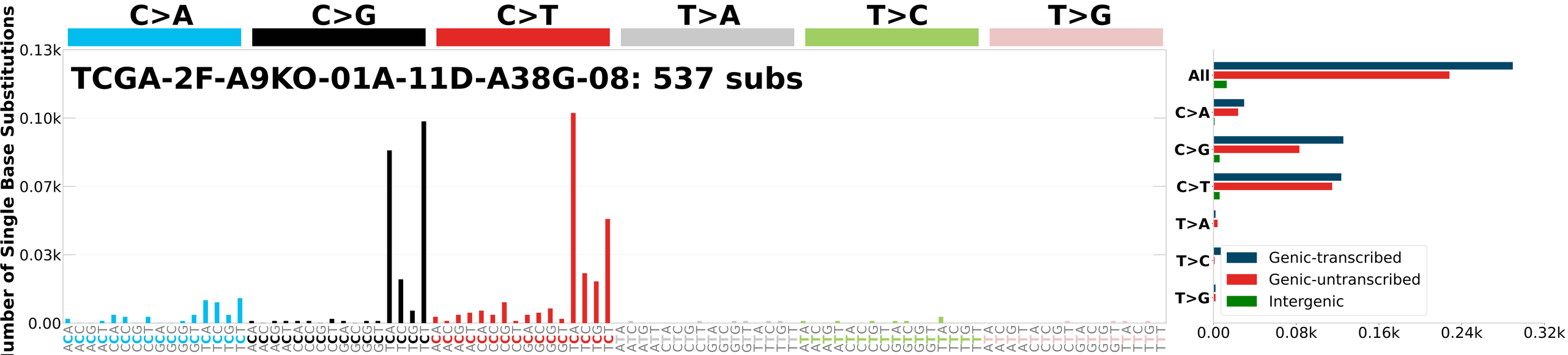
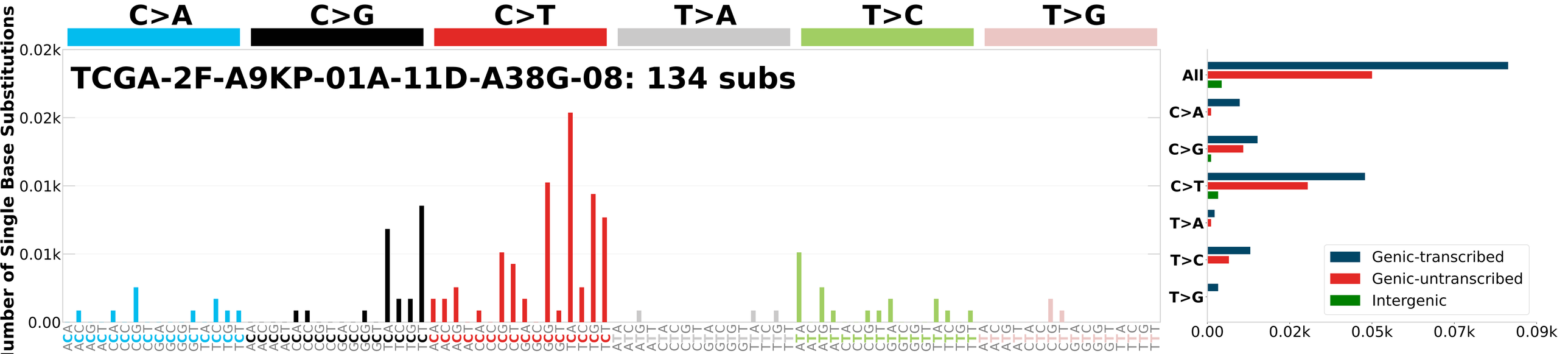
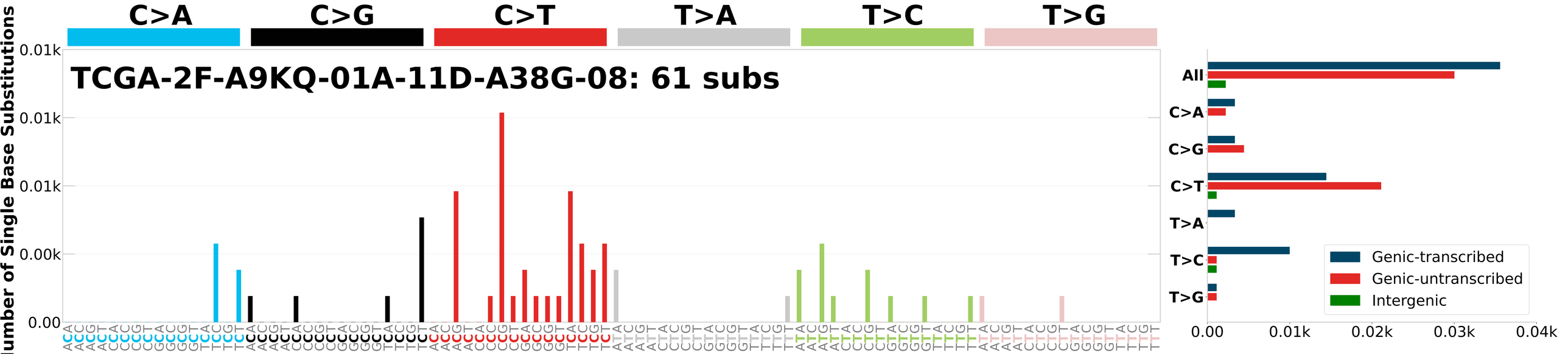
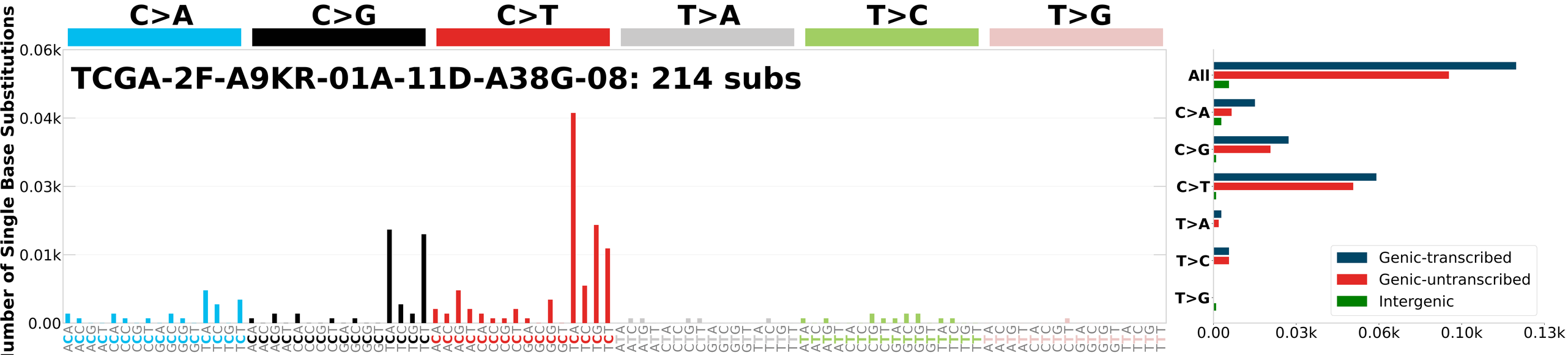
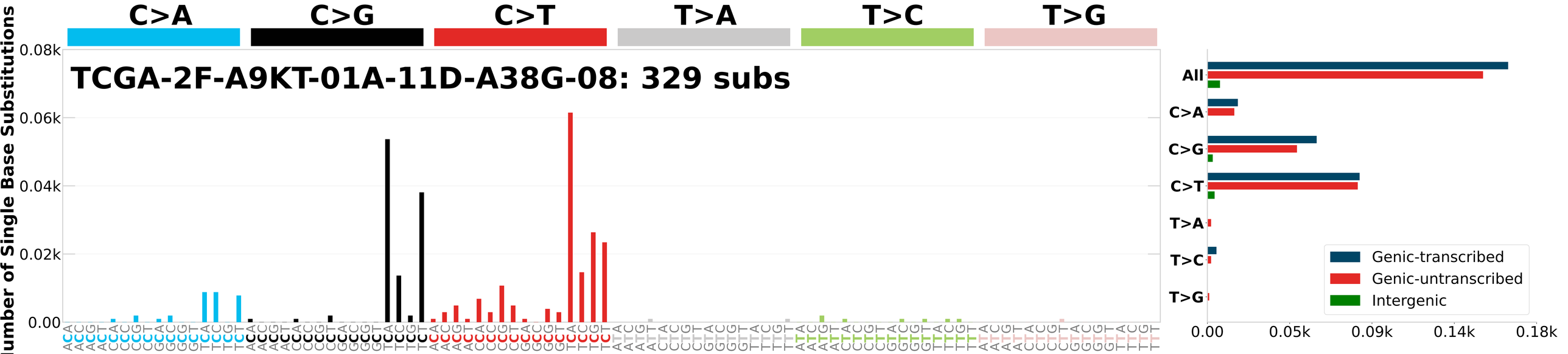
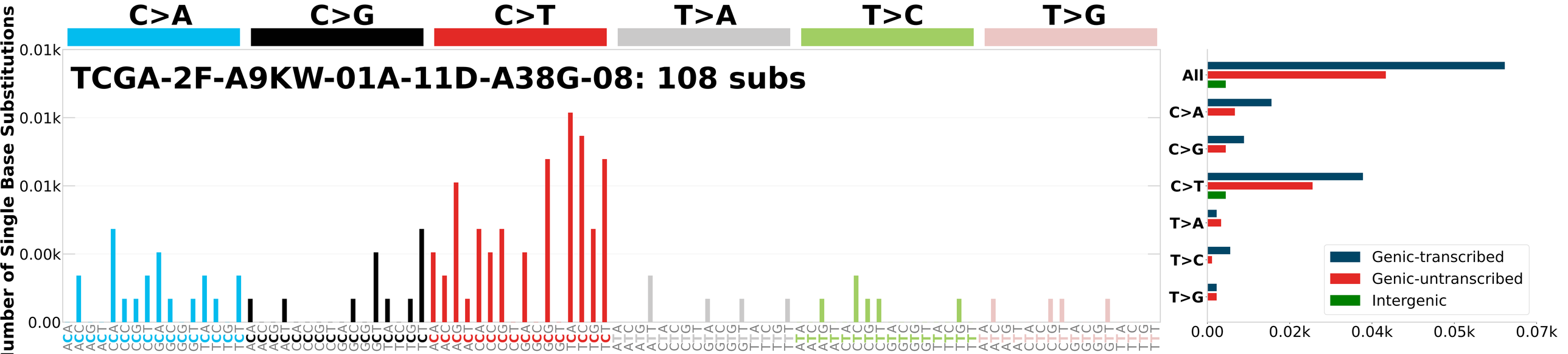

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-2F-A9KO-01A-11D-A38G-08: 537 subs
Number of Single Base Substitutions
0.13k
0.10k
0.07k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.08k
0.16k
0.24k
0.32k

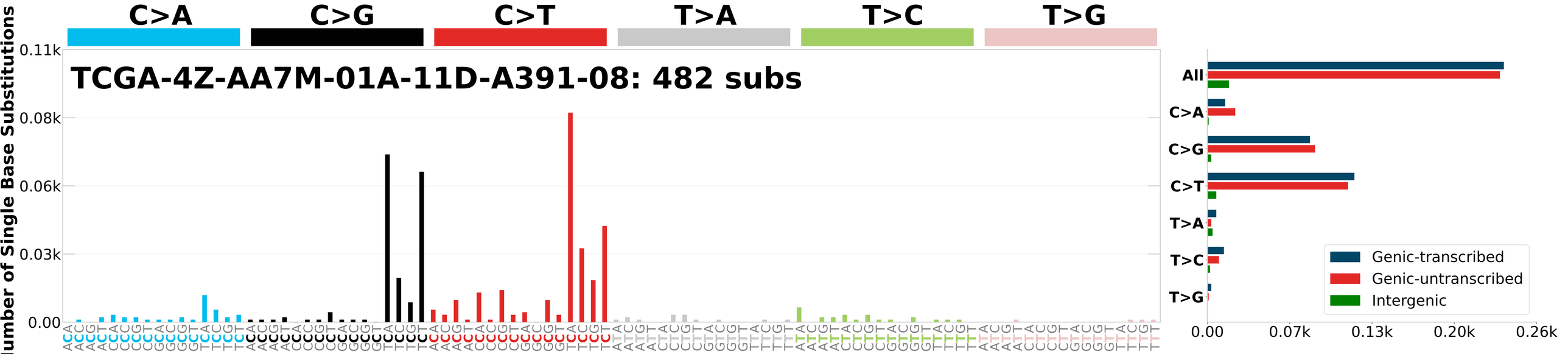

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-2F-A9KP-01A-11D-A38G-08: 134 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.09k

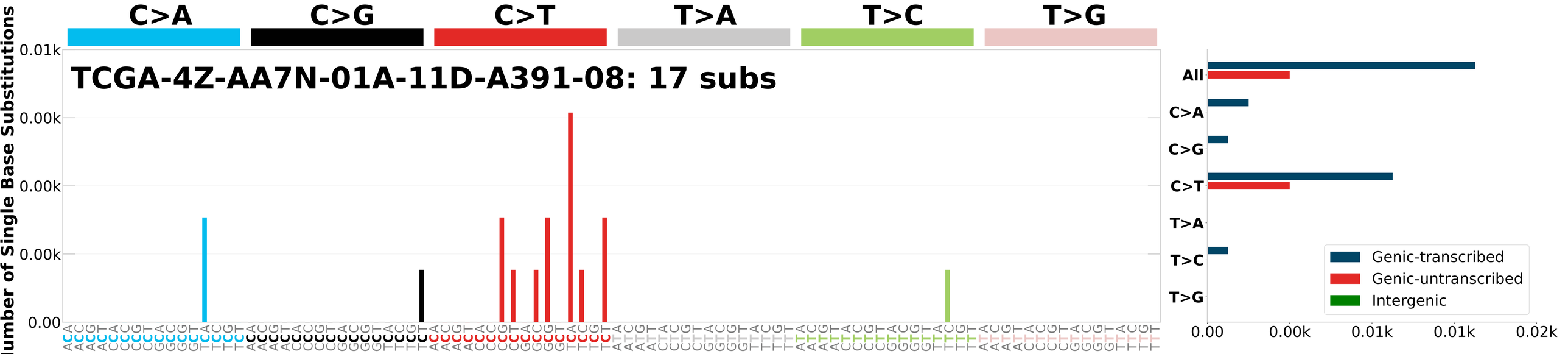

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-2F-A9KQ-01A-11D-A38G-08: 61 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

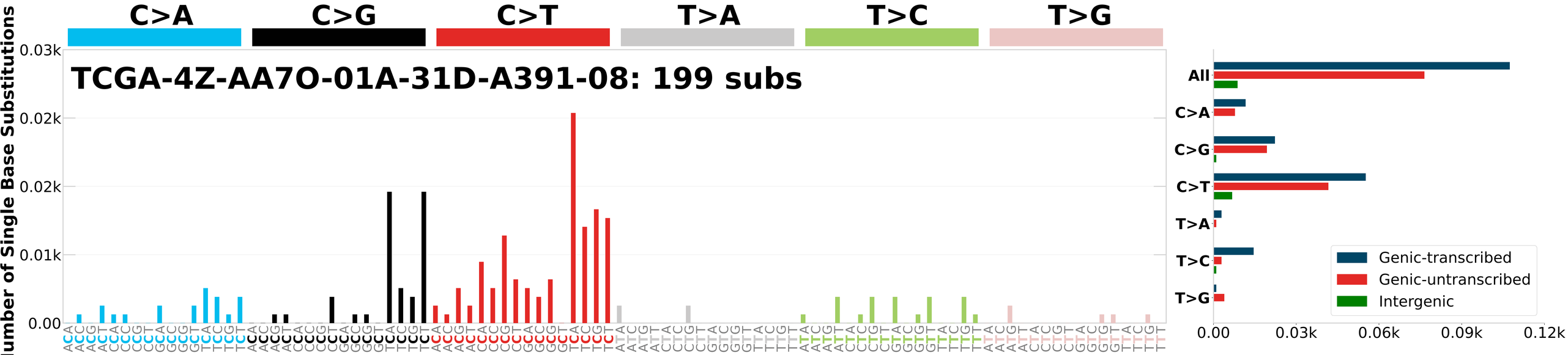

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-2F-A9KR-01A-11D-A38G-08: 214 subs
Number of Single Base Substitutions
0.06k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.10k
0.13k

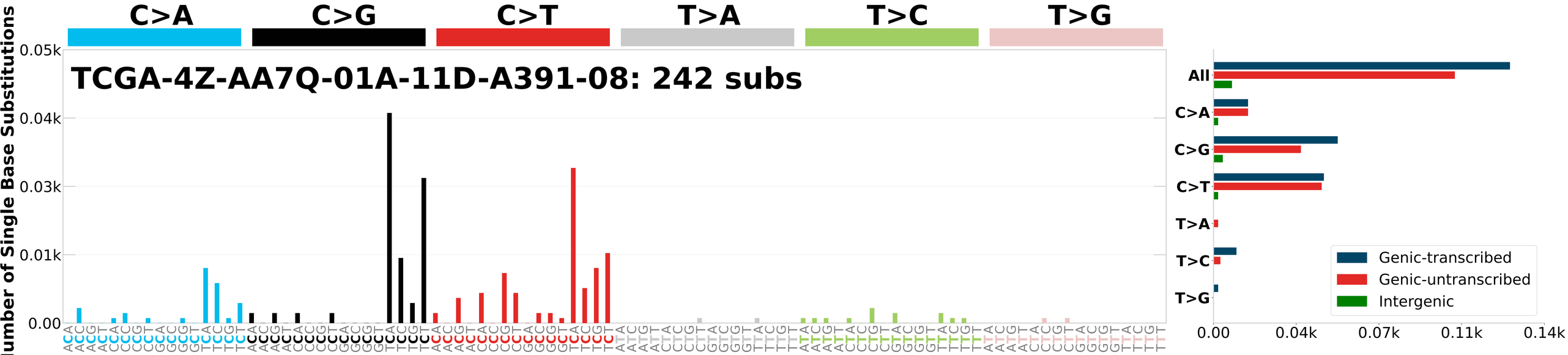

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-2F-A9KT-01A-11D-A38G-08: 329 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.09k
0.14k
0.18k

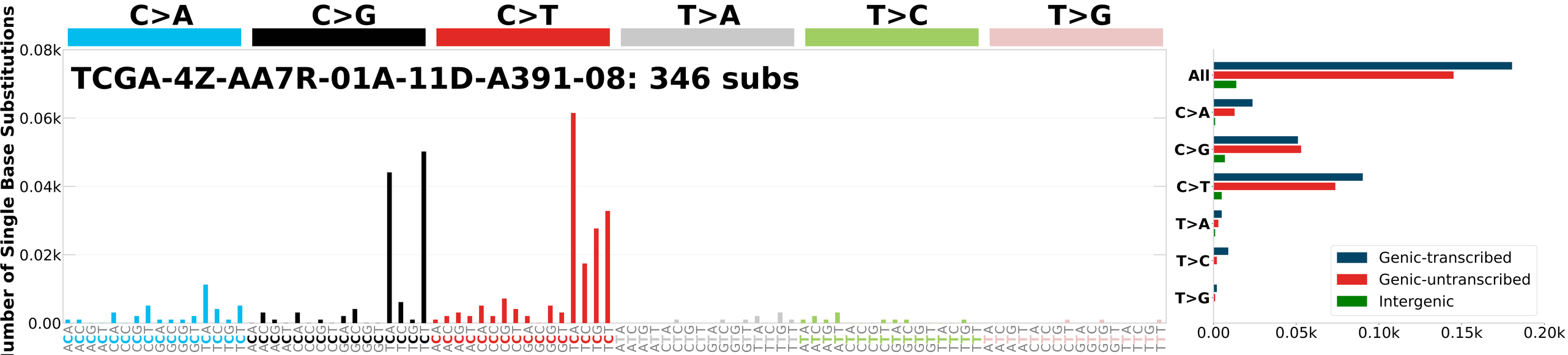

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-2F-A9KW-01A-11D-A38G-08: 108 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.05k
0.07k

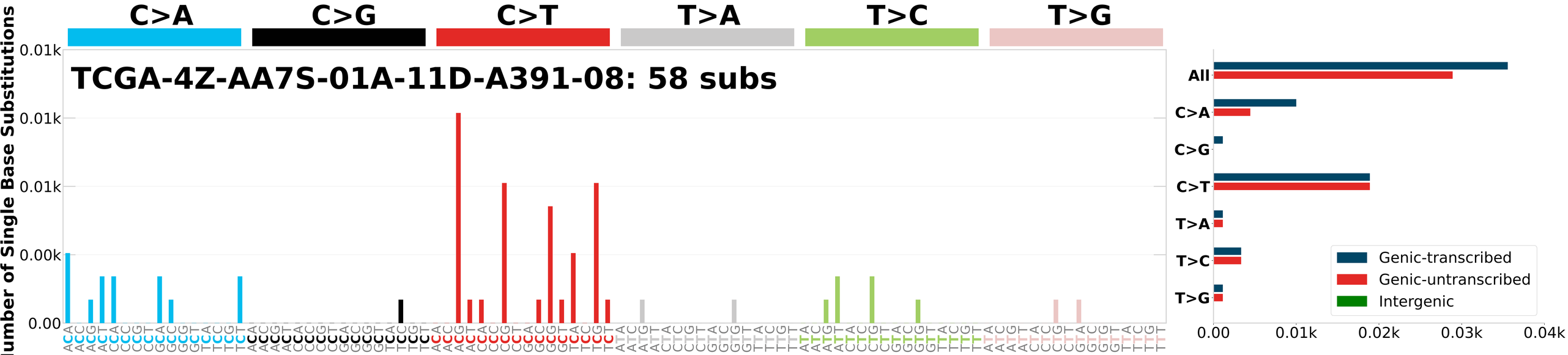

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA7M-01A-11D-A391-08: 482 subs
Number of Single Base Substitutions
0.11k
0.08k
0.06k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.13k
0.20k
0.26k

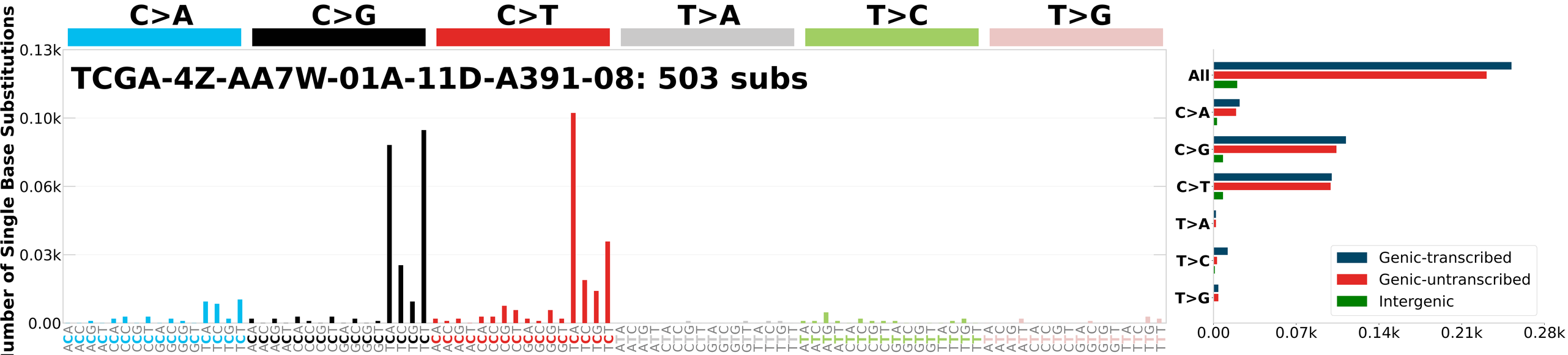

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA7N-01A-11D-A391-08: 17 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.00k
0.01k
0.01k
0.02k

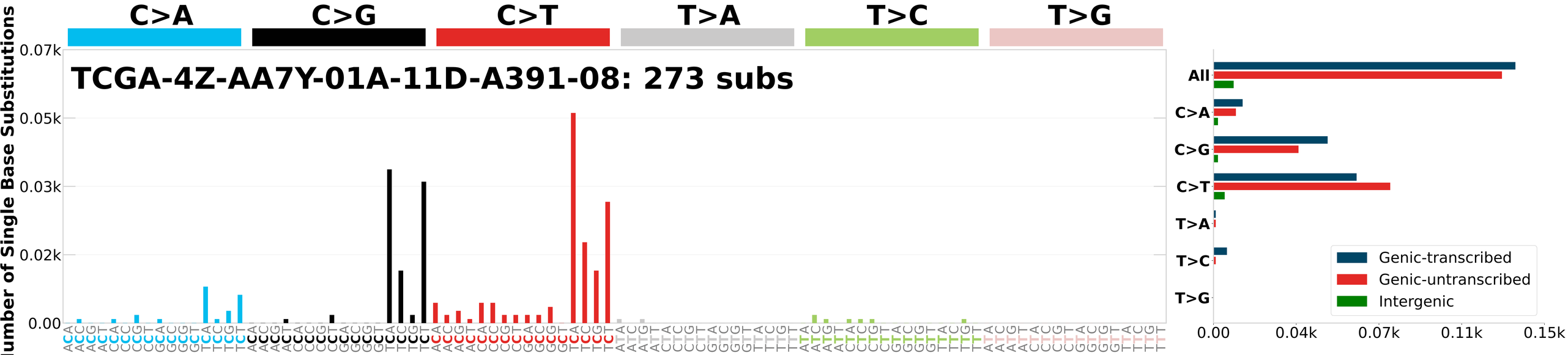

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA7O-01A-31D-A391-08: 199 subs
Number of Single Base Substitutions
0.03k
0.02k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

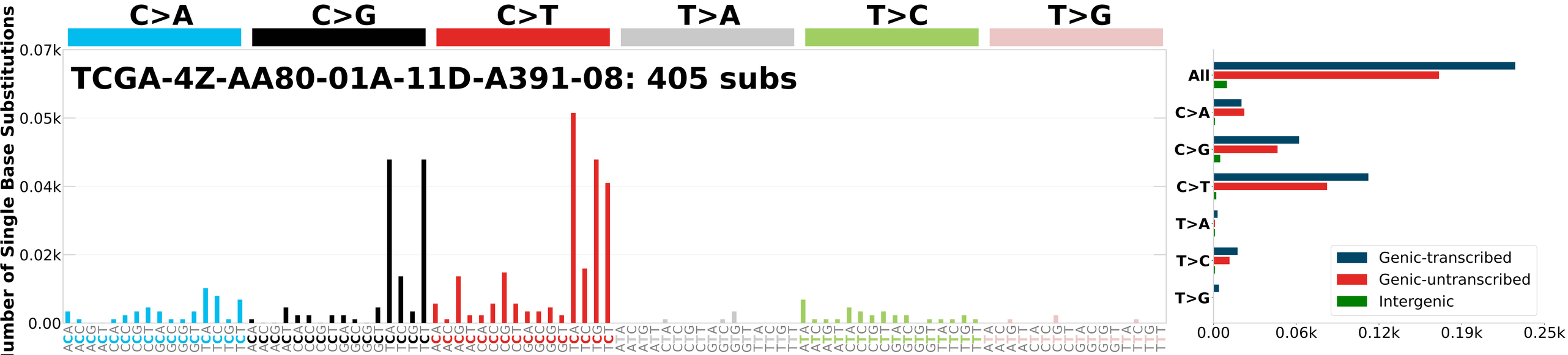

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA7Q-01A-11D-A391-08: 242 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.07k
0.11k
0.14k

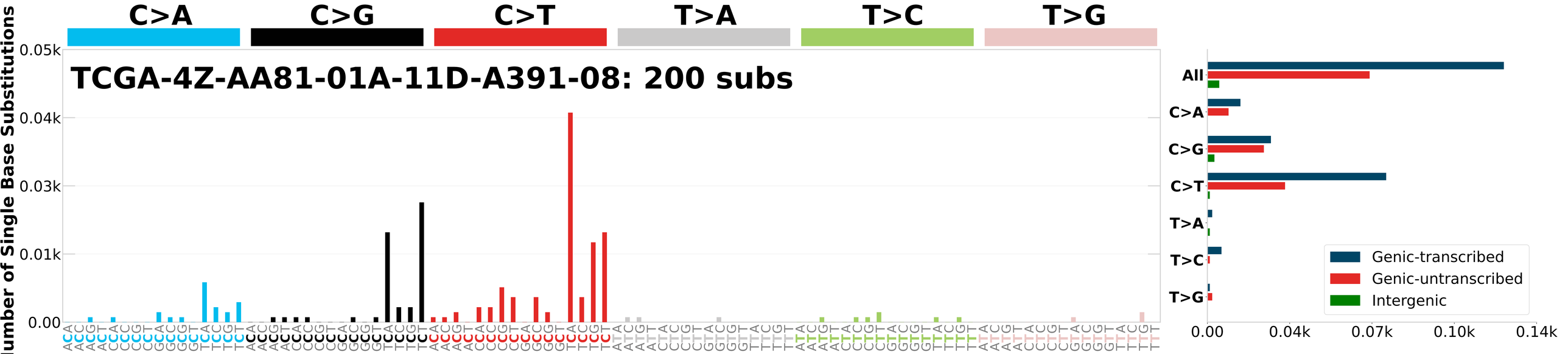

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA7R-01A-11D-A391-08: 346 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.10k
0.15k
0.20k

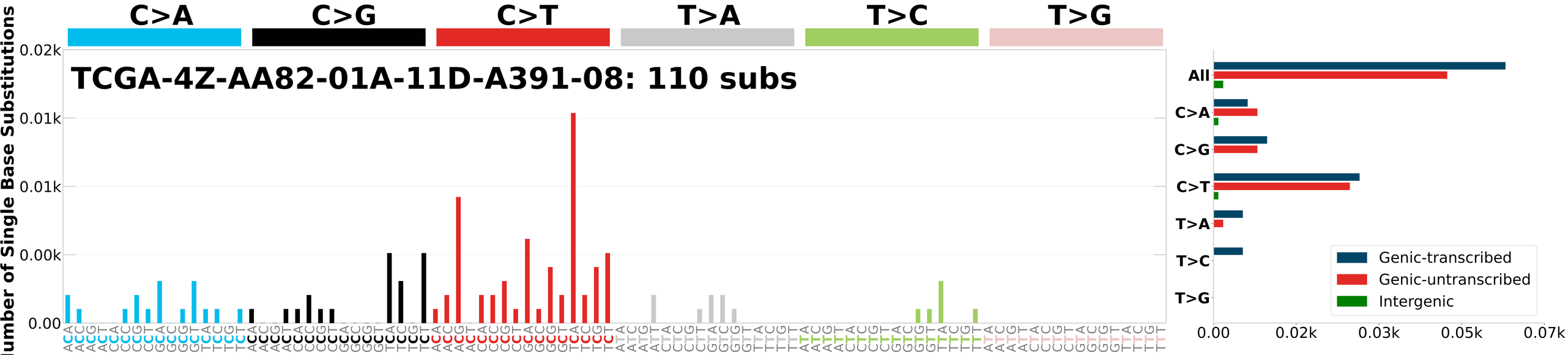

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA7S-01A-11D-A391-08: 58 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

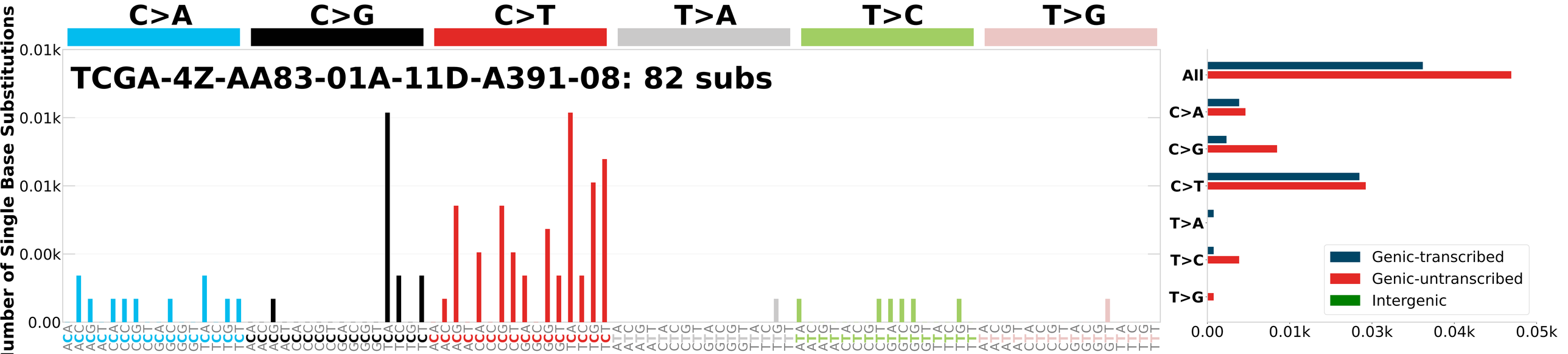

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA7W-01A-11D-A391-08: 503 subs
Number of Single Base Substitutions
0.13k
0.10k
0.06k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.14k
0.21k
0.28k

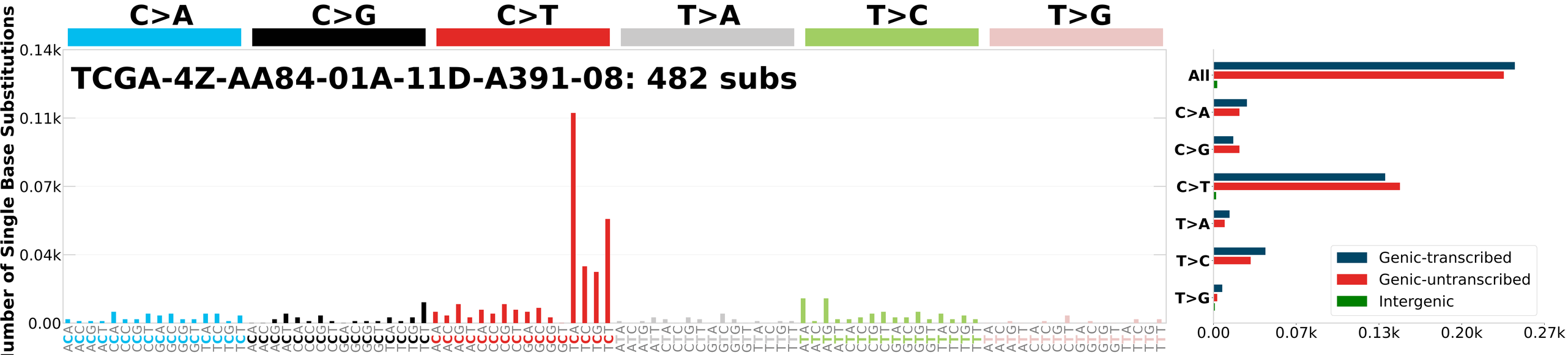

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA7Y-01A-11D-A391-08: 273 subs
Number of Single Base Substitutions
0.07k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.07k
0.11k
0.15k

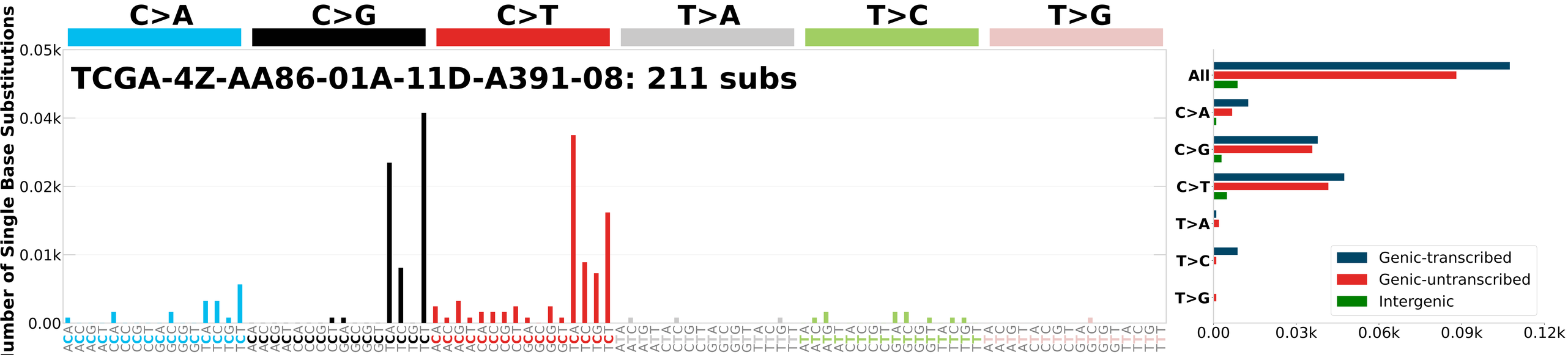

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA80-01A-11D-A391-08: 405 subs
Number of Single Base Substitutions
0.07k
0.05k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.12k
0.19k
0.25k

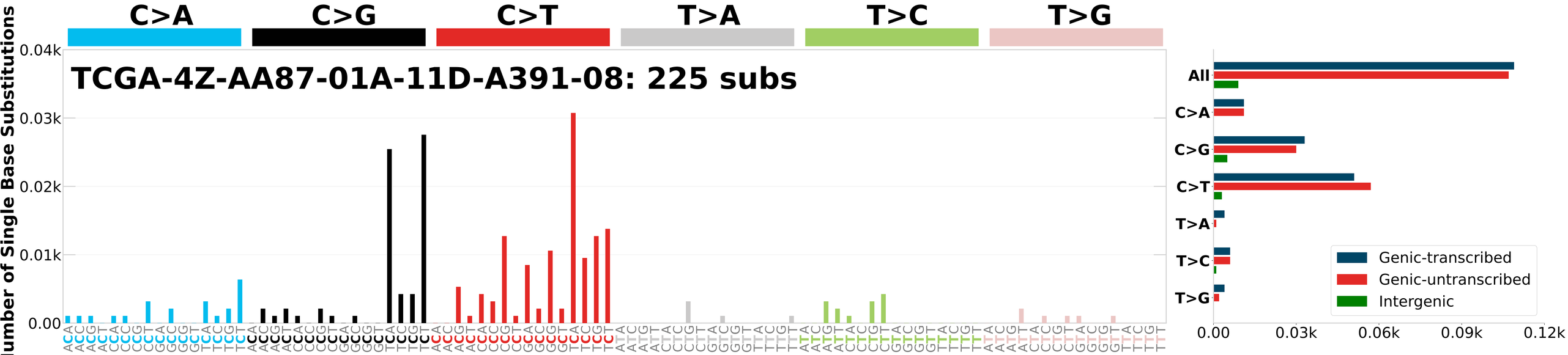

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA81-01A-11D-A391-08: 200 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.07k
0.10k
0.14k

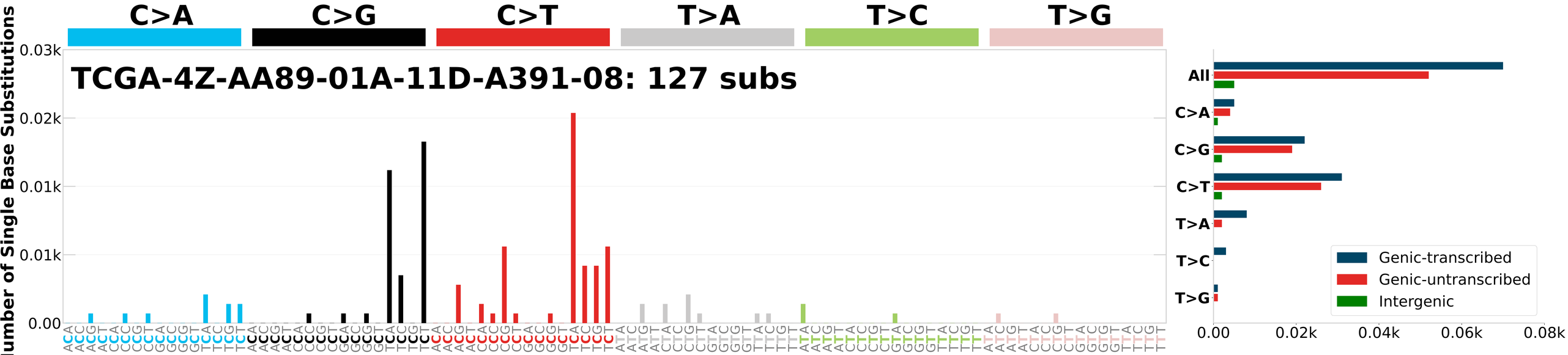

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA82-01A-11D-A391-08: 110 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.07k

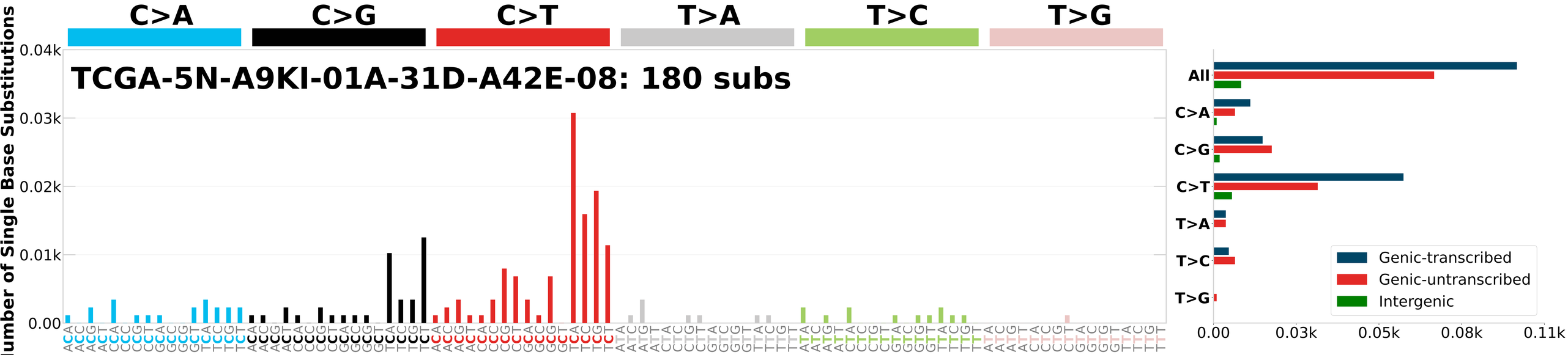

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA83-01A-11D-A391-08: 82 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

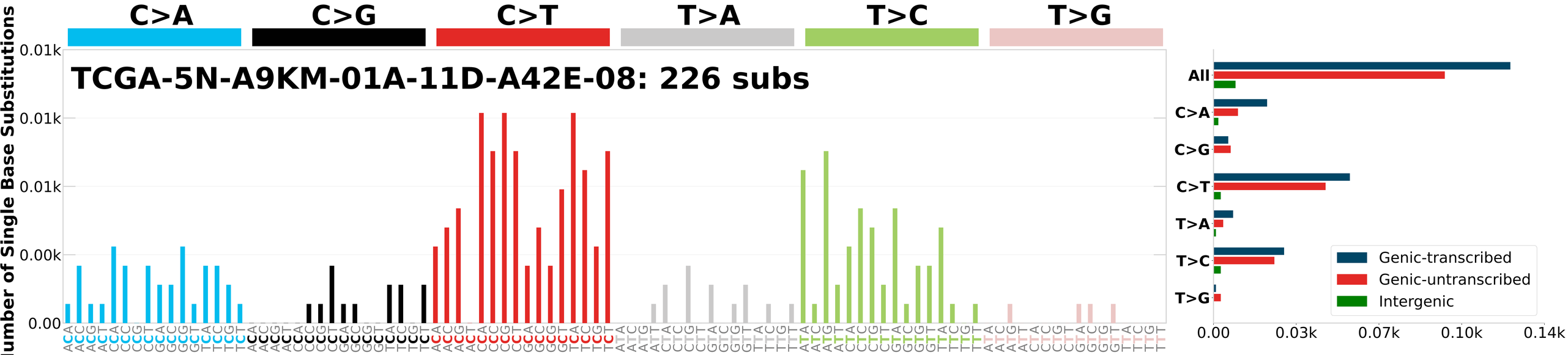

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA84-01A-11D-A391-08: 482 subs
Number of Single Base Substitutions
0.14k
0.11k
0.07k
0.04k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.13k
0.20k
0.27k

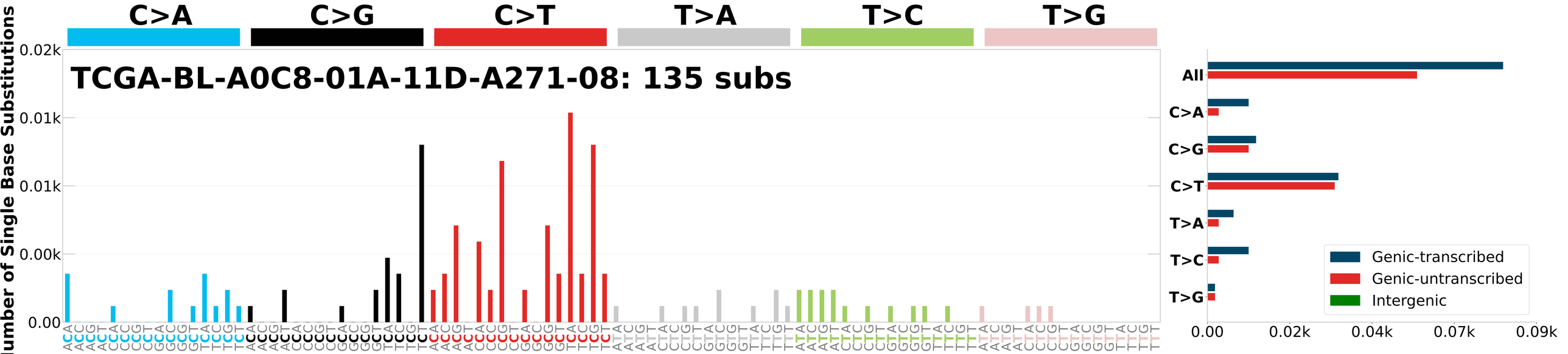

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA86-01A-11D-A391-08: 211 subs
Number of Single Base Substitutions
0.05k
0.04k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

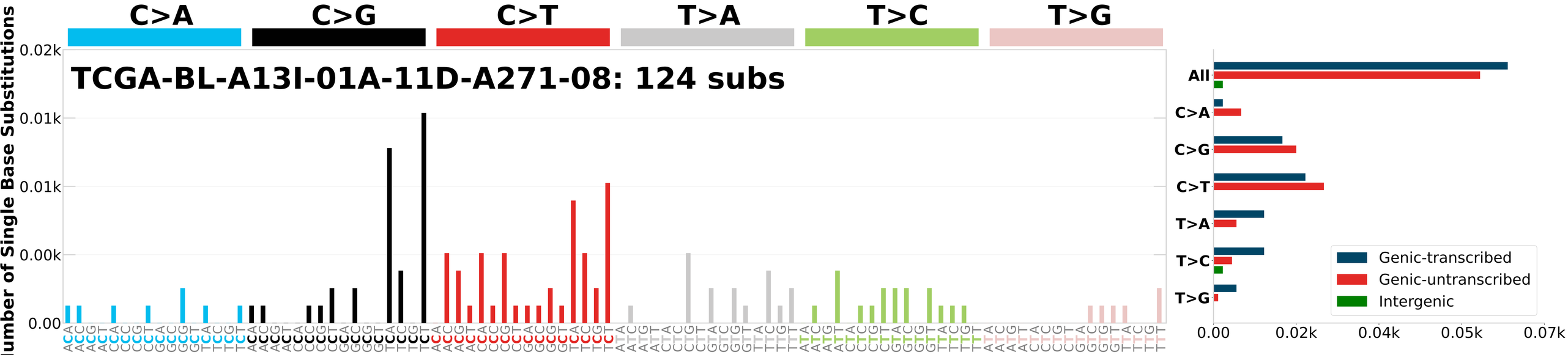

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA87-01A-11D-A391-08: 225 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

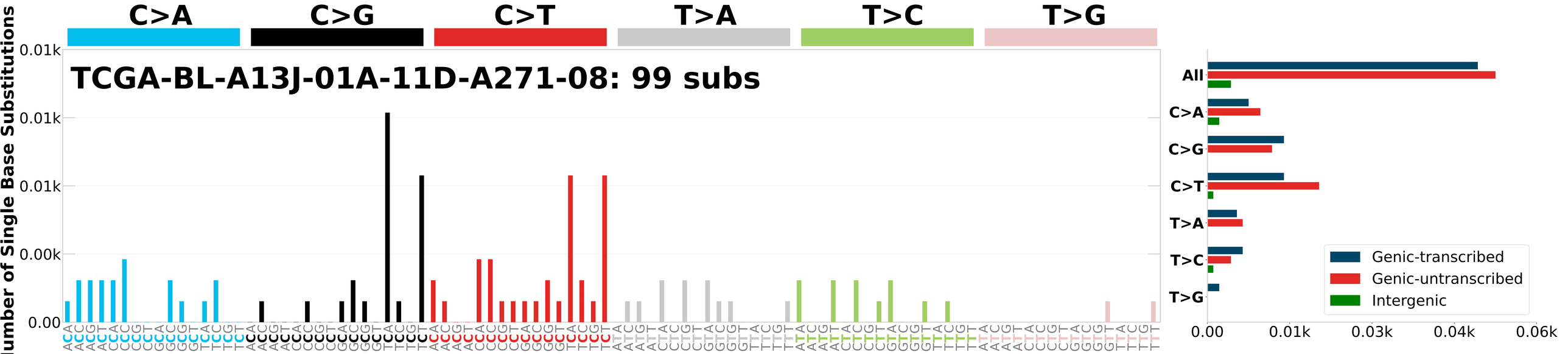

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-4Z-AA89-01A-11D-A391-08: 127 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

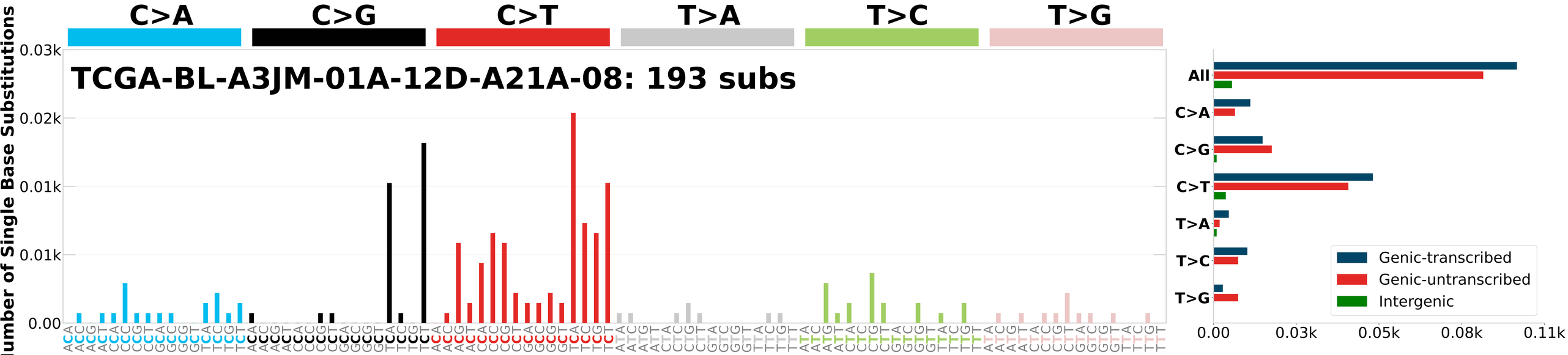

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-5N-A9KI-01A-31D-A42E-08: 180 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.11k

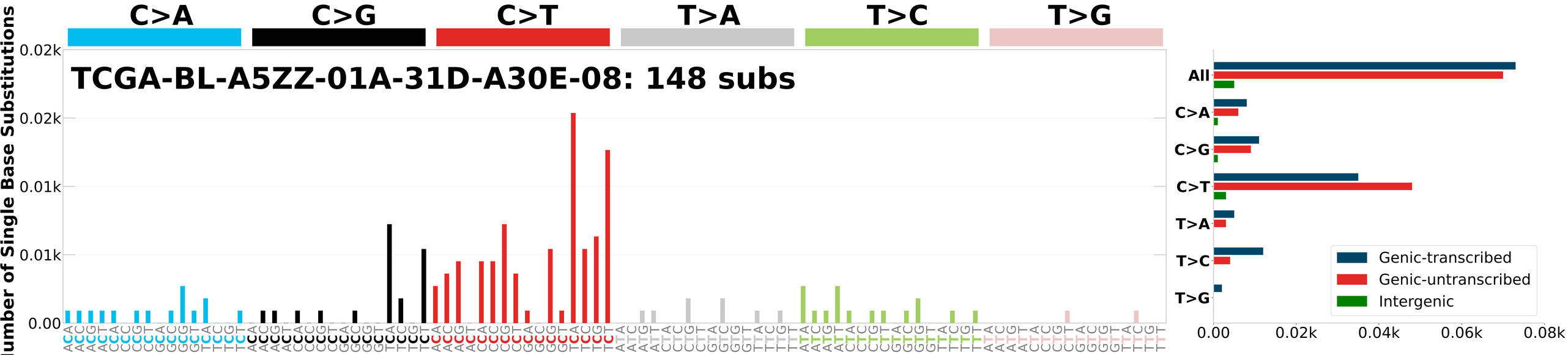

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-5N-A9KM-01A-11D-A42E-08: 226 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.14k

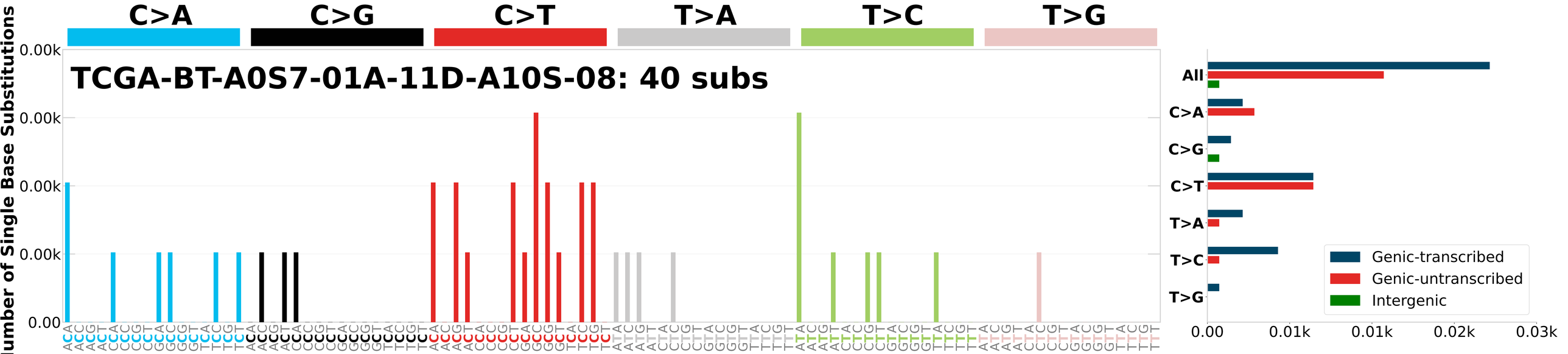

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BL-A0C8-01A-11D-A271-08: 135 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.07k
0.09k

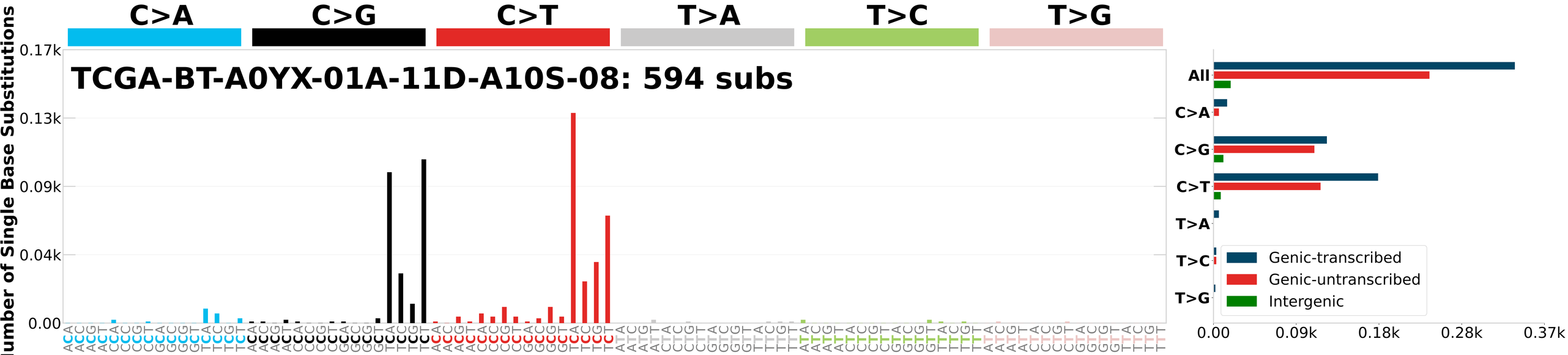

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BL-A13I-01A-11D-A271-08: 124 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.05k
0.07k

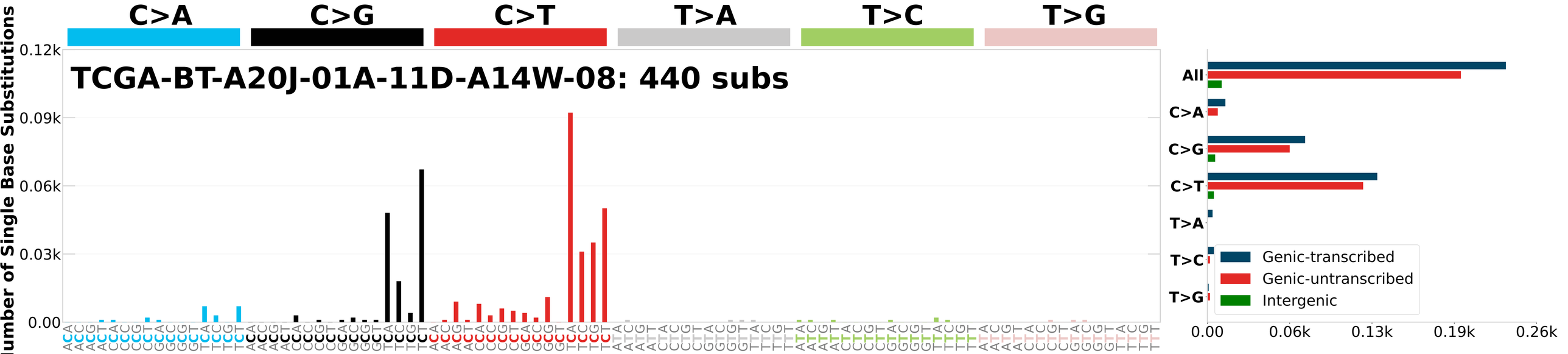

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BL-A13J-01A-11D-A271-08: 99 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

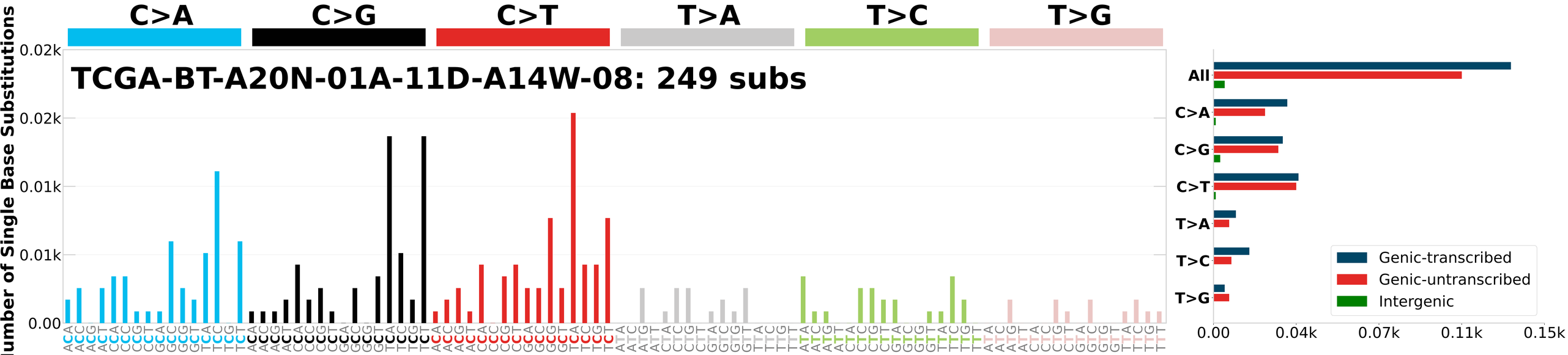

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BL-A3JM-01A-12D-A21A-08: 193 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.11k

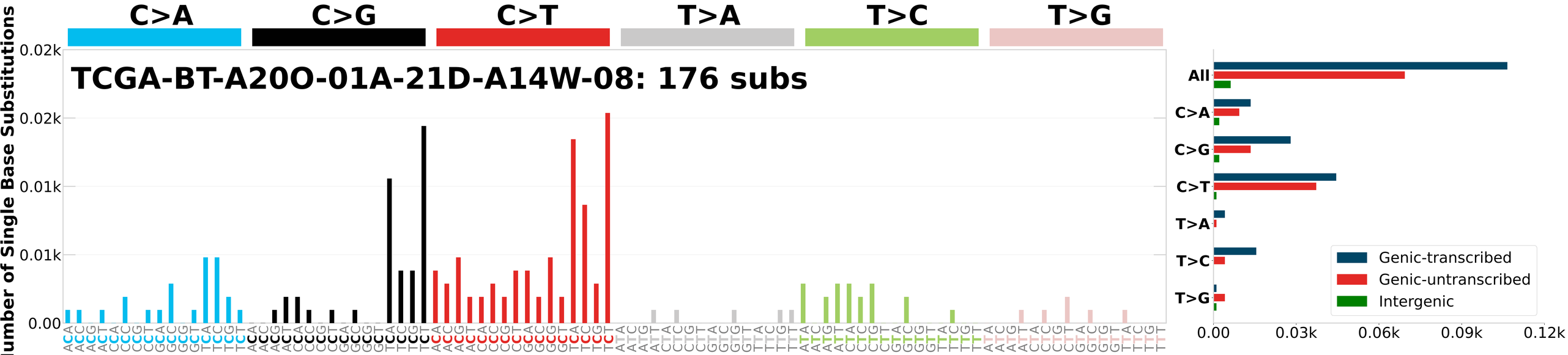

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BL-A5ZZ-01A-31D-A30E-08: 148 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

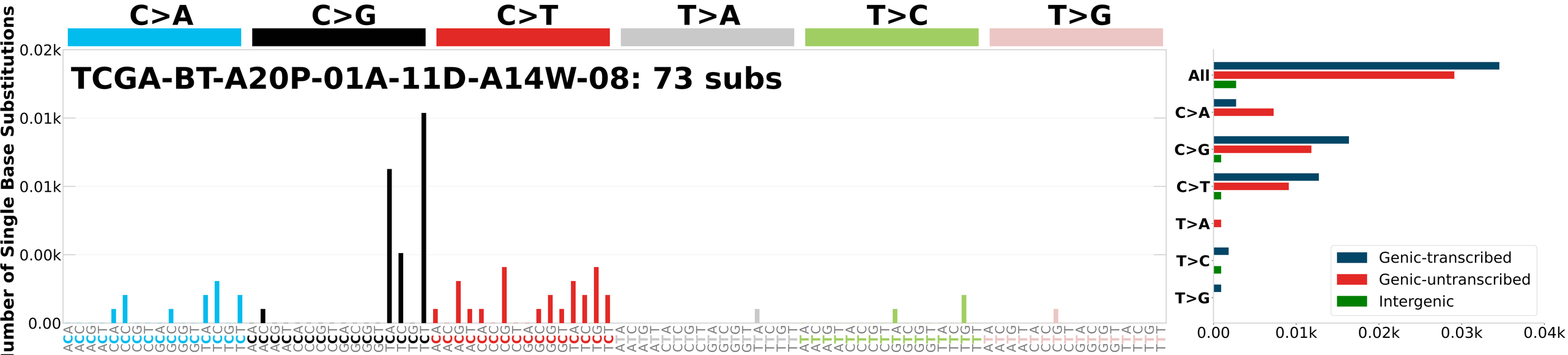

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A0S7-01A-11D-A10S-08: 40 subs
Number of Single Base Substitutions
0.00k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.02k
0.03k

