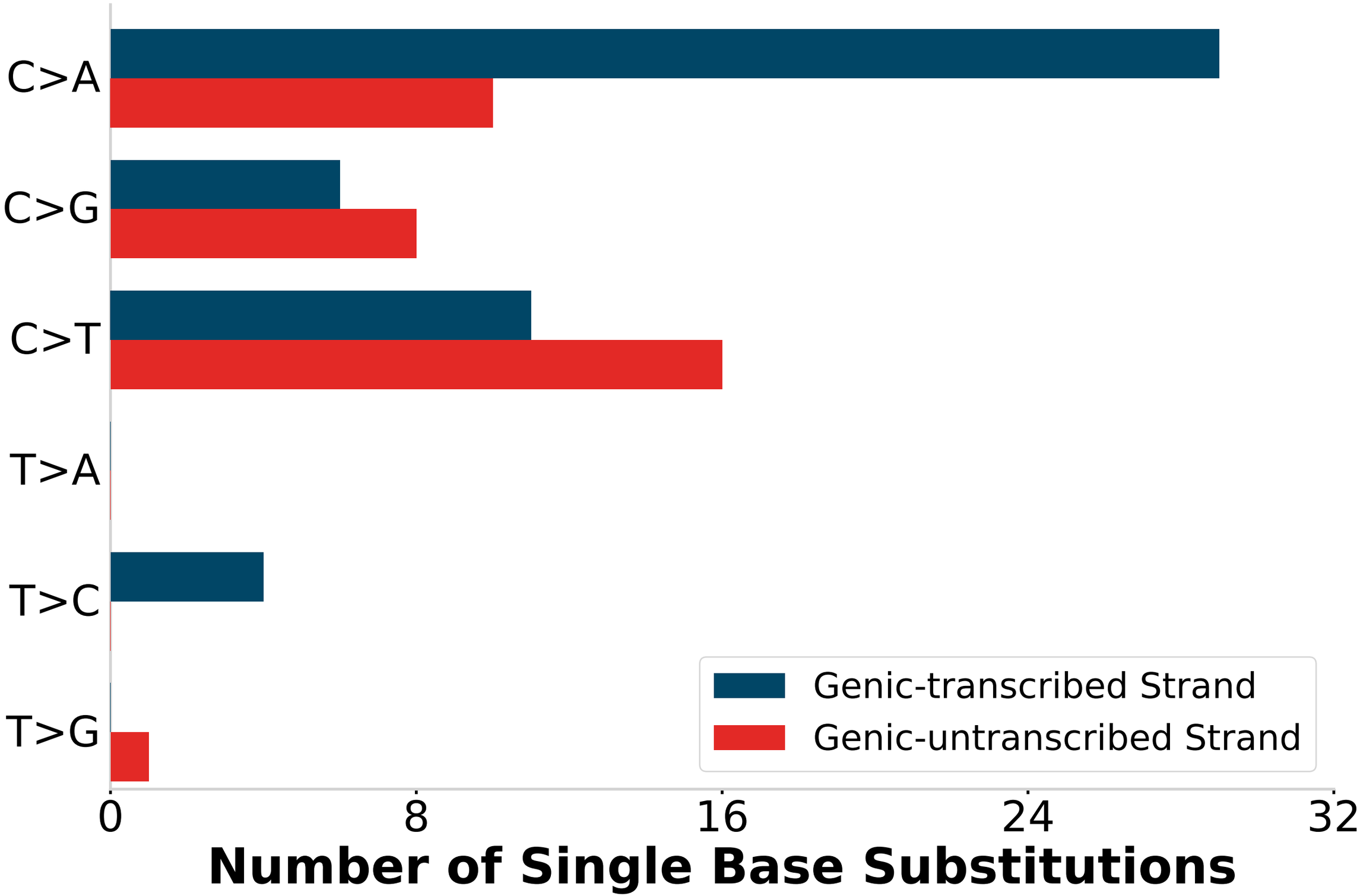
TCGA-CF-A7I0-01A-22D-A34U-08: 58 trans



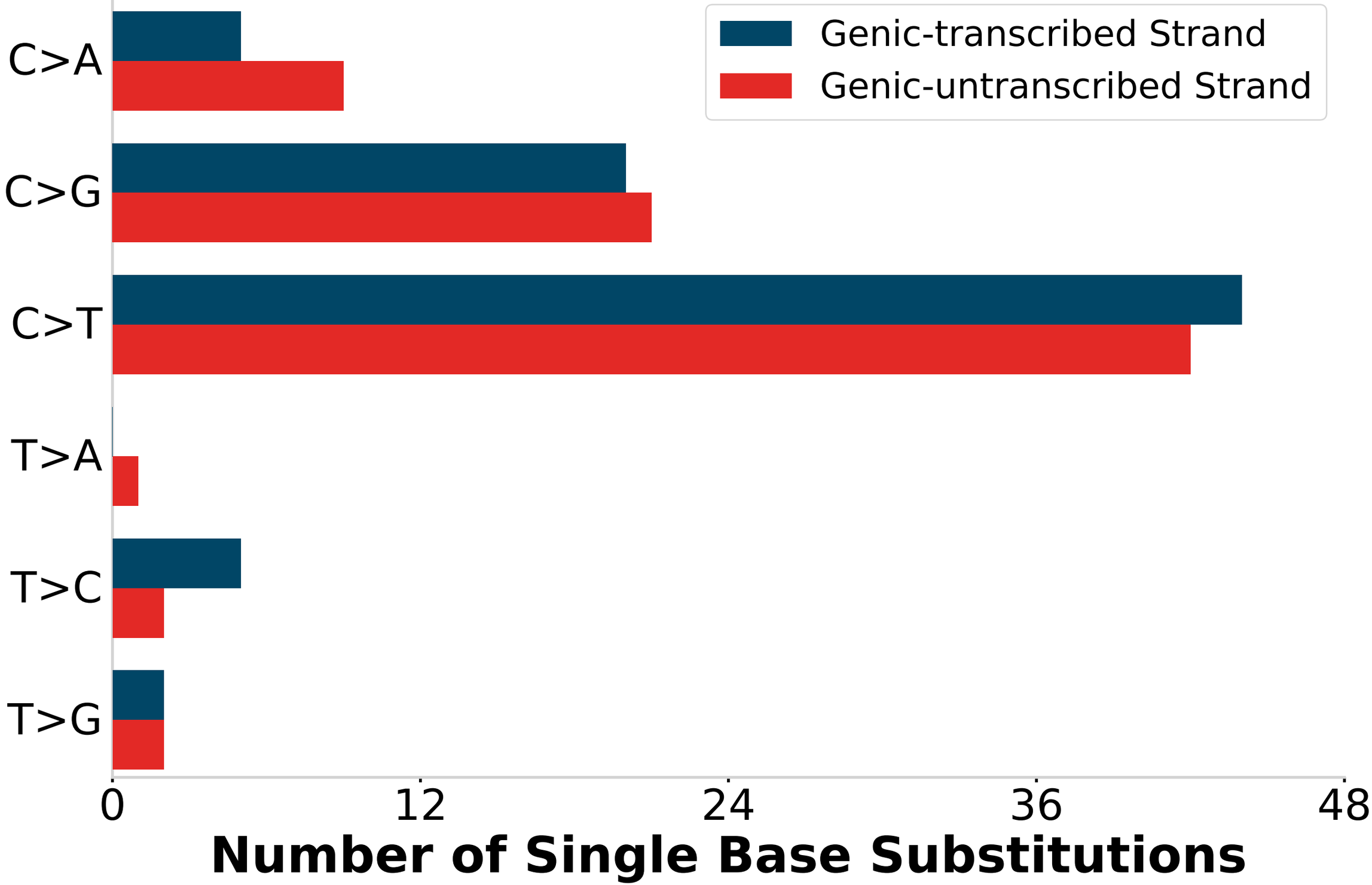
TCGA-CF-A8HX-01A-11D-A364-08: 67 trans



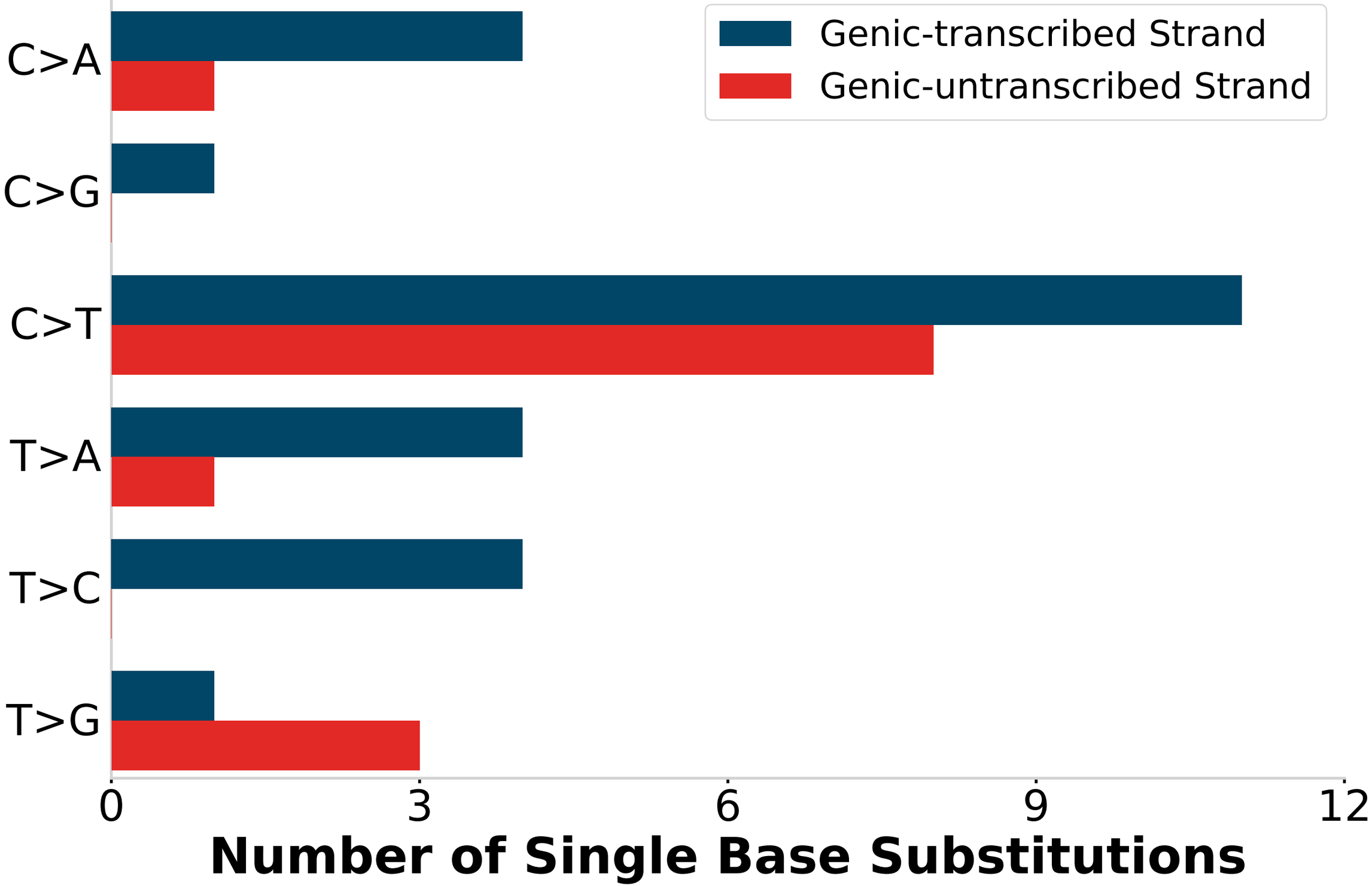
TCGA-CF-A8HY-01A-11D-A364-08: 85 trans



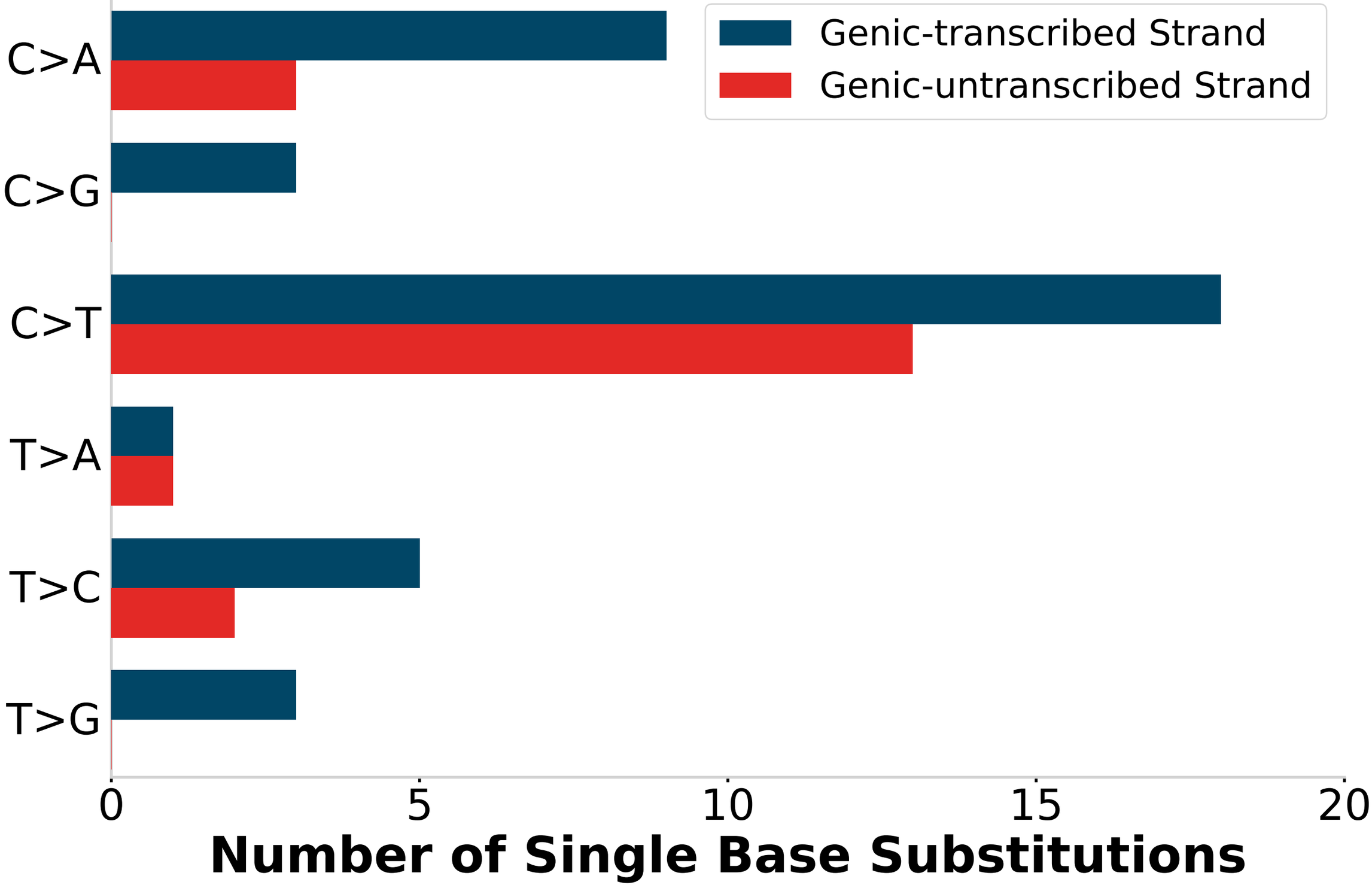
TCGA-CF-A9FF-01A-11D-A38G-08: 153 tran



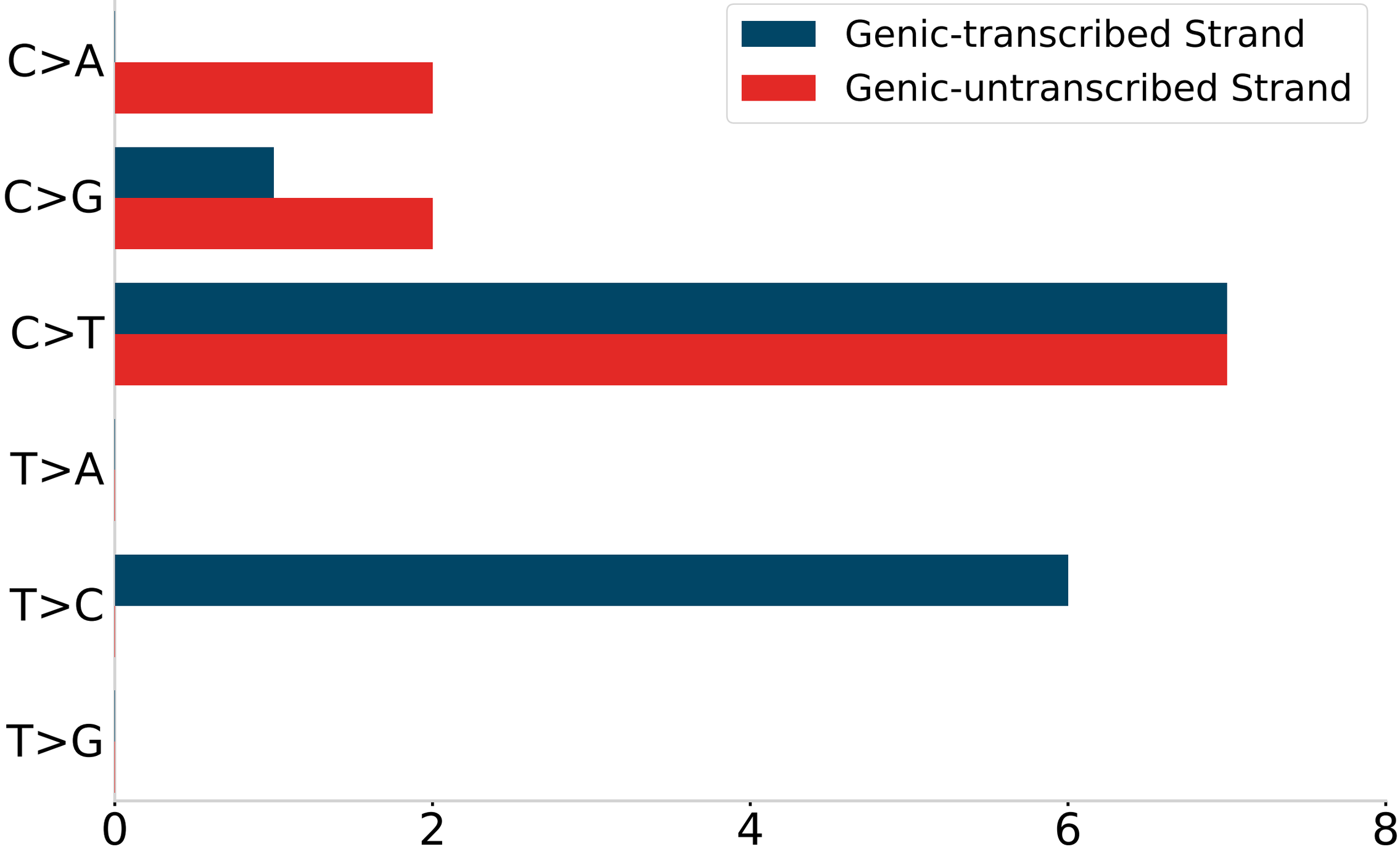
TCGA-CF-A9FH-01A-11D-A38G-08: 38 trans



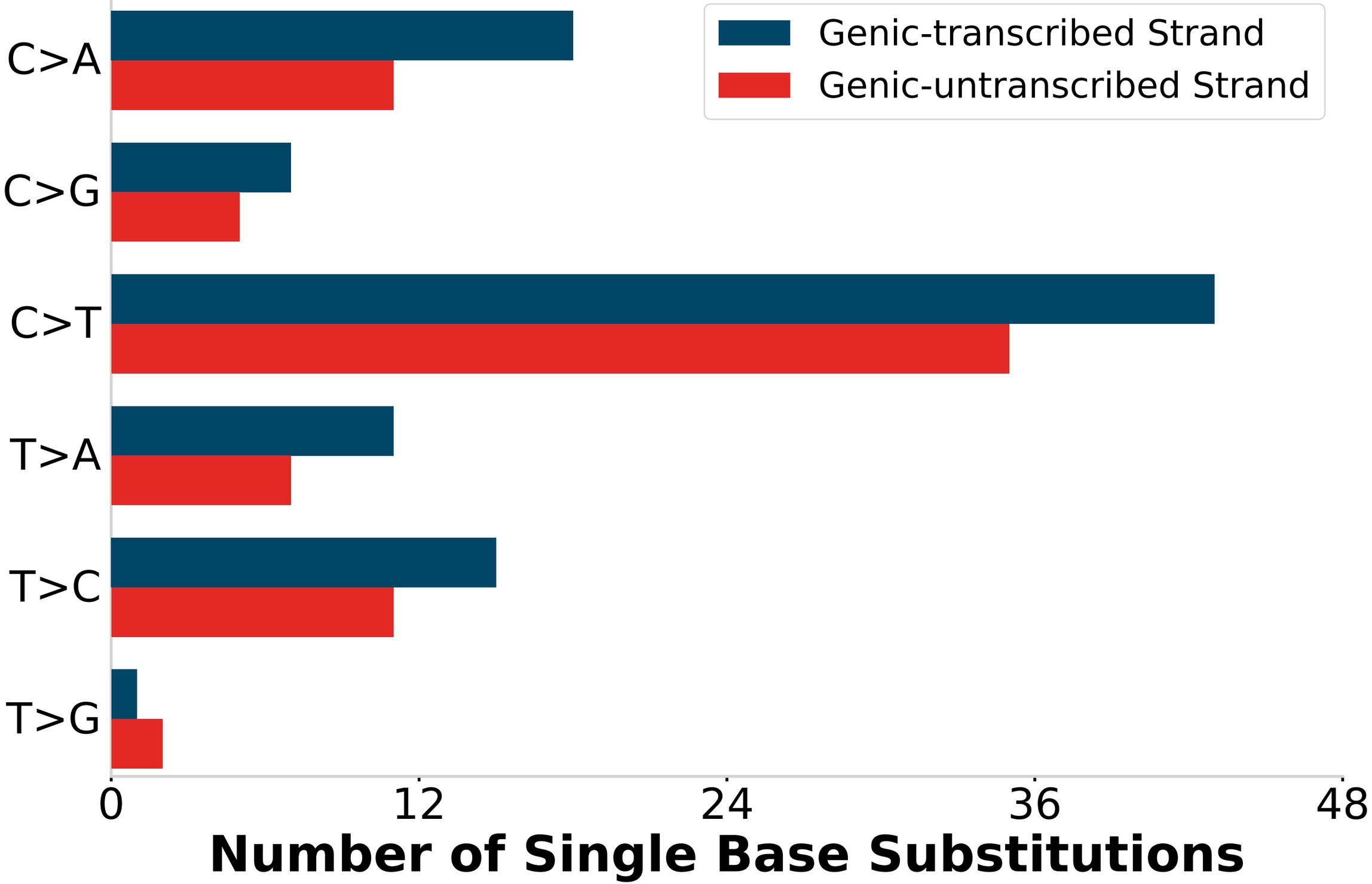
TCGA-CF-A9FL-01A-11D-A38G-08: 58 trans



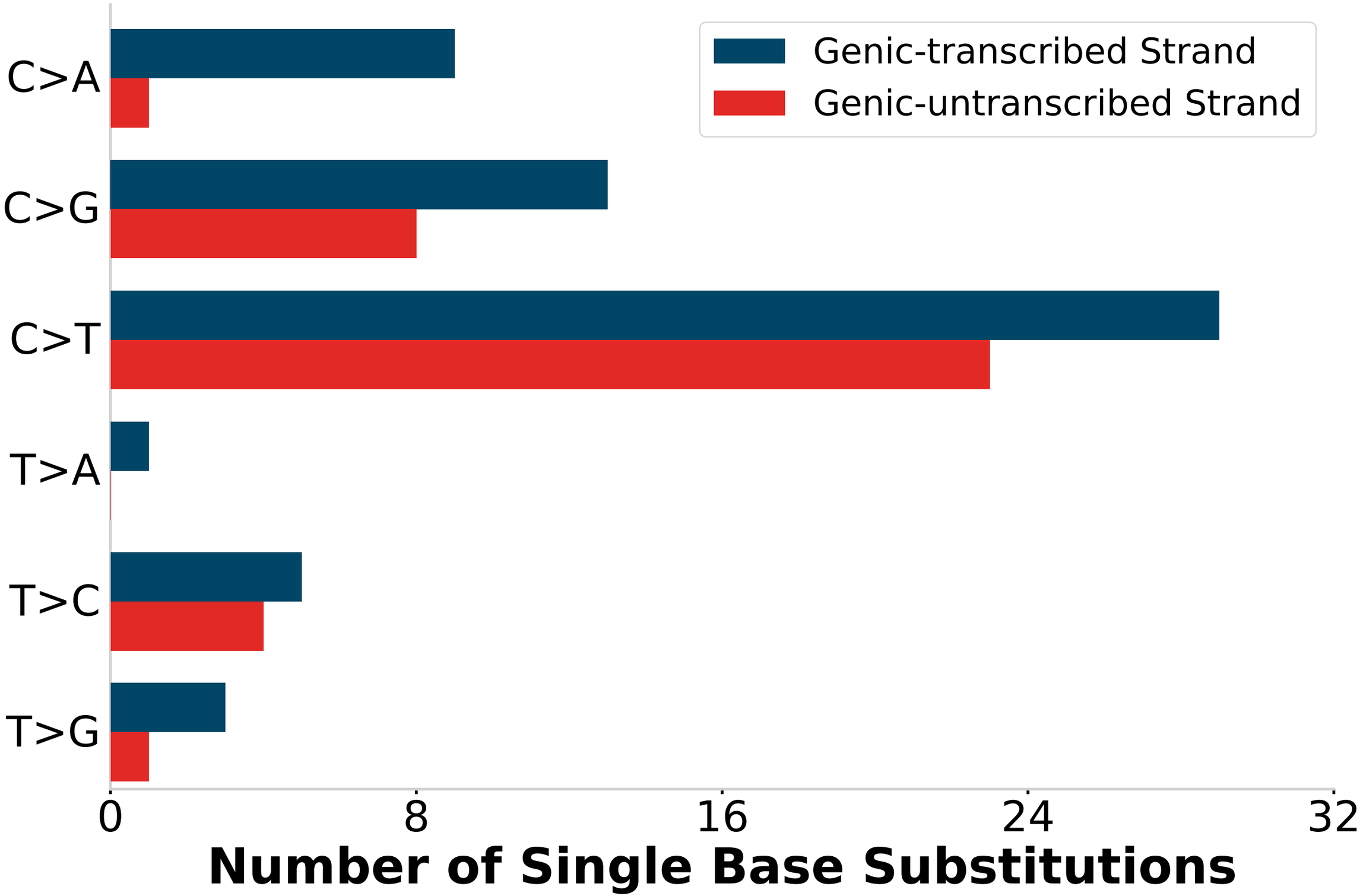
TCGA-CF-A9FM-01A-11D-A38G-08: 25 tran



TCGA-CU-A0YN-01A-21D-A10S-08: 166 tra



TCGA-CU-A0YO-01A-11D-A10S-08: 97 tran



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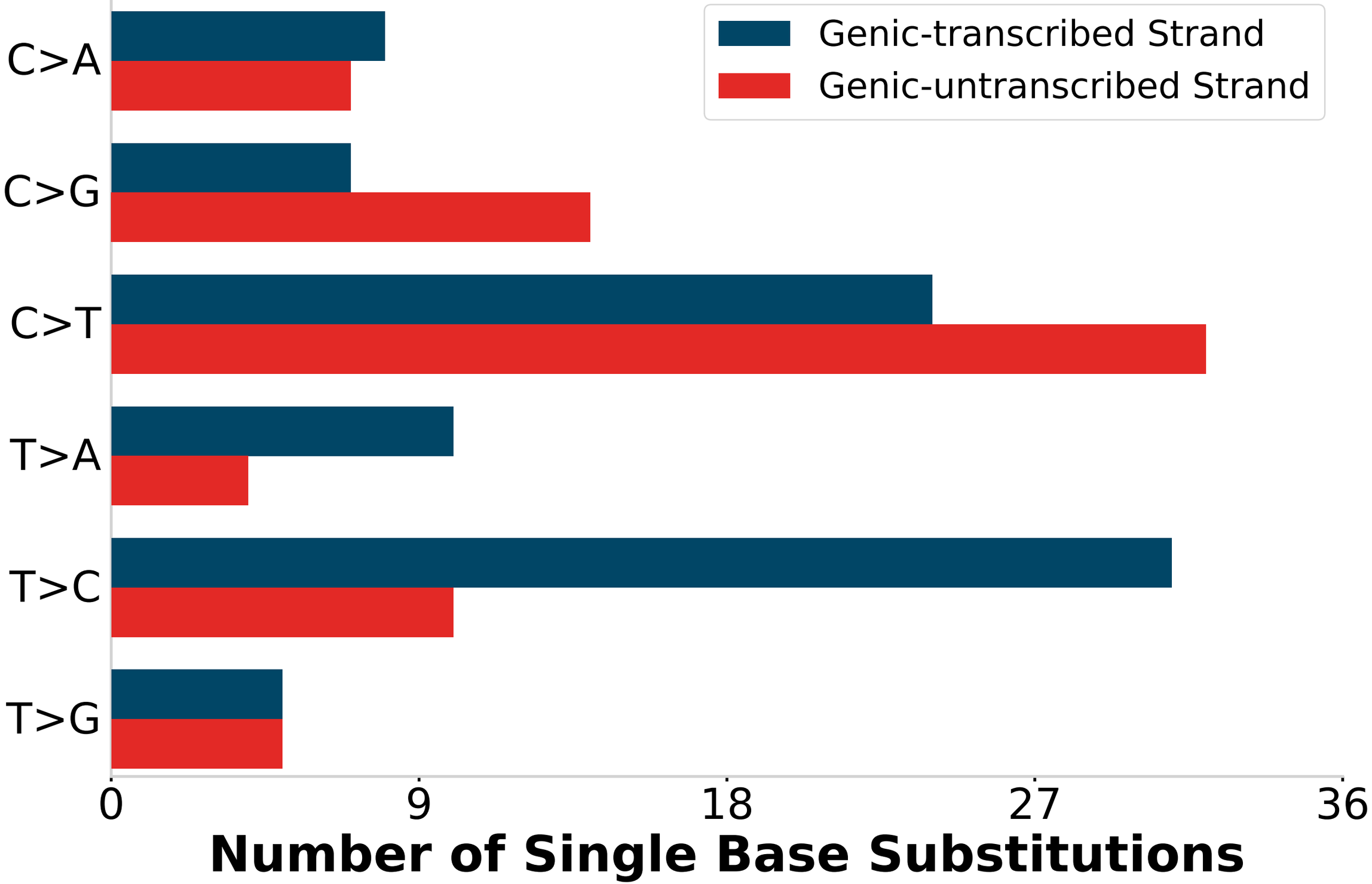
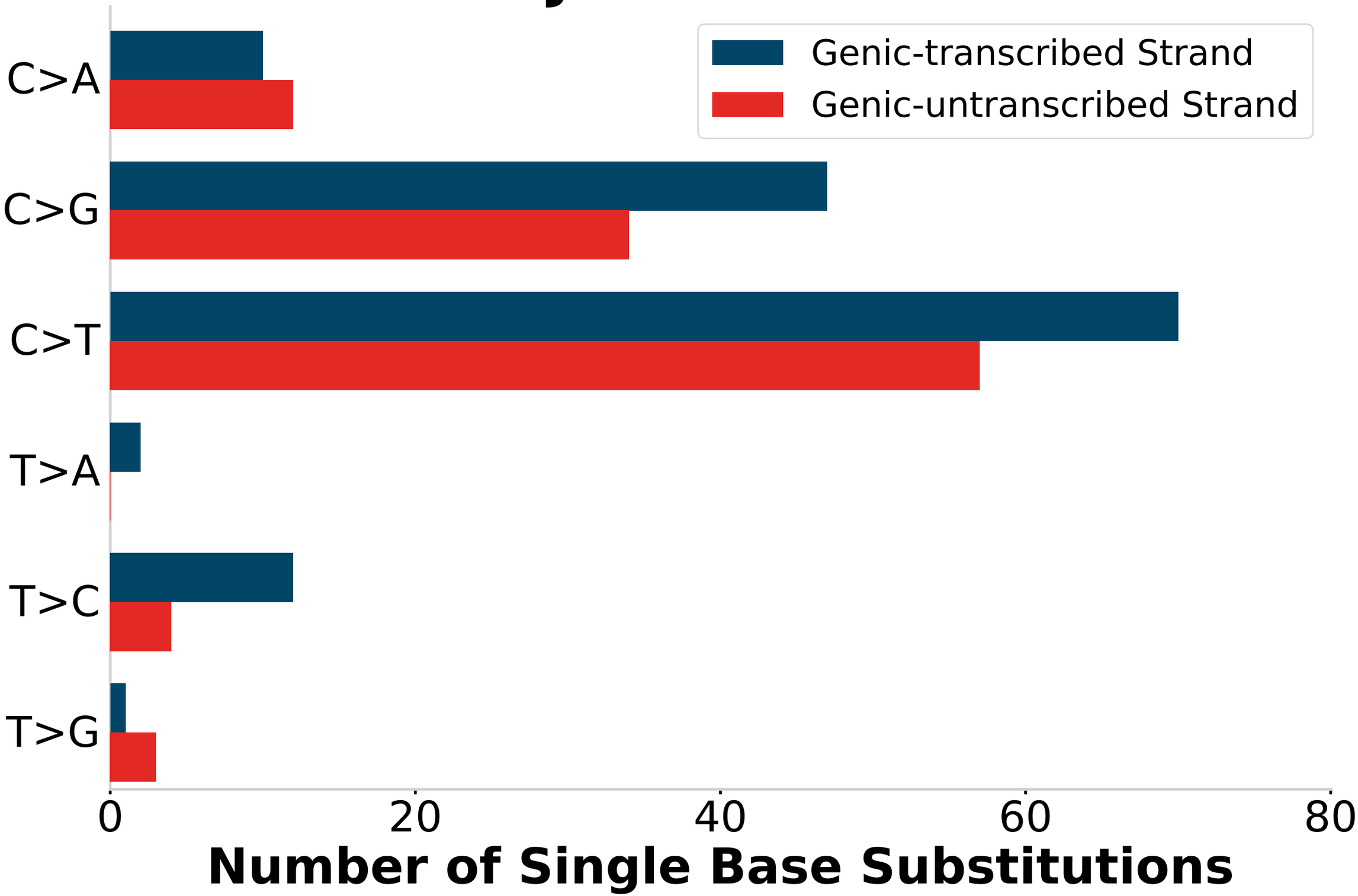
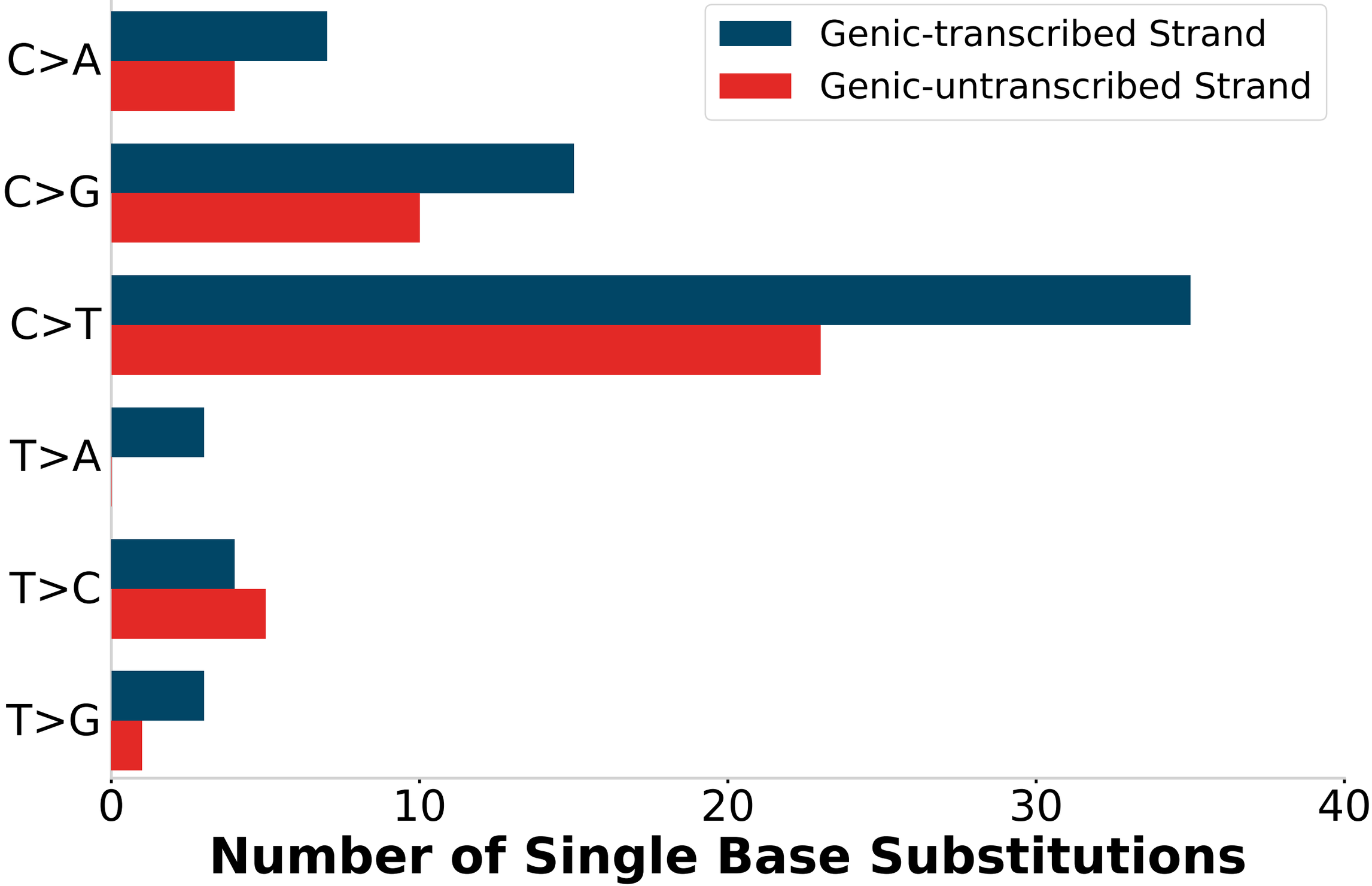


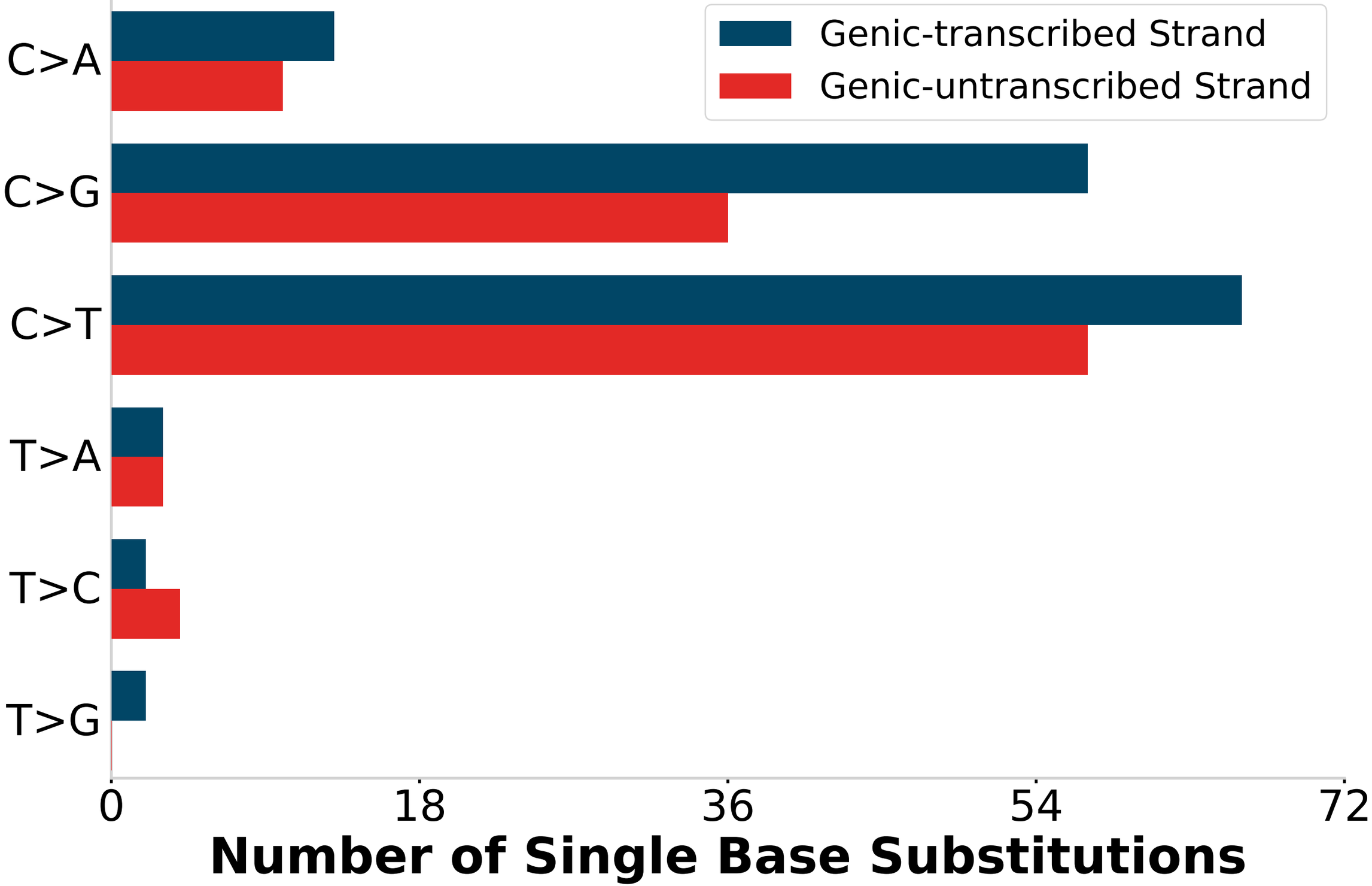
TCGA-CU-A3KJ-01A-11D-A21A-08: 252 tran



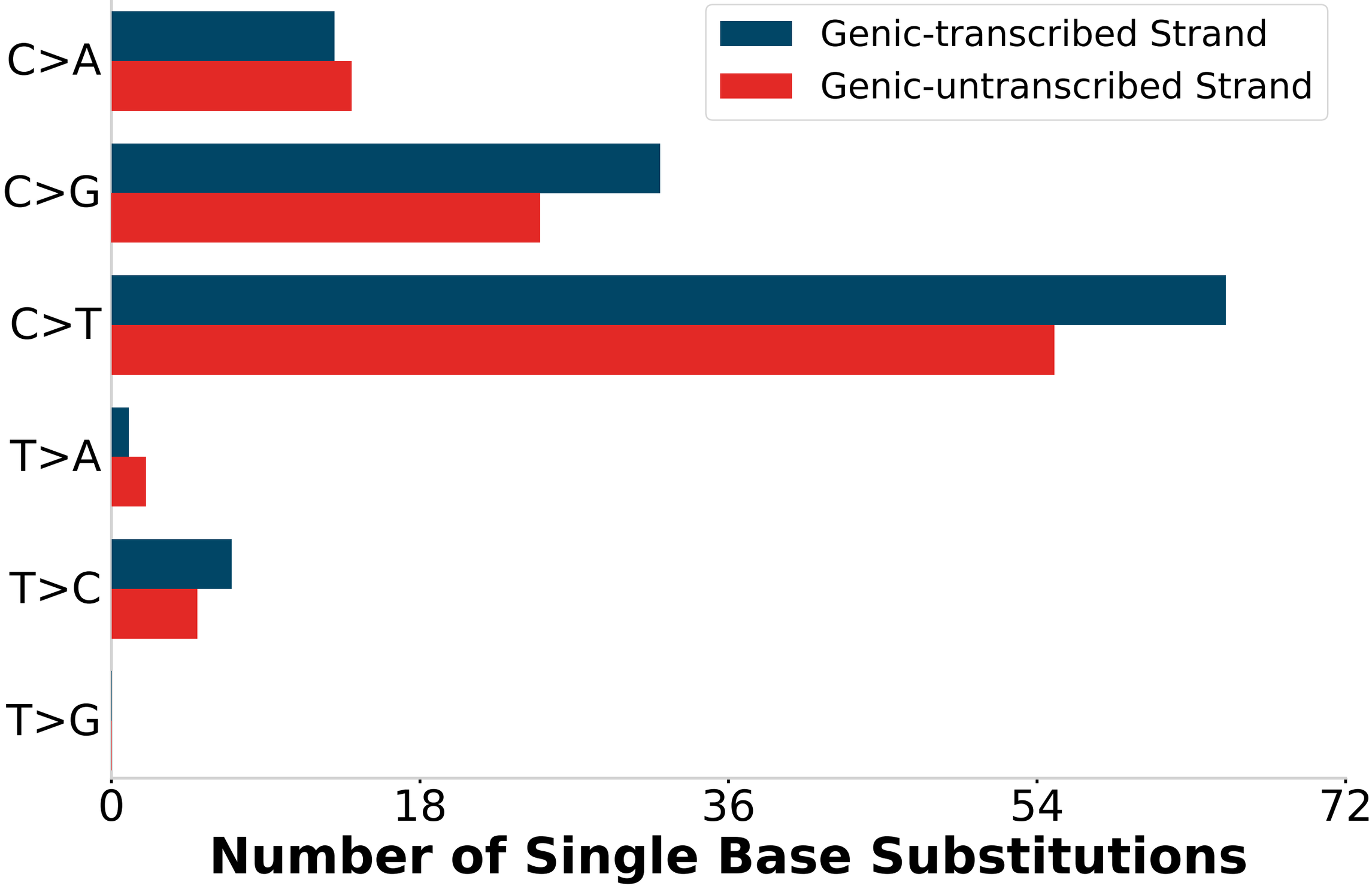
TCGA-CU-A3QU-01A-11D-A22Z-08: 110 tra



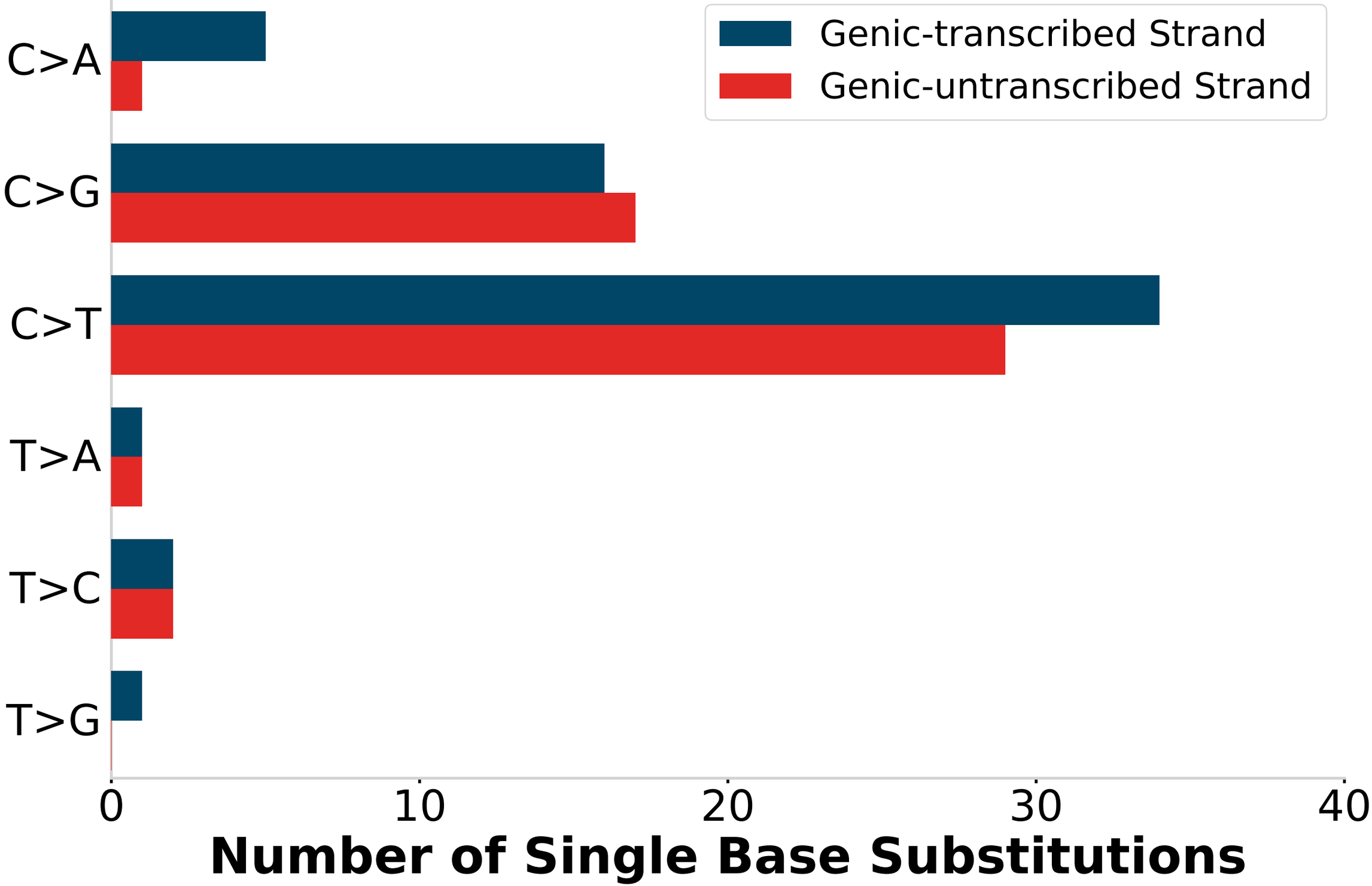
TCGA-CU-A3YL-01A-11D-A22Z-08: 253 tra



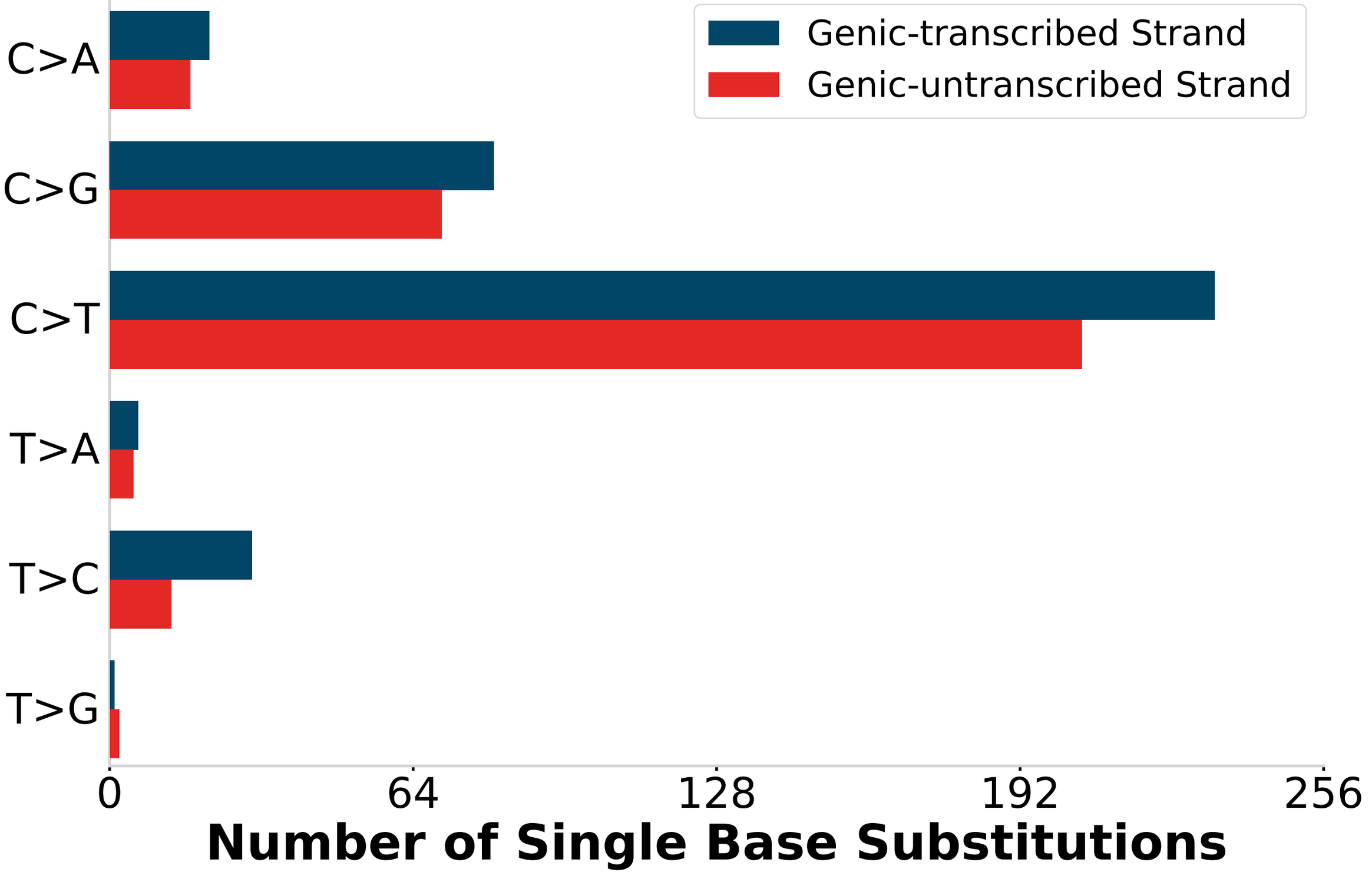
TCGA-CU-A5W6-01A-11D-A289-08: 219 tra



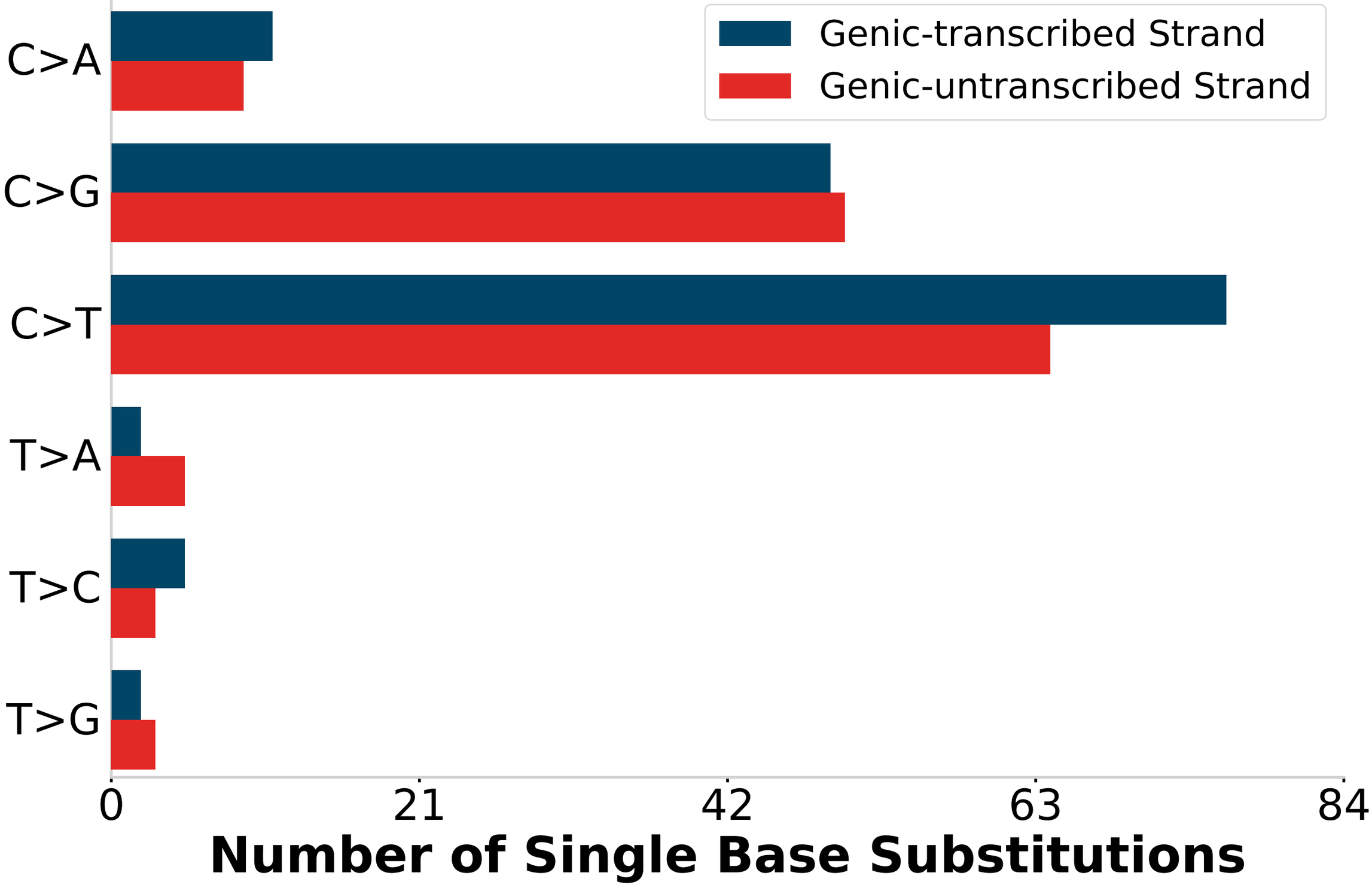
TCGA-CU-A72E-01A-12D-A339-08: 109 tra



TCGA-DK-A1A3-01A-11D-A13W-08: 684 tra



TCGA-DK-A1A5-01A-11D-A13W-08: 279 tra



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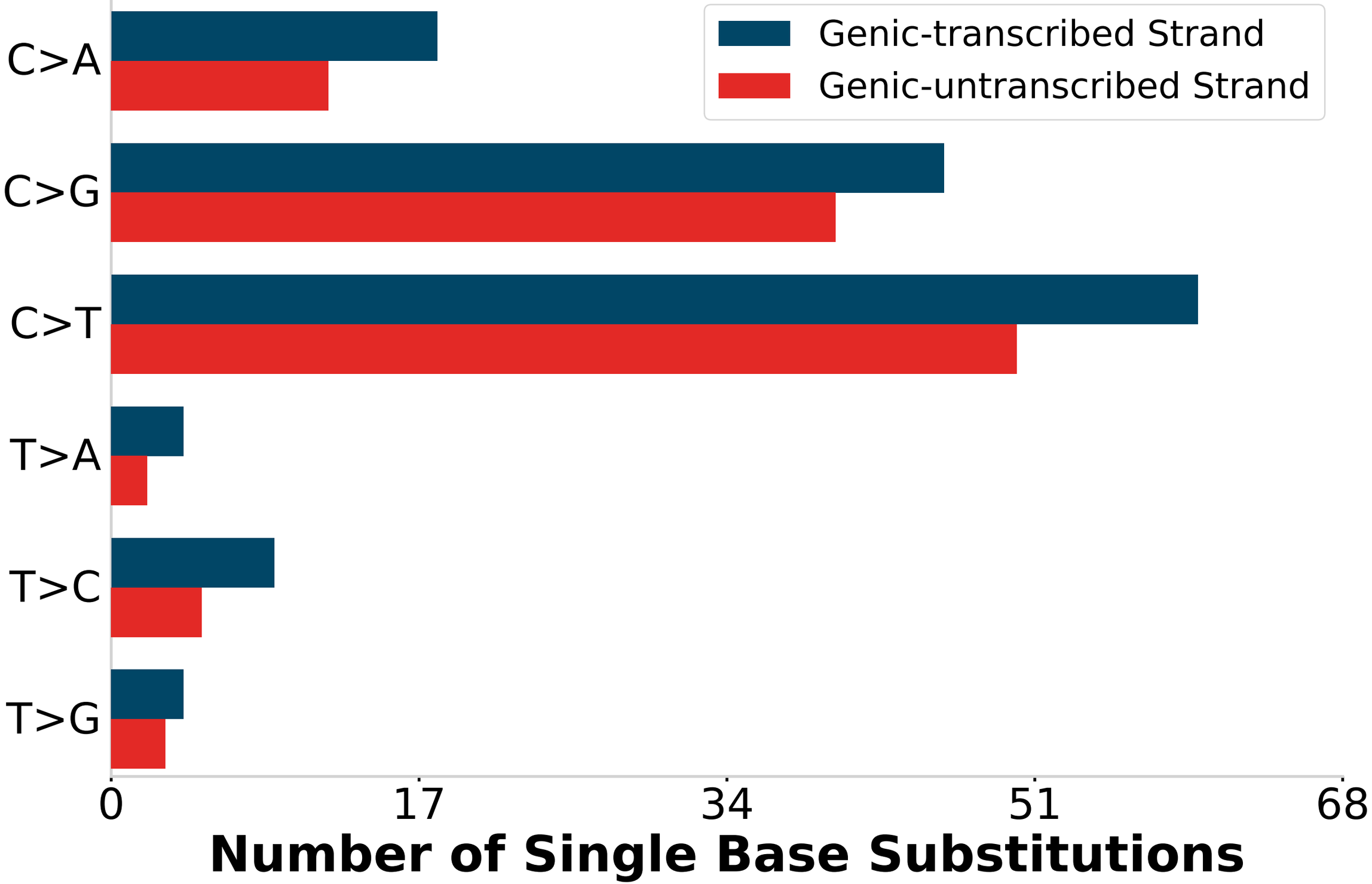
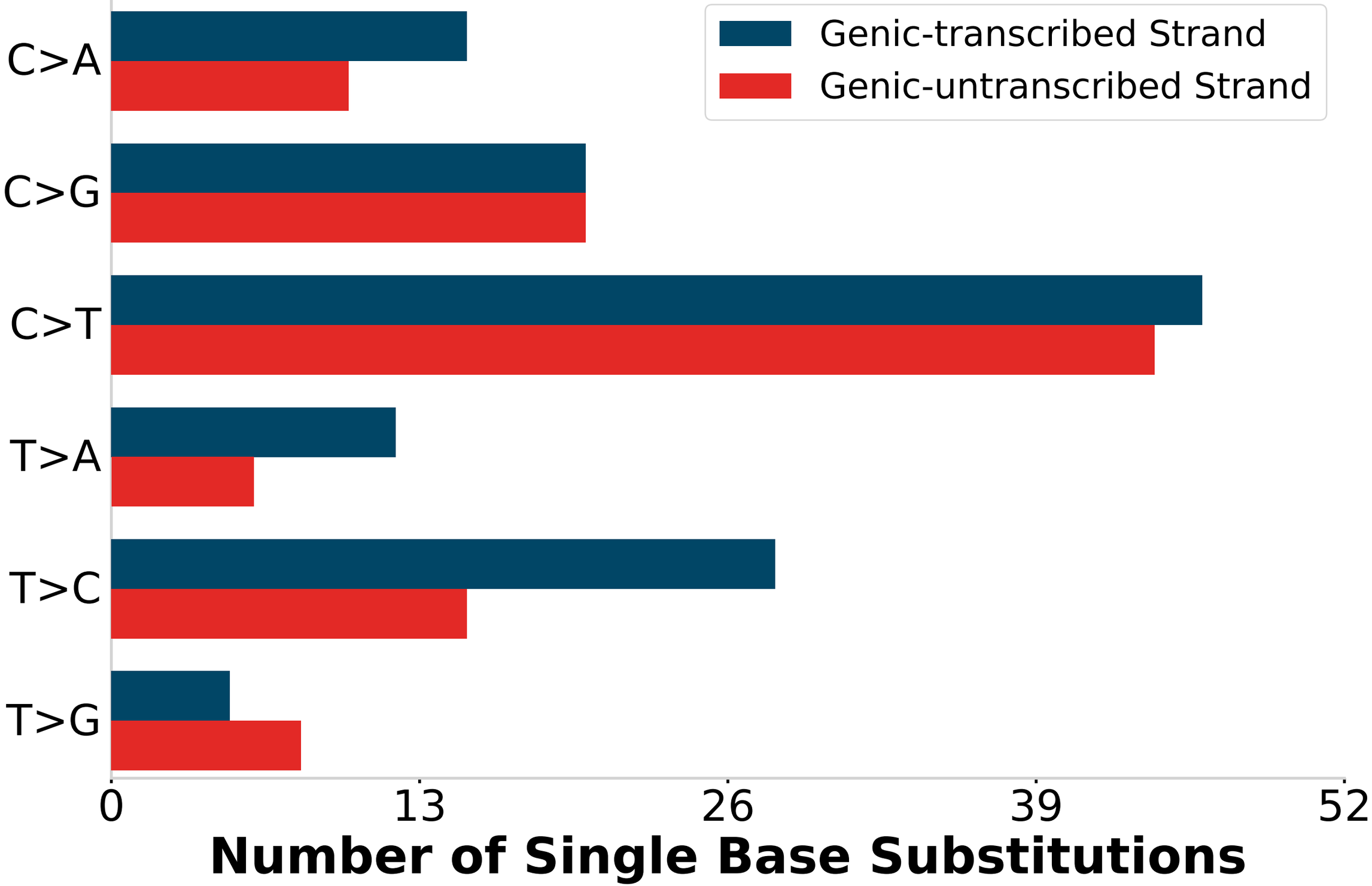
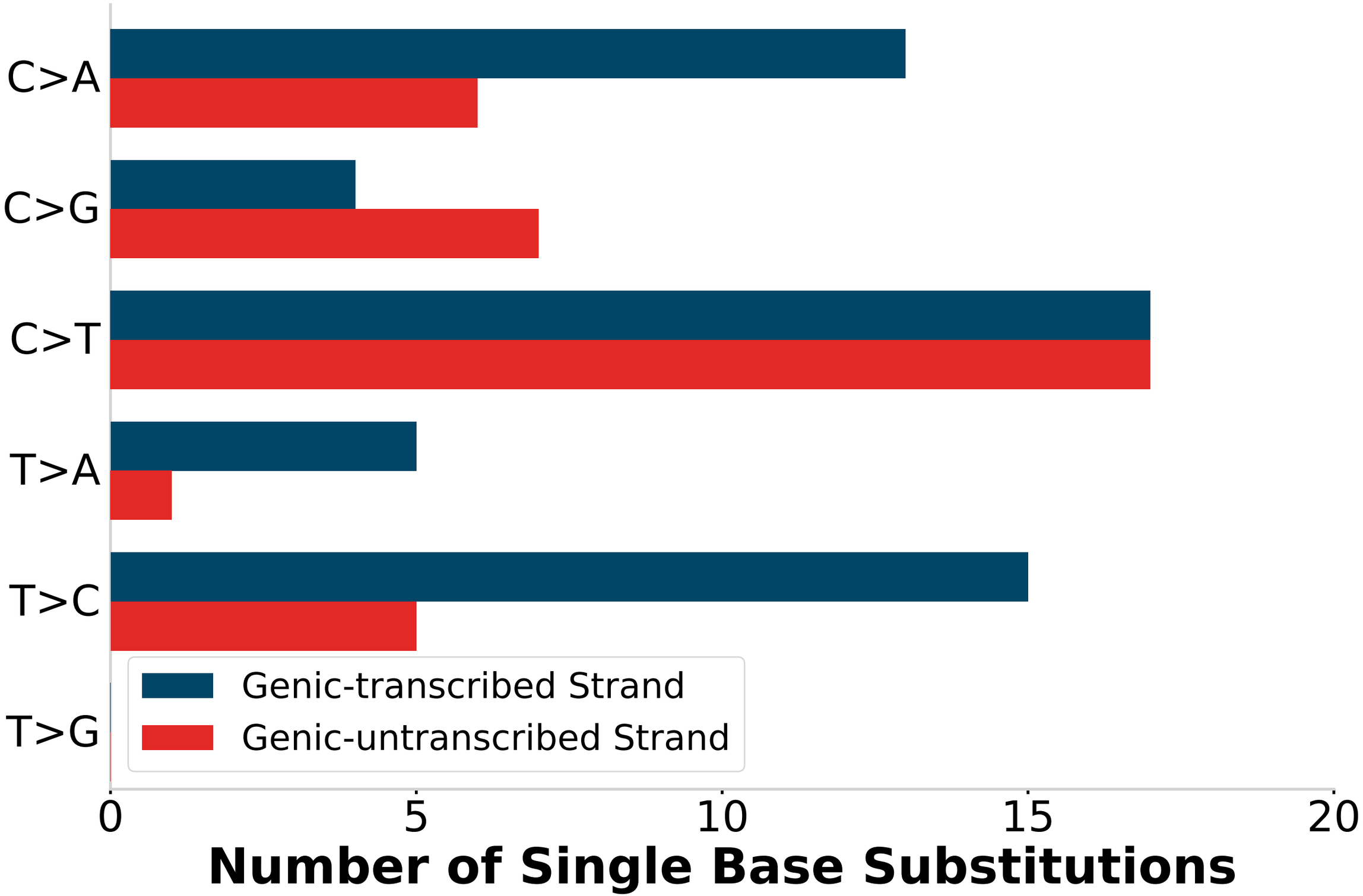


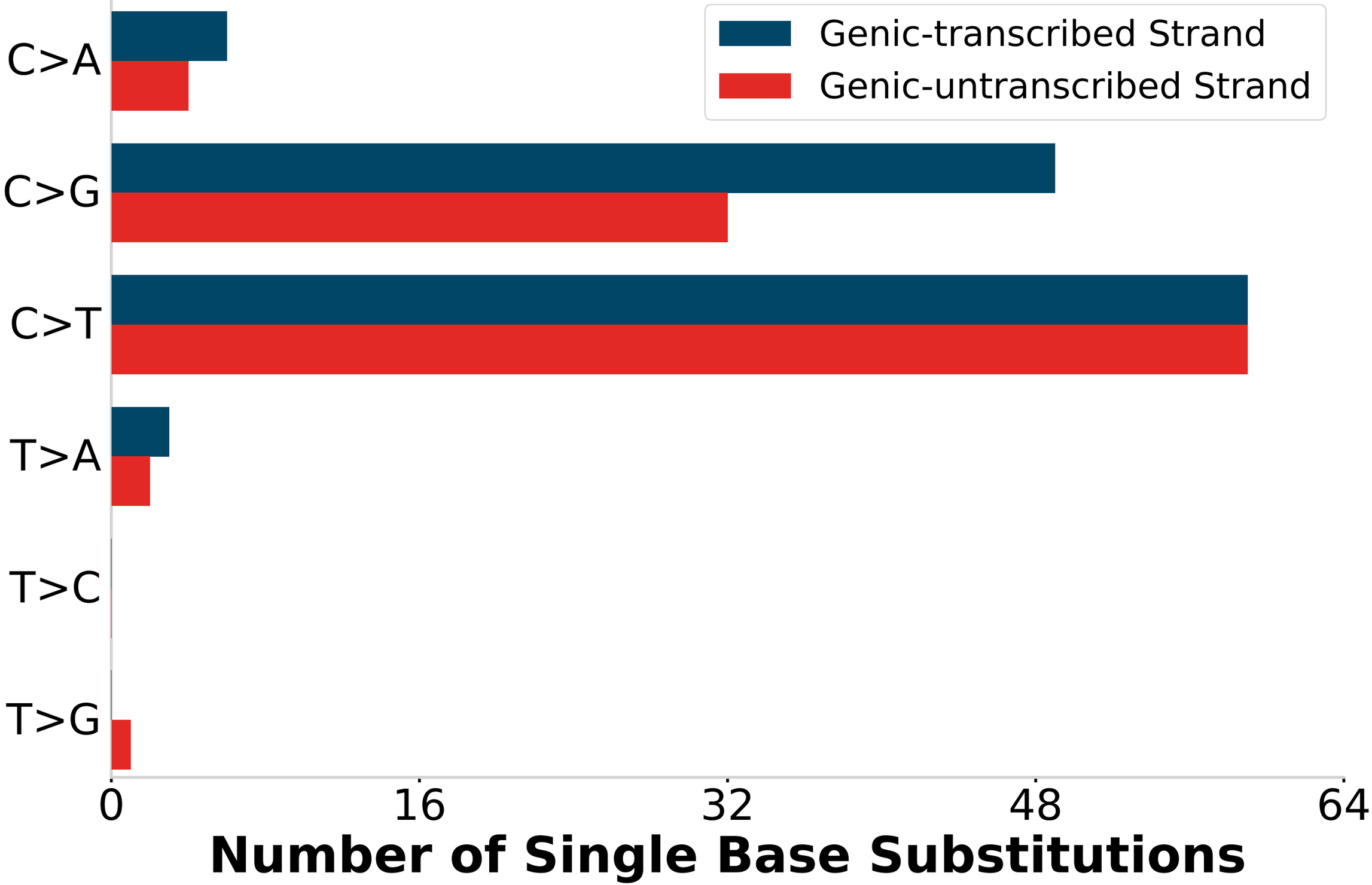
TCGA-DK-A1A7-01A-11D-A13W-08: 229 tra



TCGA-DK-A1AA-01A-11D-A13W-08: 90 tran



TCGA-DK-A1AB-01A-11D-A13W-08: 215 tra



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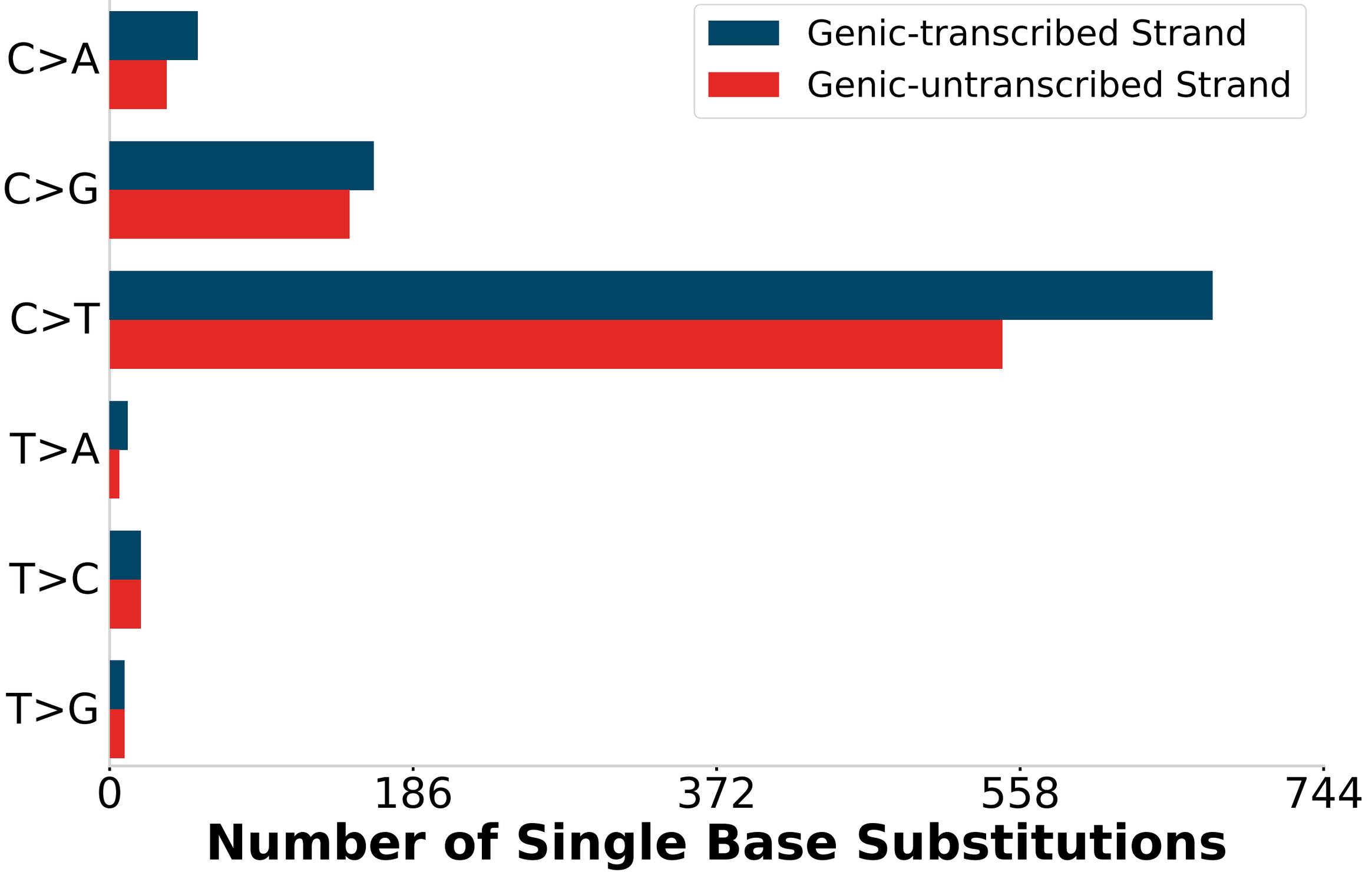
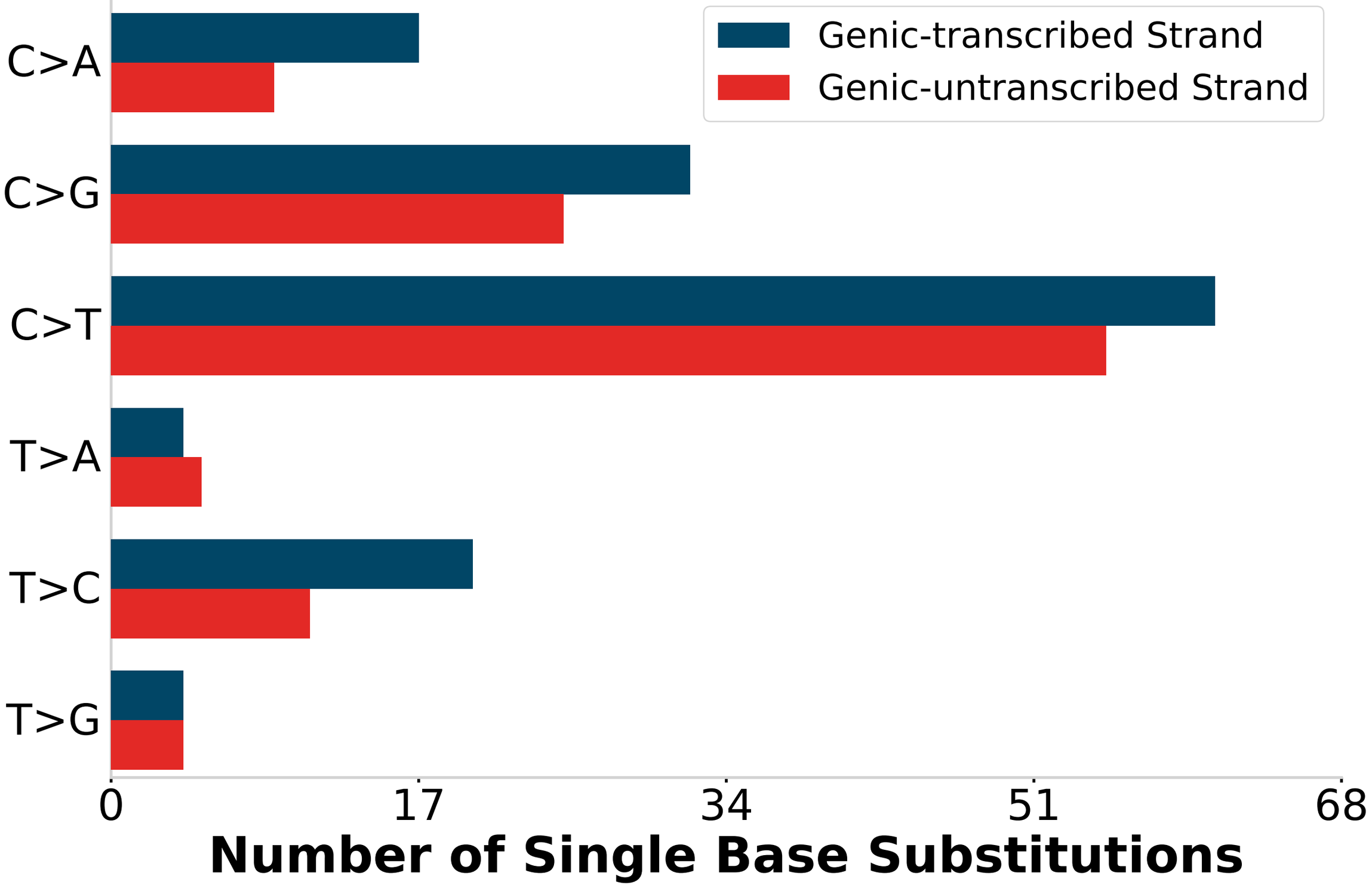
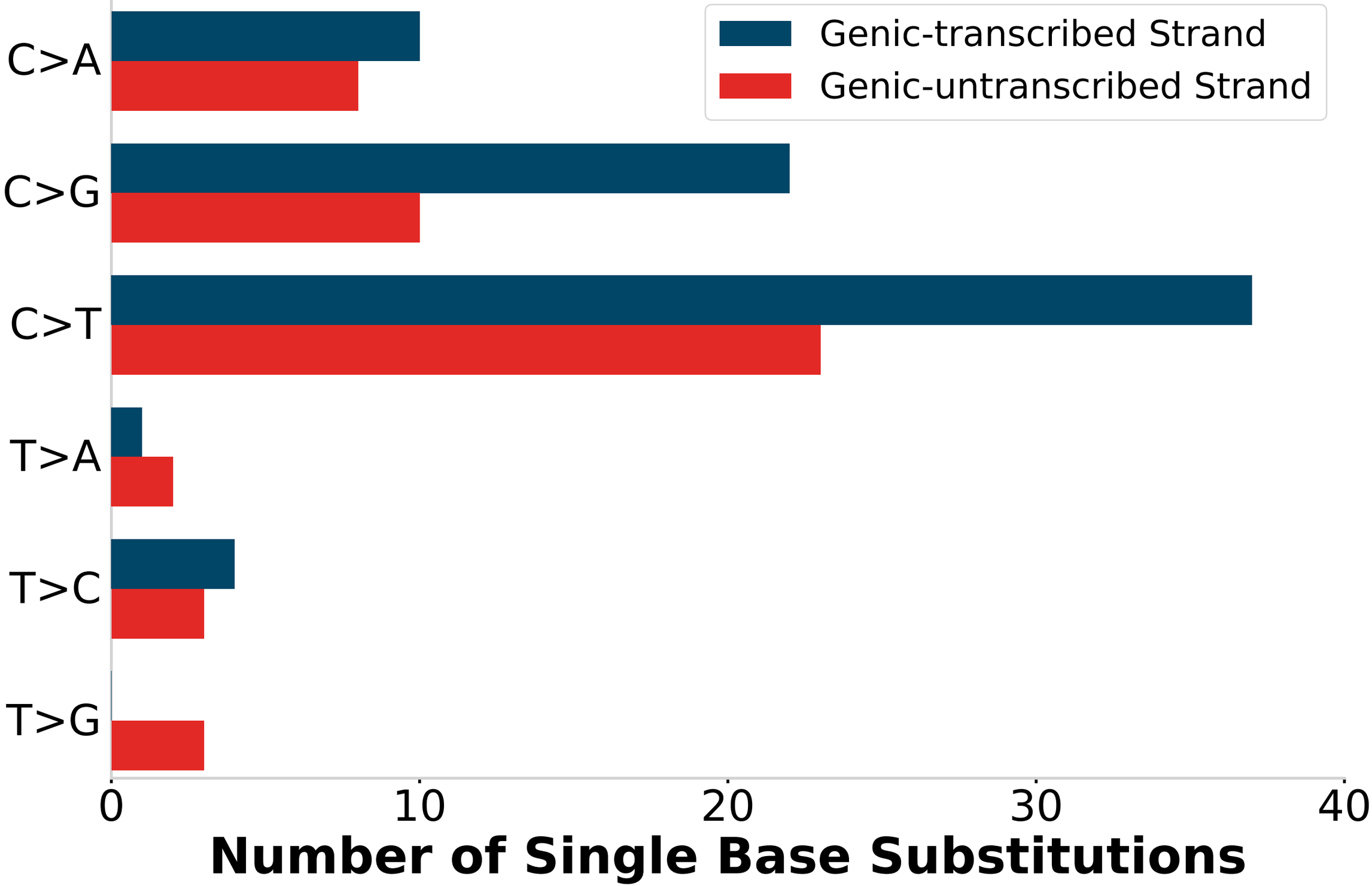


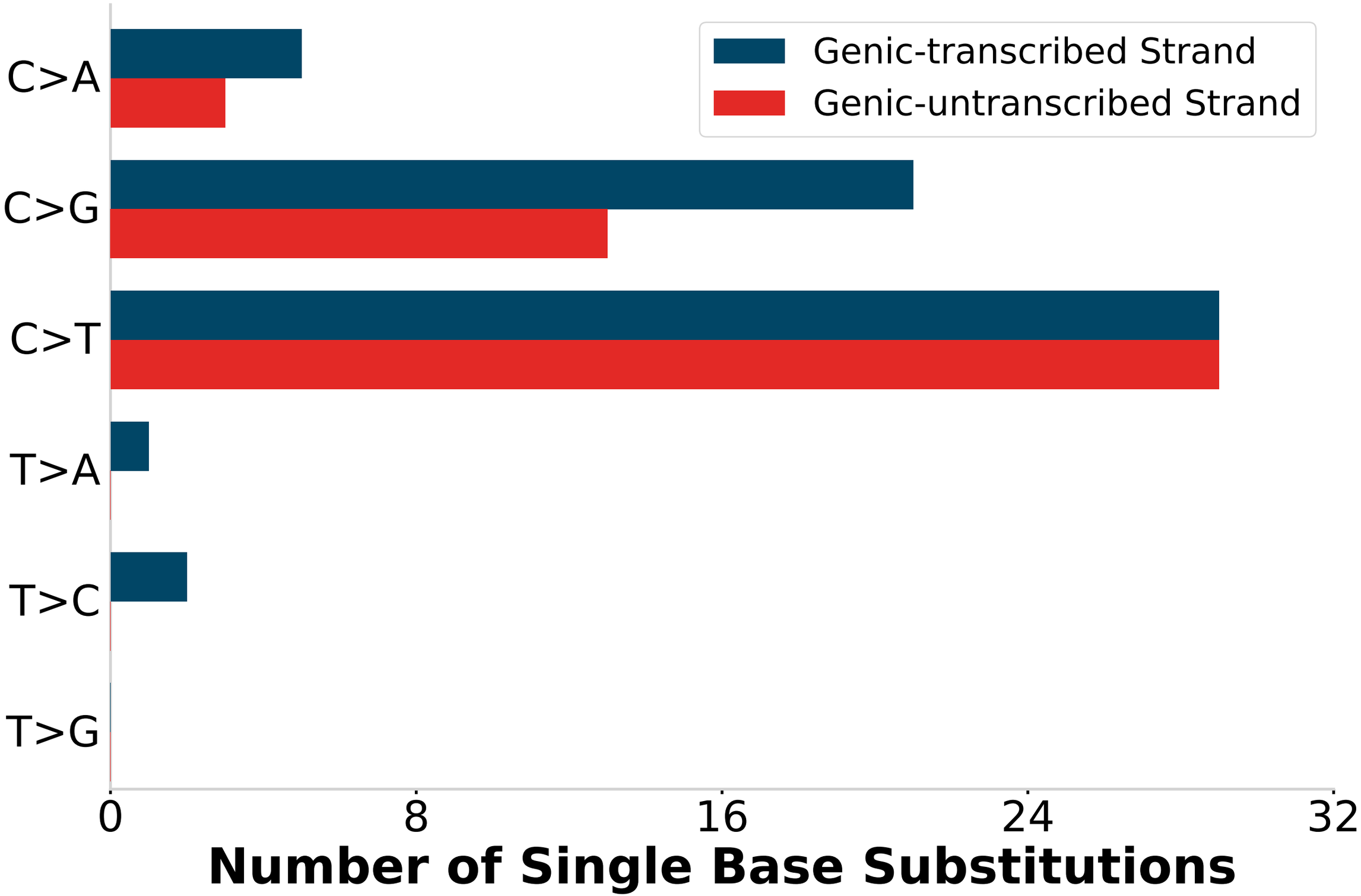
TCGA-DK-A1AD-01A-11D-A13W-08: 247 tra



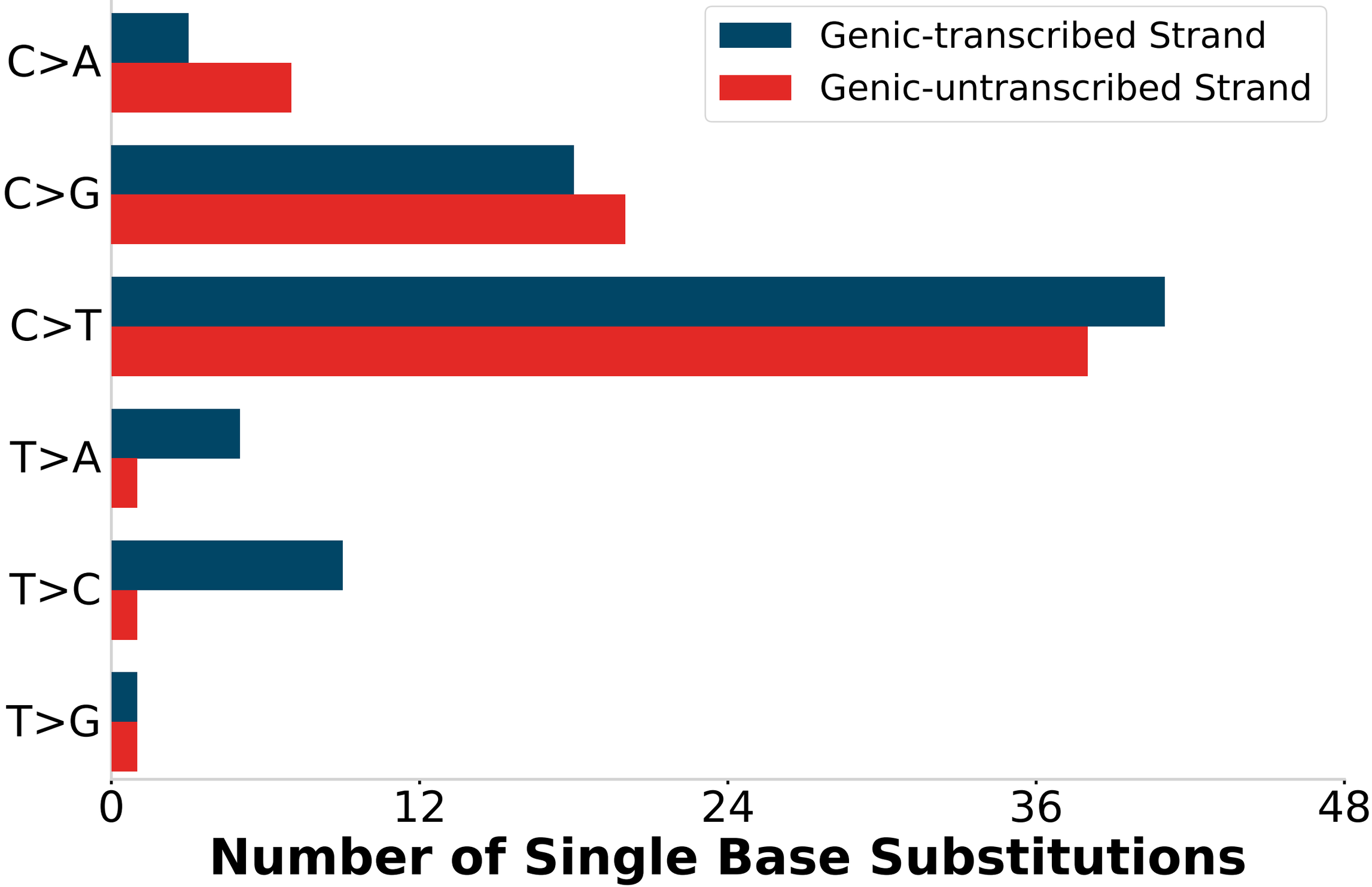
TCGA-DK-A1AE-01A-11D-A13W-08: 123 tra



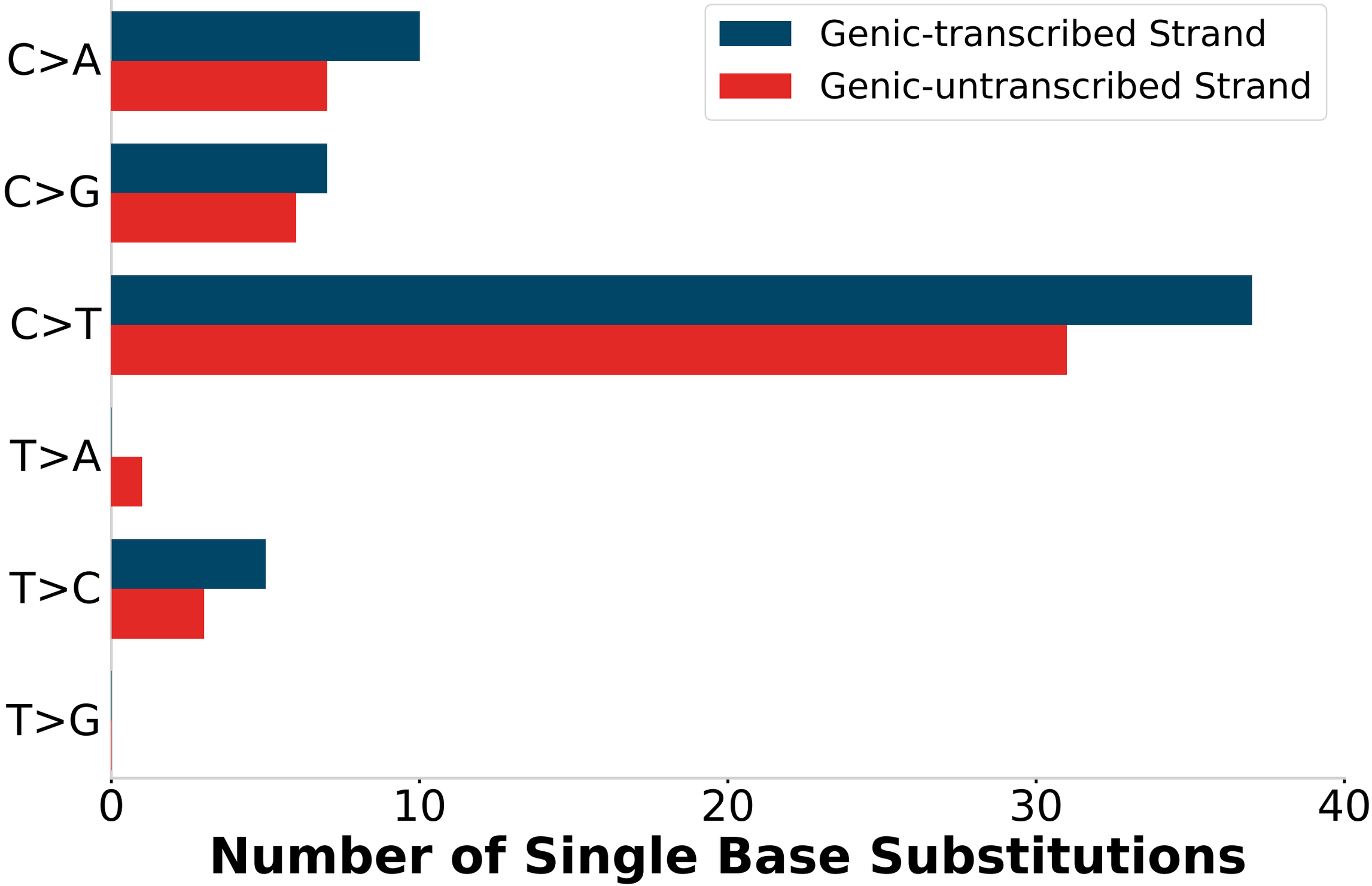
TCGA-DK-A1AF-01A-11D-A13W-08: 103 tra



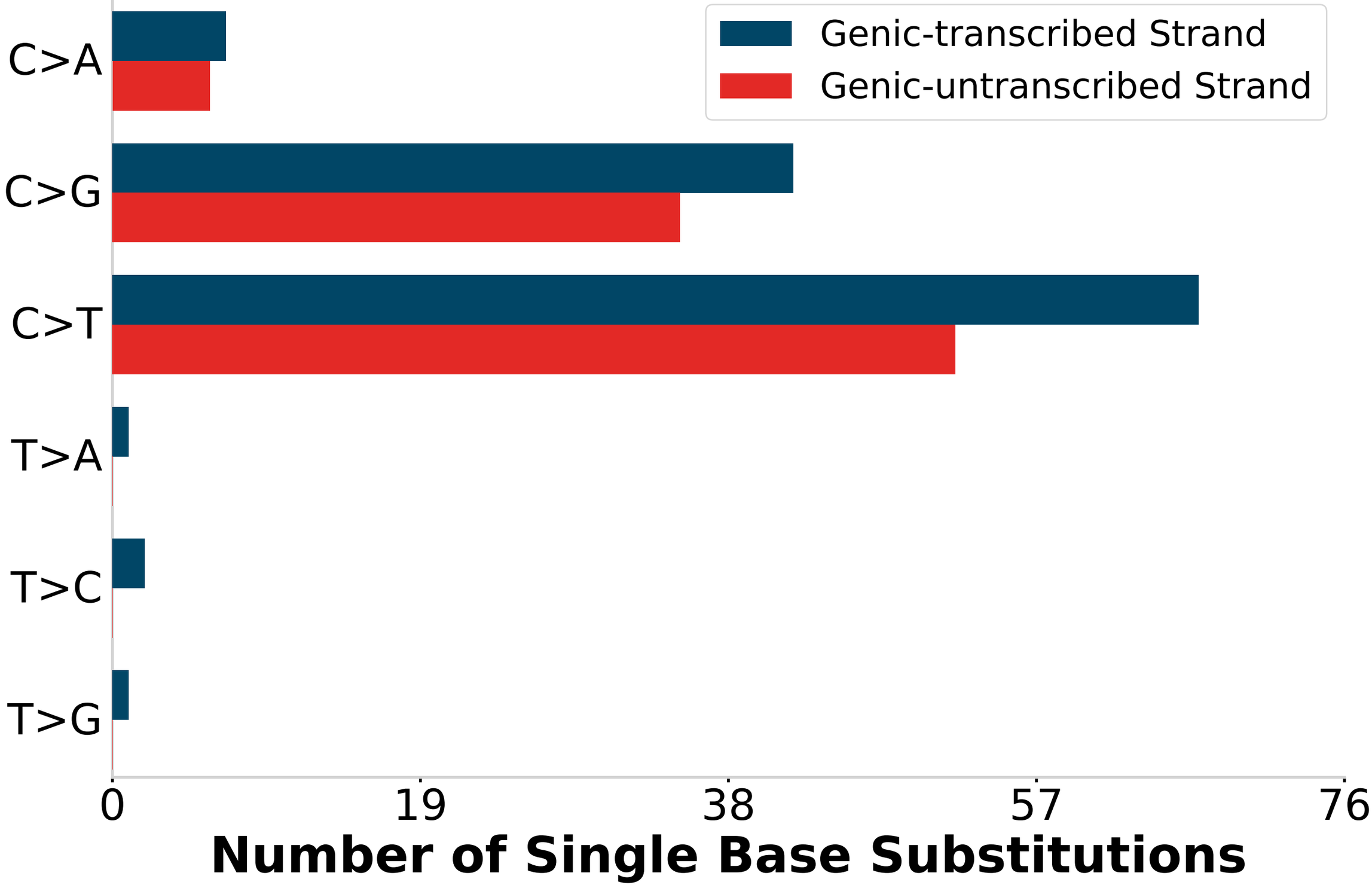
TCGA-DK-A1AG-01A-11D-A13W-08: 145 tra



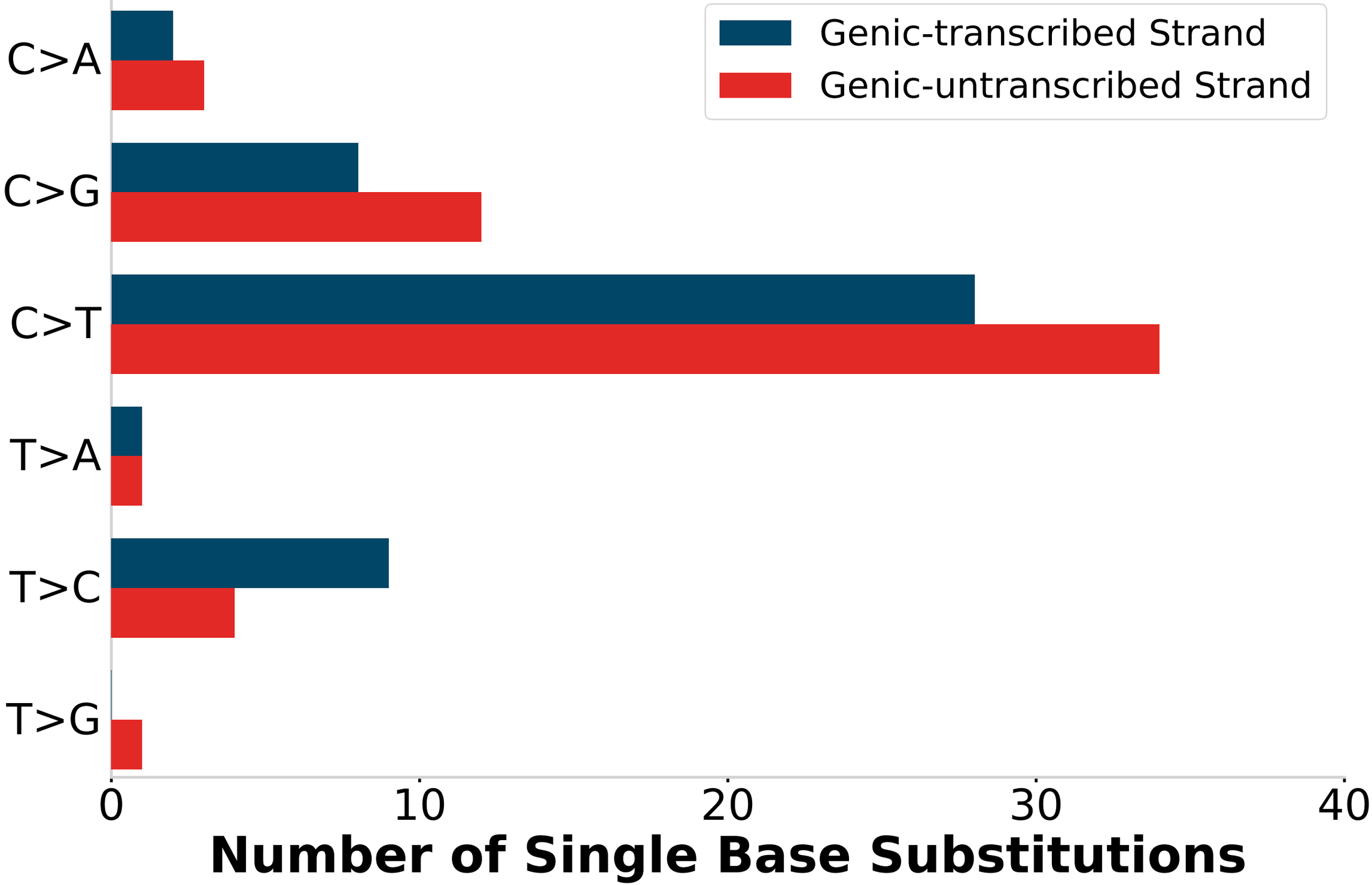
TCGA-DK-A2HX-01A-12D-A18F-08: 107 tra



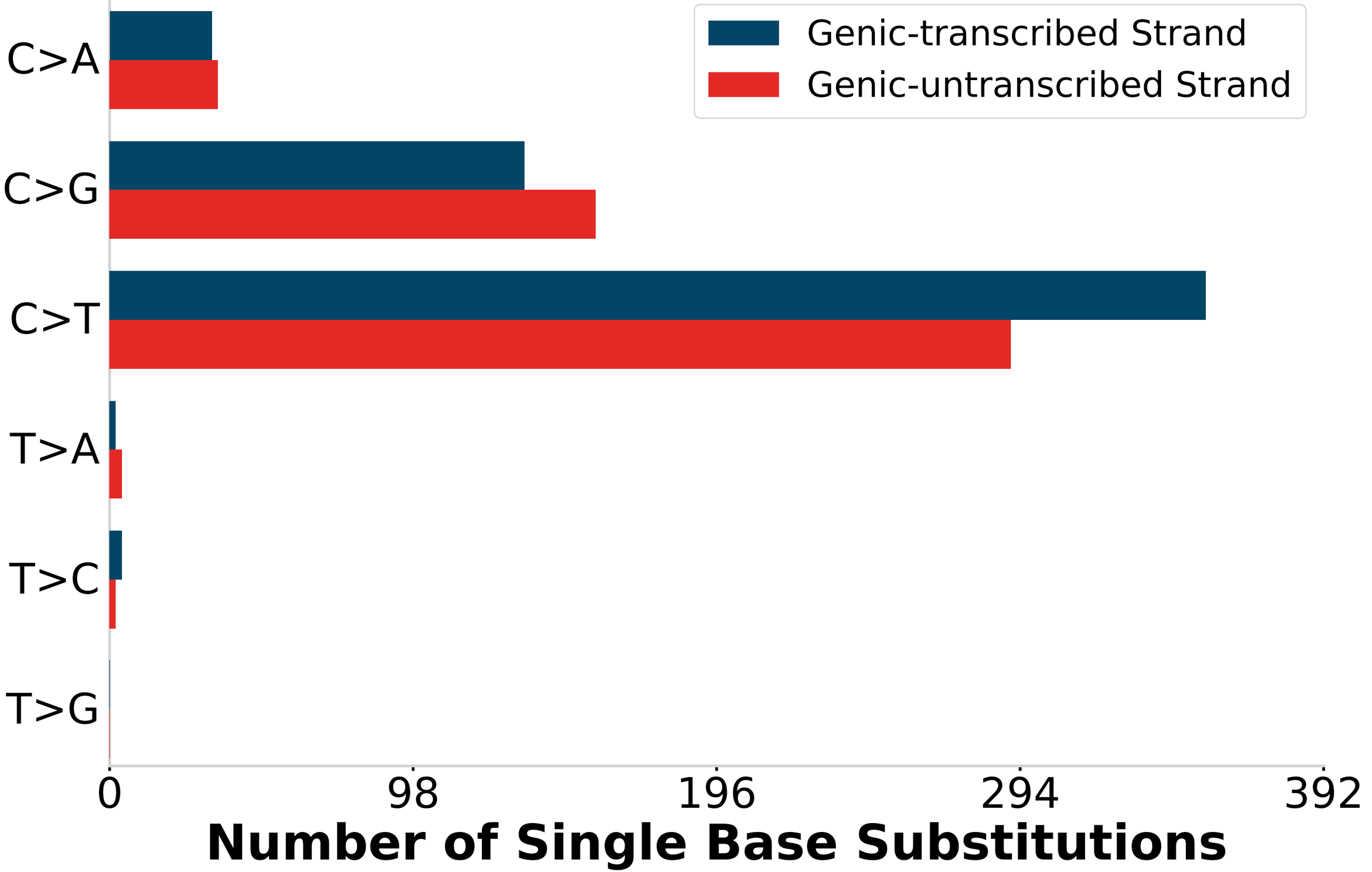
TCGA-DK-A2I1-01A-11D-A17V-08: 213 tran



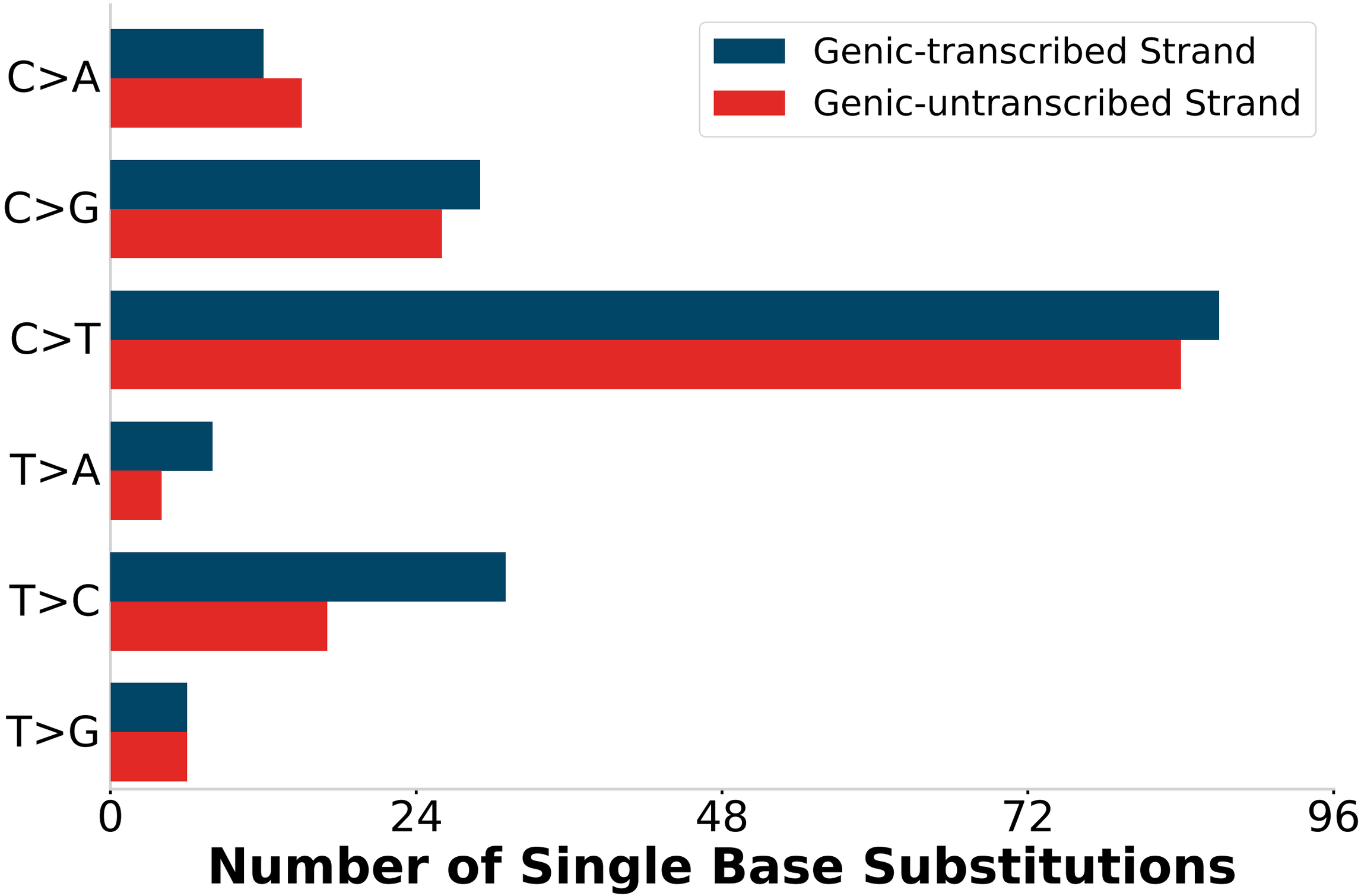
TCGA-DK-A2I2-01A-11D-A17V-08: 103 tran



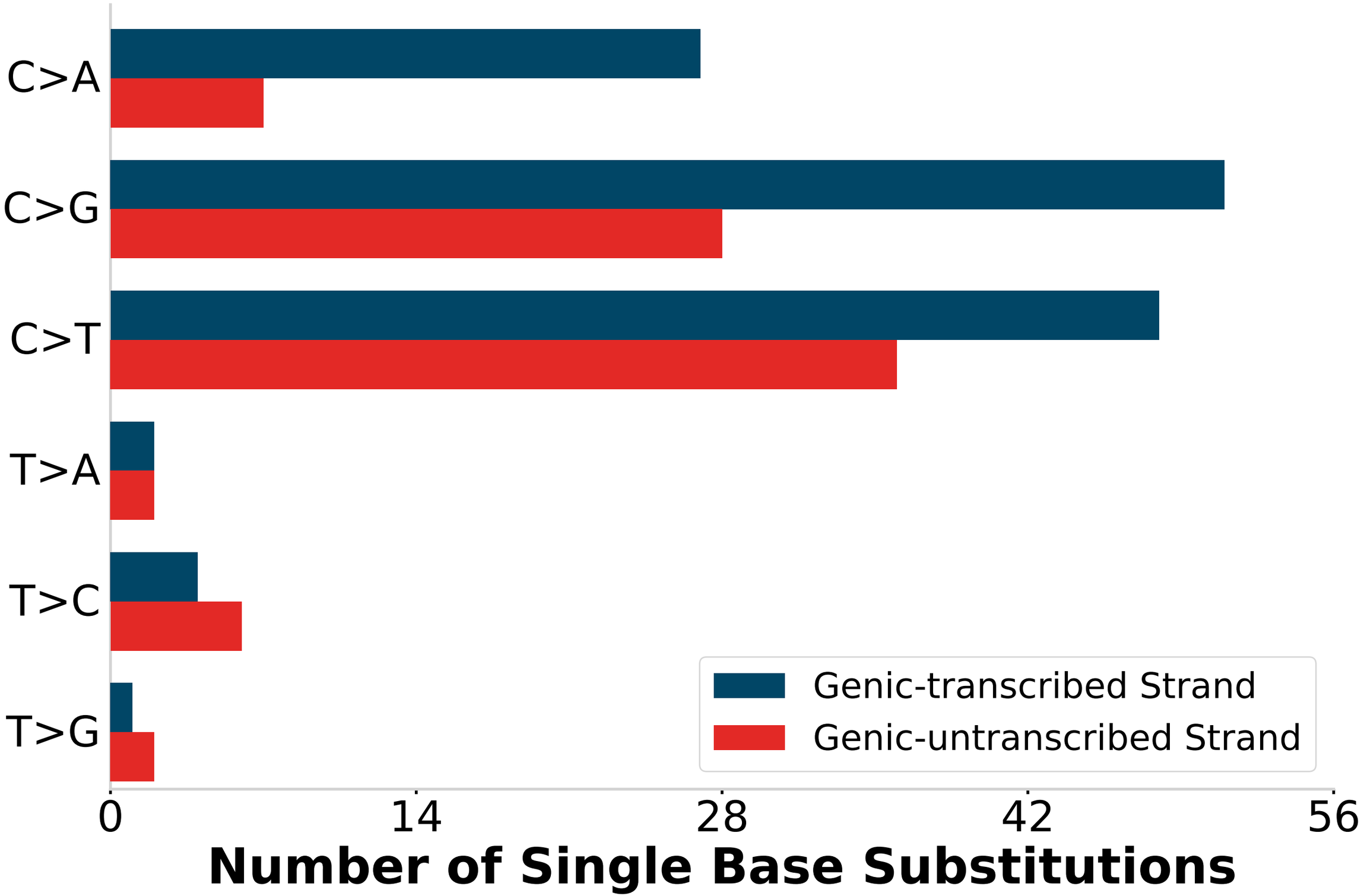
TCGA-DK-A2I4-01A-11D-A21A-08: 1,016 tr



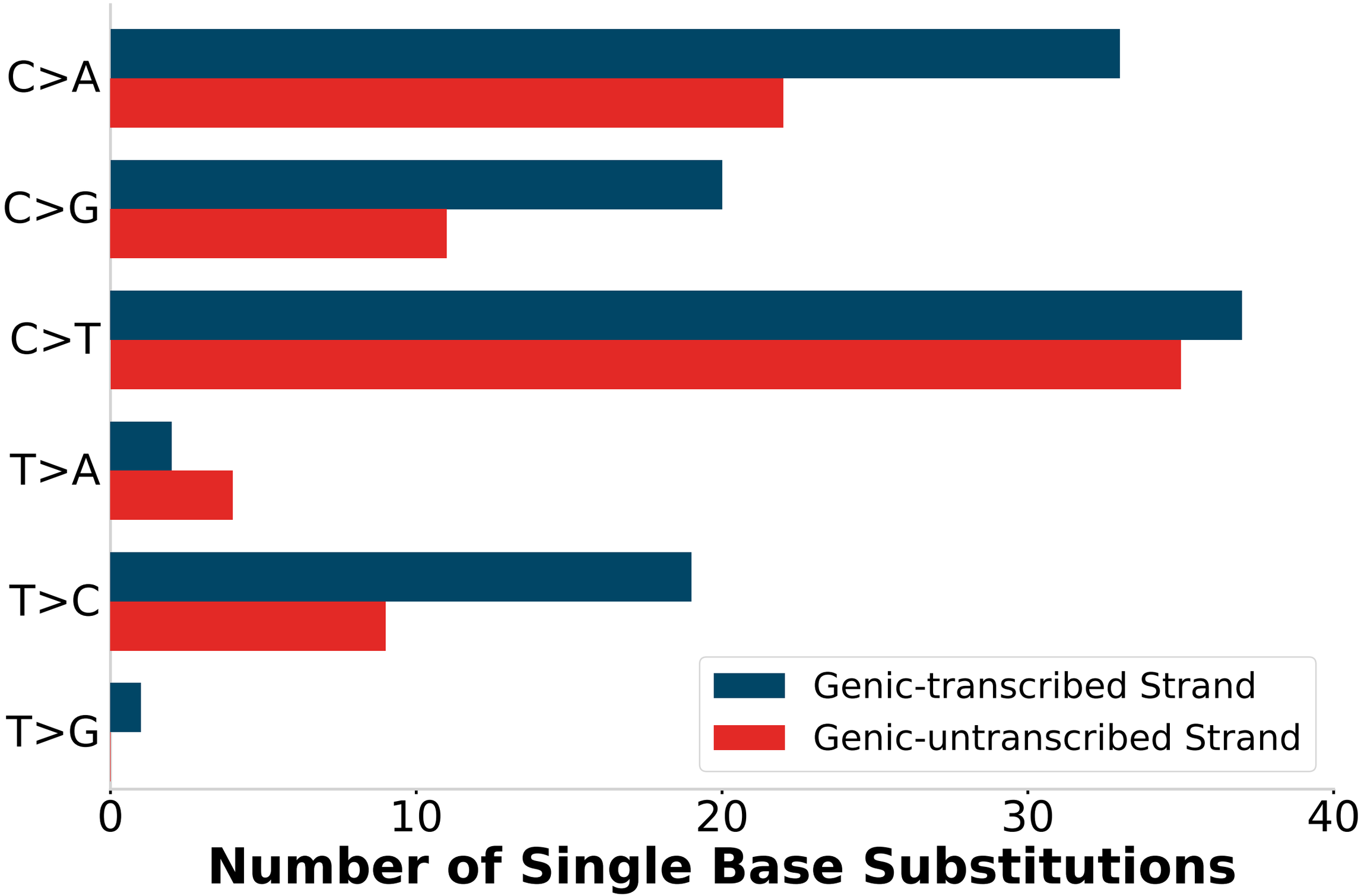
TCGA-DK-A2I6-01A-12D-A18F-08: 325 tran



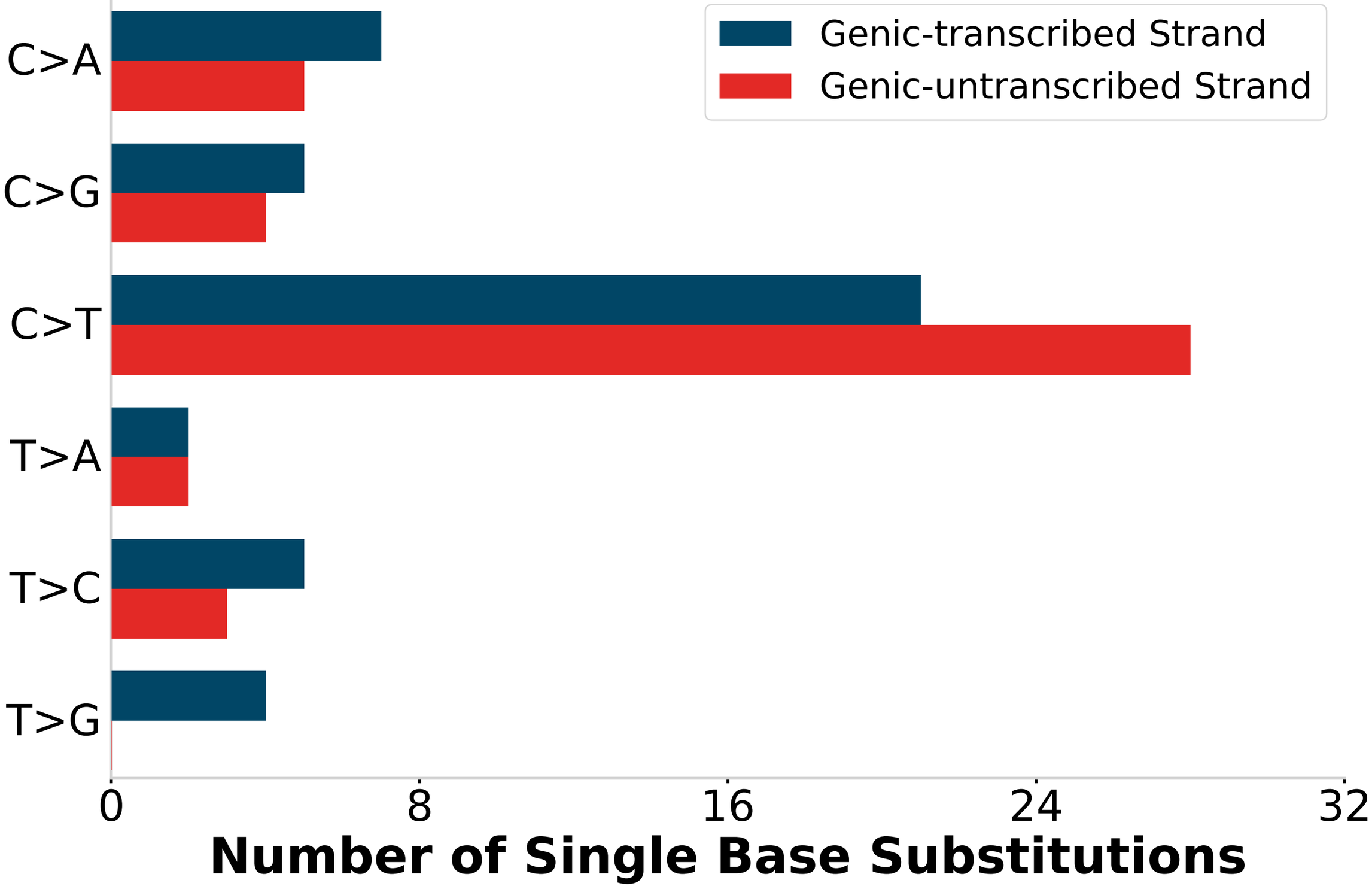
TCGA-DK-A3IK-01A-32D-A21A-08: 214 tran



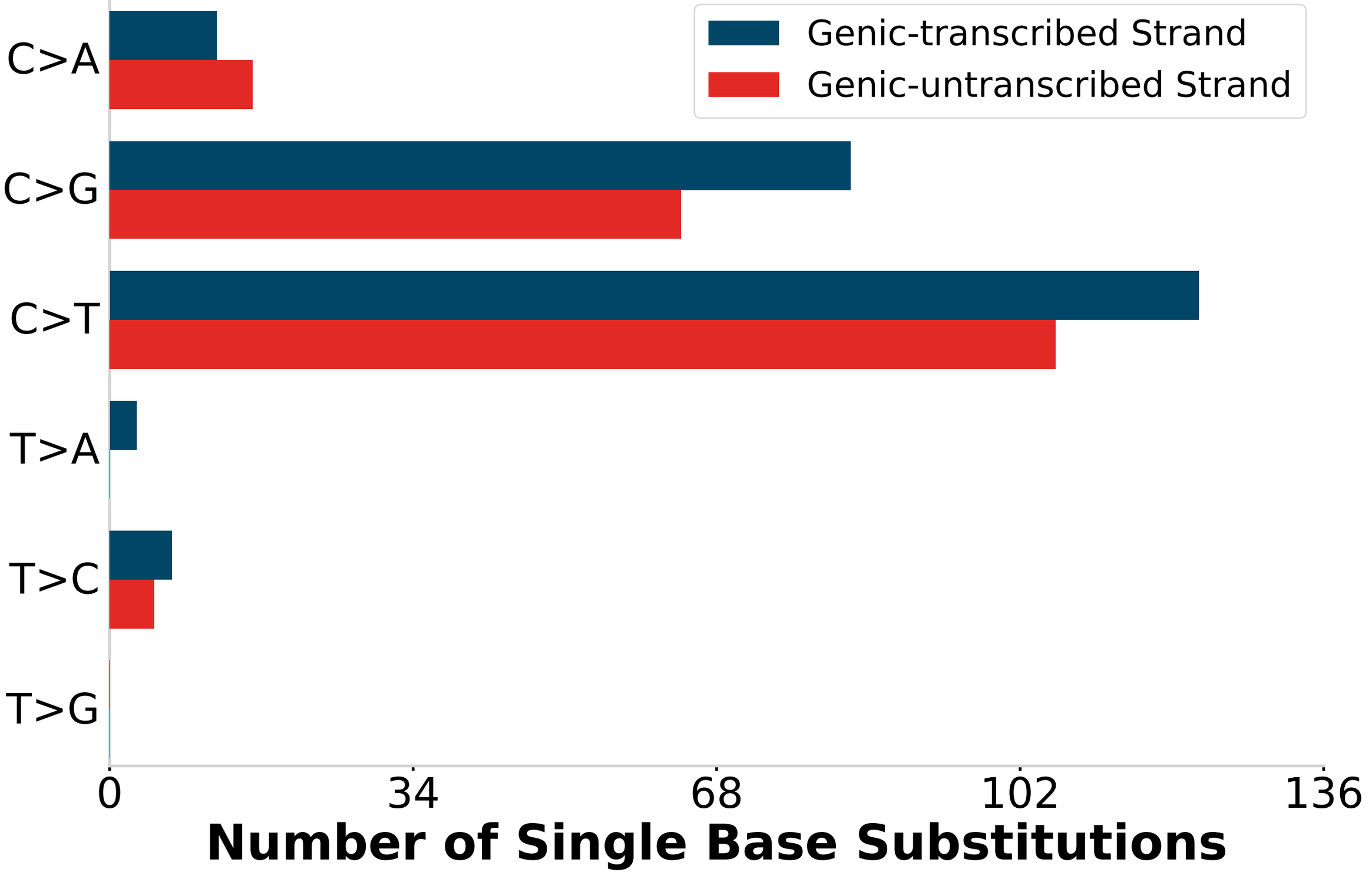
TCGA-DK-A3IL-01A-11D-A20D-08: 193 tran



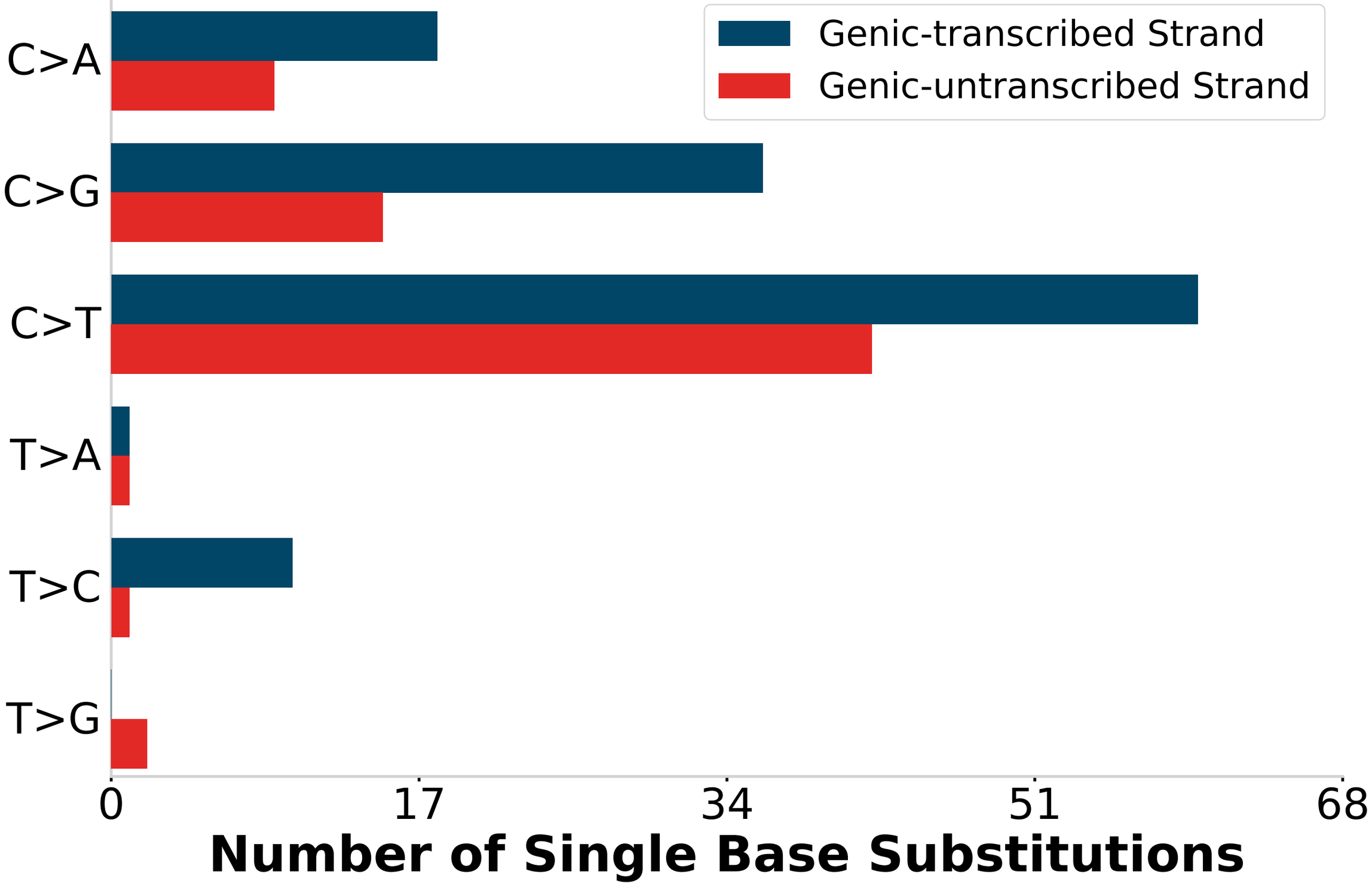
TCGA-DK-A3IM-01A-11D-A20D-08: 86 trans



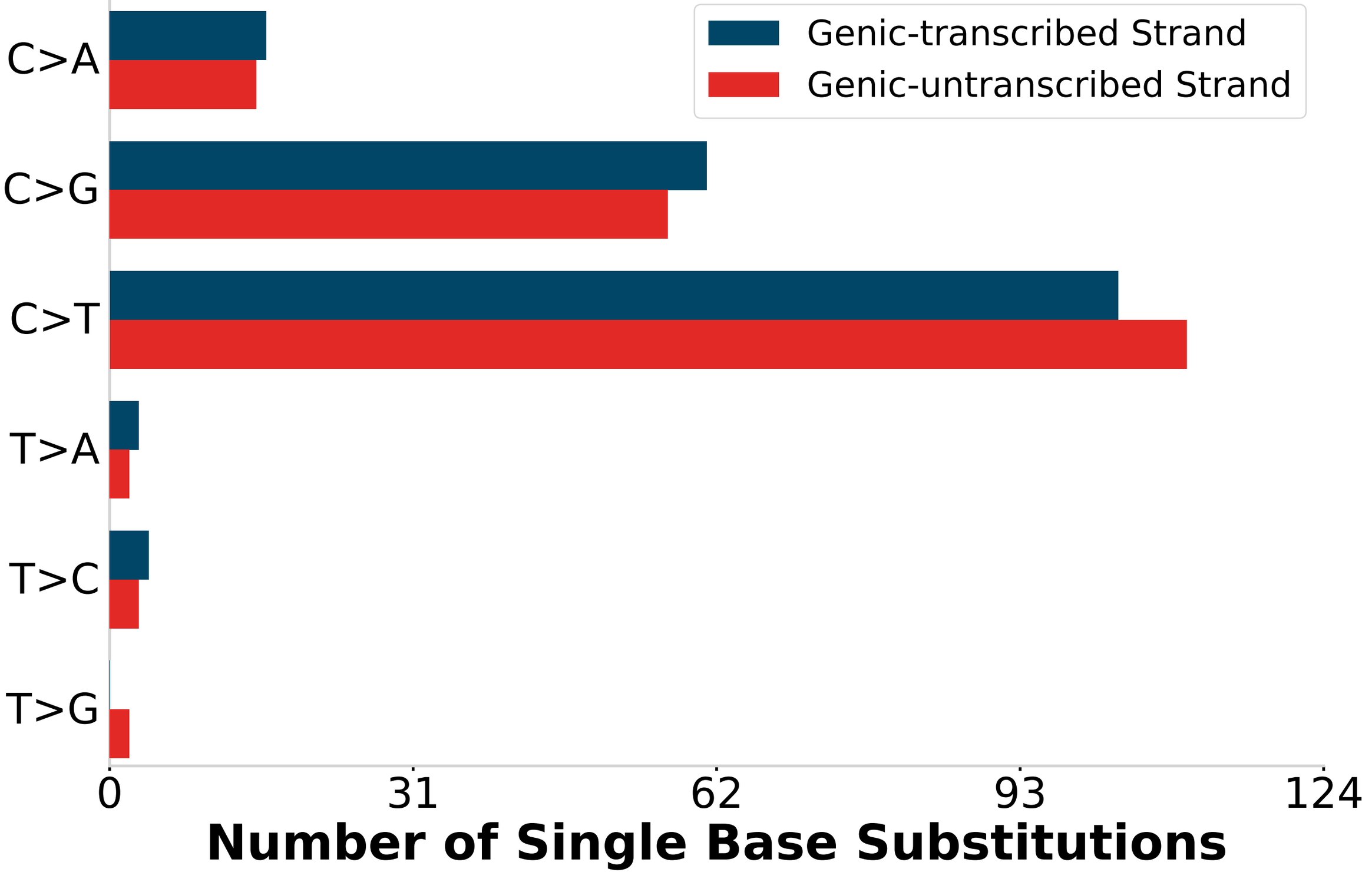
TCGA-DK-A3IN-01A-11D-A20D-08: 418 tran



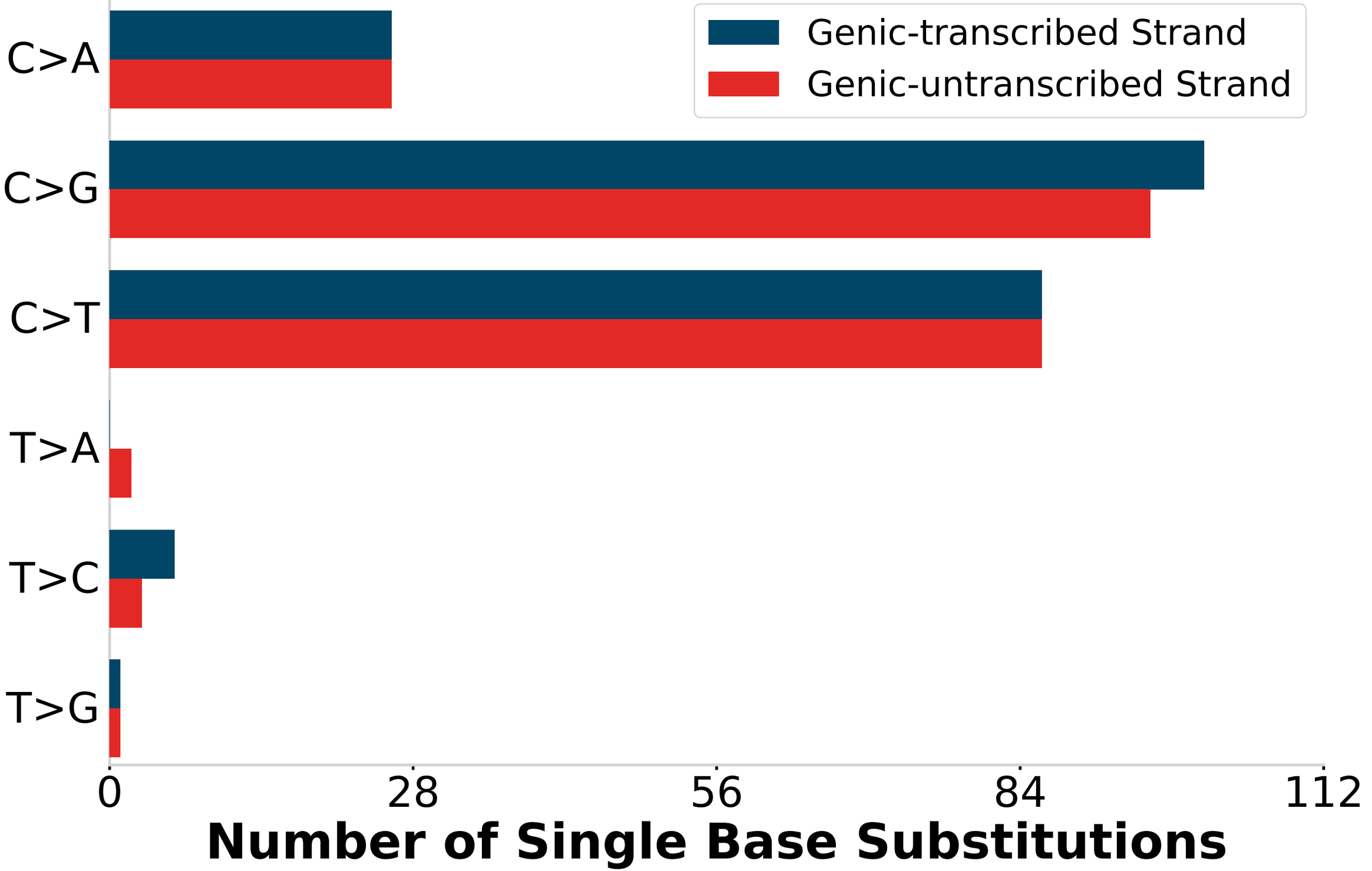
TCGA-DK-A3IQ-01A-31D-A20D-08: 195 tran



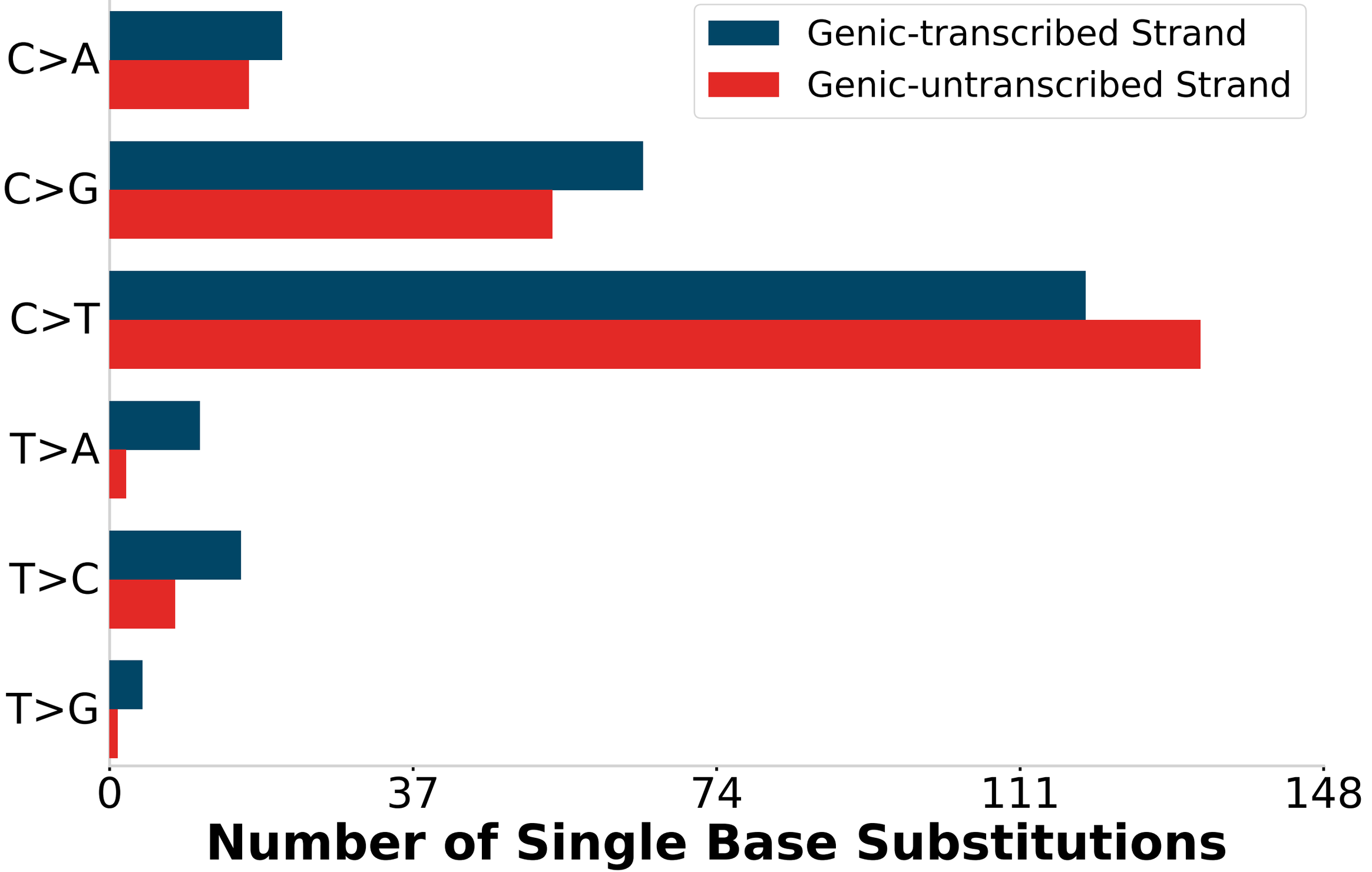
TCGA-DK-A3IS-01A-21D-A21A-08: 376 tran



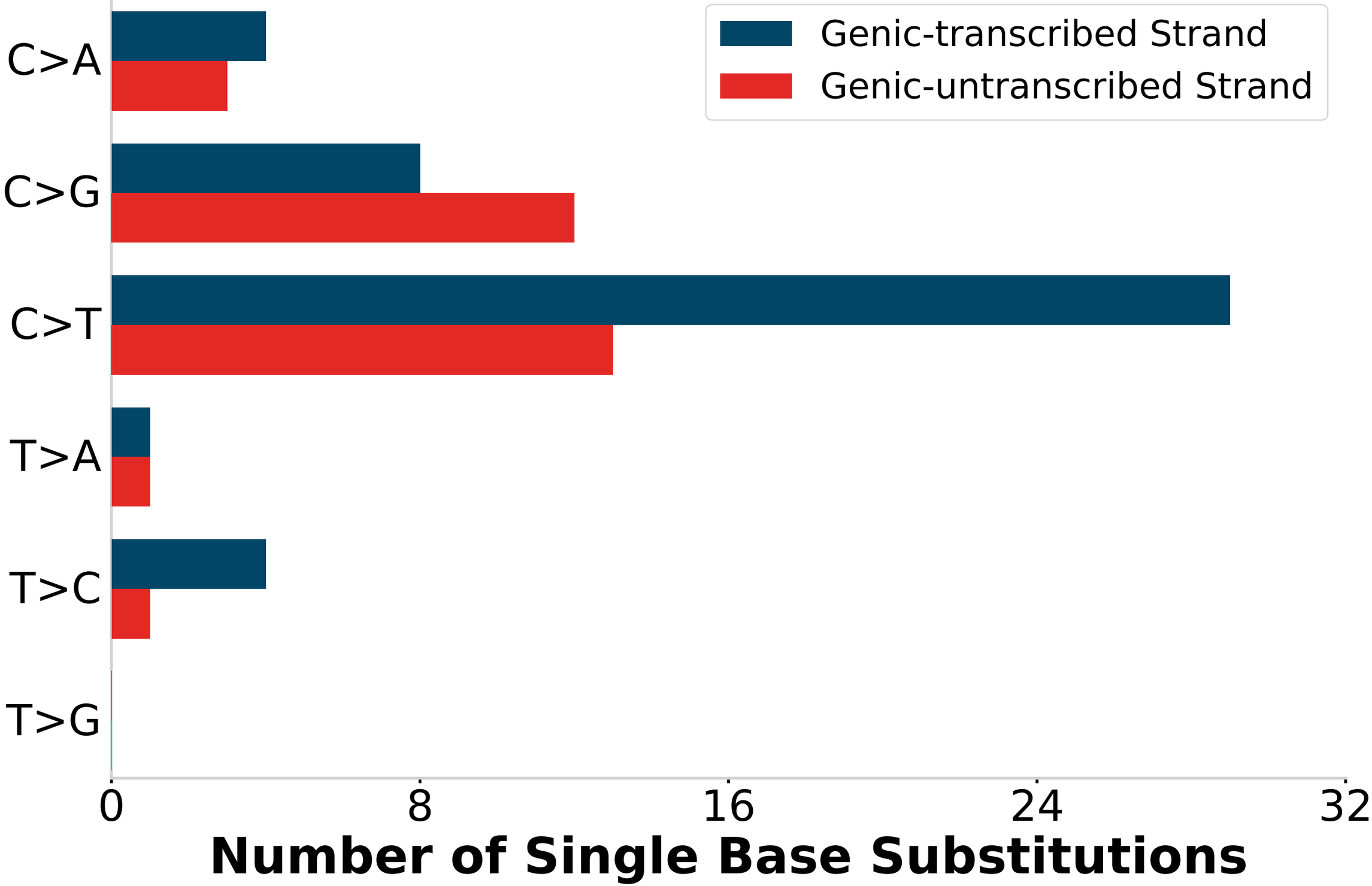
TCGA-DK-A3IT-01A-31D-A20D-08: 434 tran



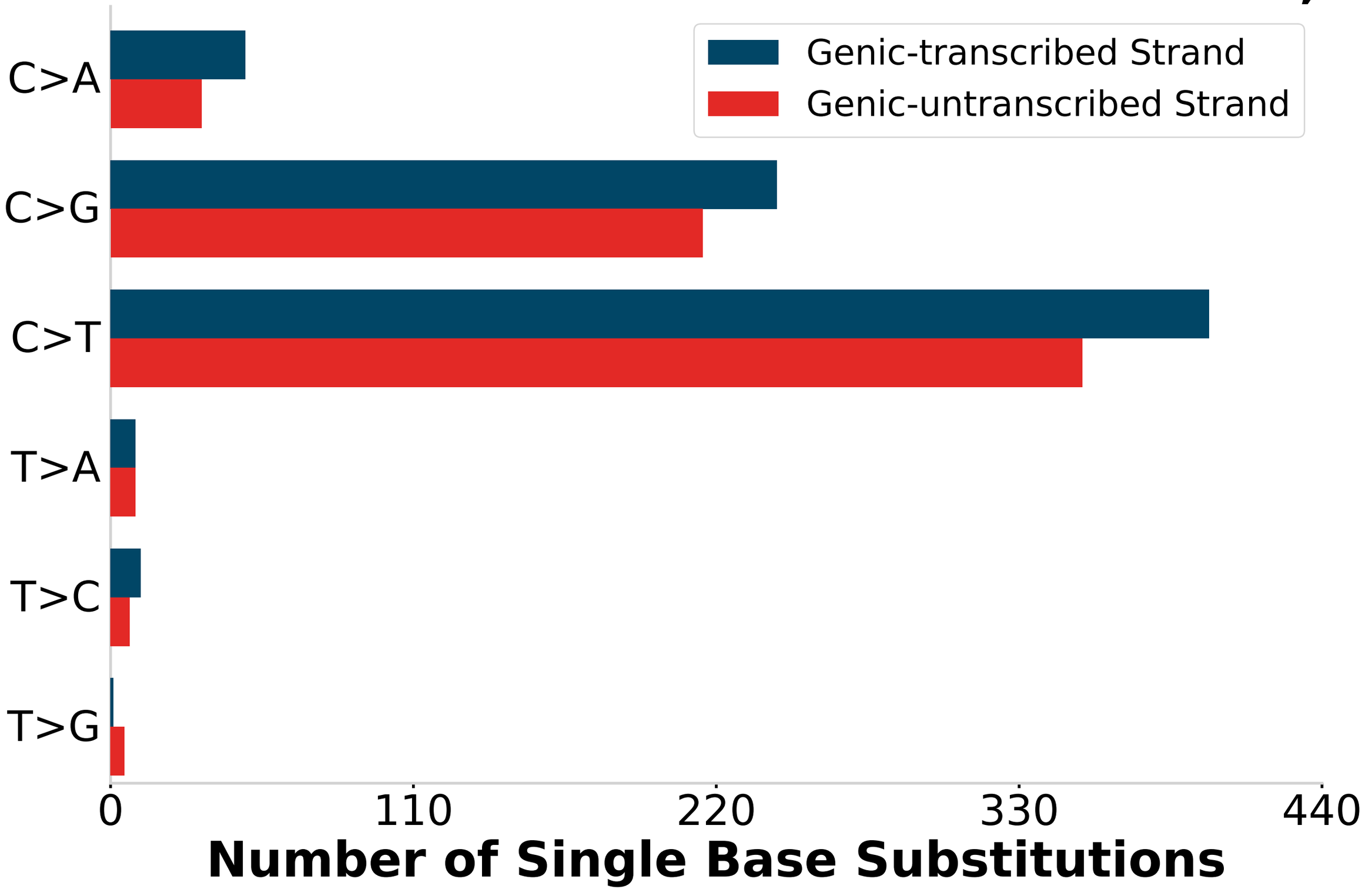
TCGA-DK-A3IU-01A-11D-A20D-08: 451 tran



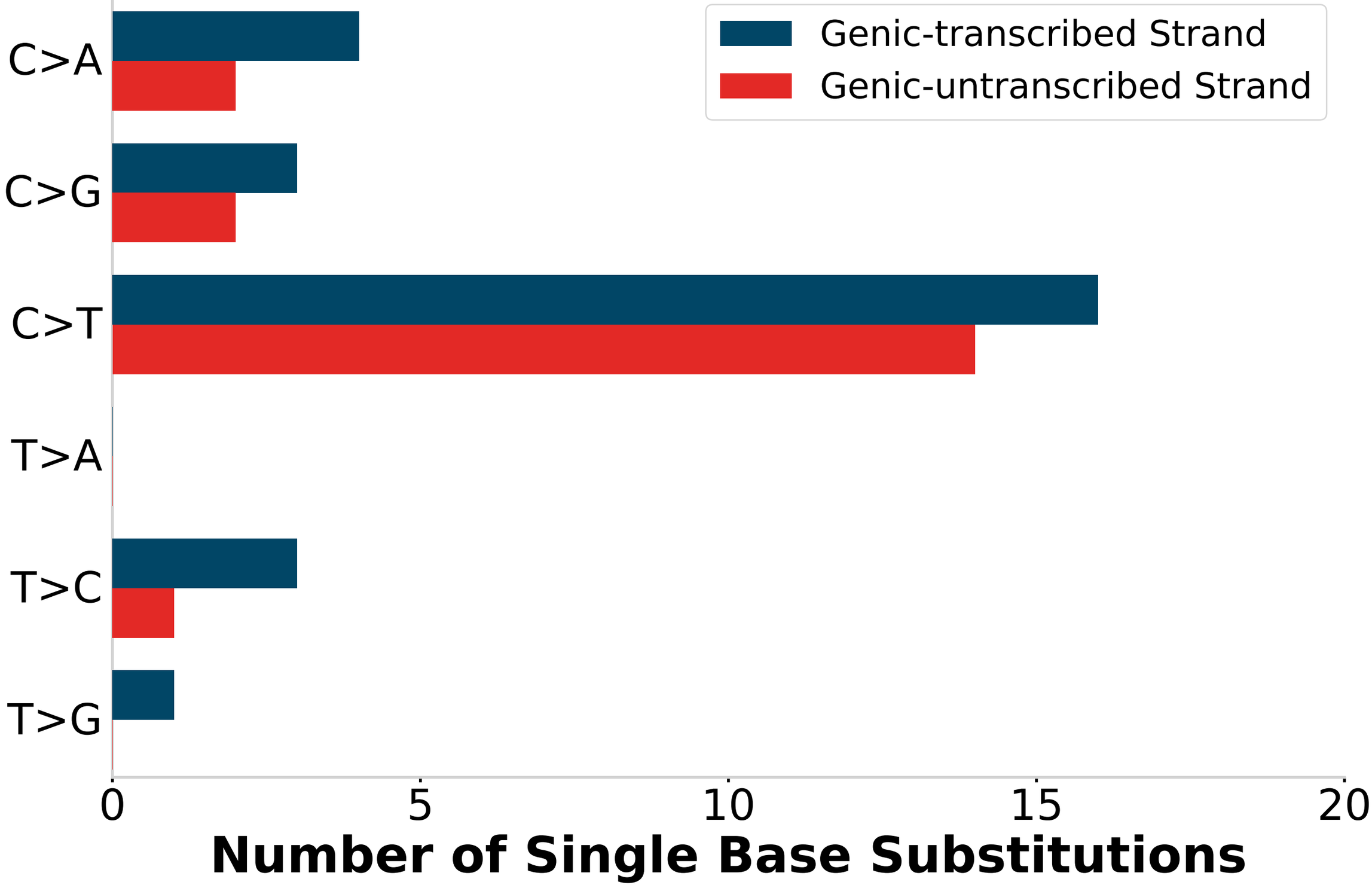
TCGA-DK-A3IV-01A-22D-A21A-08: 76 trans



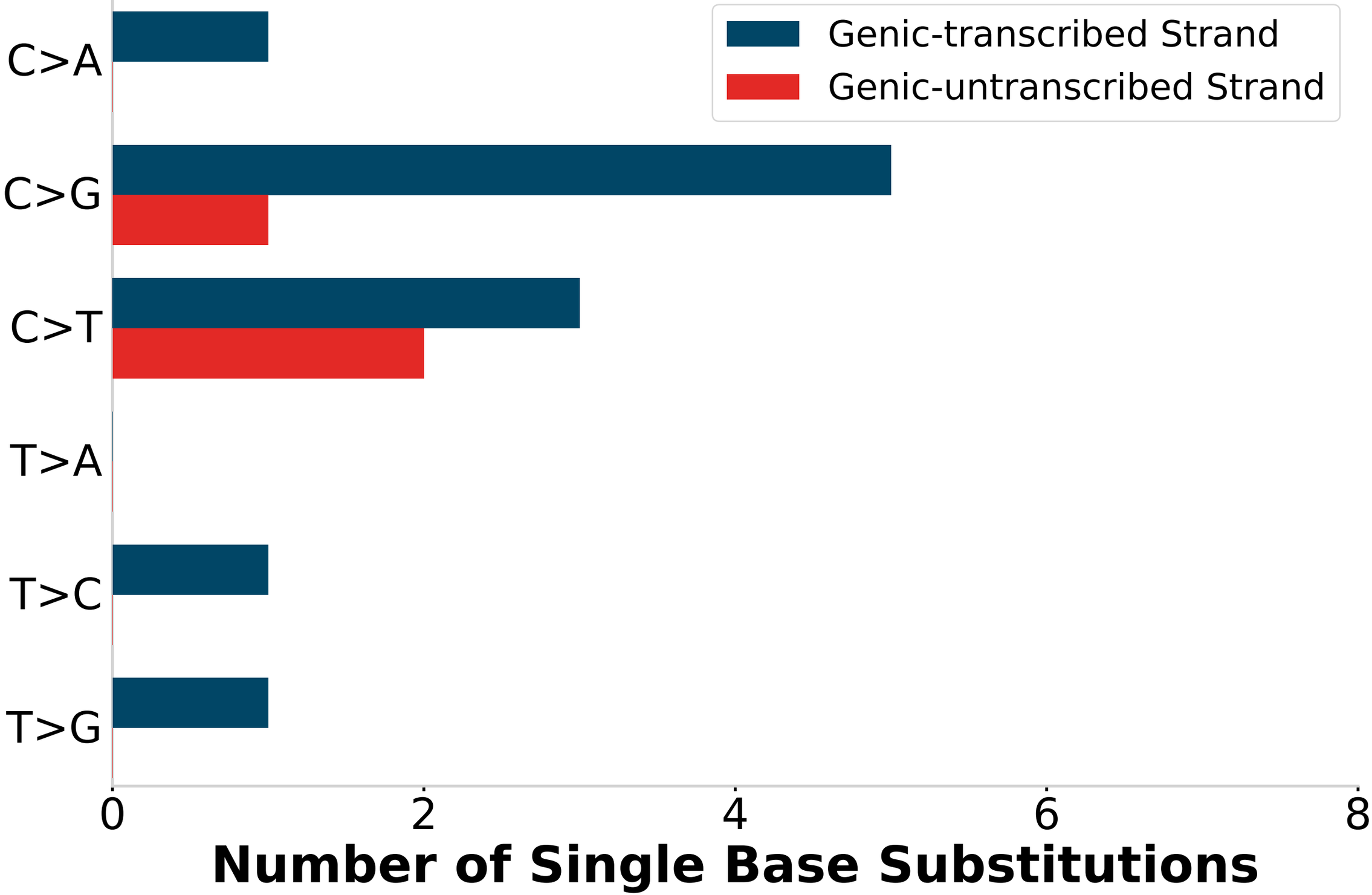
TCGA-DK-A3WW-01A-22D-A23M-08: 1,333



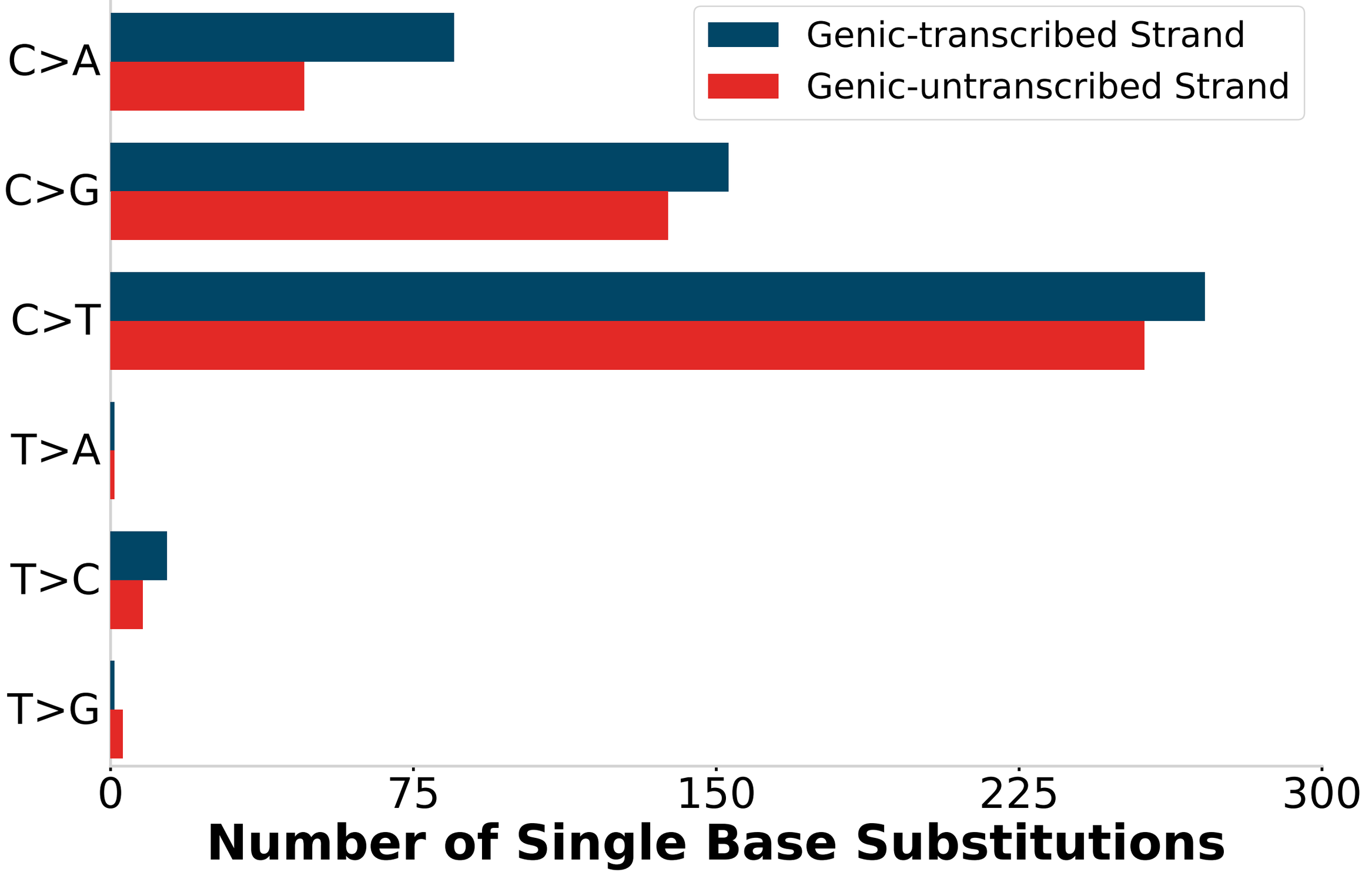
TCGA-DK-A3WX-01A-22D-A22Z-08: 46 tran



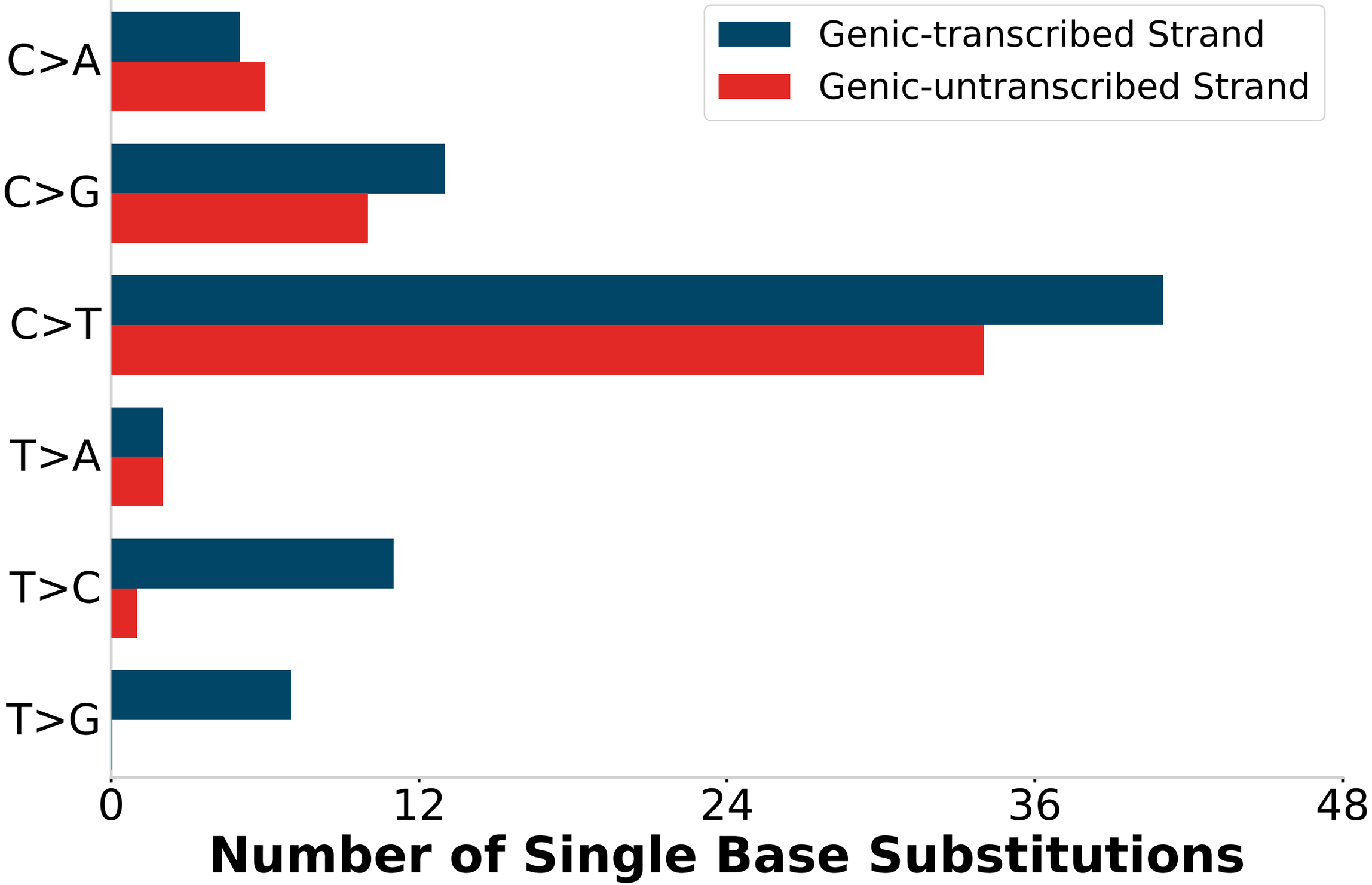
TCGA-DK-A3WY-01A-11D-A22Z-08: 14 tran



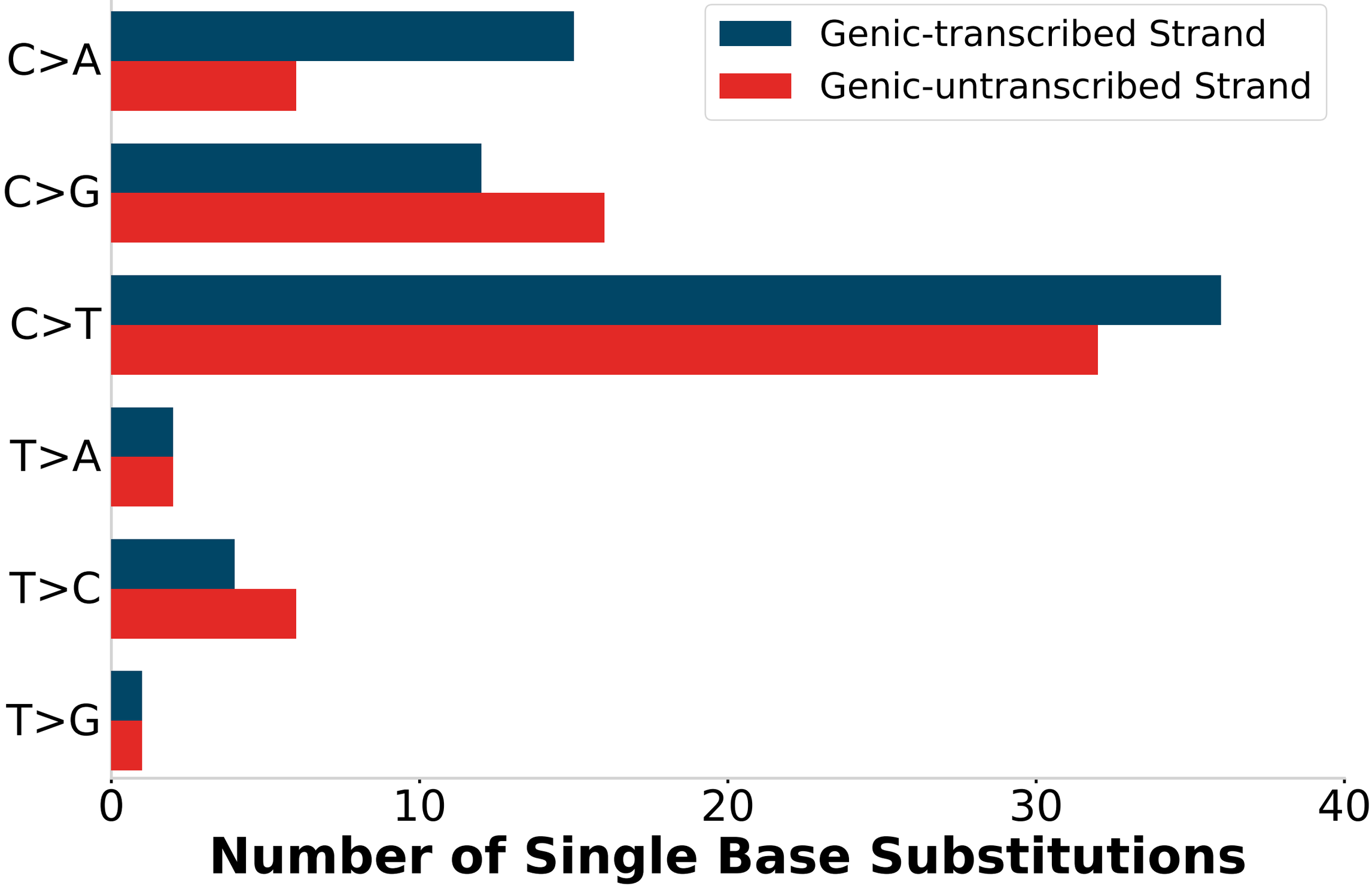
TCGA-DK-A3X1-01A-12D-A22Z-08: 979 tra



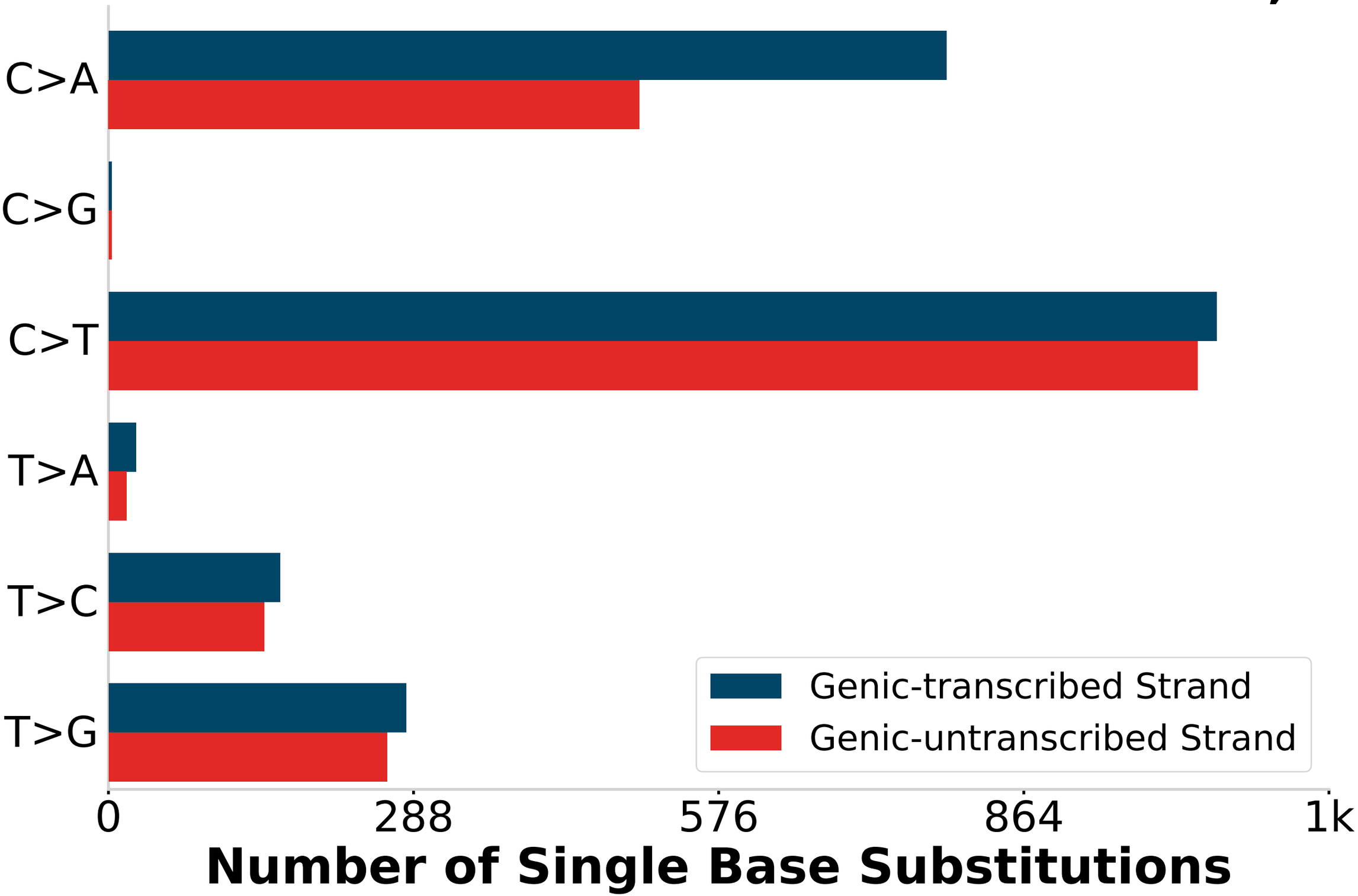
TCGA-DK-A3X2-01A-11D-A22Z-08: 132 tra



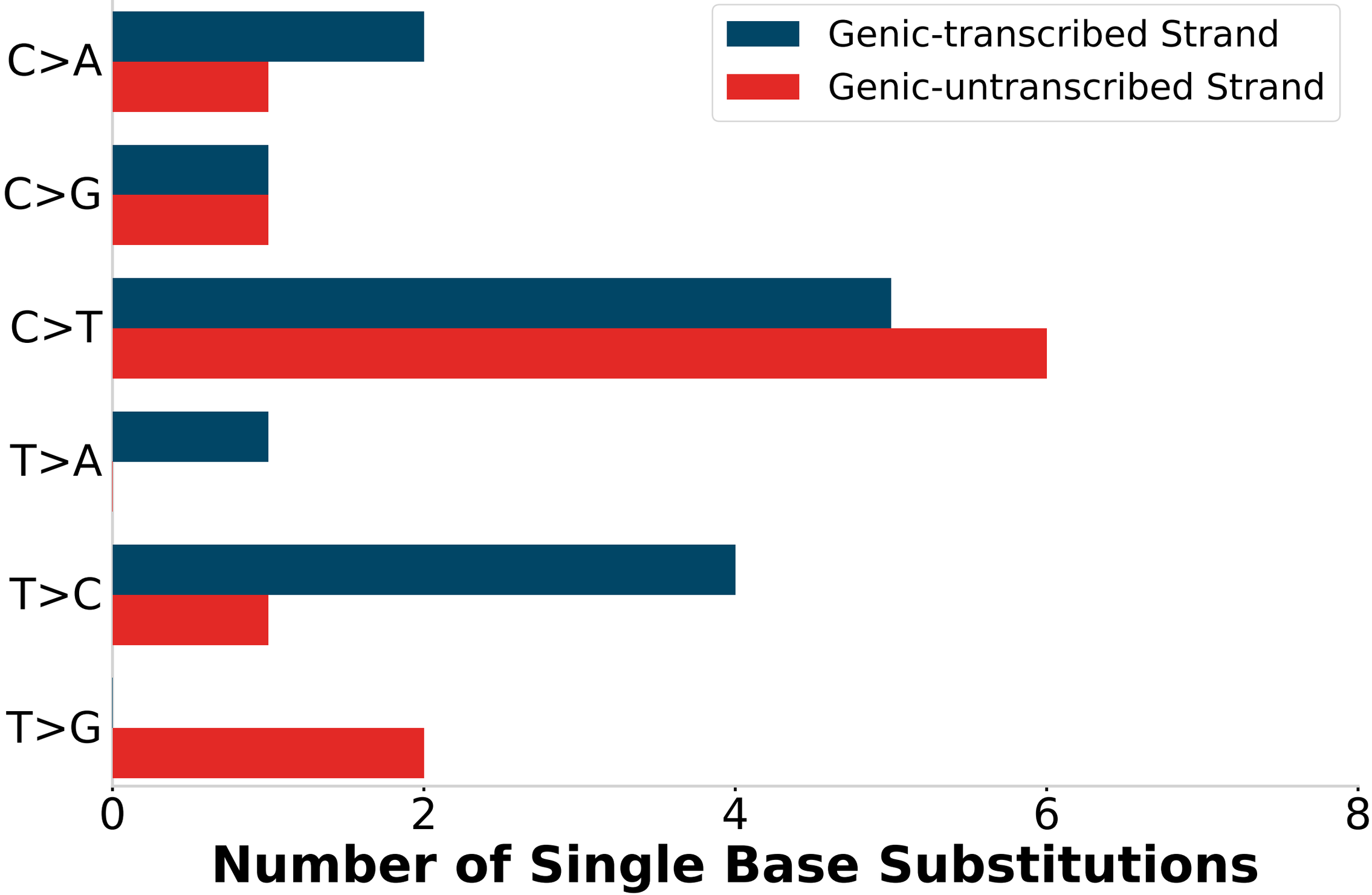
TCGA-DK-A6AV-01A-12D-A30E-08: 133 tran



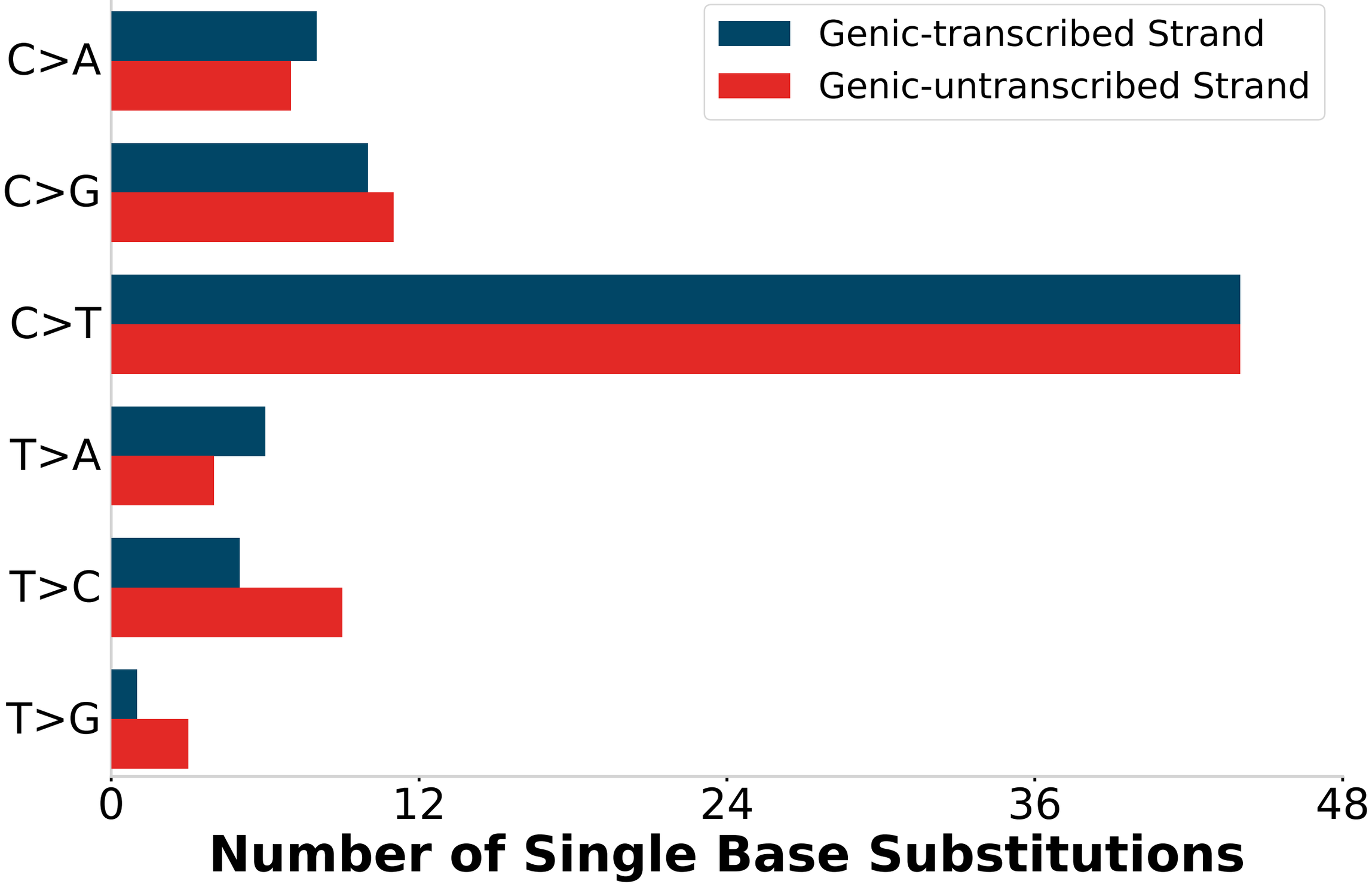
TCGA-DK-A6AW-01A-11D-A30E-08: 4,268 t



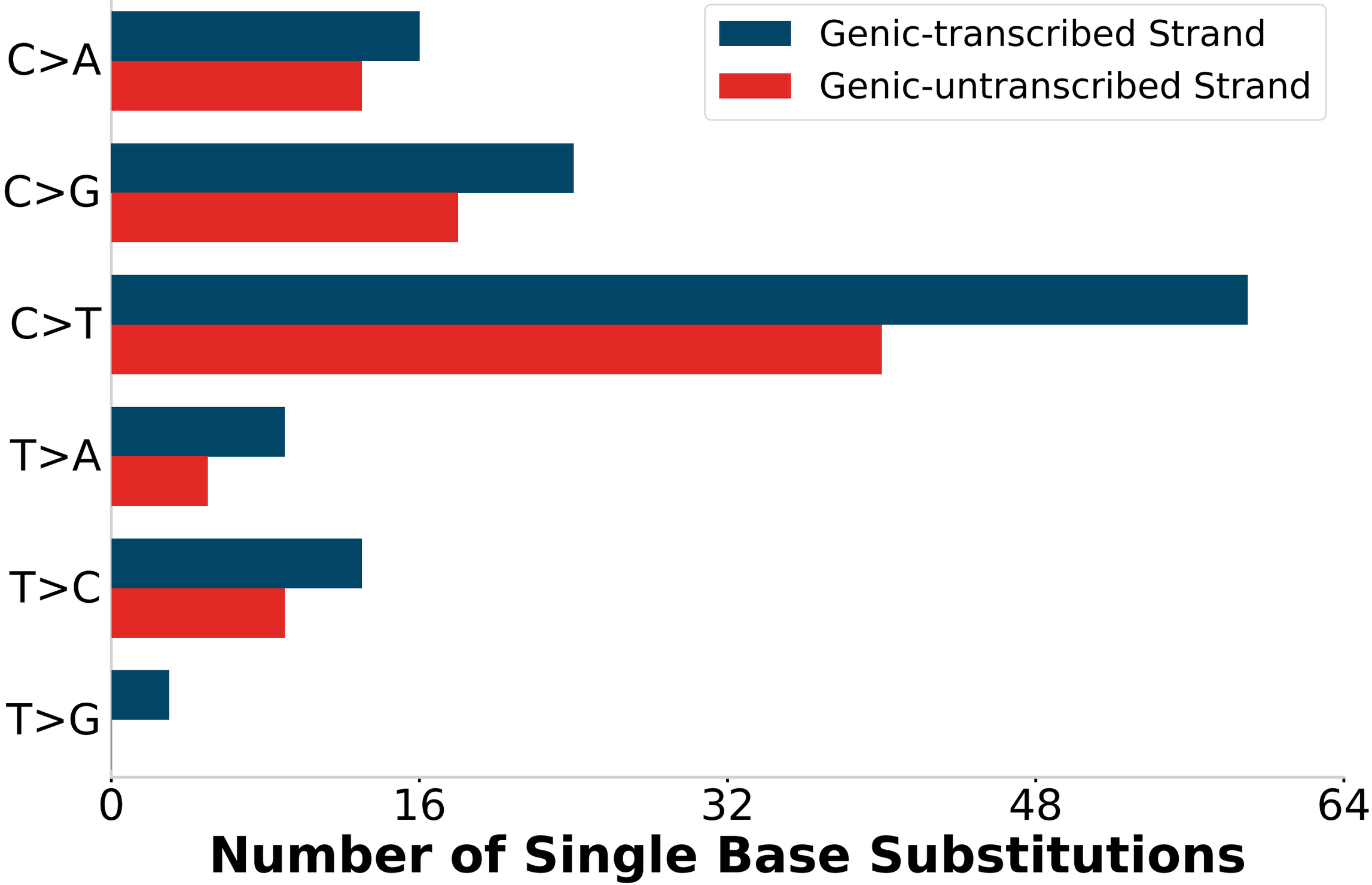
TCGA-DK-A6B0-01A-11D-A31L-08: 24 trans



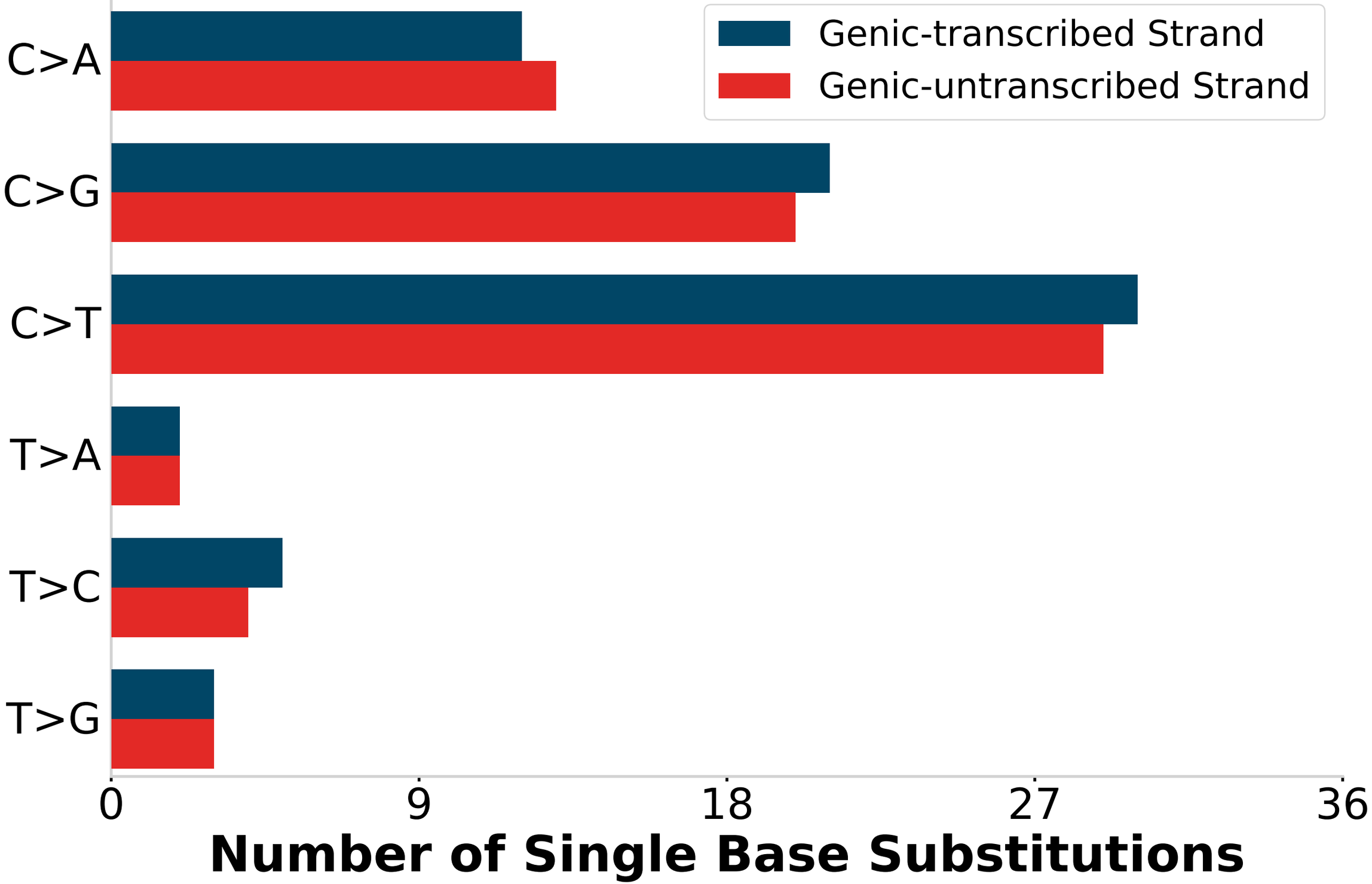
TCGA-DK-A6B1-01A-12D-A30E-08: 152 tra



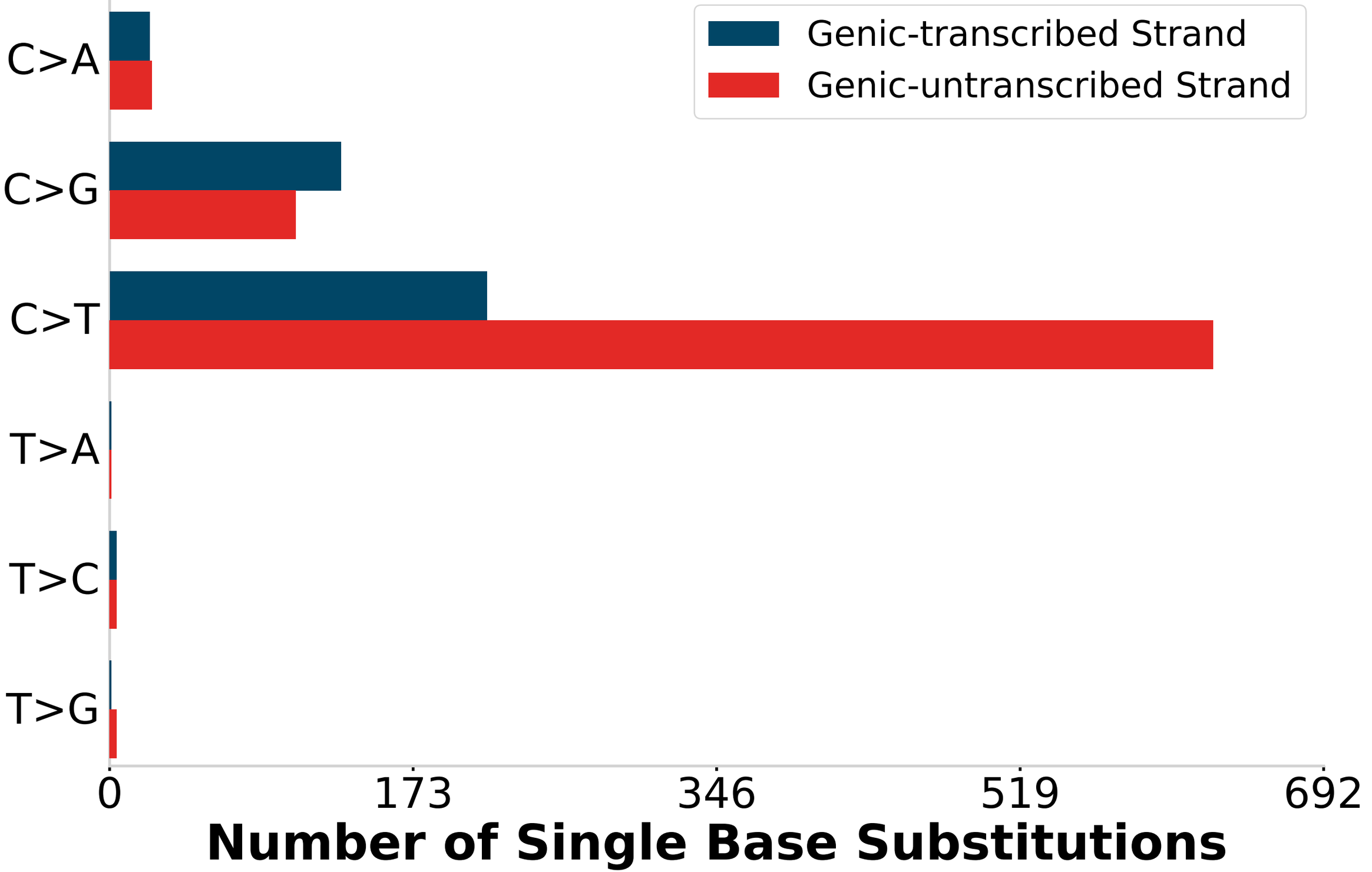
TCGA-DK-A6B2-01A-11D-A30E-08: 209 tra



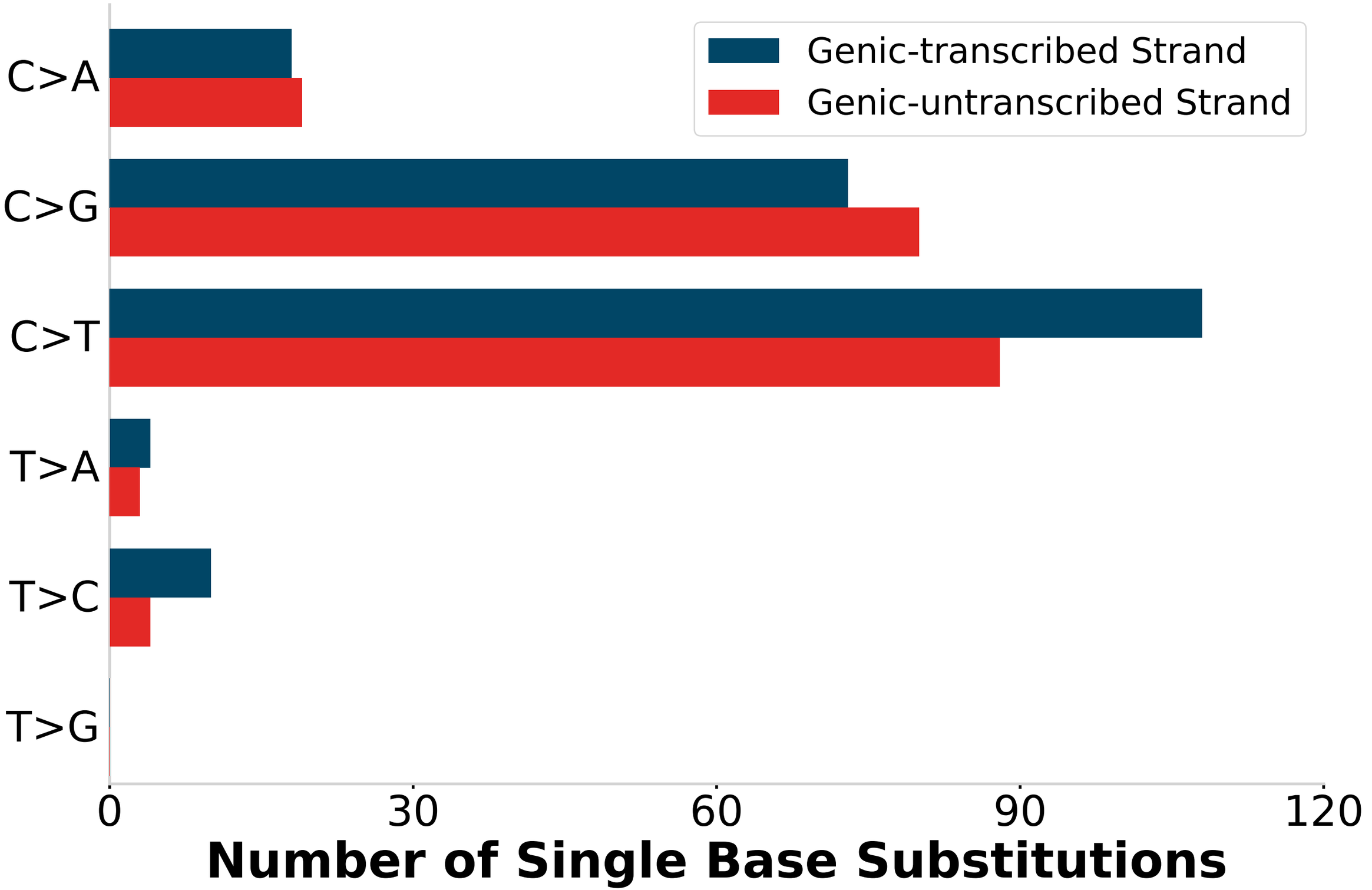
TCGA-DK-A6B5-01A-11D-A31L-08: 144 tra



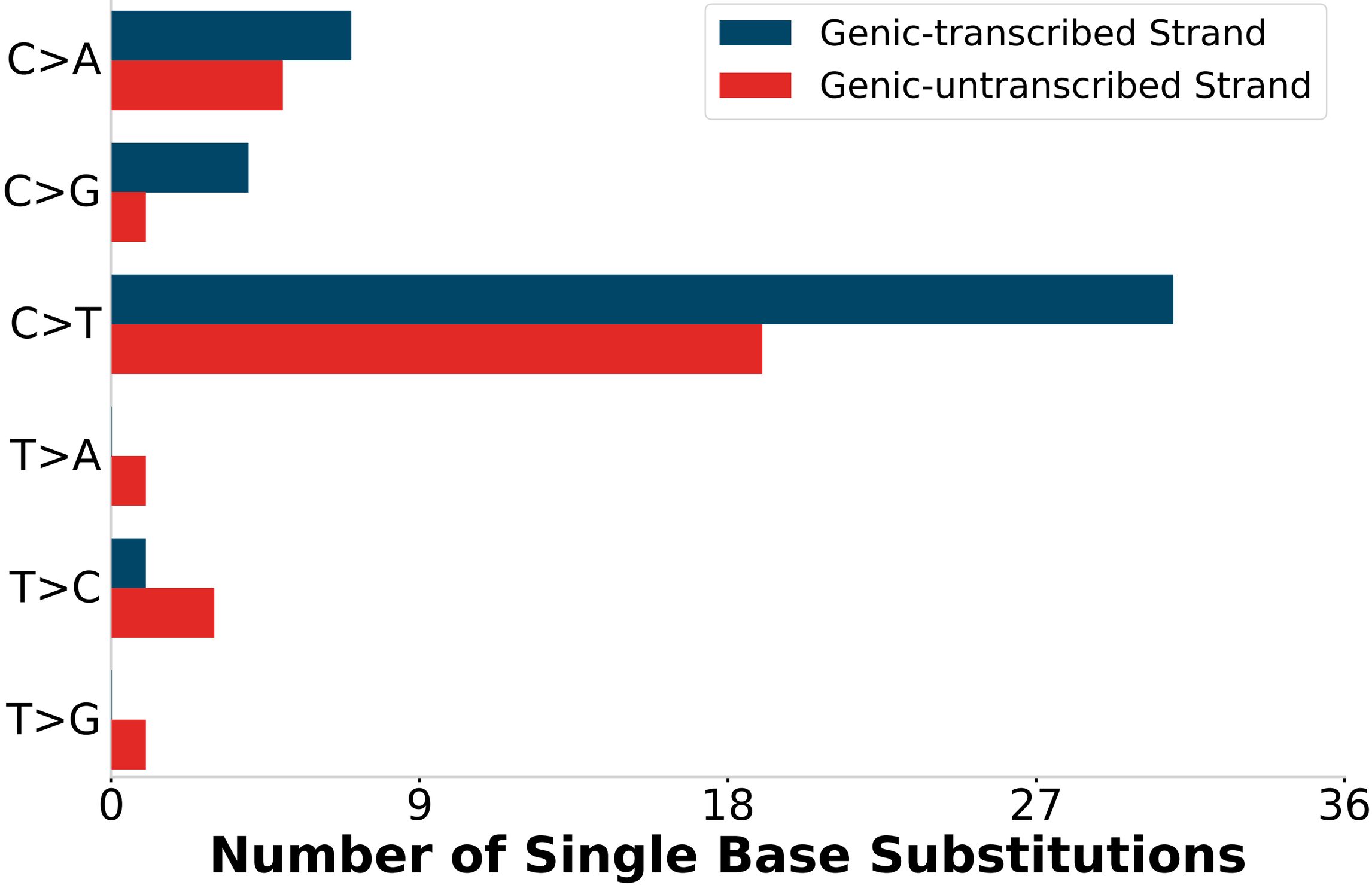
TCGA-DK-A6B6-01A-11D-A30E-08: 1,144 tr



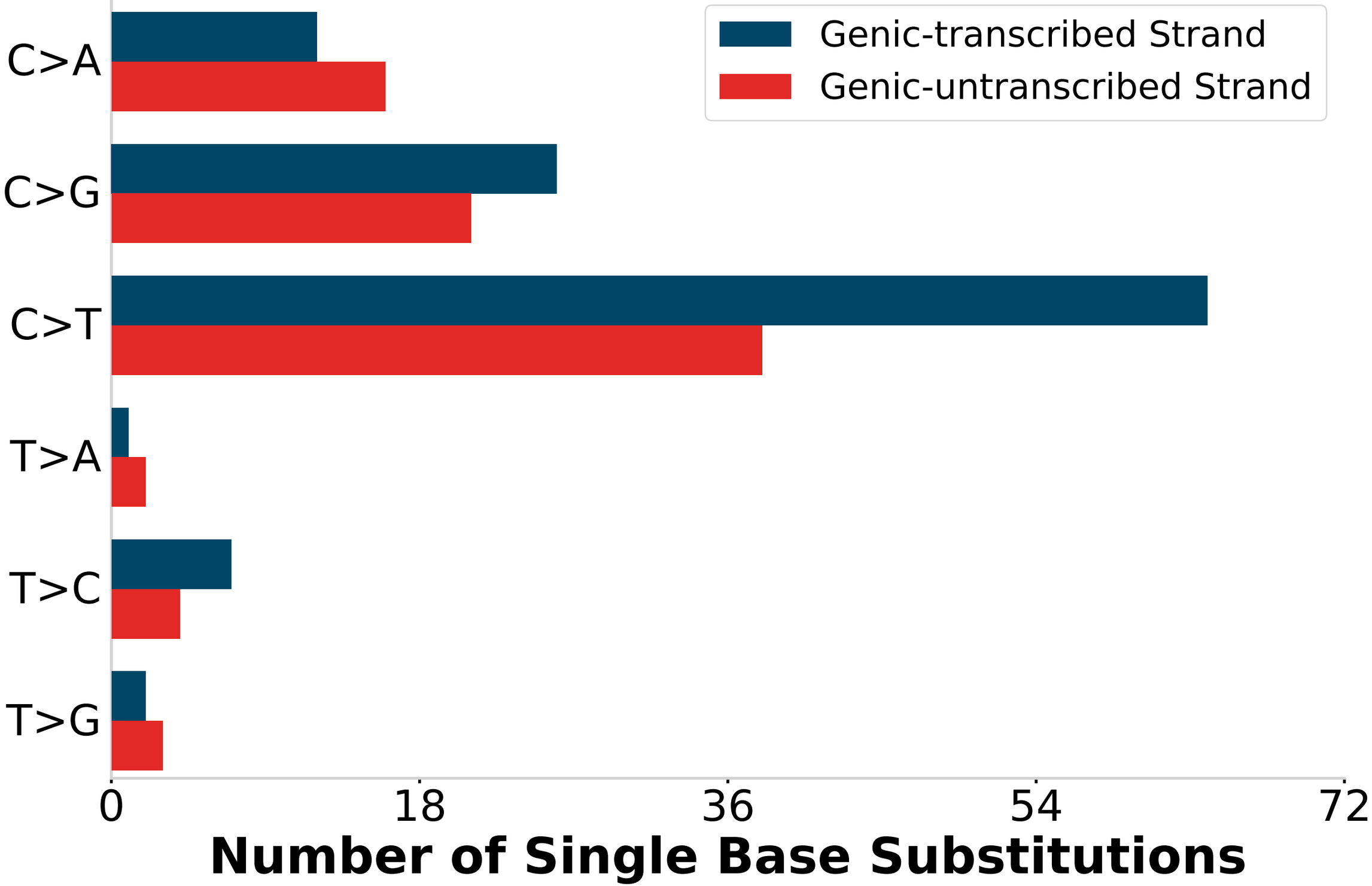
TCGA-DK-AA6L-01A-11D-A391-08: 407 tra



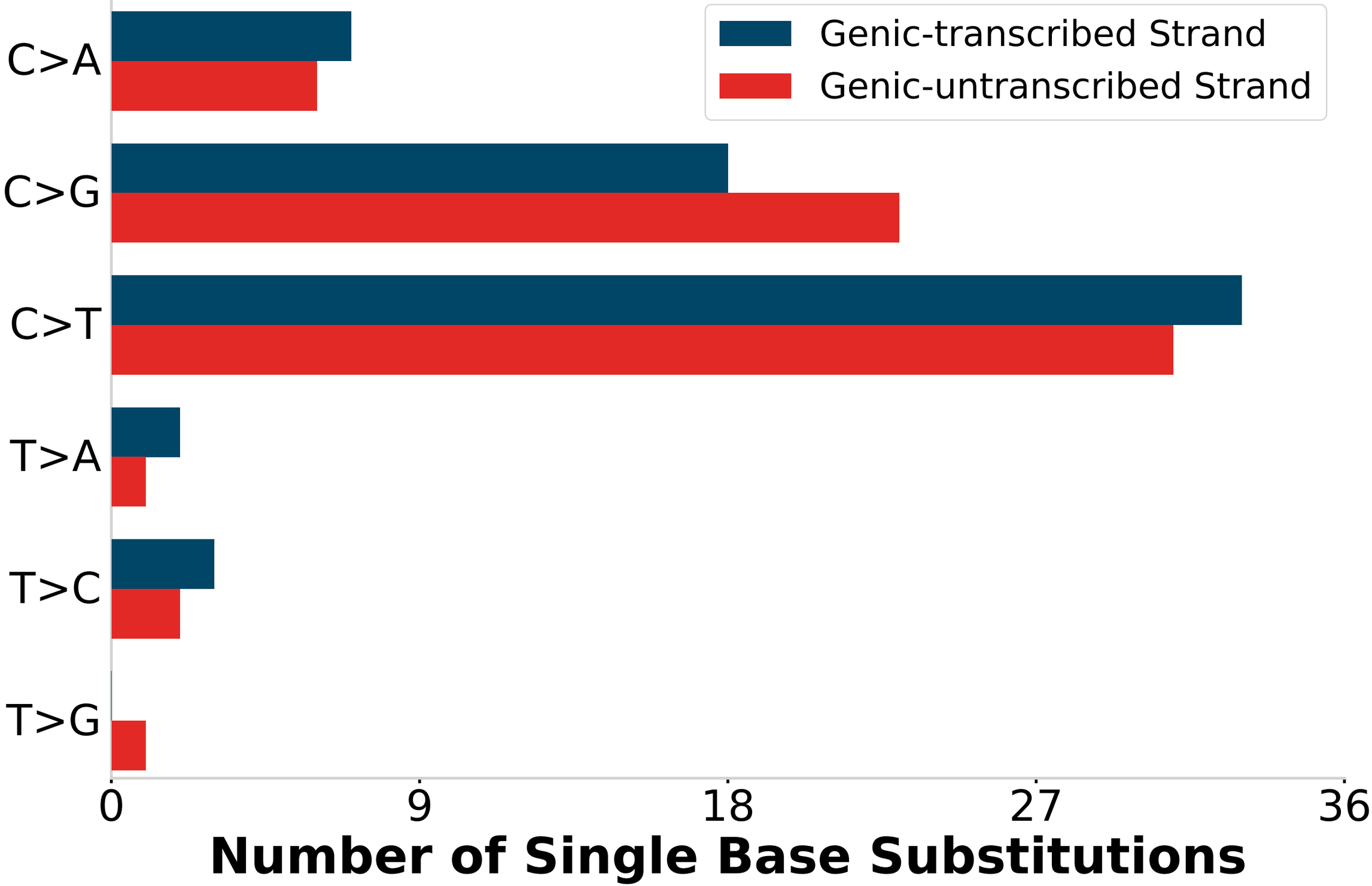
TCGA-DK-AA6M-01A-11D-A391-08: 73 tran



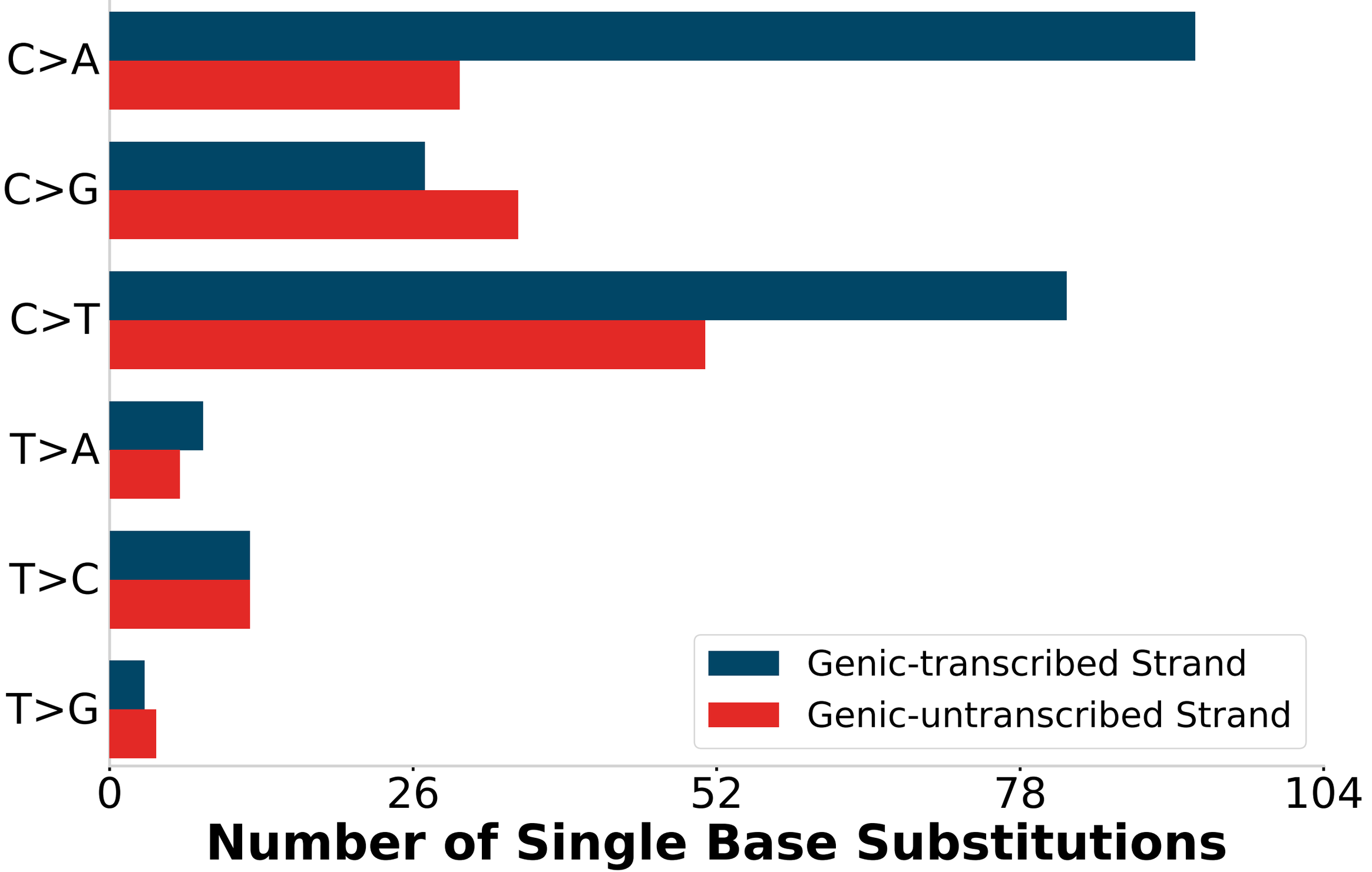
TCGA-DK-AA6P-01A-11D-A391-08: 196 tra



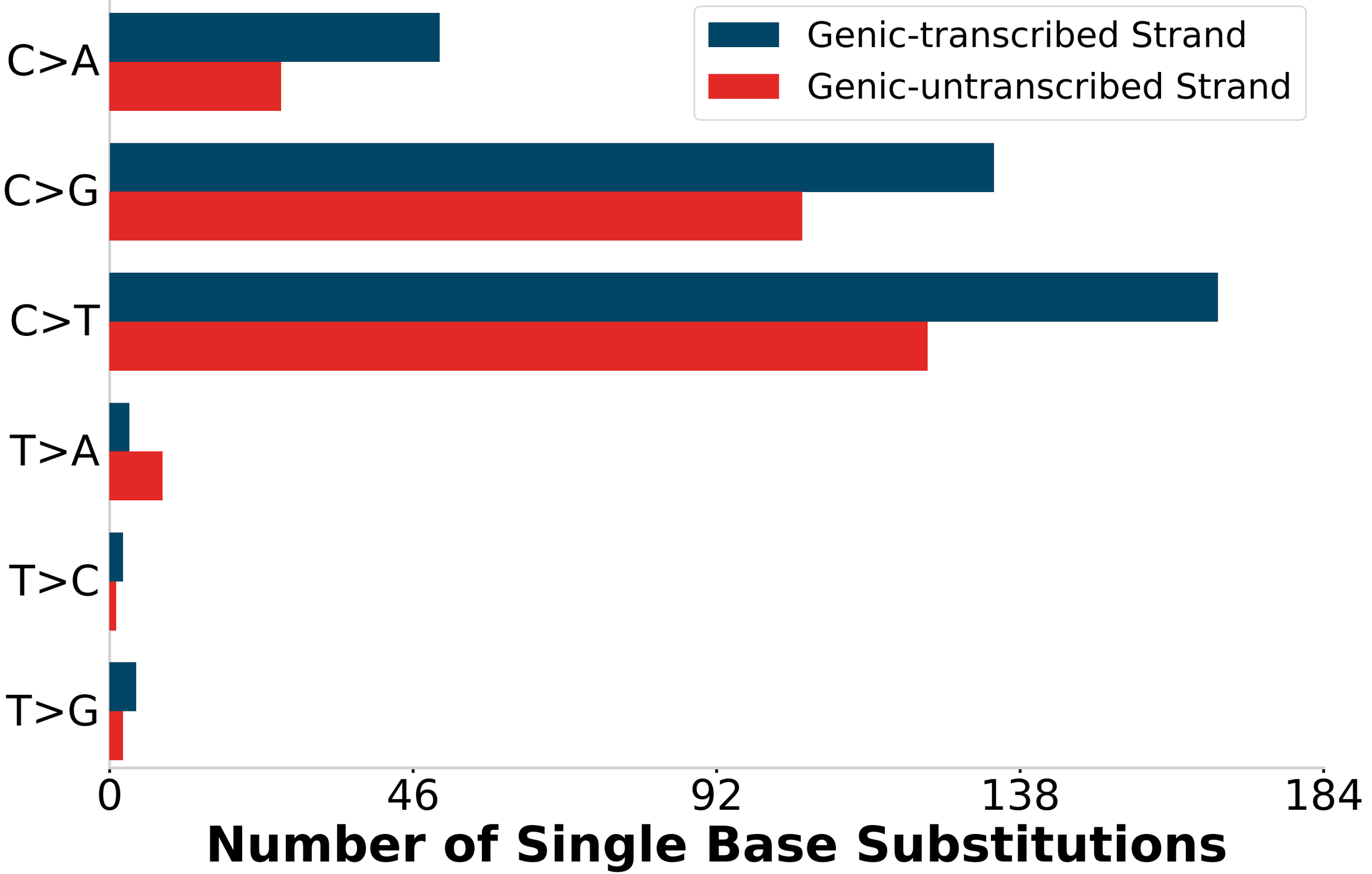
TCGA-DK-AA6Q-01A-11D-A391-08: 127 tra



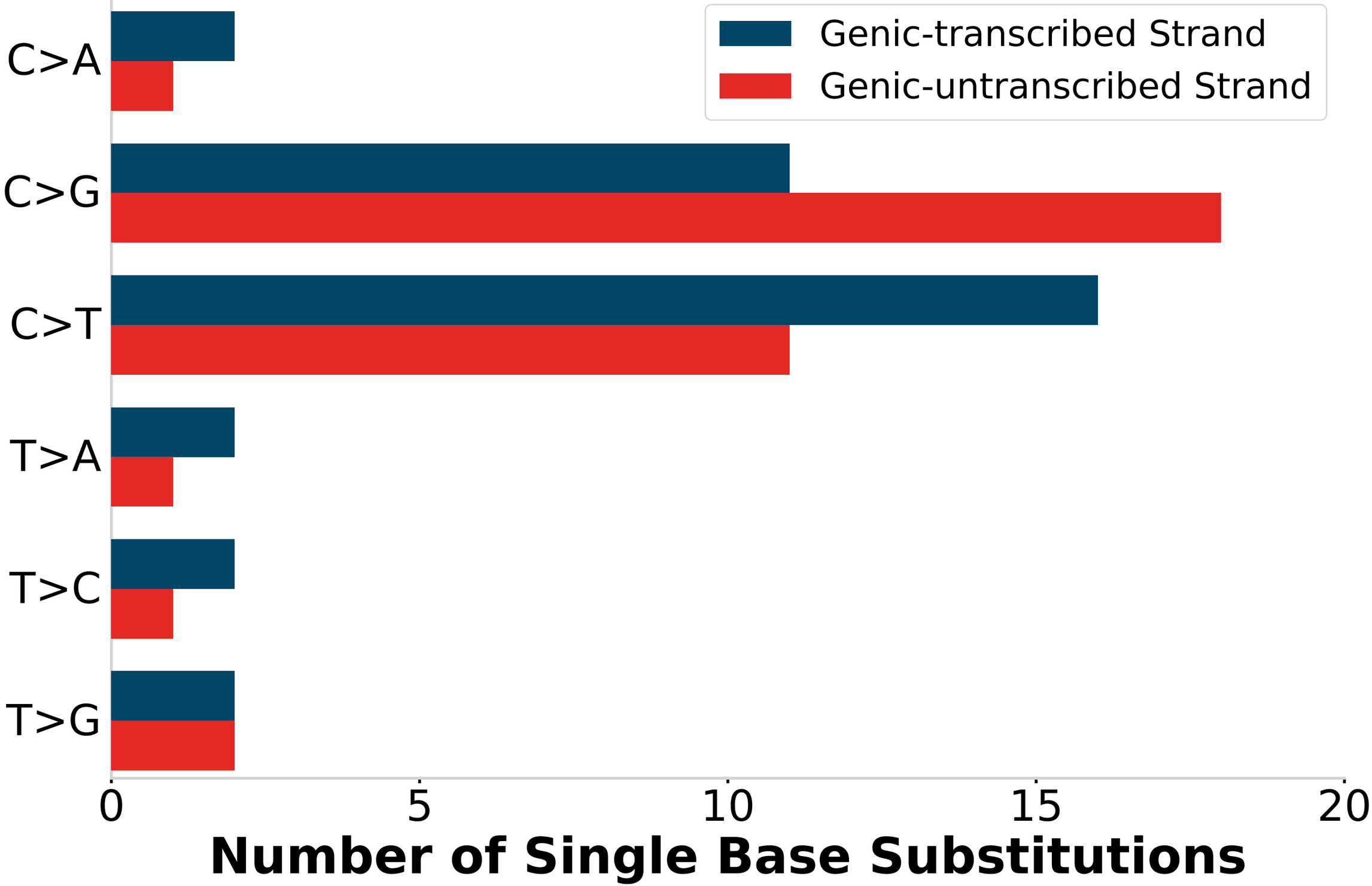
TCGA-DK-AA6R-01A-11D-A42E-08: 363 tra



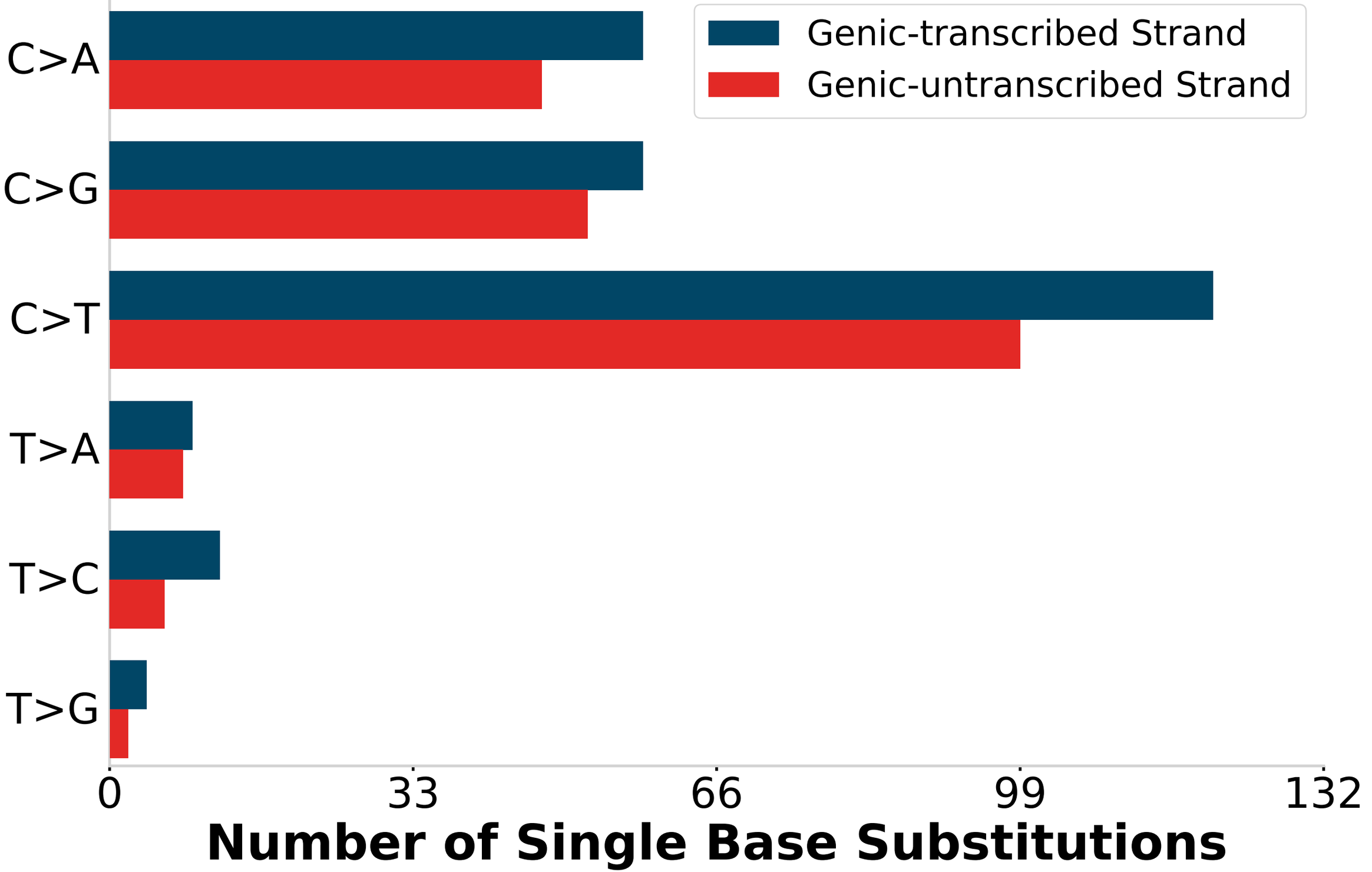
TCGA-DK-AA6S-01A-21D-A391-08: 627 tra



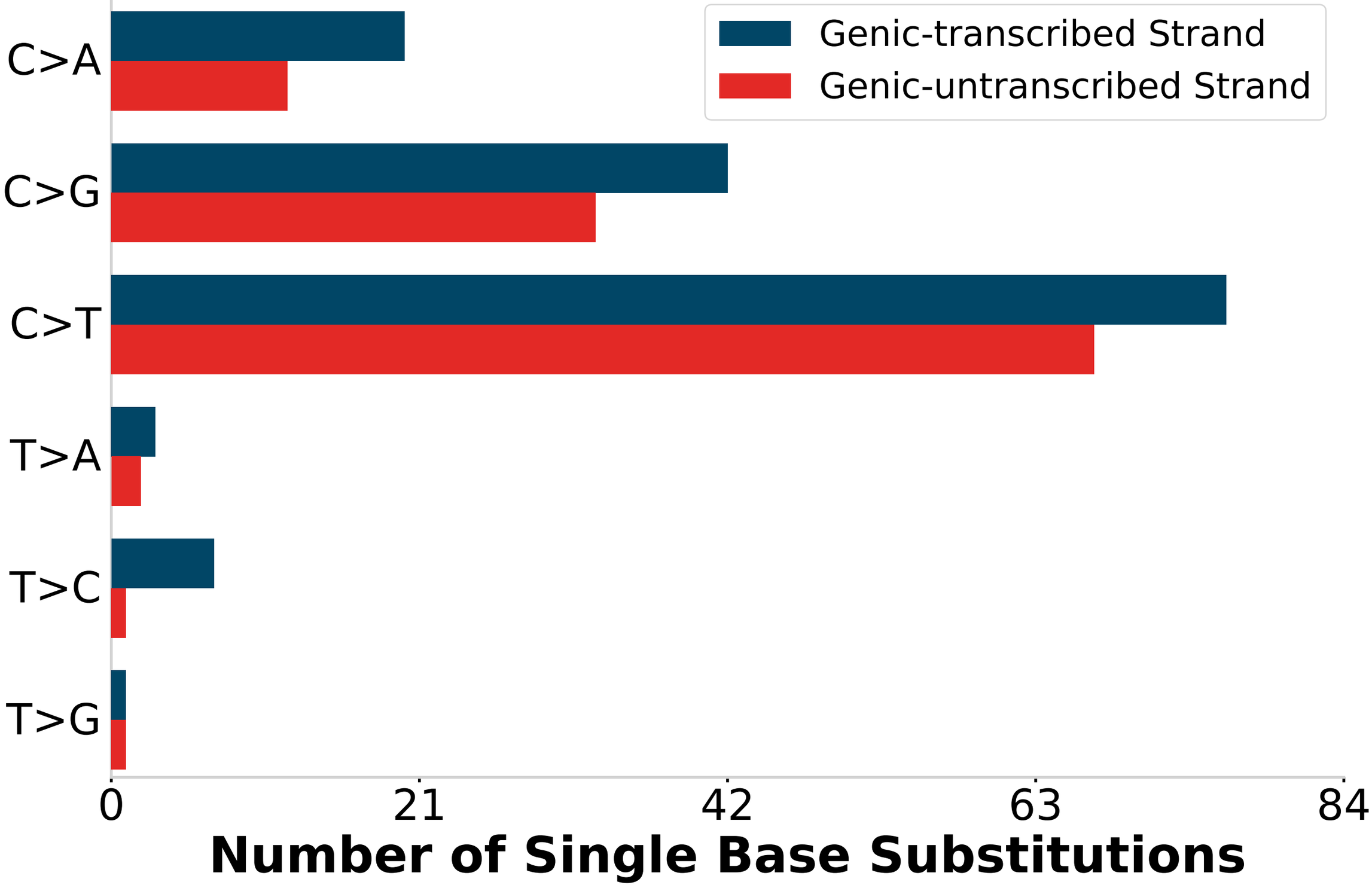
TCGA-DK-AA6T-01A-11D-A391-08: 69 trans



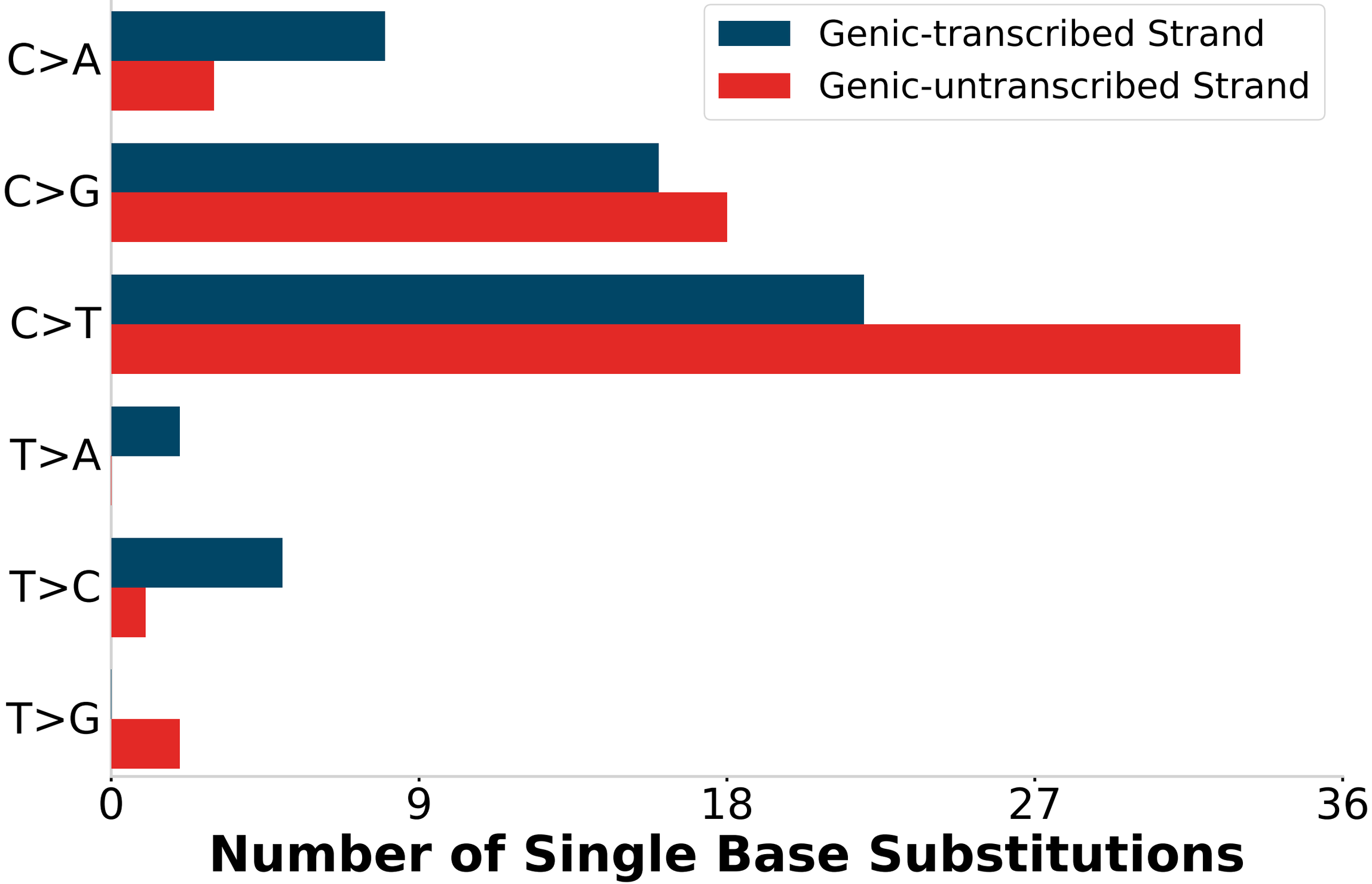
TCGA-DK-AA6U-01A-11D-A391-08: 475 tra



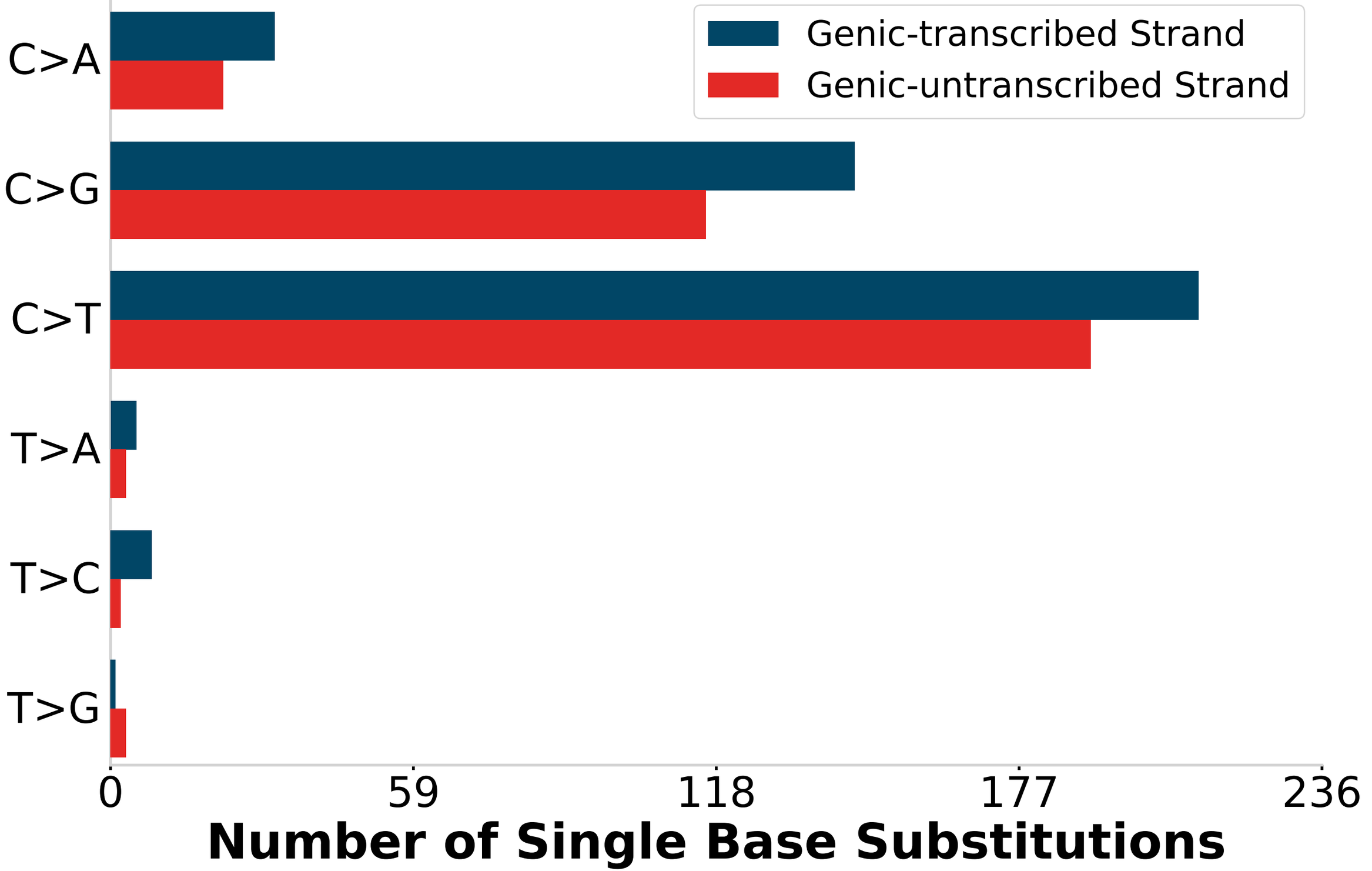
TCGA-DK-AA6W-01A-12D-A391-08: 265 tra



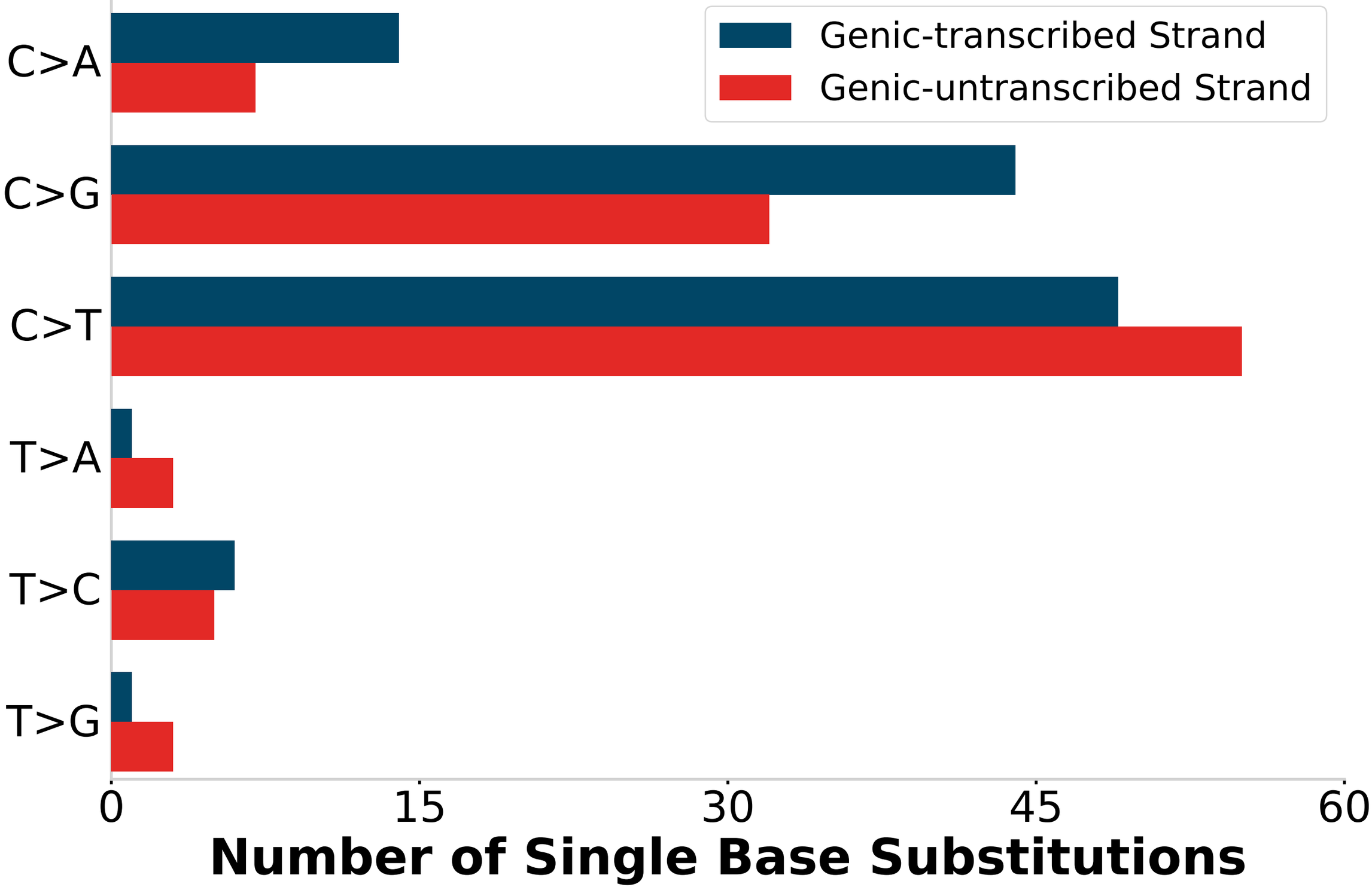
TCGA-DK-AA6X-01A-12D-A42E-08: 110 tra



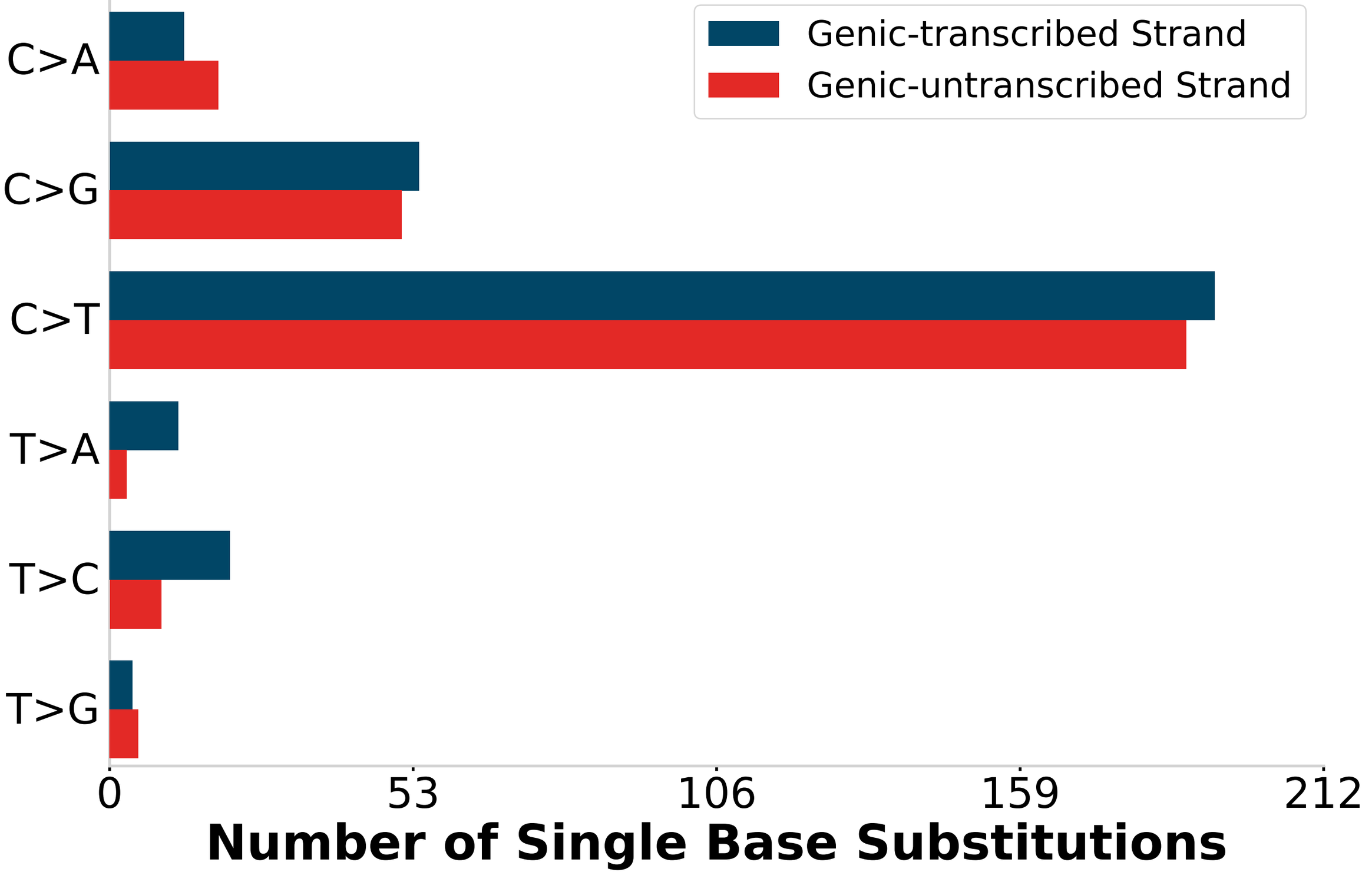
TCGA-DK-AA71-01A-31D-A391-08: 740 tra



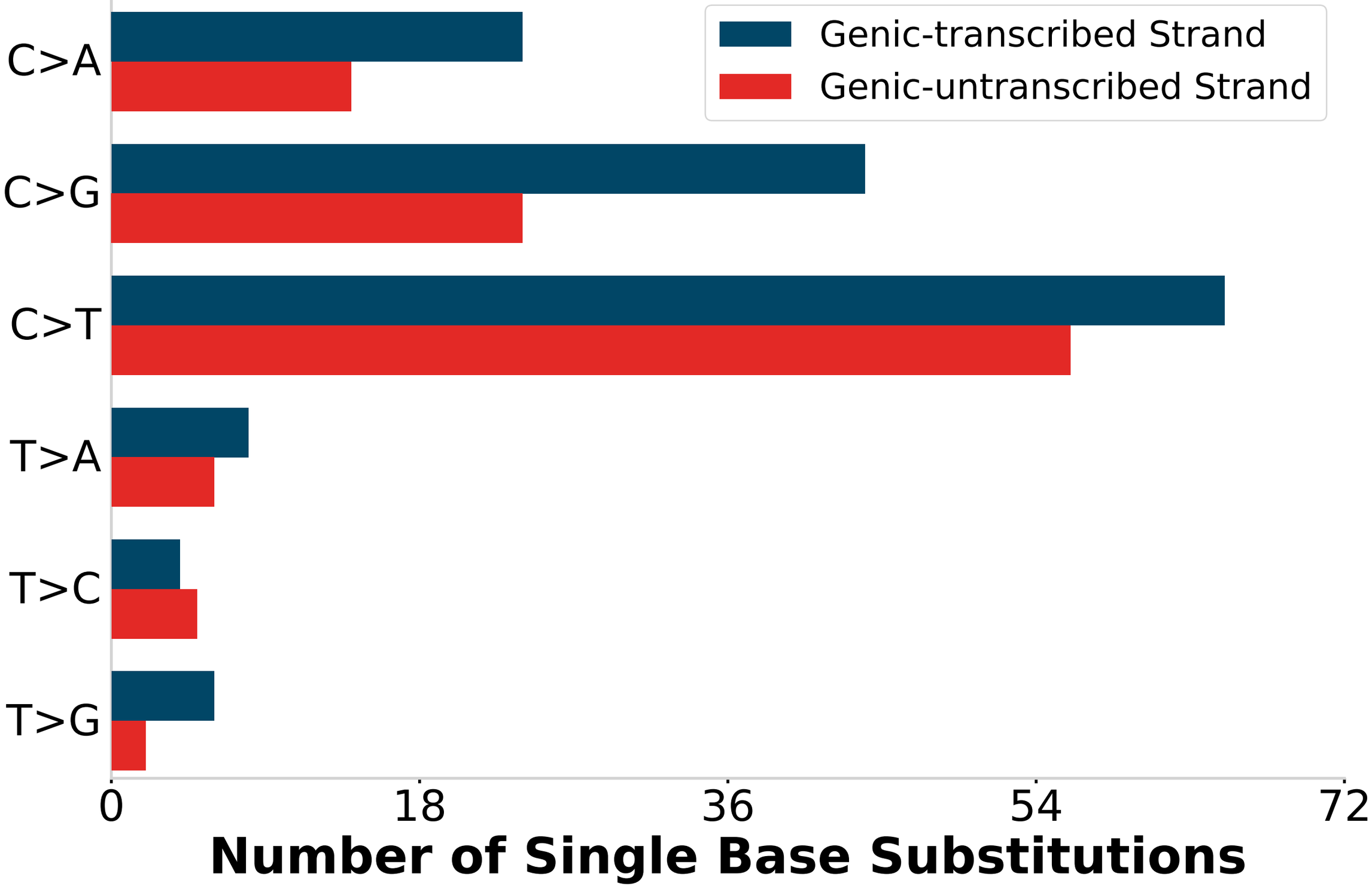
TCGA-DK-AA74-01A-11D-A391-08: 220 tra



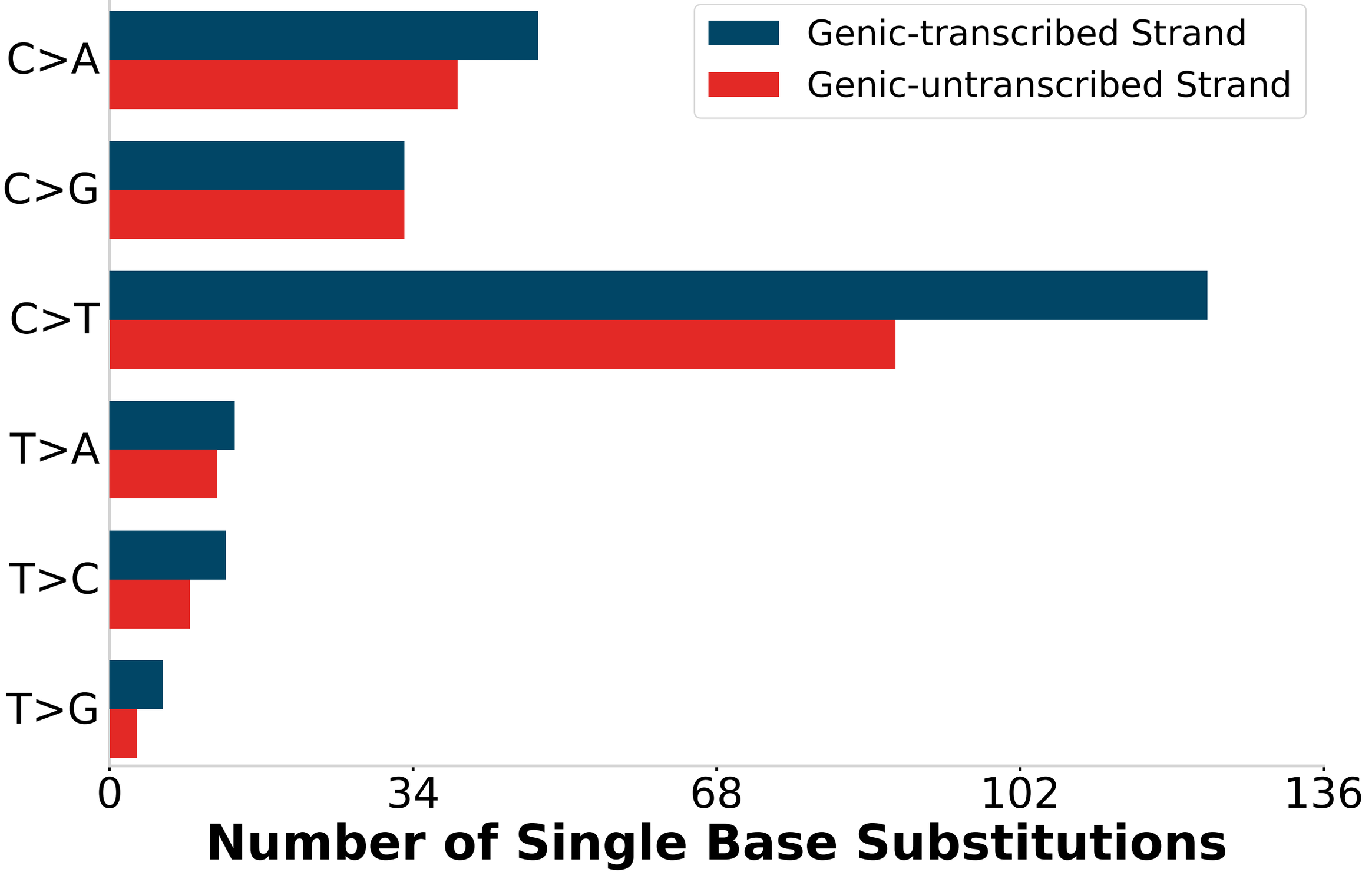
TCGA-DK-AA75-01A-11D-A391-08: 572 tra



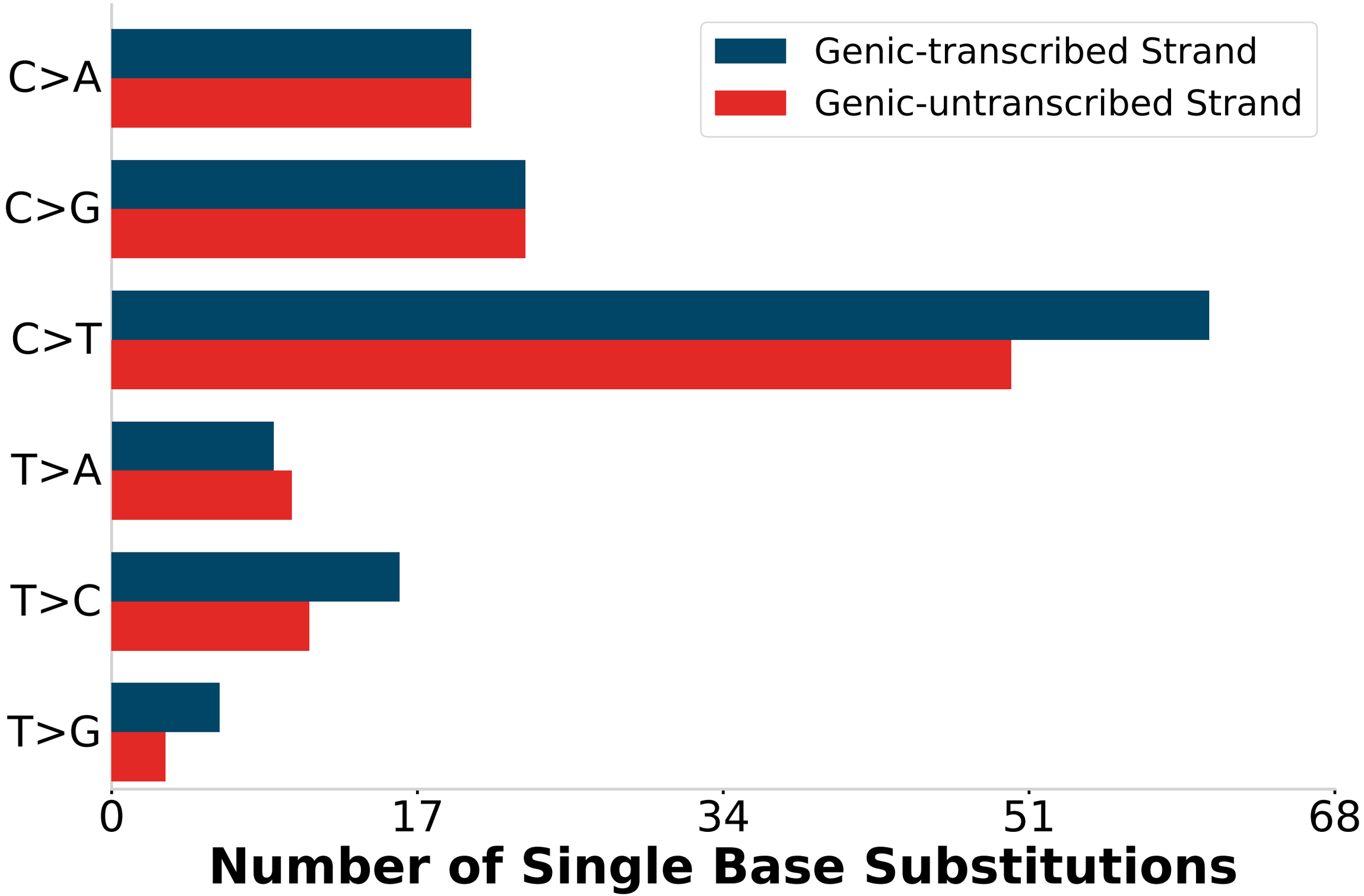
TCGA-DK-AA76-01A-11D-A391-08: 258 tra



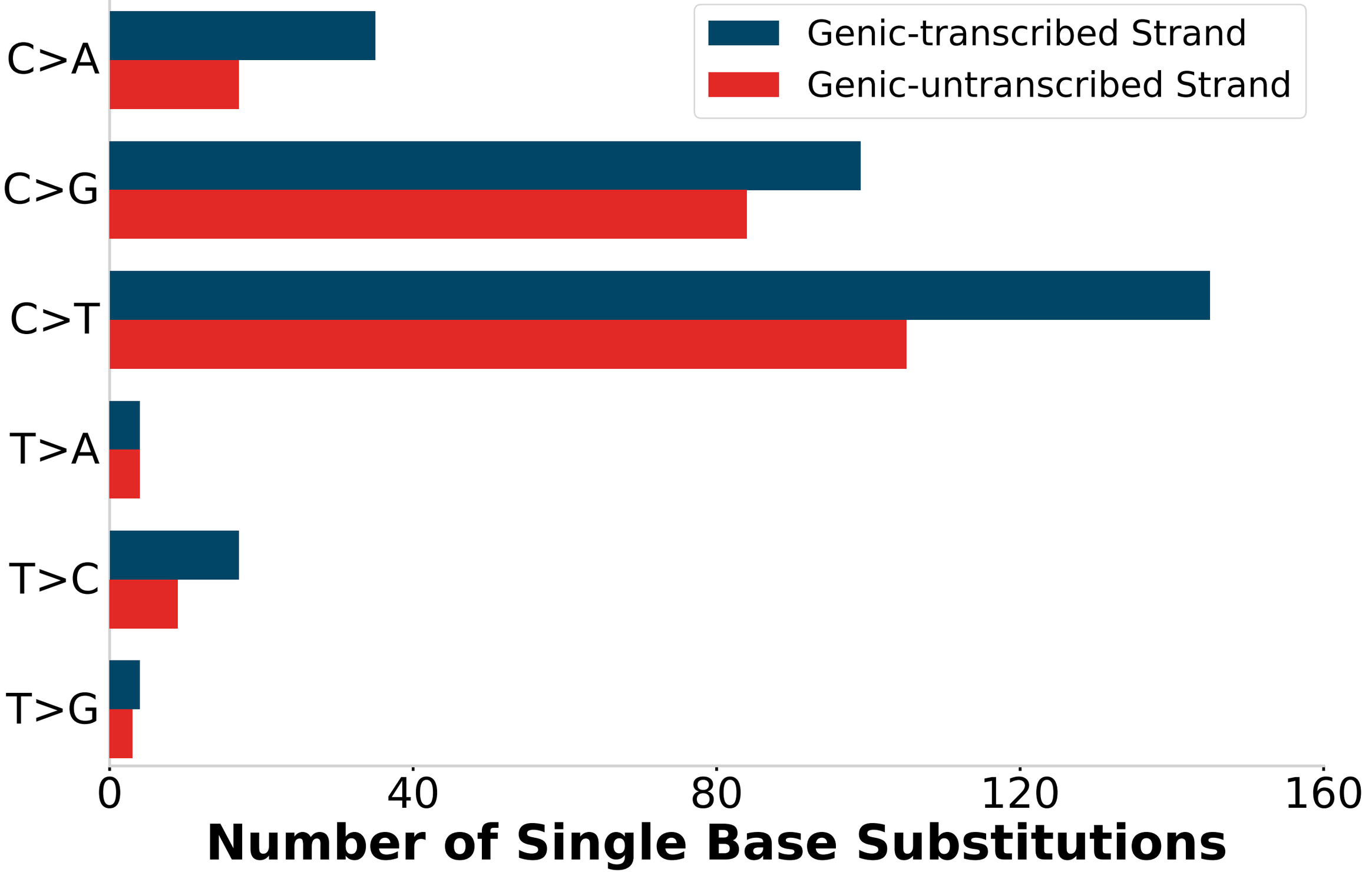
TCGA-DK-AA77-01A-11D-A391-08: 421 tra



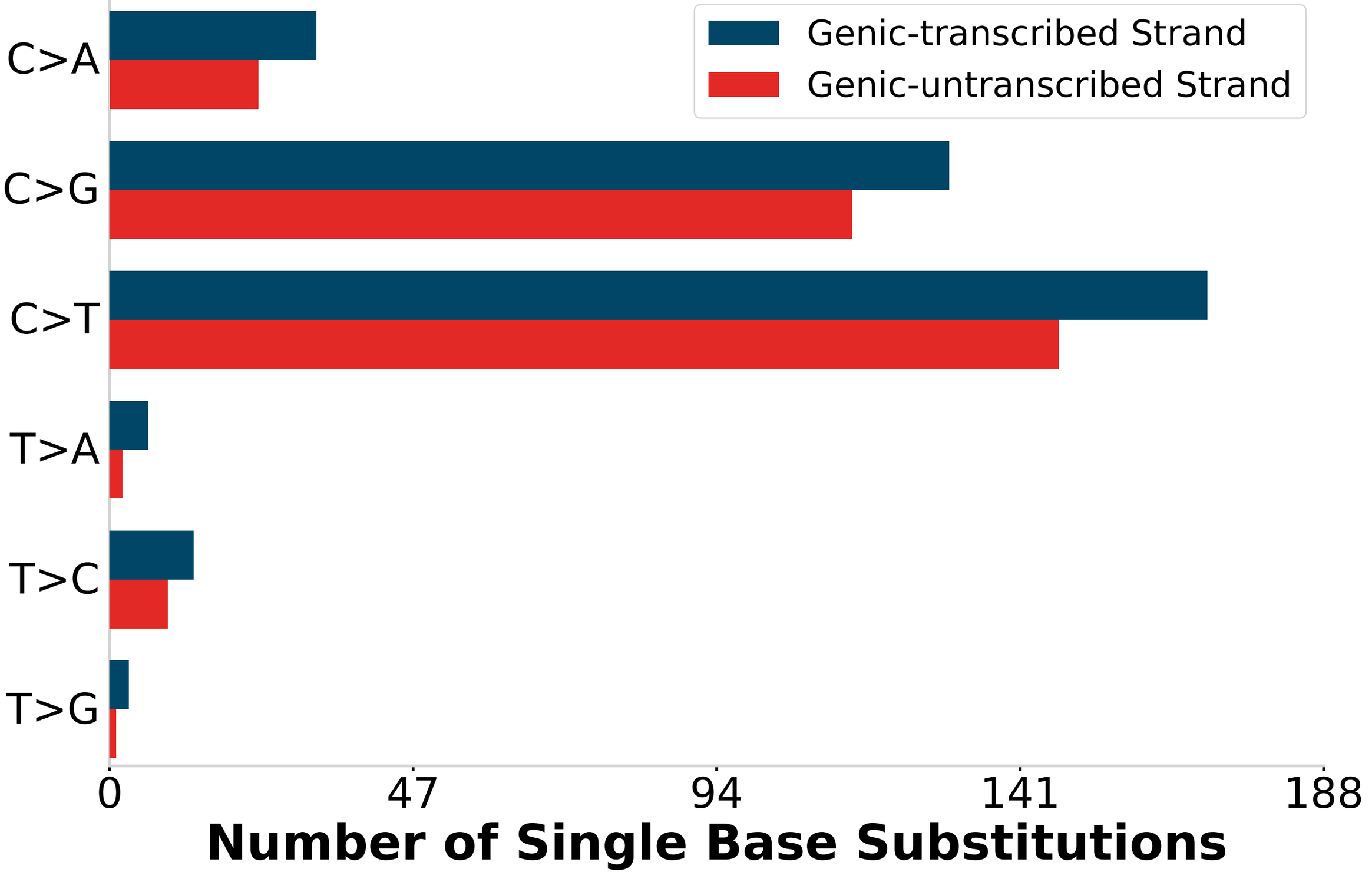
TCGA-E5-A2PC-01A-11D-A202-08: 252 tran



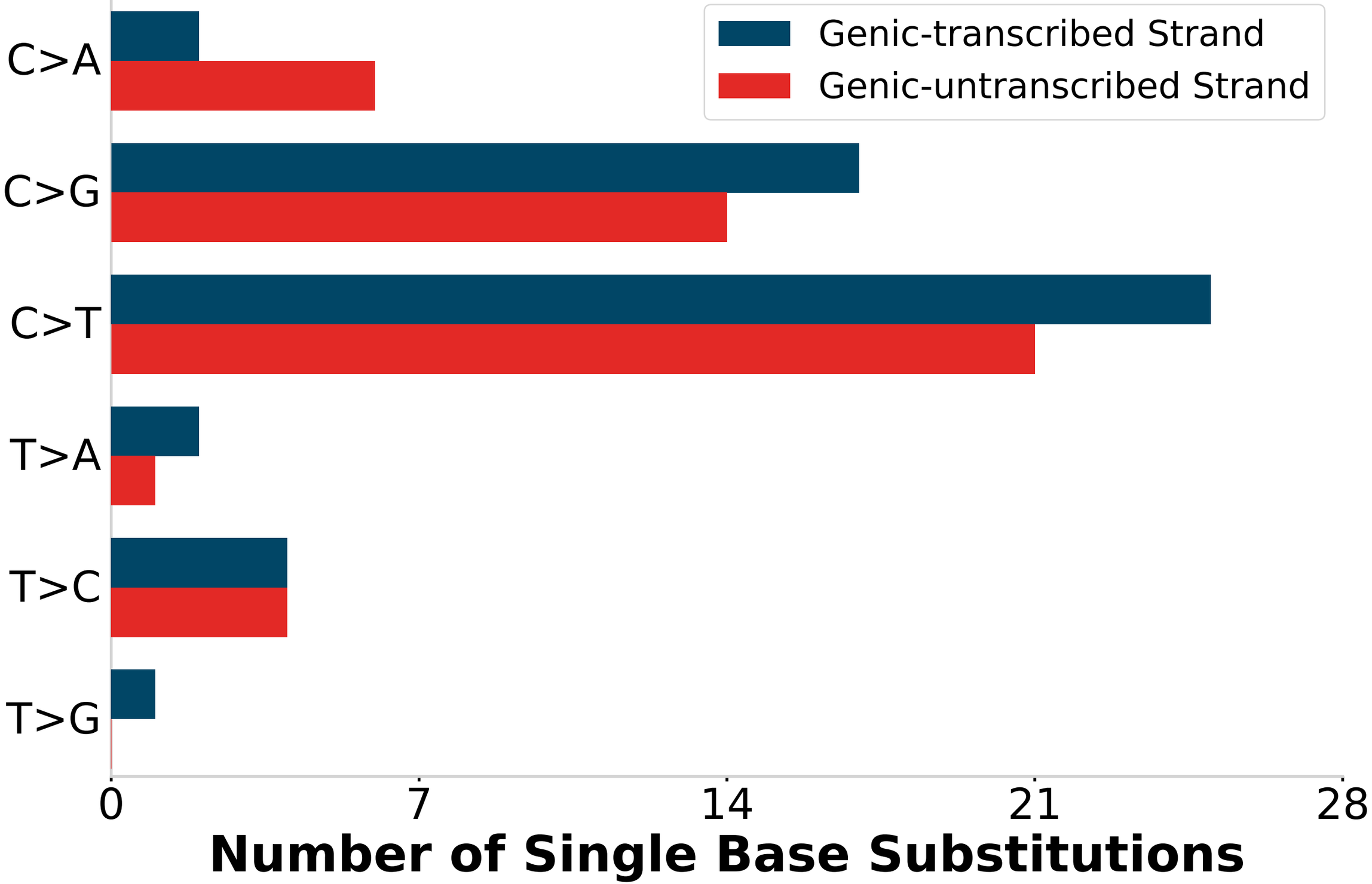
TCGA-E5-A4TZ-01A-11D-A31L-08: 526 tran



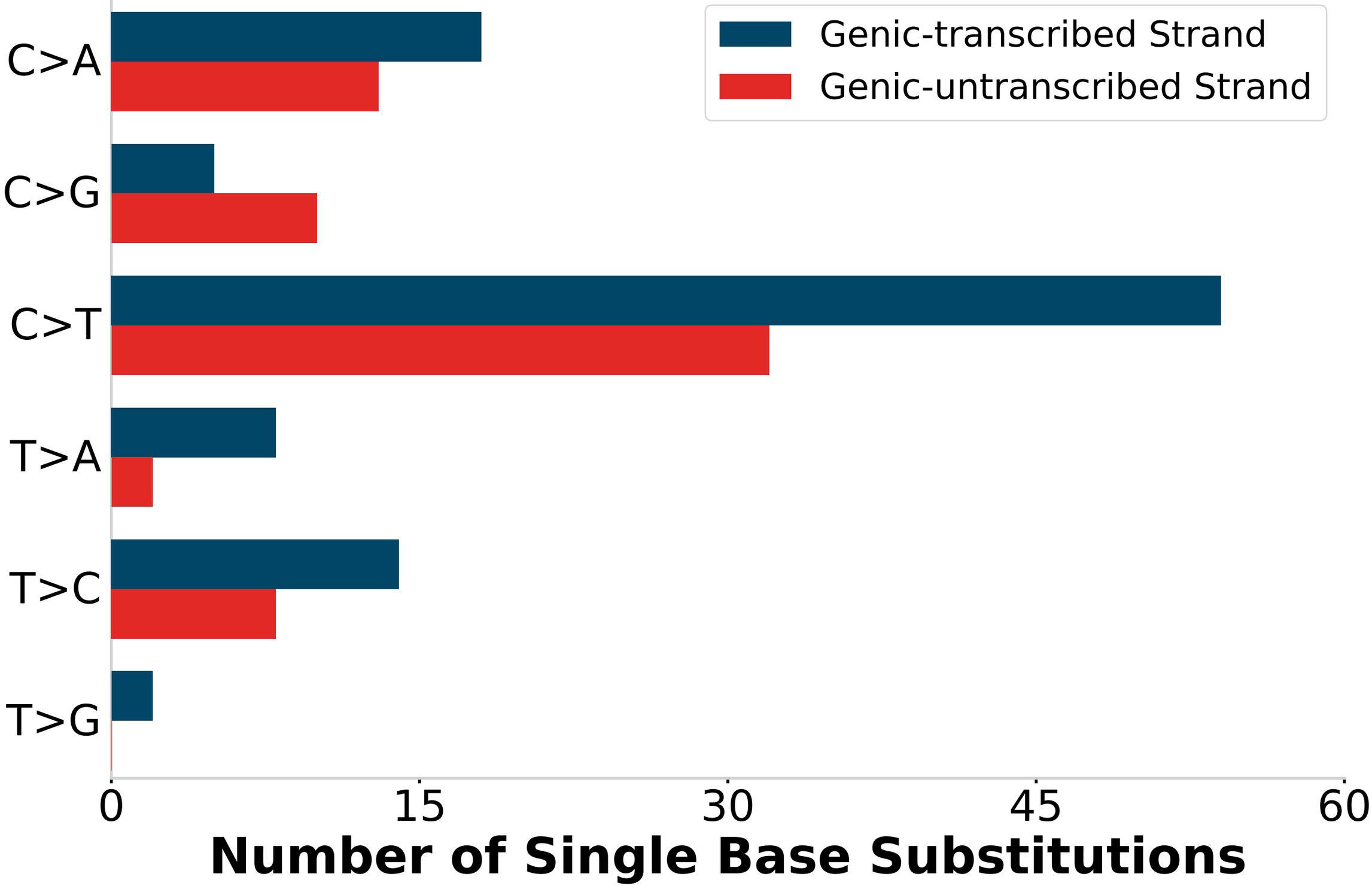
TCGA-E5-A4U1-01A-11D-A31L-08: 651 tran



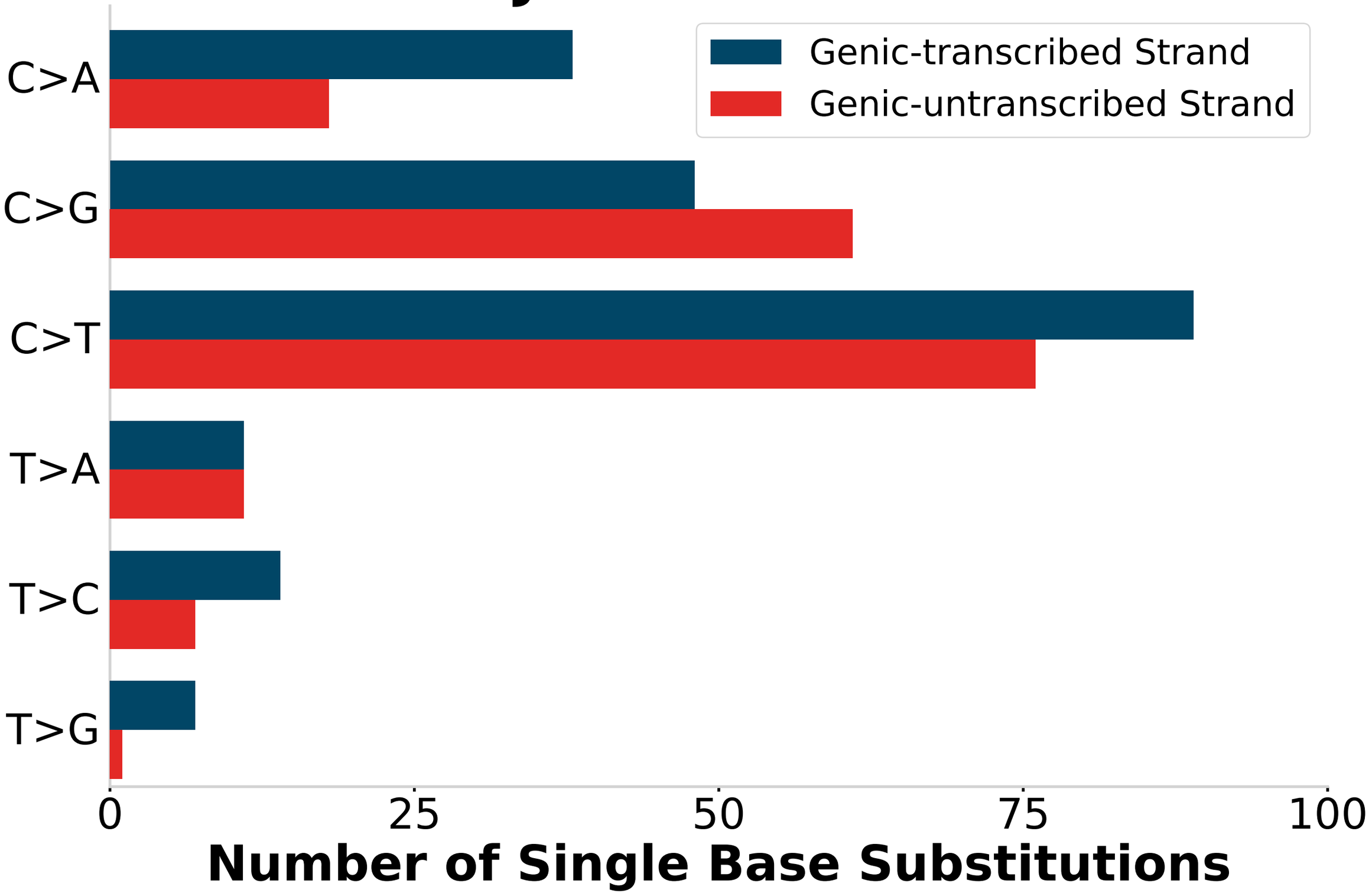
TCGA-E7-A3X6-01A-12D-A22Z-08: 97 trans



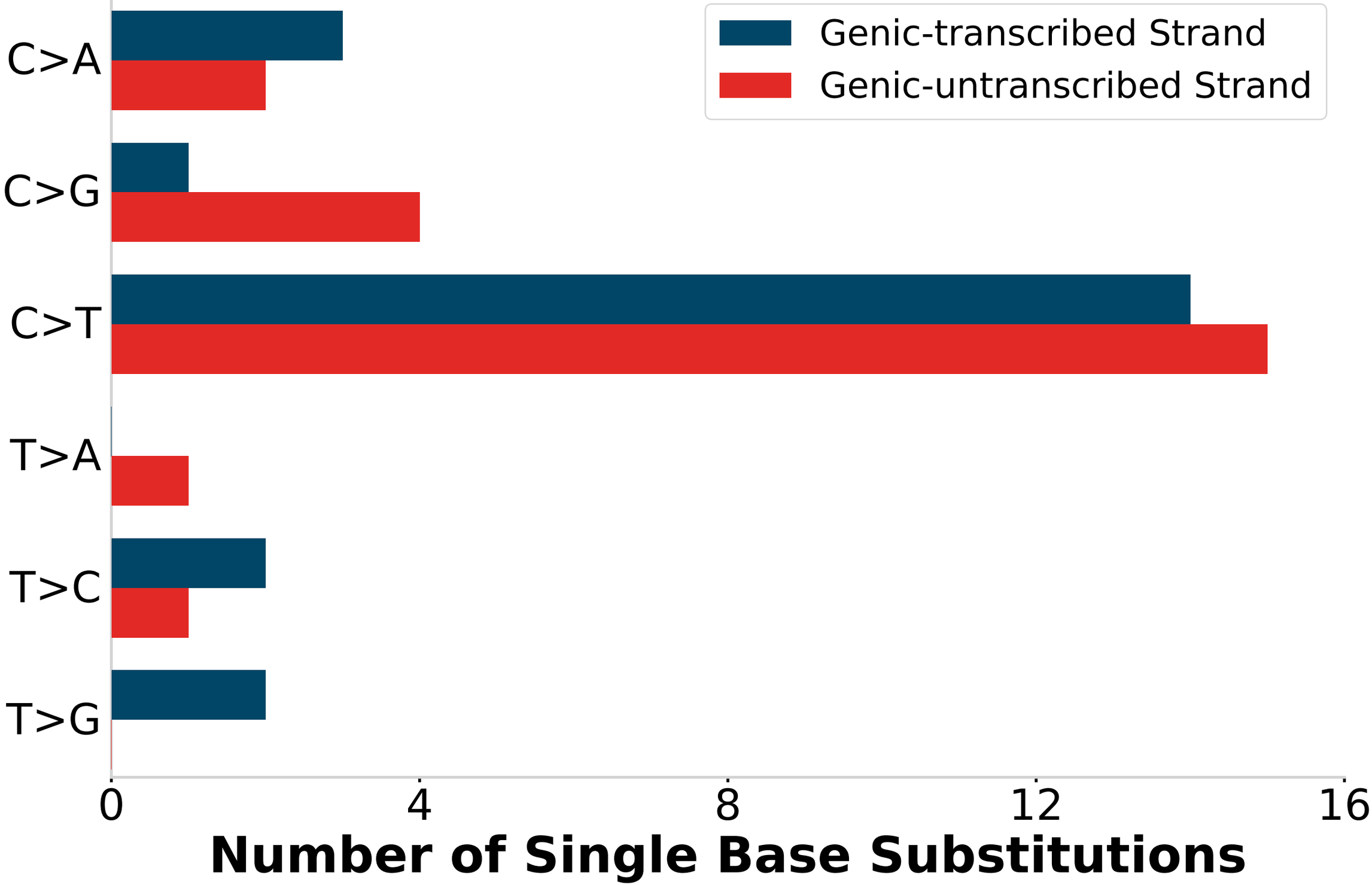
TCGA-E7-A3Y1-01A-11D-A22Z-08: 166 tran



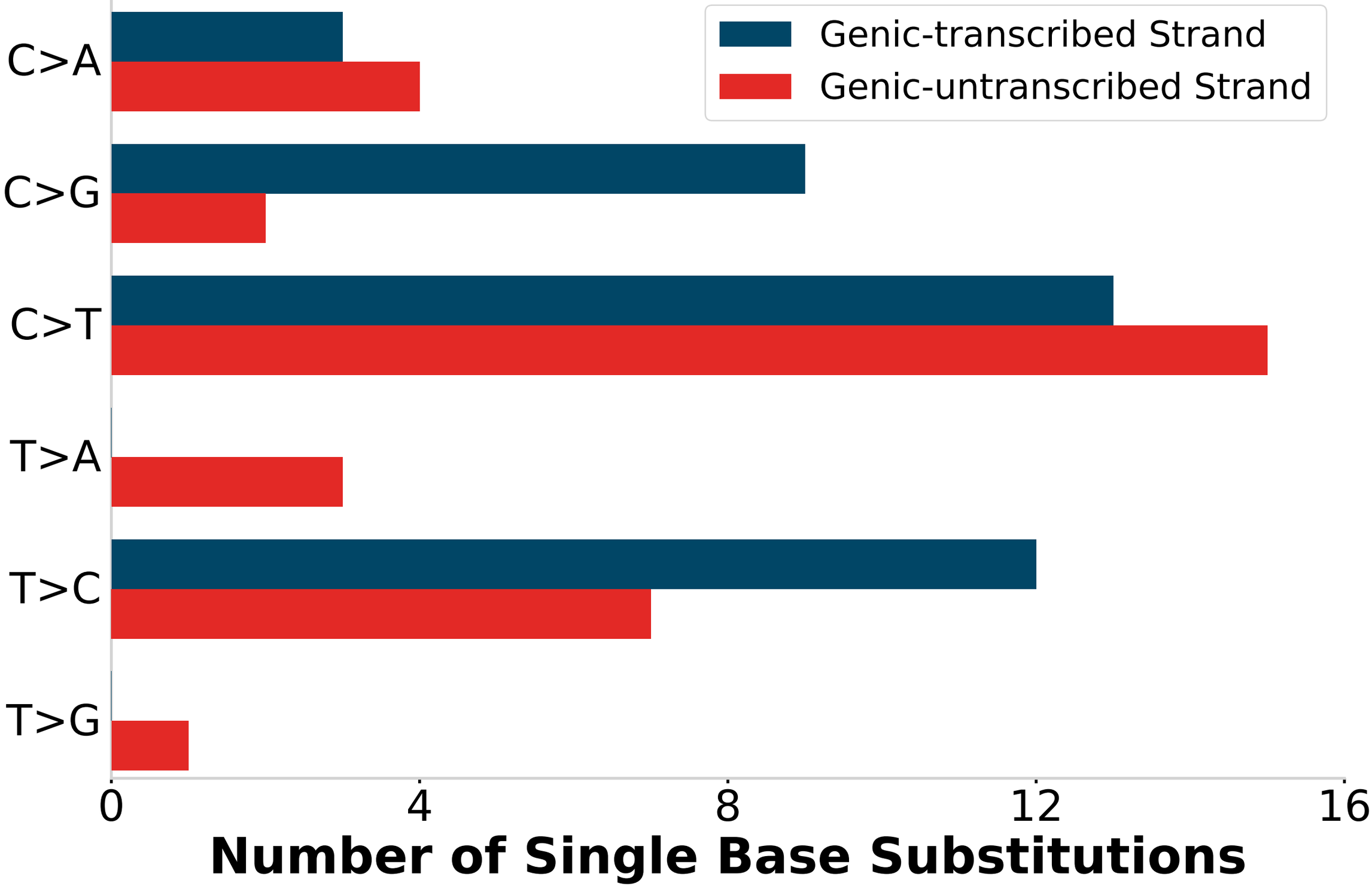
TCGA-E7-A4IJ-01A-31D-A26M-08: 381 tran



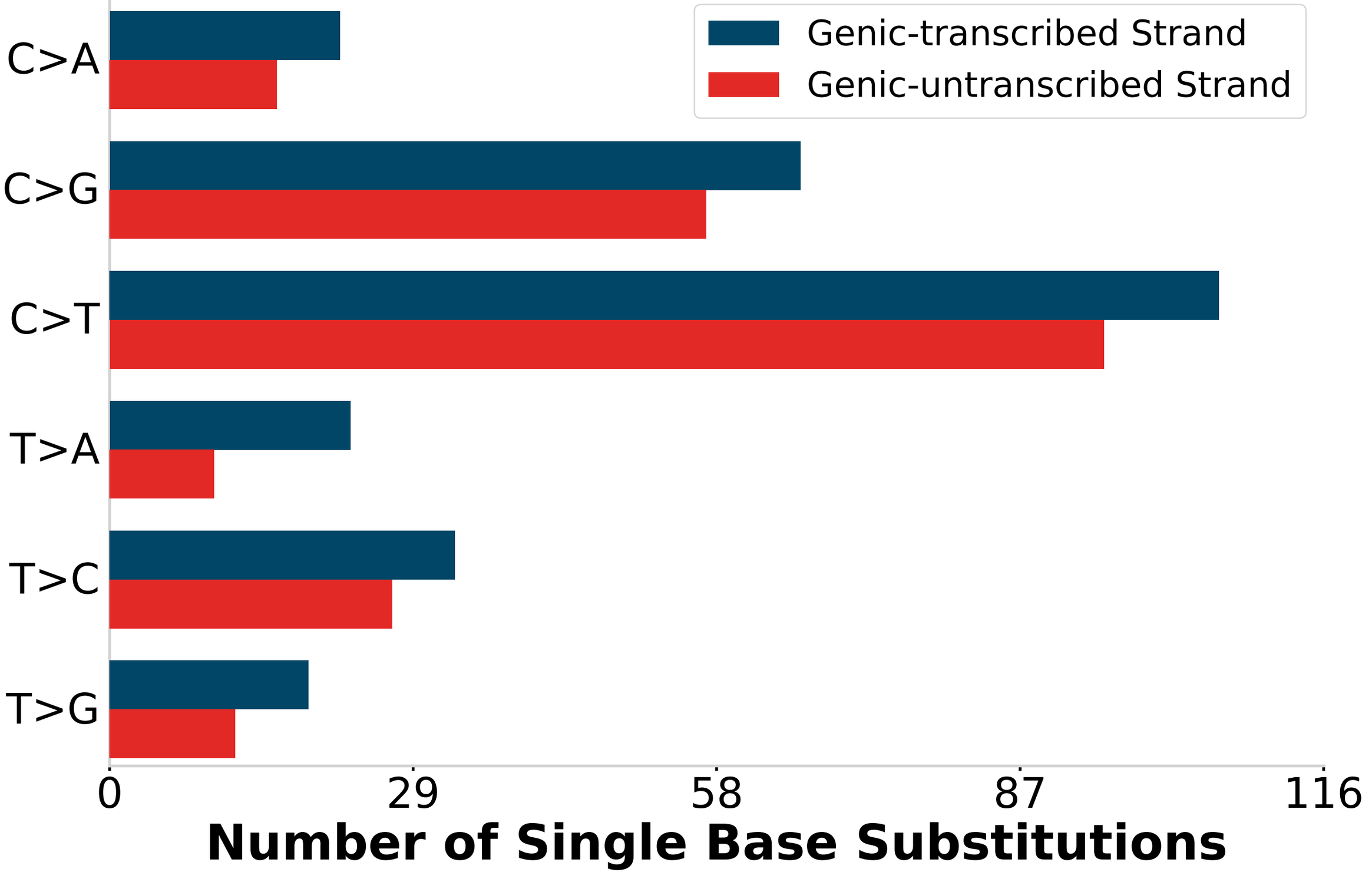
TCGA-E7-A4XJ-01A-11D-A26M-08: 45 trans



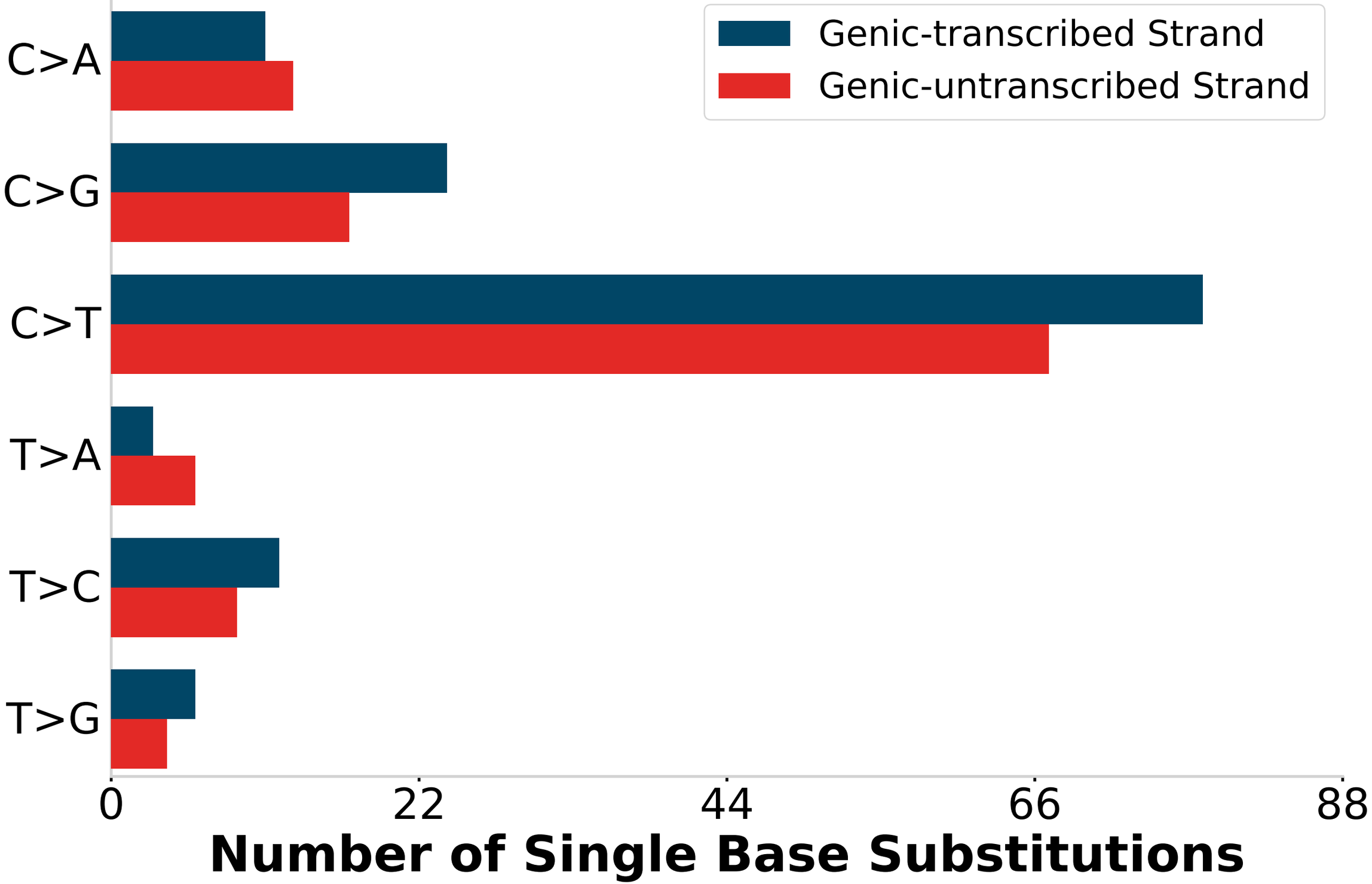
TCGA-E7-A519-01A-11D-A26M-08: 69 trans



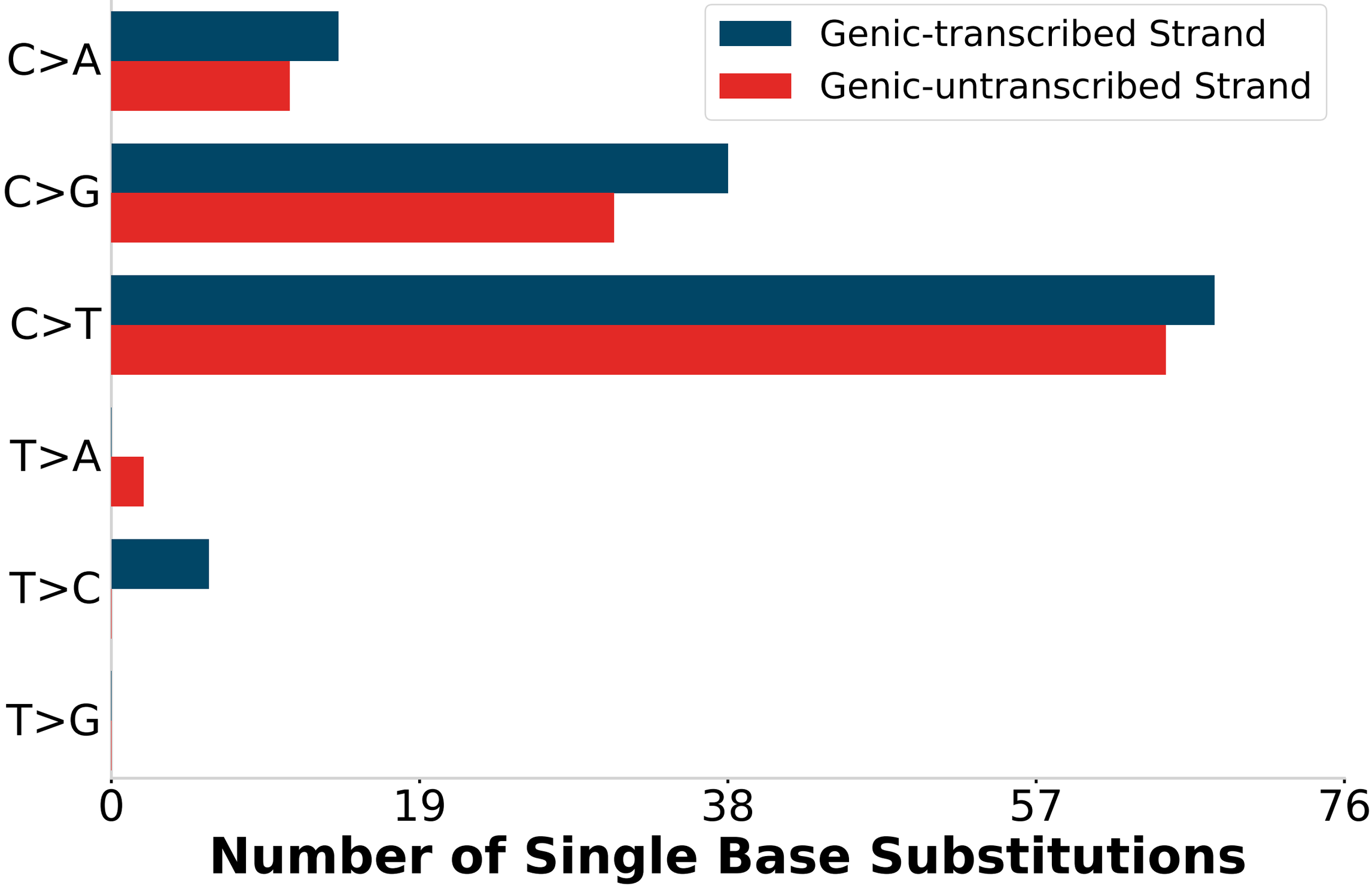
TCGA-E7-A541-01A-11D-A26M-08: 486 tra



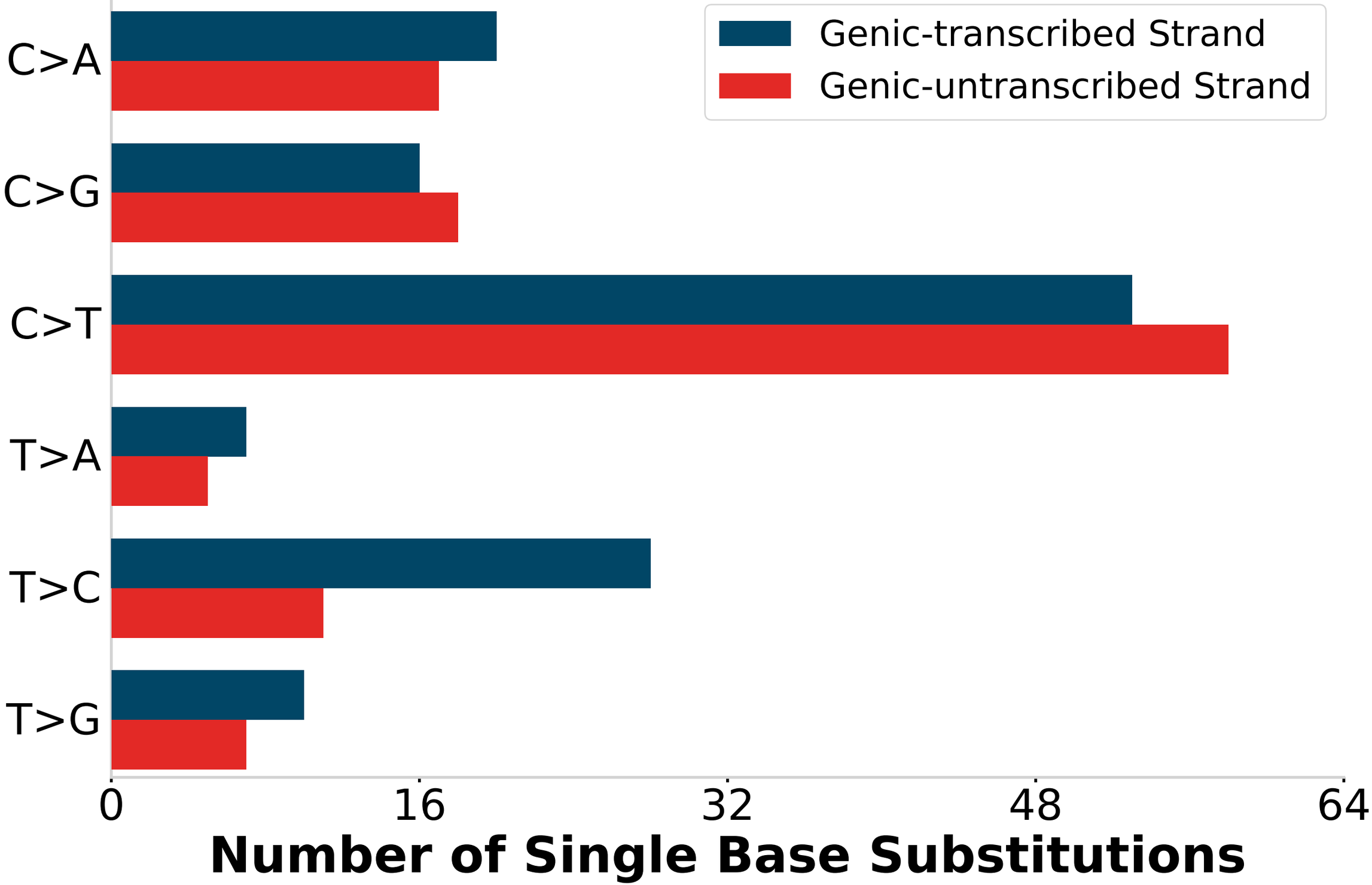
TCGA-E7-A5KE-01A-11D-A289-08: 250 tran



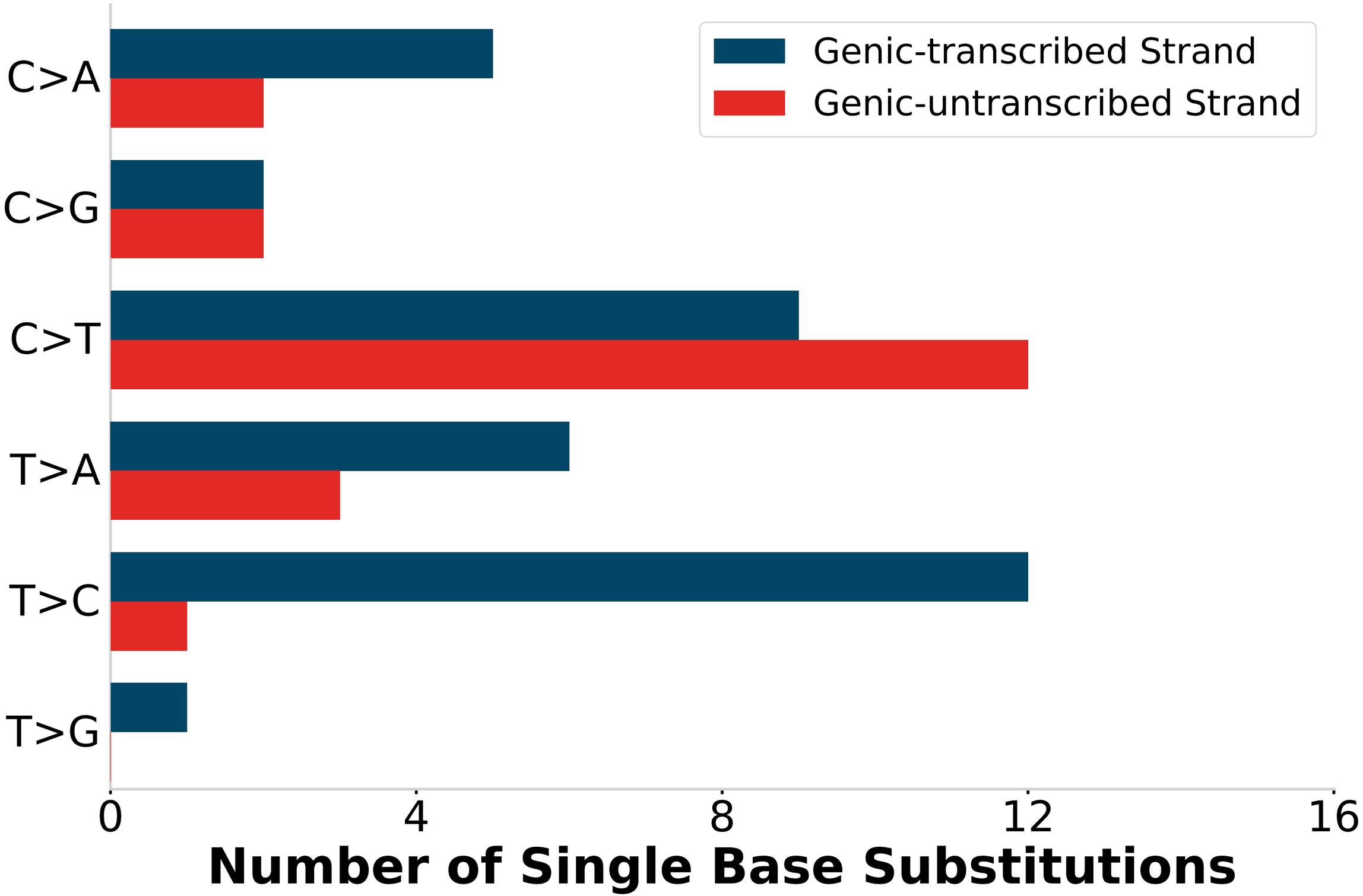
TCGA-E7-A5KF-01A-11D-A289-08: 235 tran



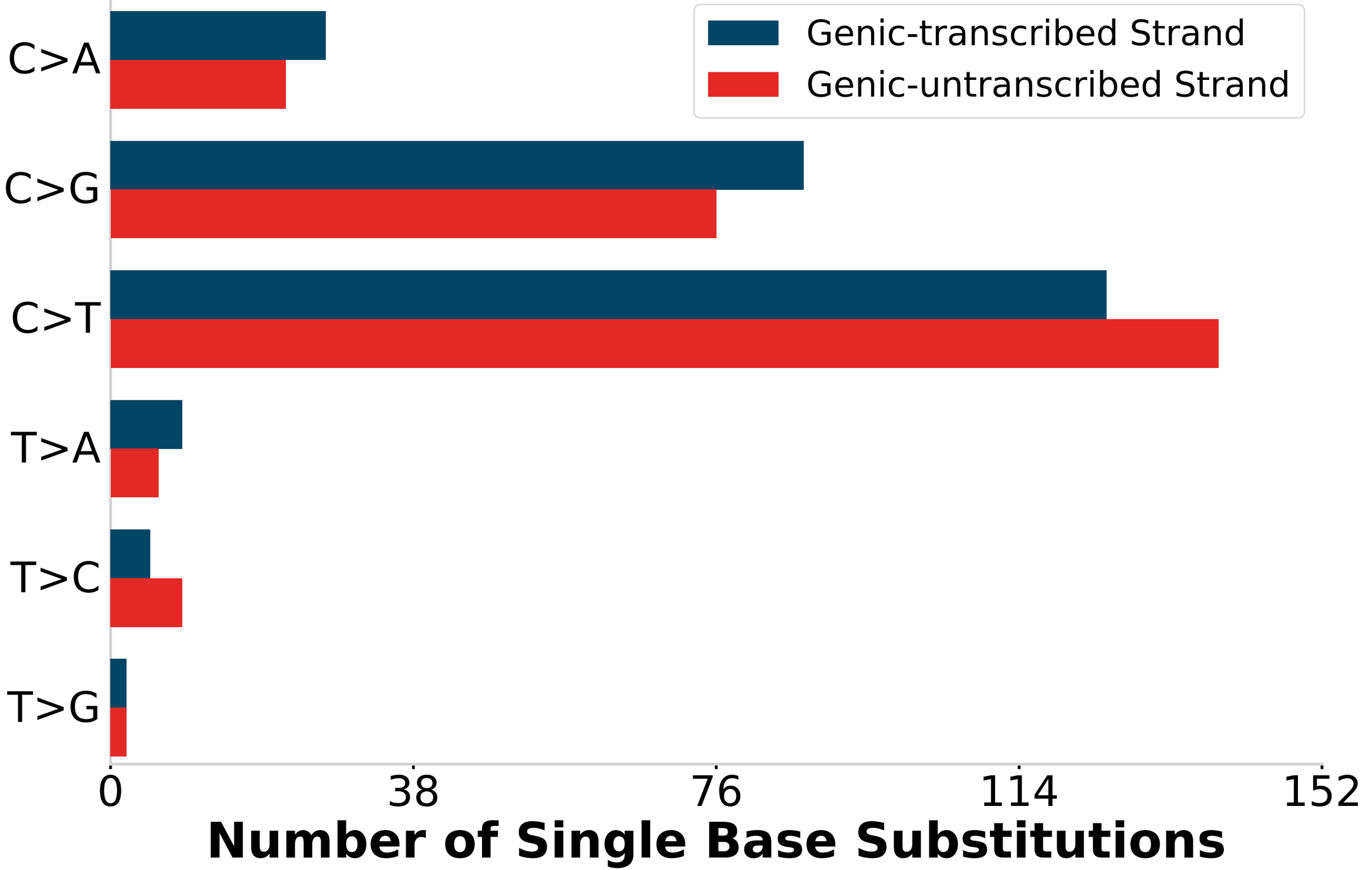
TCGA-E7-A677-01A-11D-A30E-08: 250 tran



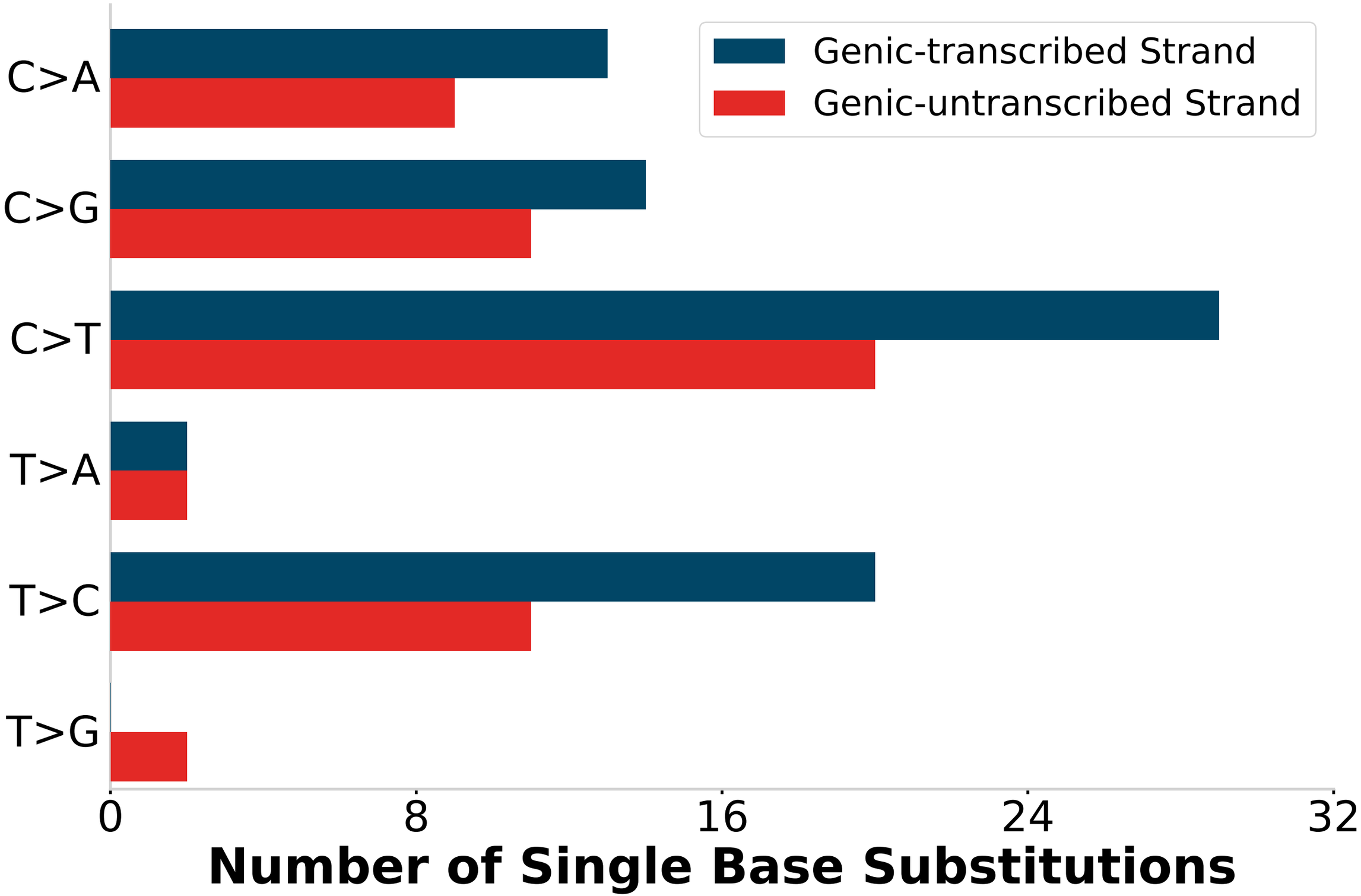
TCGA-E7-A678-01A-11D-A30E-08: 55 trans



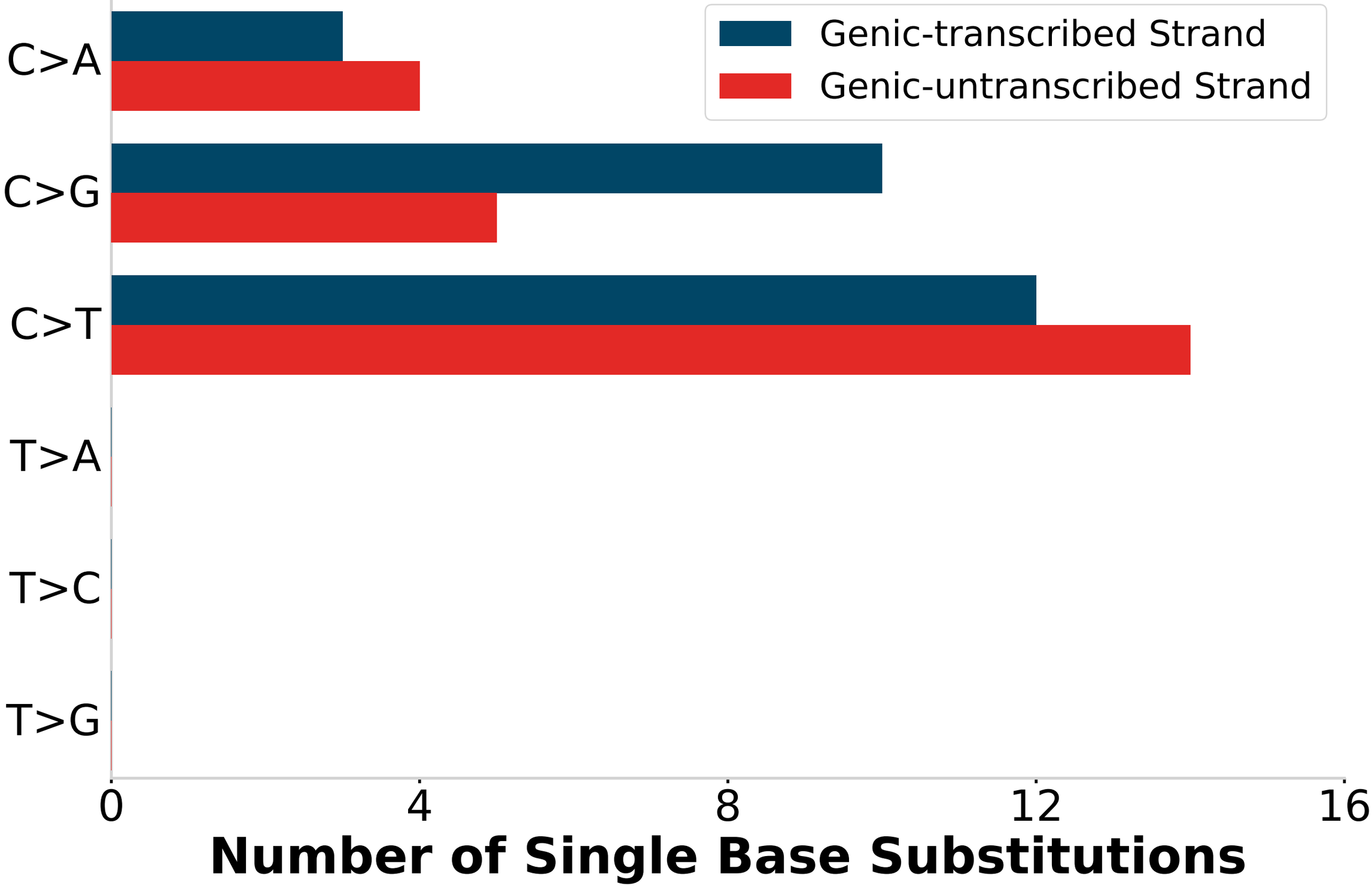
TCGA-E7-A6MD-01A-41D-A34U-08: 509 tra



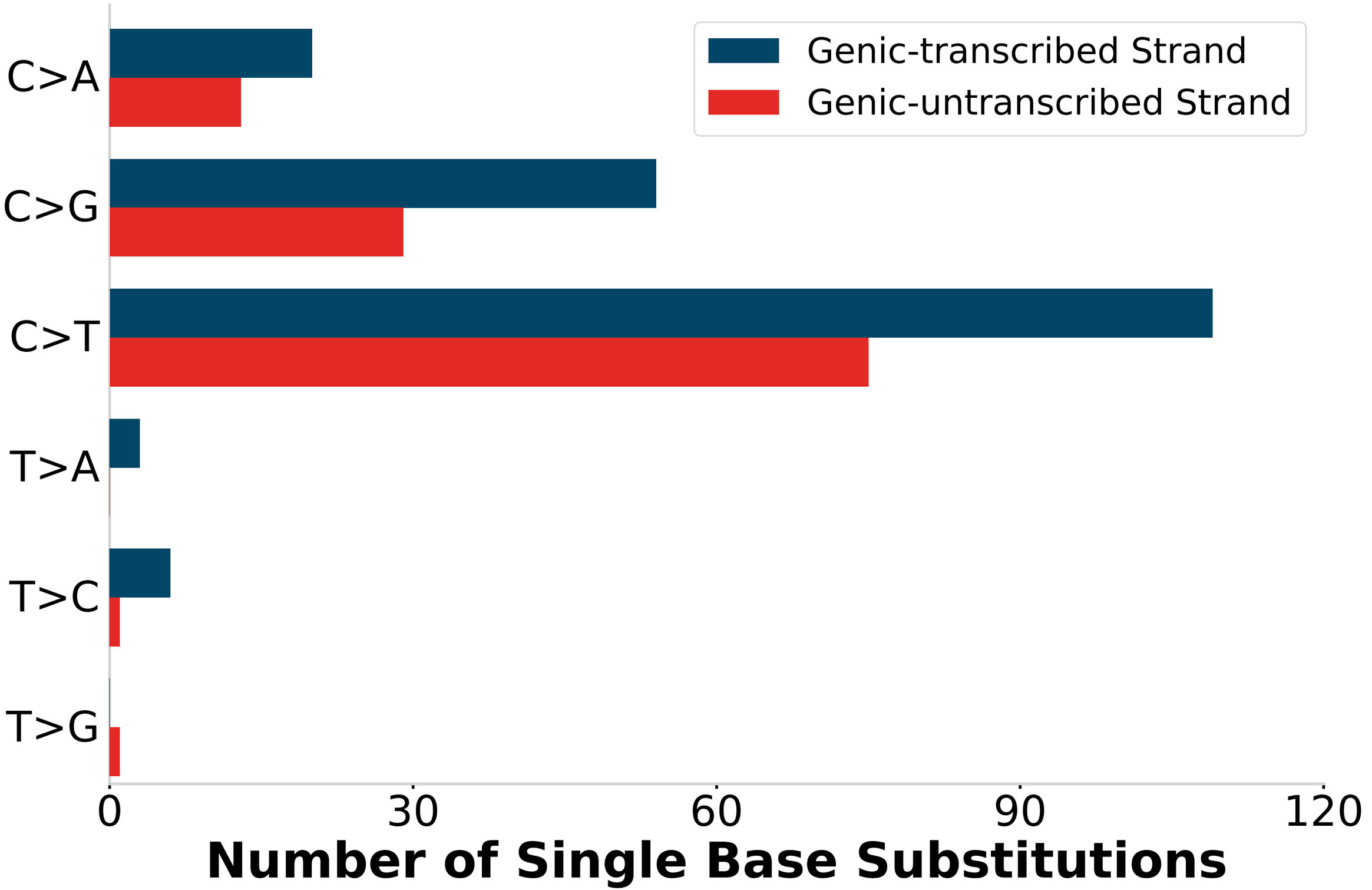
TCGA-E7-A6ME-01A-22D-A32B-08: 133 tra



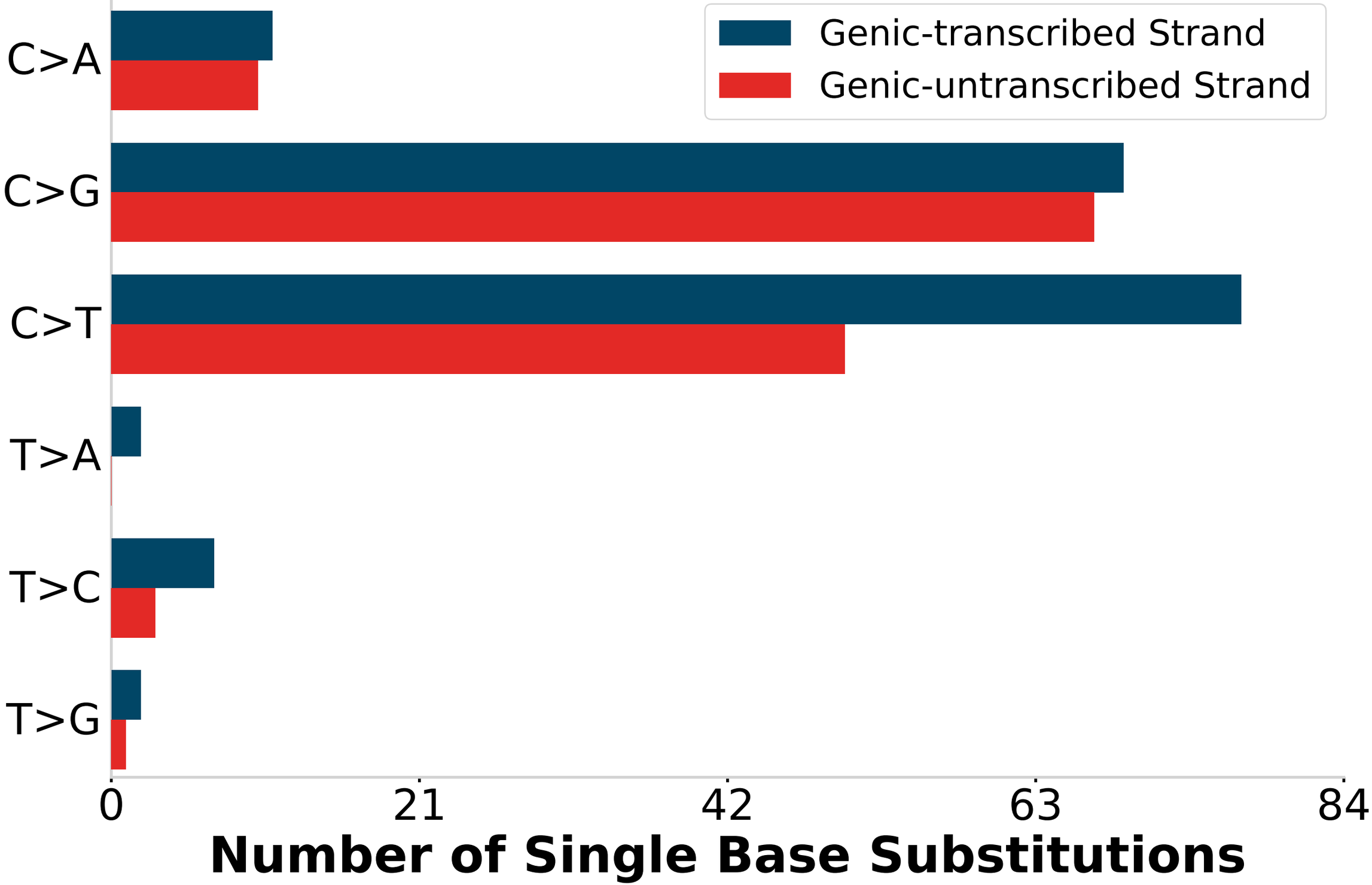
TCGA-E7-A6MF-01A-12D-A32B-08: 48 tran



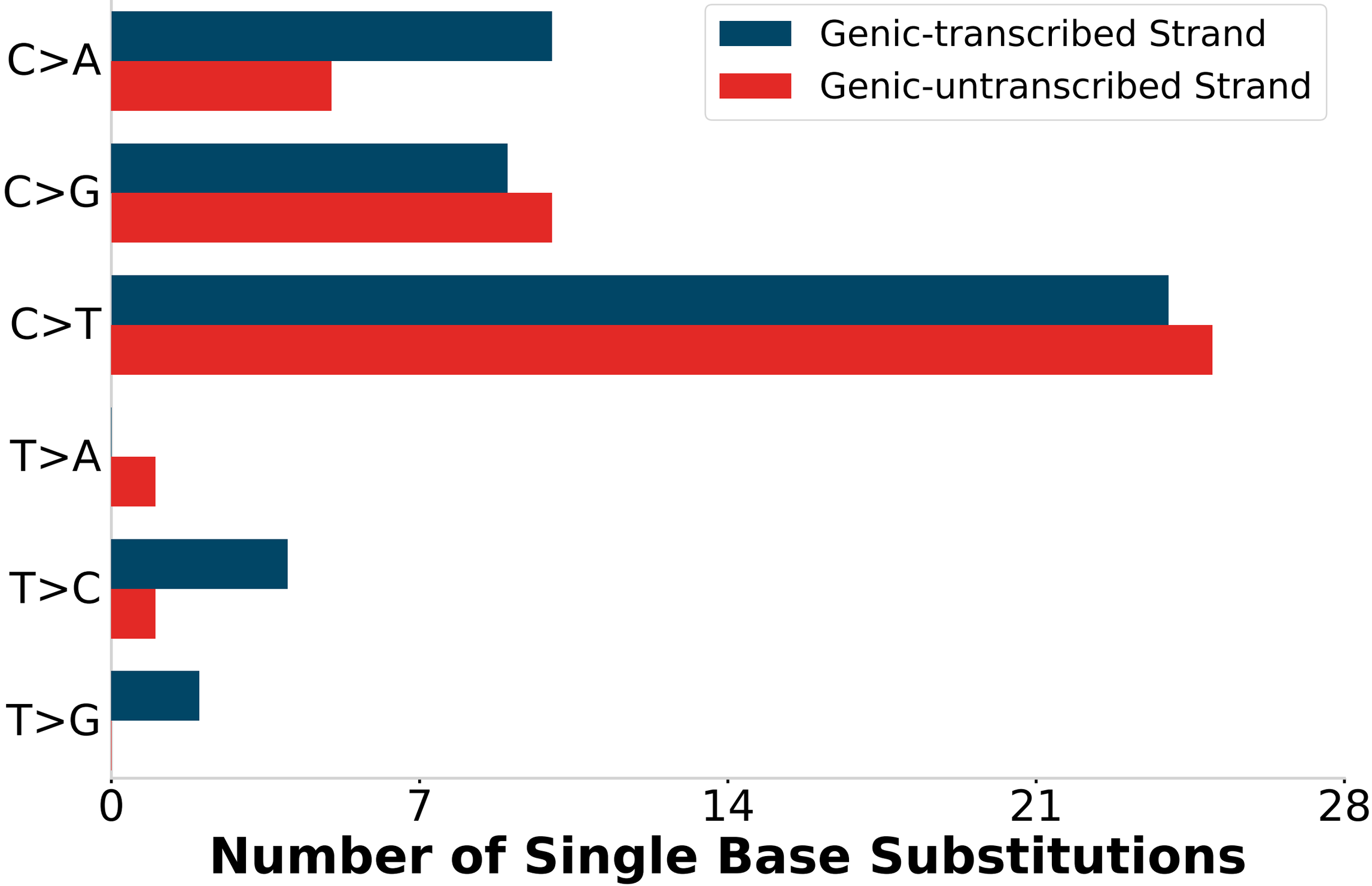
TCGA-E7-A7DU-01A-11D-A32B-08: 311 tra



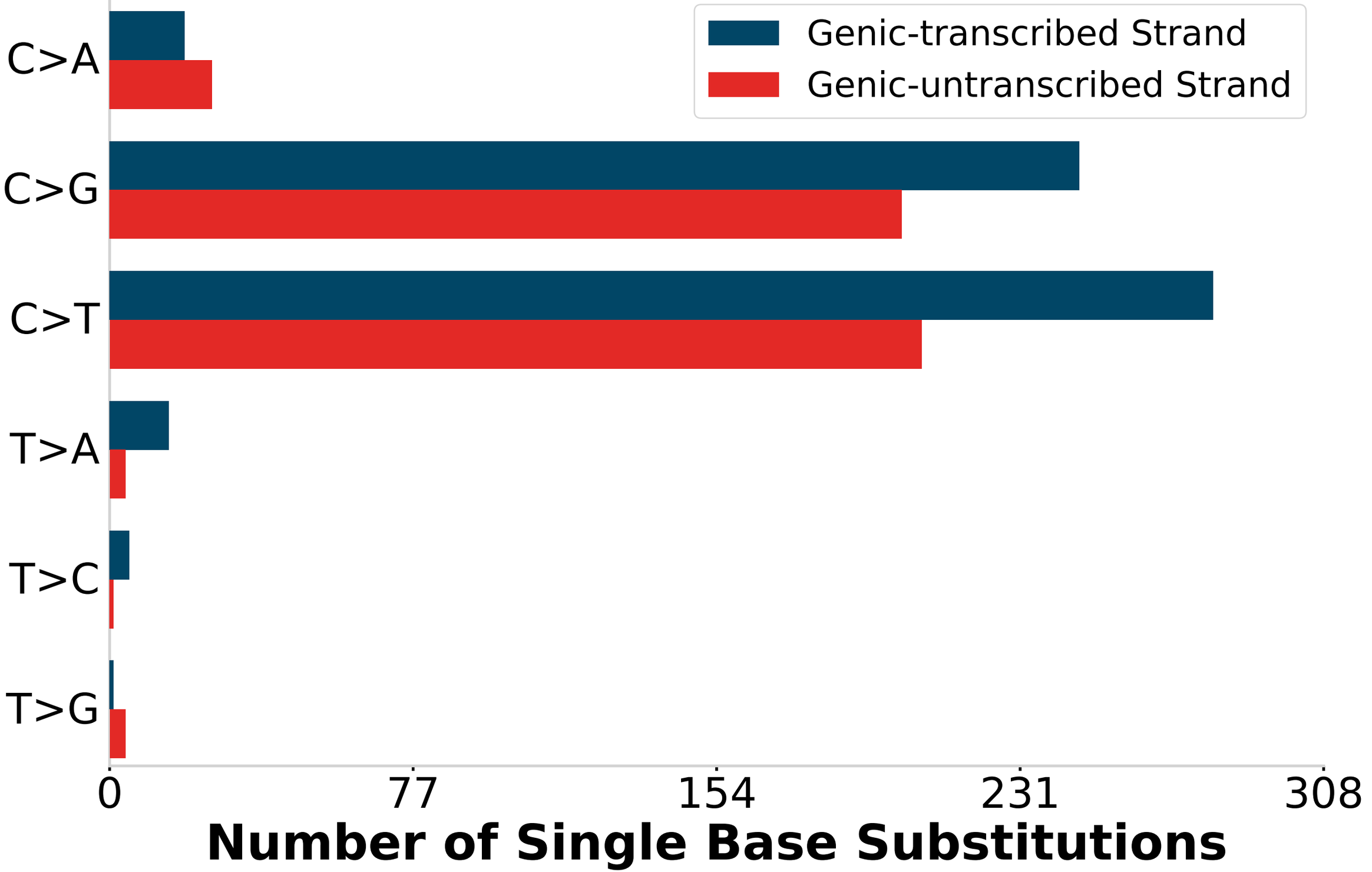
TCGA-E7-A7DV-01A-11D-A339-08: 299 tra



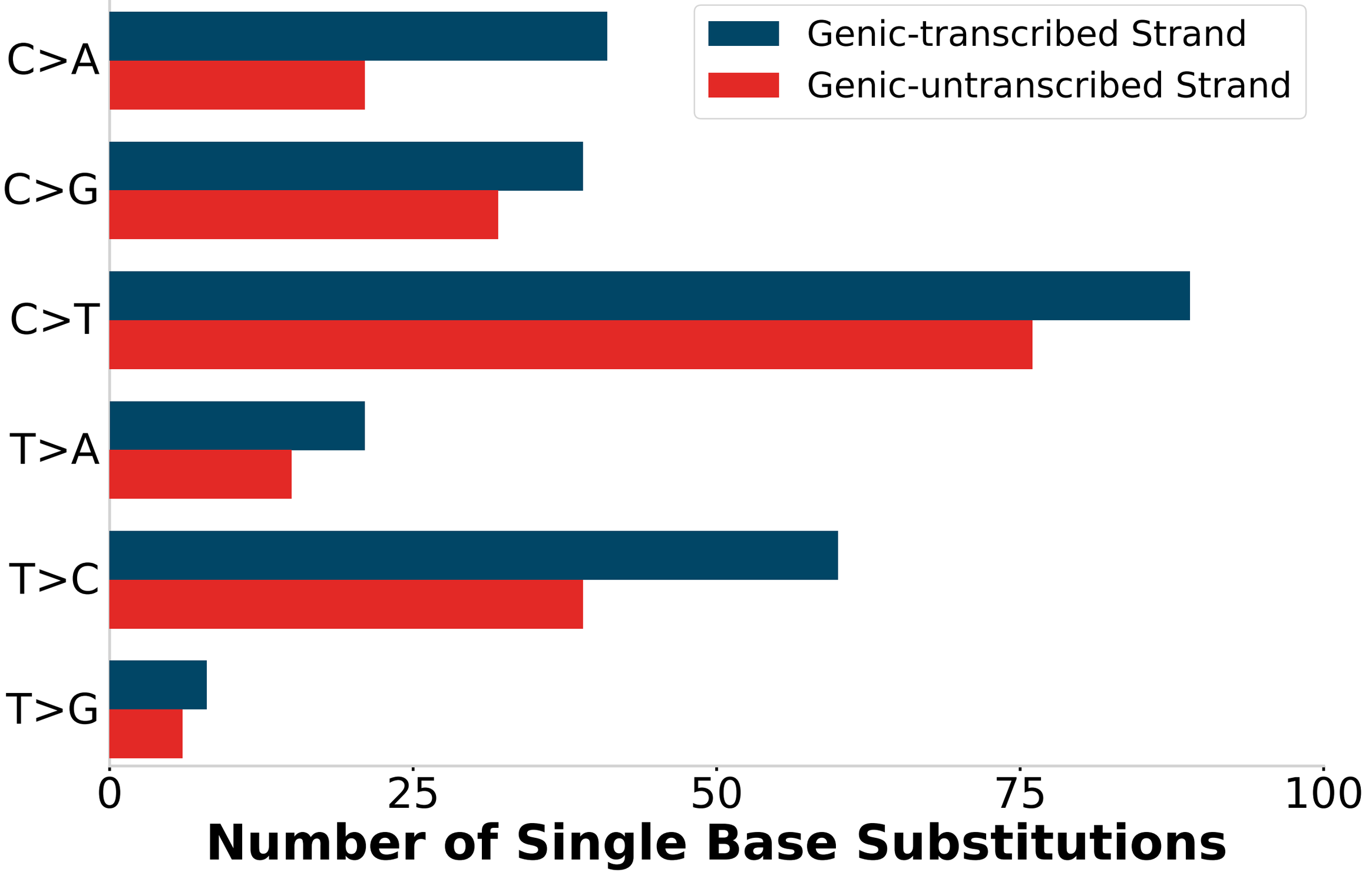
TCGA-E7-A7PW-01A-11D-A34U-08: 91 tran



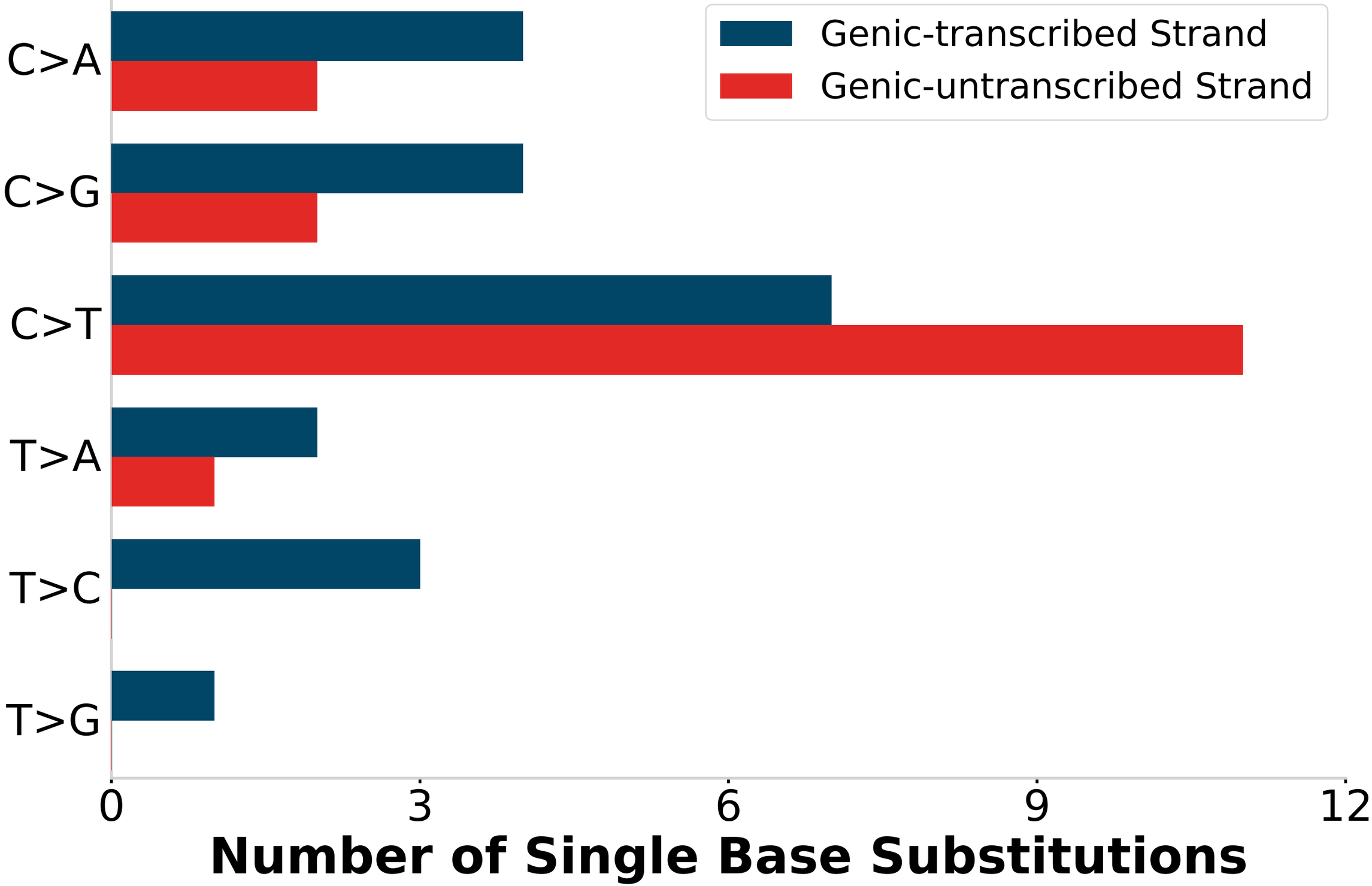
TCGA-E7-A7XN-01A-11D-A34U-08: 1,008 t



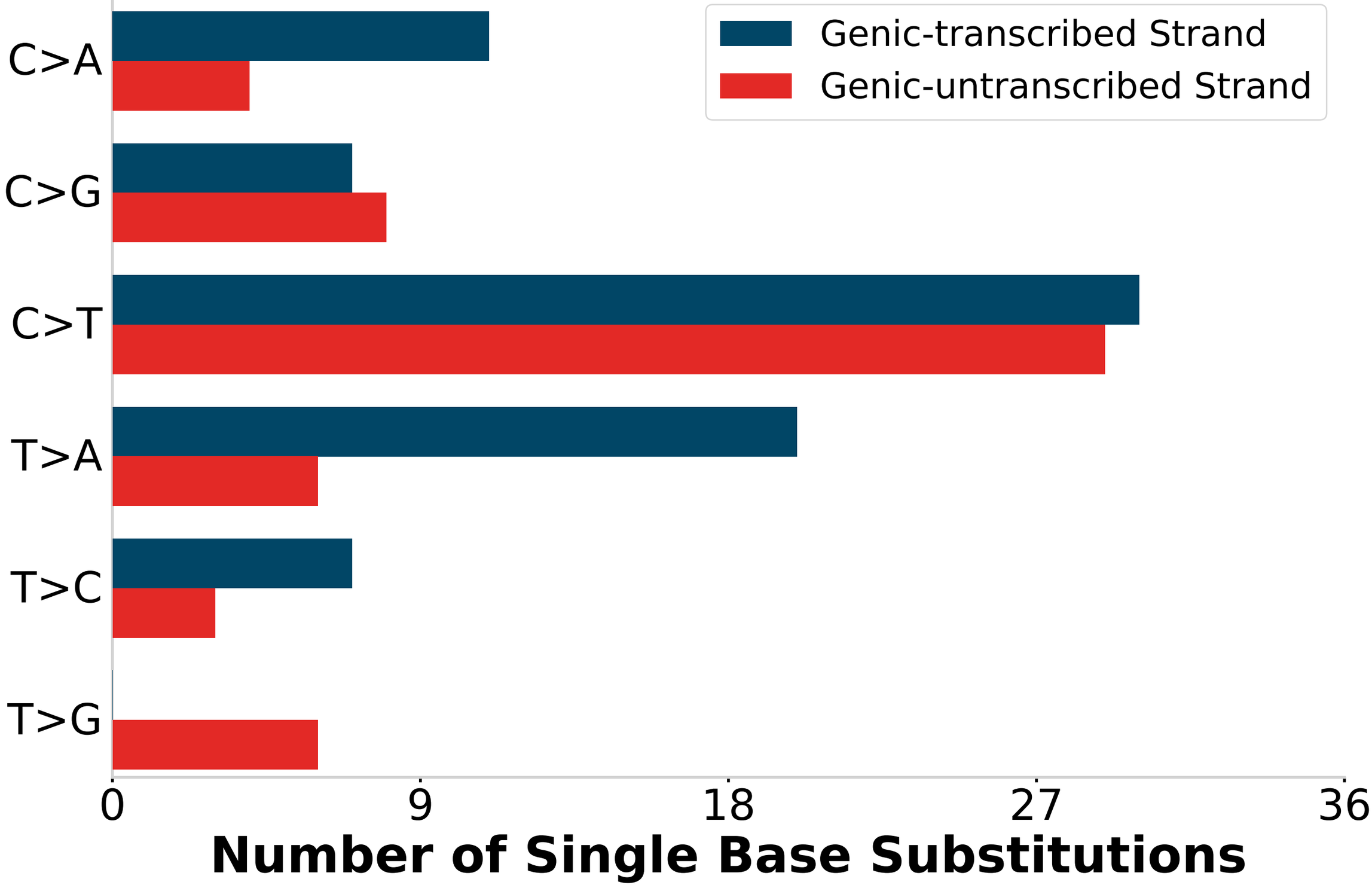
TCGA-E7-A85H-01A-11D-A34U-08: 447 tra



TCGA-E7-A8O7-01A-11D-A364-08: 37 trans



TCGA-E7-A8O8-01A-11D-A364-08: 131 tra



TCGA-E7-A97P-01A-11D-A38G-08: 214 tran

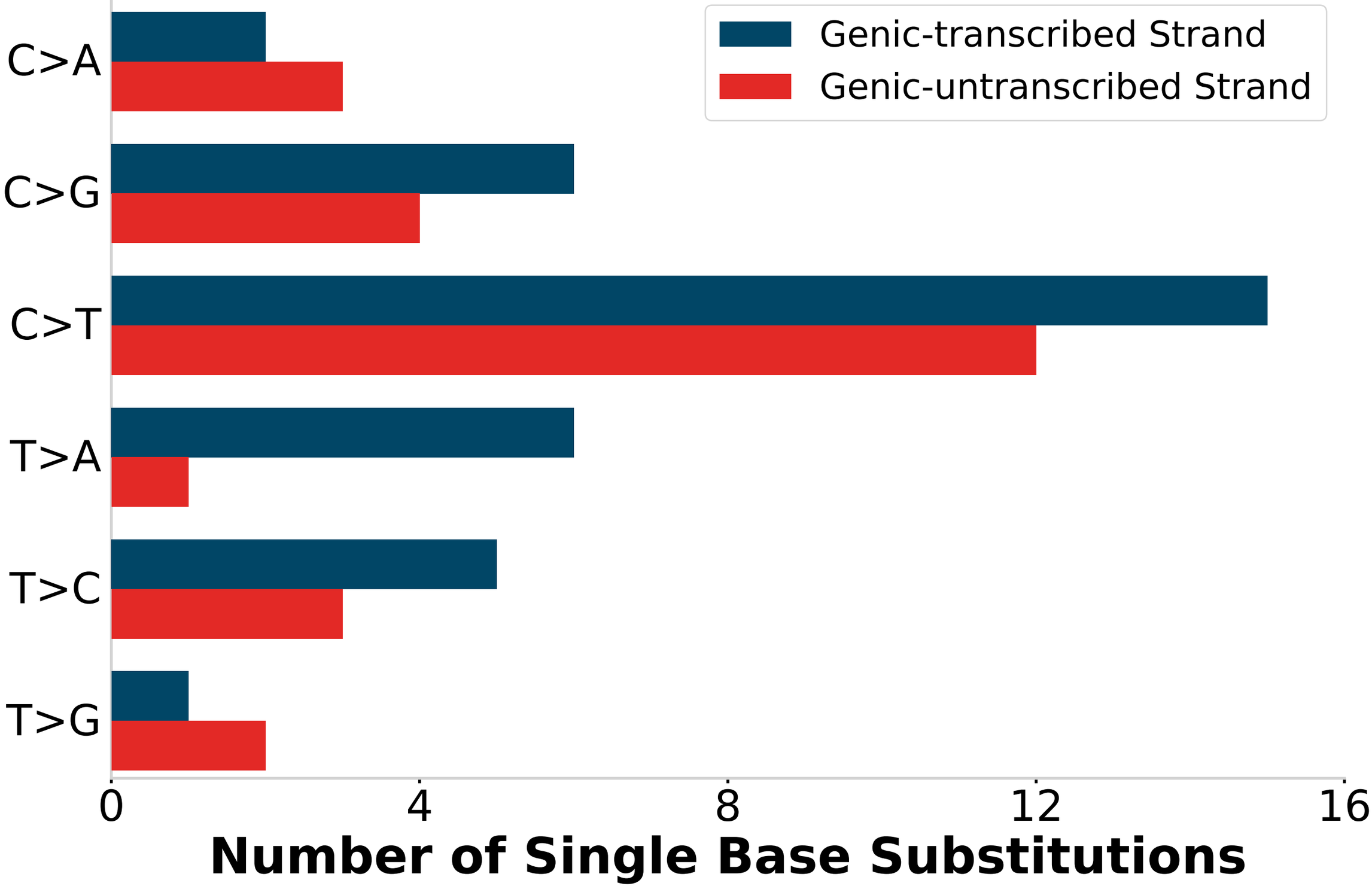
C>A
C>G
C>T
T>A
T>C
T>G

Genic-transcribed Strand
Genic-untranscribed Strand

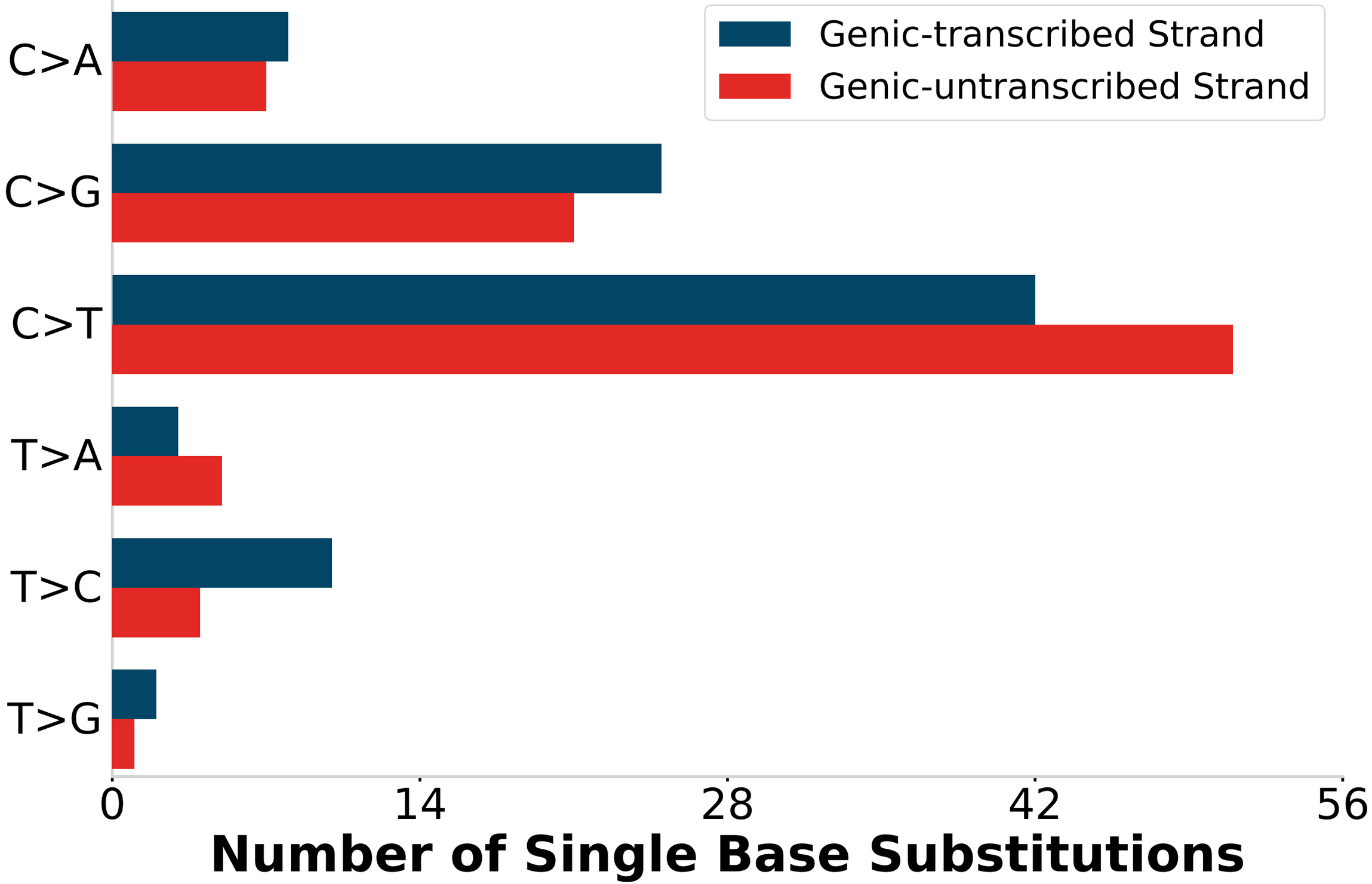
0
13
26
39
52

Number of Single Base Substitutions

TCGA-E7-A97Q-01A-11D-A38G-08: 60 trans



TCGA-FD-A3B3-01A-12D-A202-08: 179 tra



TCGA-FD-A3B4-01A-12D-A202-08: 77 trans

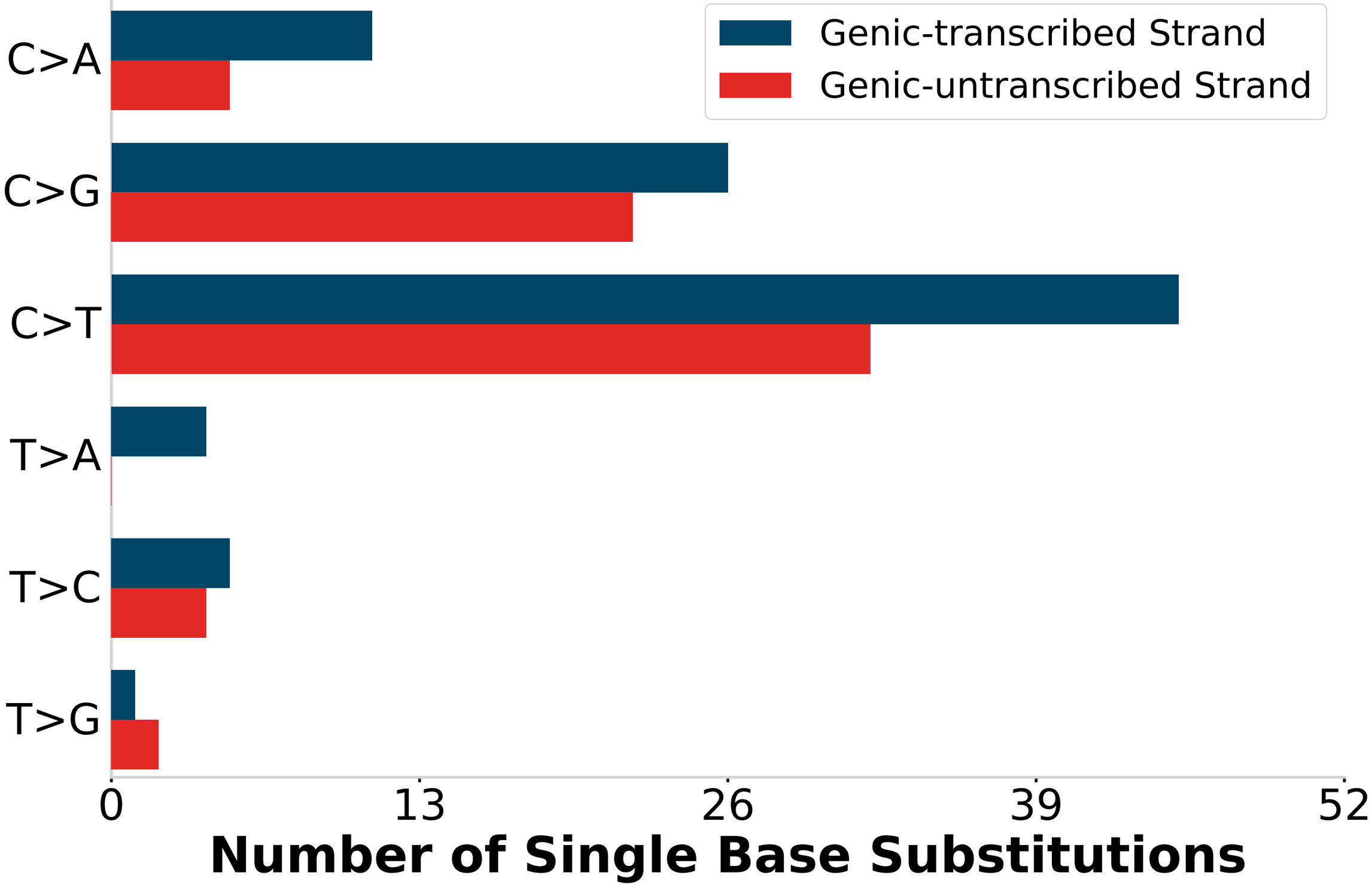
C>A
C>G
C>T
T>A
T>C
T>G

0
5
10
15
20

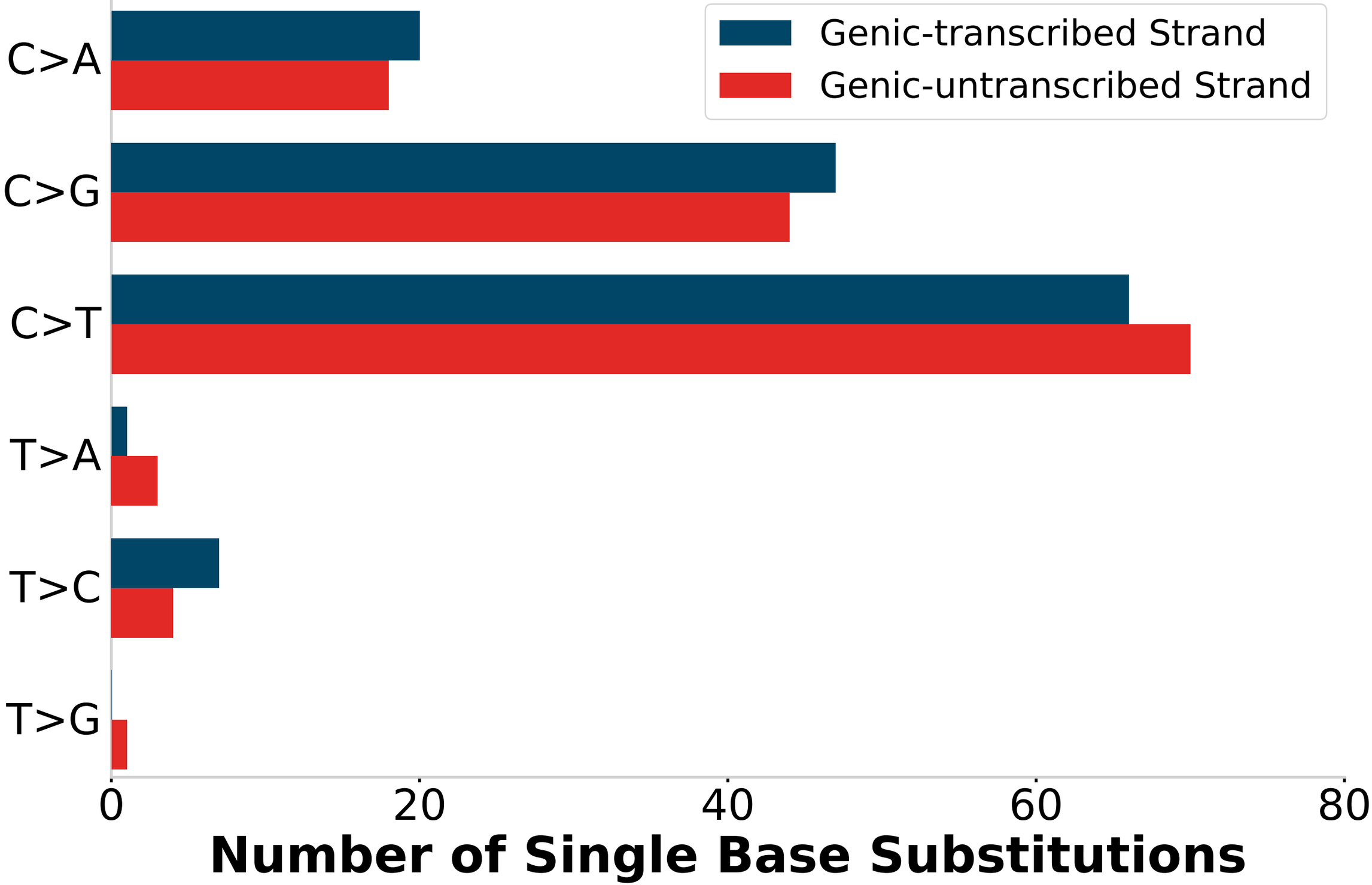
Genic-transcribed Strand
Genic-untranscribed Strand