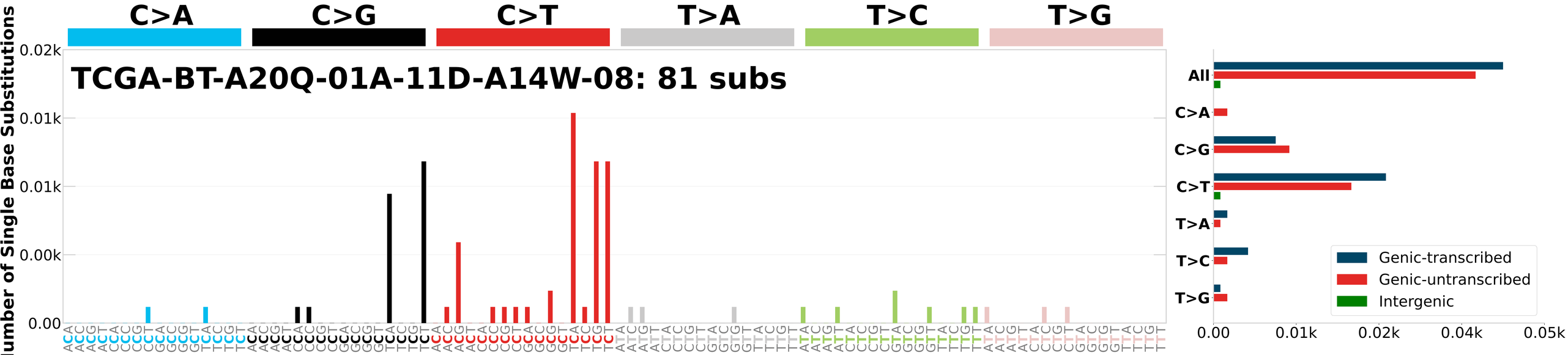

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A0YX-01A-11D-A10S-08: 594 subs
Number of Single Base Substitutions
0.17k
0.13k
0.09k
0.04k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.09k
0.18k
0.28k
0.37k

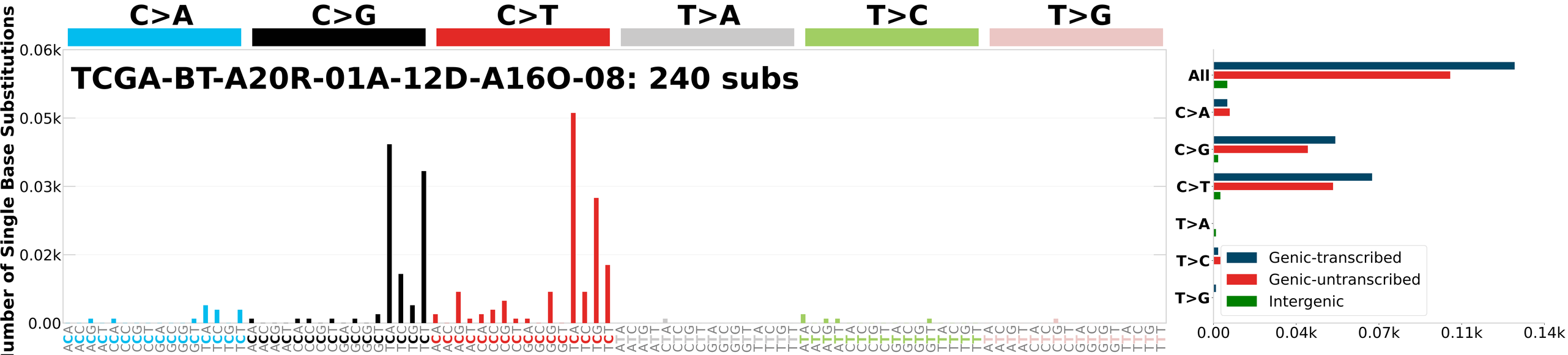

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A20J-01A-11D-A14W-08: 440 subs
Number of Single Base Substitutions
0.12k
0.09k
0.06k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.13k
0.19k
0.26k

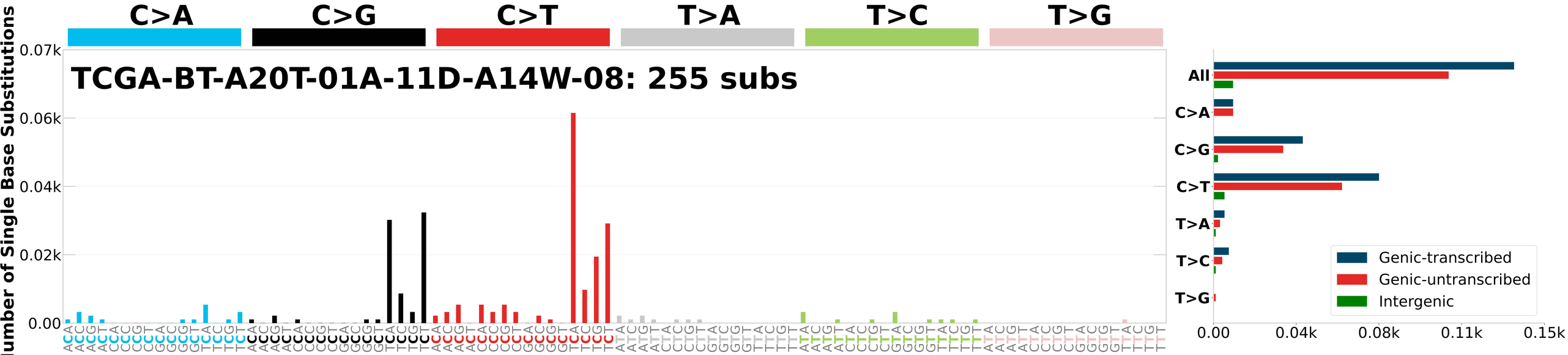

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A20N-01A-11D-A14W-08: 249 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.07k
0.11k
0.15k

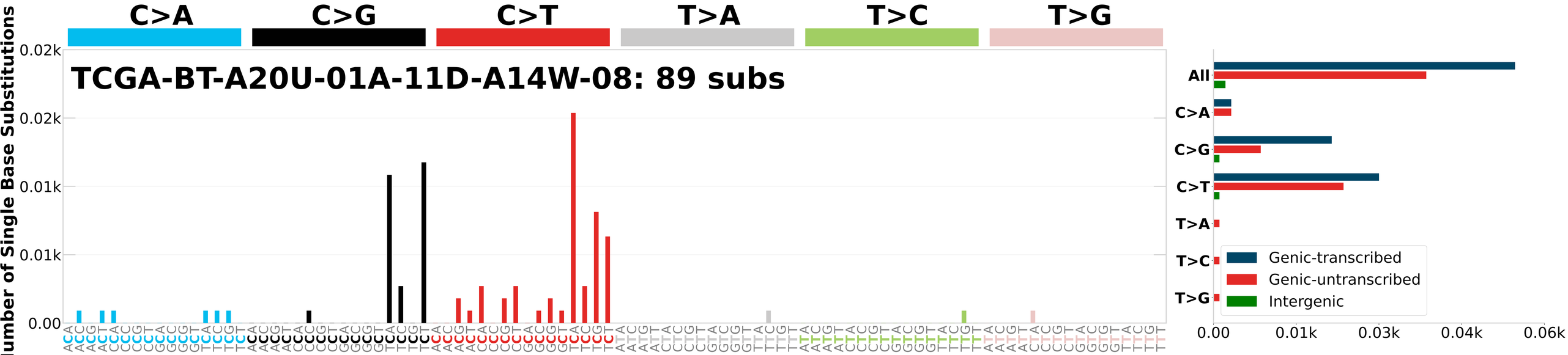

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A20O-01A-21D-A14W-08: 176 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

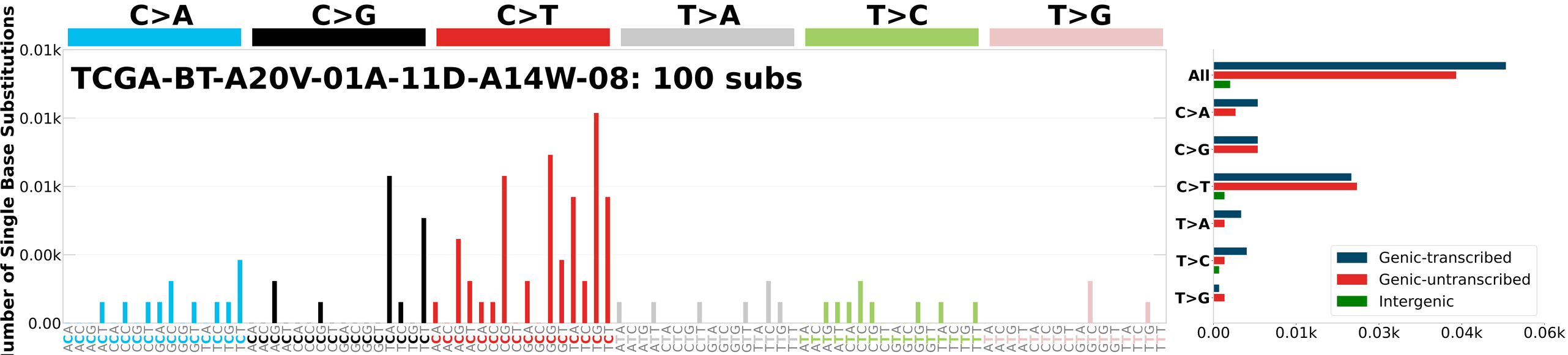

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A20P-01A-11D-A14W-08: 73 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

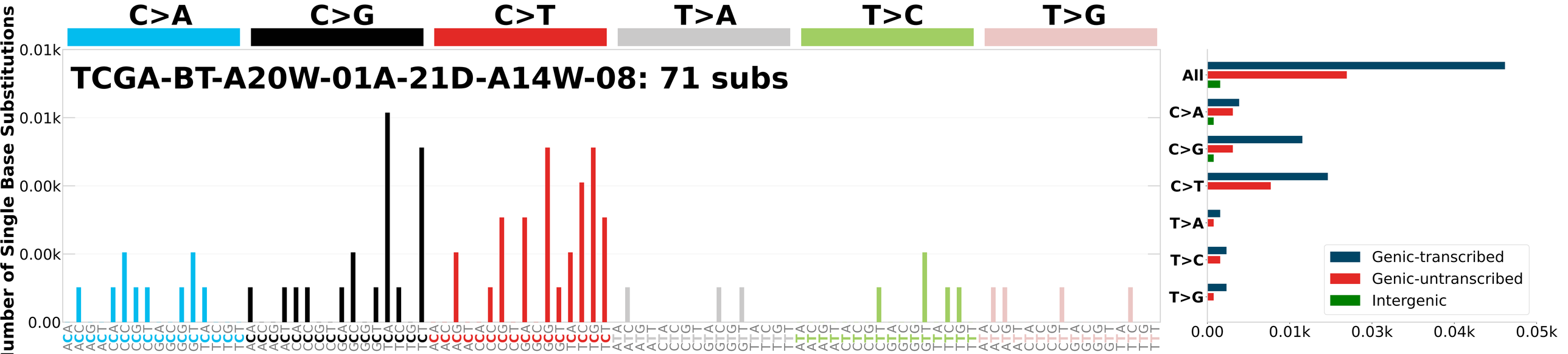

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A20Q-01A-11D-A14W-08: 81 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

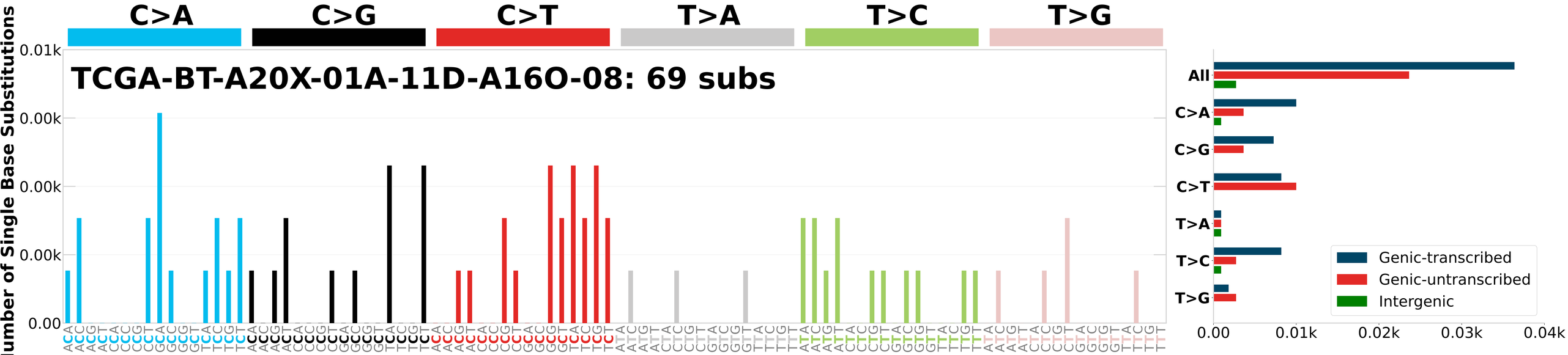

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A20R-01A-12D-A16O-08: 240 subs
Number of Single Base Substitutions
0.06k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.07k
0.11k
0.14k

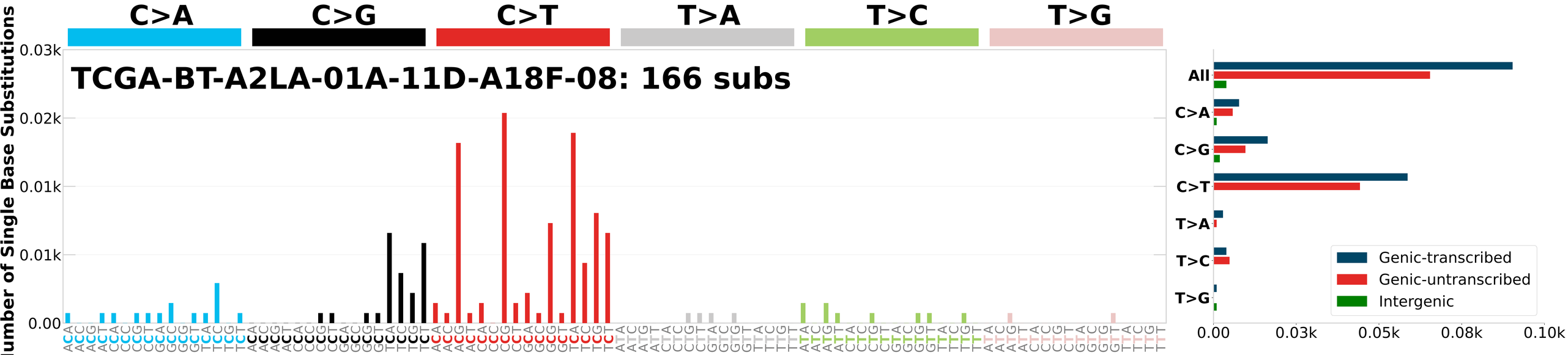

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A20T-01A-11D-A14W-08: 255 subs
Number of Single Base Substitutions
0.07k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.11k
0.15k

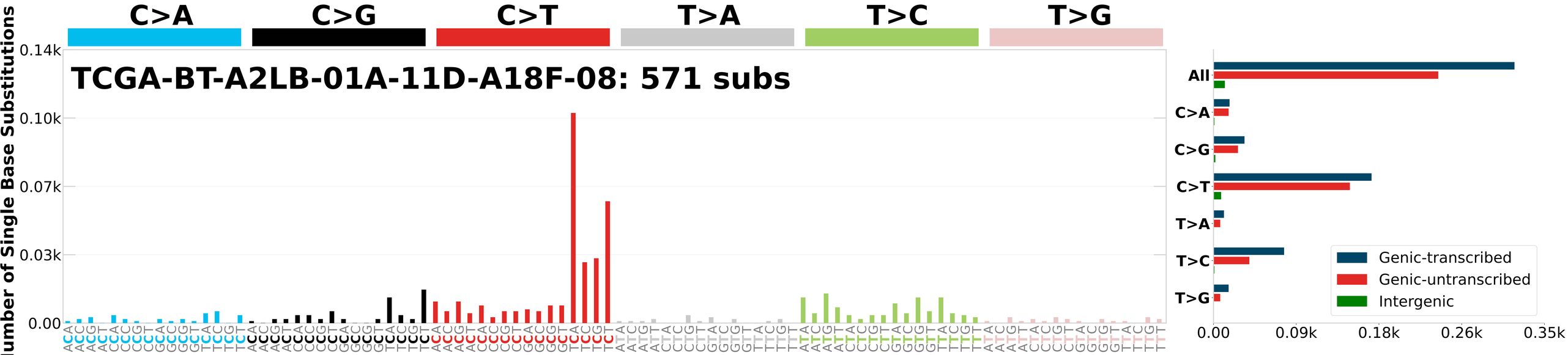

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A20U-01A-11D-A14W-08: 89 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

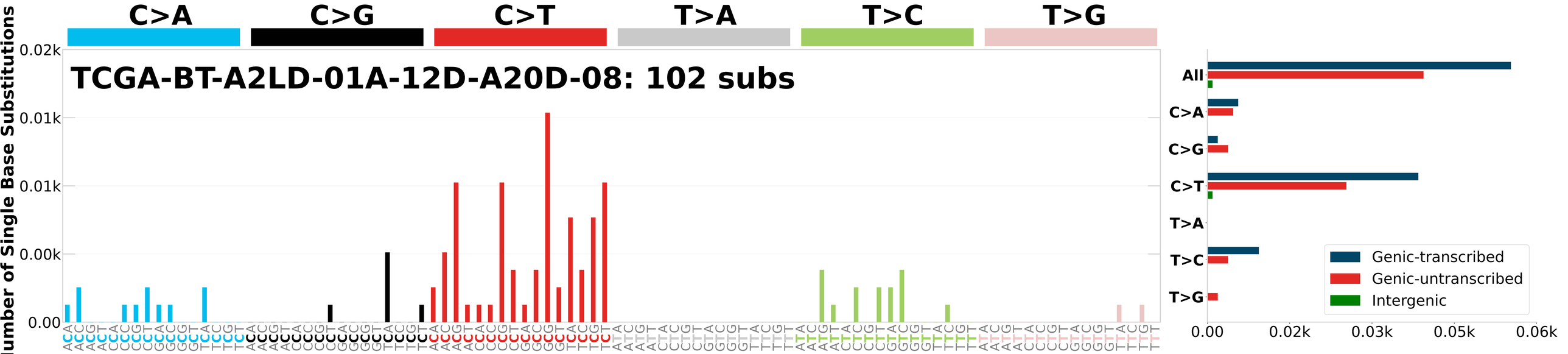

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A20V-01A-11D-A14W-08: 100 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

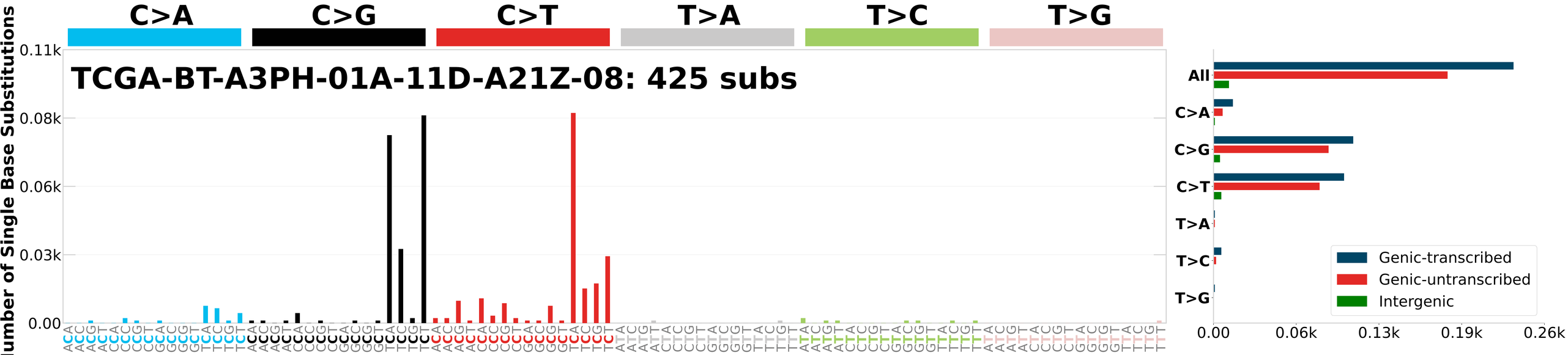

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A20W-01A-21D-A14W-08: 71 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

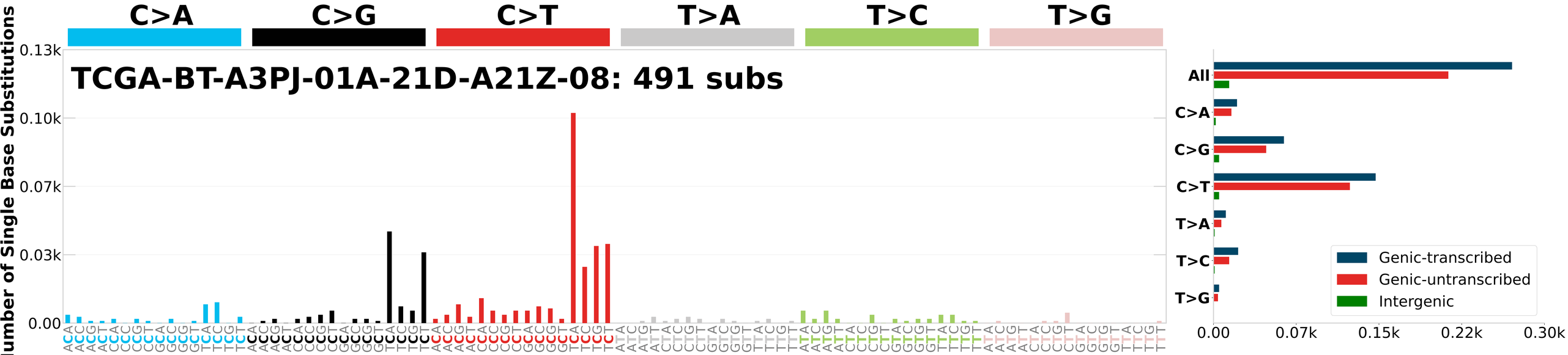

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A20X-01A-11D-A16O-08: 69 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

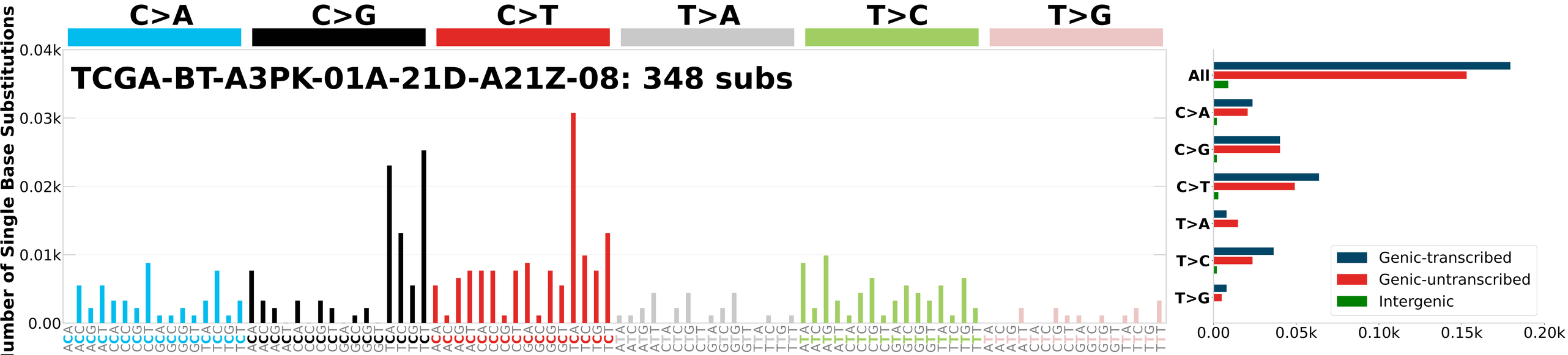

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A2LA-01A-11D-A18F-08: 166 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.10k

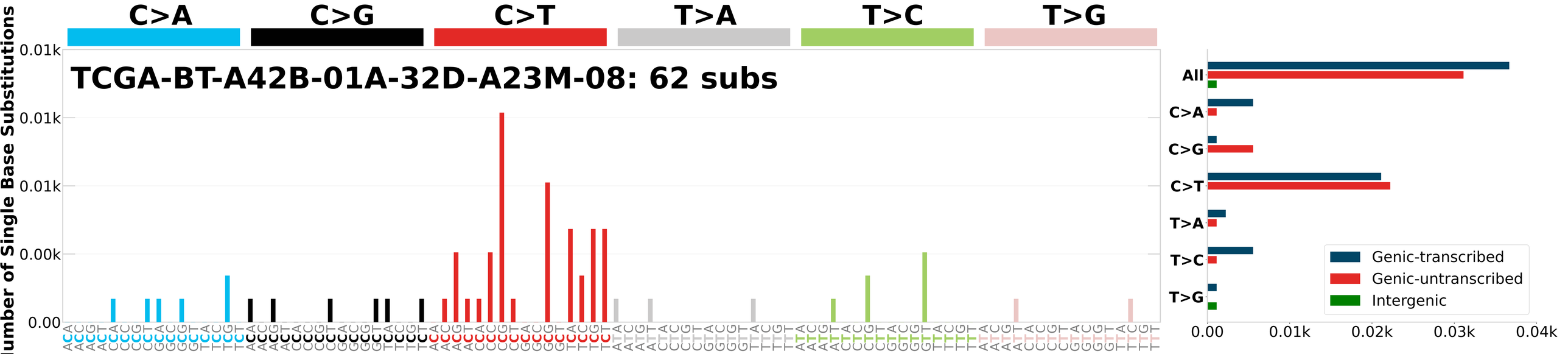

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A2LB-01A-11D-A18F-08: 571 subs
Number of Single Base Substitutions
0.14k
0.10k
0.07k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.09k
0.18k
0.26k
0.35k

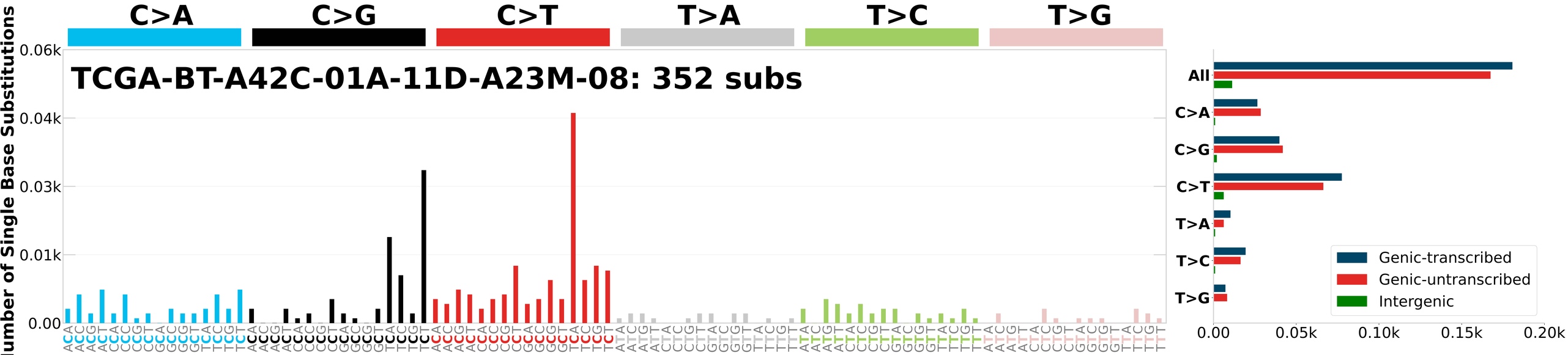

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A2LD-01A-12D-A20D-08: 102 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.06k

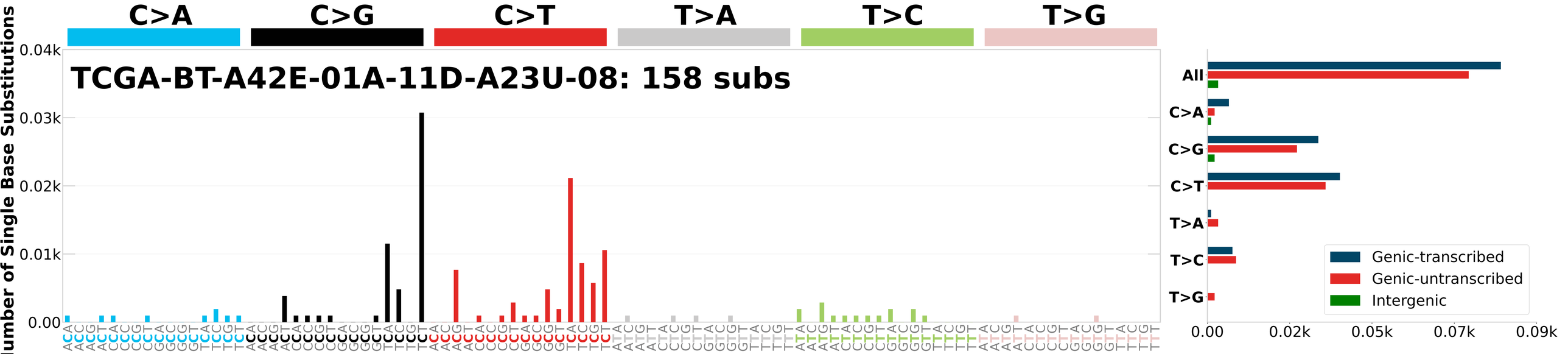

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A3PH-01A-11D-A21Z-08: 425 subs
Number of Single Base Substitutions
0.11k
0.08k
0.06k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.13k
0.19k
0.26k

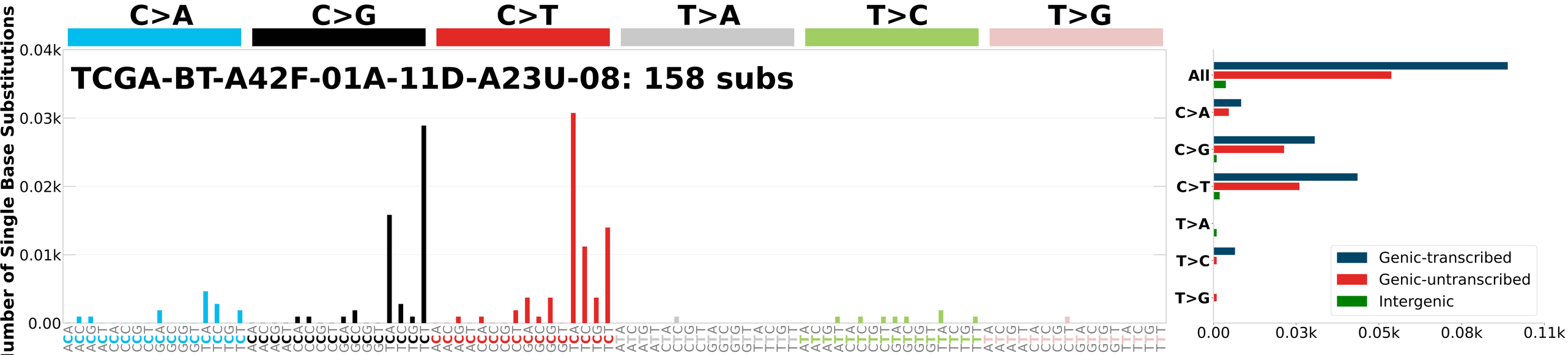

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A3PJ-01A-21D-A21Z-08: 491 subs
Number of Single Base Substitutions
0.13k
0.10k
0.07k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.15k
0.22k
0.30k

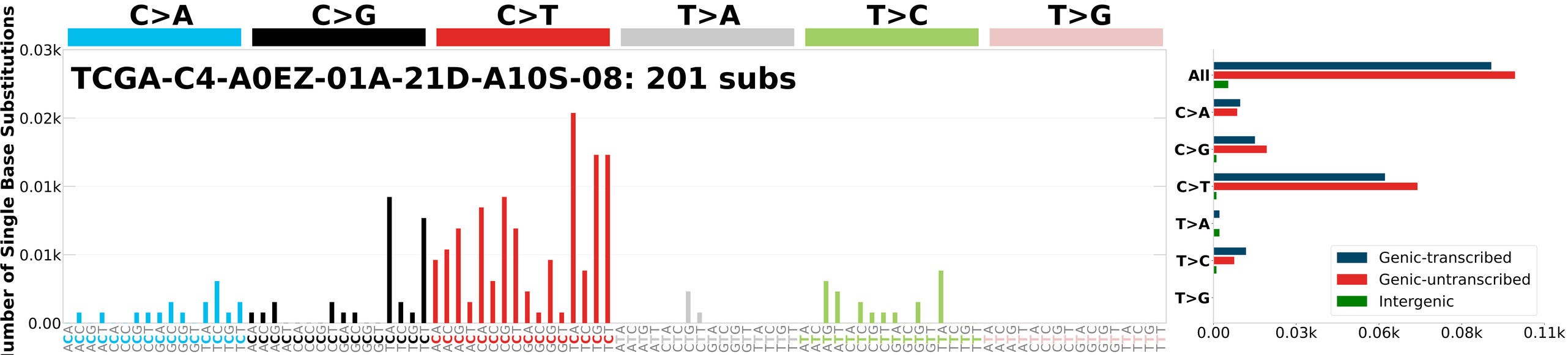

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A3PK-01A-21D-A21Z-08: 348 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.10k
0.15k
0.20k

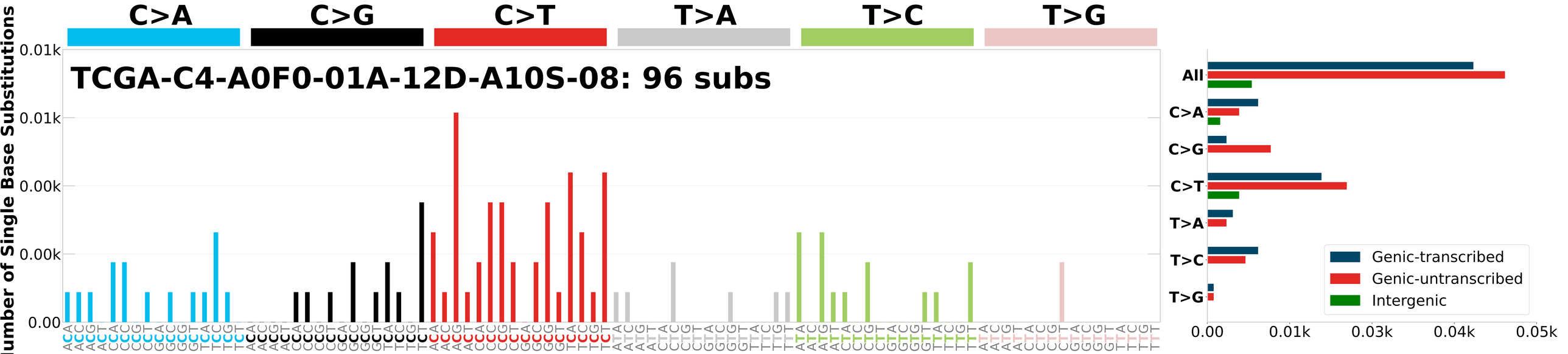

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A42B-01A-32D-A23M-08: 62 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

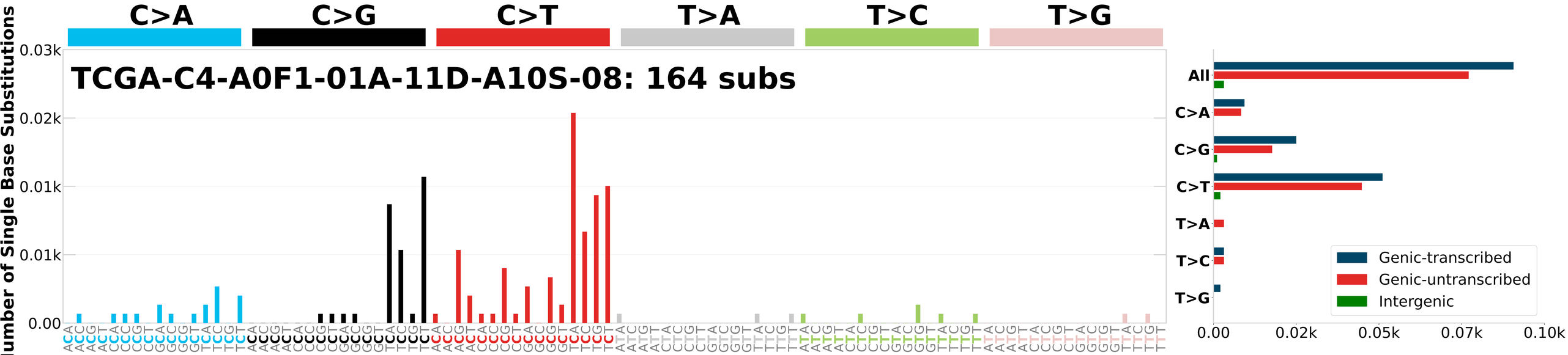

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A42C-01A-11D-A23M-08: 352 subs
Number of Single Base Substitutions
0.06k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.10k
0.15k
0.20k

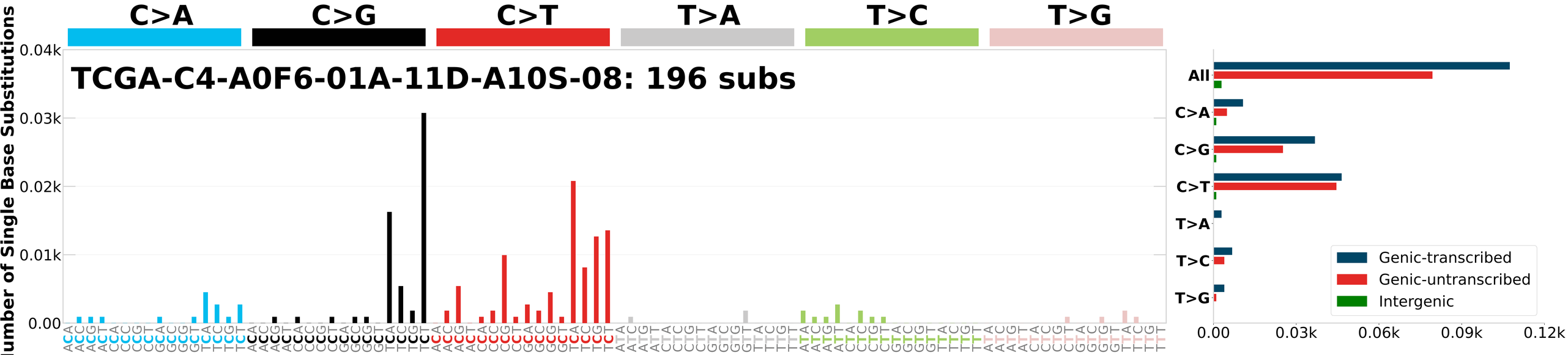

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A42E-01A-11D-A23U-08: 158 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.09k

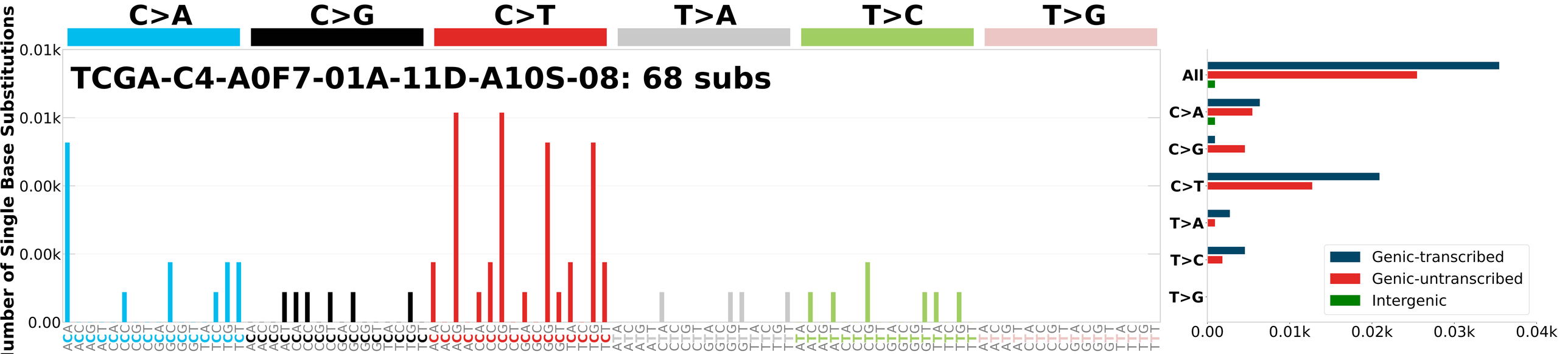

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-BT-A42F-01A-11D-A23U-08: 158 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.11k

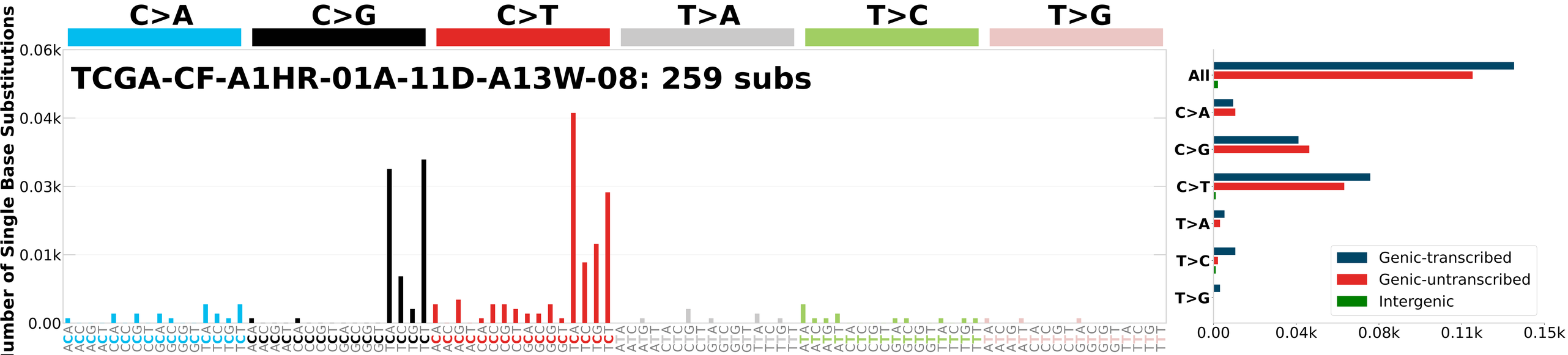

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-C4-A0EZ-01A-21D-A10S-08: 201 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.08k
0.11k

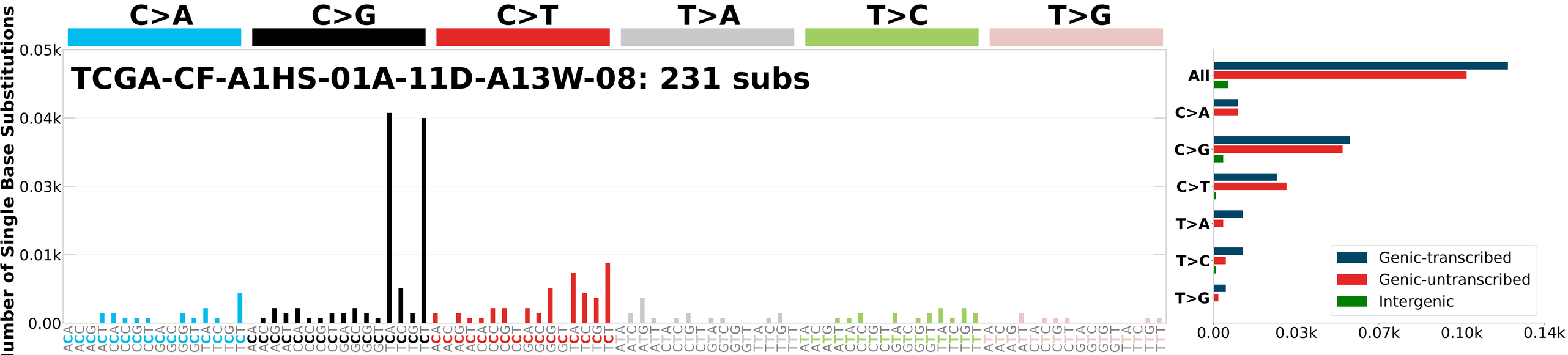

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-C4-A0F0-01A-12D-A10S-08: 96 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

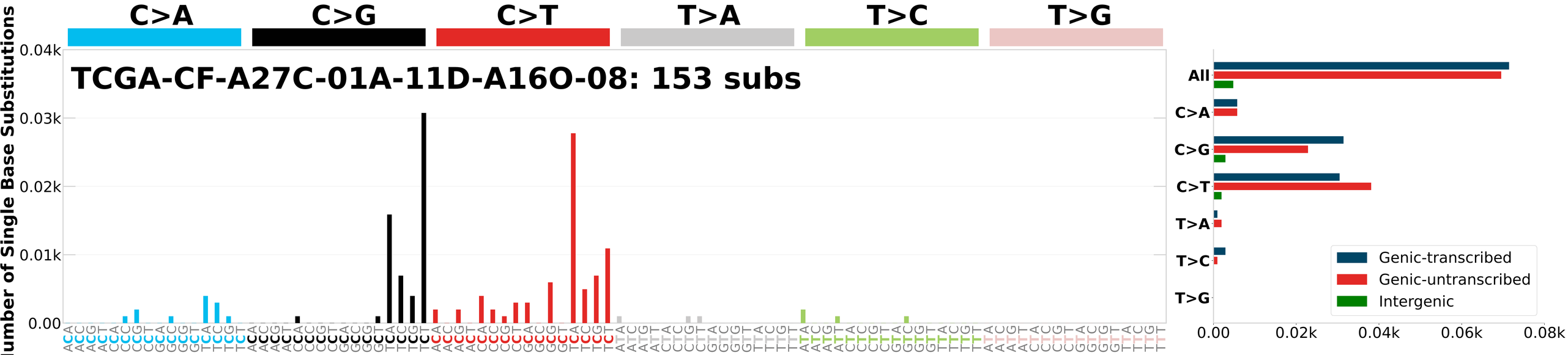

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-C4-A0F1-01A-11D-A10S-08: 164 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.10k

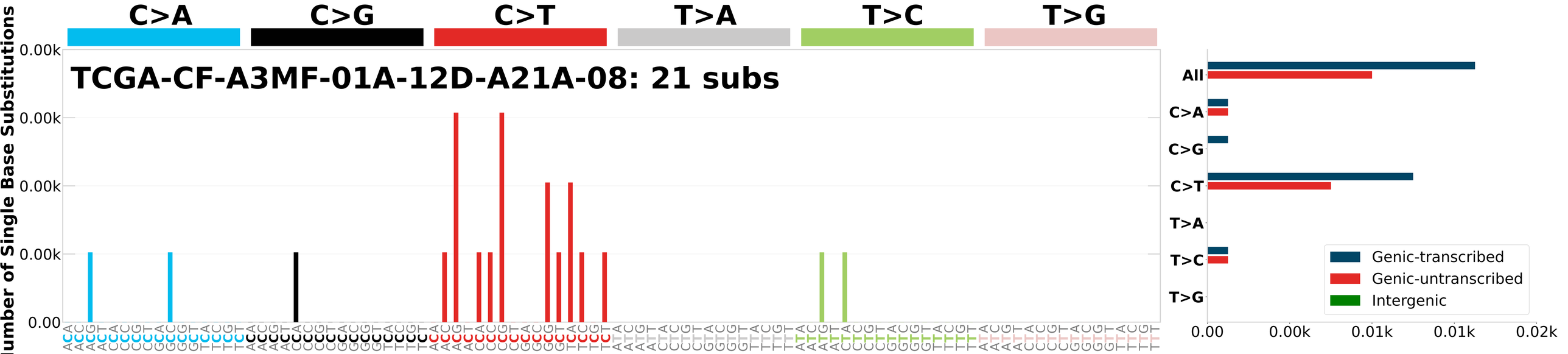

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-C4-A0F6-01A-11D-A10S-08: 196 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

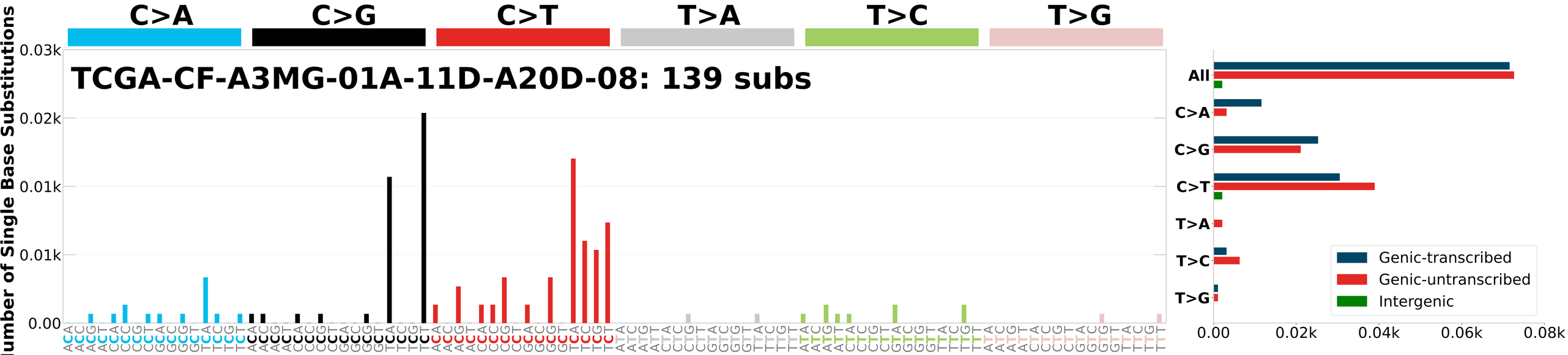

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-C4-A0F7-01A-11D-A10S-08: 68 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

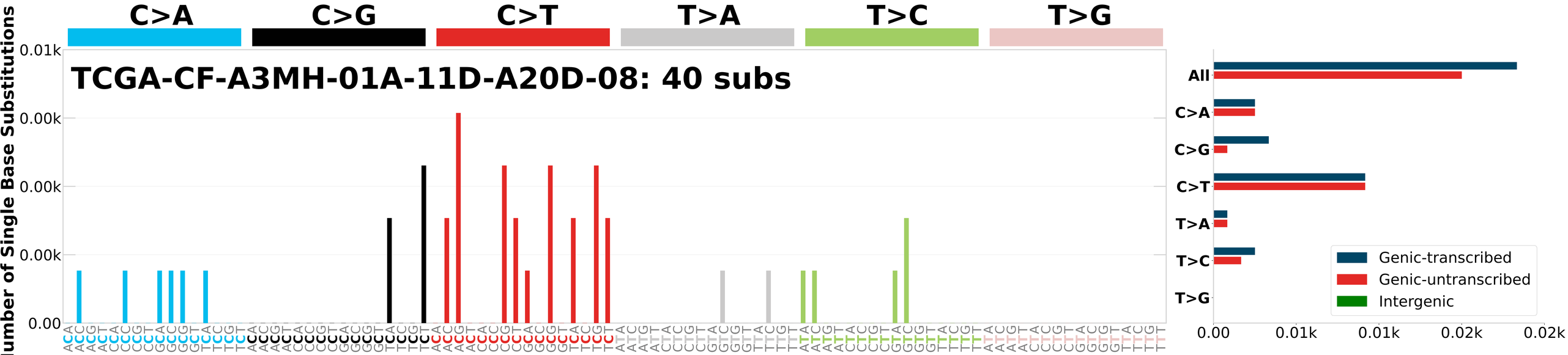

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A1HR-01A-11D-A13W-08: 259 subs
Number of Single Base Substitutions
0.06k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.11k
0.15k

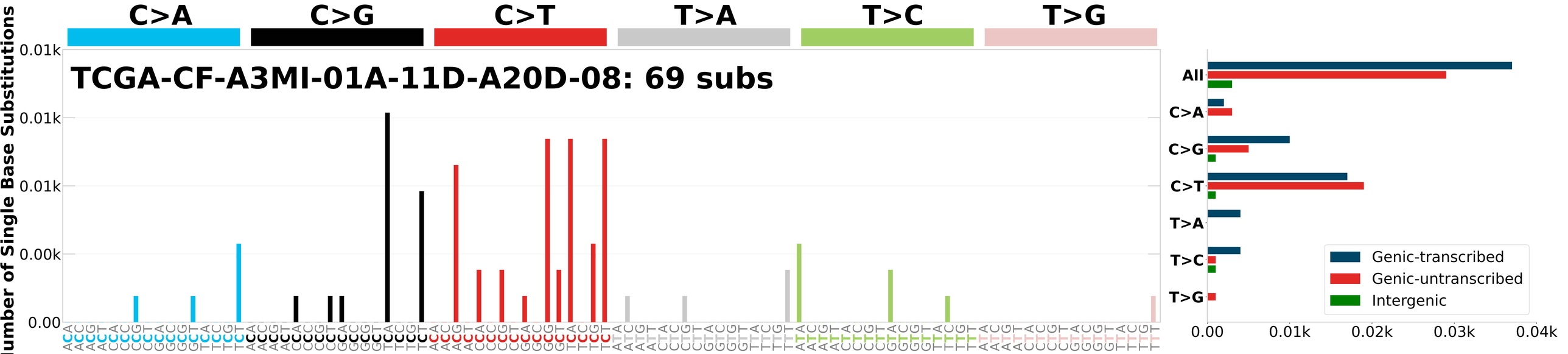

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A1HS-01A-11D-A13W-08: 231 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.14k

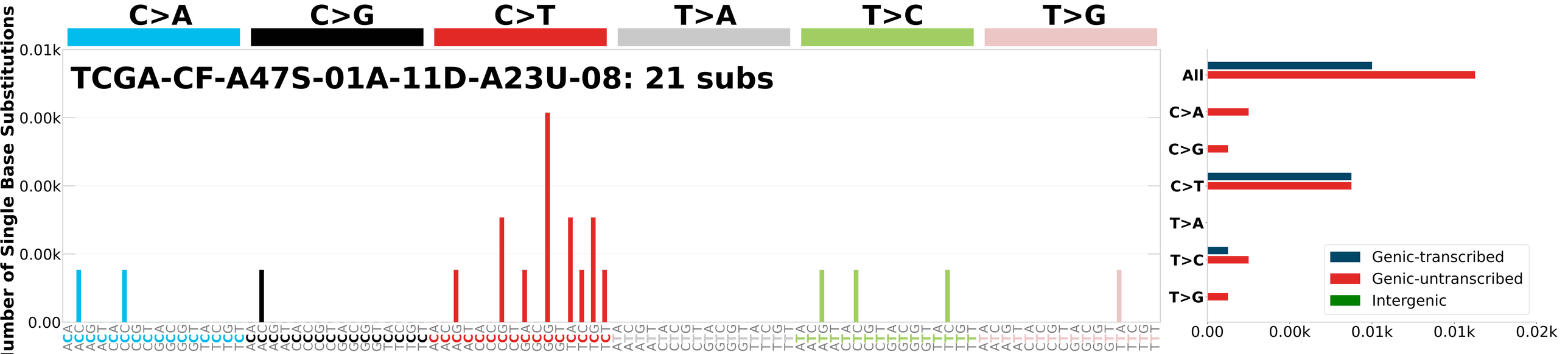

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A27C-01A-11D-A16O-08: 153 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

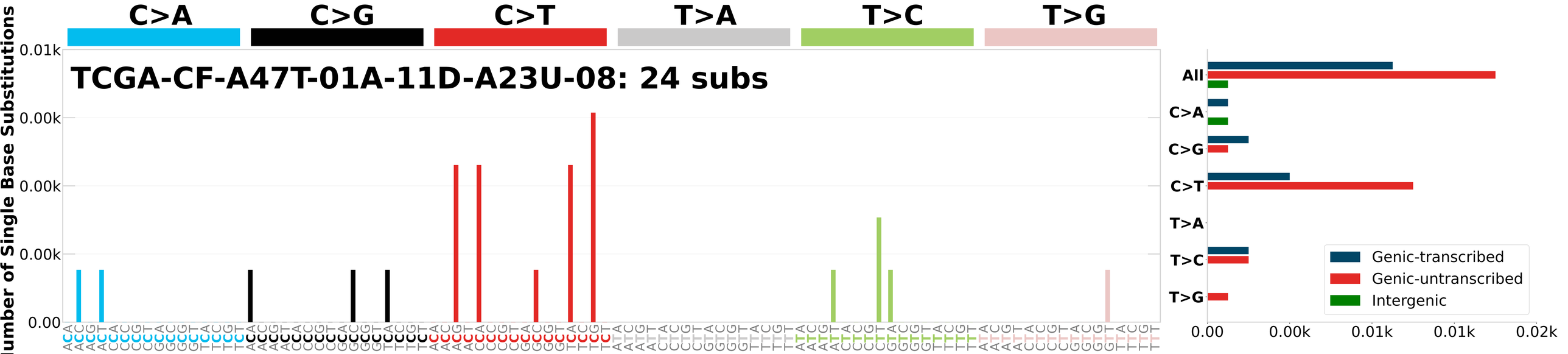

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A3MF-01A-12D-A21A-08: 21 subs
Number of Single Base Substitutions
0.00k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.00k
0.01k
0.01k
0.02k

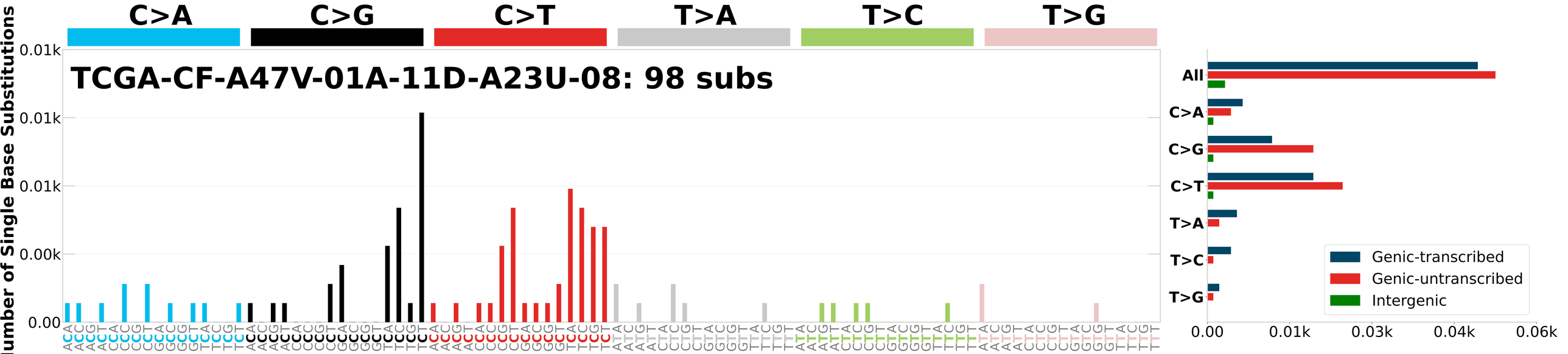

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A3MG-01A-11D-A20D-08: 139 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

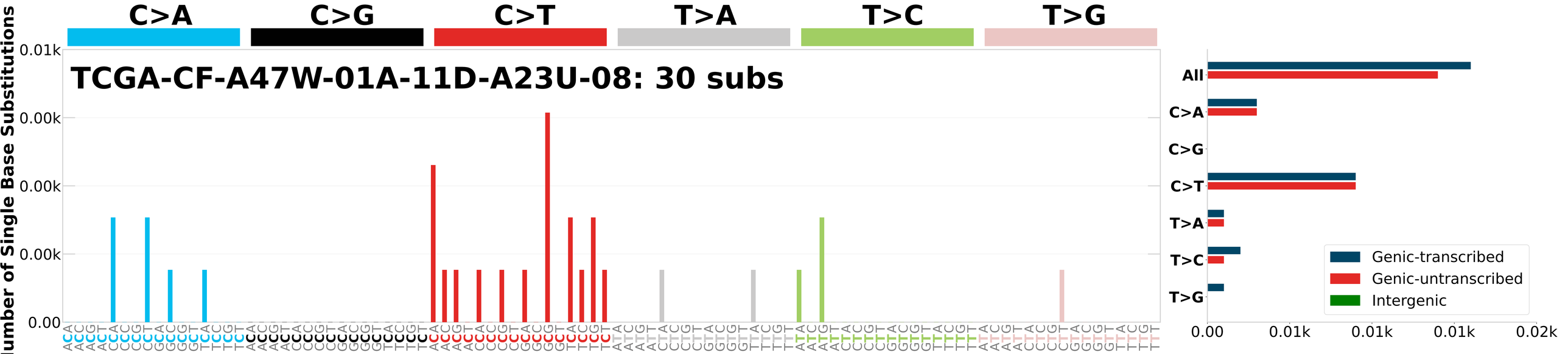

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A3MH-01A-11D-A20D-08: 40 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.02k
0.02k

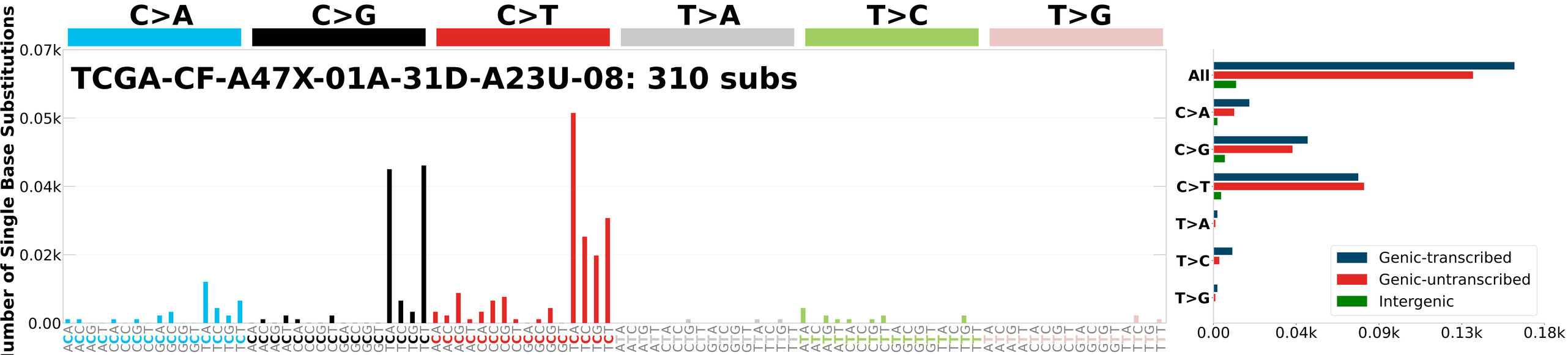

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A3MI-01A-11D-A20D-08: 69 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