Number of Single Base Substitutions

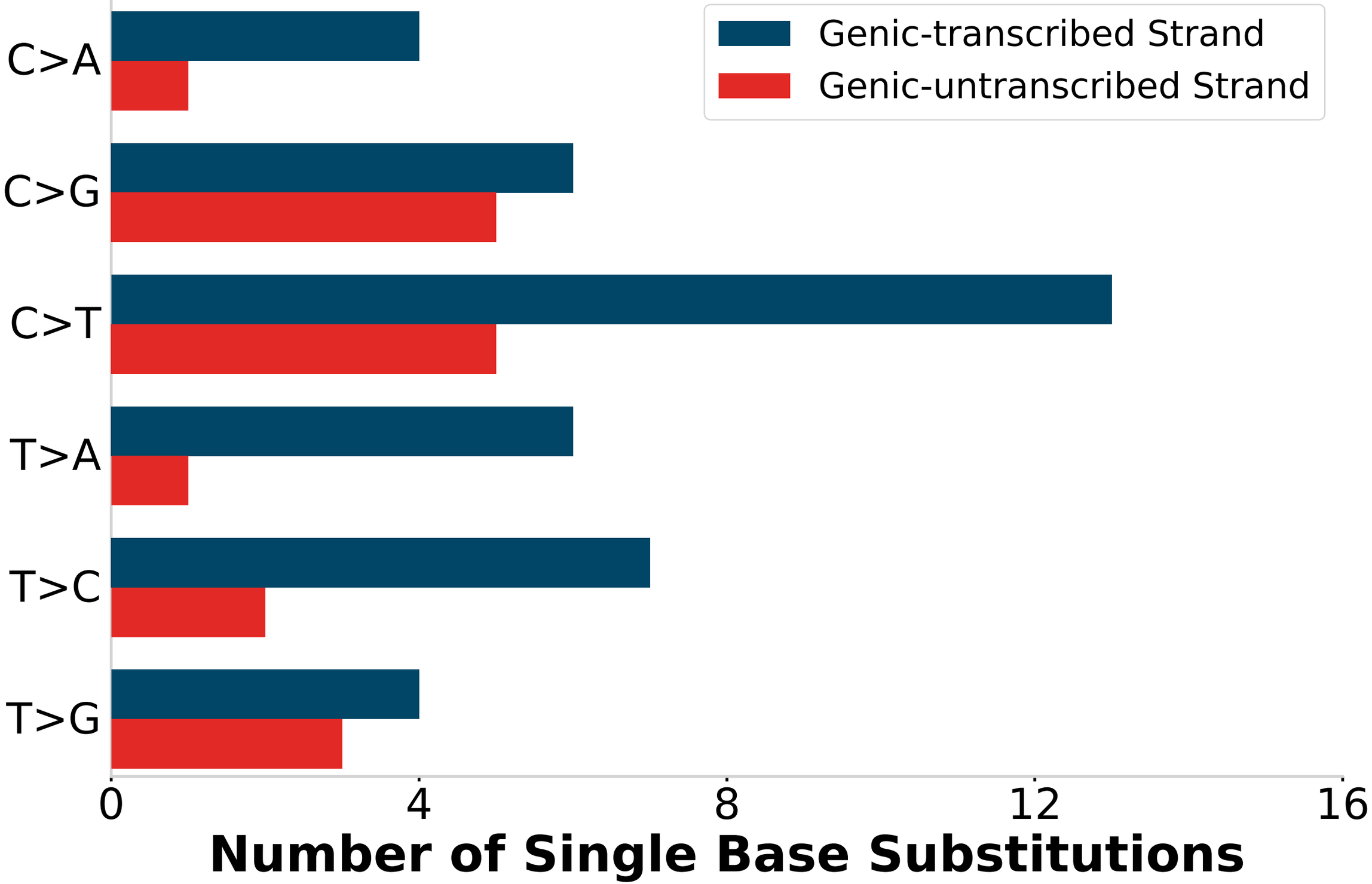
TCGA-FD-A3B5-01A-11D-A20D-08: 157 tra



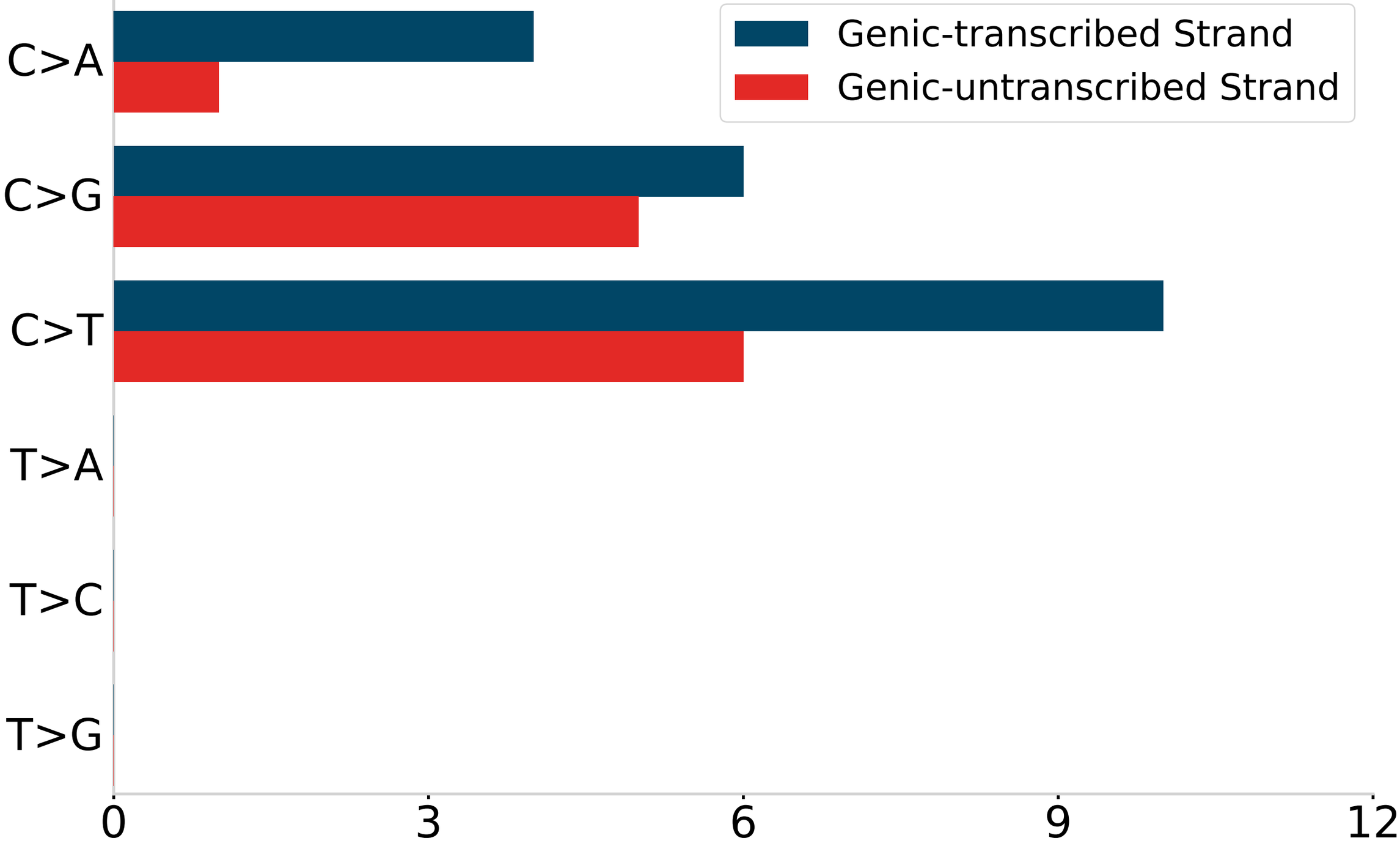
TCGA-FD-A3B6-01A-21D-A20D-08: 281 tra



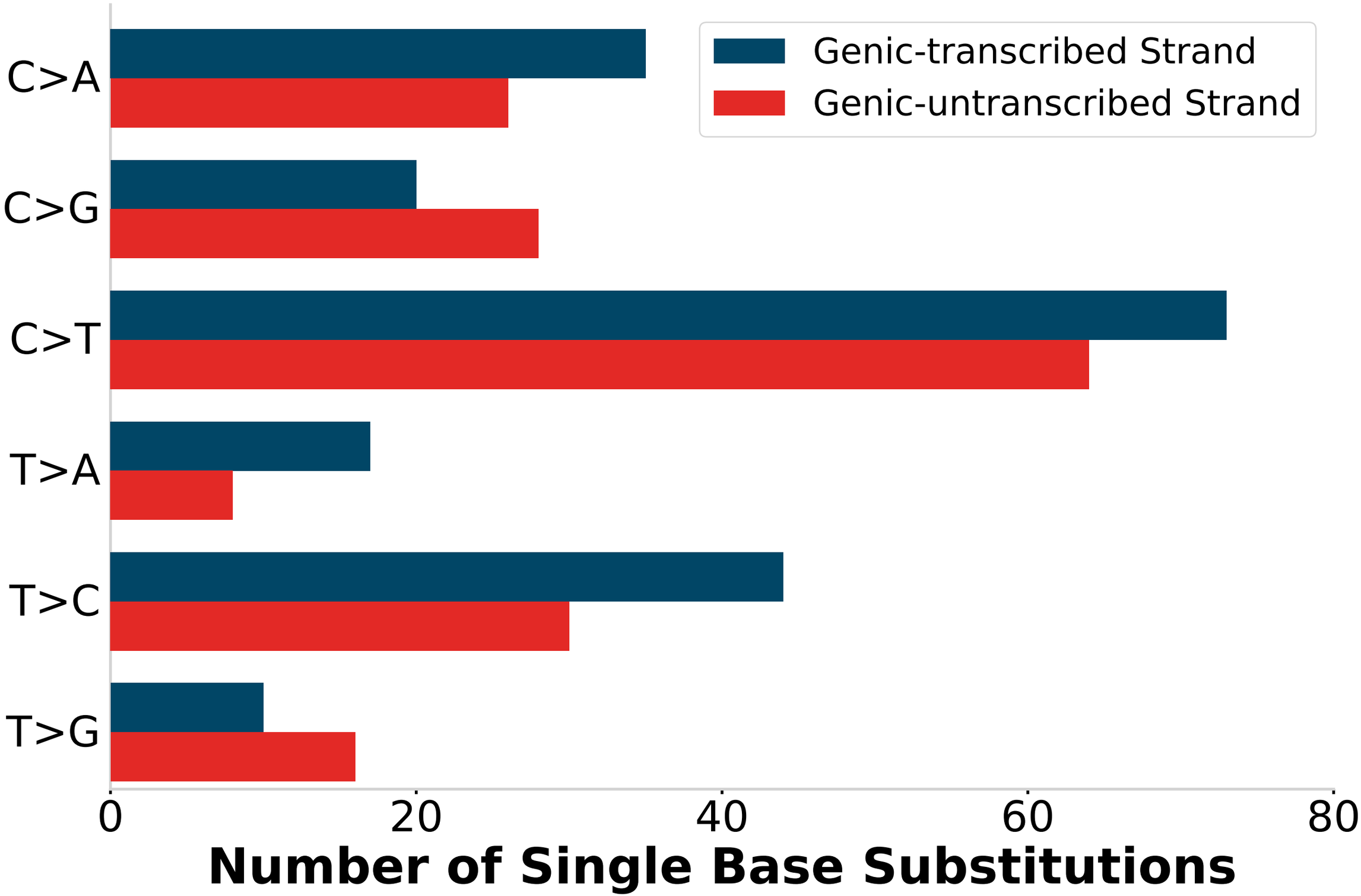
TCGA-FD-A3B7-01A-31D-A20D-08: 57 tran



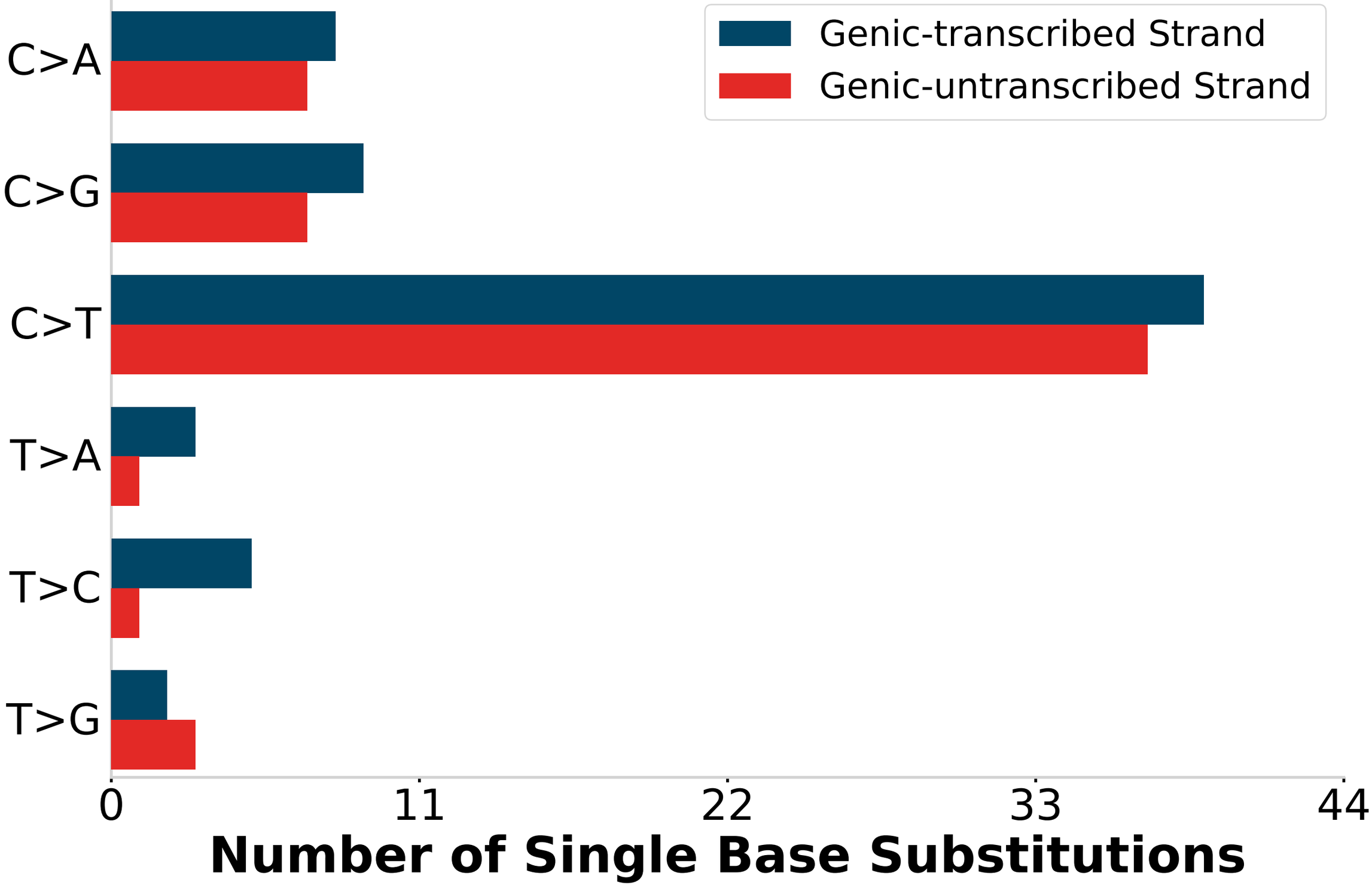
TCGA-FD-A3B8-01A-31D-A20D-08: 32 tran



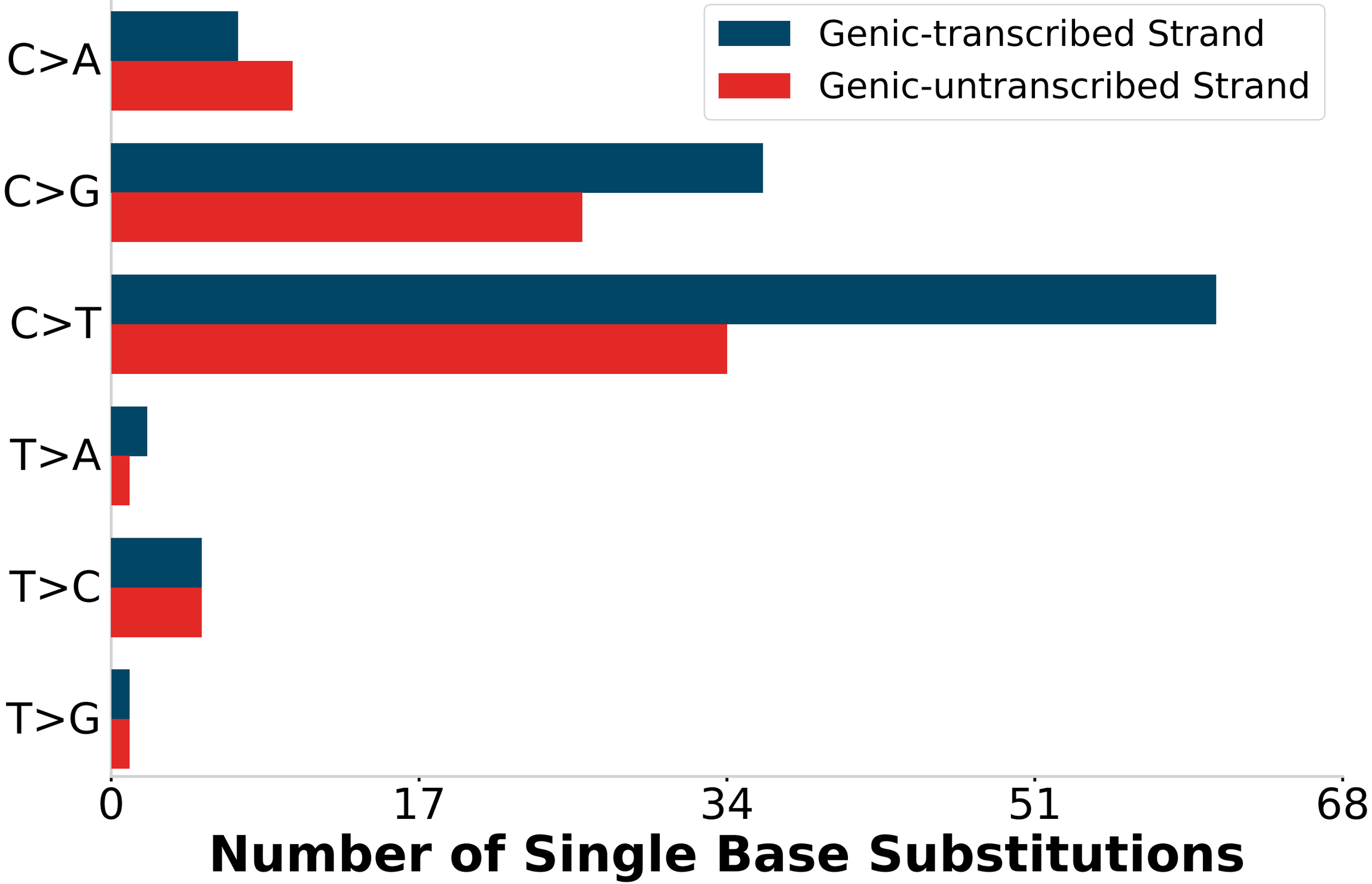
TCGA-FD-A3N5-01A-11D-A21A-08: 371 tra



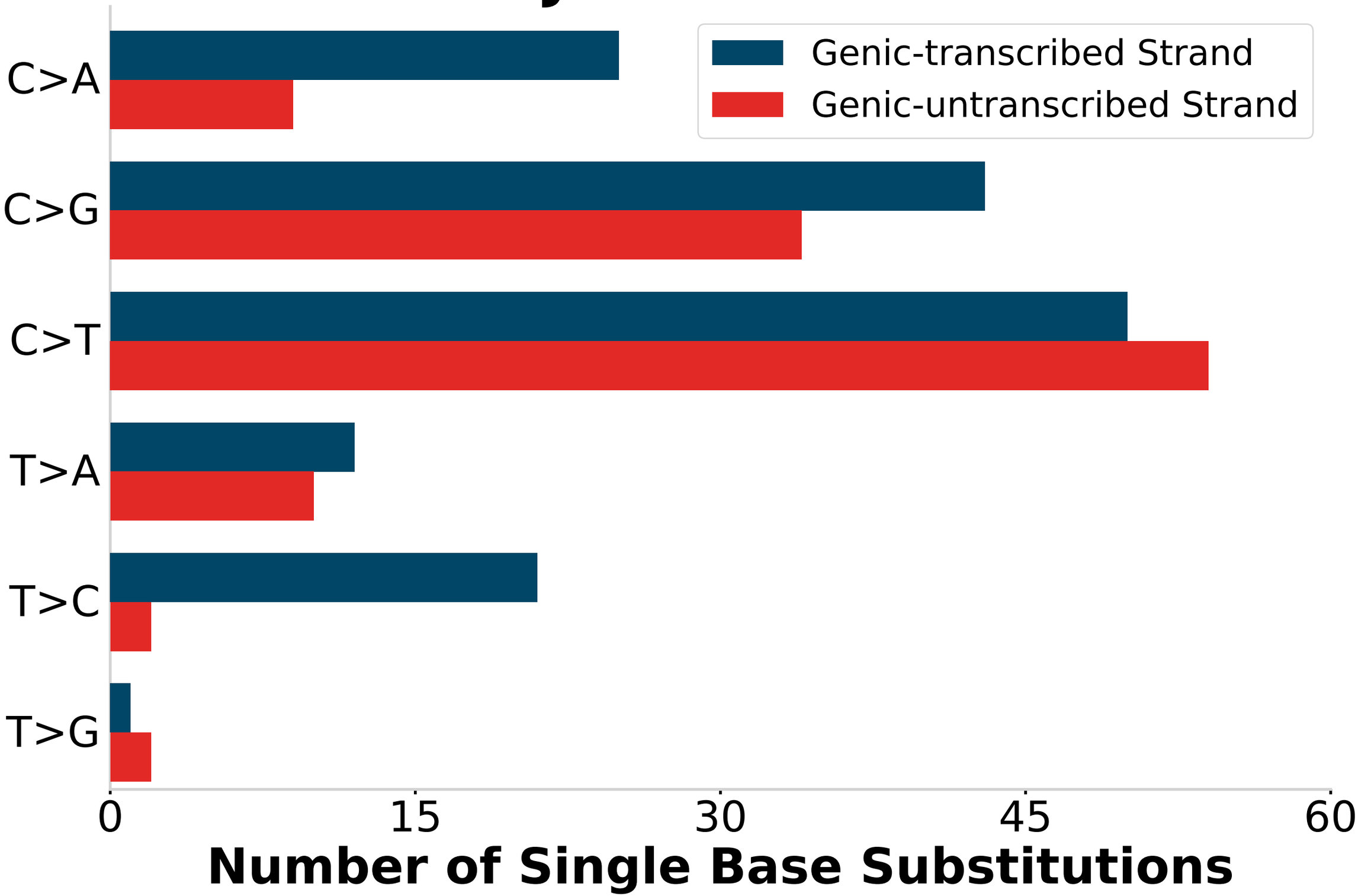
TCGA-FD-A3N6-01A-11D-A21A-08: 122 tra



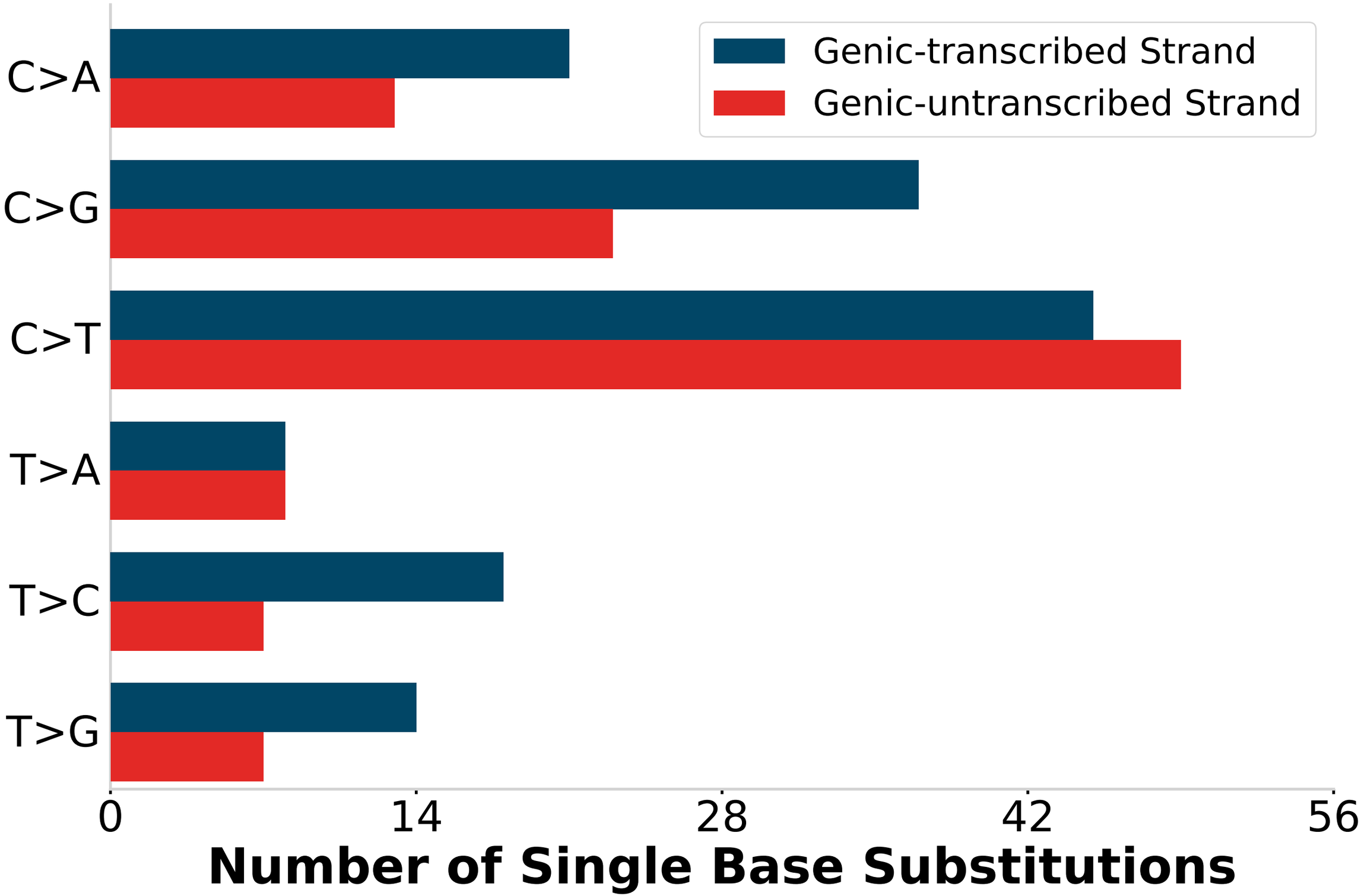
TCGA-FD-A3NA-01A-11D-A21A-08: 189 tra



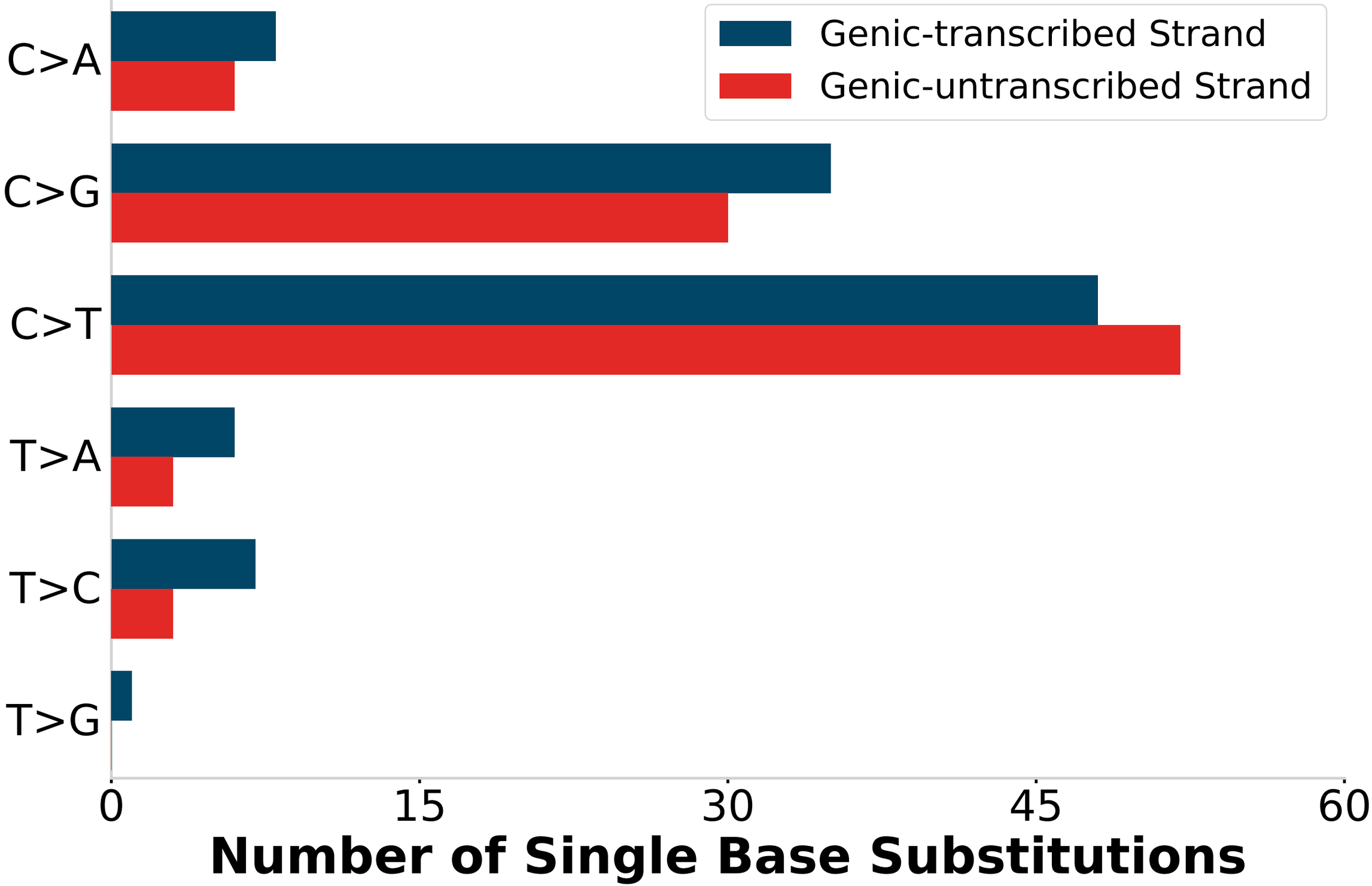
TCGA-FD-A3SJ-01A-12D-A22Z-08: 263 tran



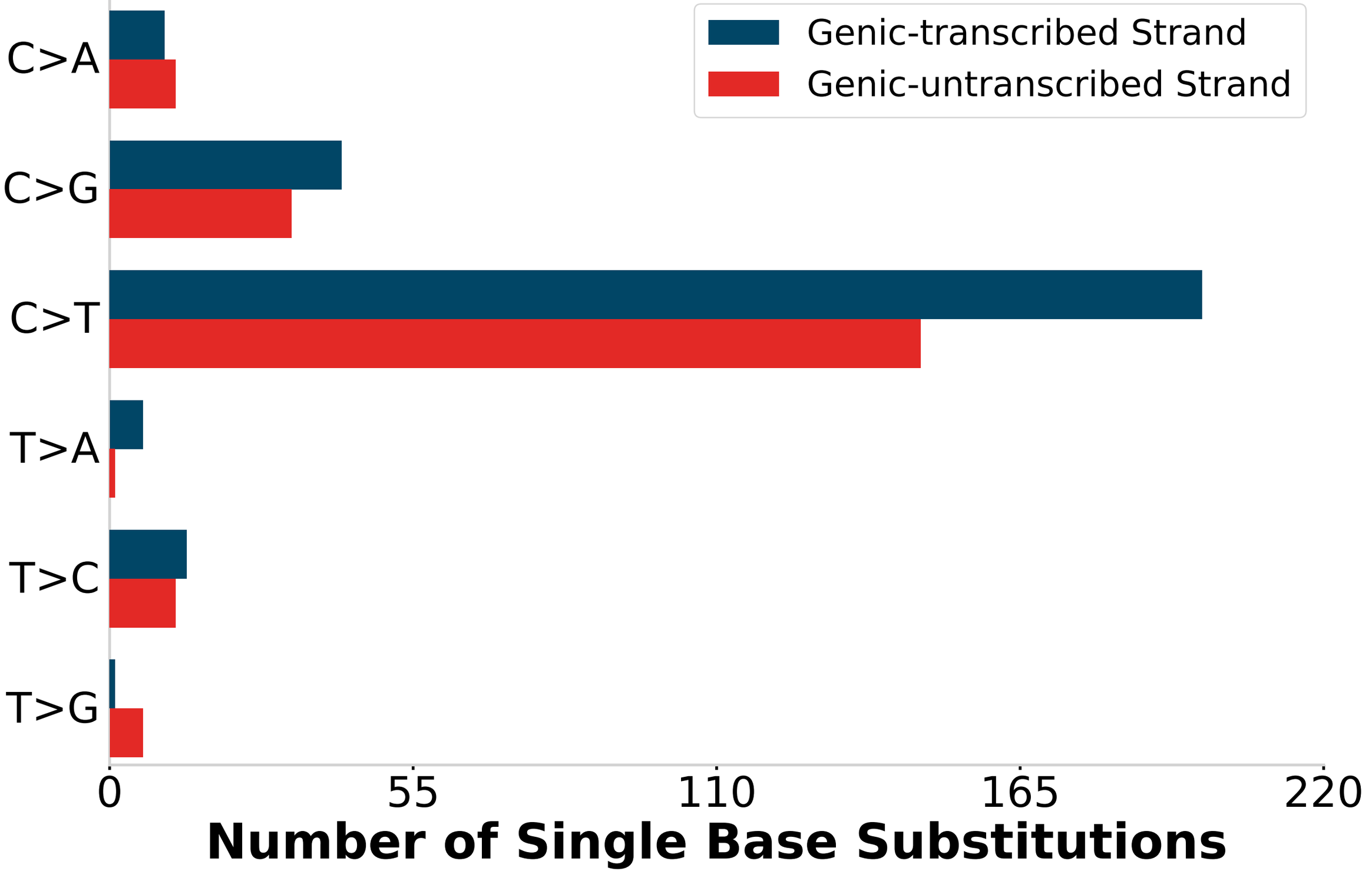
TCGA-FD-A3SL-01A-21D-A22Z-08: 250 tran



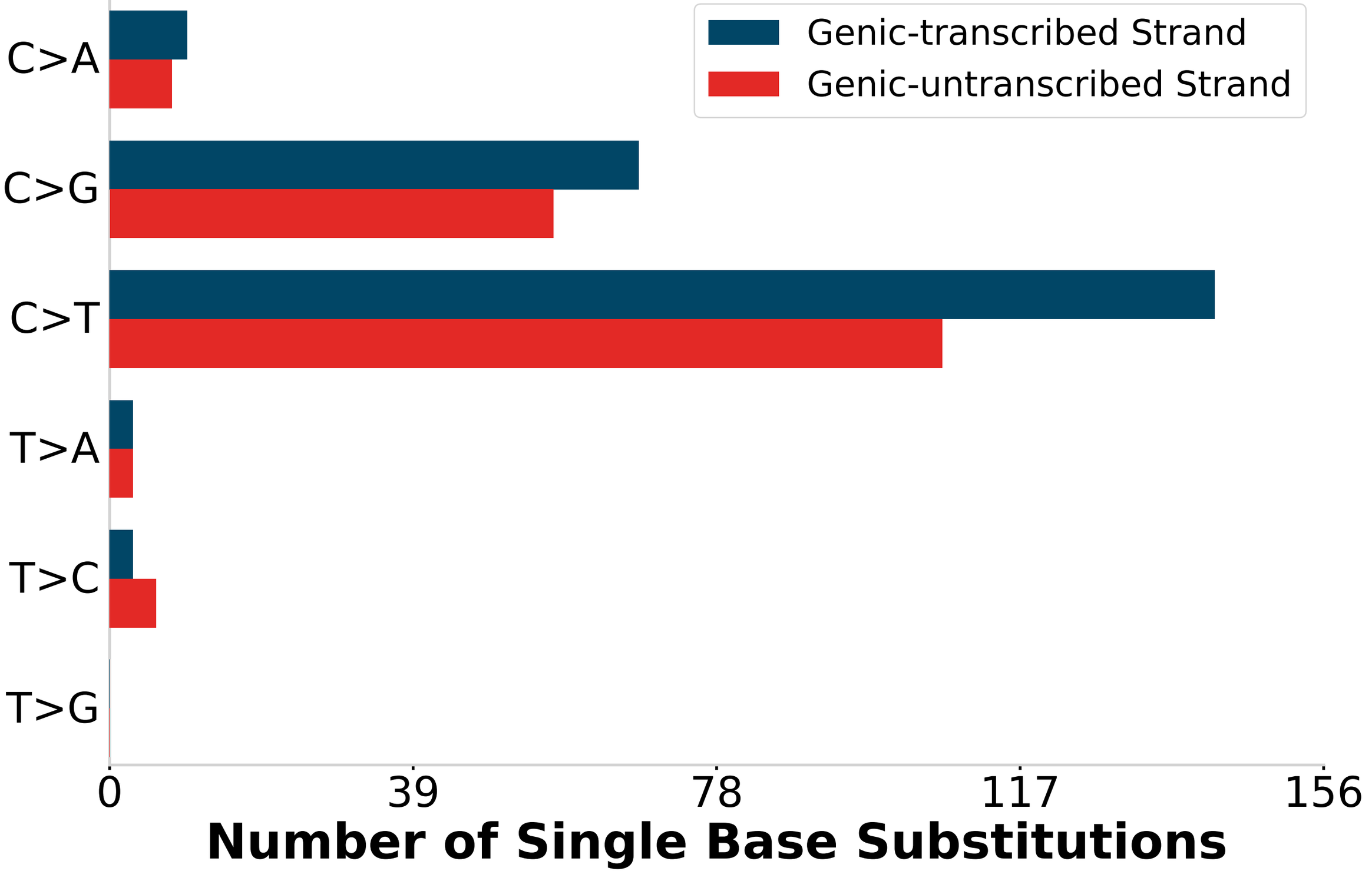
TCGA-FD-A3SM-01A-11D-A22Z-08: 199 tra



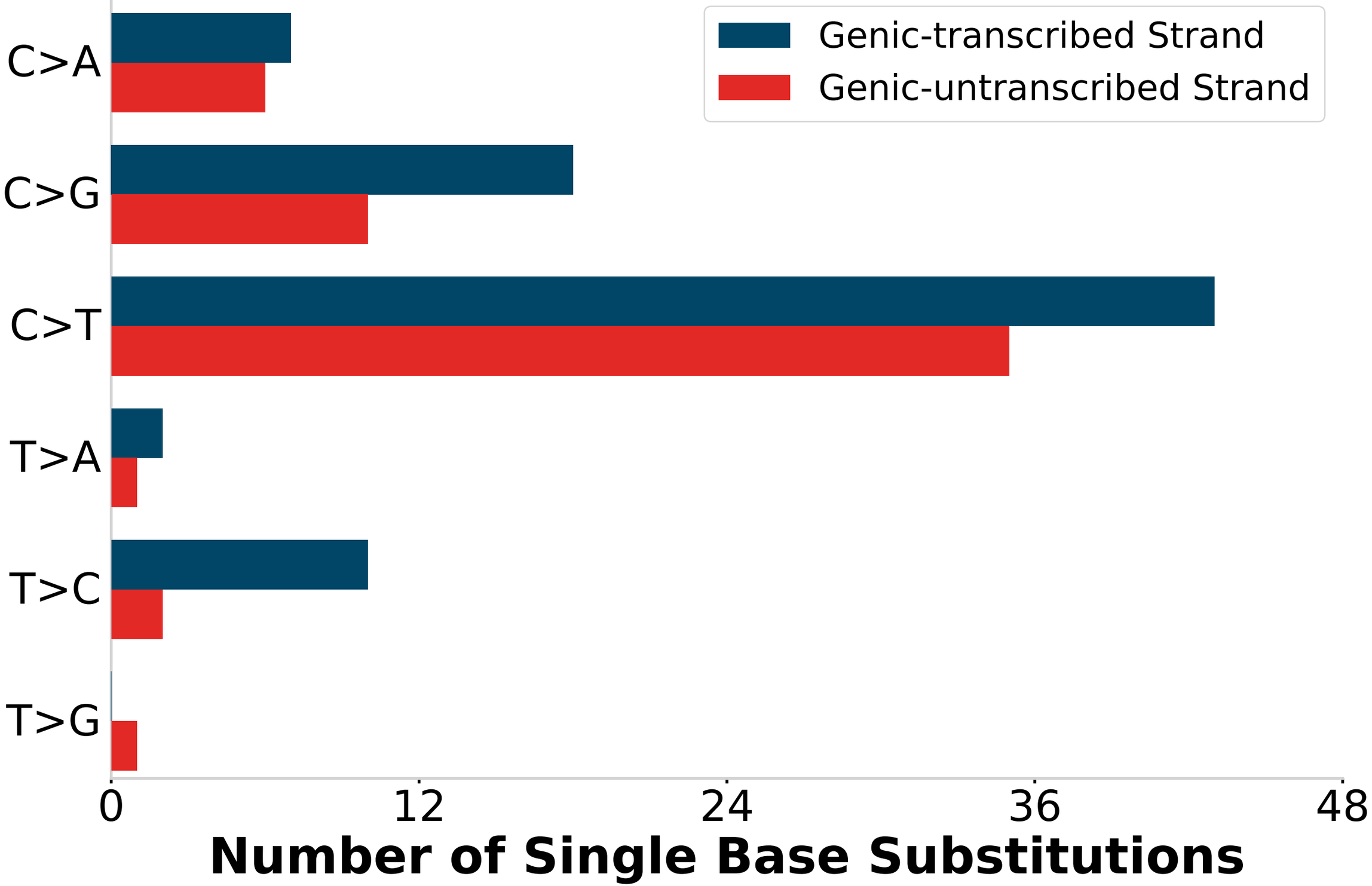
TCGA-FD-A3SN-01A-12D-A22Z-08: 482 tra



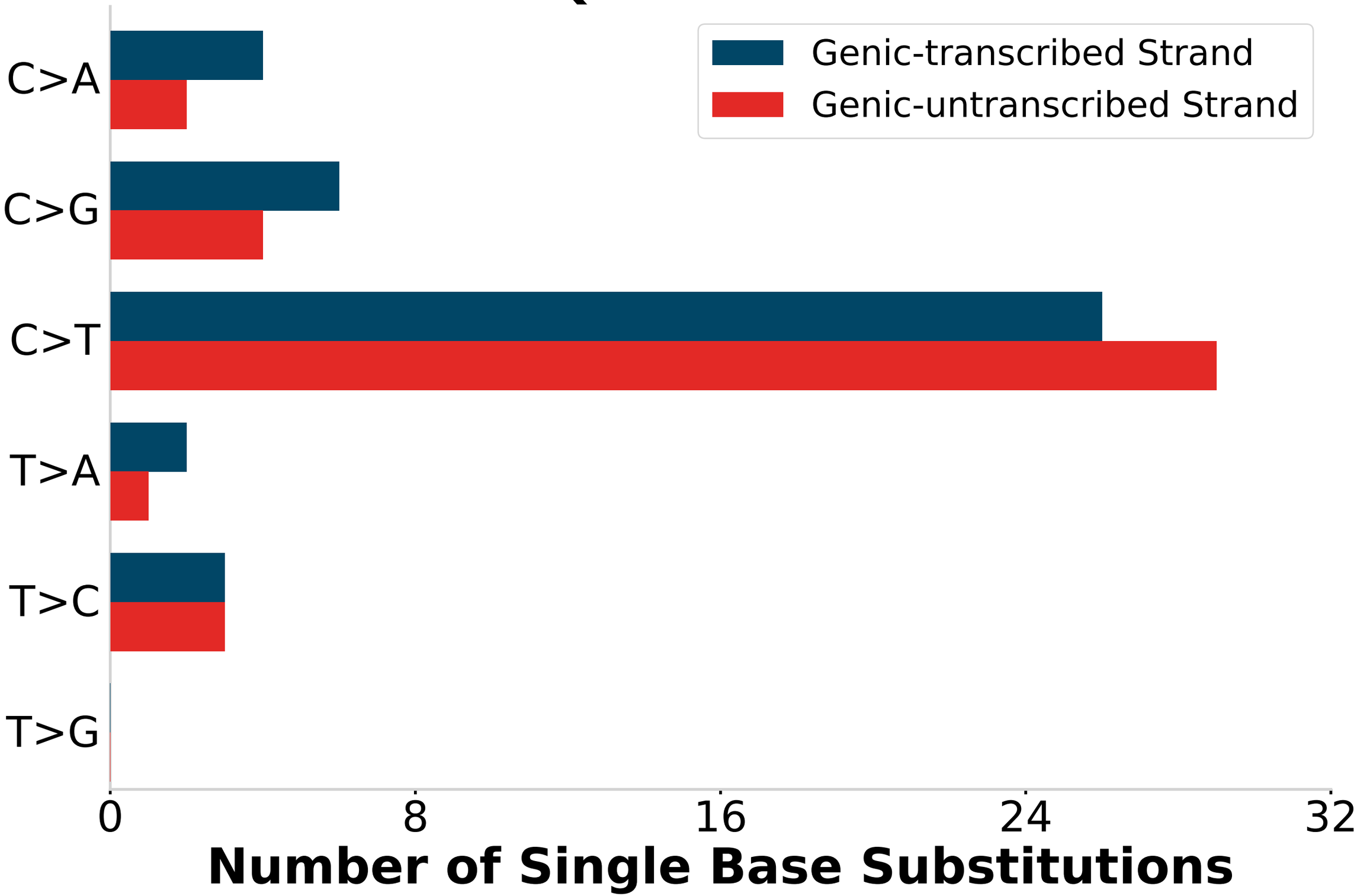
TCGA-FD-A3SO-01A-11D-A22Z-08: 407 tra



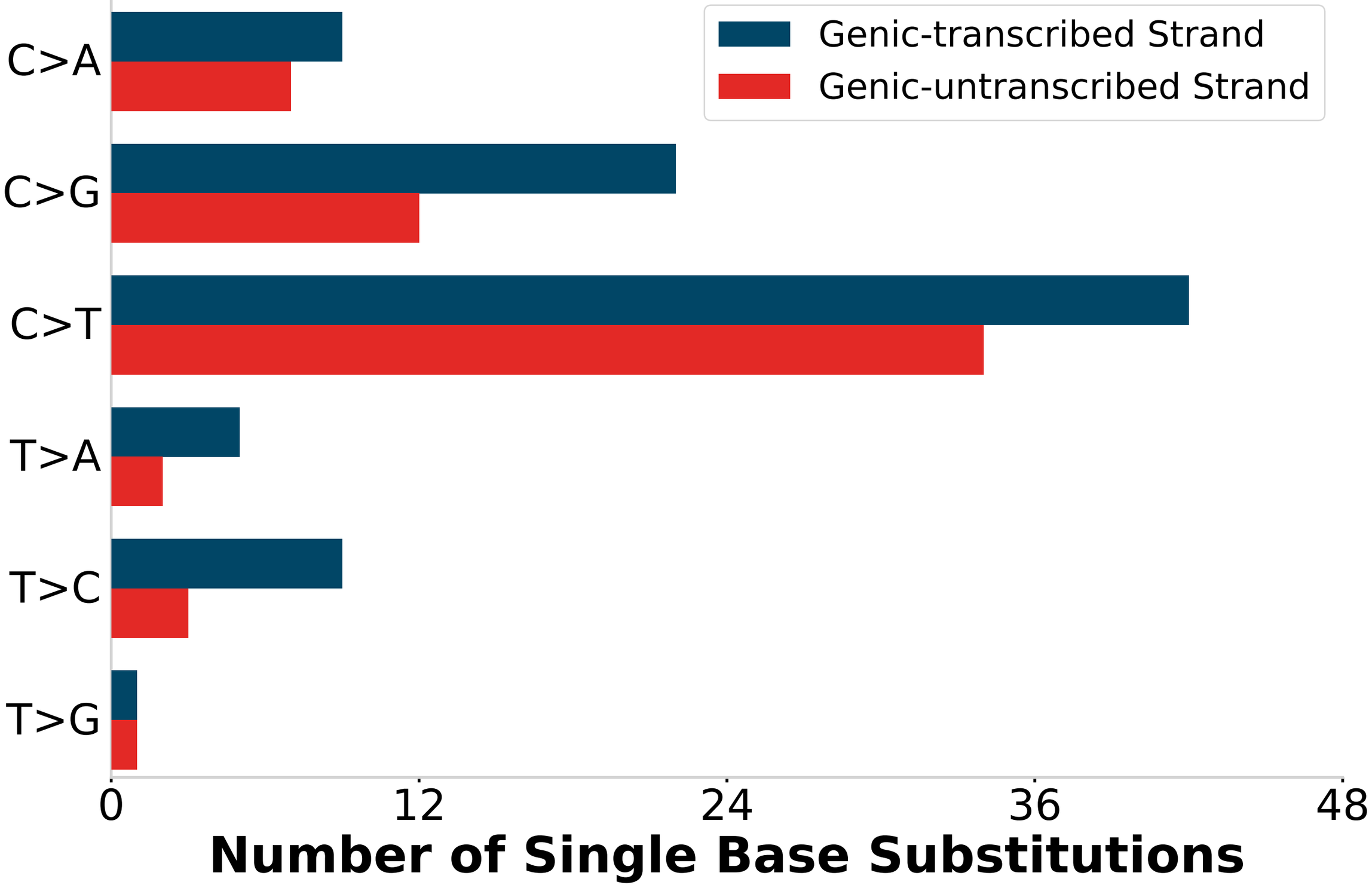
TCGA-FD-A3SP-01A-31D-A22Z-08: 135 tra



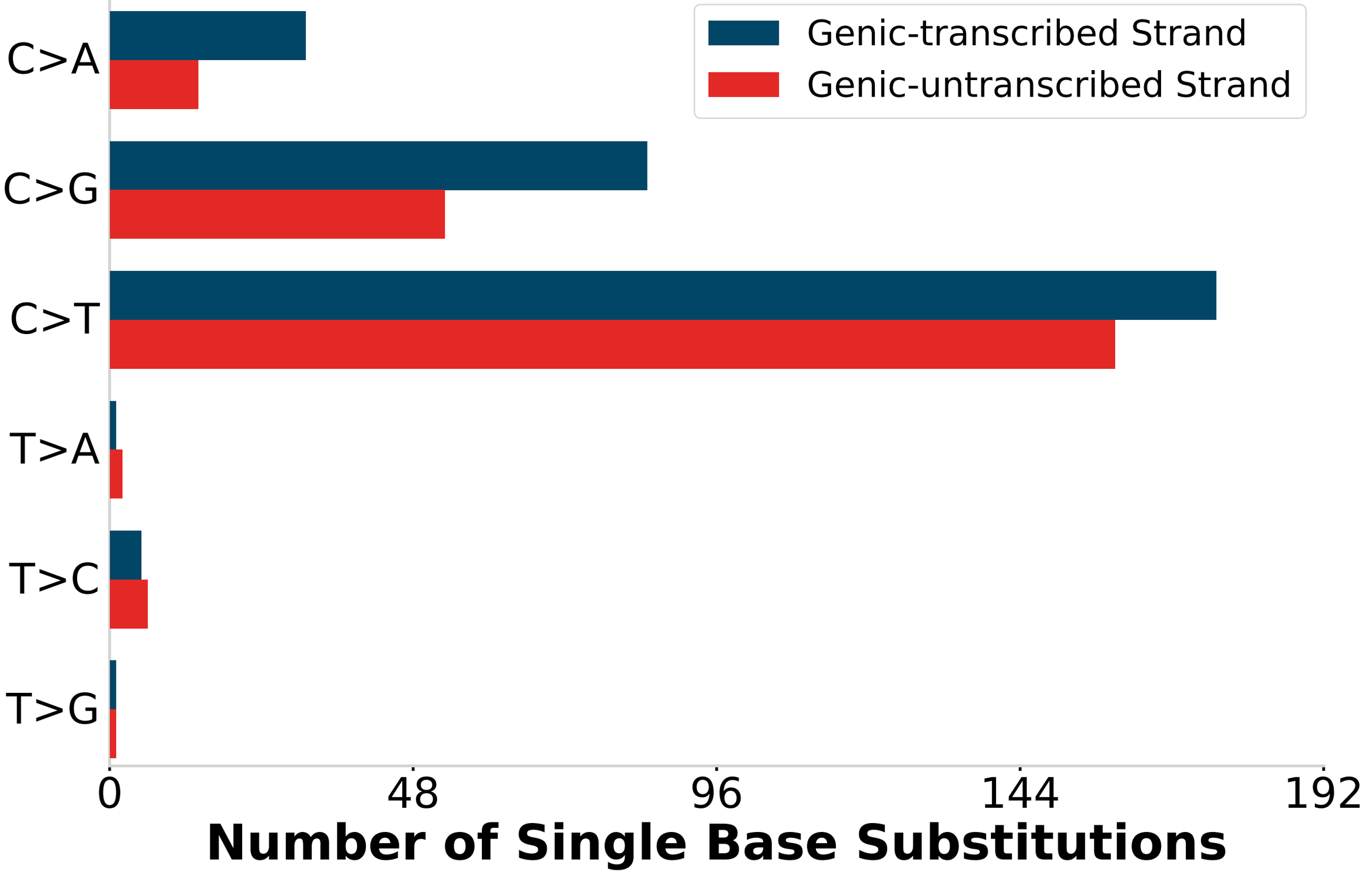
TCGA-FD-A3SQ-01A-21D-A22Z-08: 80 tran



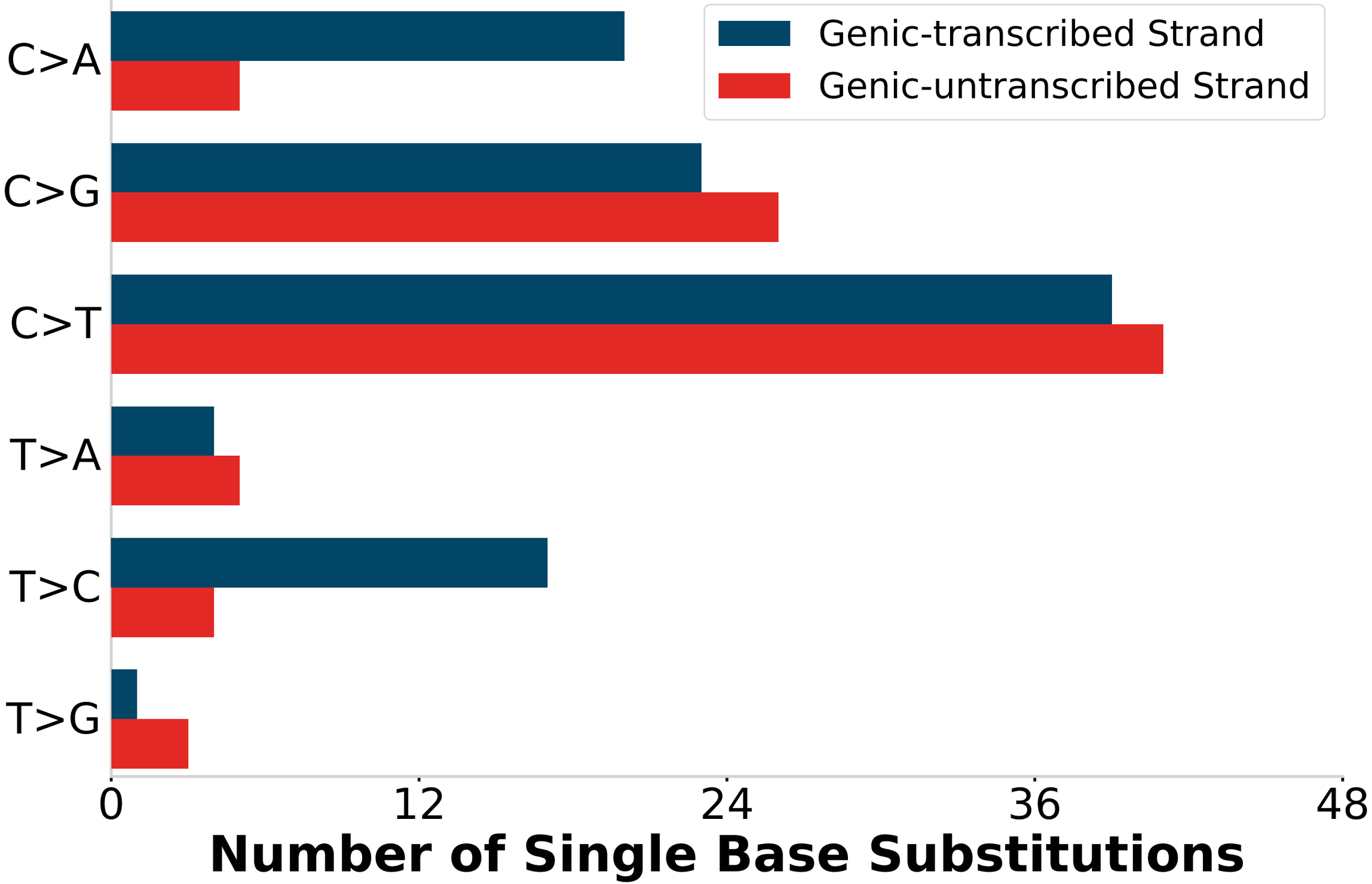
TCGA-FD-A3SR-01A-11D-A22Z-08: 147 tra



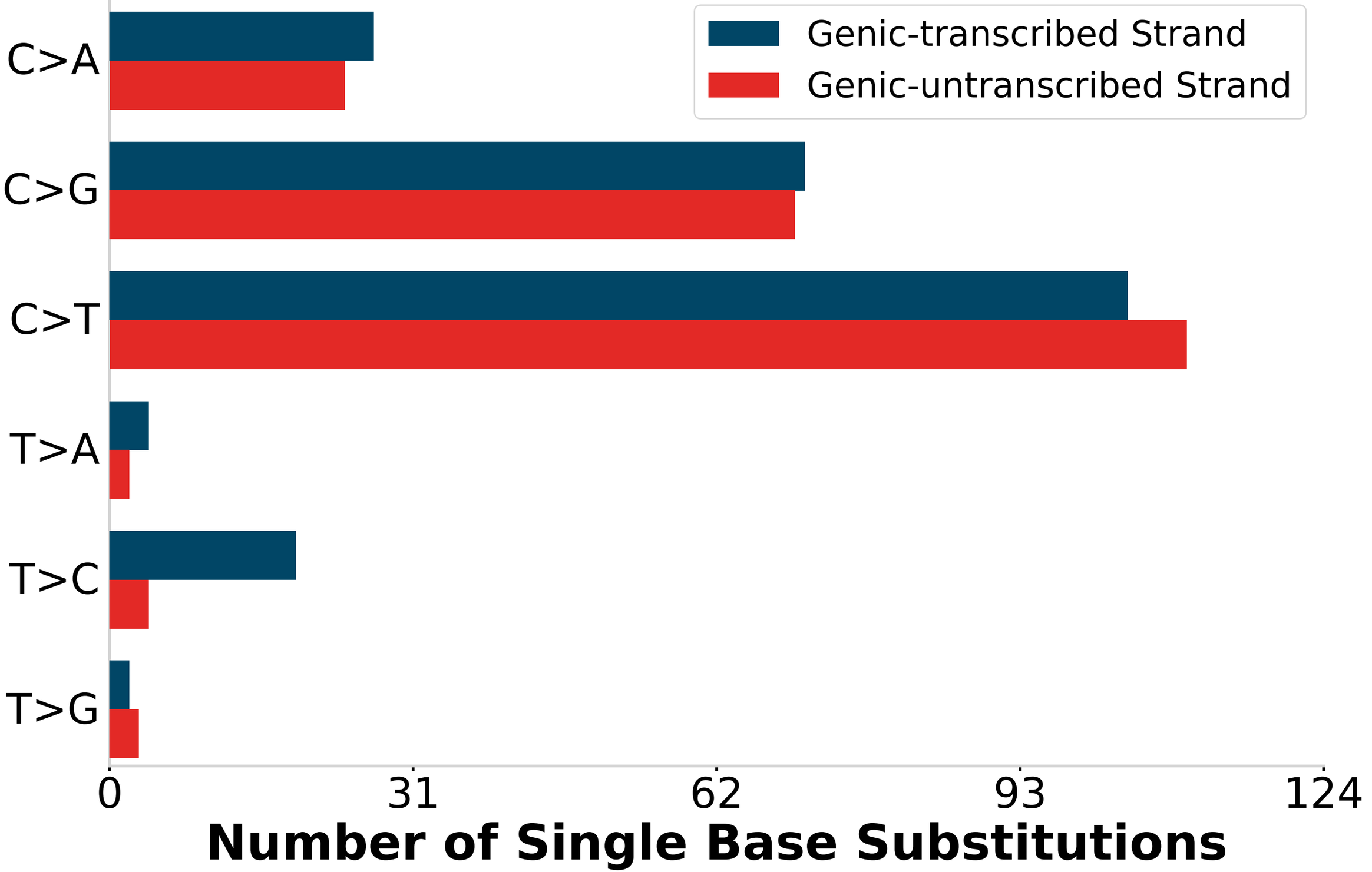
TCGA-FD-A3SS-01A-12D-A22Z-08: 533 tra



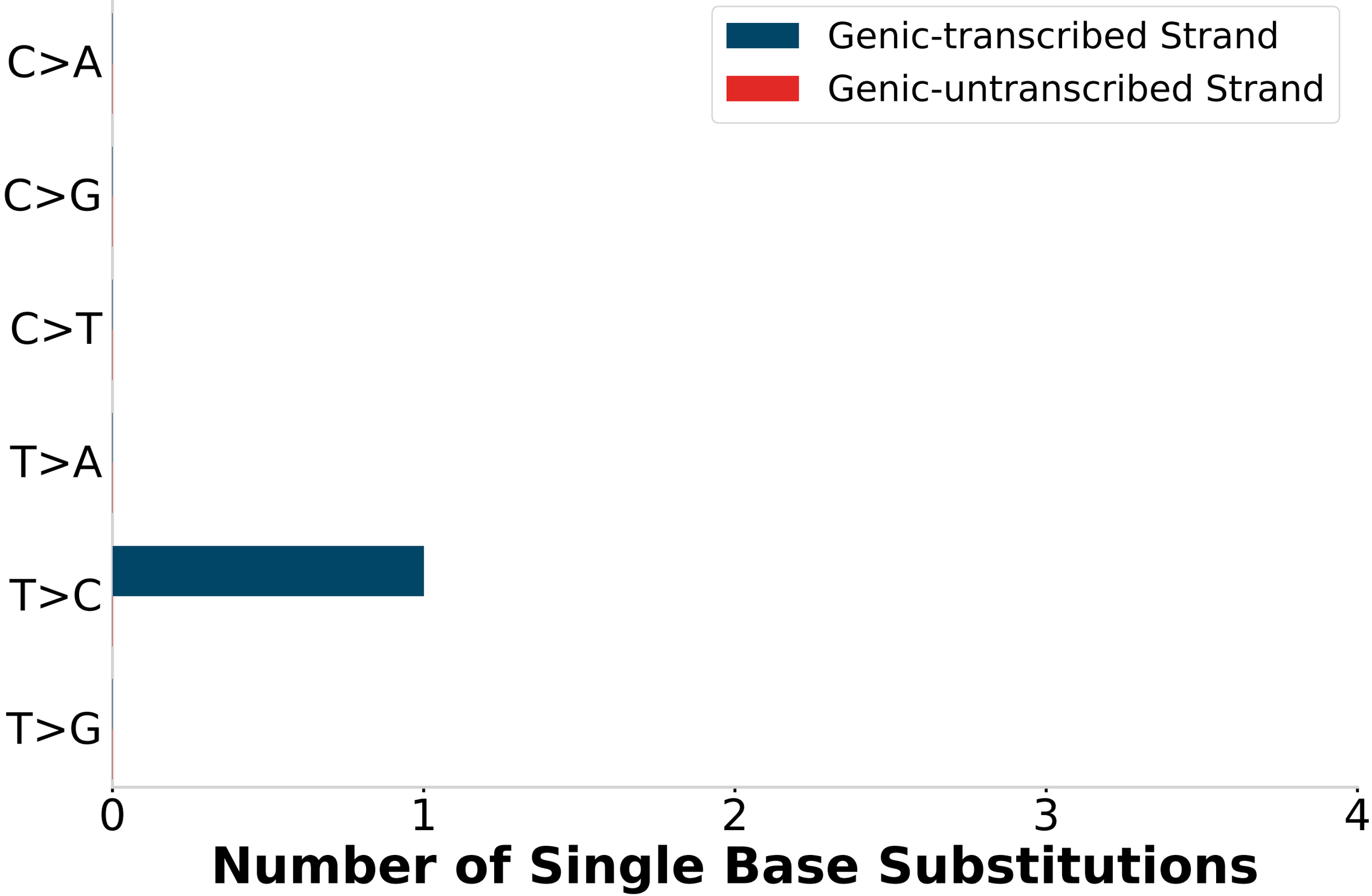
TCGA-FD-A43N-01A-11D-A23U-08: 188 tra



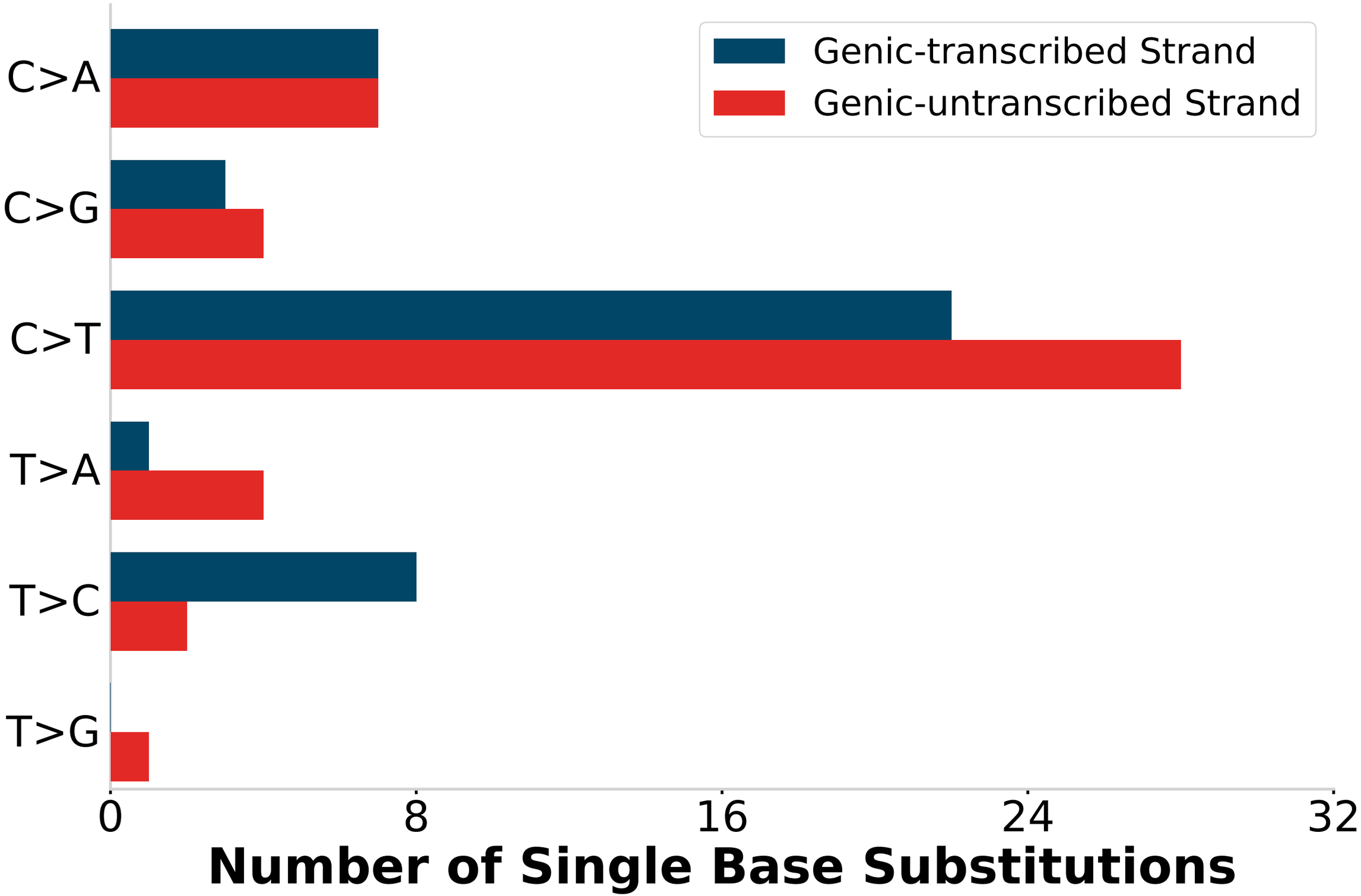
TCGA-FD-A43P-01A-31D-A23U-08: 440 tra



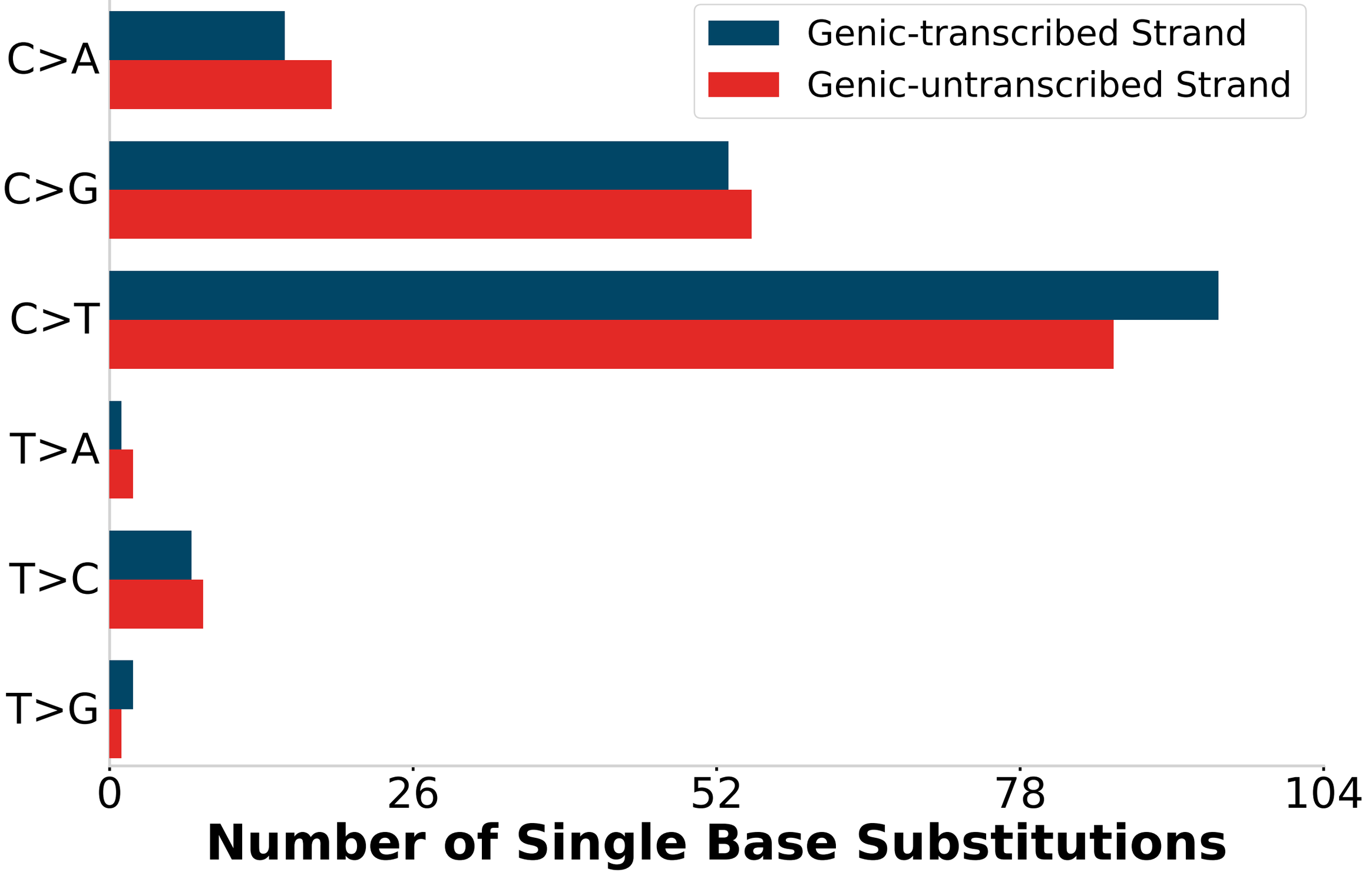
TCGA-FD-A43S-01A-21D-A23U-08: 1 transc



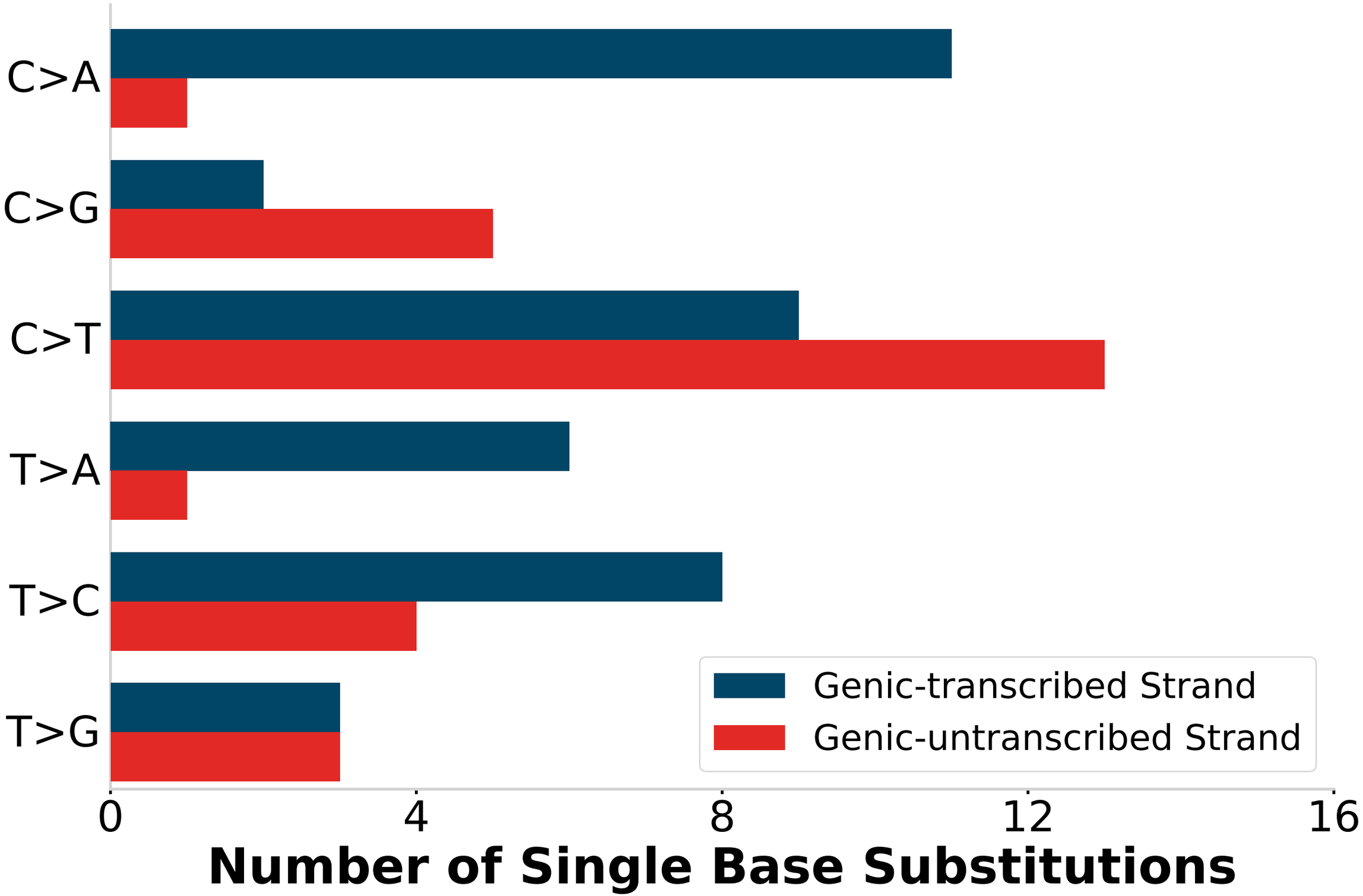
TCGA-FD-A43U-01A-11D-A23U-08: 87 tran



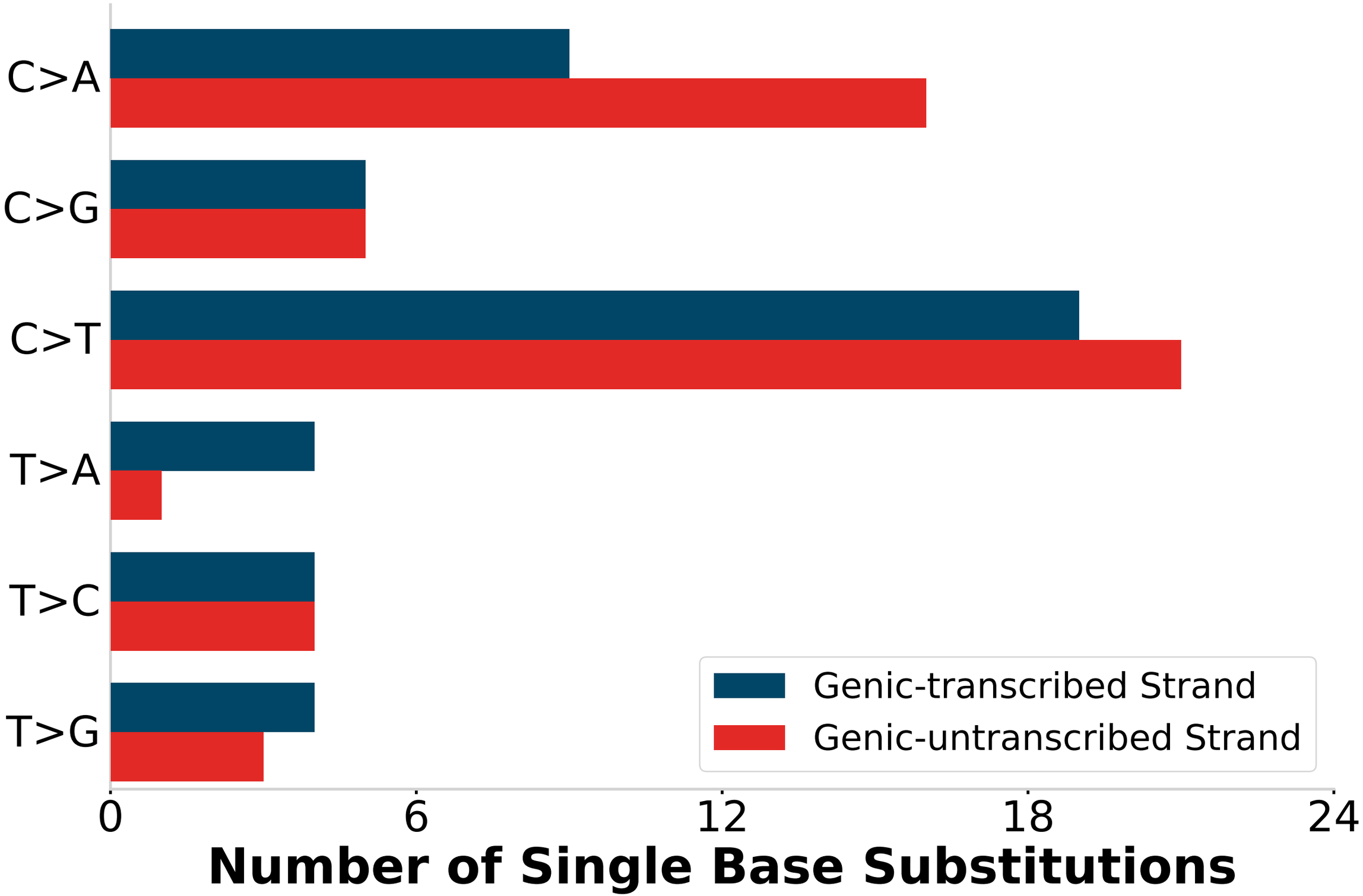
TCGA-FD-A43X-01A-11D-A23U-08: 344 tra



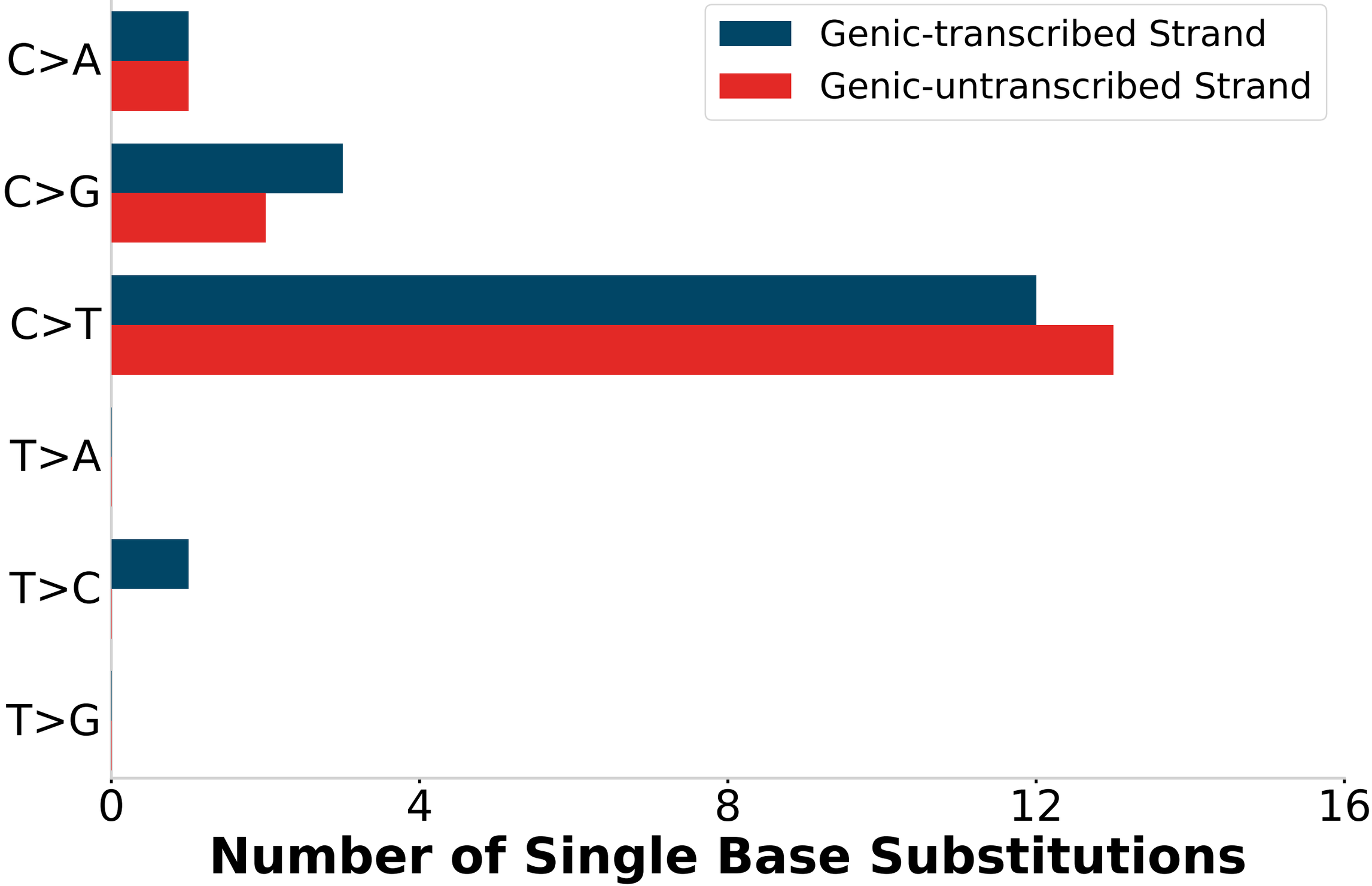
TCGA-FD-A43Y-01A-21D-A26M-08: 66 tran



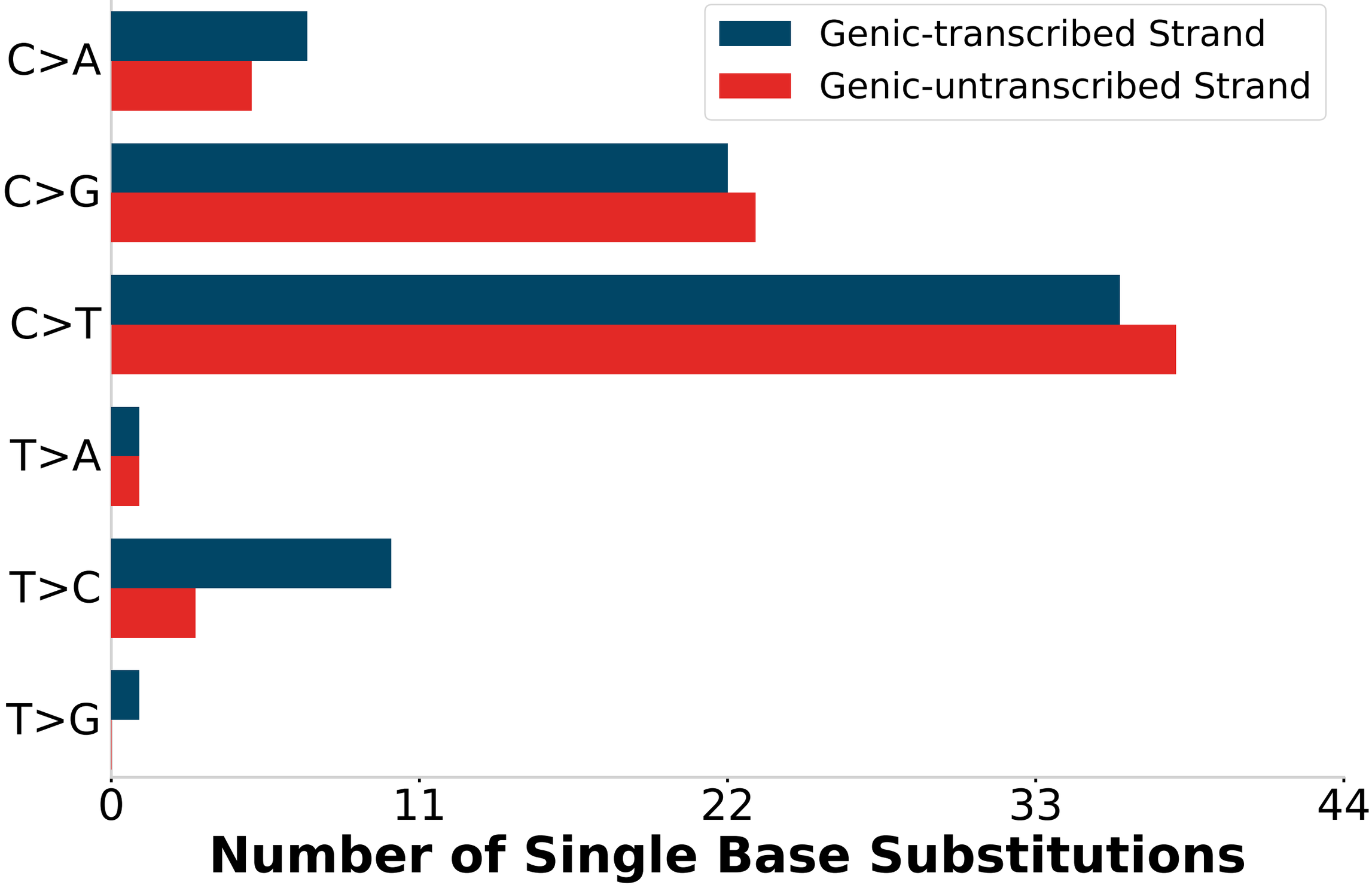
TCGA-FD-A5BR-01A-11D-A26M-08: 95 tran



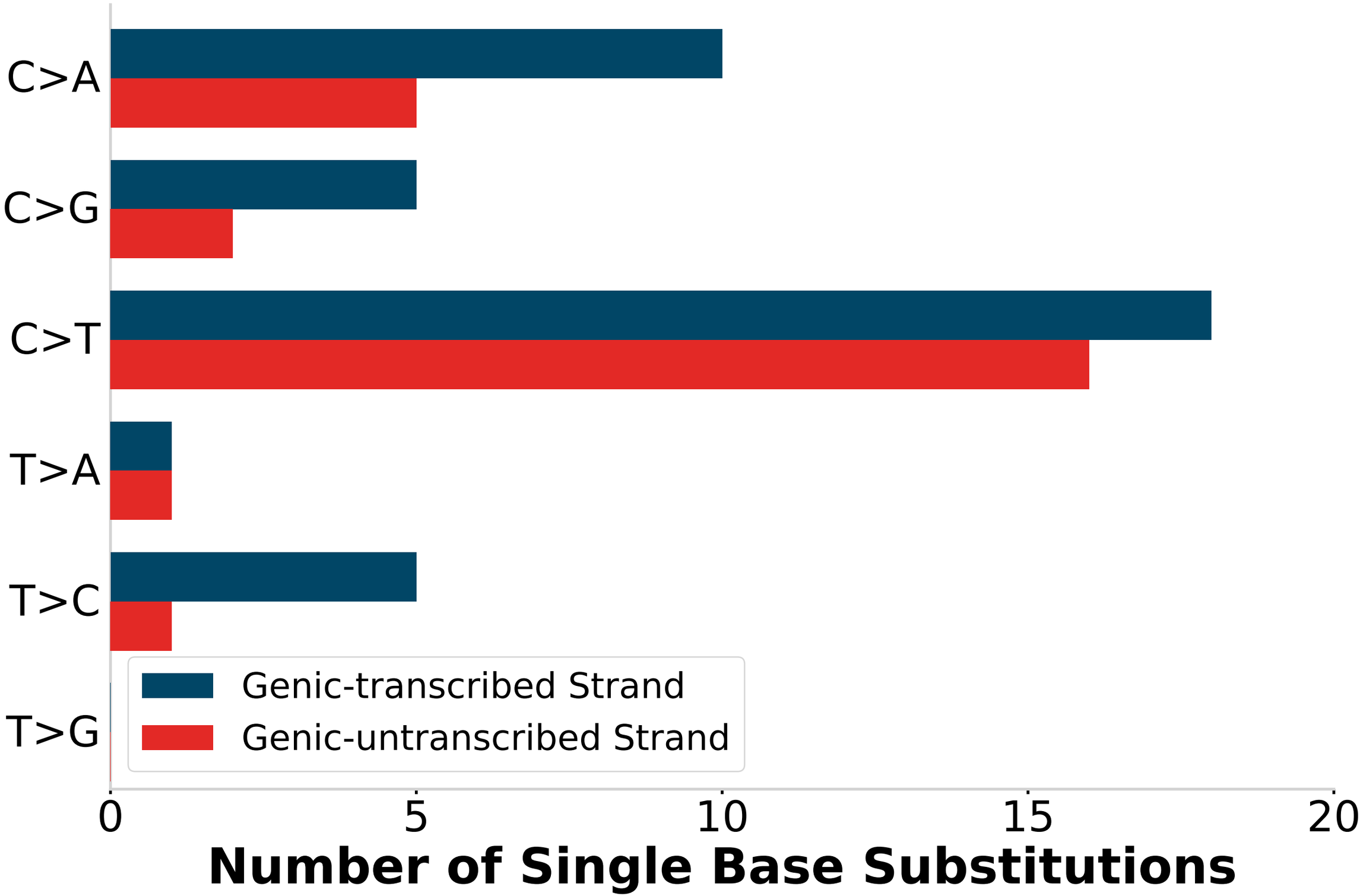
TCGA-FD-A5BS-01A-21D-A26M-08: 33 tran



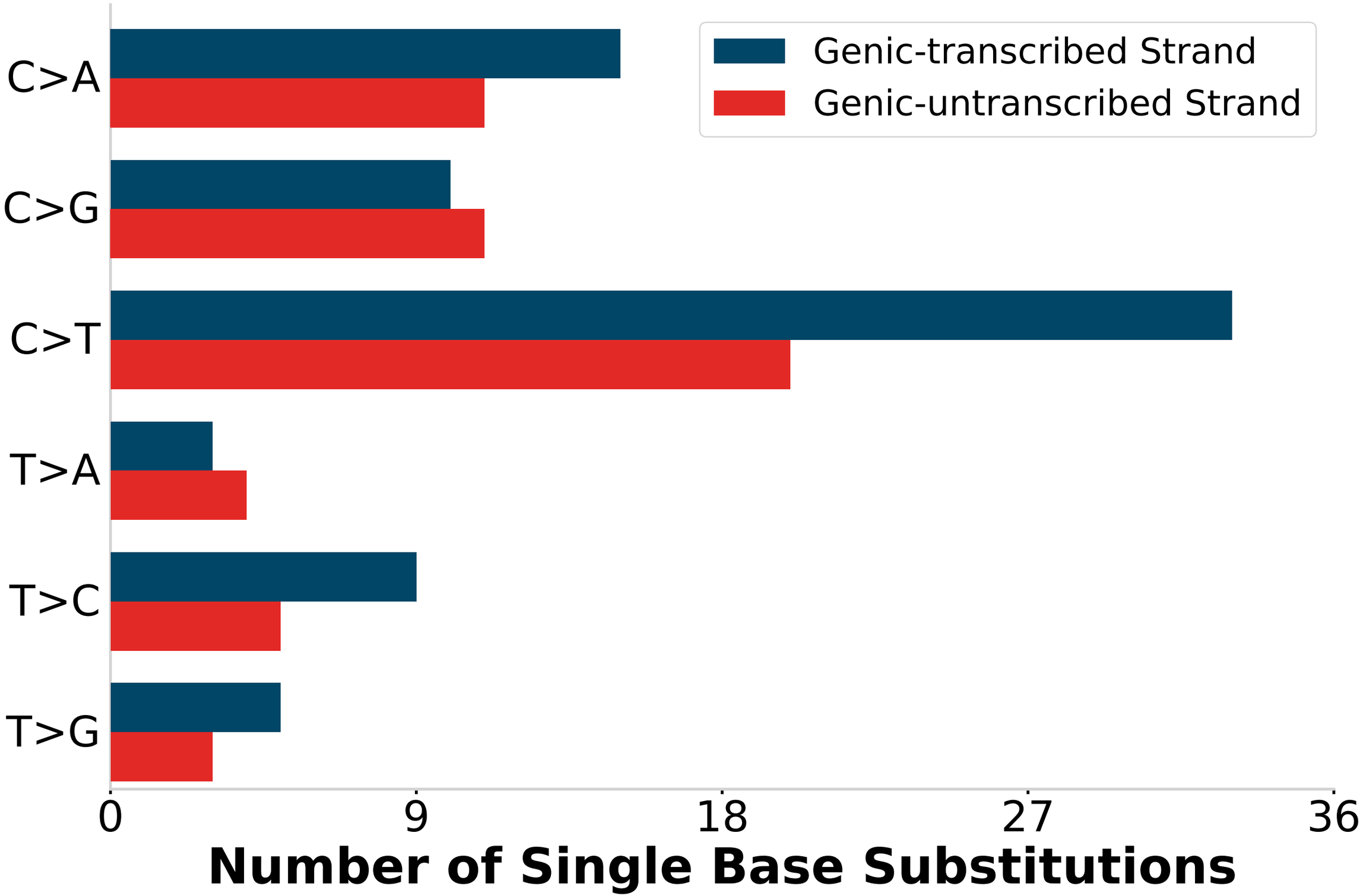
TCGA-FD-A5BT-01A-11D-A26M-08: 147 tra



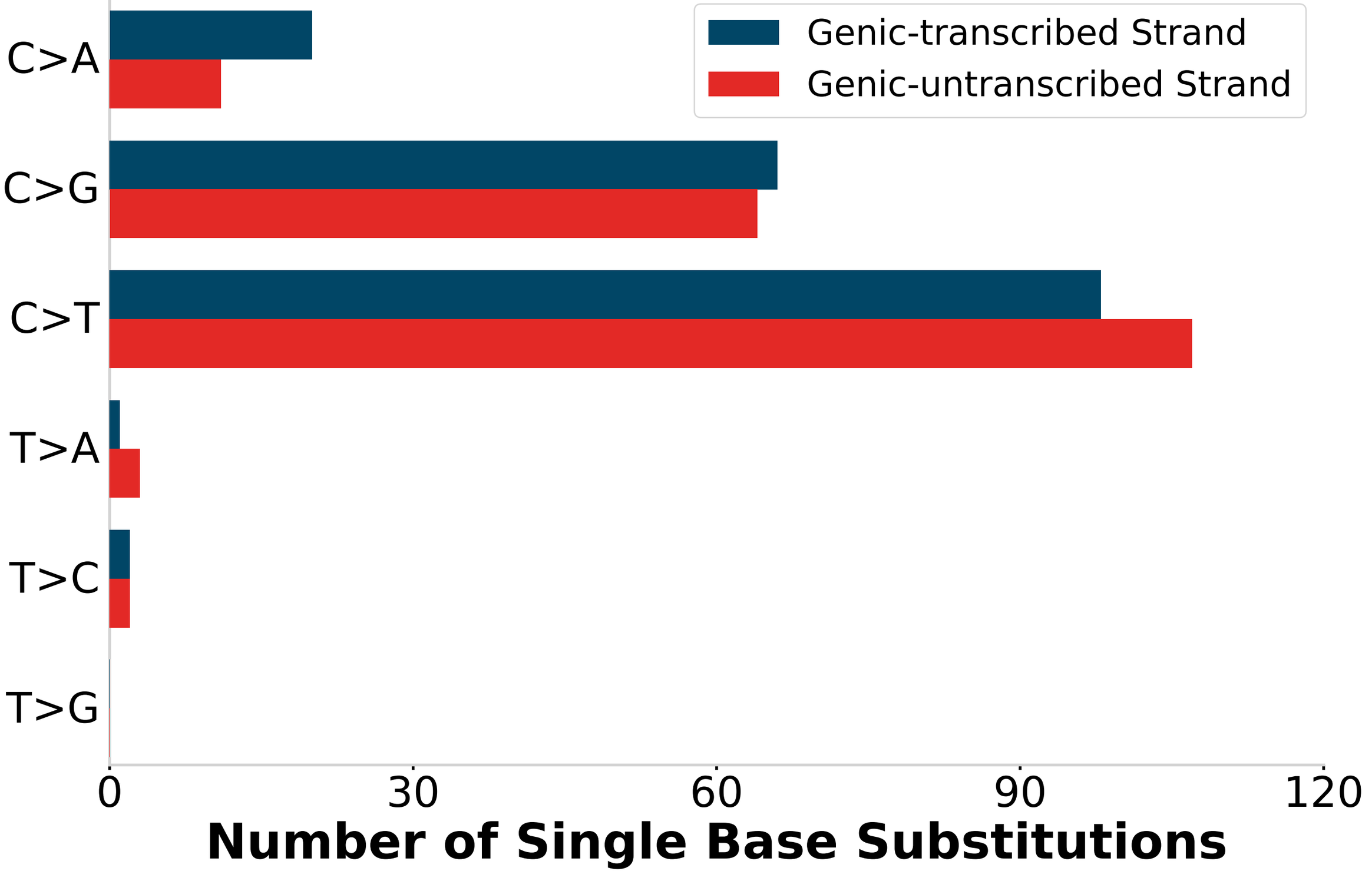
TCGA-FD-A5BU-01A-31D-A26M-08: 64 tran



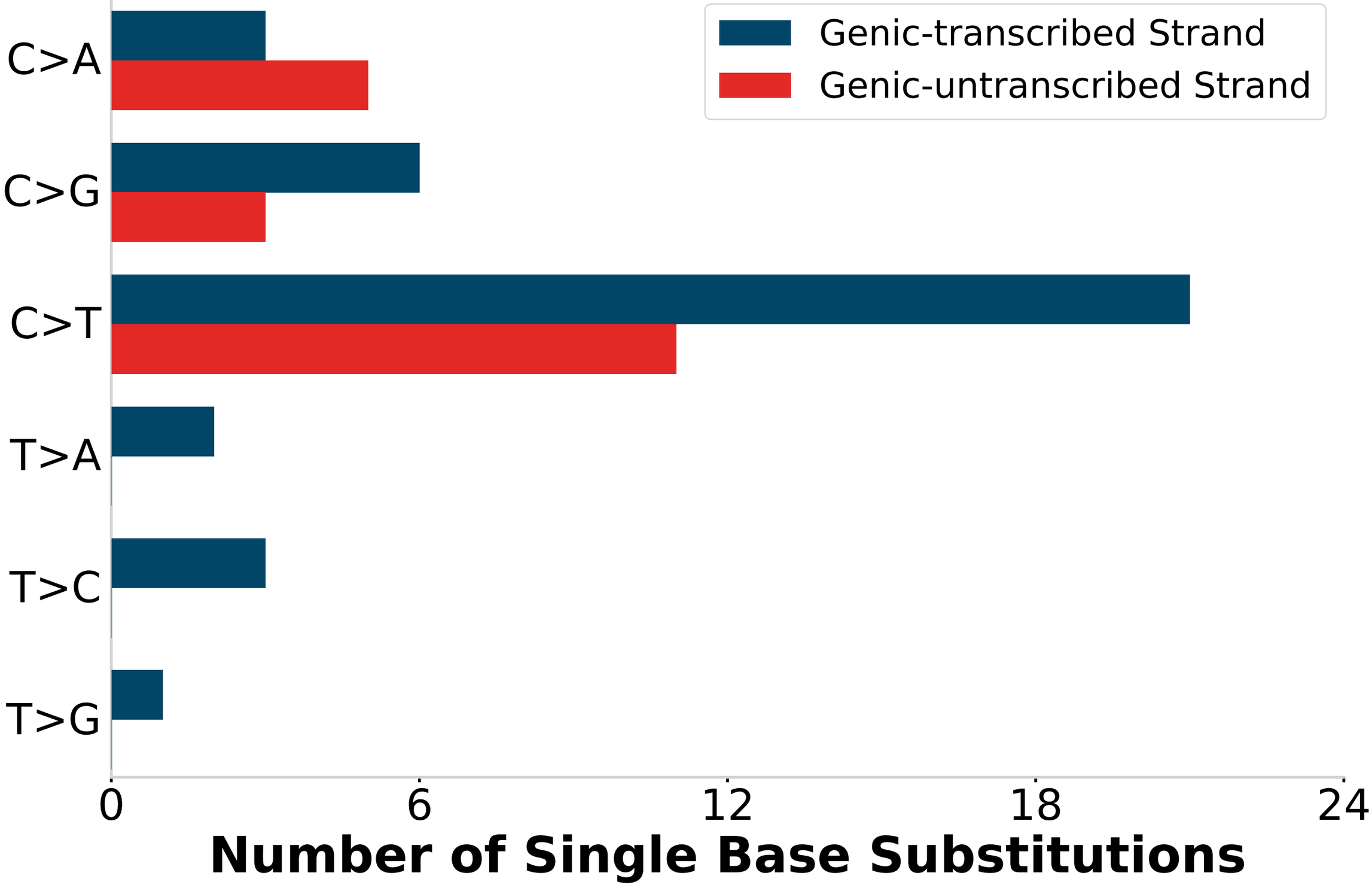
TCGA-FD-A5BV-01A-11D-A26M-08: 129 tra



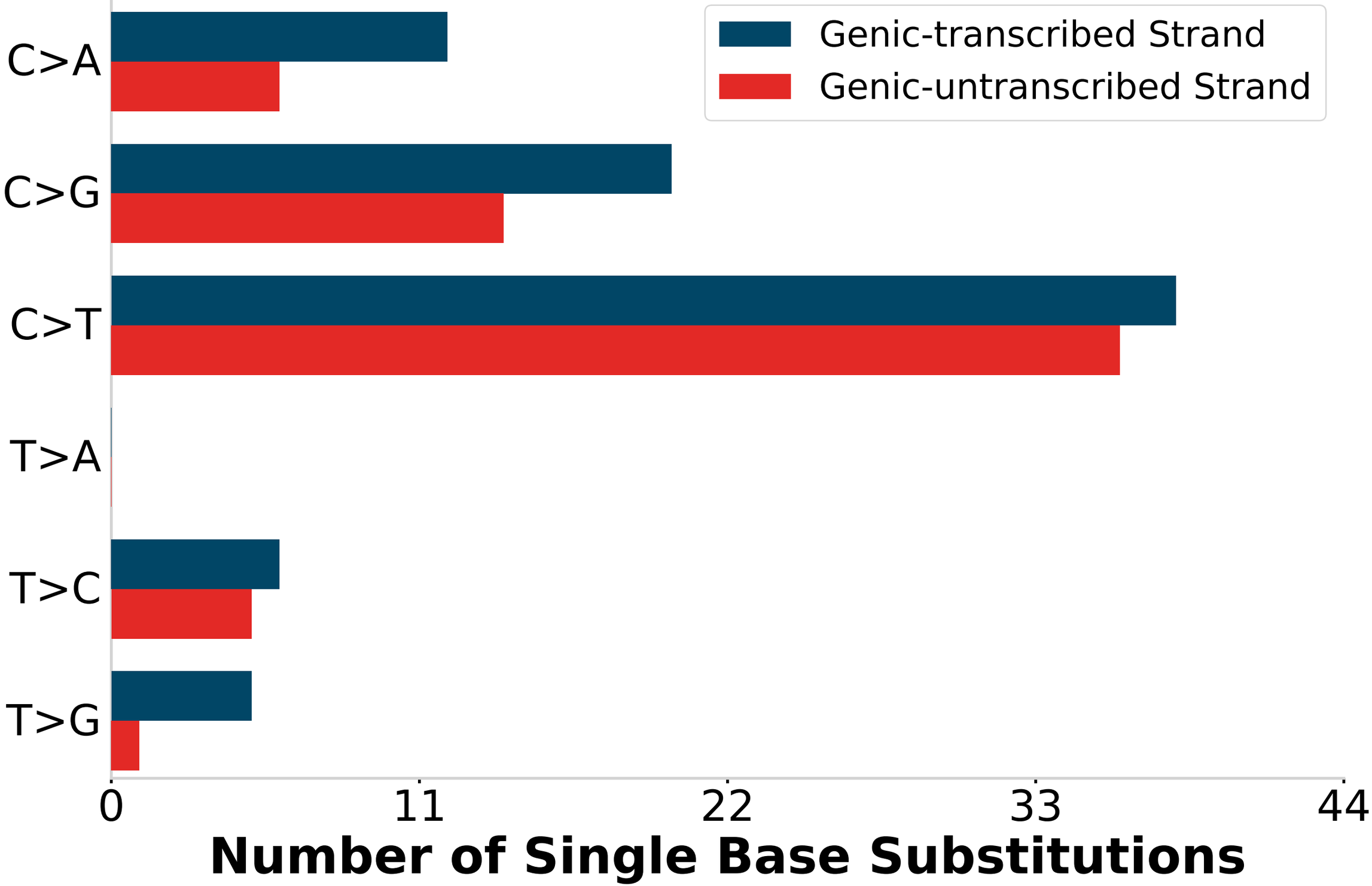
TCGA-FD-A5BX-01A-11D-A26M-08: 374 tra



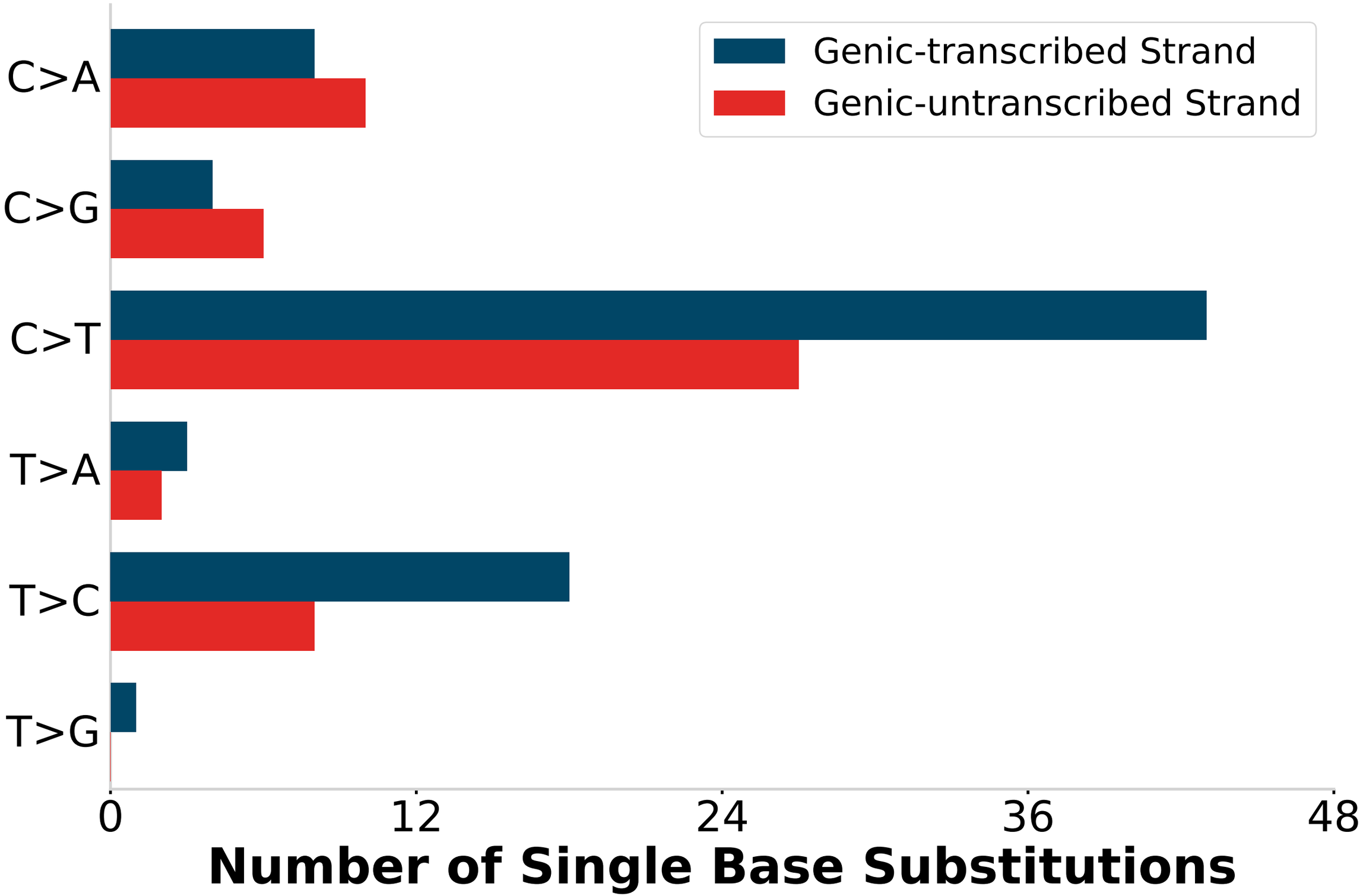
TCGA-FD-A5BY-01A-31D-A289-08: 55 trans



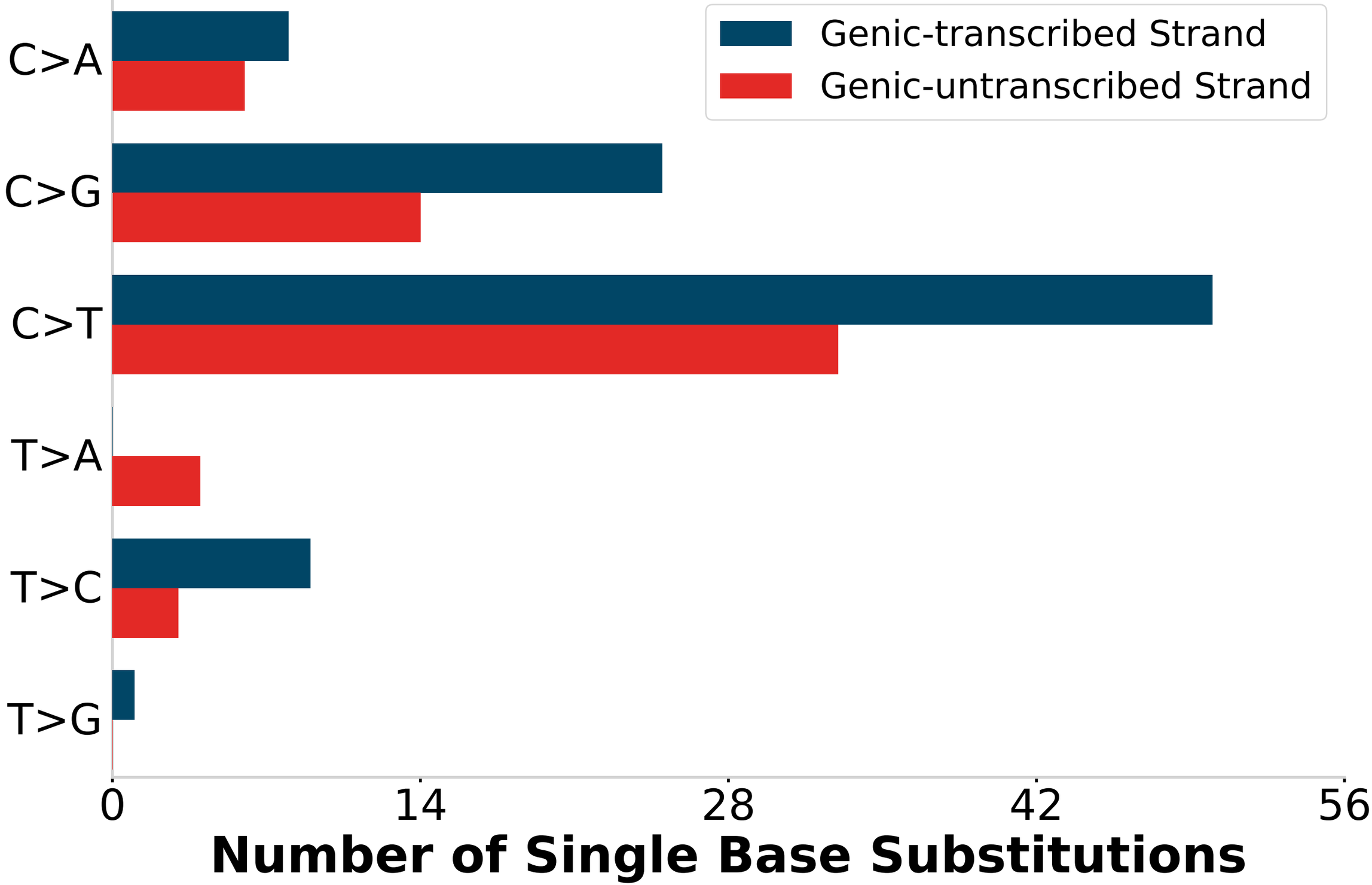
TCGA-FD-A5BZ-01A-11D-A289-08: 143 tra



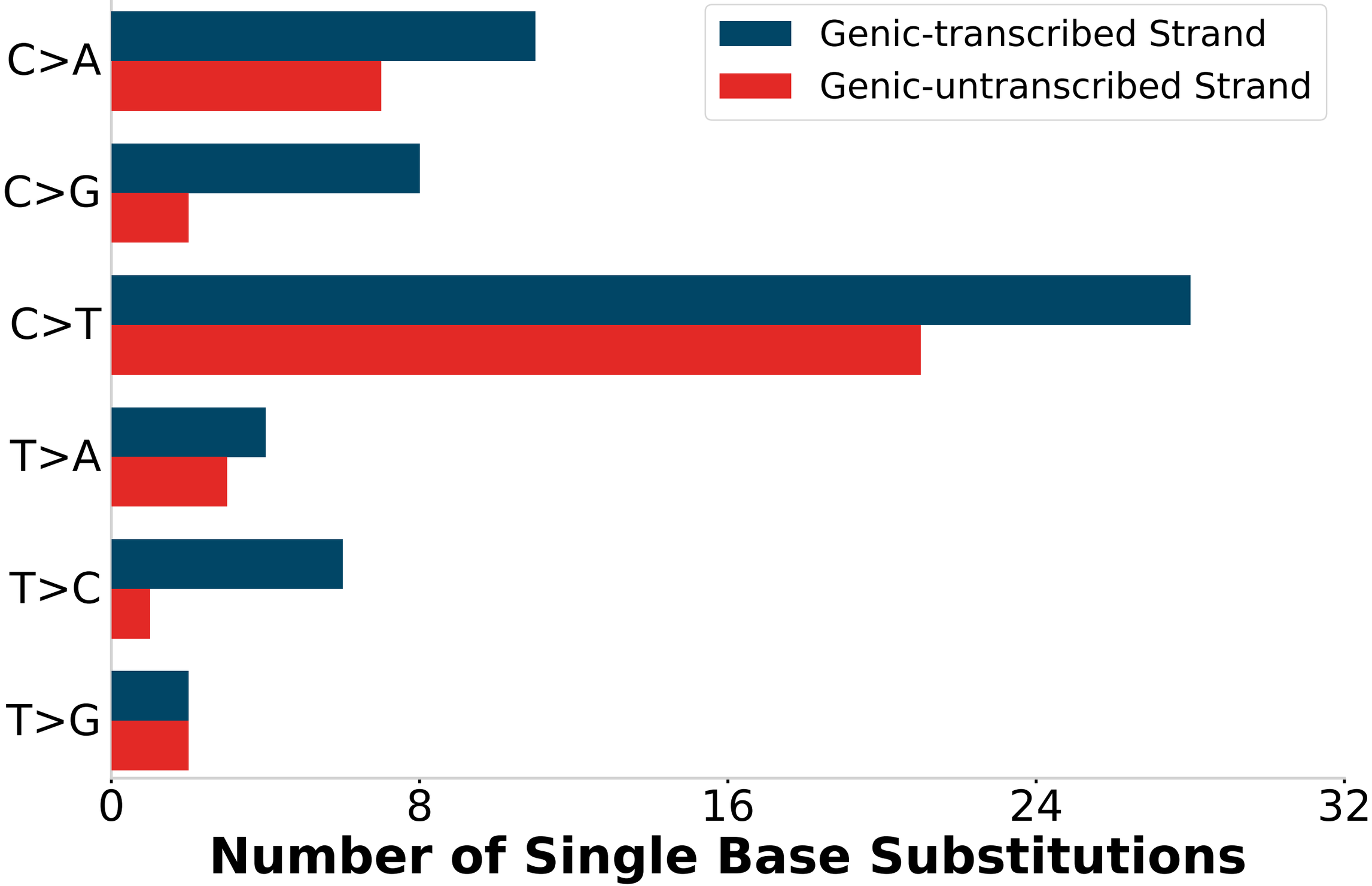
TCGA-FD-A5C0-01A-11D-A289-08: 130 tra



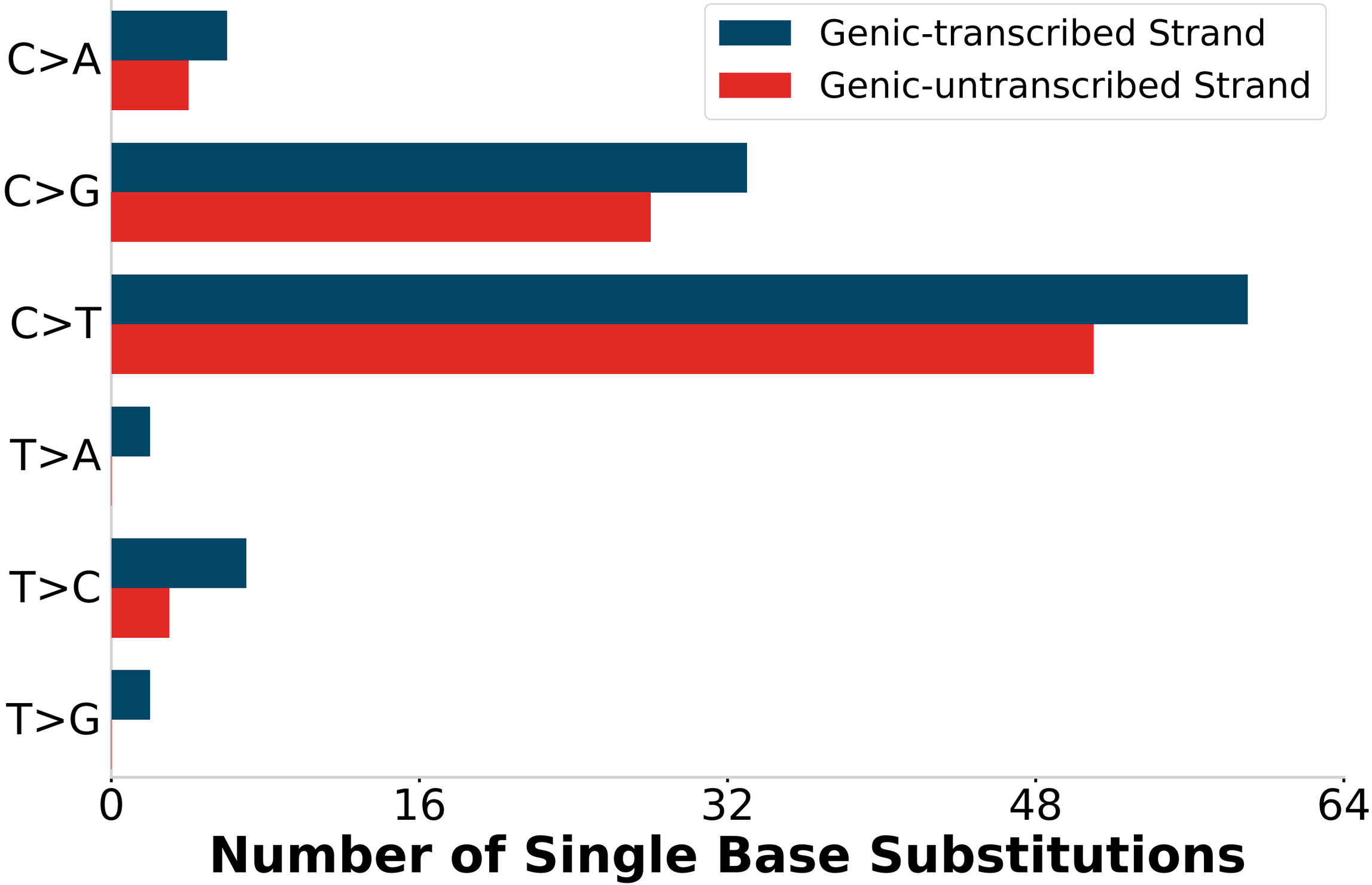
TCGA-FD-A5C1-01A-11D-A289-08: 153 tra



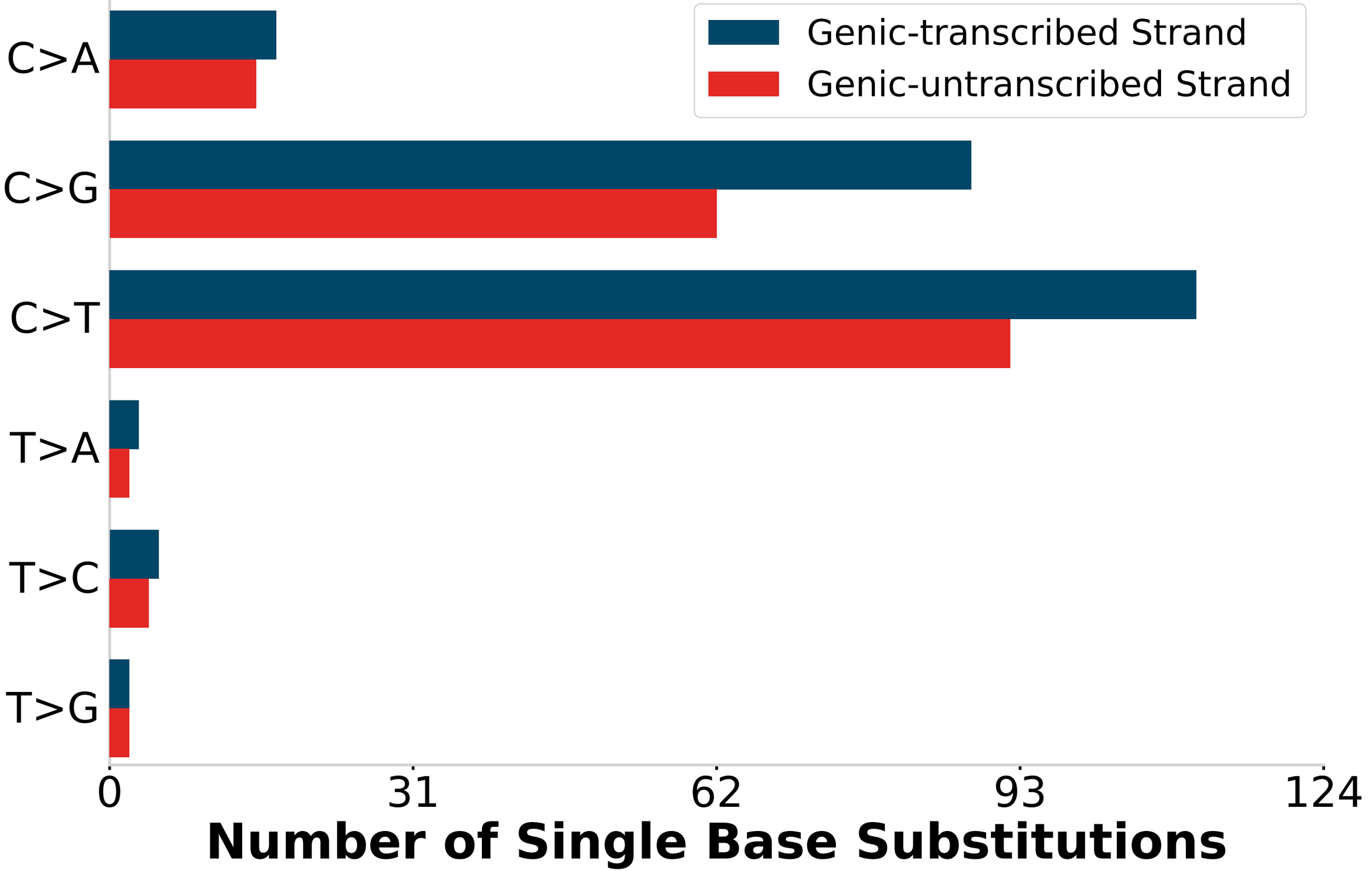
TCGA-FD-A62N-01A-11D-A30E-08: 95 trans



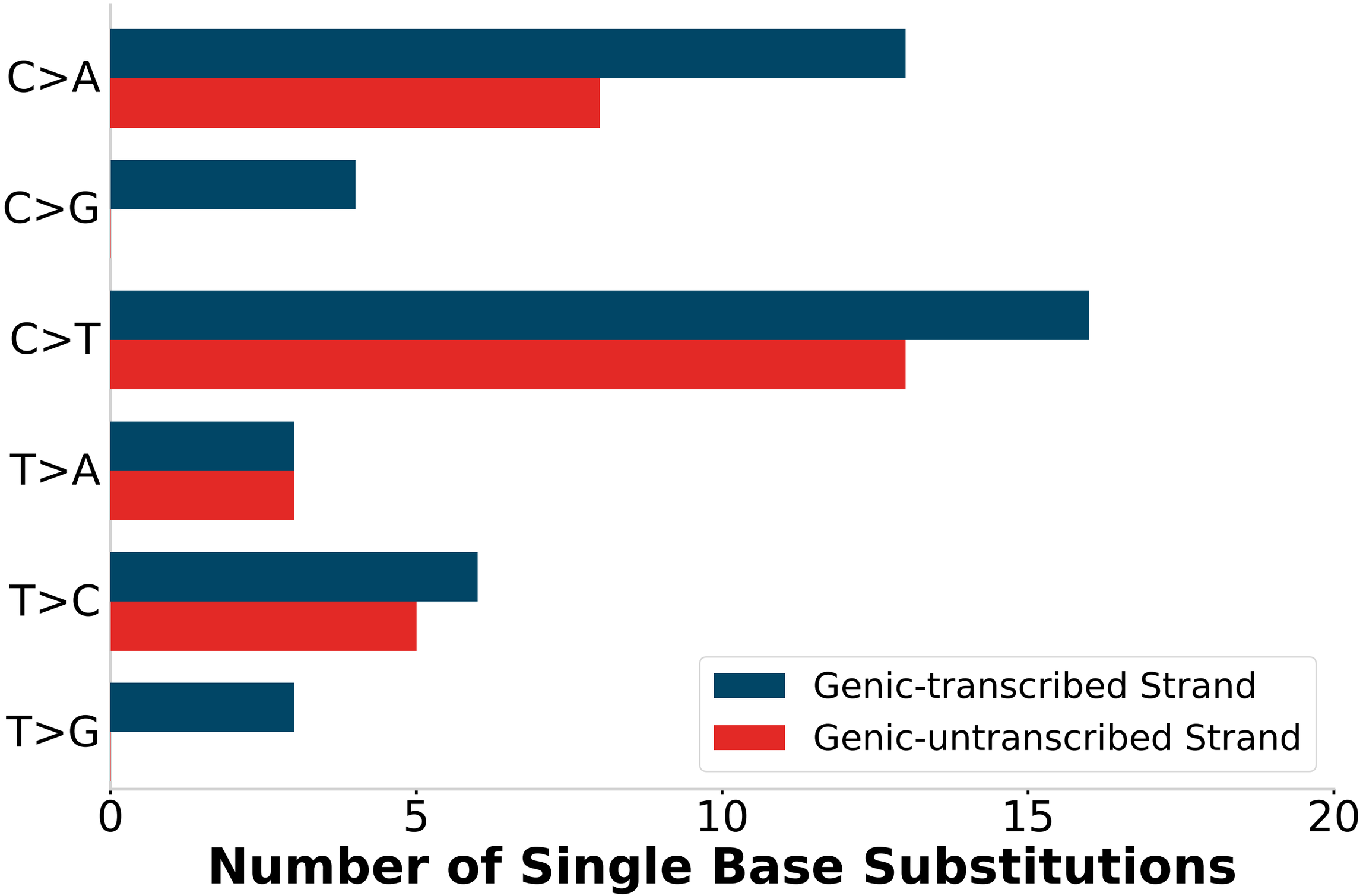
TCGA-FD-A62O-01A-11D-A30E-08: 195 tra



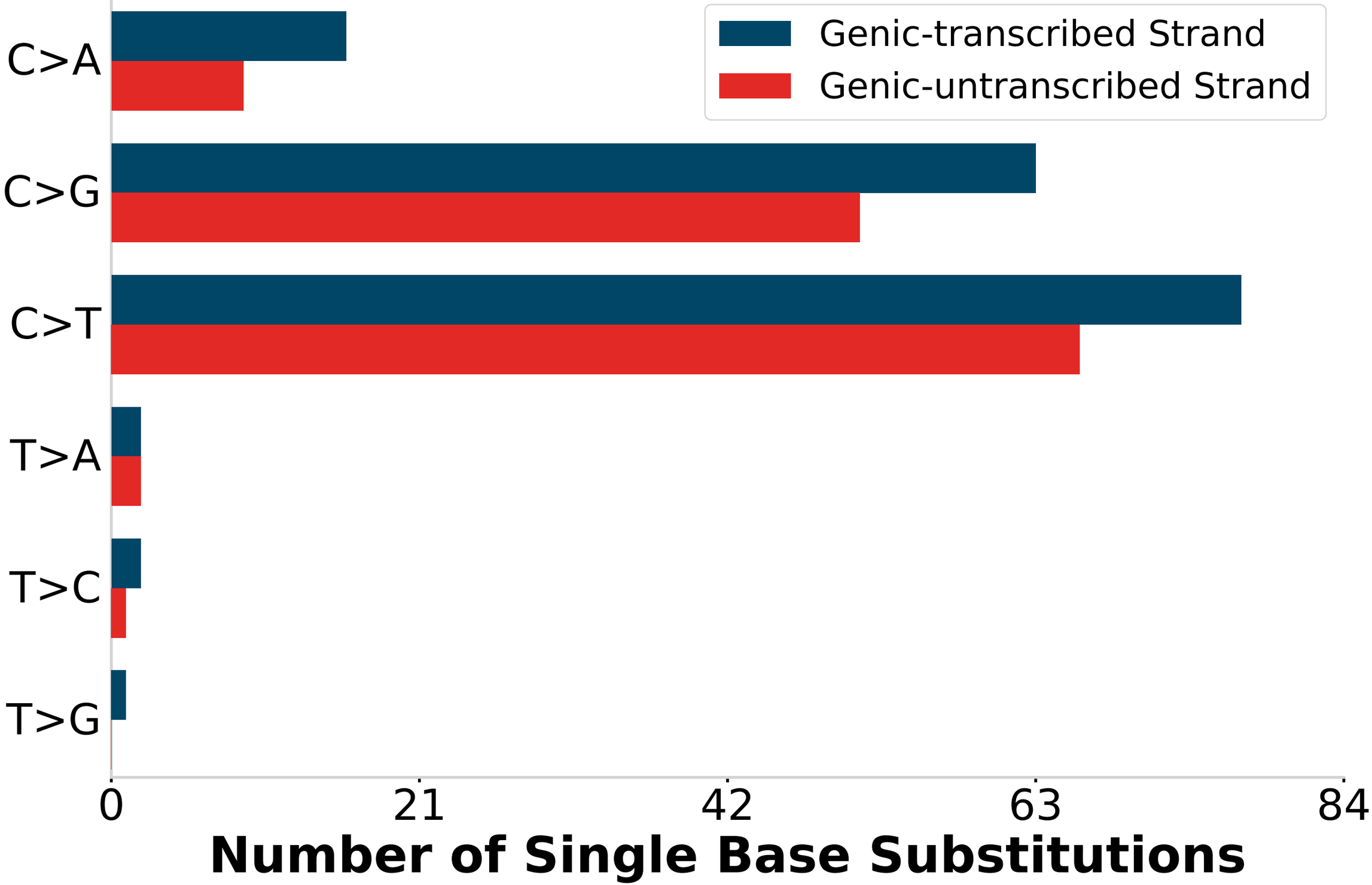
TCGA-FD-A62P-01A-32D-A30E-08: 403 tra



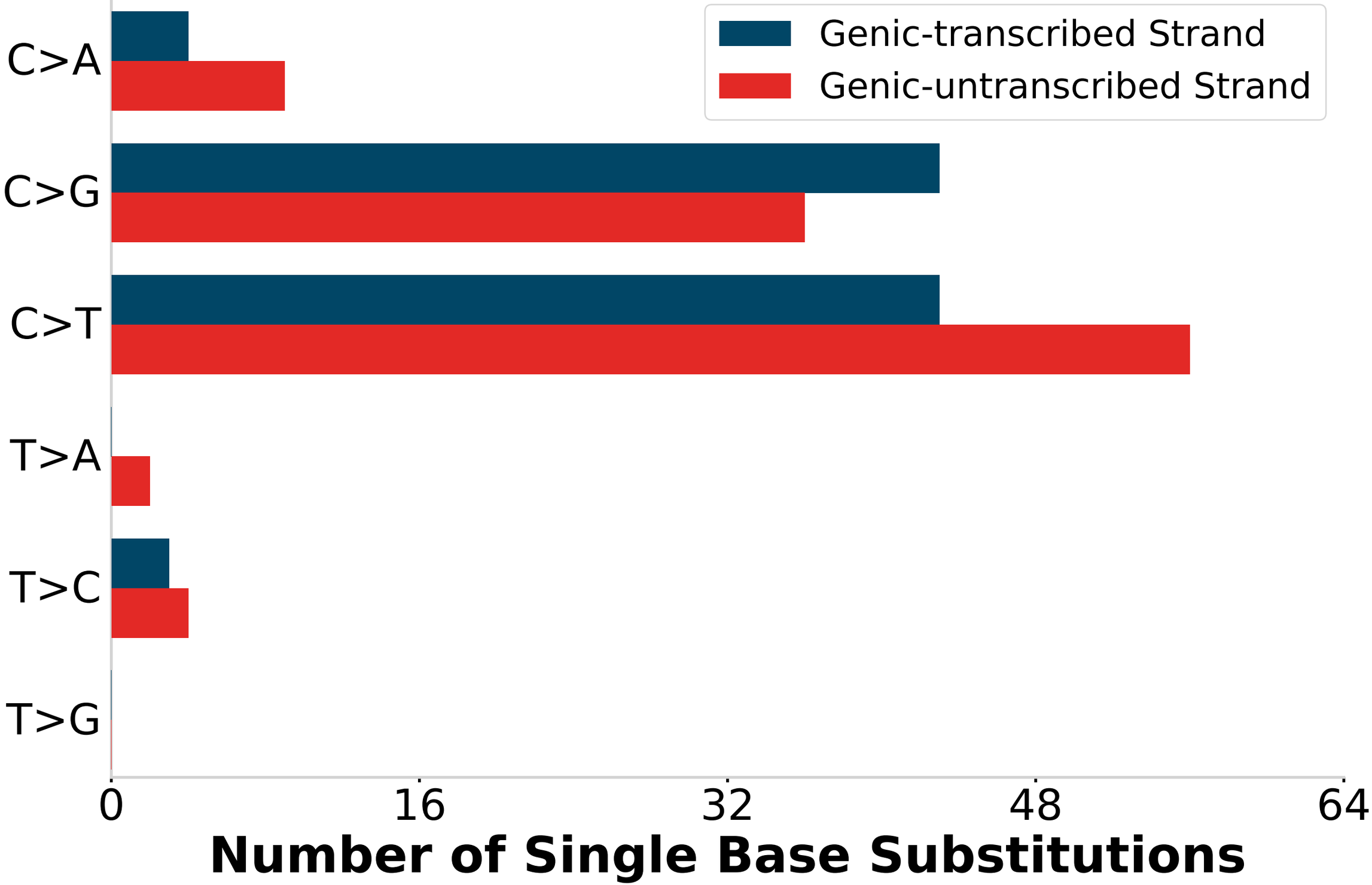
TCGA-FD-A62S-01A-11D-A30E-08: 74 trans



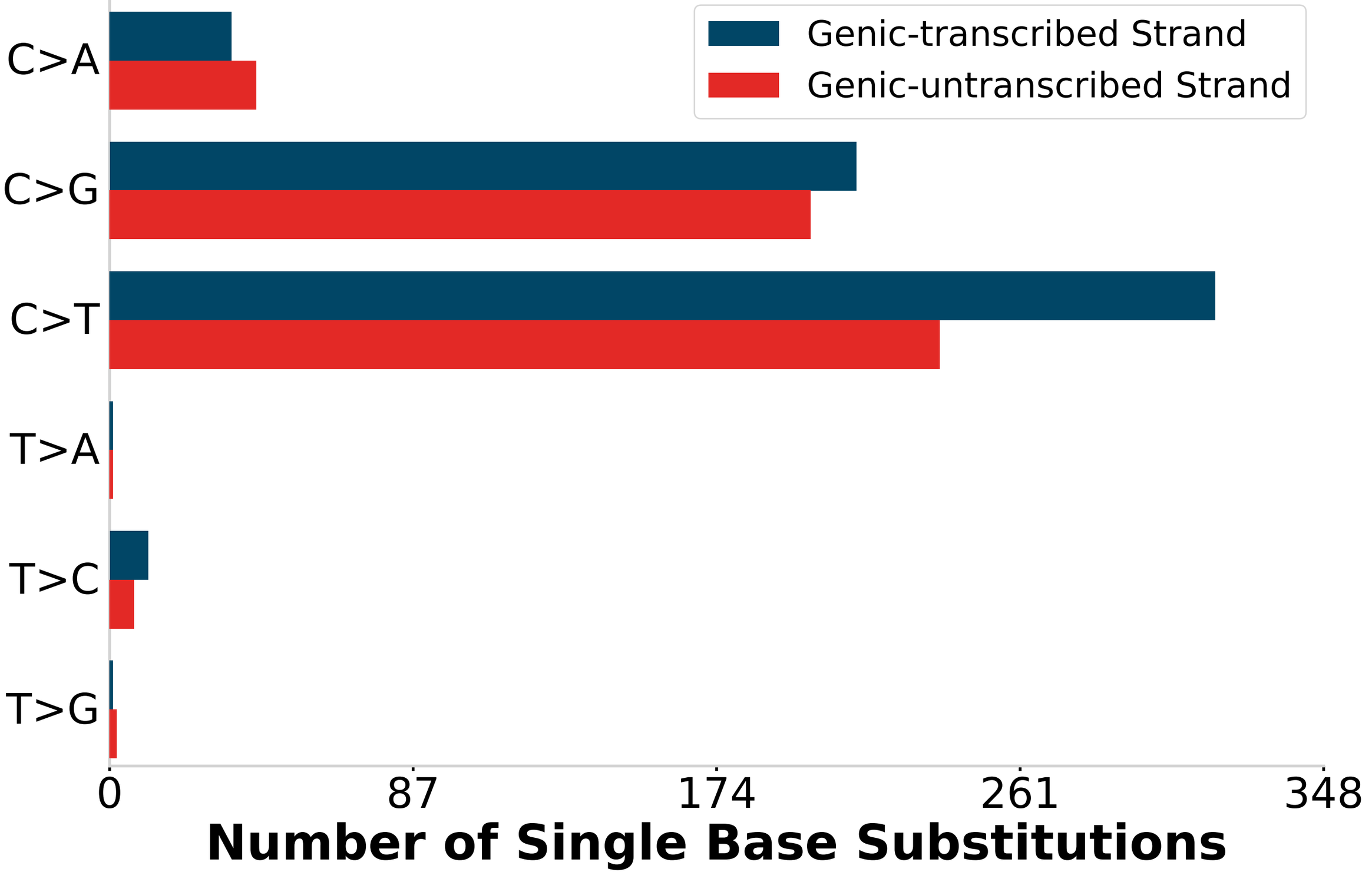
TCGA-FD-A6TA-01A-12D-A339-08: 290 tra



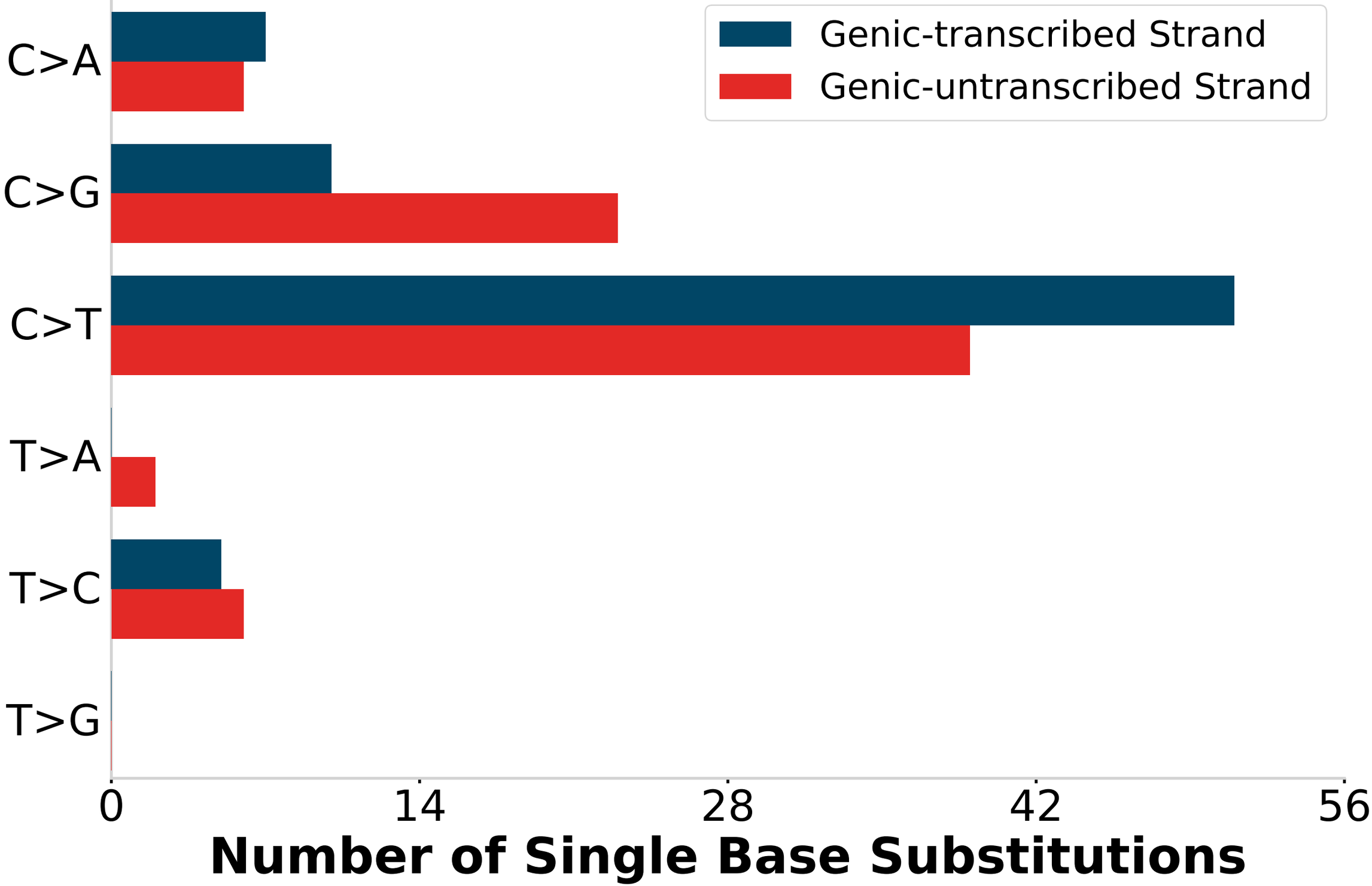
TCGA-FD-A6TB-01A-12D-A339-08: 200 tra



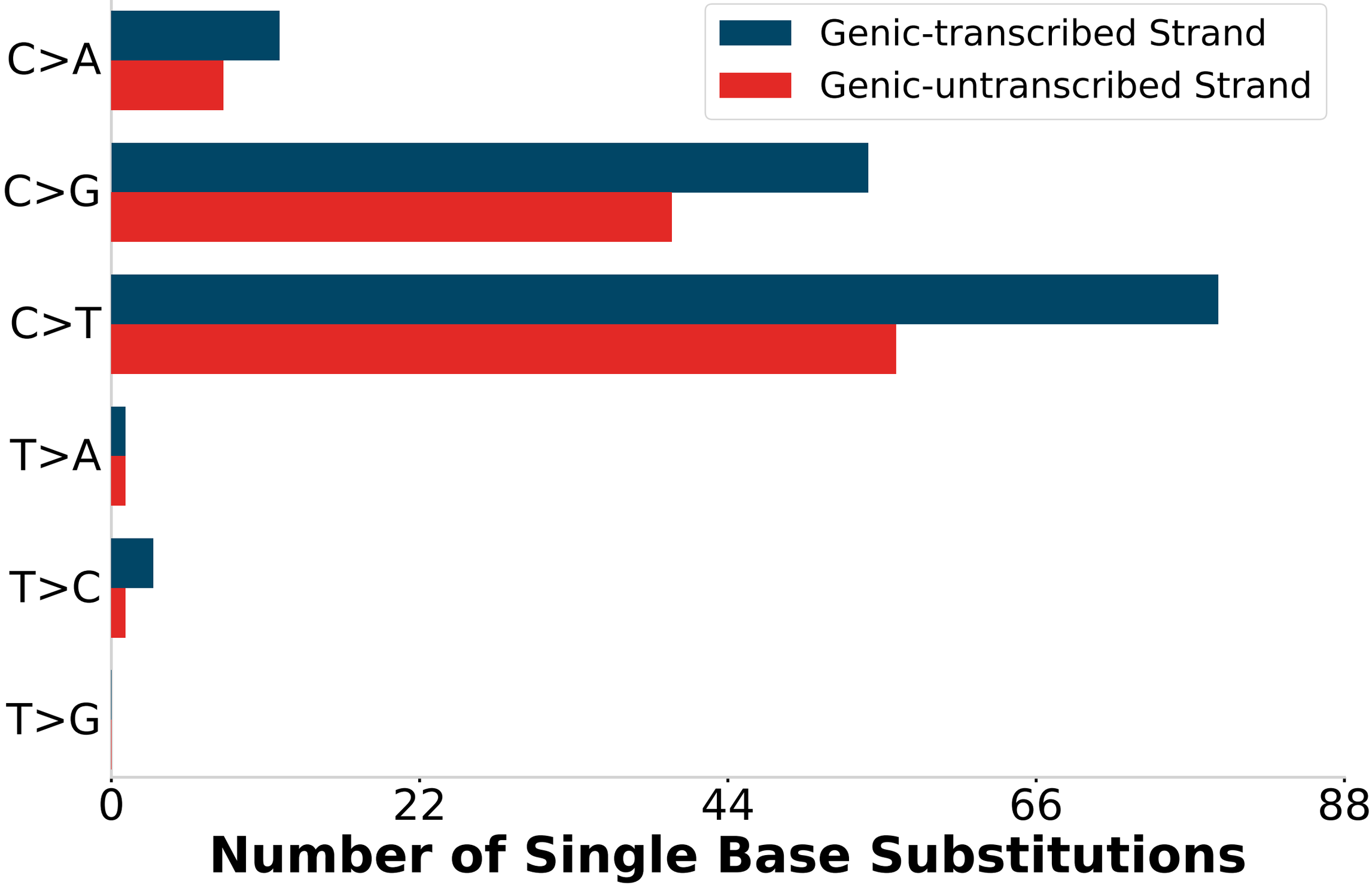
TCGA-FD-A6TC-01A-21D-A339-08: 1,070 tr



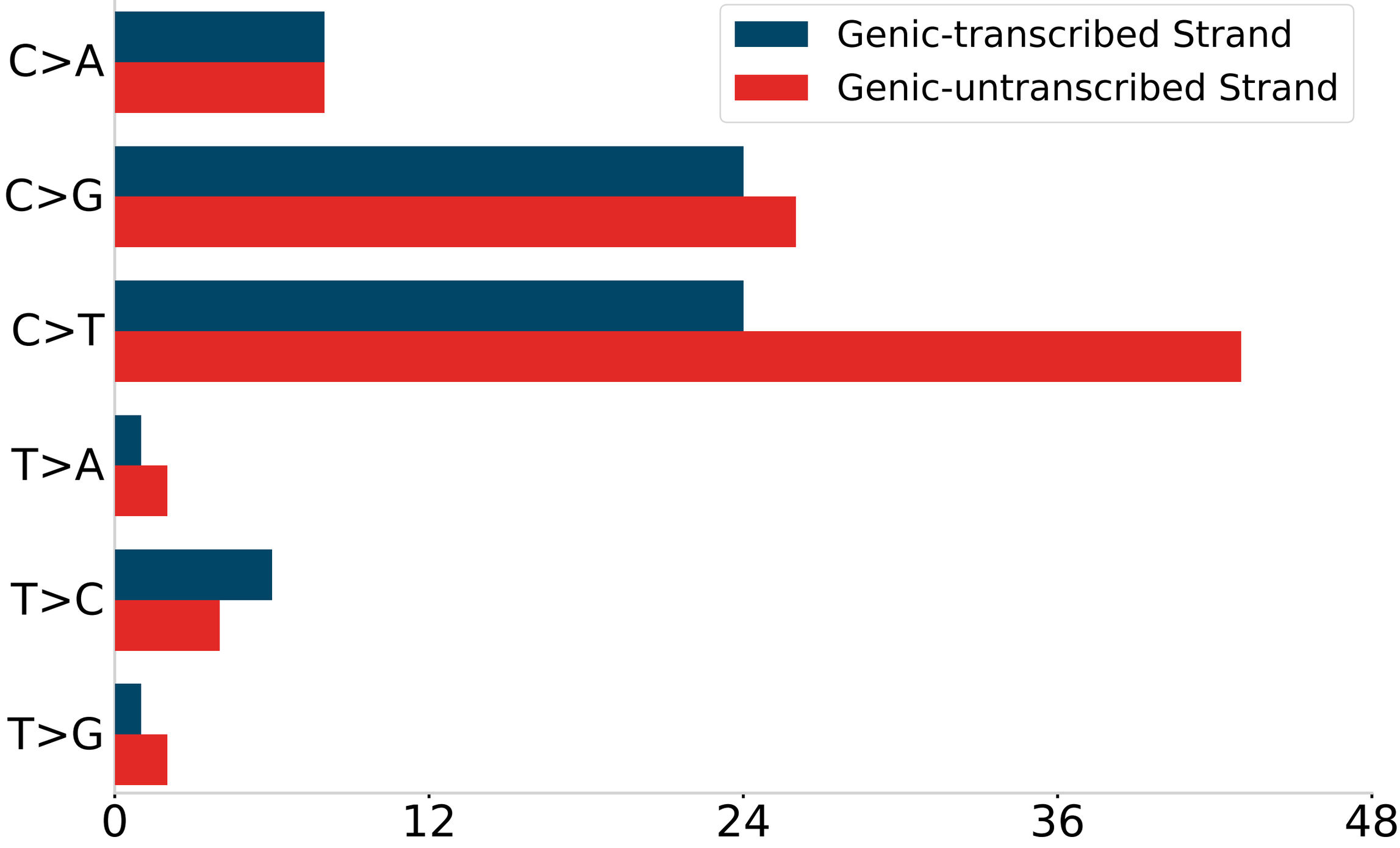
TCGA-FD-A6TD-01A-51D-A339-08: 149 tra



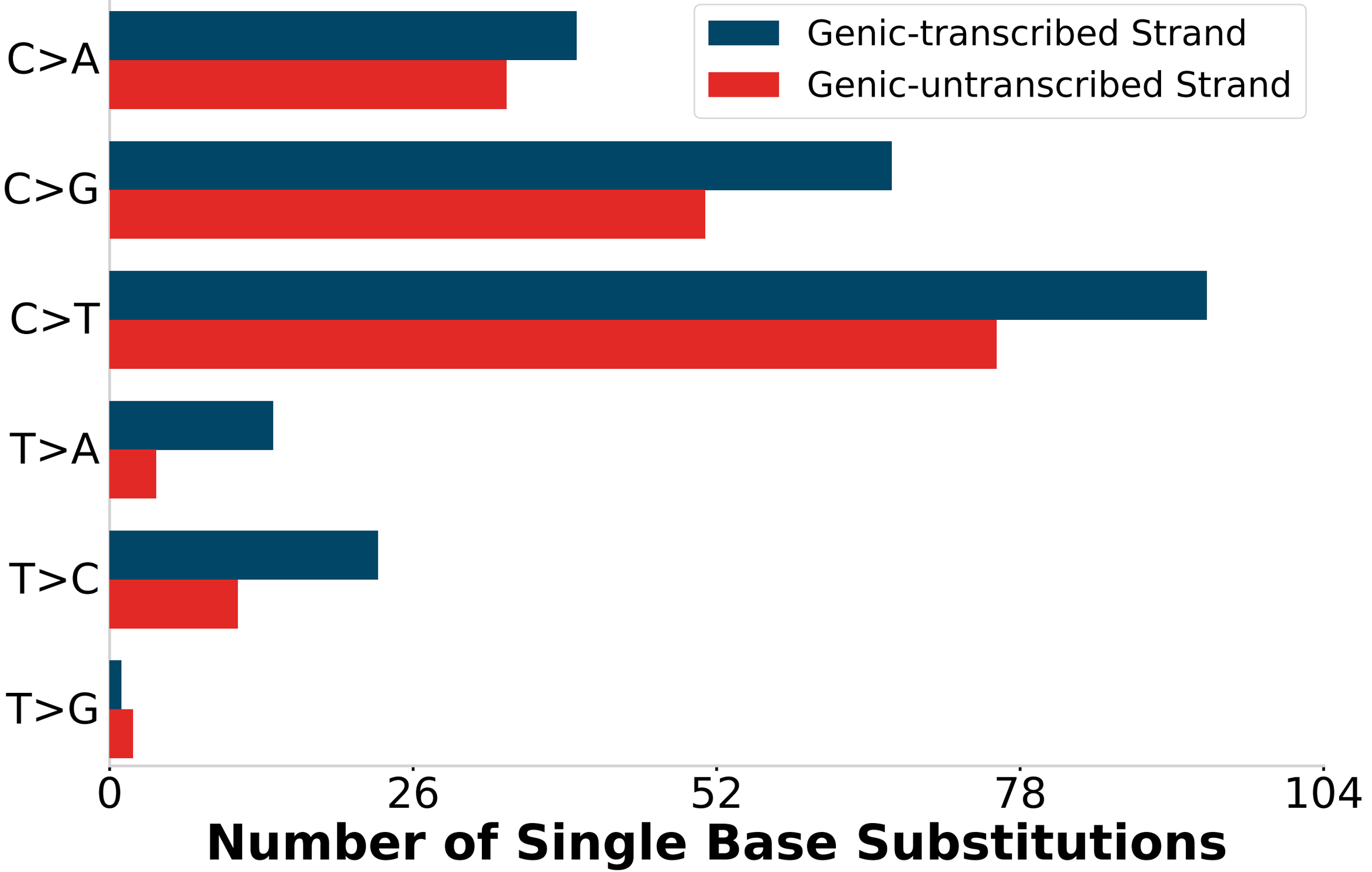
TCGA-FD-A6TE-01A-12D-A339-08: 255 tran



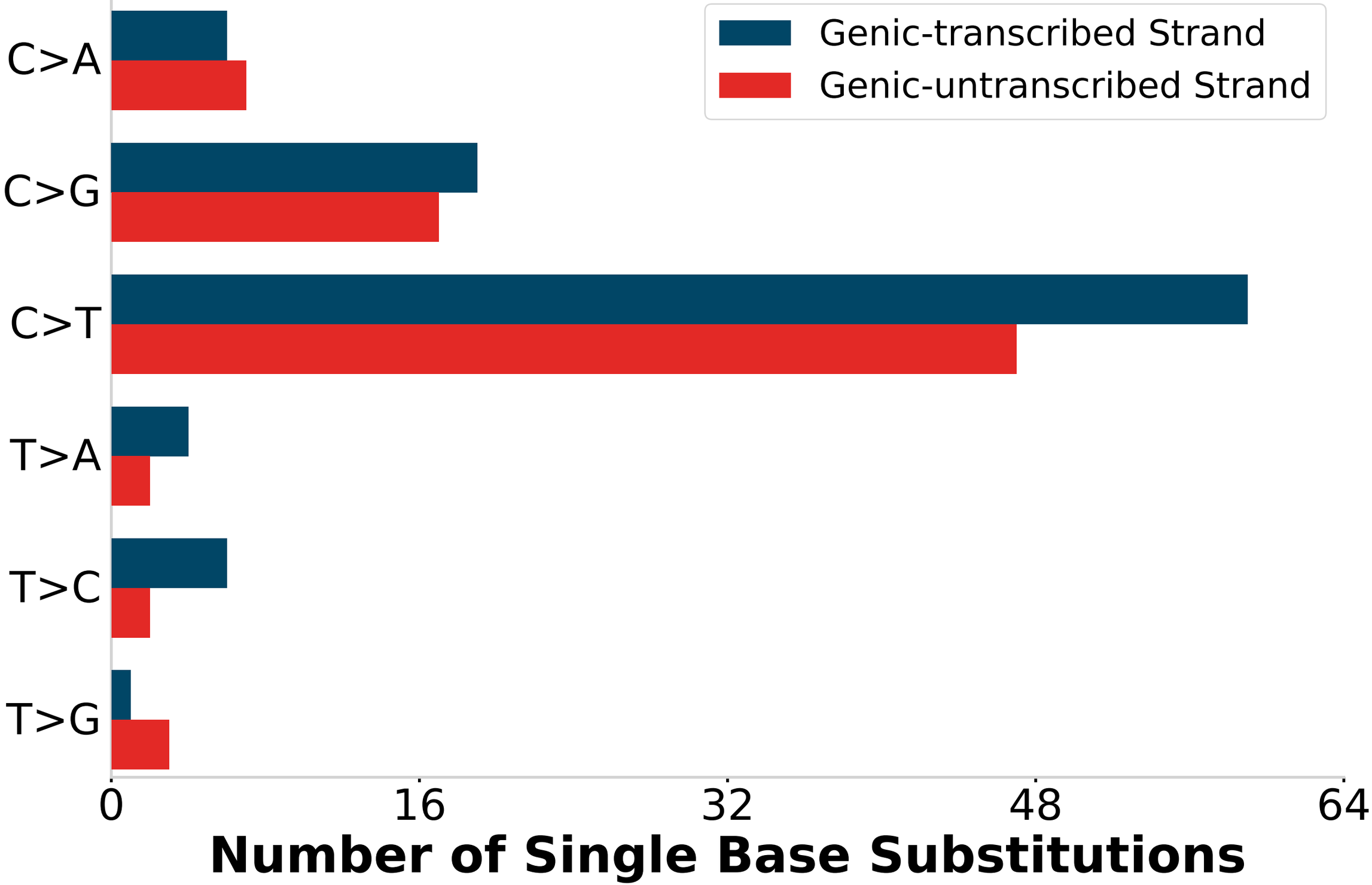
TCGA-FD-A6TF-01A-52D-A32B-08: 149 tra



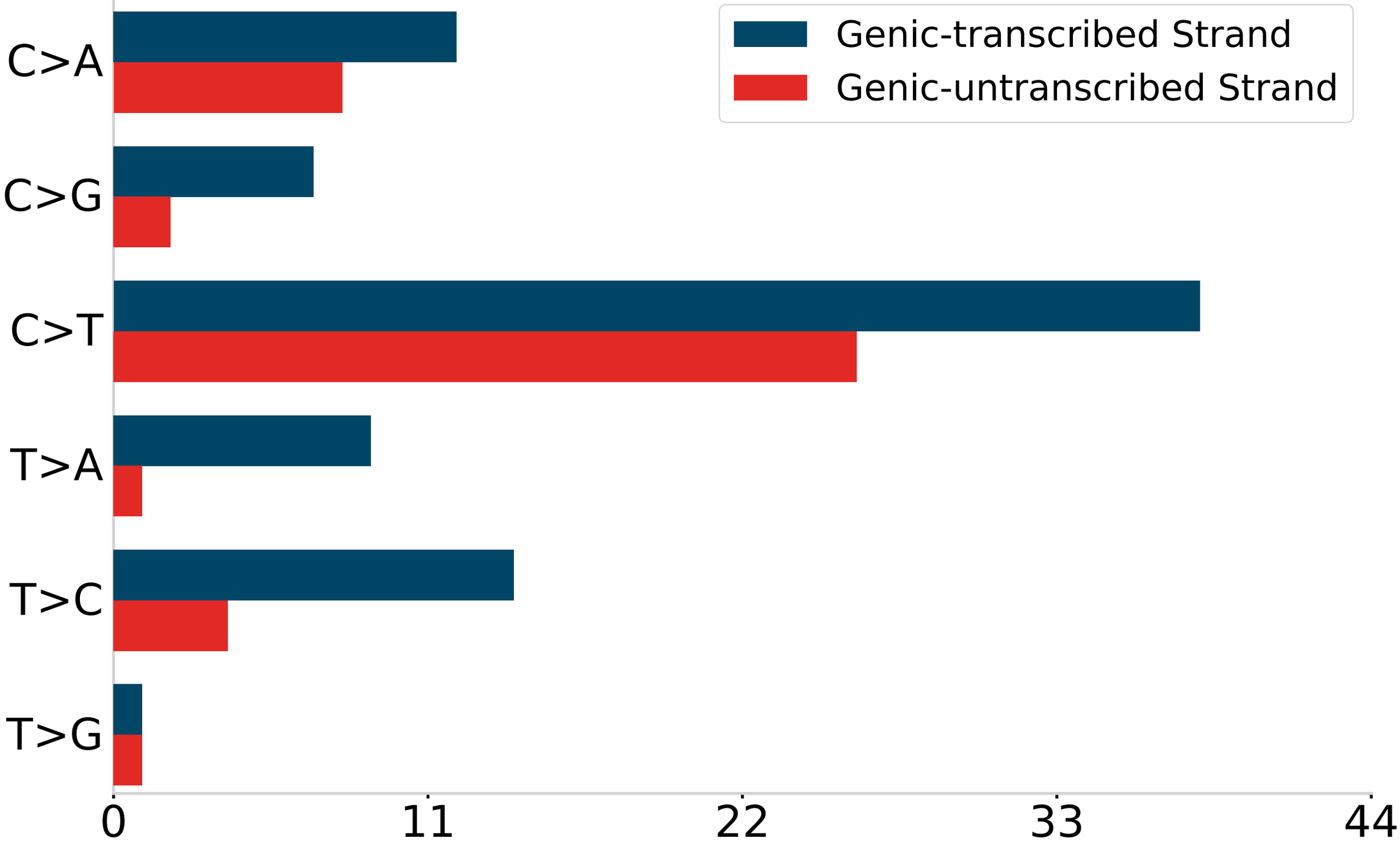
TCGA-FD-A6TG-01A-11D-A32B-08: 417 tra



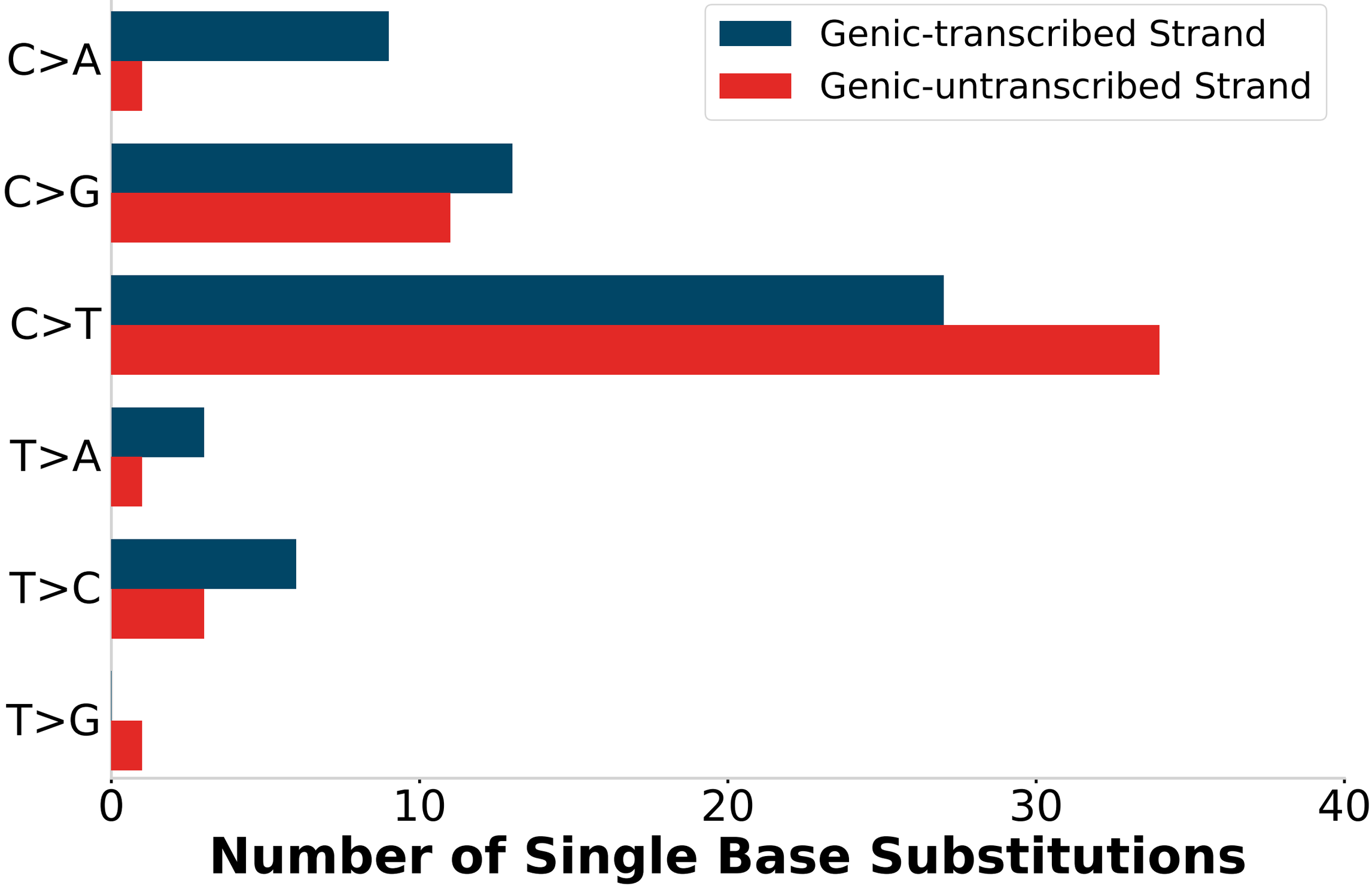
TCGA-FD-A6TH-01A-11D-A32B-08: 173 tra



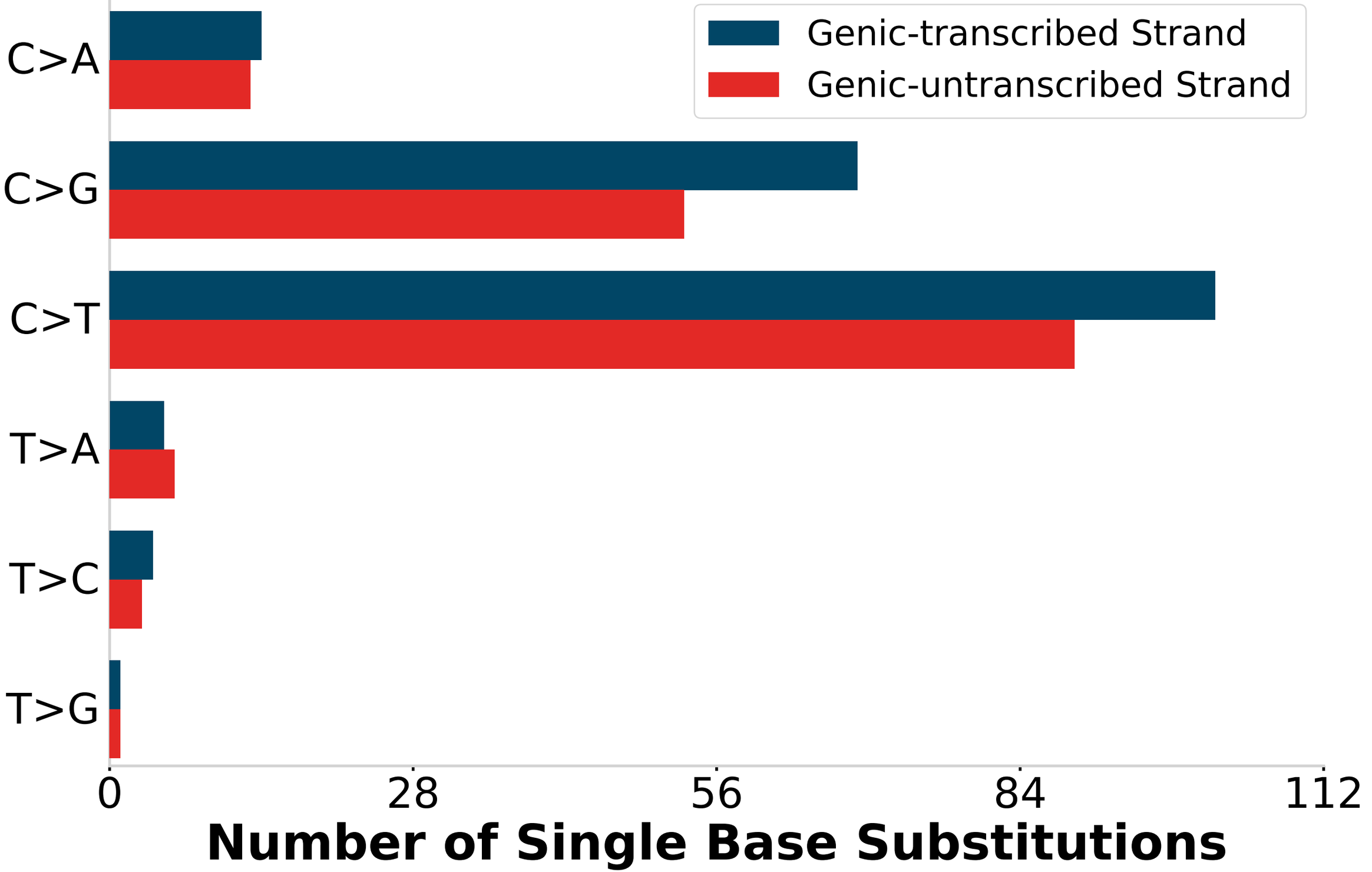
TCGA-FD-A6TI-01A-11D-A32B-08: 123 tran



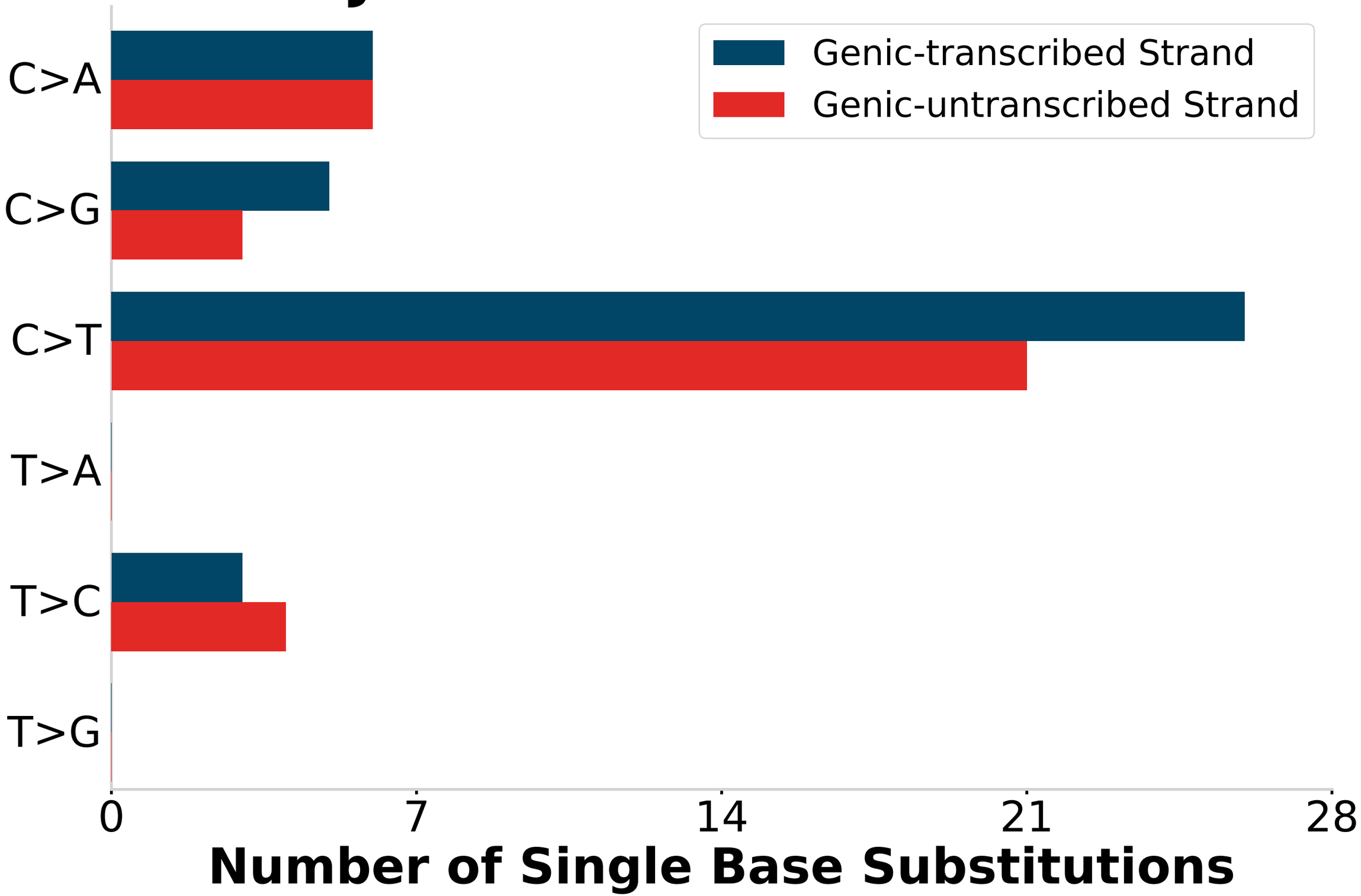
TCGA-FD-A6TK-01A-42D-A339-08: 109 tran



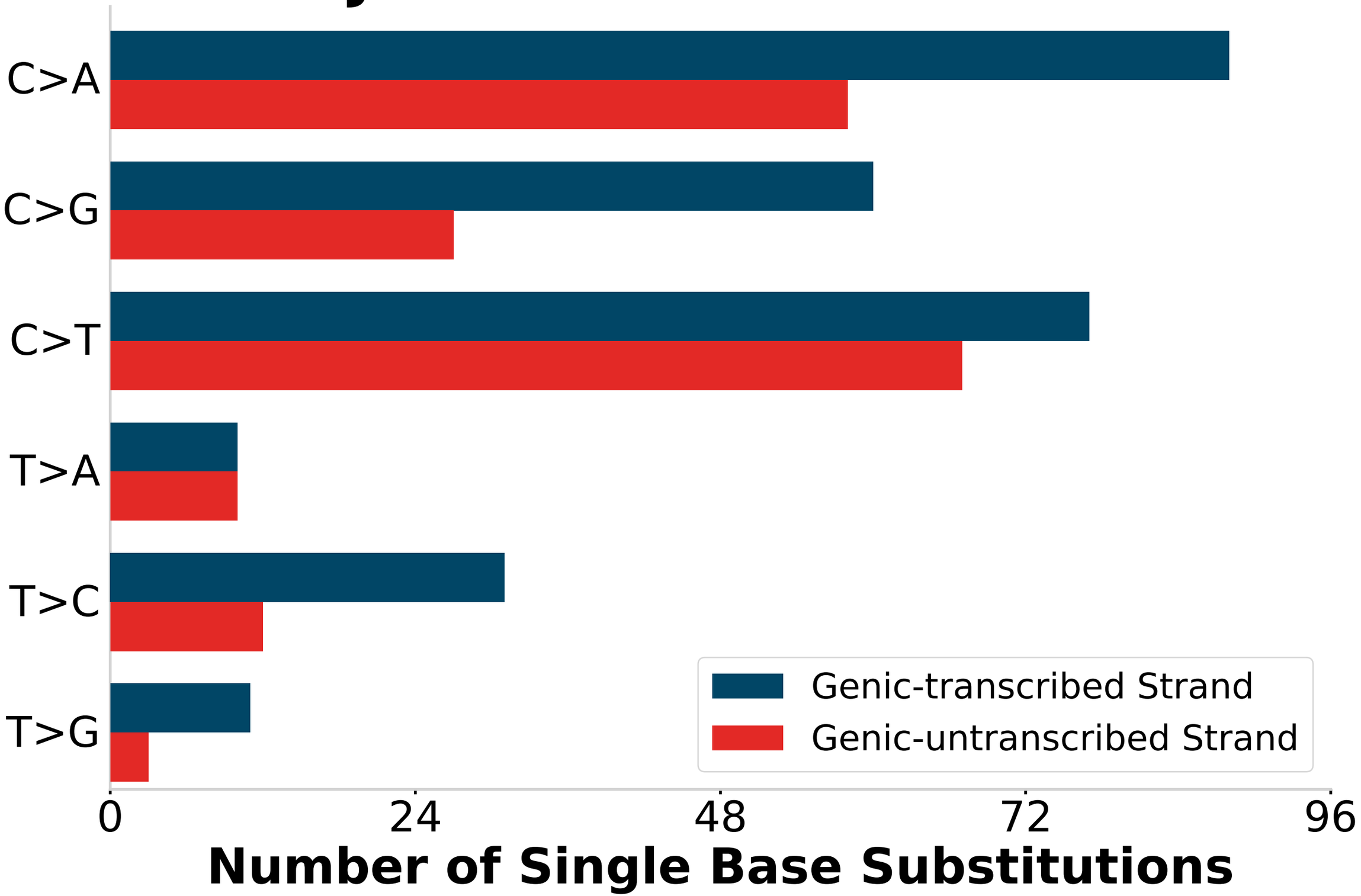
TCGA-FJ-A3Z7-01A-12D-A23M-08: 360 tran



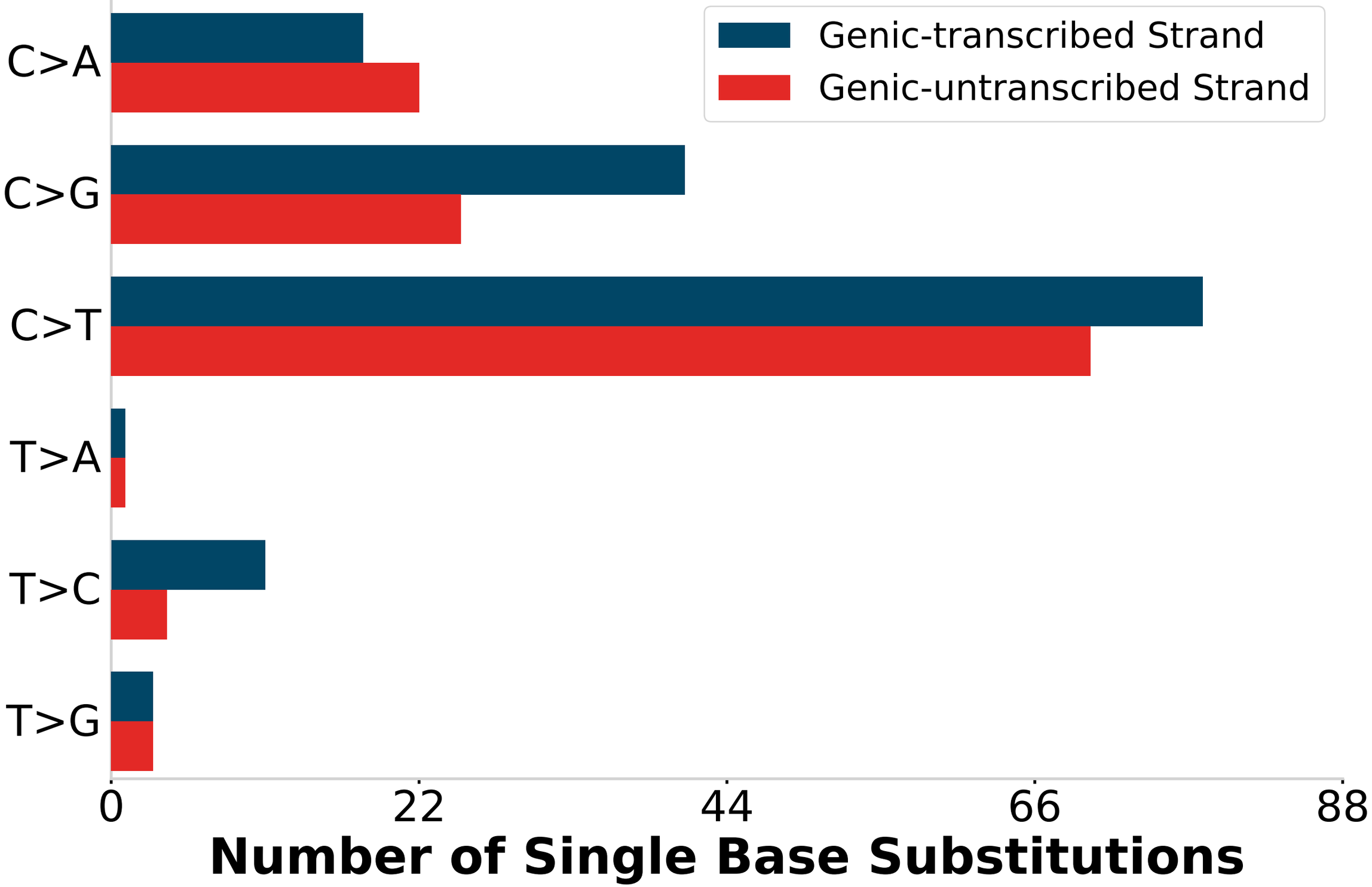
TCGA-FJ-A3Z9-01A-11D-A26M-08: 74 trans



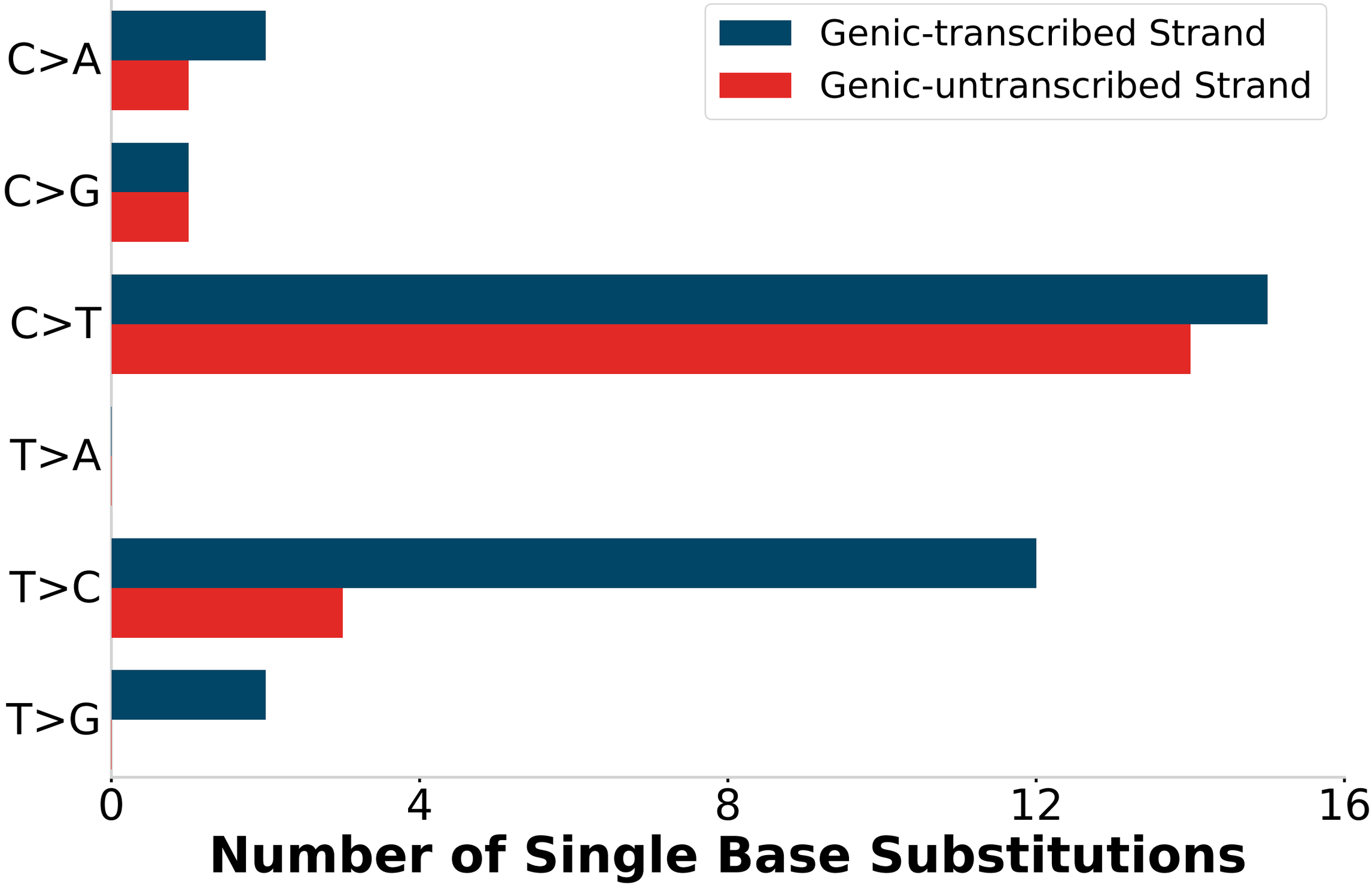
TCGA-FJ-A3ZE-01A-11D-A23M-08: 454 tran



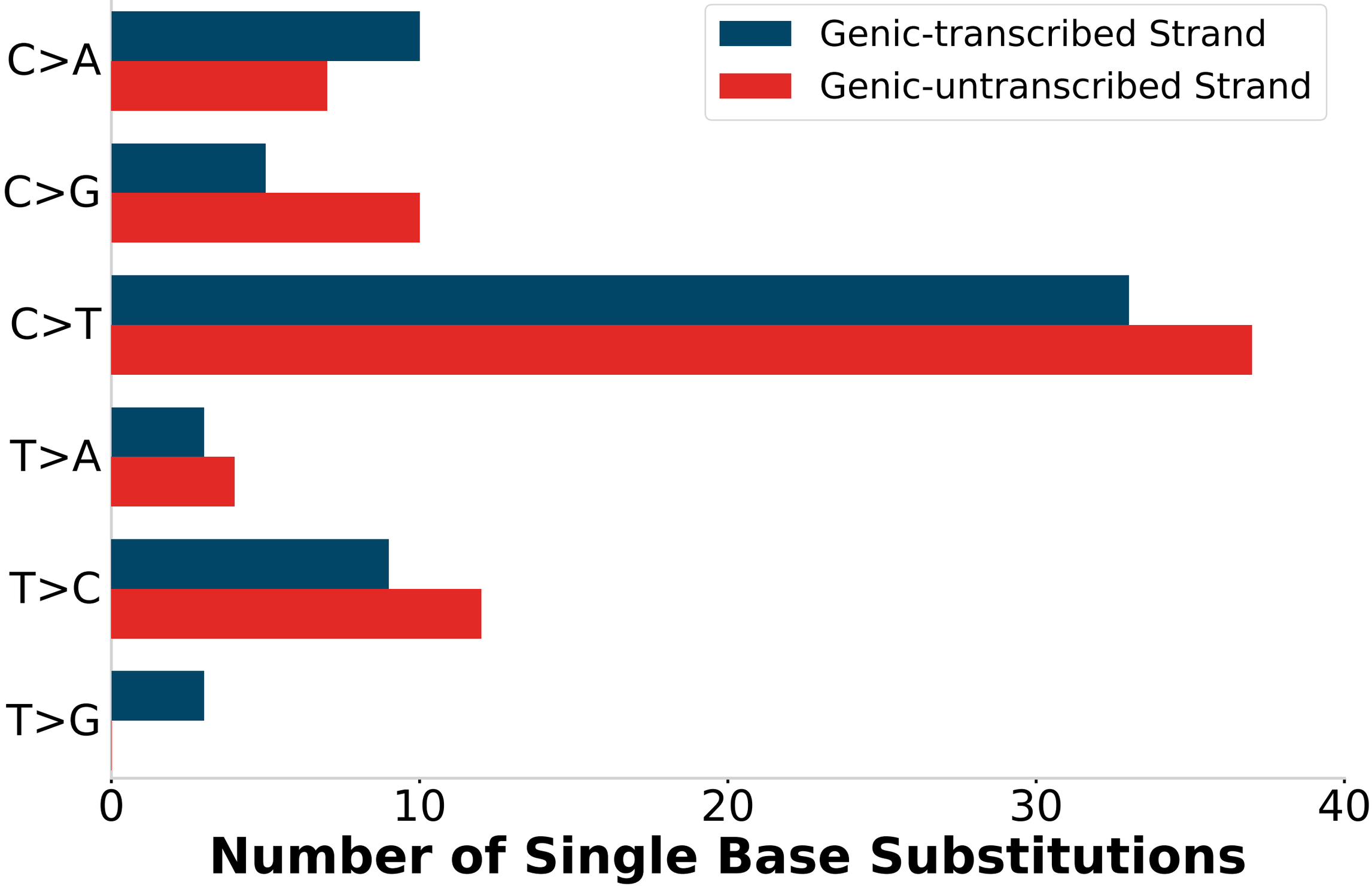
TCGA-FJ-A3ZF-01A-11D-A23M-08: 277 tran



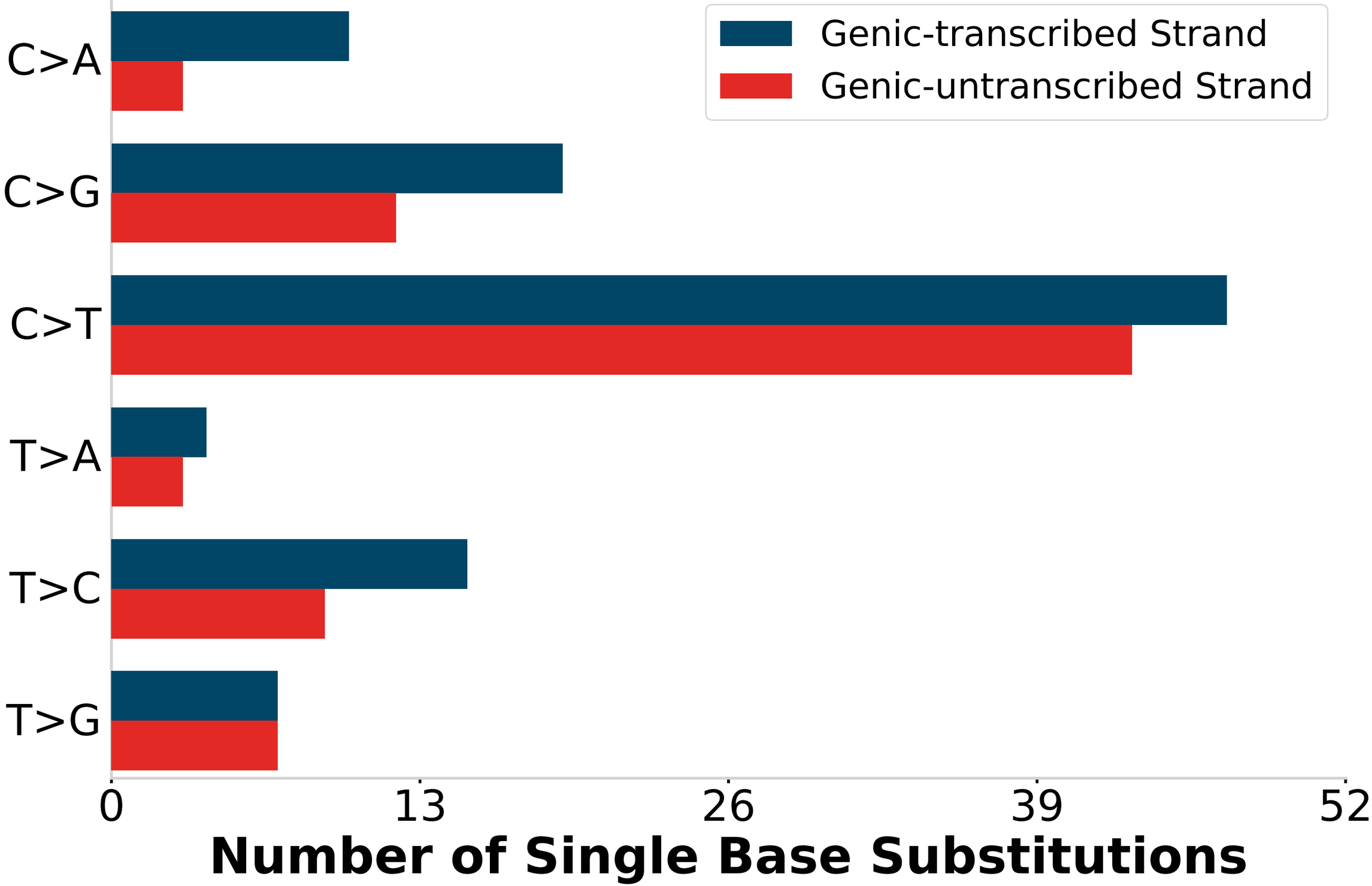
TCGA-FJ-A871-01A-11D-A34U-08: 51 trans



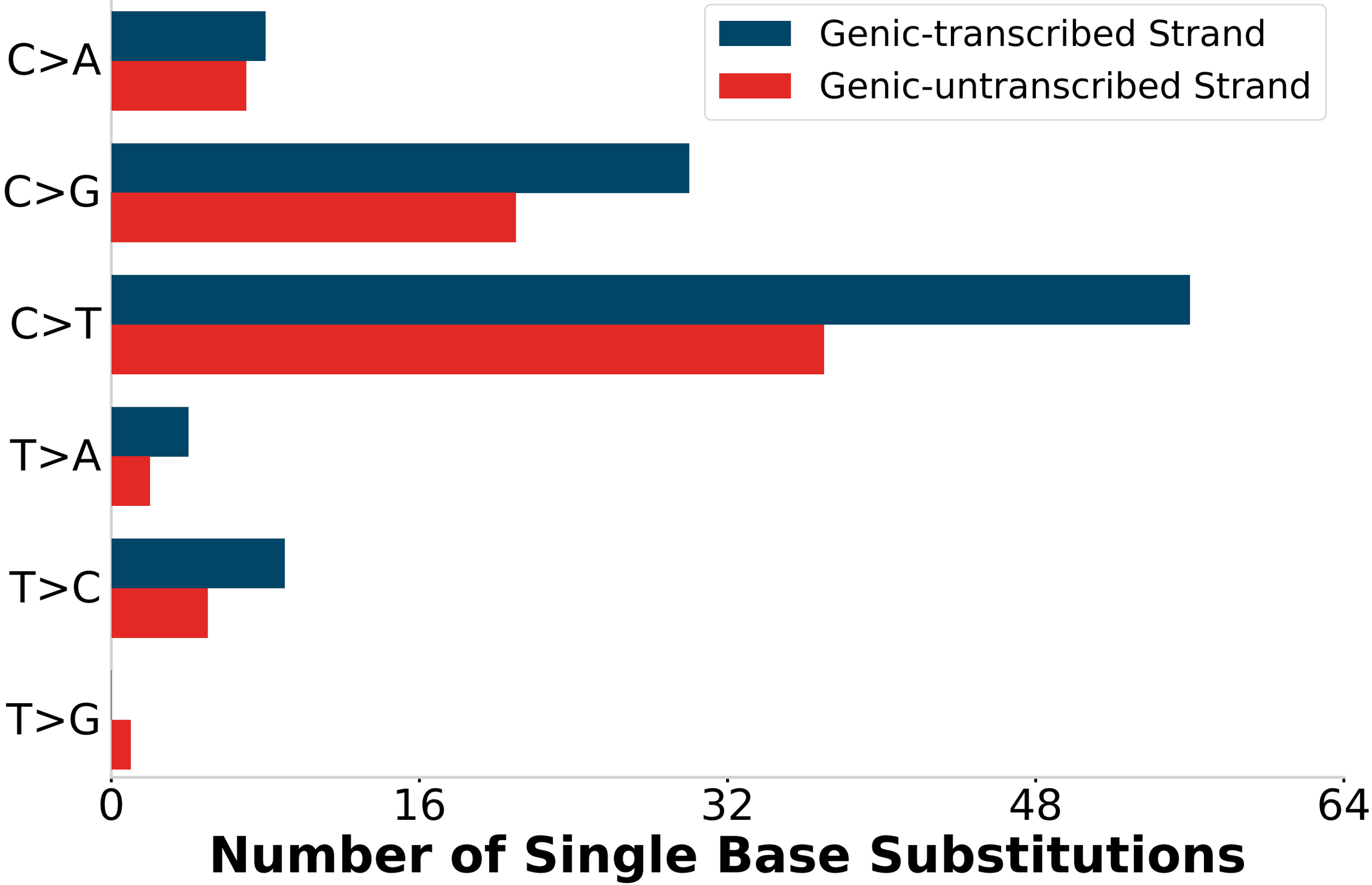
TCGA-FT-A3EE-01A-11D-A202-08: 133 tran



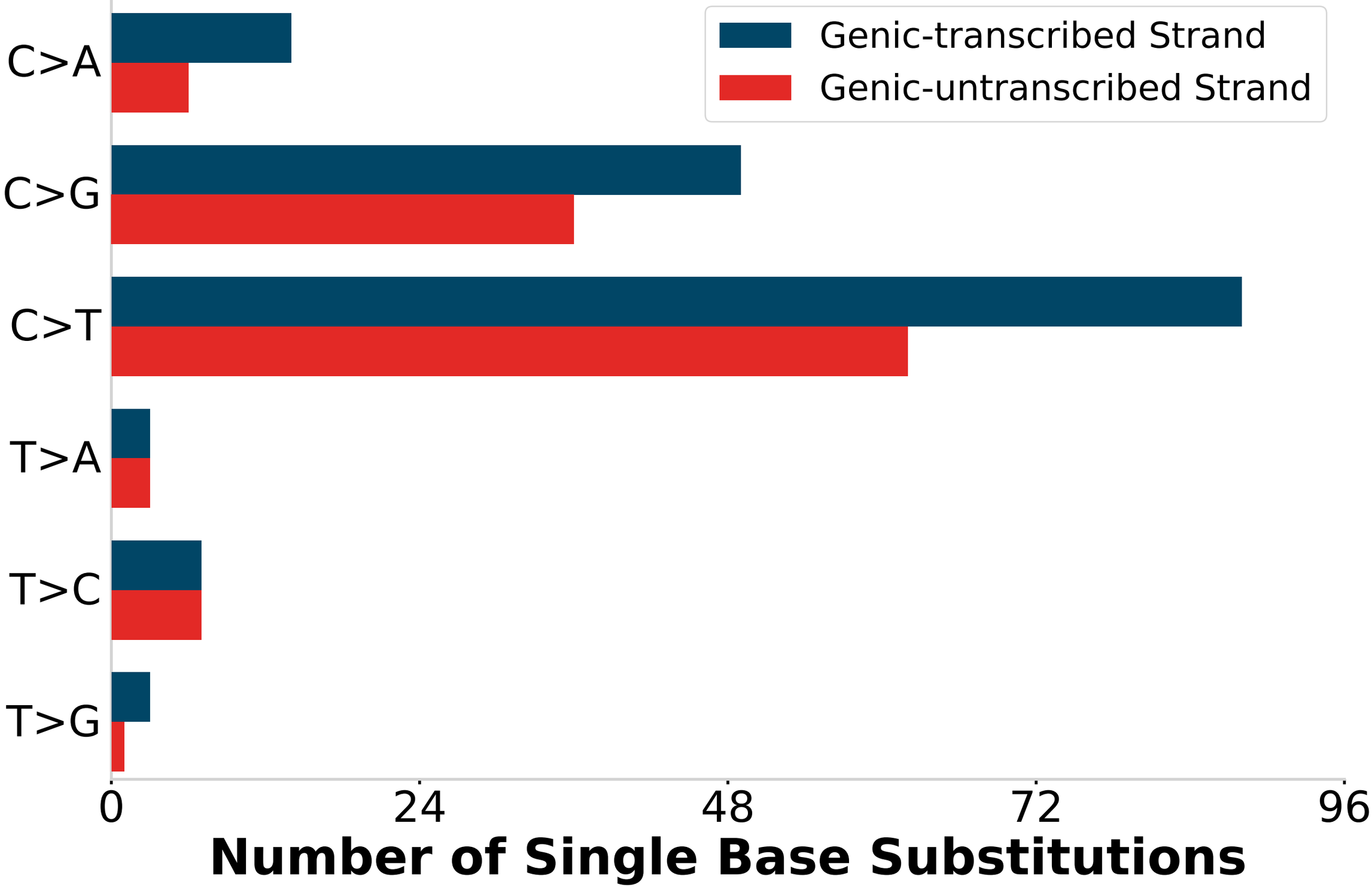
TCGA-FT-A61P-01A-11D-A30E-08: 179 tran



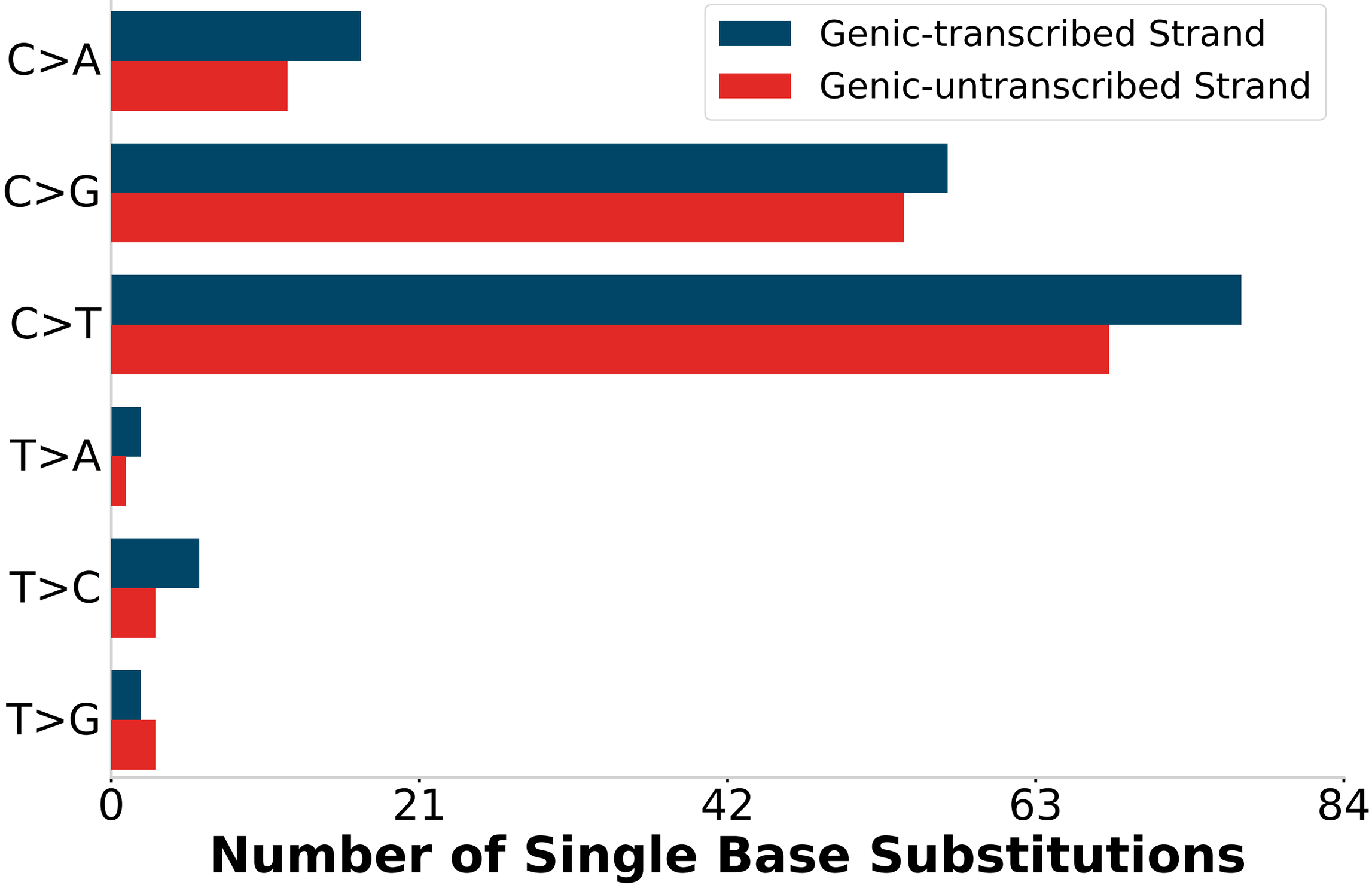
TCGA-G2-A2EC-01A-11D-A17V-08: 180 tra



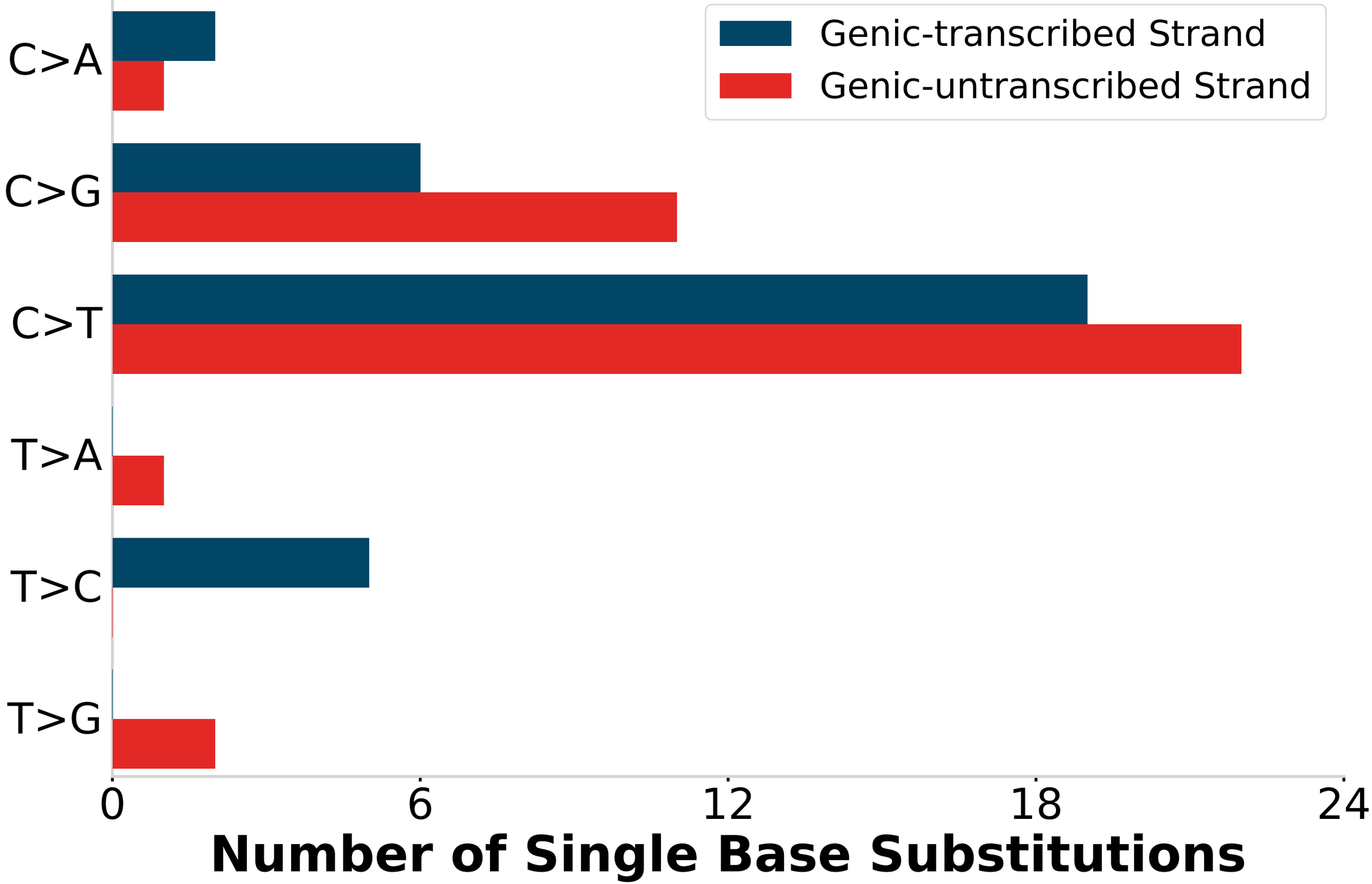
TCGA-G2-A2EF-01A-12D-A18F-08: 279 tran



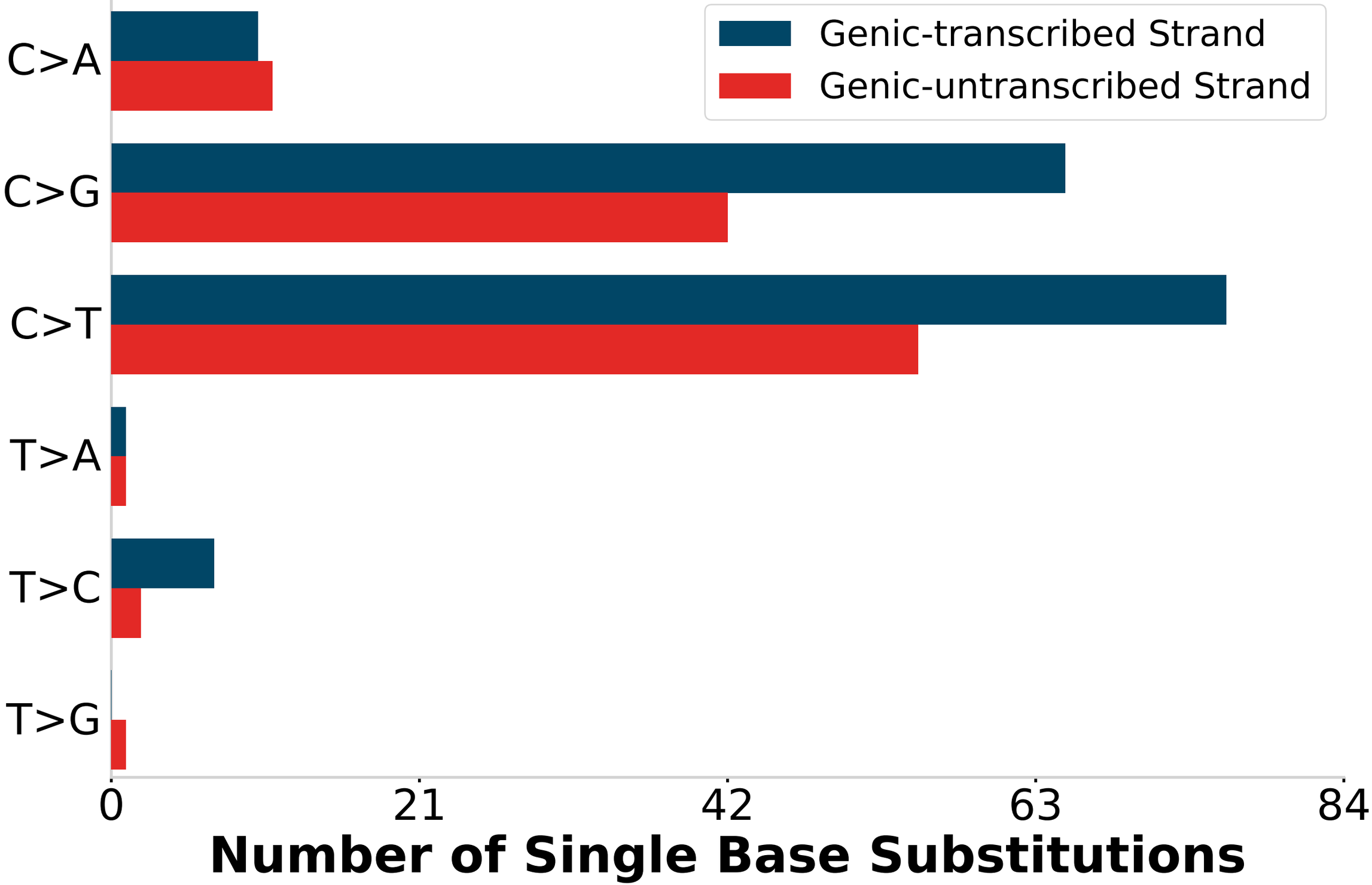
TCGA-G2-A2EJ-01A-11D-A17V-08: 302 tran



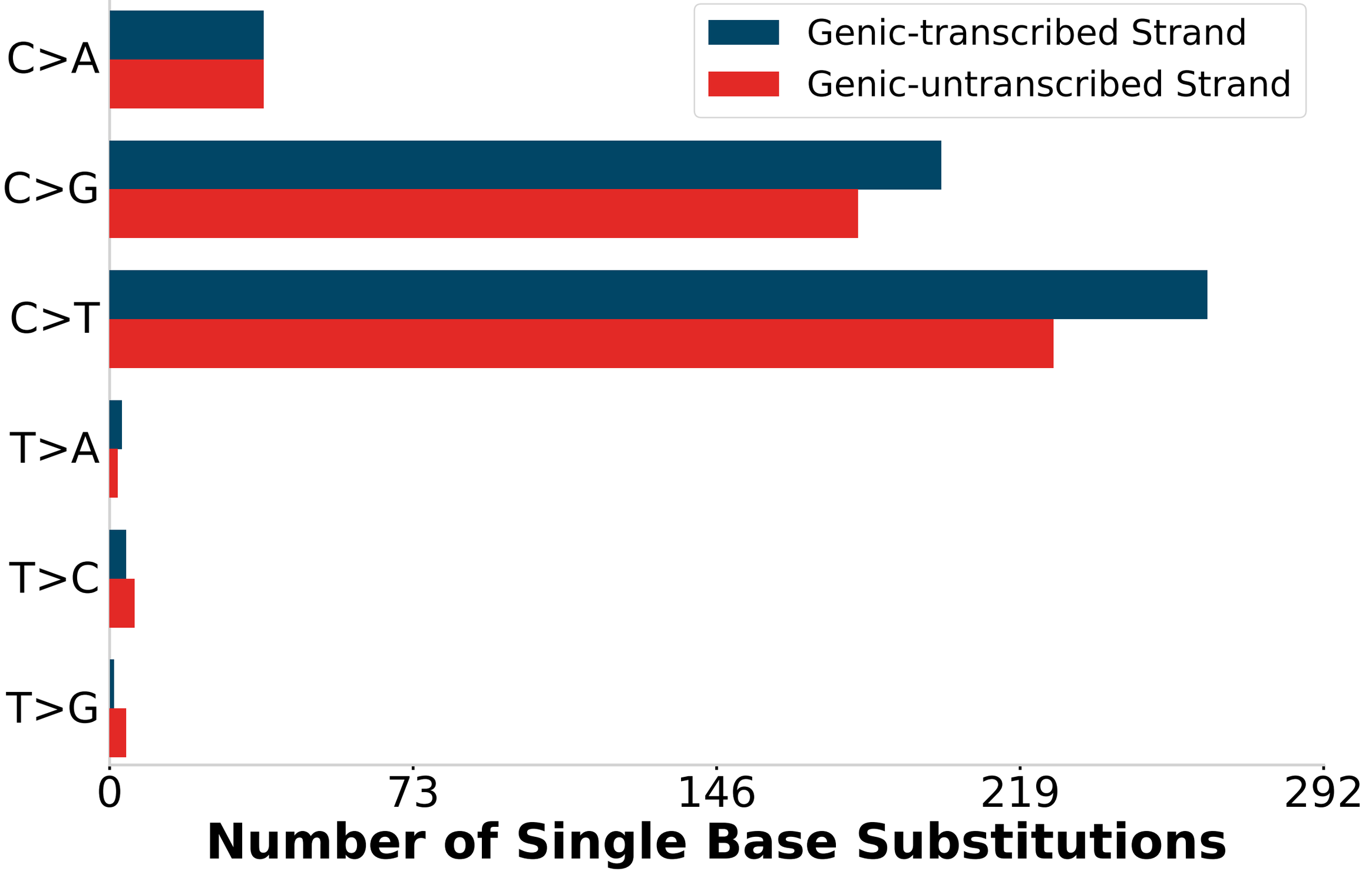
TCGA-G2-A2EK-01A-22D-A18F-08: 69 trans



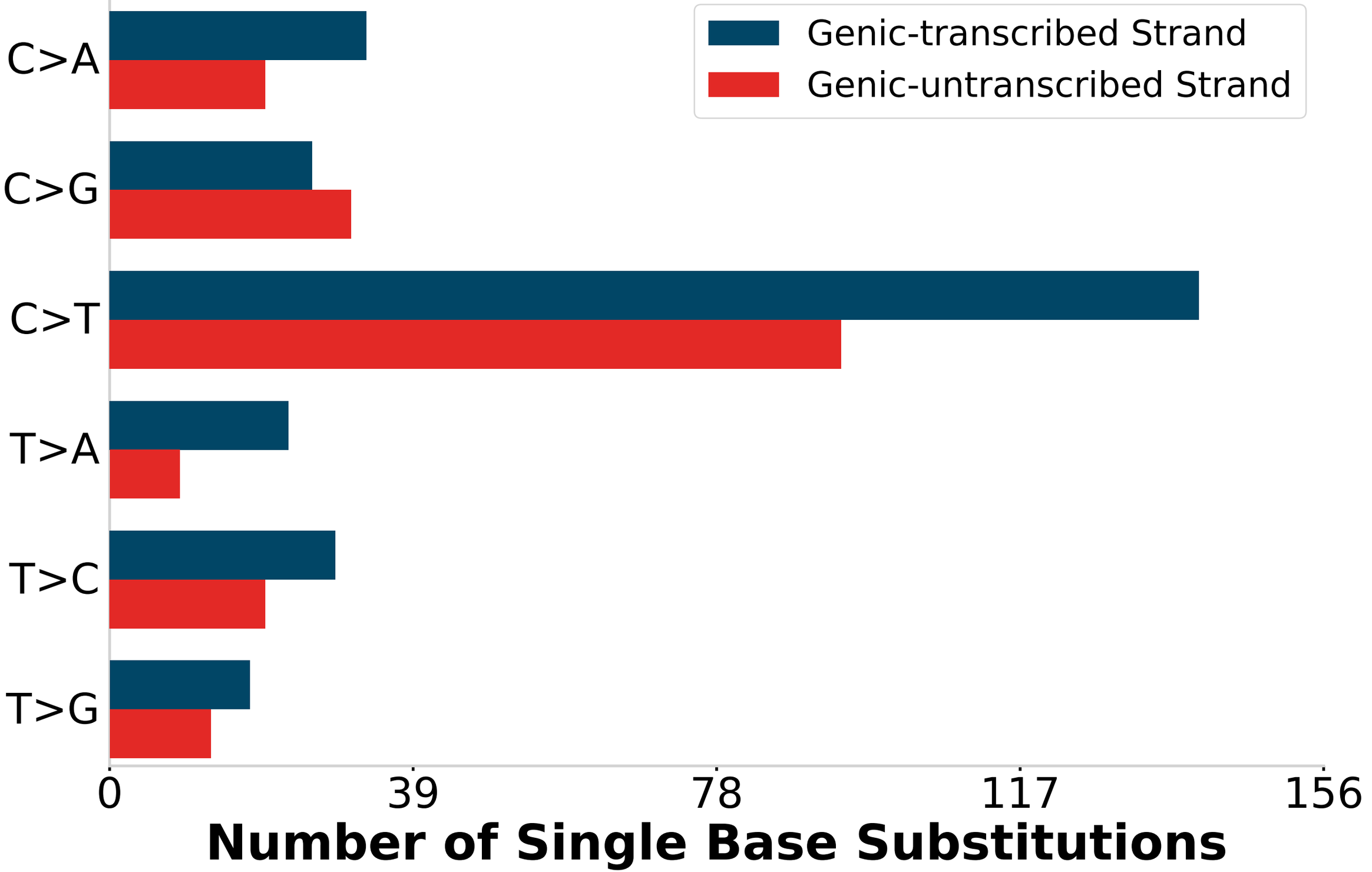
TCGA-G2-A2EL-01A-12D-A18F-08: 271 tran



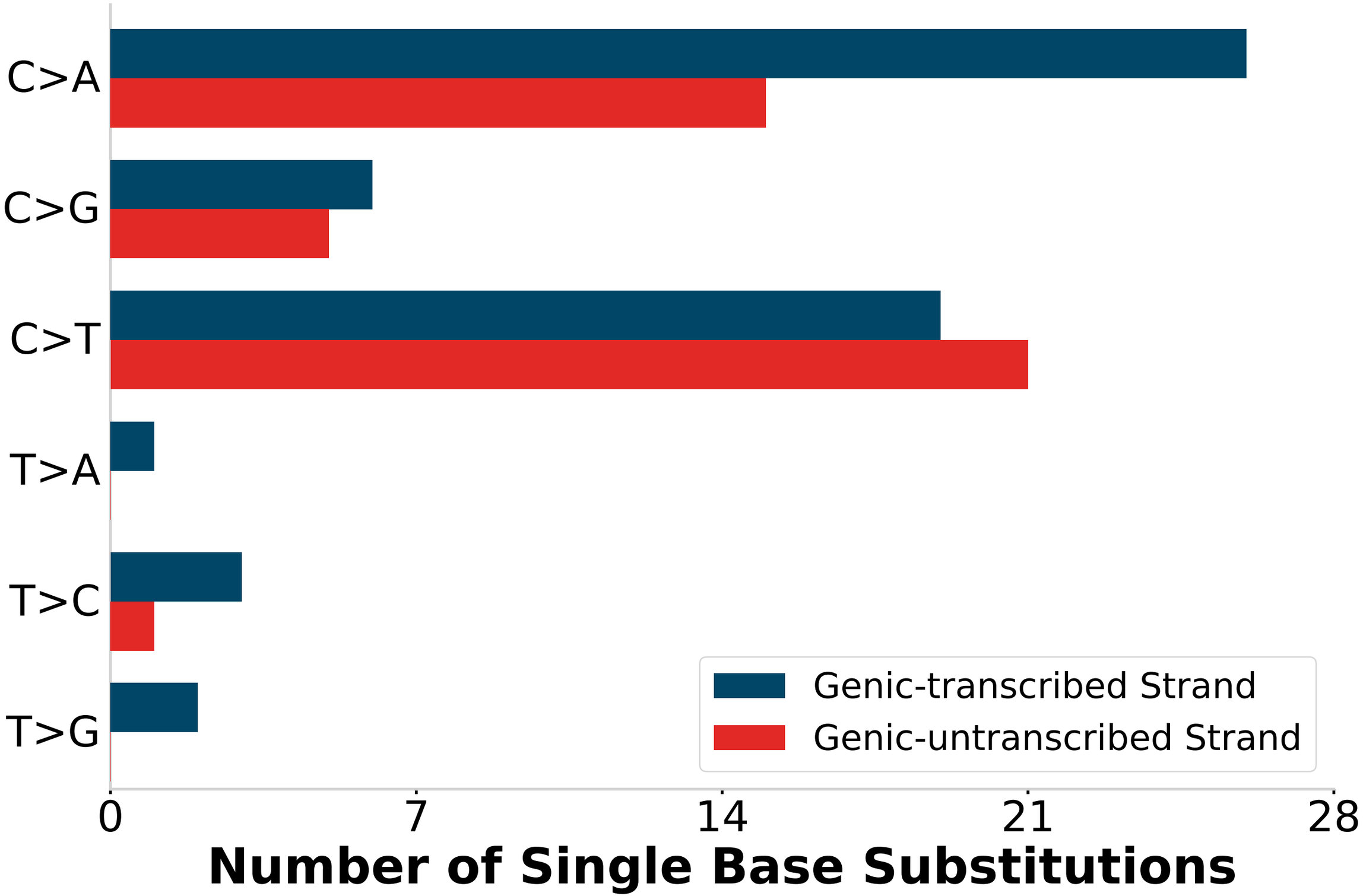
TCGA-G2-A2EO-01A-11D-A17V-08: 965 tra



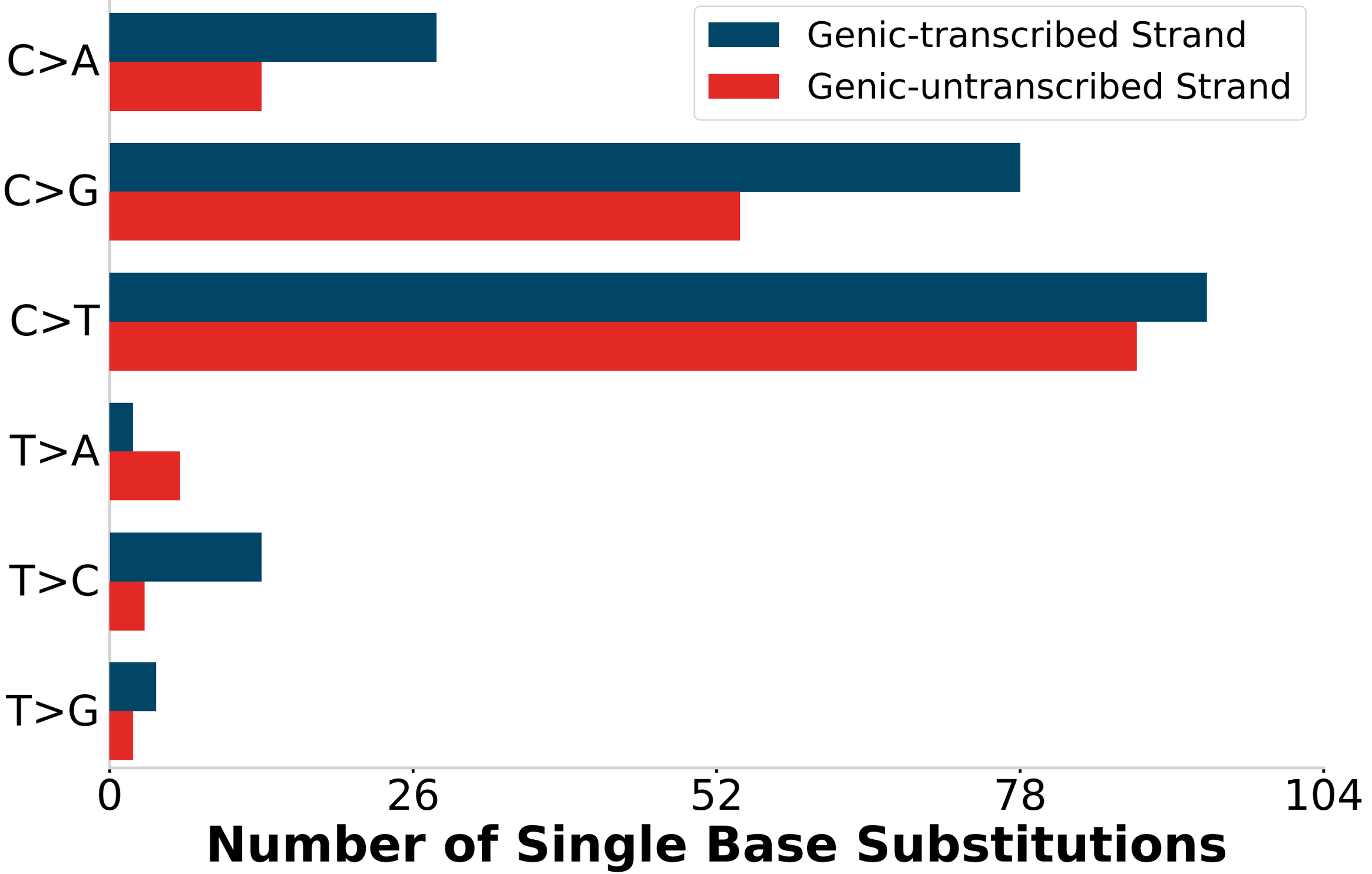
TCGA-G2-A2ES-01A-11D-A17V-08: 456 tra



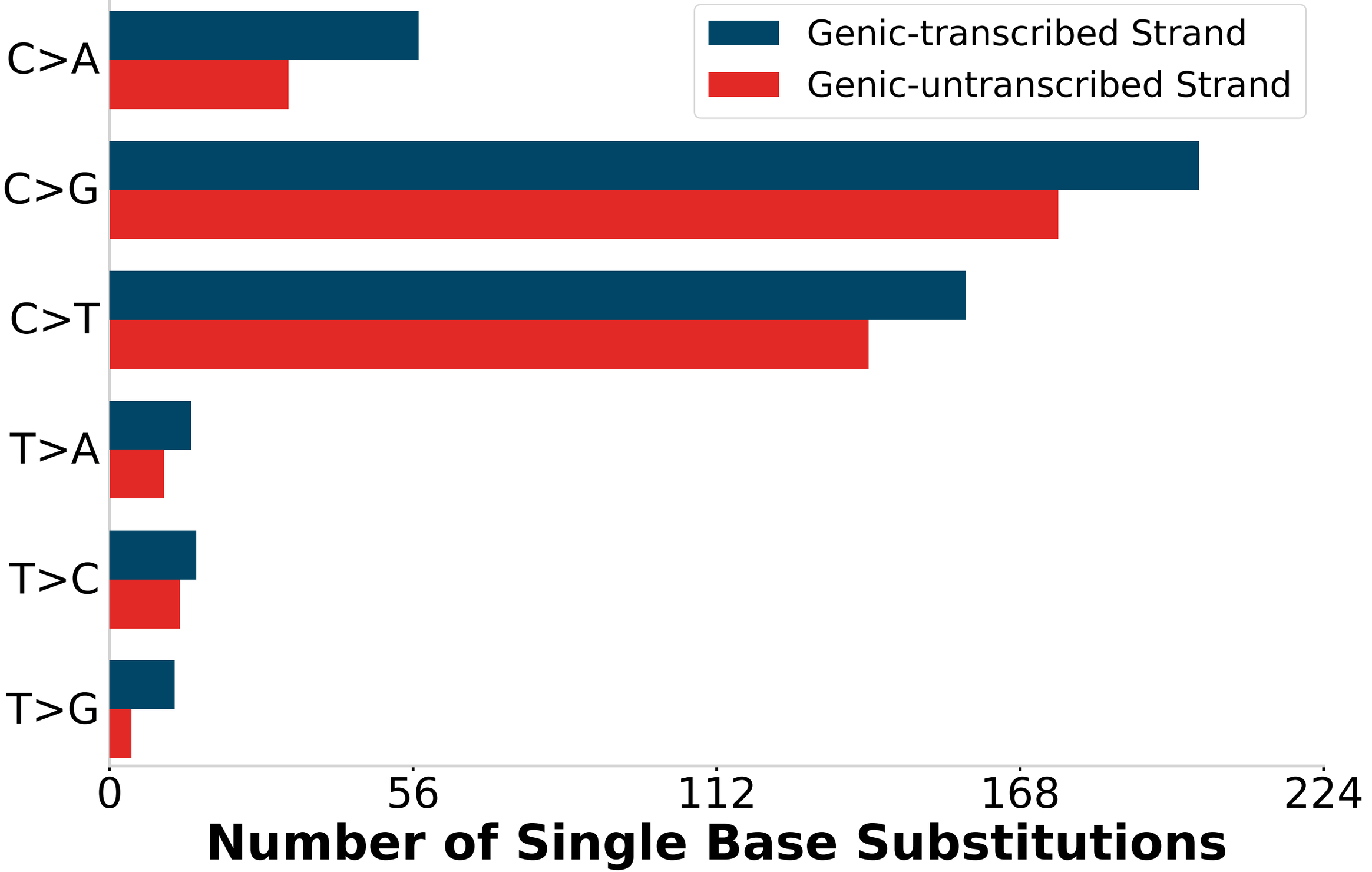
TCGA-G2-A3IB-01A-11D-A20D-08: 99 trans



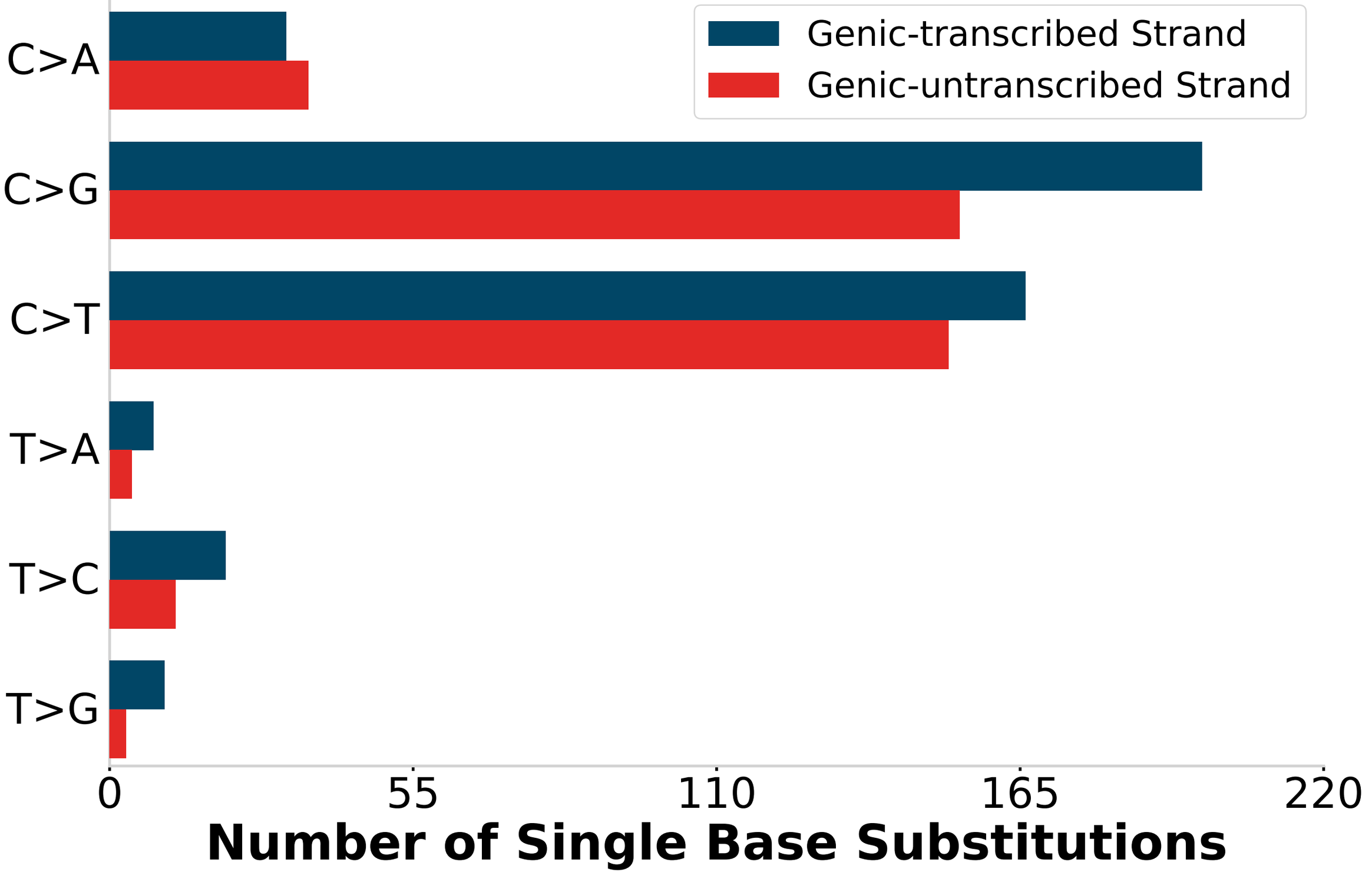
TCGA-G2-A3IE-01A-11D-A20D-08: 385 tran



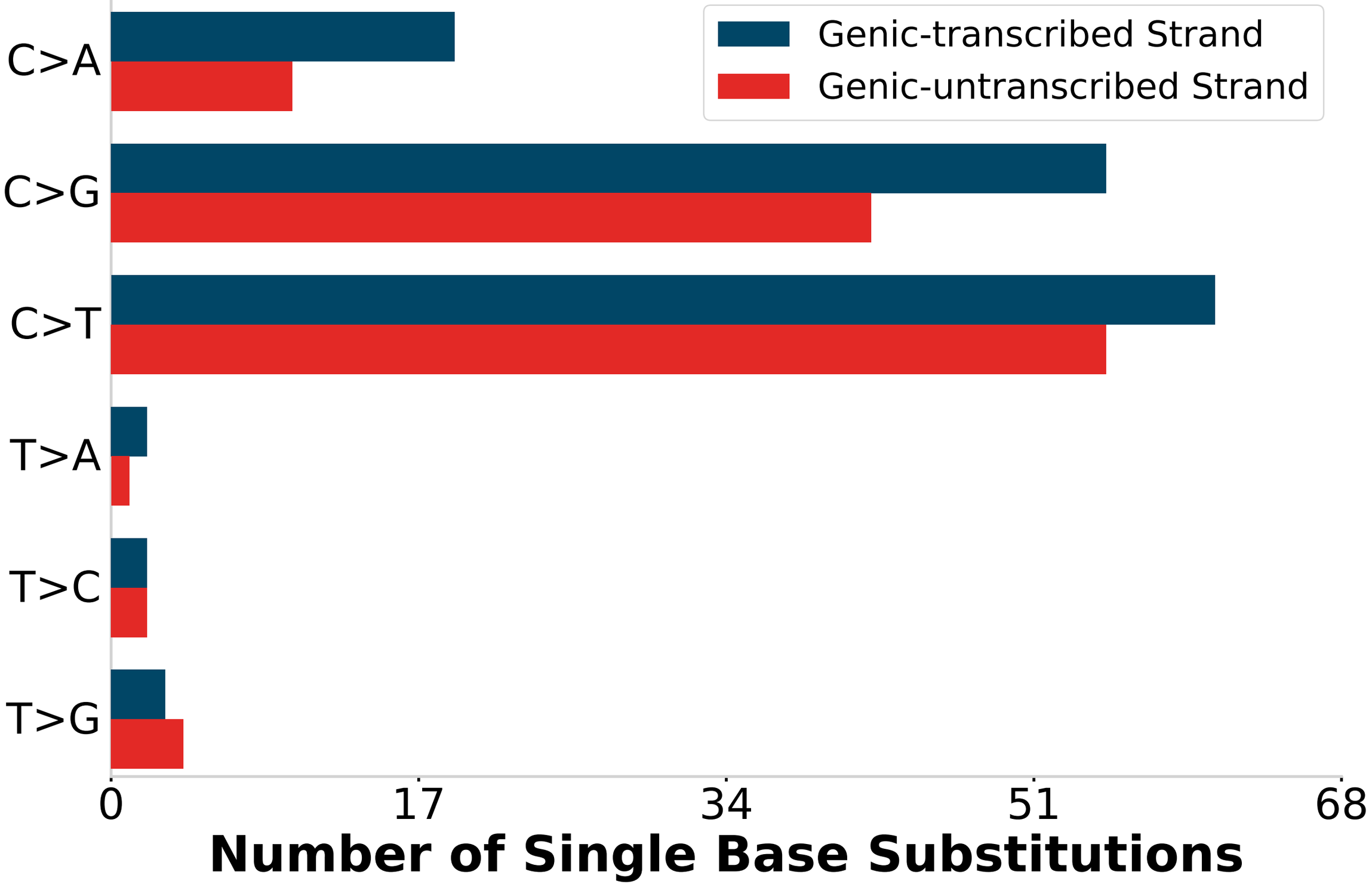
TCGA-G2-A3VY-01A-11D-A22Z-08: 834 tran



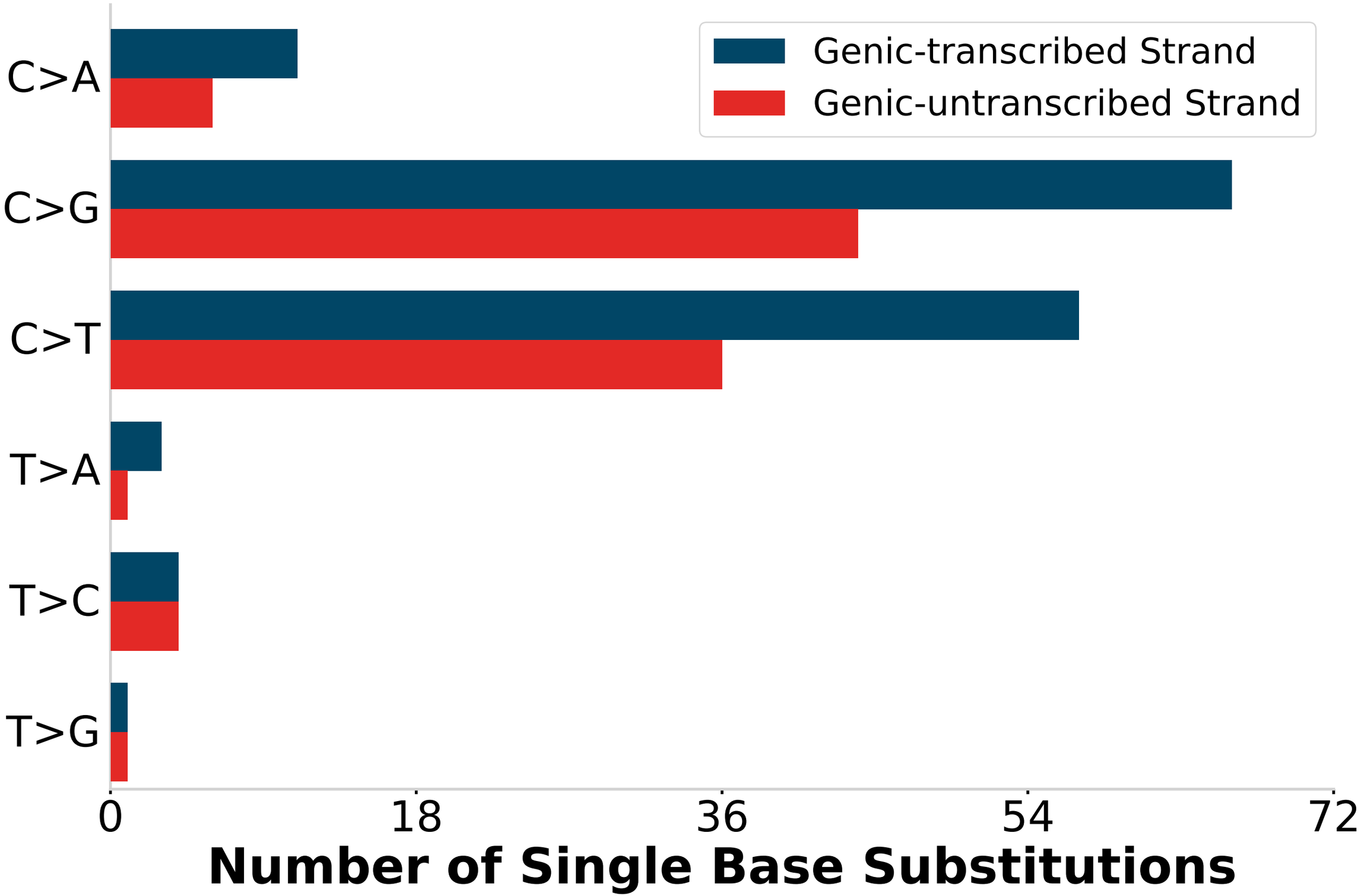
TCGA-G2-AA3B-01A-11D-A391-08: 796 tra



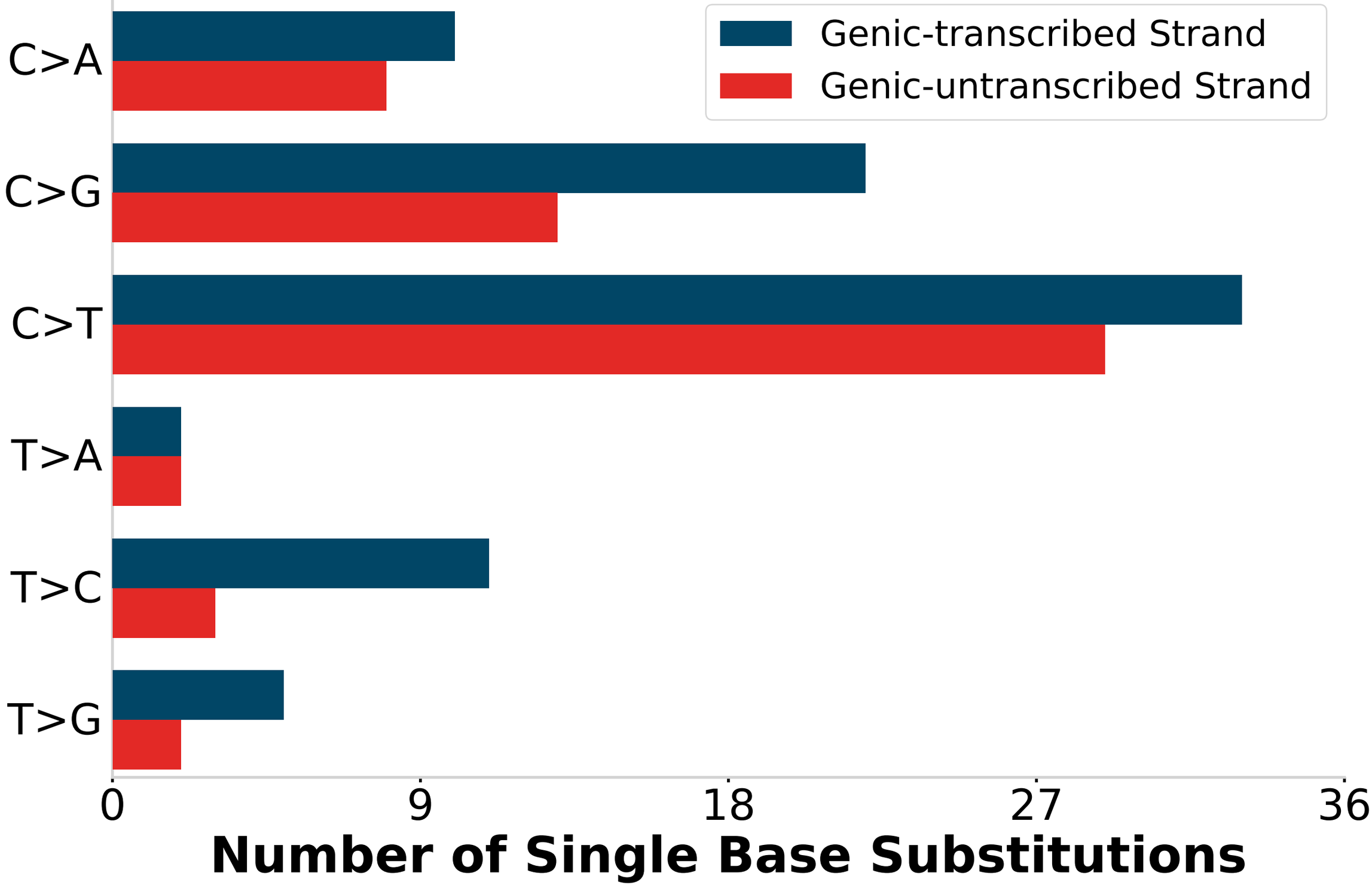
TCGA-G2-AA3C-01A-21D-A391-08: 256 tra



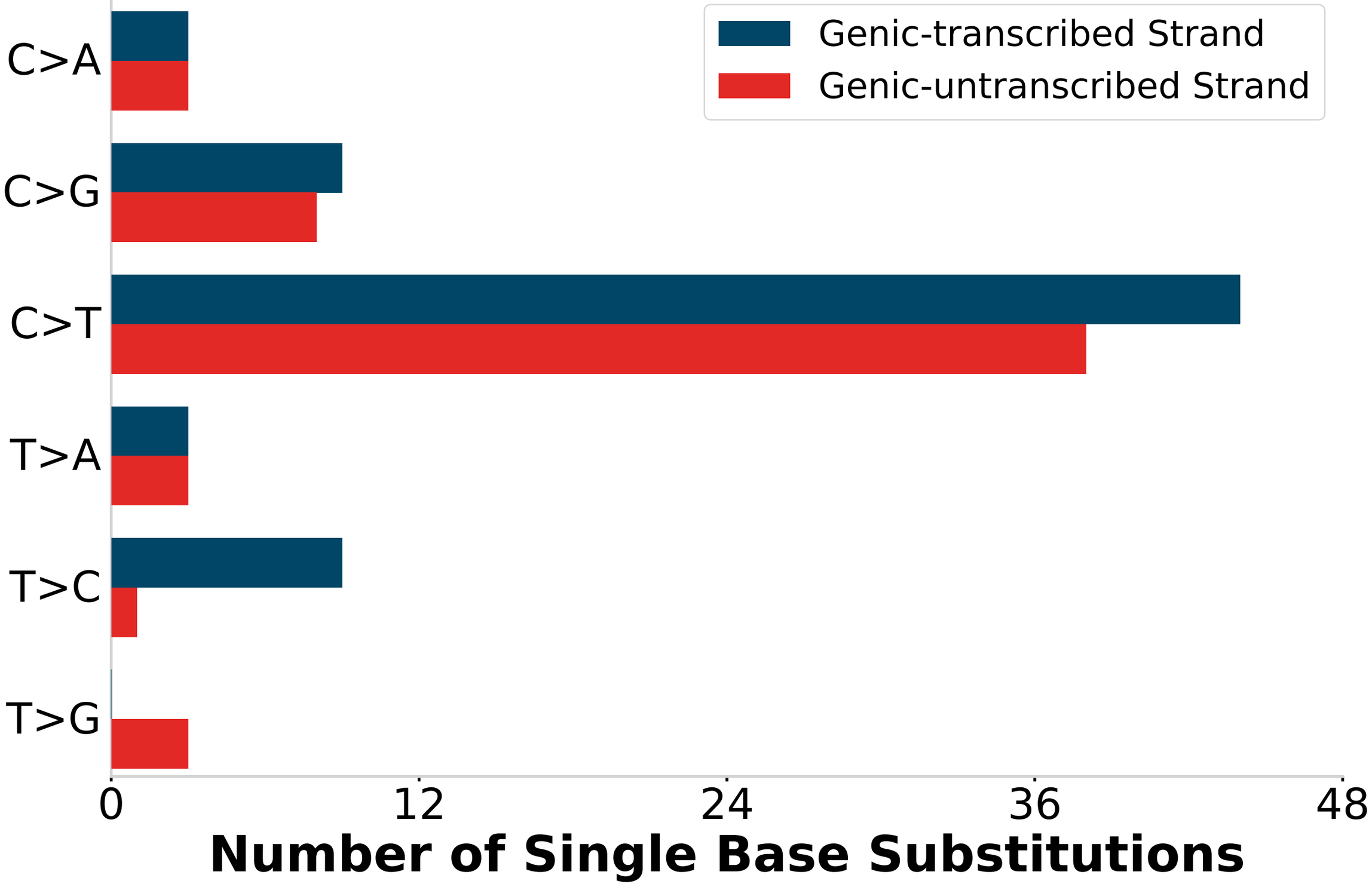
TCGA-G2-AA3D-01A-11D-A391-08: 234 tra



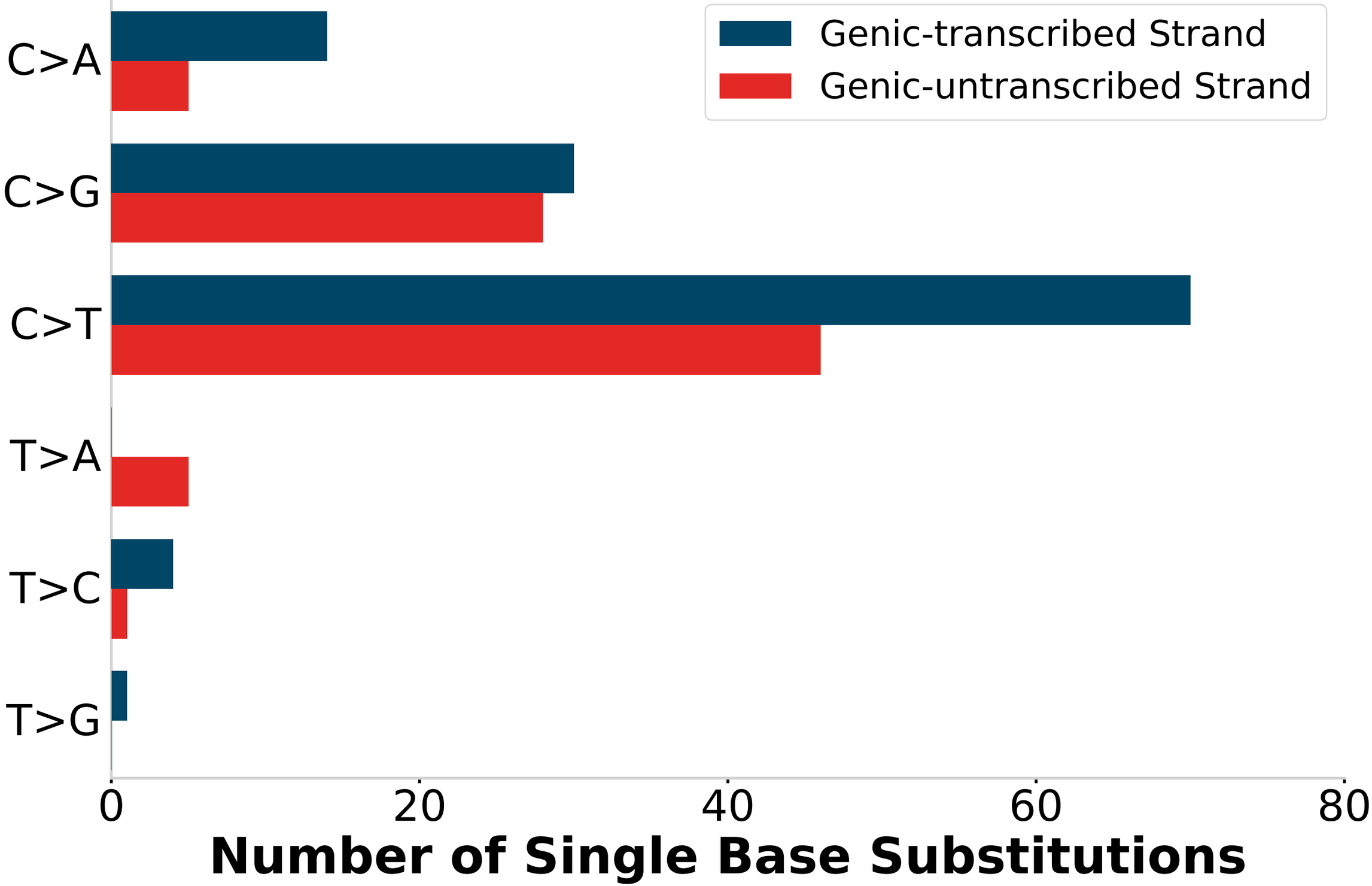
TCGA-G2-AA3F-01A-12D-A42E-08: 140 tra



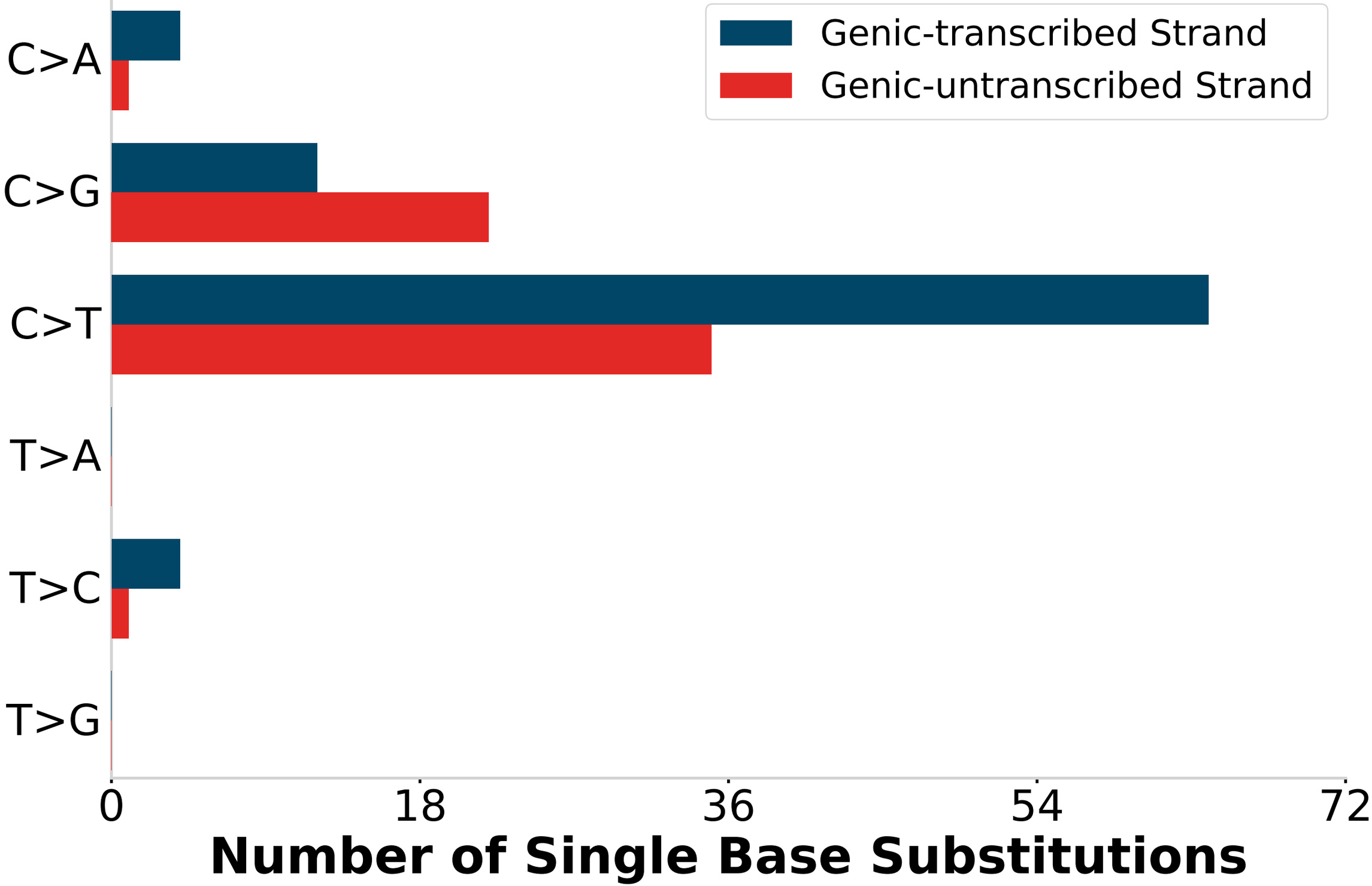
TCGA-GC-A3BM-01A-11D-A22Z-08: 124 tra



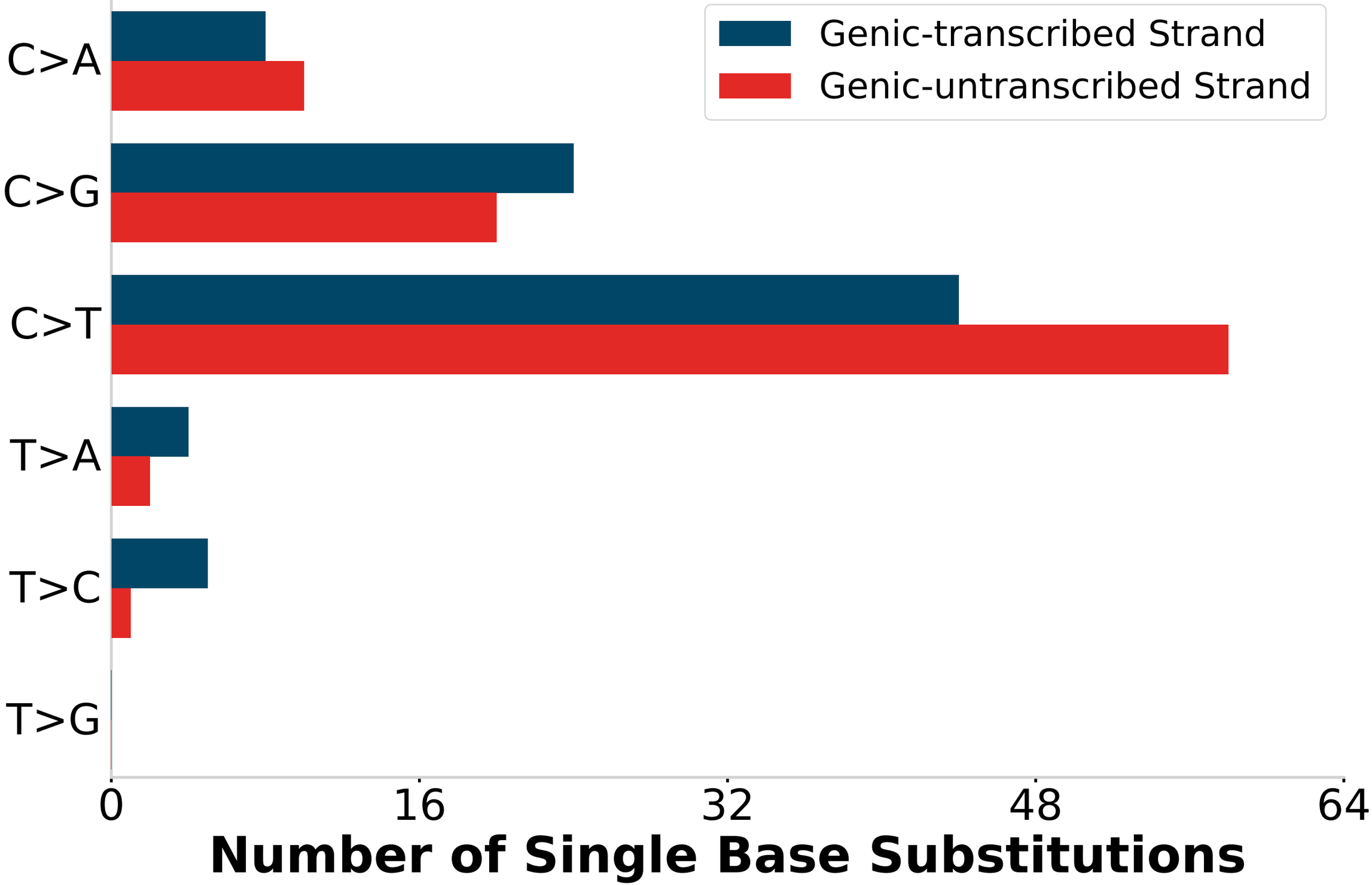
TCGA-GC-A3I6-01A-11D-A20D-08: 204 tran



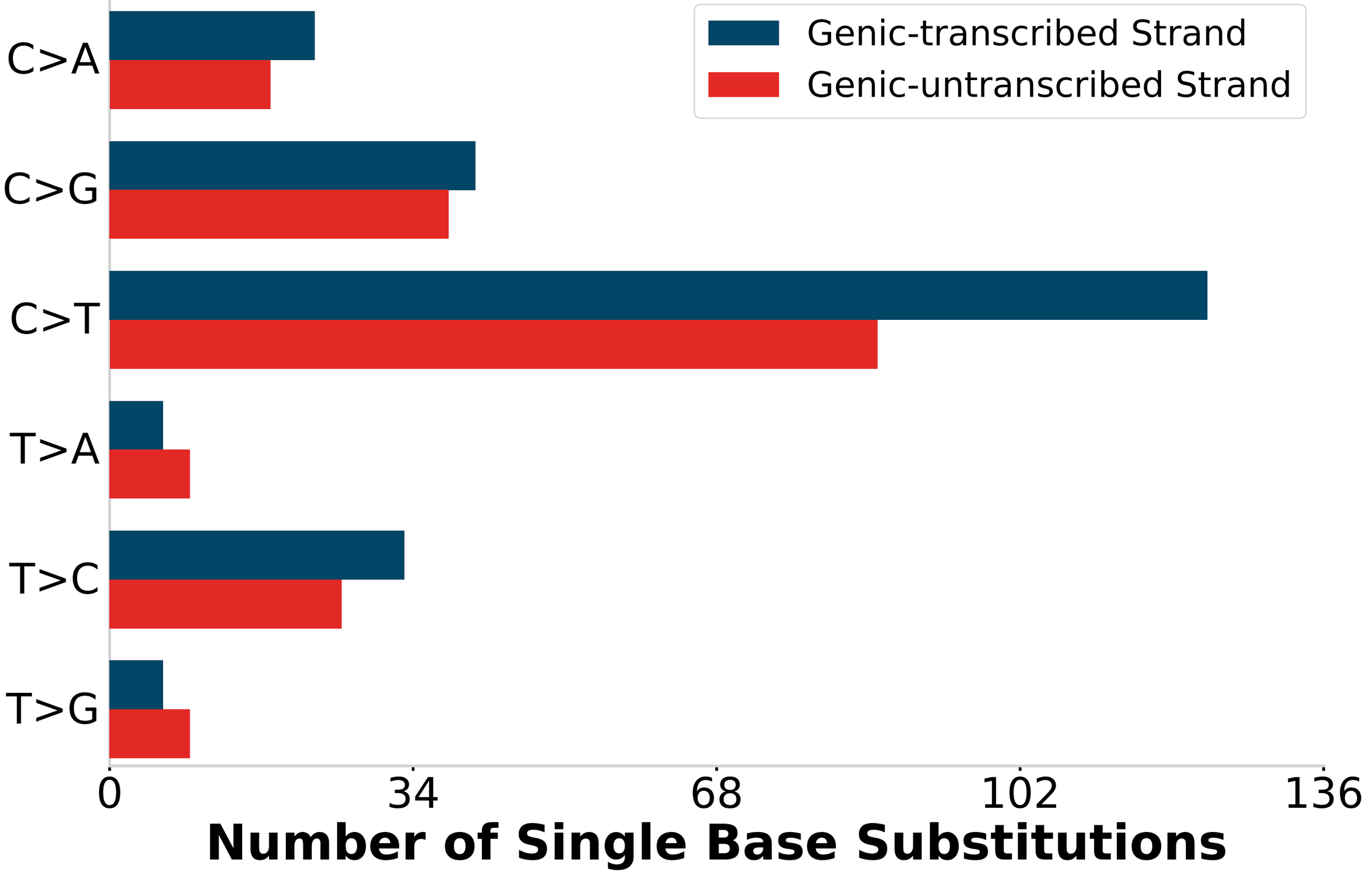
TCGA-GC-A3OO-01A-11D-A22Z-08: 143 tra



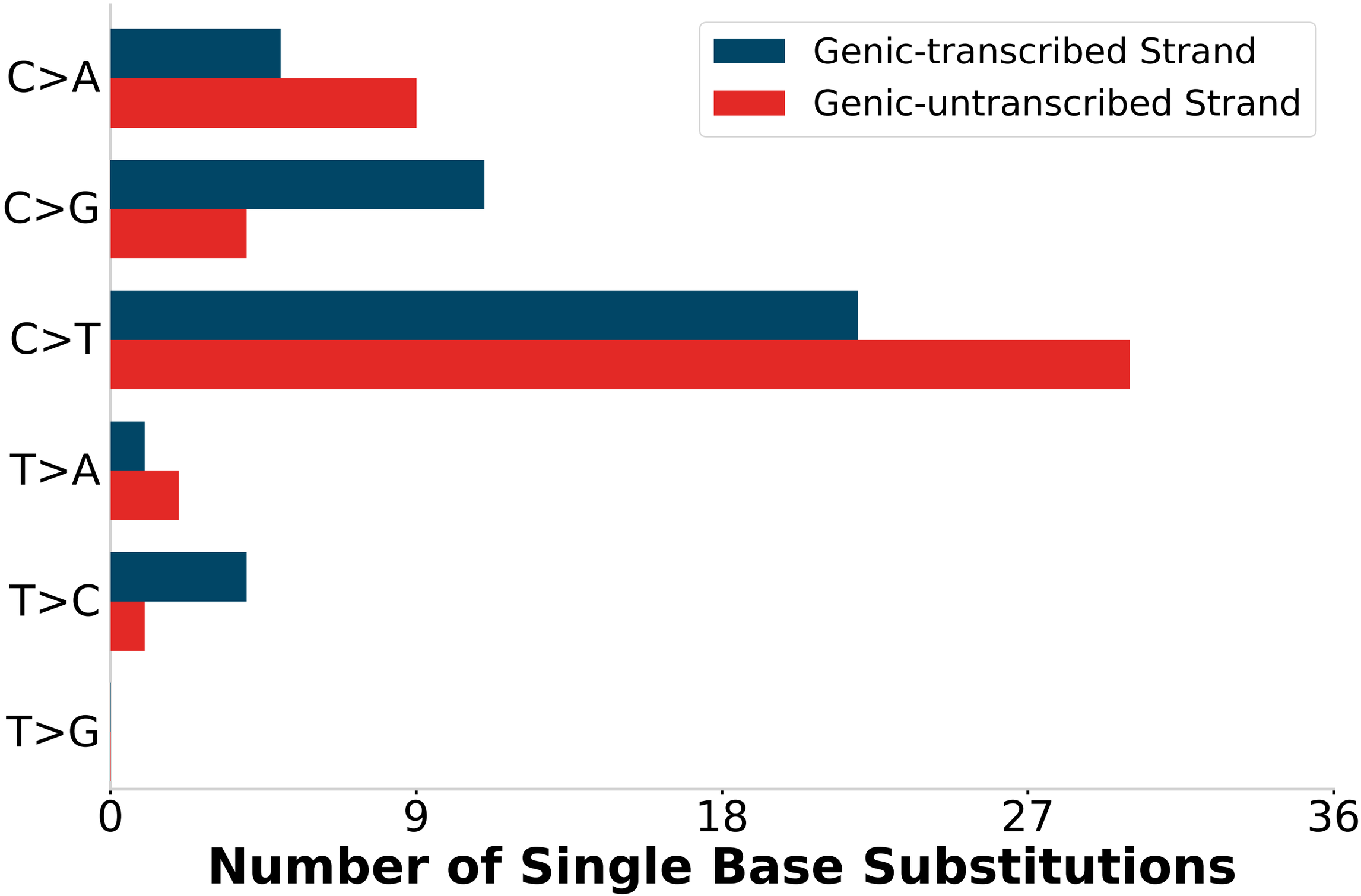
TCGA-GC-A3RB-01A-12D-A21Z-08: 176 tra



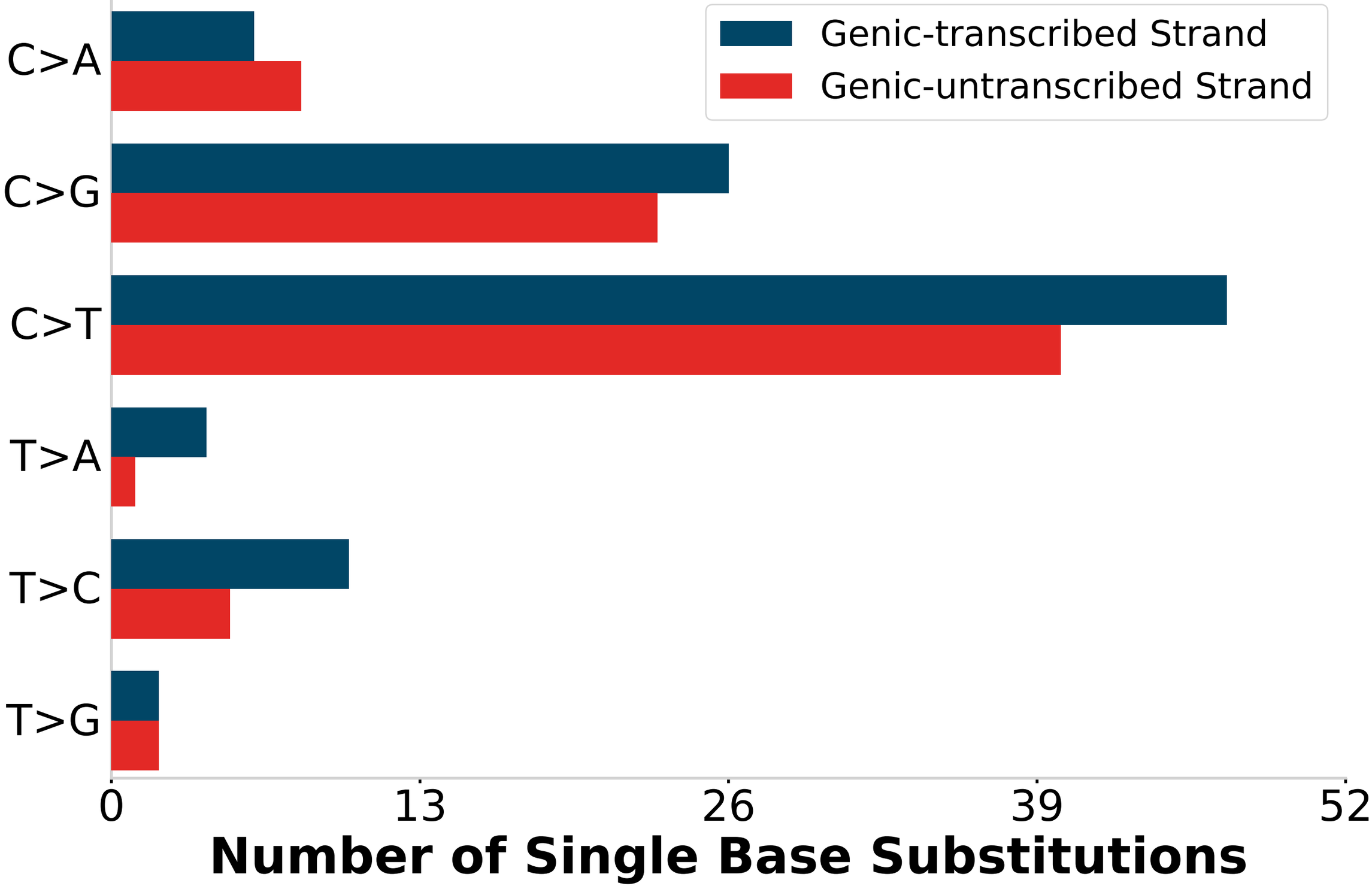
TCGA-GC-A3RC-01A-11D-A22Z-08: 418 tra



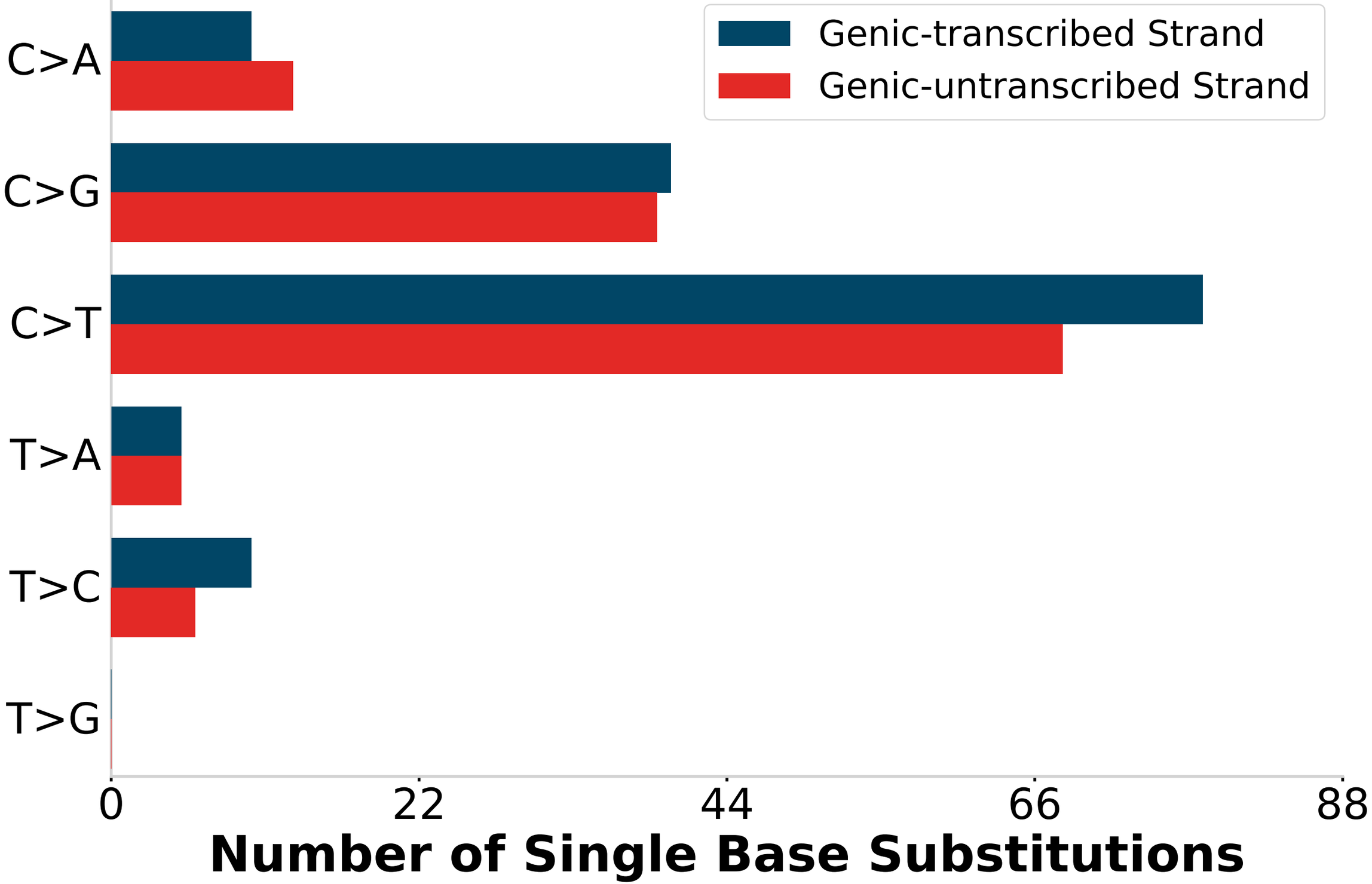
TCGA-GC-A3RD-01A-12D-A22Z-08: 89 tran



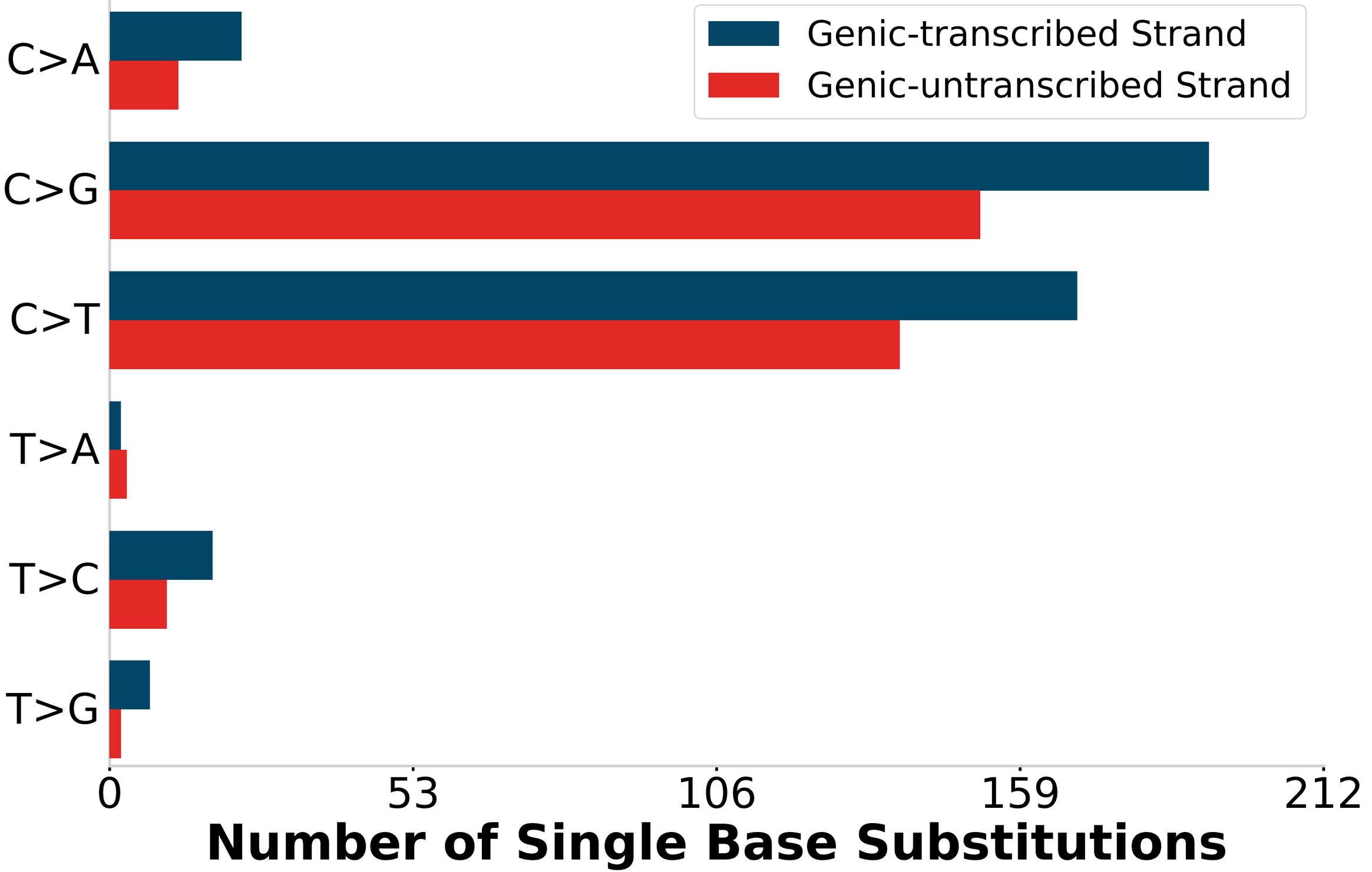
TCGA-GC-A3WC-01A-31D-A22Z-08: 174 tra



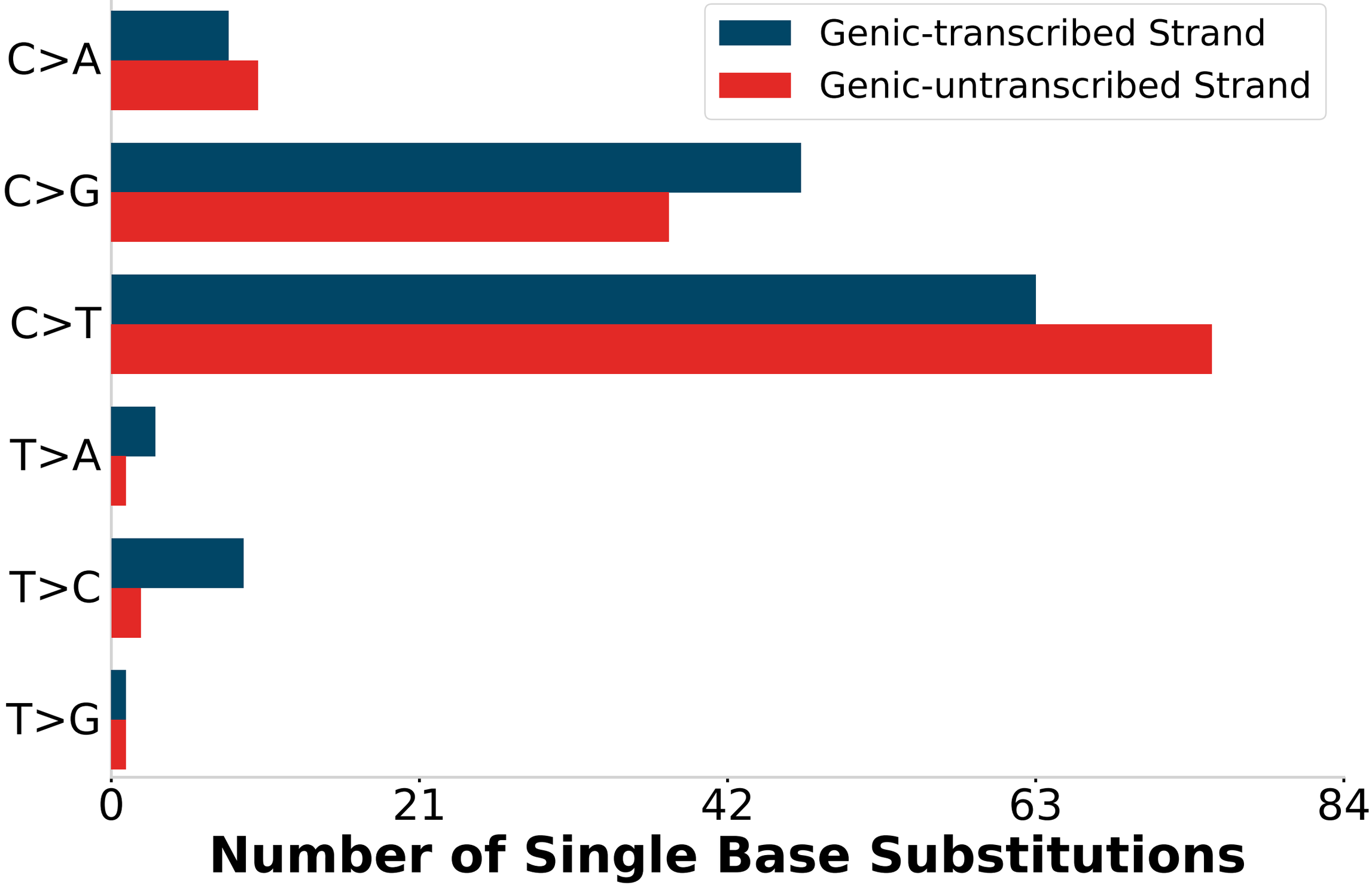
TCGA-GC-A3YS-01A-11D-A23M-08: 274 tra



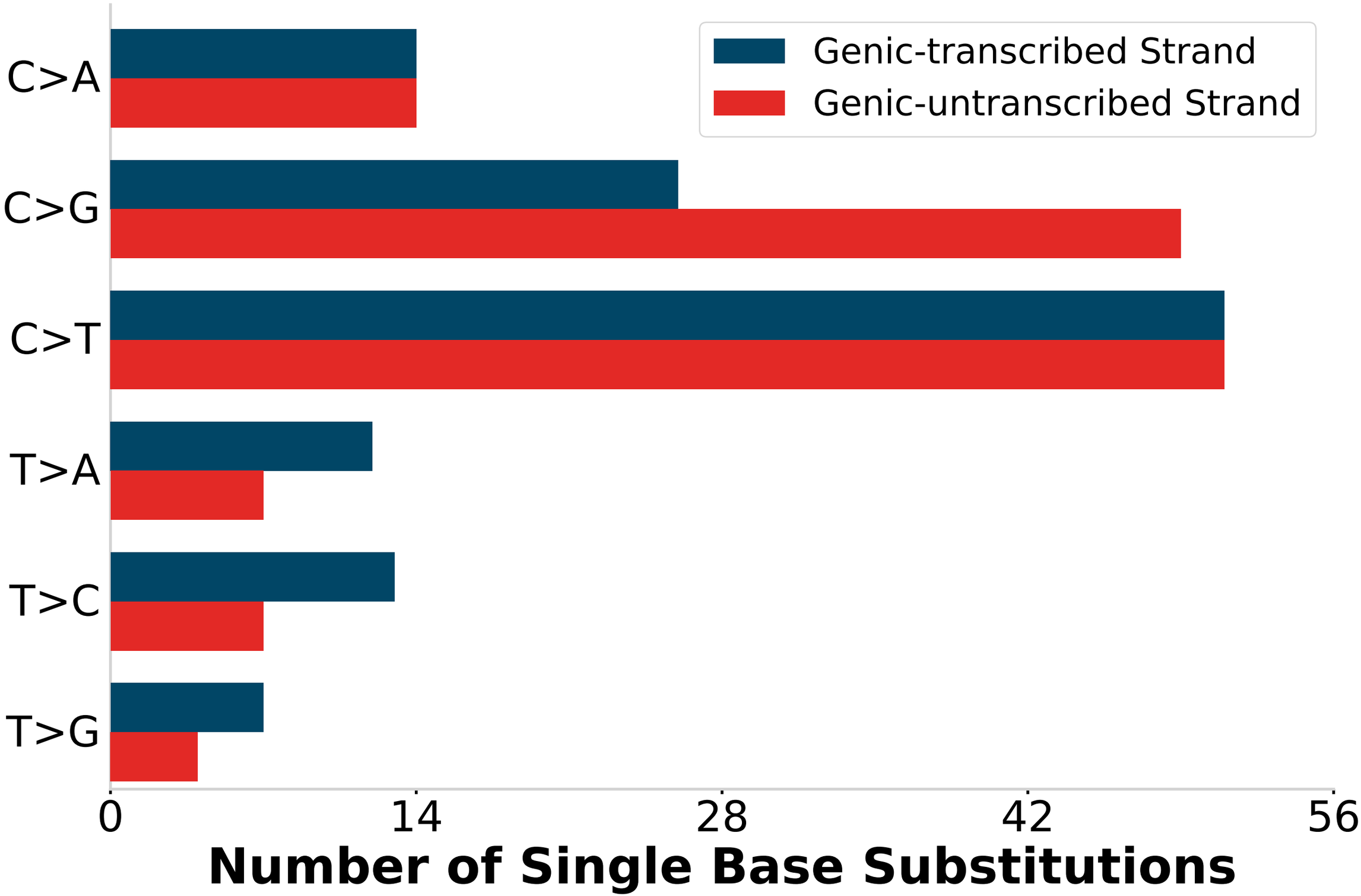
TCGA-GC-A4ZW-01A-11D-A26M-08: 728 tra



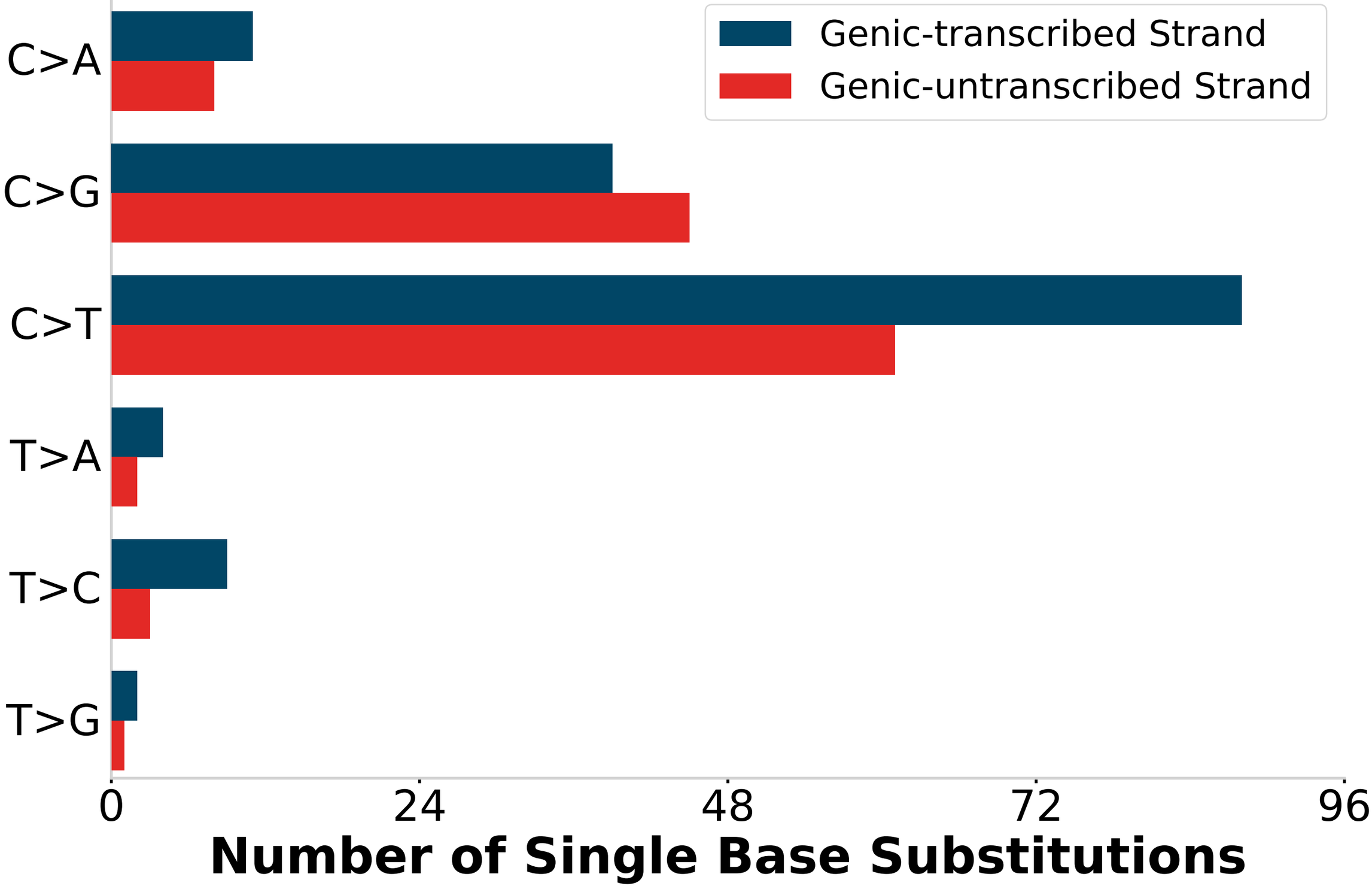
TCGA-GC-A6I1-01A-12D-A31L-08: 258 tran



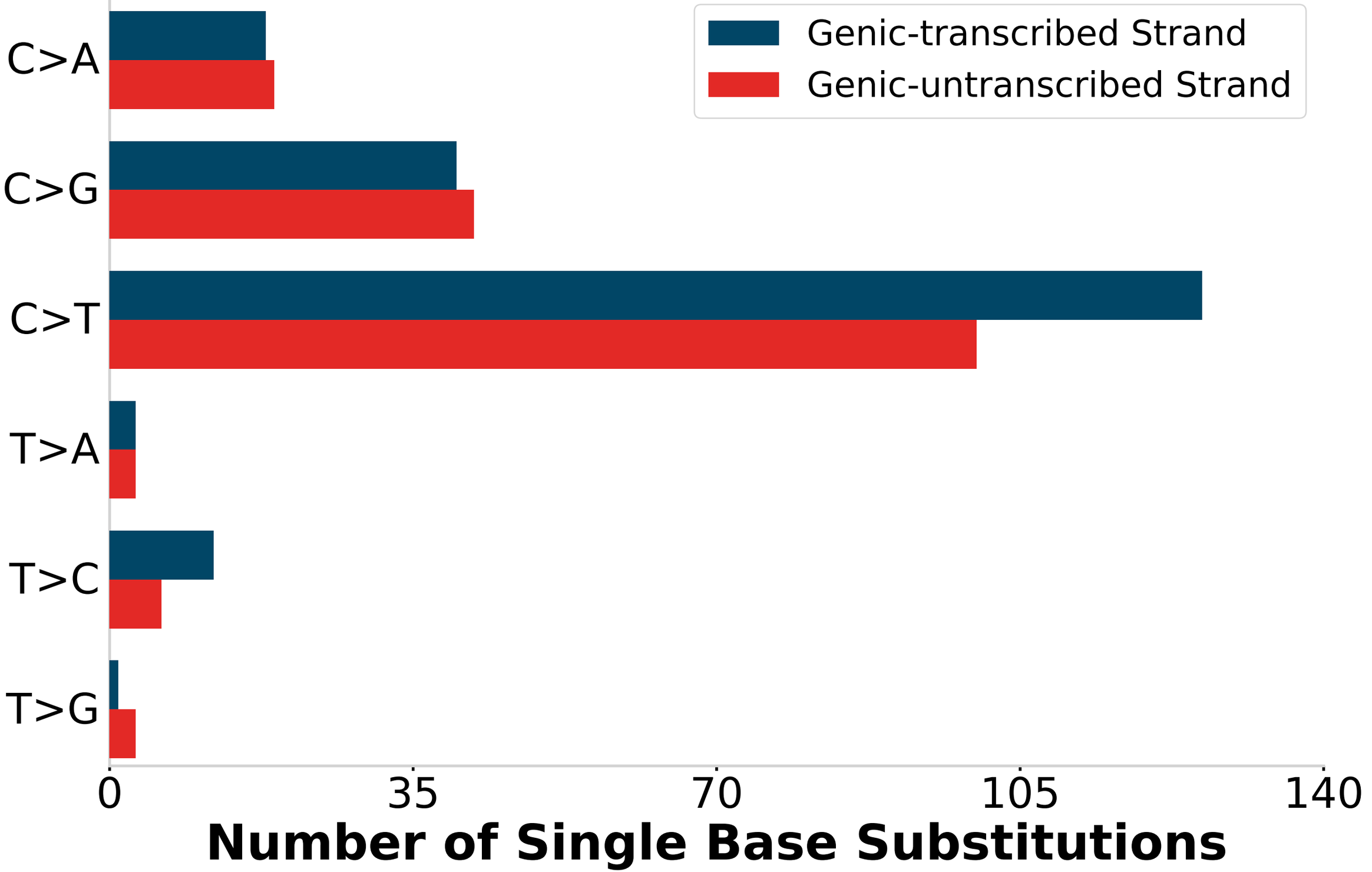
TCGA-GC-A6I3-01A-11D-A31L-08: 255 tran



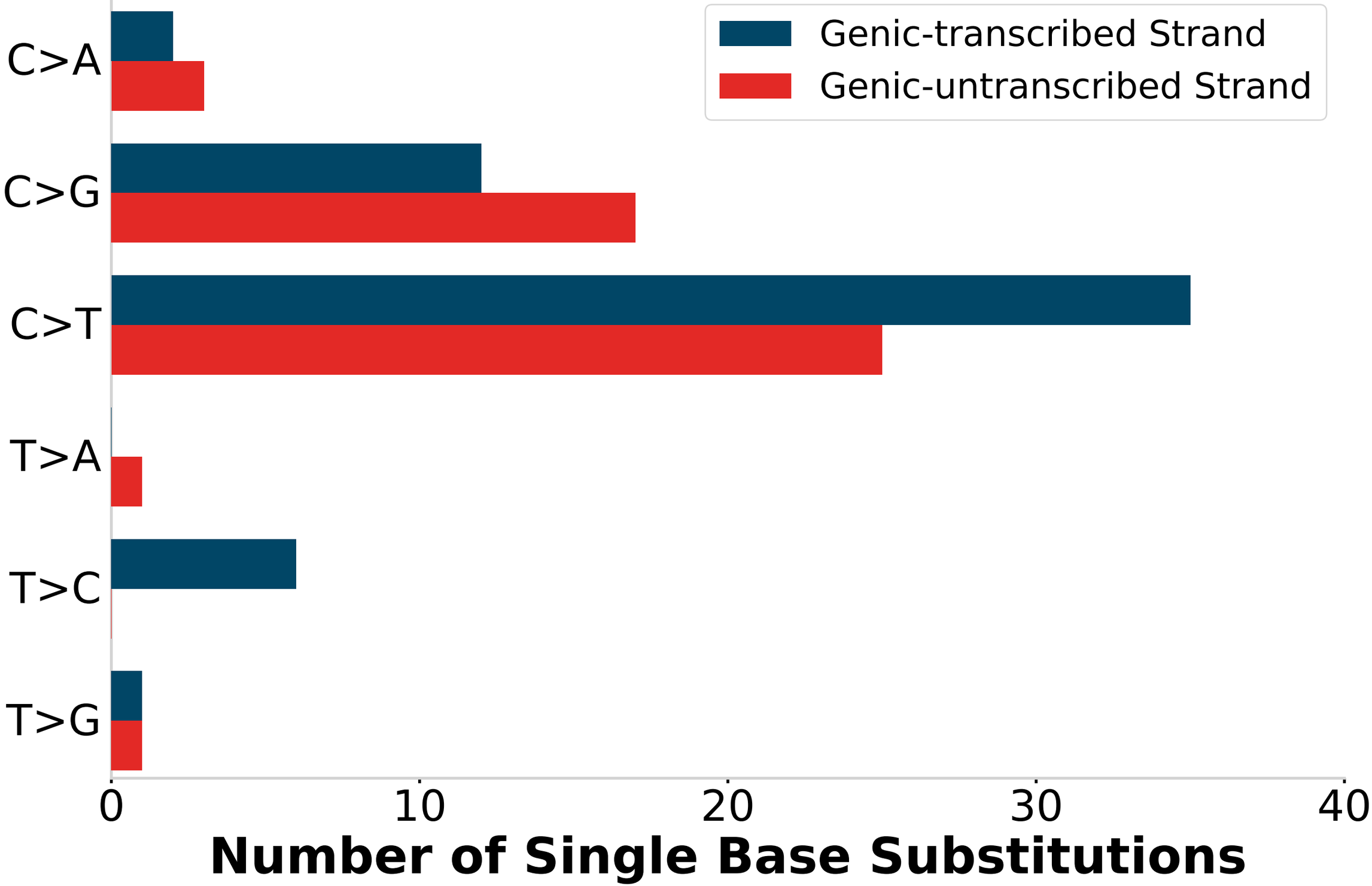