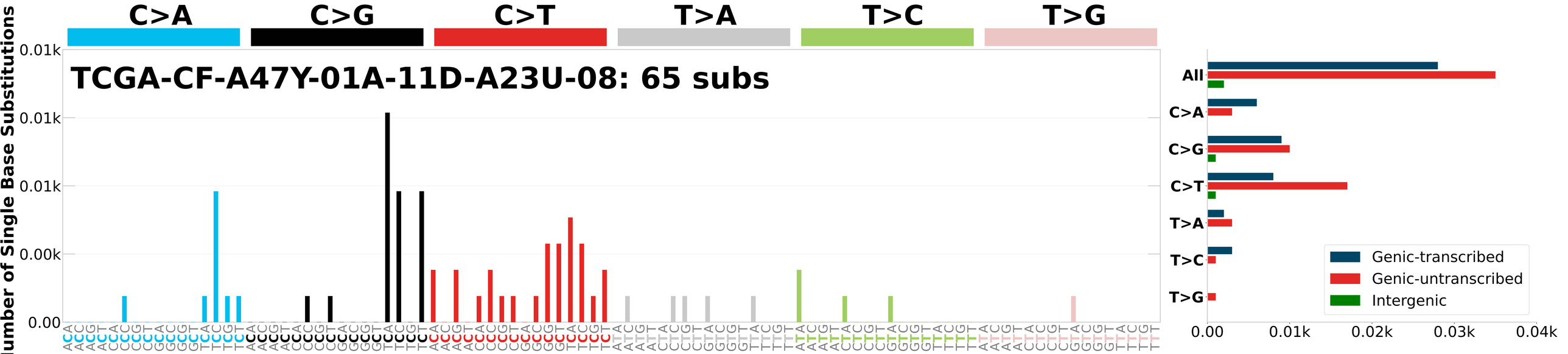

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A47S-01A-11D-A23U-08: 21 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.00k
0.01k
0.01k
0.02k

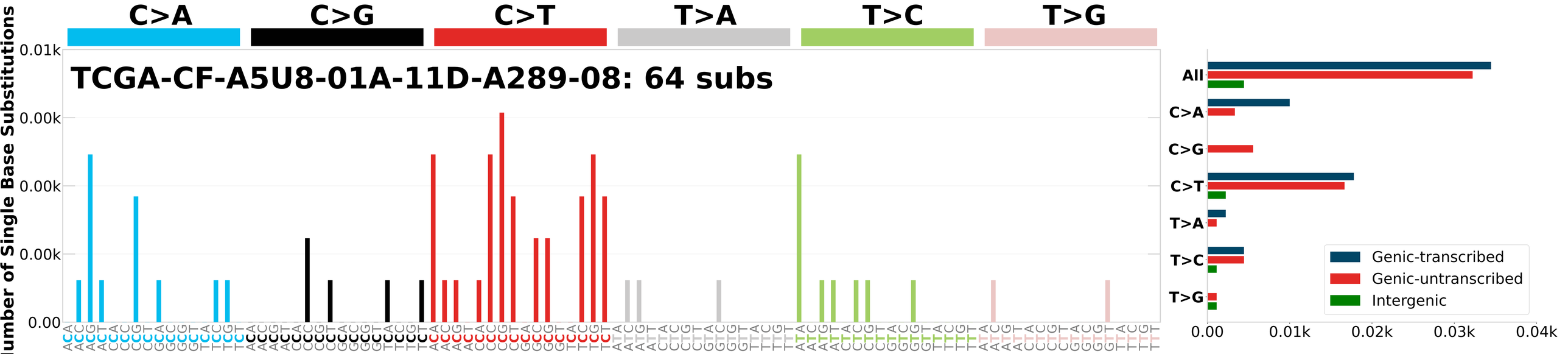

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A47T-01A-11D-A23U-08: 24 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.00k
0.01k
0.01k
0.02k

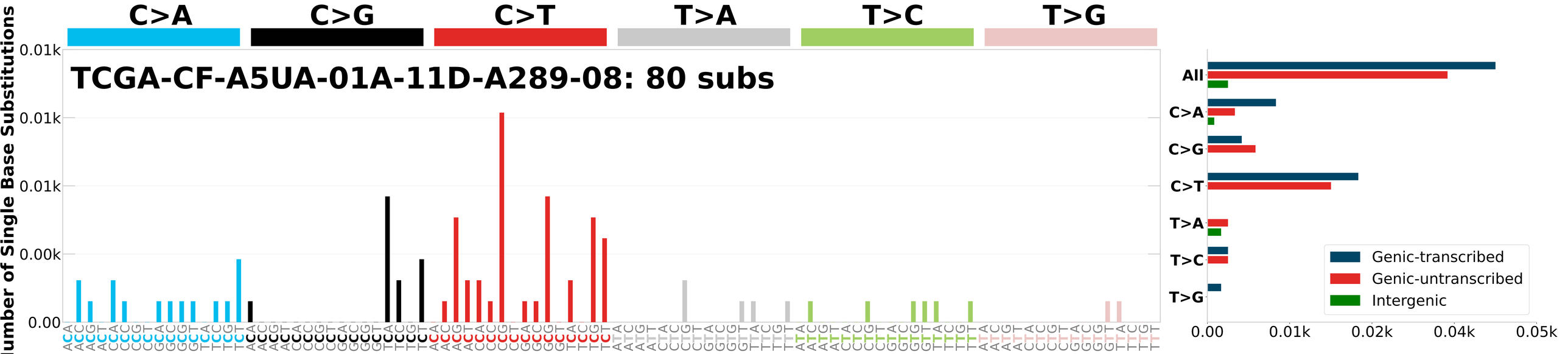

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A47V-01A-11D-A23U-08: 98 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

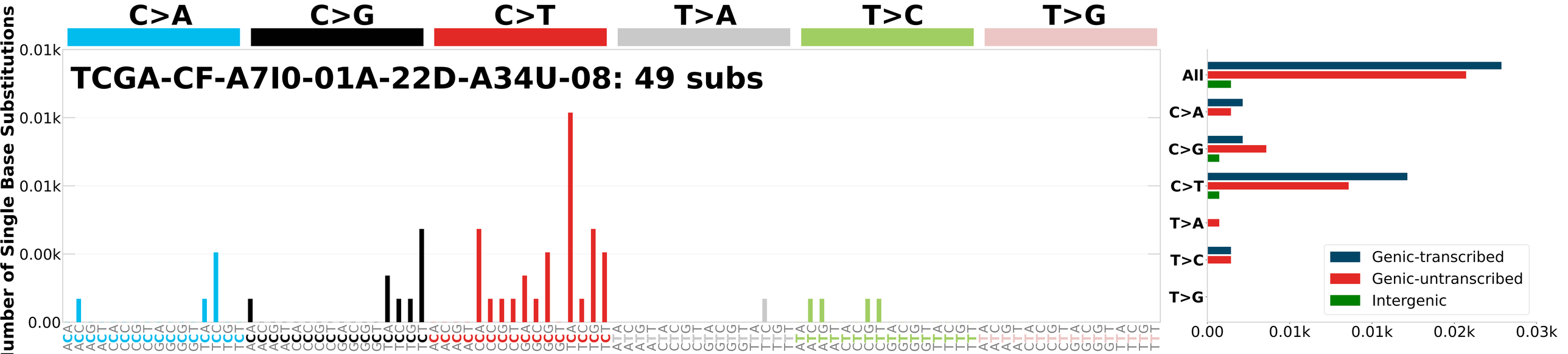

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A47W-01A-11D-A23U-08: 30 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.01k
0.02k

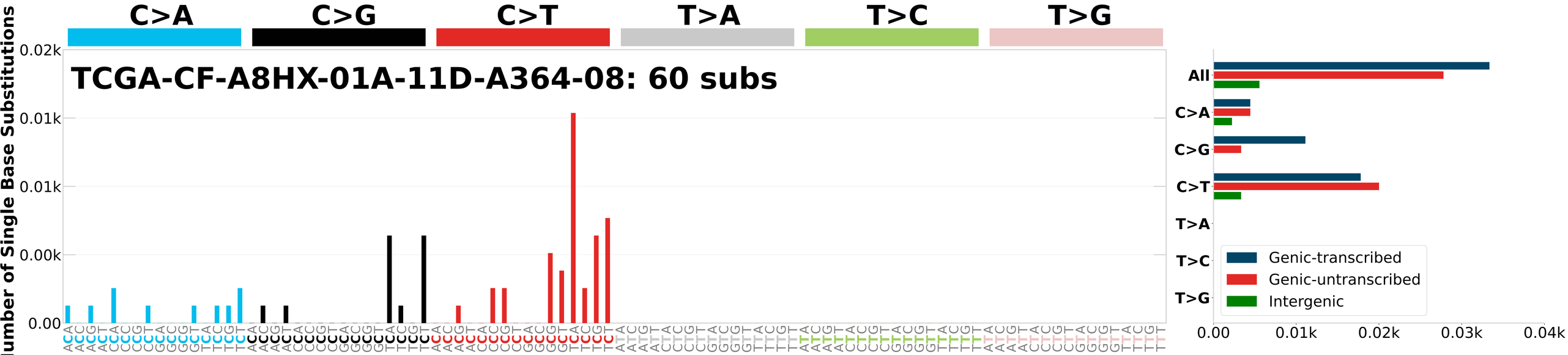

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A47X-01A-31D-A23U-08: 310 subs
Number of Single Base Substitutions
0.07k
0.05k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.09k
0.13k
0.18k

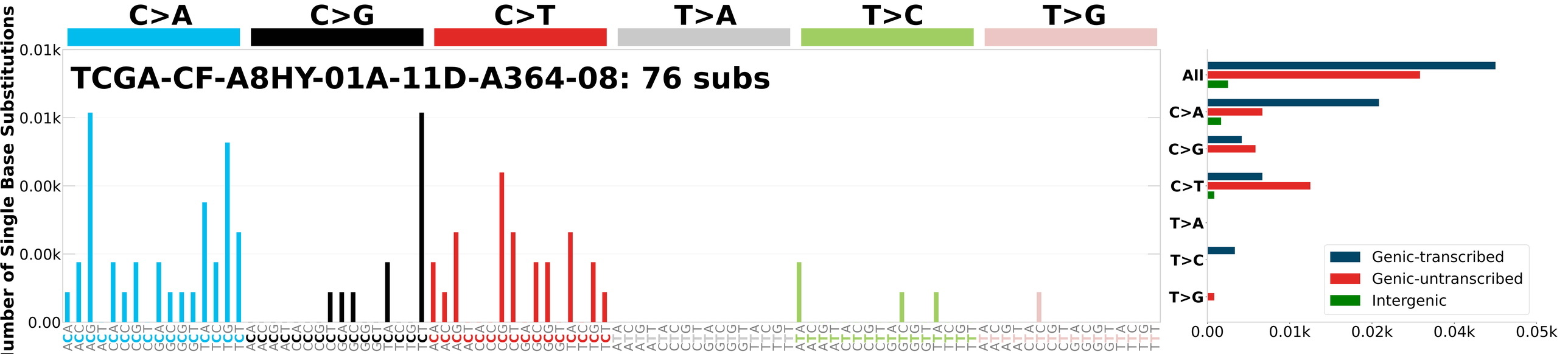

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A47Y-01A-11D-A23U-08: 65 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

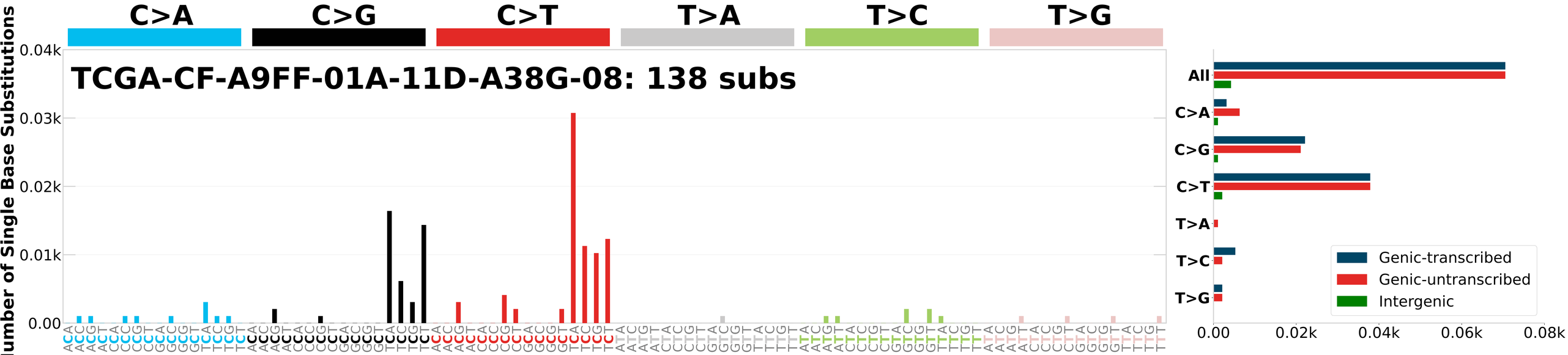

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A5U8-01A-11D-A289-08: 64 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

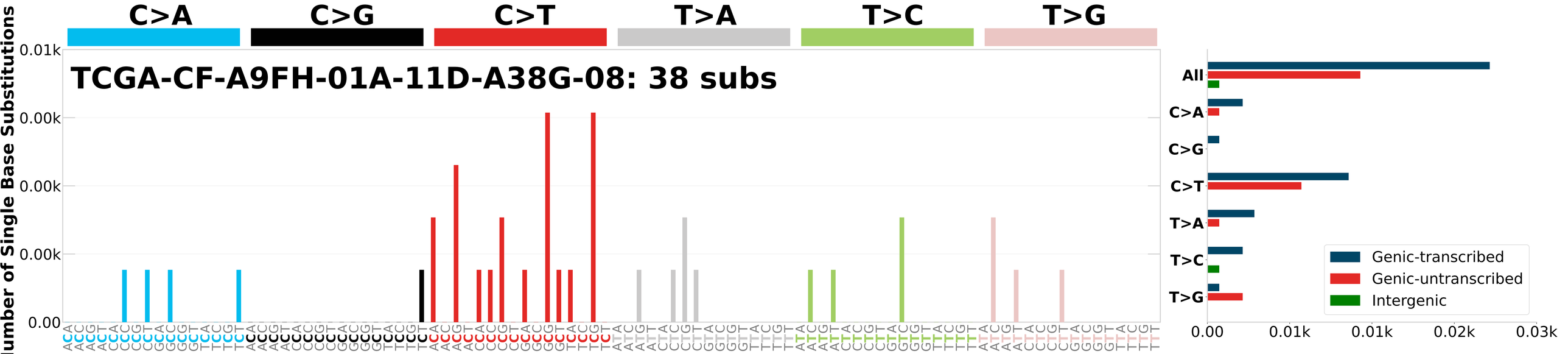

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A5UA-01A-11D-A289-08: 80 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

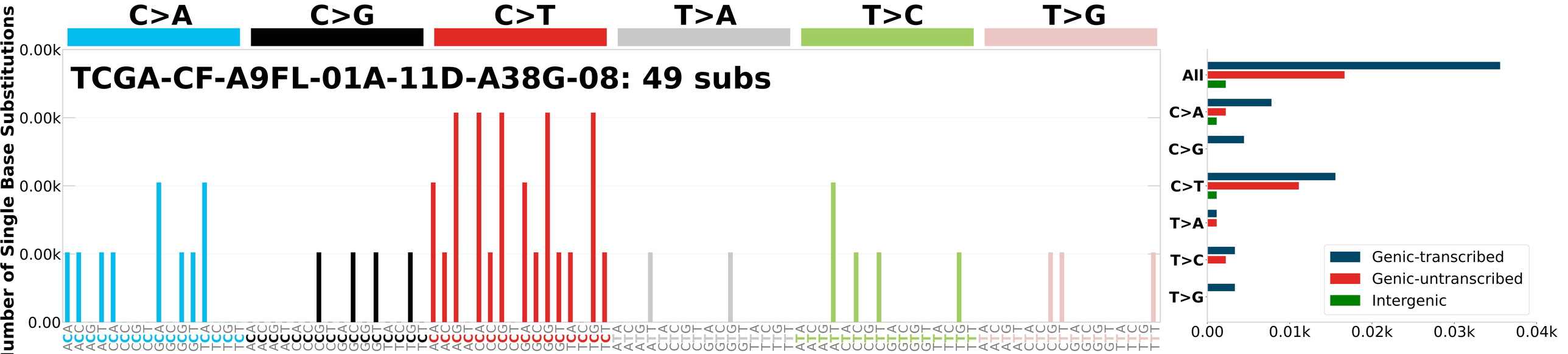

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A7I0-01A-22D-A34U-08: 49 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.02k
0.03k

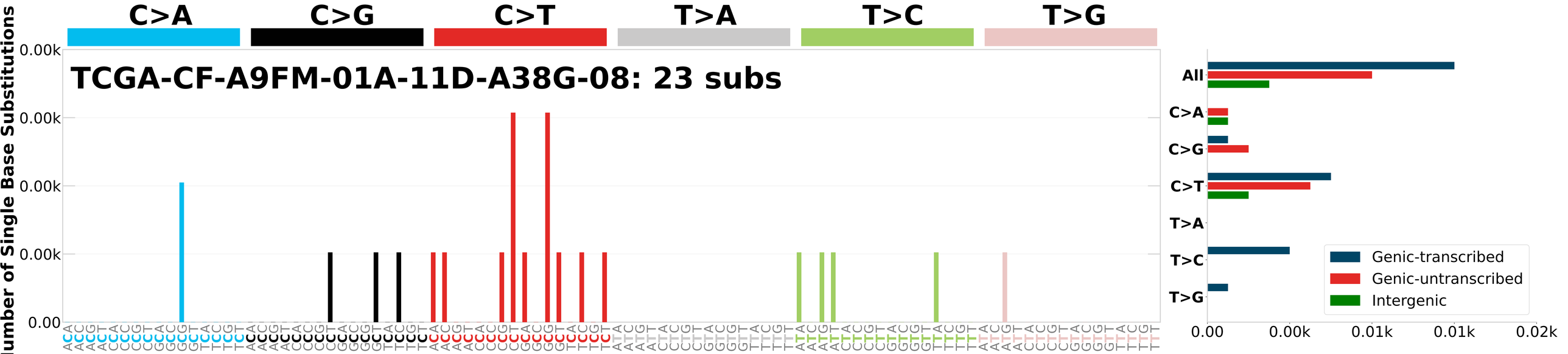

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A8HX-01A-11D-A364-08: 60 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

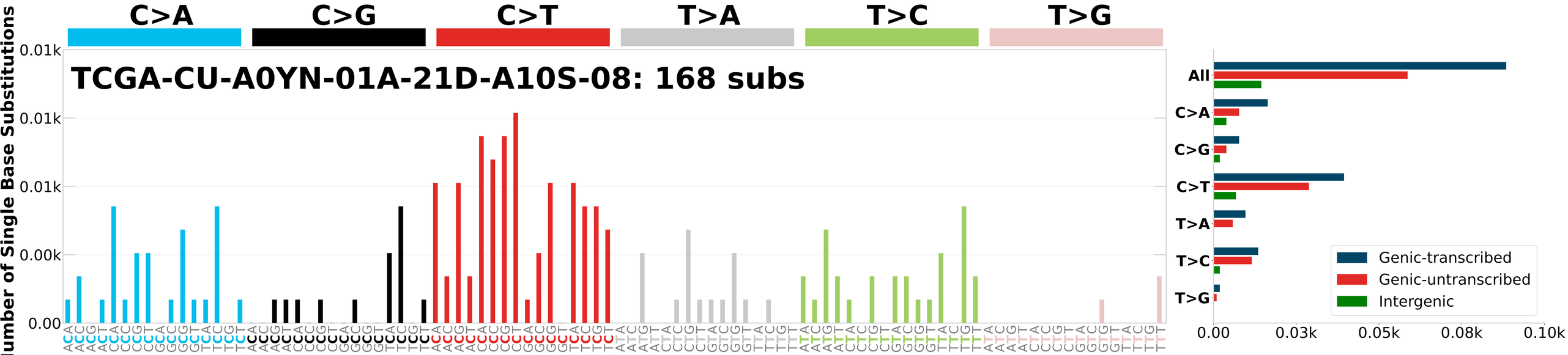

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A8HY-01A-11D-A364-08: 76 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

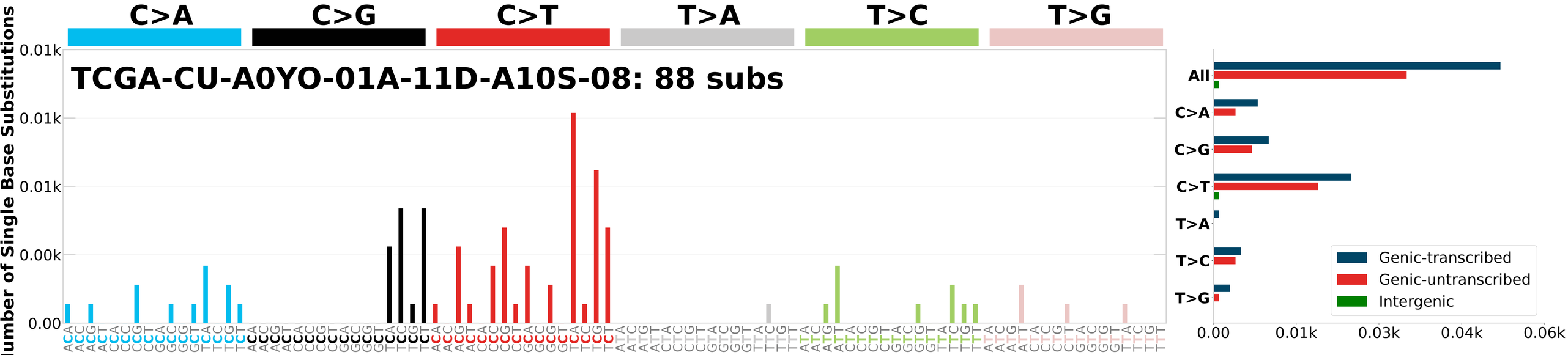

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A9FF-01A-11D-A38G-08: 138 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

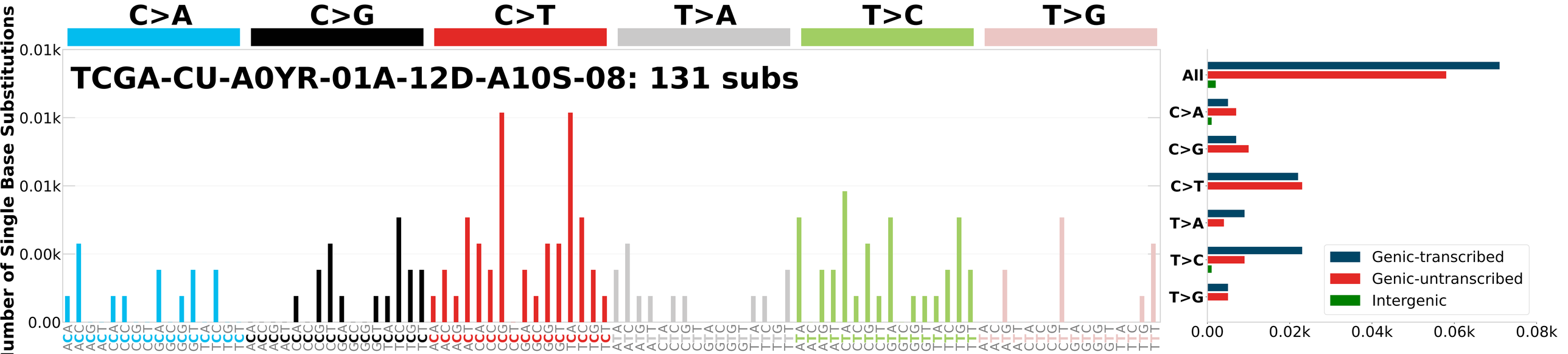

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A9FH-01A-11D-A38G-08: 38 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.02k
0.03k

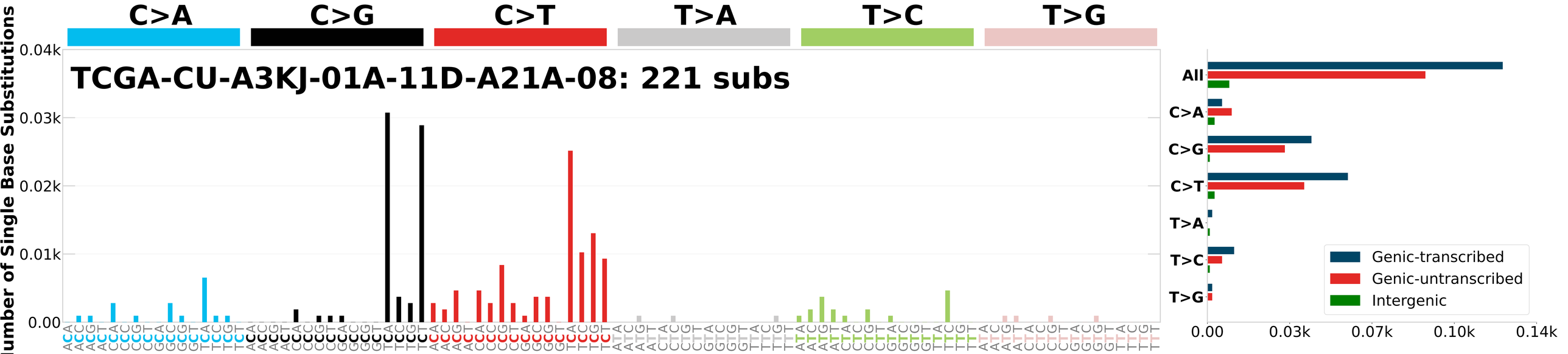

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A9FL-01A-11D-A38G-08: 49 subs
Number of Single Base Substitutions
0.00k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

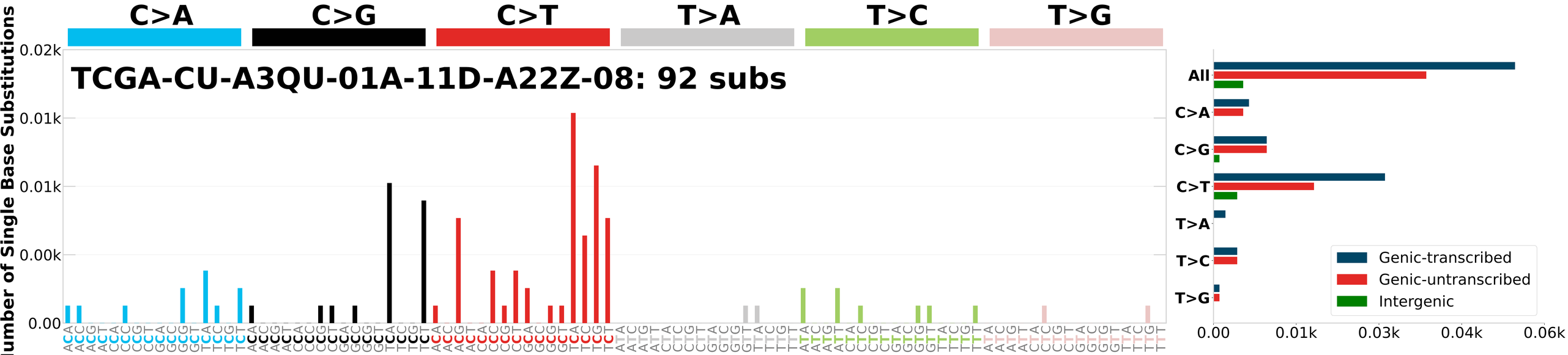

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CF-A9FM-01A-11D-A38G-08: 23 subs
Number of Single Base Substitutions
0.00k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.00k
0.01k
0.01k
0.02k

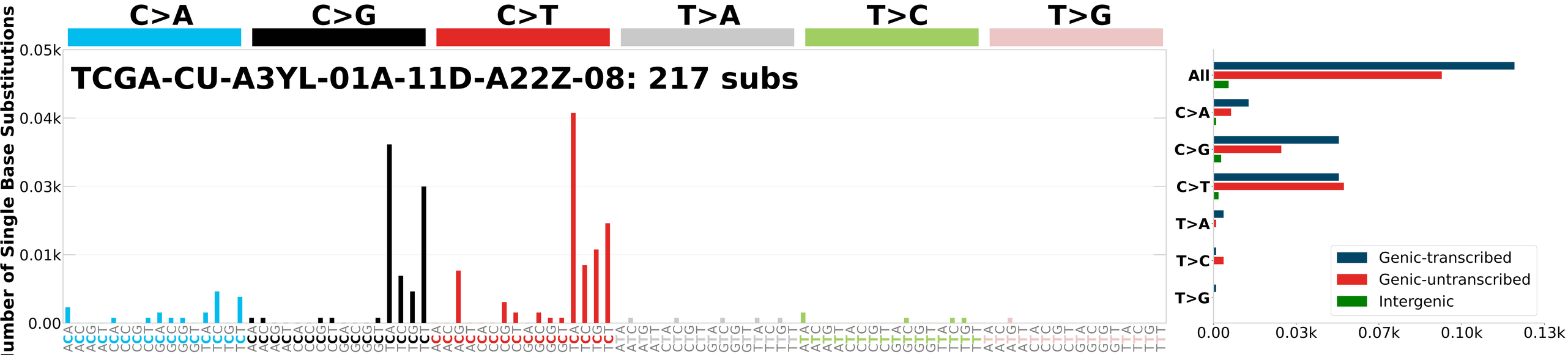

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CU-A0YN-01A-21D-A10S-08: 168 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.10k

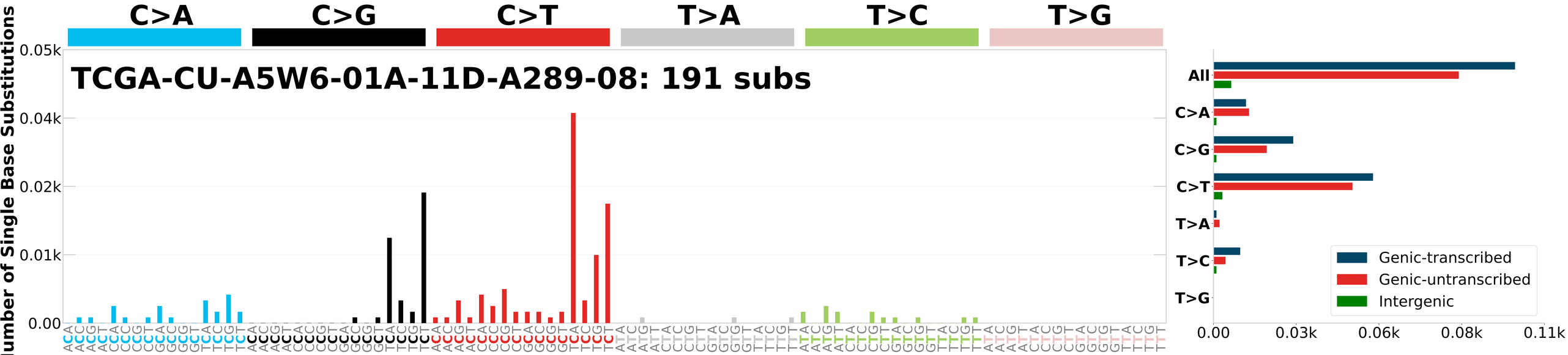

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CU-A0YO-01A-11D-A10S-08: 88 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

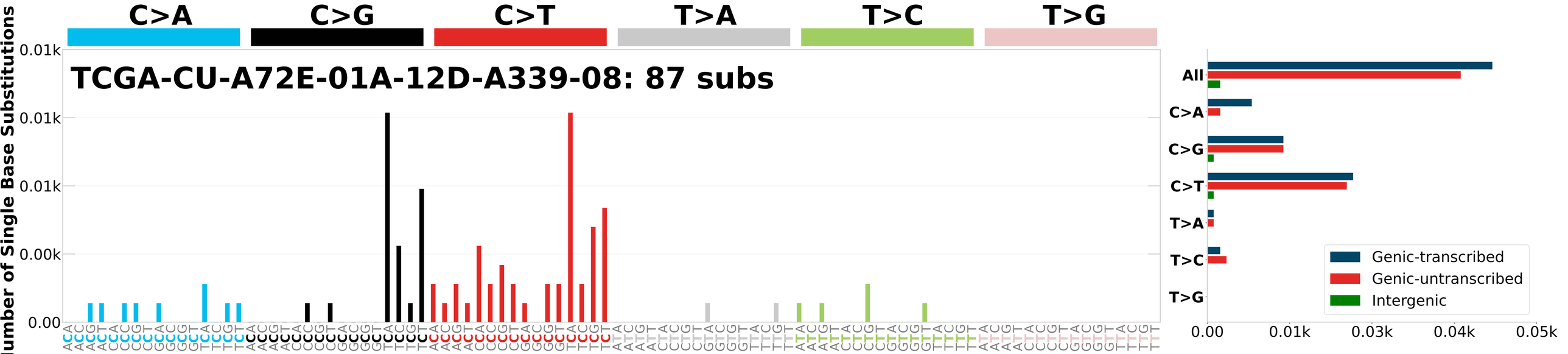

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CU-A0YR-01A-12D-A10S-08: 131 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

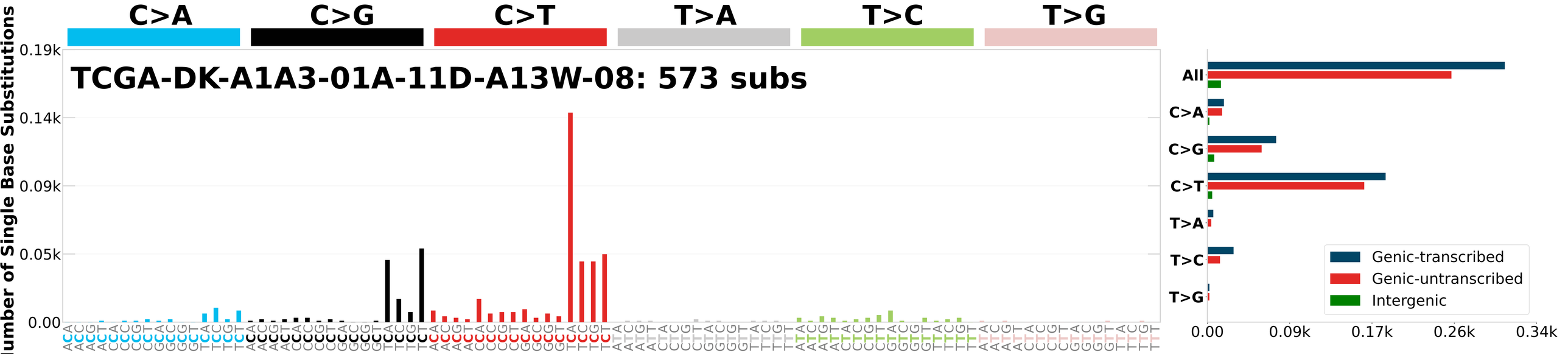

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CU-A3KJ-01A-11D-A21A-08: 221 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.14k

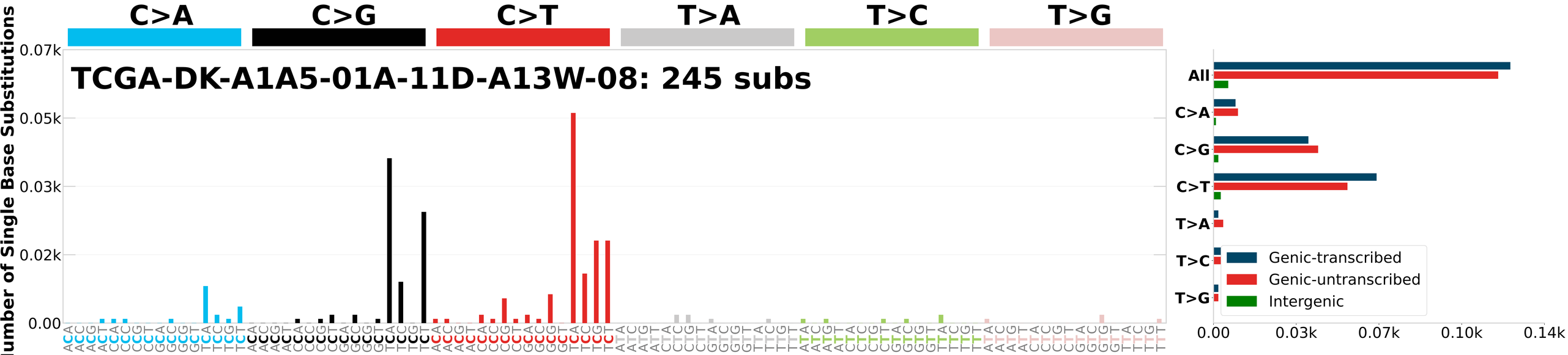

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CU-A3QU-01A-11D-A22Z-08: 92 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

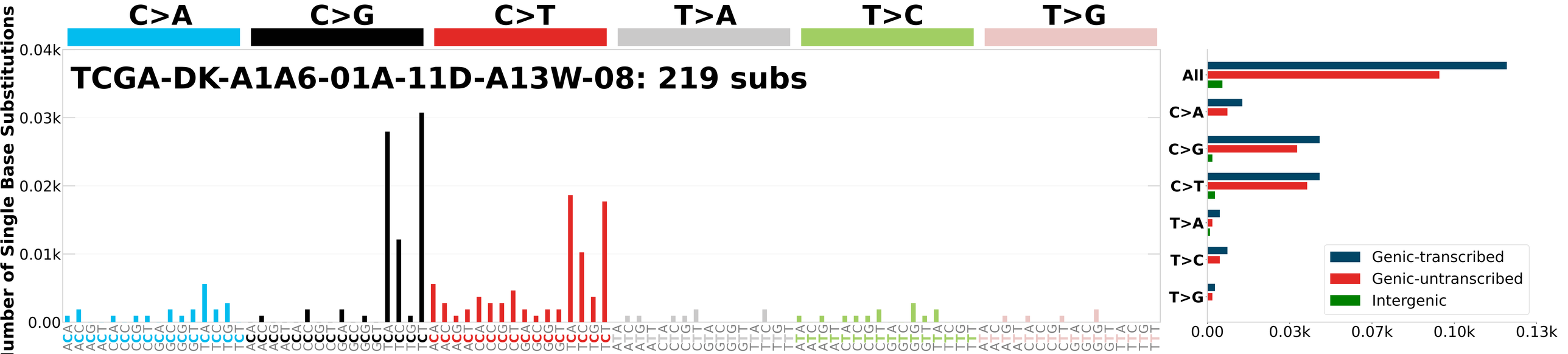

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CU-A3YL-01A-11D-A22Z-08: 217 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.13k

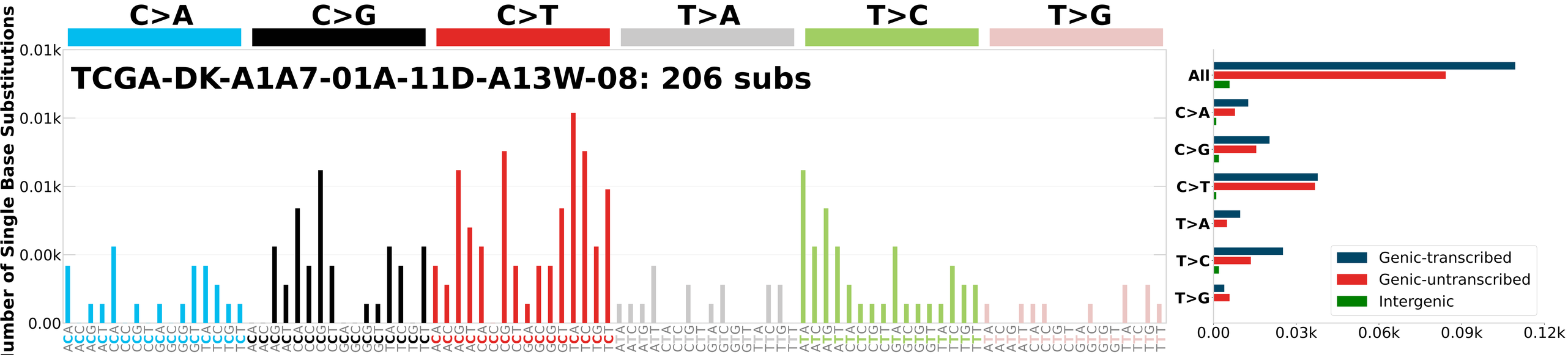

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CU-A5W6-01A-11D-A289-08: 191 subs
Number of Single Base Substitutions
0.05k
0.04k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.08k
0.11k

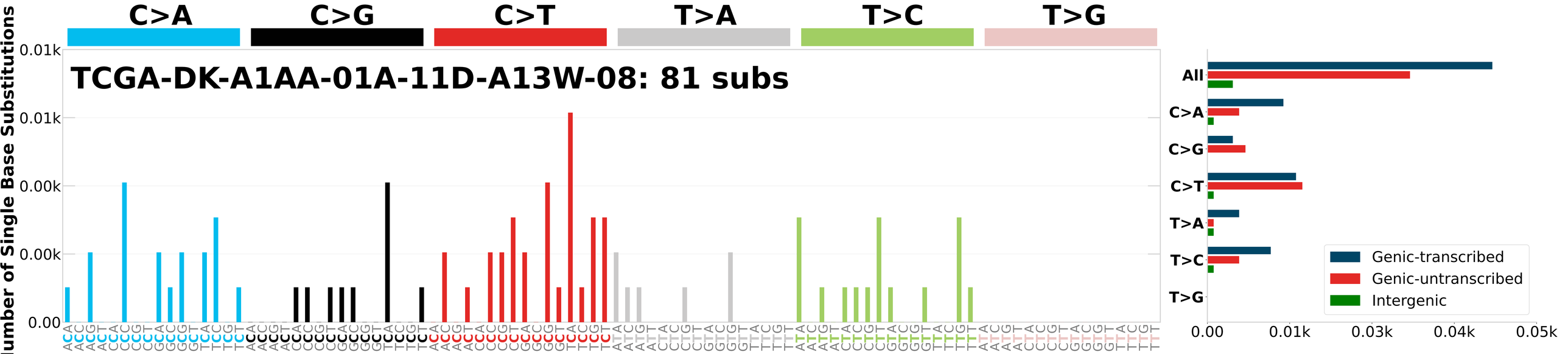

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-CU-A72E-01A-12D-A339-08: 87 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

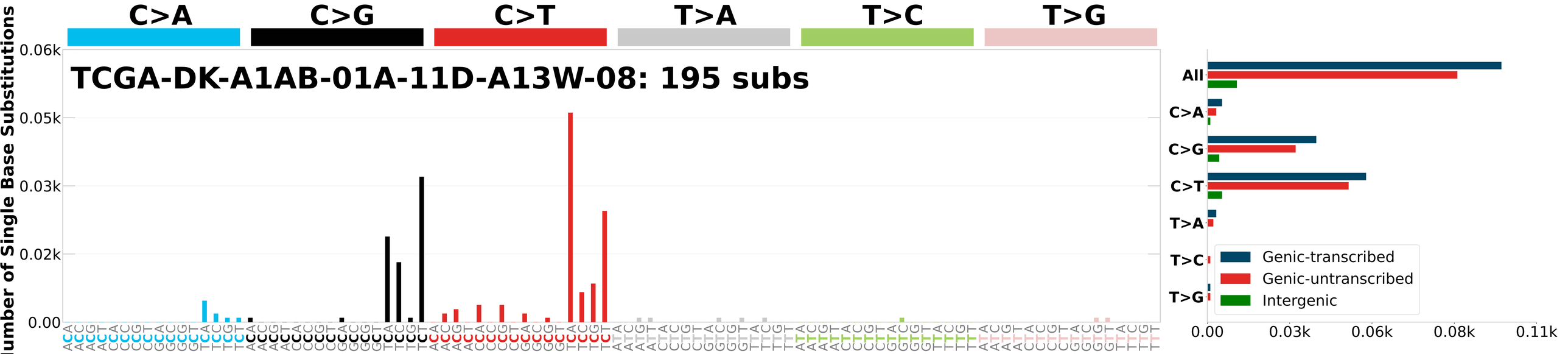

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A1A3-01A-11D-A13W-08: 573 subs
Number of Single Base Substitutions
0.19k
0.14k
0.09k
0.05k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.09k
0.17k
0.26k
0.34k

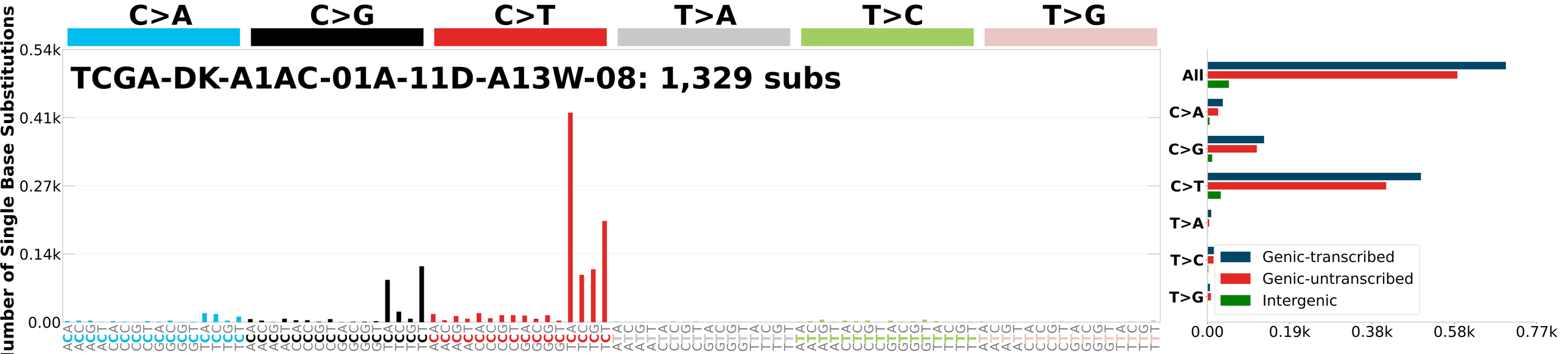

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A1A5-01A-11D-A13W-08: 245 subs
Number of Single Base Substitutions
0.07k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.14k

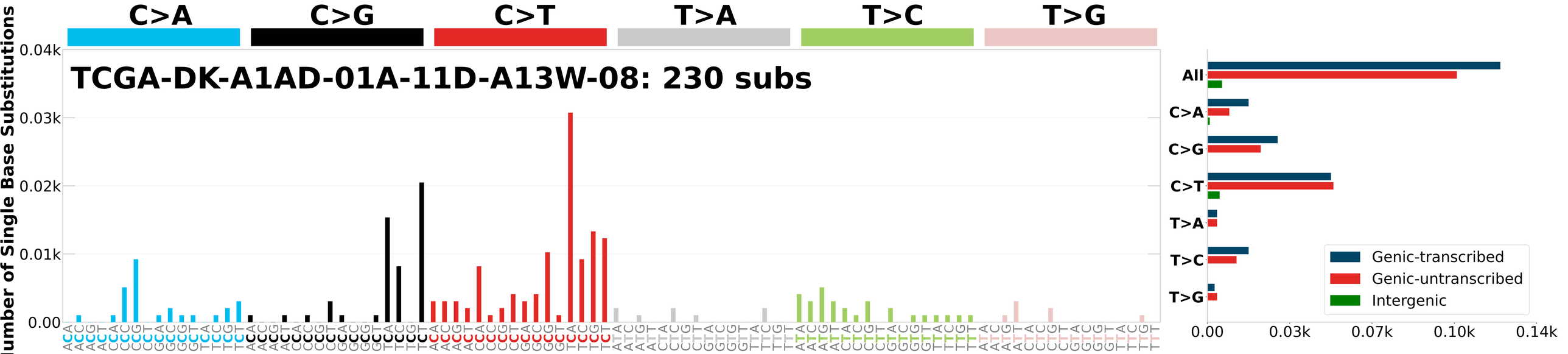

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A1A6-01A-11D-A13W-08: 219 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.13k

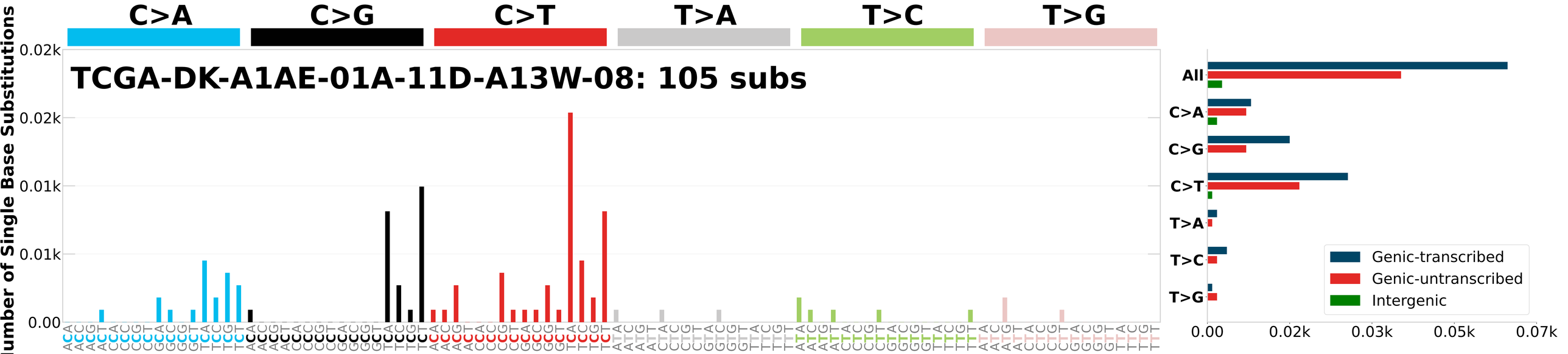

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A1A7-01A-11D-A13W-08: 206 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

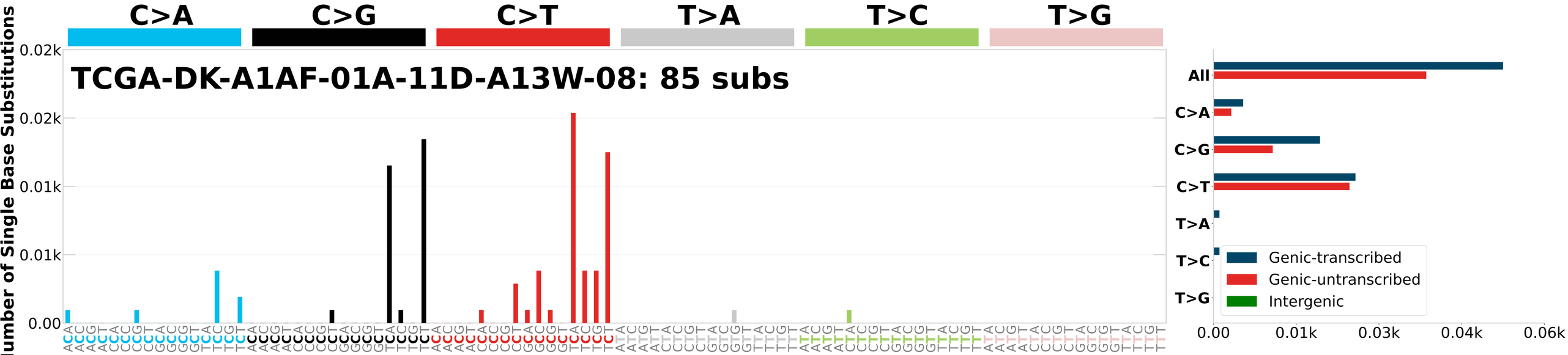

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A1AA-01A-11D-A13W-08: 81 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

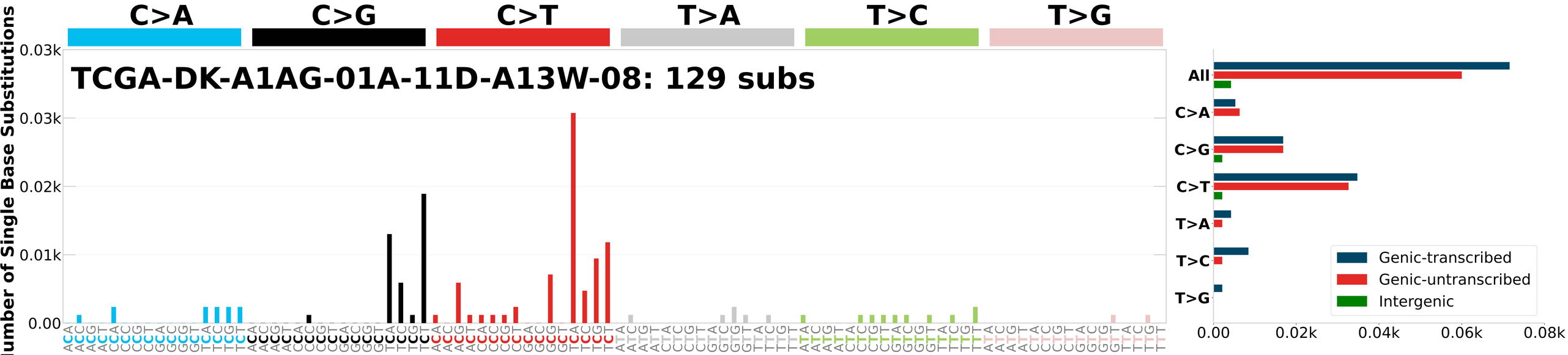

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A1AB-01A-11D-A13W-08: 195 subs
Number of Single Base Substitutions
0.06k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.08k
0.11k

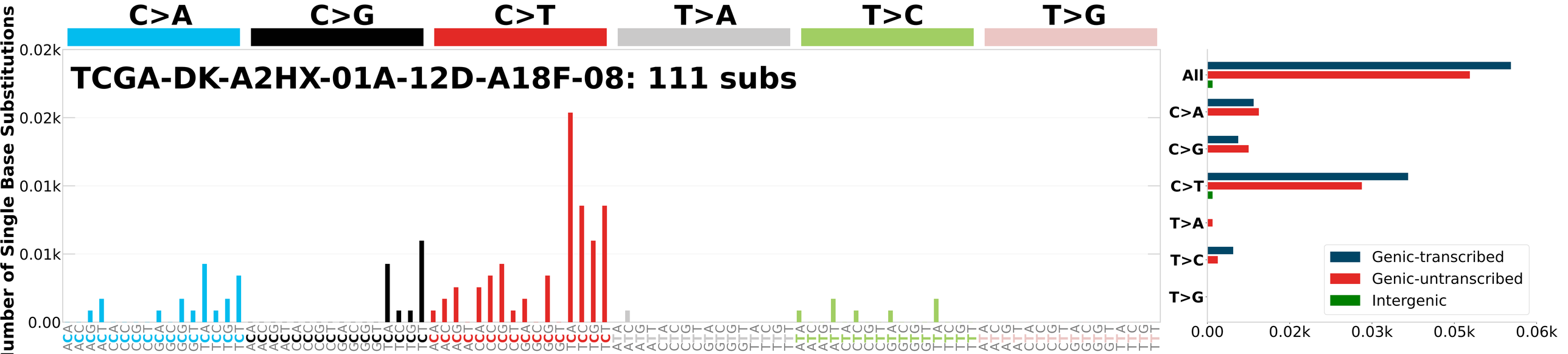

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A1AC-01A-11D-A13W-08: 1,329 subs
Number of Single Base Substitutions
0.54k
0.41k
0.27k
0.14k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.19k
0.38k
0.58k
0.77k

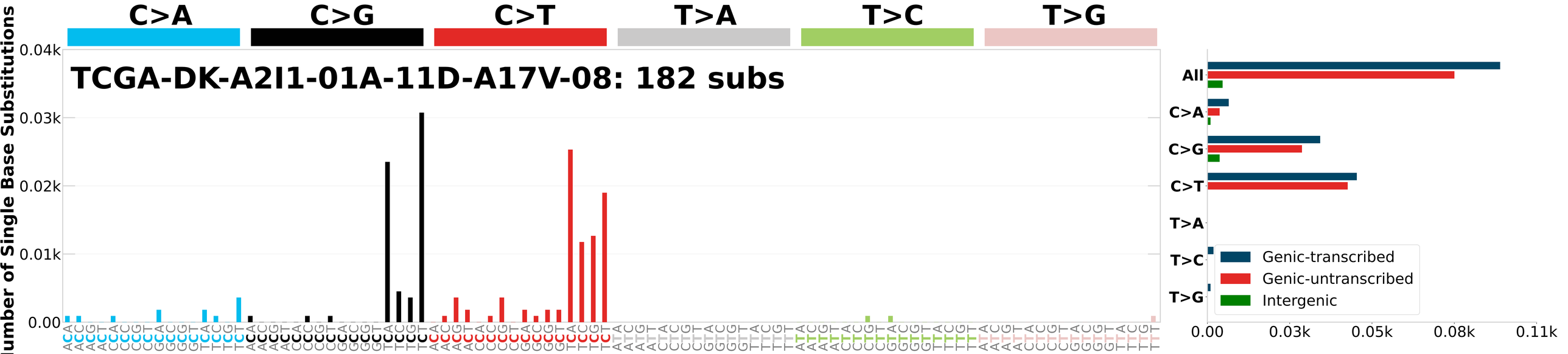

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A1AD-01A-11D-A13W-08: 230 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.14k

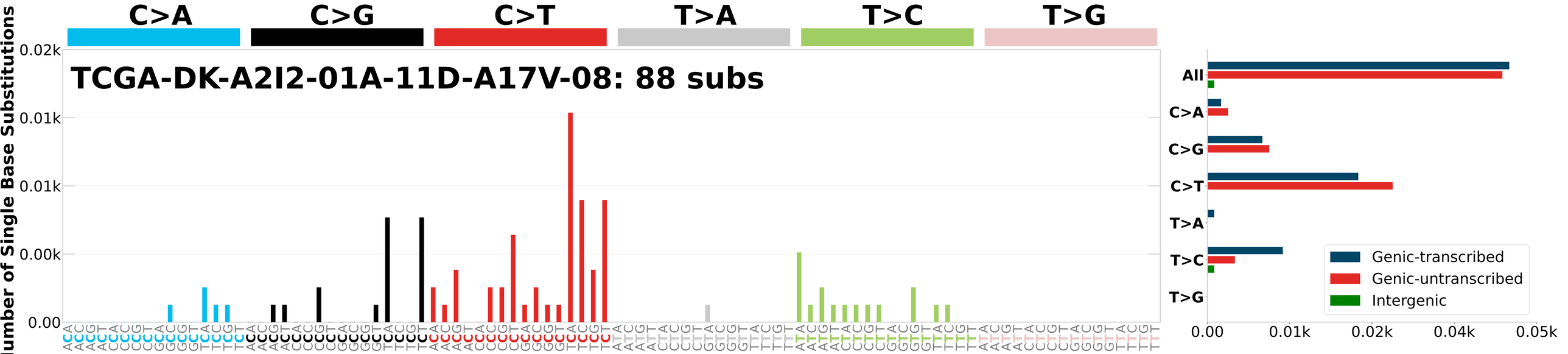

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A1AE-01A-11D-A13W-08: 105 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.07k

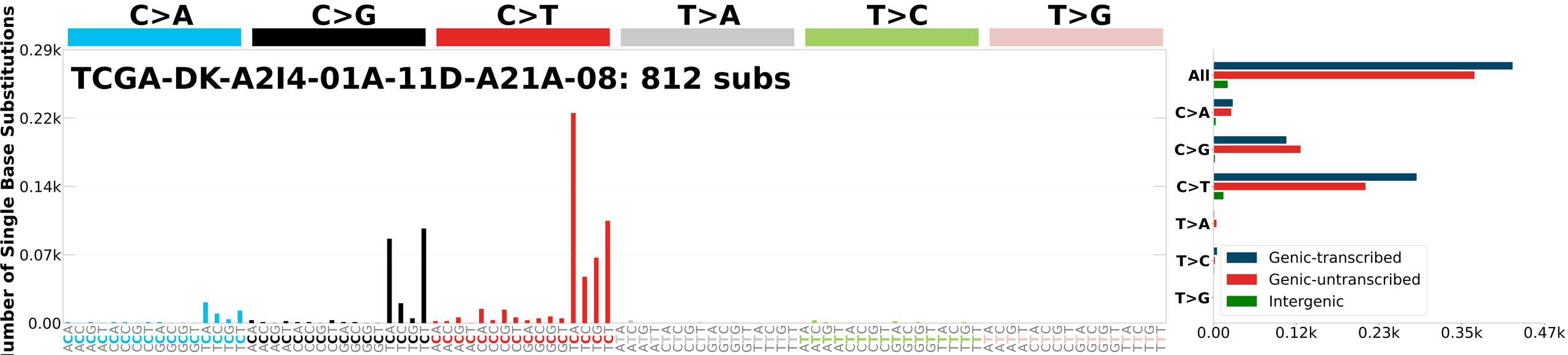

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A1AF-01A-11D-A13W-08: 85 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

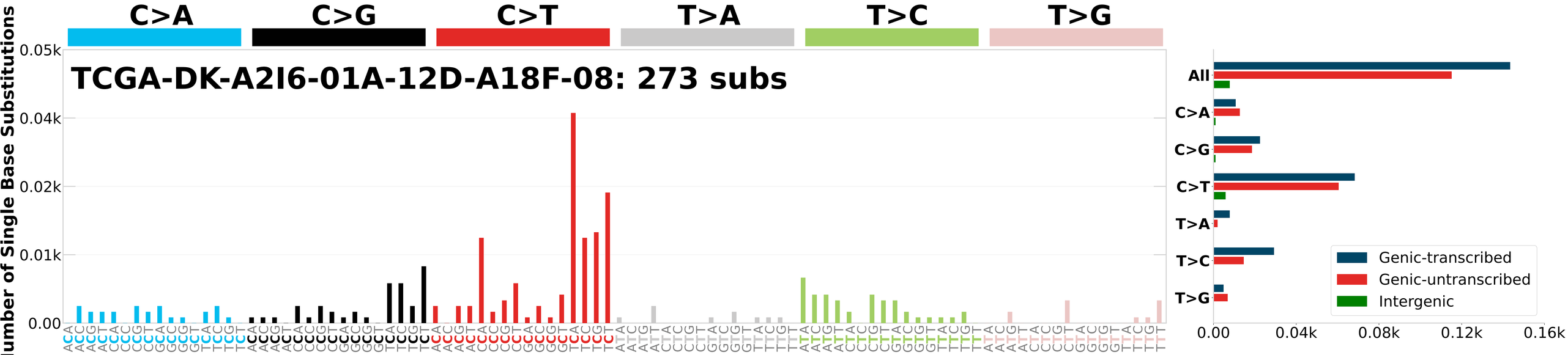

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A1AG-01A-11D-A13W-08: 129 subs
Number of Single Base Substitutions
0.03k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

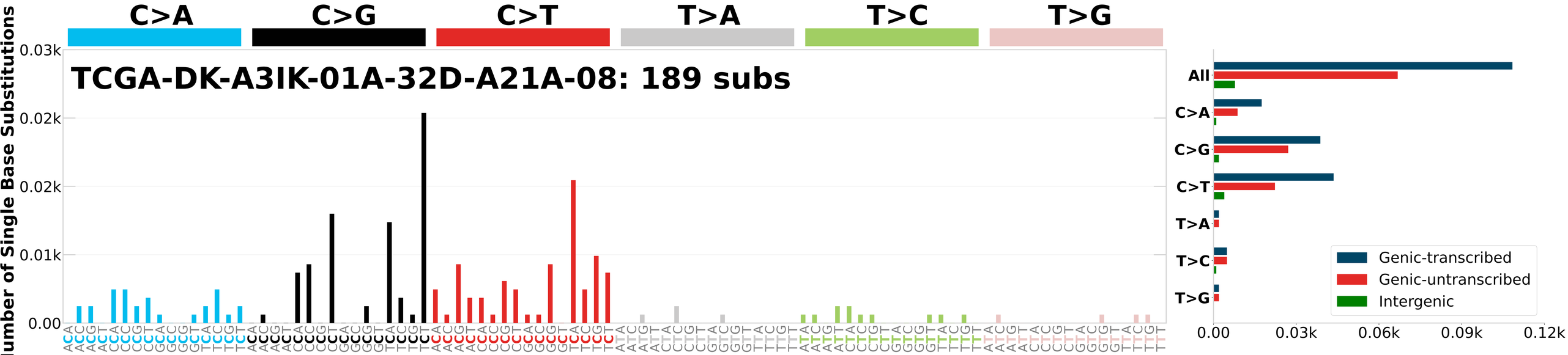

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A2HX-01A-12D-A18F-08: 111 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.06k