TCGA-GD-A2C5-01A-12D-A17V-08: 273 tra



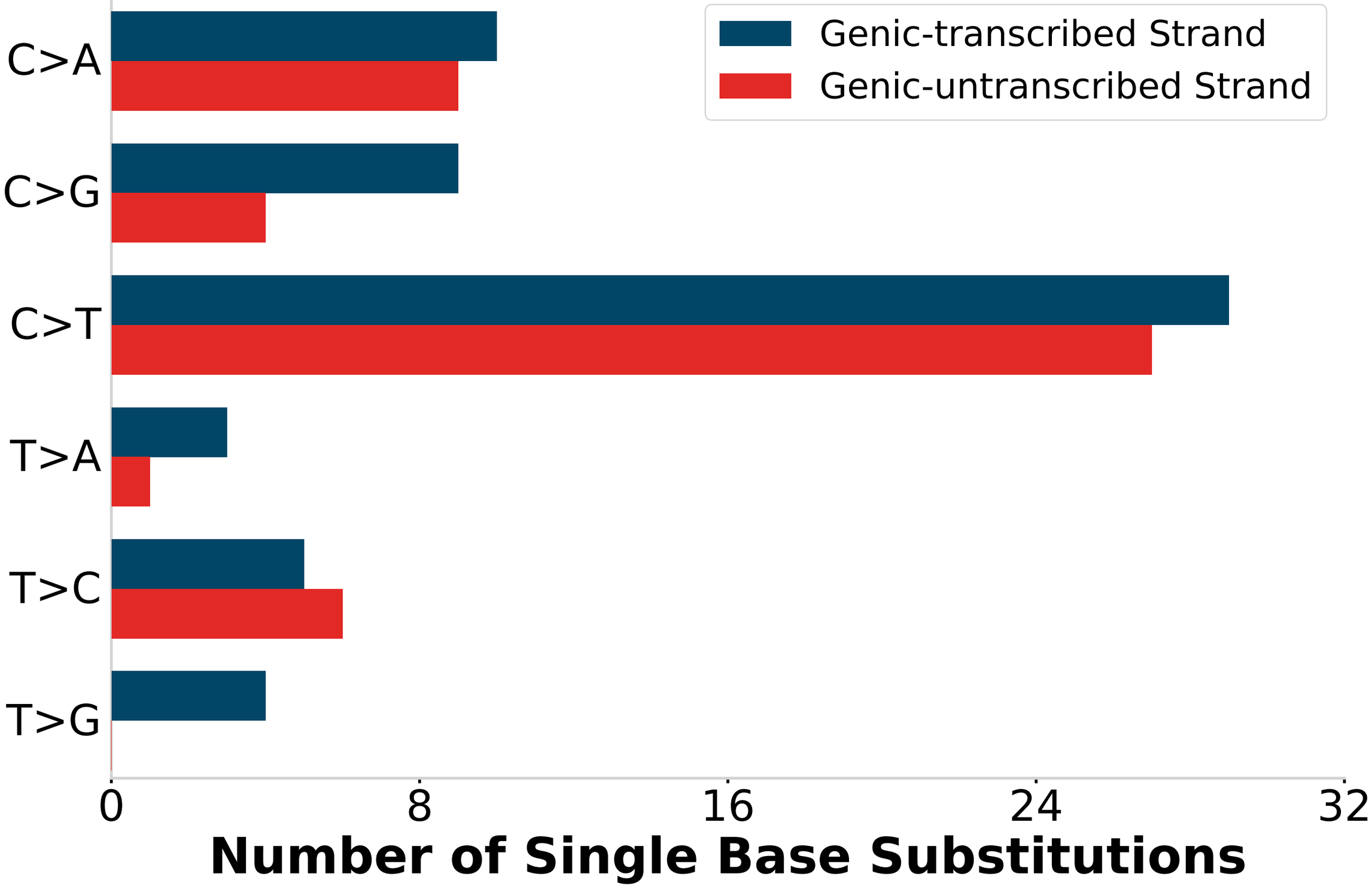
TCGA-GD-A3OP-01A-21D-A21Z-08: 373 tra



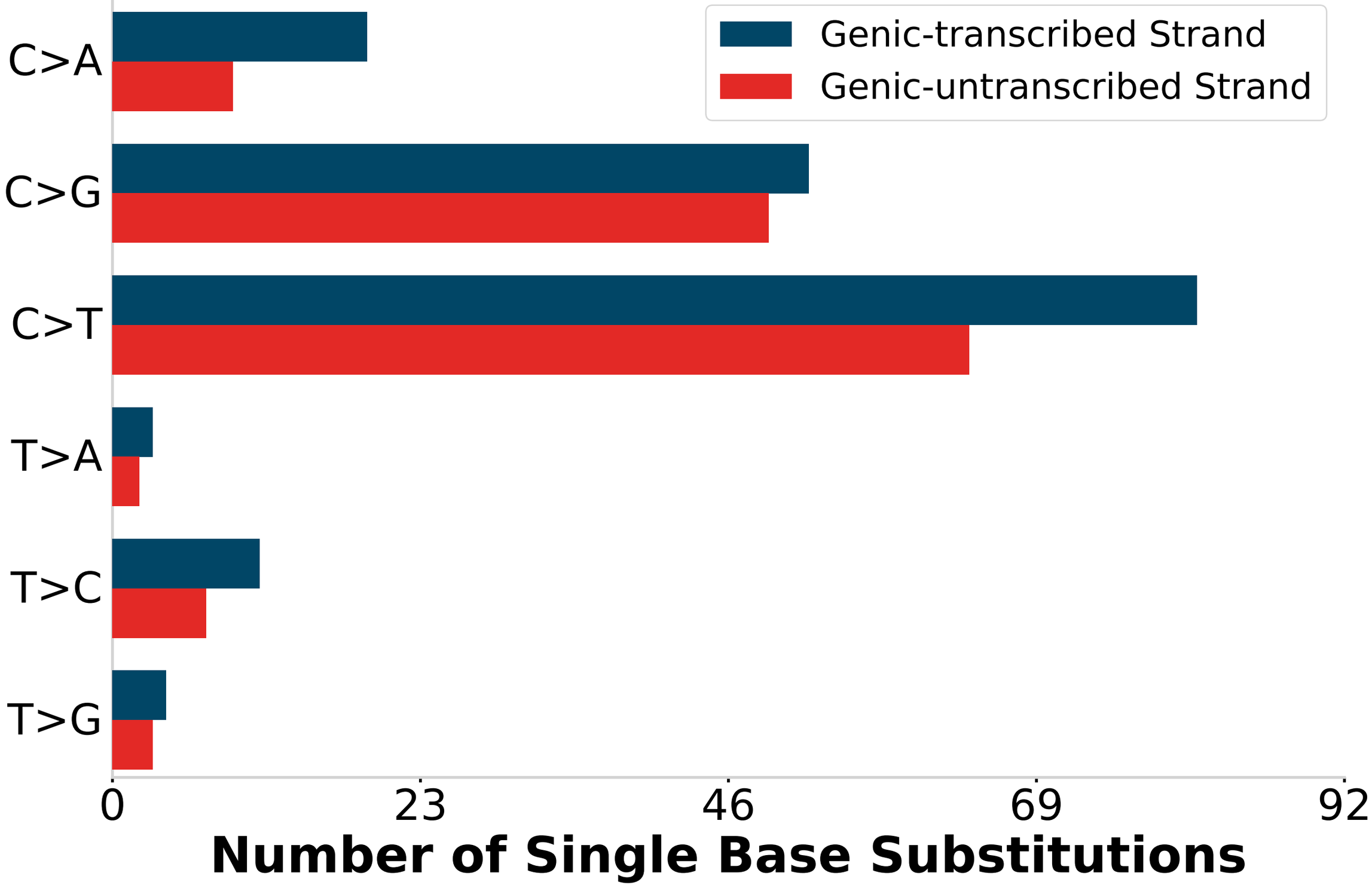
TCGA-GD-A3OQ-01A-32D-A21Z-08: 103 tra



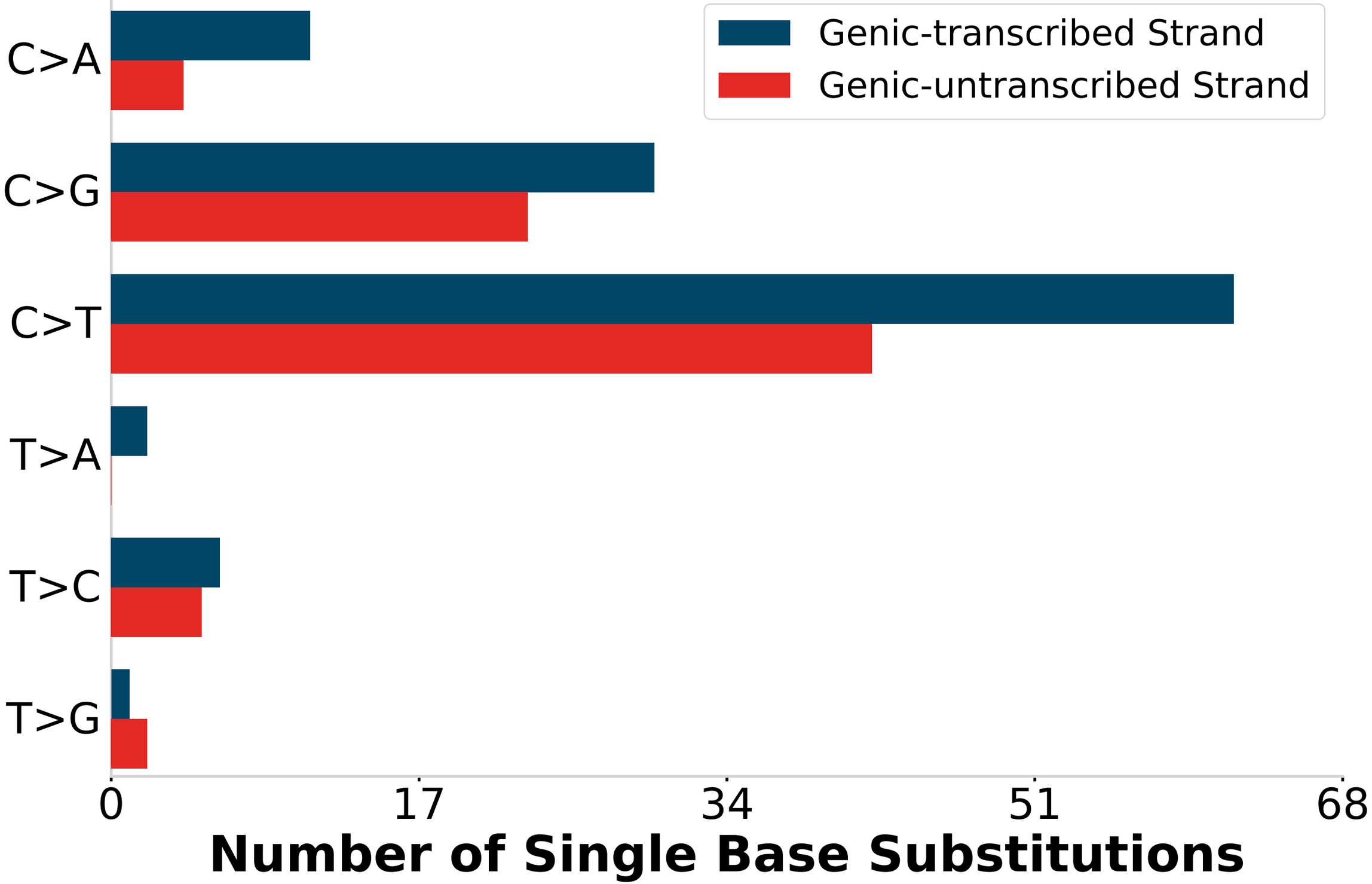
TCGA-GD-A3OS-01A-12D-A21Z-08: 107 tra



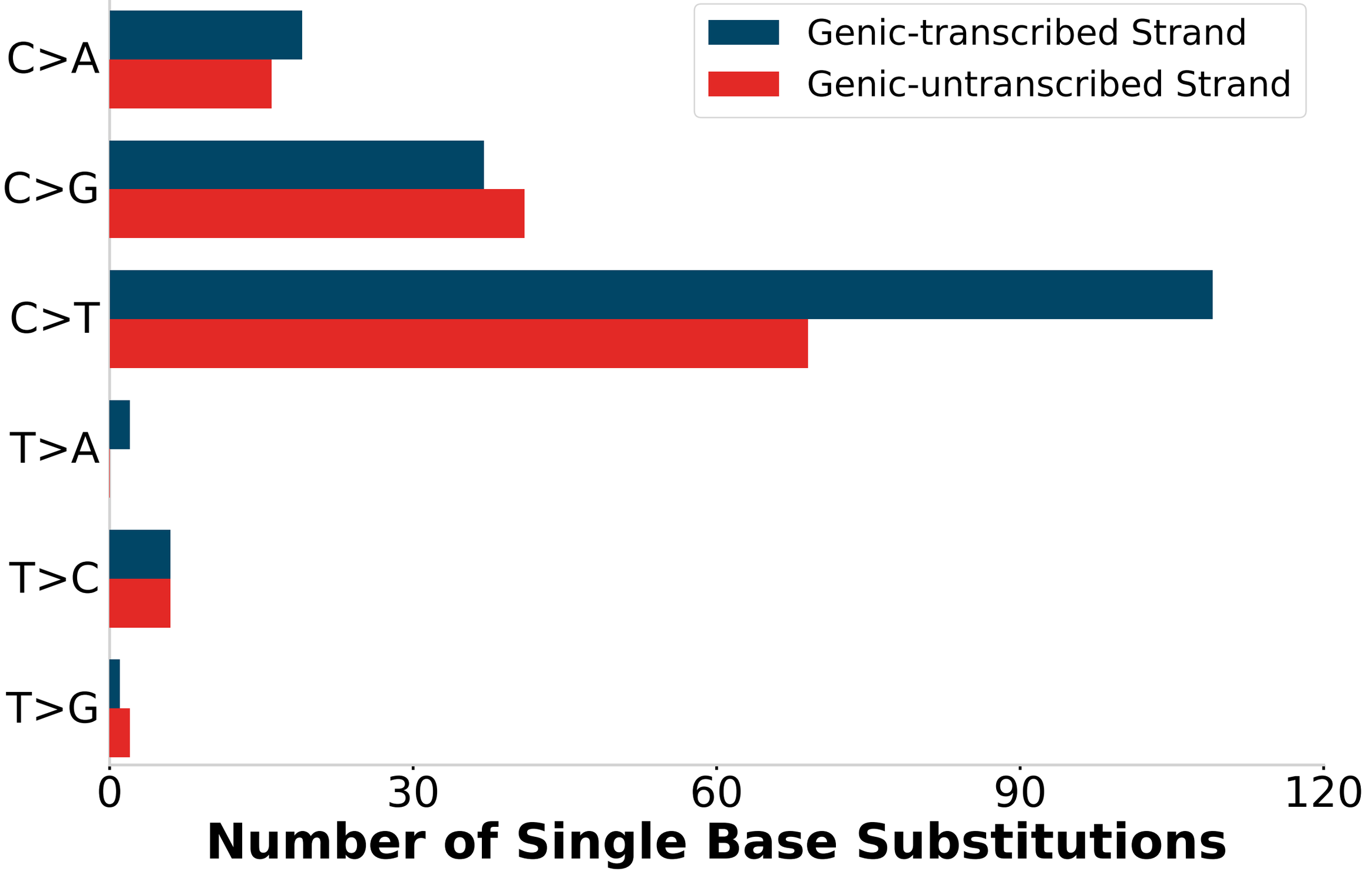
TCGA-GD-A6C6-01A-21D-A31L-08: 304 tra



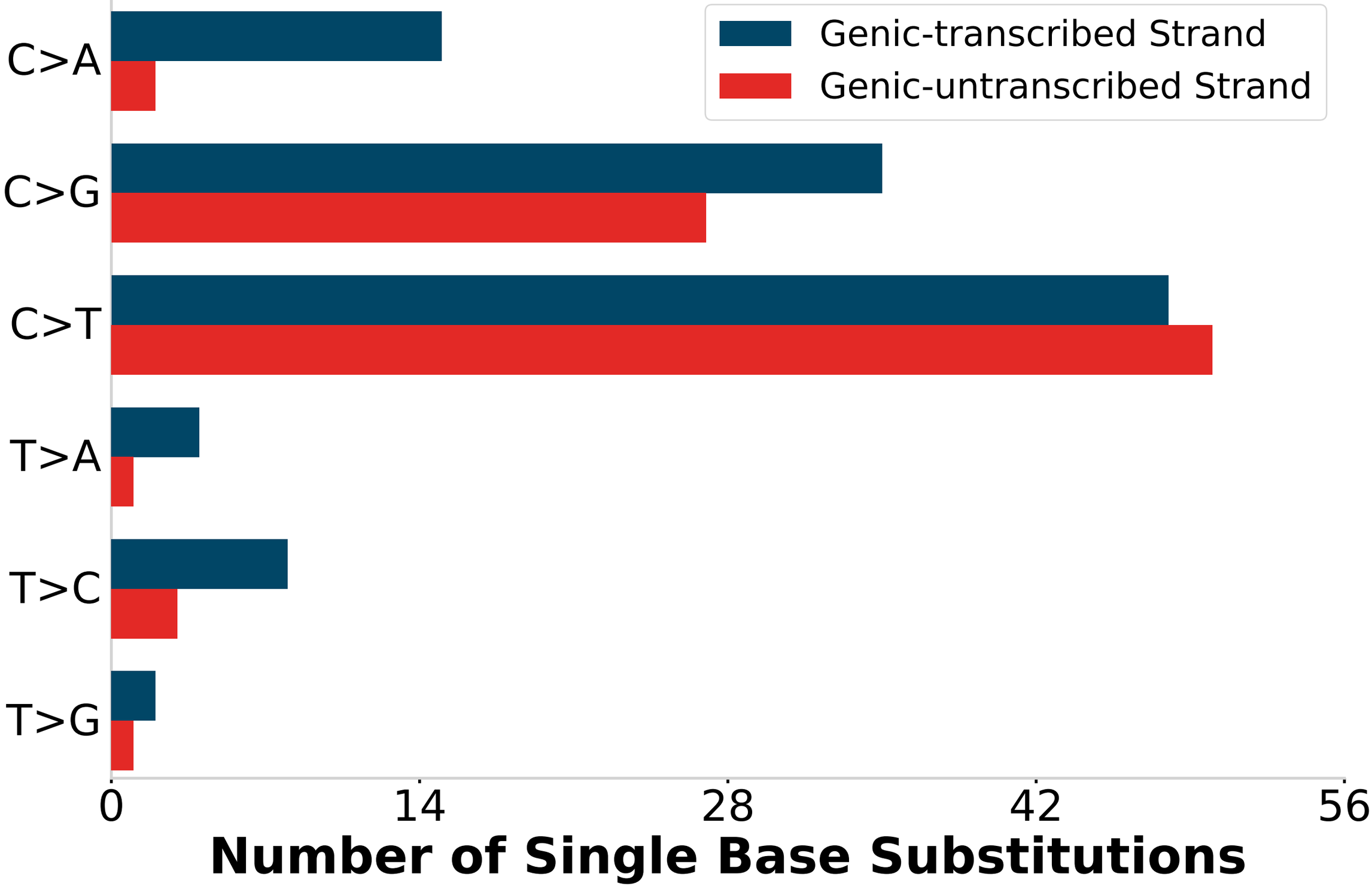
TCGA-GD-A76B-01A-11D-A32B-08: 188 tra



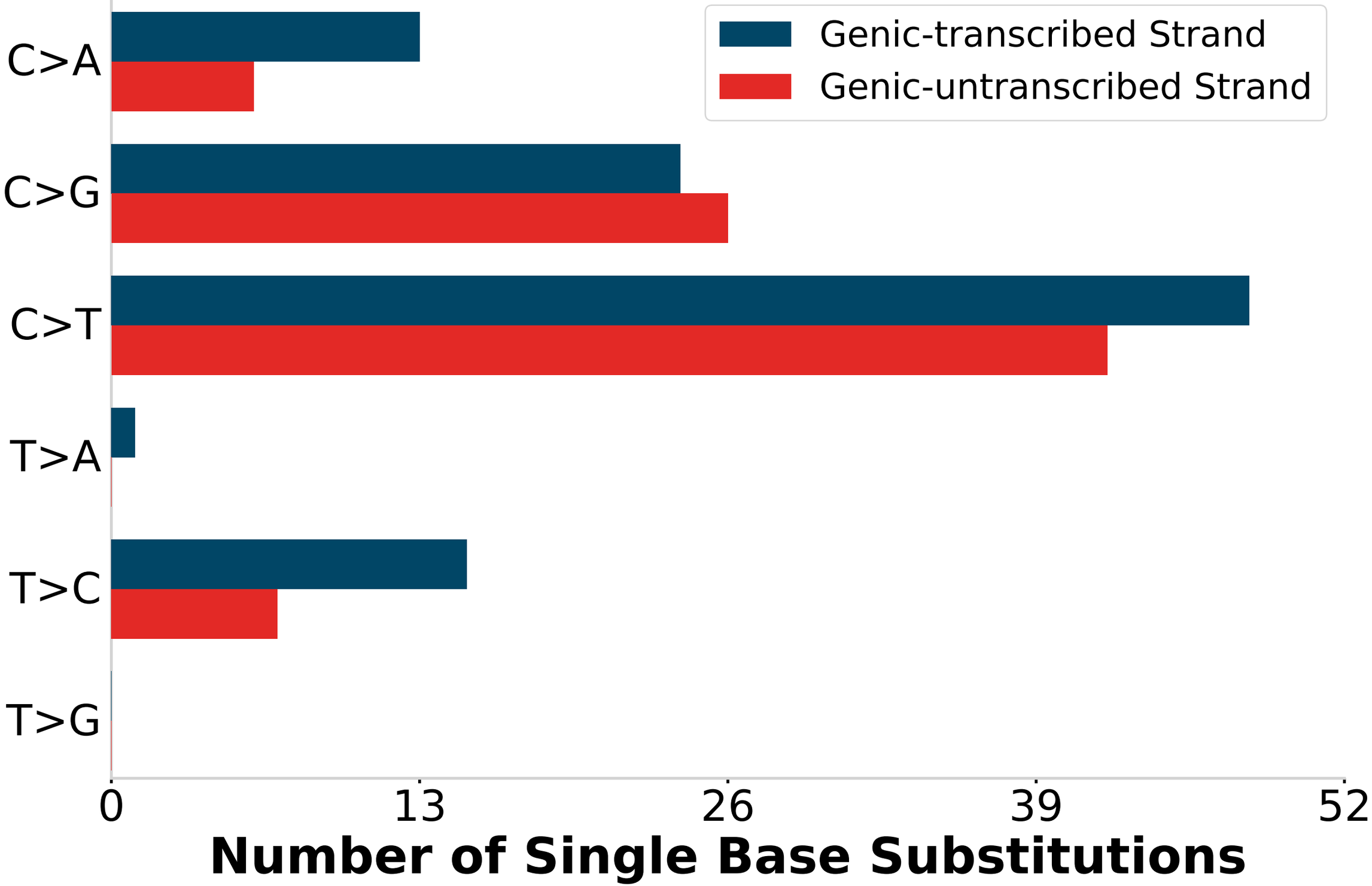
TCGA-GU-A42P-01A-11D-A23U-08: 308 tra



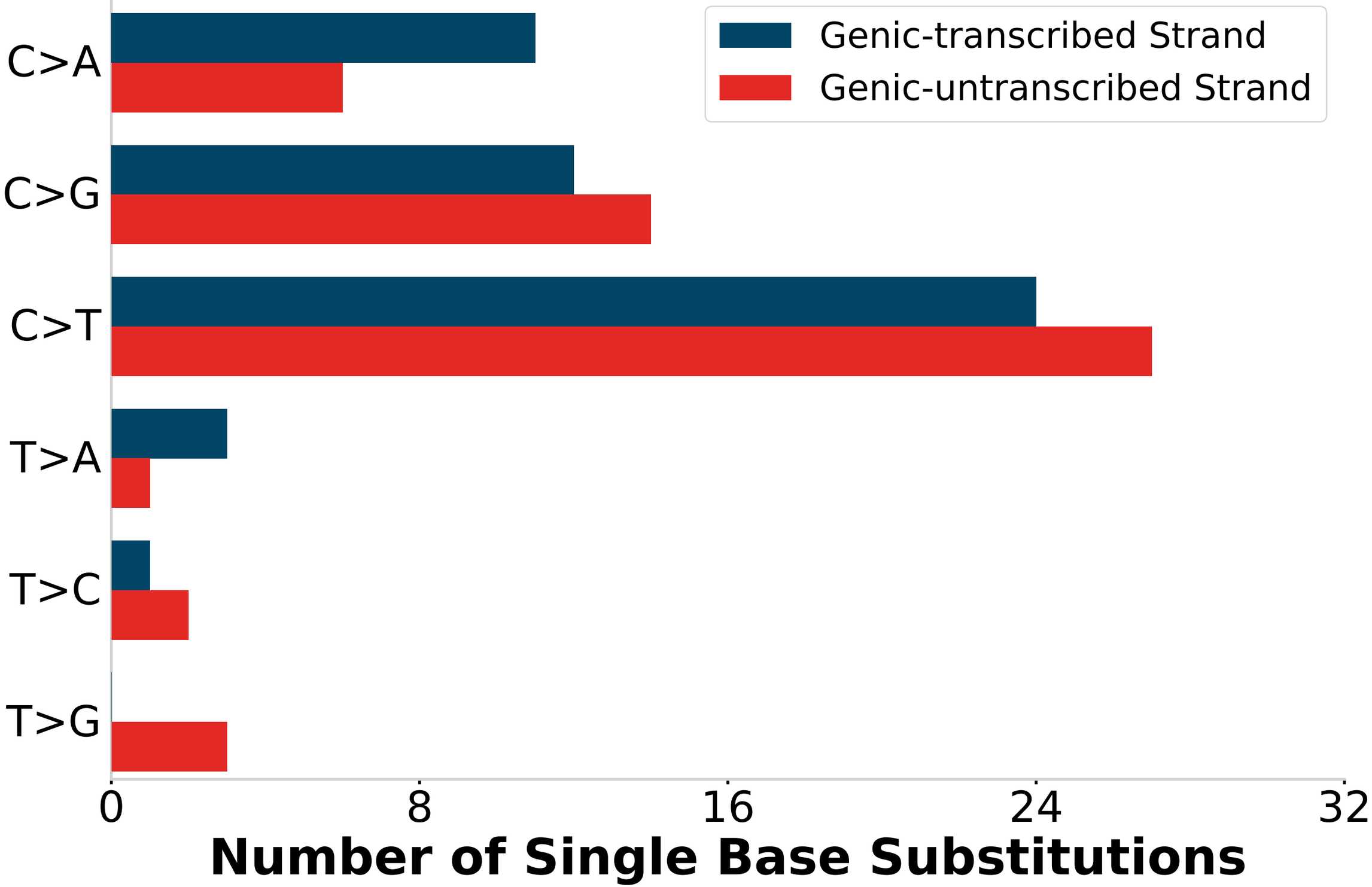
TCGA-GU-A42Q-01A-11D-A23U-08: 196 tra



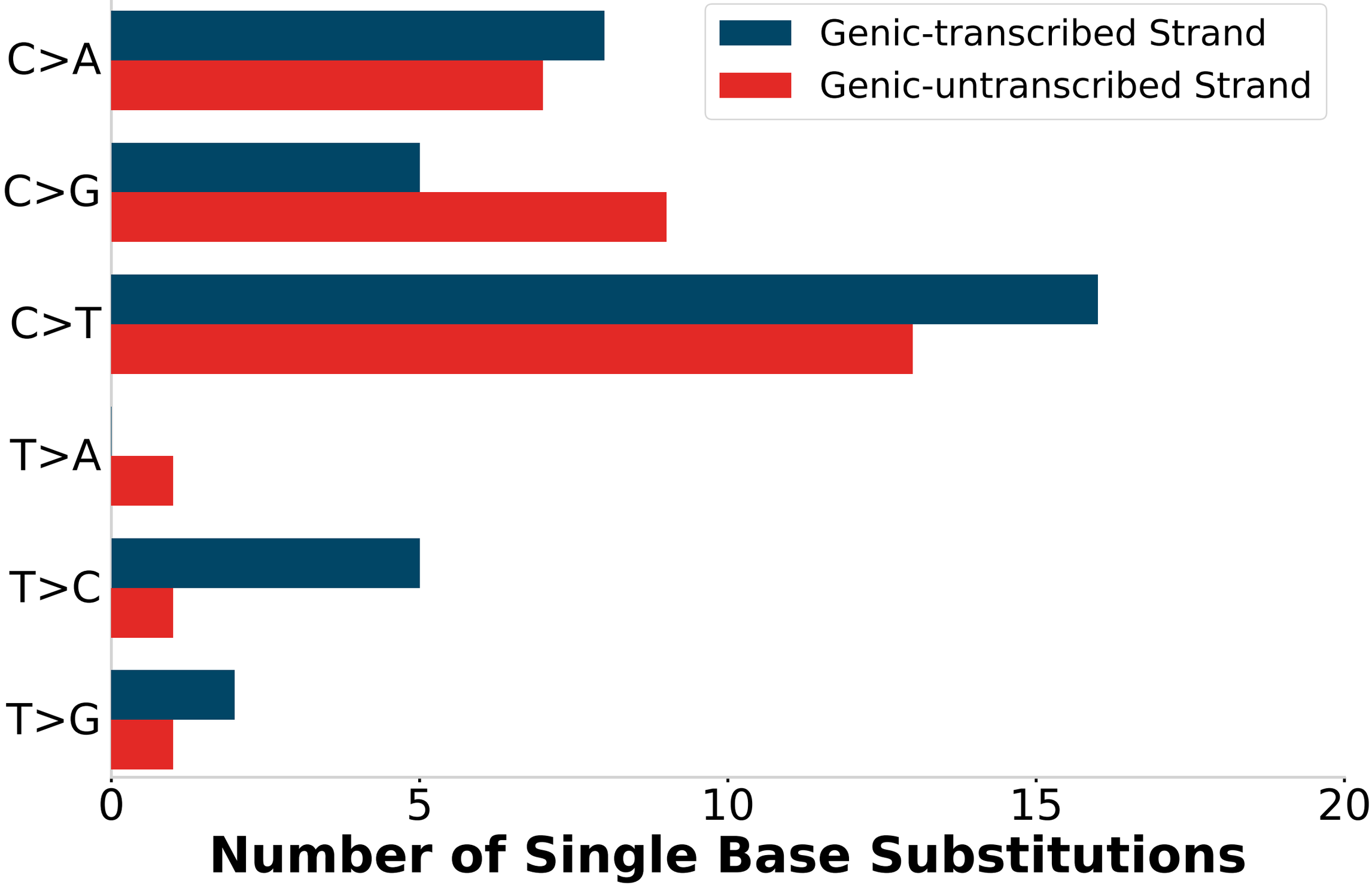
TCGA-GU-A42R-01A-11D-A23M-08: 182 tra



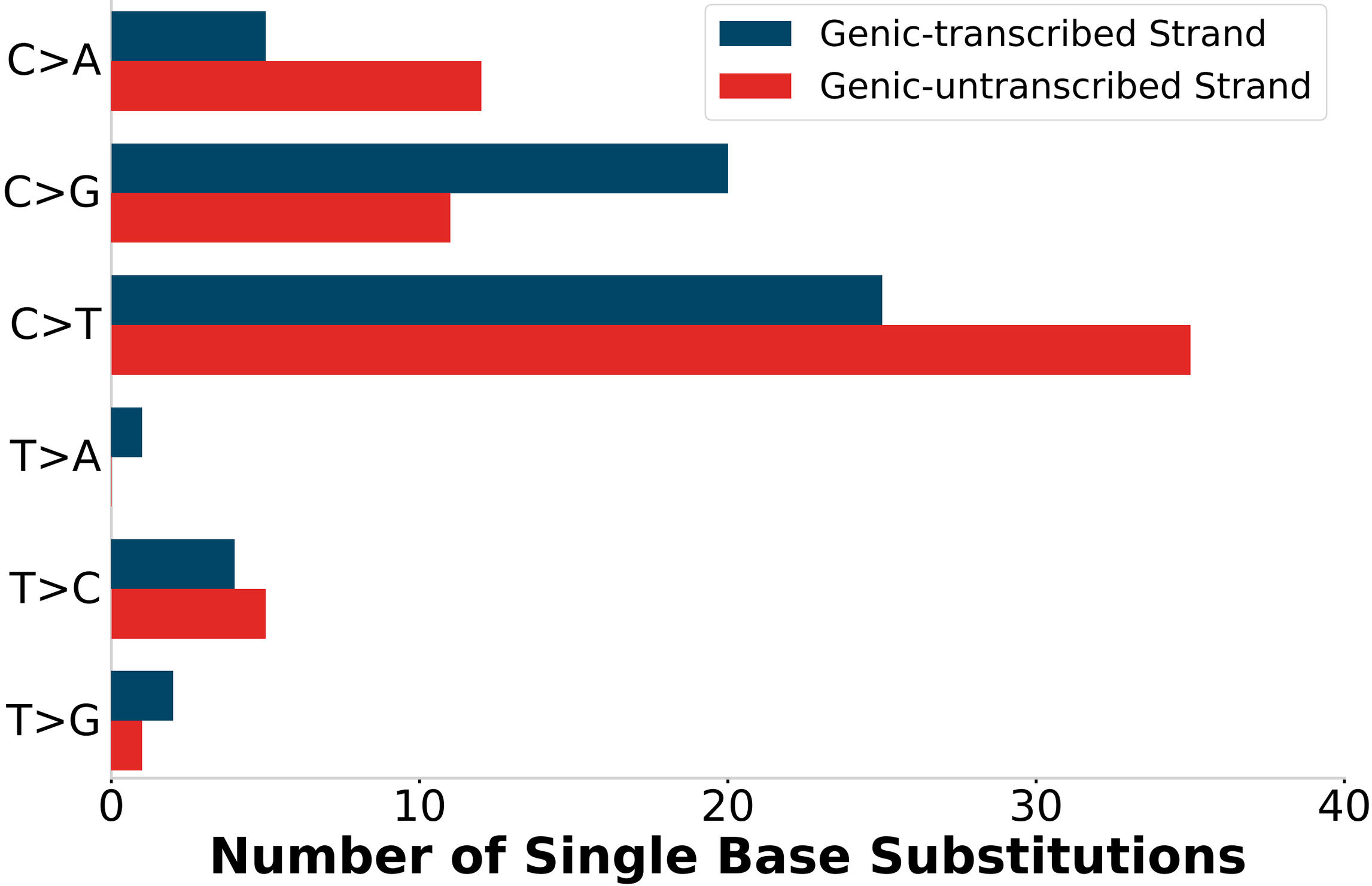
TCGA-GU-A762-01A-11D-A339-08: 104 tra



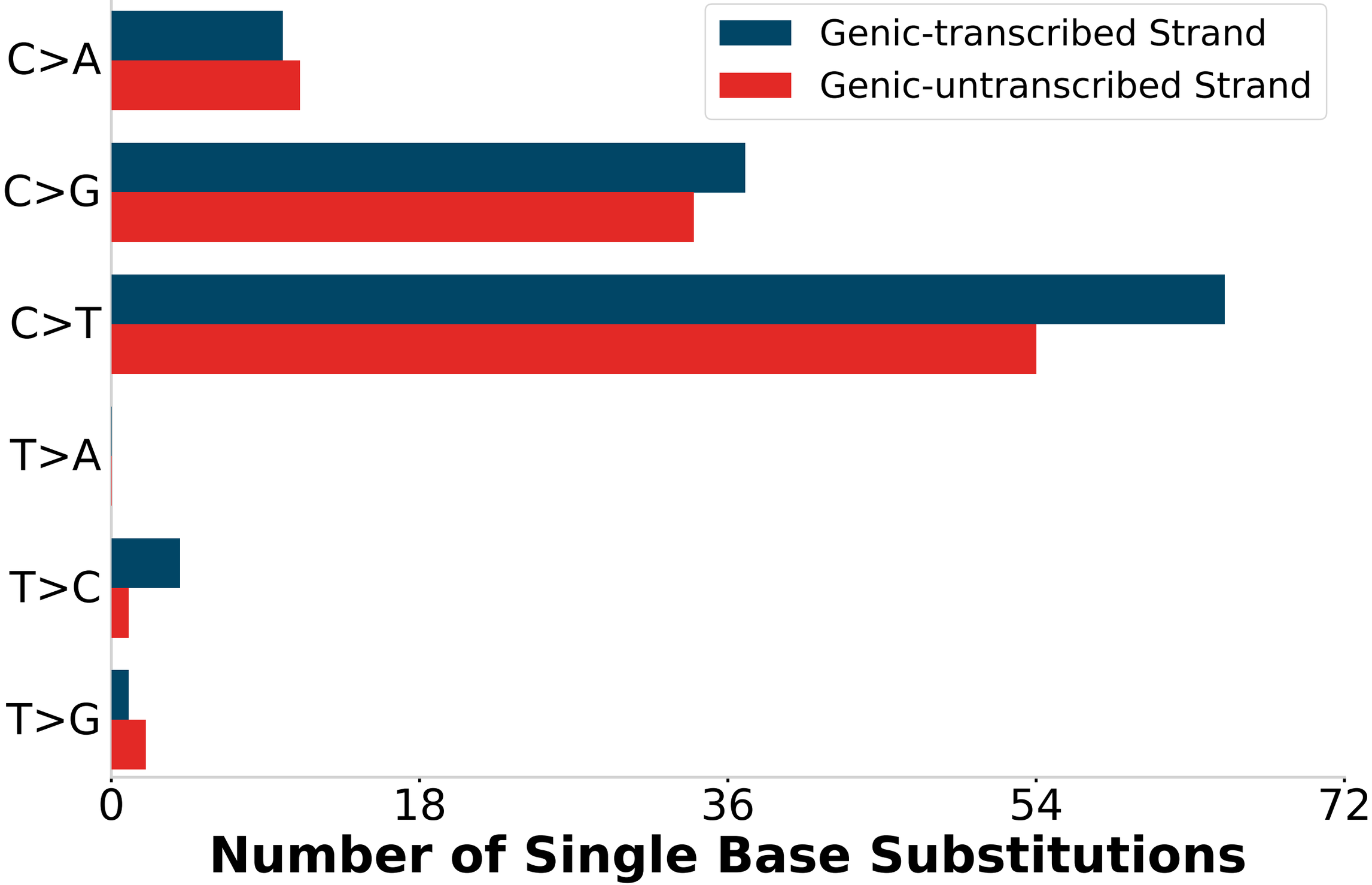
TCGA-GU-A763-01A-11D-A32B-08: 68 tran



TCGA-GU-A764-01A-11D-A34U-08: 121 tra



TCGA-GU-A766-01A-11D-A32B-08: 219 tra



TCGA-GU-A767-01A-11D-A32B-08: 425 tra

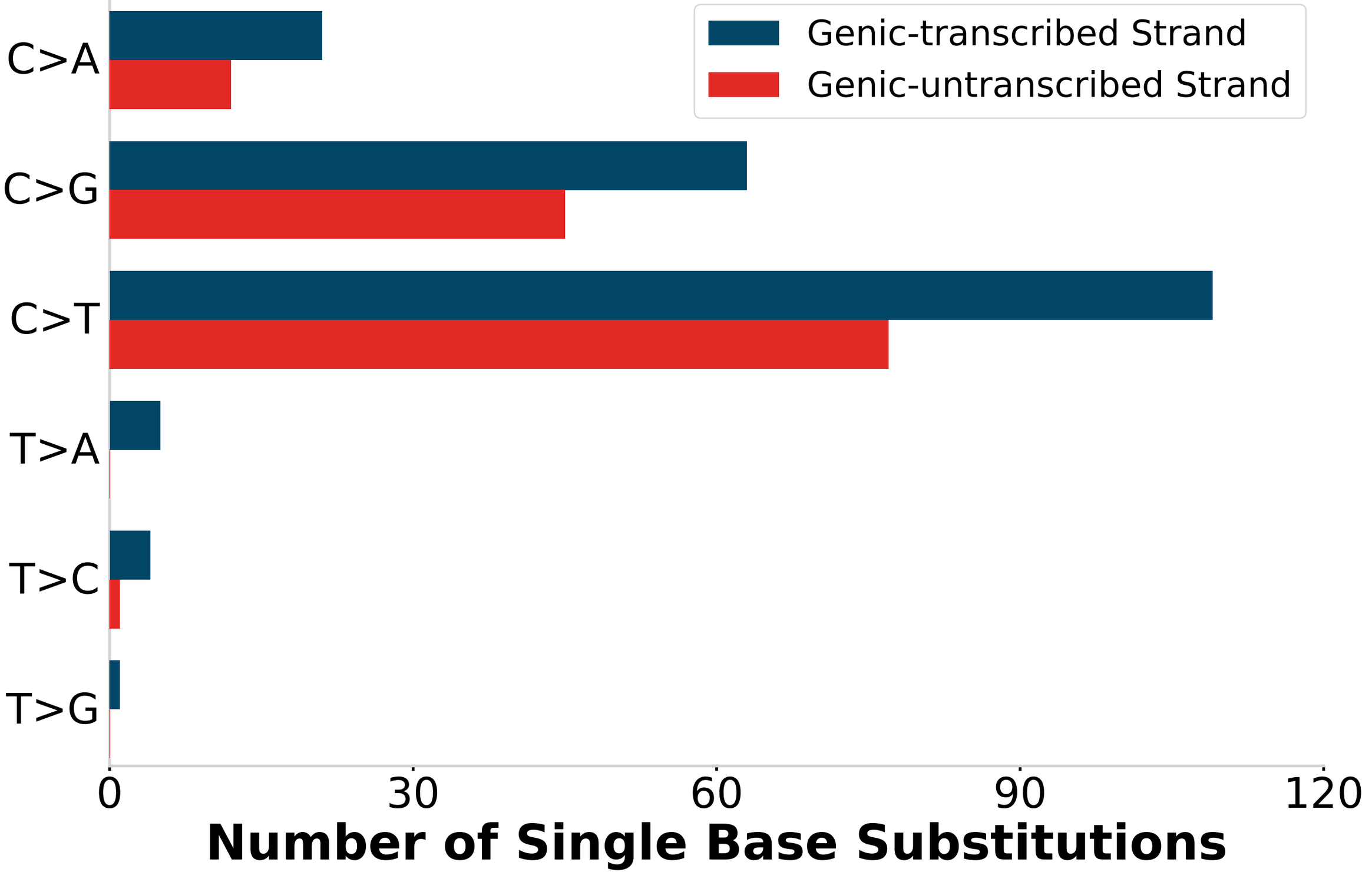
C>A
C>G
C>T
T>A
T>C
T>G

Genic-transcribed Strand
Genic-untranscribed Strand

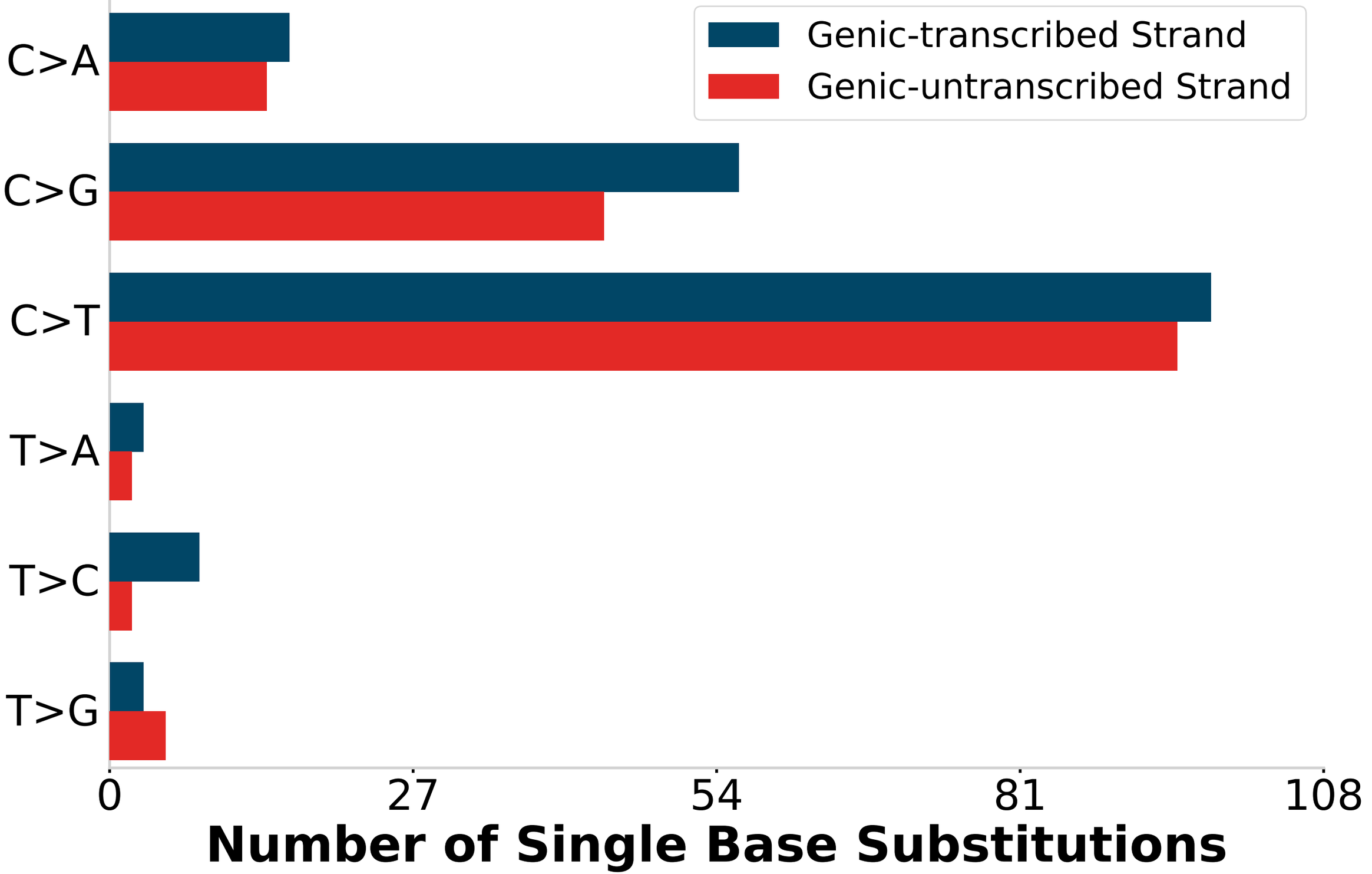
0
25
50
75
100

Number of Single Base Substitutions

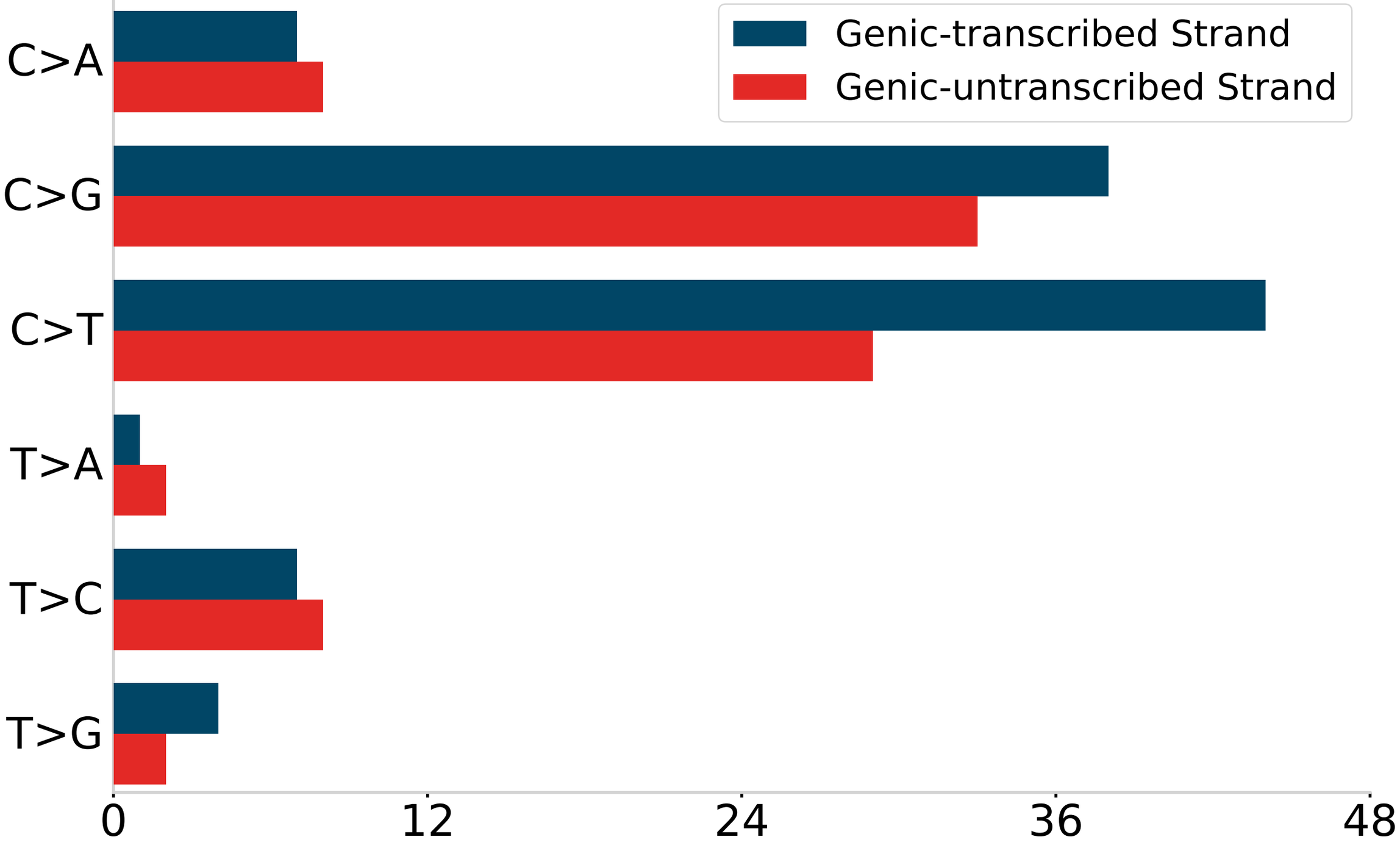
TCGA-GU-AATO-01A-11D-A391-08: 338 tra



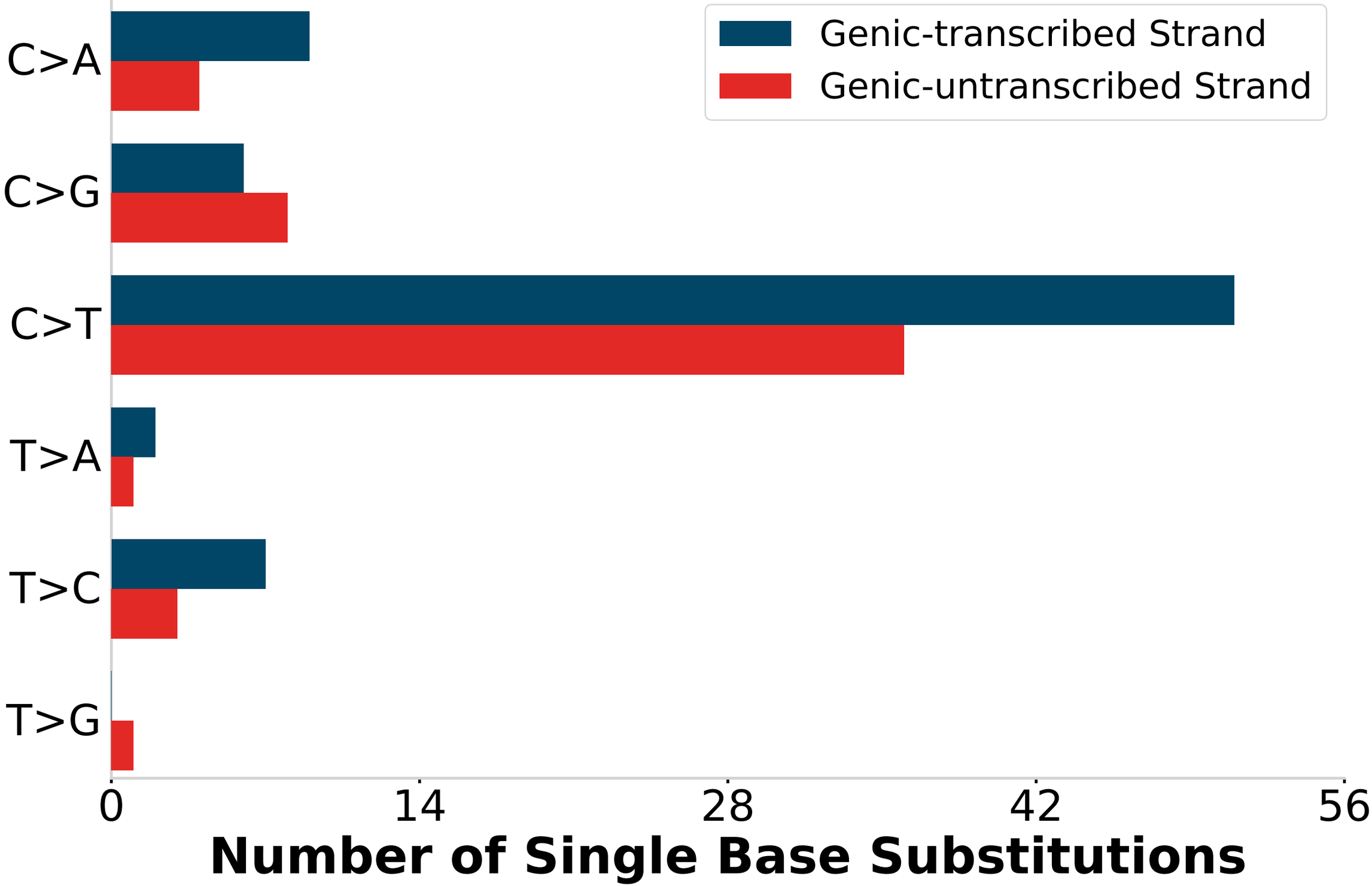
TCGA-GU-AATP-01A-11D-A391-08: 346 tra



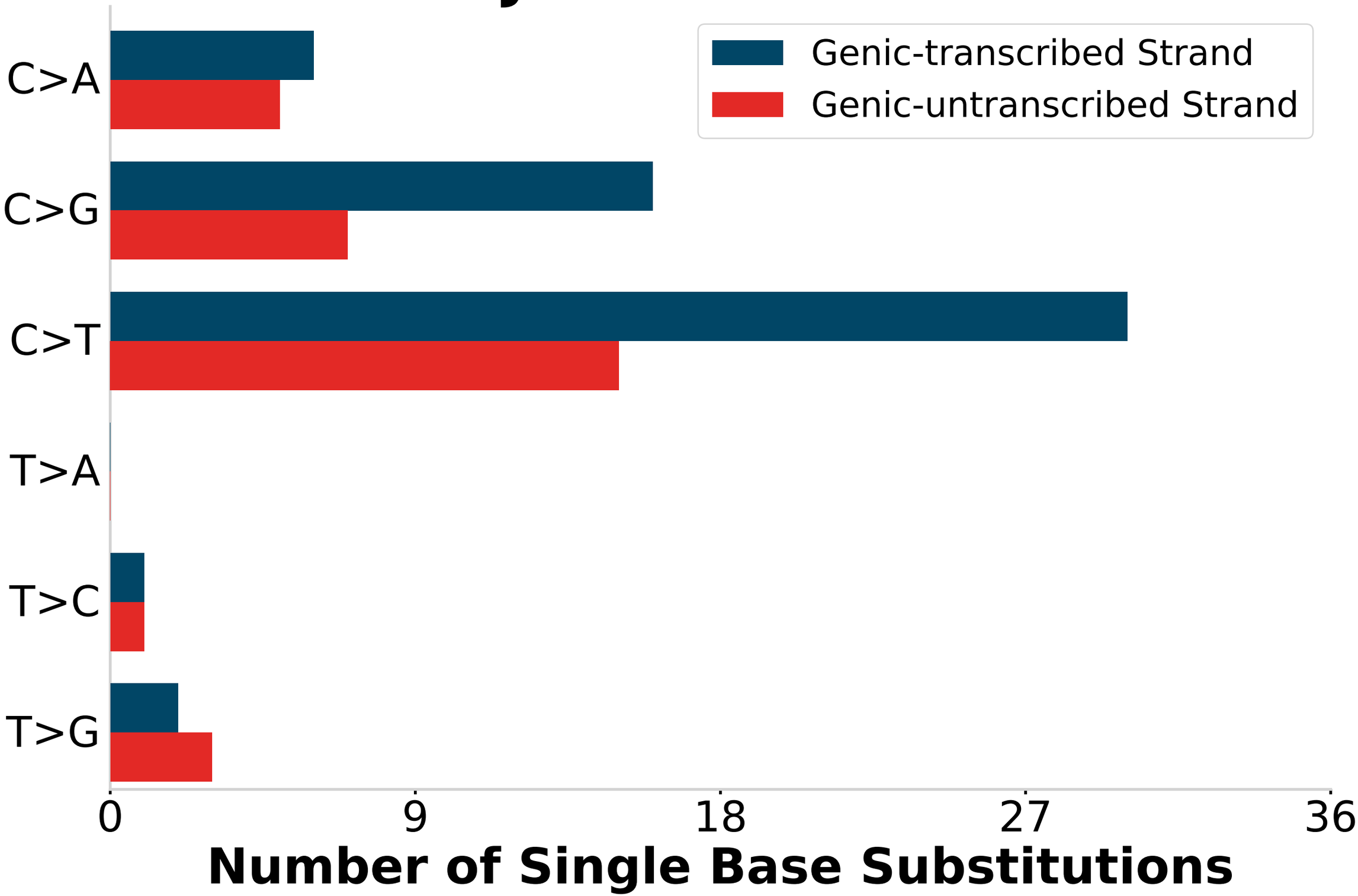
TCGA-GU-AATQ-01A-11D-A391-08: 183 tra



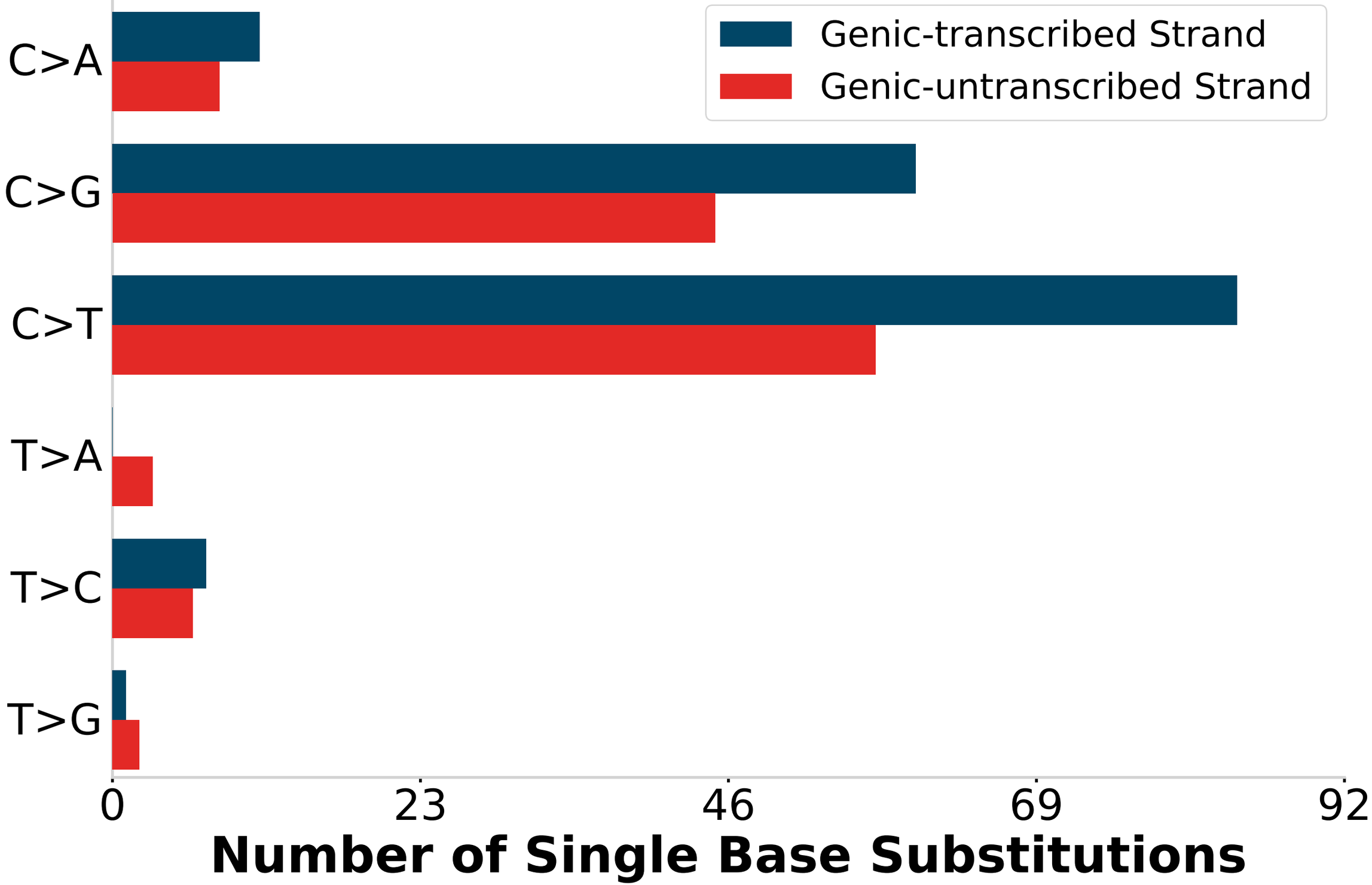
TCGA-GV-A3JV-01A-11D-A21Z-08: 128 tran



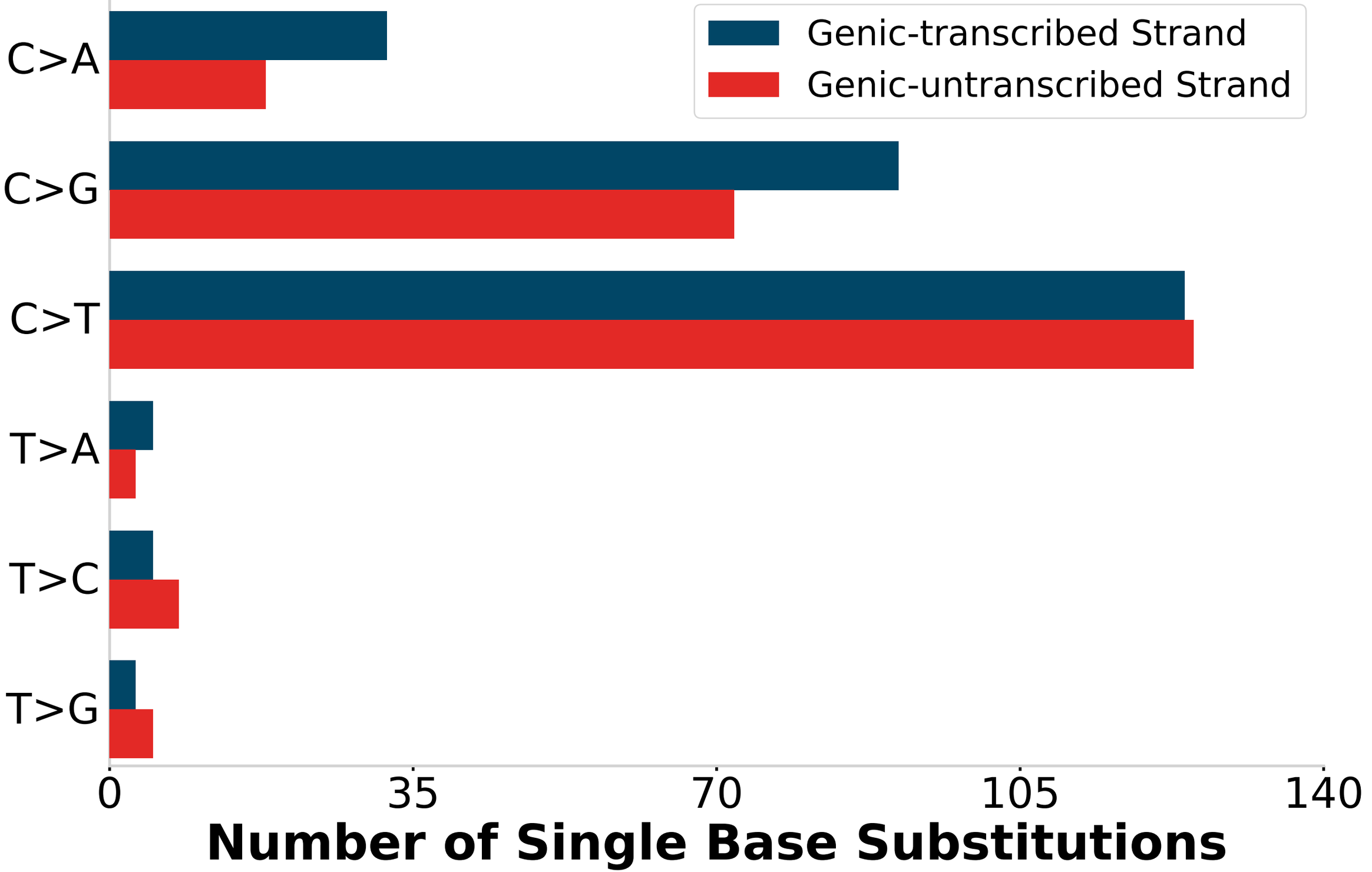
TCGA-GV-A3JW-01A-11D-A20D-08: 86 tran



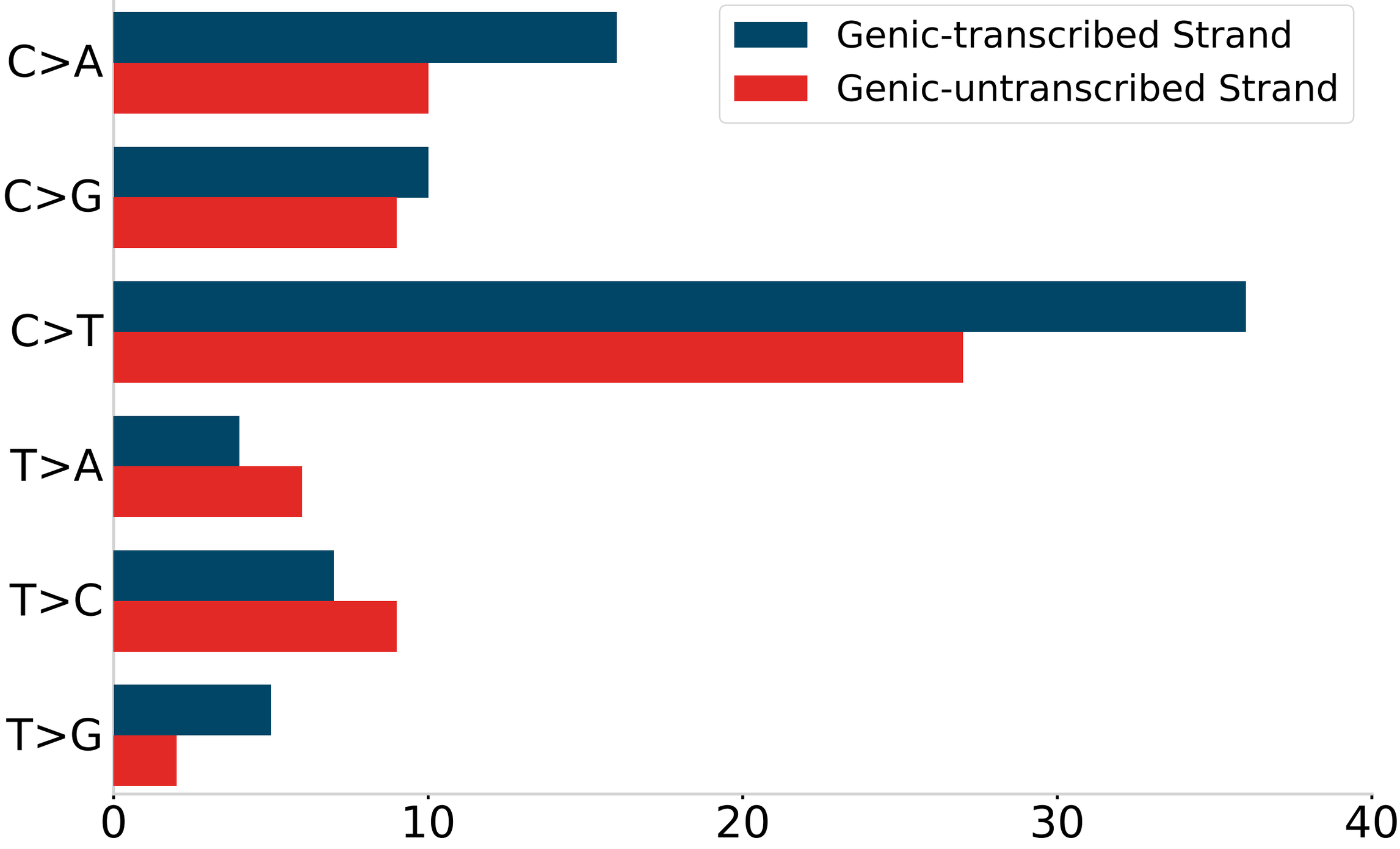
TCGA-GV-A3JX-01A-11D-A20D-08: 284 tran



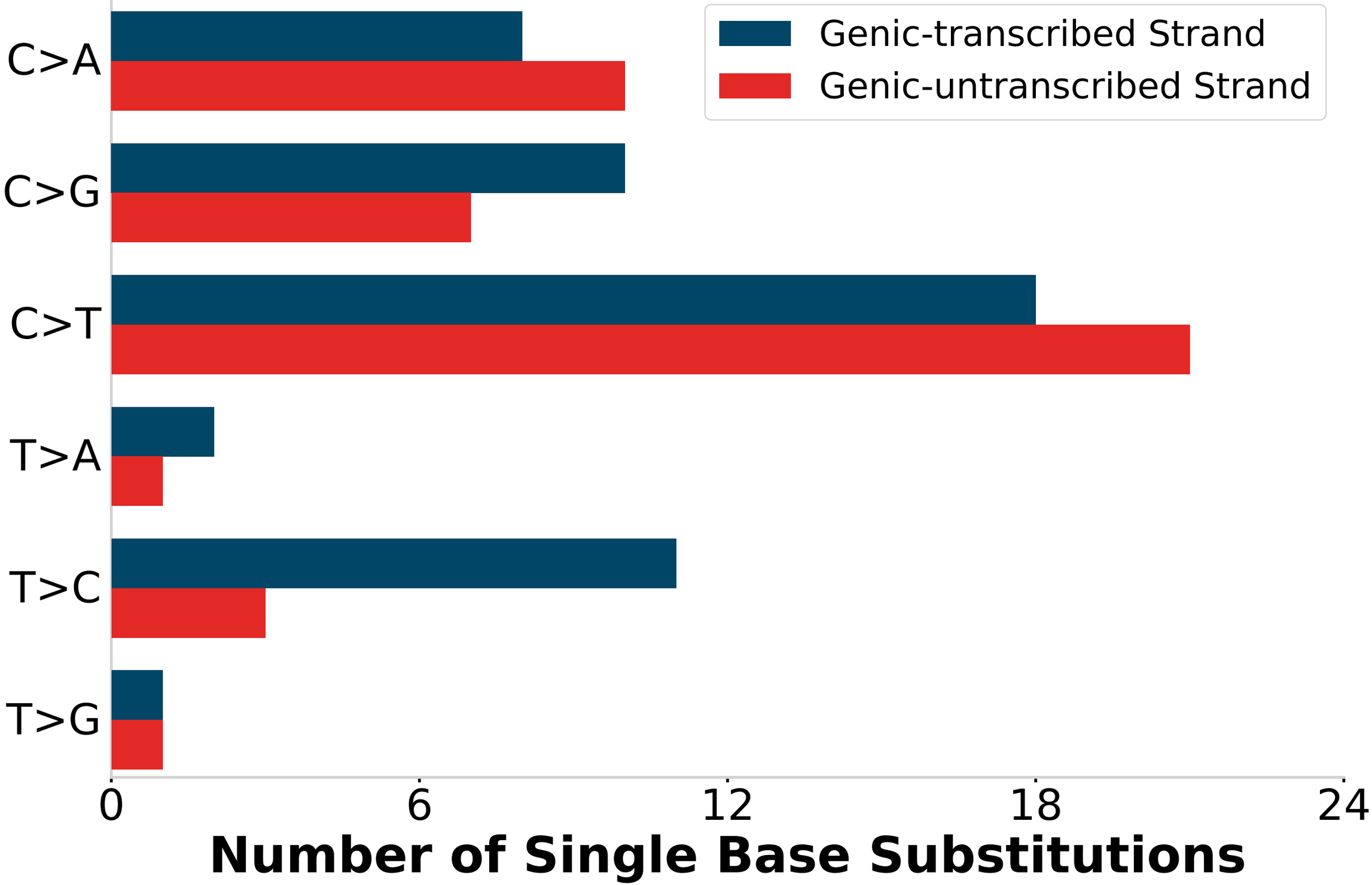
TCGA-GV-A3JZ-01A-11D-A21A-08: 491 tran



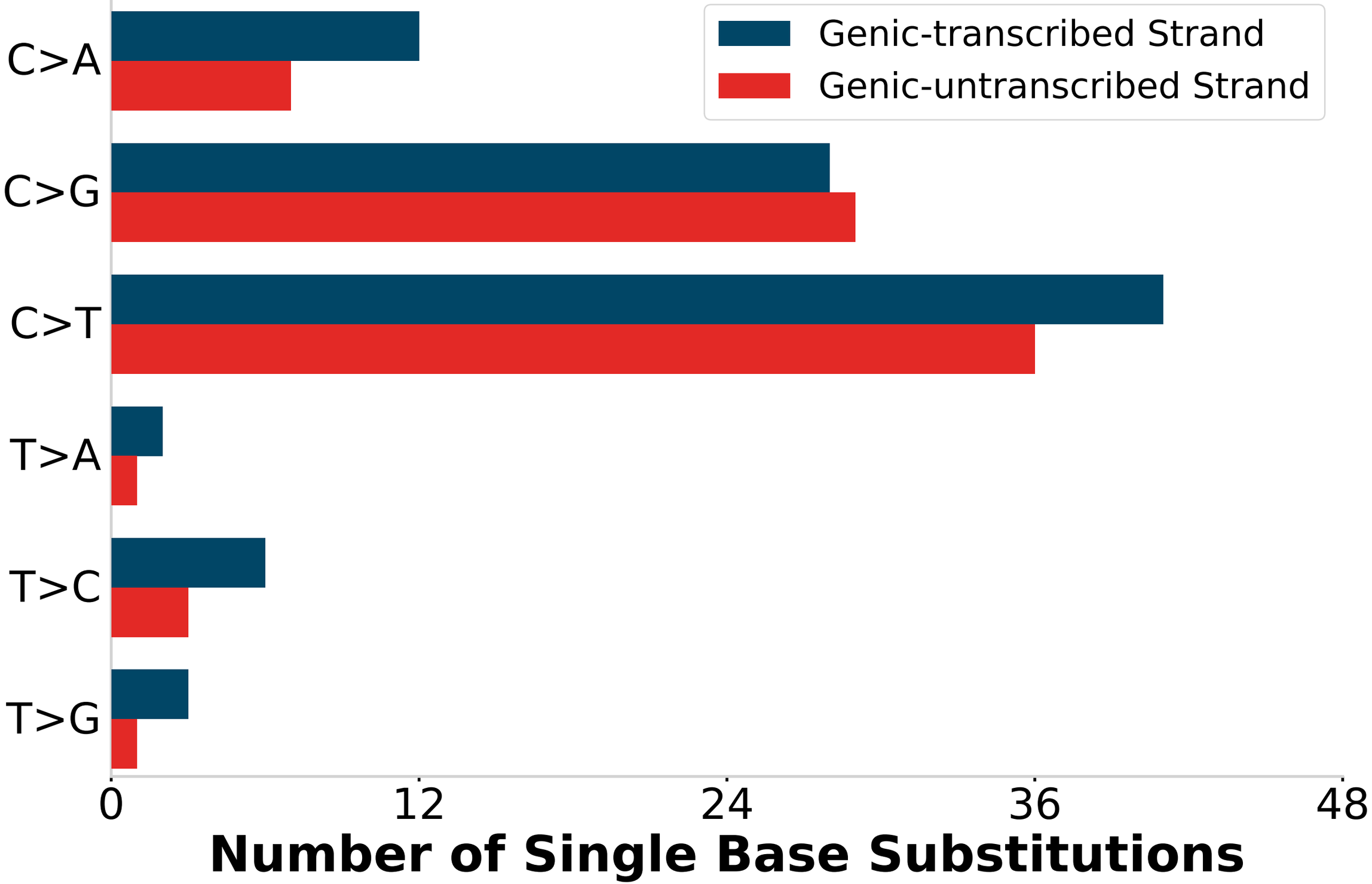
TCGA-GV-A3QF-01A-31D-A22Z-08: 141 tra



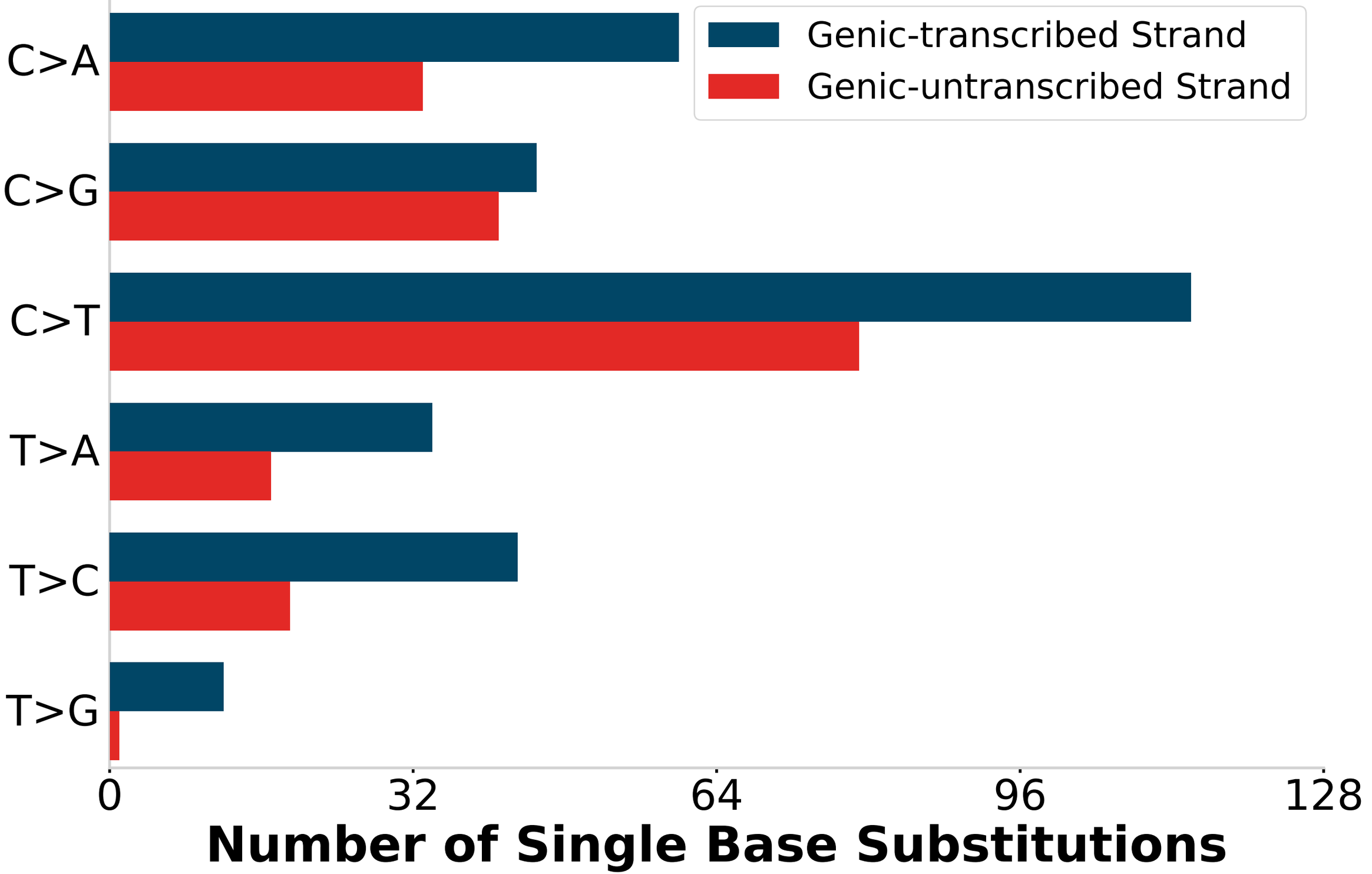
TCGA-GV-A3QG-01A-11D-A21Z-08: 93 tran



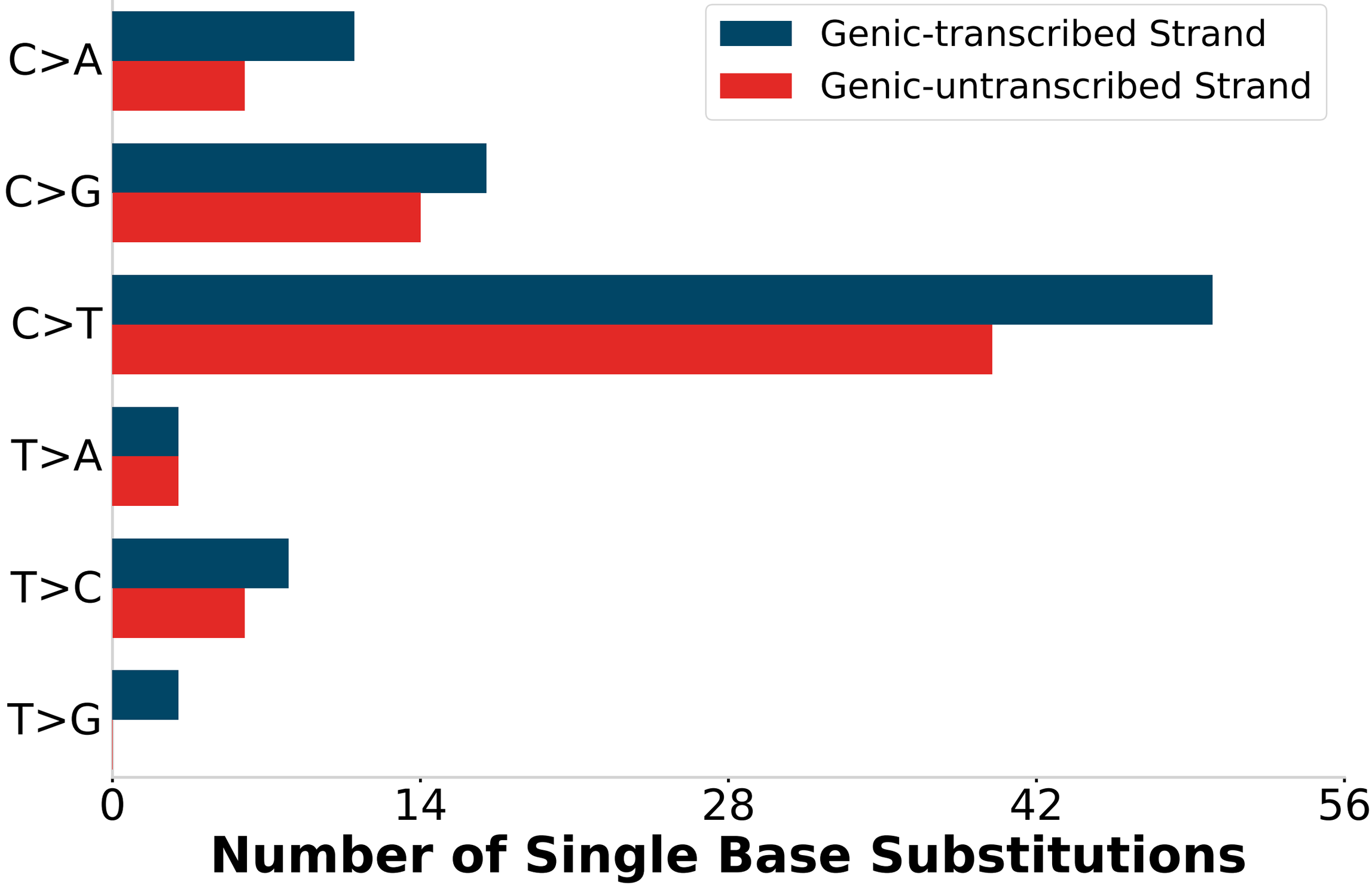
TCGA-GV-A3QH-01A-11D-A21Z-08: 169 tra



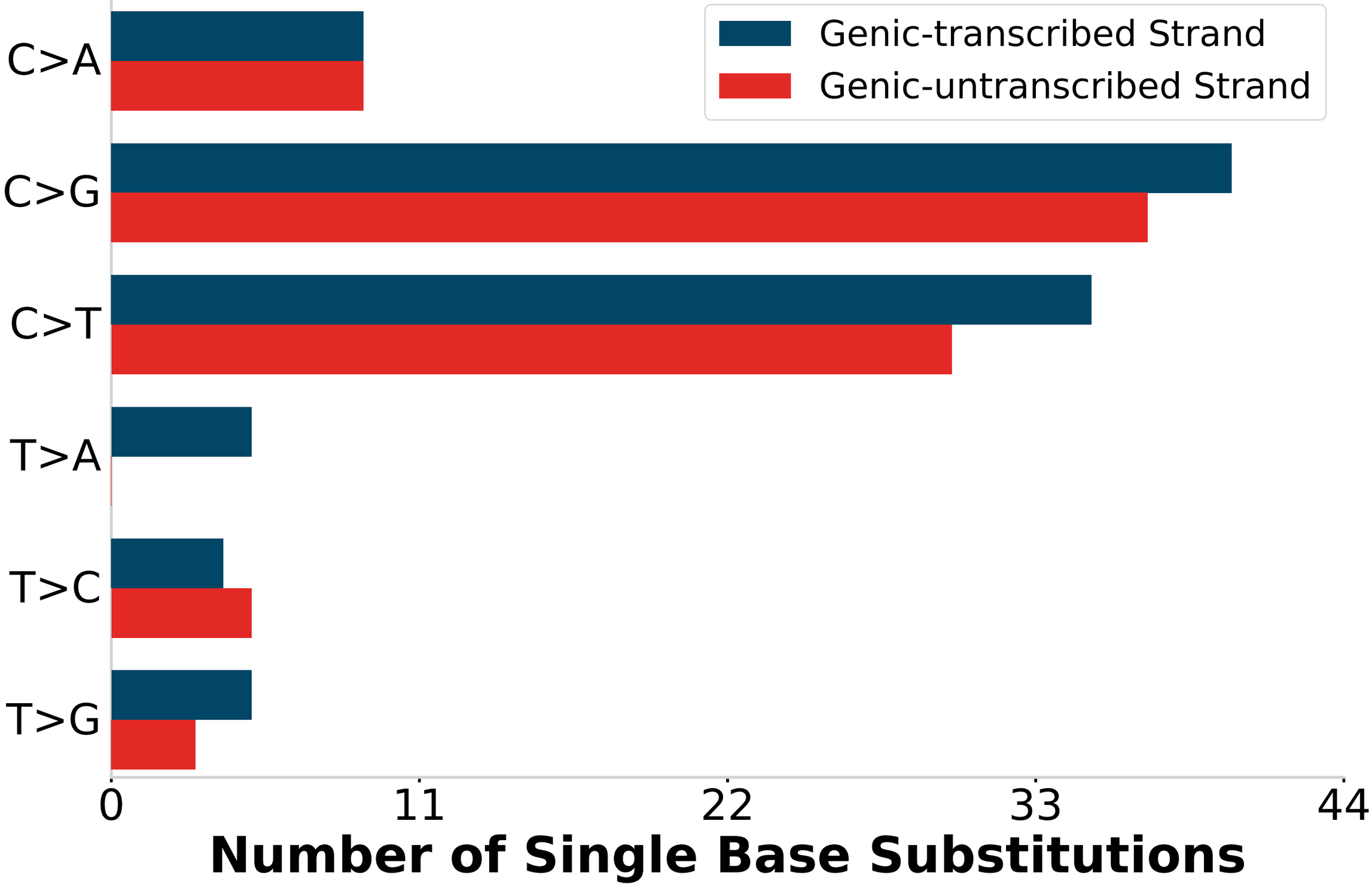
TCGA-GV-A3QI-01A-11D-A21Z-08: 498 tran



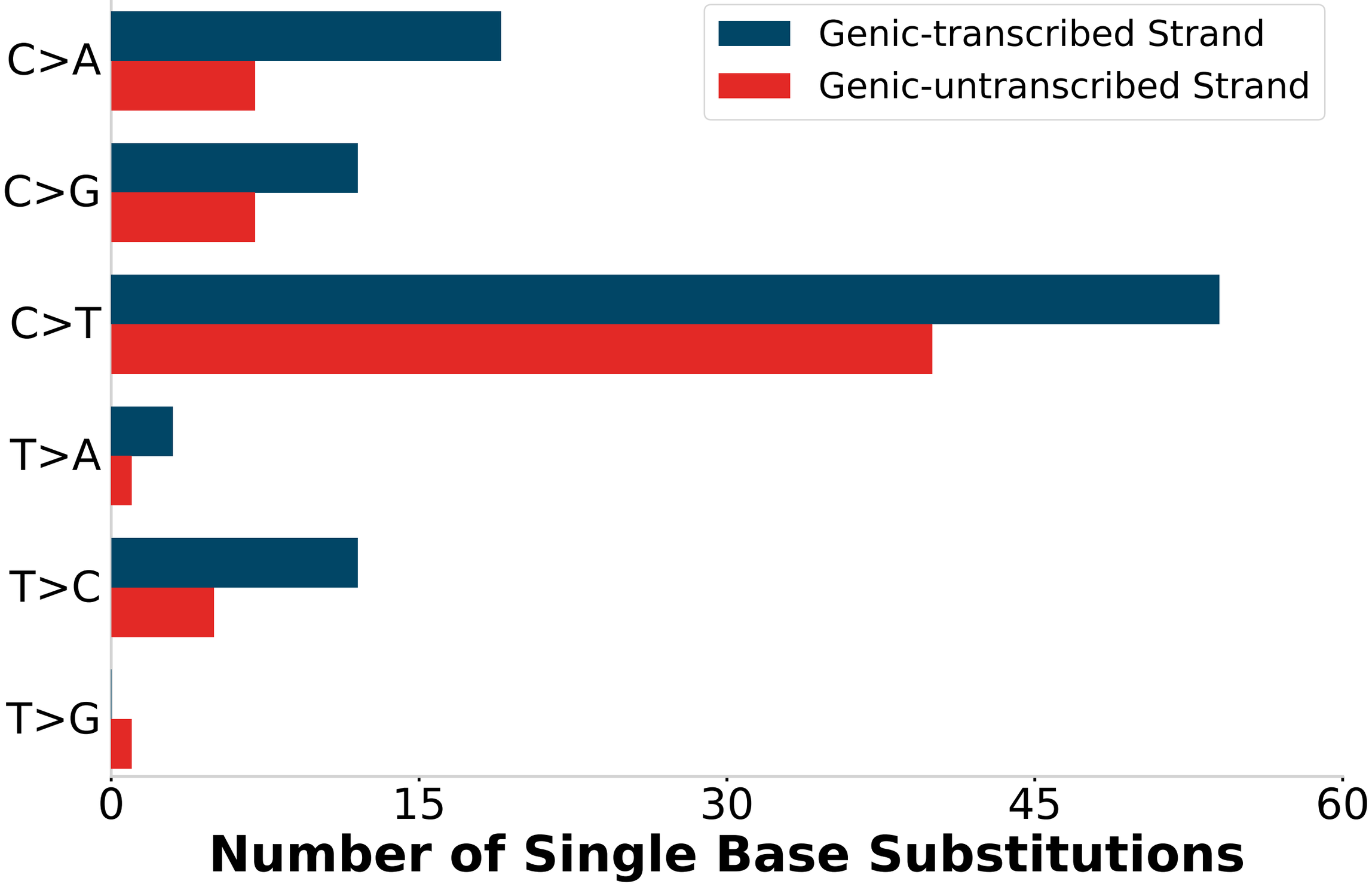
TCGA-GV-A3QK-01B-11D-A23M-08: 161 tra



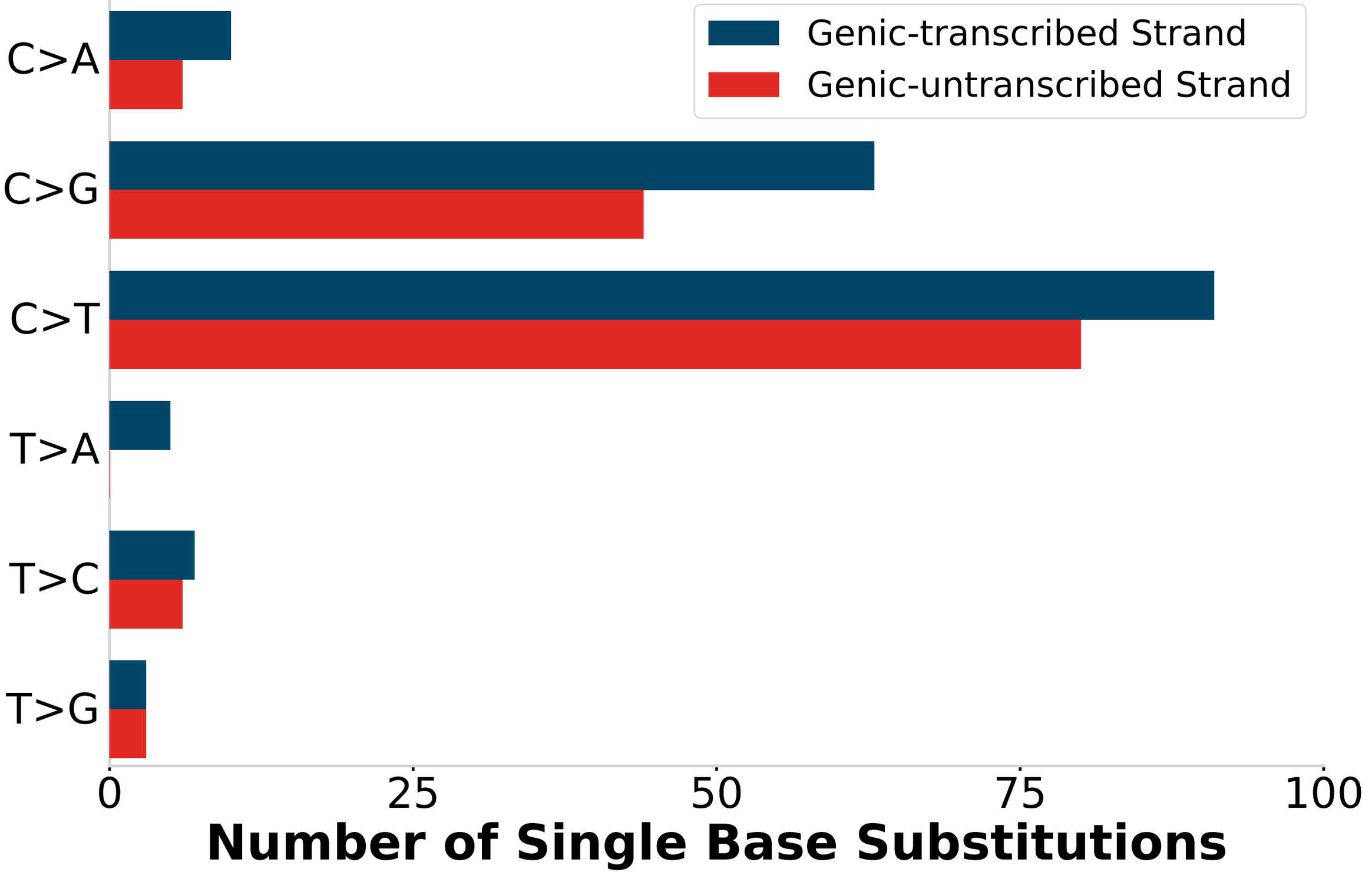
TCGA-GV-A40E-01A-12D-A23M-08: 182 tra



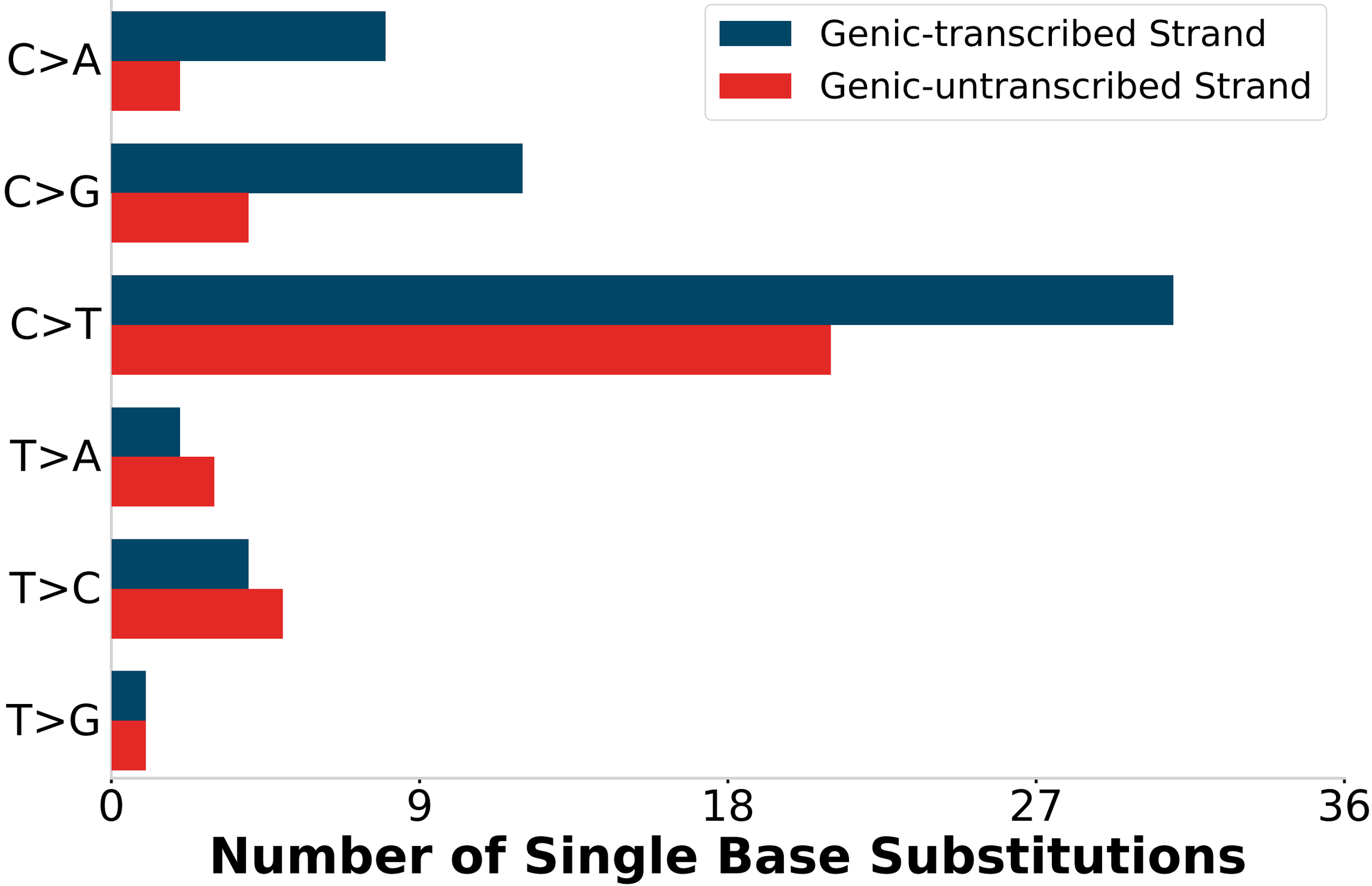
TCGA-GV-A40G-01A-11D-A23M-08: 161 tra



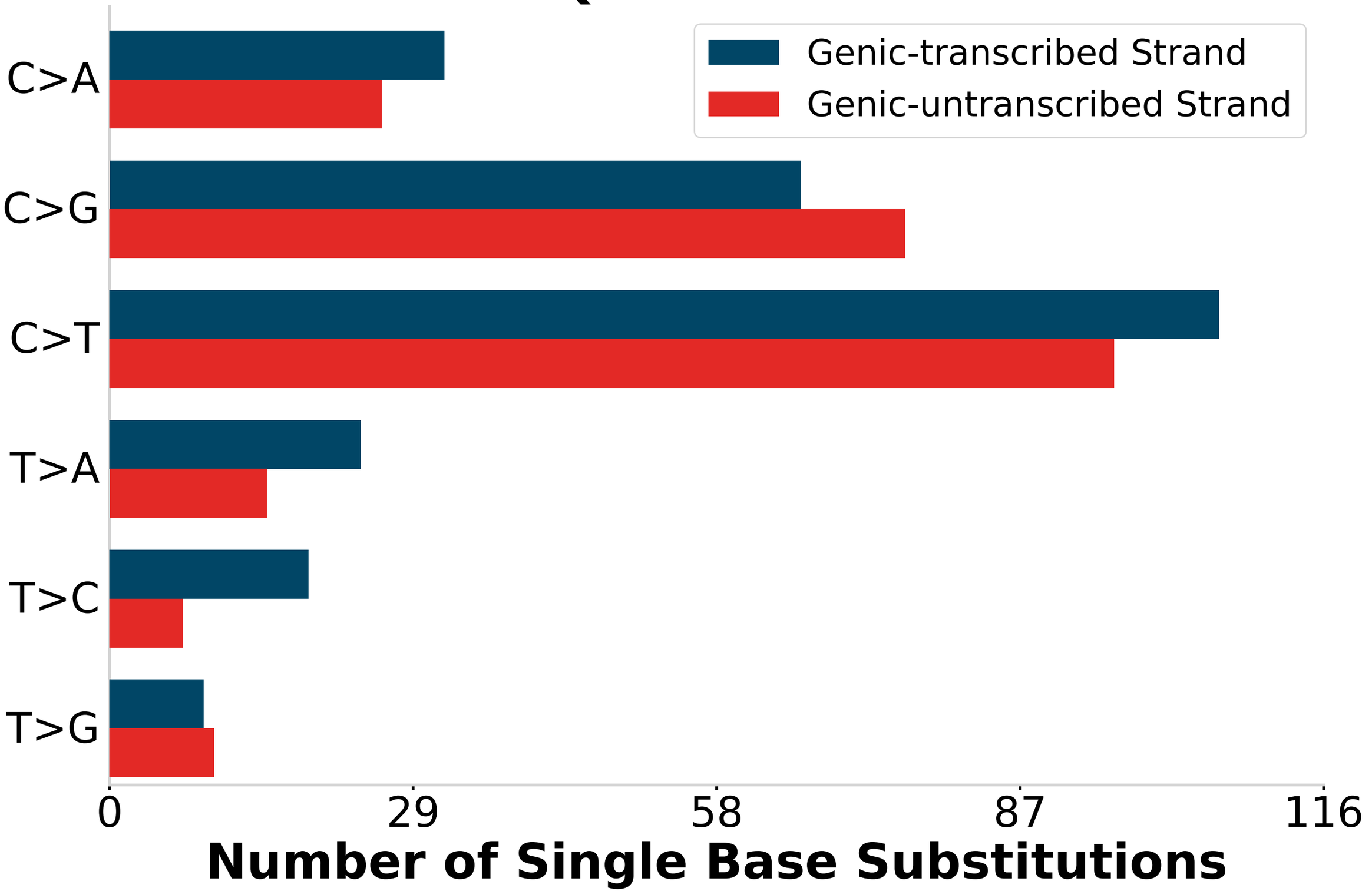
TCGA-GV-A6ZA-01A-12D-A339-08: 318 tra



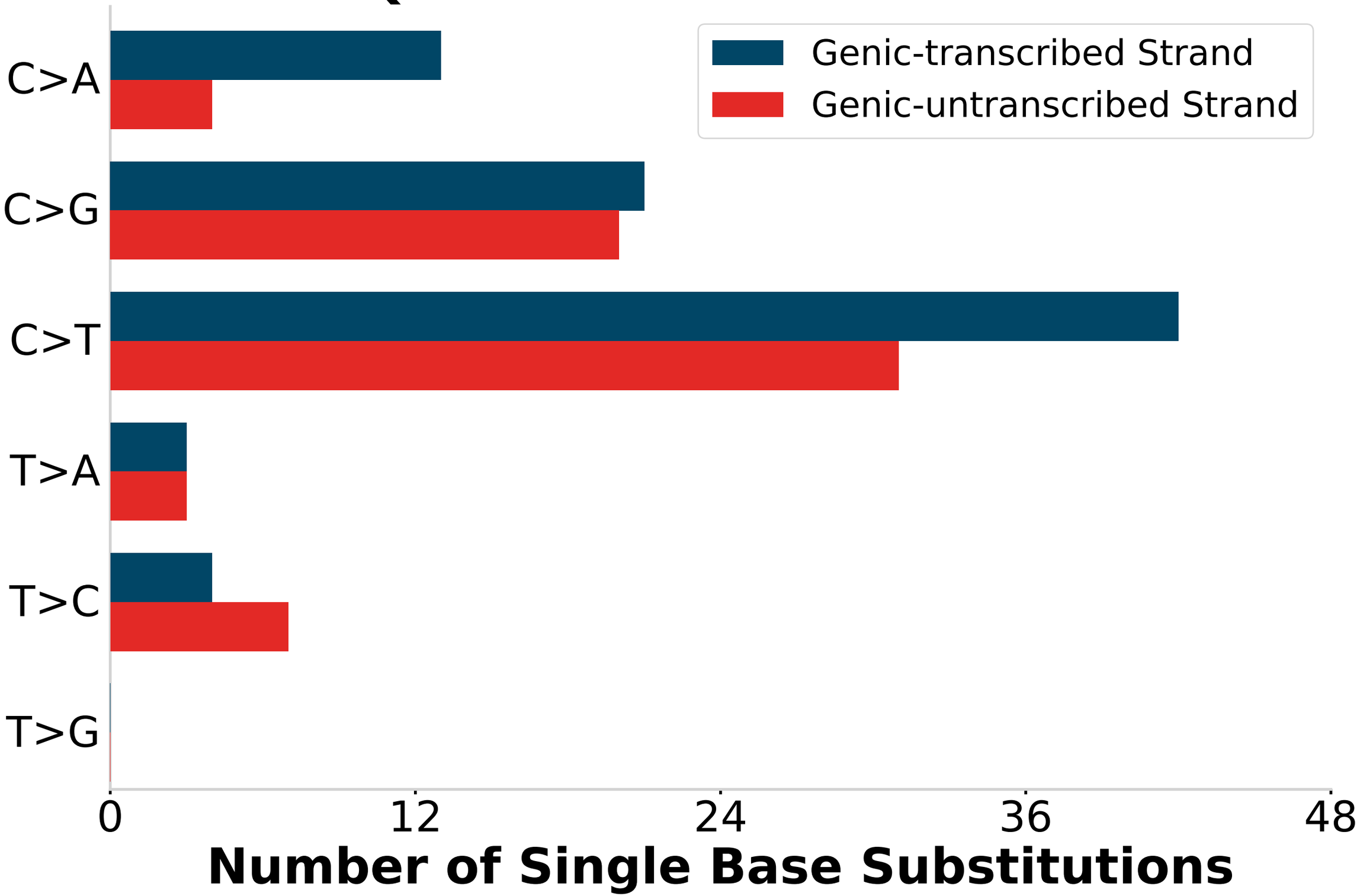
TCGA-H4-A2HO-01A-11D-A17V-08: 94 tran



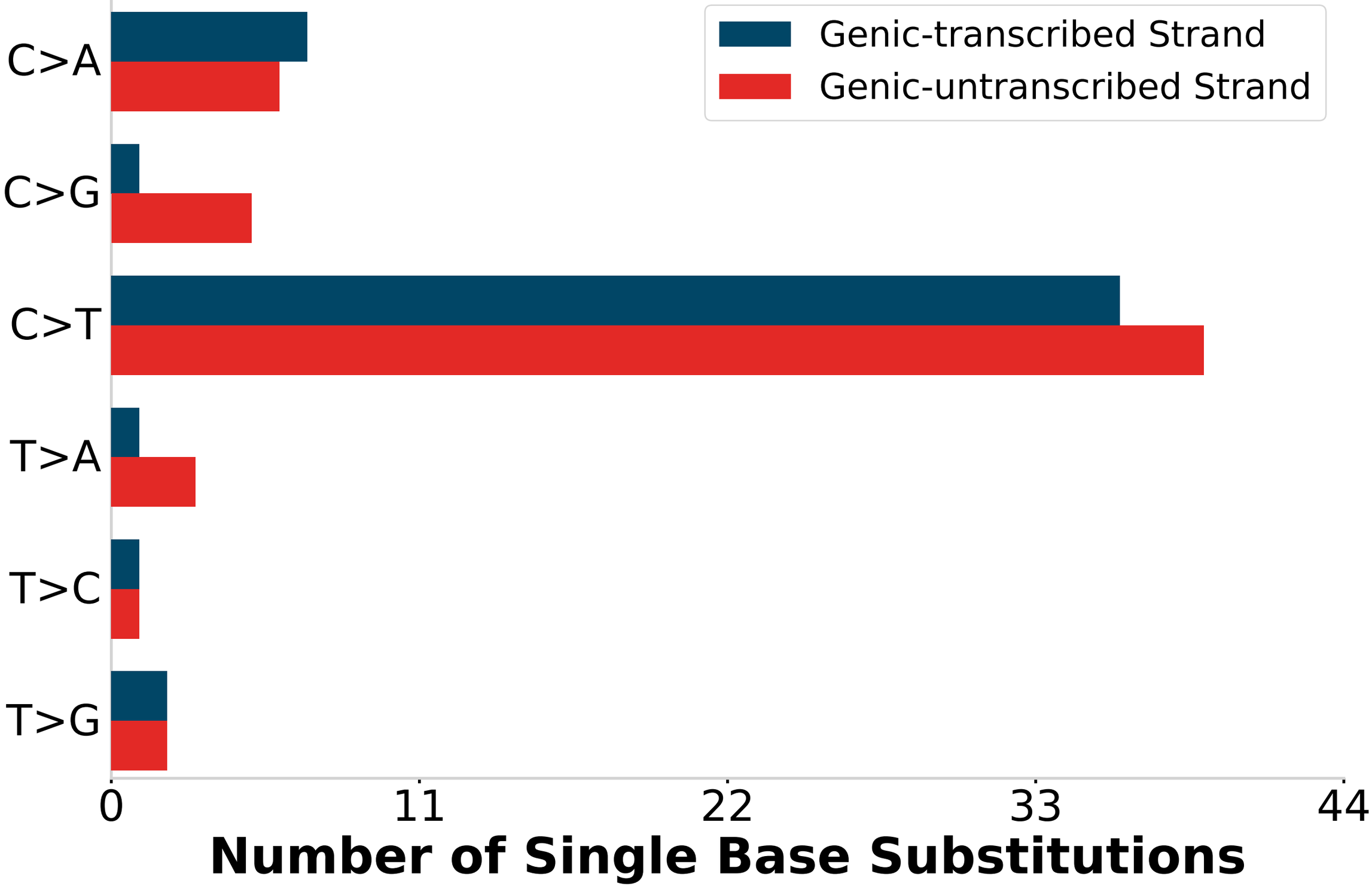
TCGA-H4-A2HQ-01A-11D-A17V-08: 486 tra



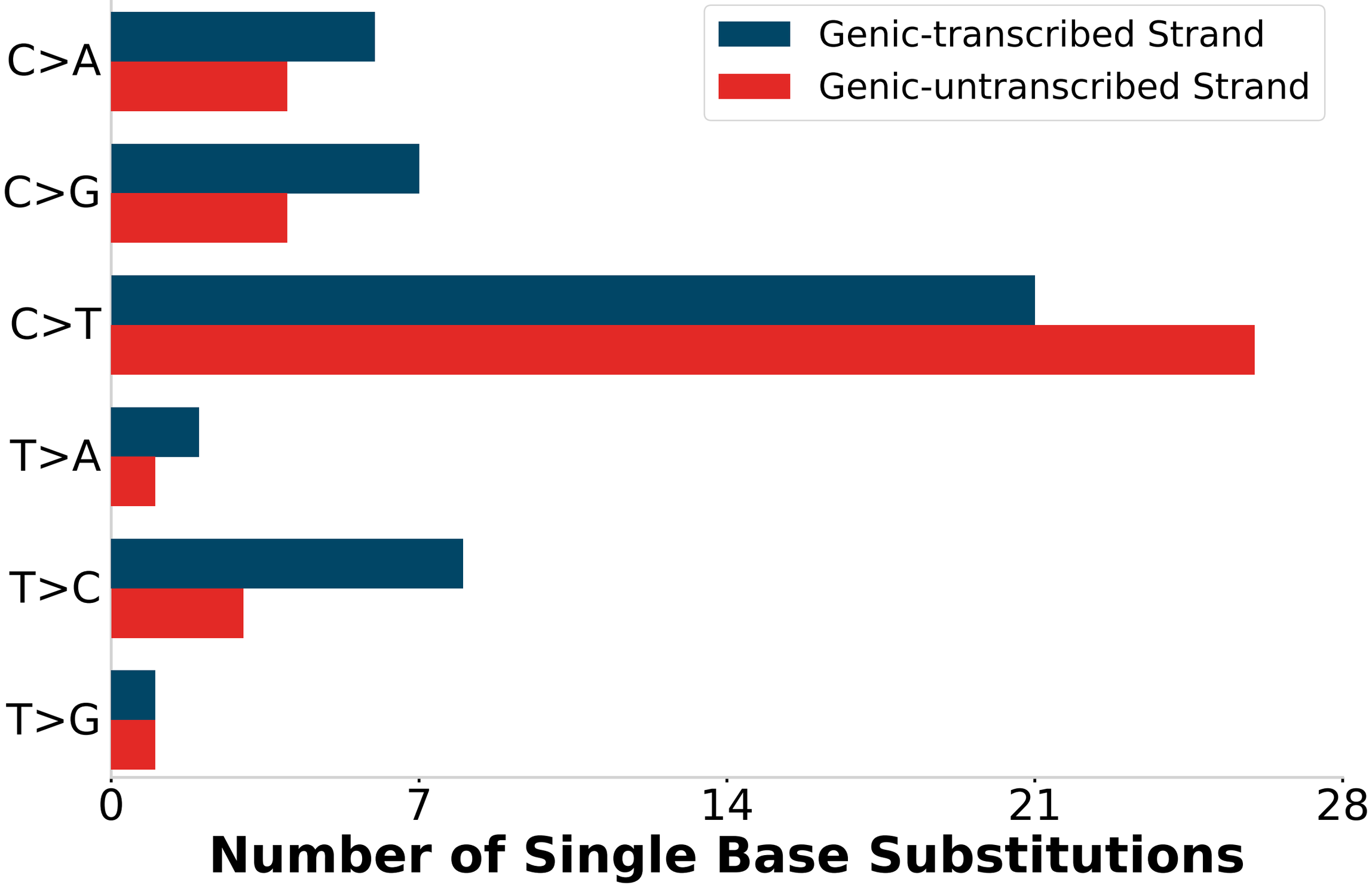
TCGA-HQ-A2OE-01A-11D-A202-08: 148 tra



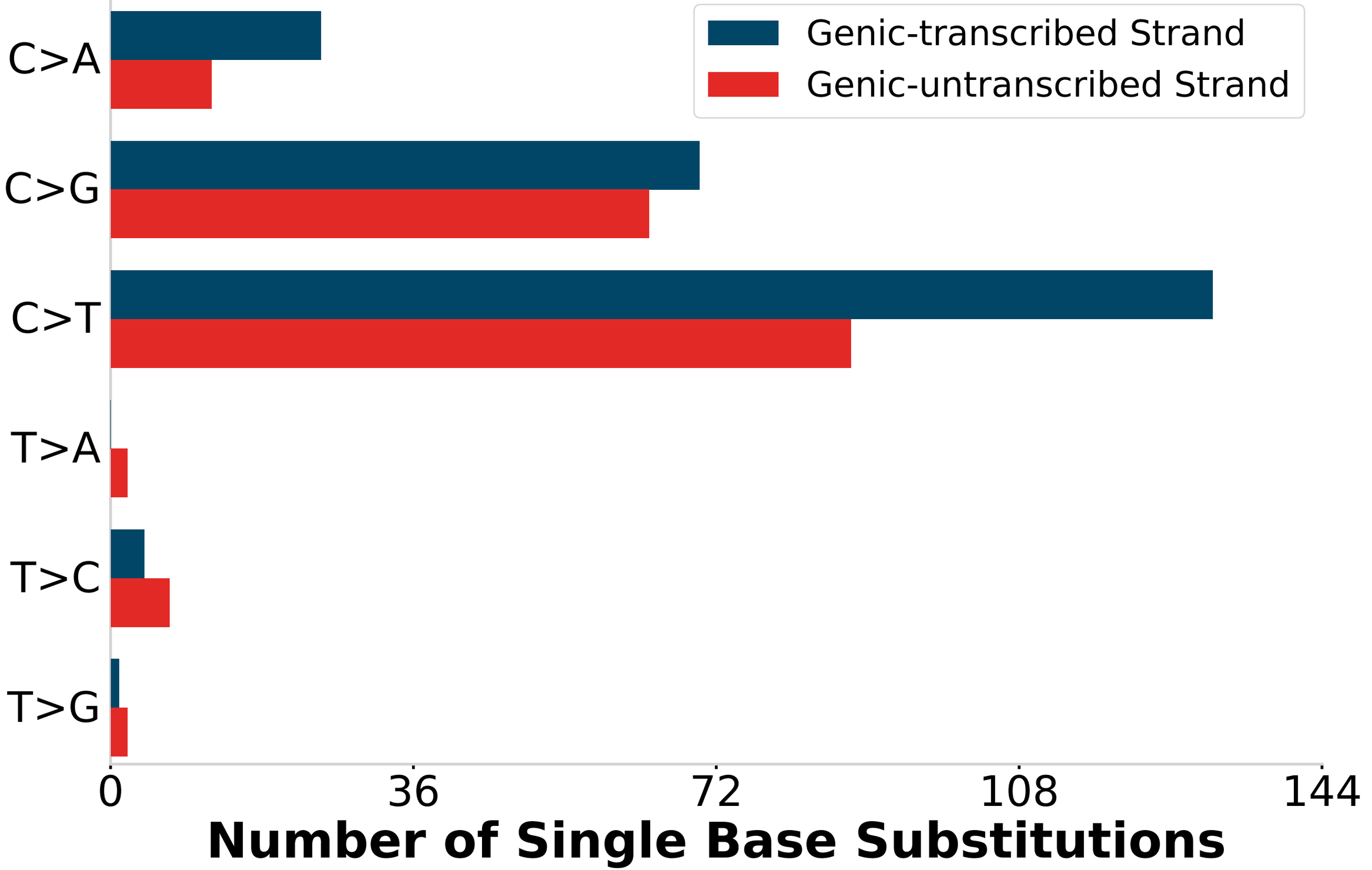
TCGA-HQ-A2OF-01A-11D-A26M-08: 104 tra



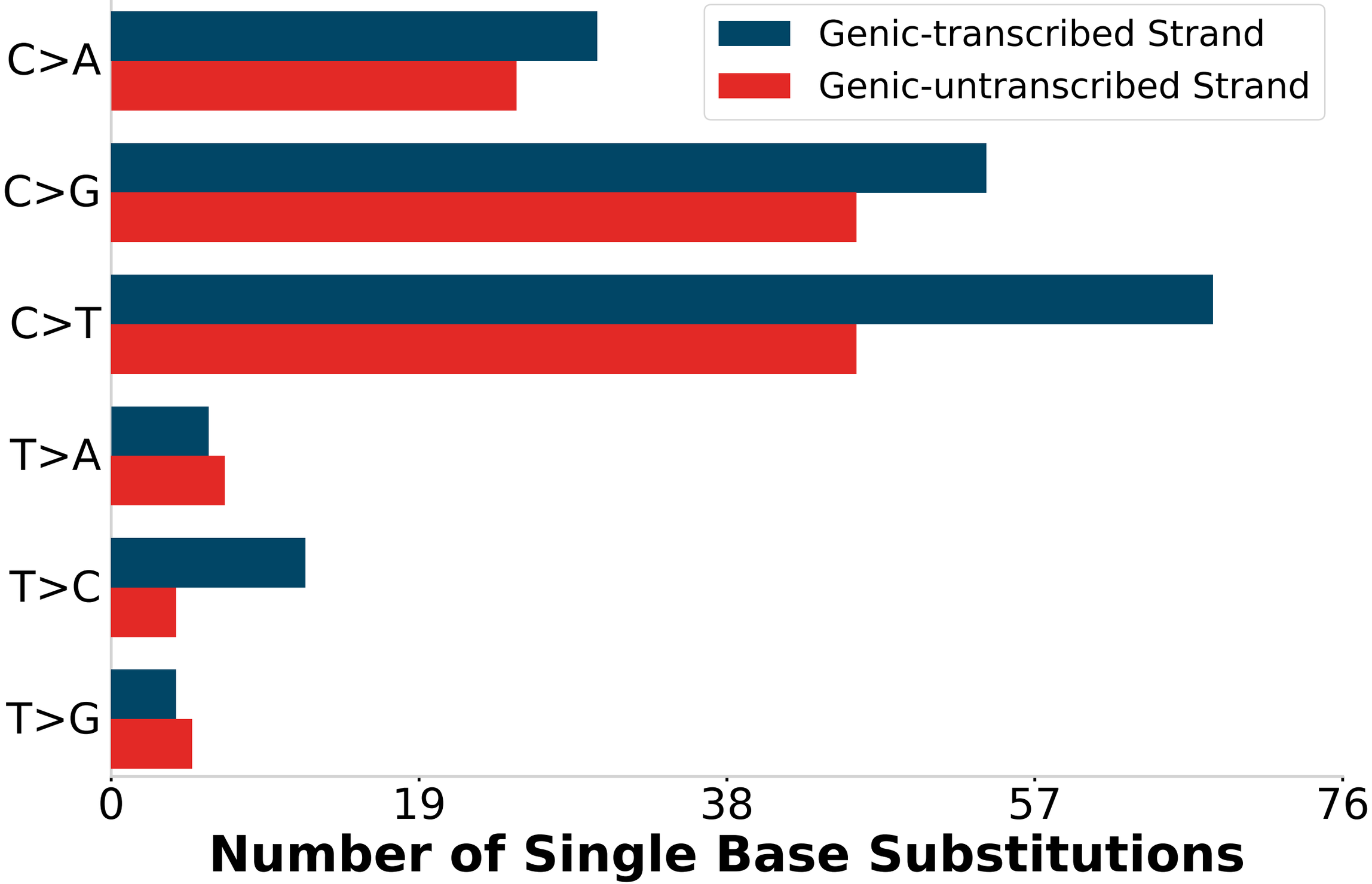
TCGA-HQ-A5ND-01A-11D-A26M-08: 84 tra



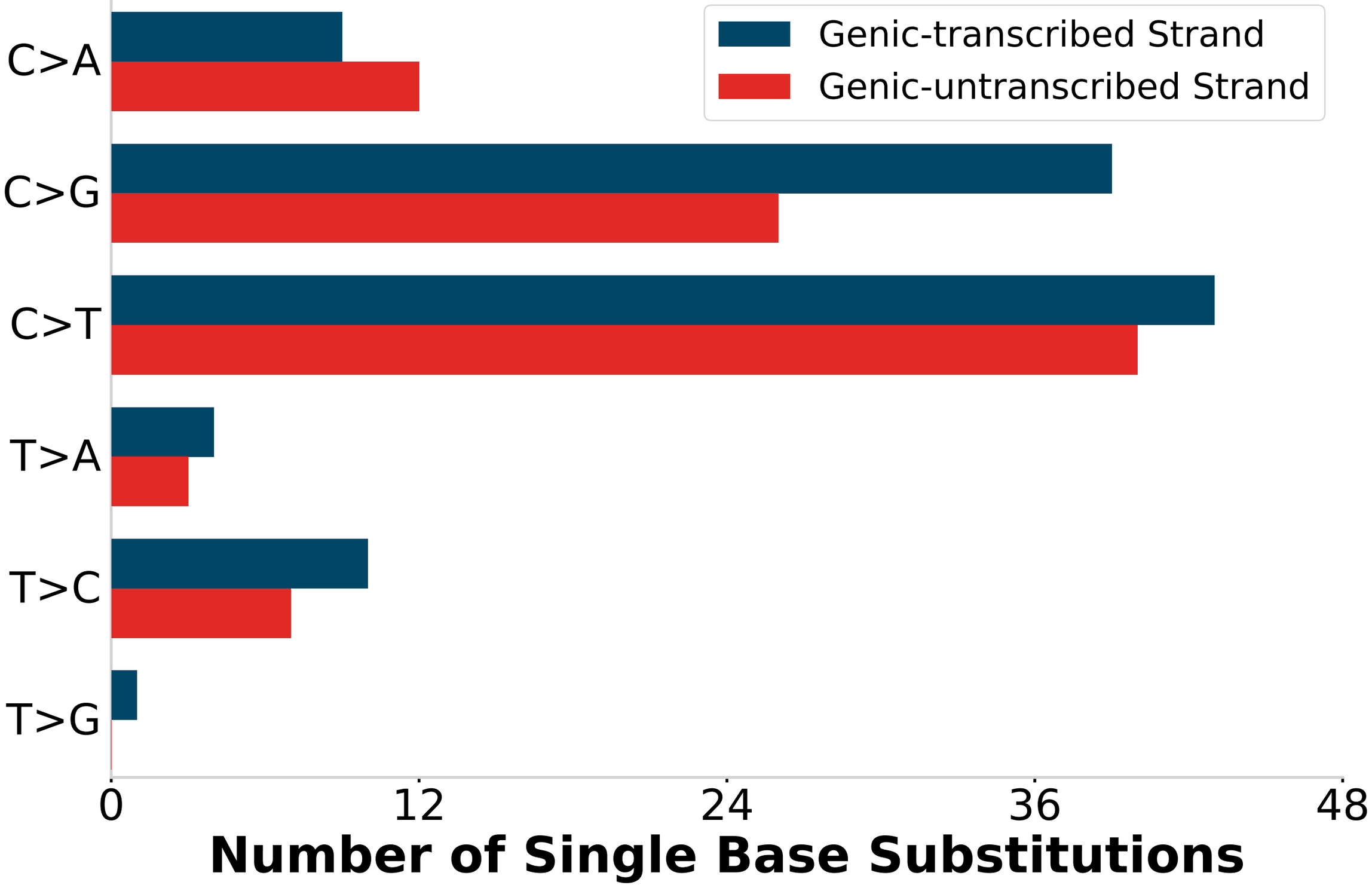
TCGA-HQ-A5NE-01A-12D-A289-08: 406 tra



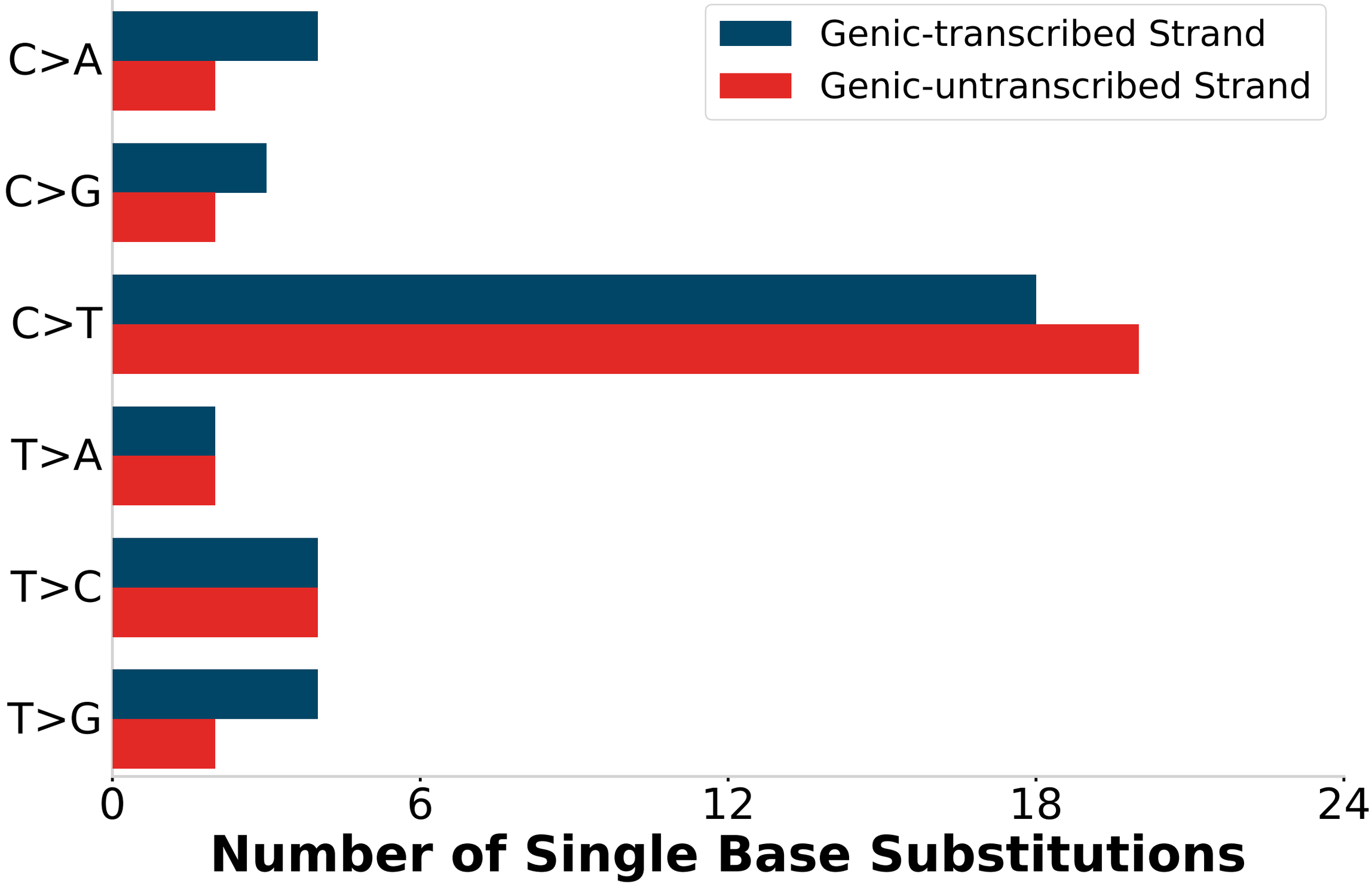
TCGA-K4-A3WS-01A-11D-A22Z-08: 307 tra



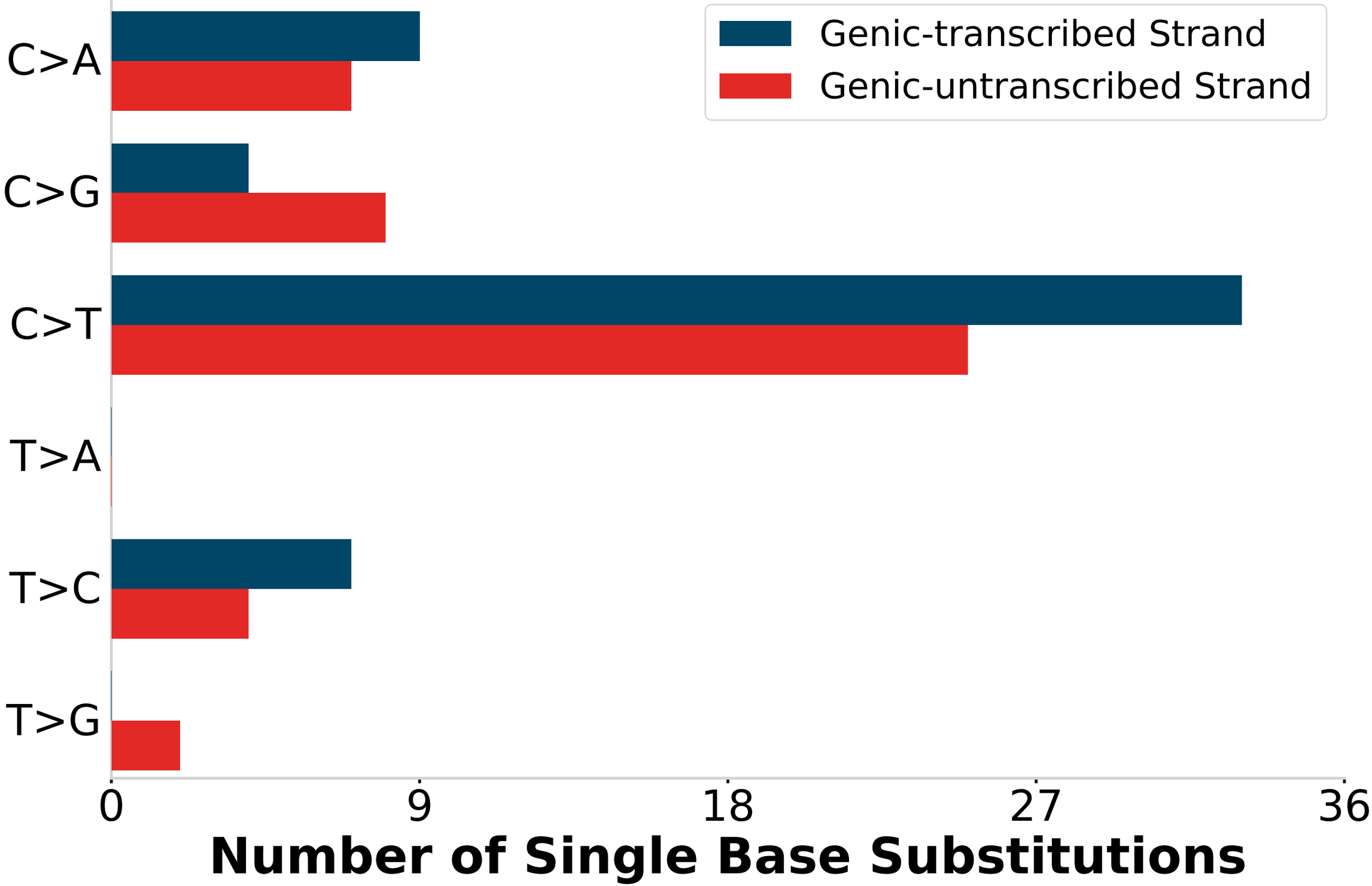
TCGA-K4-A3WU-01B-11D-A23M-08: 194 tra



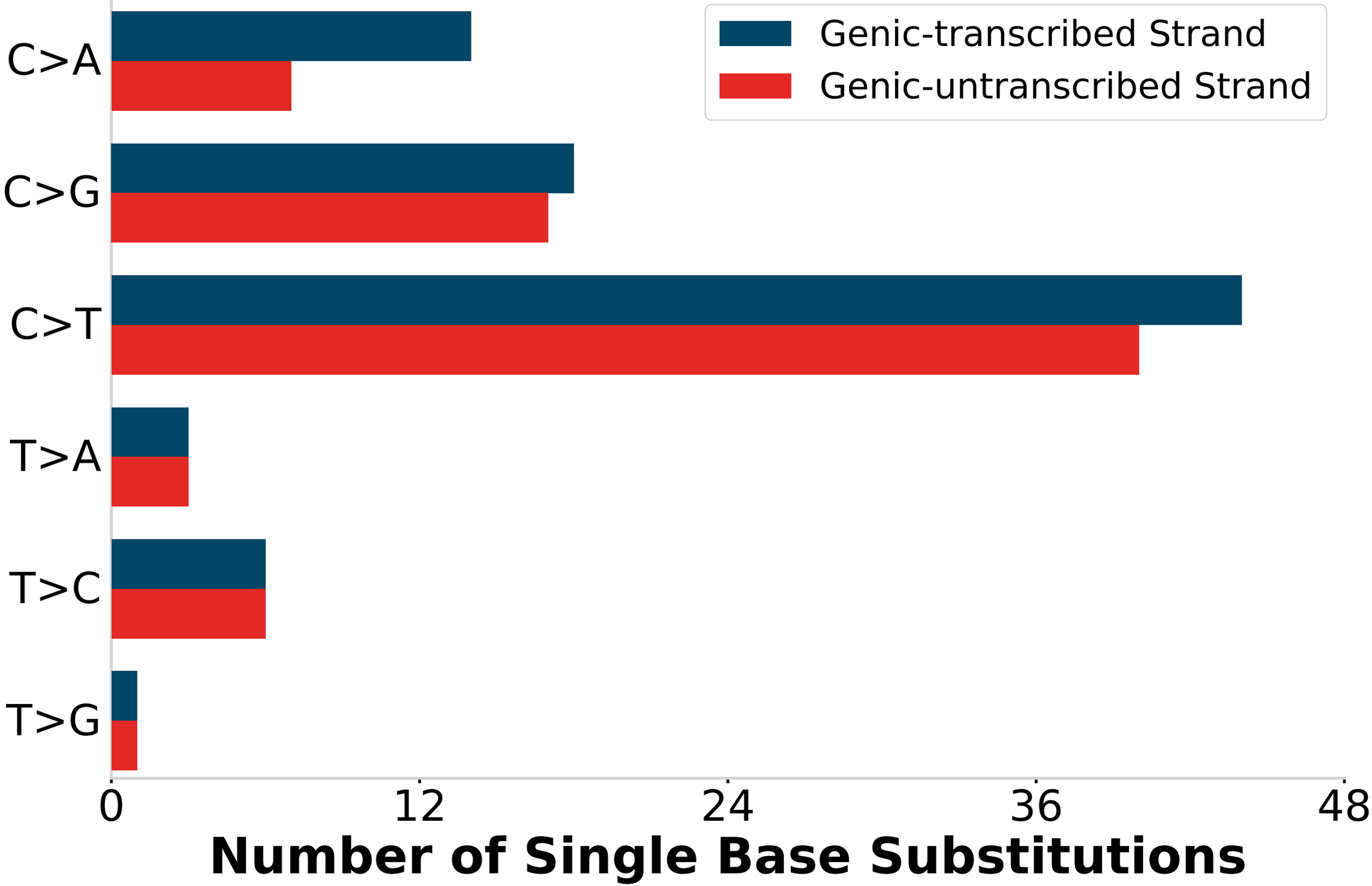
TCGA-K4-A3WV-01A-11D-A22Z-08: 67 tran



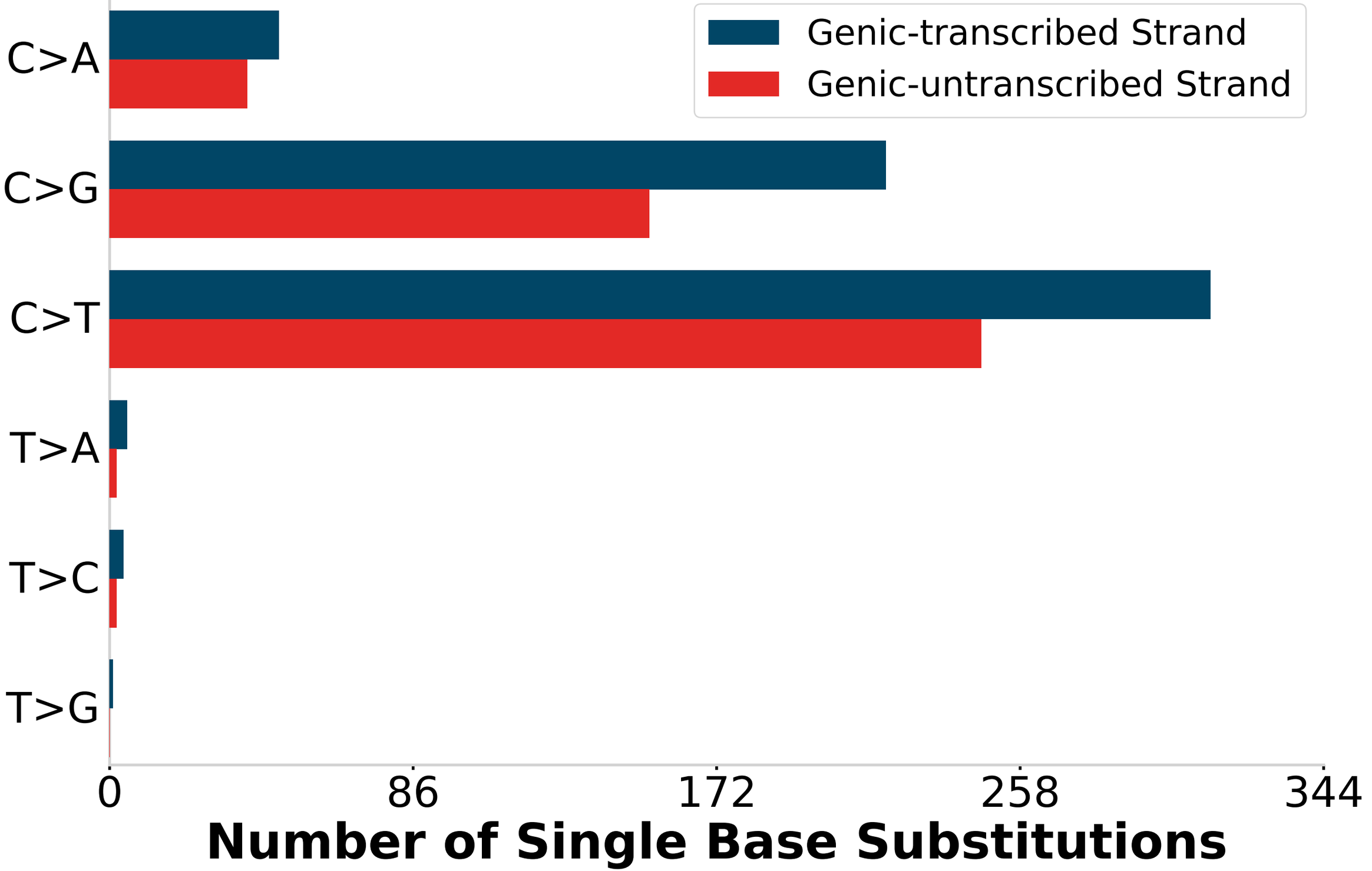
TCGA-K4-A4AB-01B-12D-A289-08: 99 trans



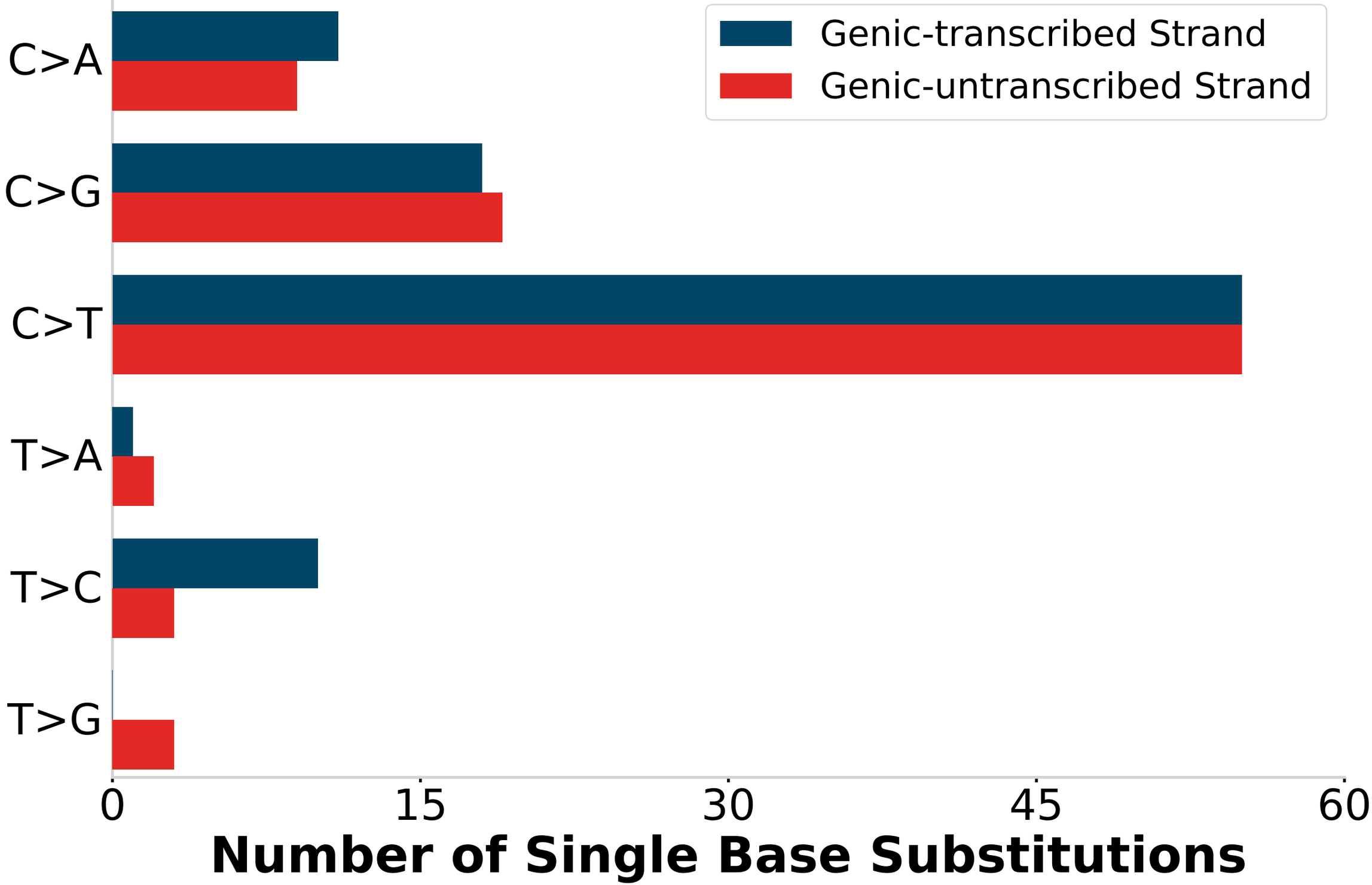
TCGA-K4-A4AC-01A-21D-A26M-08: 160 tra



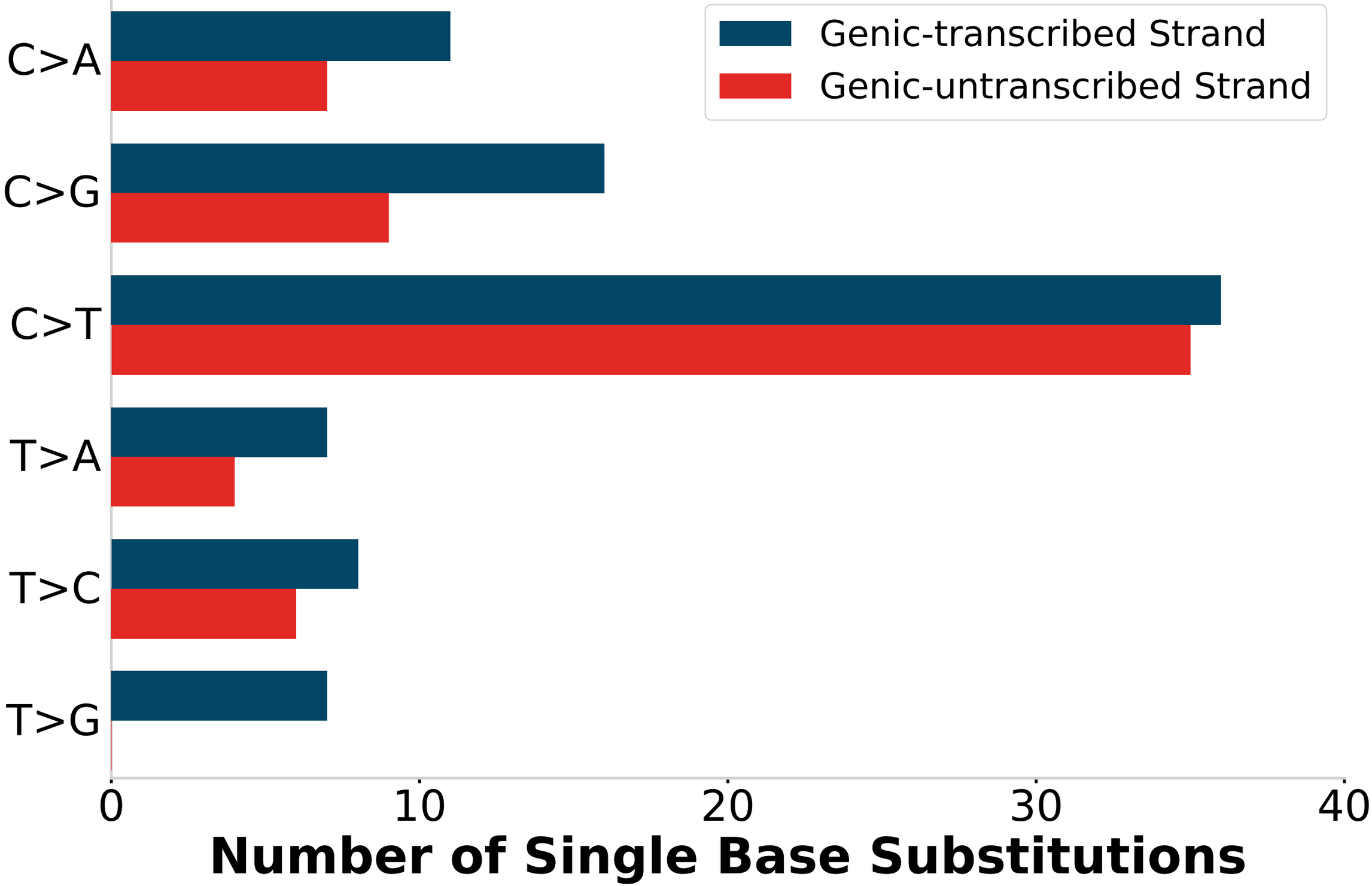
TCGA-K4-A54R-01A-11D-A26M-08: 1,033 t



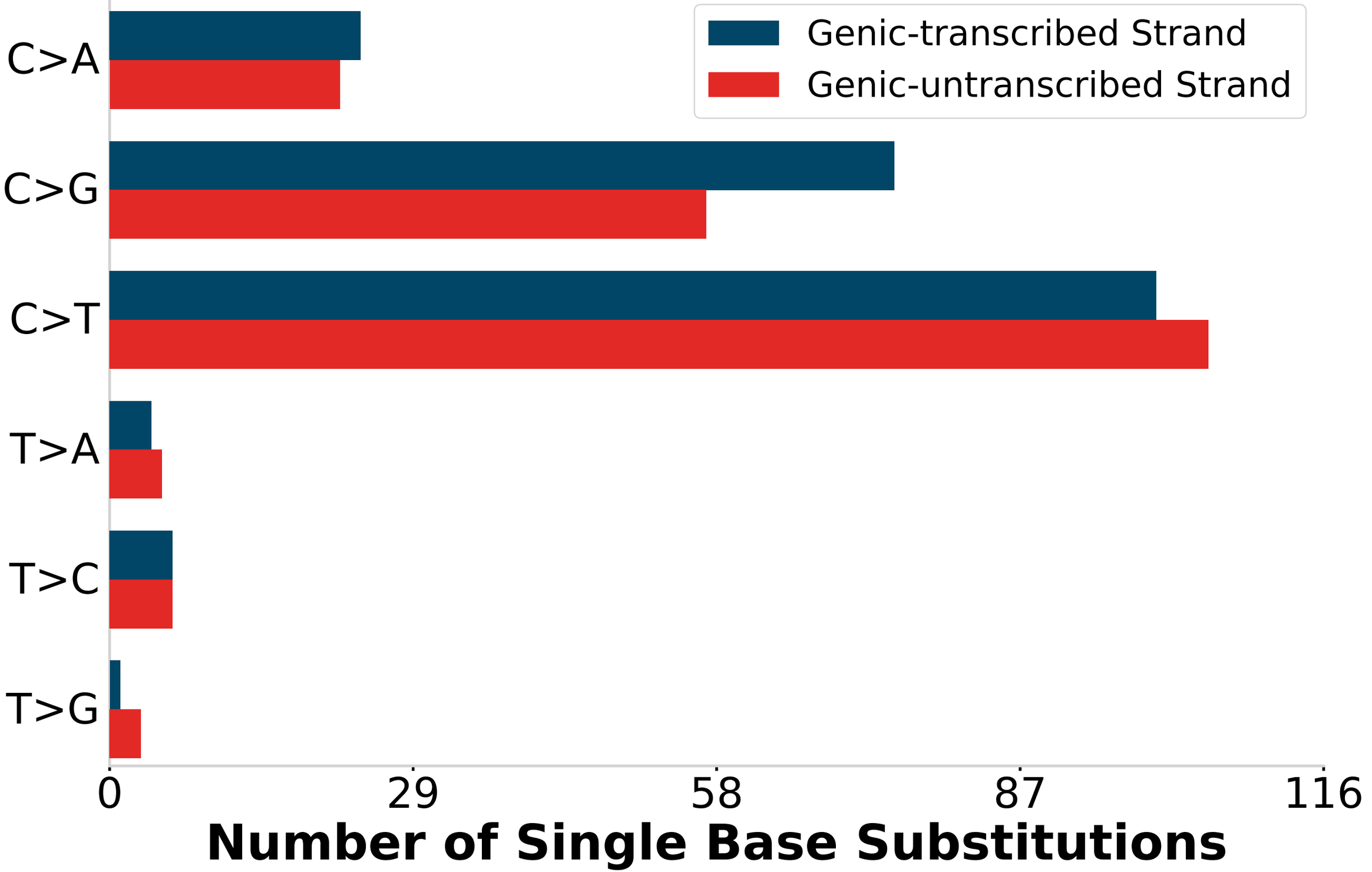
TCGA-K4-A5RH-01A-11D-A30E-08: 186 tra



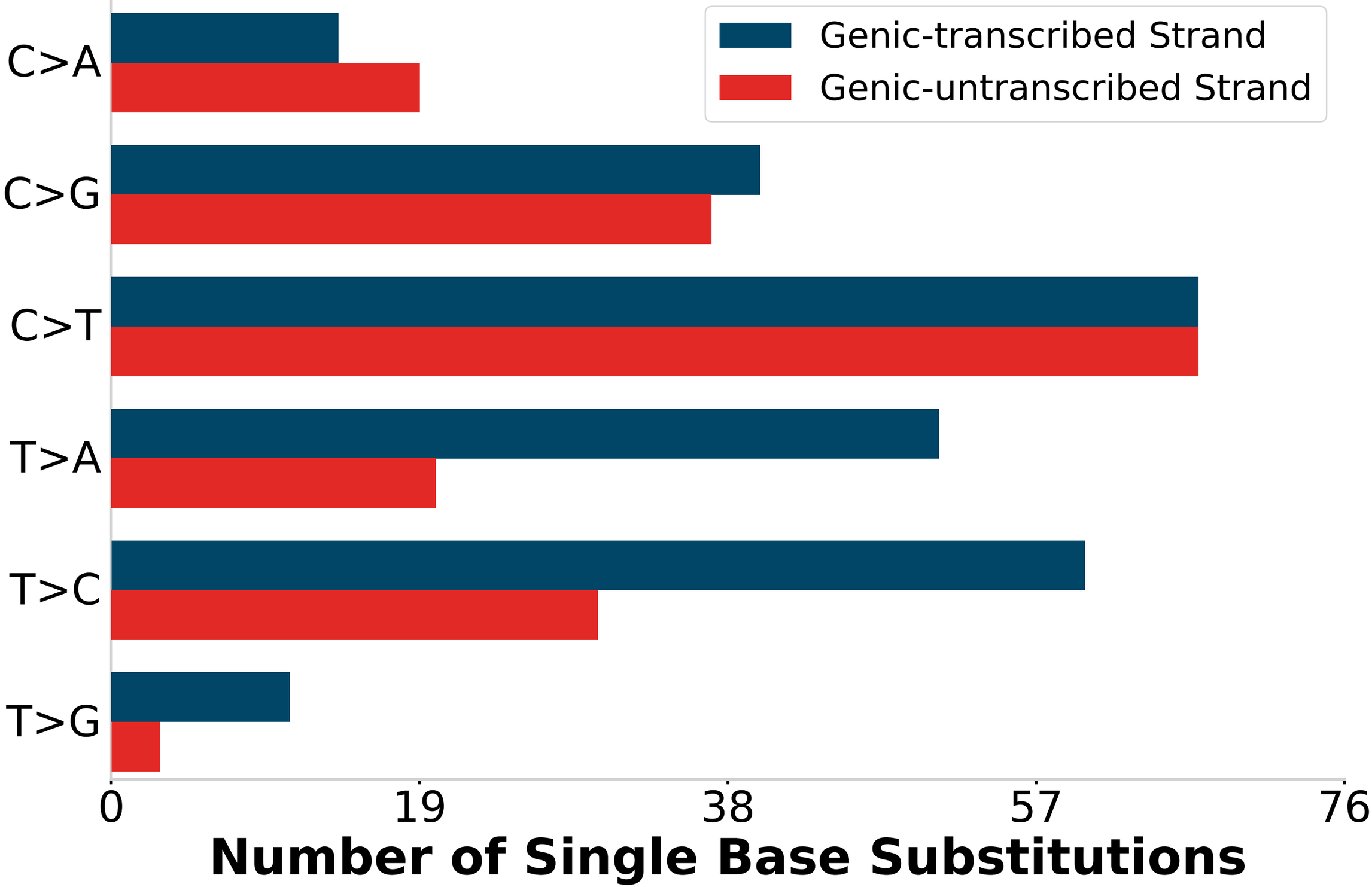
TCGA-K4-A5RI-01A-11D-A289-08: 146 tran



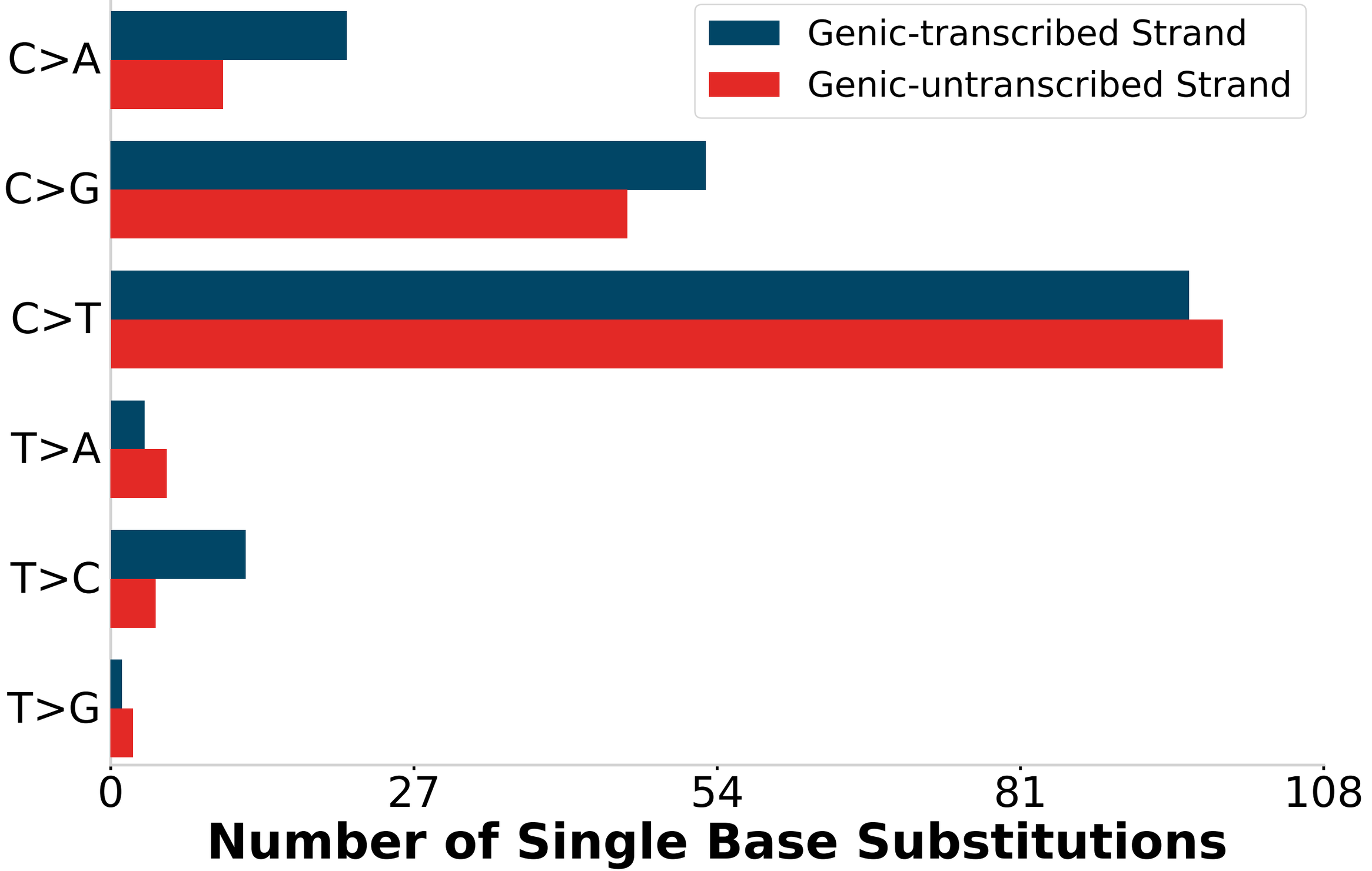
TCGA-K4-A5RJ-01A-11D-A289-08: 408 tran



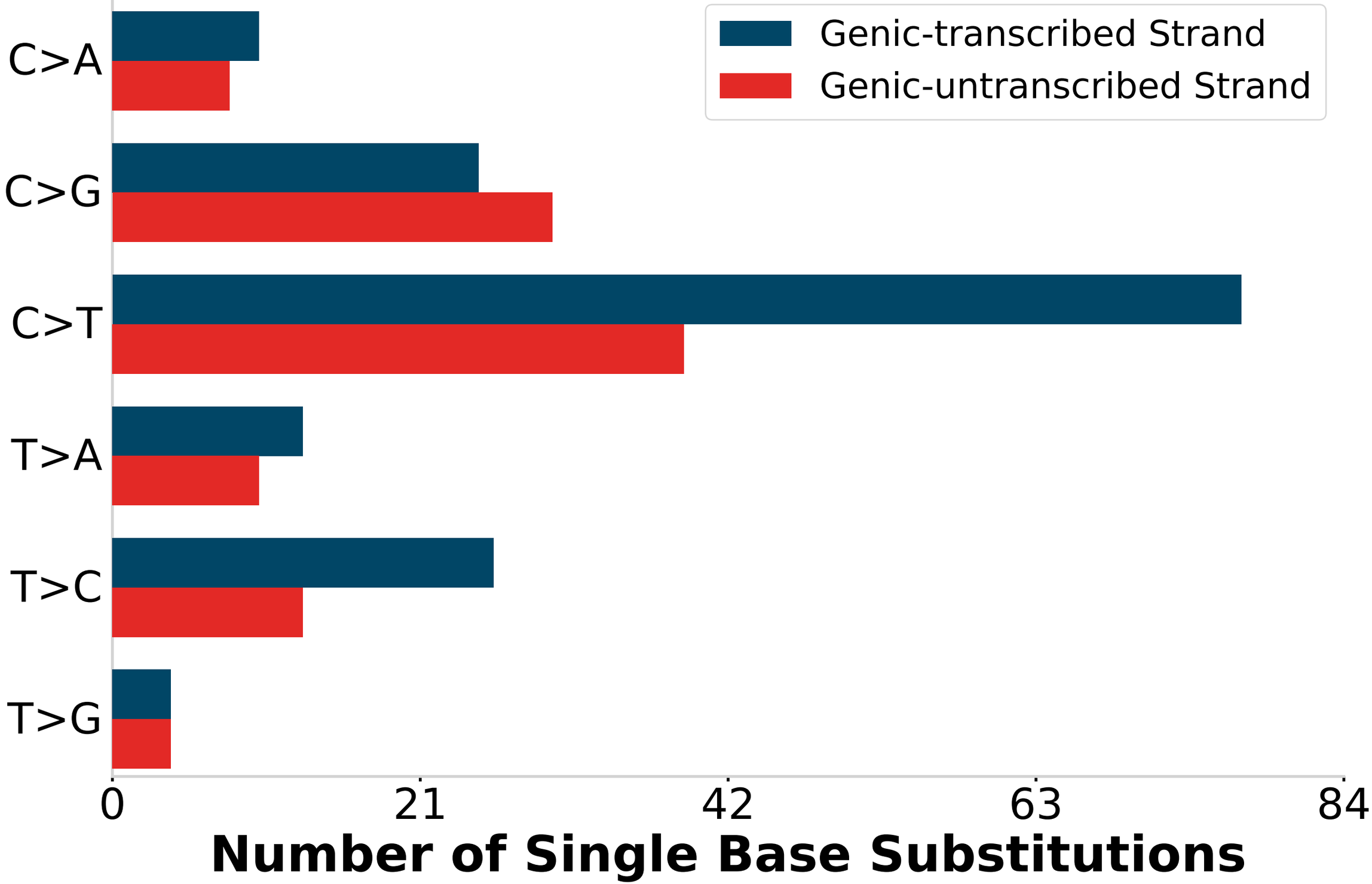
TCGA-K4-A6FZ-01A-11D-A31L-08: 419 tran



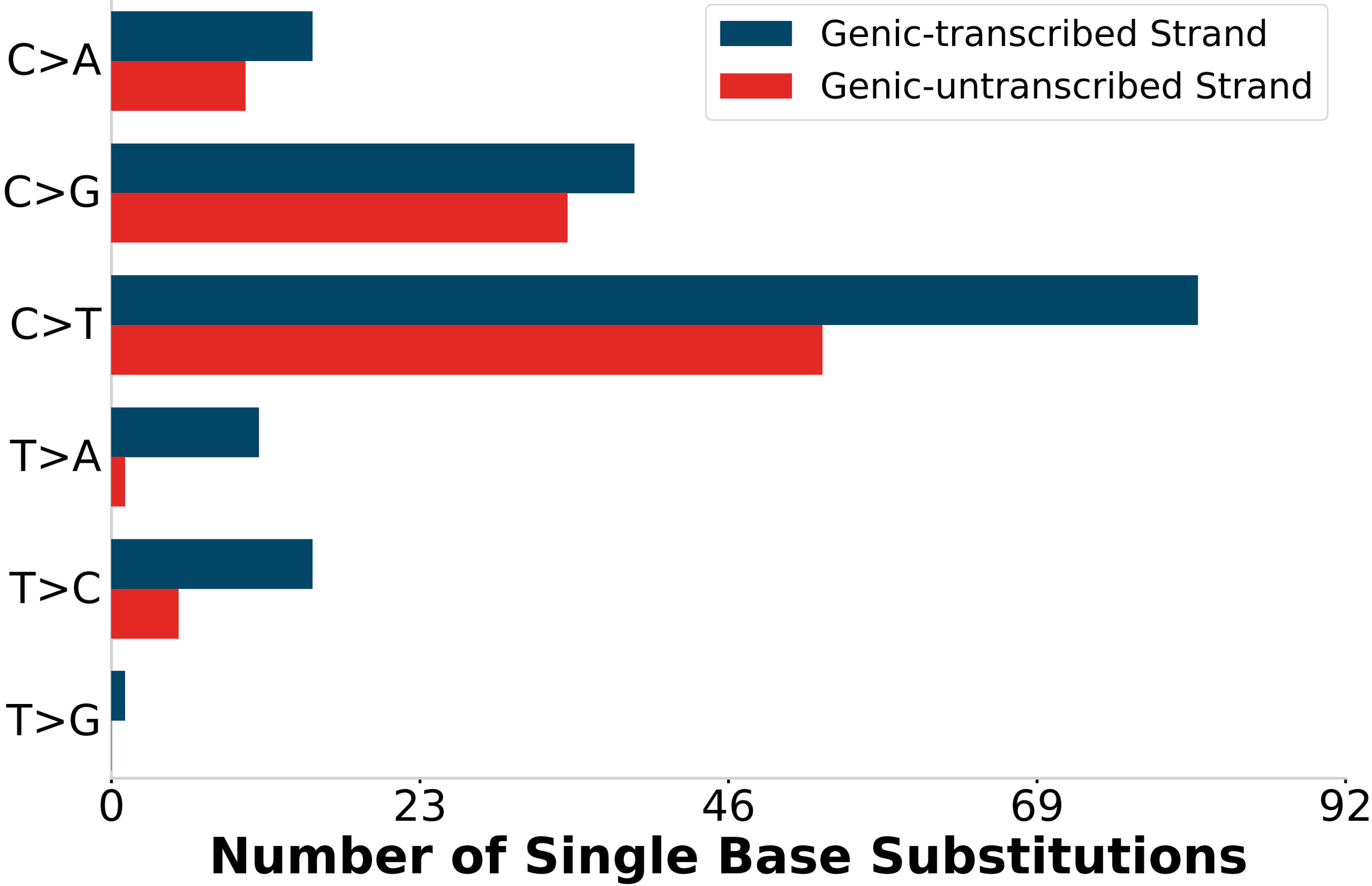
TCGA-K4-A6MB-01A-11D-A31L-08: 352 tra



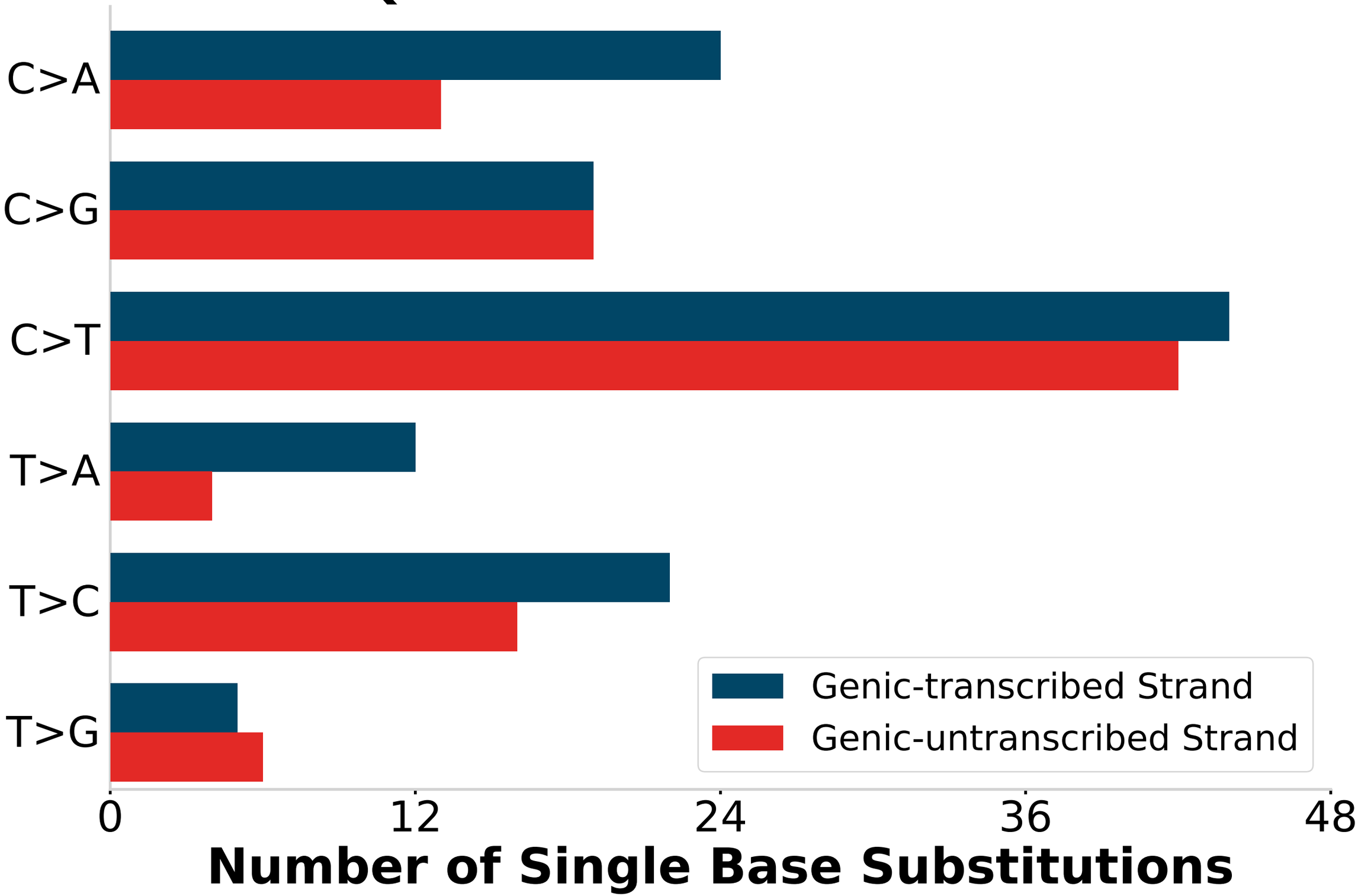
TCGA-K4-A83P-01A-11D-A34U-08: 259 tra



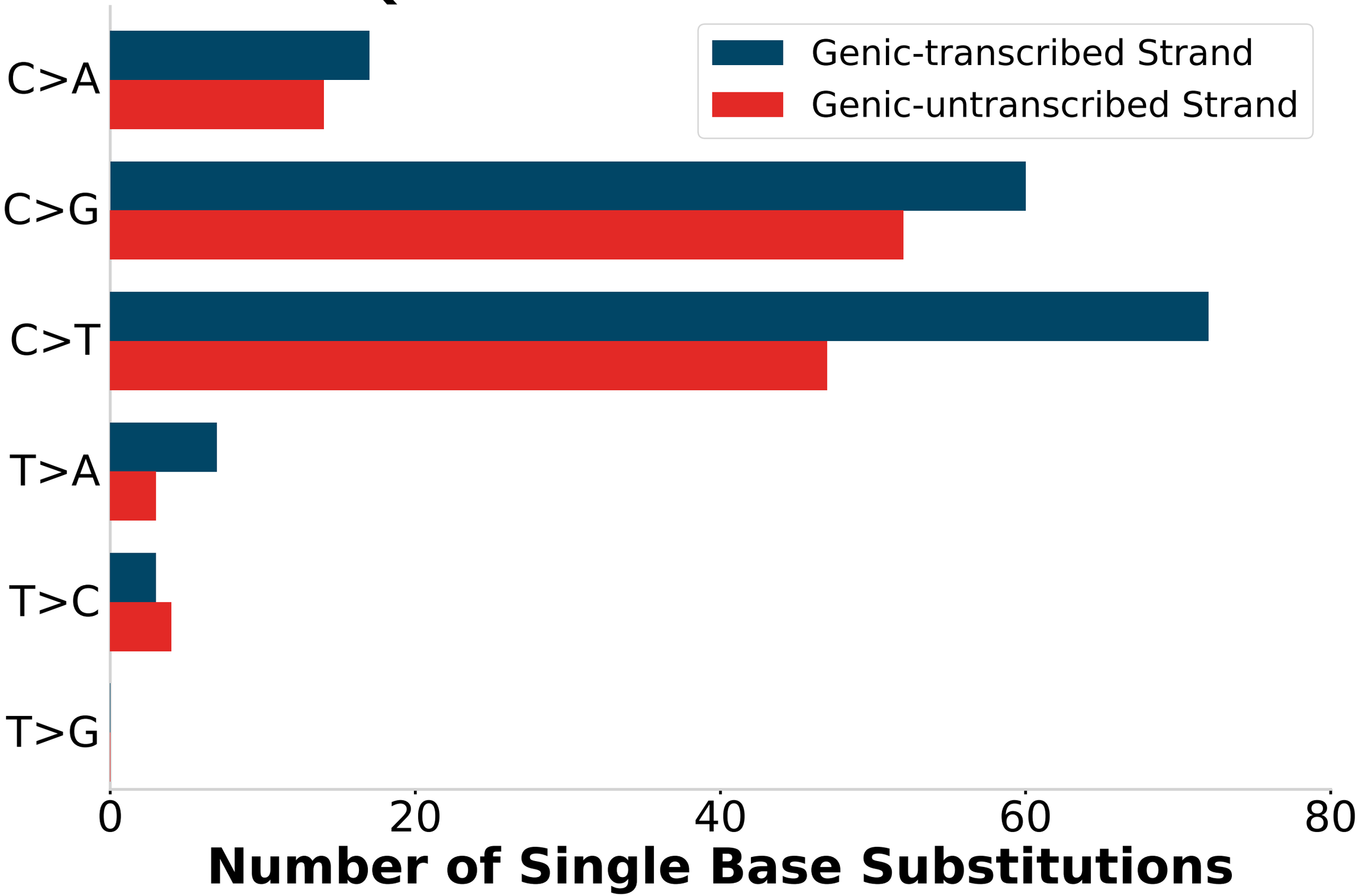
TCGA-K4-AAQO-01A-11D-A38G-08: 265 tra



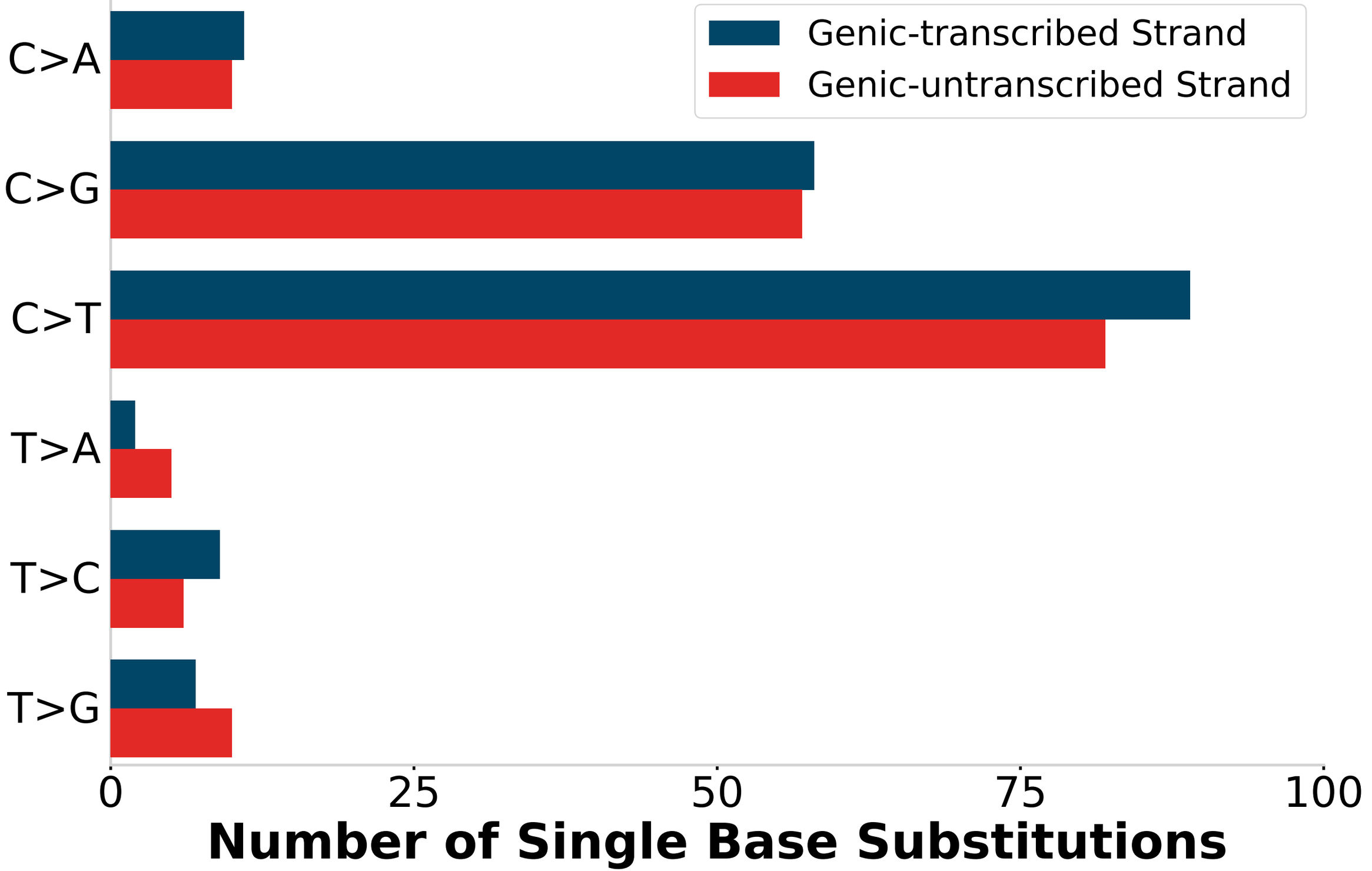
TCGA-KQ-A41N-01A-11D-A339-08: 226 tra



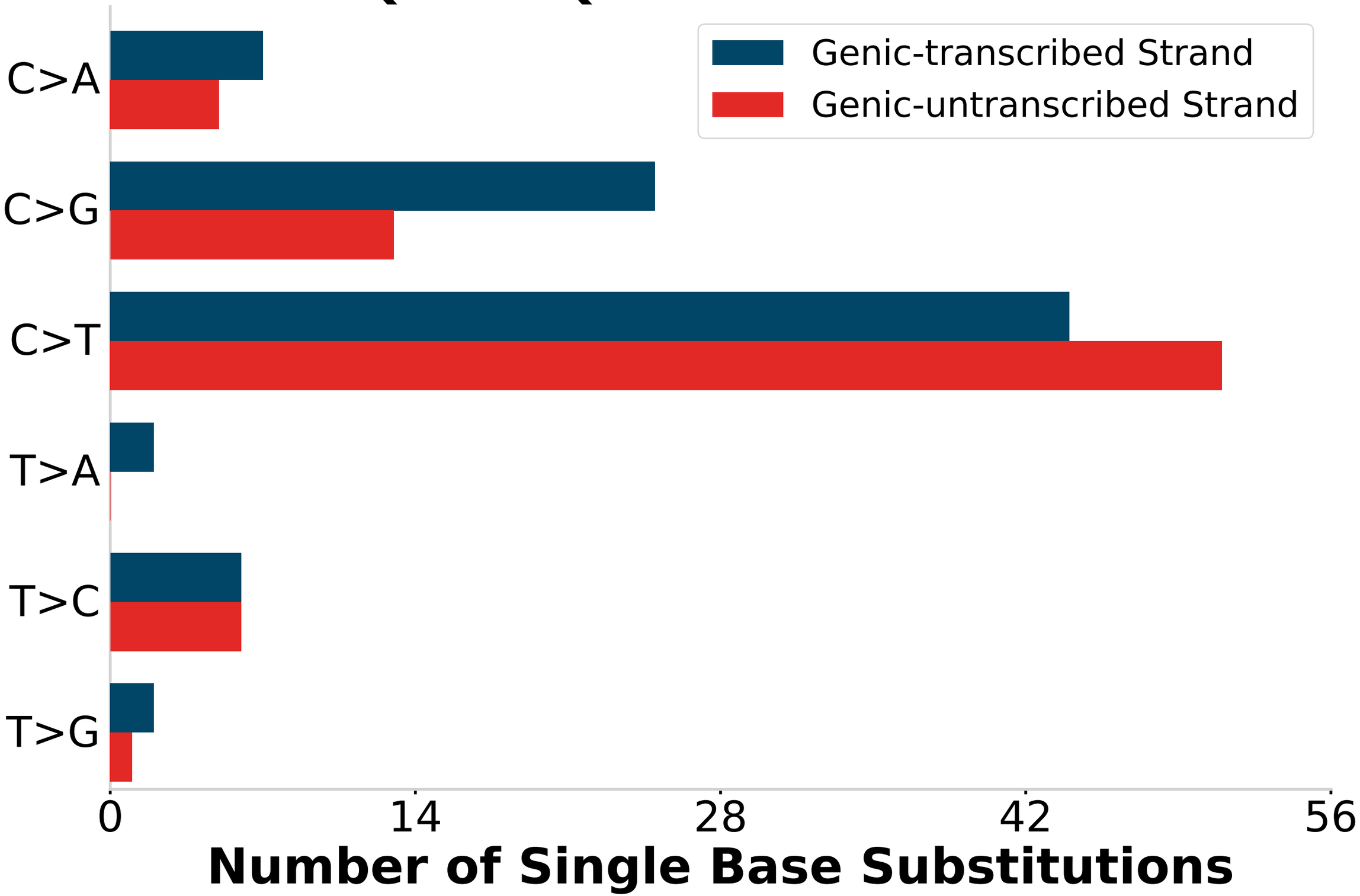
TCGA-KQ-A41O-01A-12D-A34U-08: 279 tra



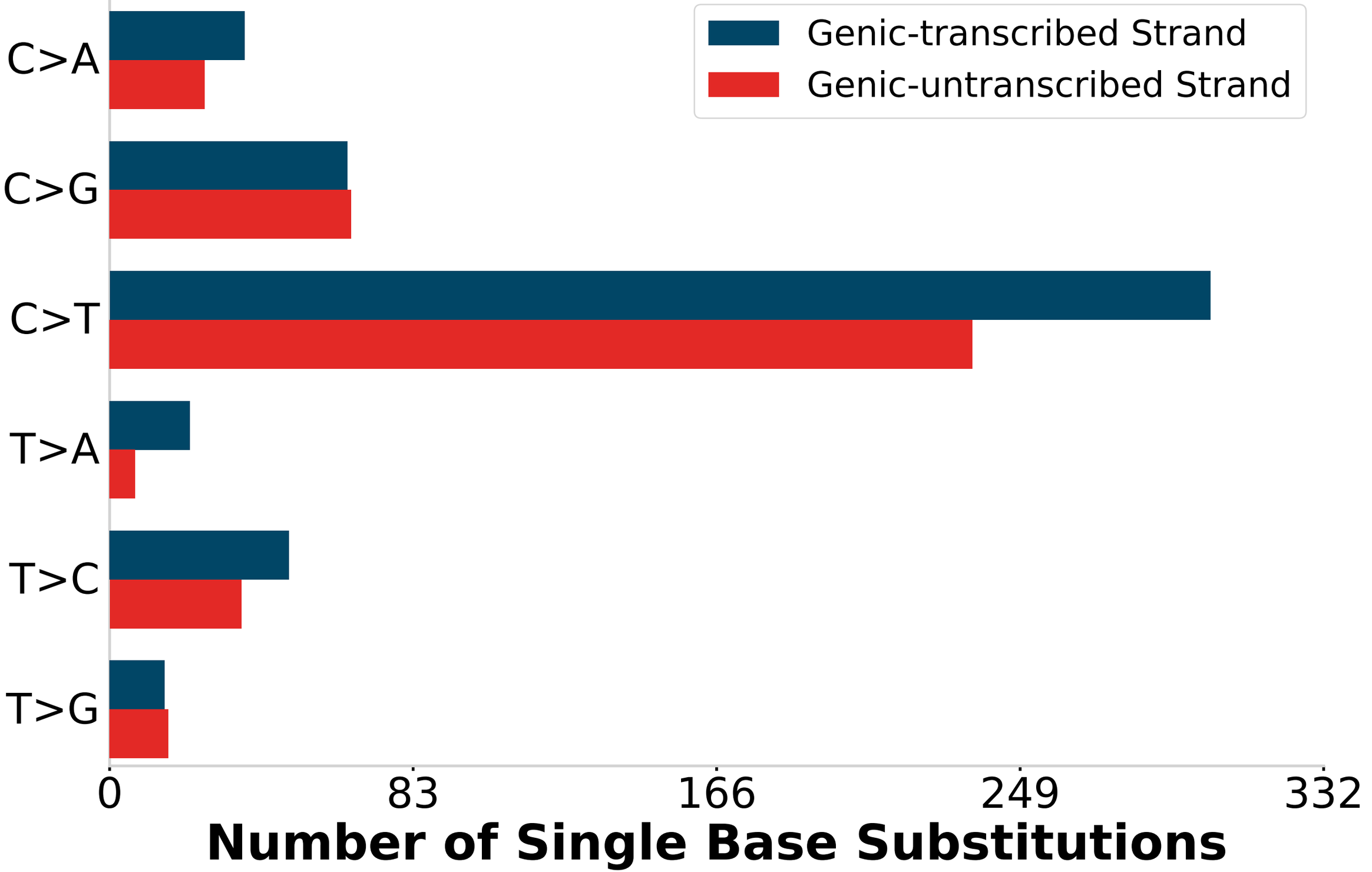
TCGA-KQ-A41P-01A-12D-A339-08: 346 tra



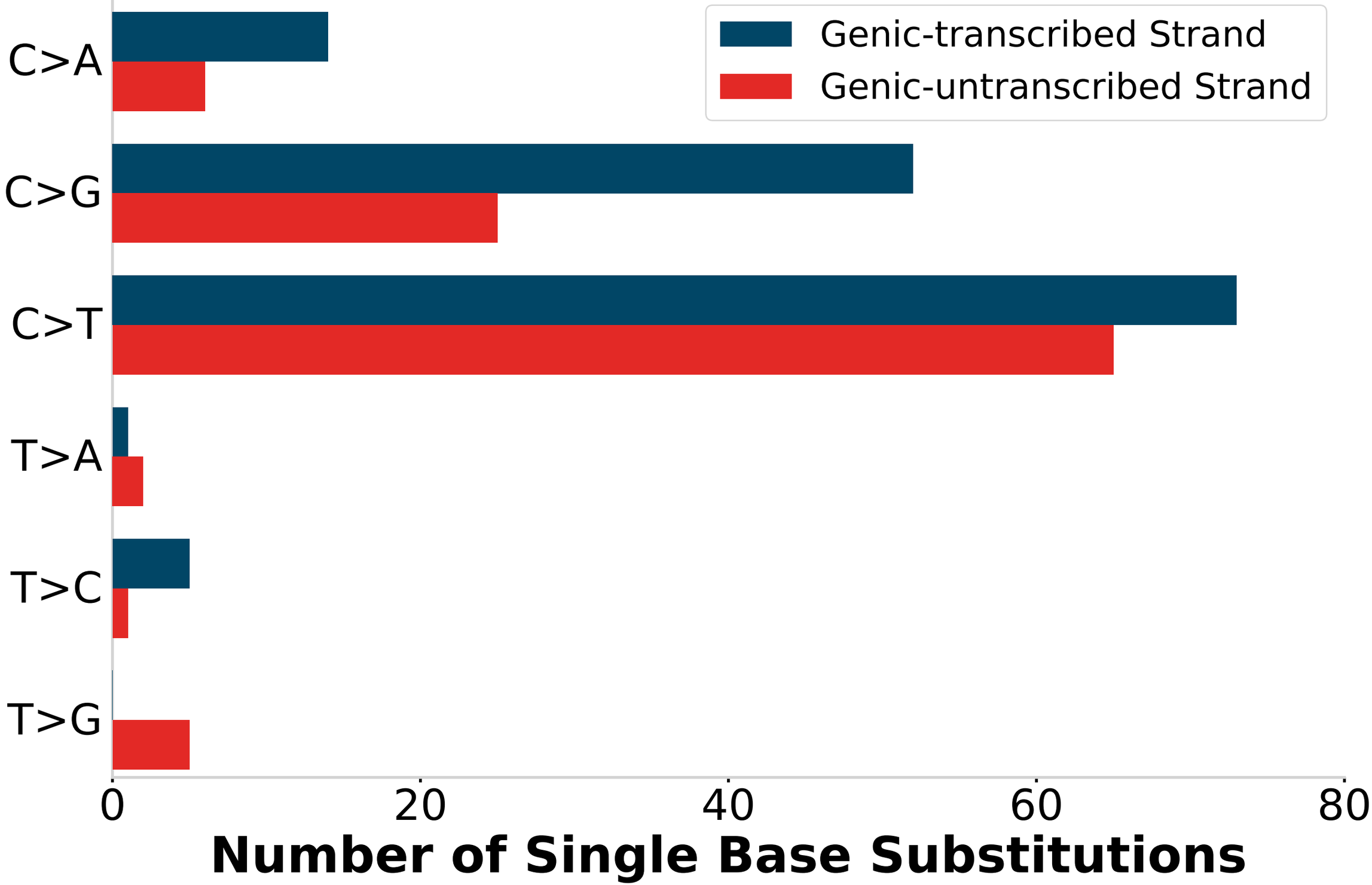
TCGA-KQ-A41Q-01A-11D-A339-08: 162 tra



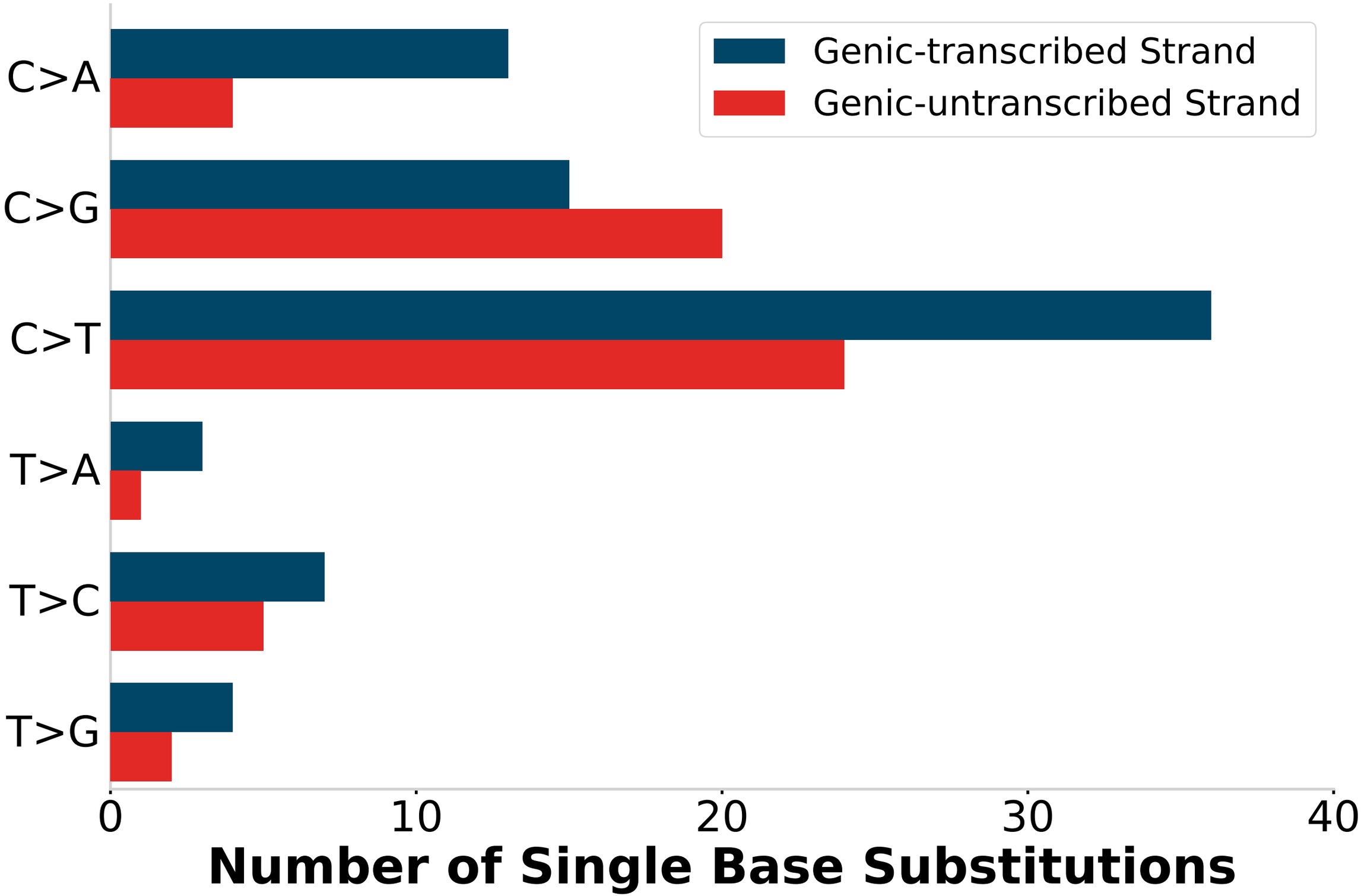
TCGA-KQ-A41R-01A-21D-A34U-08: 876 tra



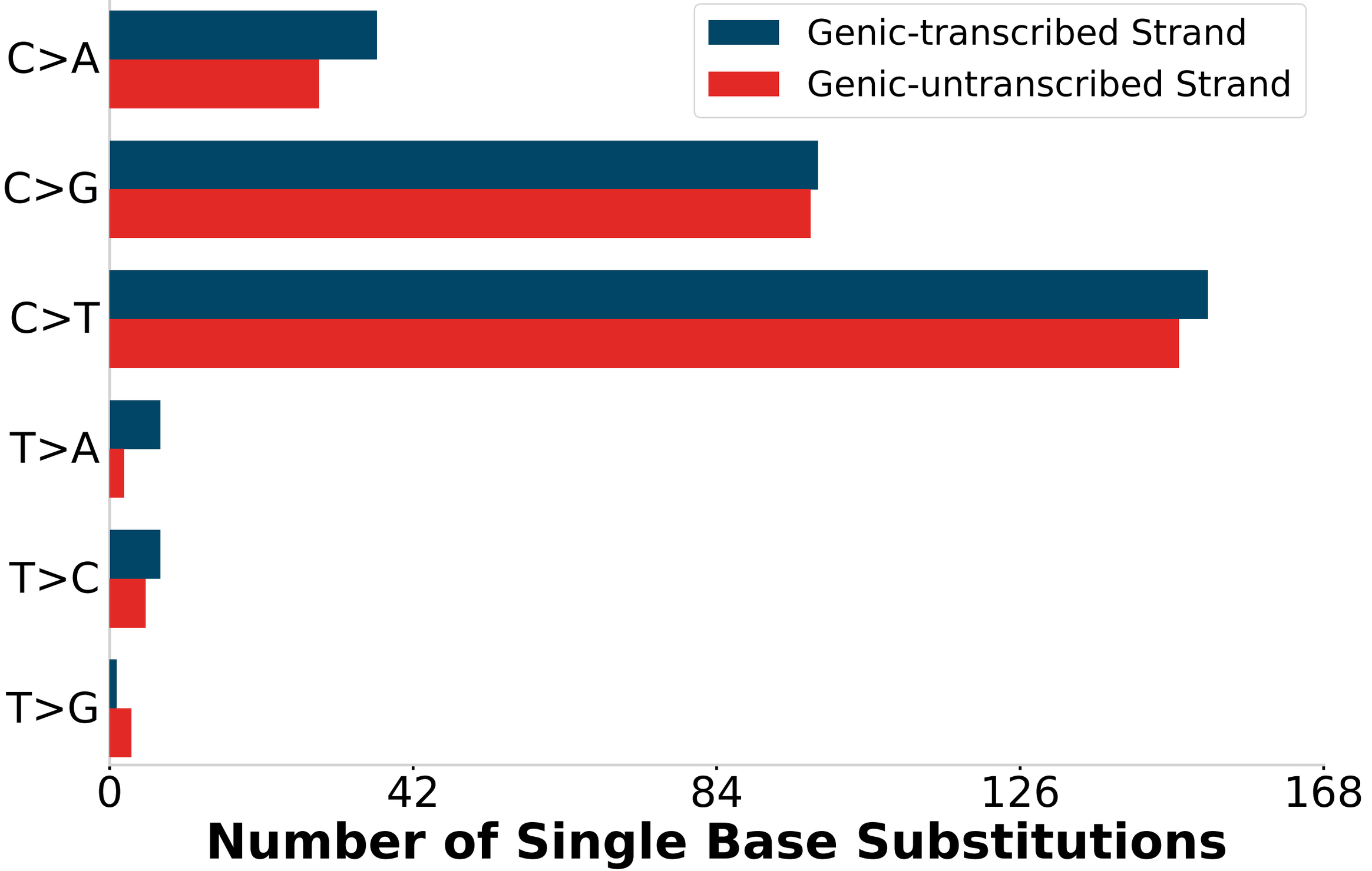
TCGA-KQ-A41S-01A-12D-A339-08: 249 tra



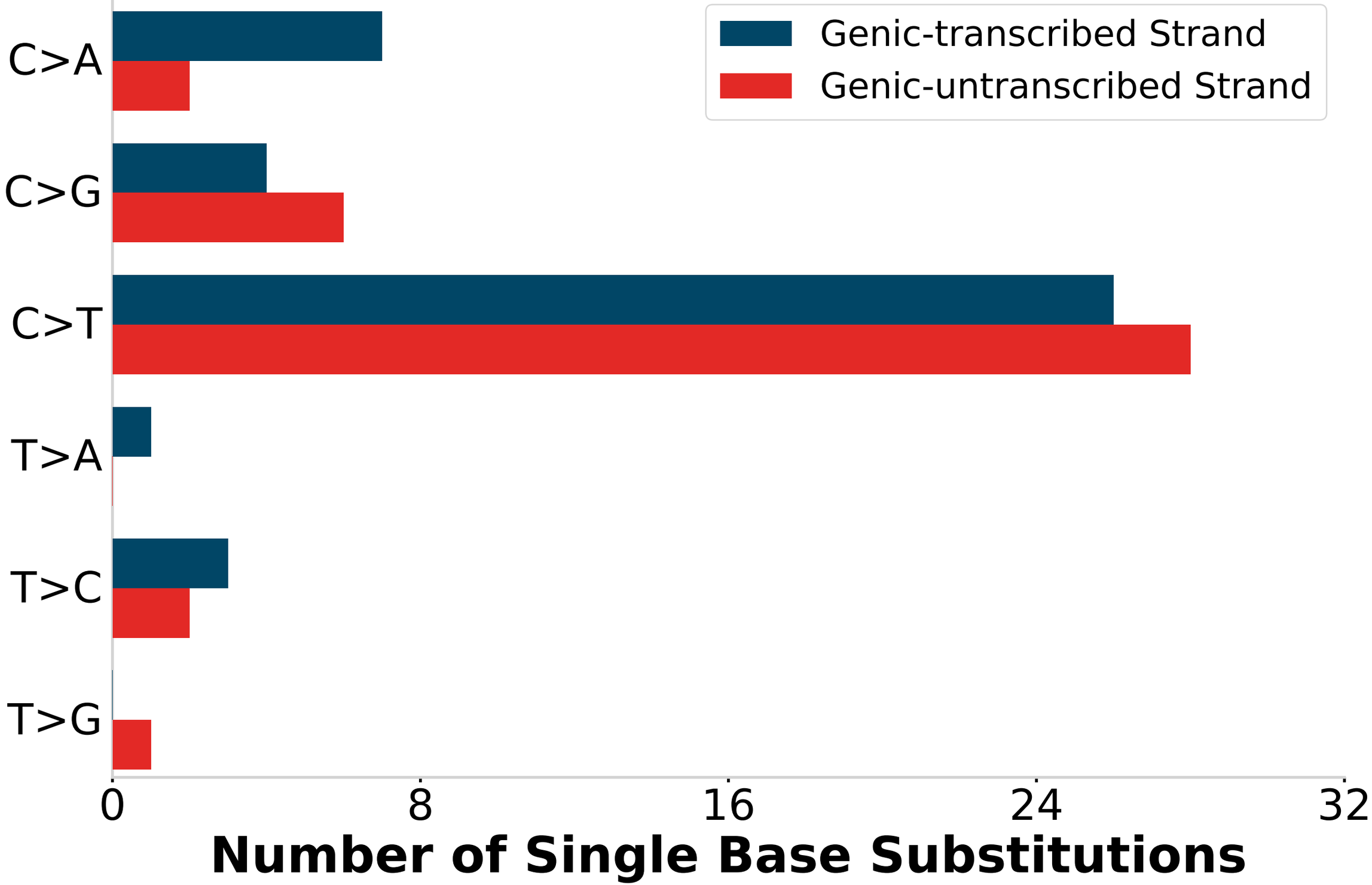
TCGA-LC-A66R-01A-41D-A30E-08: 134 tran



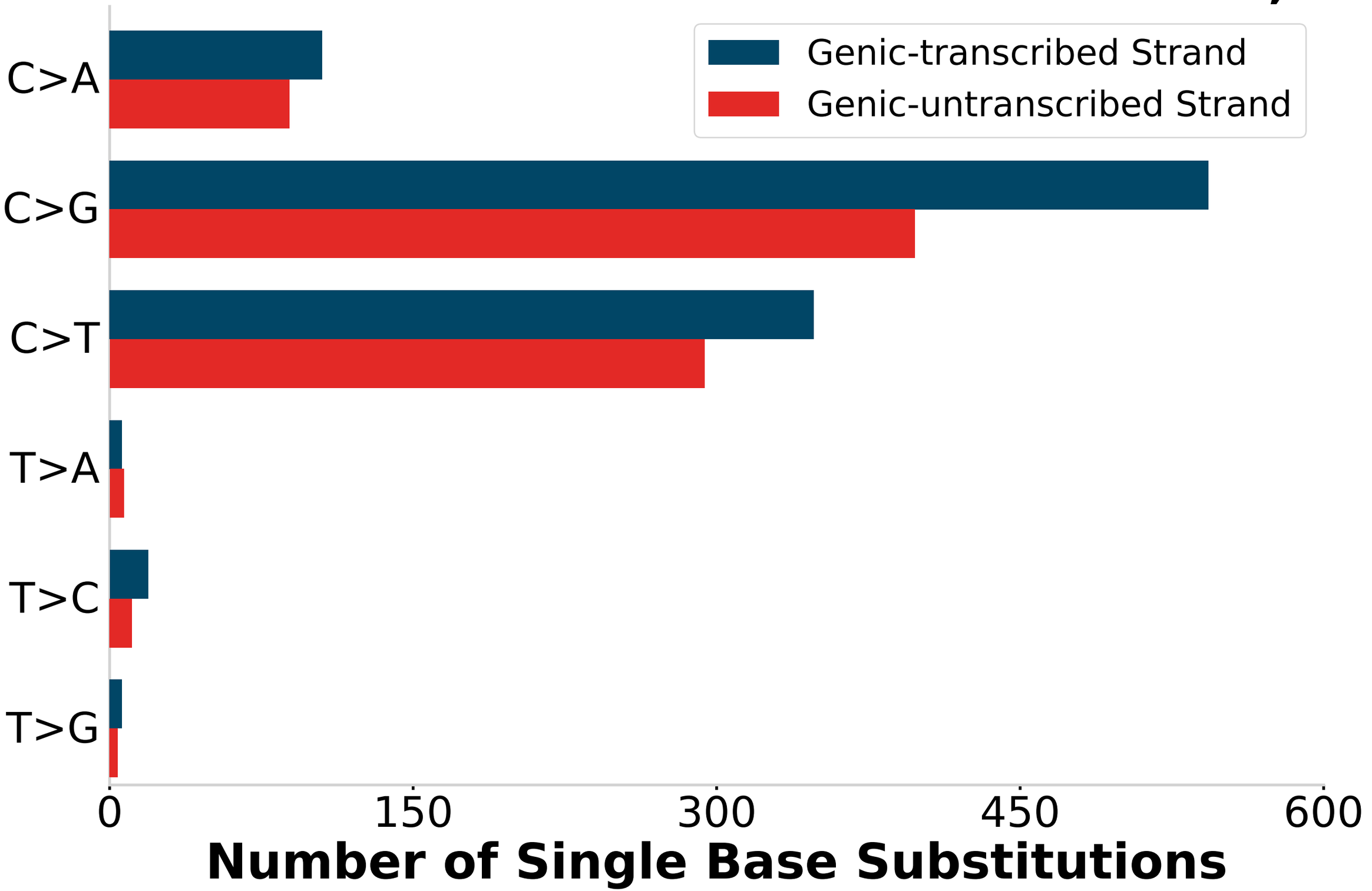
TCGA-LT-A5Z6-01A-11D-A289-08: 586 tran



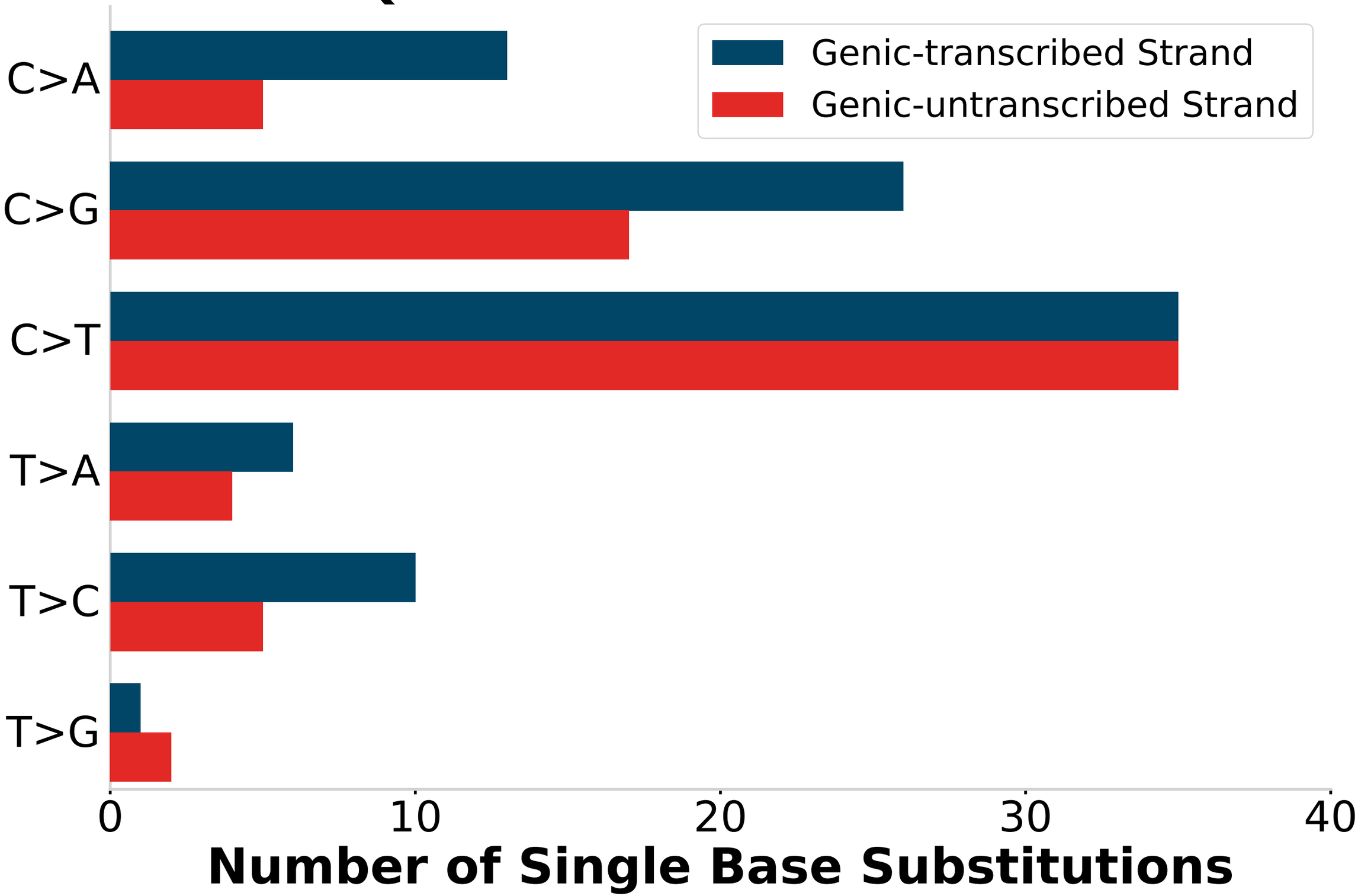
TCGA-LT-A8JT-01A-11D-A364-08: 80 transc



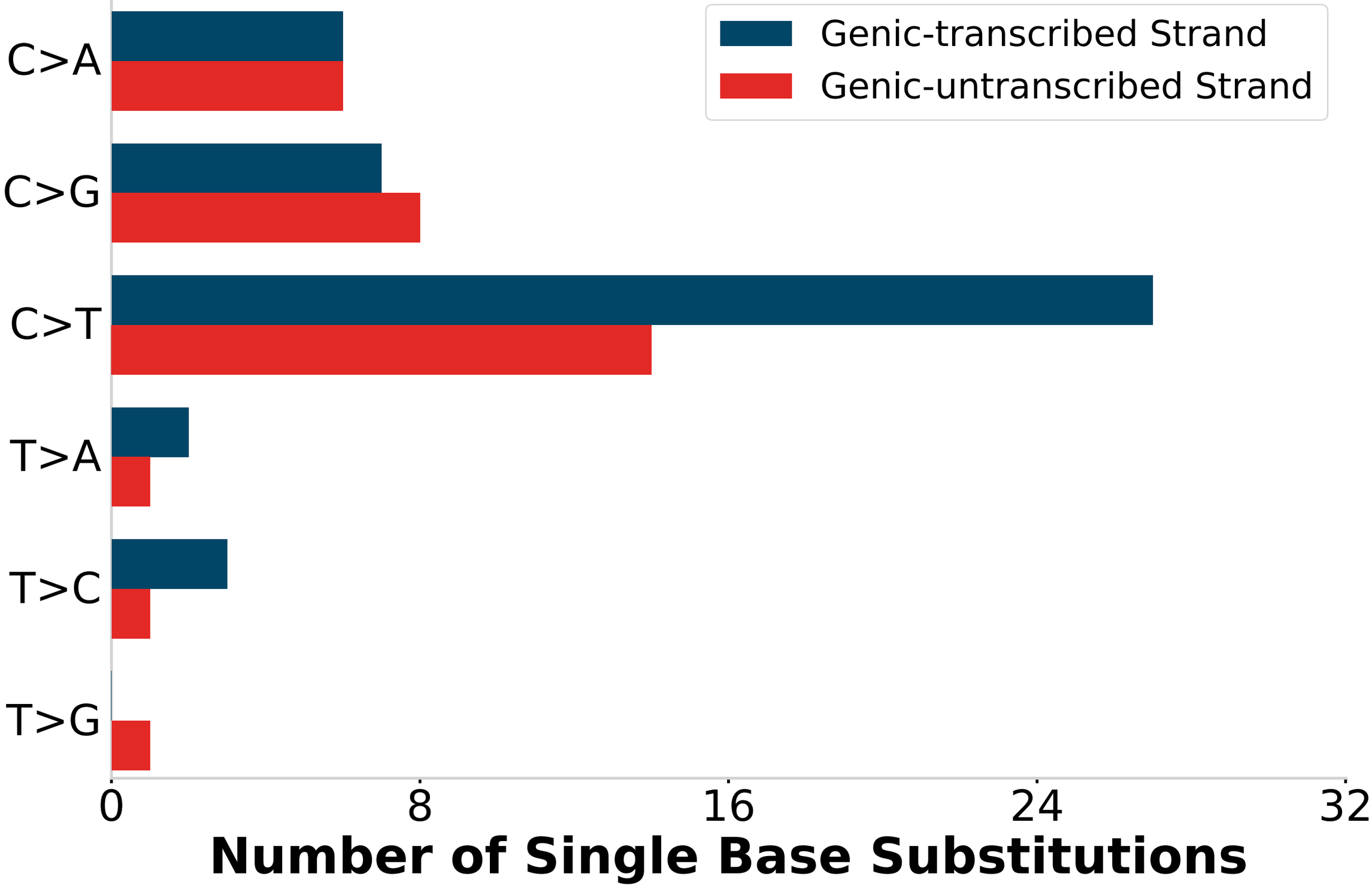
TCGA-MV-A51V-01A-11D-A26M-08: 1,830 t



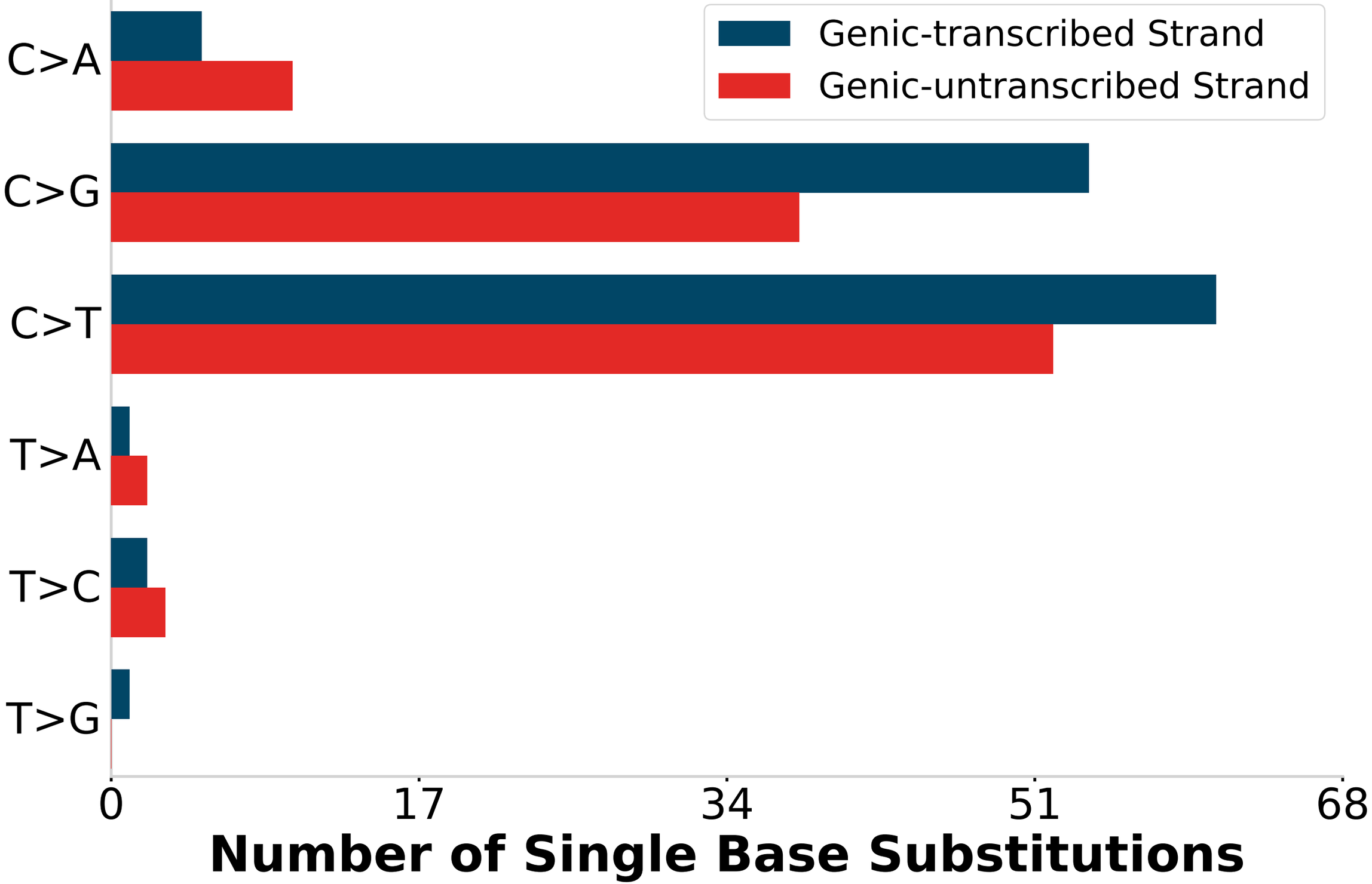
TCGA-PQ-A6FI-01A-11D-A31L-08: 159 tran



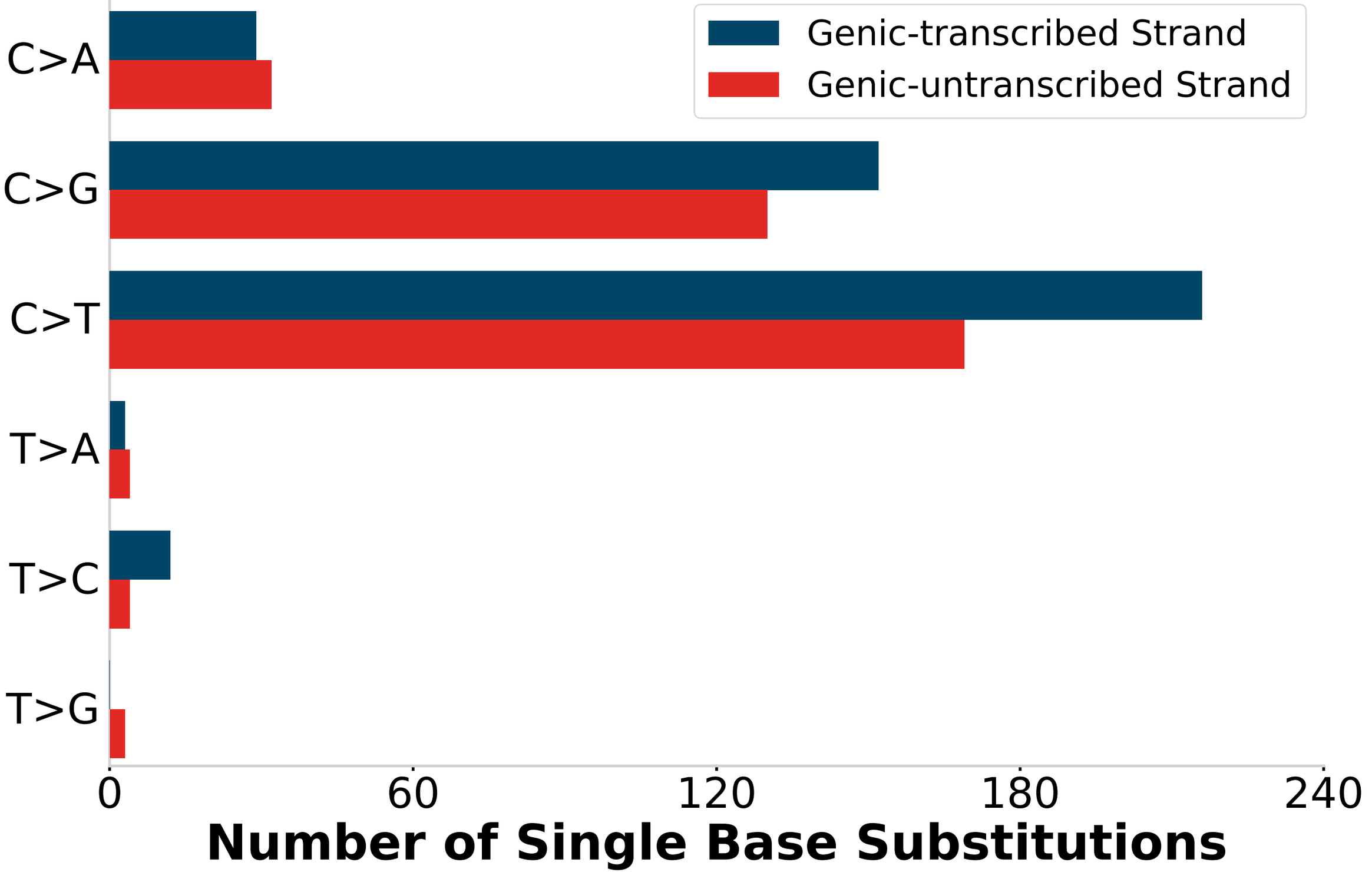
TCGA-PQ-A6FN-01A-11D-A31L-08: 76 trans

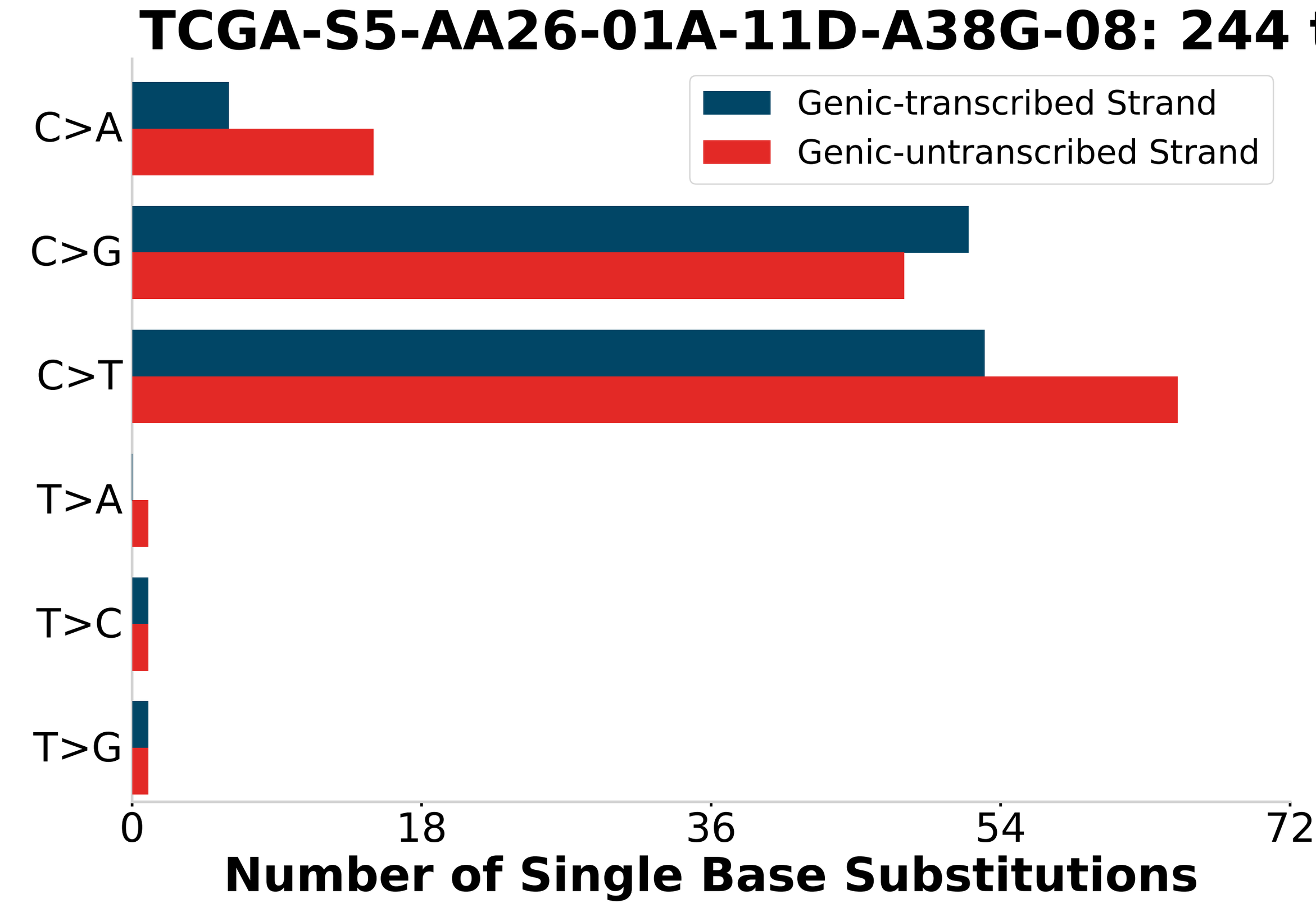


TCGA-R3-A69X-01A-22D-A30E-08: 229 tran

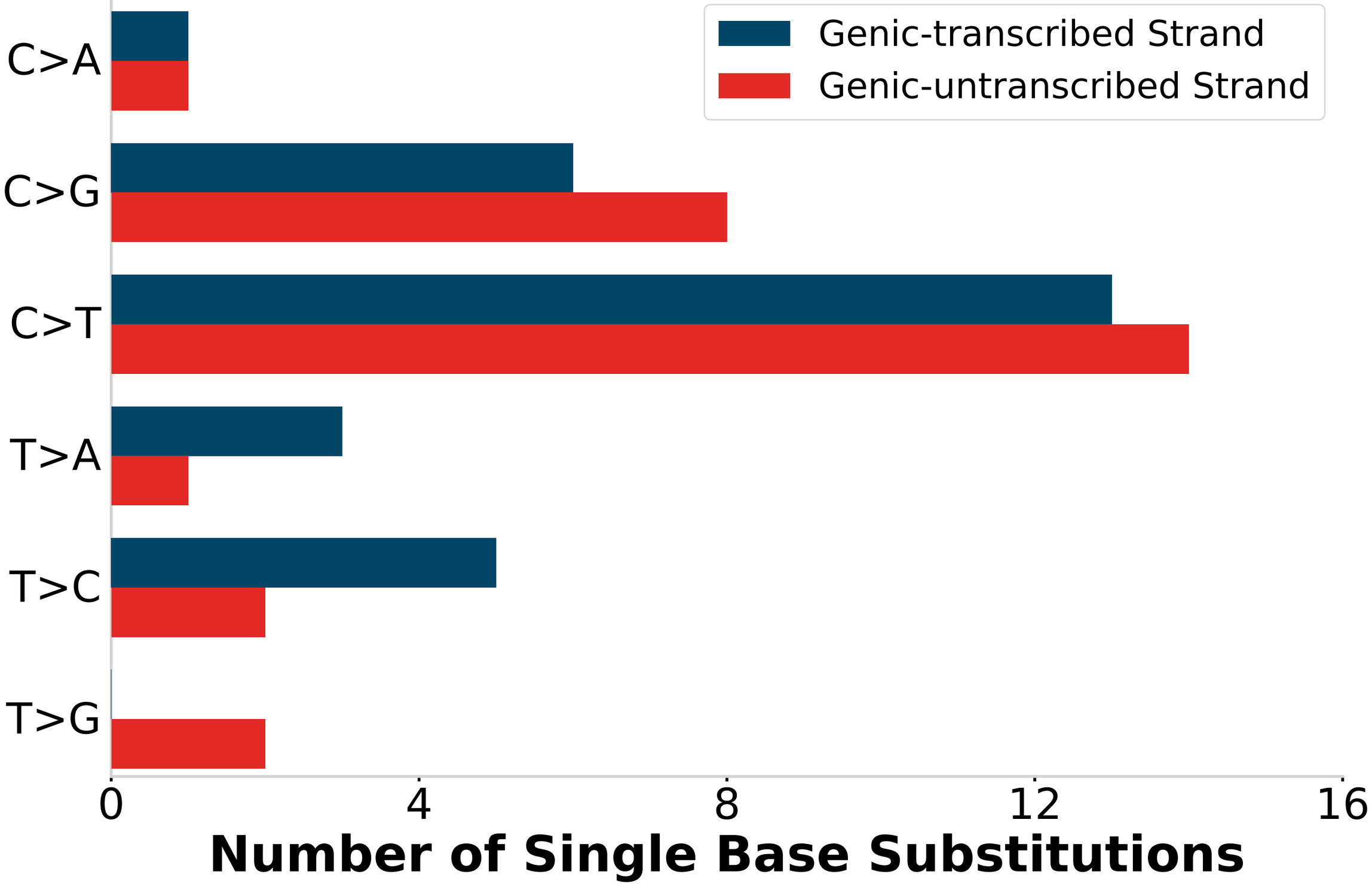


TCGA-S5-A6DX-01A-11D-A31L-08: 754 tran

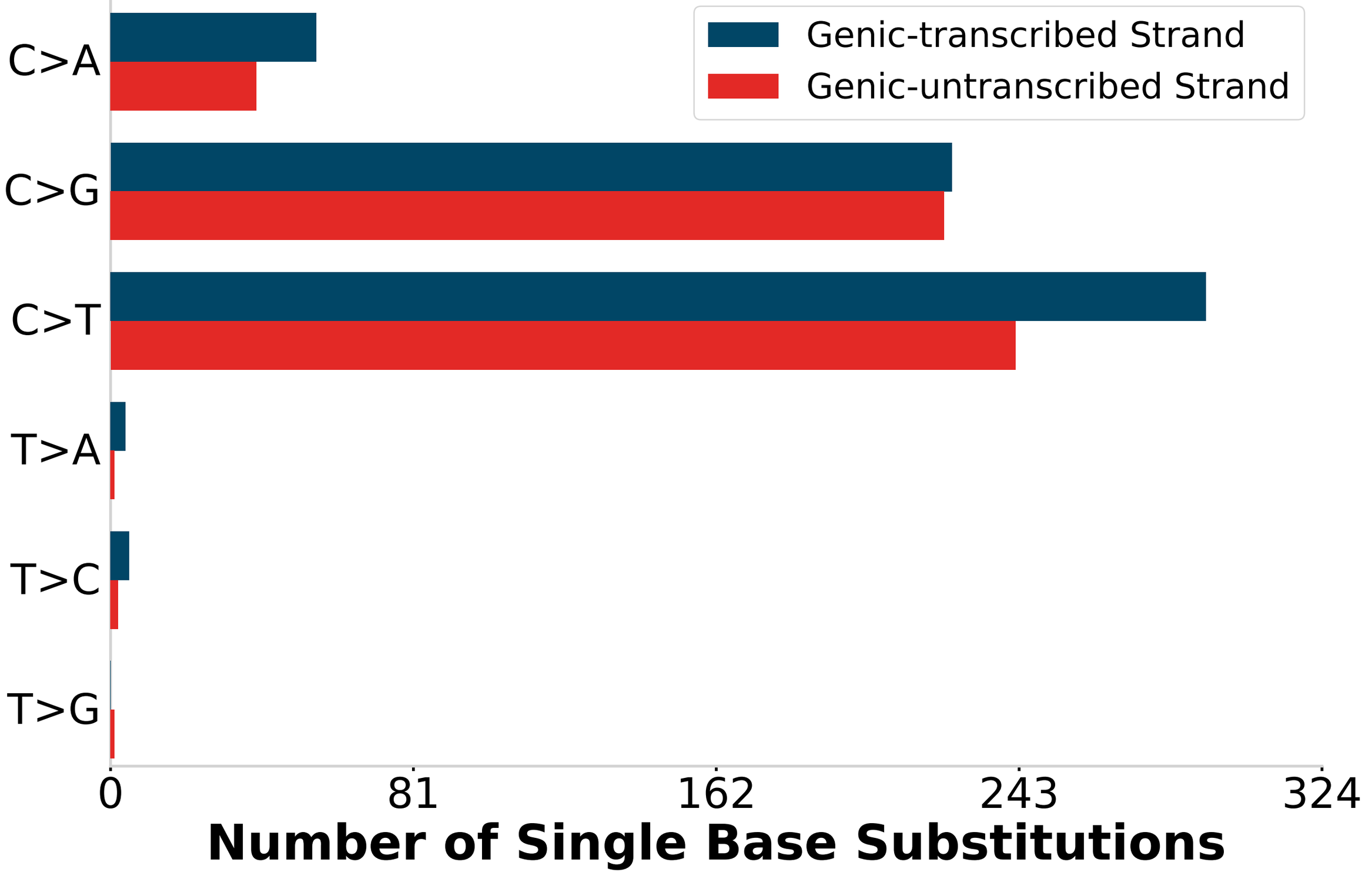



TCGA-S5-AA26-01A-11D-A38G-08: 244 tra
Genic-transcribed Strand
Genic-untranscribed Strand
C>A
C>G
C>T
T>A
T>C
T>G
0
18
36
54
72
Number of Single Base Substitutions

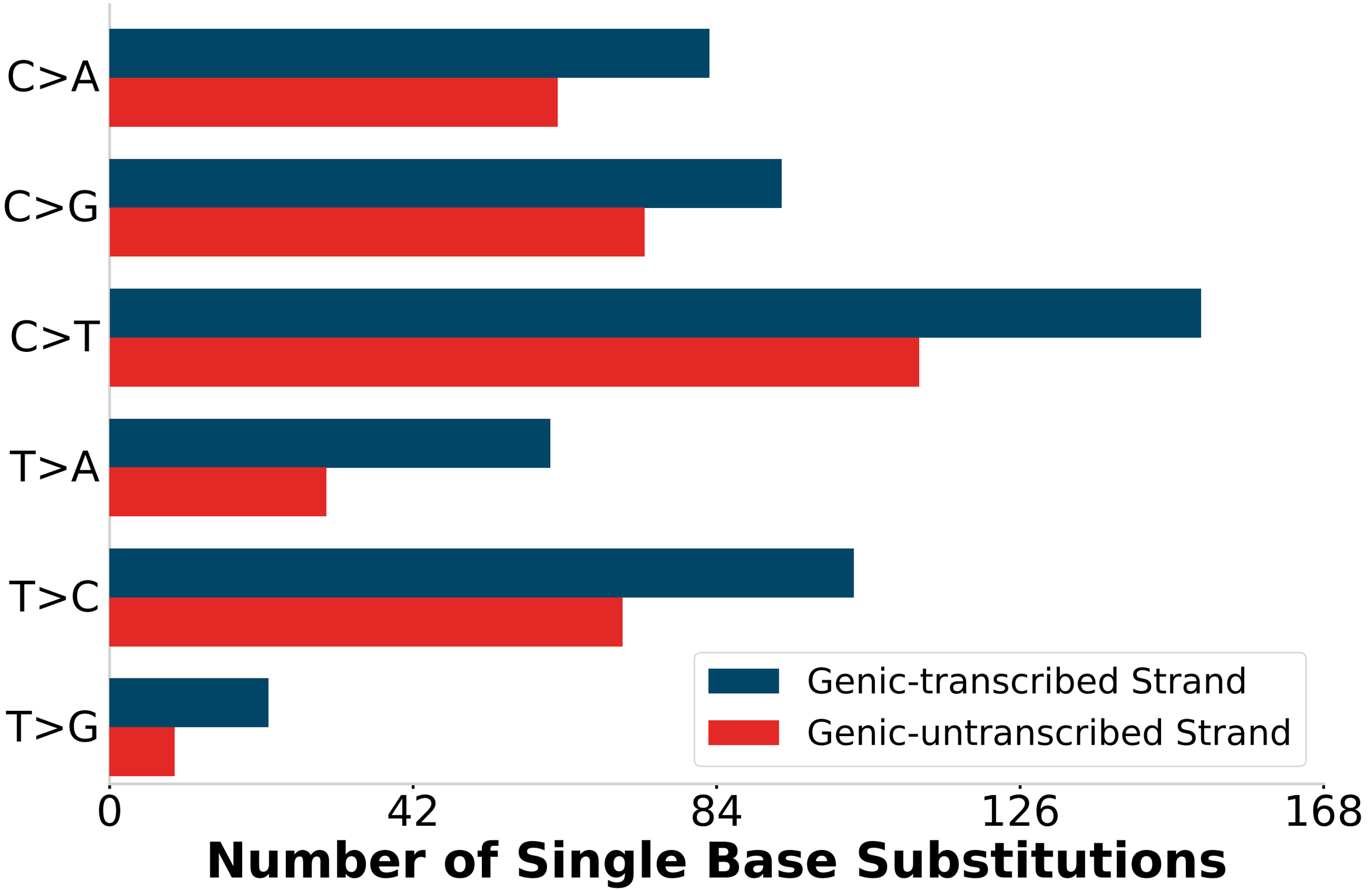
TCGA-SY-A9G0-01A-12D-A38G-08: 56 trans



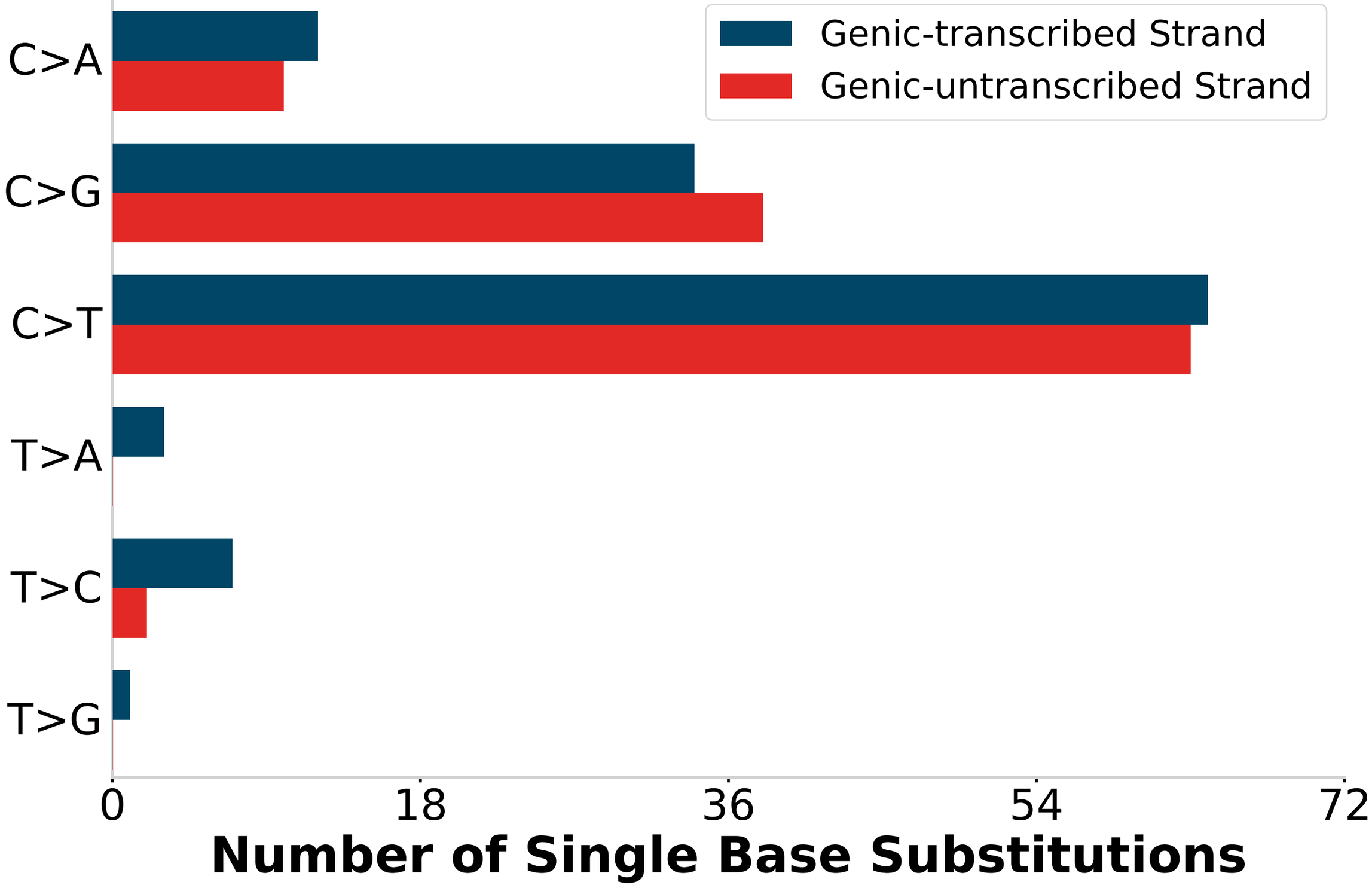
TCGA-SY-A9G5-01A-11D-A38G-08: 1,090 tr



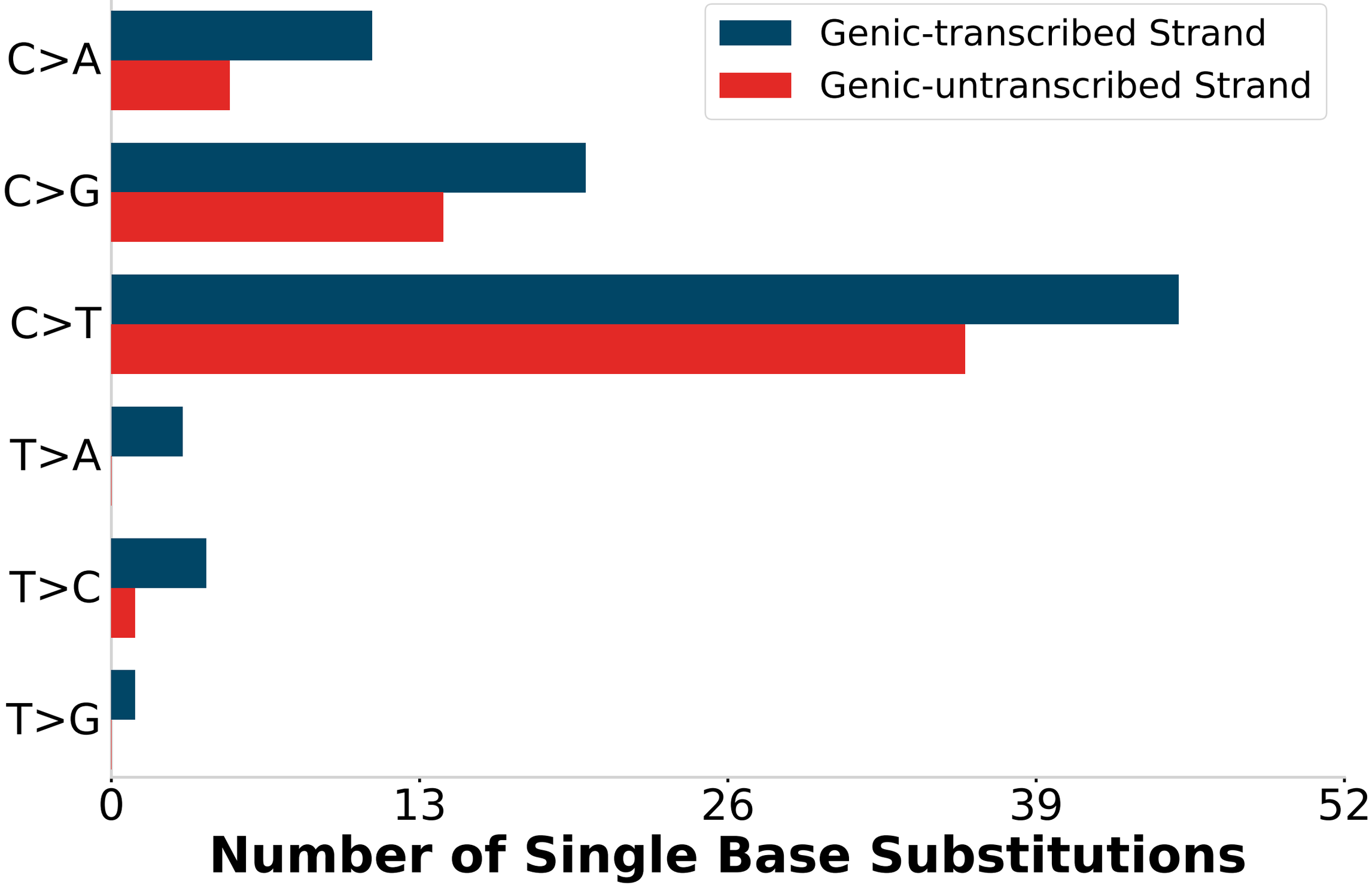
TCGA-UY-A78K-01A-11D-A339-08: 871 tran



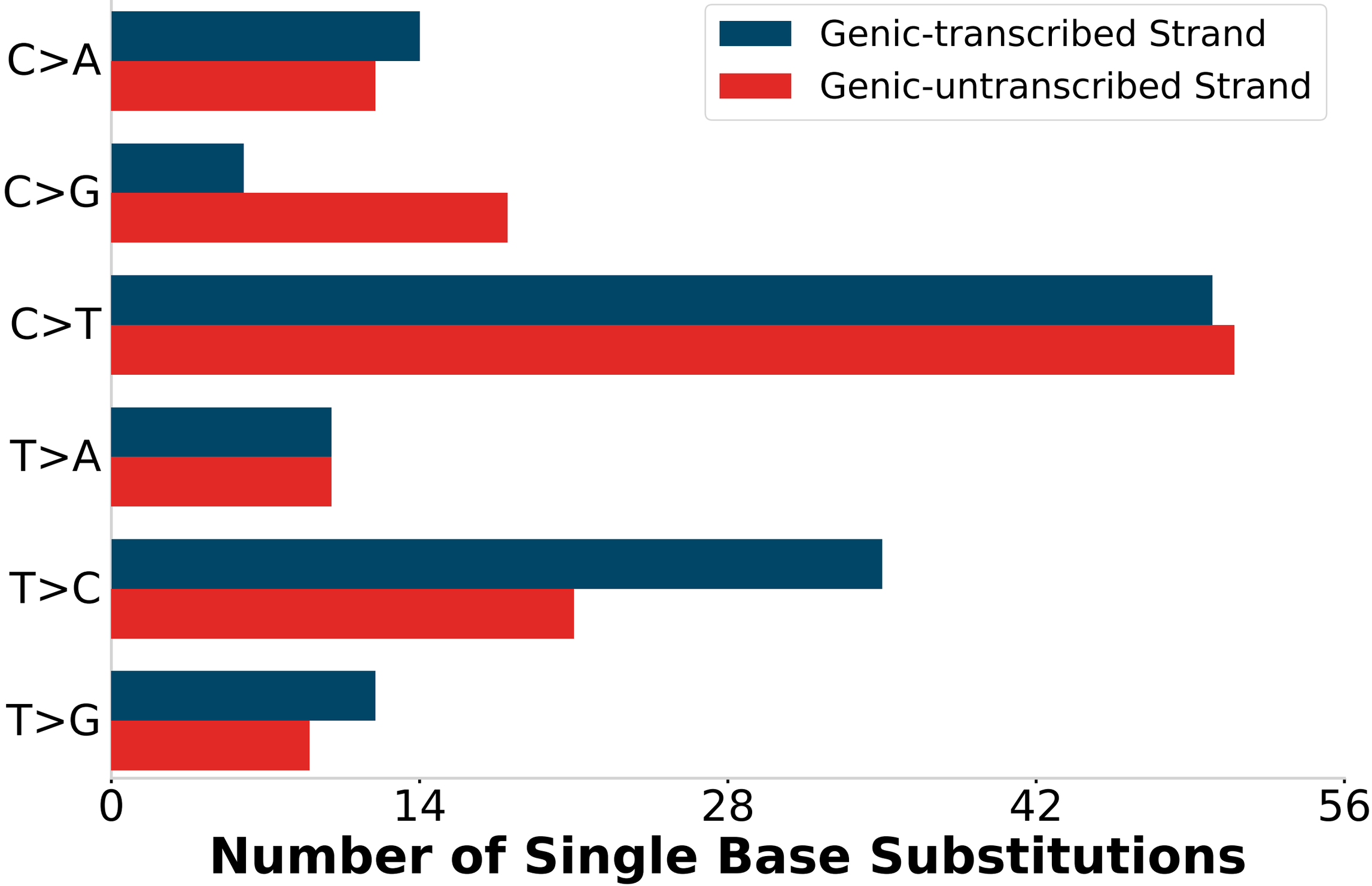
TCGA-UY-A78L-01A-12D-A339-08: 234 tran



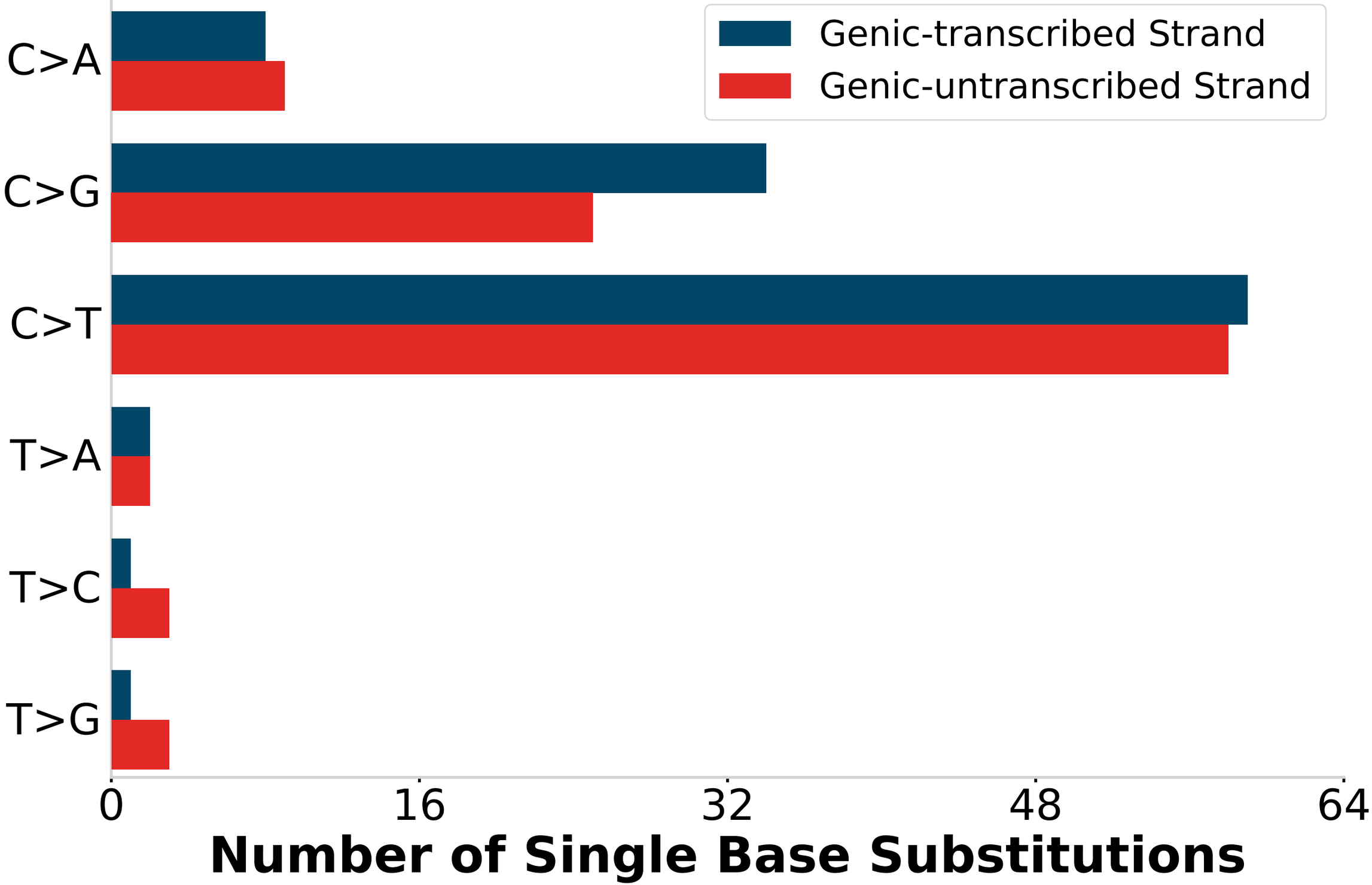
TCGA-UY-A78M-01A-21D-A34U-08: 140 tra



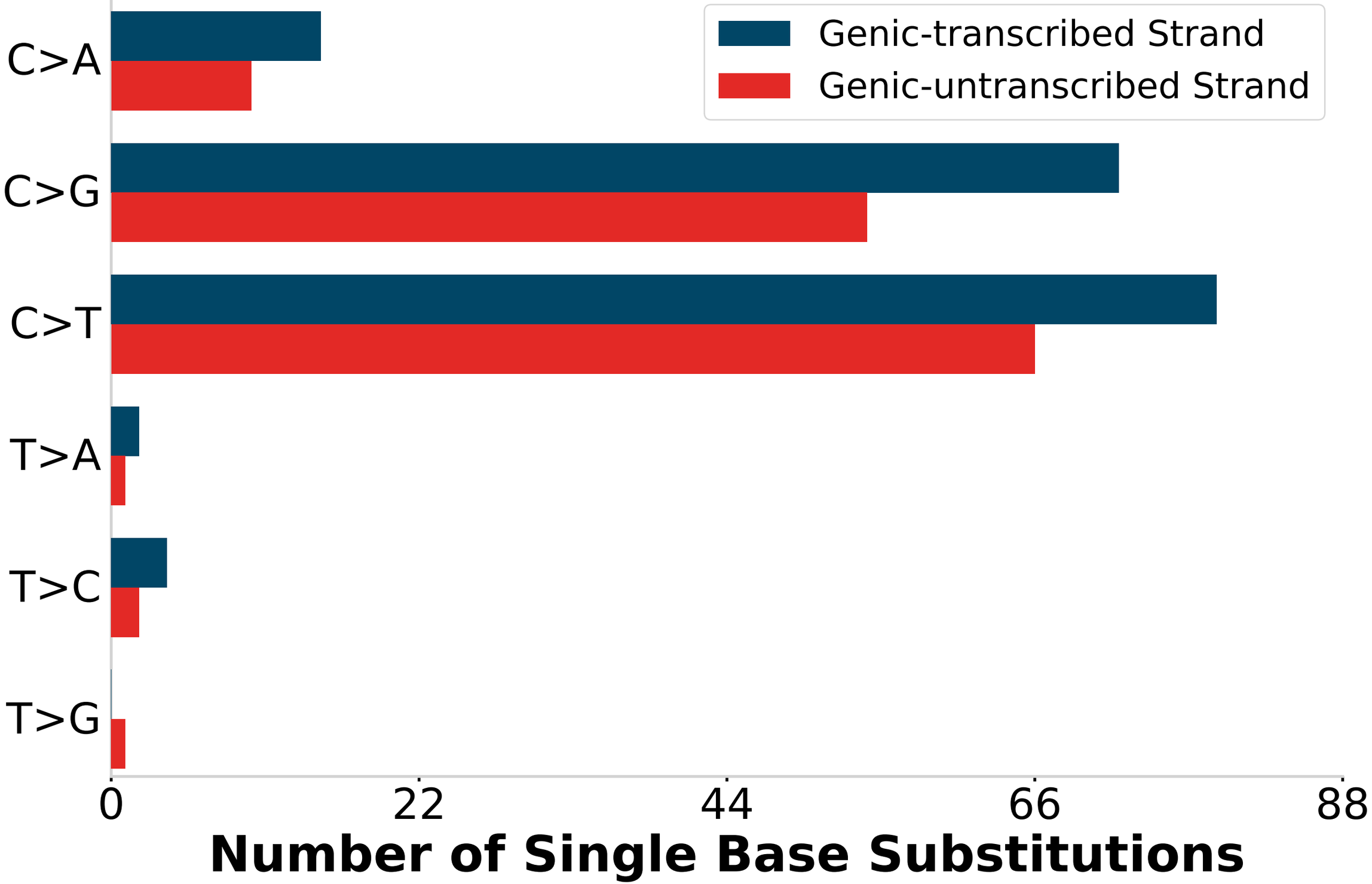
TCGA-UY-A78N-01A-12D-A339-08: 248 tra



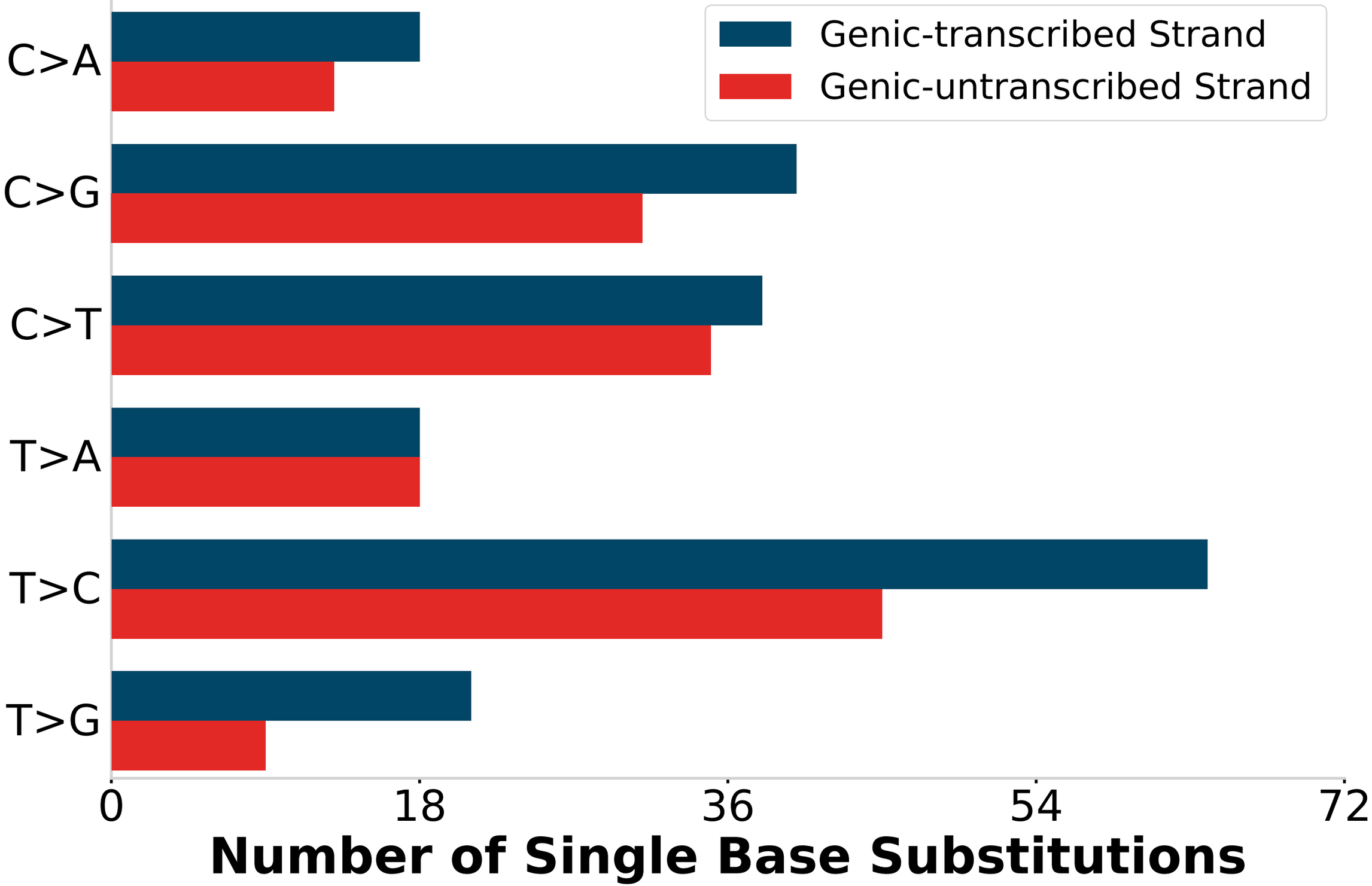
TCGA-UY-A78O-01A-12D-A339-08: 205 tra



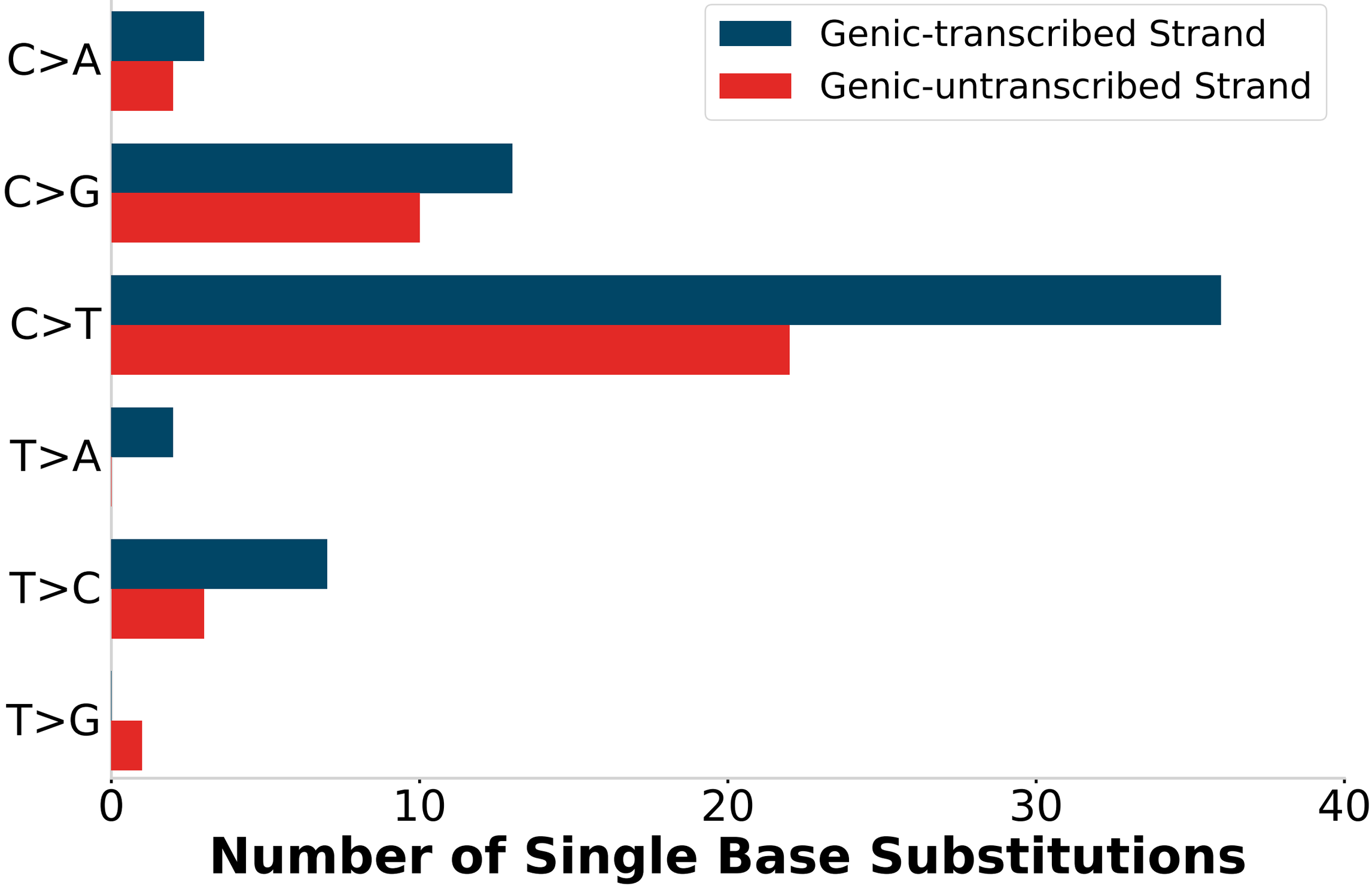
TCGA-UY-A78P-01A-12D-A364-08: 306 tran



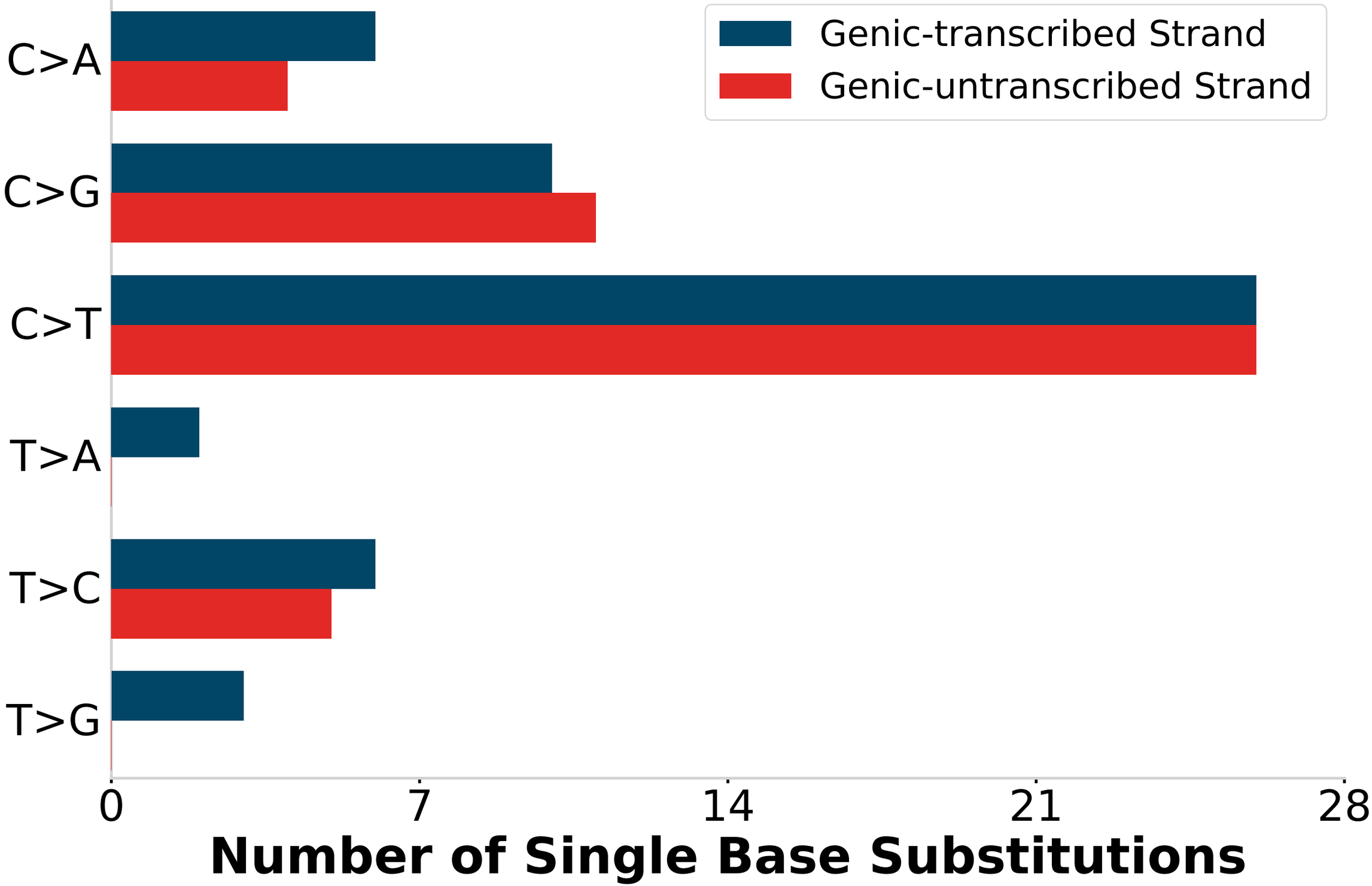
TCGA-UY-A8OB-01A-12D-A42E-08: 350 tra



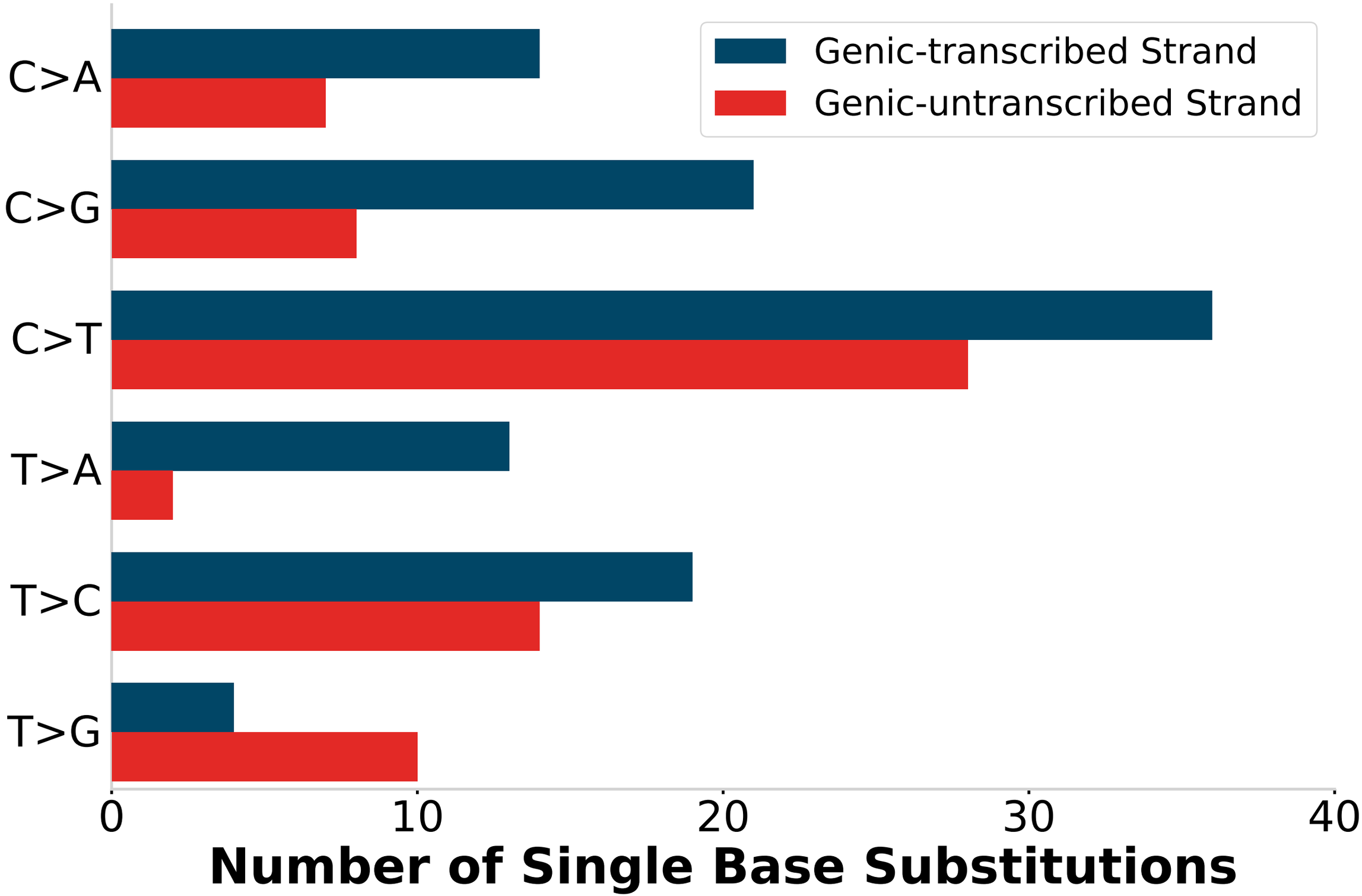
TCGA-UY-A8OC-01A-11D-A364-08: 99 trans



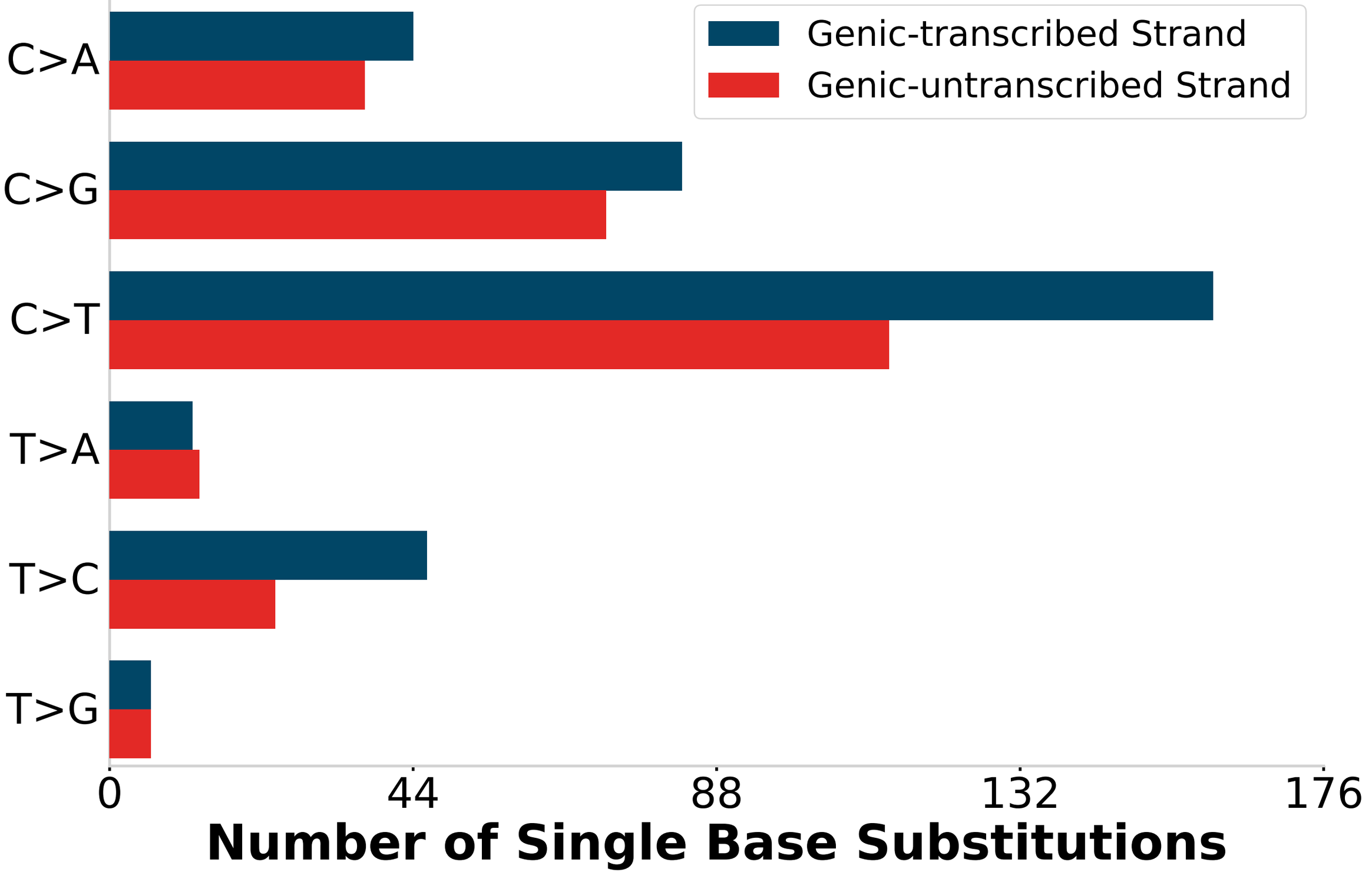
TCGA-UY-A8OD-01A-11D-A364-08: 99 tran



TCGA-UY-A9PA-01A-11D-A38G-08: 176 tra



TCGA-UY-A9PB-01A-11D-A38G-08: 616 tra



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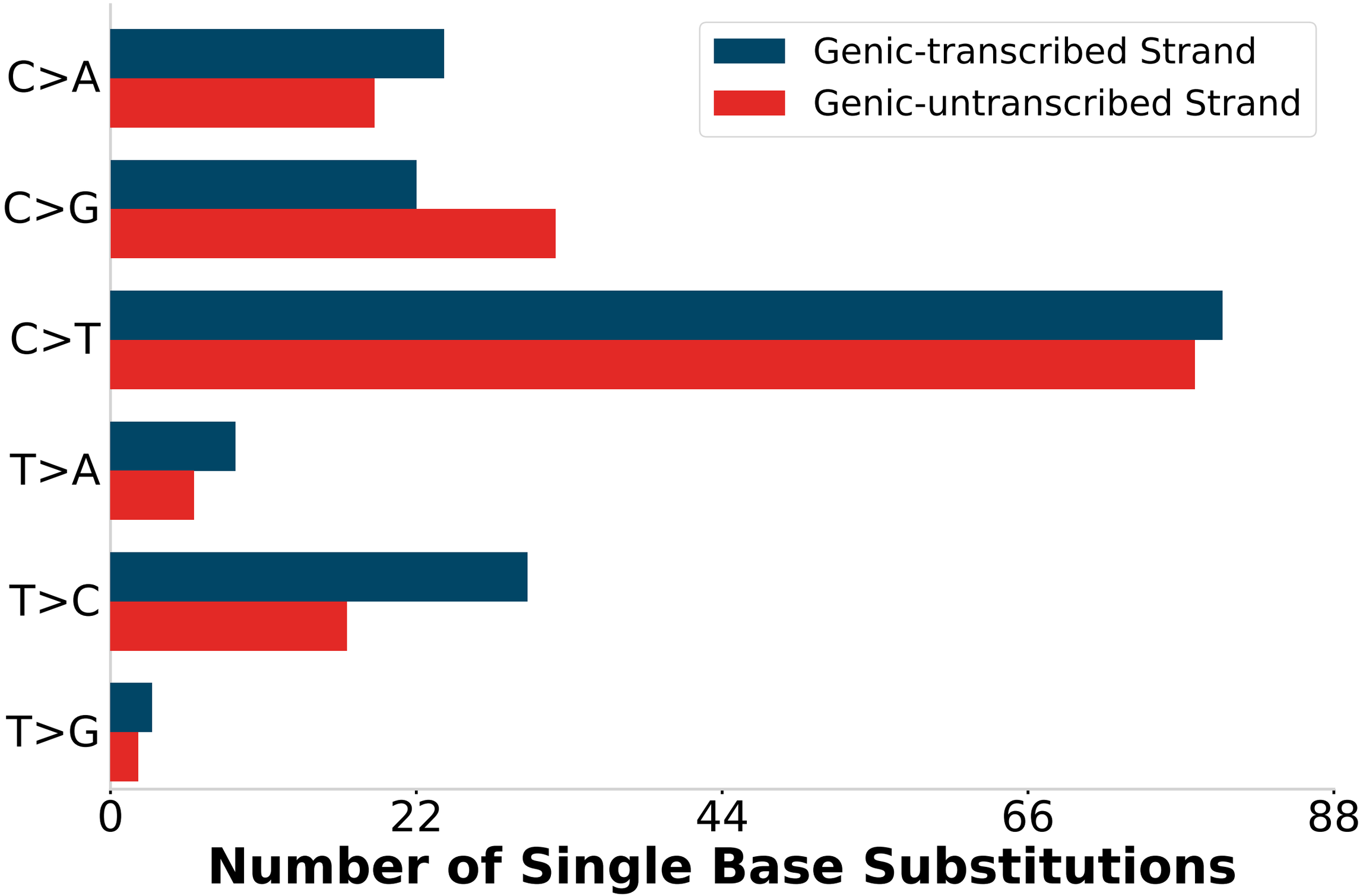
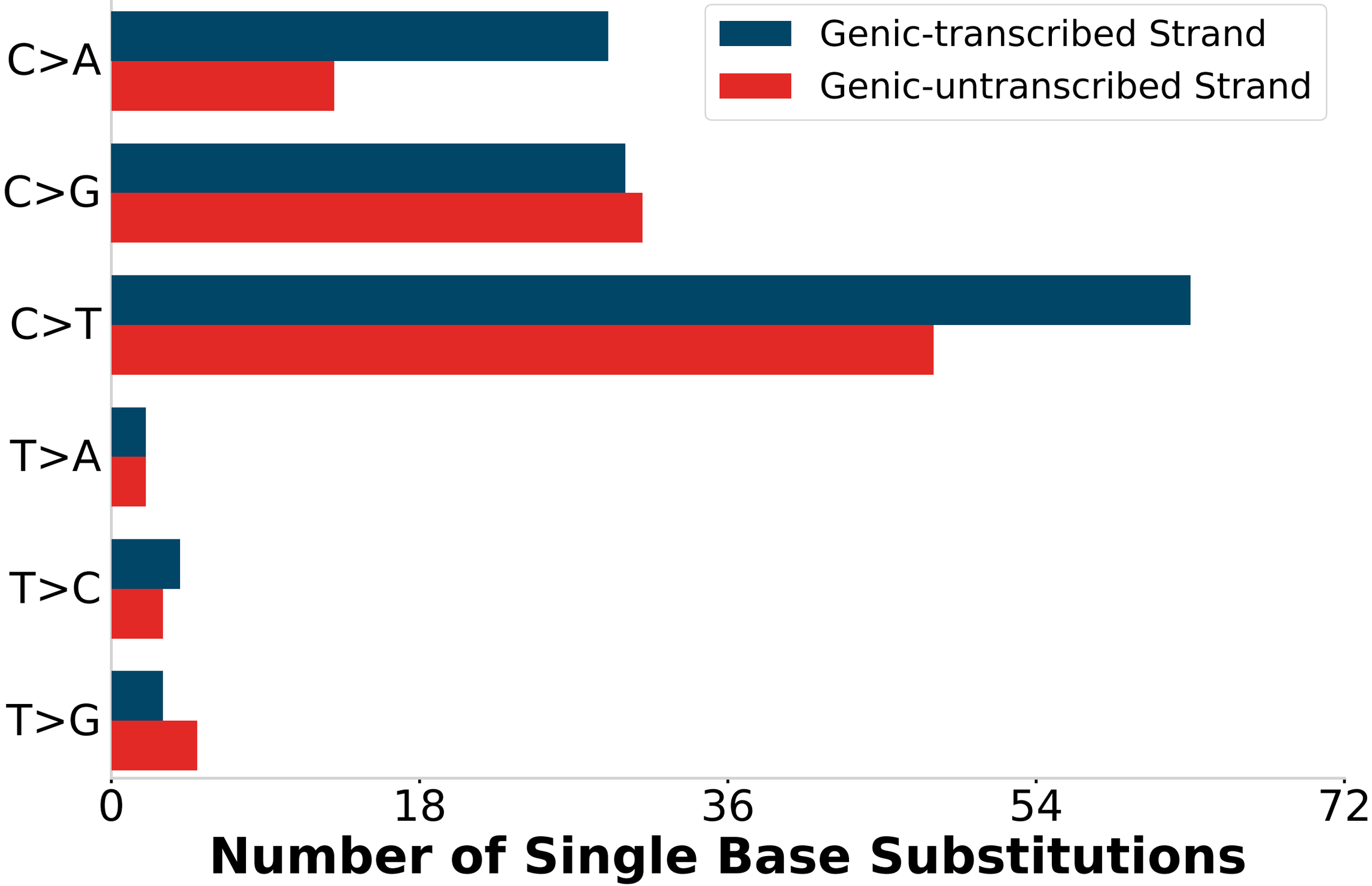
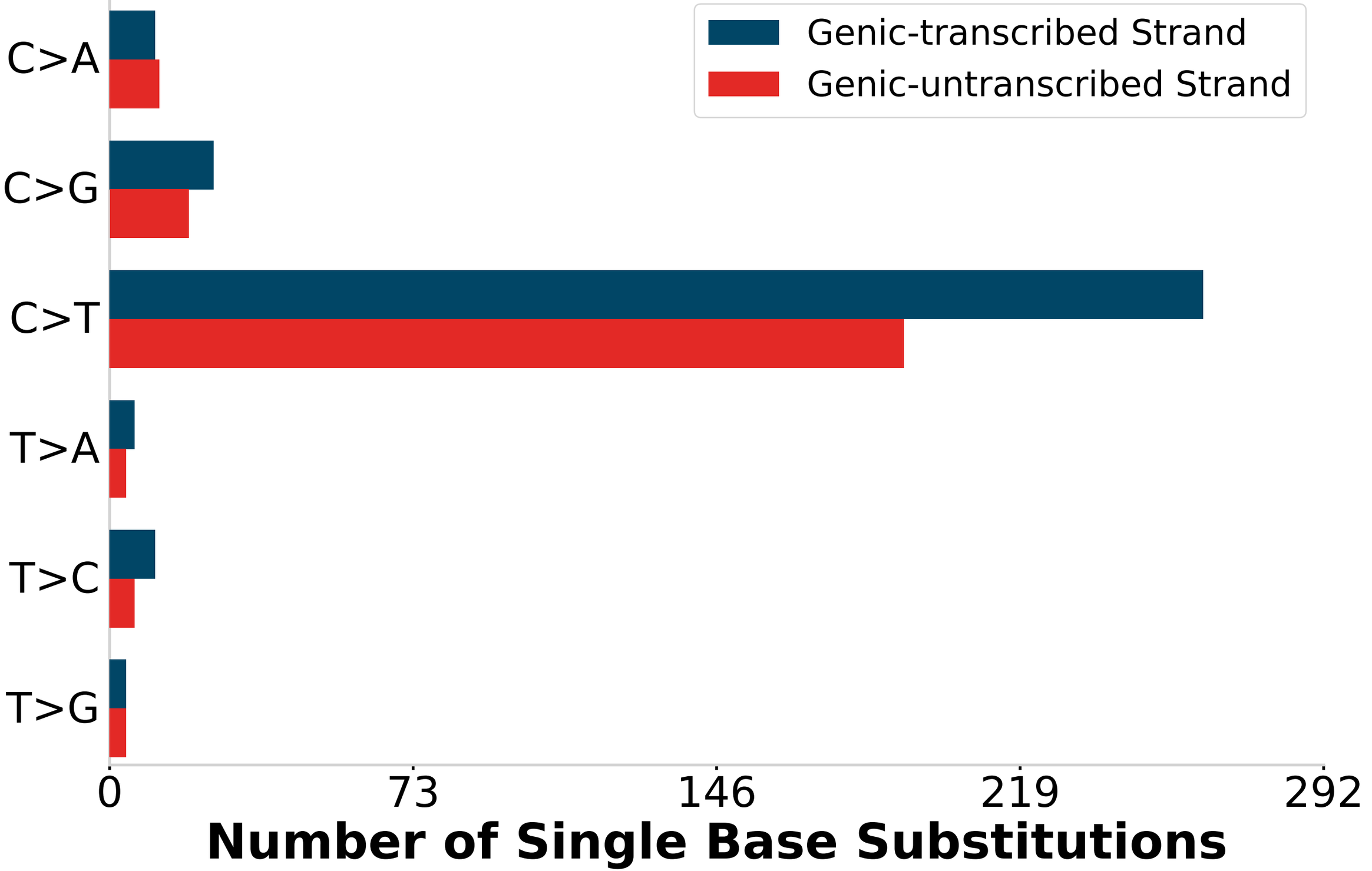