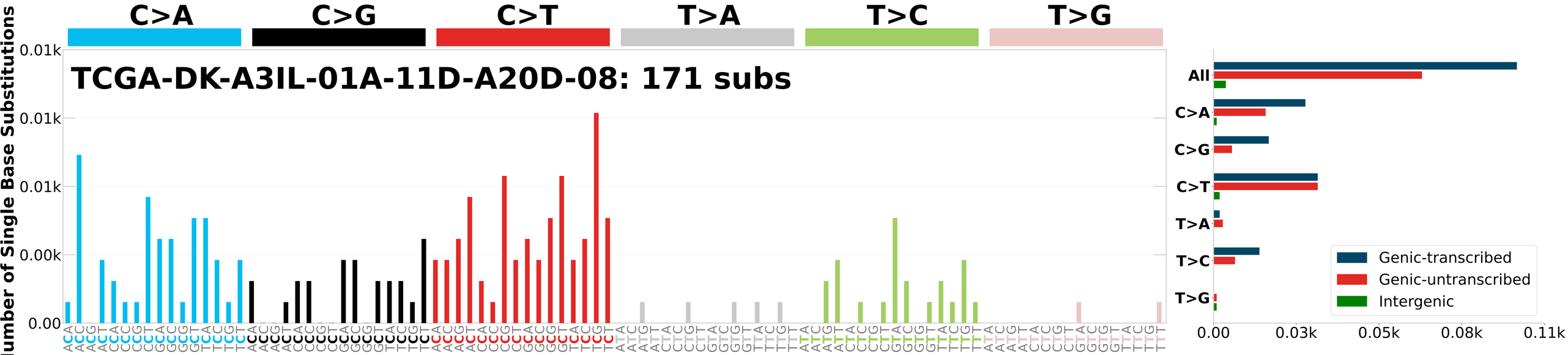

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A2I1-01A-11D-A17V-08: 182 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.11k

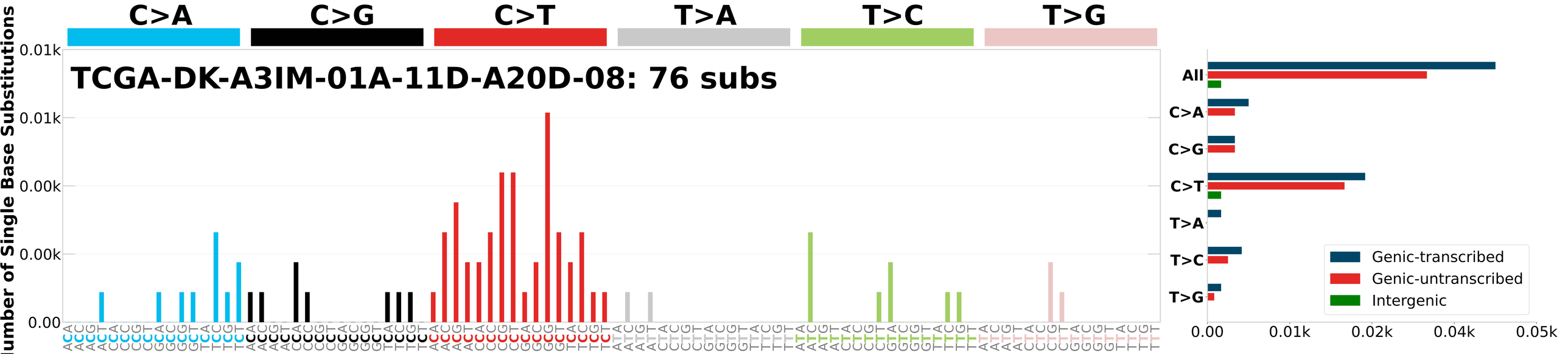

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A2I2-01A-11D-A17V-08: 88 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

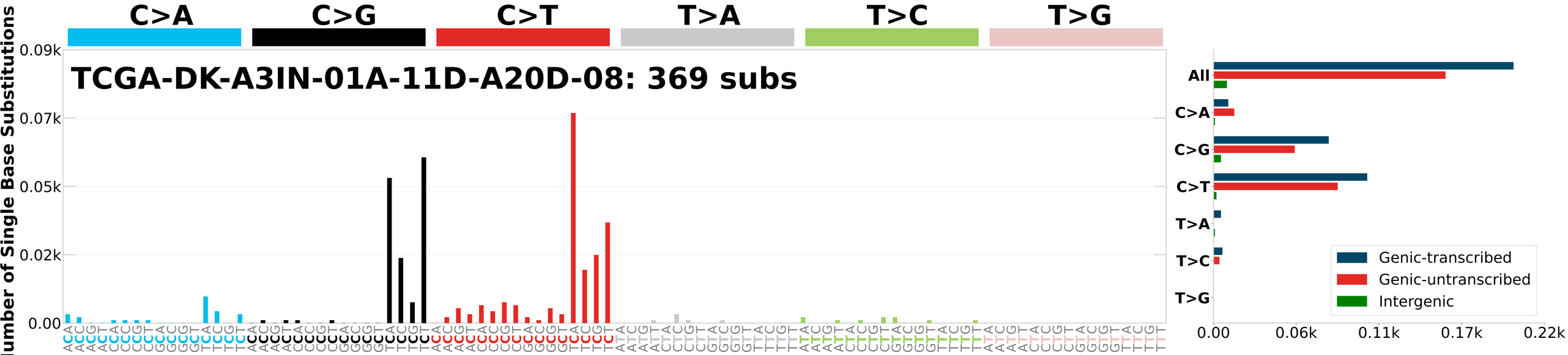

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A2I4-01A-11D-A21A-08: 812 subs
Number of Single Base Substitutions
0.29k
0.22k
0.14k
0.07k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.12k
0.23k
0.35k
0.47k

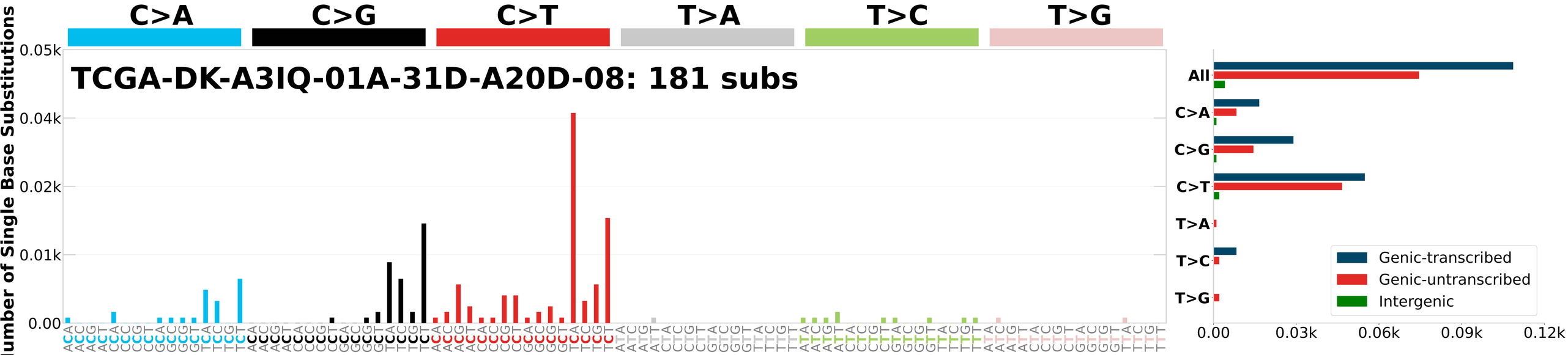

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A2I6-01A-12D-A18F-08: 273 subs
Number of Single Base Substitutions
0.05k
0.04k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.12k
0.16k

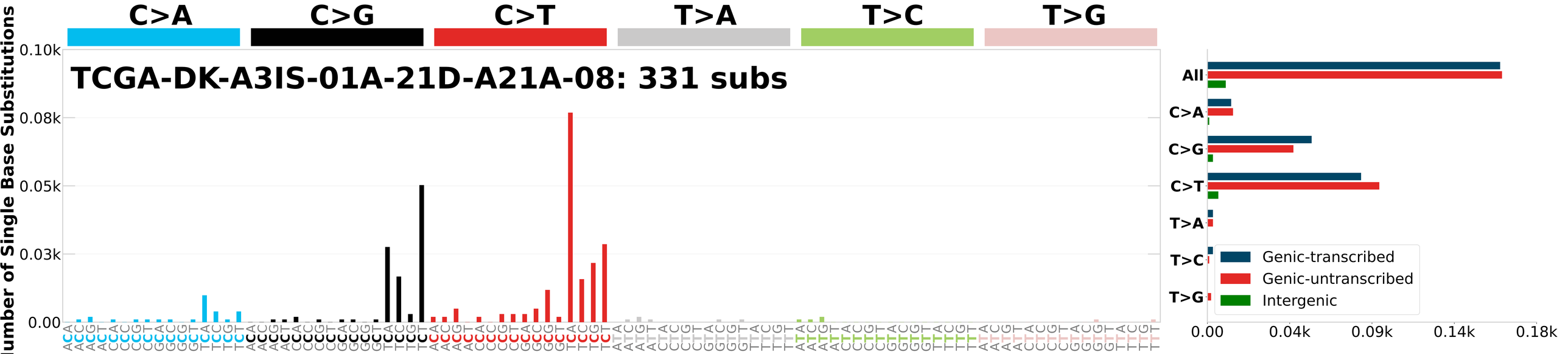

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A3IK-01A-32D-A21A-08: 189 subs
Number of Single Base Substitutions
0.03k
0.02k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

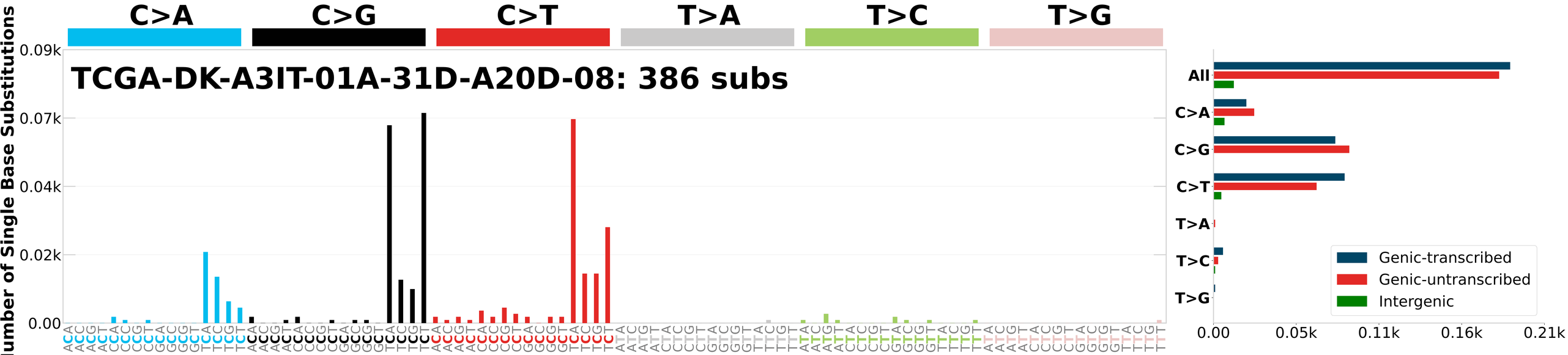

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A3IL-01A-11D-A20D-08: 171 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.11k

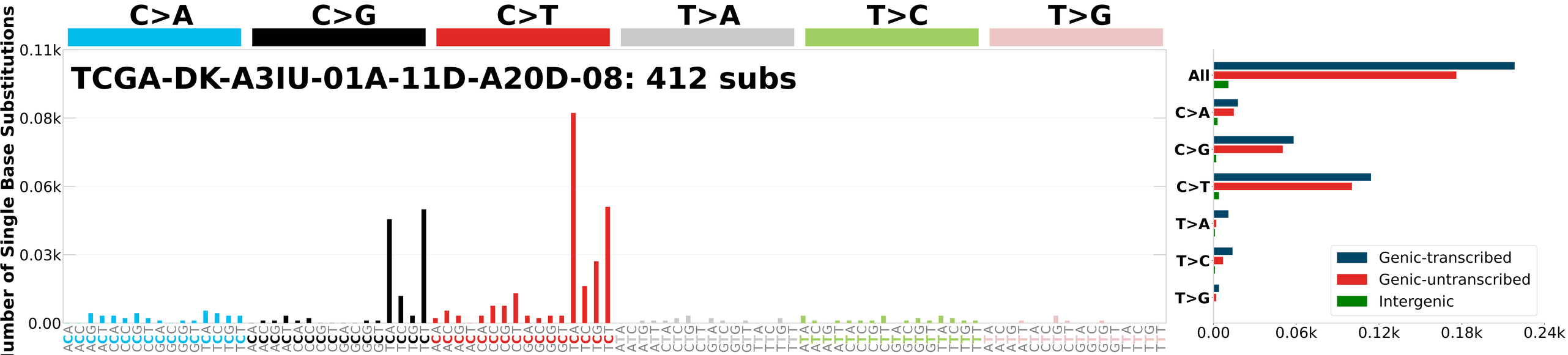

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A3IM-01A-11D-A20D-08: 76 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

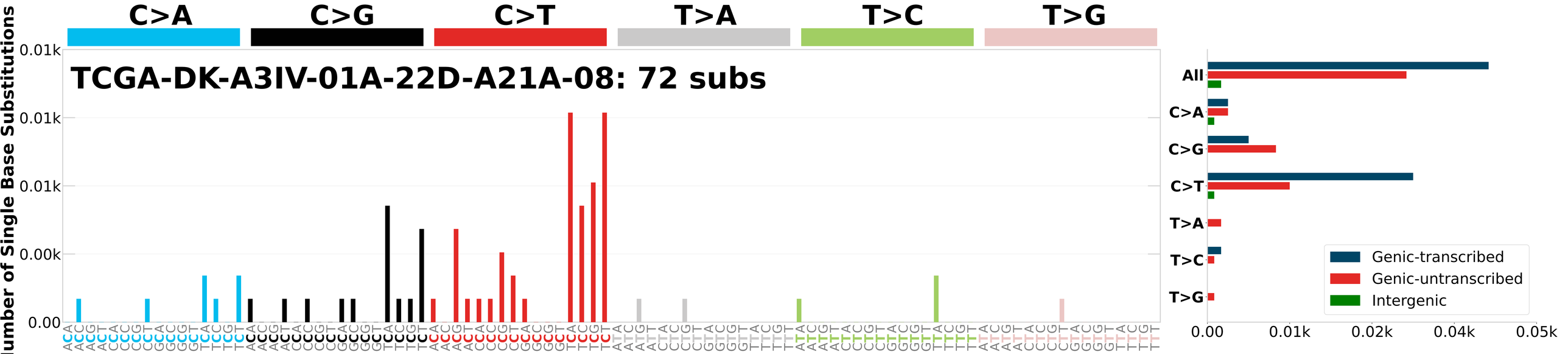

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A3IN-01A-11D-A20D-08: 369 subs
Number of Single Base Substitutions
0.09k
0.07k
0.05k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.11k
0.17k
0.22k

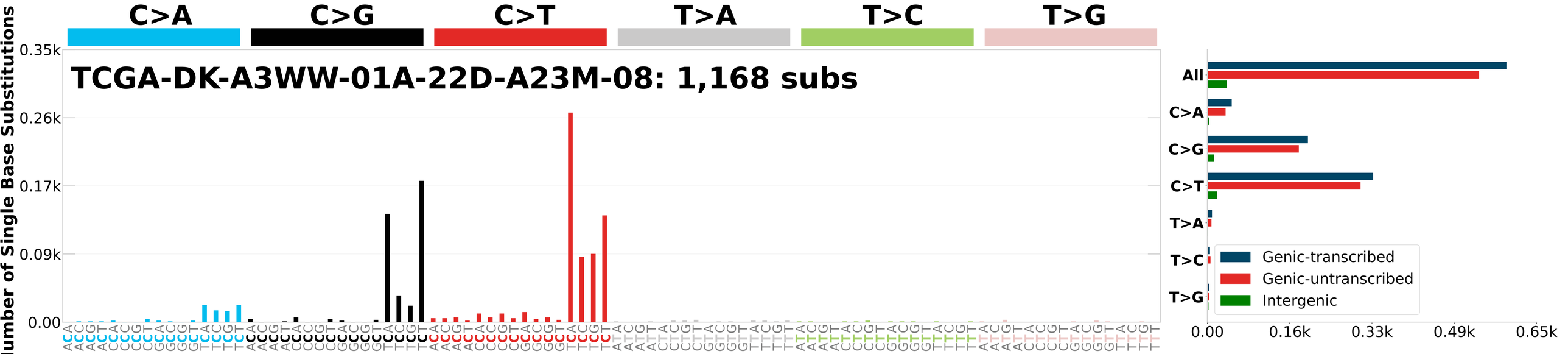

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A3IQ-01A-31D-A20D-08: 181 subs
Number of Single Base Substitutions
0.05k
0.04k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

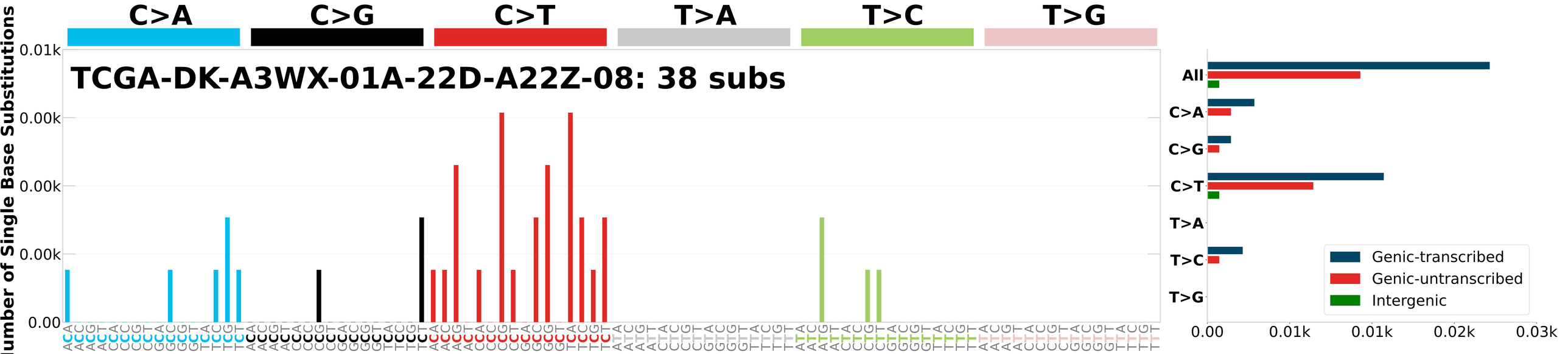

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A3IS-01A-21D-A21A-08: 331 subs
Number of Single Base Substitutions
0.10k
0.08k
0.05k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.09k
0.14k
0.18k

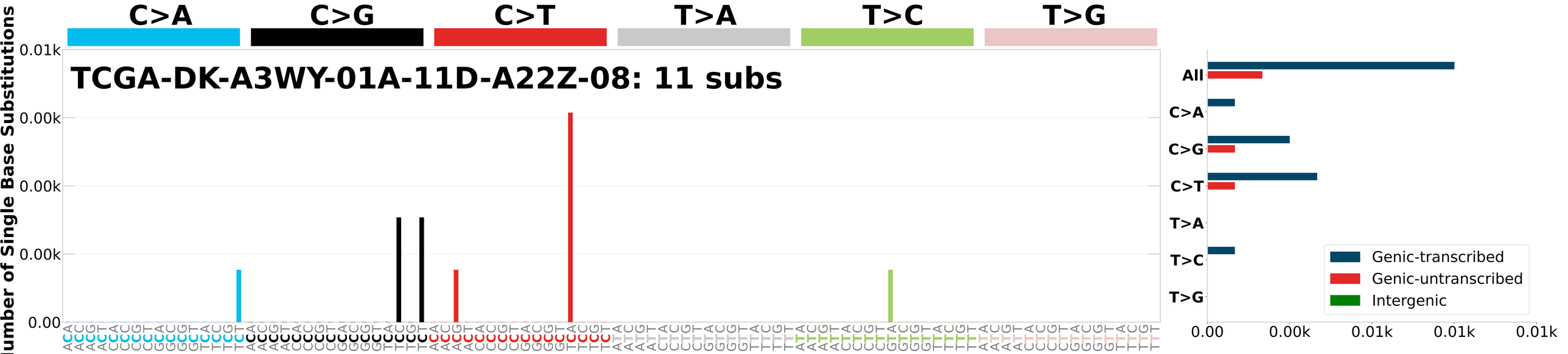

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A3IT-01A-31D-A20D-08: 386 subs
Number of Single Base Substitutions
0.09k
0.07k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.11k
0.16k
0.21k

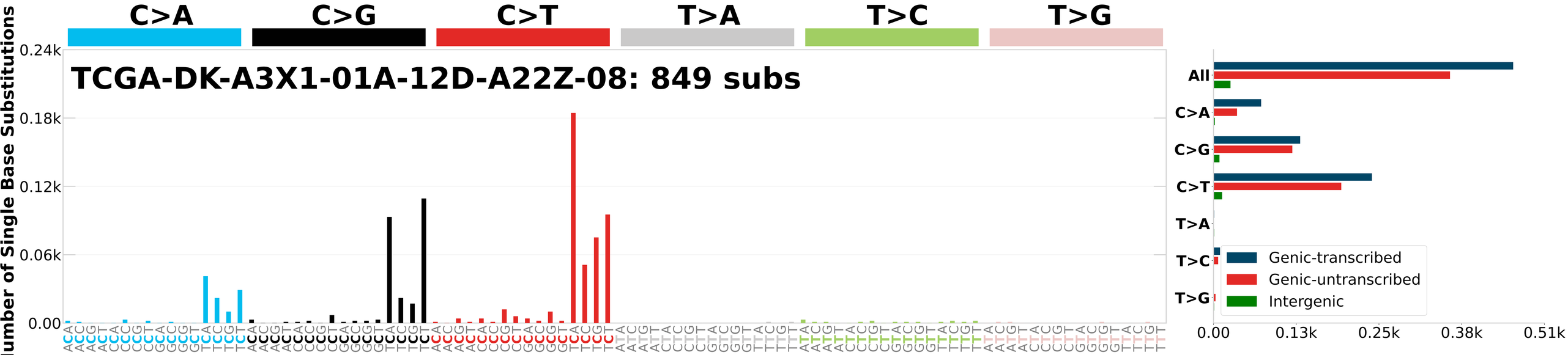

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A3IU-01A-11D-A20D-08: 412 subs
Number of Single Base Substitutions
0.11k
0.08k
0.06k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.12k
0.18k
0.24k

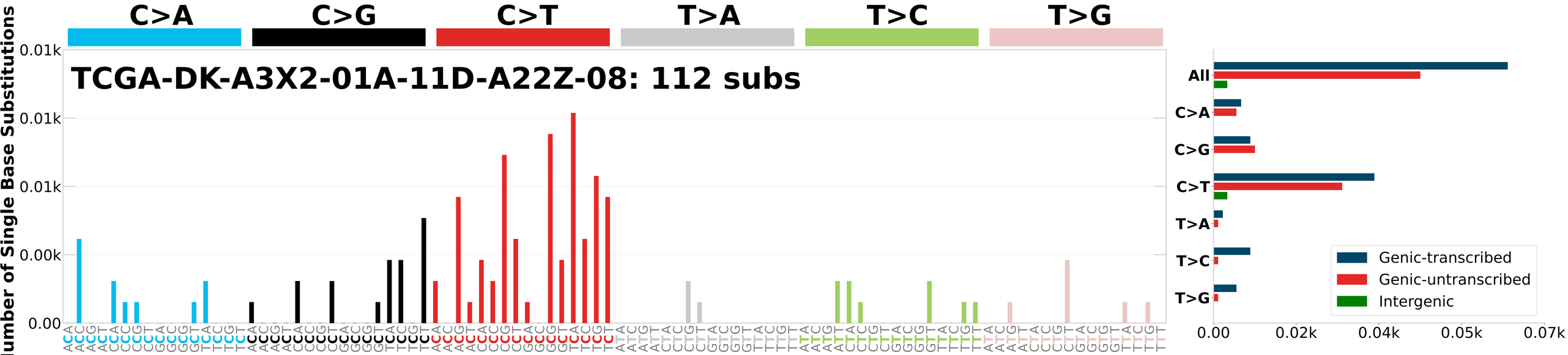

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A3IV-01A-22D-A21A-08: 72 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

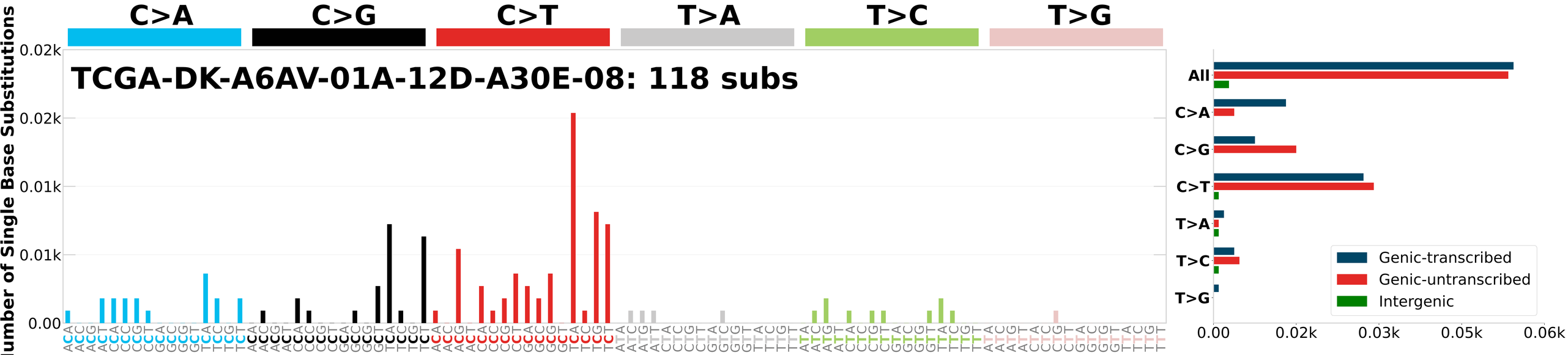

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A3WW-01A-22D-A23M-08: 1,168 subs
Number of Single Base Substitutions
0.35k
0.26k
0.17k
0.09k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.16k
0.33k
0.49k
0.65k

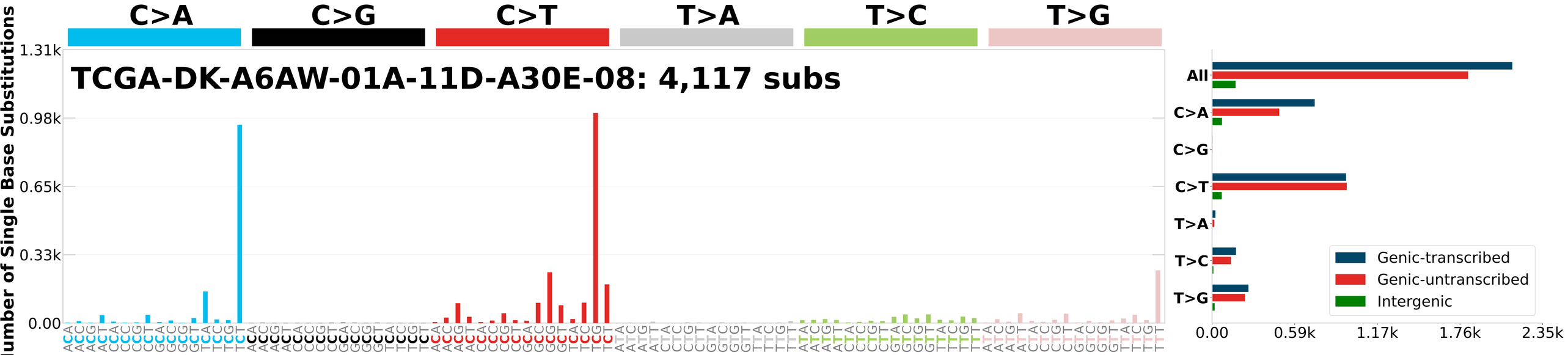

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A3WX-01A-22D-A22Z-08: 38 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.02k
0.03k

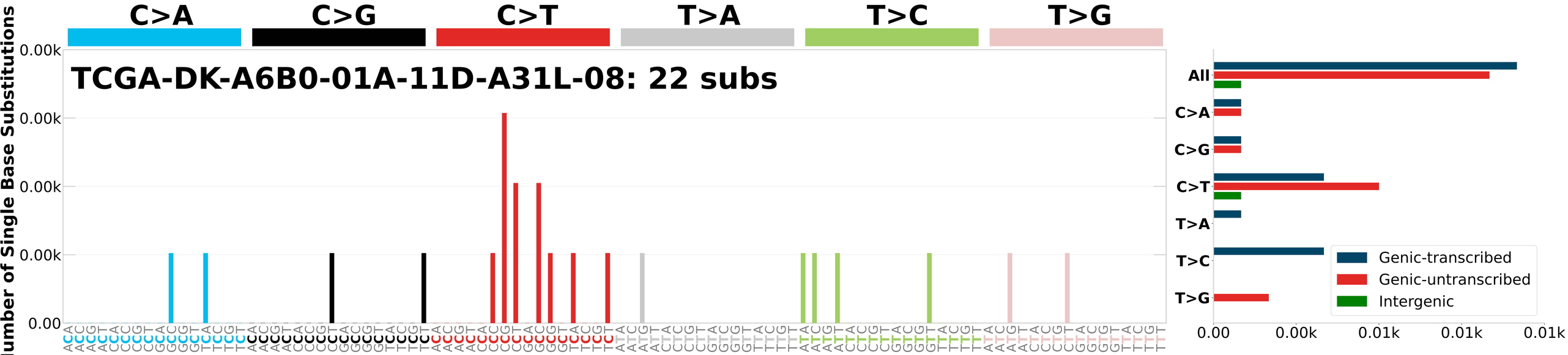

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A3WY-01A-11D-A22Z-08: 11 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.00k
0.01k
0.01k
0.01k

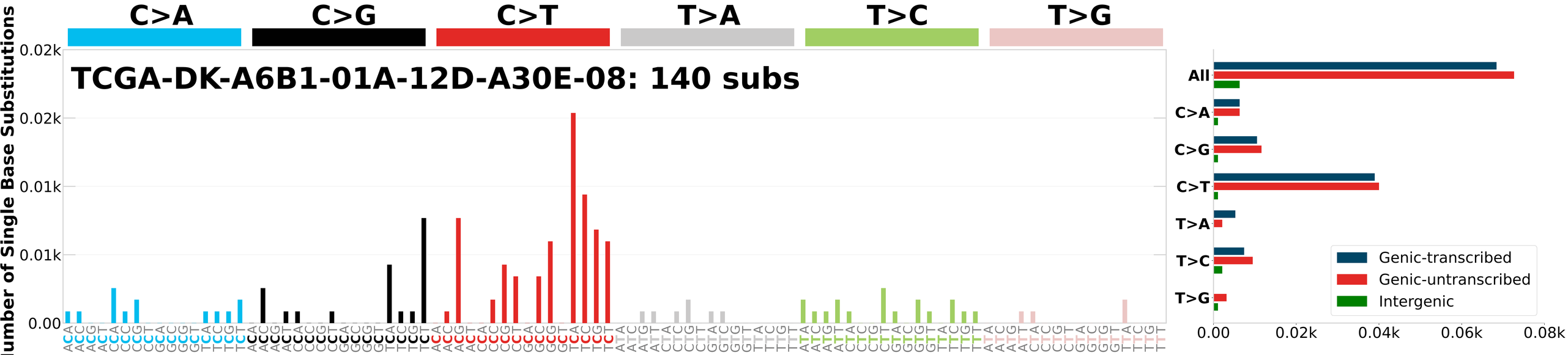

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A3X1-01A-12D-A22Z-08: 849 subs
Number of Single Base Substitutions
0.24k
0.18k
0.12k
0.06k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.13k
0.25k
0.38k
0.51k

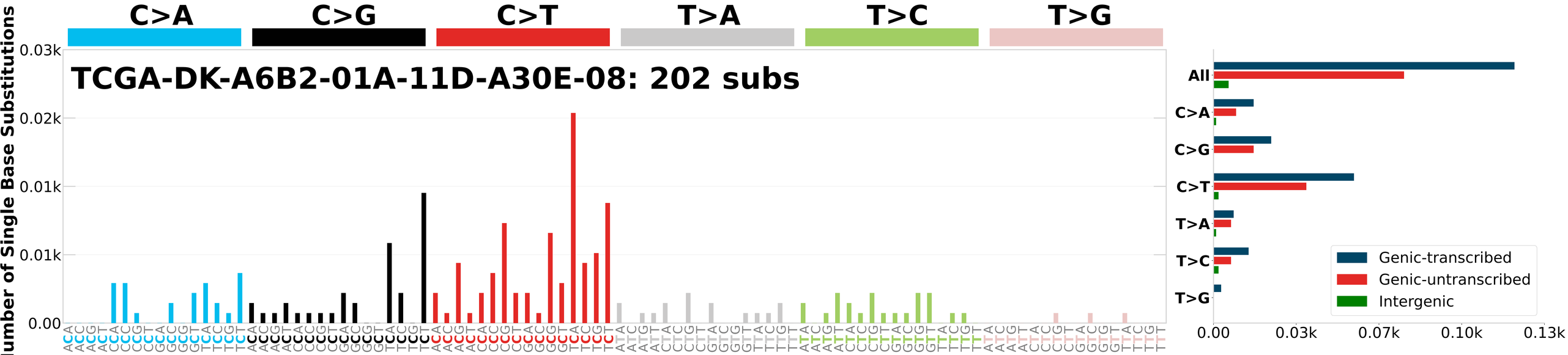

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A3X2-01A-11D-A22Z-08: 112 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.05k
0.07k

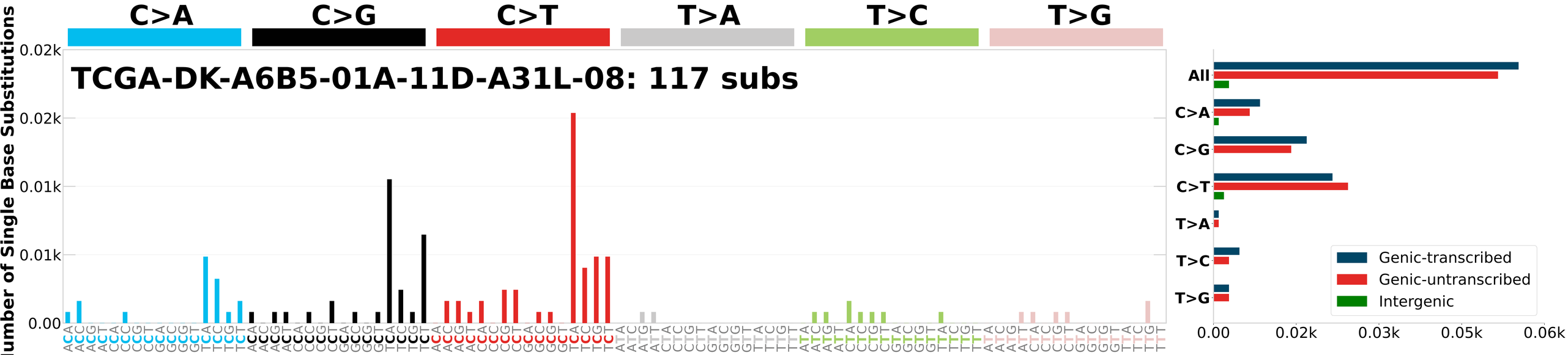

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A6AV-01A-12D-A30E-08: 118 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.06k

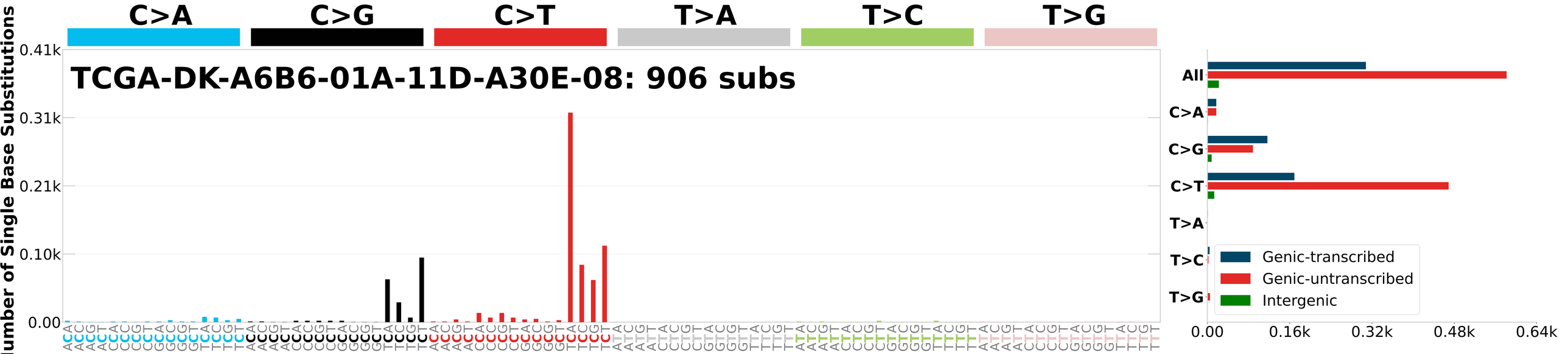

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A6AW-01A-11D-A30E-08: 4,117 subs
Number of Single Base Substitutions
1.31k
0.98k
0.65k
0.33k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.59k
1.17k
1.76k
2.35k

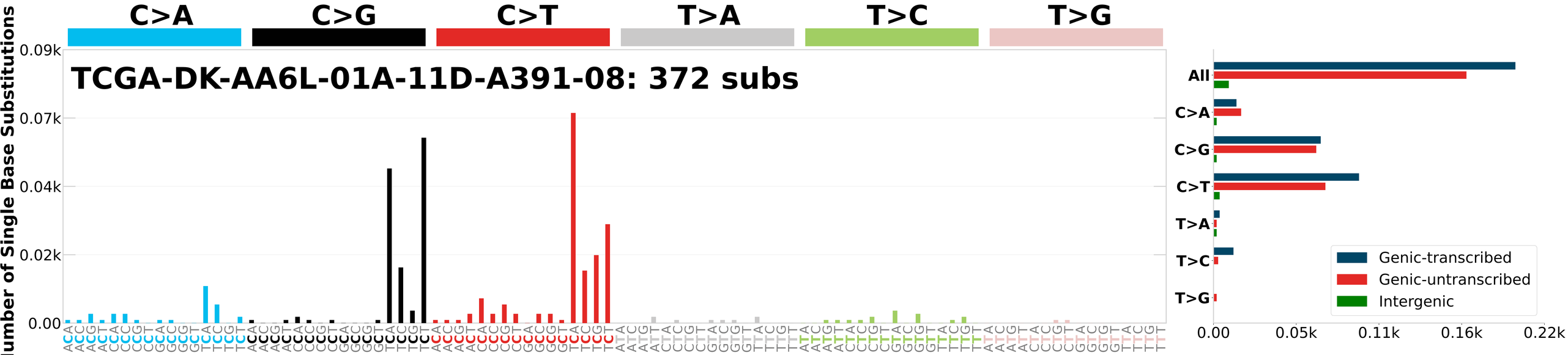

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A6B0-01A-11D-A31L-08: 22 subs
Number of Single Base Substitutions
0.00k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.00k
0.01k
0.01k
0.01k

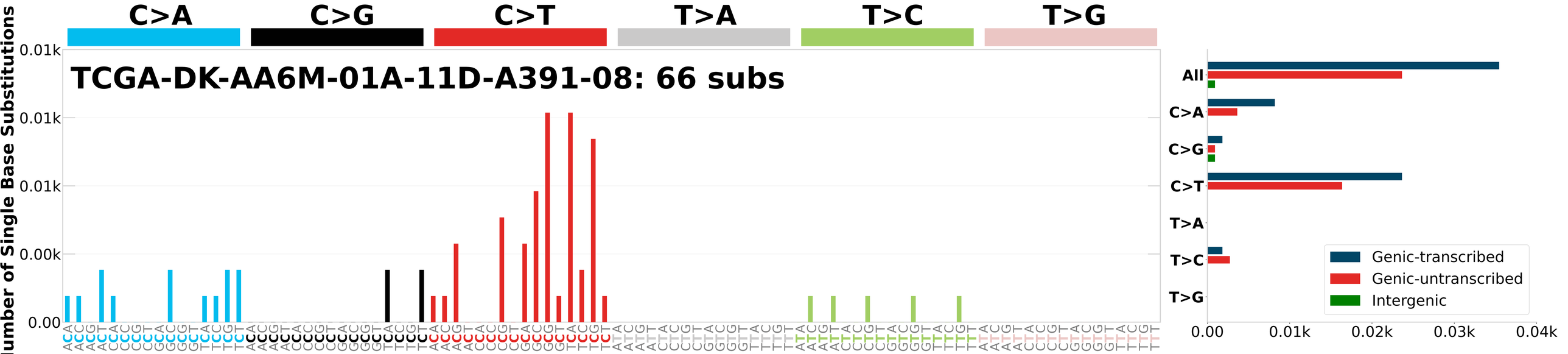

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A6B1-01A-12D-A30E-08: 140 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

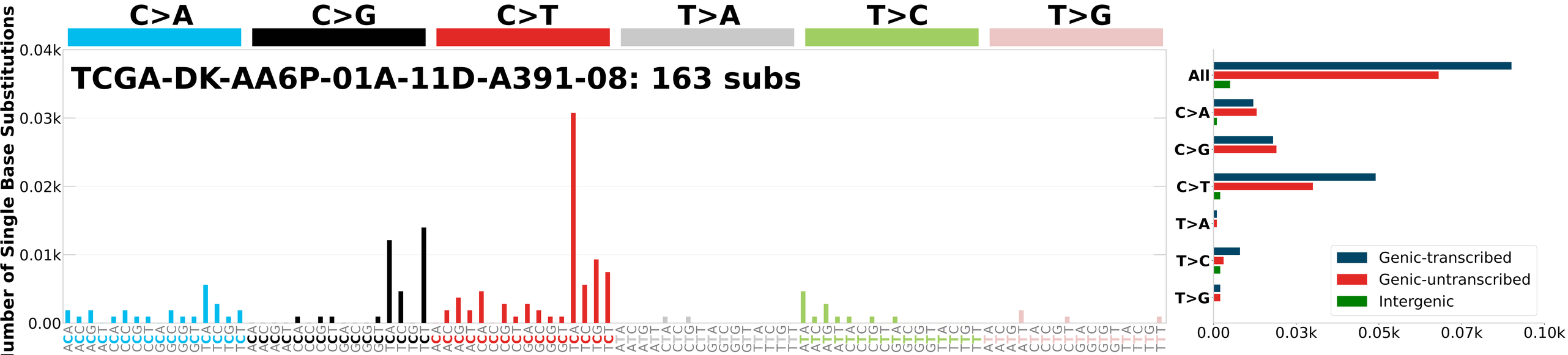

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A6B2-01A-11D-A30E-08: 202 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.13k

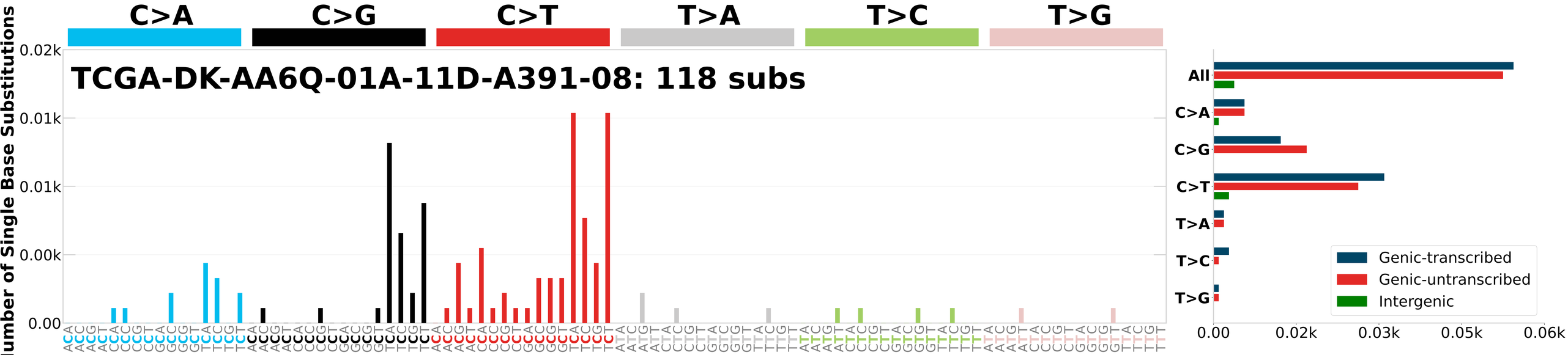

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A6B5-01A-11D-A31L-08: 117 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.06k

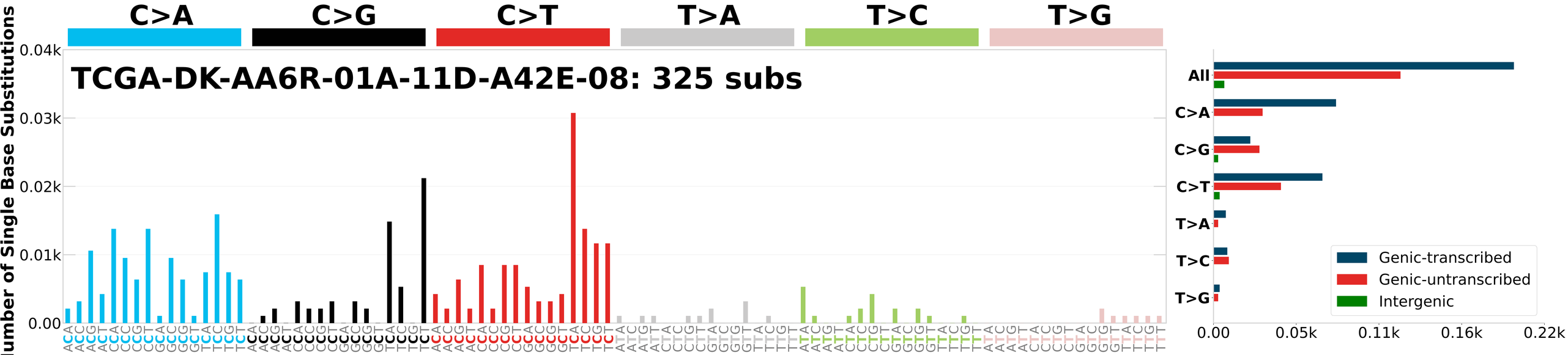

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-A6B6-01A-11D-A30E-08: 906 subs
Number of Single Base Substitutions
0.41k
0.31k
0.21k
0.10k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.16k
0.32k
0.48k
0.64k

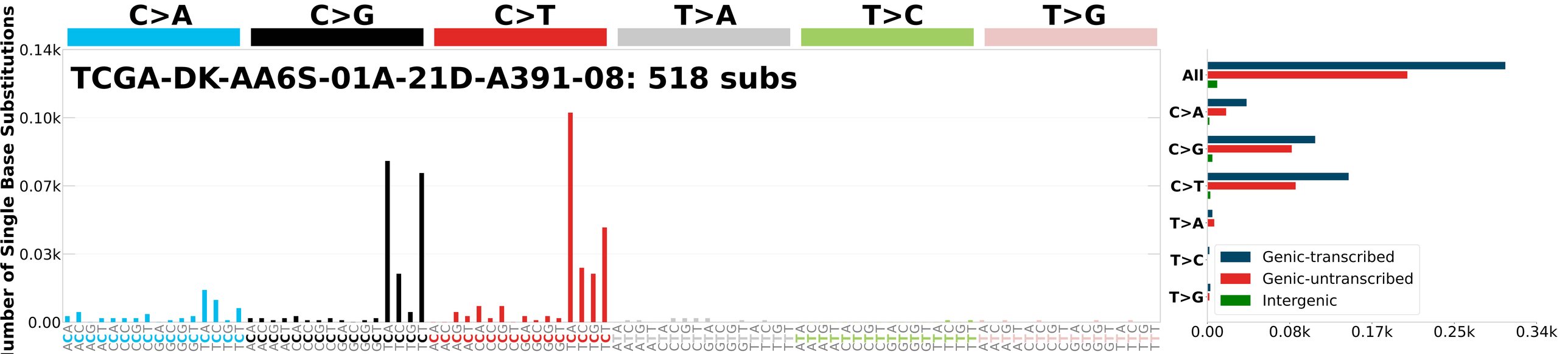

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA6L-01A-11D-A391-08: 372 subs
Number of Single Base Substitutions
0.09k
0.07k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.11k
0.16k
0.22k

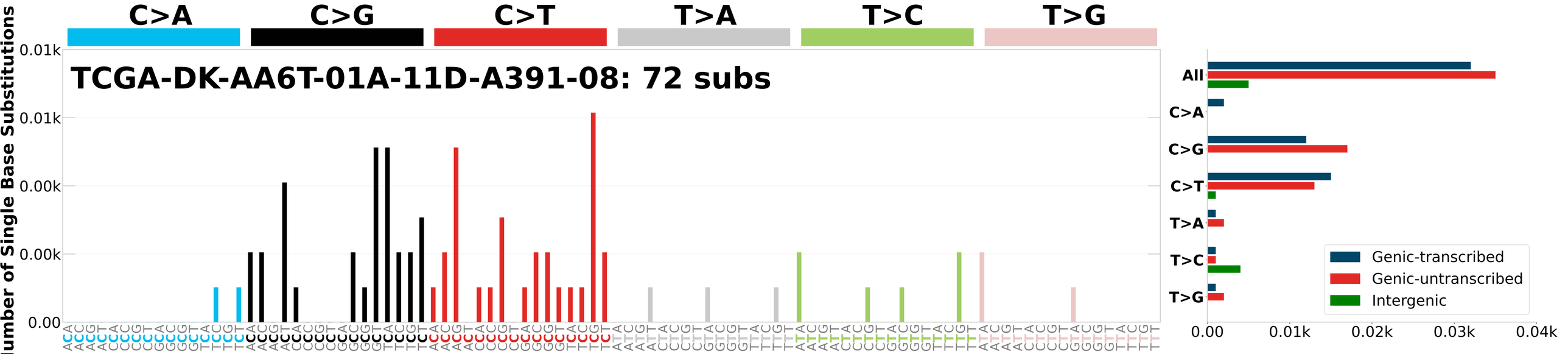

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA6M-01A-11D-A391-08: 66 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

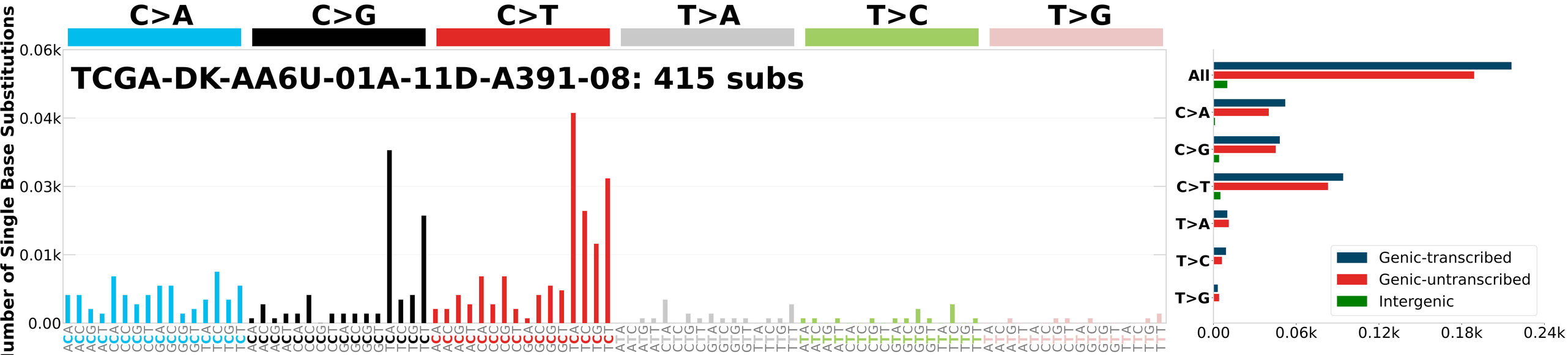

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA6P-01A-11D-A391-08: 163 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.07k
0.10k

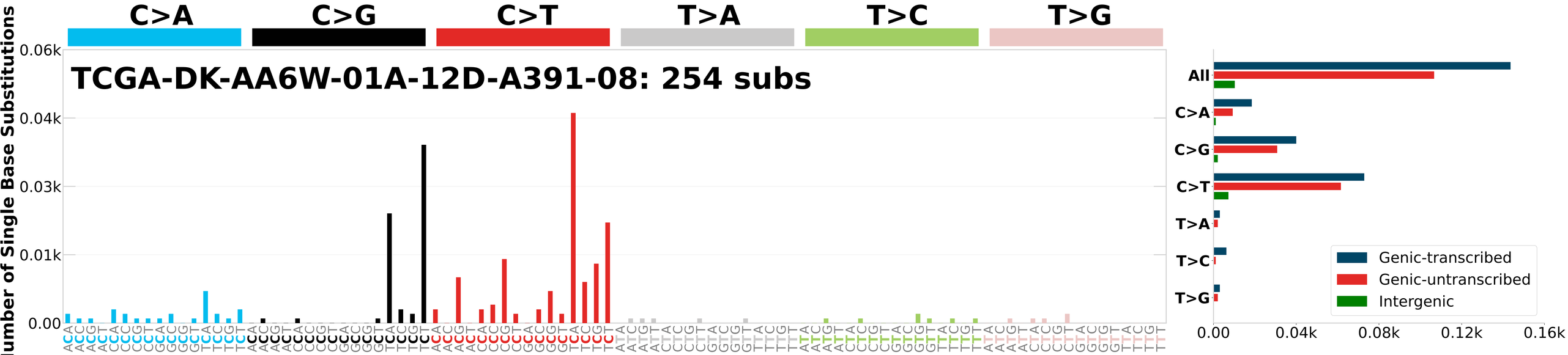

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA6Q-01A-11D-A391-08: 118 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.06k

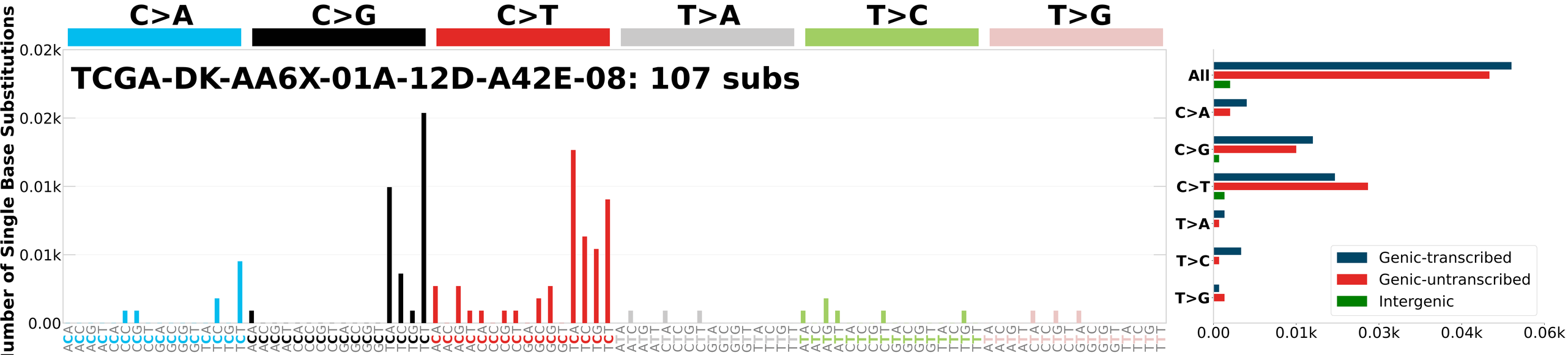

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA6R-01A-11D-A42E-08: 325 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.11k
0.16k
0.22k

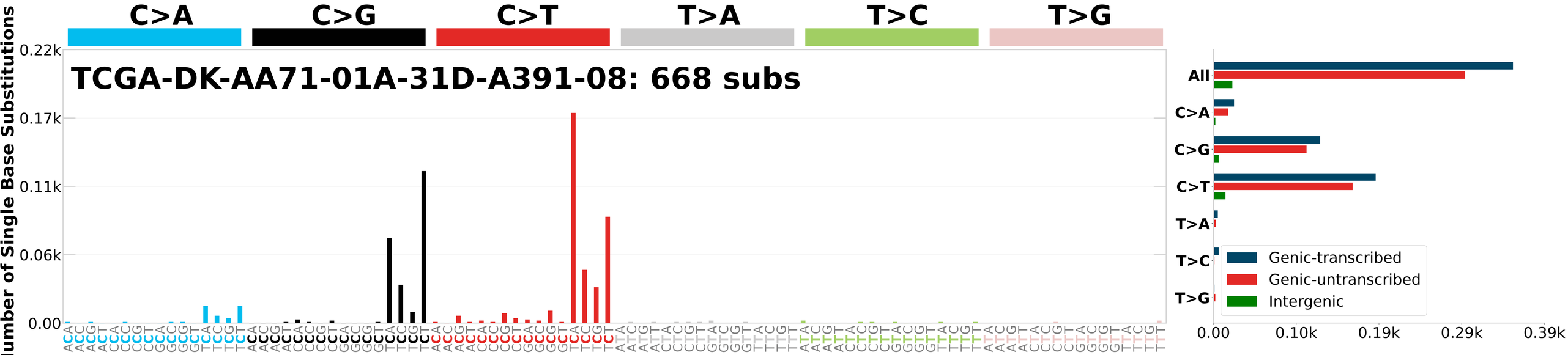

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA6S-01A-21D-A391-08: 518 subs
Number of Single Base Substitutions
0.14k
0.10k
0.07k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.08k
0.17k
0.25k
0.34k

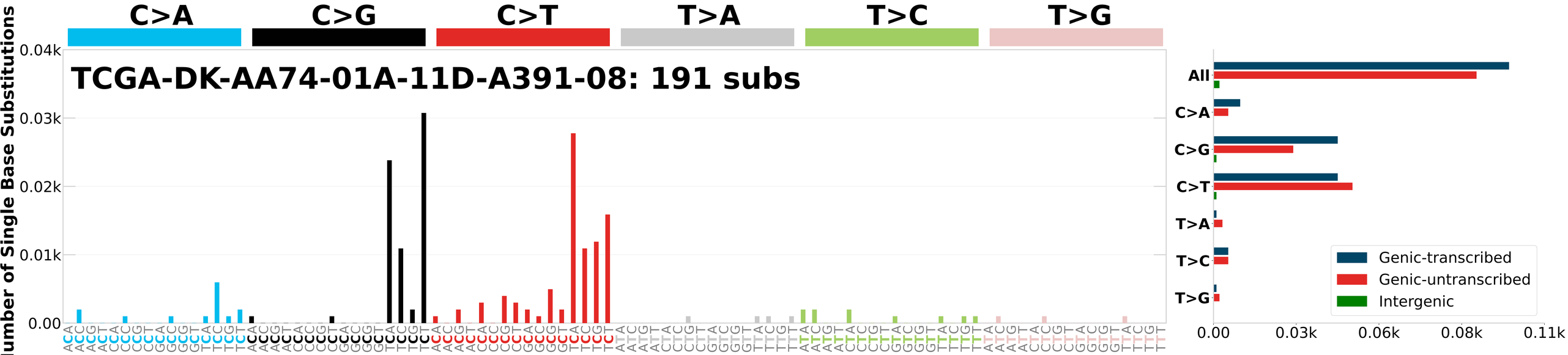

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA6T-01A-11D-A391-08: 72 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

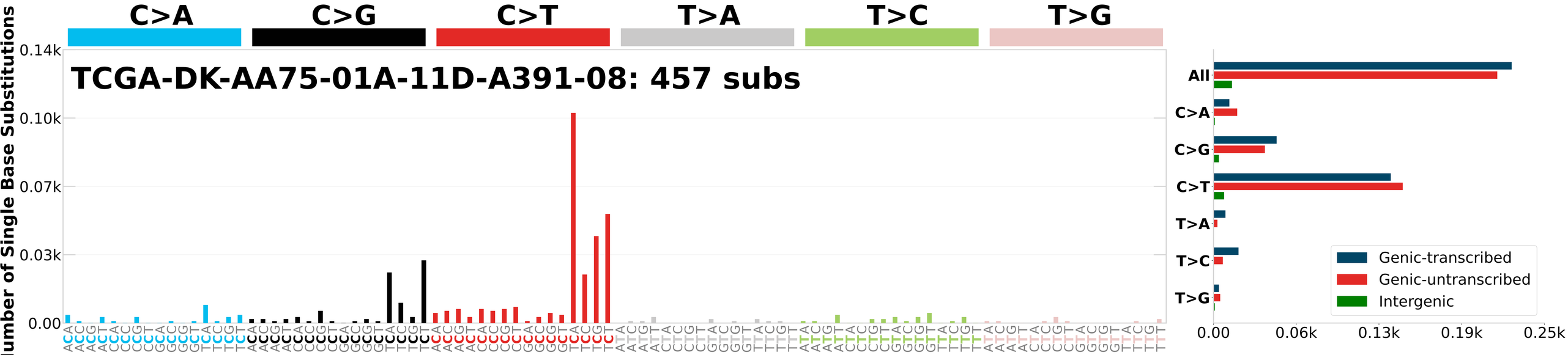

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA6U-01A-11D-A391-08: 415 subs
Number of Single Base Substitutions
0.06k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.12k
0.18k
0.24k

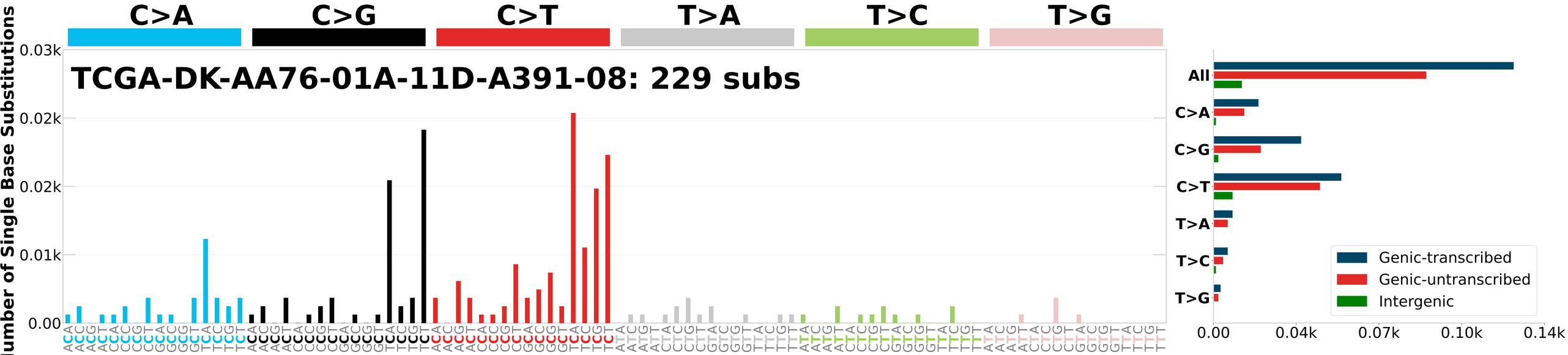

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA6W-01A-12D-A391-08: 254 subs
Number of Single Base Substitutions
0.06k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.12k
0.16k

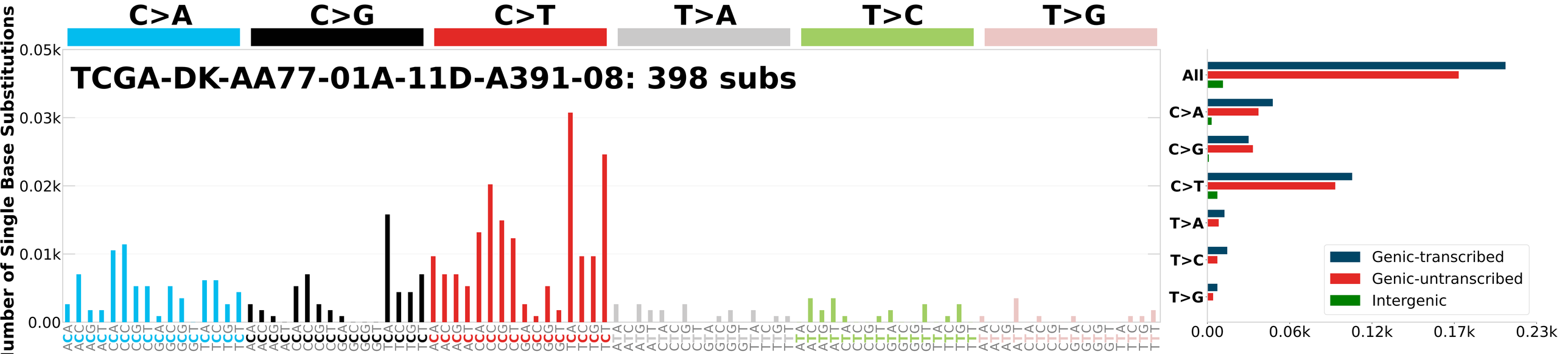

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA6X-01A-12D-A42E-08: 107 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

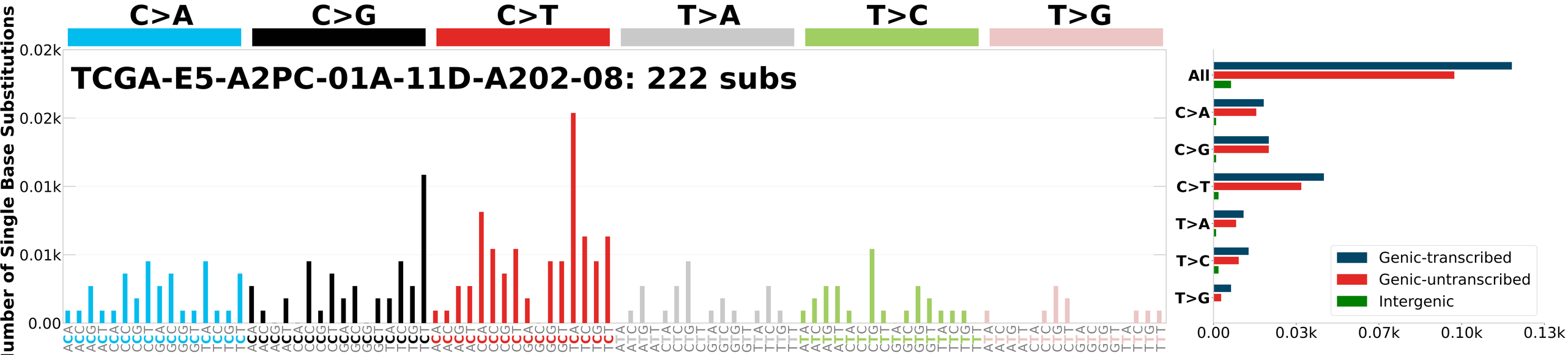

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA71-01A-31D-A391-08: 668 subs
Number of Single Base Substitutions
0.22k
0.17k
0.11k
0.06k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.10k
0.19k
0.29k
0.39k

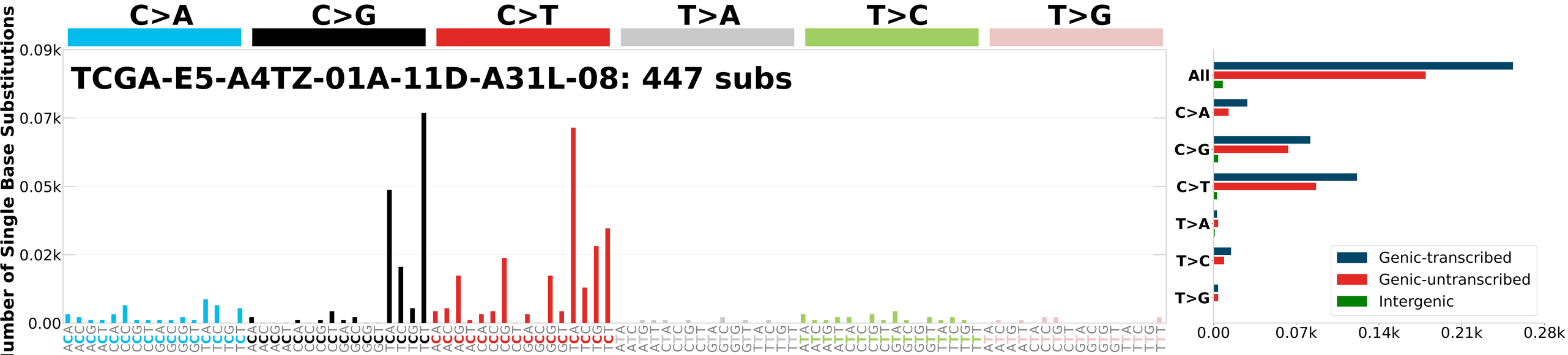

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA74-01A-11D-A391-08: 191 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.08k
0.11k

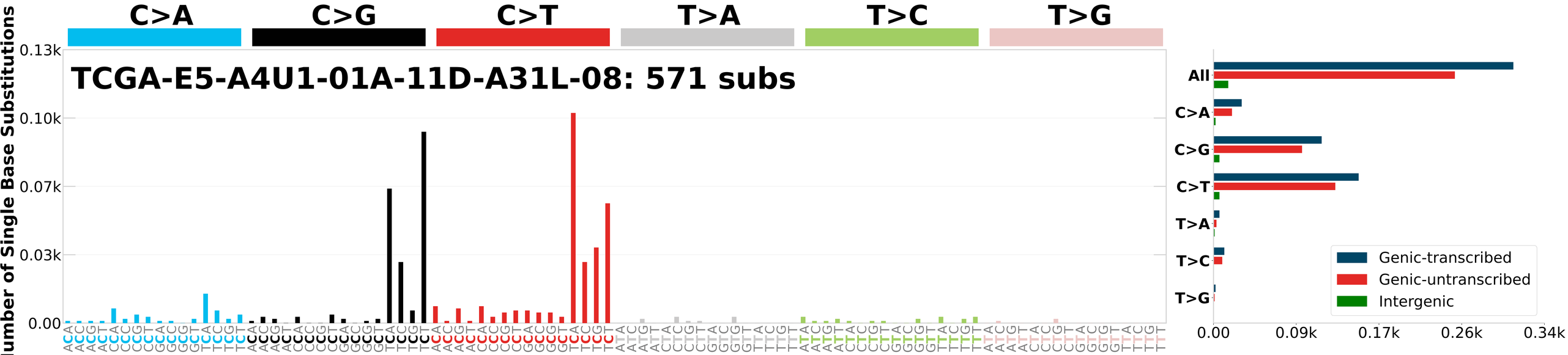

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA75-01A-11D-A391-08: 457 subs
Number of Single Base Substitutions
0.14k
0.10k
0.07k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.13k
0.19k
0.25k

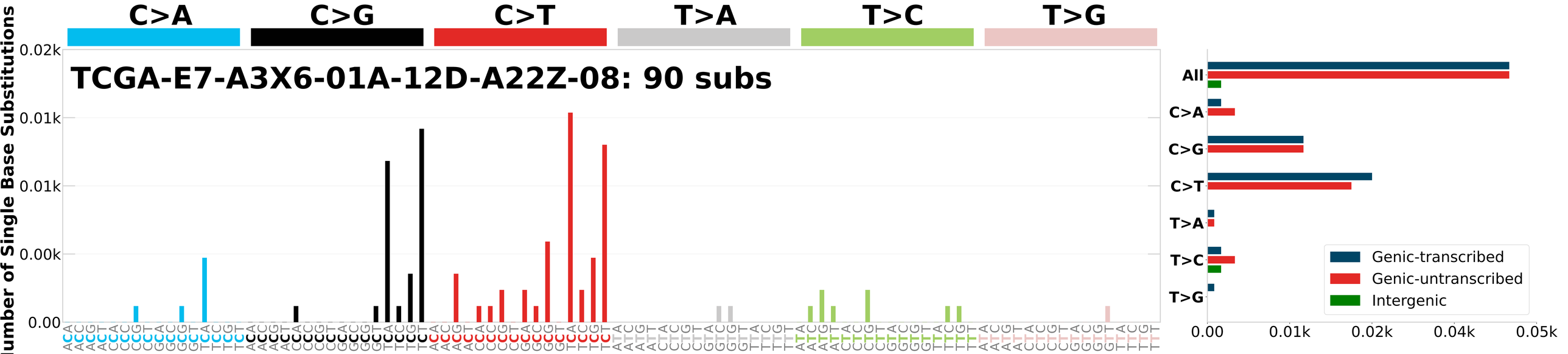

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA76-01A-11D-A391-08: 229 subs
Number of Single Base Substitutions
0.03k
0.02k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.07k
0.10k
0.14k

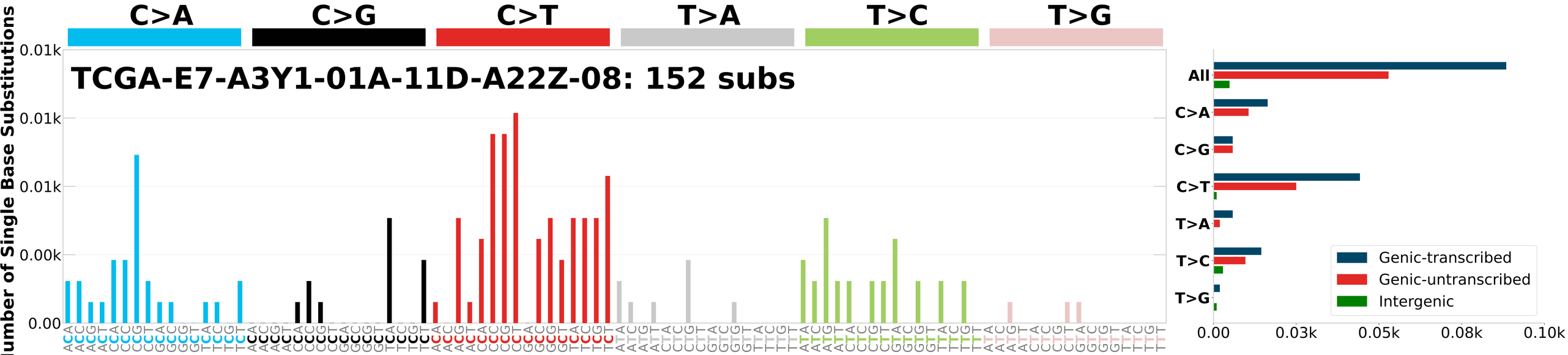

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-DK-AA77-01A-11D-A391-08: 398 subs
Number of Single Base Substitutions
0.05k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.12k
0.17k
0.23k

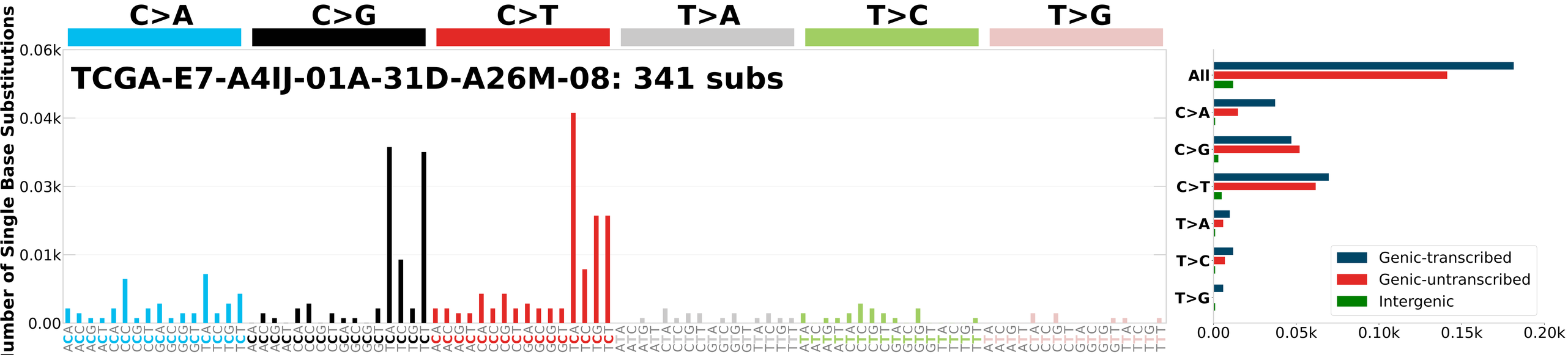

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E5-A2PC-01A-11D-A202-08: 222 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.13k

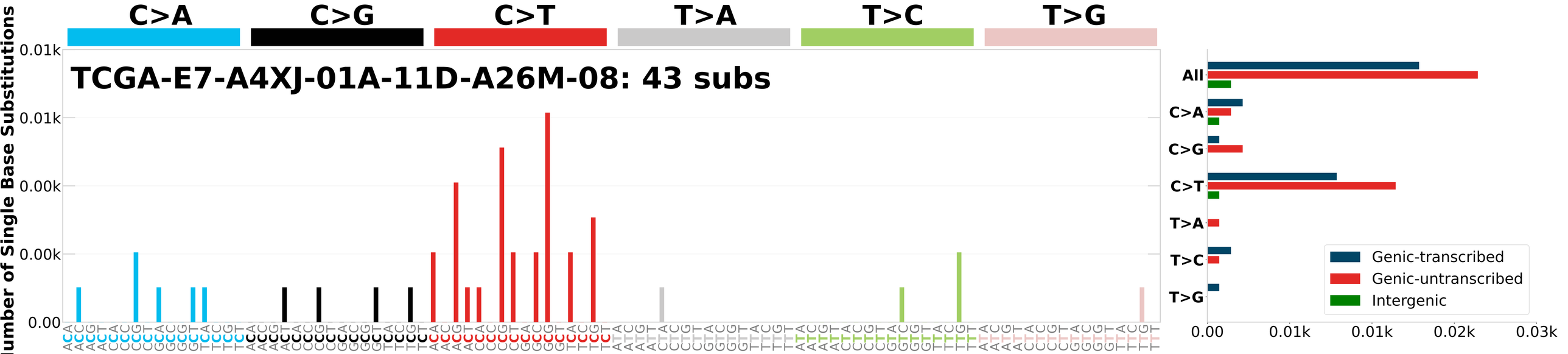

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E5-A4TZ-01A-11D-A31L-08: 447 subs
Number of Single Base Substitutions
0.09k
0.07k
0.05k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.14k
0.21k
0.28k

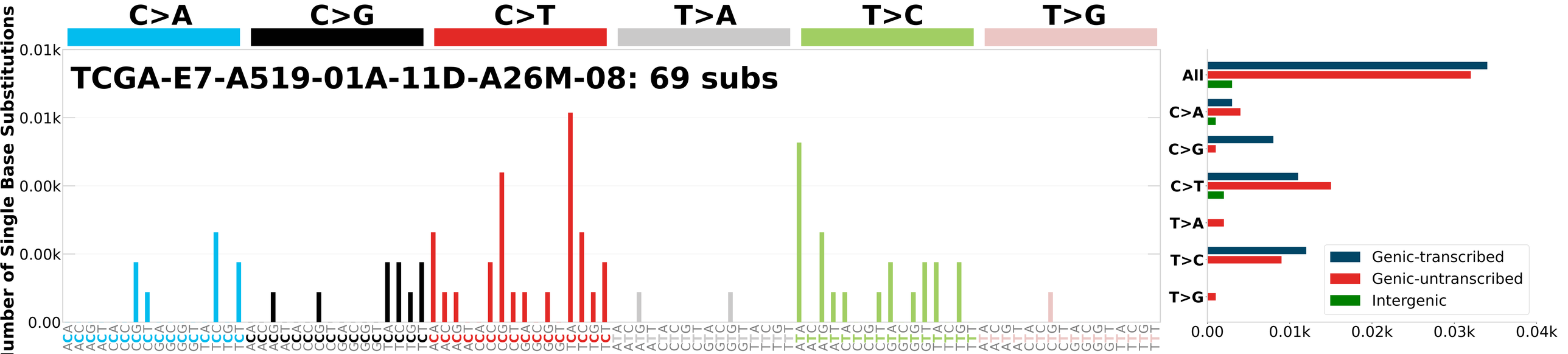

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E5-A4U1-01A-11D-A31L-08: 571 subs
Number of Single Base Substitutions
0.13k
0.10k
0.07k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.09k
0.17k
0.26k
0.34k

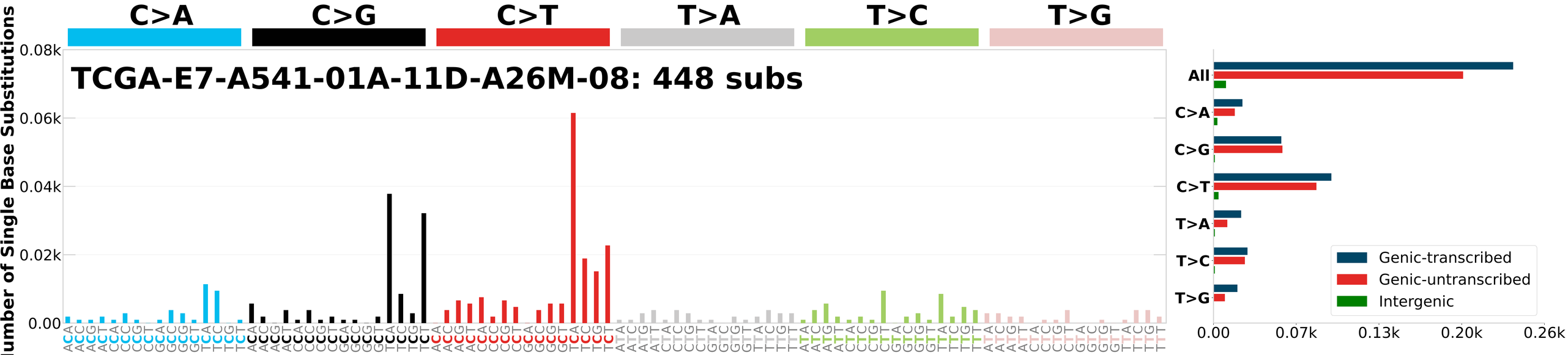

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A3X6-01A-12D-A22Z-08: 90 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

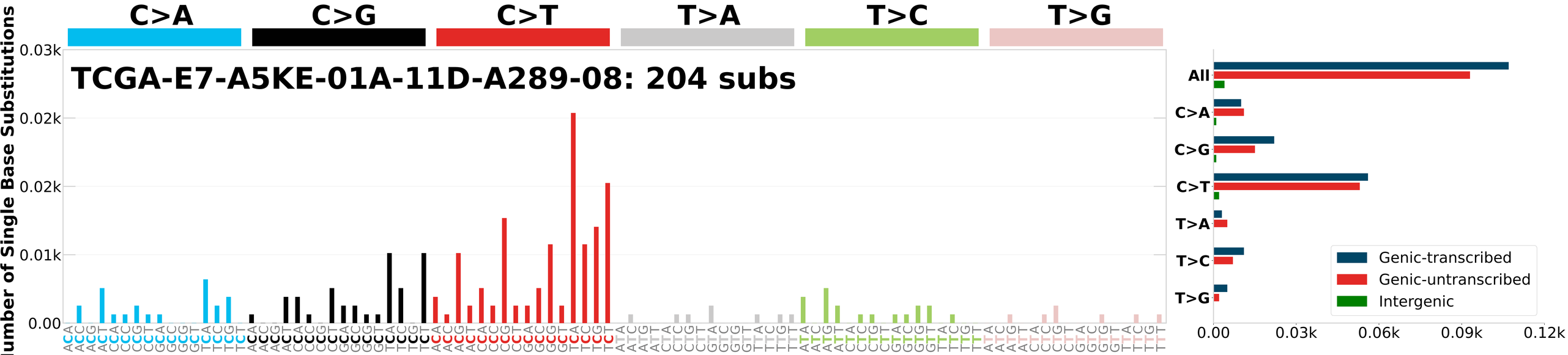

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A3Y1-01A-11D-A22Z-08: 152 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.10k

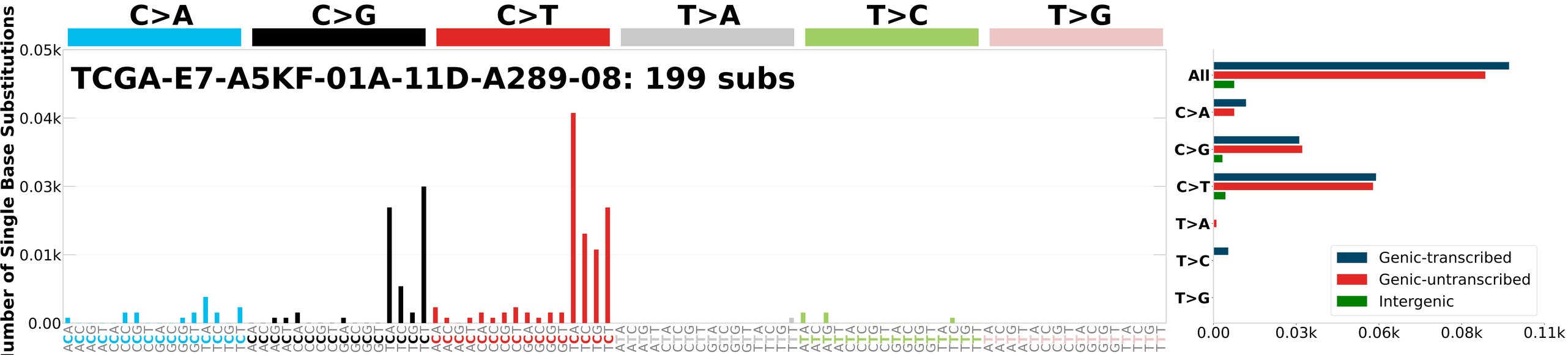

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A4IJ-01A-31D-A26M-08: 341 subs
Number of Single Base Substitutions
0.06k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.10k
0.15k
0.20k

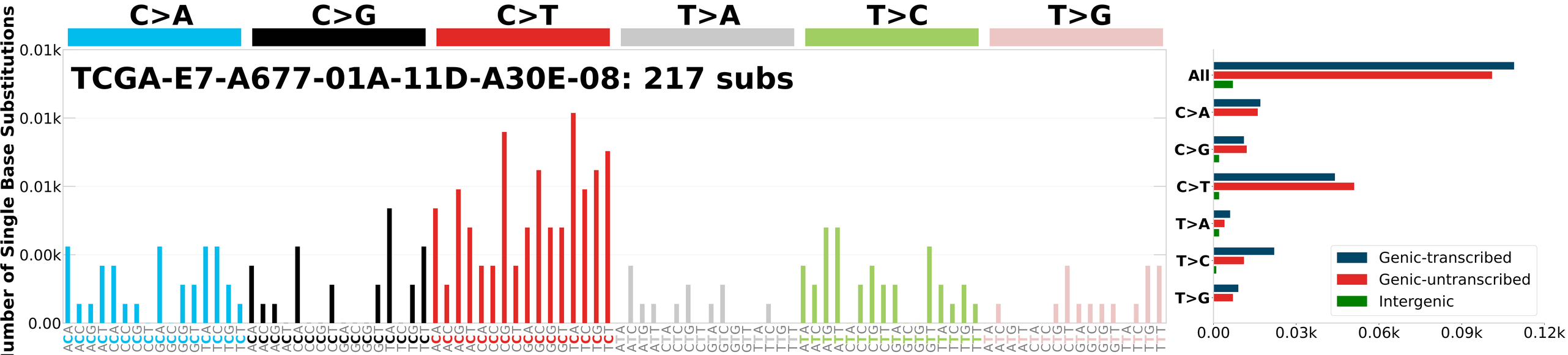

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A4XJ-01A-11D-A26M-08: 43 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.02k
0.03k

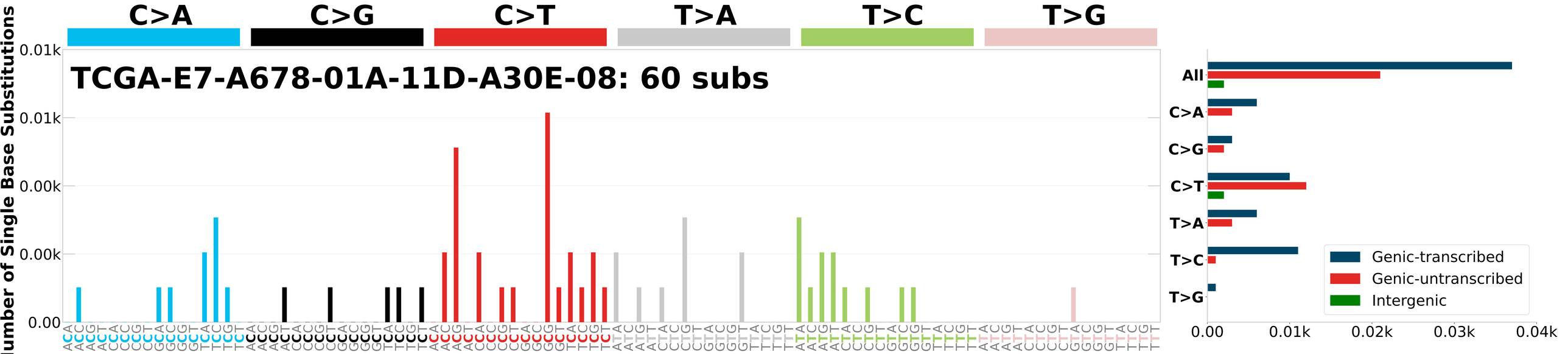

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A519-01A-11D-A26M-08: 69 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

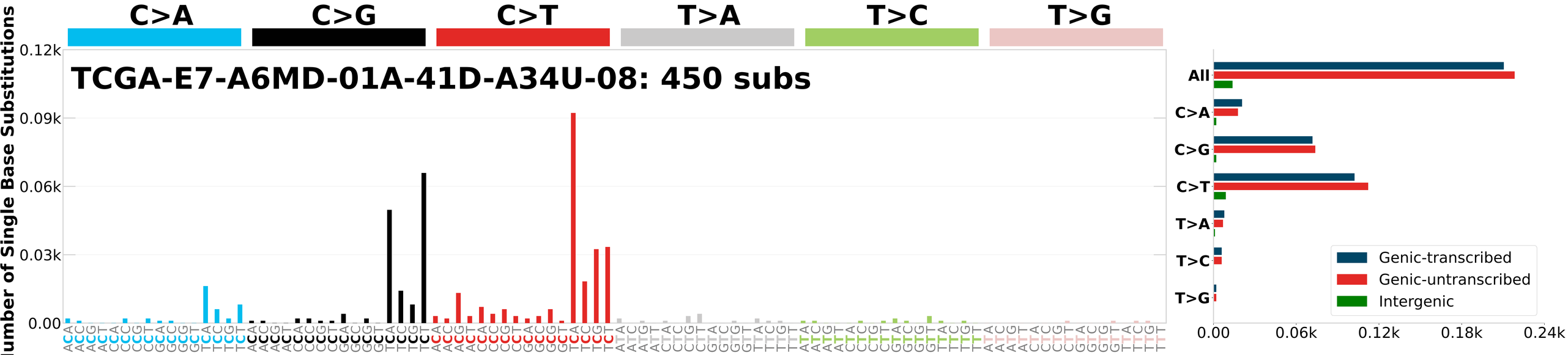

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A541-01A-11D-A26M-08: 448 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.13k
0.20k
0.26k

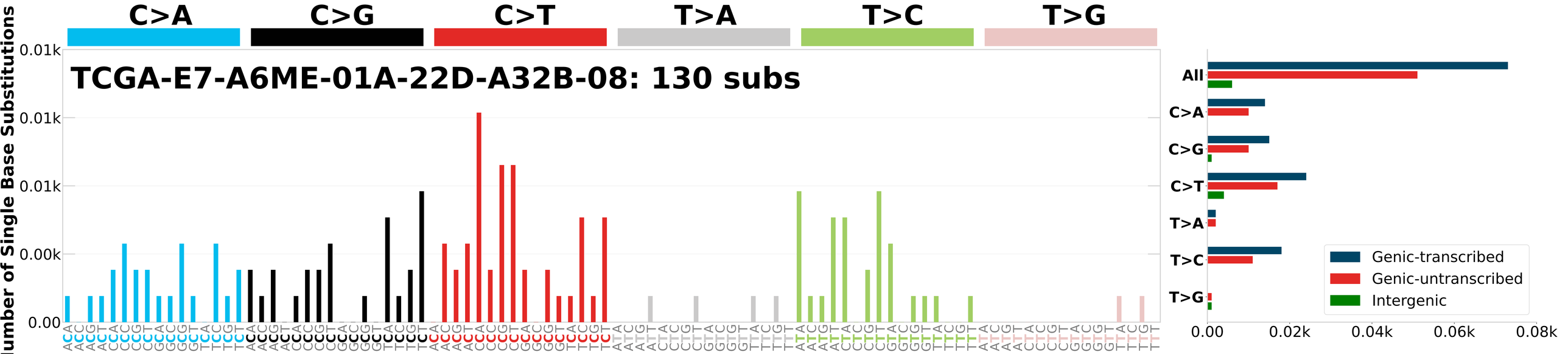

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A5KE-01A-11D-A289-08: 204 subs
Number of Single Base Substitutions
0.03k
0.02k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

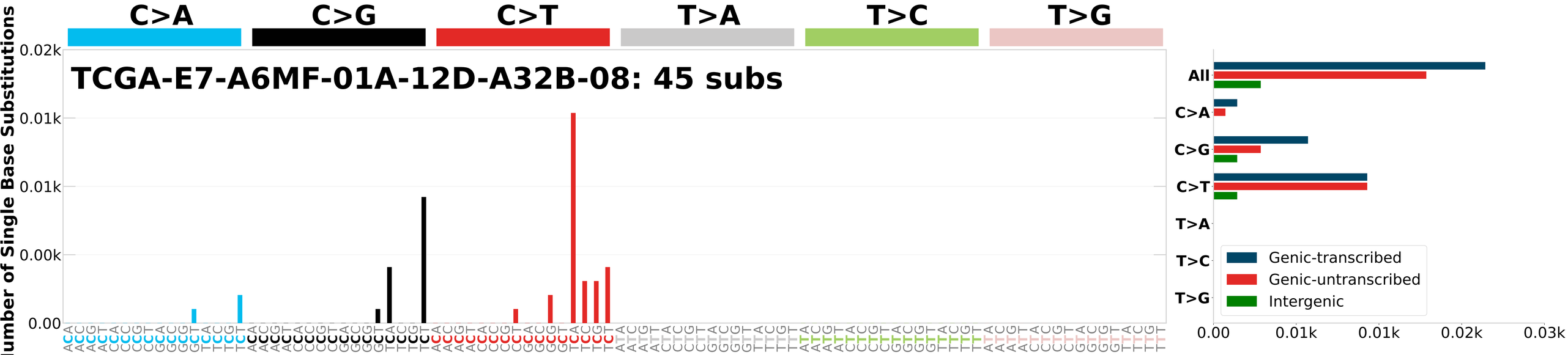

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A5KF-01A-11D-A289-08: 199 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.08k
0.11k

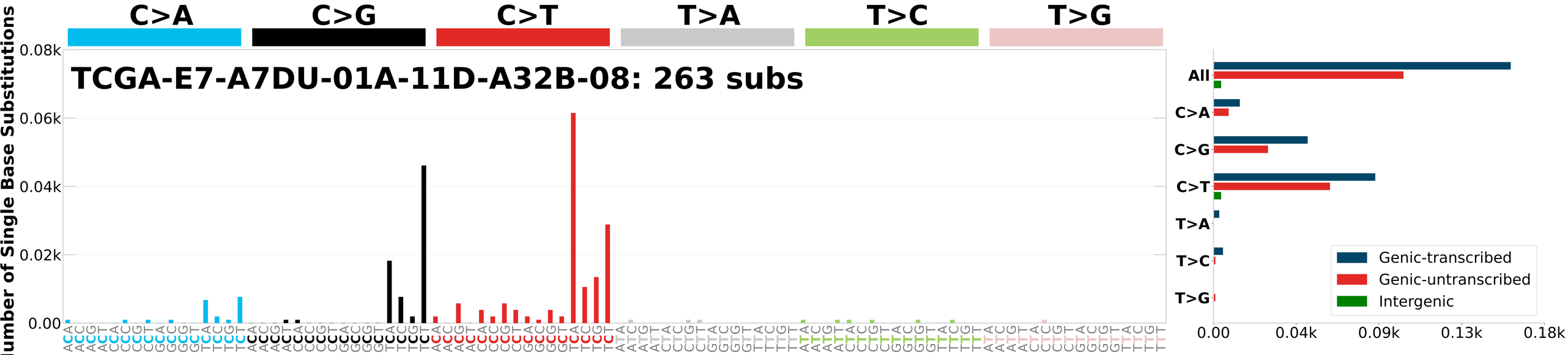

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A677-01A-11D-A30E-08: 217 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

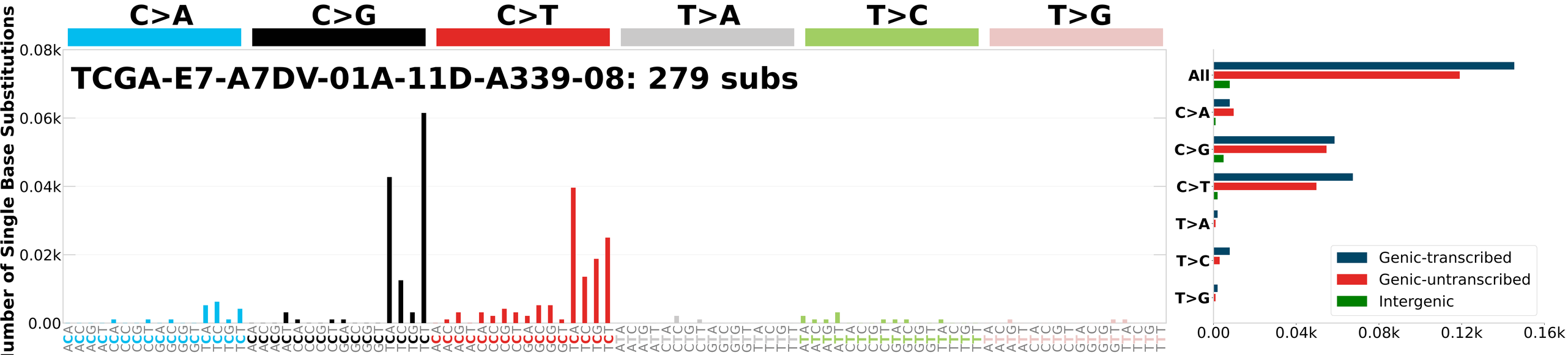

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A678-01A-11D-A30E-08: 60 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

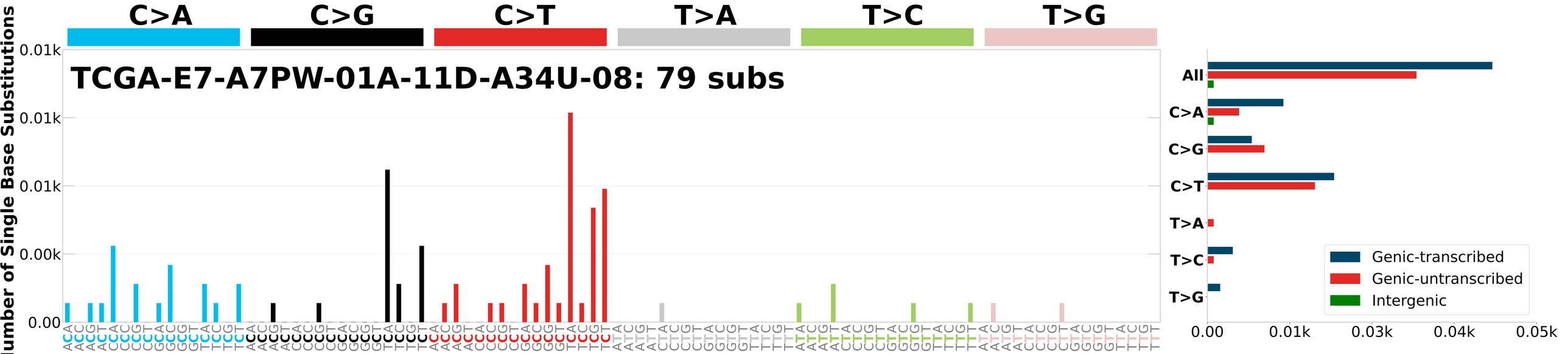

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A6MD-01A-41D-A34U-08: 450 subs
Number of Single Base Substitutions
0.12k
0.09k
0.06k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.12k
0.18k
0.24k

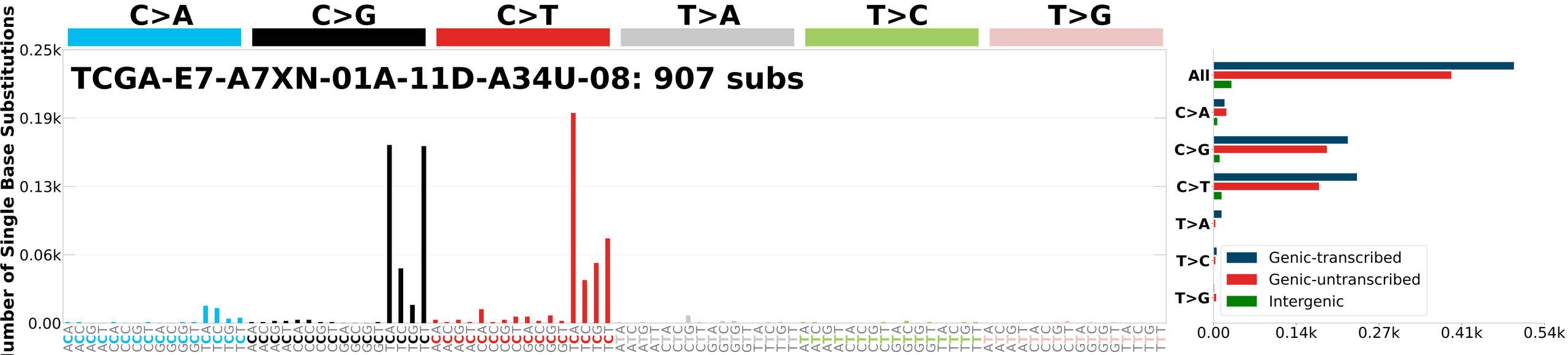

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A6ME-01A-22D-A32B-08: 130 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

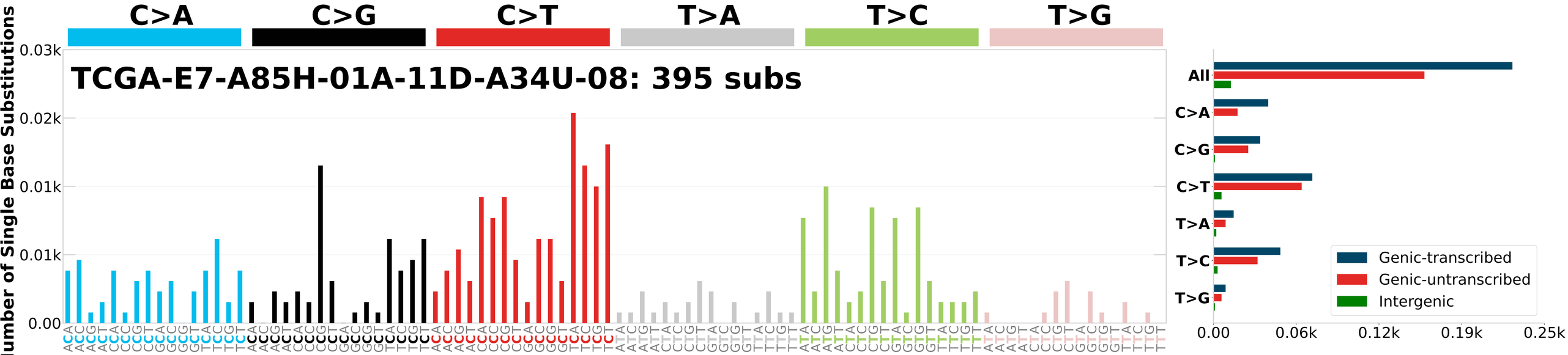

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A6MF-01A-12D-A32B-08: 45 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.02k
0.03k

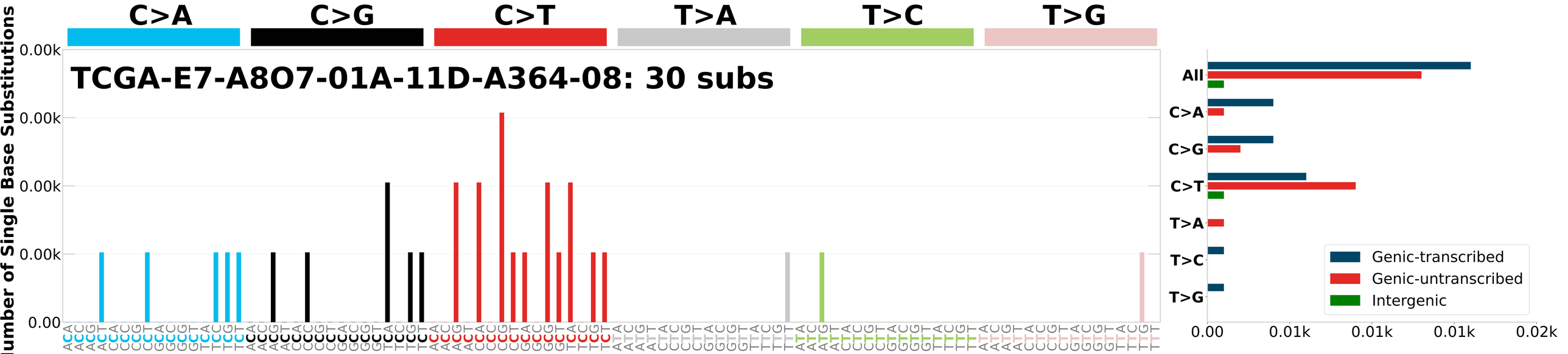

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A7DU-01A-11D-A32B-08: 263 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.09k
0.13k
0.18k

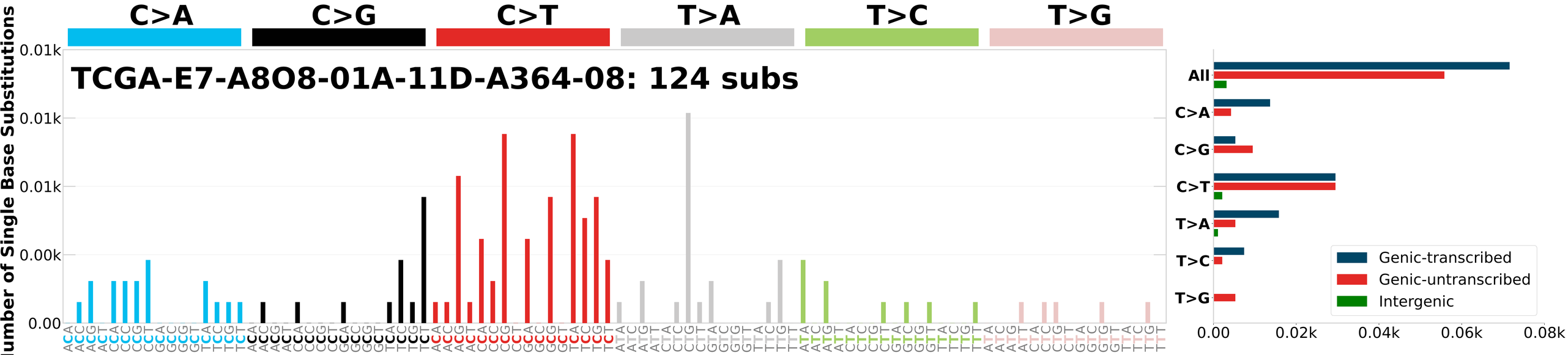

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A7DV-01A-11D-A339-08: 279 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.12k
0.16k

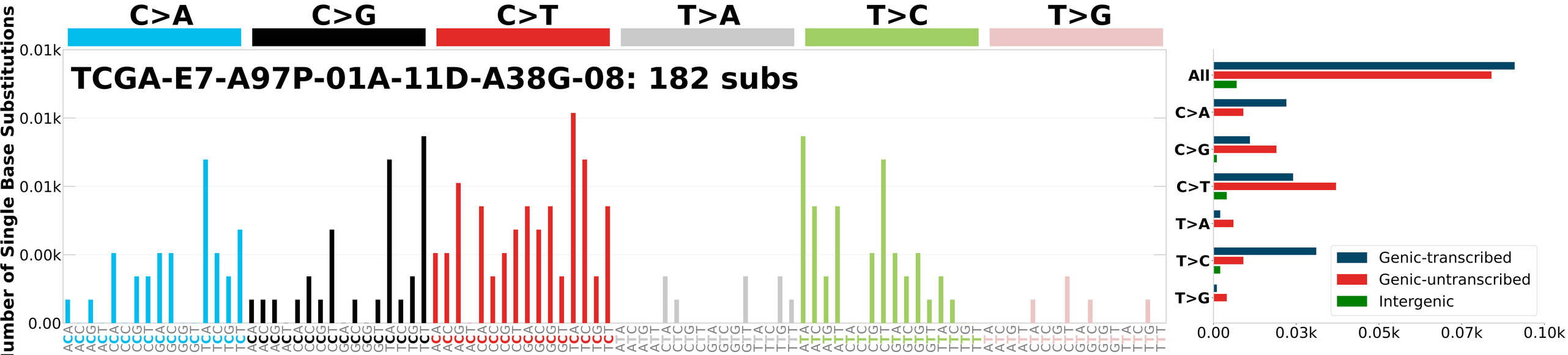

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A7PW-01A-11D-A34U-08: 79 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

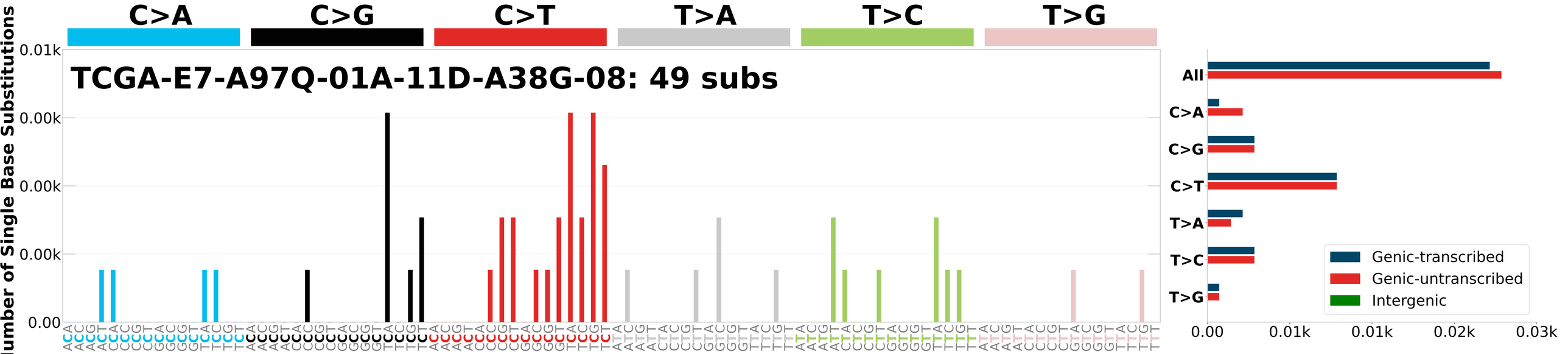

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A7XN-01A-11D-A34U-08: 907 subs
Number of Single Base Substitutions
0.25k
0.19k
0.13k
0.06k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.14k
0.27k
0.41k
0.54k

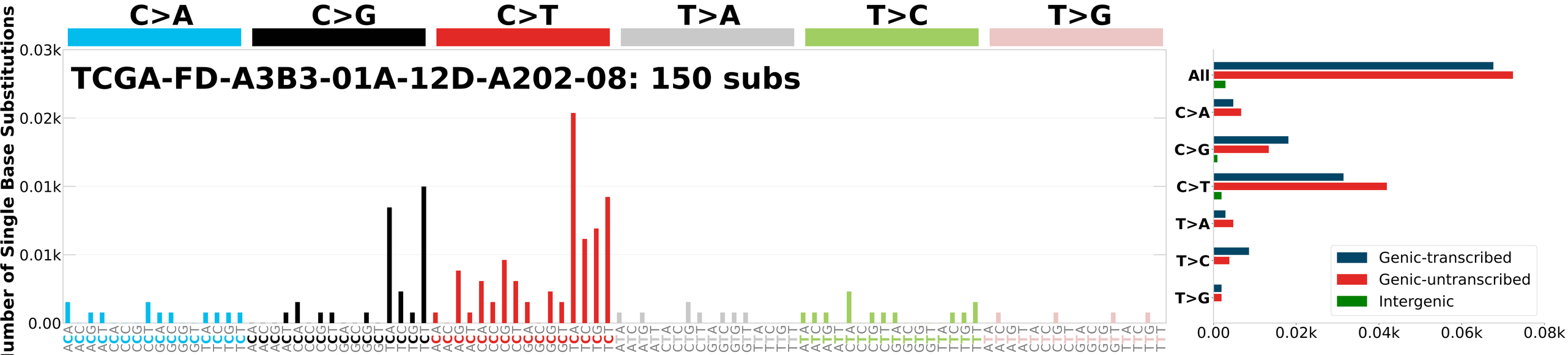

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A85H-01A-11D-A34U-08: 395 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.12k
0.19k
0.25k

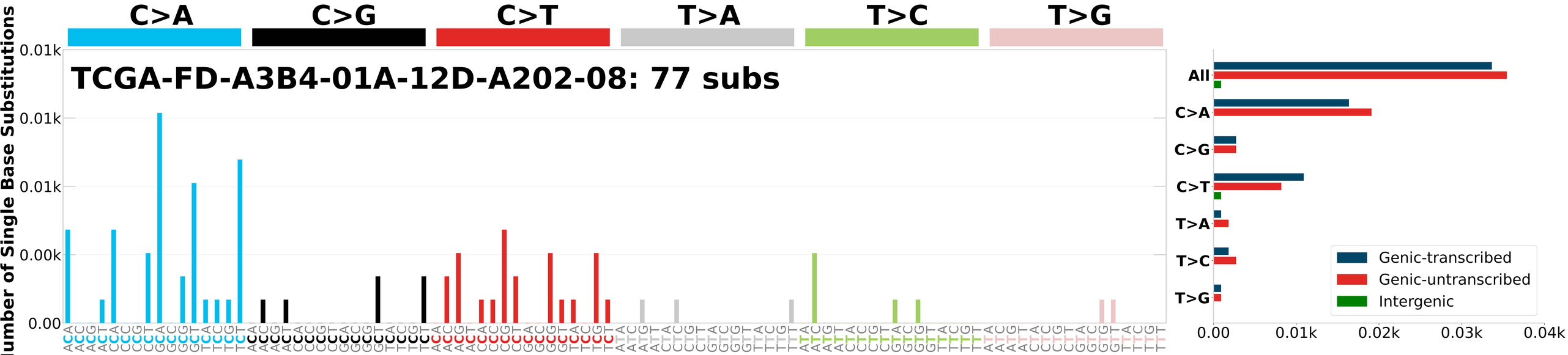

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A8O7-01A-11D-A364-08: 30 subs
Number of Single Base Substitutions
0.00k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.01k
0.02k

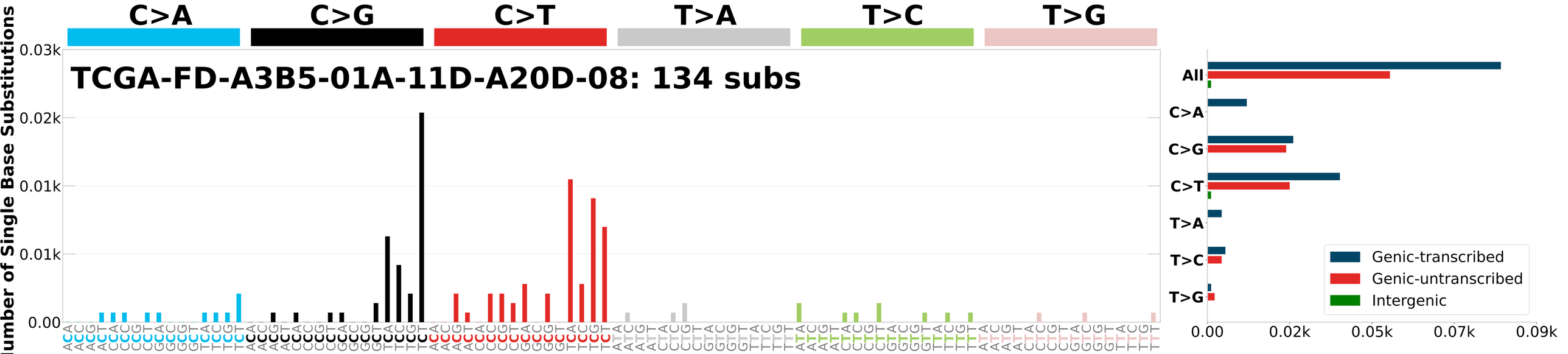

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A8O8-01A-11D-A364-08: 124 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

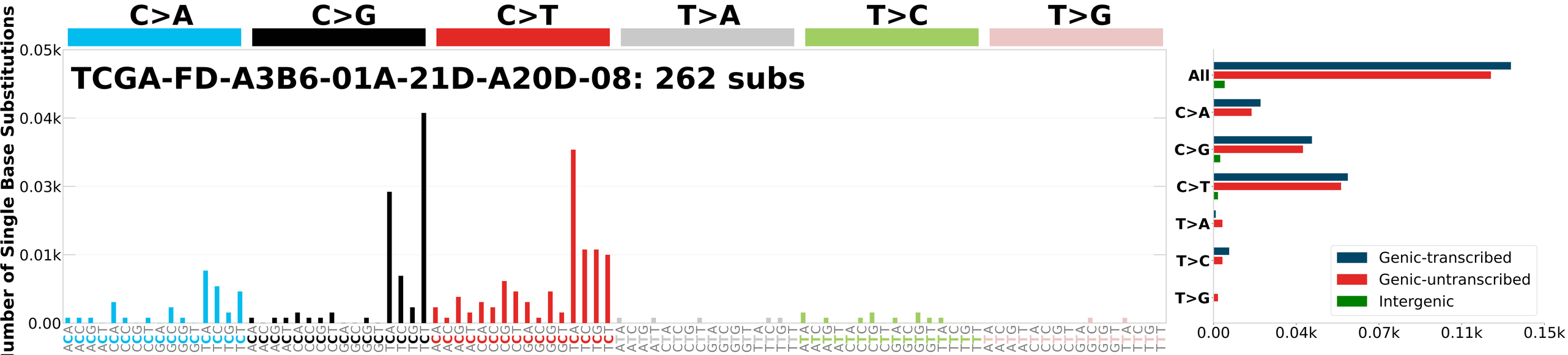

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A97P-01A-11D-A38G-08: 182 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.07k
0.10k

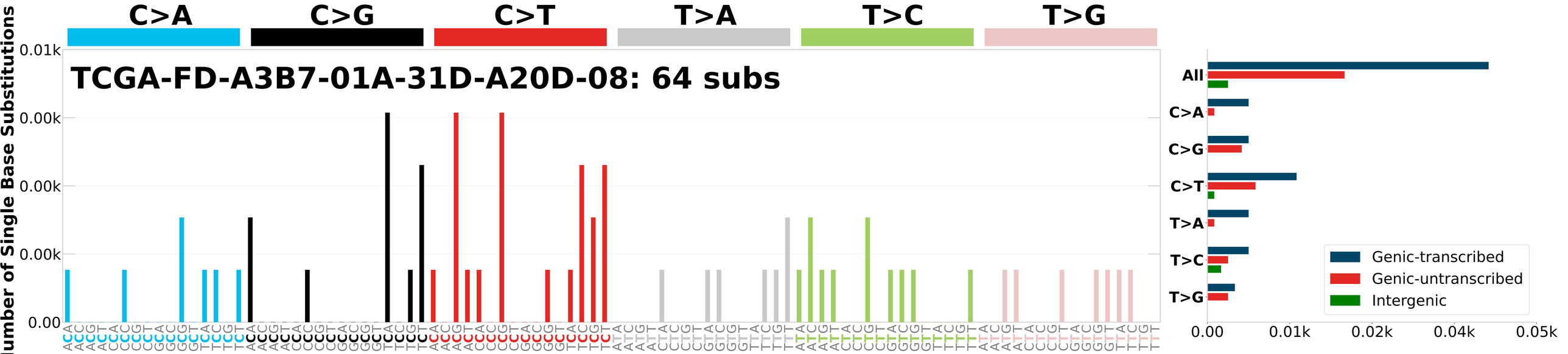

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-E7-A97Q-01A-11D-A38G-08: 49 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.02k
0.03k

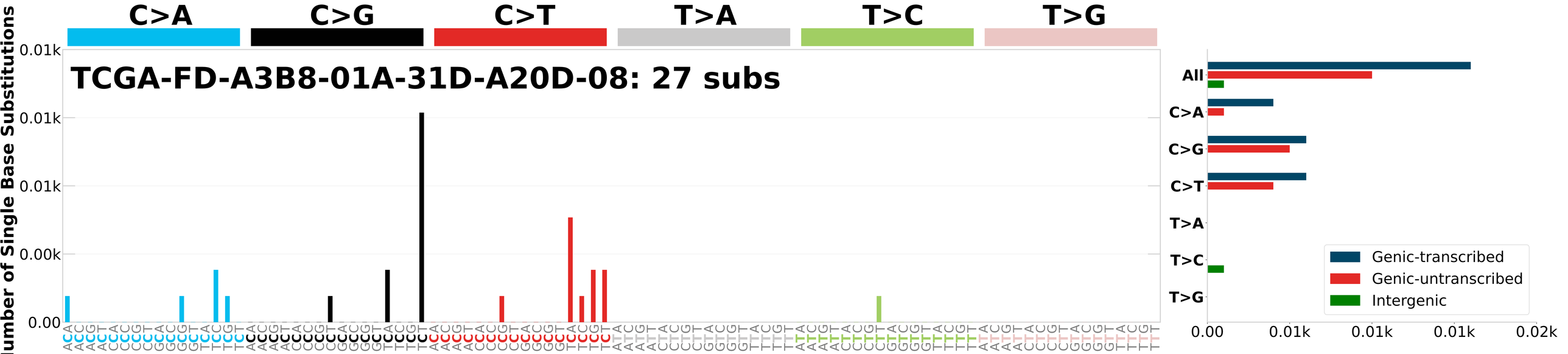

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3B3-01A-12D-A202-08: 150 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

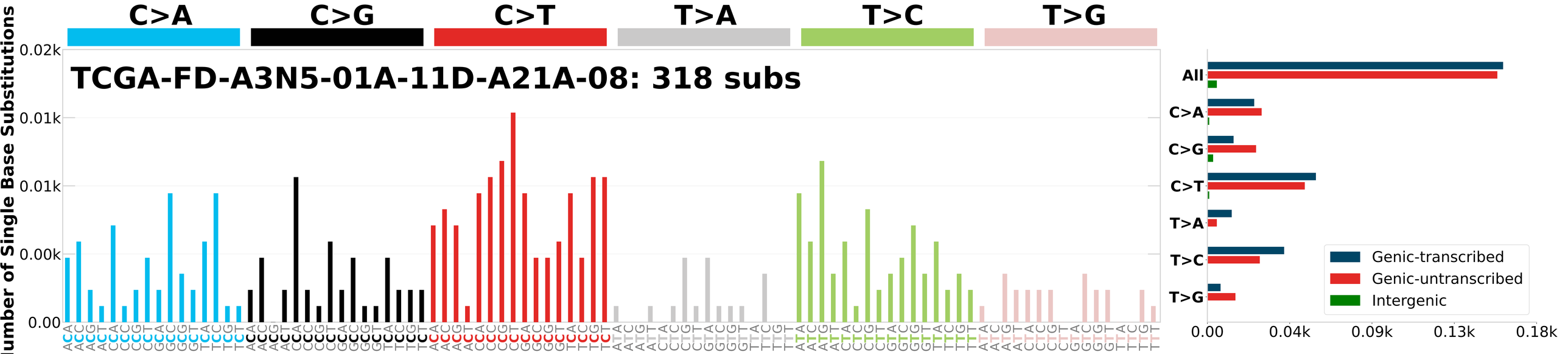

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3B4-01A-12D-A202-08: 77 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

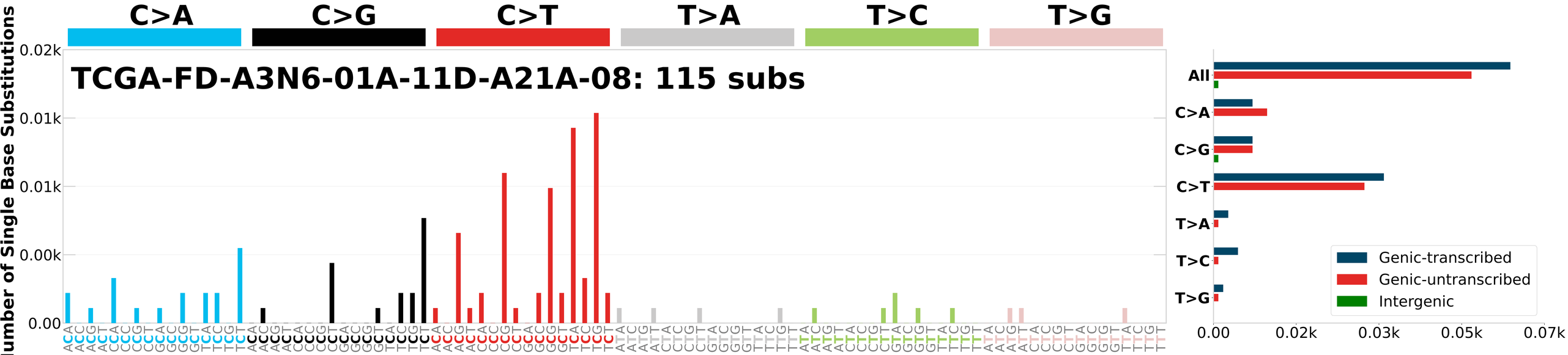

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3B5-01A-11D-A20D-08: 134 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.09k