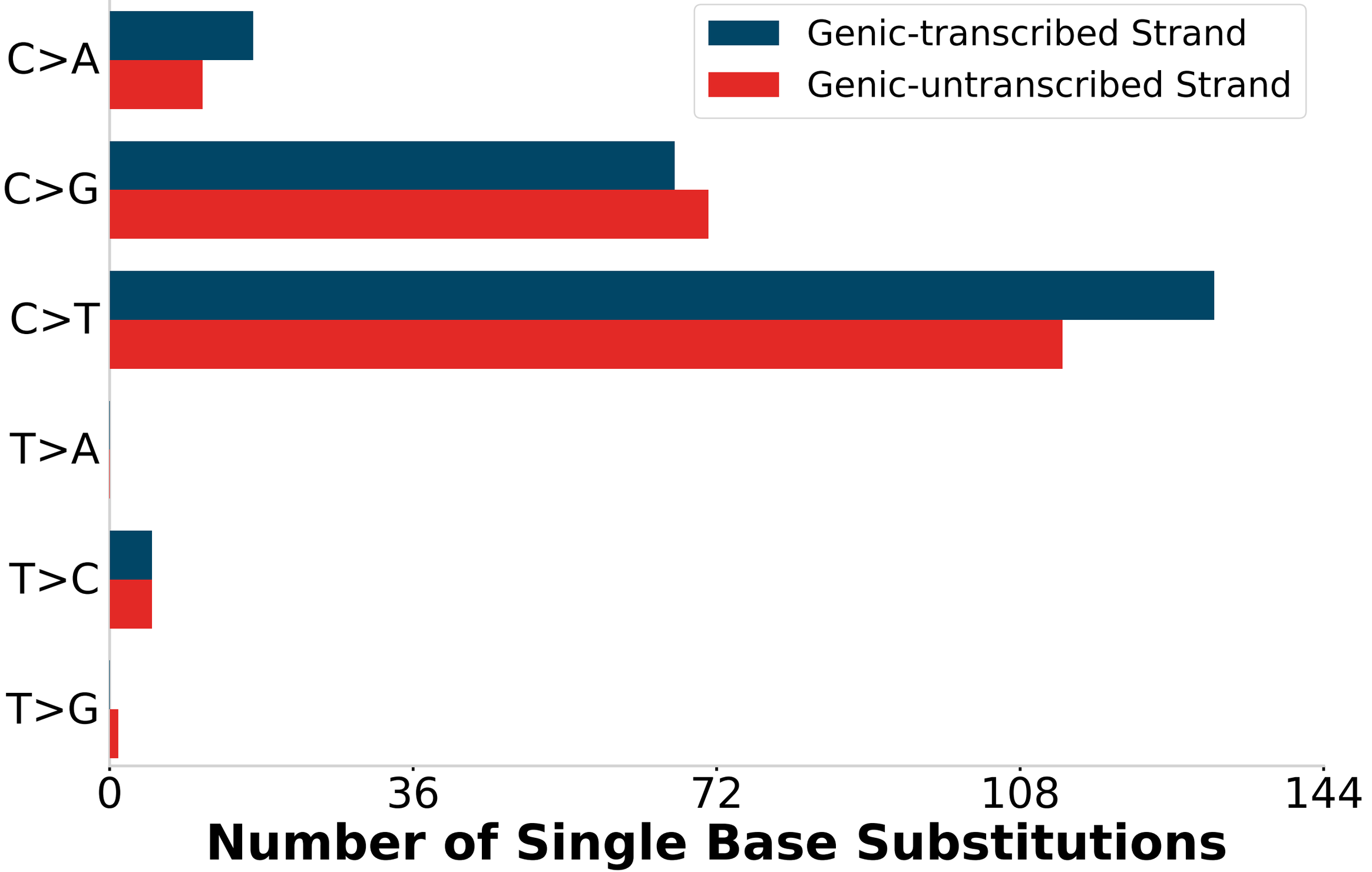
TCGA-UY-A9PE-01A-11D-A38G-08: 233 tra



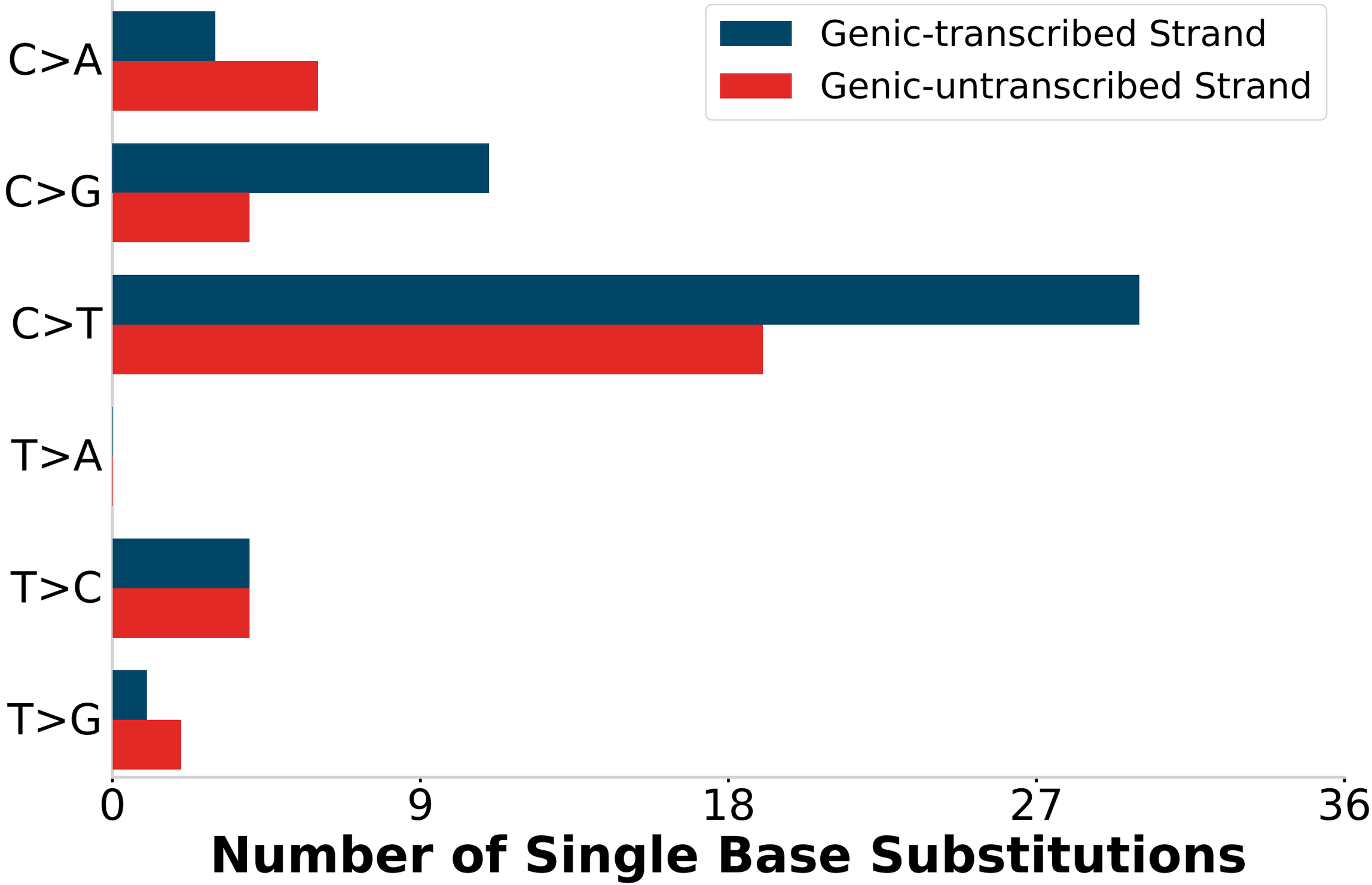
TCGA-UY-A9PF-01A-11D-A38G-08: 556 tran



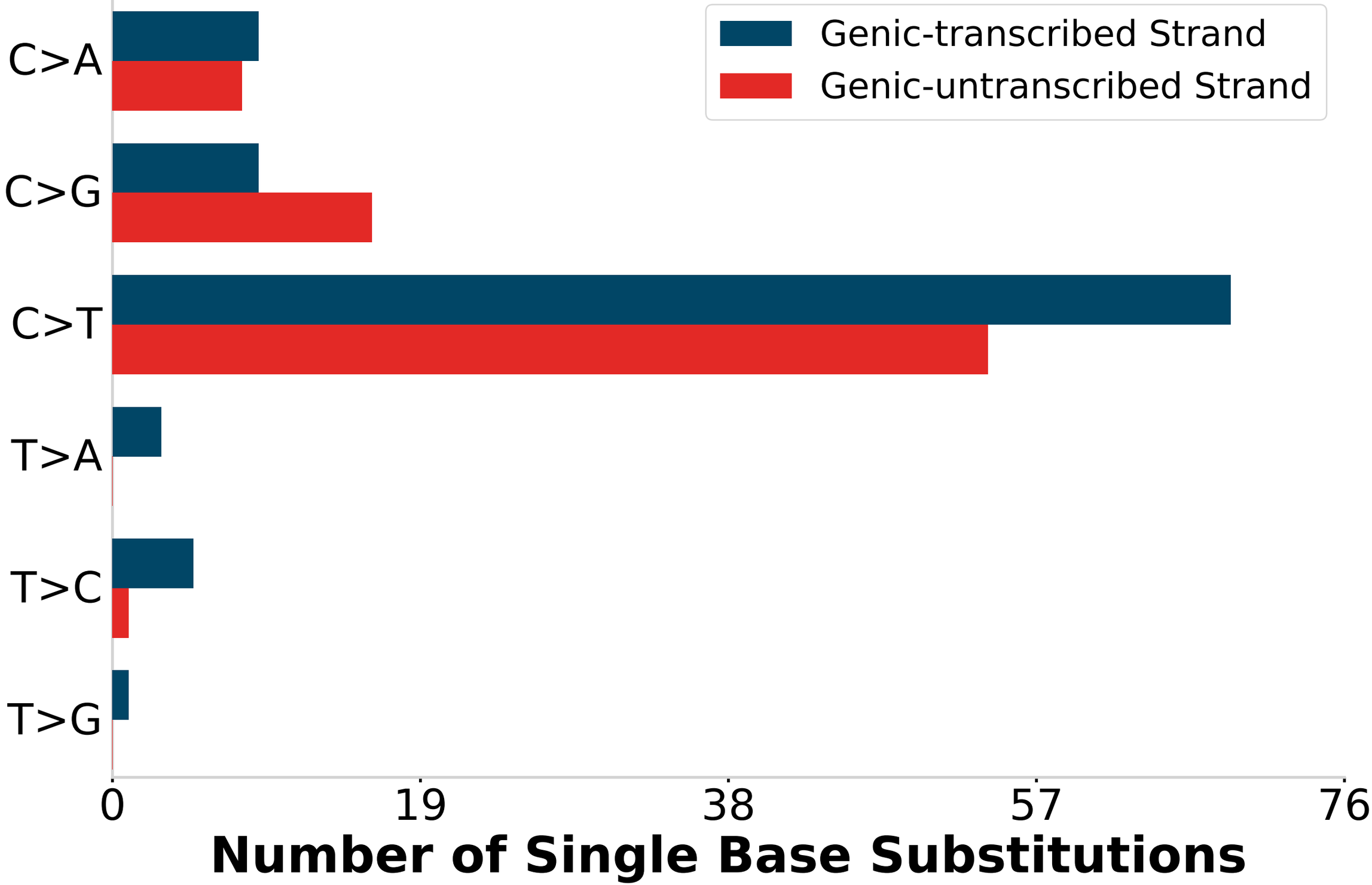
TCGA-UY-A9PH-01A-11D-A38G-08: 421 tra



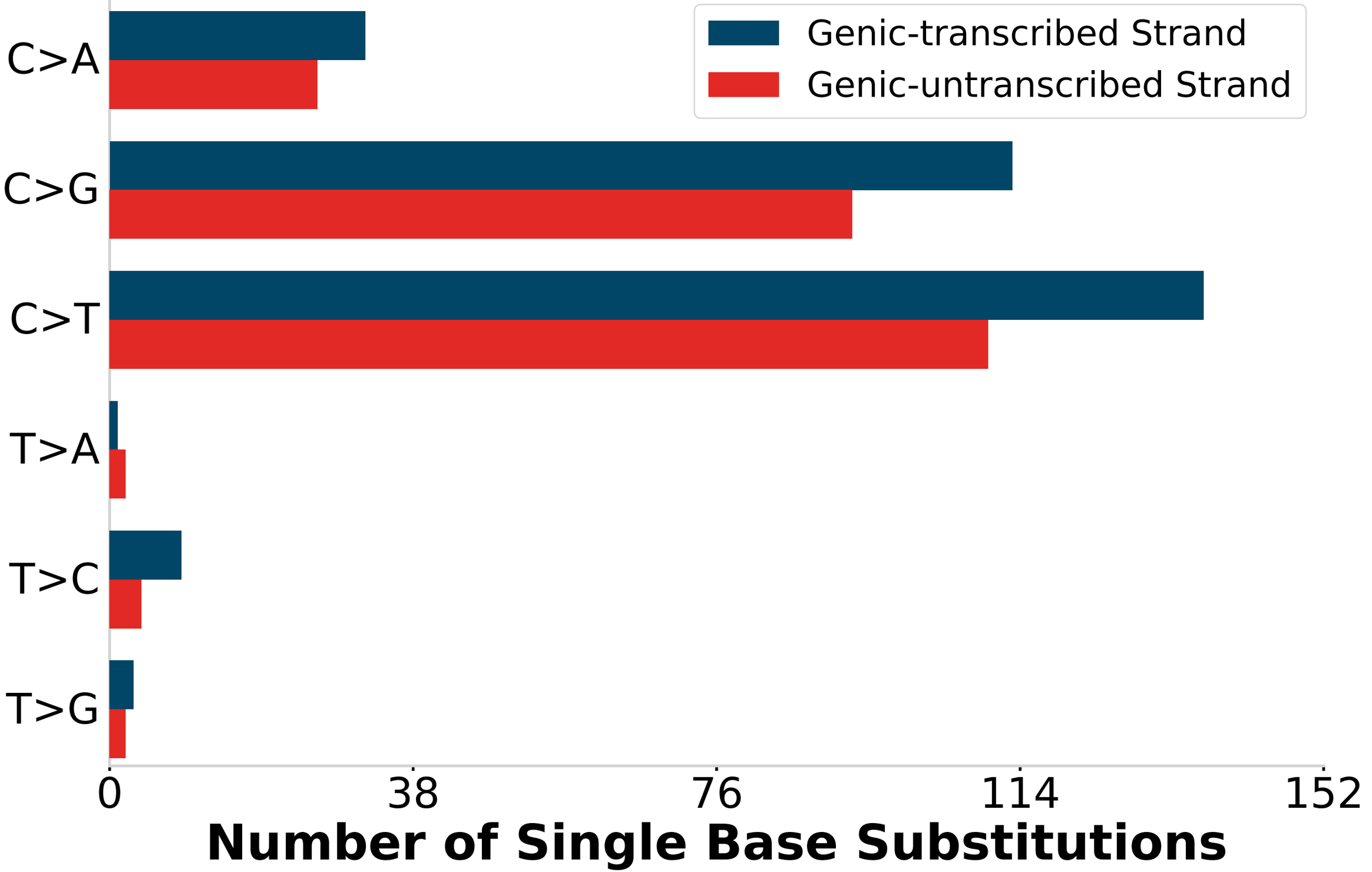
TCGA-XF-A8HB-01A-11D-A364-08: 84 trans



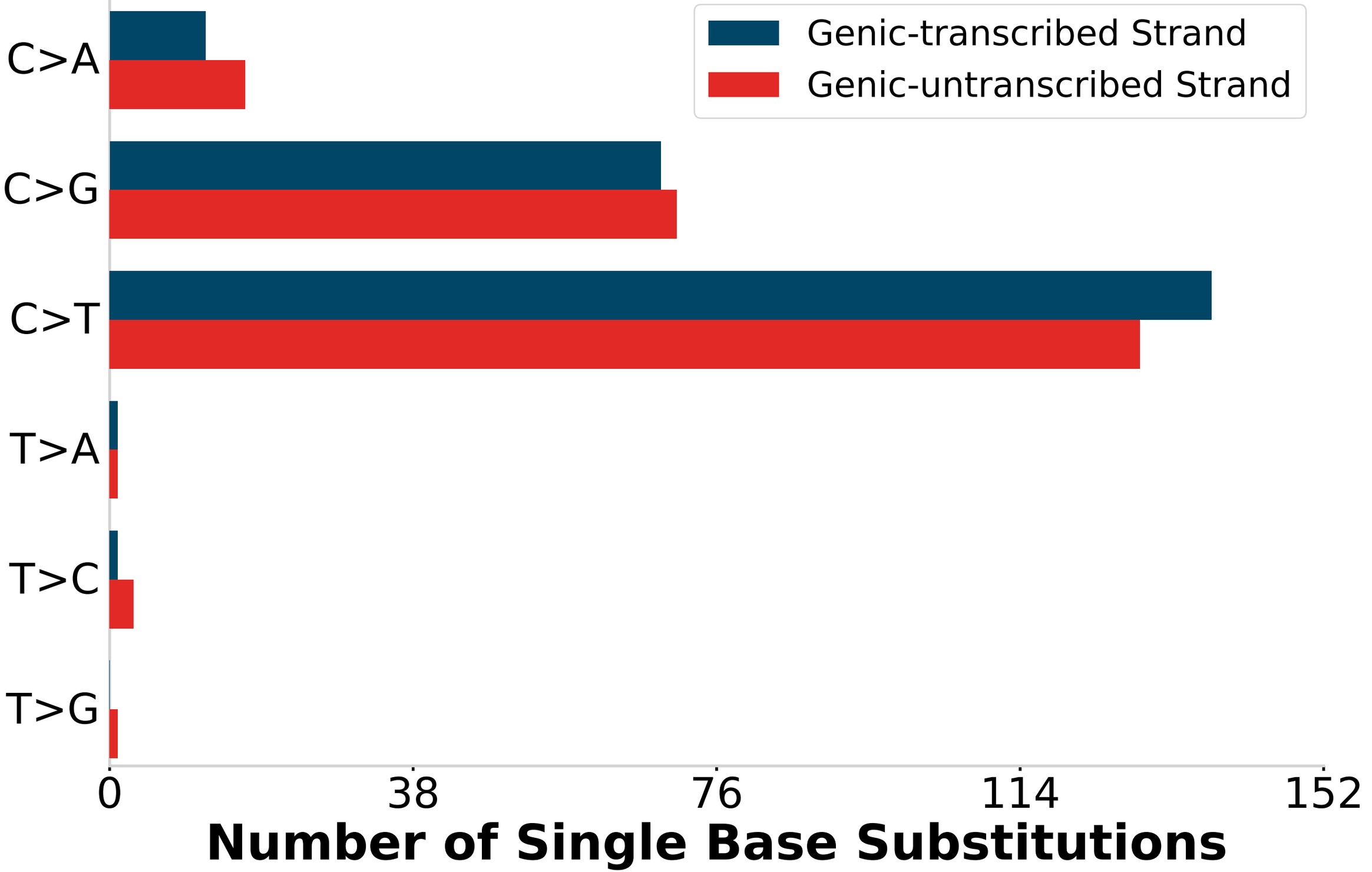
TCGA-XF-A8HC-01A-11D-A364-08: 175 tra



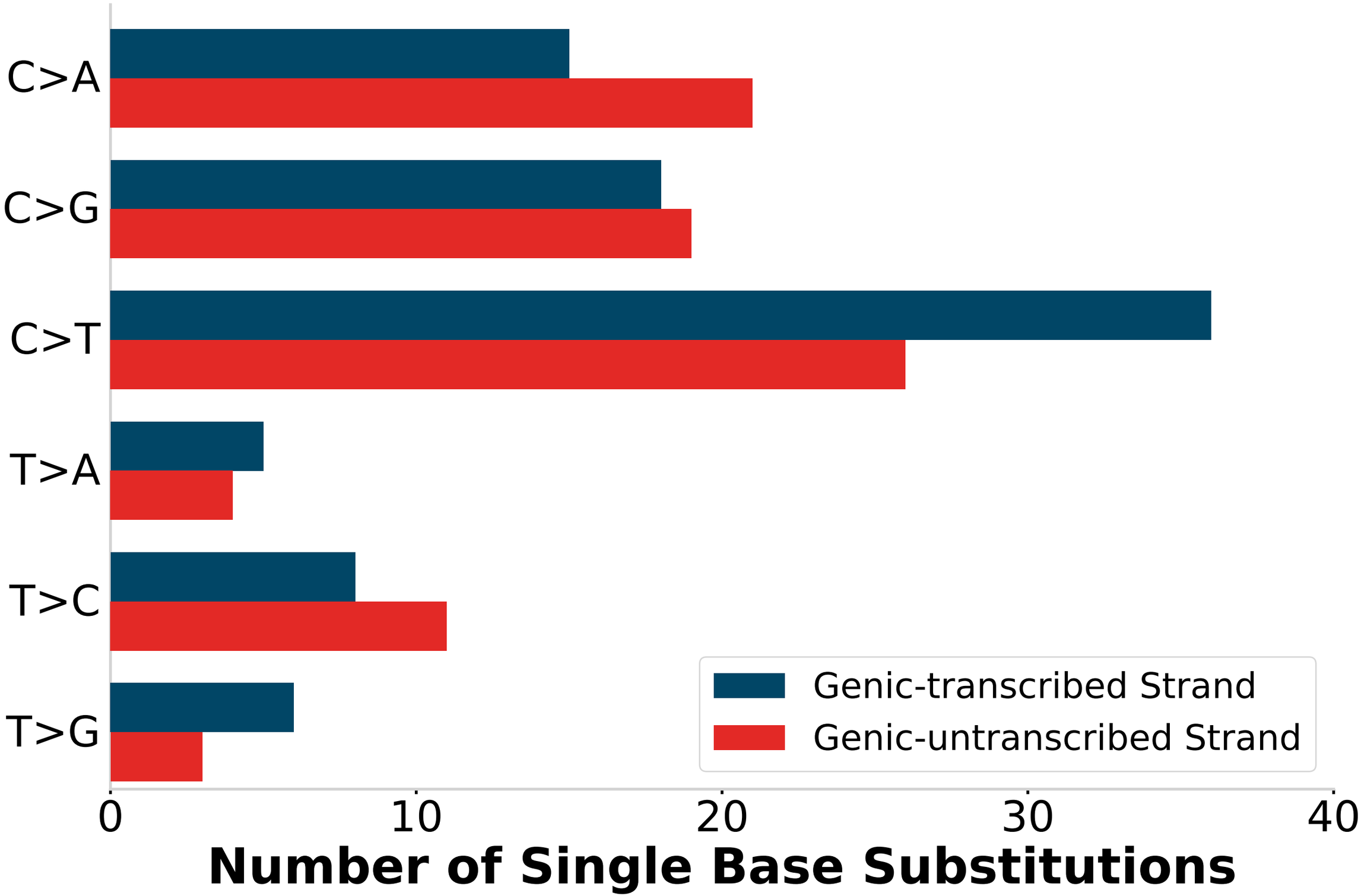
TCGA-XF-A8HD-01A-11D-A364-08: 532 tra



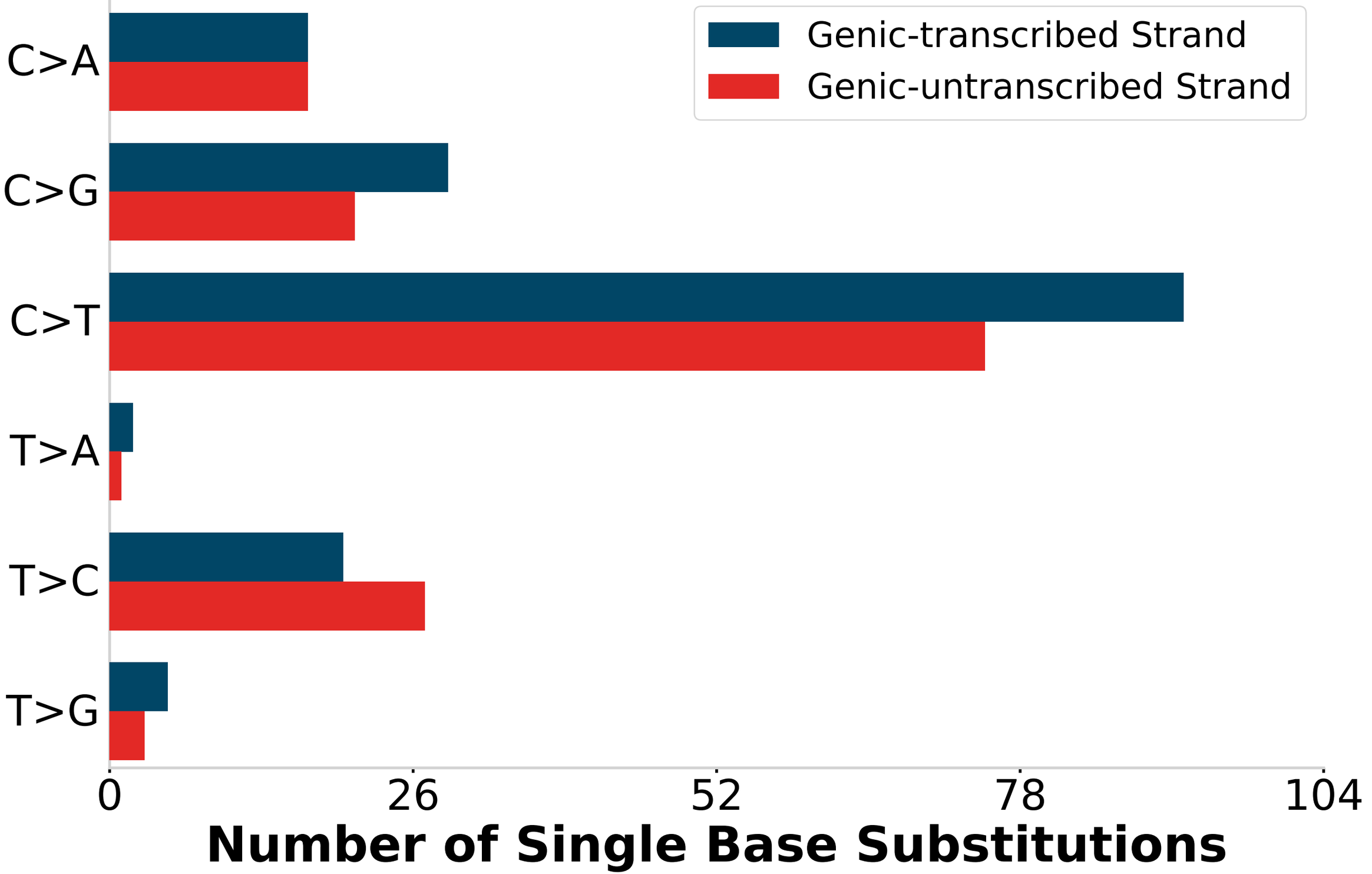
TCGA-XF-A8HE-01A-11D-A364-08: 443 tran



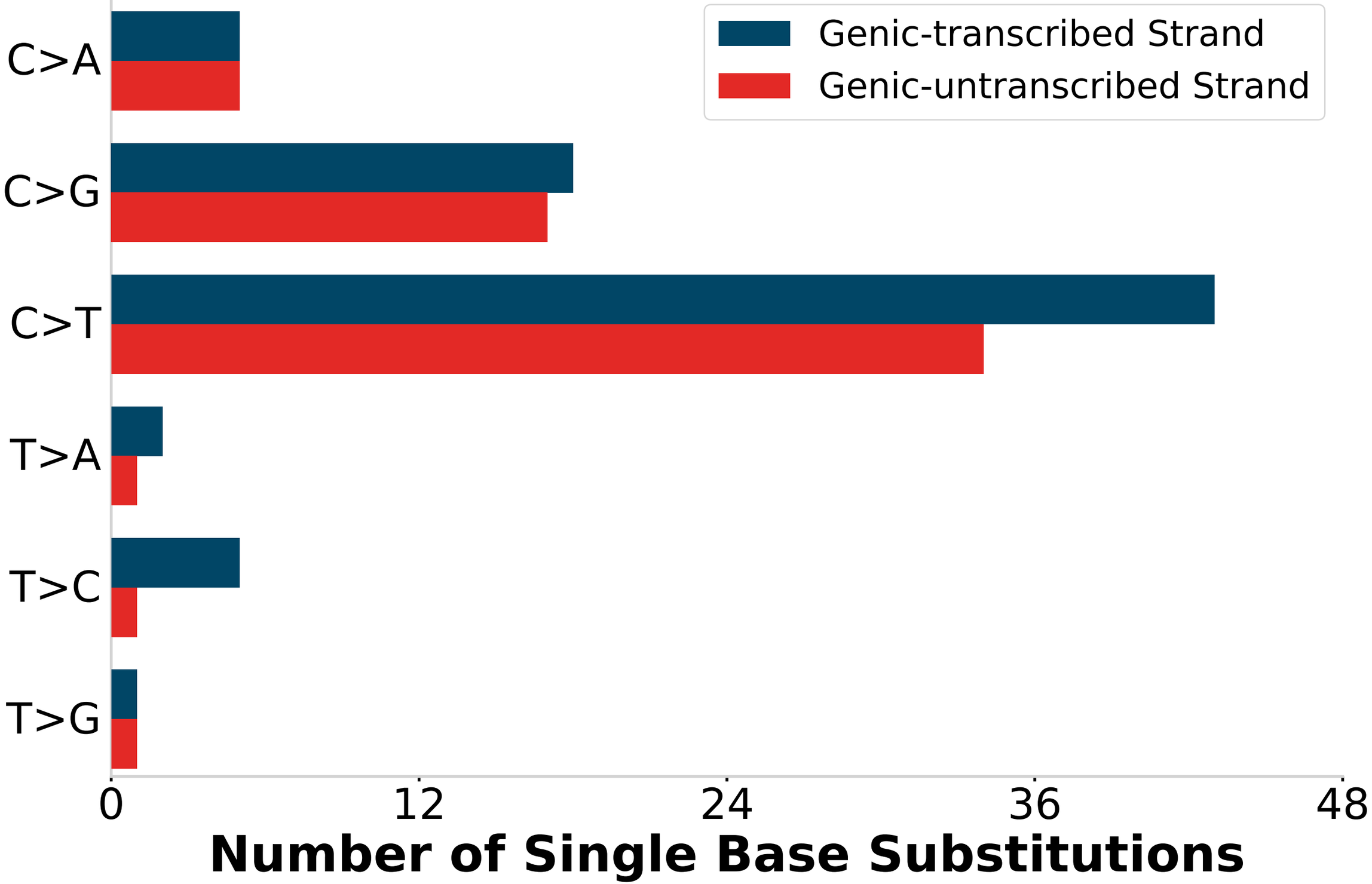
TCGA-XF-A8HF-01A-11D-A364-08: 172 tran



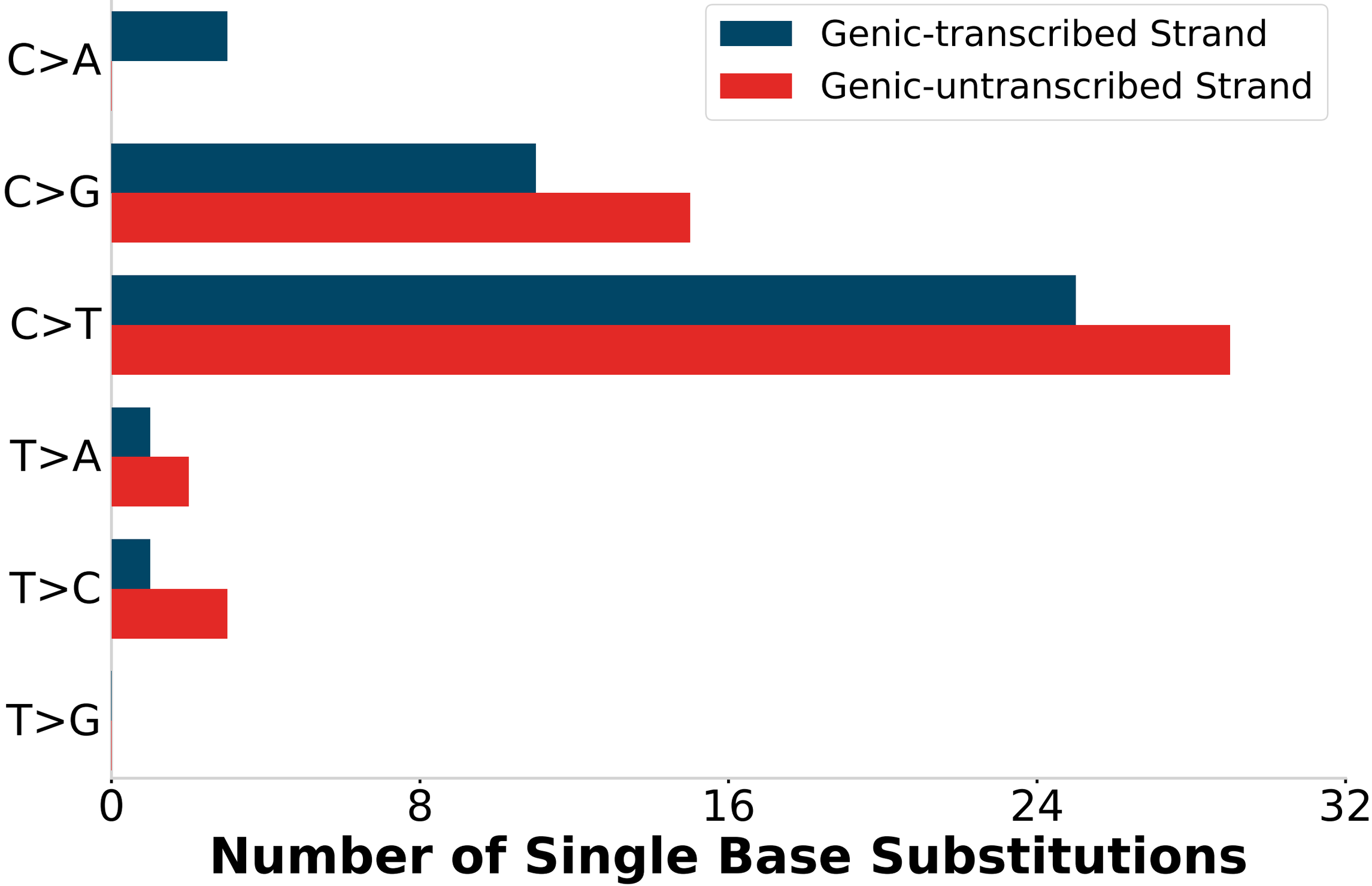
TCGA-XF-A8HG-01A-11D-A364-08: 309 tra



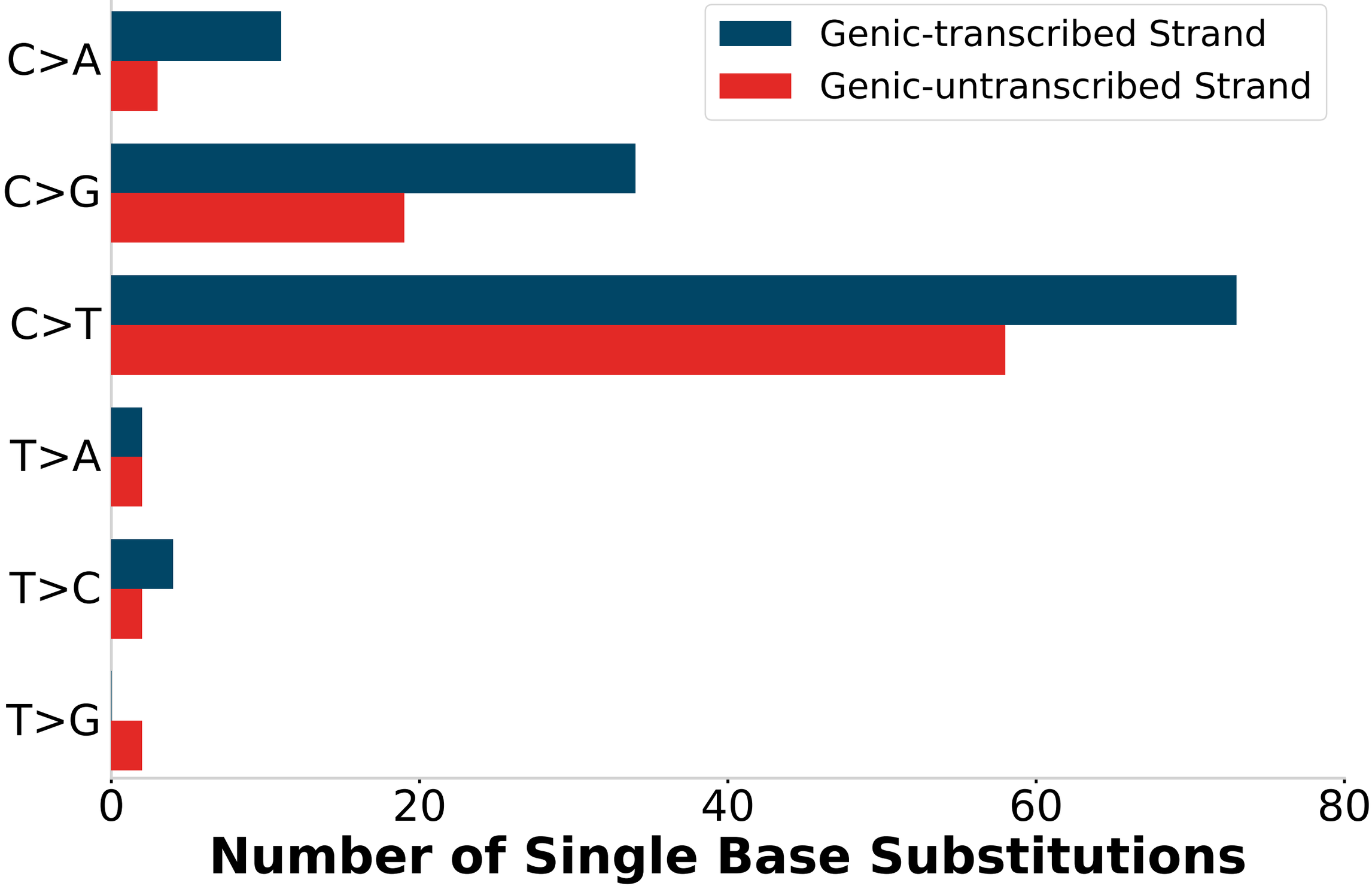
TCGA-XF-A8HH-01A-11D-A38G-08: 133 tra



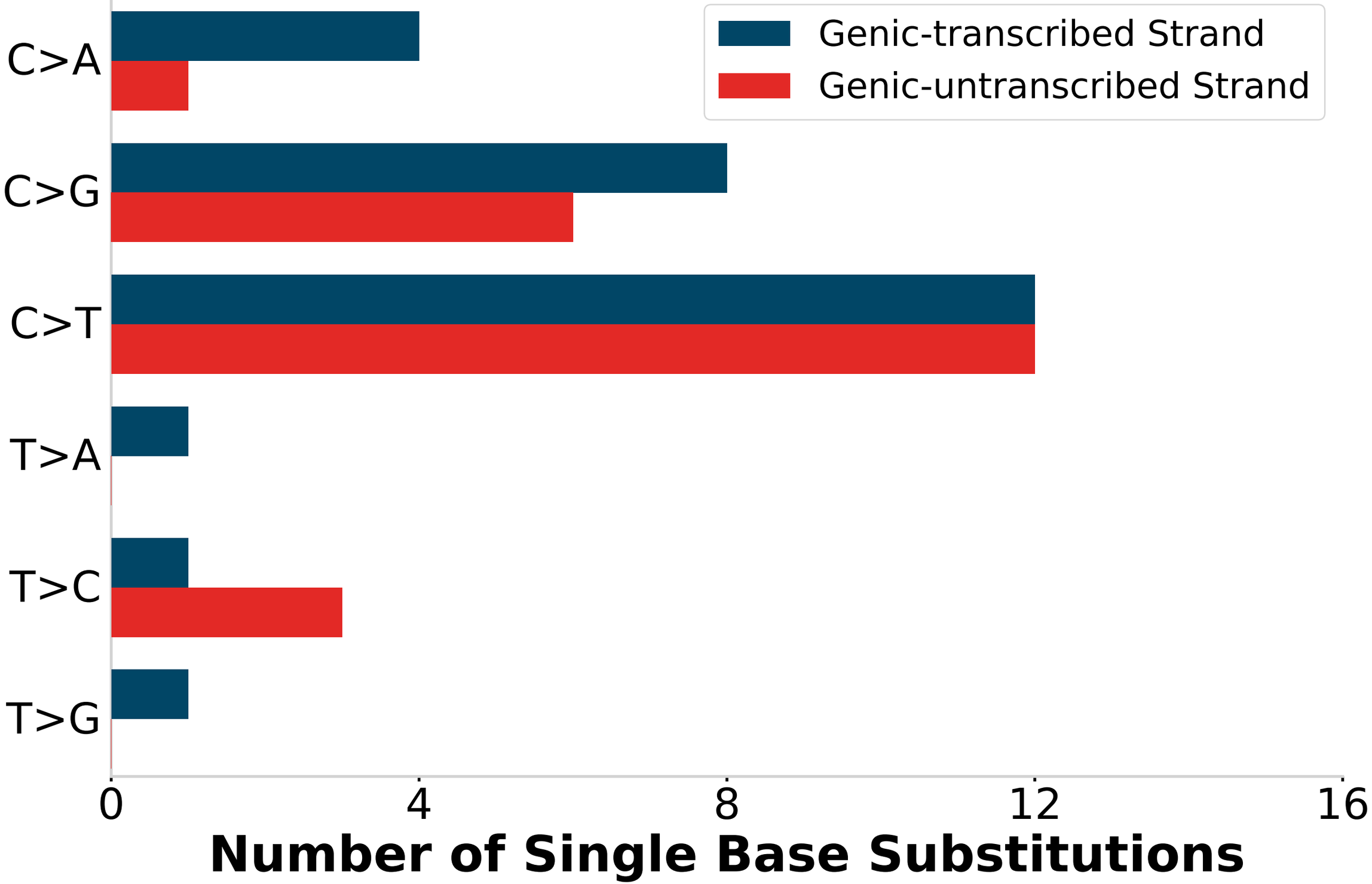
TCGA-XF-A8HI-01A-11D-A38G-08: 90 trans



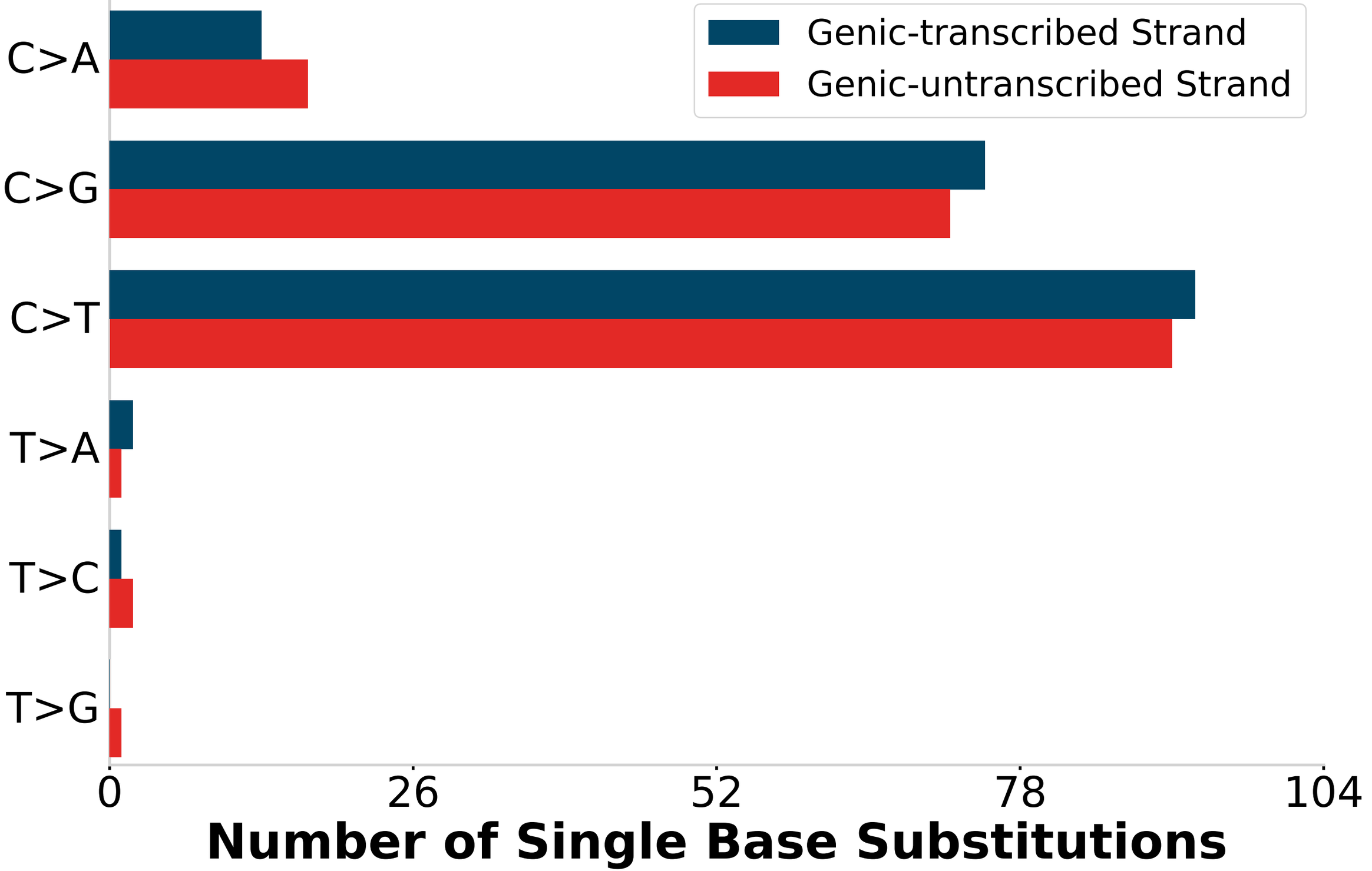
TCGA-XF-A9SG-01A-12D-A42E-08: 210 tran



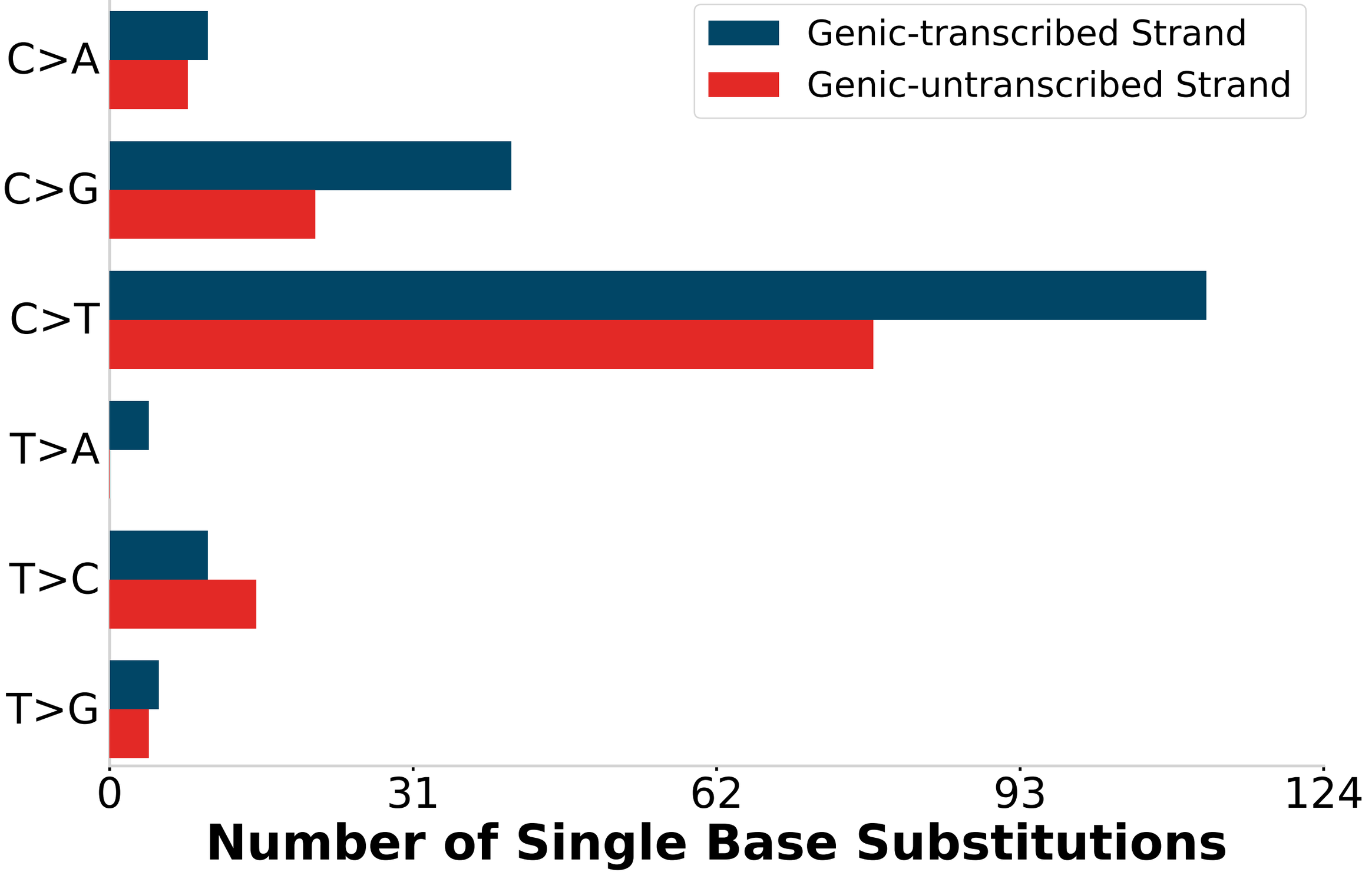
TCGA-XF-A9SH-01A-11D-A391-08: 49 trans



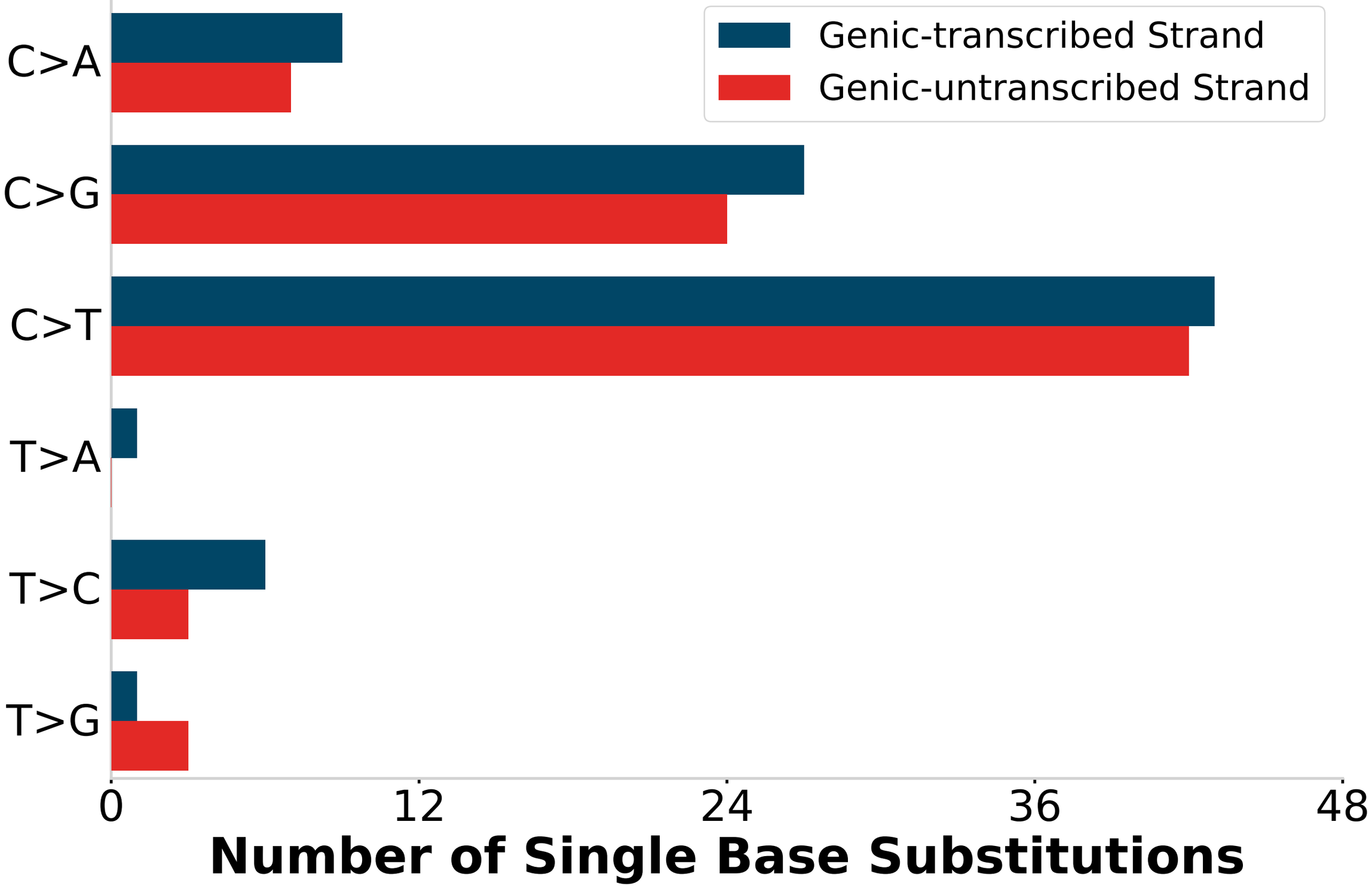
TCGA-XF-A9SI-01A-11D-A391-08: 368 tran



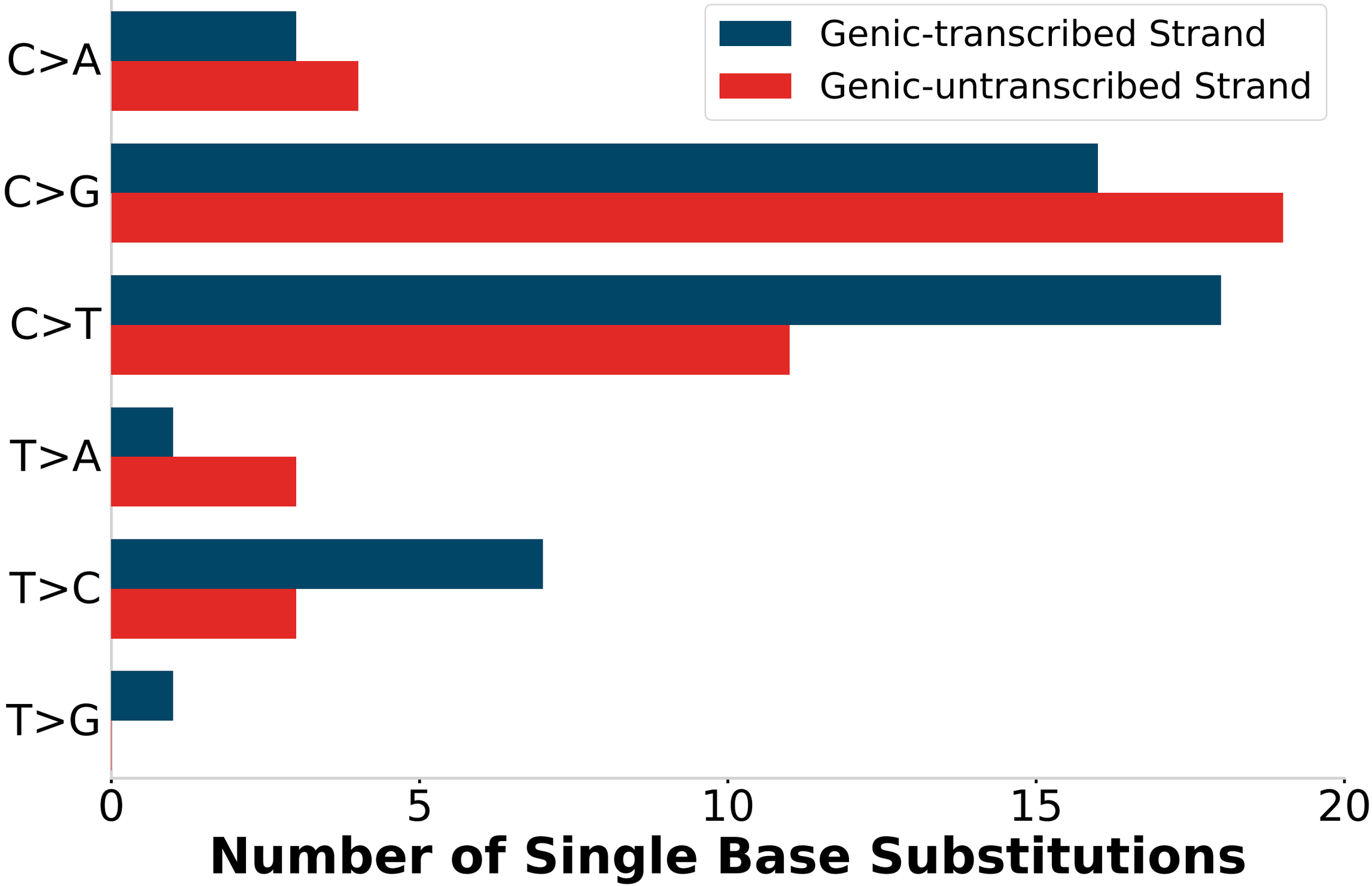
TCGA-XF-A9SJ-01A-11D-A391-08: 308 tran



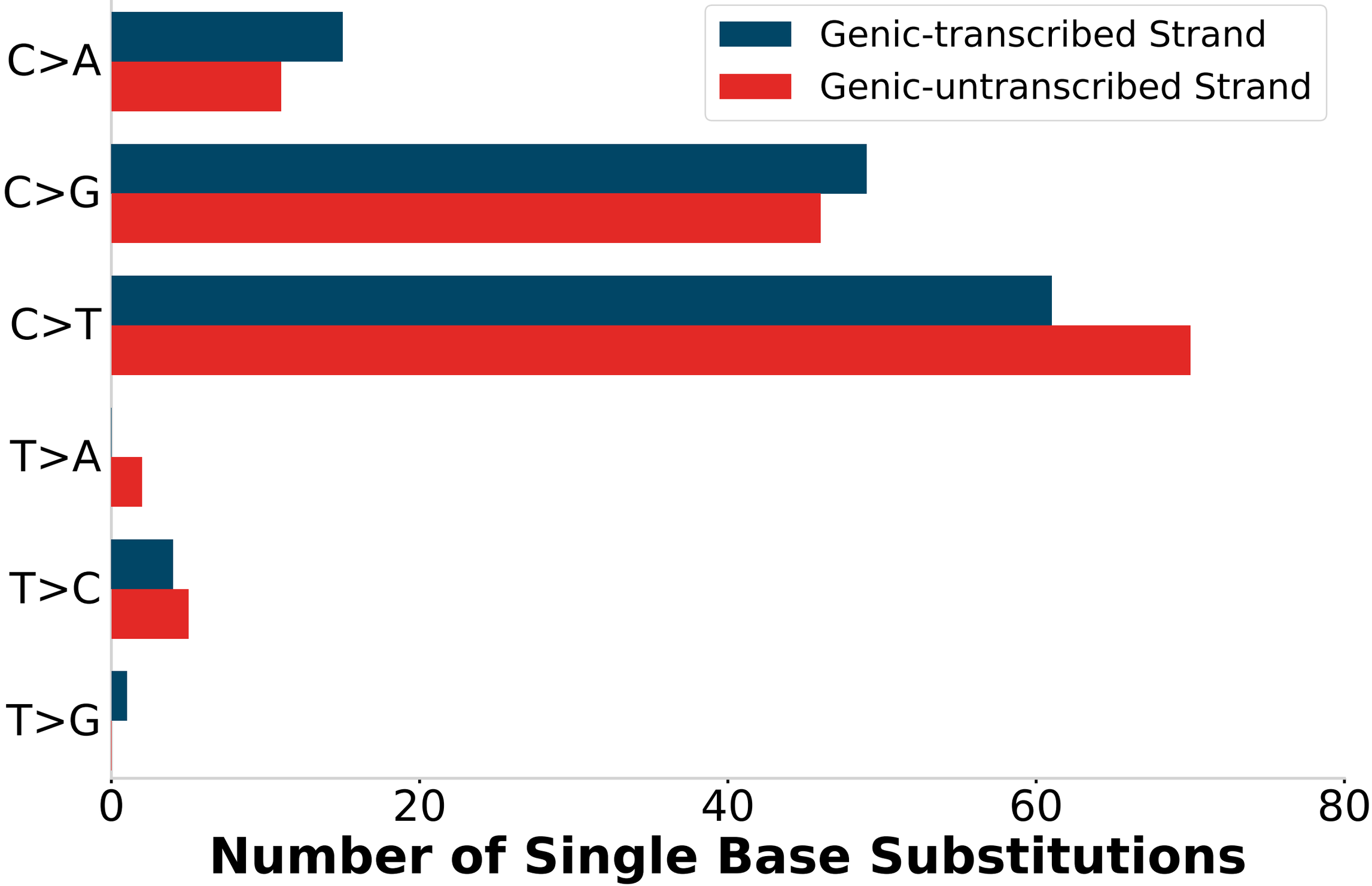
TCGA-XF-A9SK-01A-11D-A42E-08: 166 tran



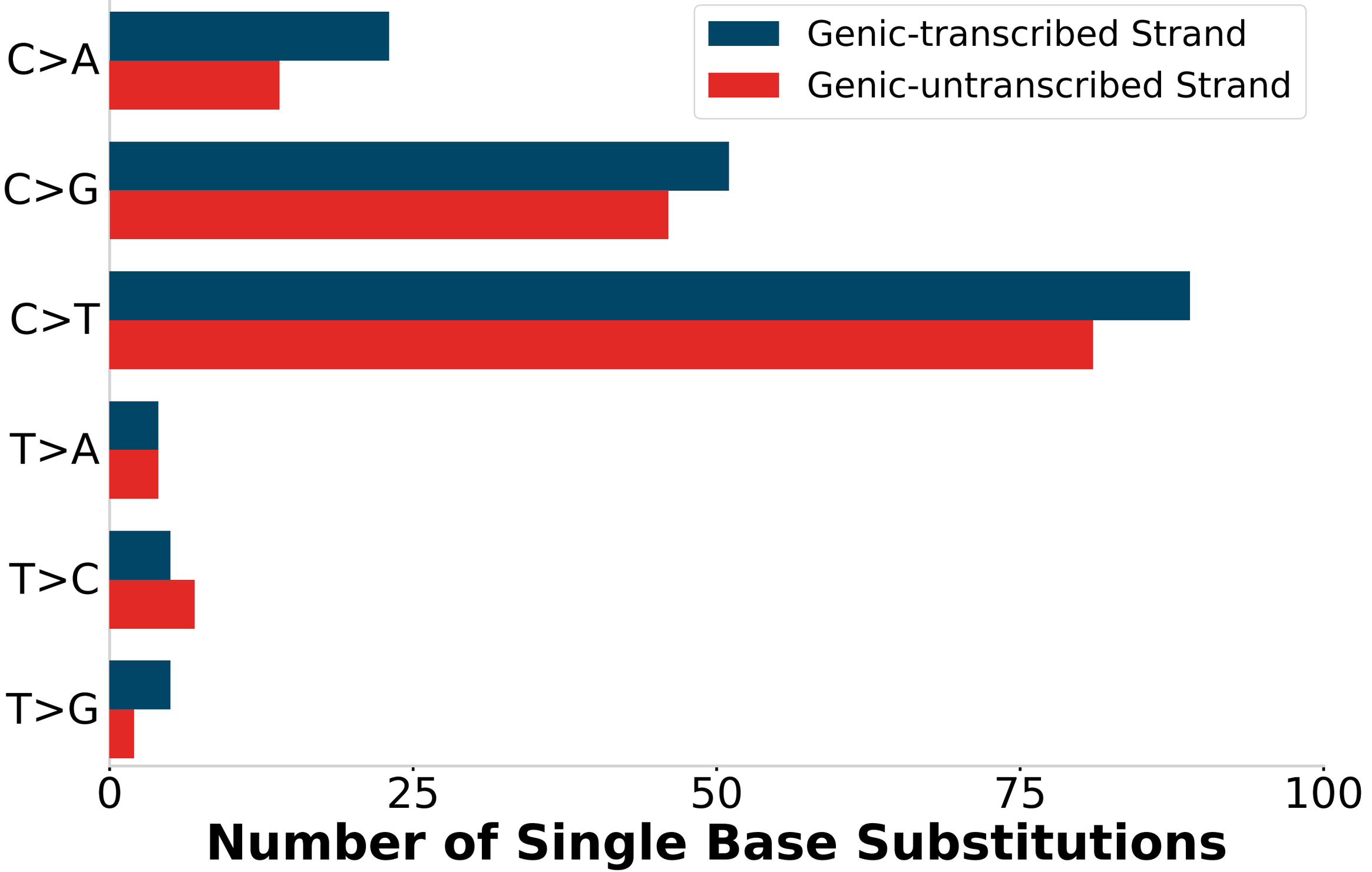
TCGA-XF-A9SL-01A-11D-A391-08: 86 trans



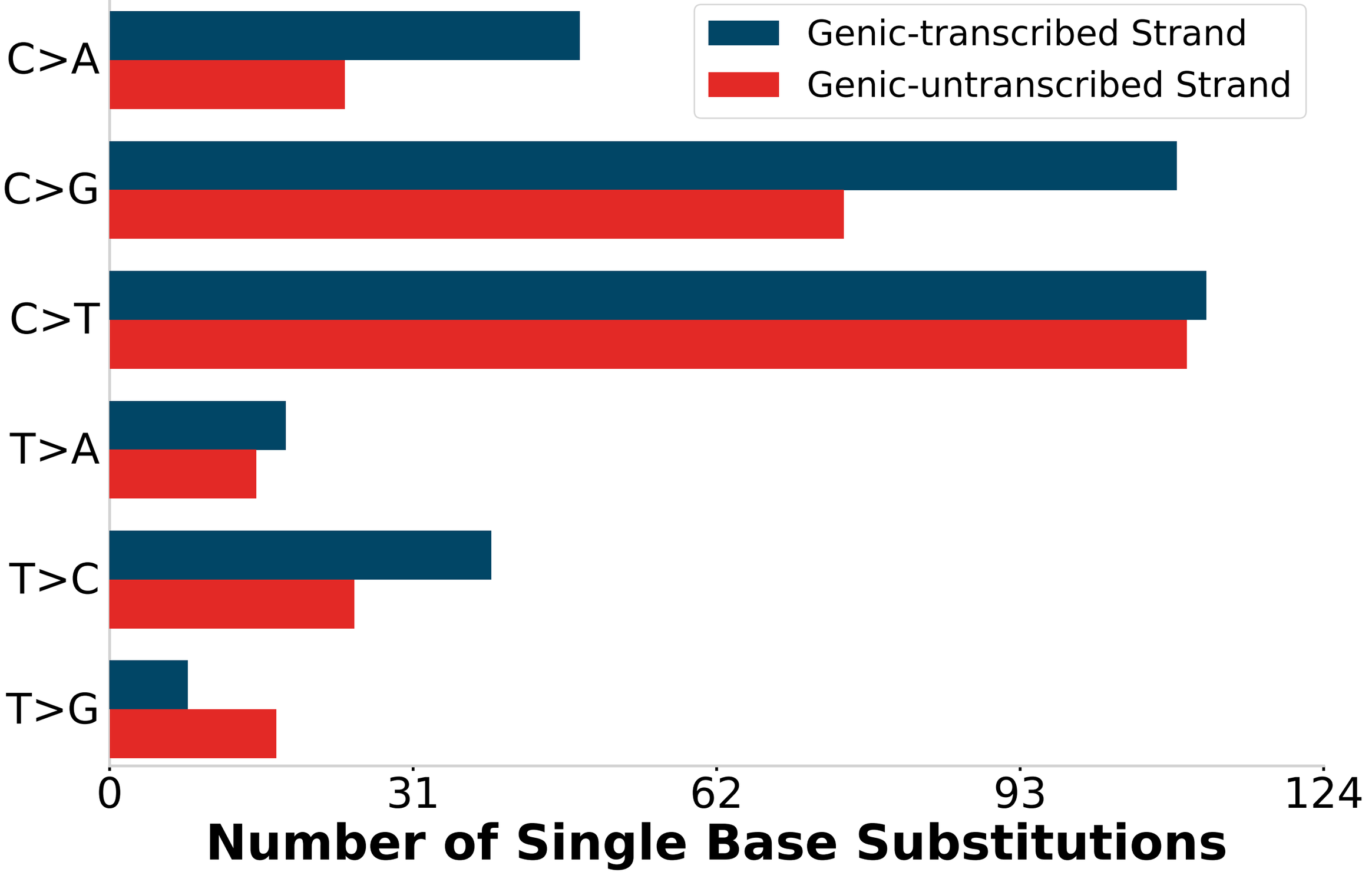
TCGA-XF-A9SM-01A-11D-A42E-08: 264 tra



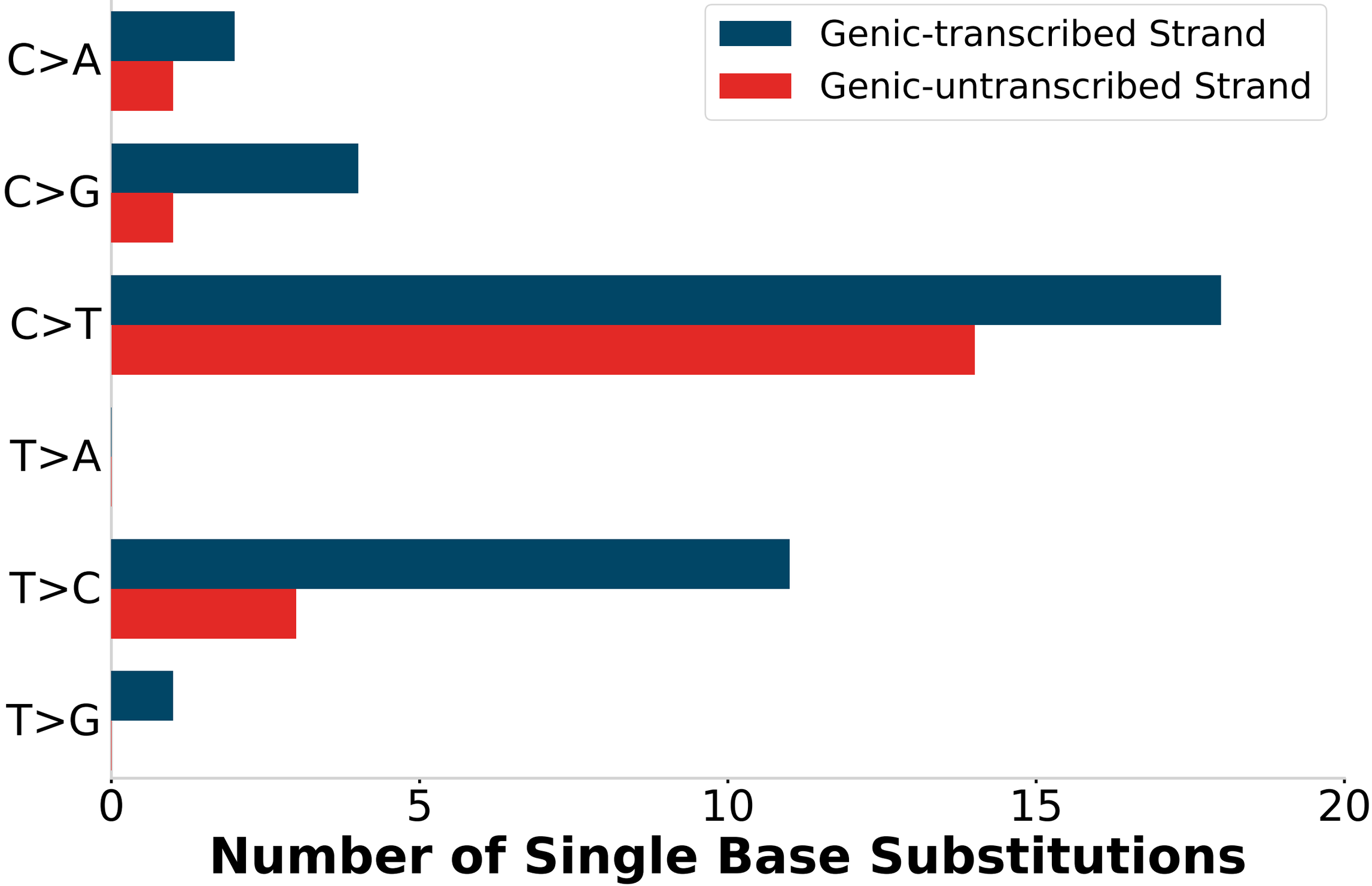
TCGA-XF-A9SP-01A-11D-A391-08: 331 tran



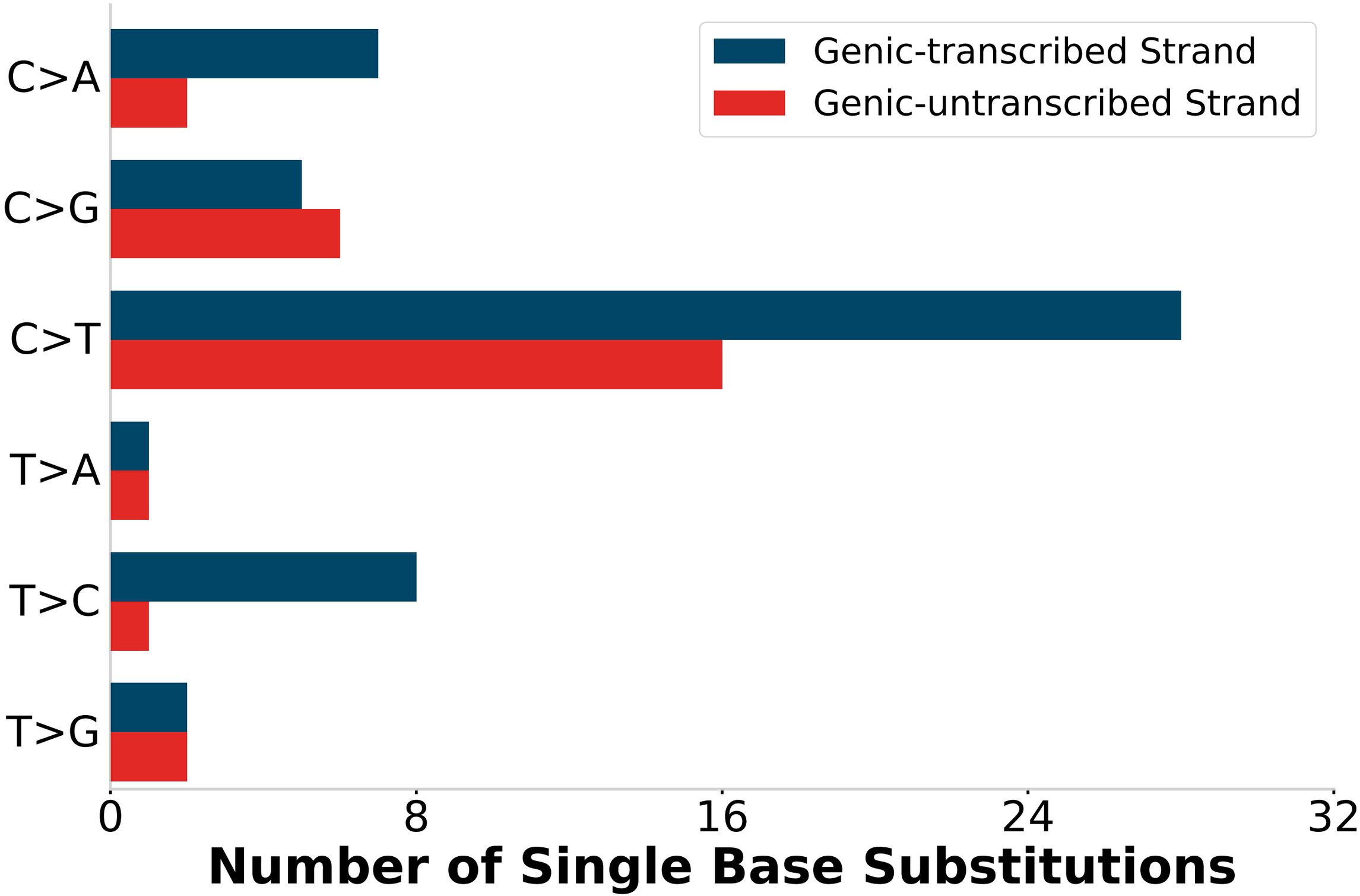
TCGA-XF-A9ST-01A-11D-A42E-08: 600 tran



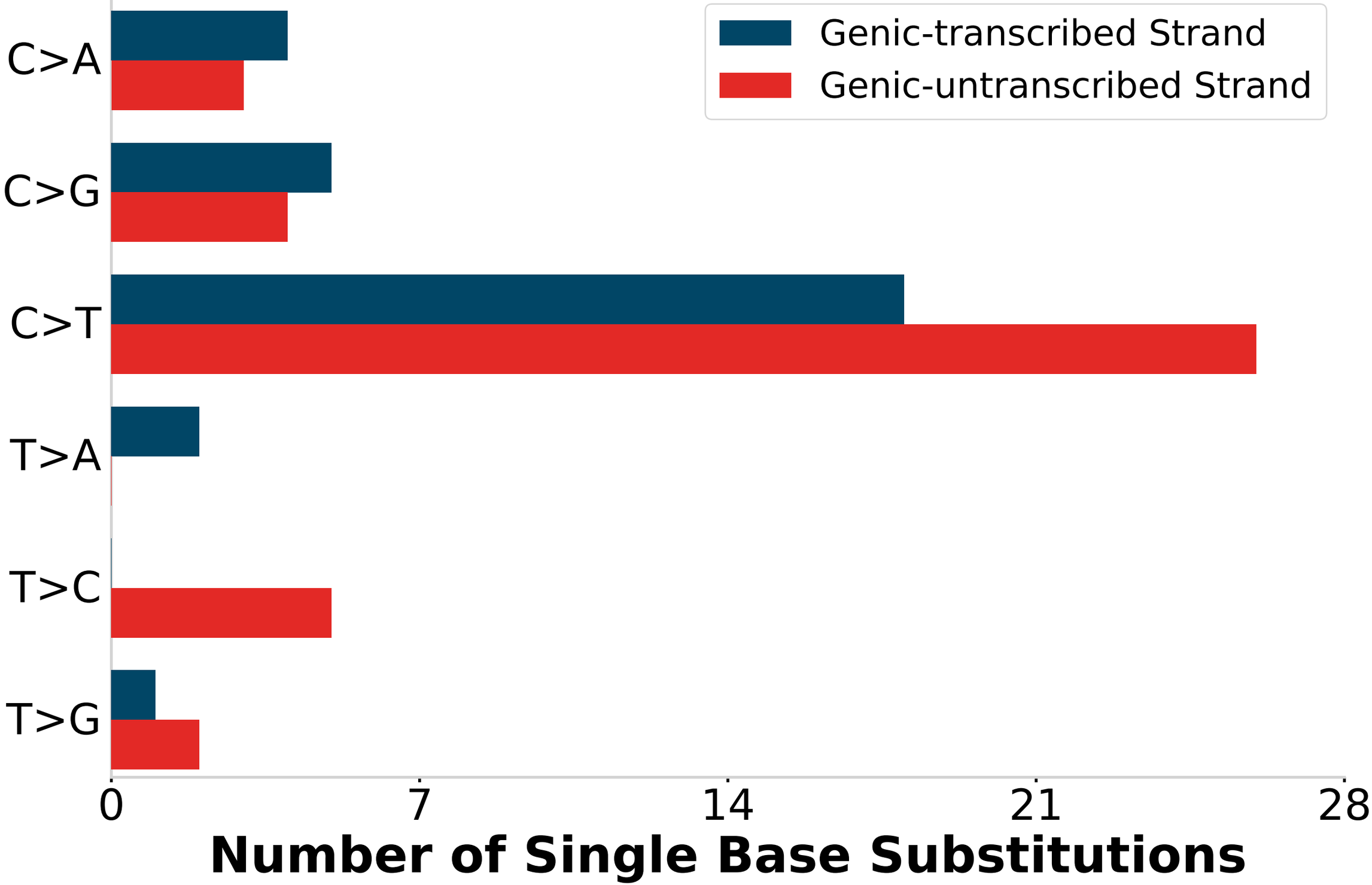
TCGA-XF-A9SU-01A-31D-A391-08: 55 trans



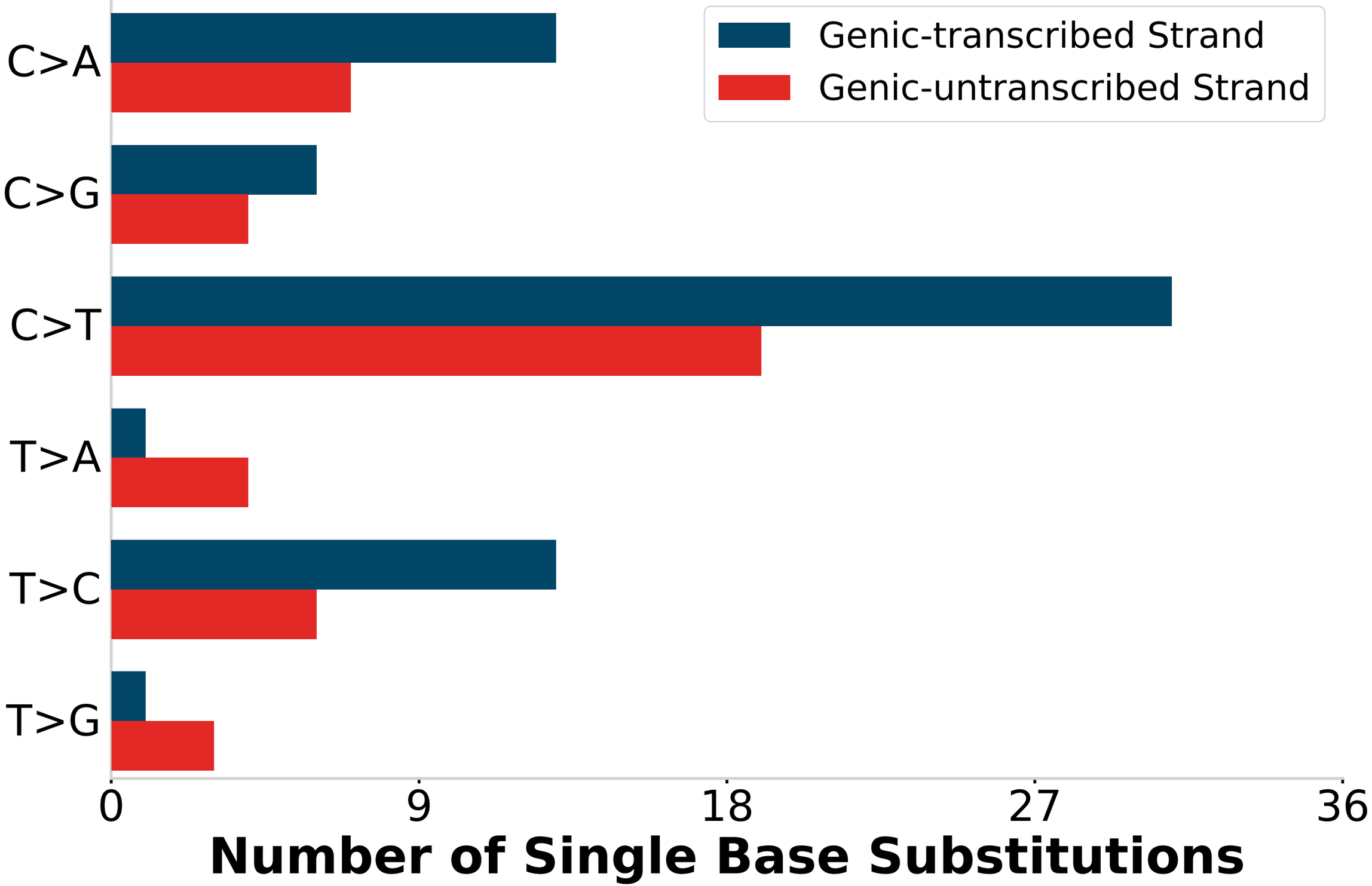
TCGA-XF-A9SV-01A-21D-A42E-08: 79 trans



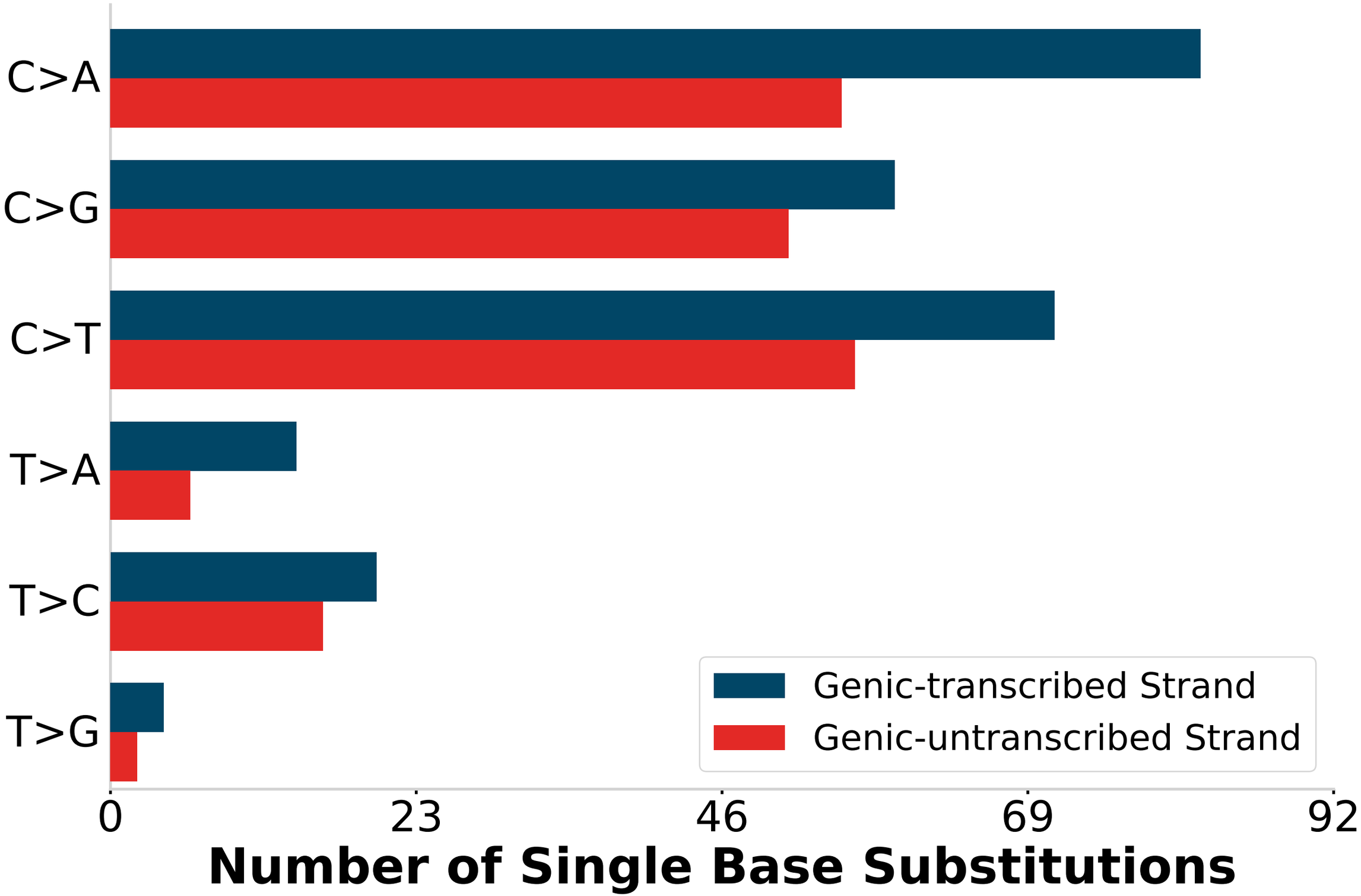
TCGA-XF-A9SW-01A-11D-A42E-08: 70 tran



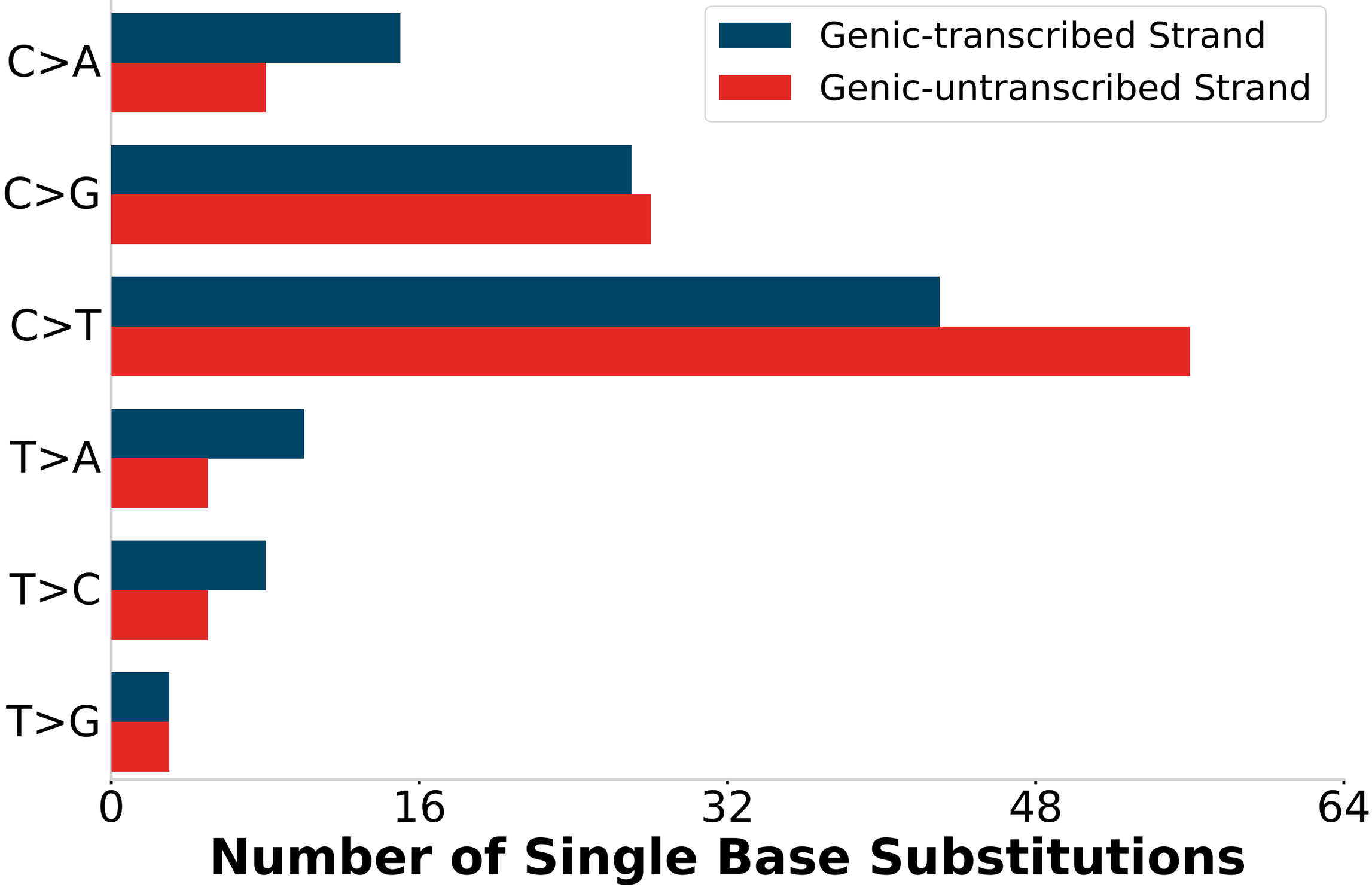
TCGA-XF-A9SX-01A-21D-A391-08: 108 tran



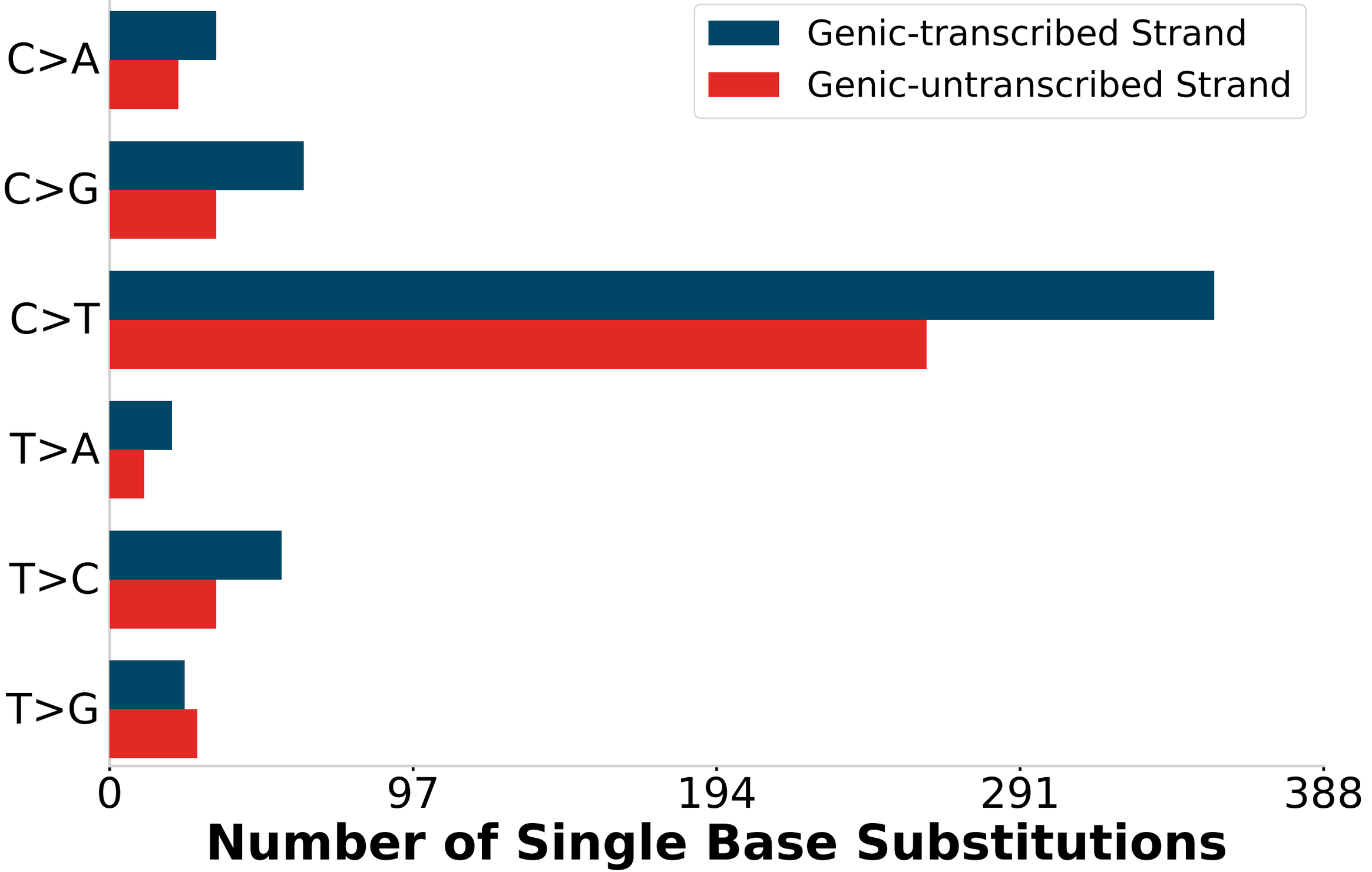
TCGA-XF-A9SY-01A-21D-A42E-08: 436 tran



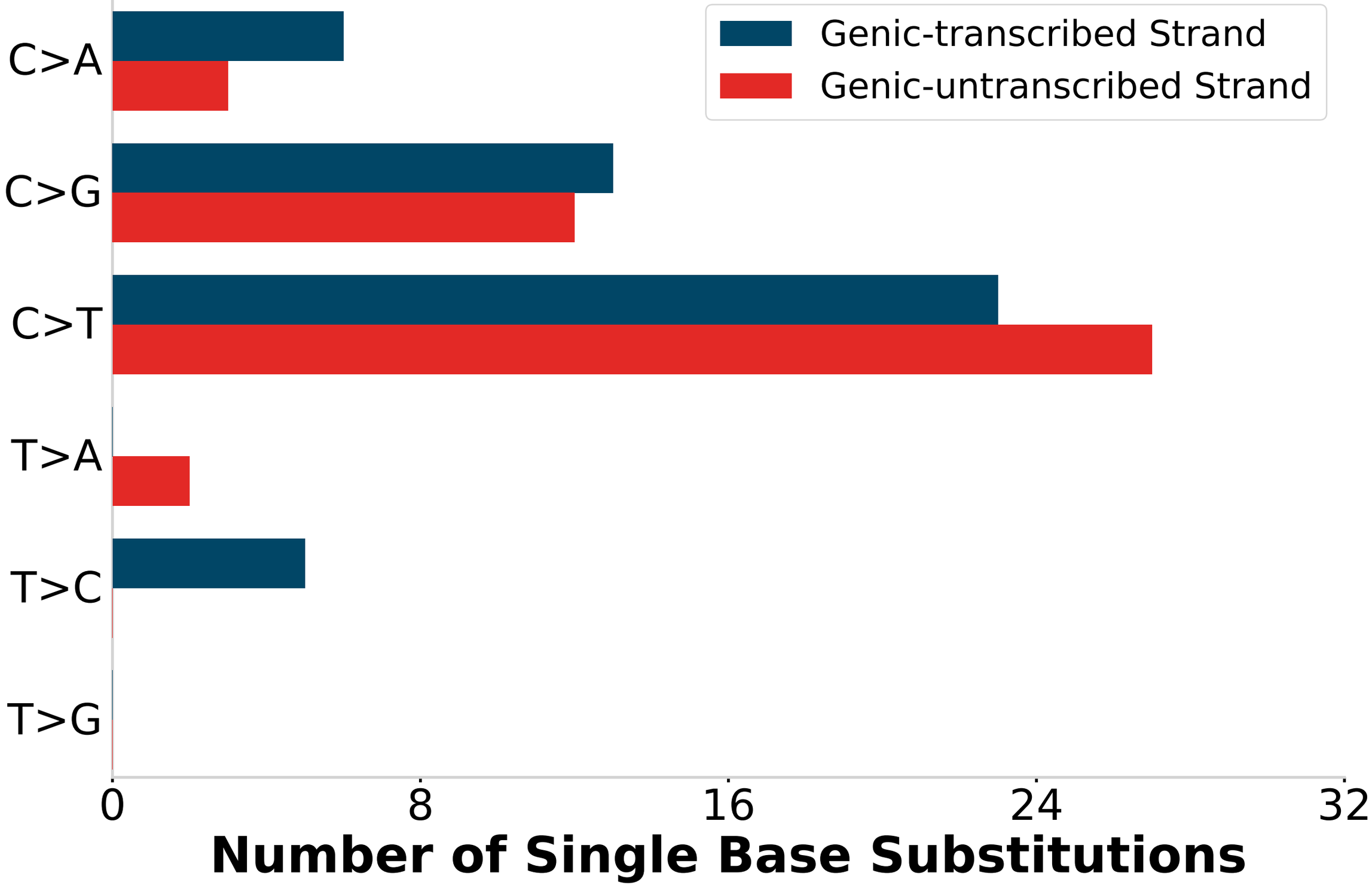
TCGA-XF-A9SZ-01A-11D-A391-08: 211 tran



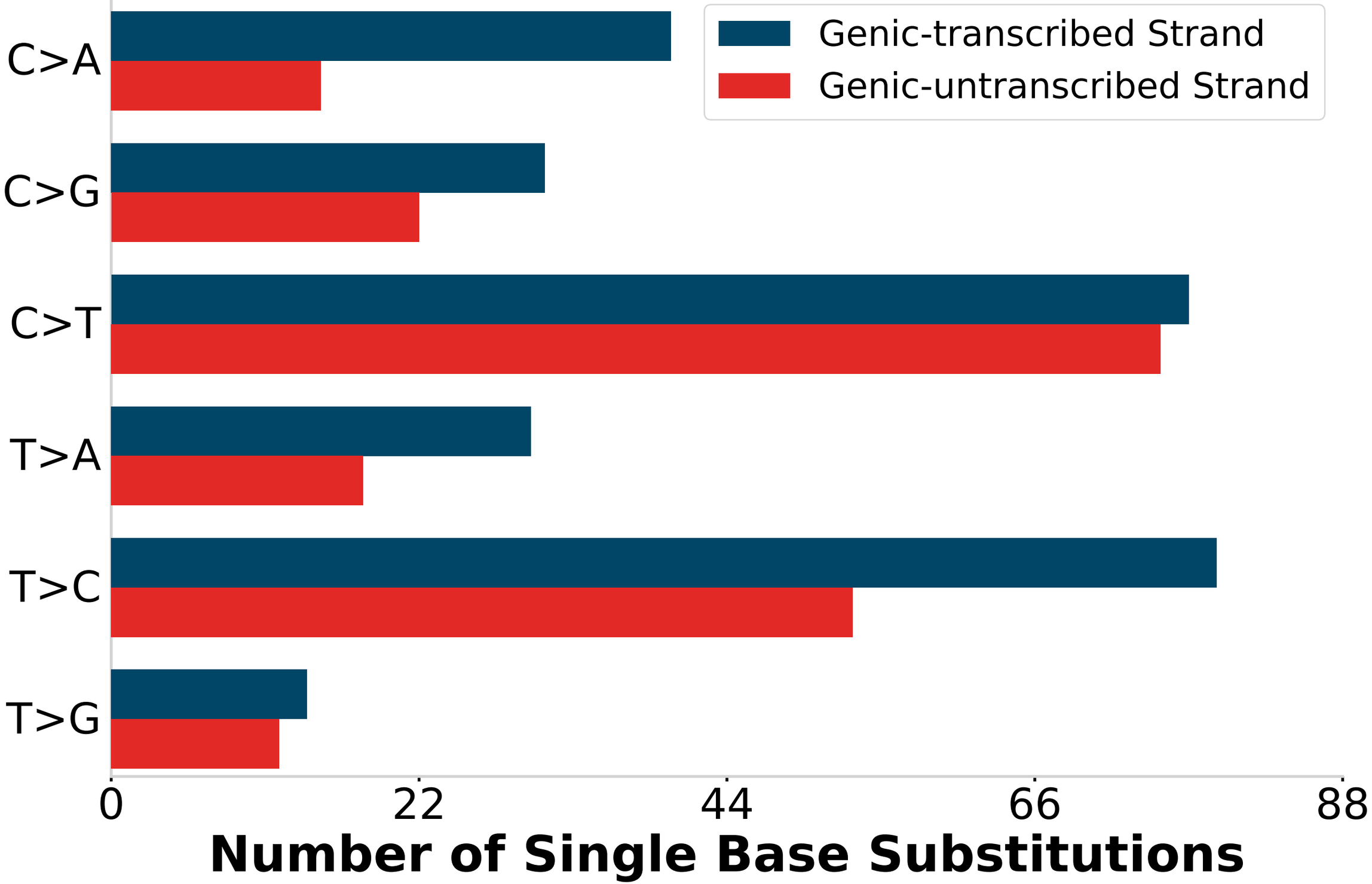
TCGA-XF-A9T0-01A-11D-A391-08: 938 tran



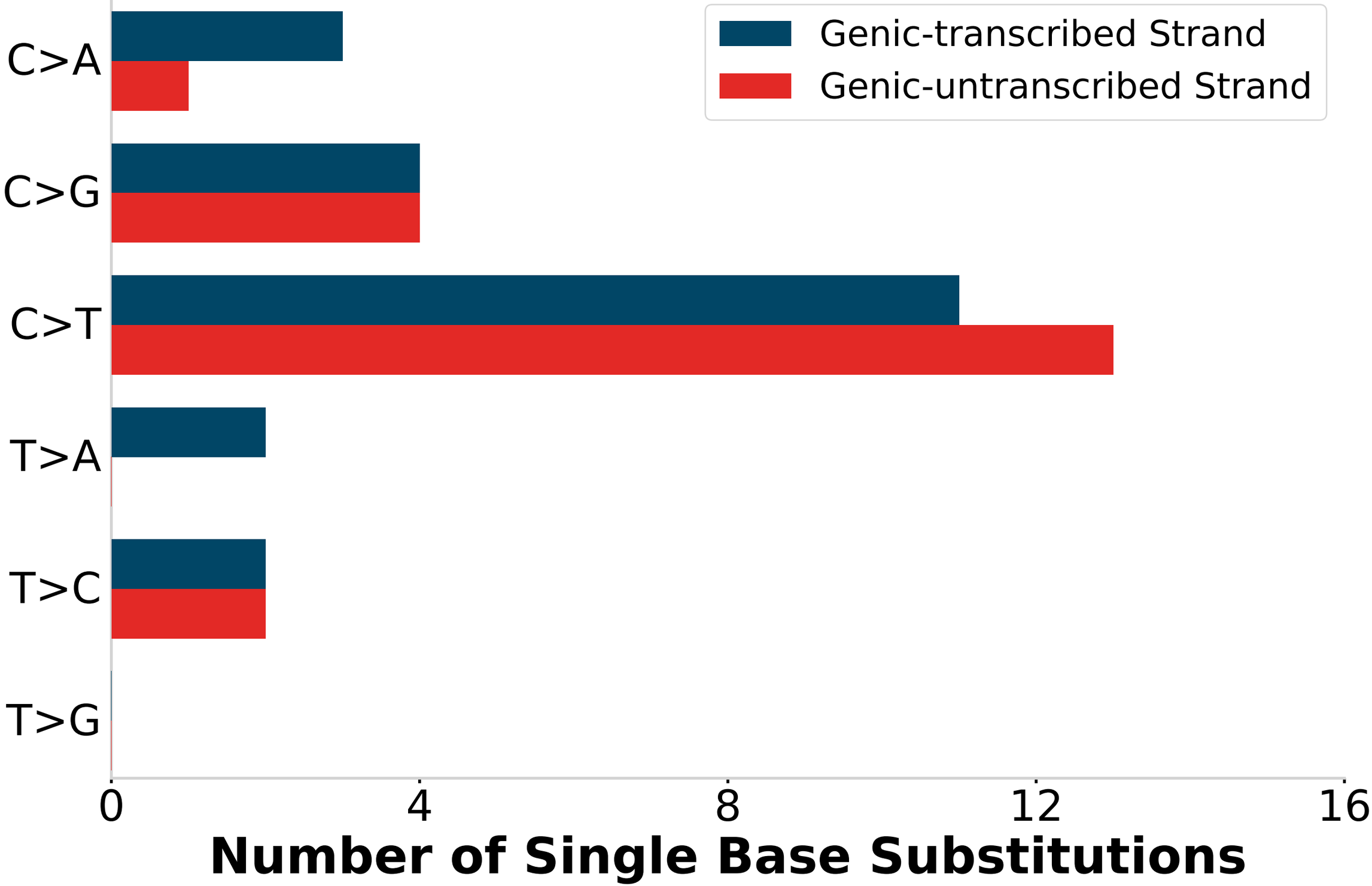
TCGA-XF-A9T2-01A-11D-A42E-08: 91 trans



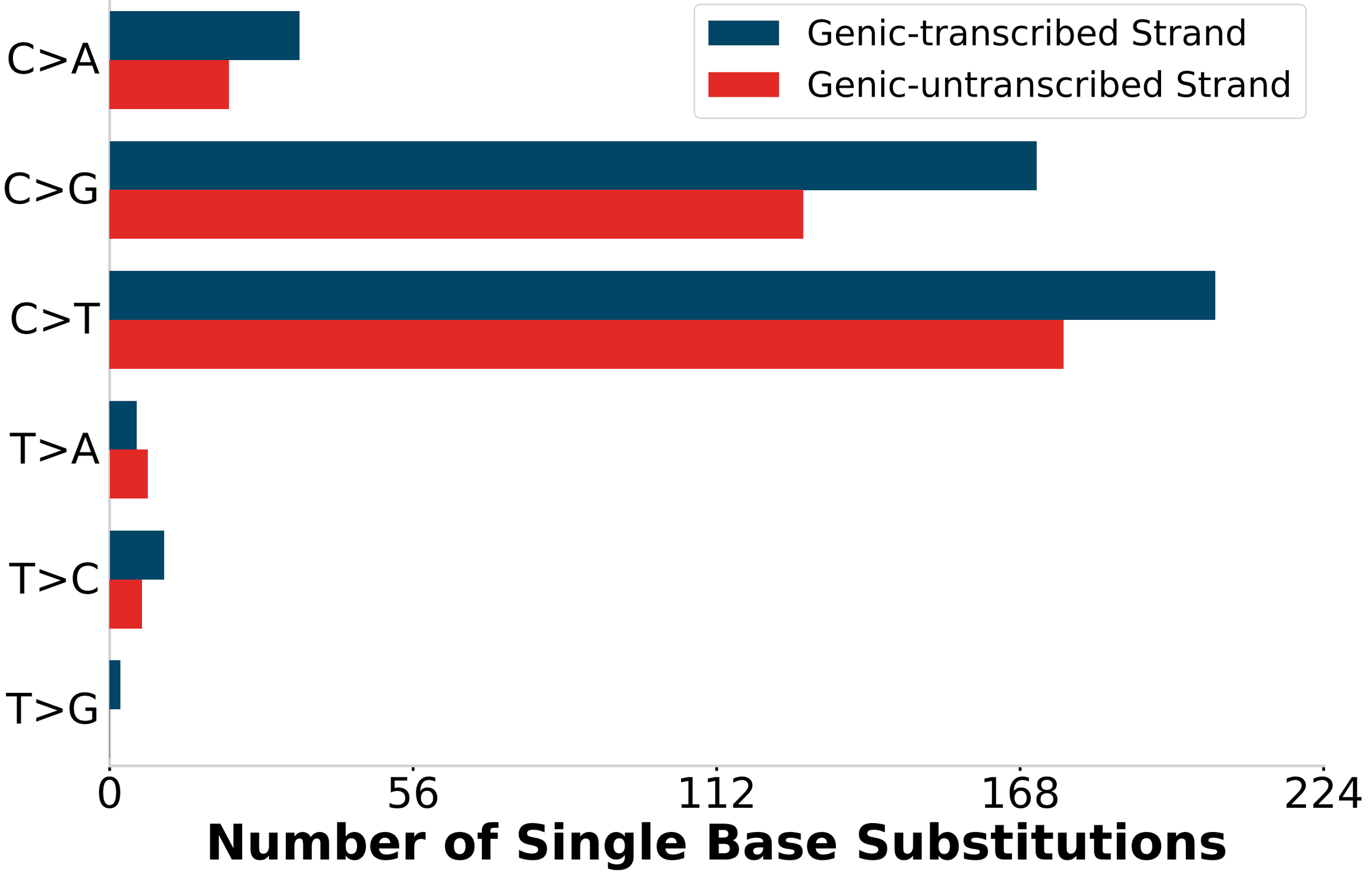
TCGA-XF-A9T3-01A-11D-A42E-08: 466 tran



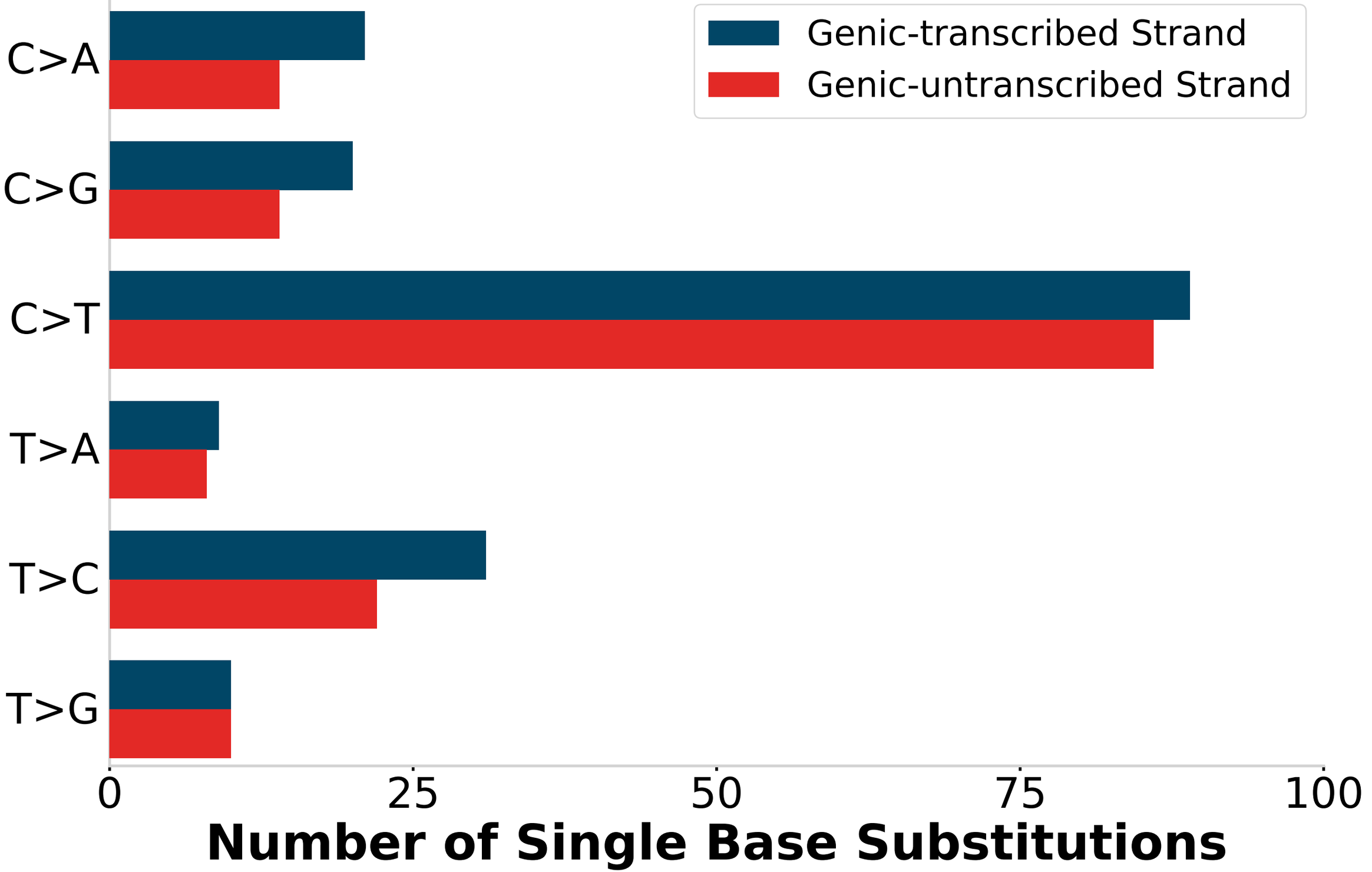
TCGA-XF-A9T4-01A-11D-A391-08: 42 trans



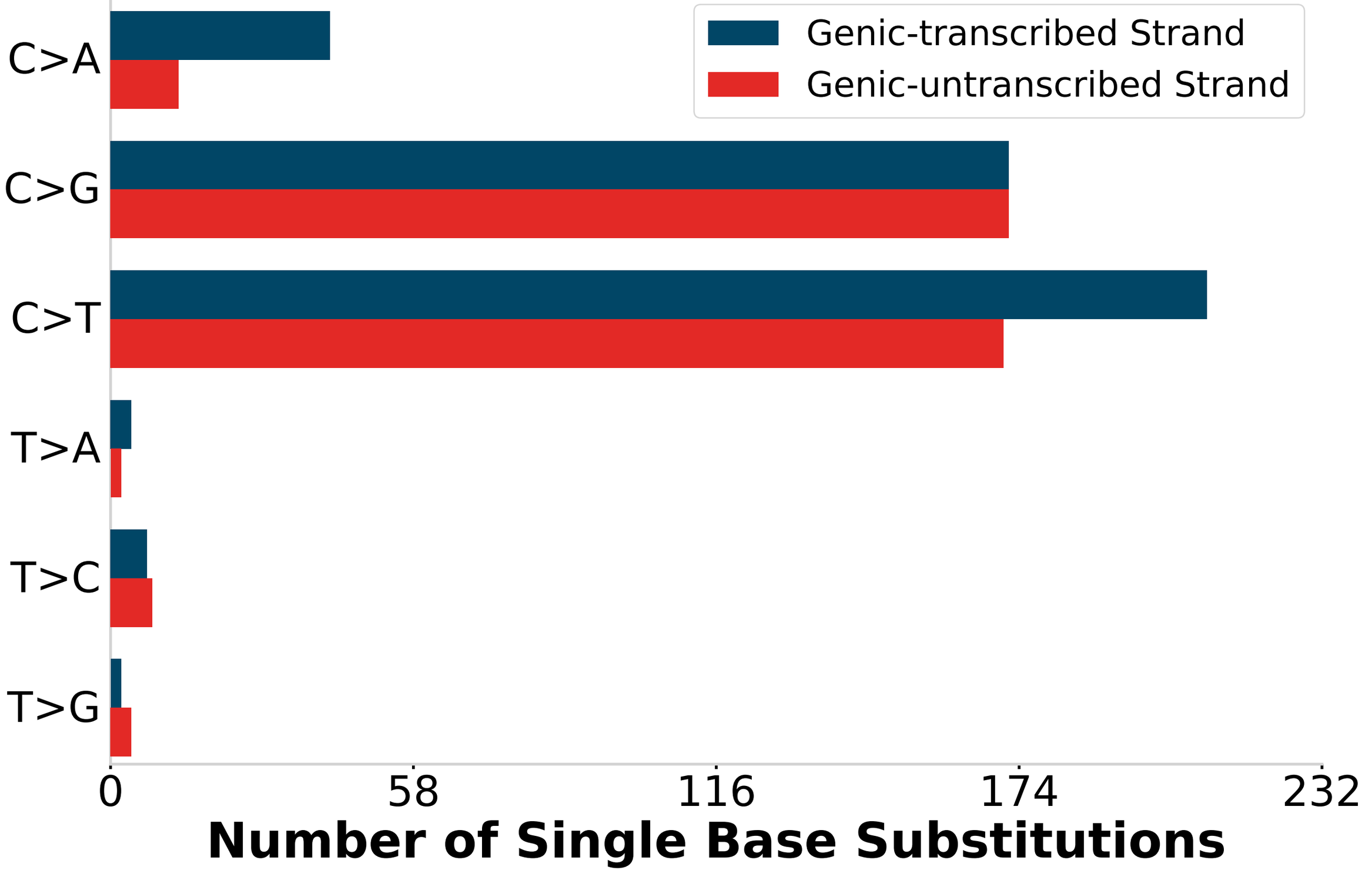
TCGA-XF-A9T5-01A-11D-A42E-08: 766 tran



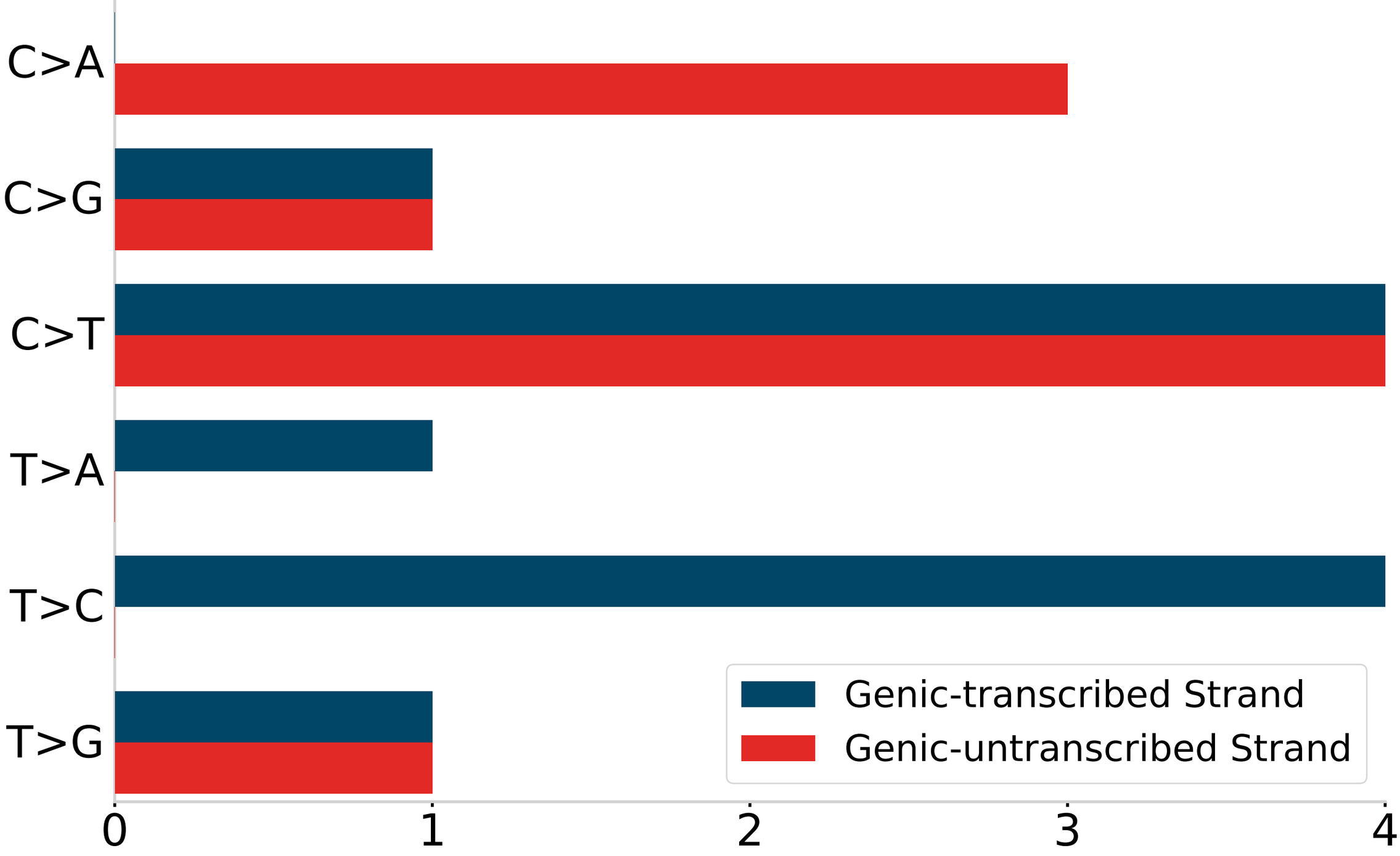
TCGA-XF-A9T6-01A-11D-A42E-08: 334 tran



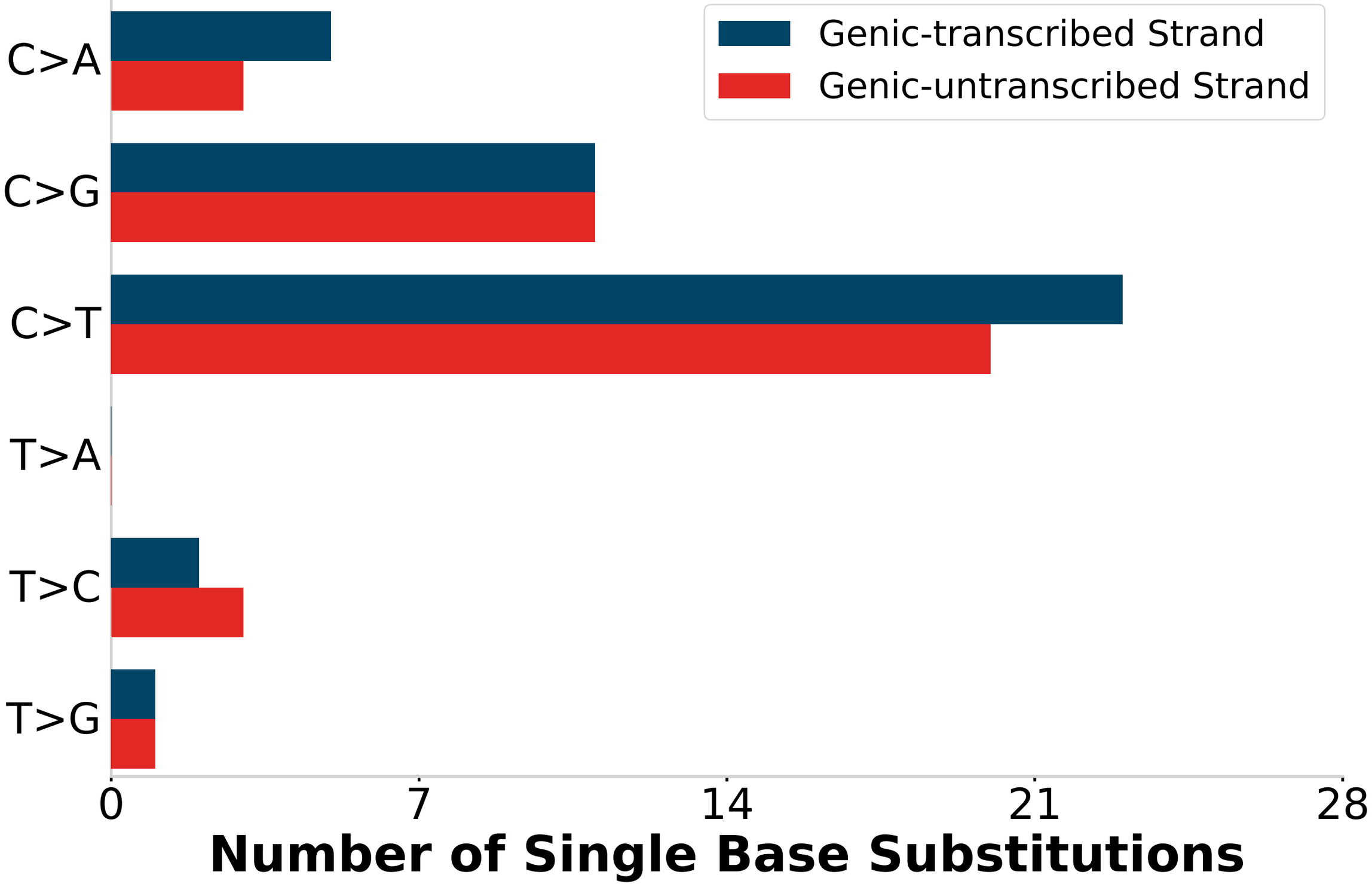
TCGA-XF-A9T8-01A-11D-A391-08: 807 tran



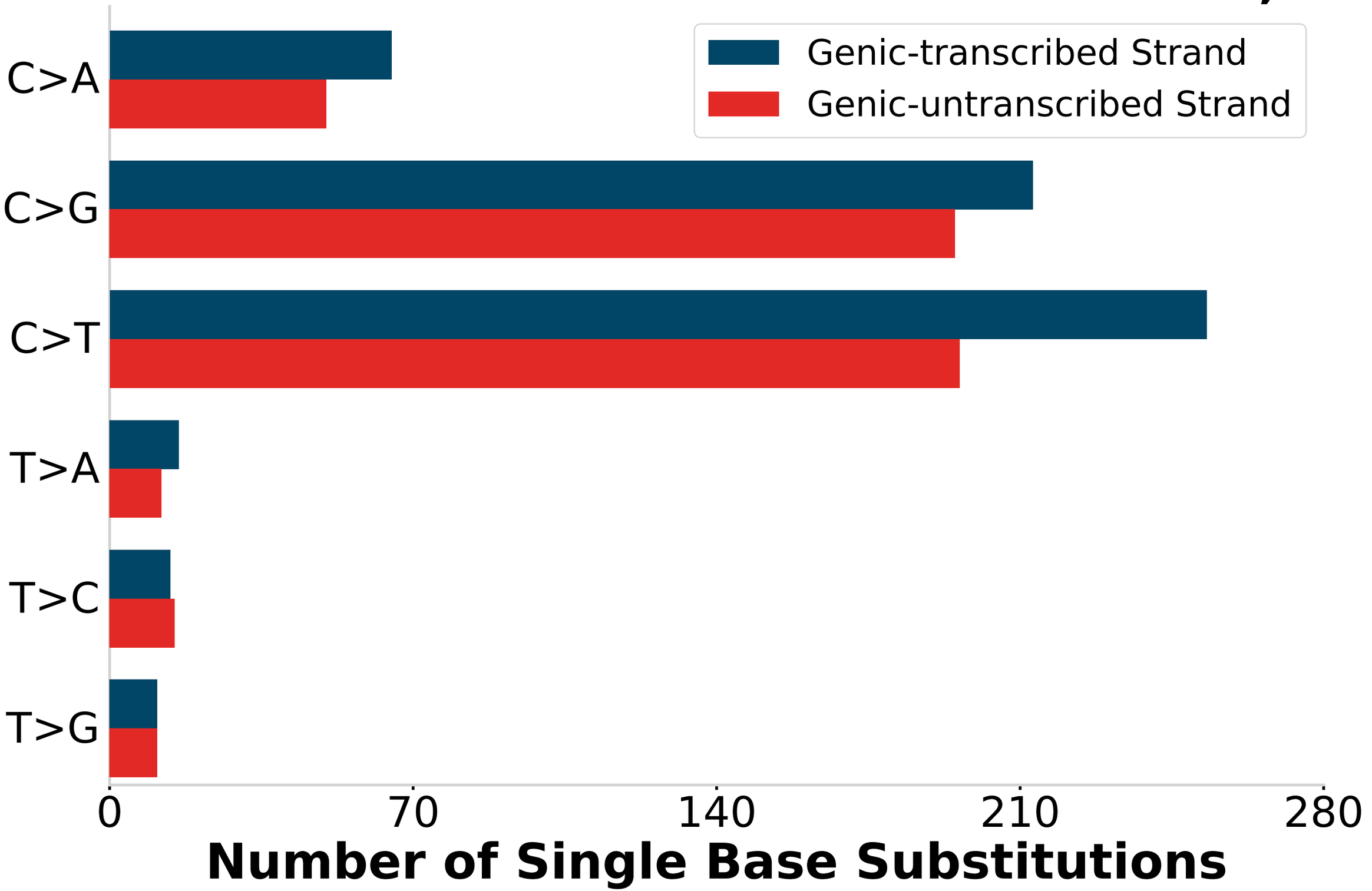
TCGA-XF-AAME-01A-12D-A42E-08: 20 tran



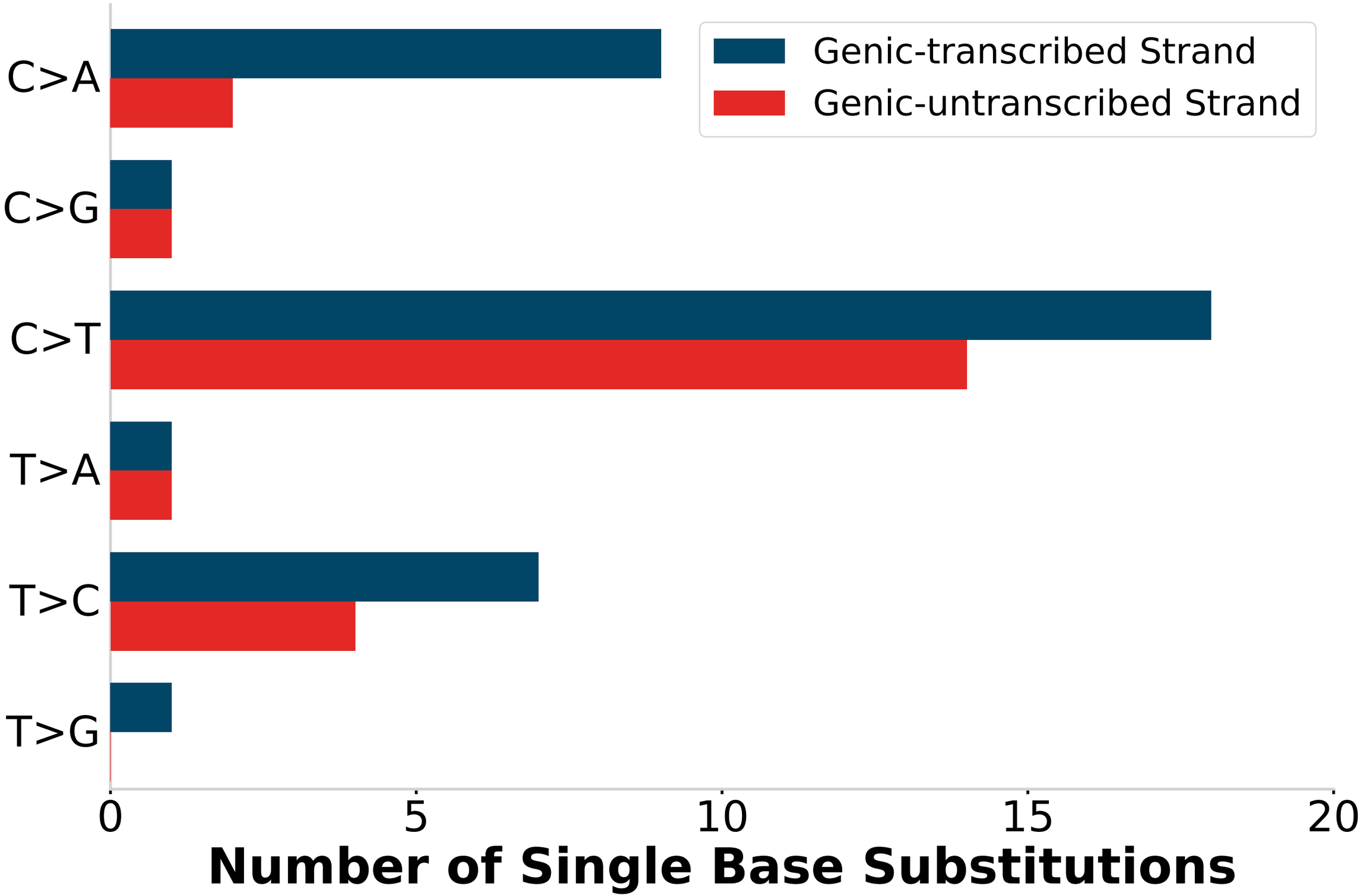
TCGA-XF-AAMF-01A-21D-A42E-08: 80 trans



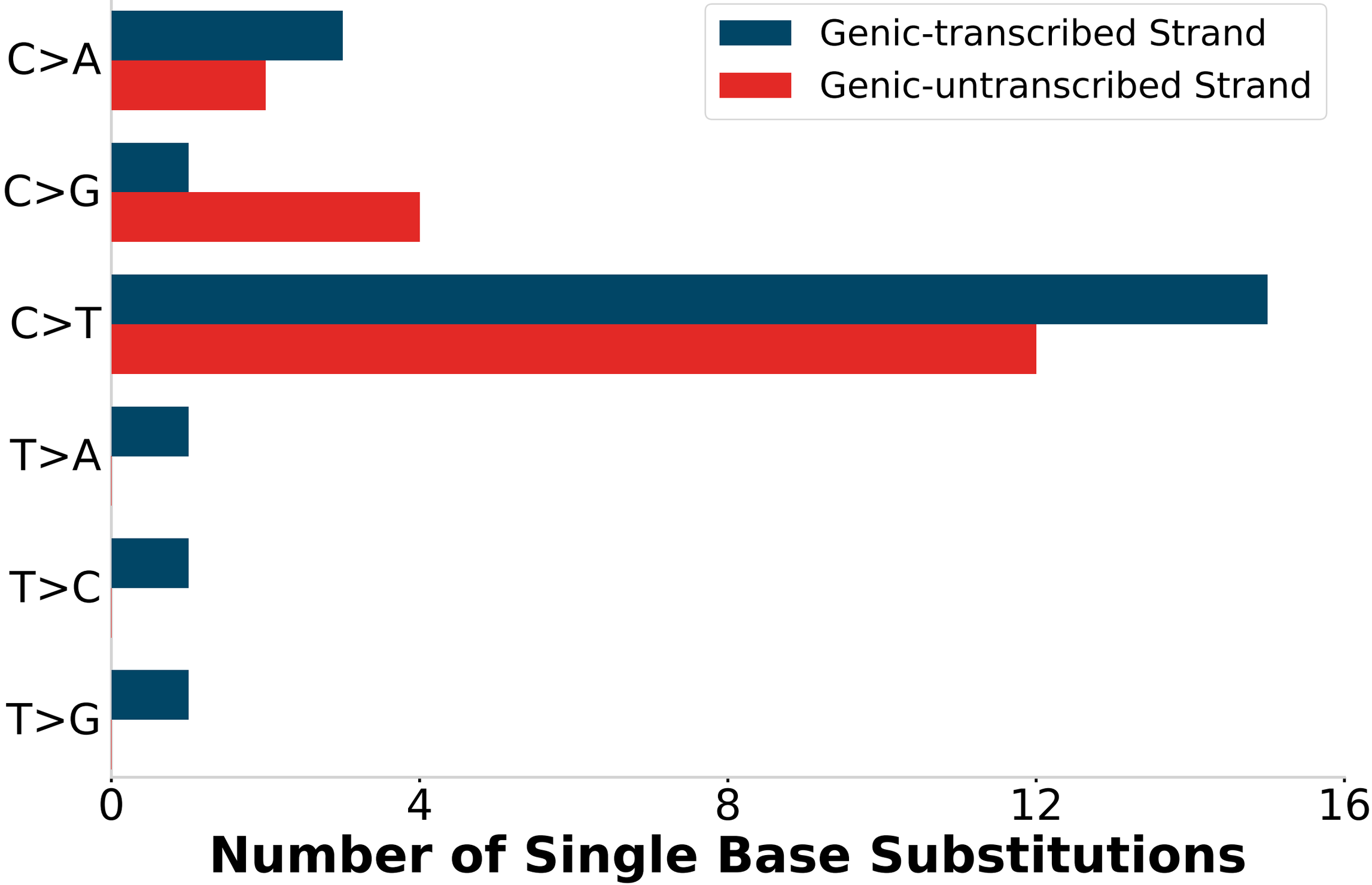
TCGA-XF-AAMG-01A-11D-A42E-08: 1,051 t



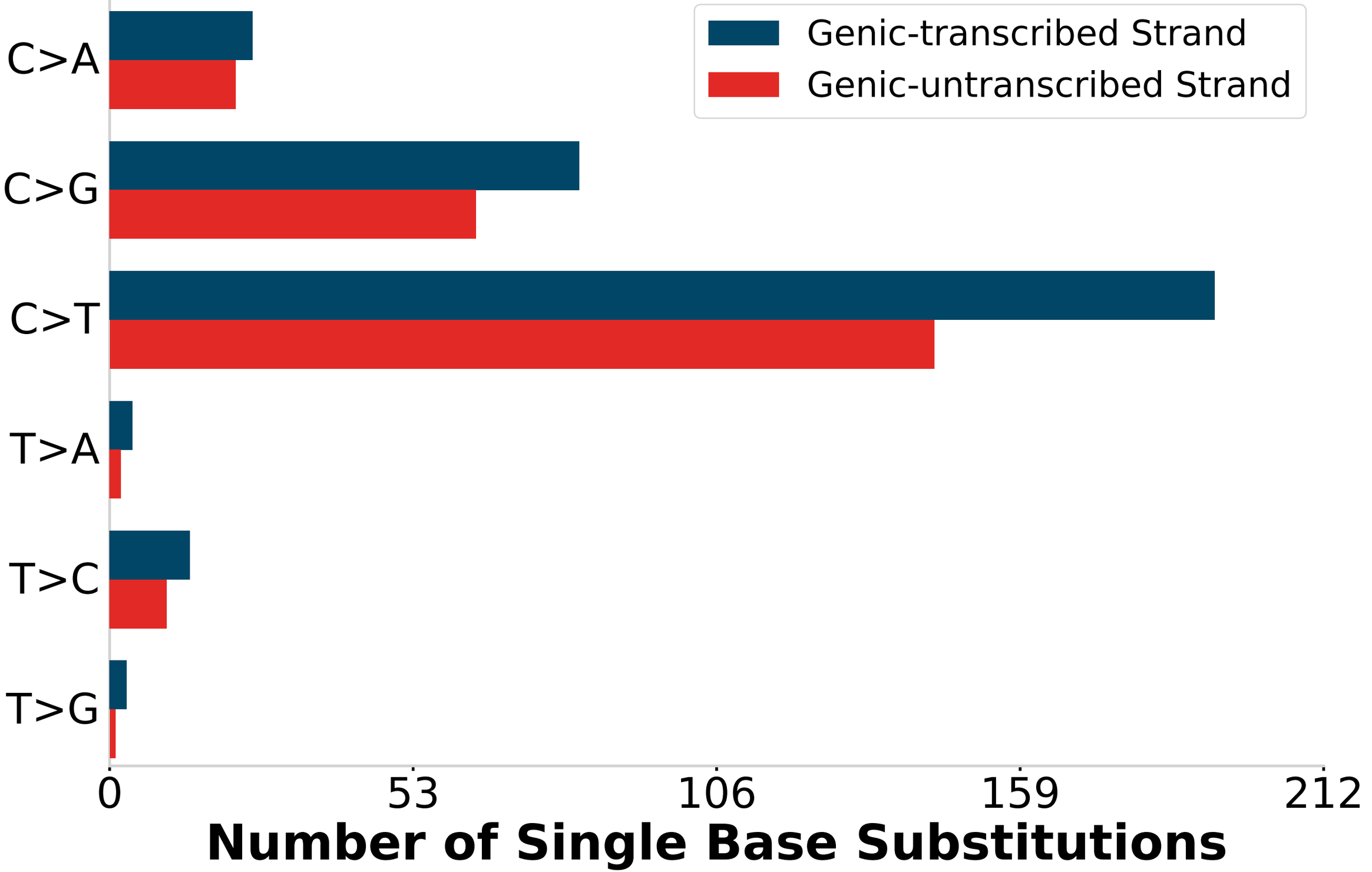
TCGA-XF-AAMH-01A-11D-A42E-08: 59 tran



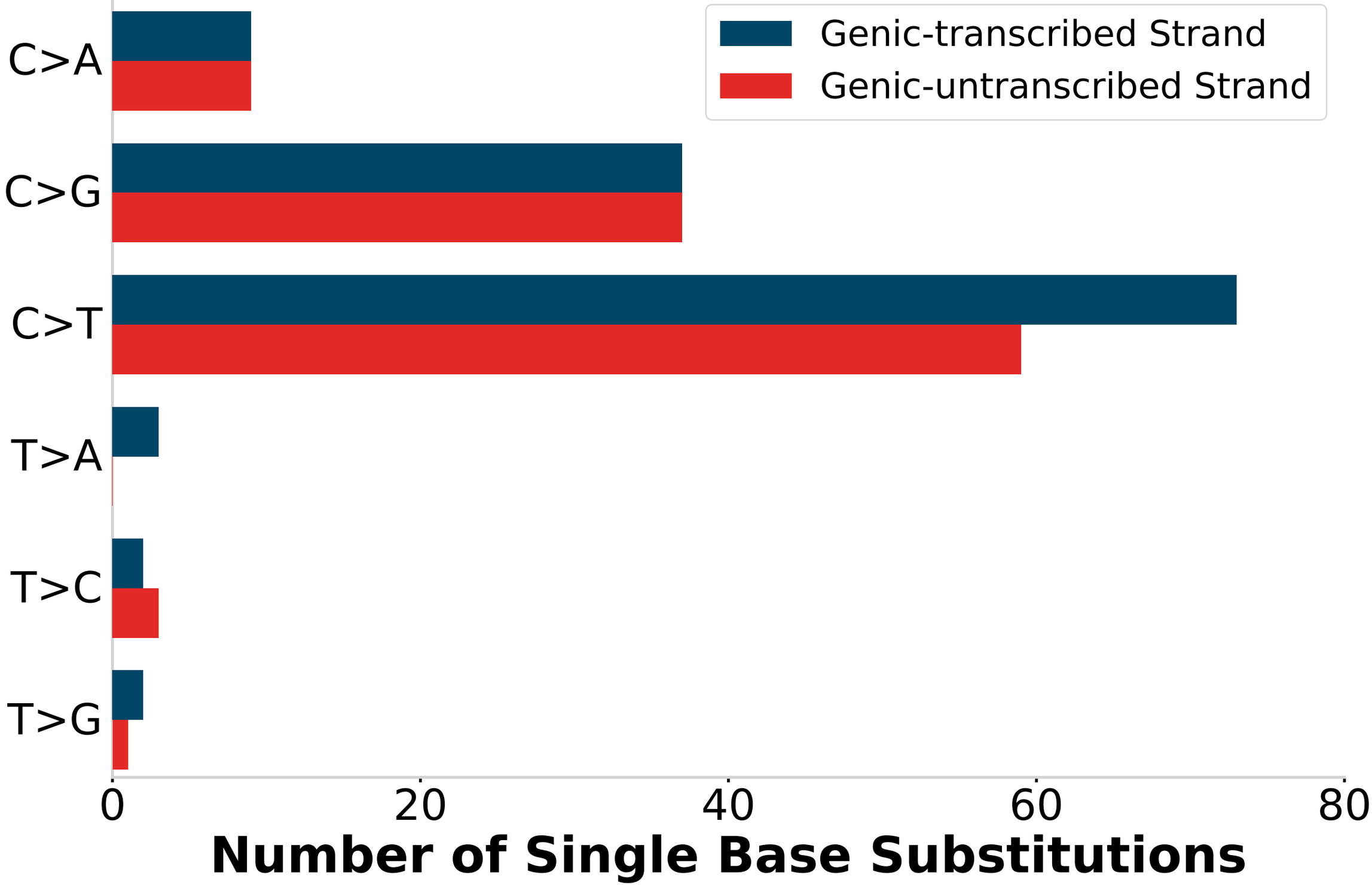
TCGA-XF-AAMJ-01A-11D-A42E-08: 40 trans



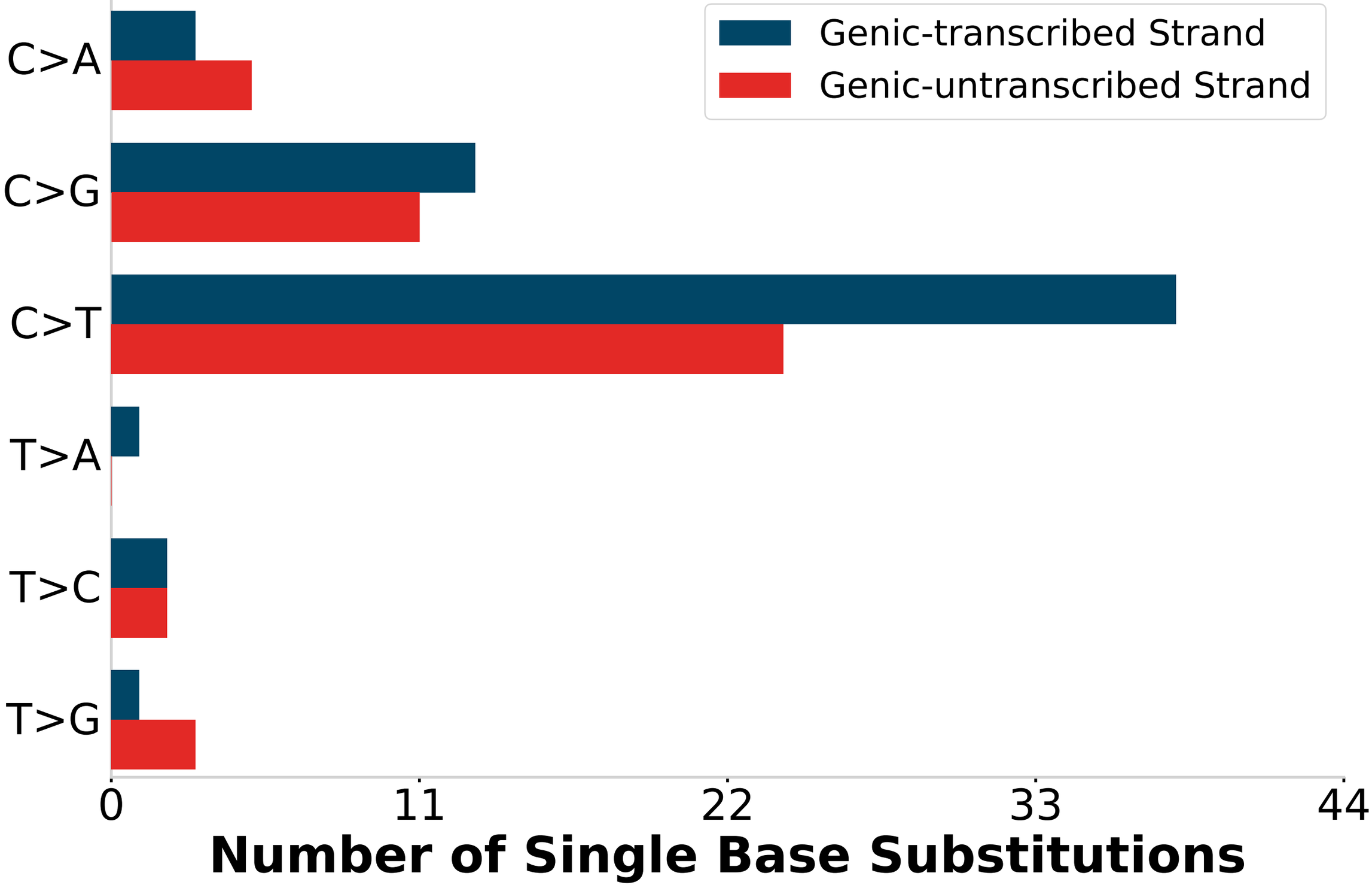
TCGA-XF-AAML-01A-11D-A42E-08: 564 tra



TCGA-XF-AAMQ-01A-11D-A42E-08: 235 tra



TCGA-XF-AAMR-01A-31D-A42E-08: 103 tra



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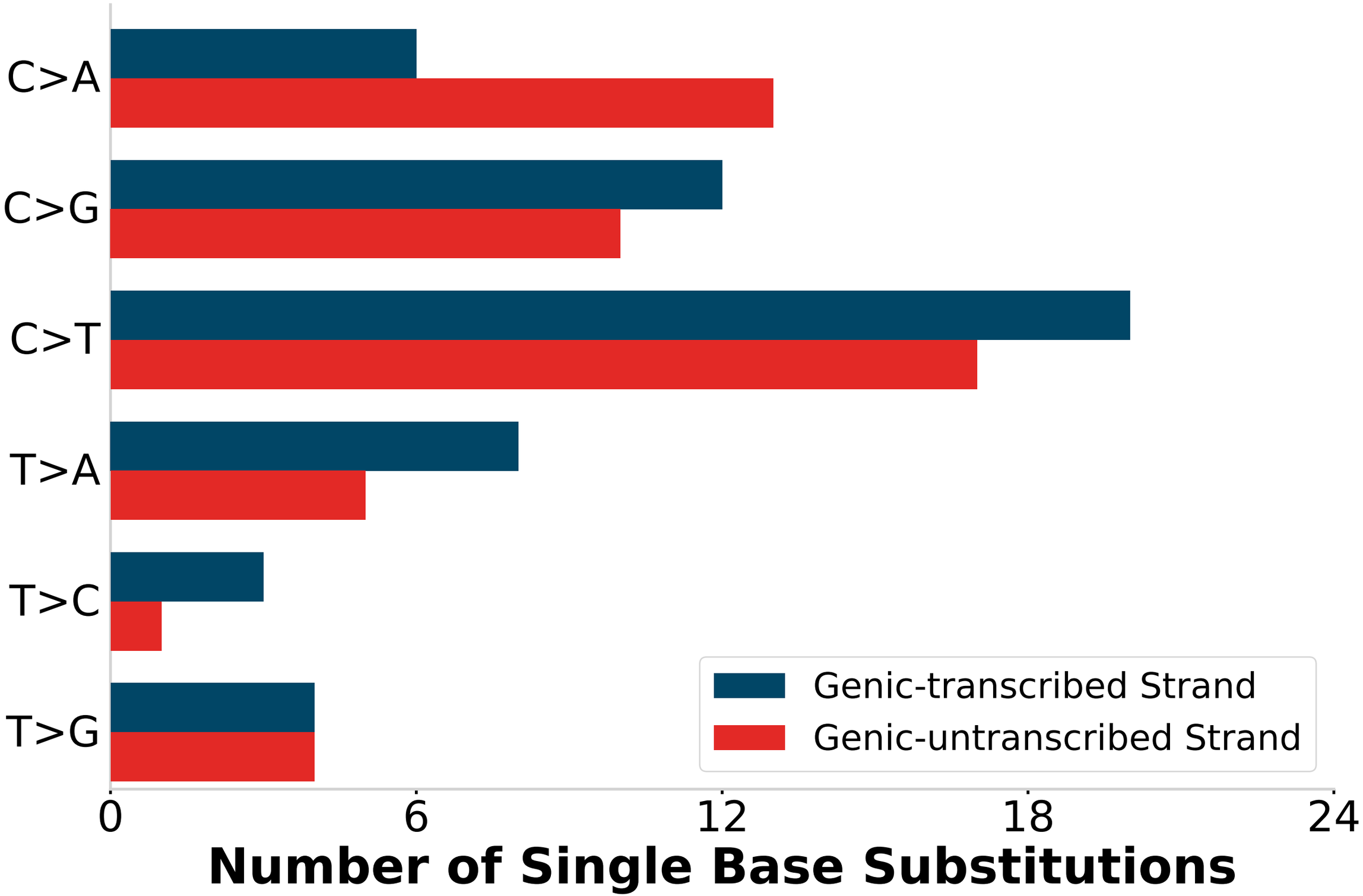
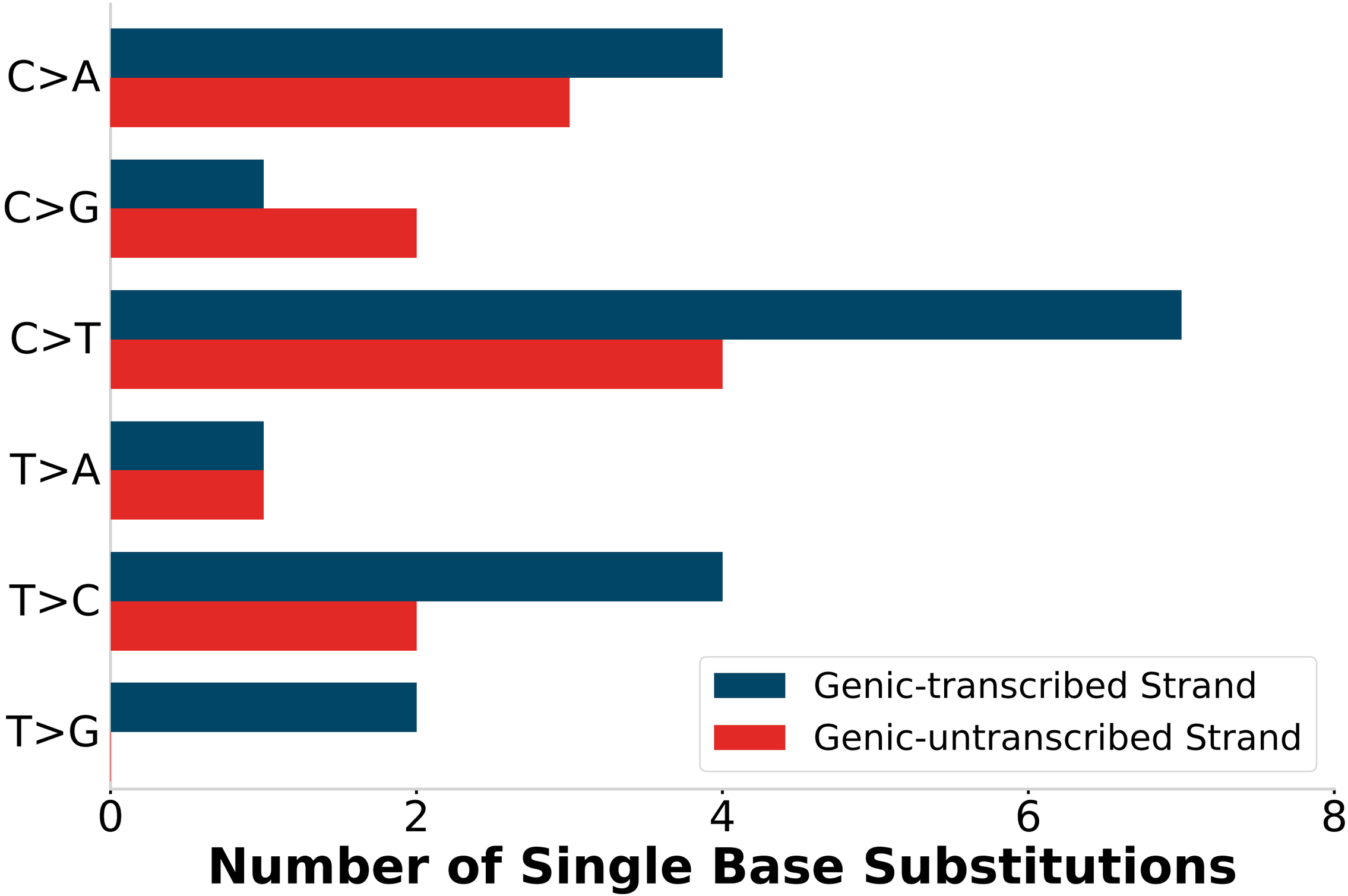
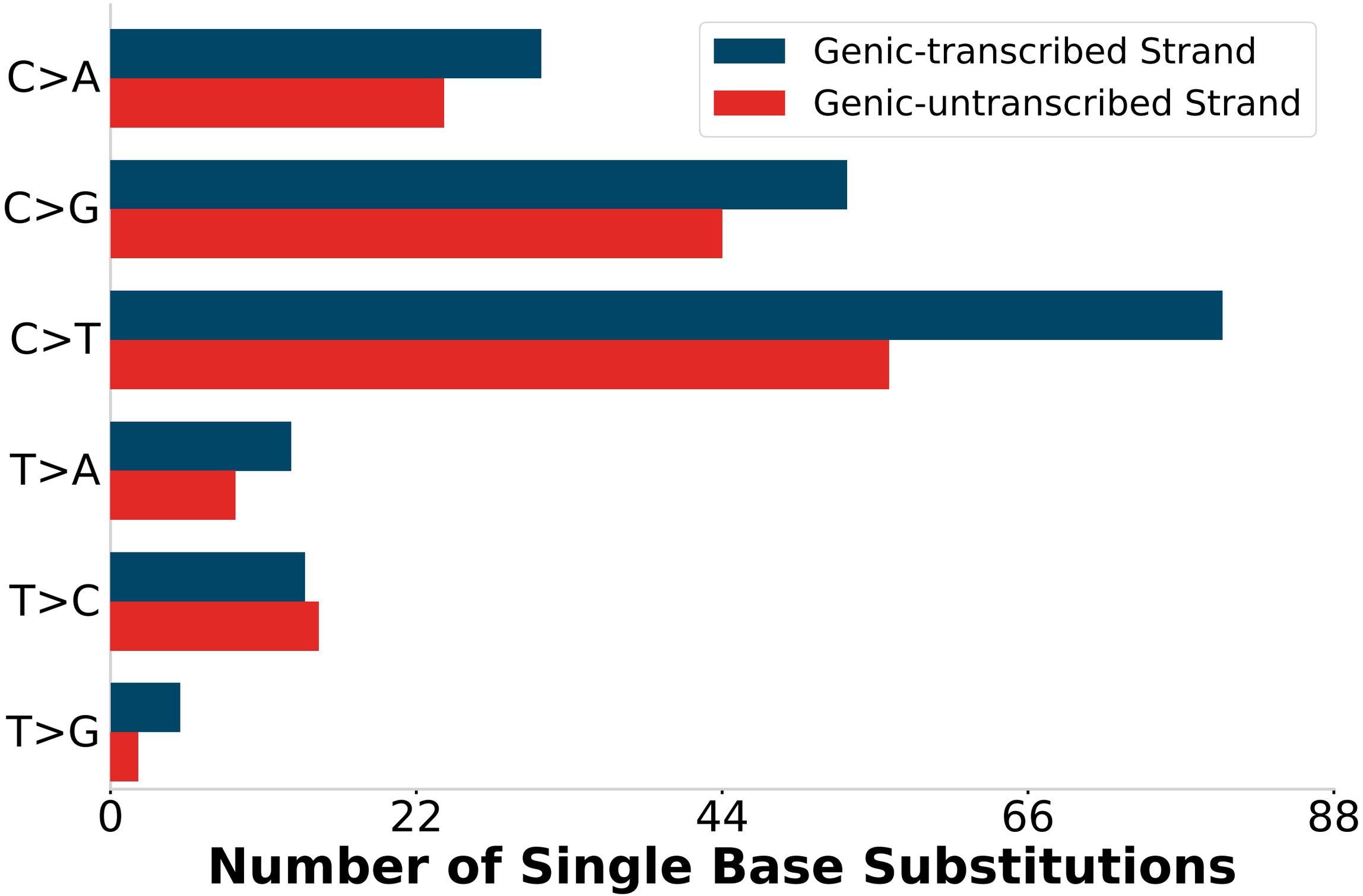