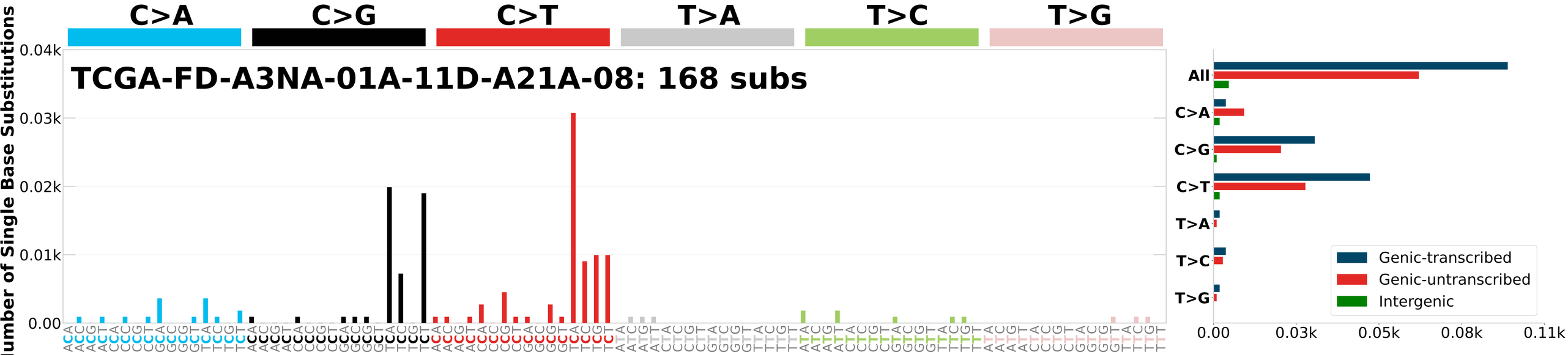

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3B6-01A-21D-A20D-08: 262 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.07k
0.11k
0.15k

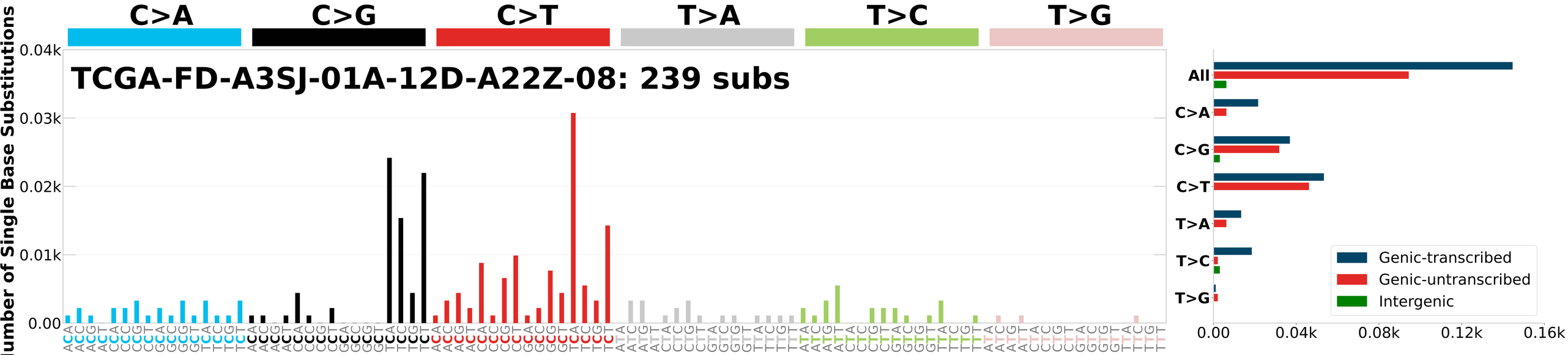

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3B7-01A-31D-A20D-08: 64 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

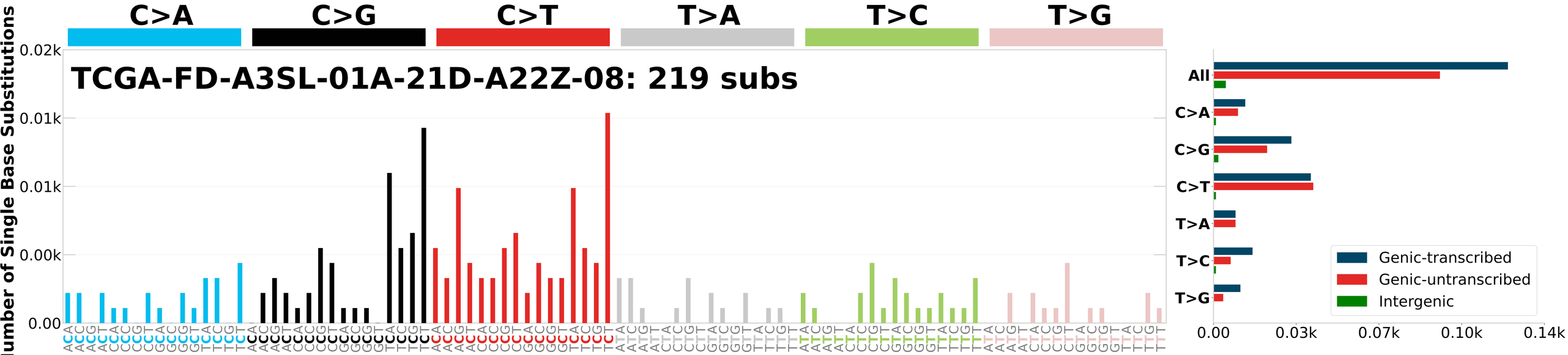

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3B8-01A-31D-A20D-08: 27 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.01k
0.02k

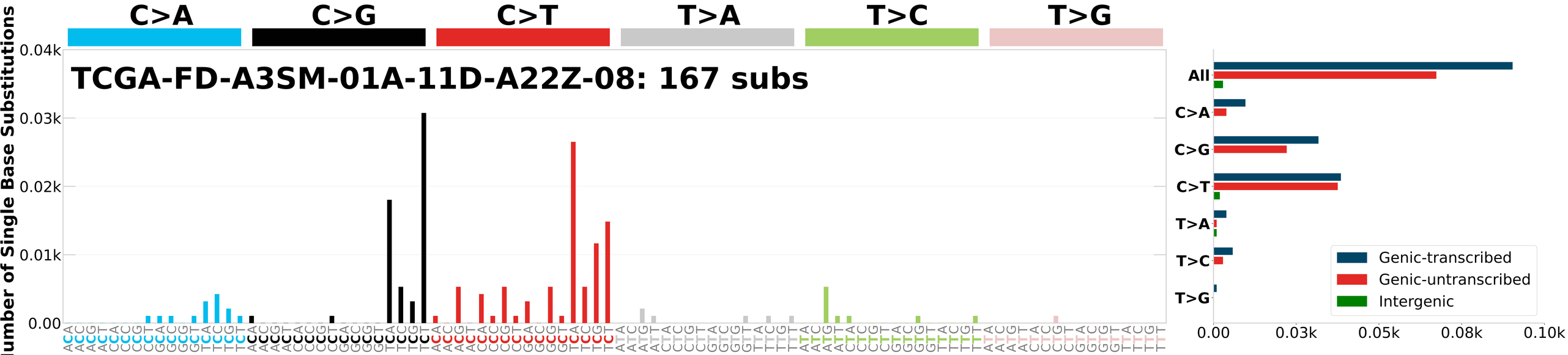

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3N5-01A-11D-A21A-08: 318 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.09k
0.13k
0.18k

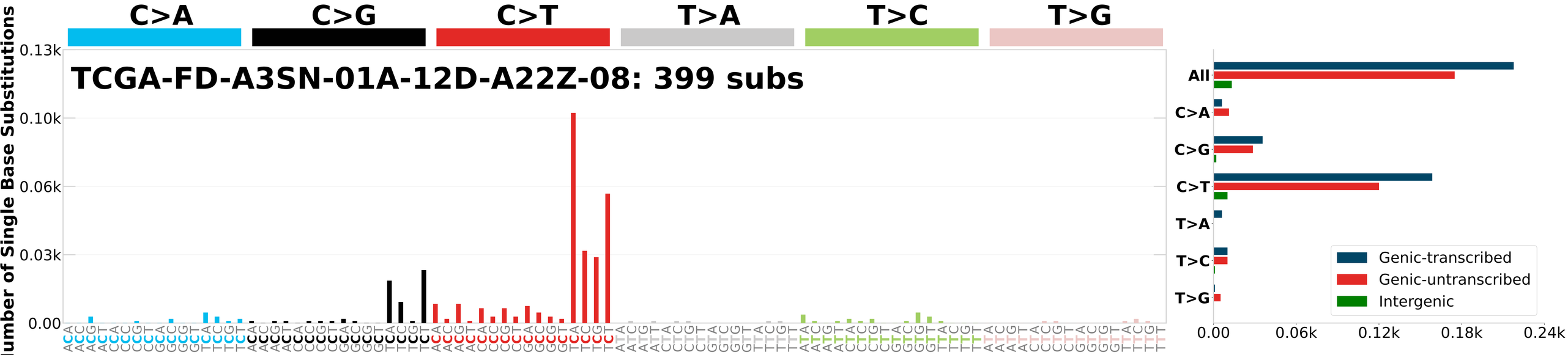

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3N6-01A-11D-A21A-08: 115 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.07k

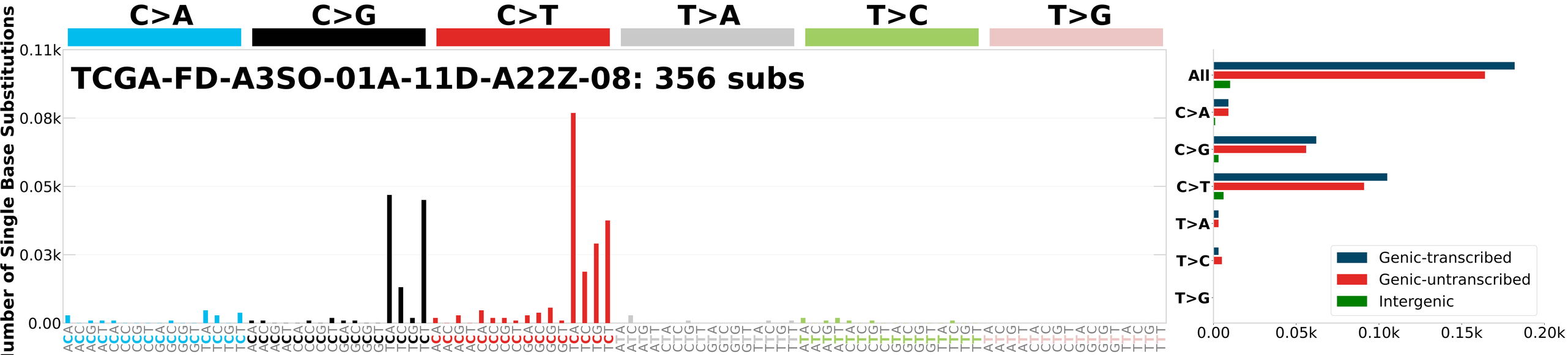

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3NA-01A-11D-A21A-08: 168 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.11k

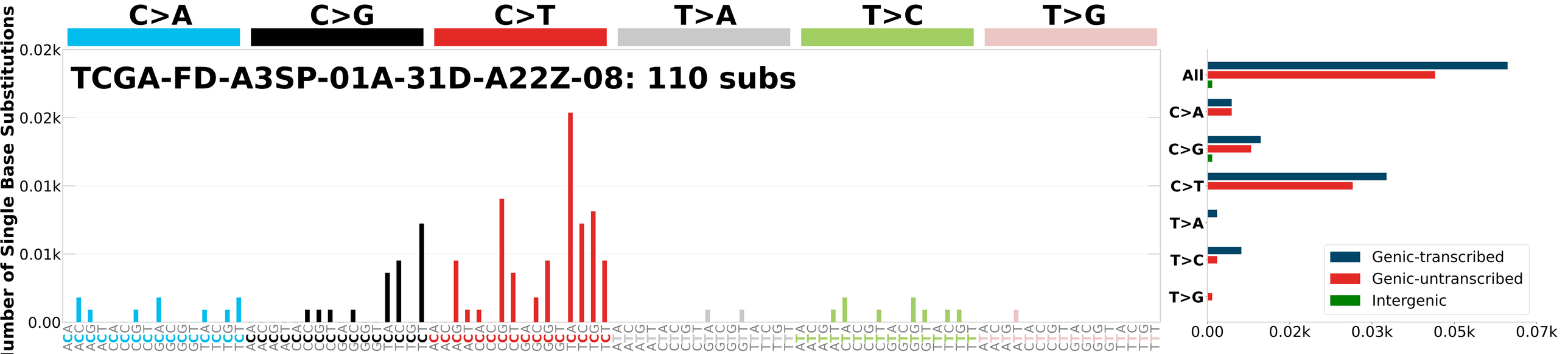

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3SJ-01A-12D-A22Z-08: 239 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.12k
0.16k

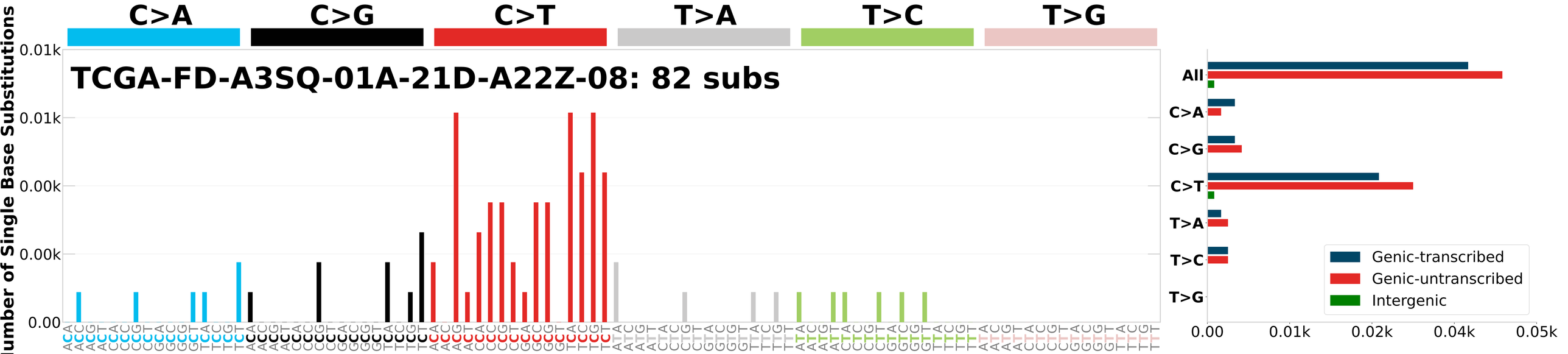

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3SL-01A-21D-A22Z-08: 219 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.14k

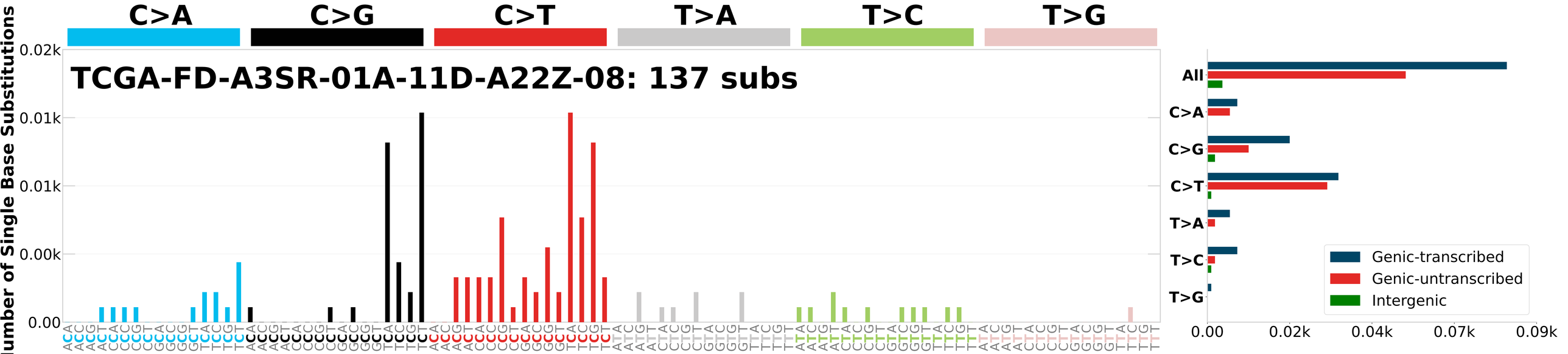

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3SM-01A-11D-A22Z-08: 167 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.10k

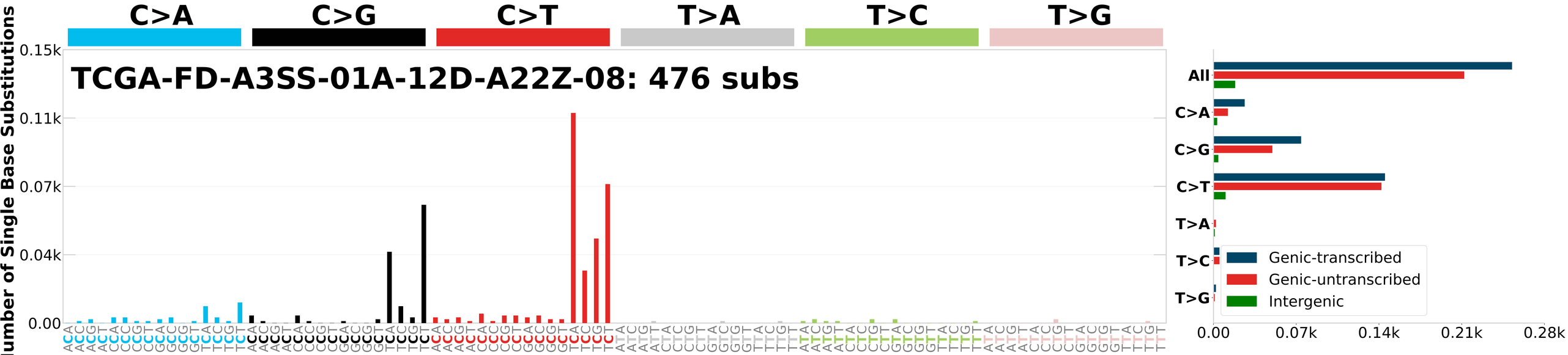

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3SN-01A-12D-A22Z-08: 399 subs
Number of Single Base Substitutions
0.13k
0.10k
0.06k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.12k
0.18k
0.24k

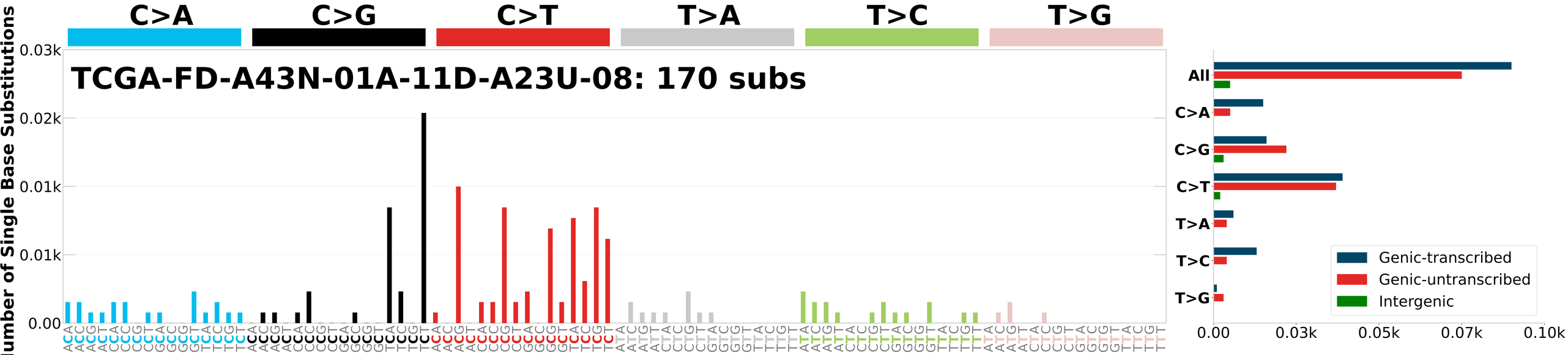

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3SO-01A-11D-A22Z-08: 356 subs
Number of Single Base Substitutions
0.11k
0.08k
0.05k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.10k
0.15k
0.20k

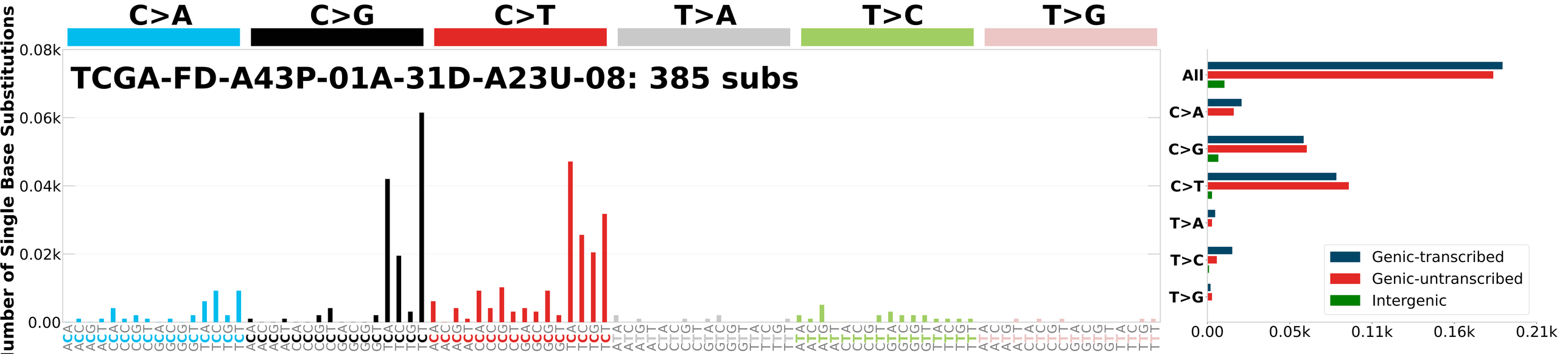

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3SP-01A-31D-A22Z-08: 110 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.07k

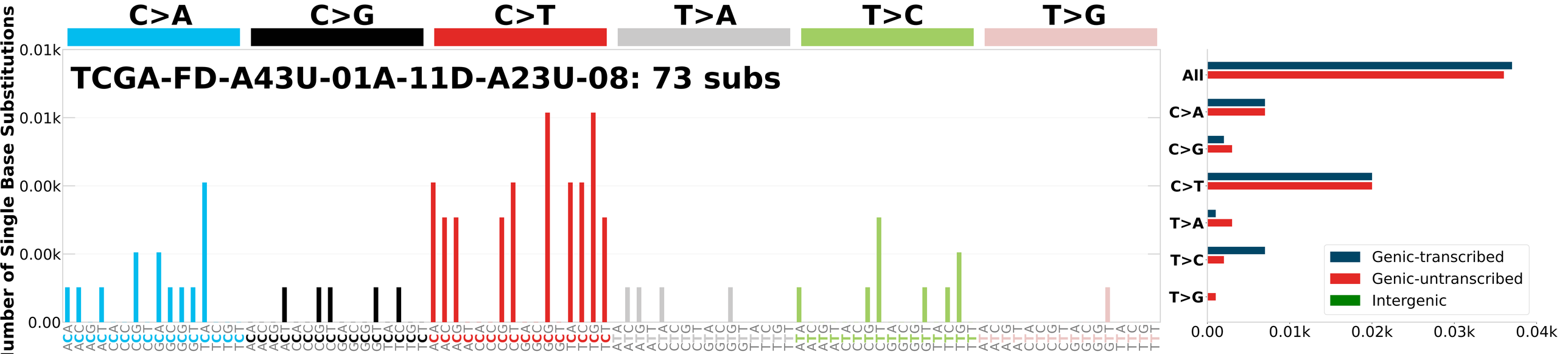

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3SQ-01A-21D-A22Z-08: 82 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

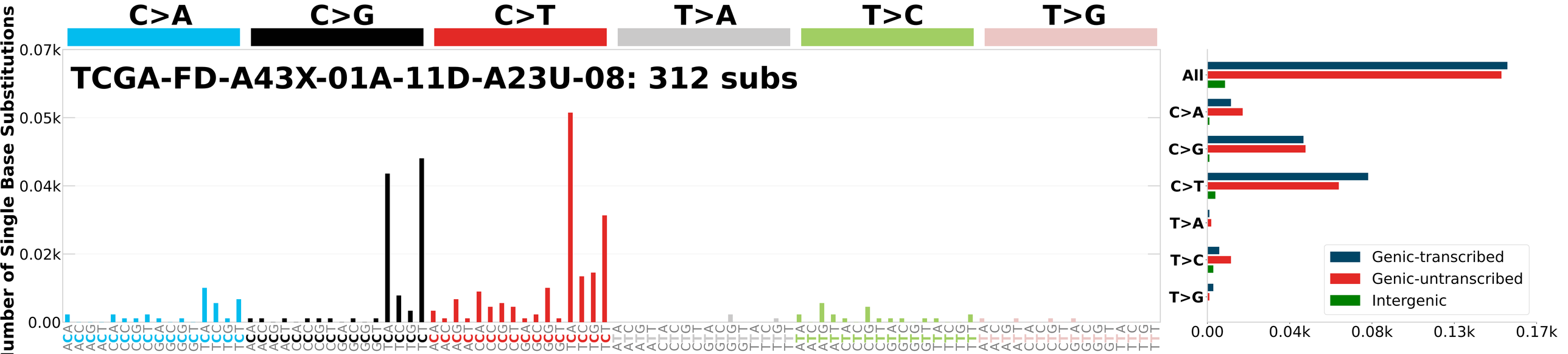

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3SR-01A-11D-A22Z-08: 137 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.07k
0.09k

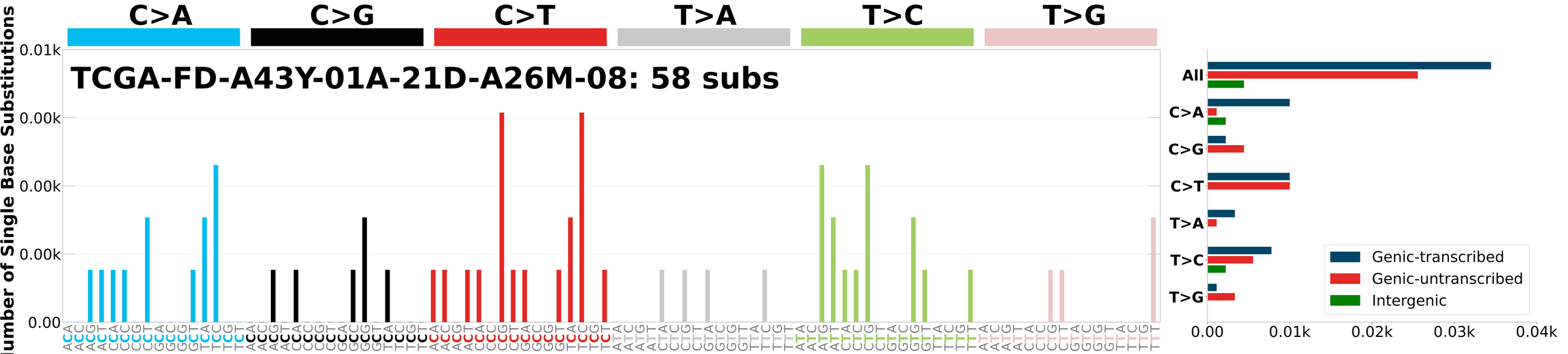

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A3SS-01A-12D-A22Z-08: 476 subs
Number of Single Base Substitutions
0.15k
0.11k
0.07k
0.04k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.14k
0.21k
0.28k

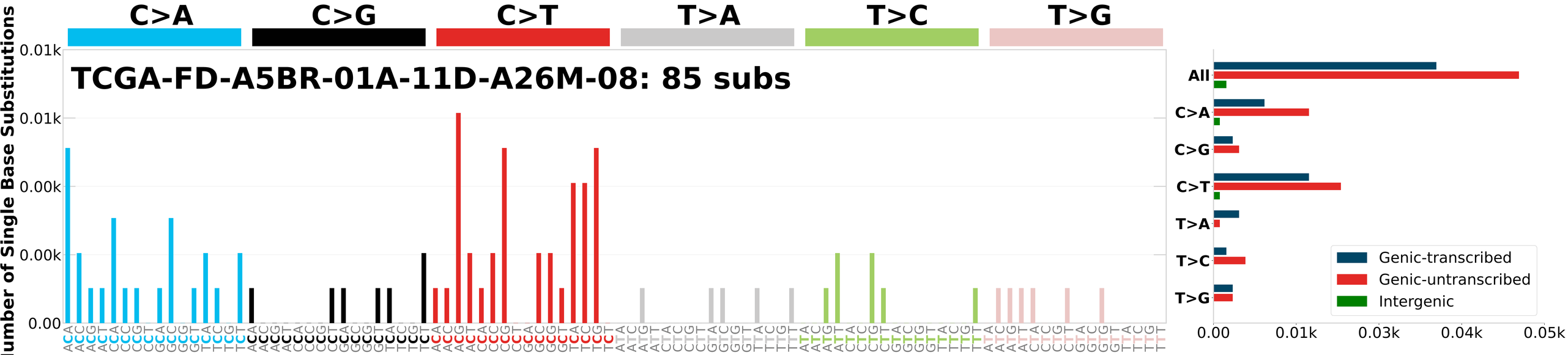

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A43N-01A-11D-A23U-08: 170 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.07k
0.10k

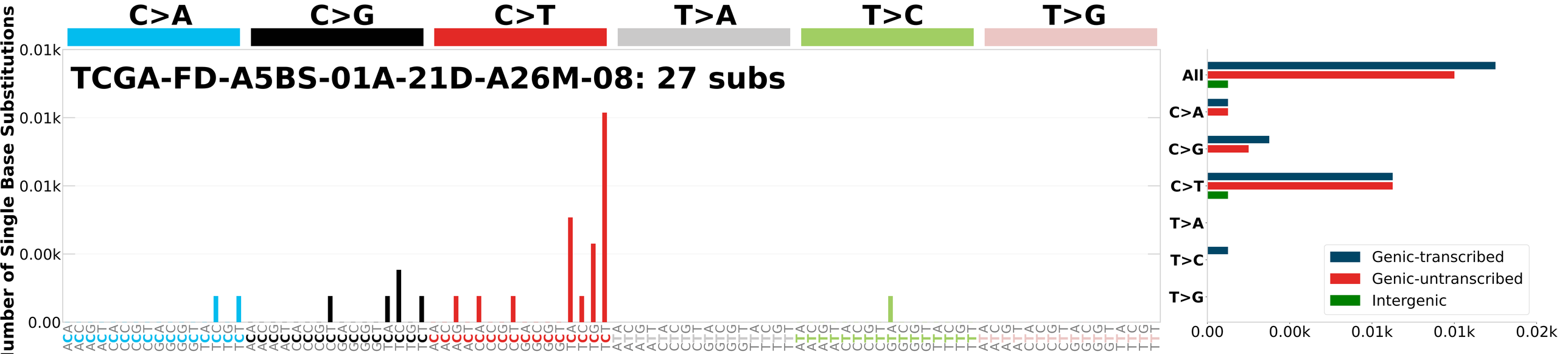

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A43P-01A-31D-A23U-08: 385 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.11k
0.16k
0.21k

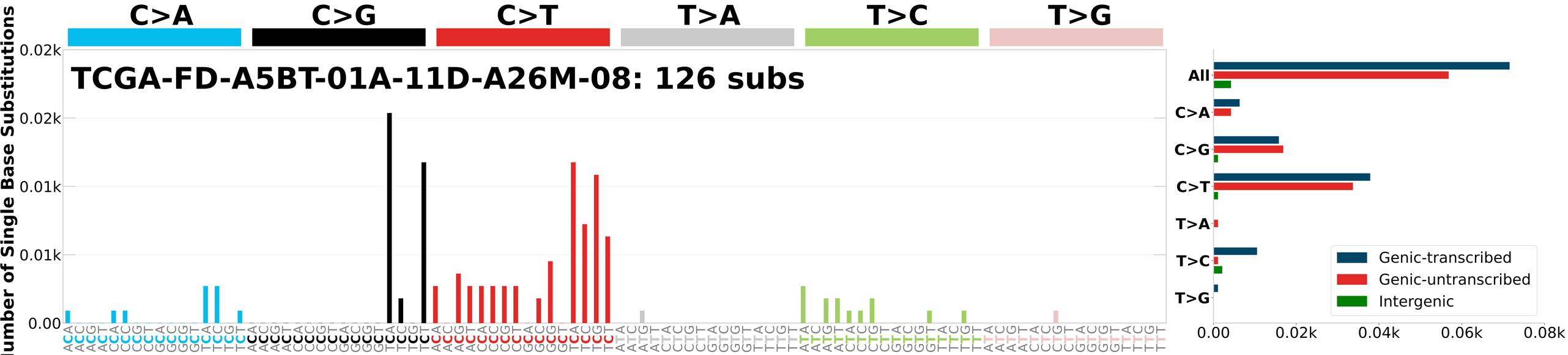

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A43U-01A-11D-A23U-08: 73 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

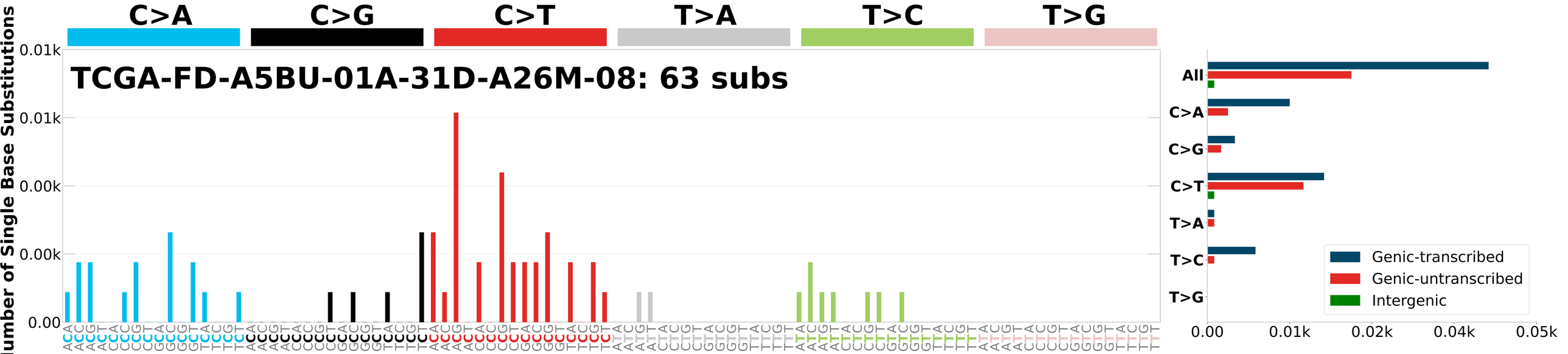

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A43X-01A-11D-A23U-08: 312 subs
Number of Single Base Substitutions
0.07k
0.05k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.13k
0.17k

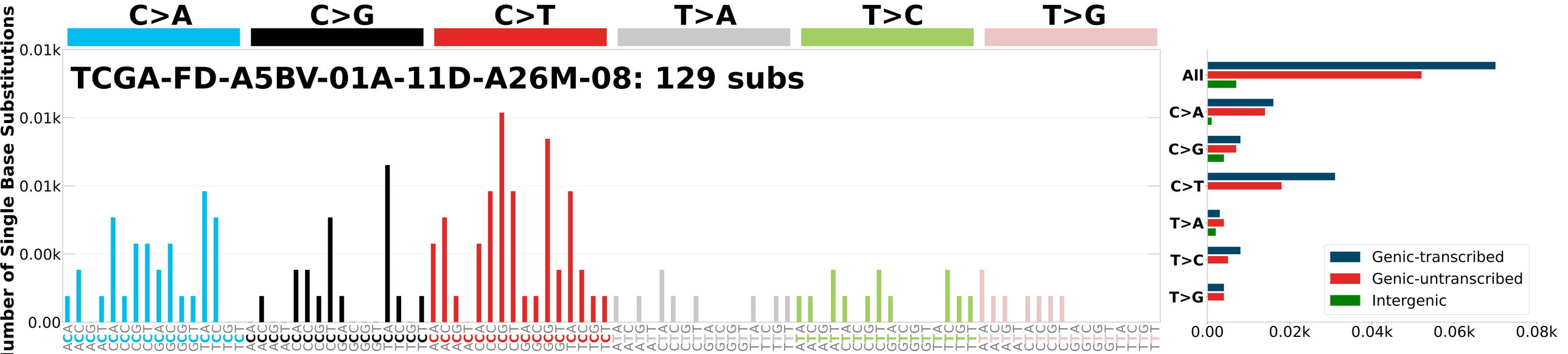

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A43Y-01A-21D-A26M-08: 58 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

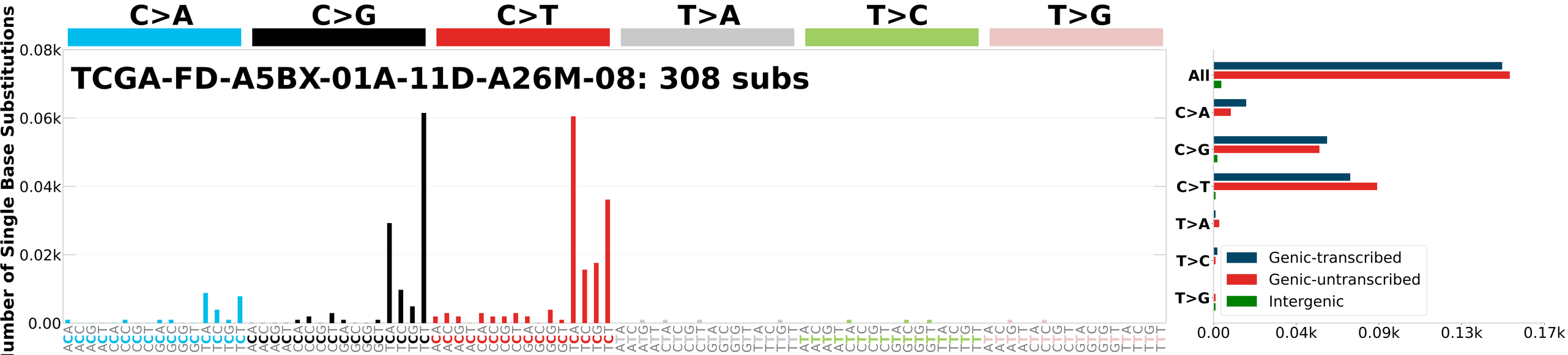

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A5BR-01A-11D-A26M-08: 85 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

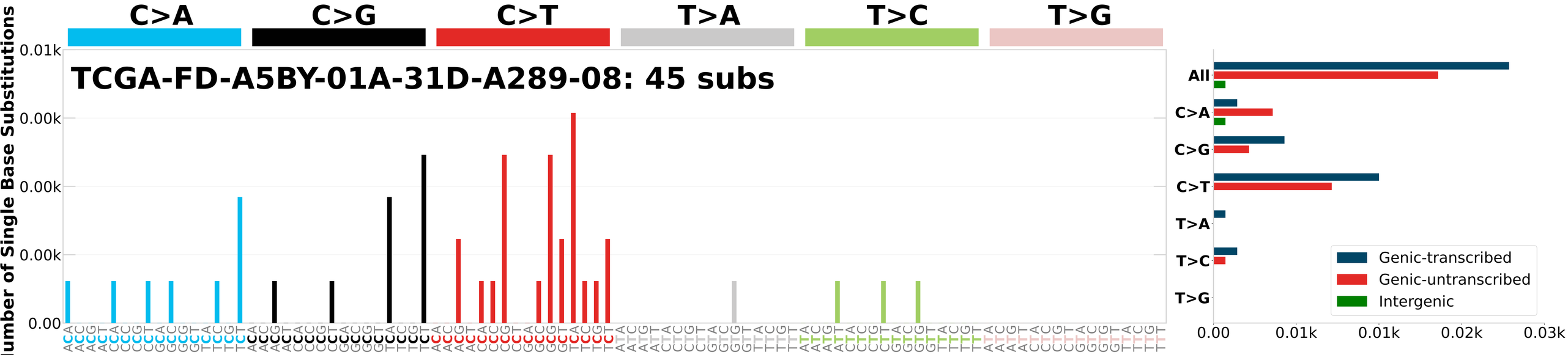

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A5BS-01A-21D-A26M-08: 27 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.00k
0.01k
0.01k
0.02k

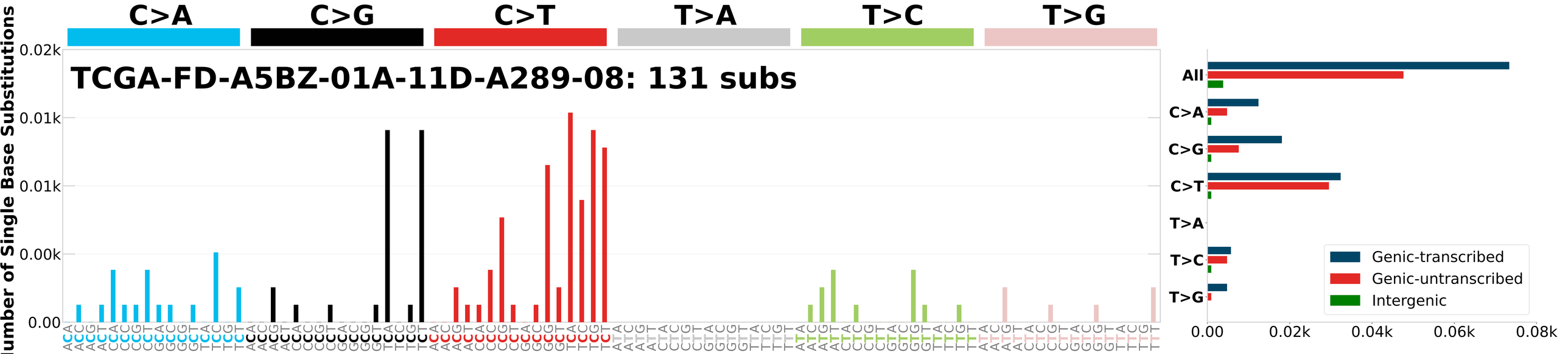

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A5BT-01A-11D-A26M-08: 126 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

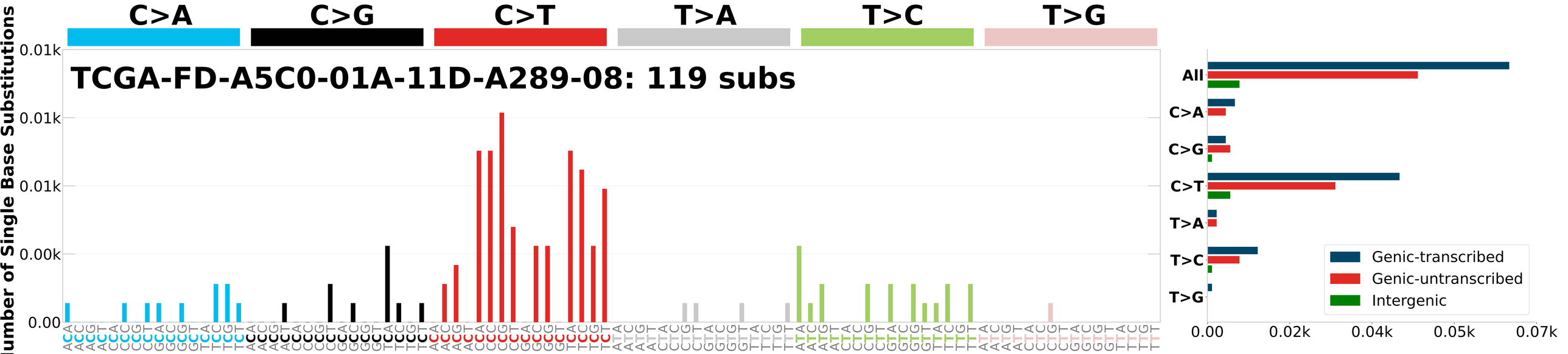

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A5BU-01A-31D-A26M-08: 63 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

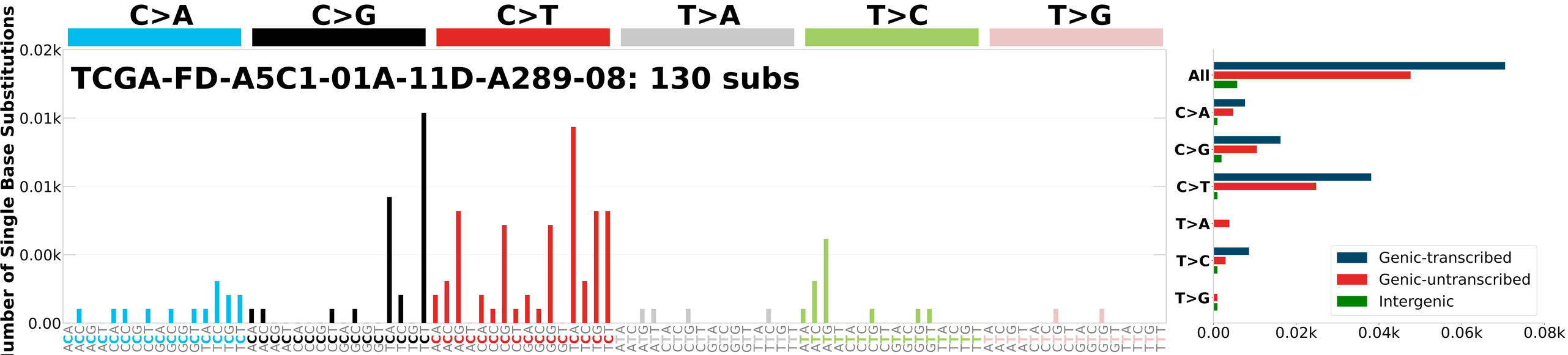

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A5BV-01A-11D-A26M-08: 129 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

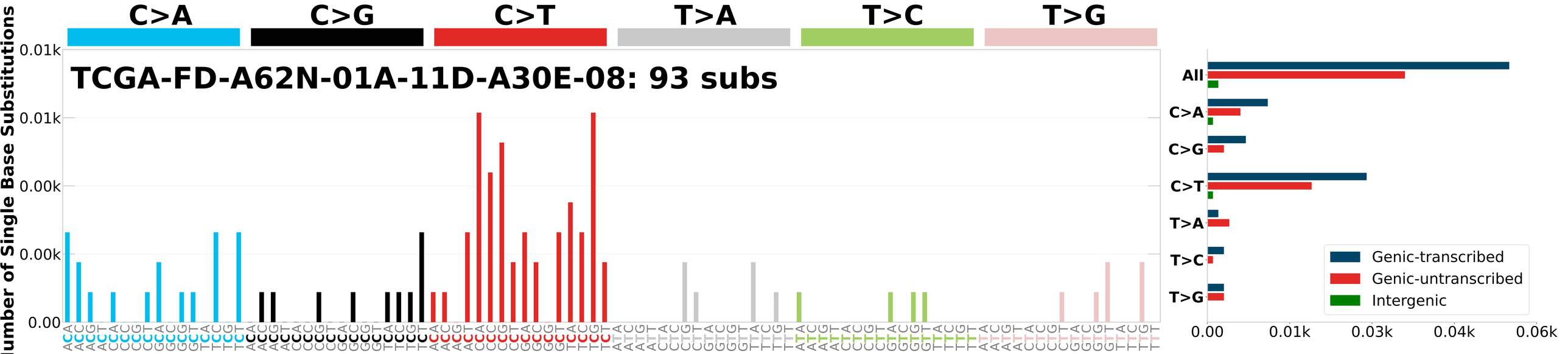

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A5BX-01A-11D-A26M-08: 308 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.09k
0.13k
0.17k

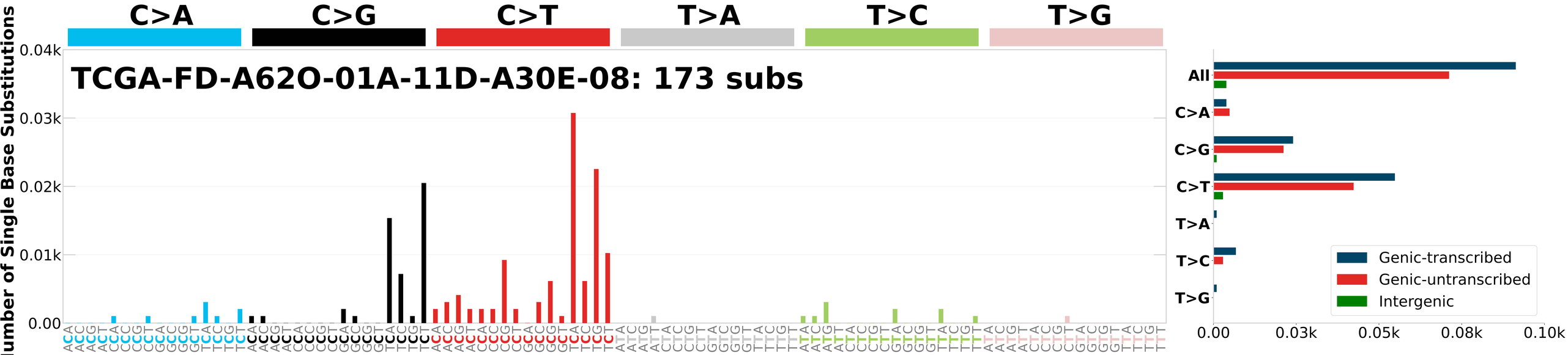

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A5BY-01A-31D-A289-08: 45 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.02k
0.03k

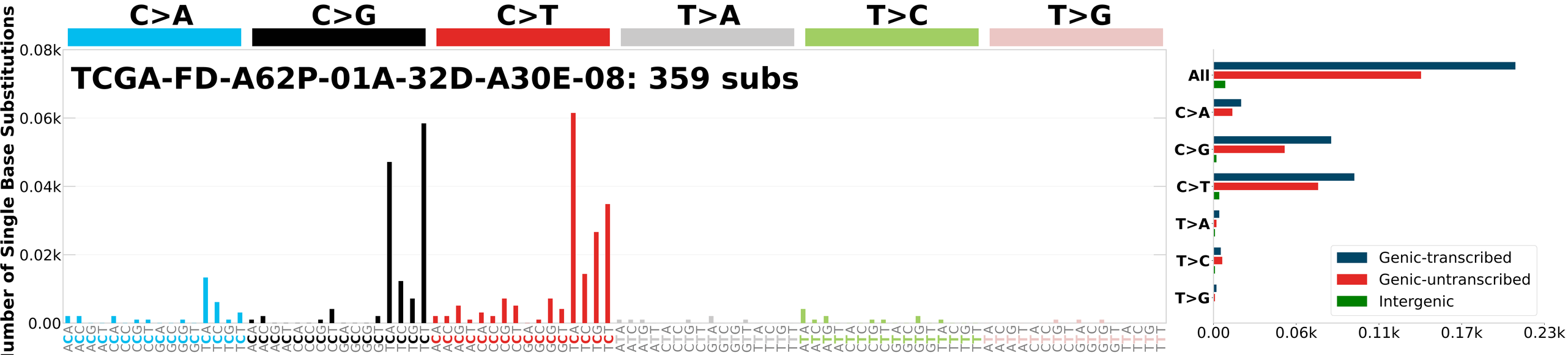

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A5BZ-01A-11D-A289-08: 131 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

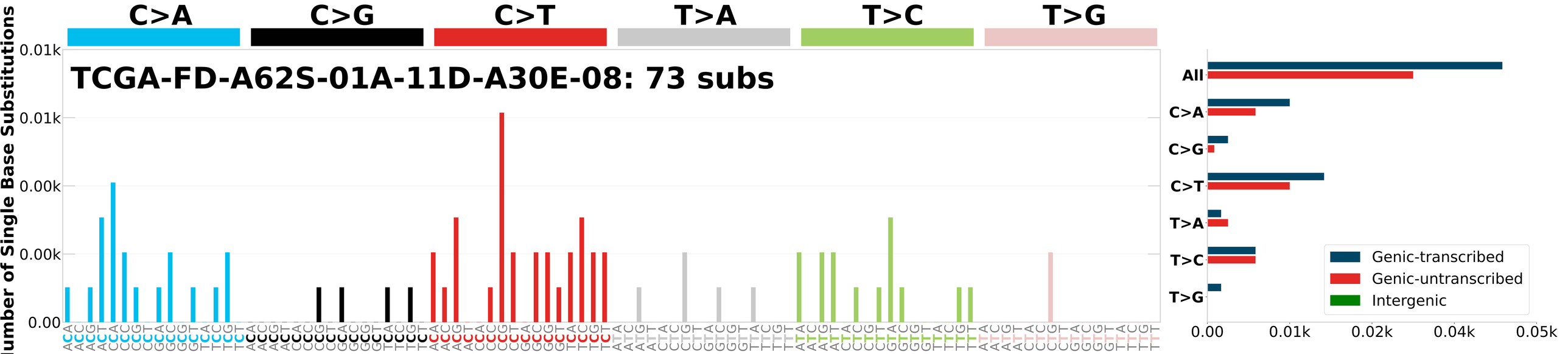

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A5C0-01A-11D-A289-08: 119 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.05k
0.07k

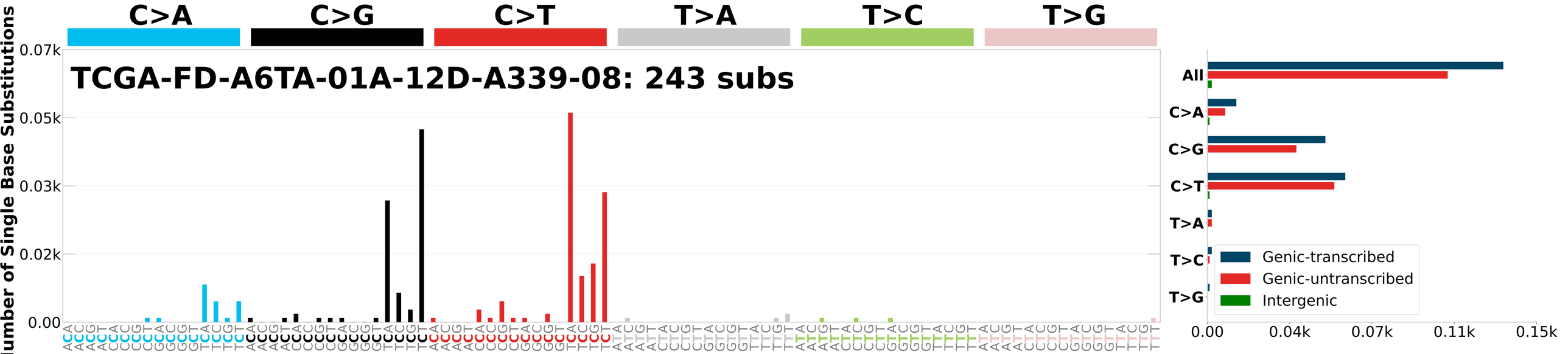

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A5C1-01A-11D-A289-08: 130 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

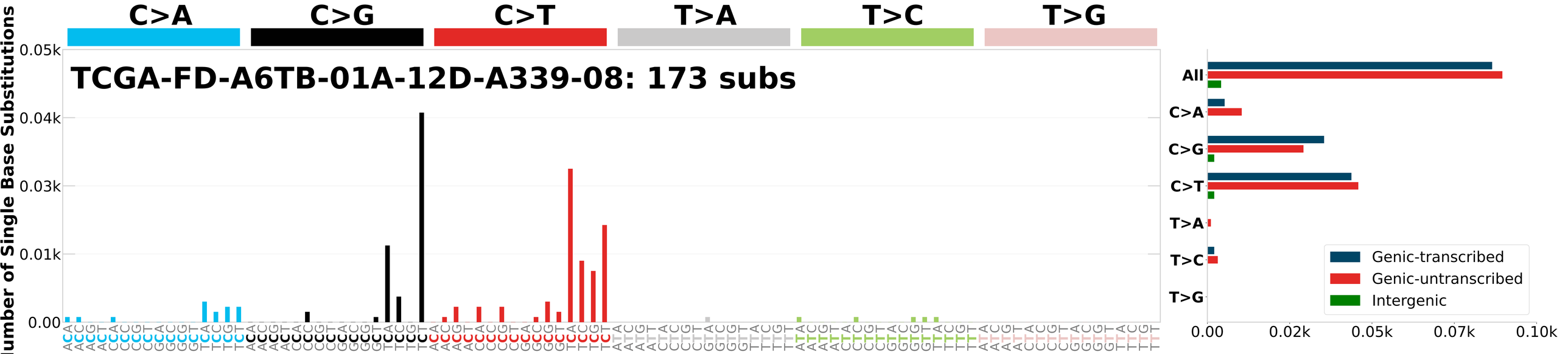

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A62N-01A-11D-A30E-08: 93 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

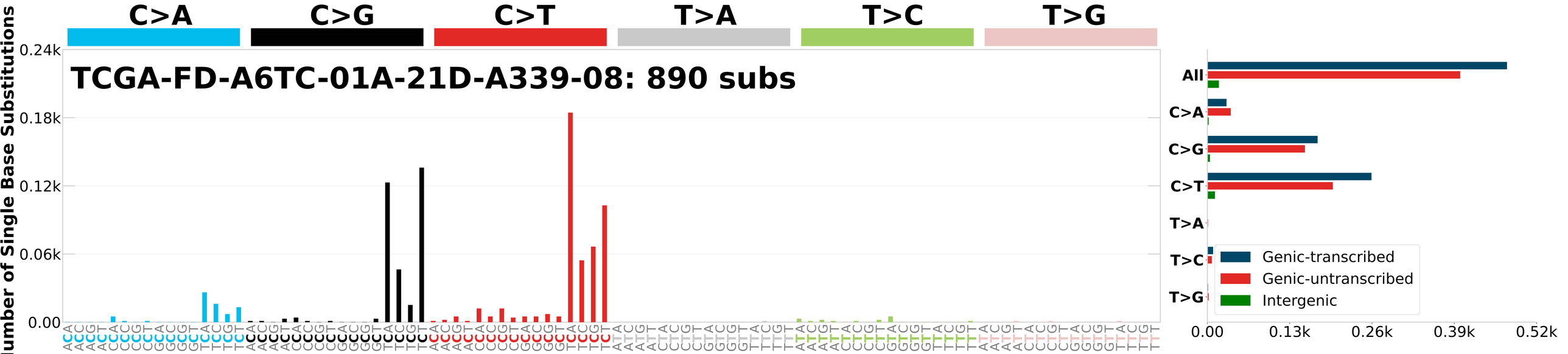

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A62O-01A-11D-A30E-08: 173 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.10k

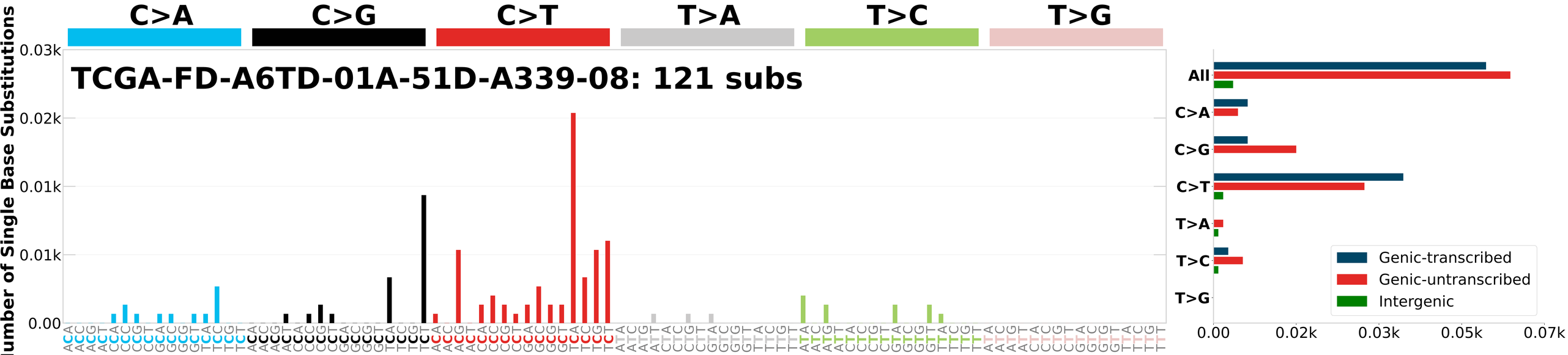

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A62P-01A-32D-A30E-08: 359 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.11k
0.17k
0.23k

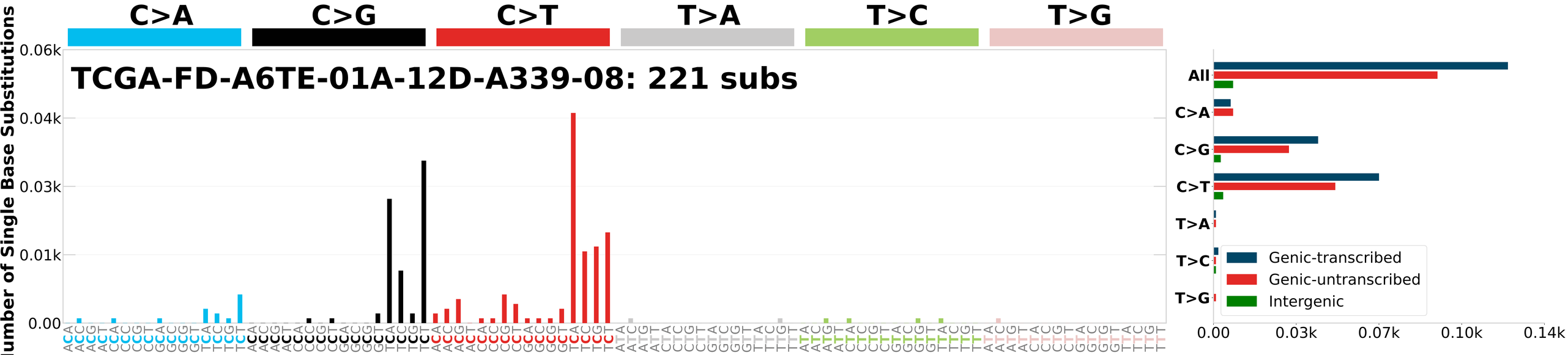

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A62S-01A-11D-A30E-08: 73 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

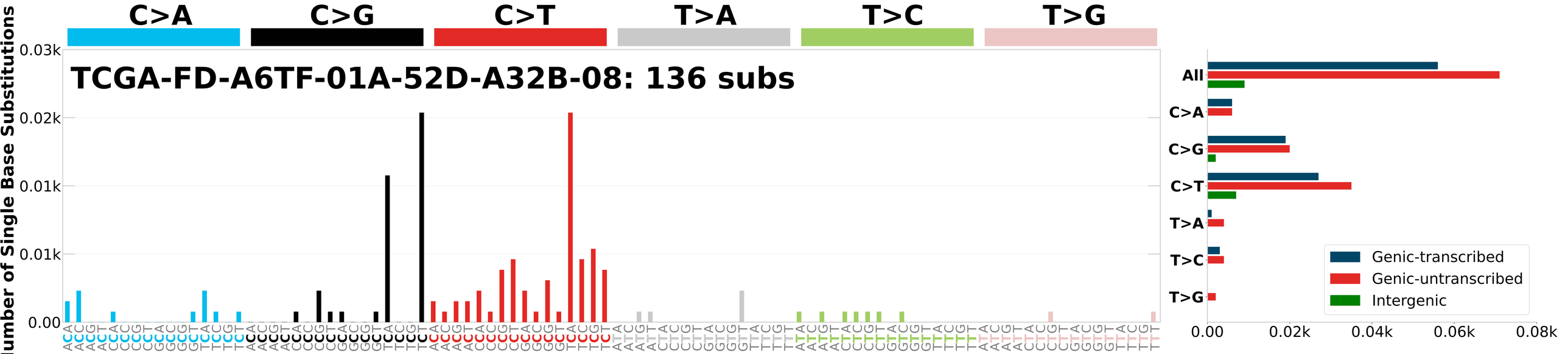

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A6TA-01A-12D-A339-08: 243 subs
Number of Single Base Substitutions
0.07k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.07k
0.11k
0.15k

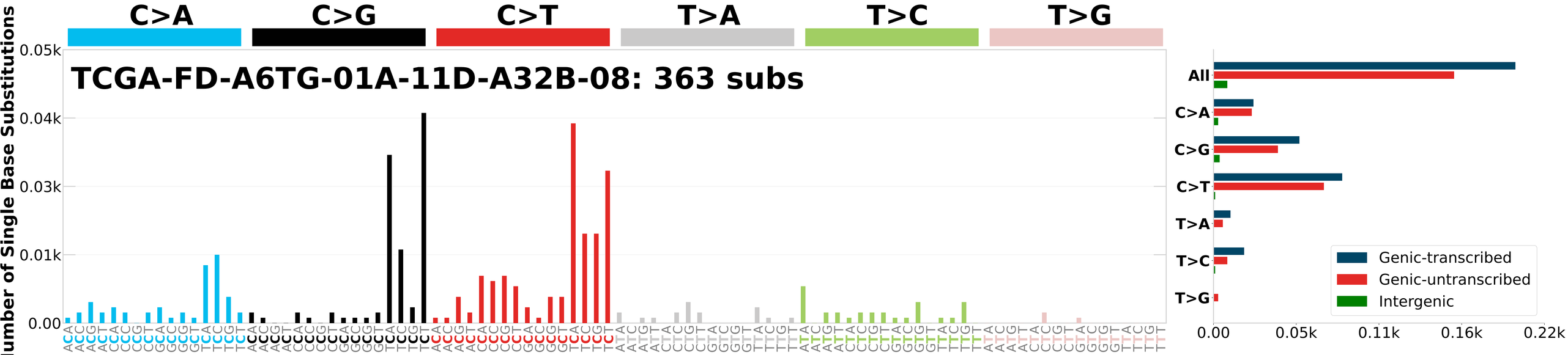

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A6TB-01A-12D-A339-08: 173 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.10k

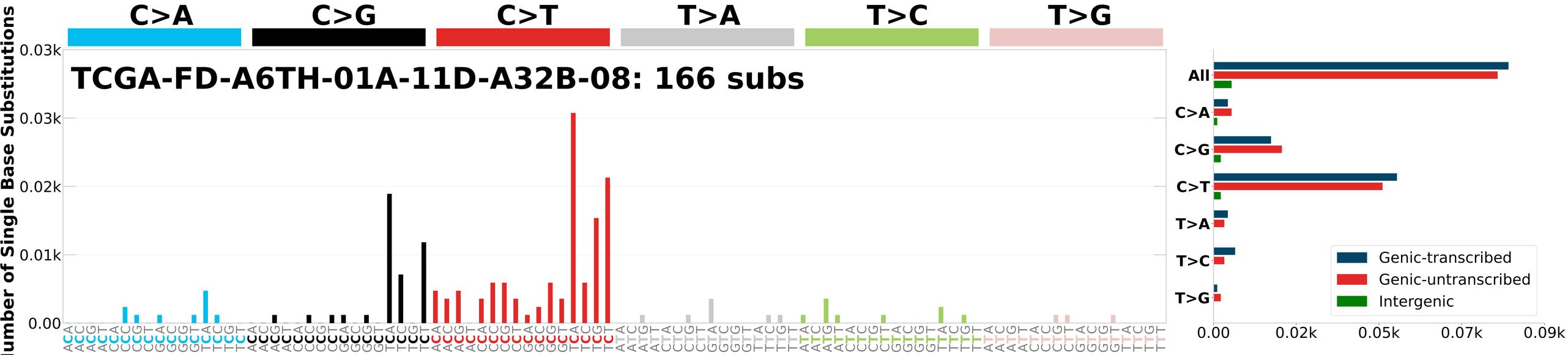

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A6TC-01A-21D-A339-08: 890 subs
Number of Single Base Substitutions
0.24k
0.18k
0.12k
0.06k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.13k
0.26k
0.39k
0.52k

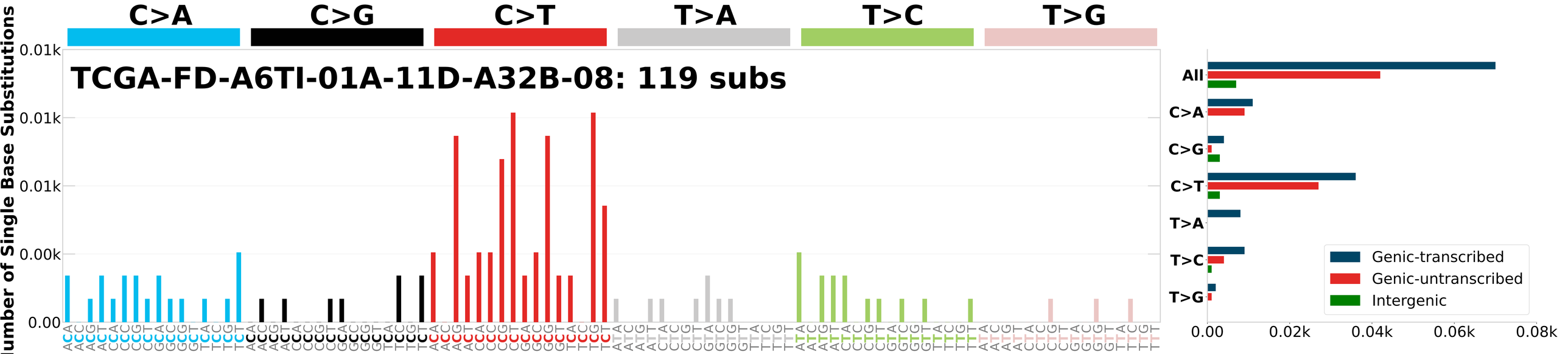

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A6TD-01A-51D-A339-08: 121 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.07k

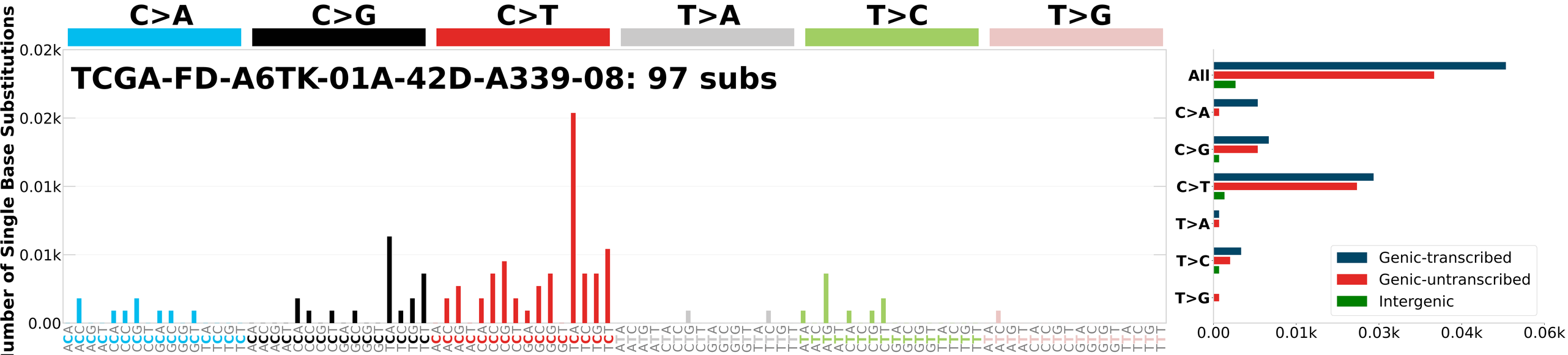

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A6TE-01A-12D-A339-08: 221 subs
Number of Single Base Substitutions
0.06k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.14k

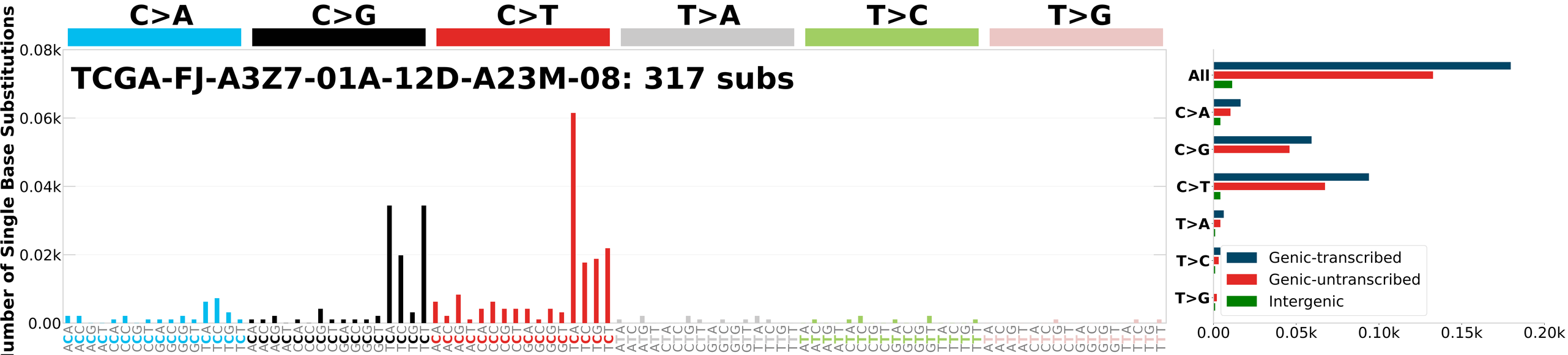

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A6TF-01A-52D-A32B-08: 136 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

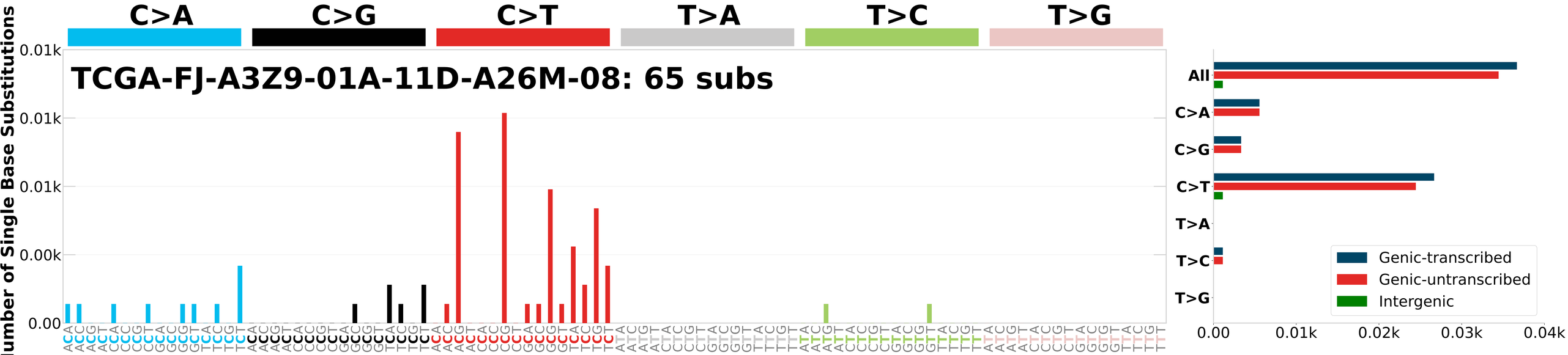

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A6TG-01A-11D-A32B-08: 363 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.11k
0.16k
0.22k

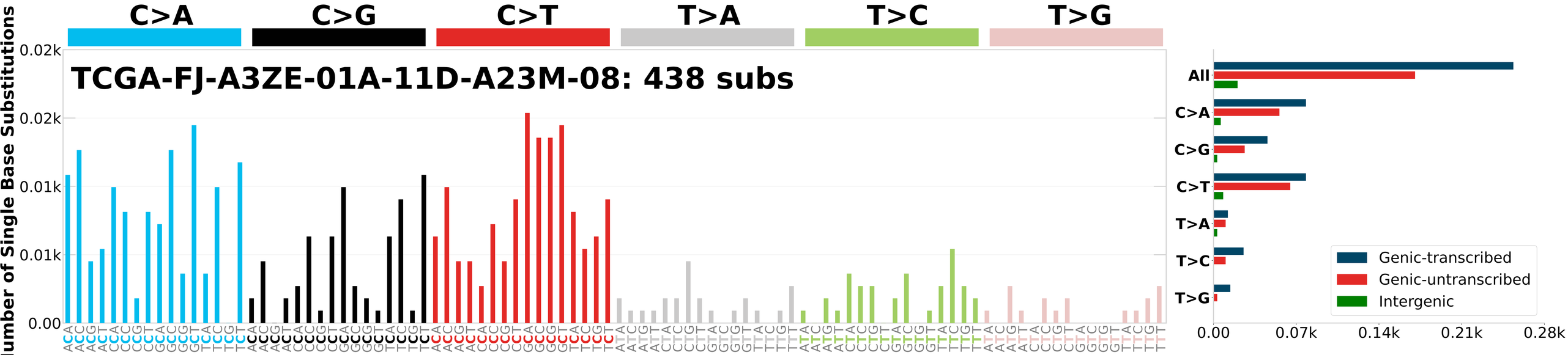

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A6TH-01A-11D-A32B-08: 166 subs
Number of Single Base Substitutions
0.03k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.09k

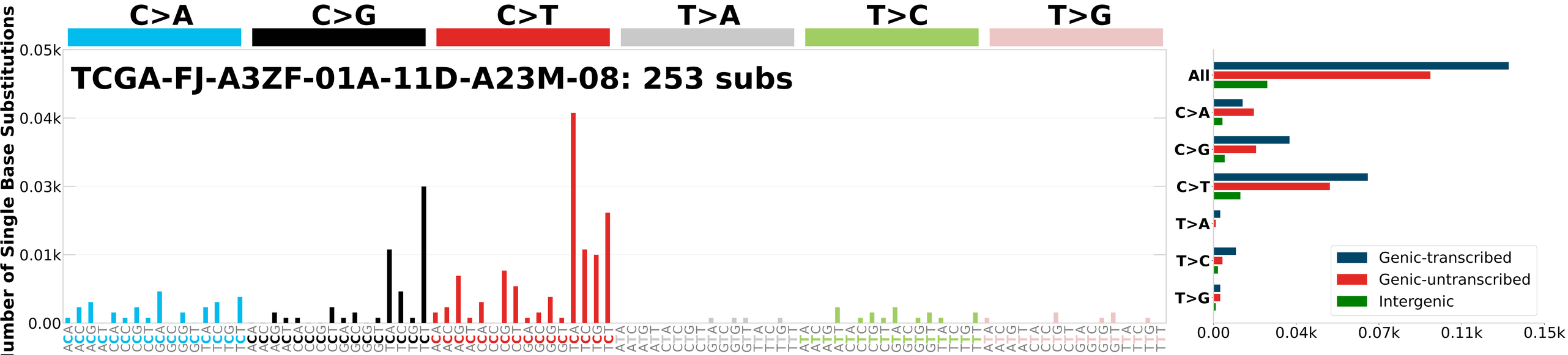

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A6TI-01A-11D-A32B-08: 119 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

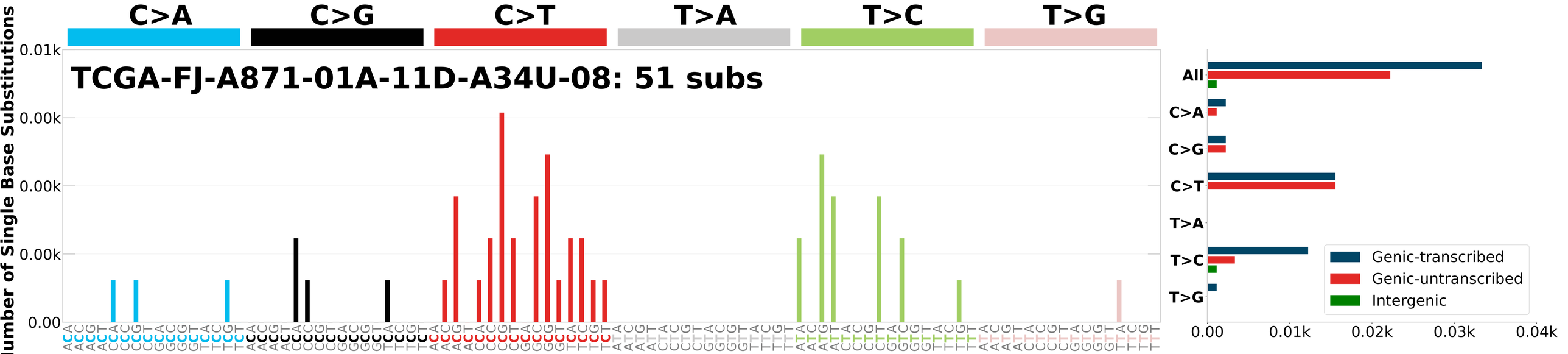

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FD-A6TK-01A-42D-A339-08: 97 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

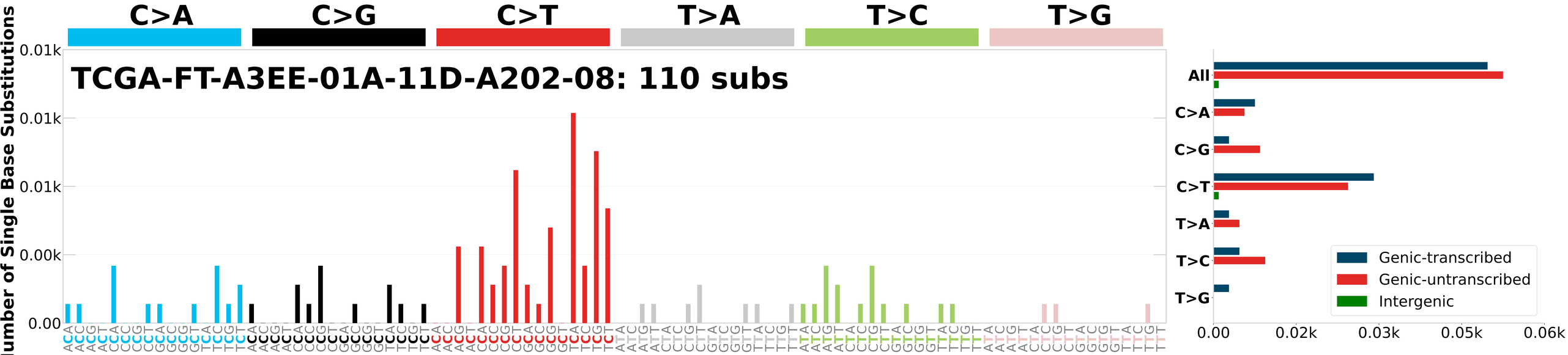

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FJ-A3Z7-01A-12D-A23M-08: 317 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.10k
0.15k
0.20k

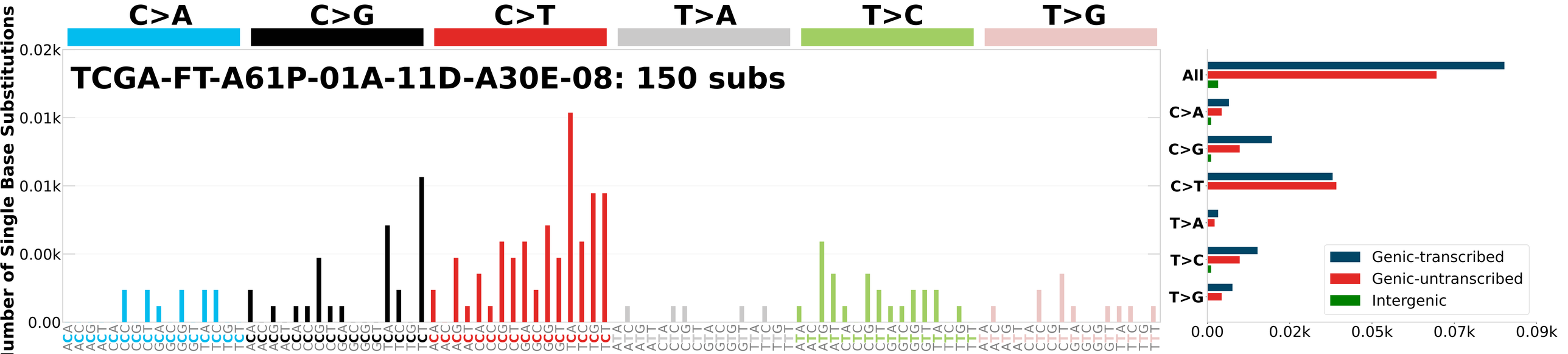

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FJ-A3Z9-01A-11D-A26M-08: 65 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

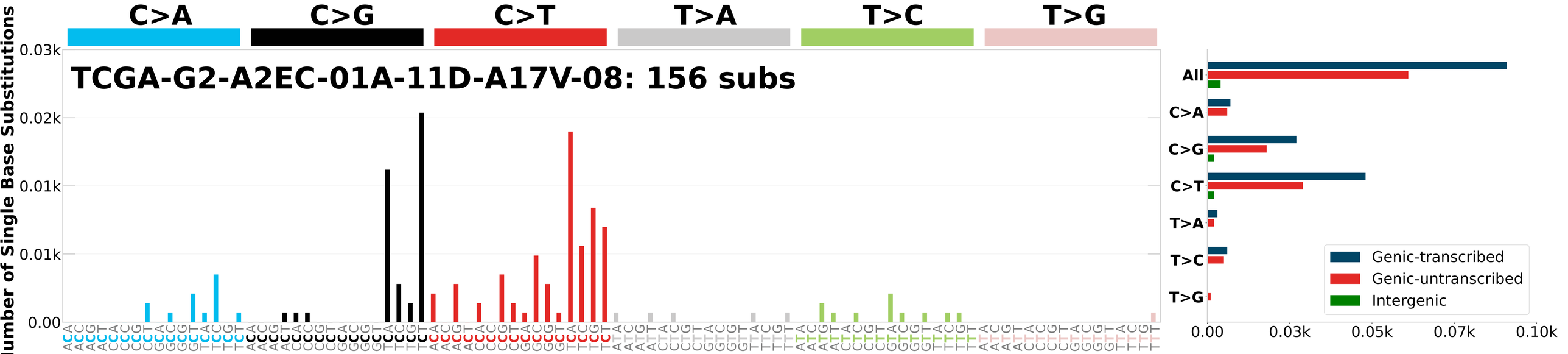

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FJ-A3ZE-01A-11D-A23M-08: 438 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.14k
0.21k
0.28k

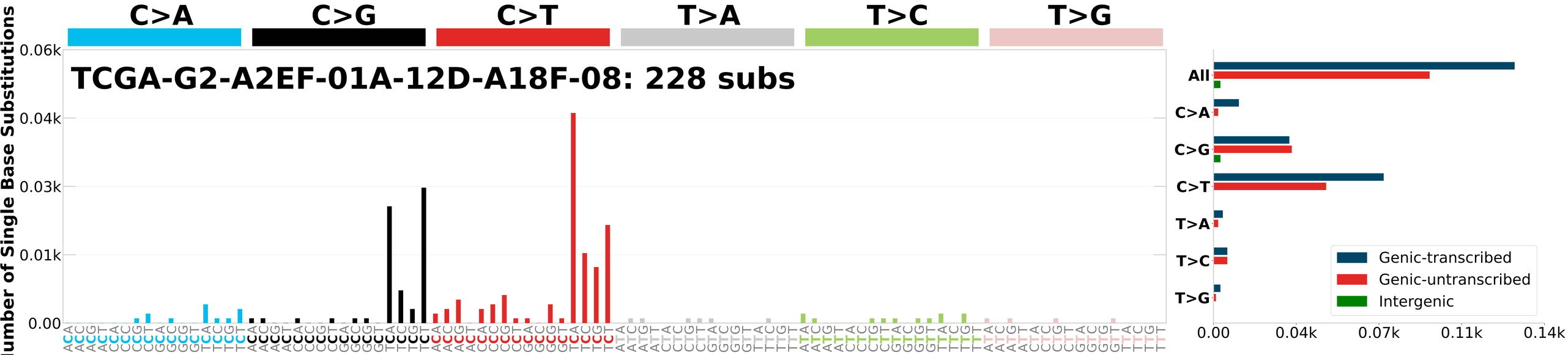

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FJ-A3ZF-01A-11D-A23M-08: 253 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.07k
0.11k
0.15k

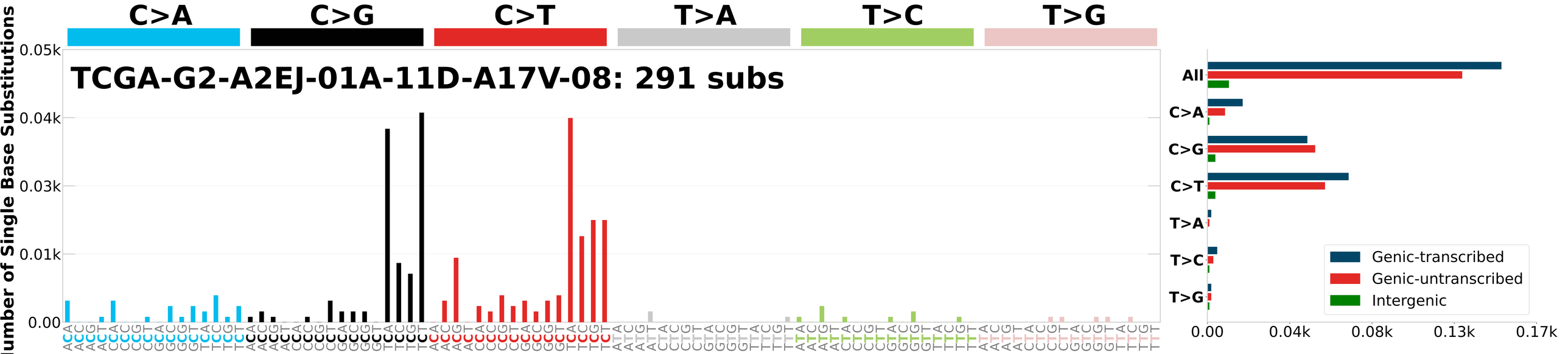

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FJ-A871-01A-11D-A34U-08: 51 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

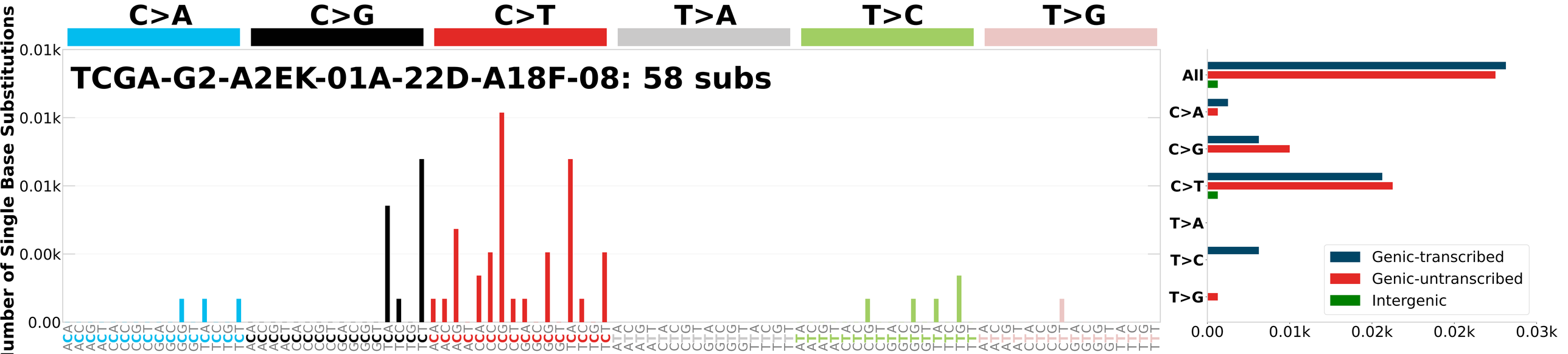

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FT-A3EE-01A-11D-A202-08: 110 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.06k

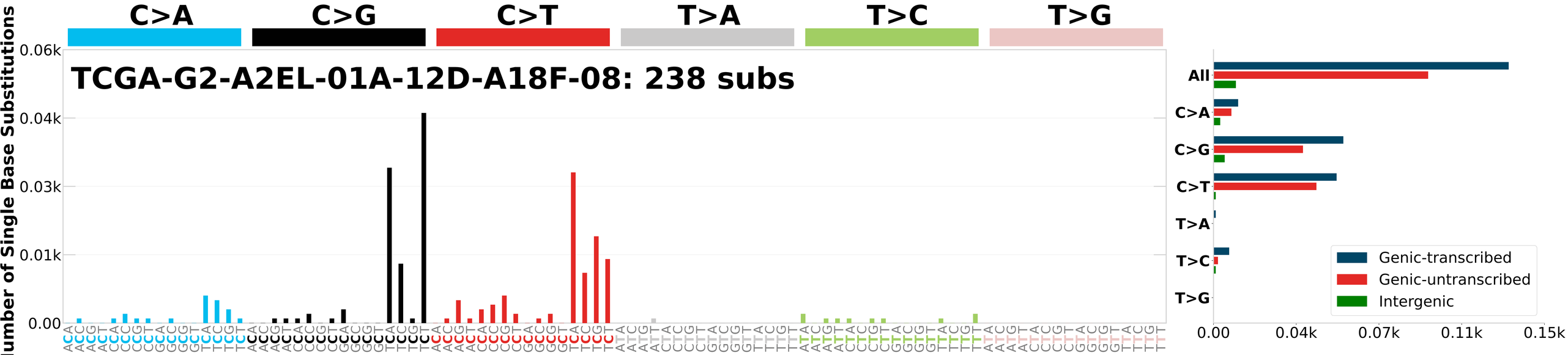

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-FT-A61P-01A-11D-A30E-08: 150 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.09k

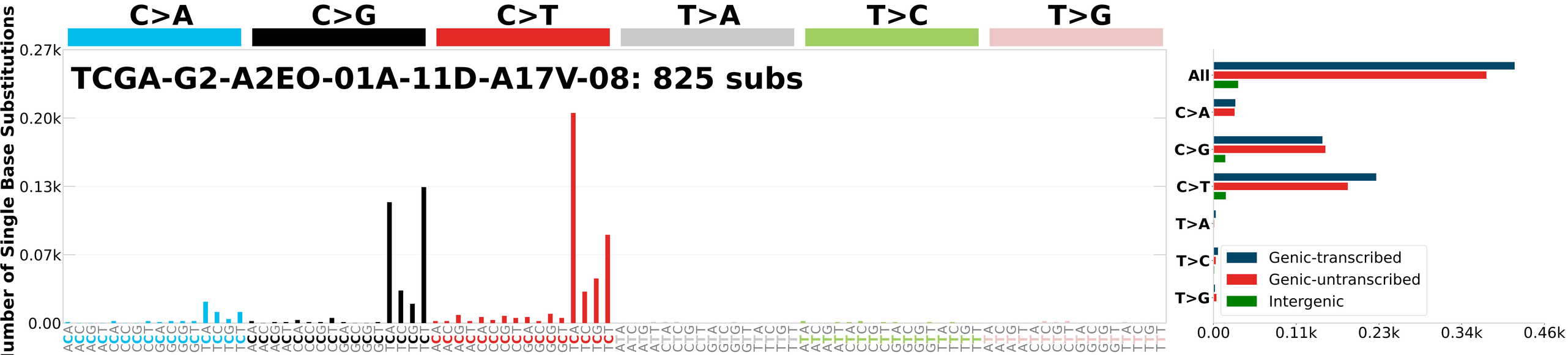

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-G2-A2EC-01A-11D-A17V-08: 156 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.07k
0.10k

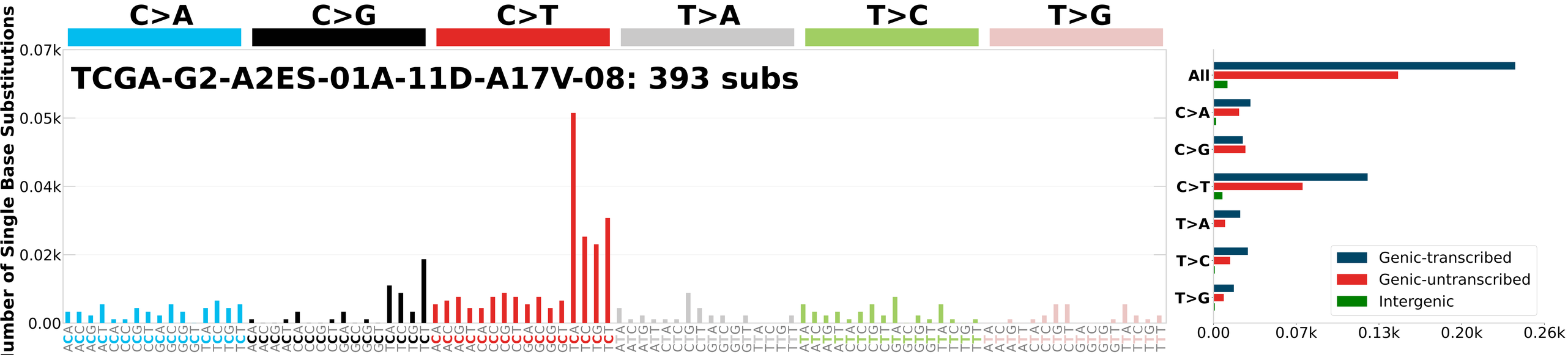

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-G2-A2EF-01A-12D-A18F-08: 228 subs
Number of Single Base Substitutions
0.06k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.07k
0.11k
0.14k

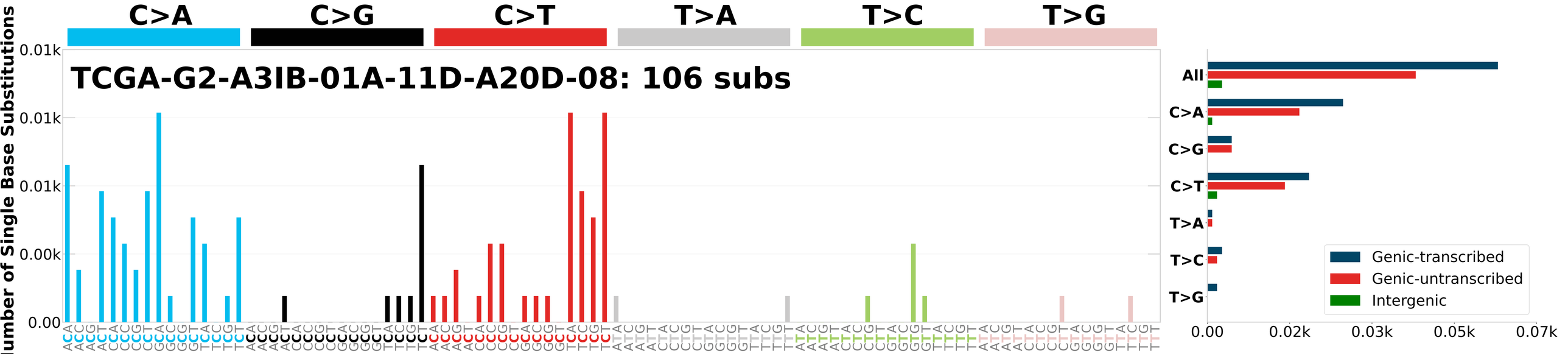

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-G2-A2EJ-01A-11D-A17V-08: 291 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.13k
0.17k

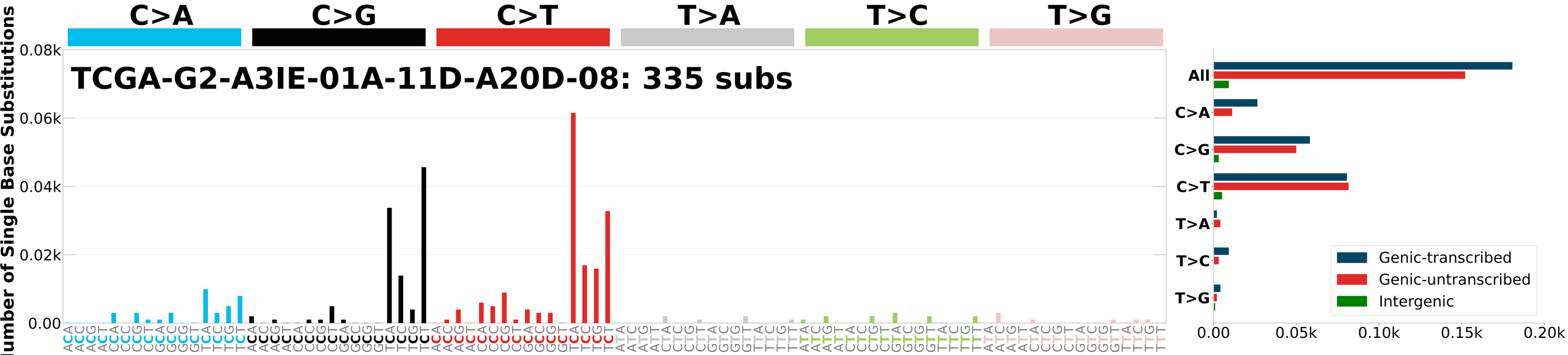

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-G2-A2EK-01A-22D-A18F-08: 58 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.02k
0.03k

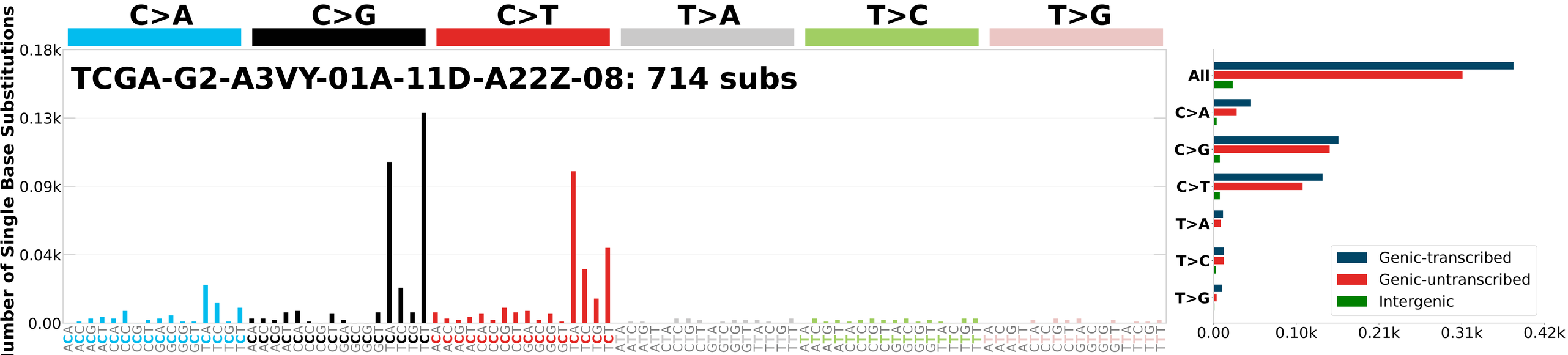

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-G2-A2EL-01A-12D-A18F-08: 238 subs
Number of Single Base Substitutions
0.06k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.07k
0.11k
0.15k

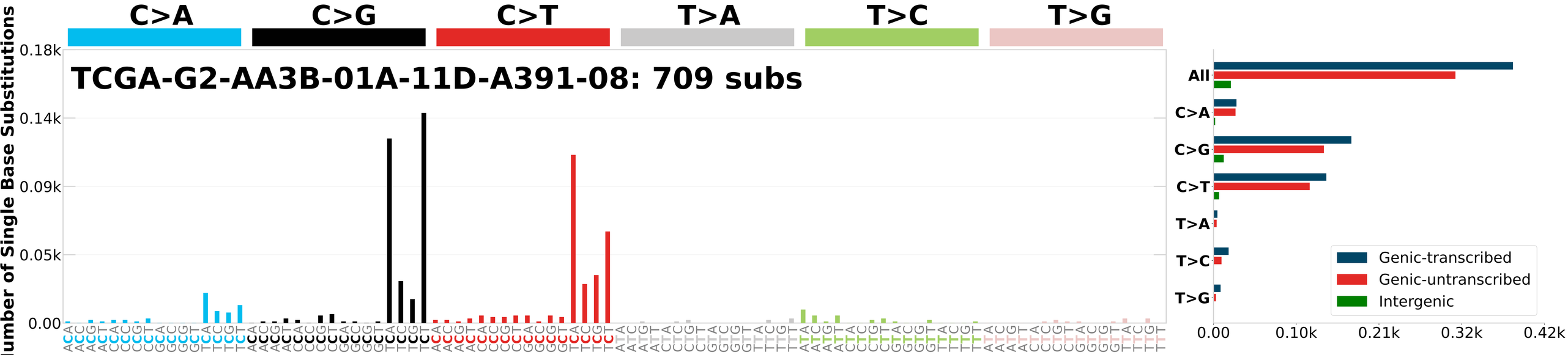

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-G2-A2EO-01A-11D-A17V-08: 825 subs
Number of Single Base Substitutions
0.27k
0.20k
0.13k
0.07k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.11k
0.23k
0.34k
0.46k

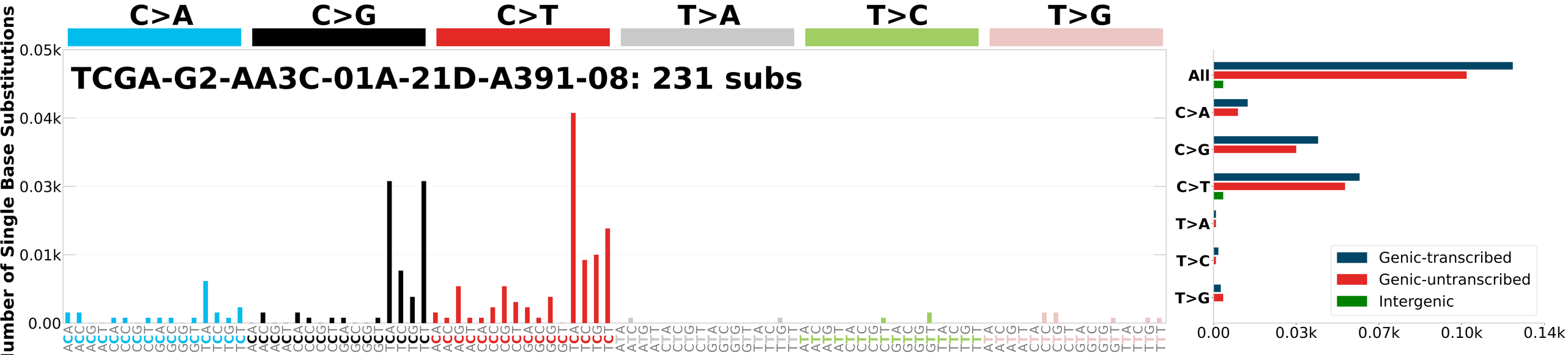

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-G2-A2ES-01A-11D-A17V-08: 393 subs
Number of Single Base Substitutions
0.07k
0.05k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.13k
0.20k
0.26k

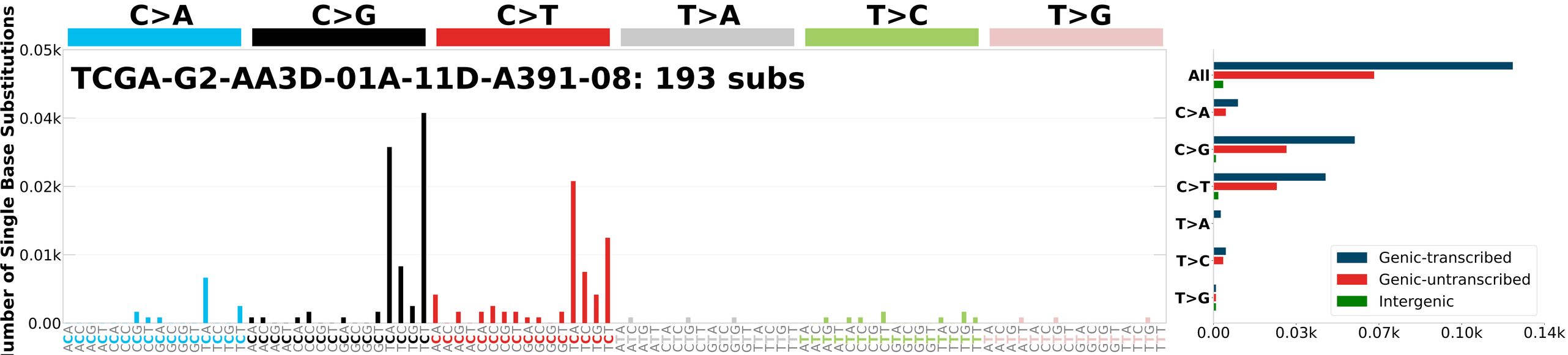

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-G2-A3IB-01A-11D-A20D-08: 106 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.07k

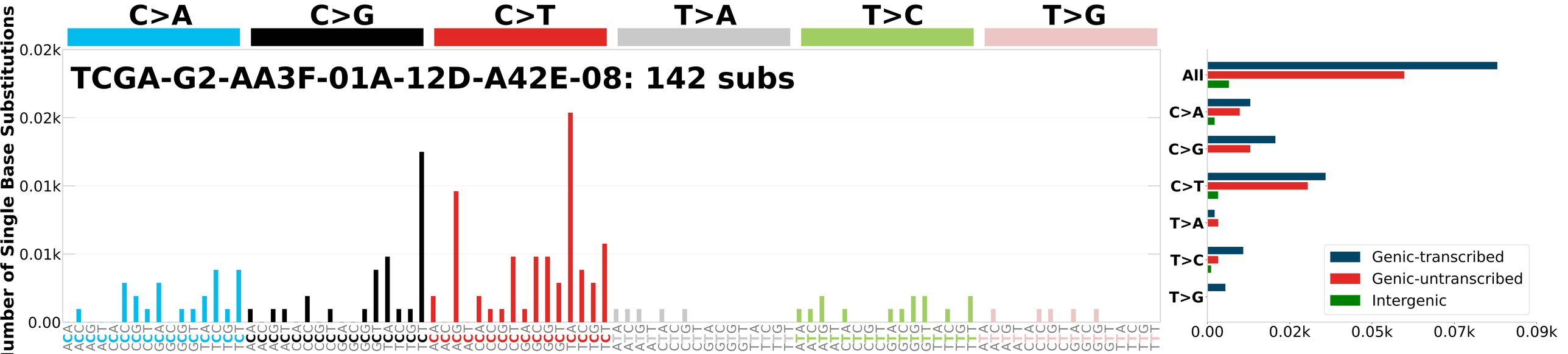

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-G2-A3IE-01A-11D-A20D-08: 335 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.10k
0.15k
0.20k

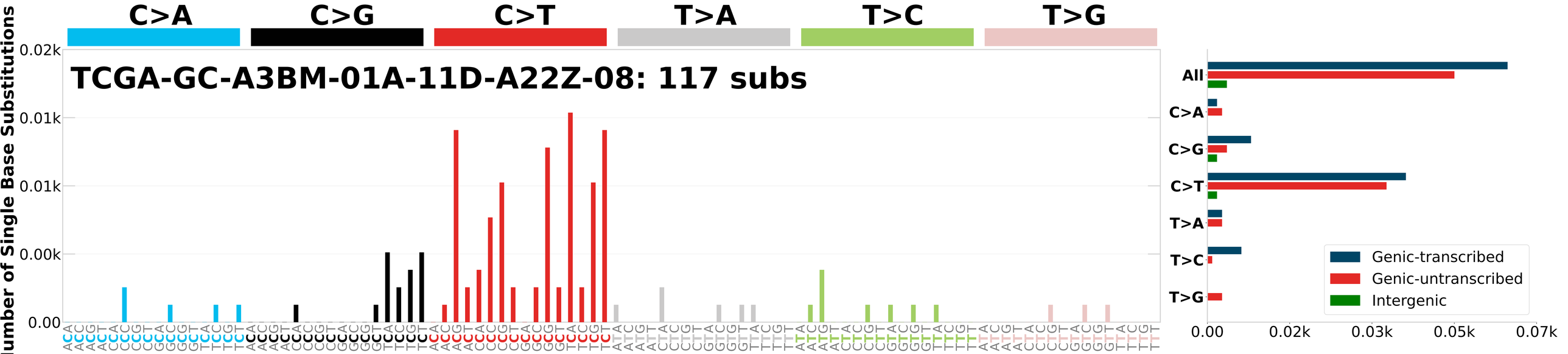

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-G2-A3VY-01A-11D-A22Z-08: 714 subs
Number of Single Base Substitutions
0.18k
0.13k
0.09k
0.04k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.10k
0.21k
0.31k
0.42k

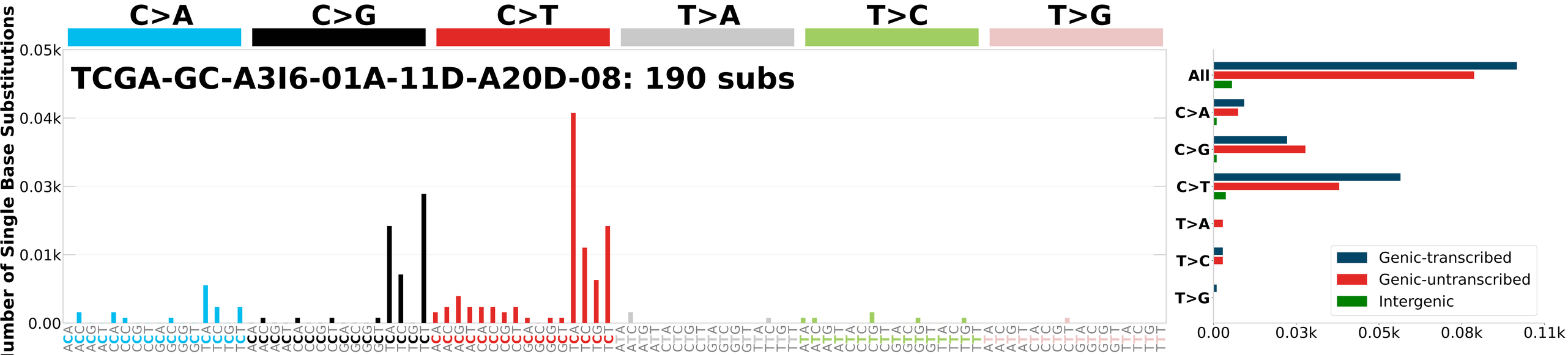

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-G2-AA3B-01A-11D-A391-08: 709 subs
Number of Single Base Substitutions
0.18k
0.14k
0.09k
0.05k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.10k
0.21k
0.32k
0.42k

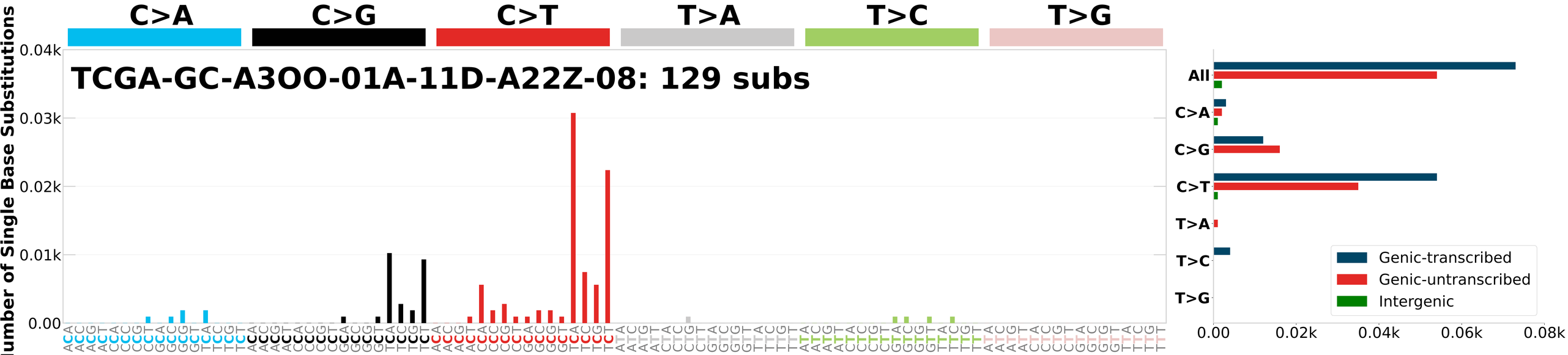

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-G2-AA3C-01A-21D-A391-08: 231 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.14k

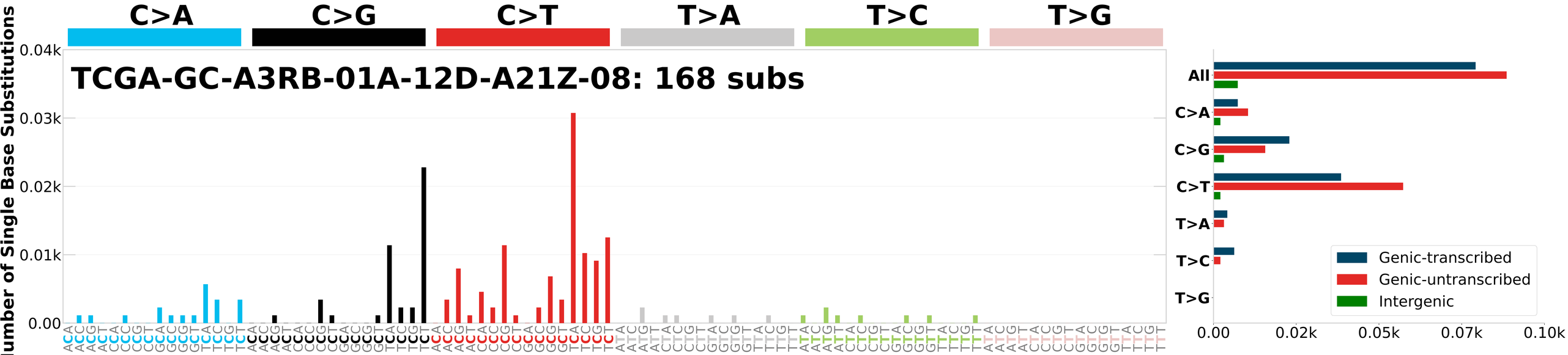

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-G2-AA3D-01A-11D-A391-08: 193 subs
Number of Single Base Substitutions
0.05k
0.04k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.14k

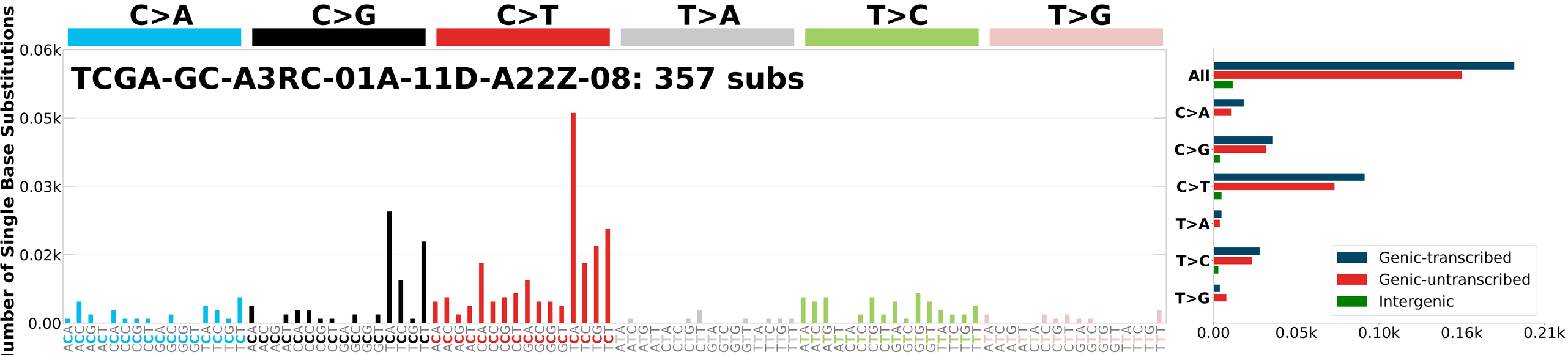

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-G2-AA3F-01A-12D-A42E-08: 142 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.09k

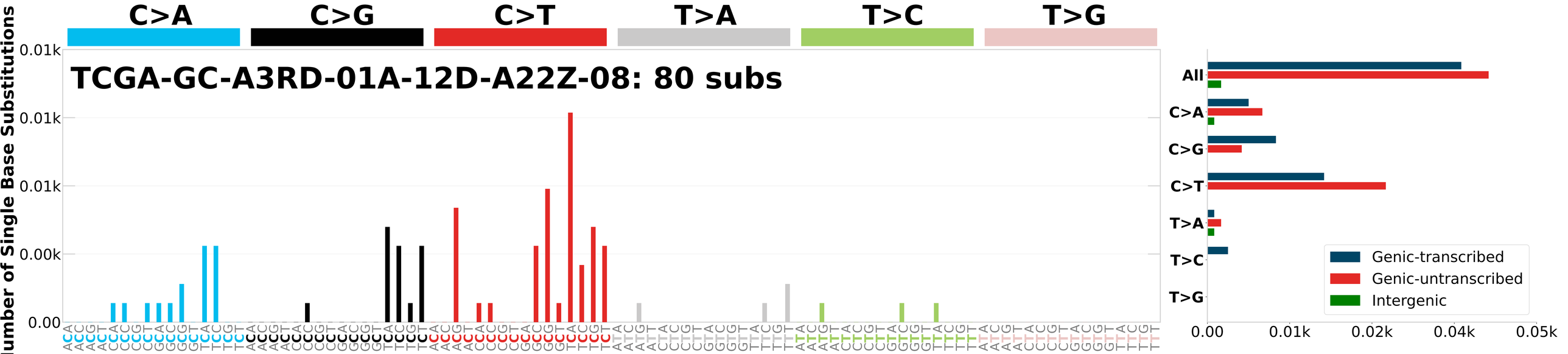

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GC-A3BM-01A-11D-A22Z-08: 117 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.07k

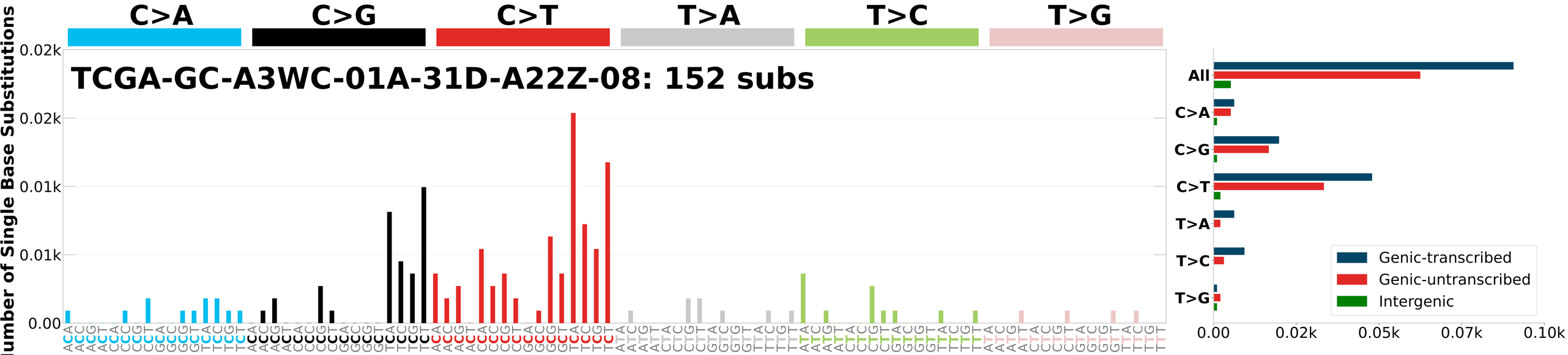

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GC-A3I6-01A-11D-A20D-08: 190 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.11k

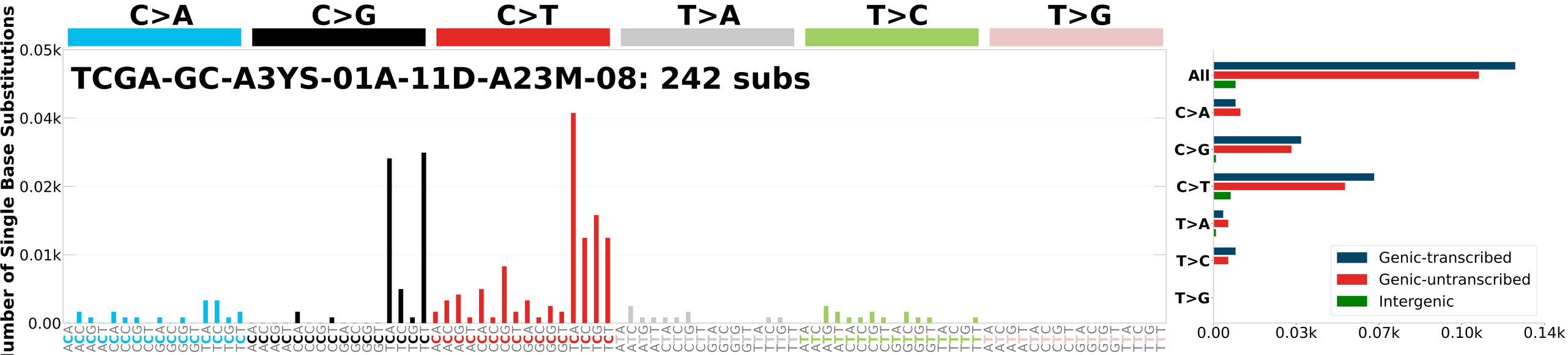

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GC-A3OO-01A-11D-A22Z-08: 129 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

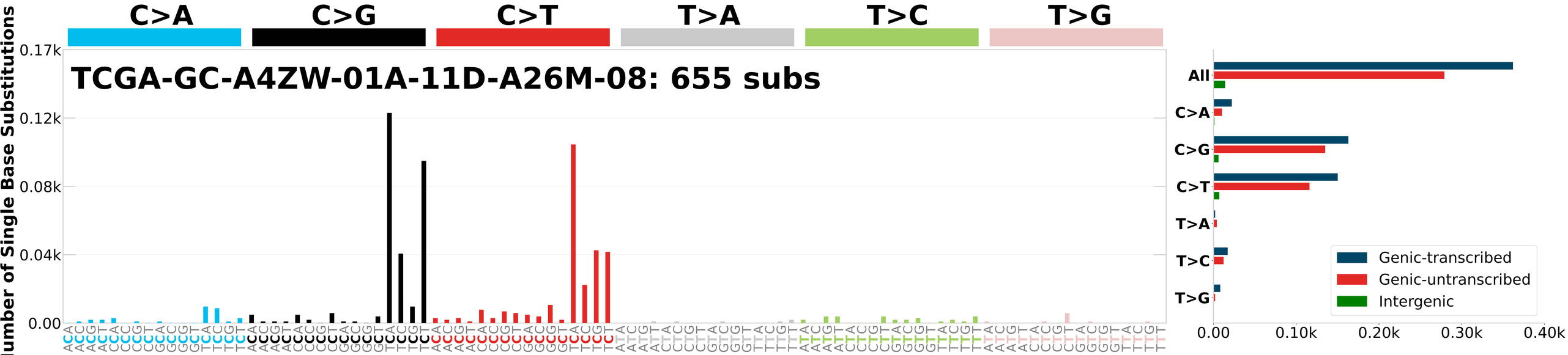

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GC-A3RB-01A-12D-A21Z-08: 168 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.10k