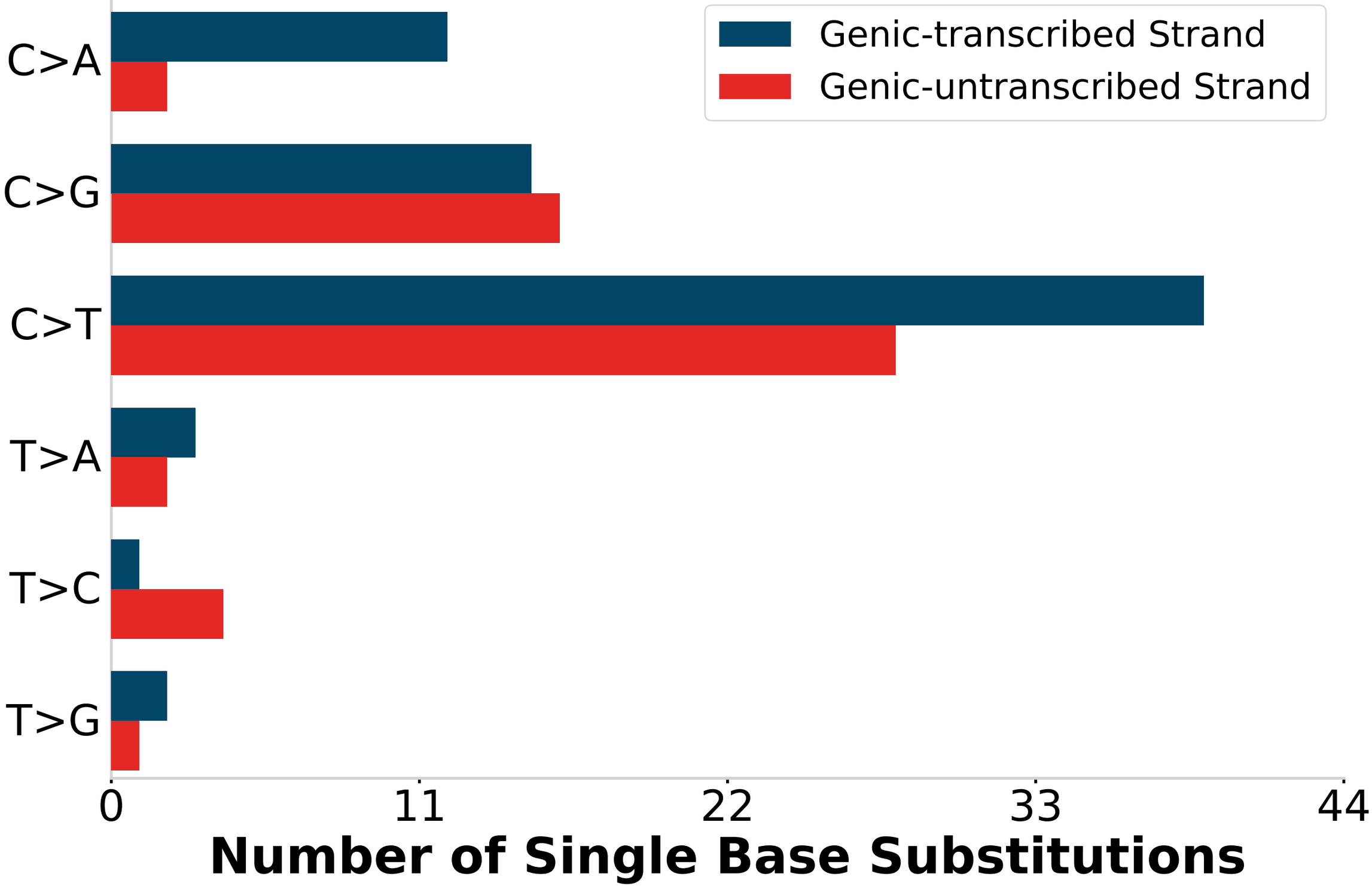
TCGA-XF-AAMW-01A-11D-A42E-08: 31 tran



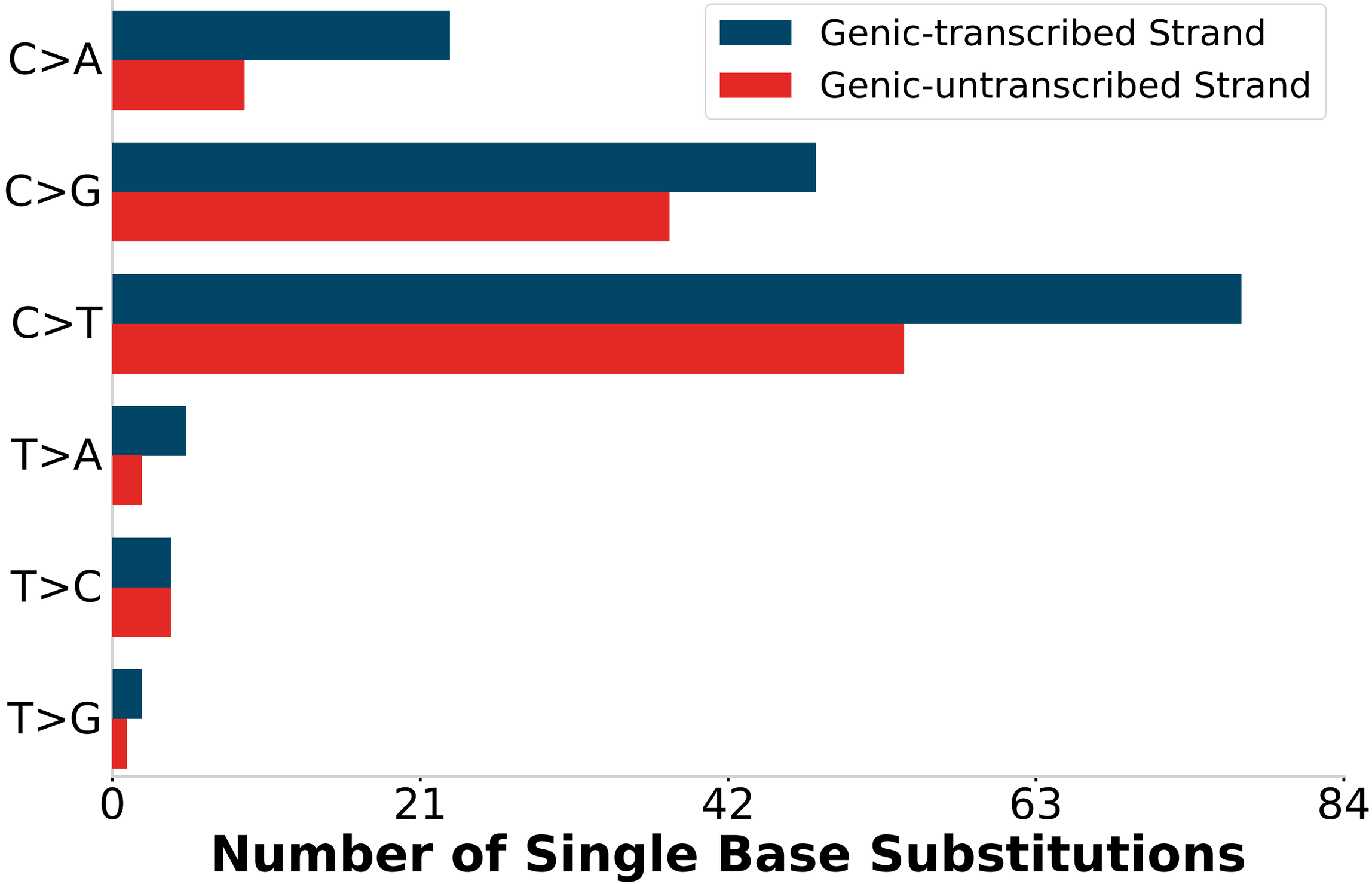
TCGA-XF-AAMX-01A-11D-A42E-08: 346 tra



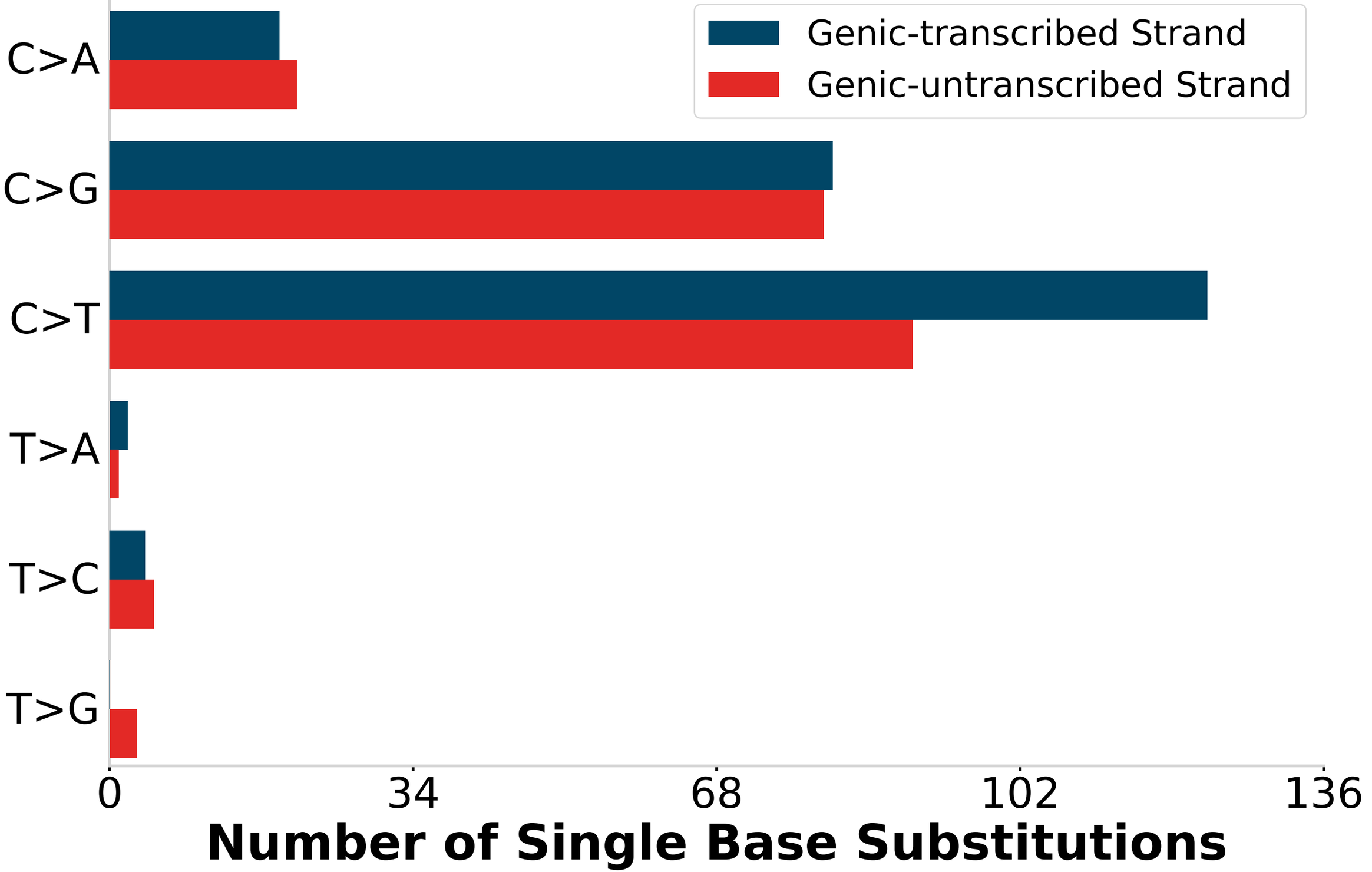
TCGA-XF-AAMY-01A-11D-A42E-08: 125 tra



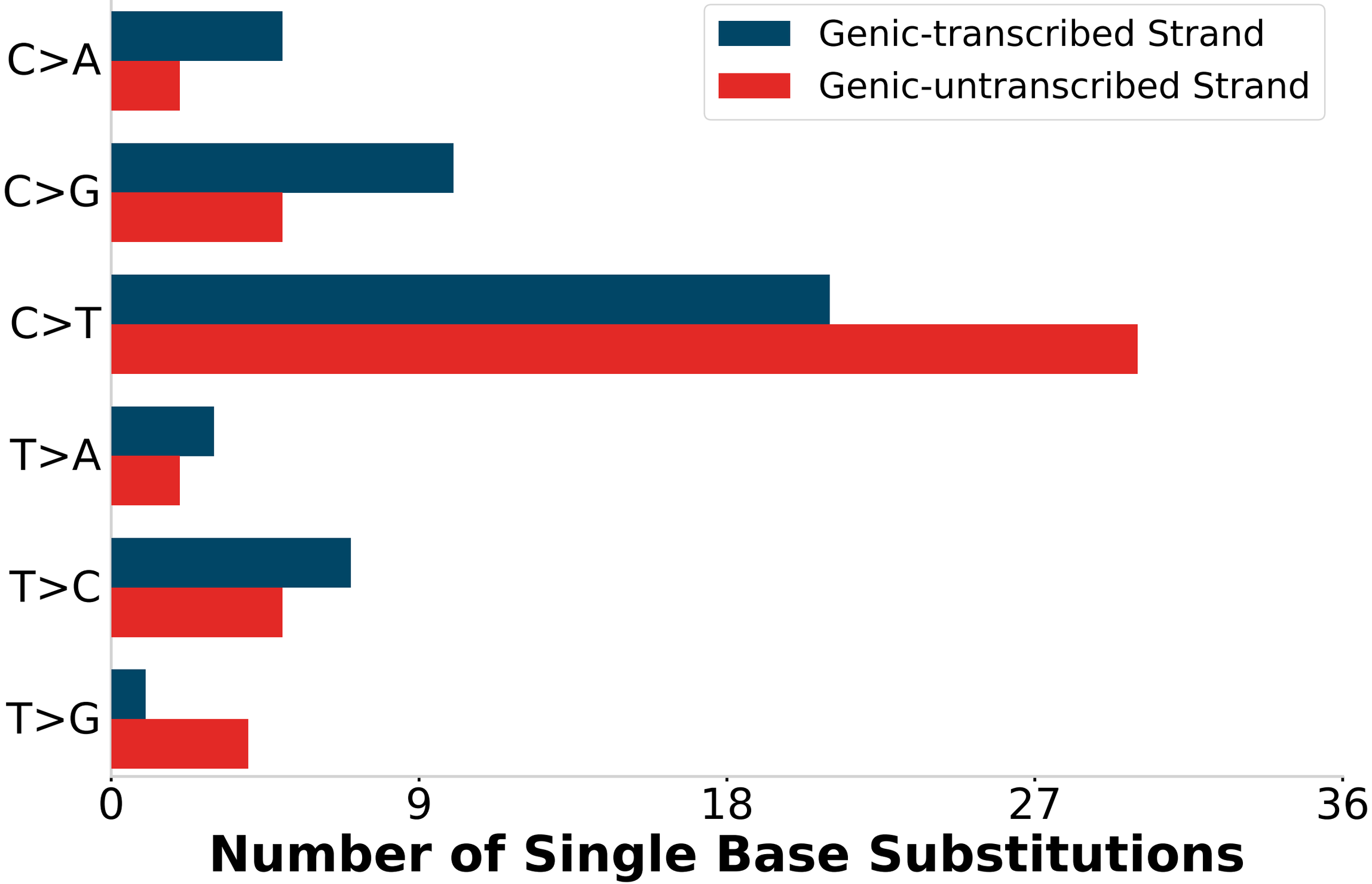
TCGA-XF-AAMZ-01A-11D-A42E-08: 267 tra



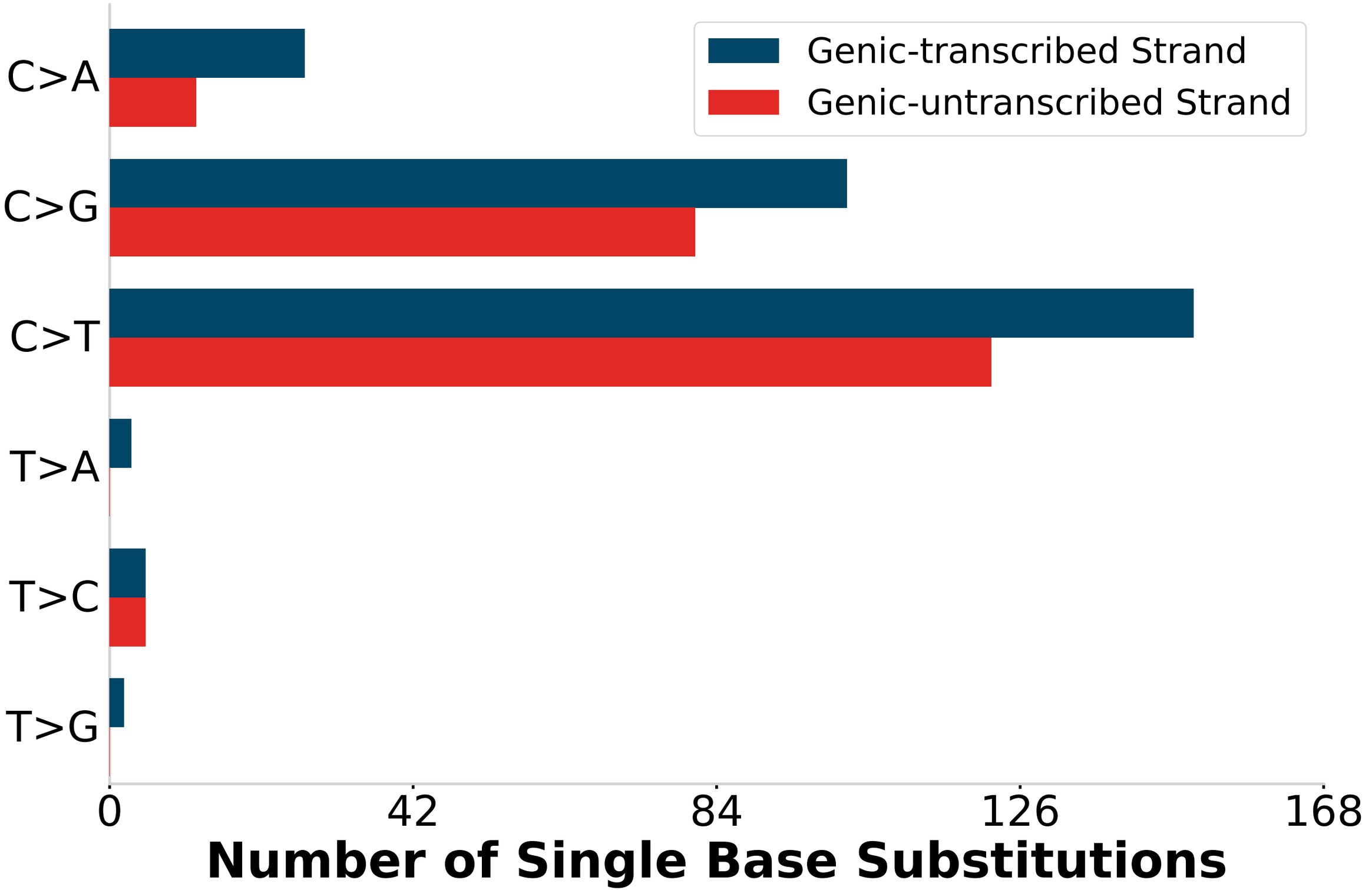
TCGA-XF-AAN0-01A-11D-A42E-08: 429 tra



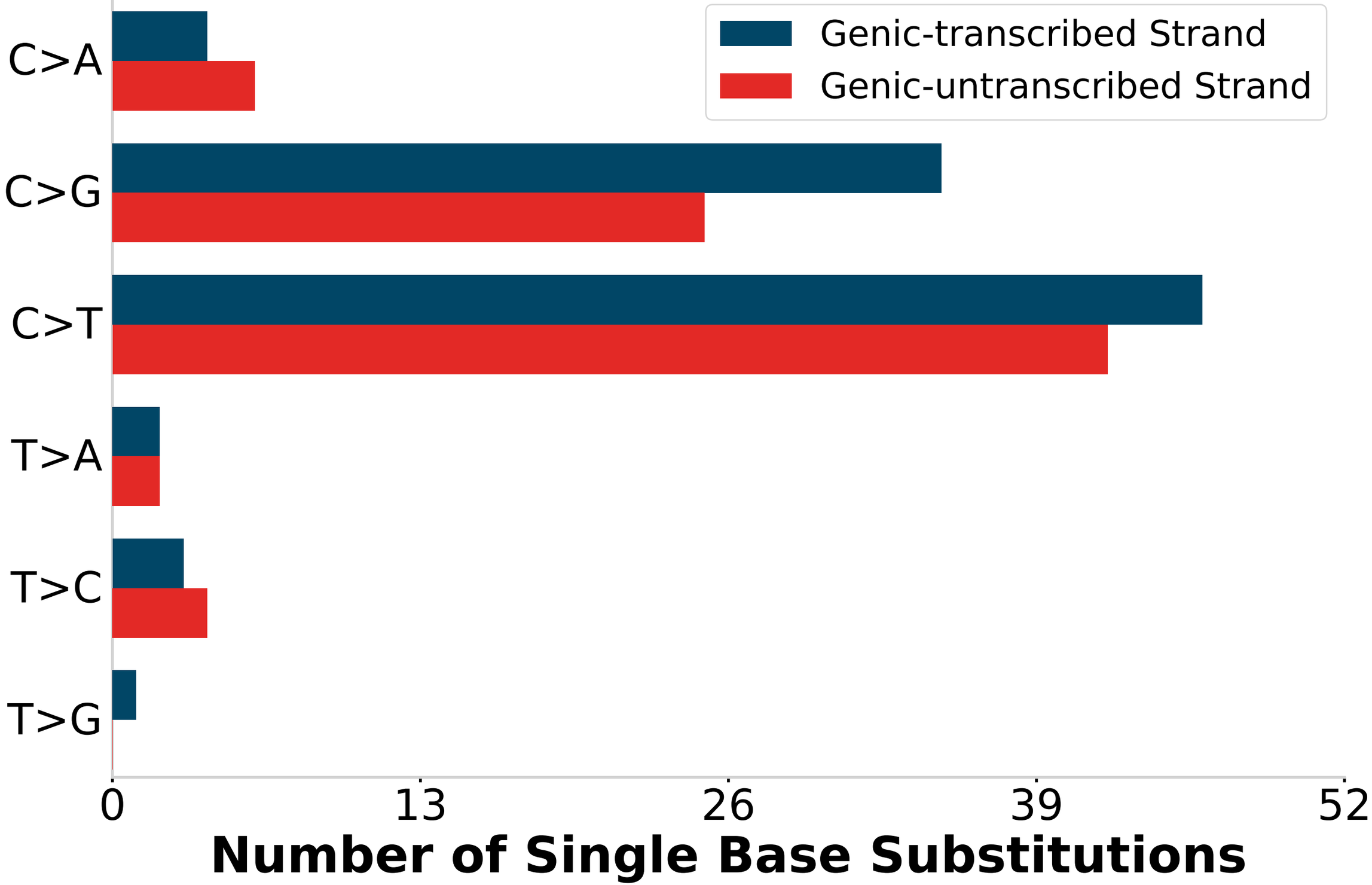
TCGA-XF-AAN1-01A-31D-A42E-08: 95 trans



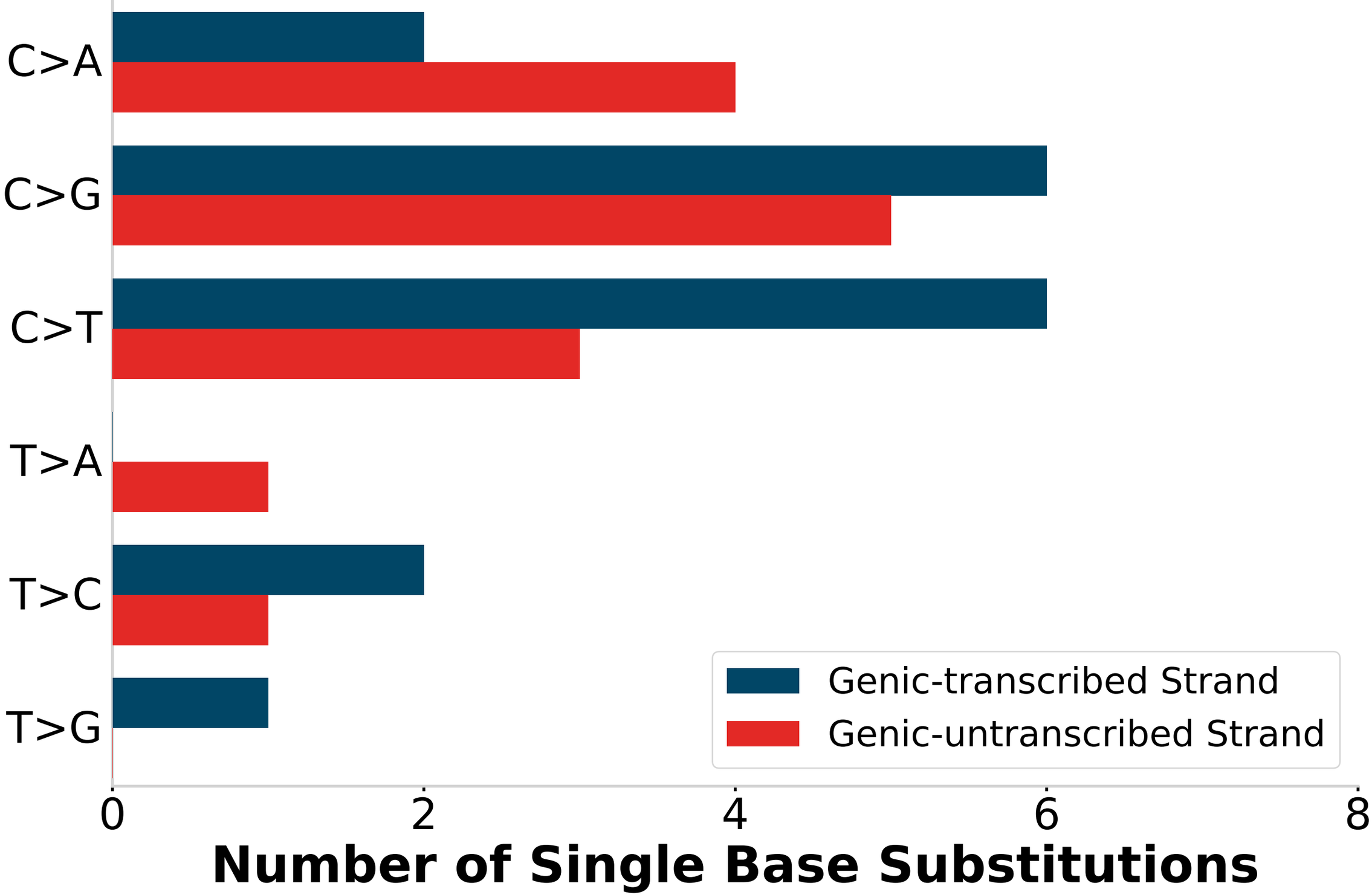
TCGA-XF-AAN2-01A-11D-A42E-08: 509 tra



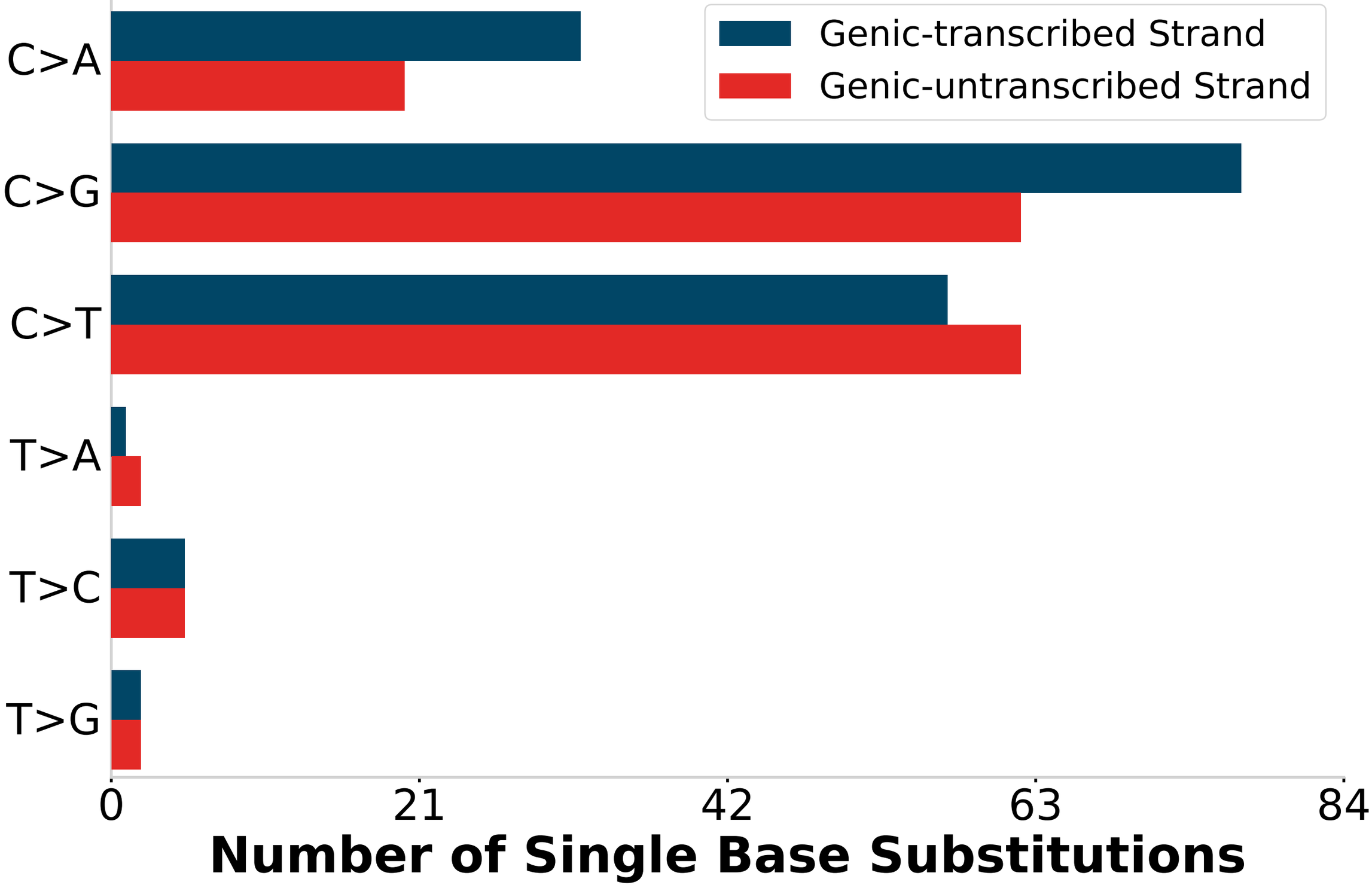
TCGA-XF-AAN3-01A-11D-A42E-08: 170 tra



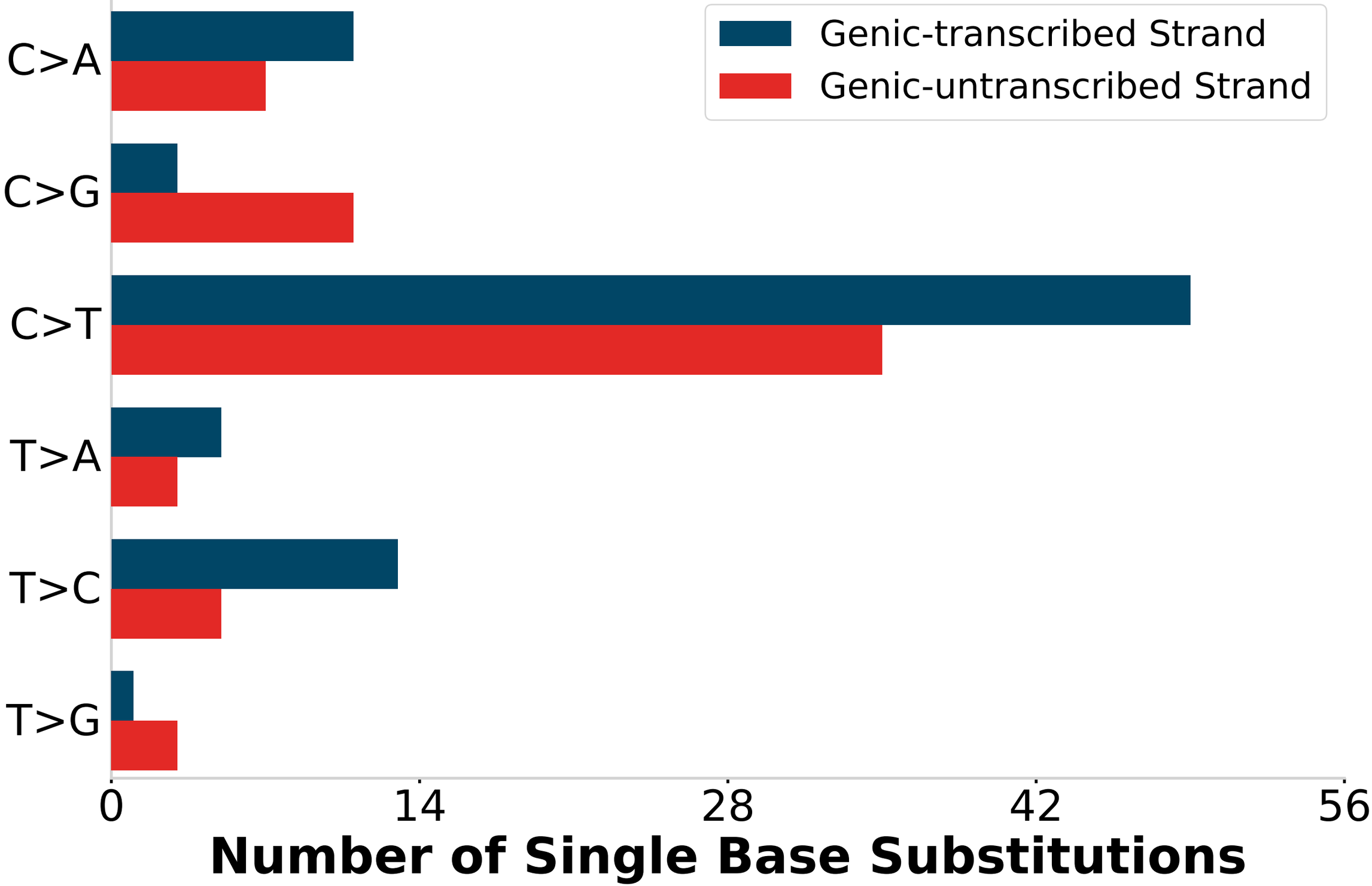
TCGA-XF-AAN4-01A-11D-A42E-08: 31 trans



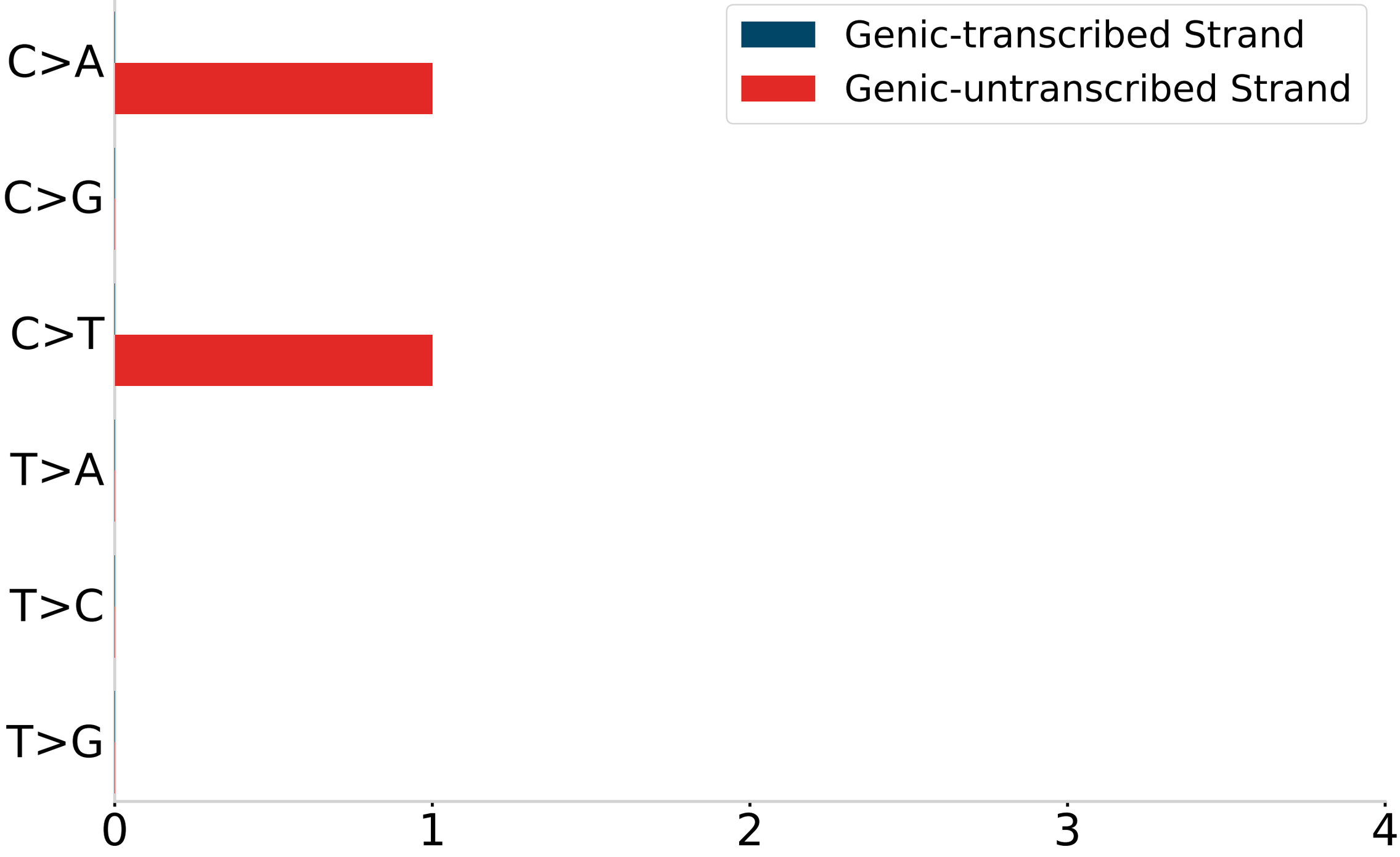
TCGA-XF-AAN5-01A-11D-A42E-08: 327 tra



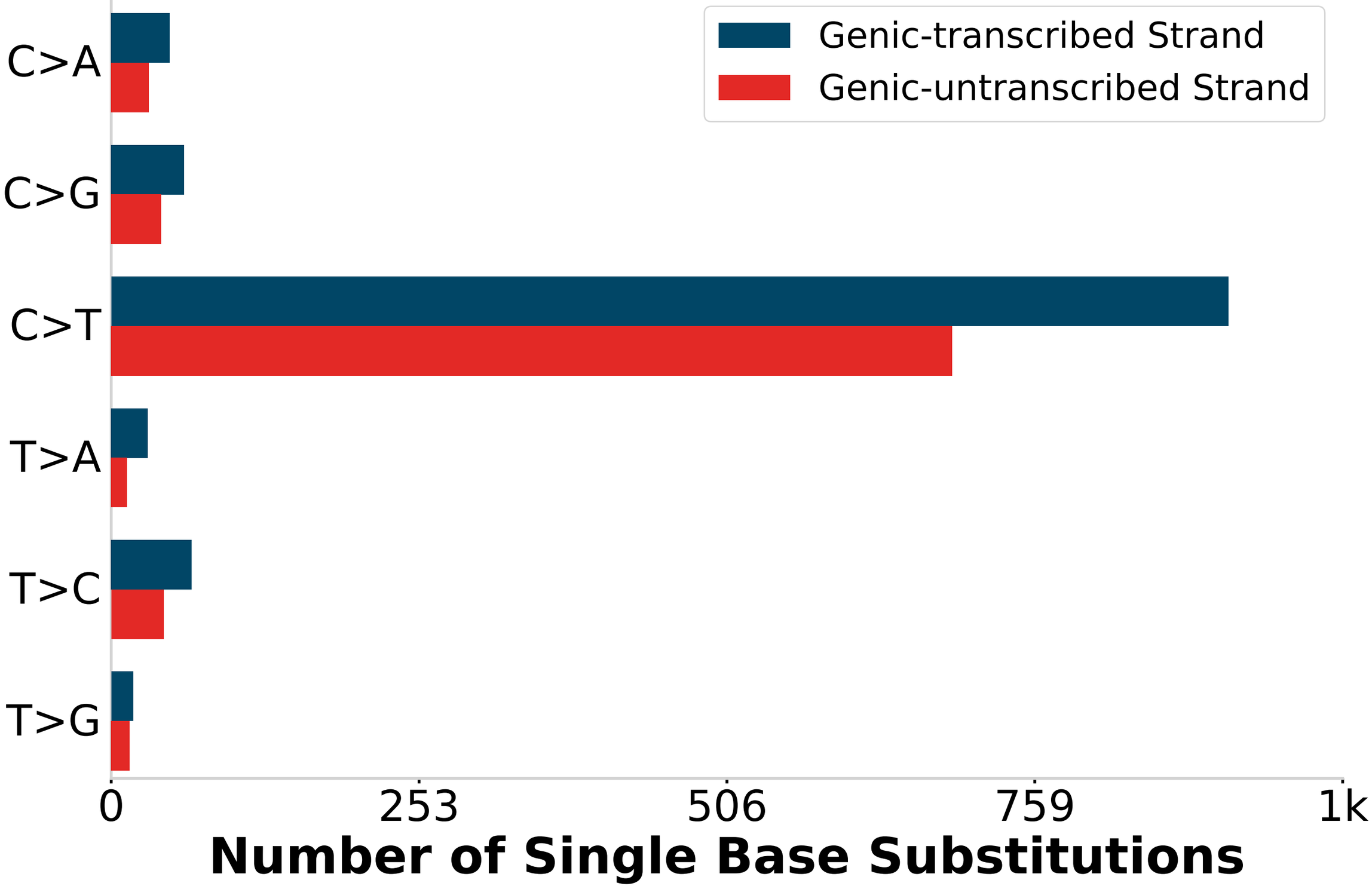
TCGA-XF-AAN7-01A-11D-A42E-08: 146 tra



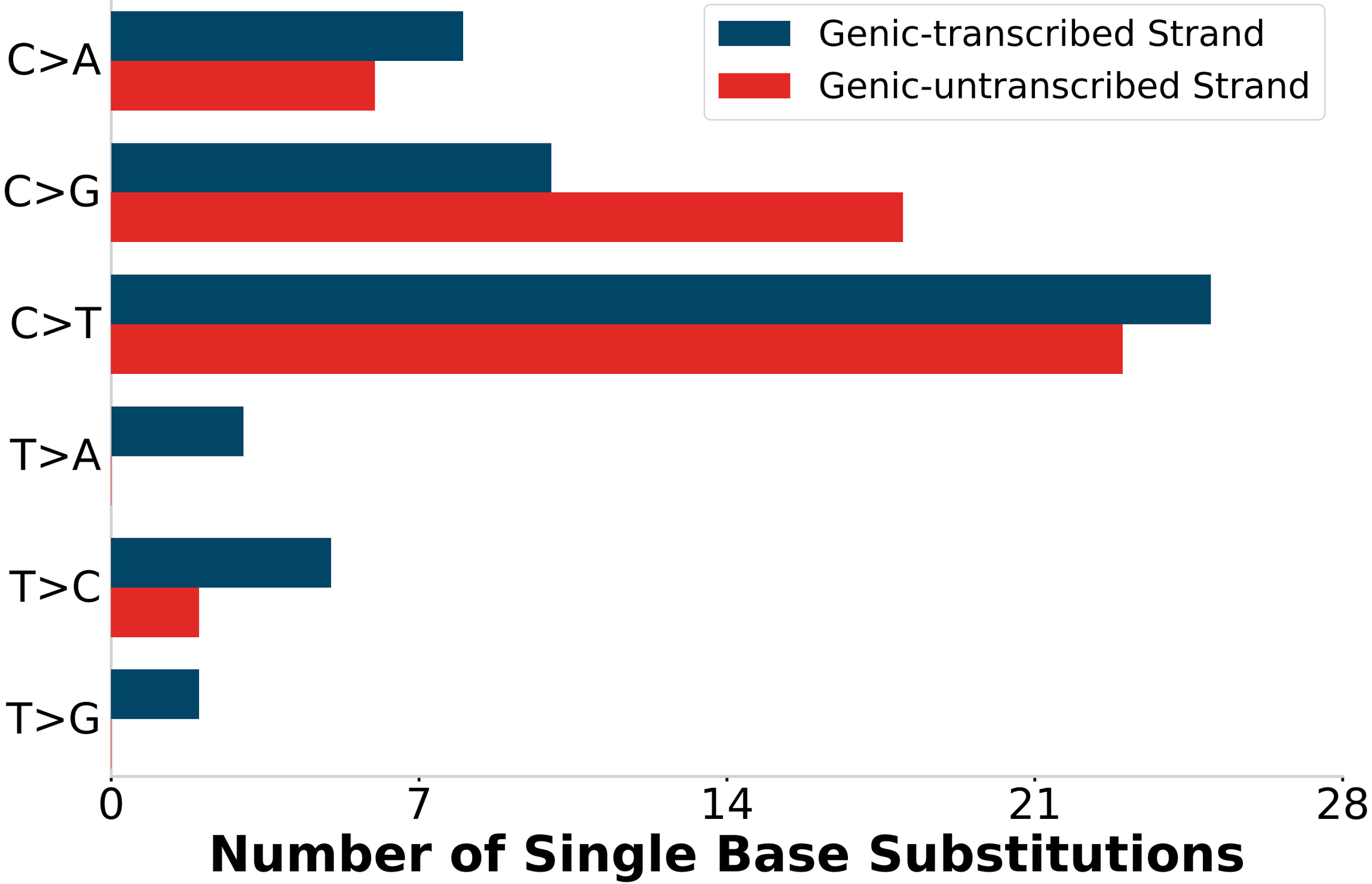
TCGA-XF-AAN8-01A-11D-A42E-08: 2 transc



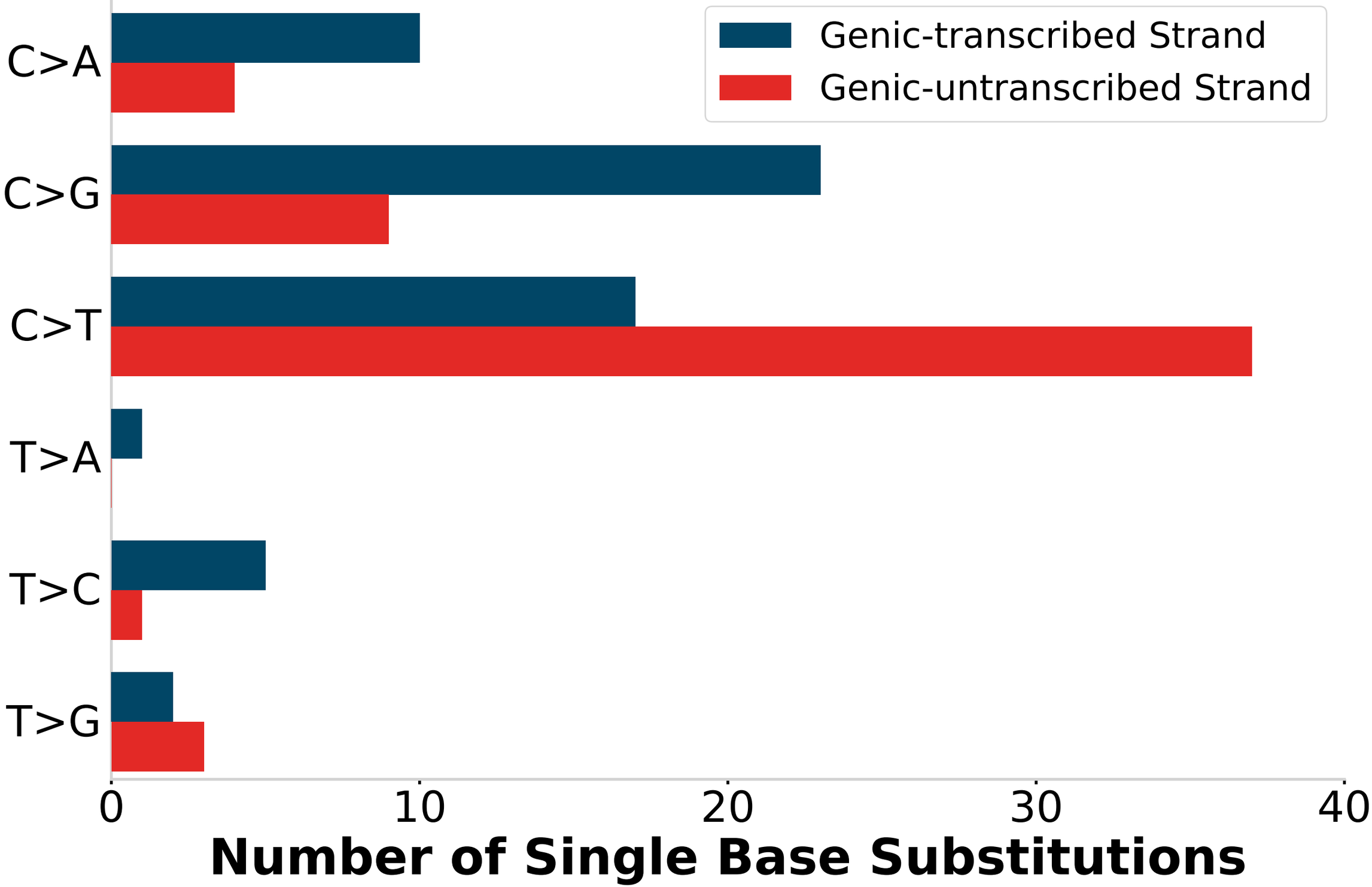
TCGA-YC-A89H-01A-11D-A364-08: 1,974 tr



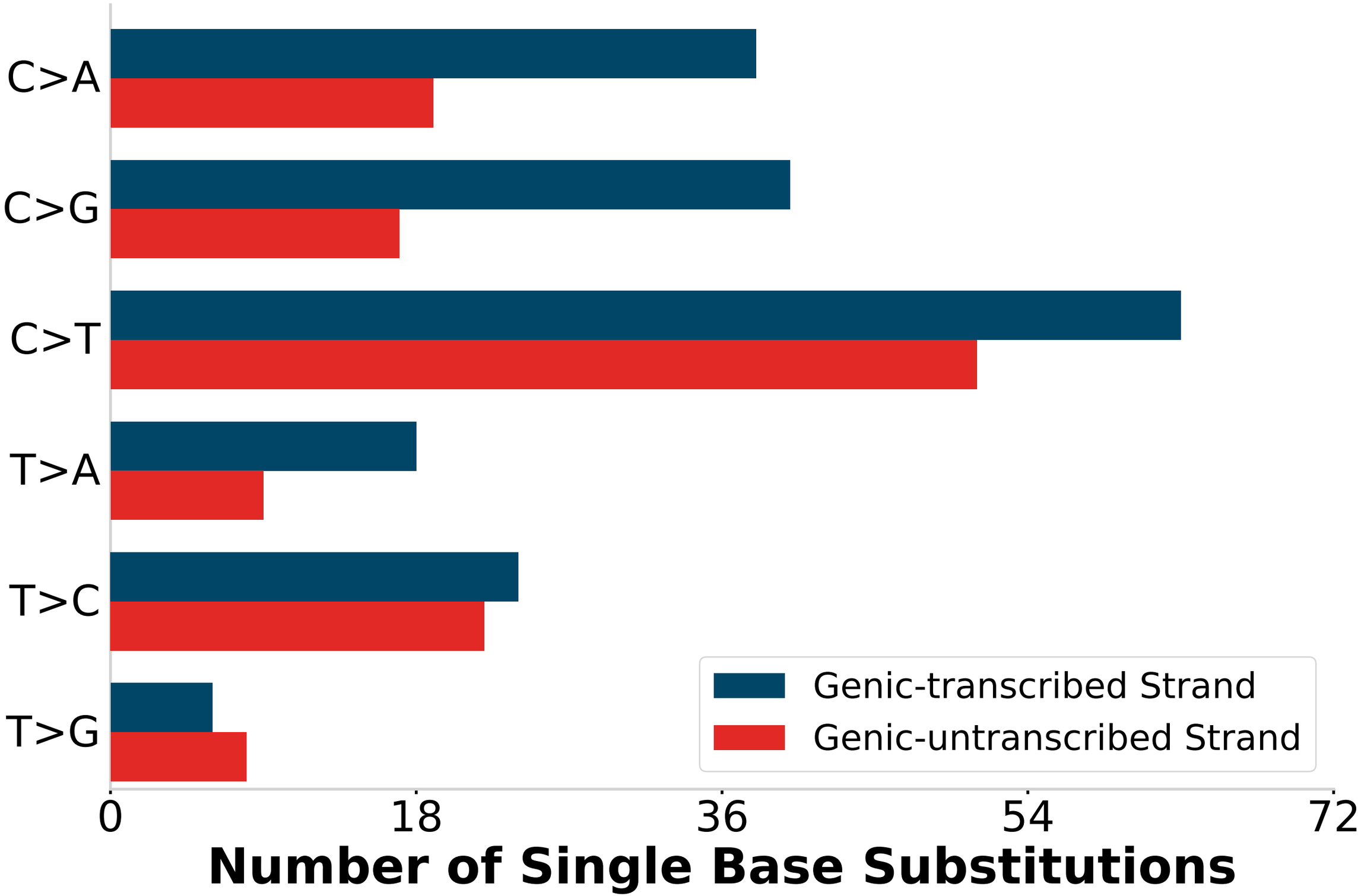
TCGA-YC-A8S6-01A-31D-A38G-08: 102 tran



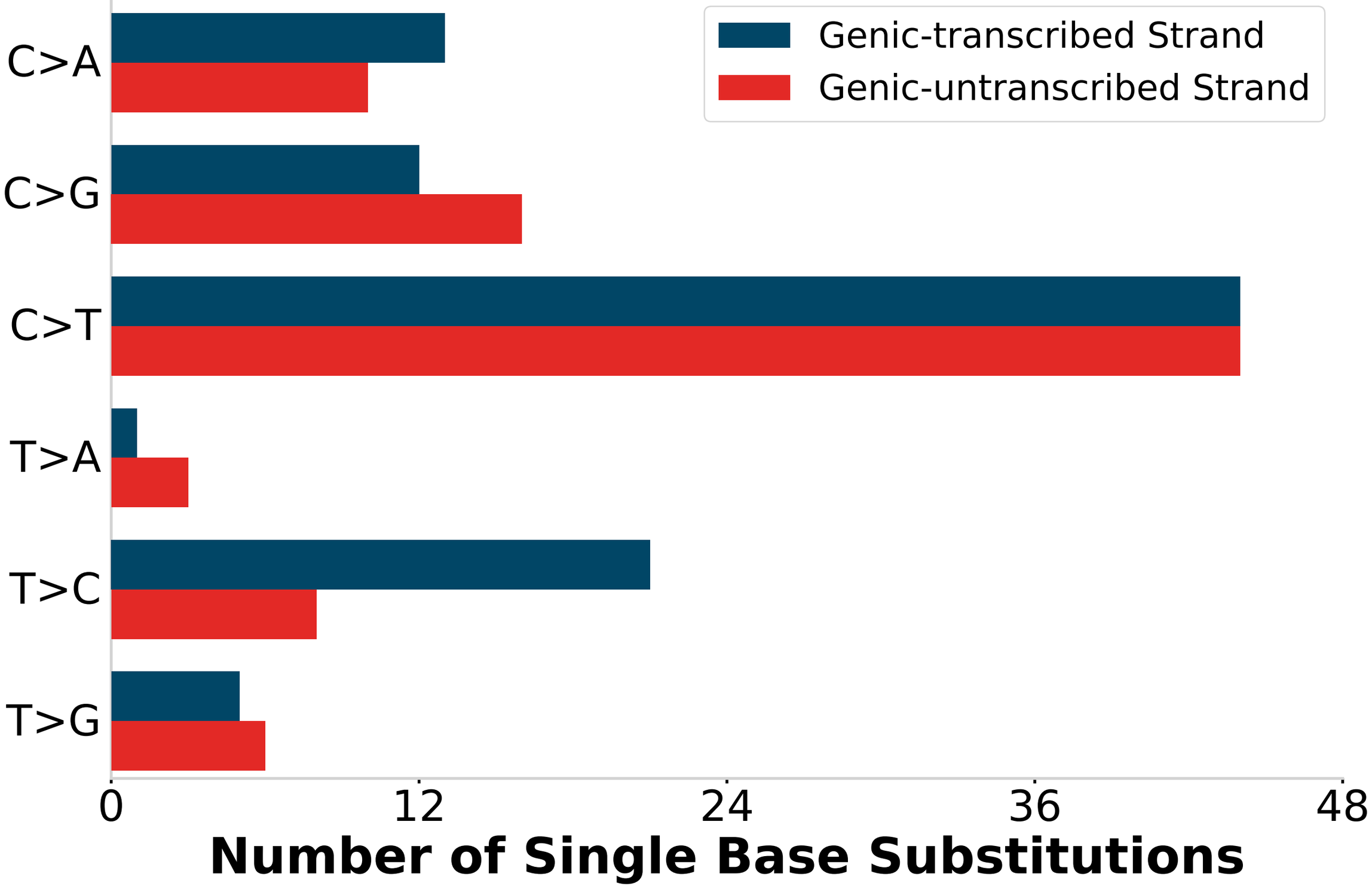
TCGA-YC-A9TC-01A-22D-A391-08: 112 tran



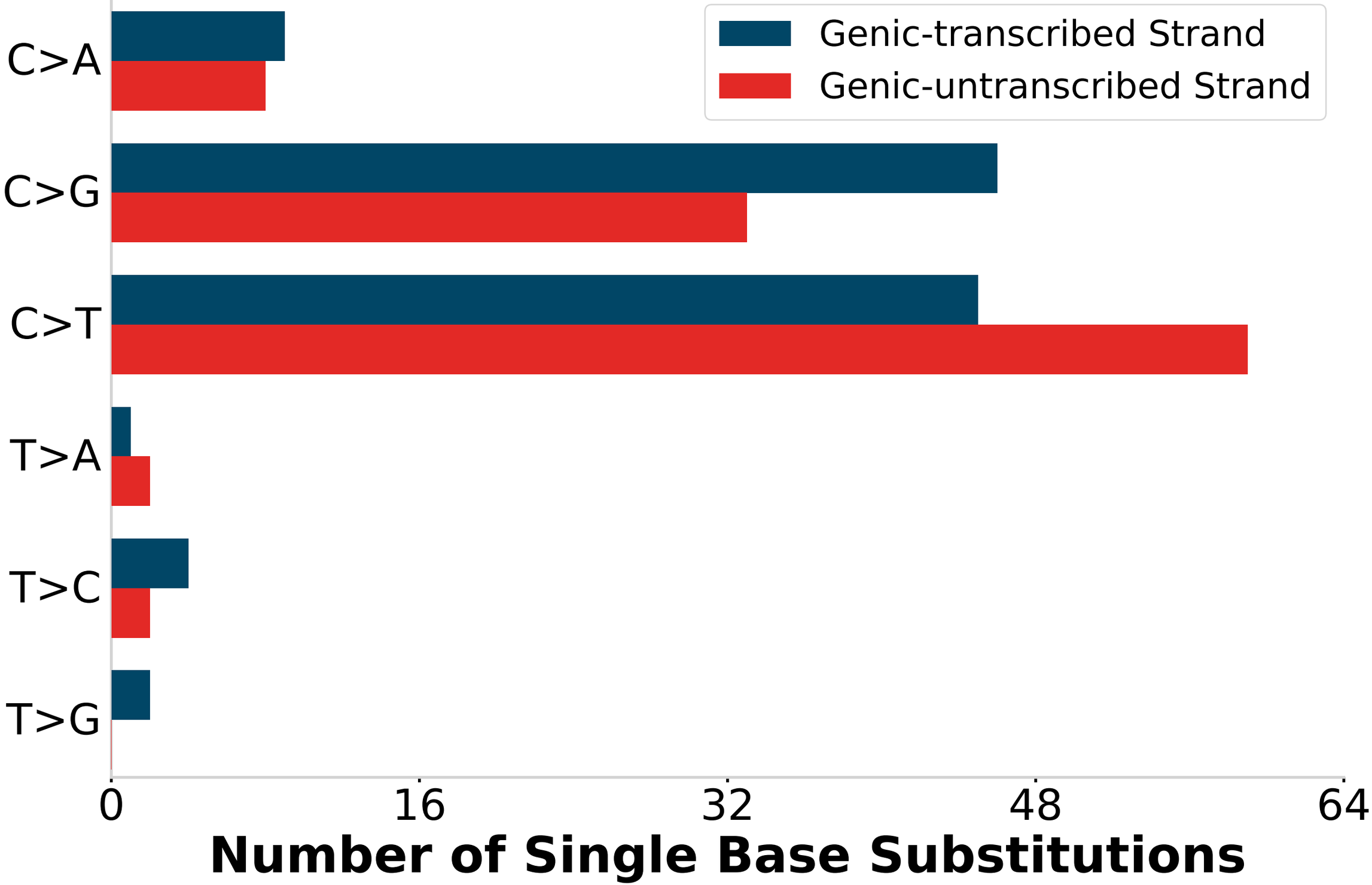
TCGA-YF-AA3L-01A-11D-A38G-08: 315 tran



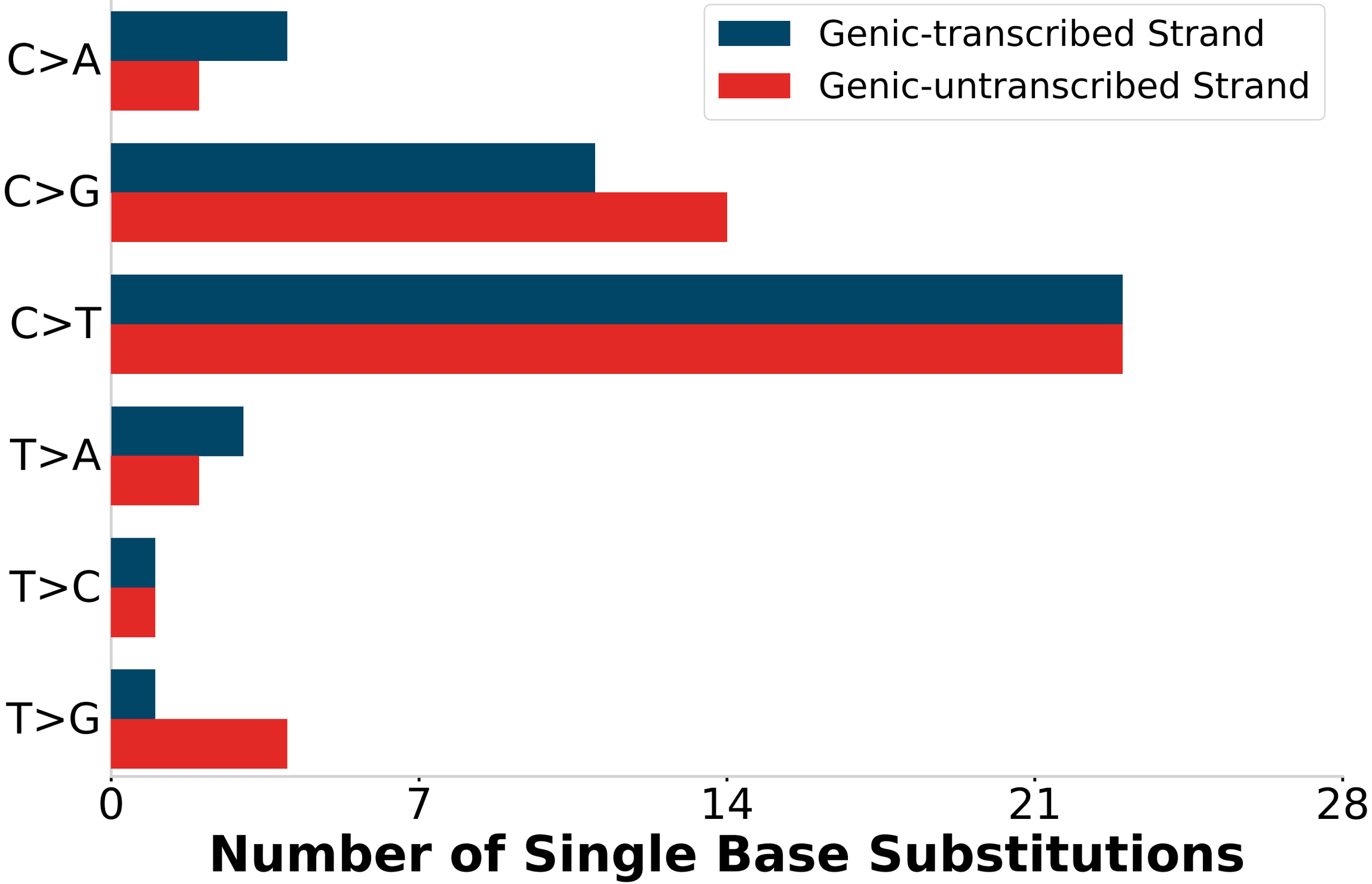
TCGA-YF-AA3M-01A-11D-A42E-08: 183 tra



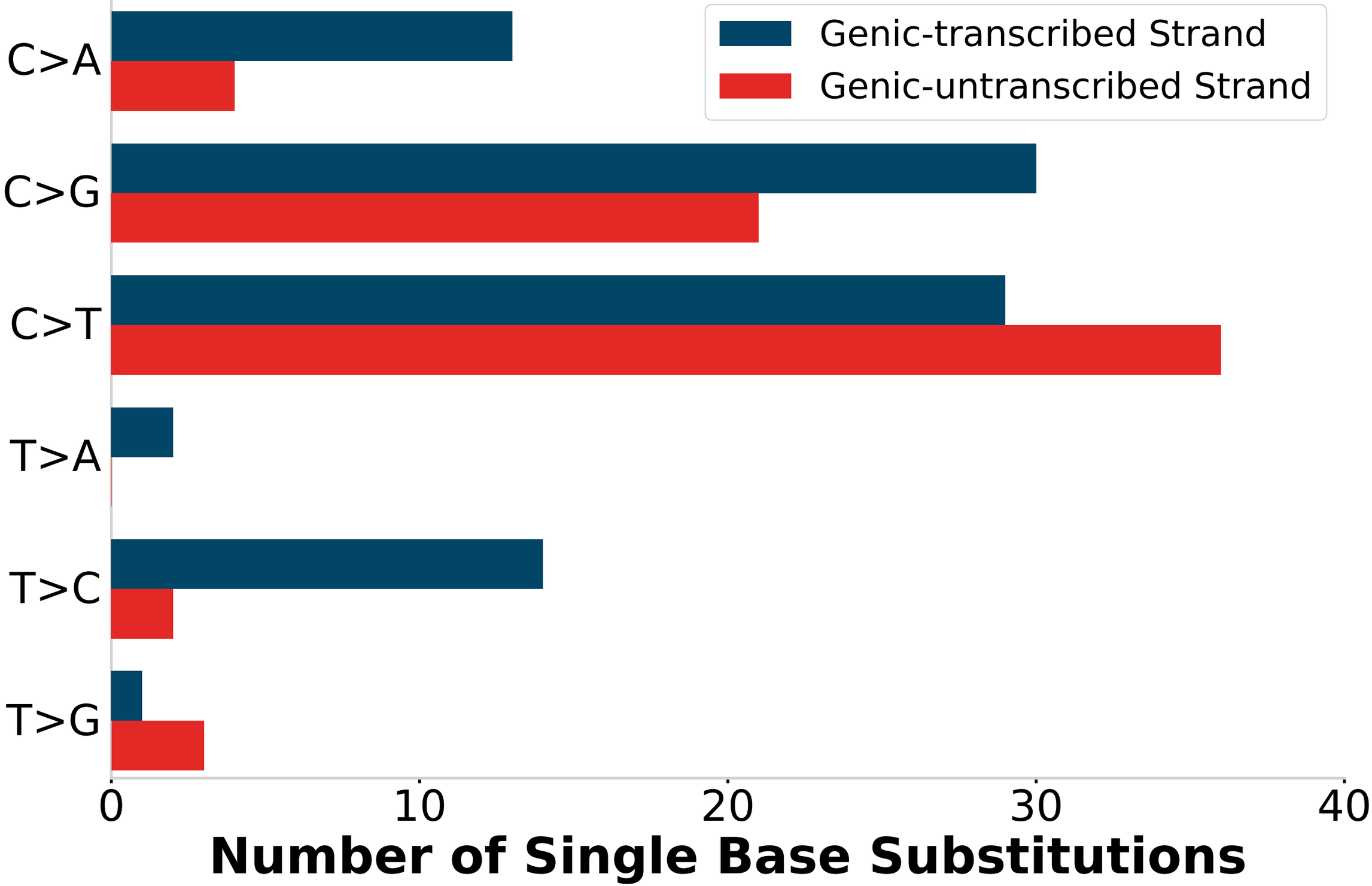
TCGA-ZF-A9R0-01A-11D-A38G-08: 211 tra



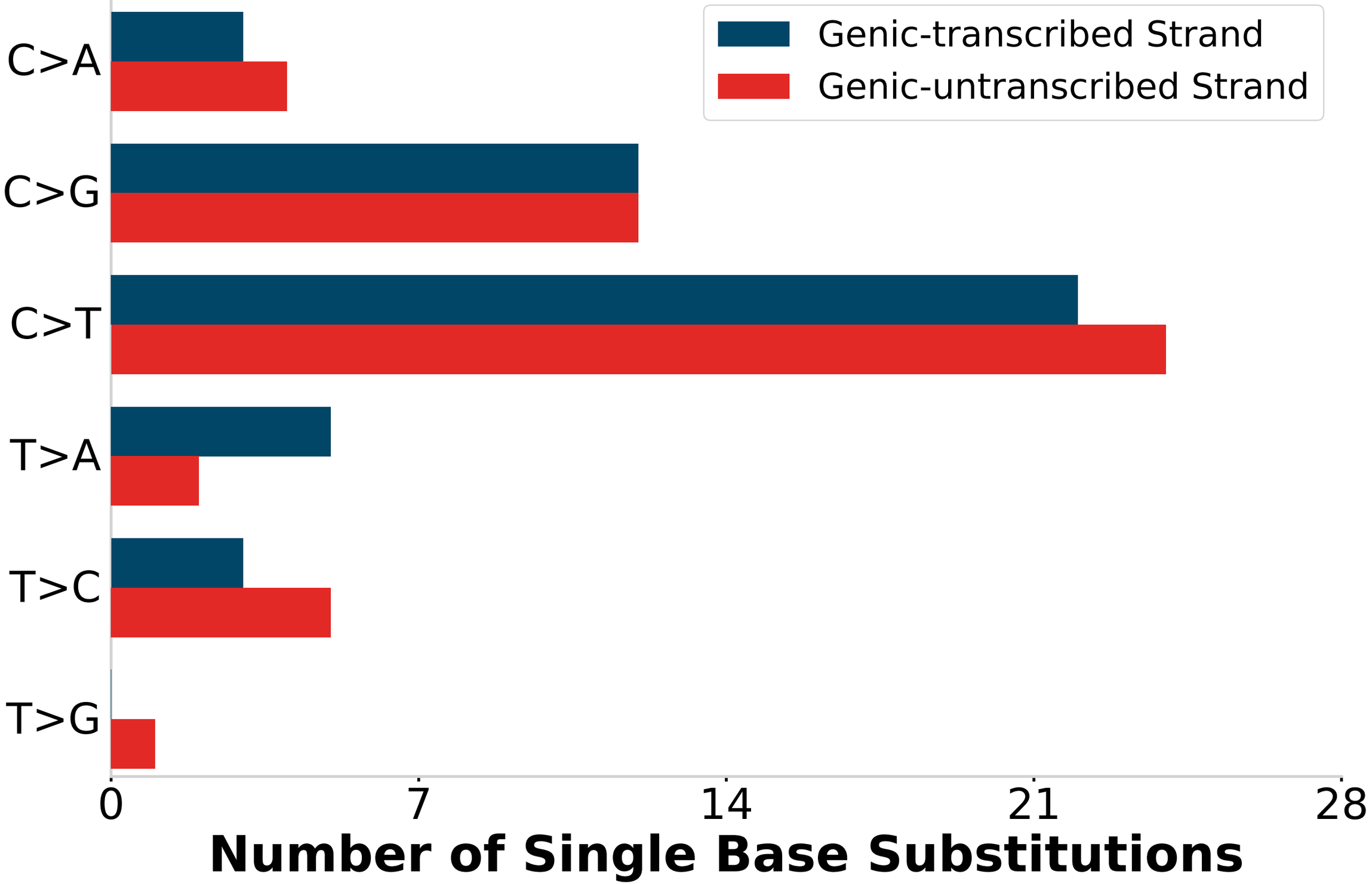
TCGA-ZF-A9R1-01A-11D-A391-08: 89 trans



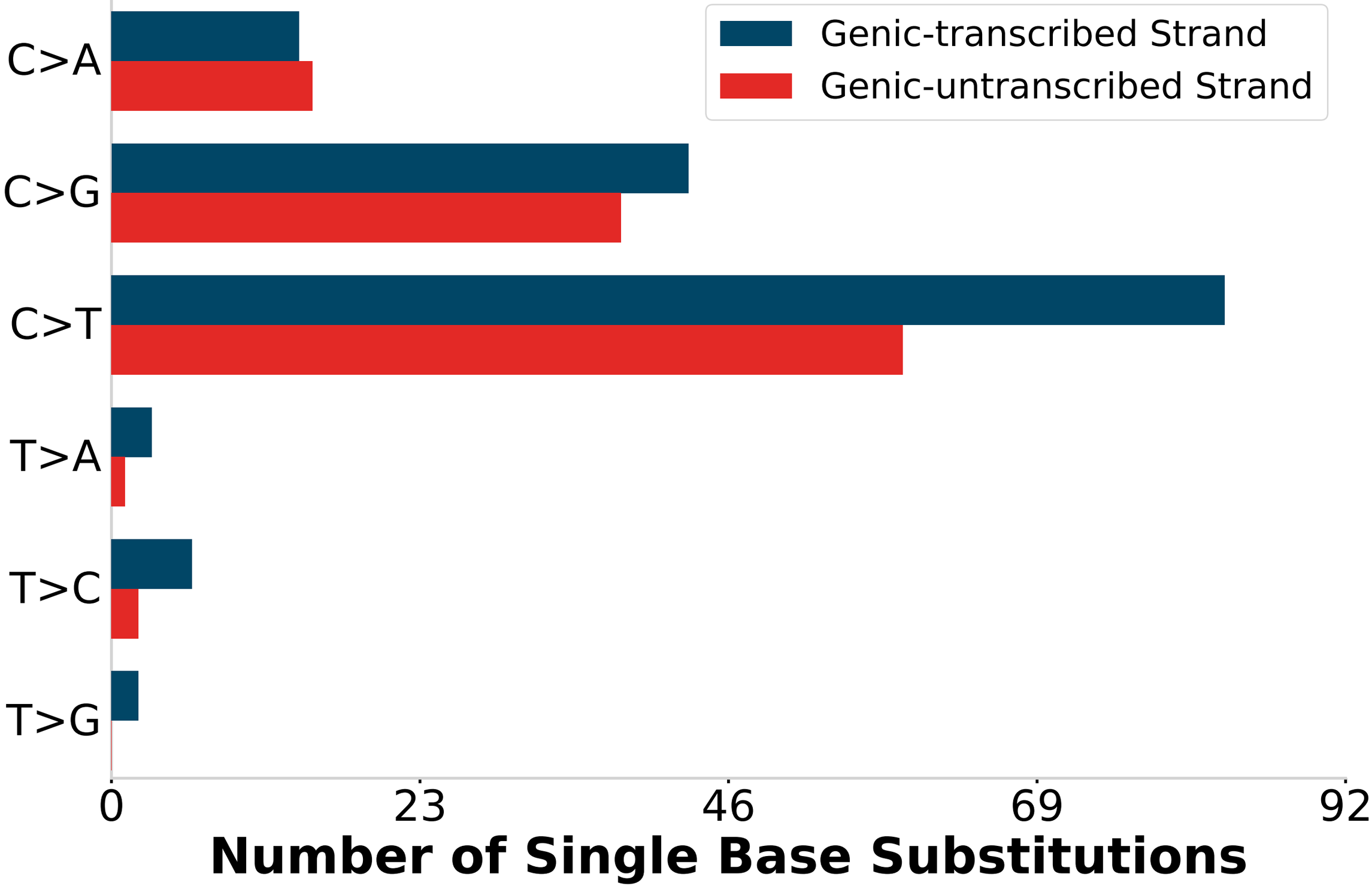
TCGA-ZF-A9R2-01A-11D-A391-08: 155 tran



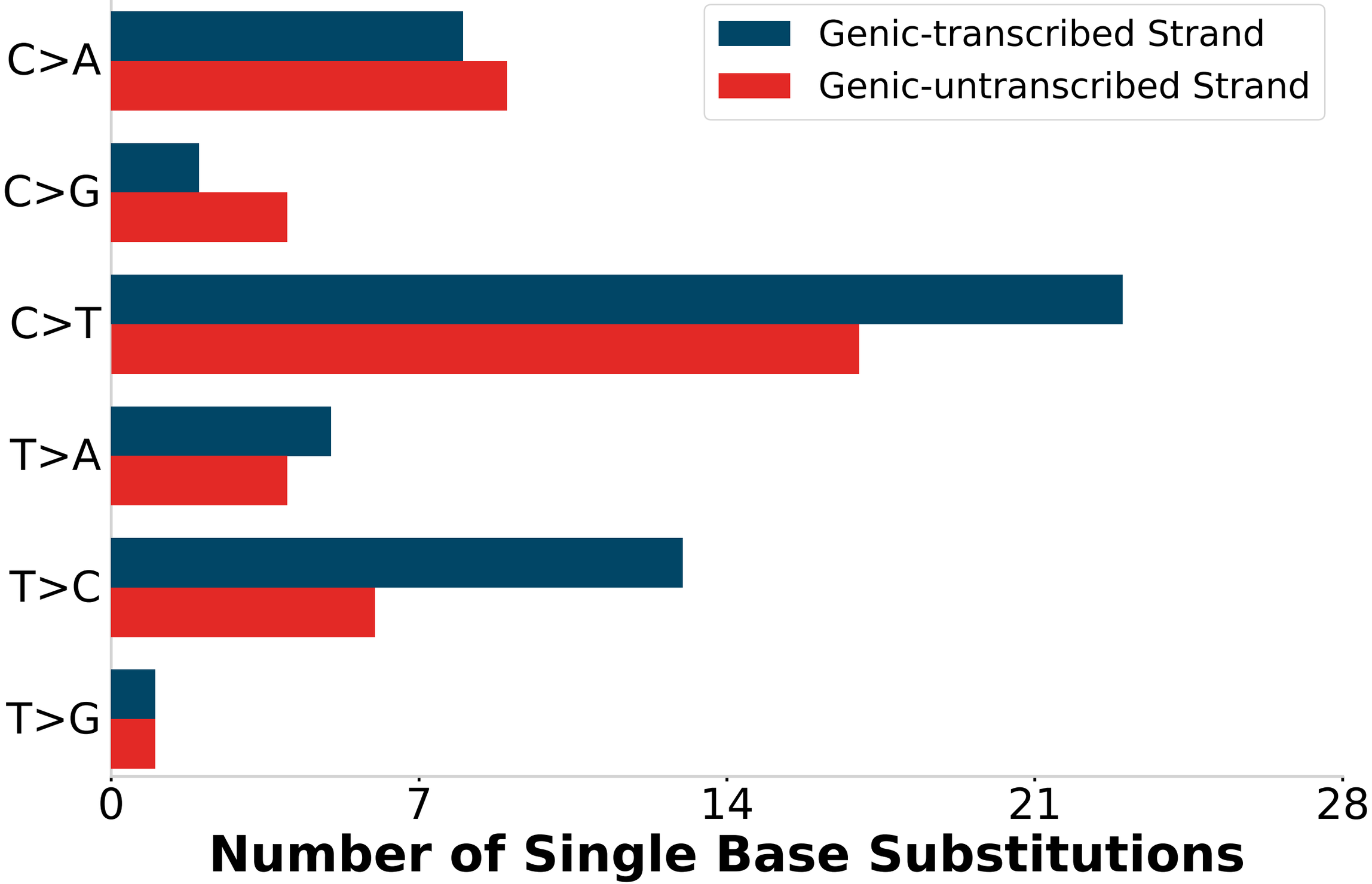
TCGA-ZF-A9R3-01A-11D-A38G-08: 93 trans



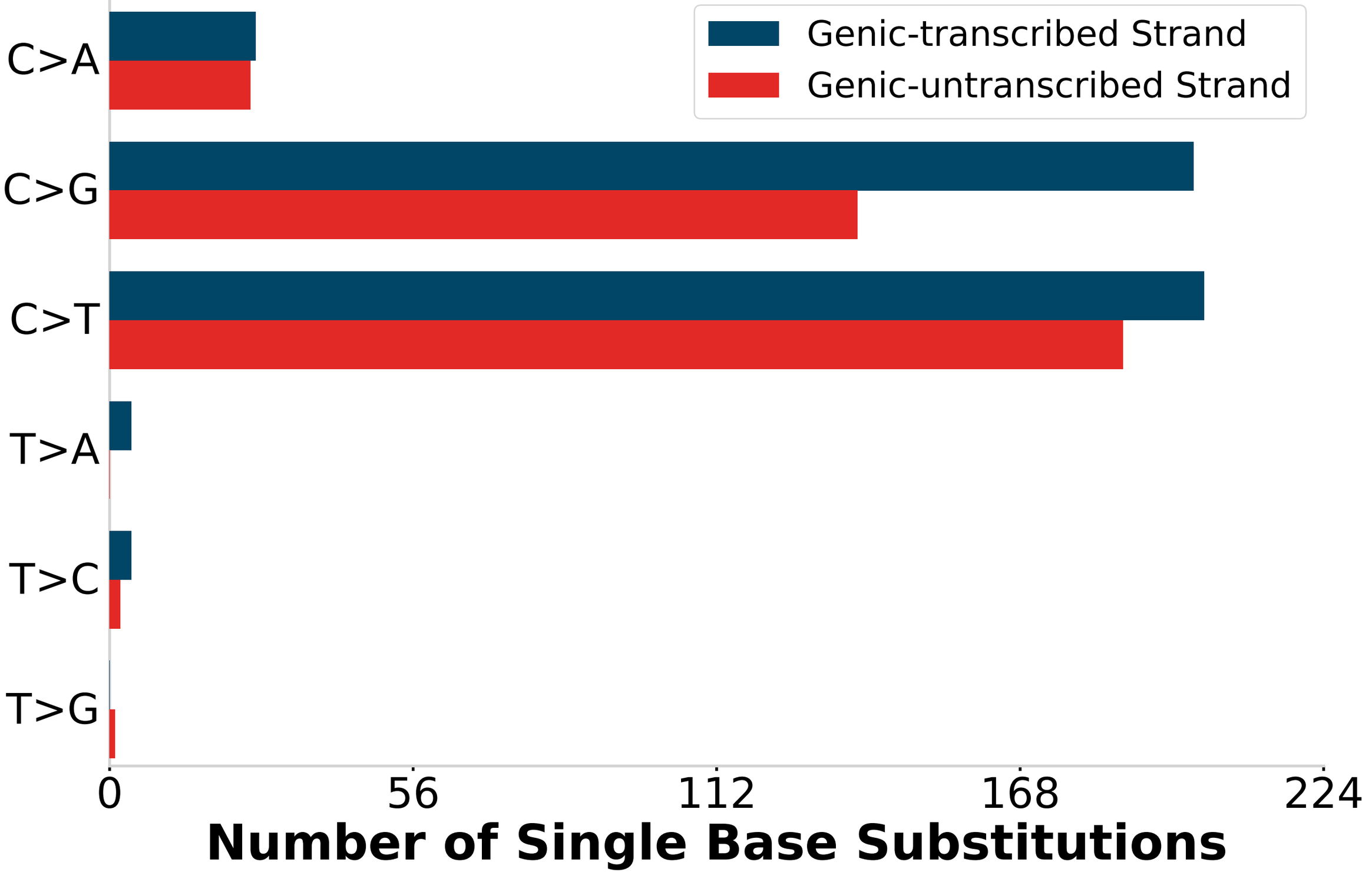
TCGA-ZF-A9R4-01A-11D-A38G-08: 266 tra



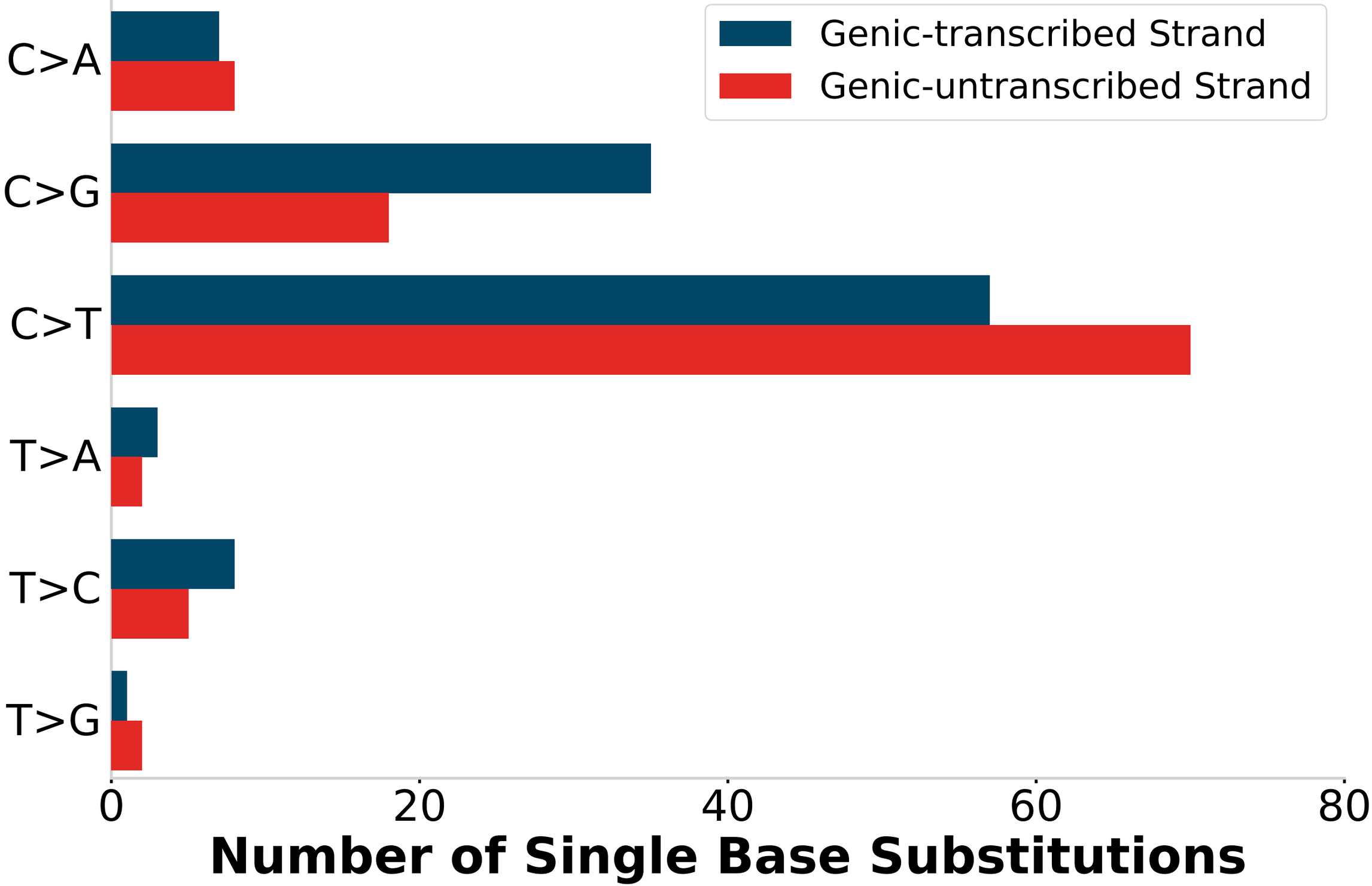
TCGA-ZF-A9R5-01A-12D-A42E-08: 93 trans



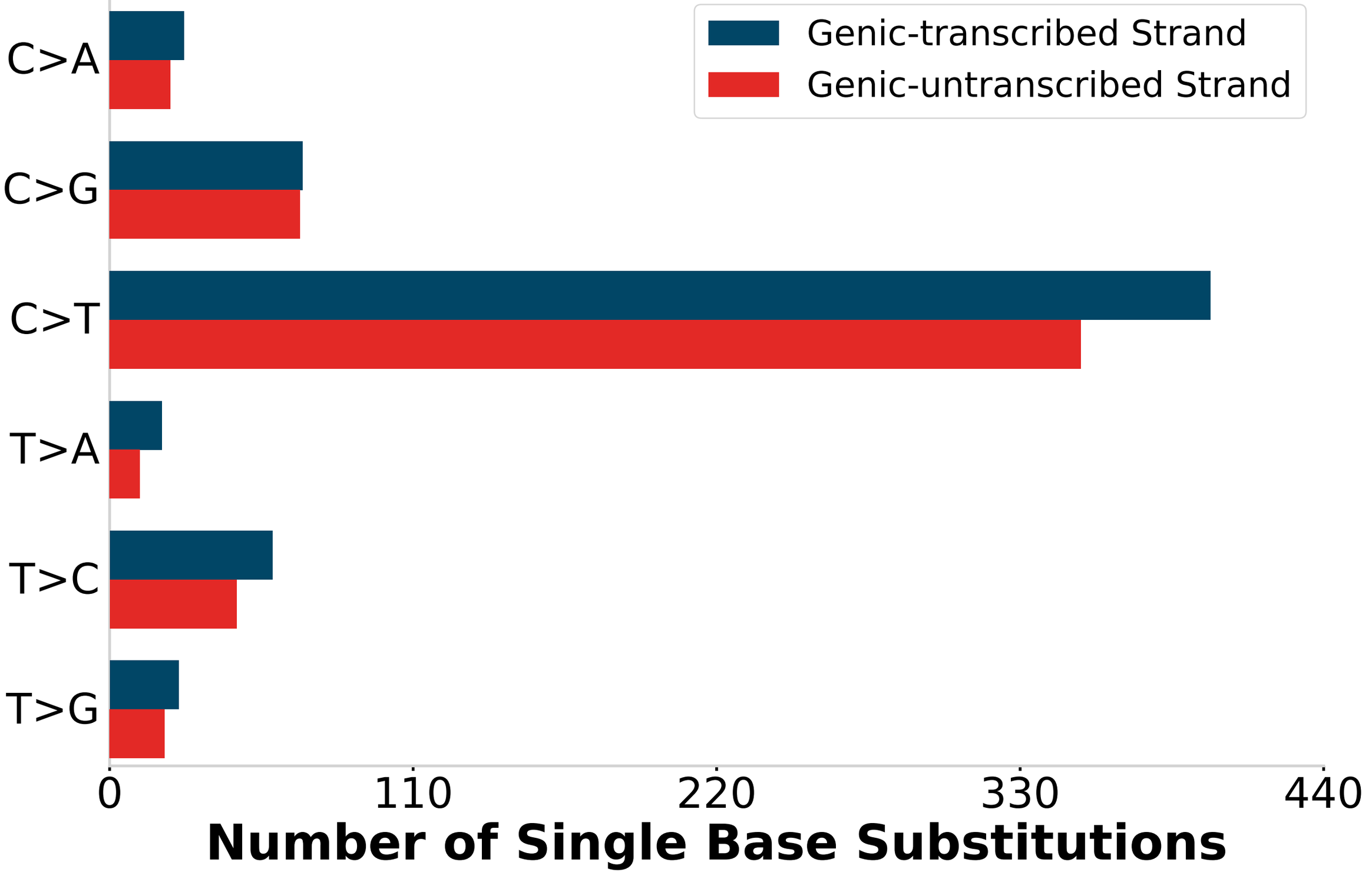
TCGA-ZF-A9R7-01A-11D-A38G-08: 791 tra



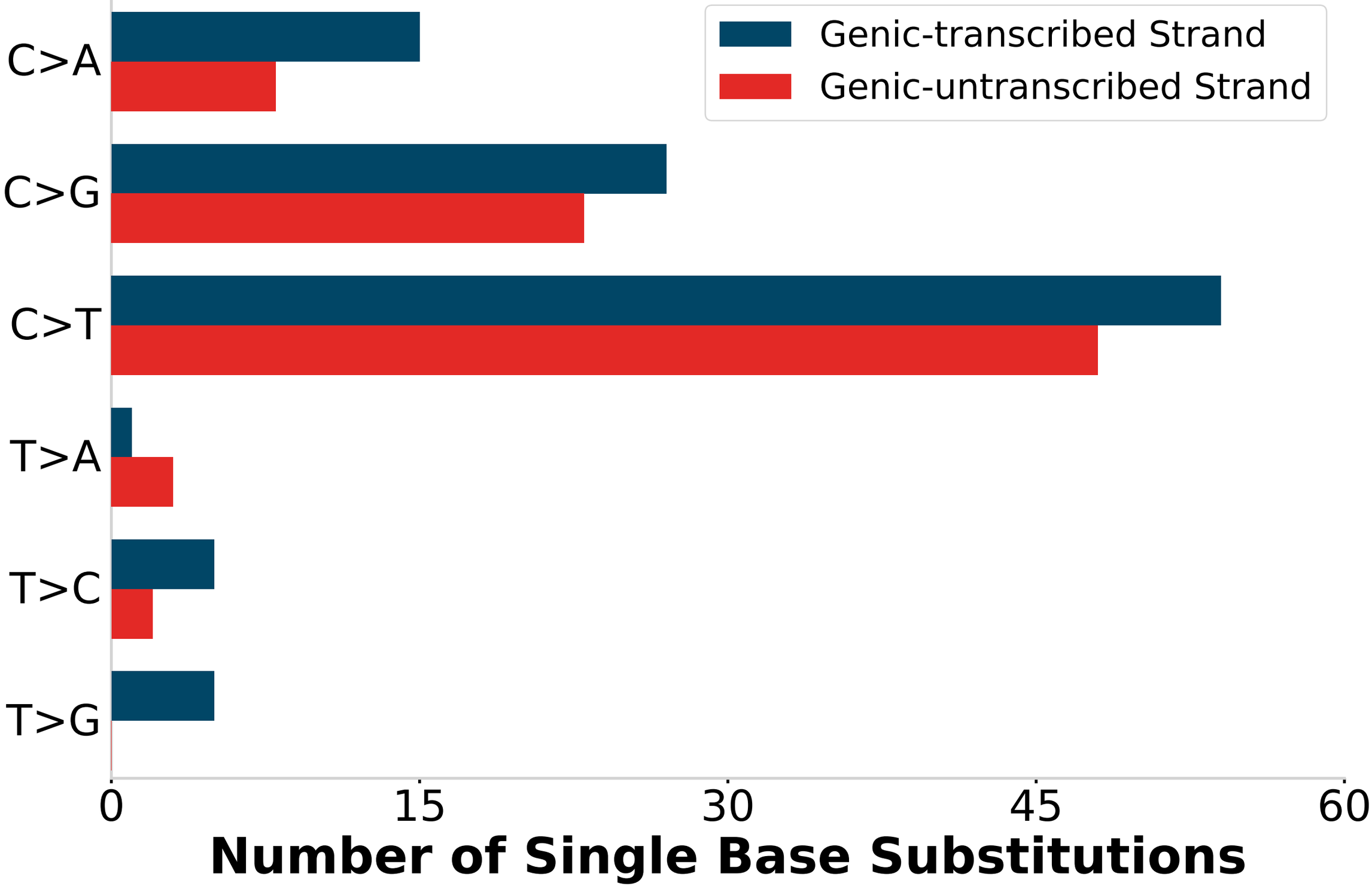
TCGA-ZF-A9R9-01A-11D-A38G-08: 216 tra



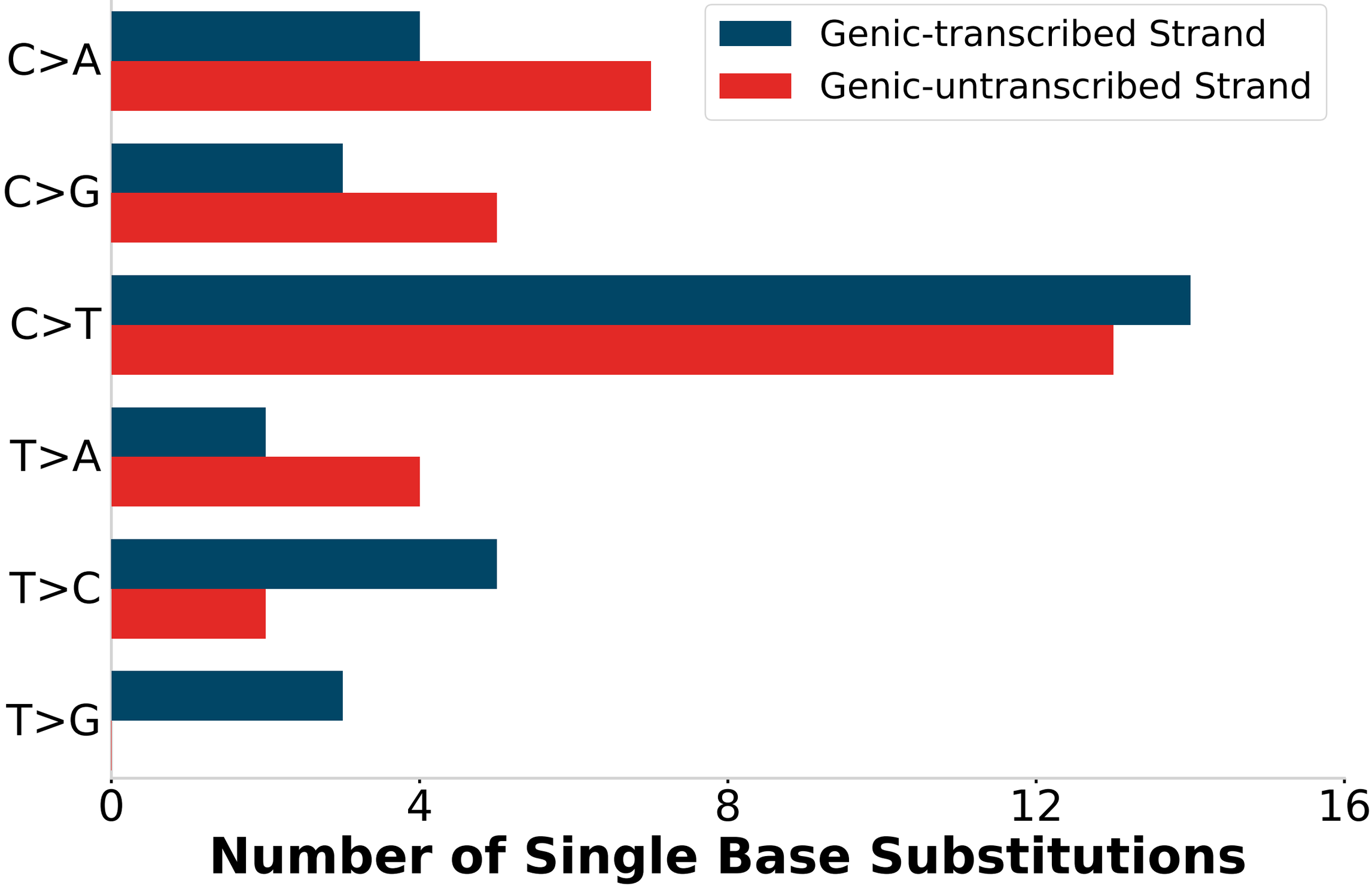
TCGA-ZF-A9RC-01A-11D-A38G-08: 1,119 tr



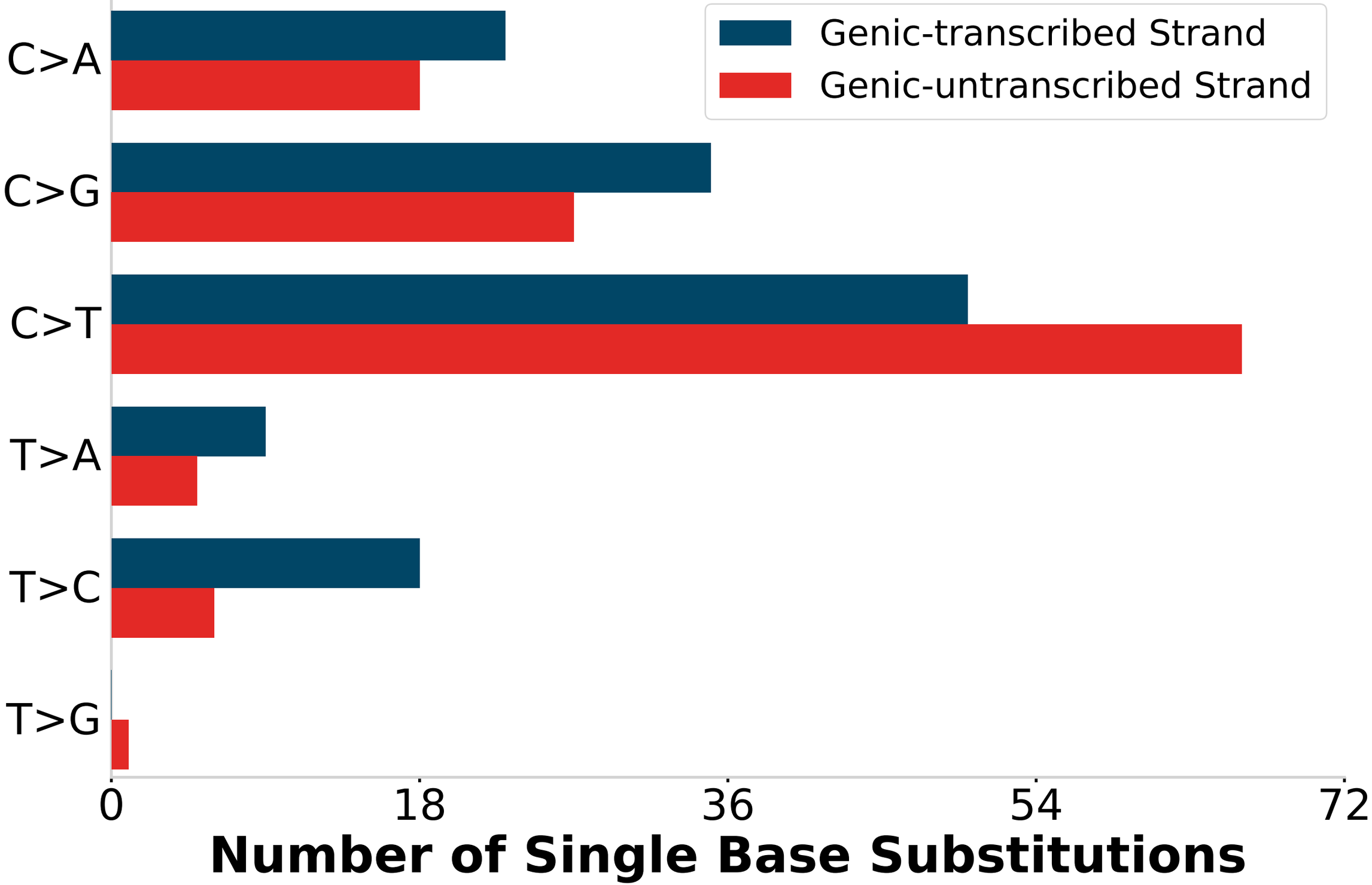
TCGA-ZF-A9RD-01A-11D-A42E-08: 191 tra



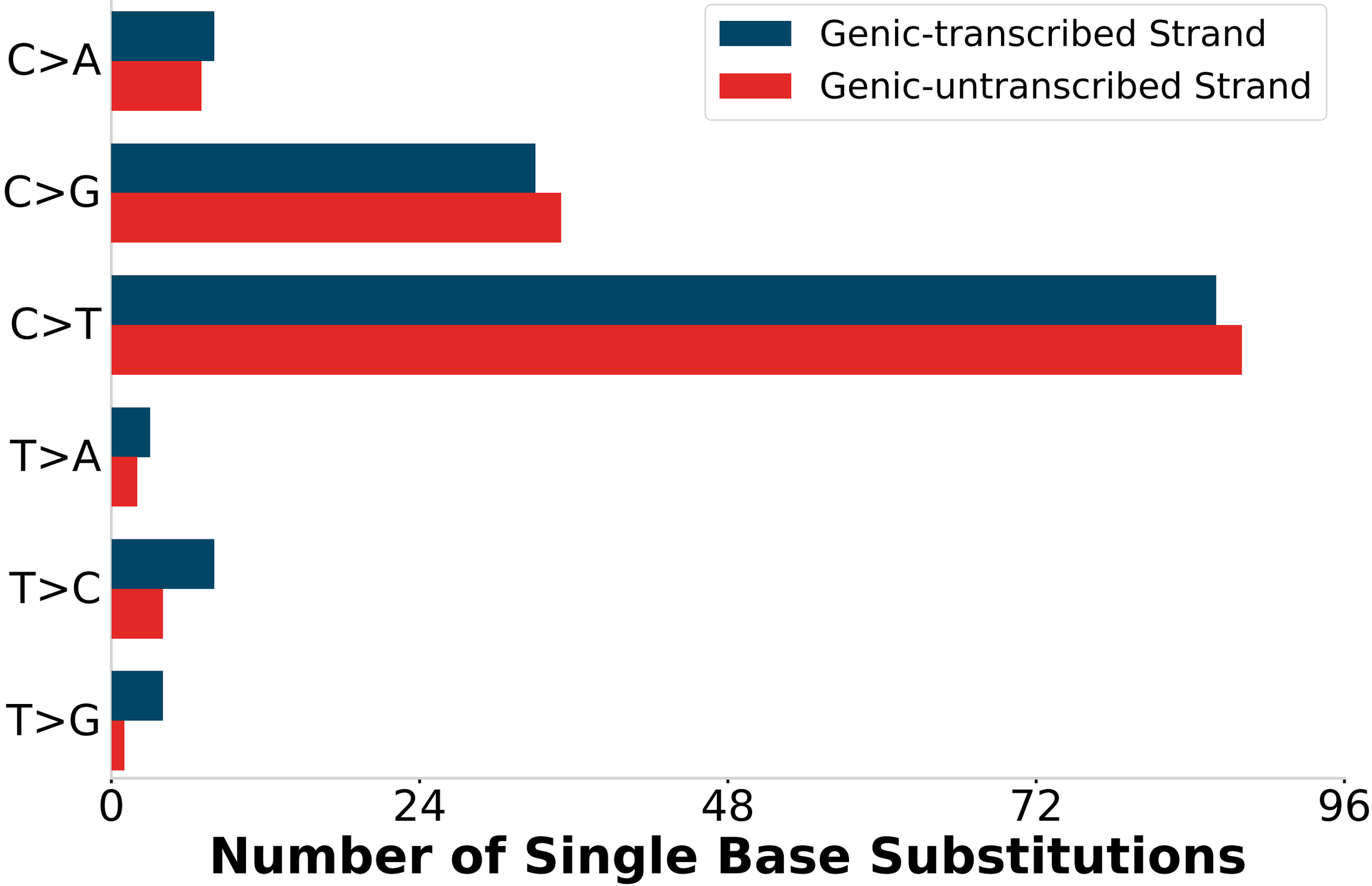
TCGA-ZF-A9RE-01A-11D-A38G-08: 62 trans



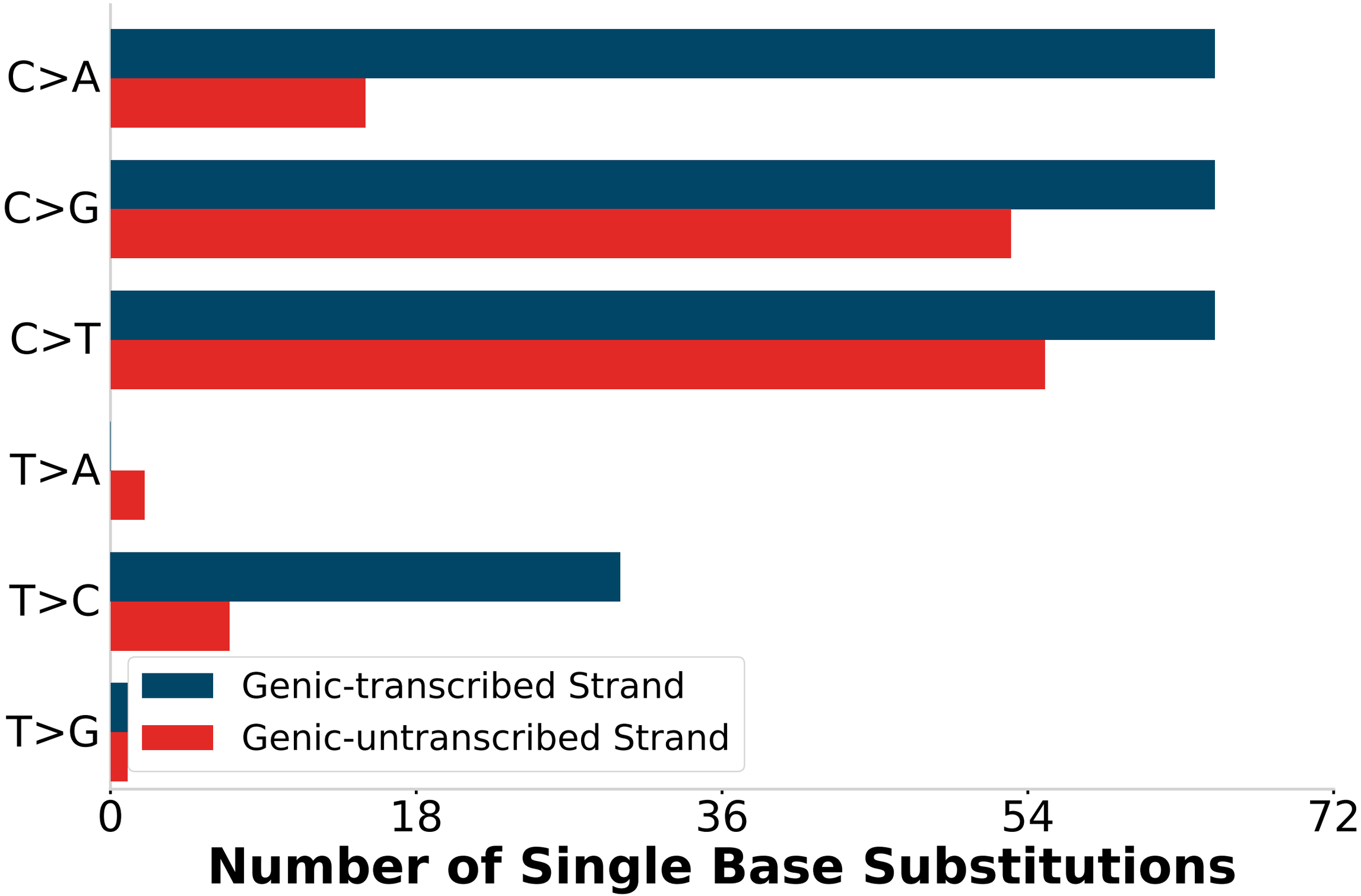
TCGA-ZF-A9RF-01A-11D-A38G-08: 258 tra



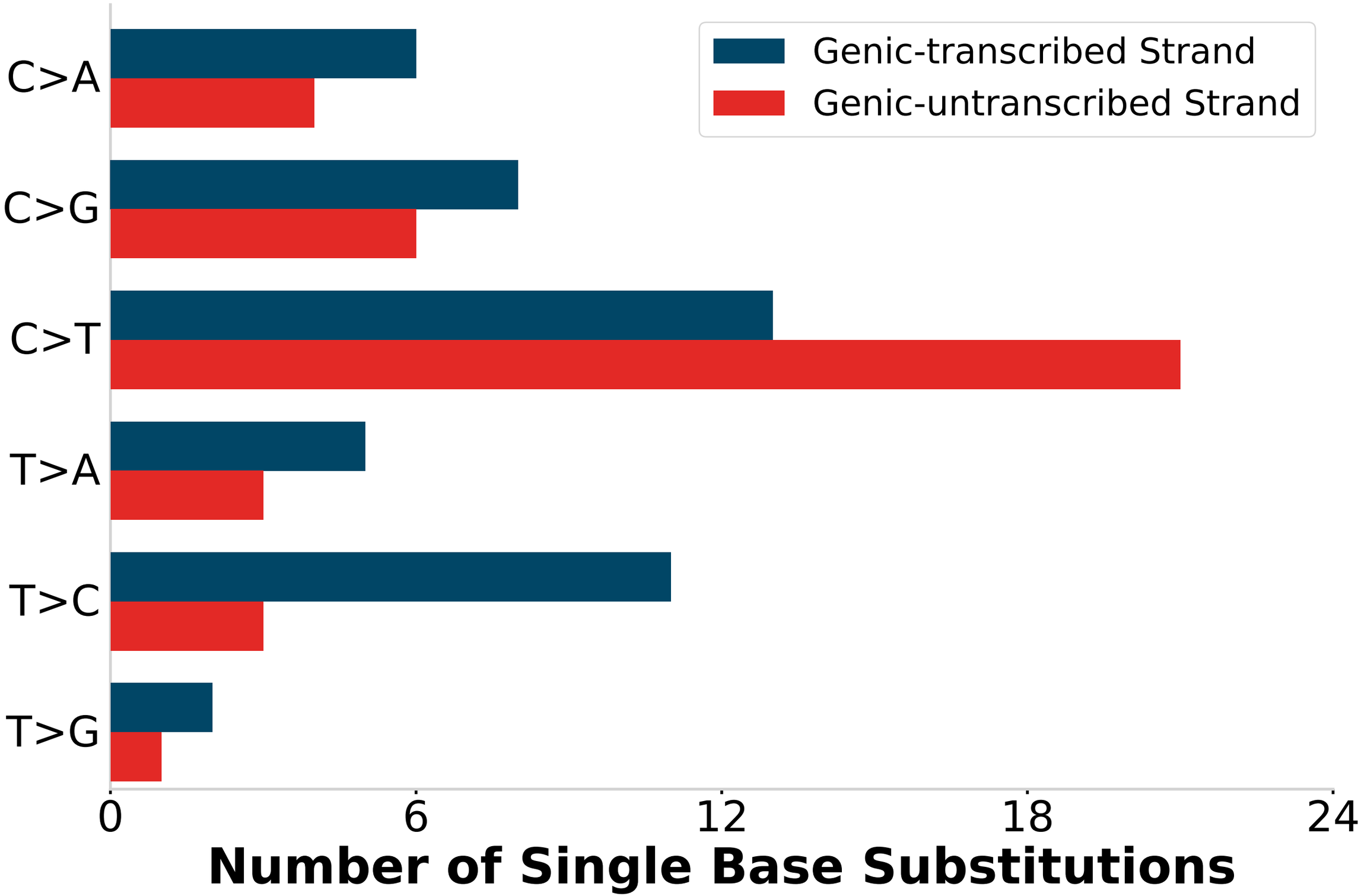
TCGA-ZF-A9RG-01A-21D-A42E-08: 279 tra



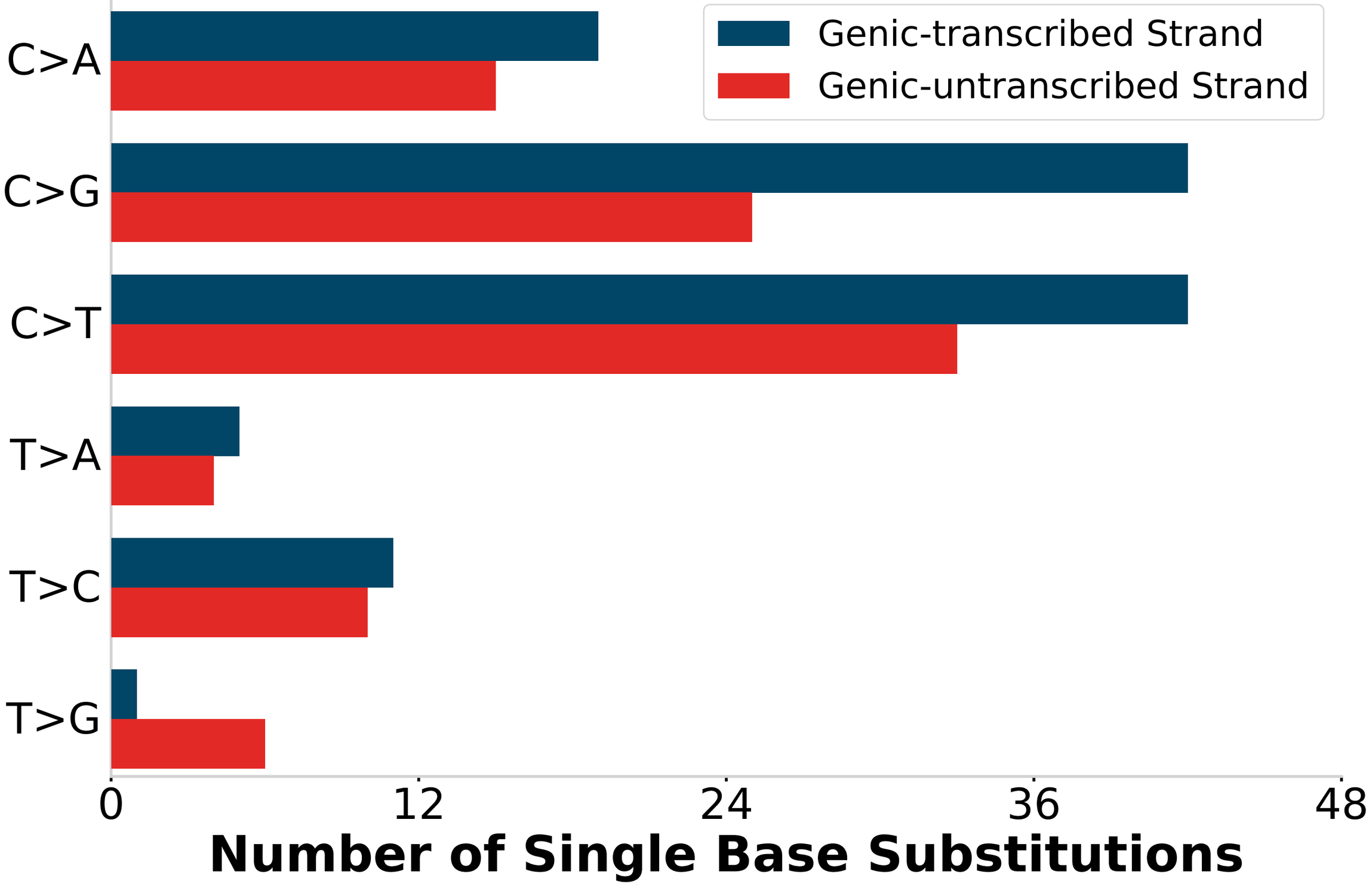
TCGA-ZF-A9RL-01A-11D-A38G-08: 359 tra



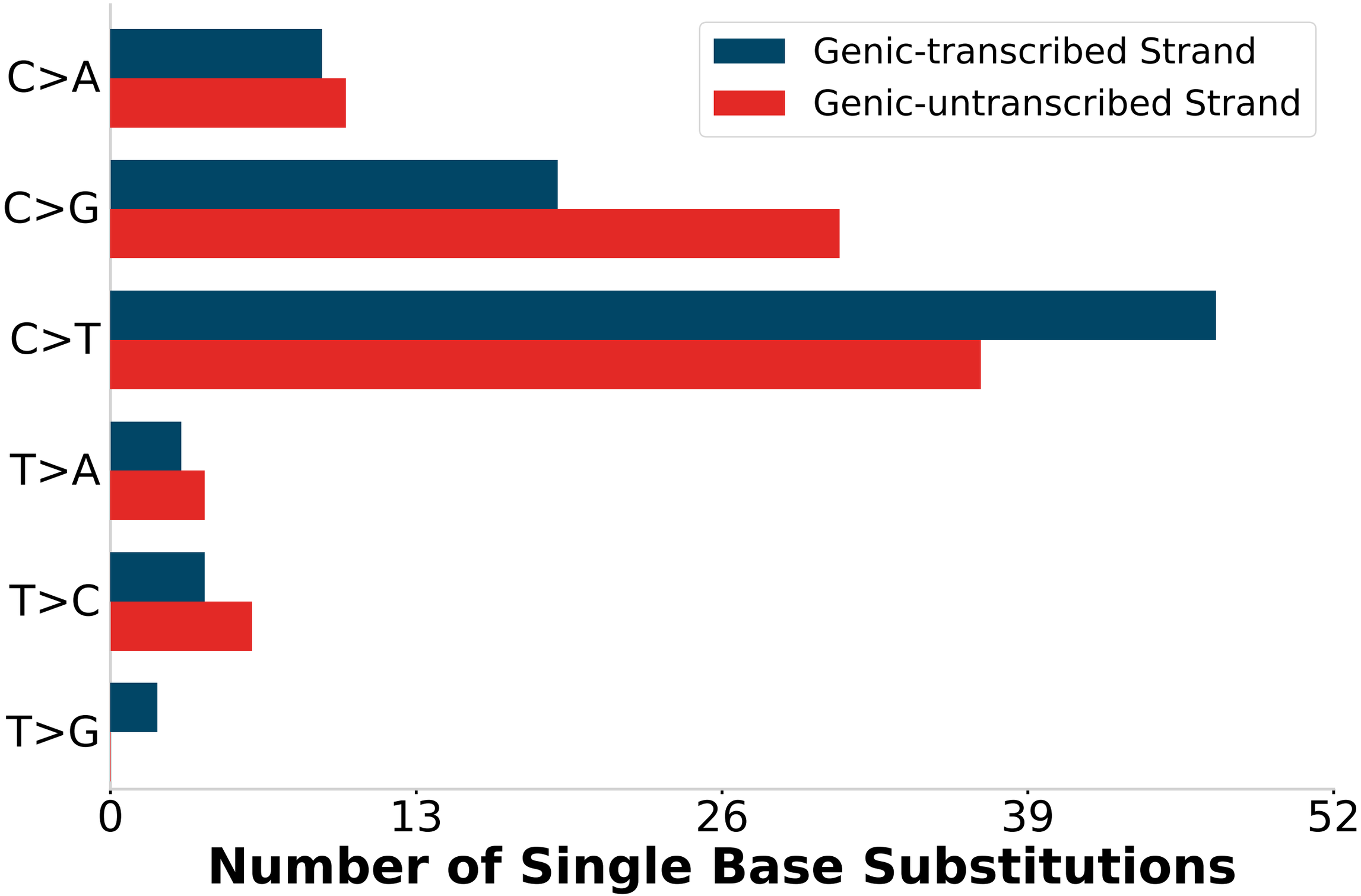
TCGA-ZF-A9RM-01A-11D-A38G-08: 83 tran



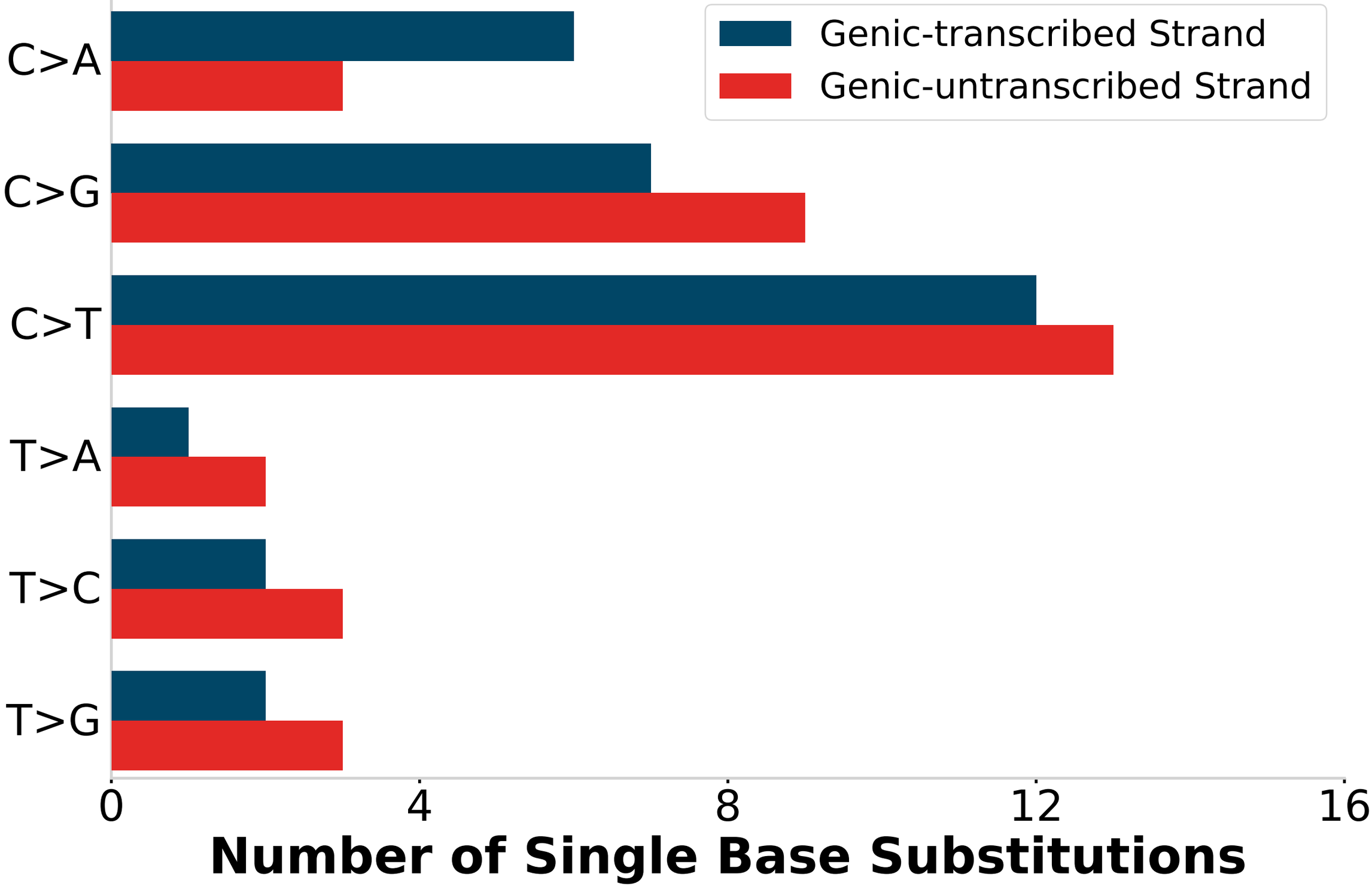
TCGA-ZF-A9RN-01A-11D-A42E-08: 213 tra



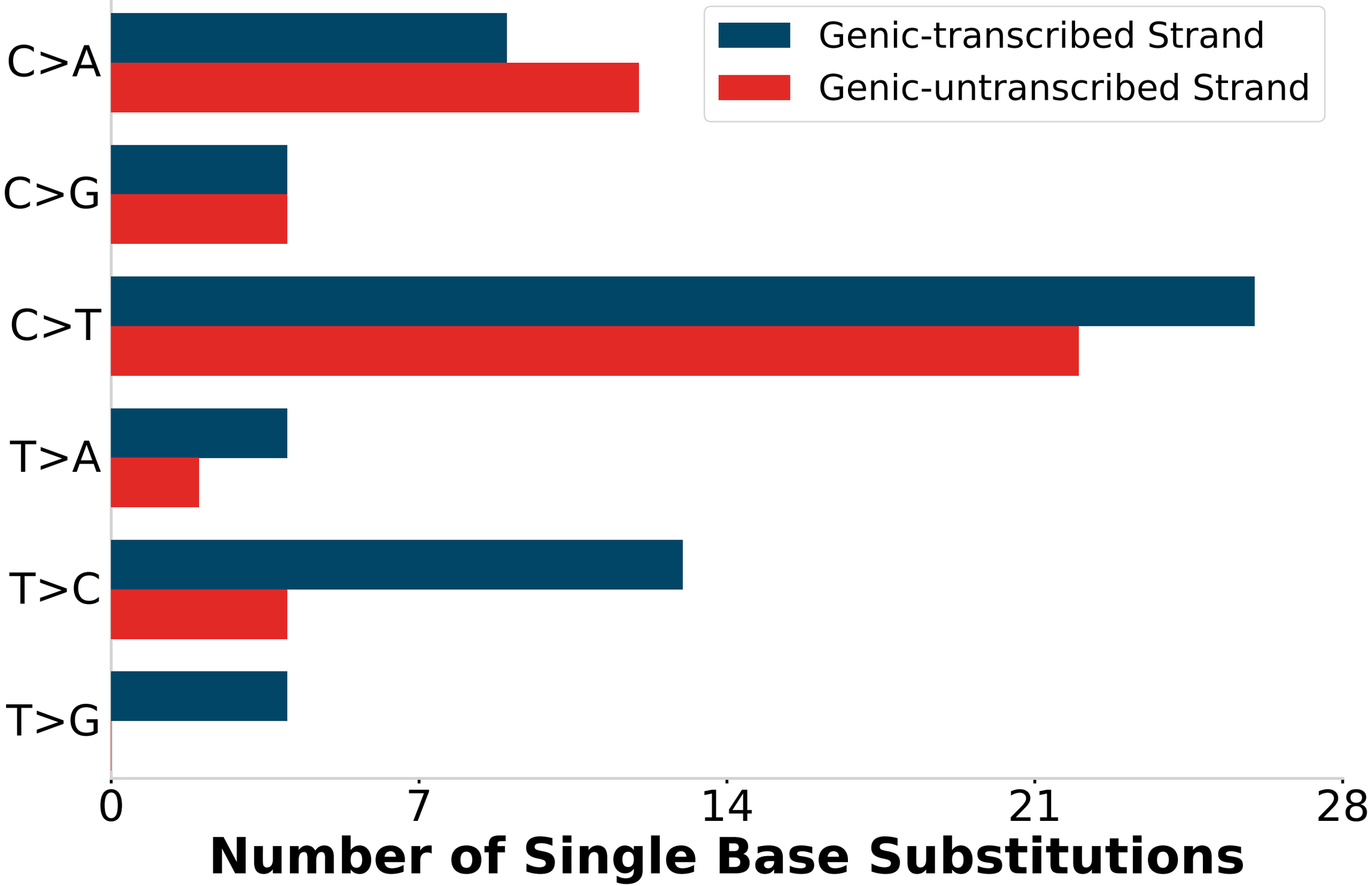
TCGA-ZF-AA4N-01A-11D-A38G-08: 172 tra



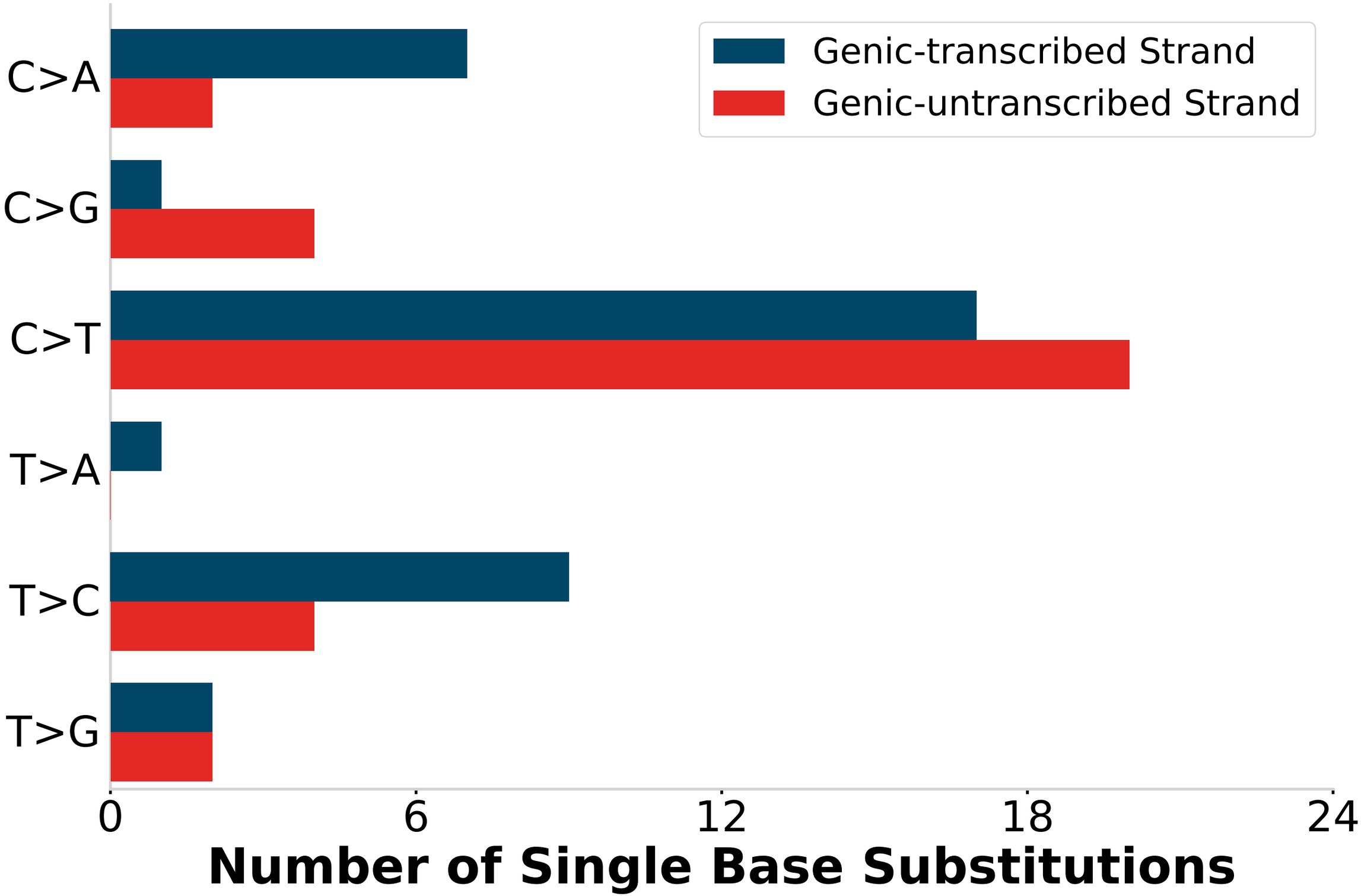
TCGA-ZF-AA4R-01A-11D-A38G-08: 63 trans



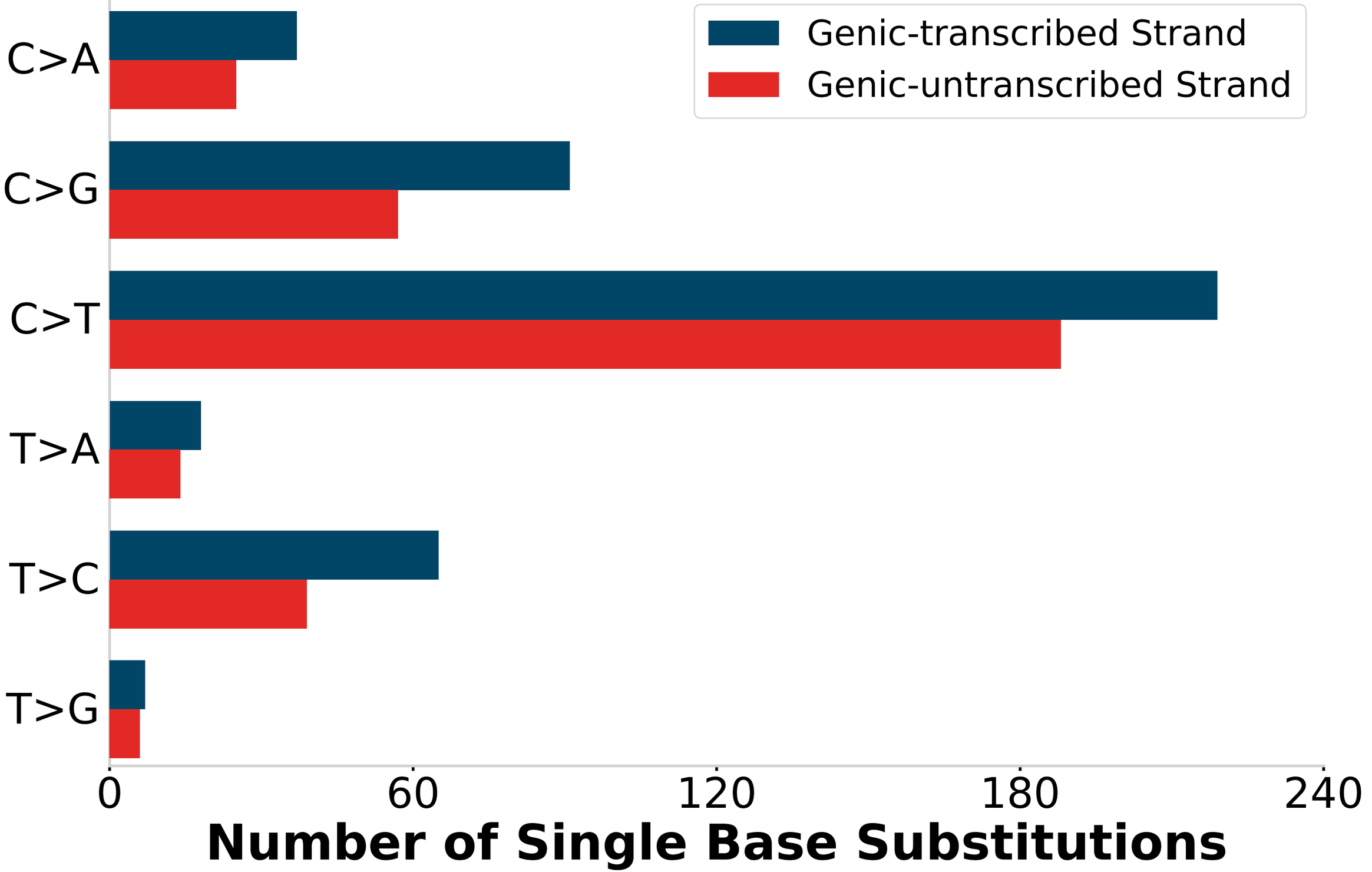
TCGA-ZF-AA4T-01A-11D-A38G-08: 104 tran



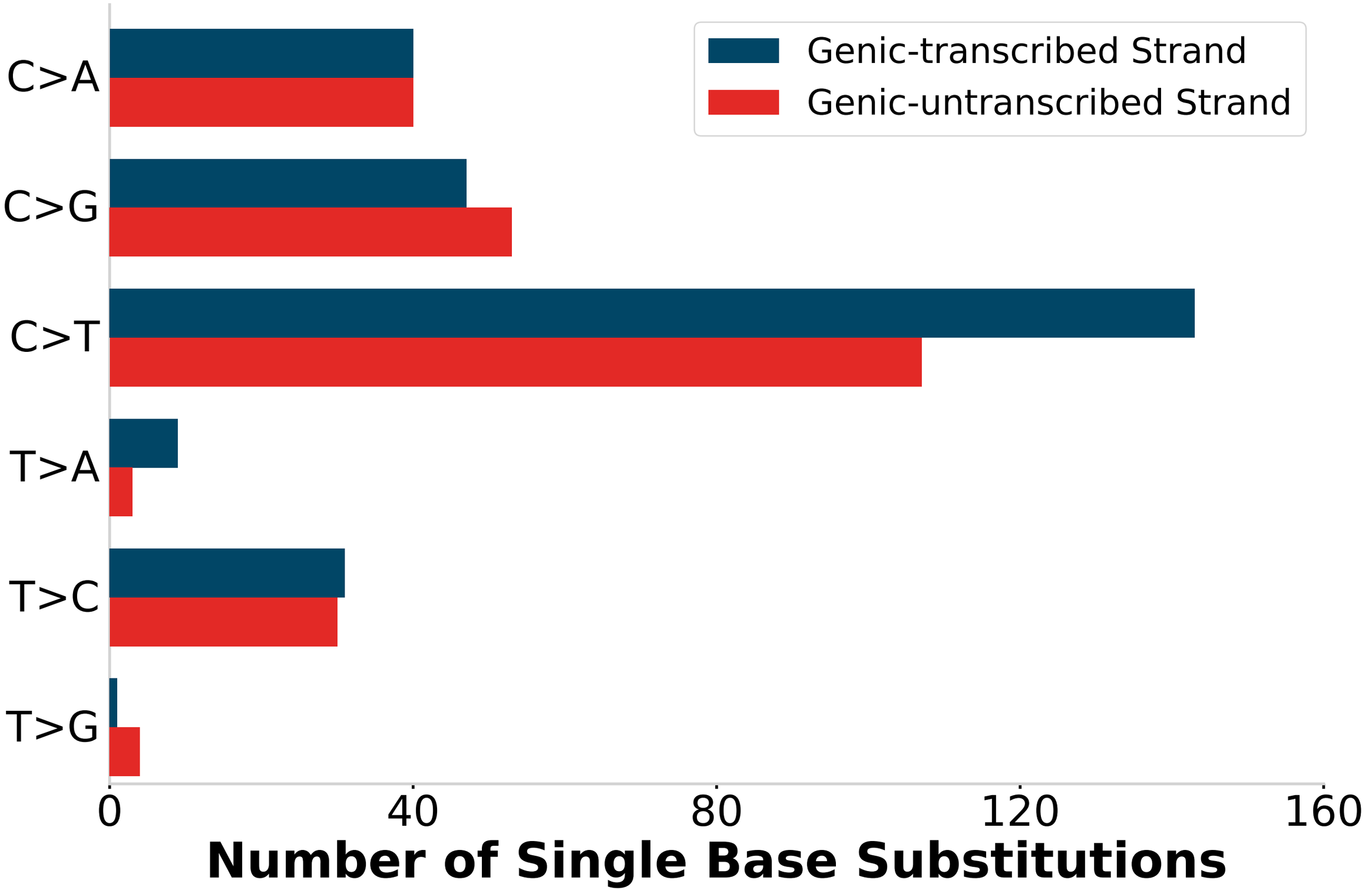
TCGA-ZF-AA4U-01A-11D-A38G-08: 69 tran

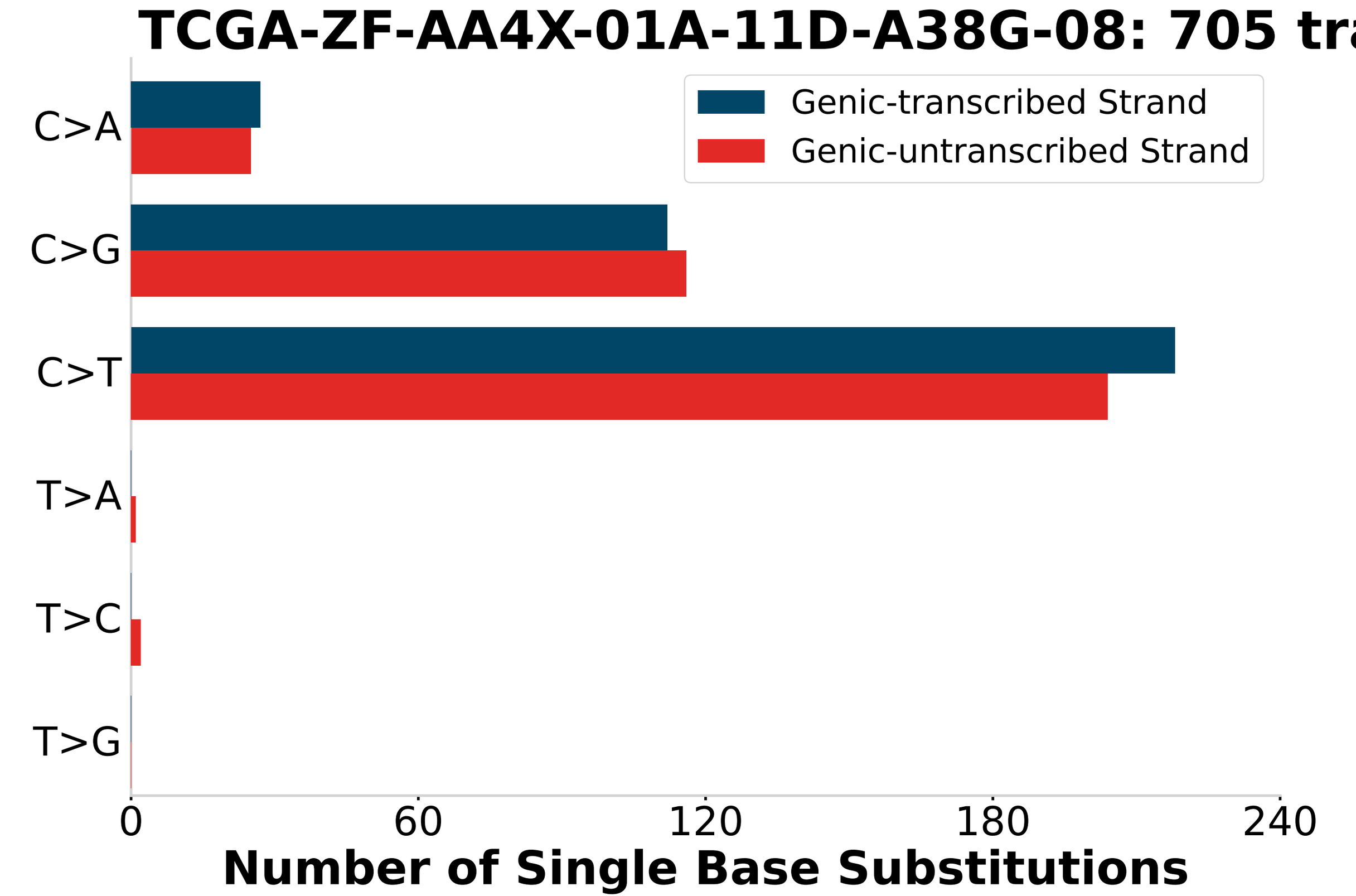


TCGA-ZF-AA4V-01A-11D-A38G-08: 766 tra

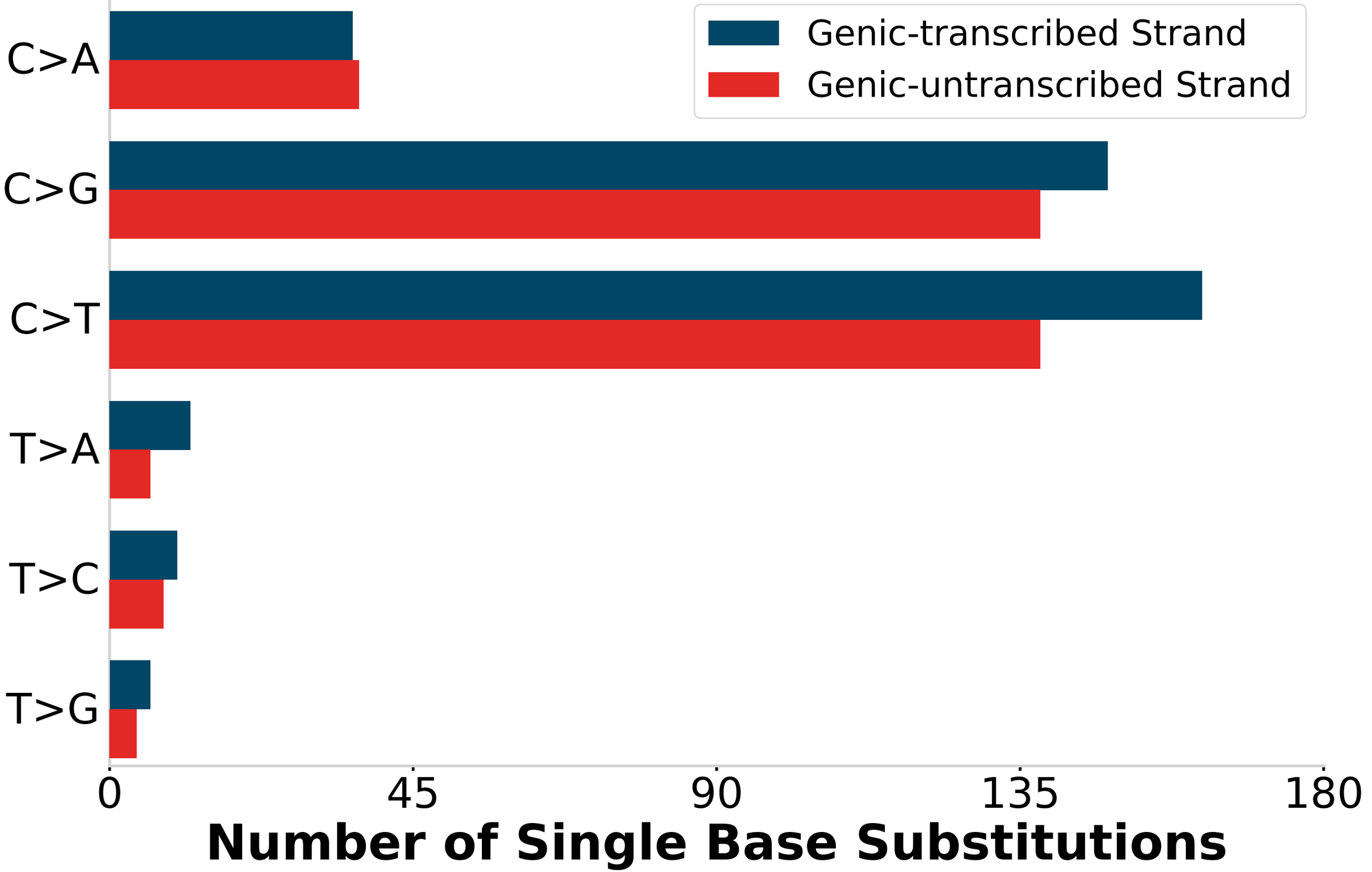


TCGA-ZF-AA4W-01A-12D-A38G-08: 508 tra

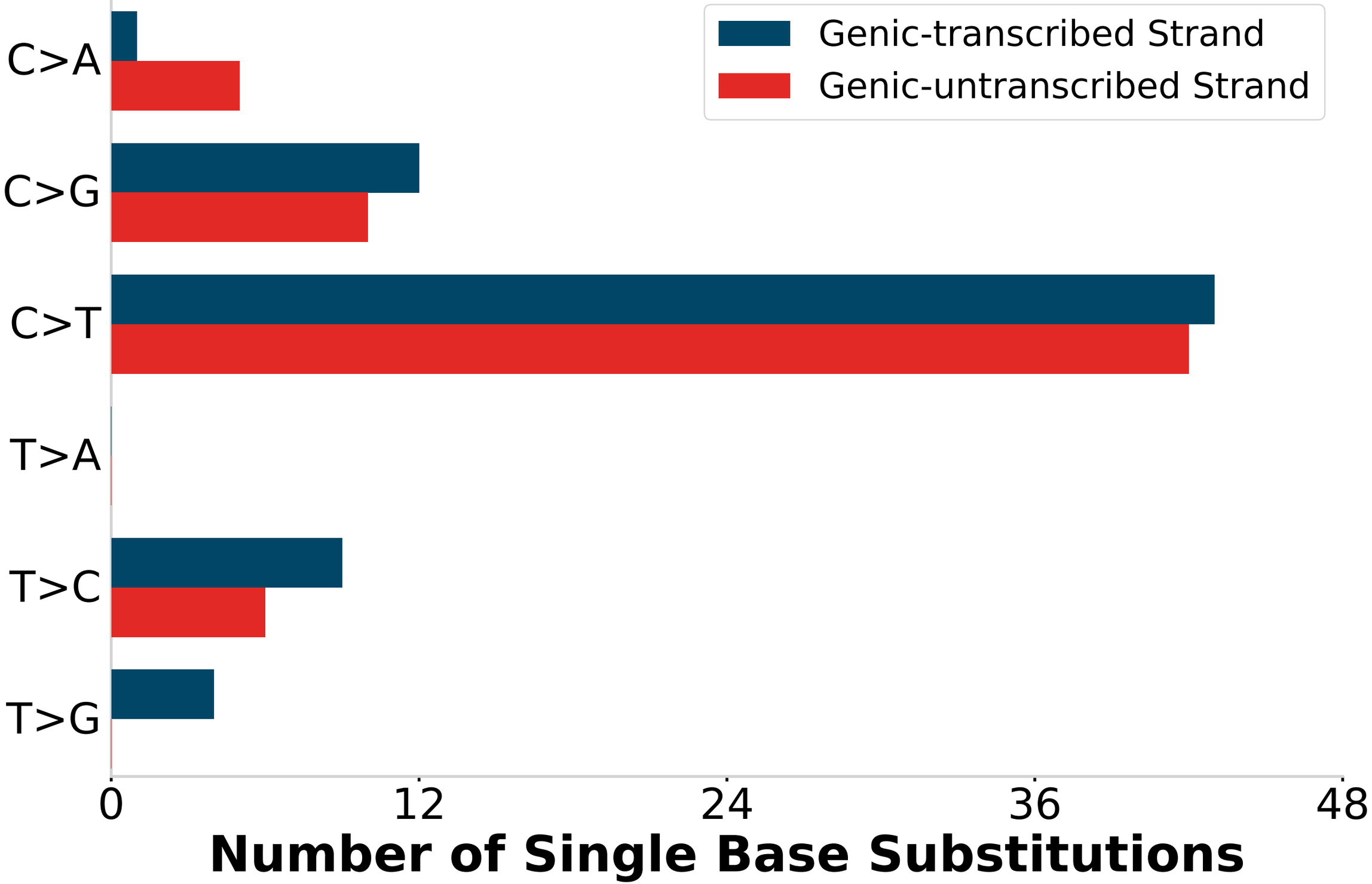



TCGA-ZF-AA4X-01A-11D-A38G-08: 705 tra
Genic-transcribed Strand
Genic-untranscribed Strand
C>A
C>G
C>T
T>A
T>C
T>G
0
60
120
180
240
Number of Single Base Substitutions

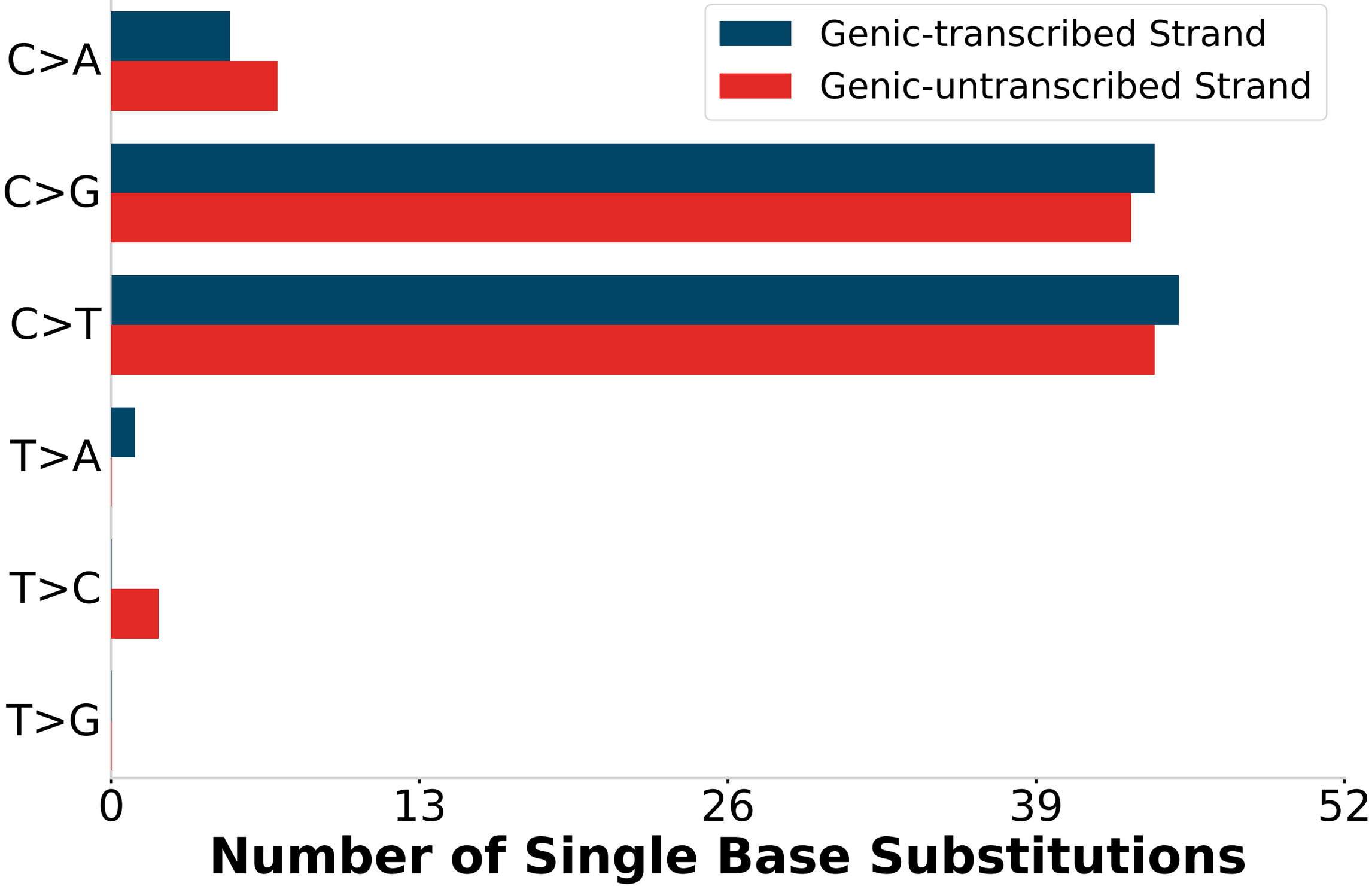
TCGA-ZF-AA51-01A-21D-A391-08: 705 tran



TCGA-ZF-AA52-01A-12D-A391-08: 132 tran



TCGA-ZF-AA53-01A-11D-A391-08: 191 tran



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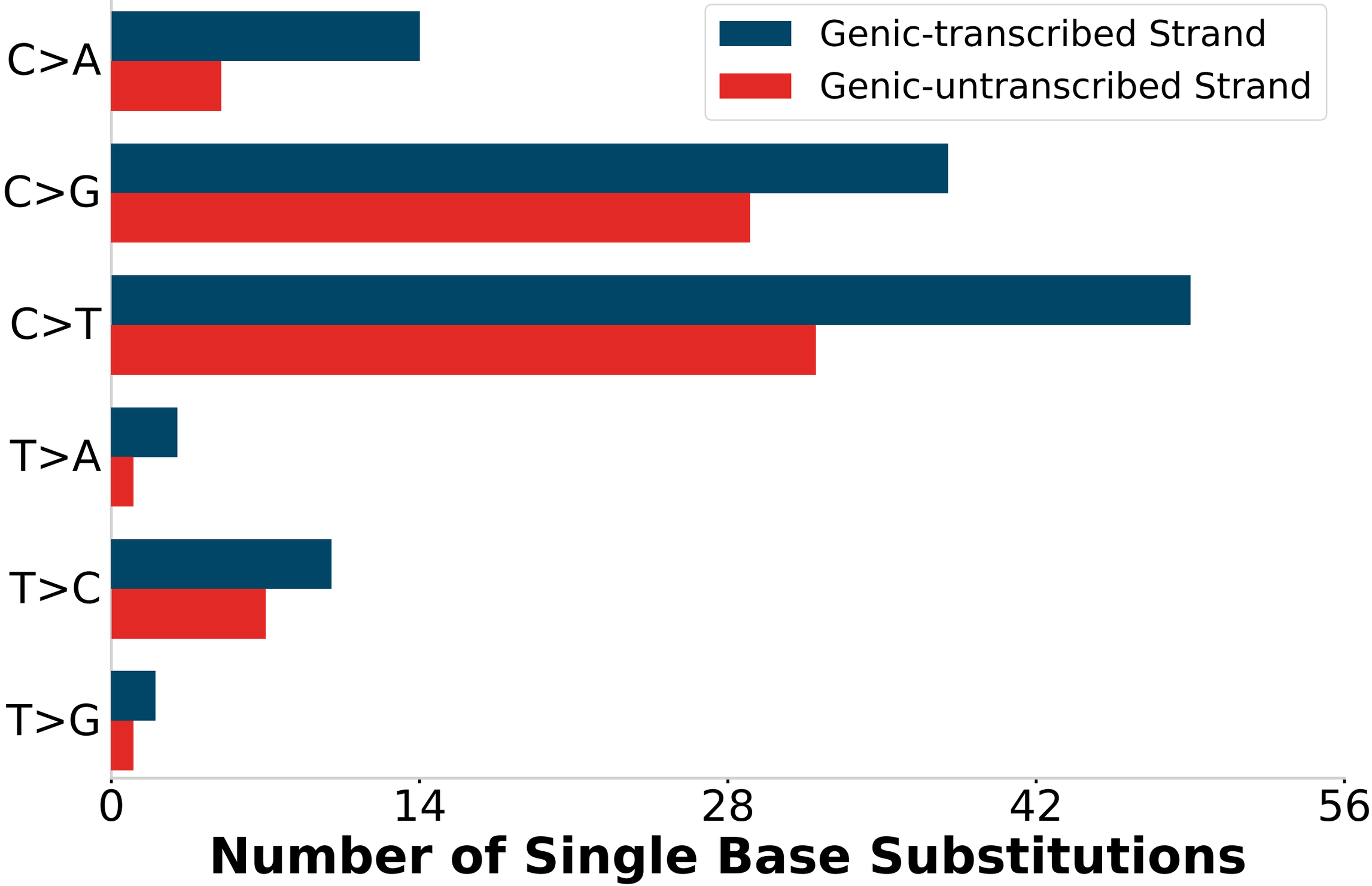
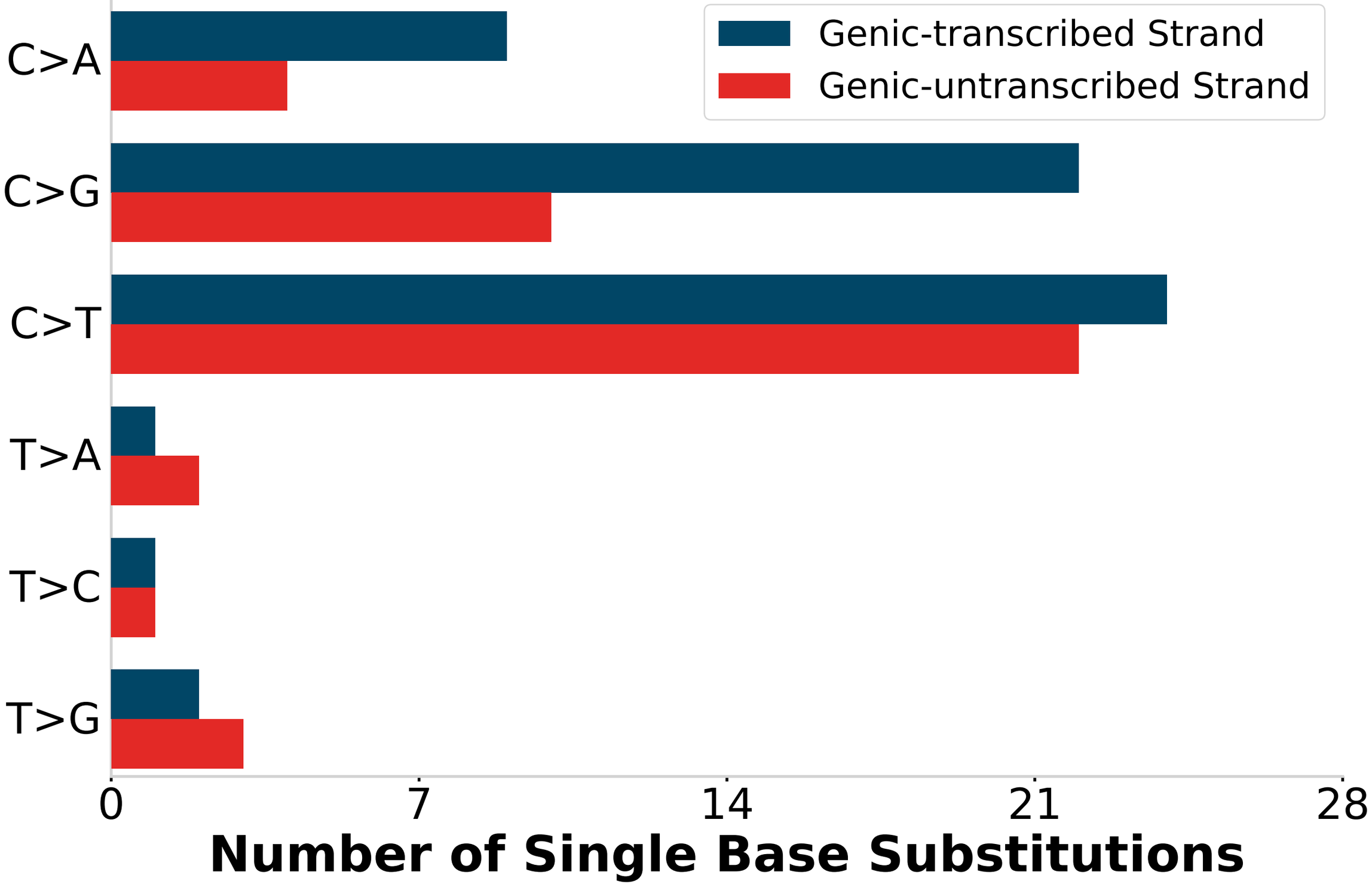
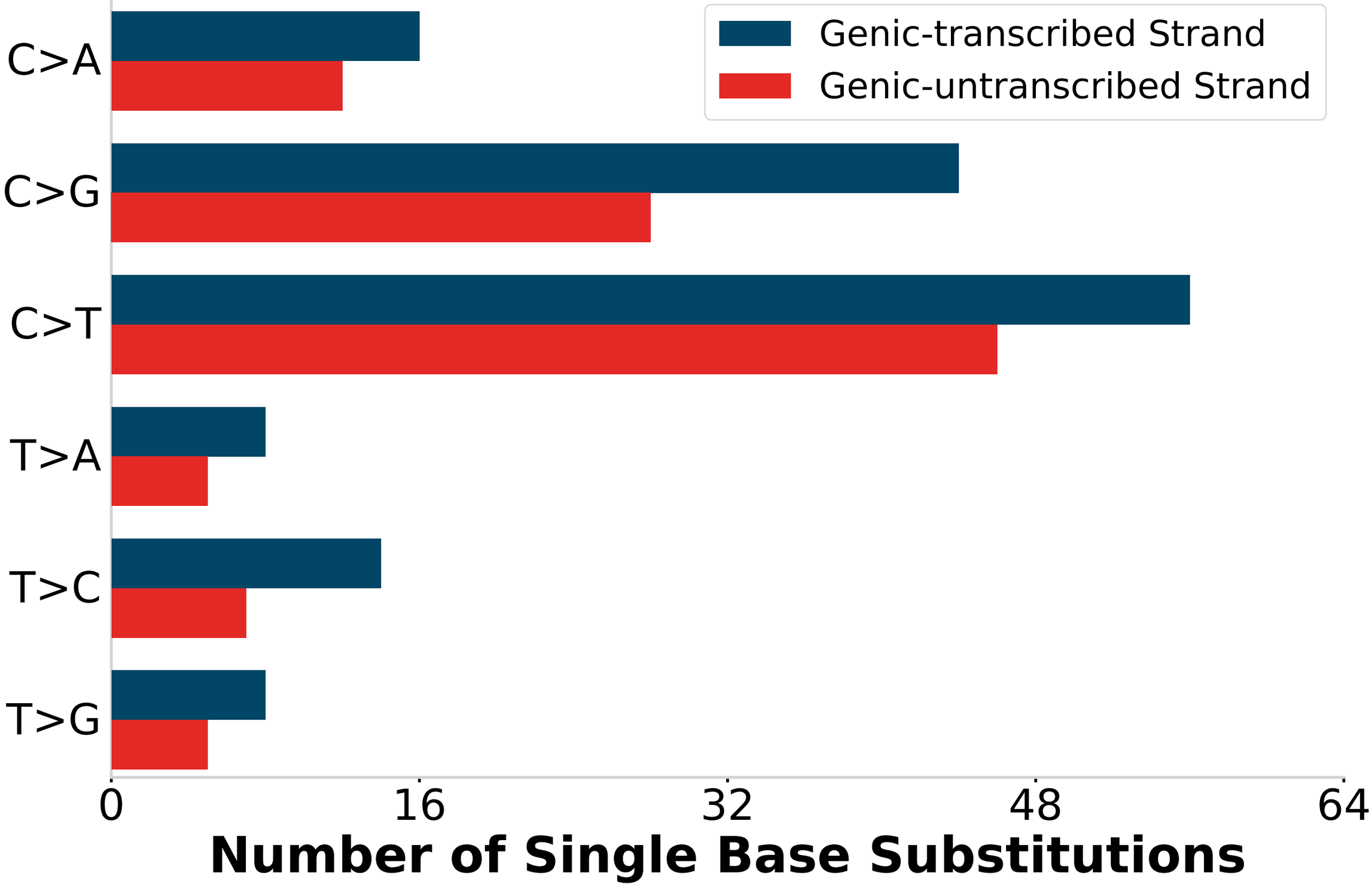


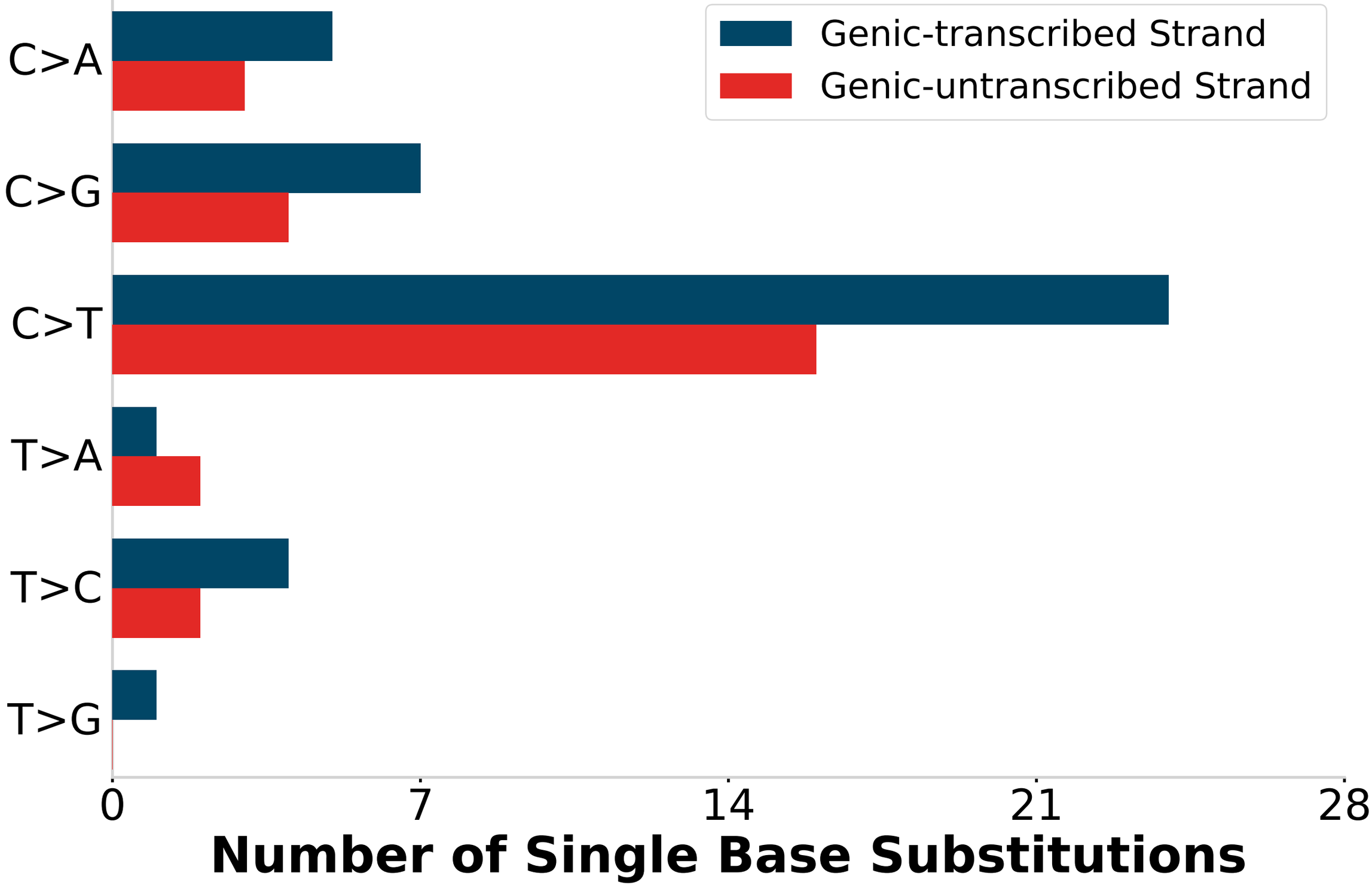
TCGA-ZF-AA56-01A-31D-A391-08: 101 tran



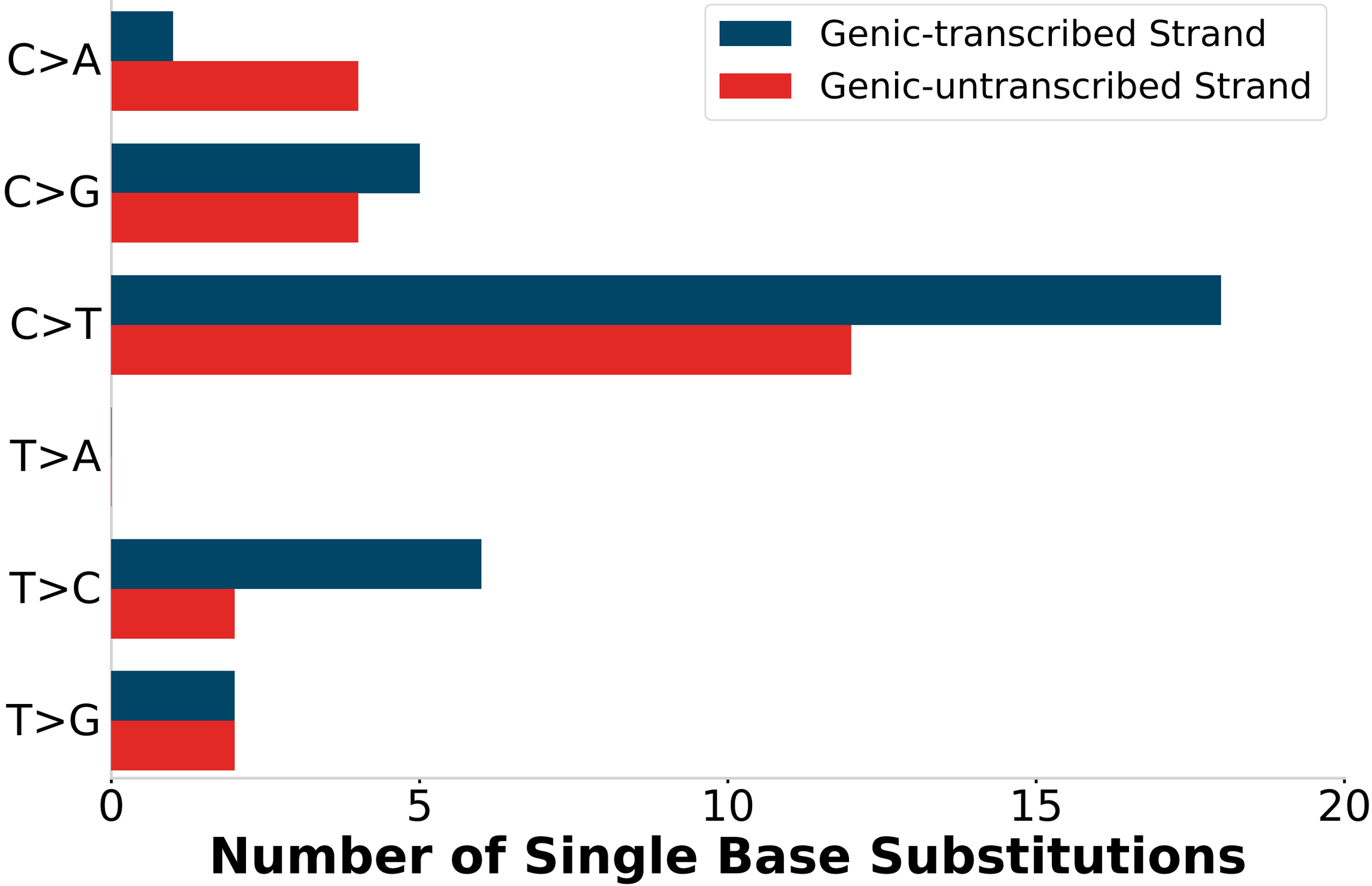
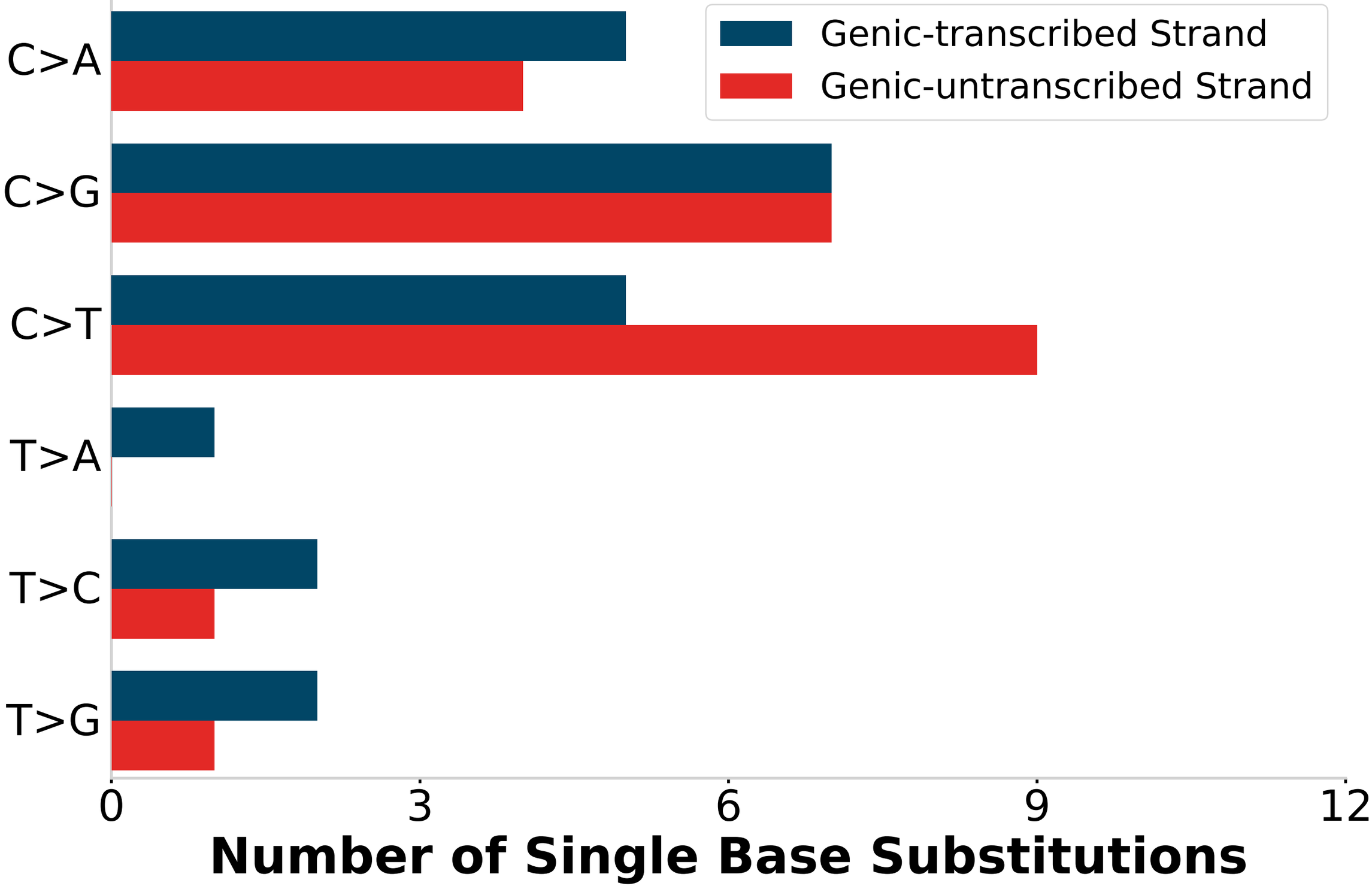
TCGA-ZF-AA58-01A-12D-A42E-08: 249 tran



TCGA-ZF-AA5H-01A-11D-A391-08: 69 trans



TCGA-ZF-AA5N-01A-11D-A42E-08: 56 trans



TCGA-ZF-AA5P-01A-11D-A391-08: 44 trans