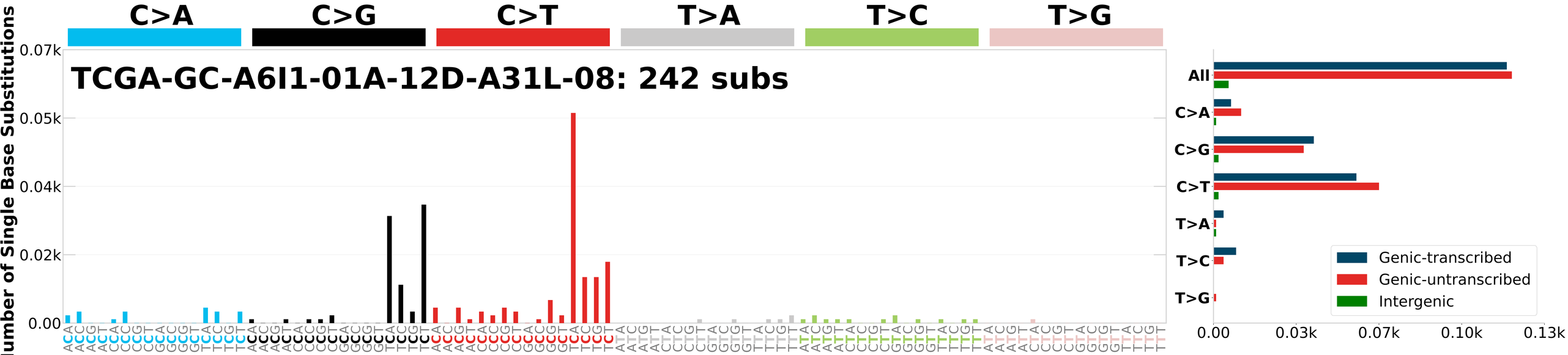

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GC-A3RC-01A-11D-A22Z-08: 357 subs
Number of Single Base Substitutions
0.06k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.10k
0.16k
0.21k

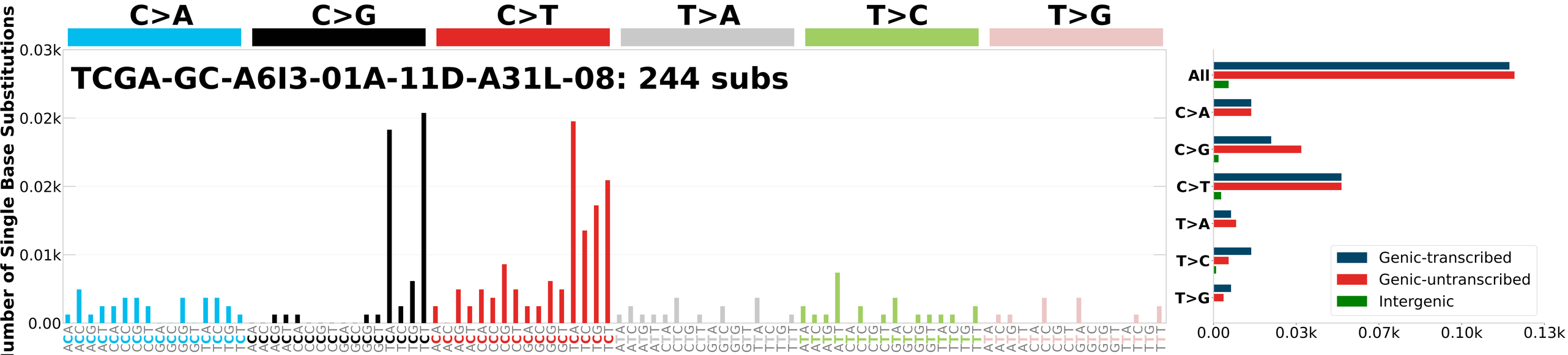

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GC-A3RD-01A-12D-A22Z-08: 80 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

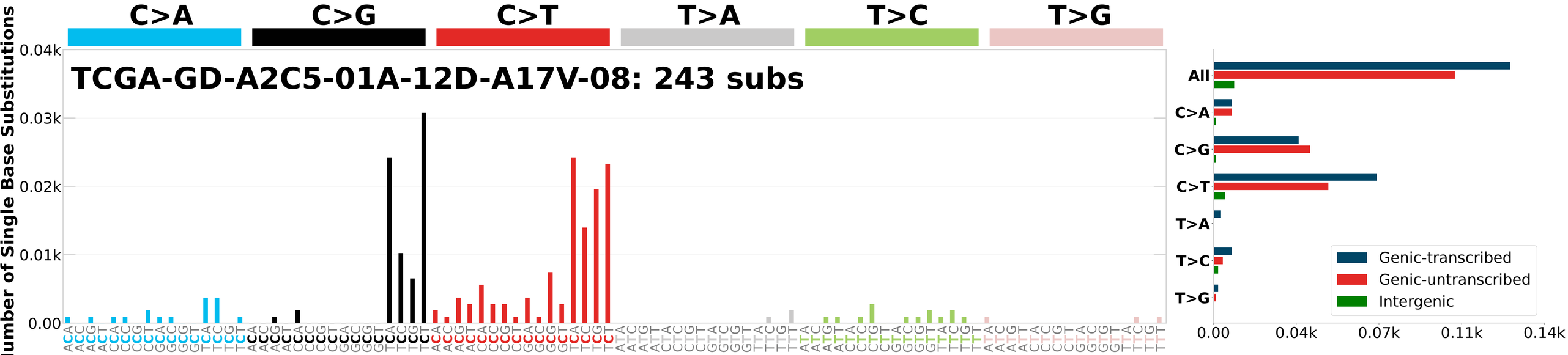

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GC-A3WC-01A-31D-A22Z-08: 152 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.10k

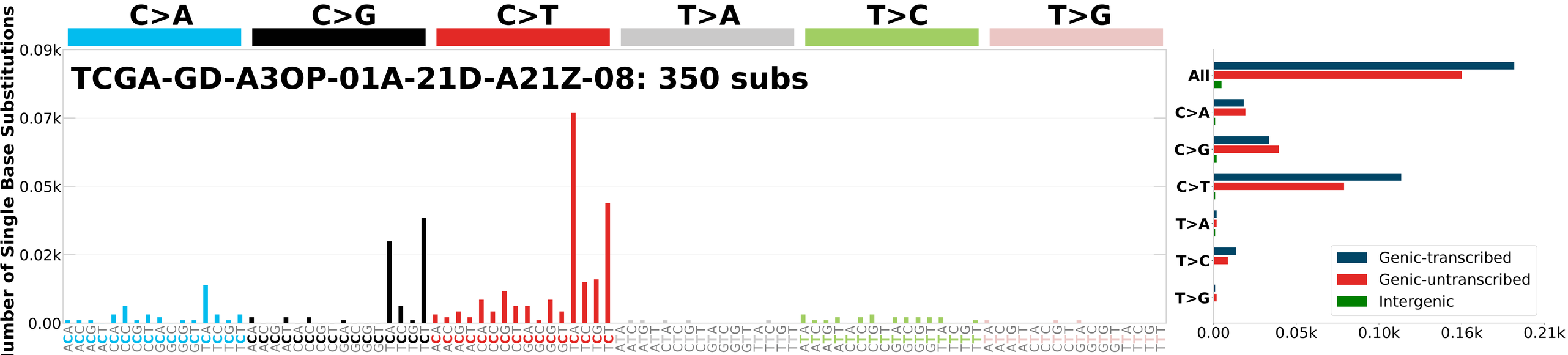

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GC-A3YS-01A-11D-A23M-08: 242 subs
Number of Single Base Substitutions
0.05k
0.04k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.14k

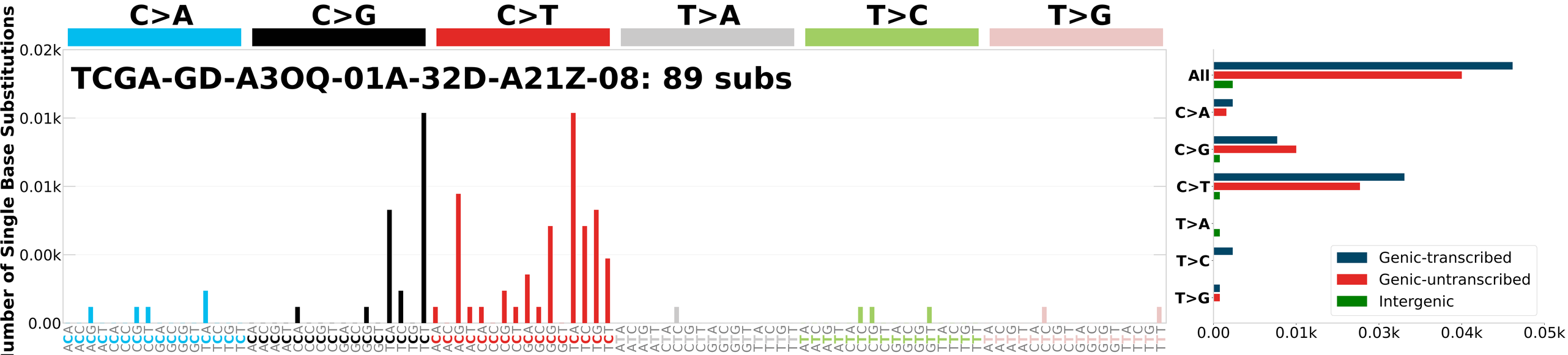

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GC-A4ZW-01A-11D-A26M-08: 655 subs
Number of Single Base Substitutions
0.17k
0.12k
0.08k
0.04k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.10k
0.20k
0.30k
0.40k

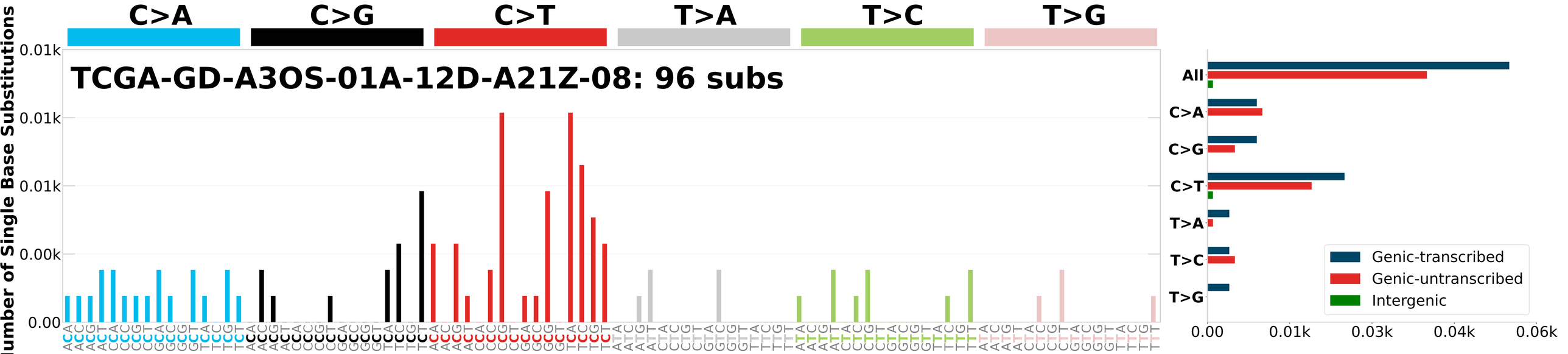

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GC-A6I1-01A-12D-A31L-08: 242 subs
Number of Single Base Substitutions
0.07k
0.05k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.13k

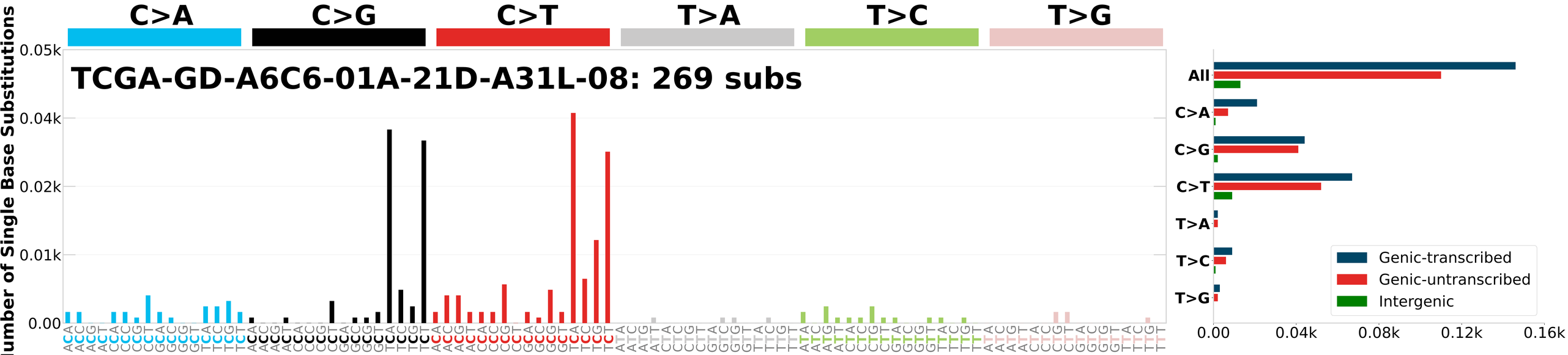

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GC-A6I3-01A-11D-A31L-08: 244 subs
Number of Single Base Substitutions
0.03k
0.02k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.13k

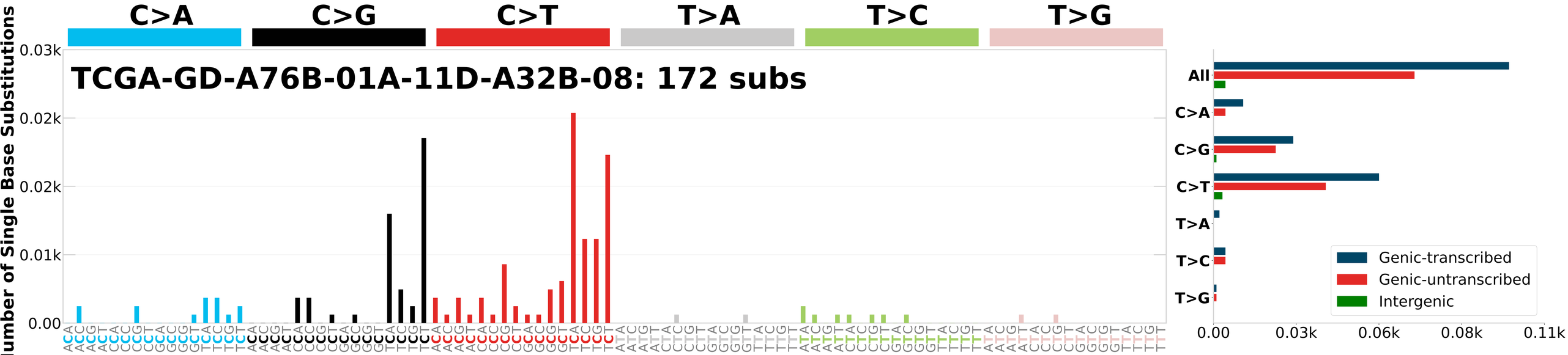

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GD-A2C5-01A-12D-A17V-08: 243 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.07k
0.11k
0.14k

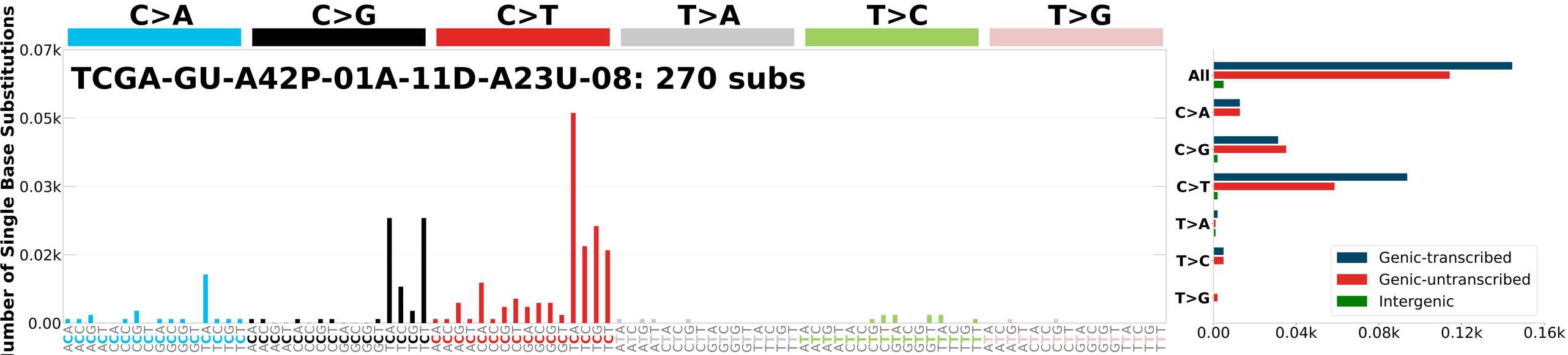

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GD-A3OP-01A-21D-A21Z-08: 350 subs
Number of Single Base Substitutions
0.09k
0.07k
0.05k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.10k
0.16k
0.21k

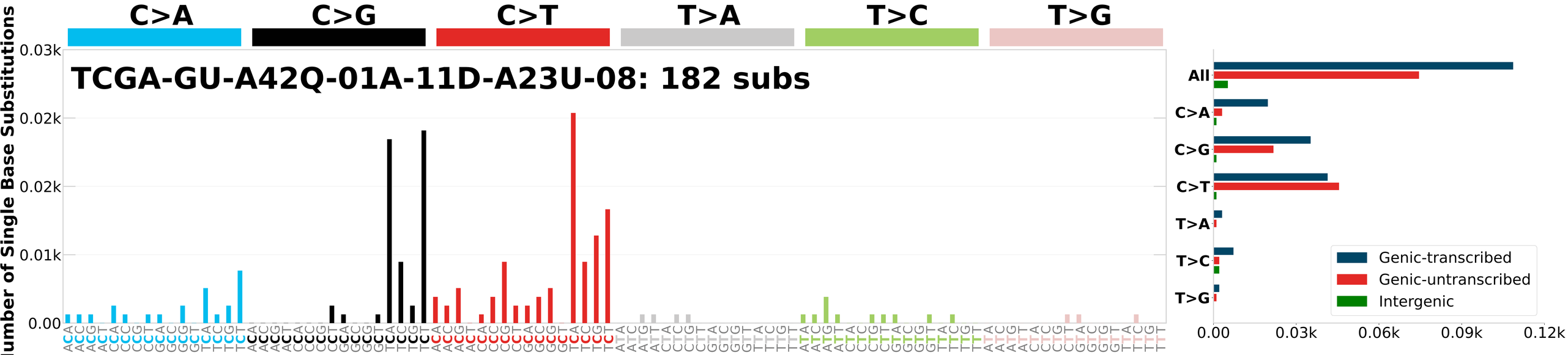

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GD-A3OQ-01A-32D-A21Z-08: 89 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

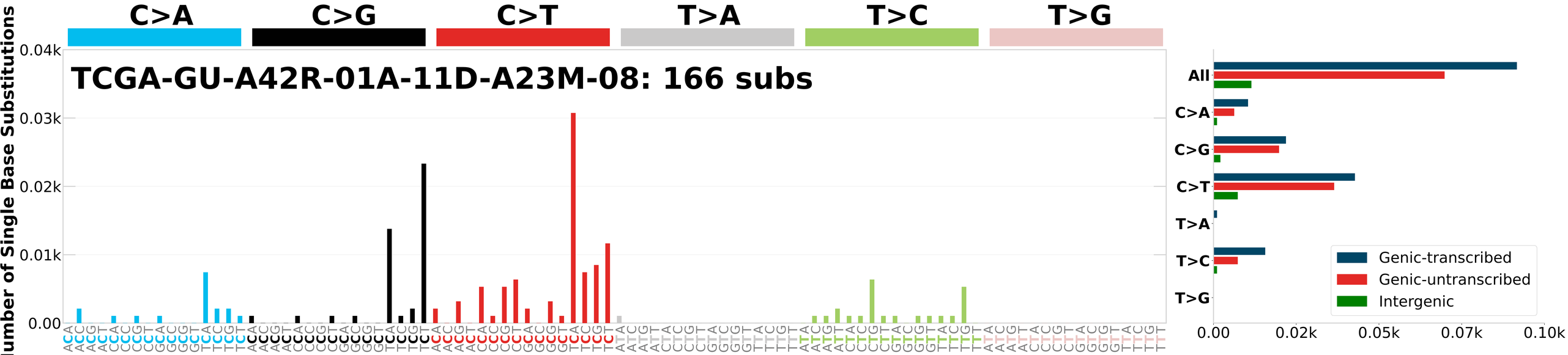

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GD-A3OS-01A-12D-A21Z-08: 96 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

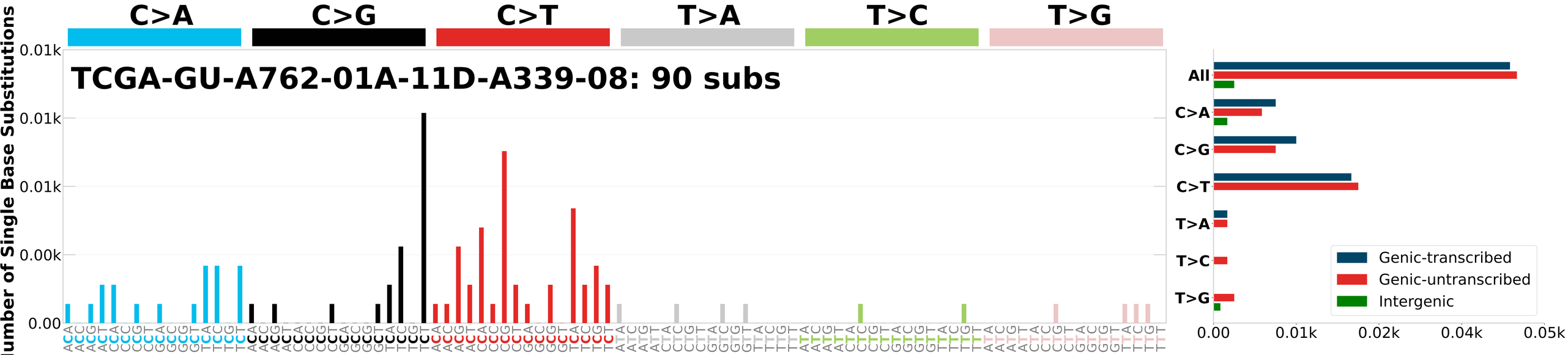

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GD-A6C6-01A-21D-A31L-08: 269 subs
Number of Single Base Substitutions
0.05k
0.04k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.12k
0.16k

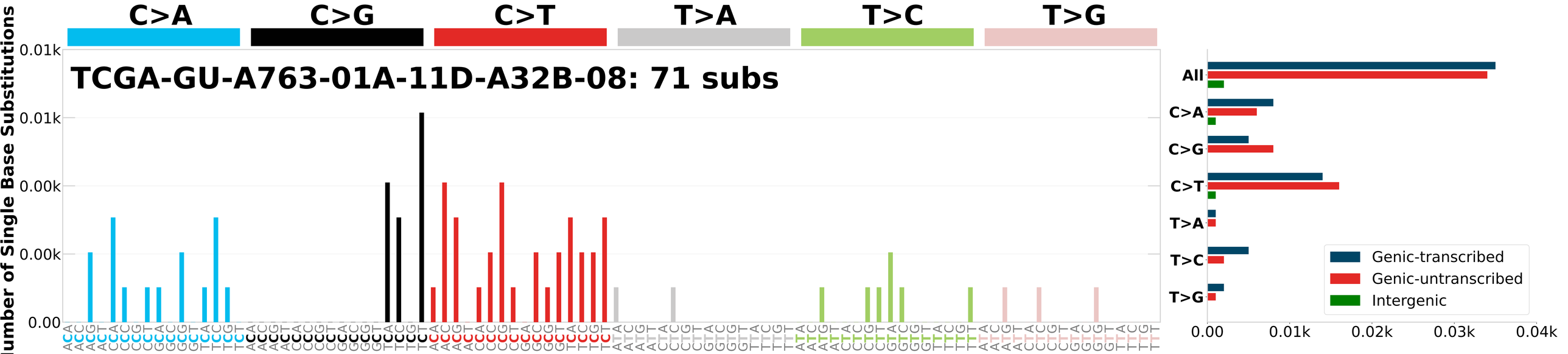

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GD-A76B-01A-11D-A32B-08: 172 subs
Number of Single Base Substitutions
0.03k
0.02k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.08k
0.11k

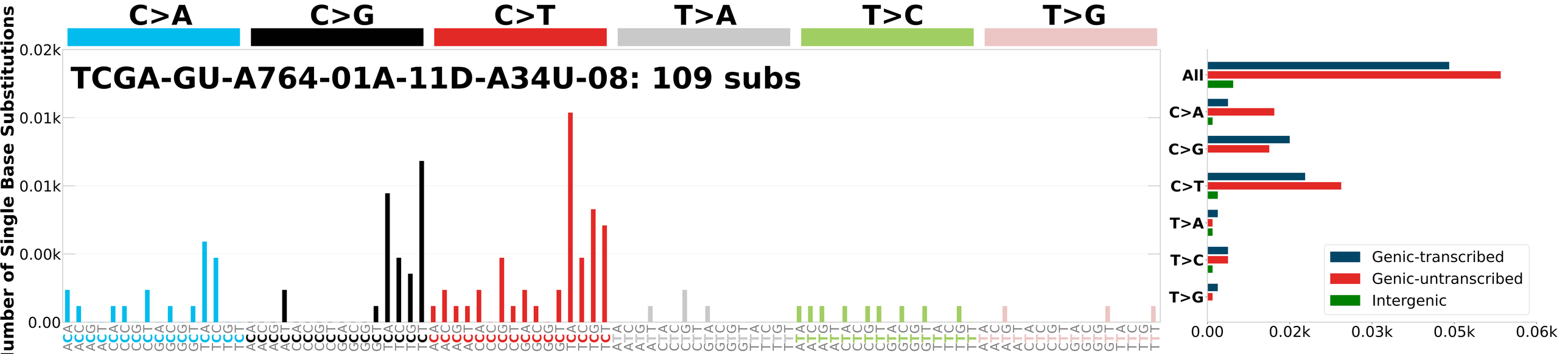

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GU-A42P-01A-11D-A23U-08: 270 subs
Number of Single Base Substitutions
0.07k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.12k
0.16k

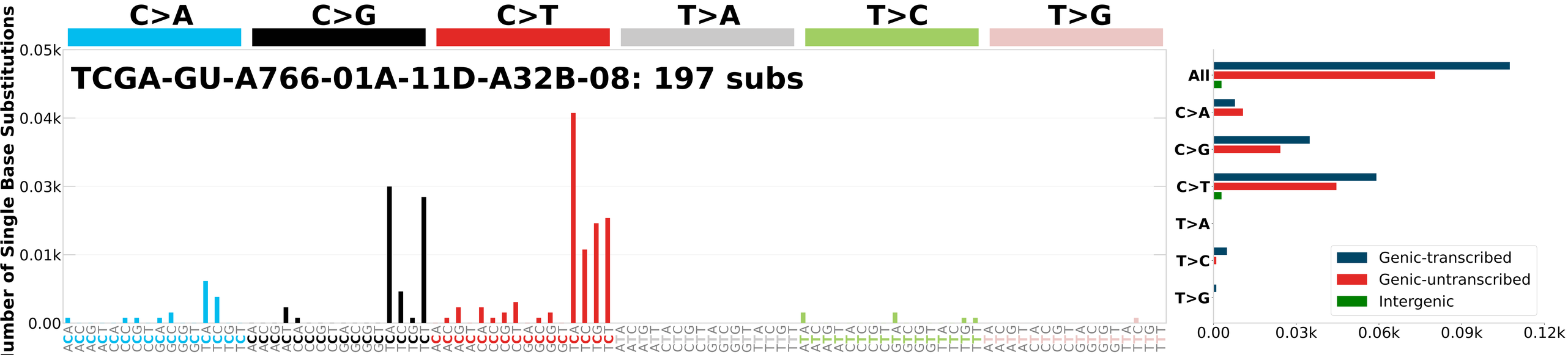

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GU-A42Q-01A-11D-A23U-08: 182 subs
Number of Single Base Substitutions
0.03k
0.02k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

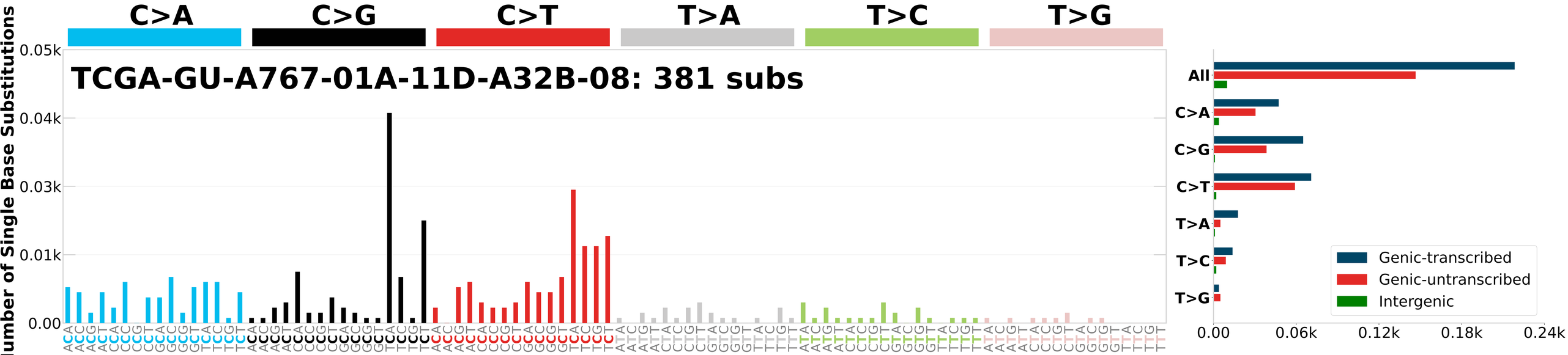

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GU-A42R-01A-11D-A23M-08: 166 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.10k

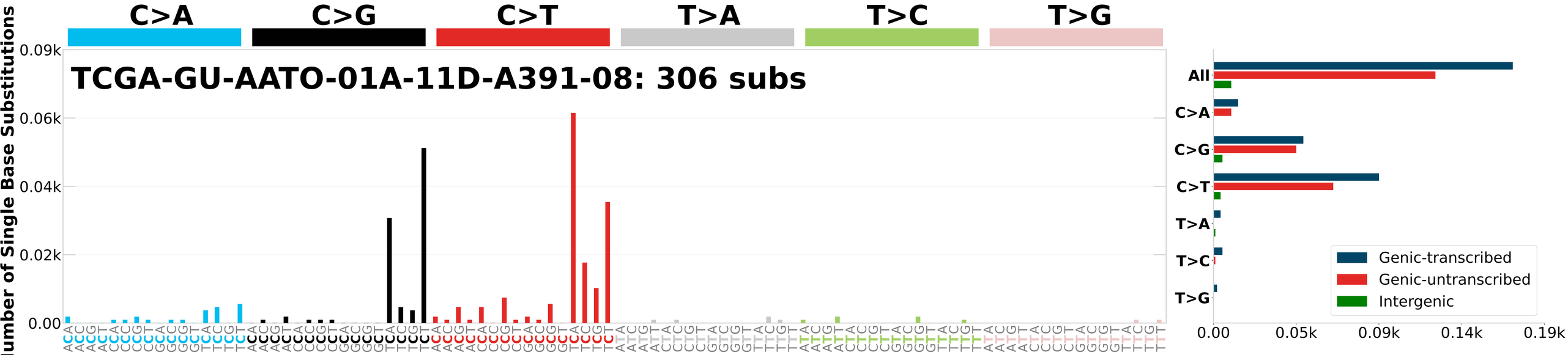

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GU-A762-01A-11D-A339-08: 90 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

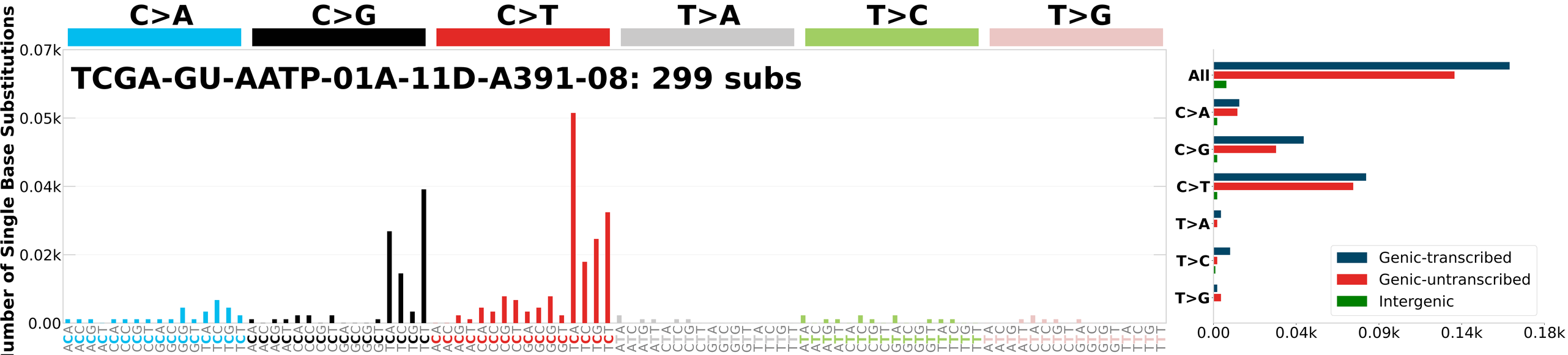

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GU-A763-01A-11D-A32B-08: 71 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

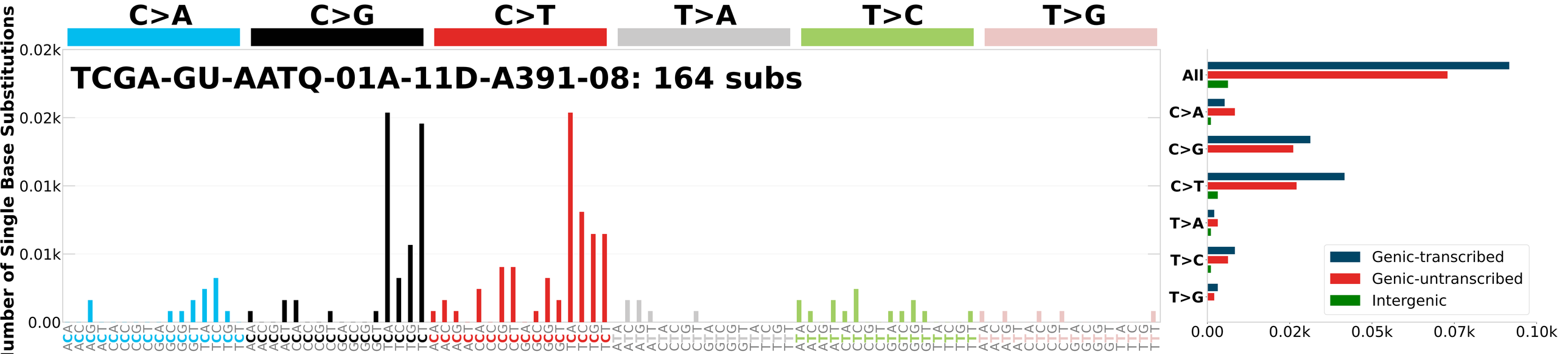

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GU-A764-01A-11D-A34U-08: 109 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.06k

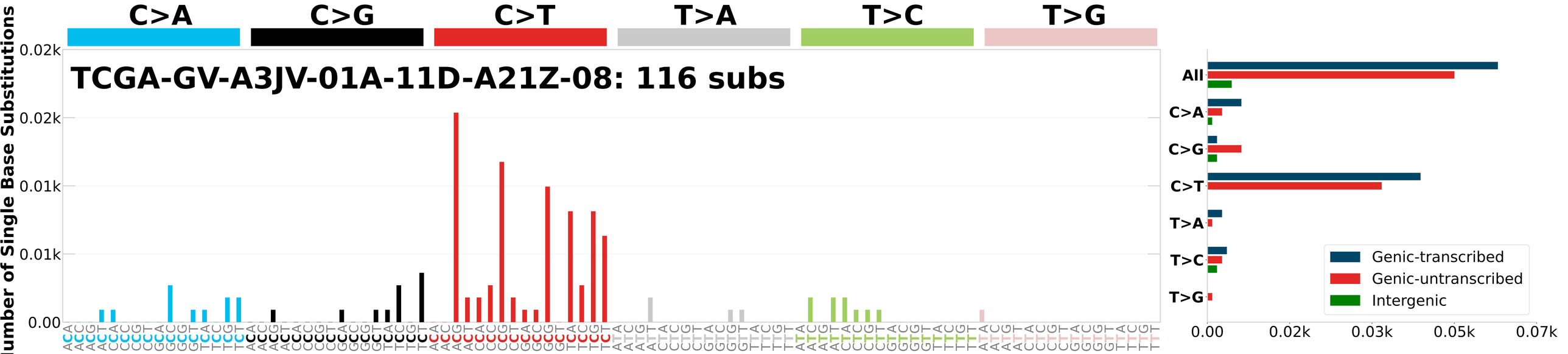

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GU-A766-01A-11D-A32B-08: 197 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

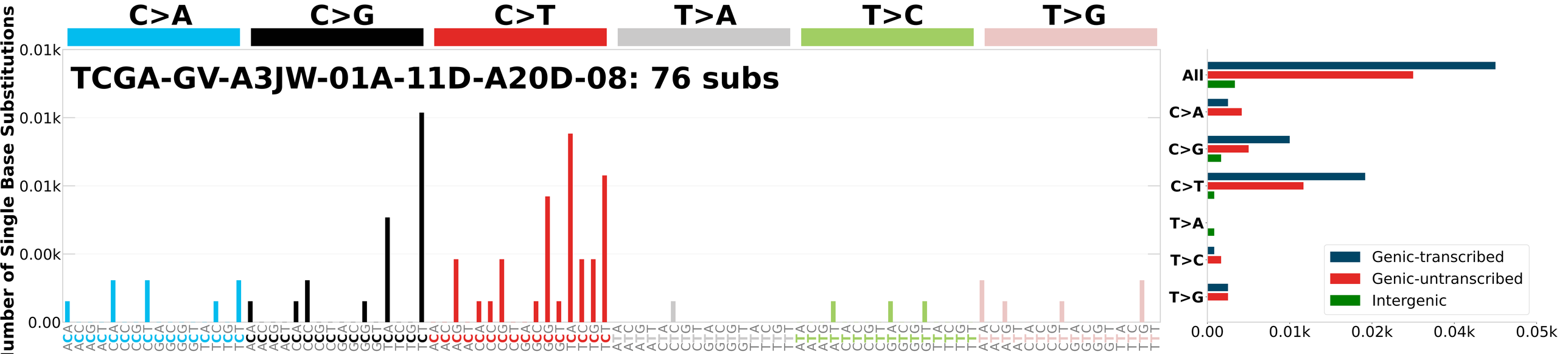

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GU-A767-01A-11D-A32B-08: 381 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.12k
0.18k
0.24k

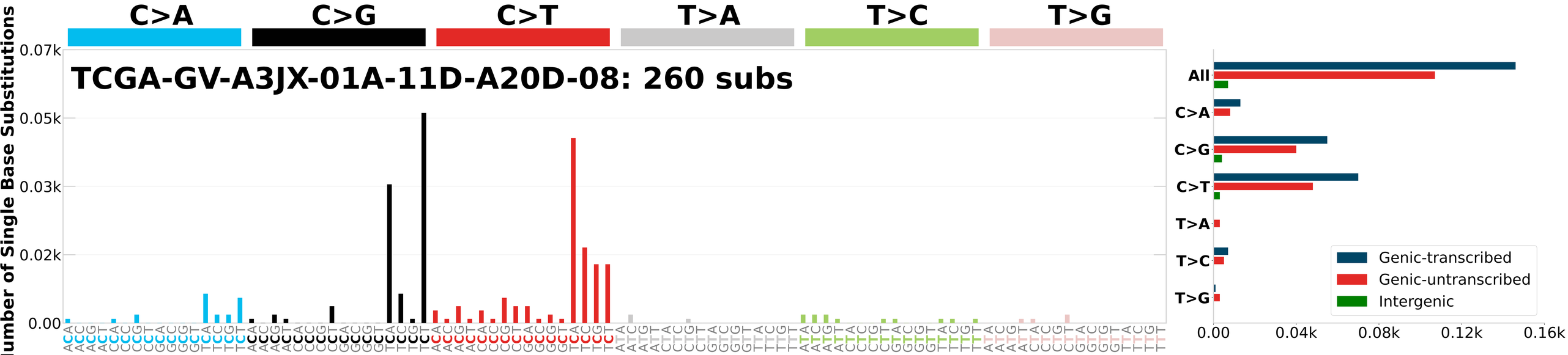

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GU-AATO-01A-11D-A391-08: 306 subs
Number of Single Base Substitutions
0.09k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.09k
0.14k
0.19k

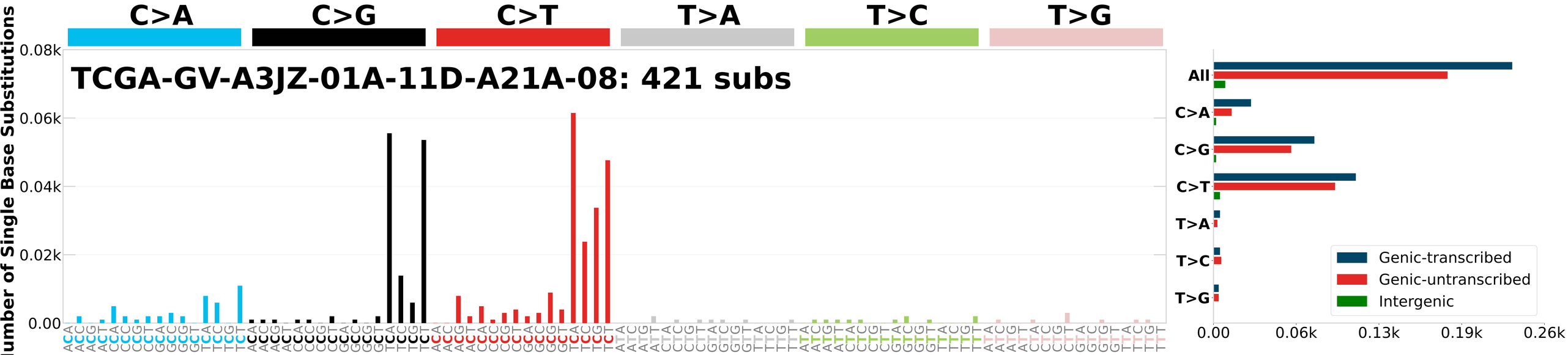

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GU-AATP-01A-11D-A391-08: 299 subs
Number of Single Base Substitutions
0.07k
0.05k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.09k
0.14k
0.18k

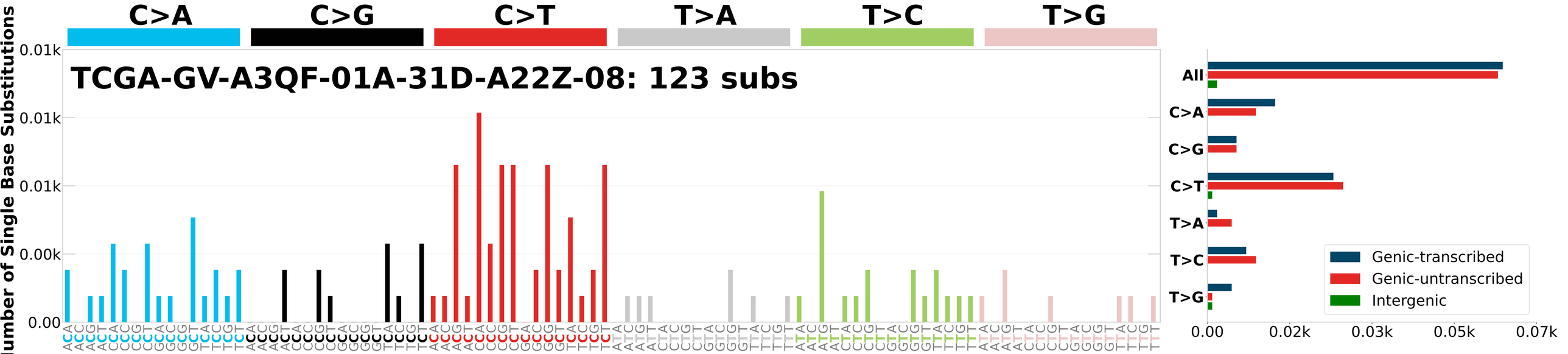

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GU-AATQ-01A-11D-A391-08: 164 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.10k

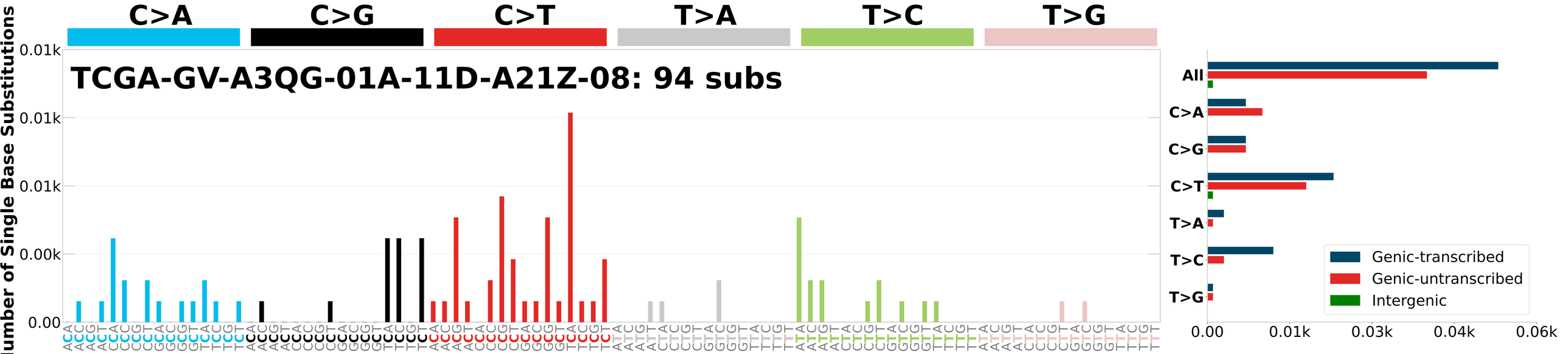

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GV-A3JV-01A-11D-A21Z-08: 116 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.07k

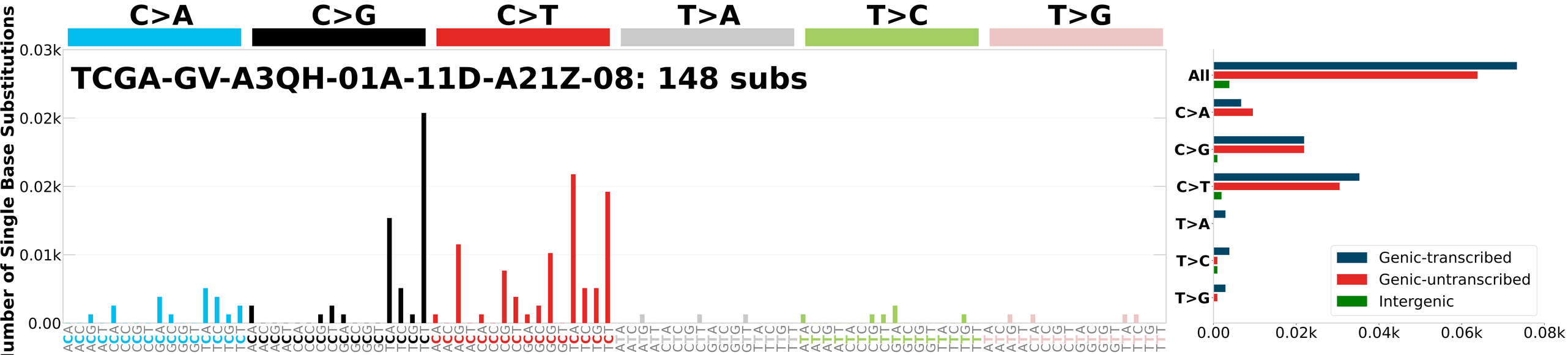

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GV-A3JW-01A-11D-A20D-08: 76 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

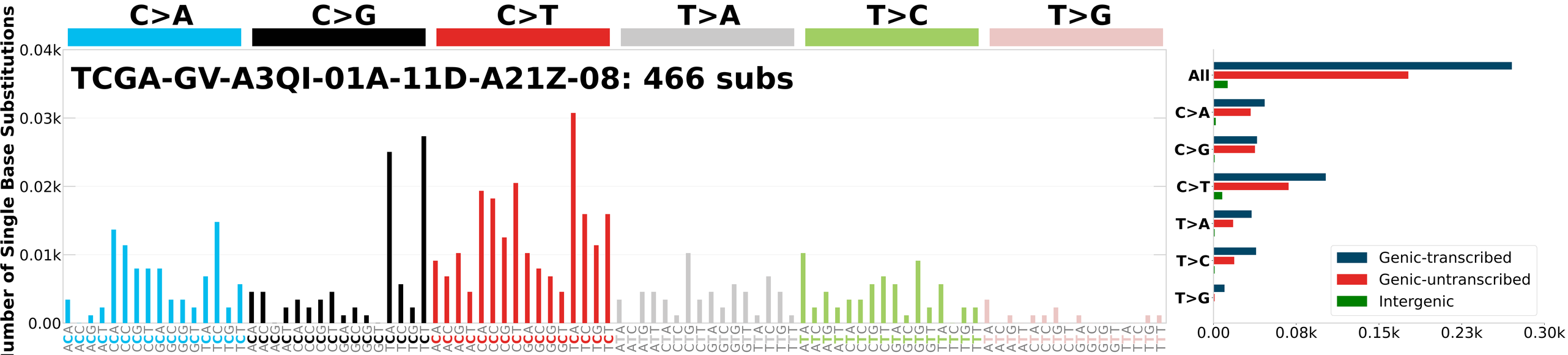

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GV-A3JX-01A-11D-A20D-08: 260 subs
Number of Single Base Substitutions
0.07k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.12k
0.16k

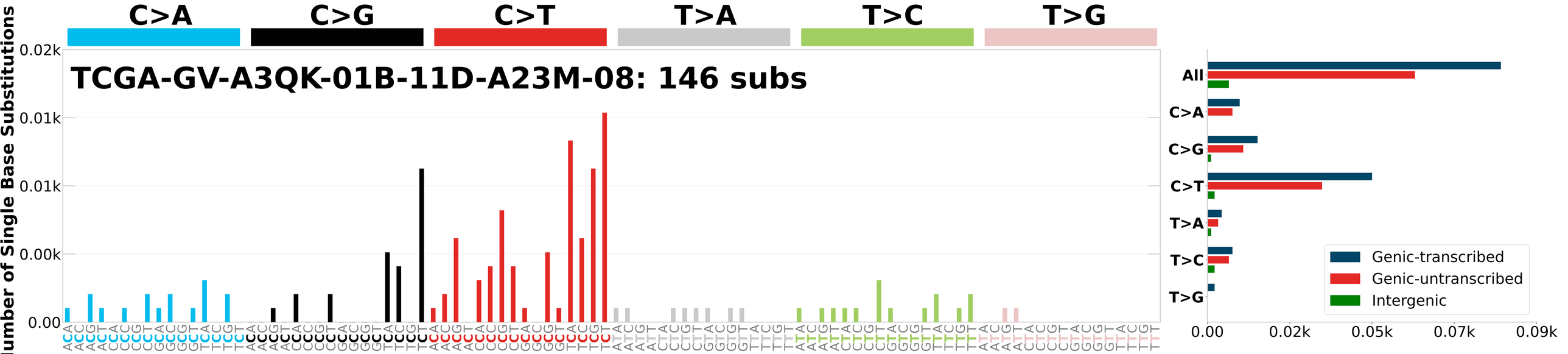

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GV-A3JZ-01A-11D-A21A-08: 421 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.13k
0.19k
0.26k

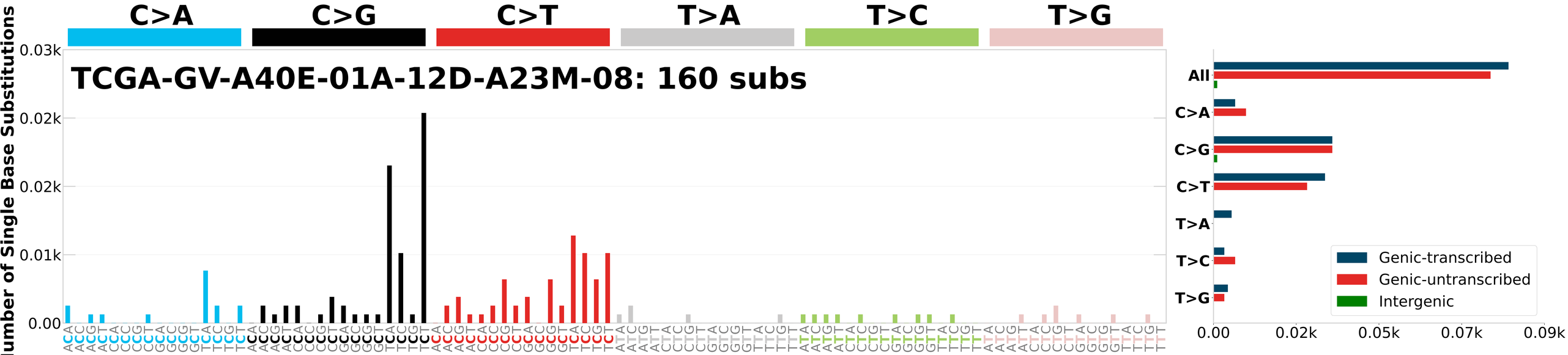

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GV-A3QF-01A-31D-A22Z-08: 123 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.07k

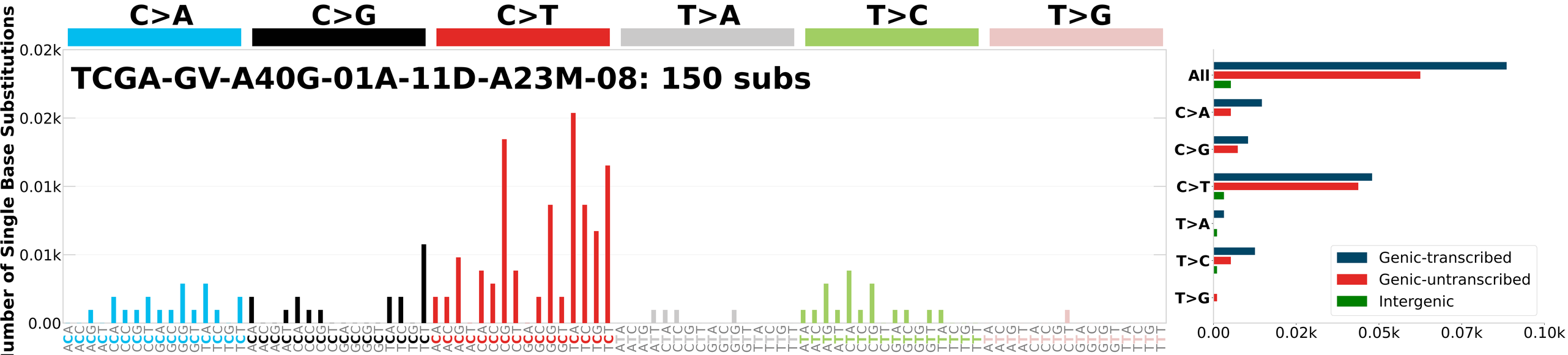

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GV-A3QG-01A-11D-A21Z-08: 94 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

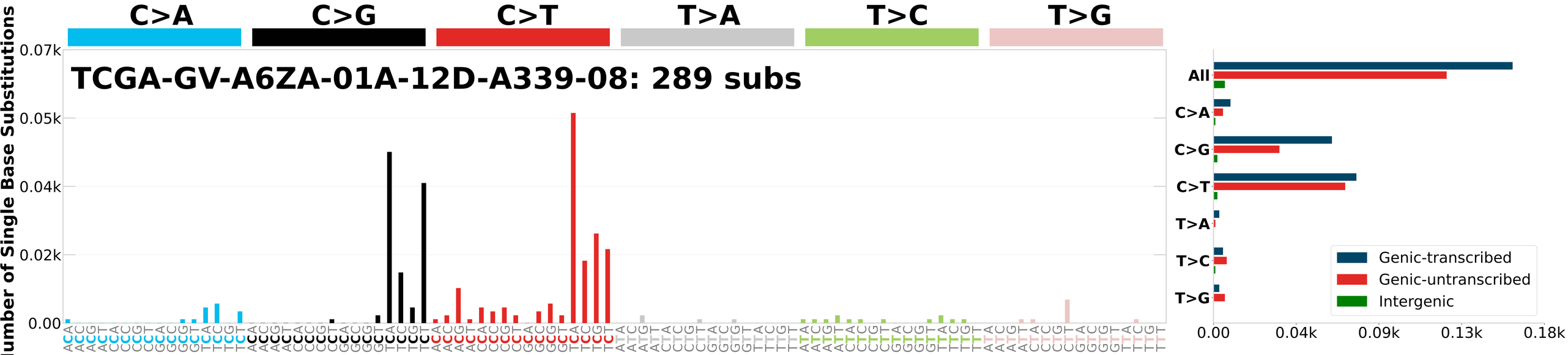

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GV-A3QH-01A-11D-A21Z-08: 148 subs
Number of Single Base Substitutions
0.03k
0.02k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

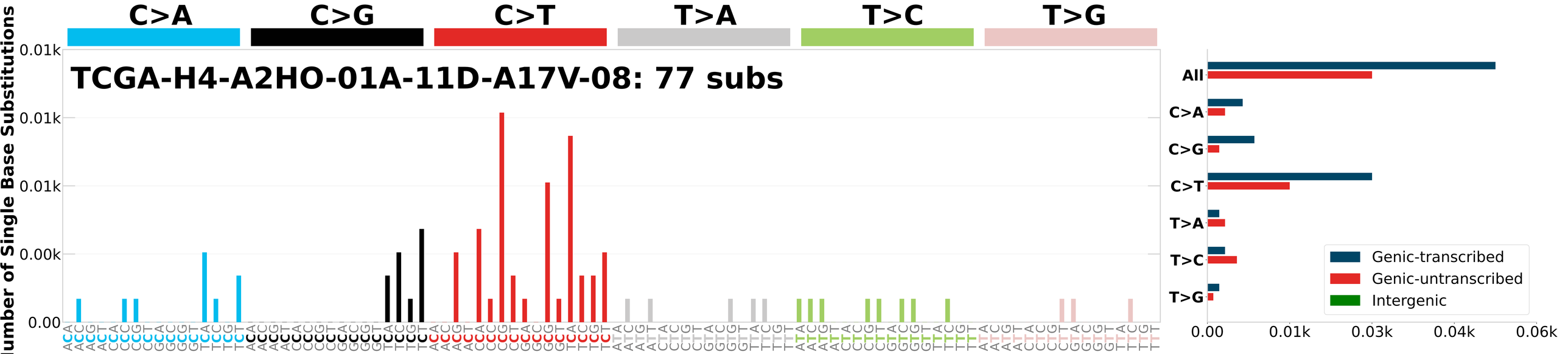

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GV-A3QI-01A-11D-A21Z-08: 466 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.08k
0.15k
0.23k
0.30k

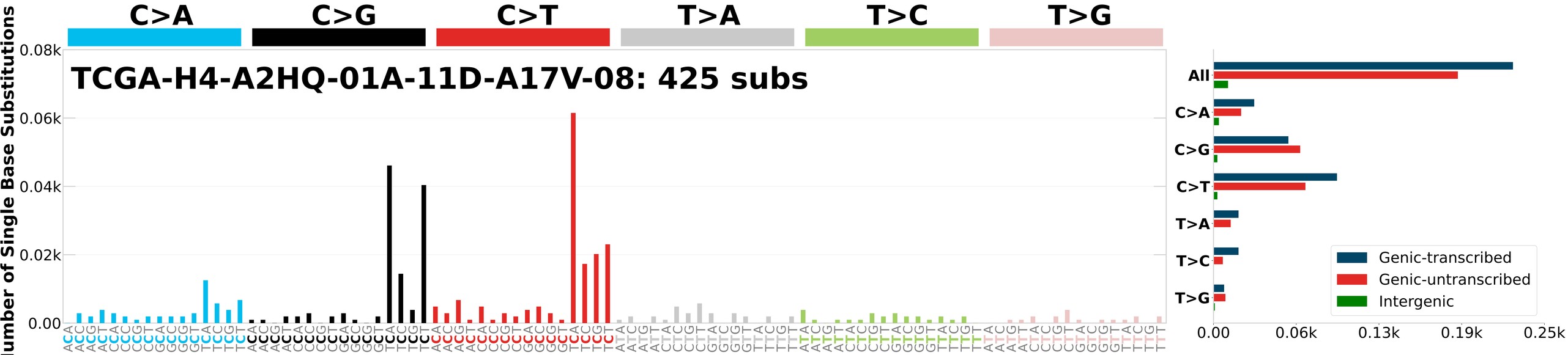

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GV-A3QK-01B-11D-A23M-08: 146 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.09k

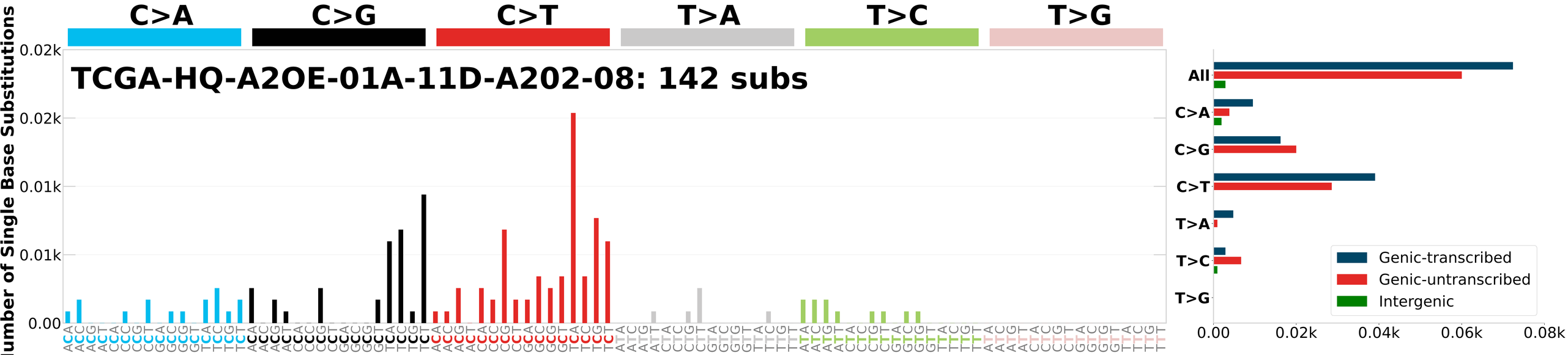

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GV-A40E-01A-12D-A23M-08: 160 subs
Number of Single Base Substitutions
0.03k
0.02k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.09k

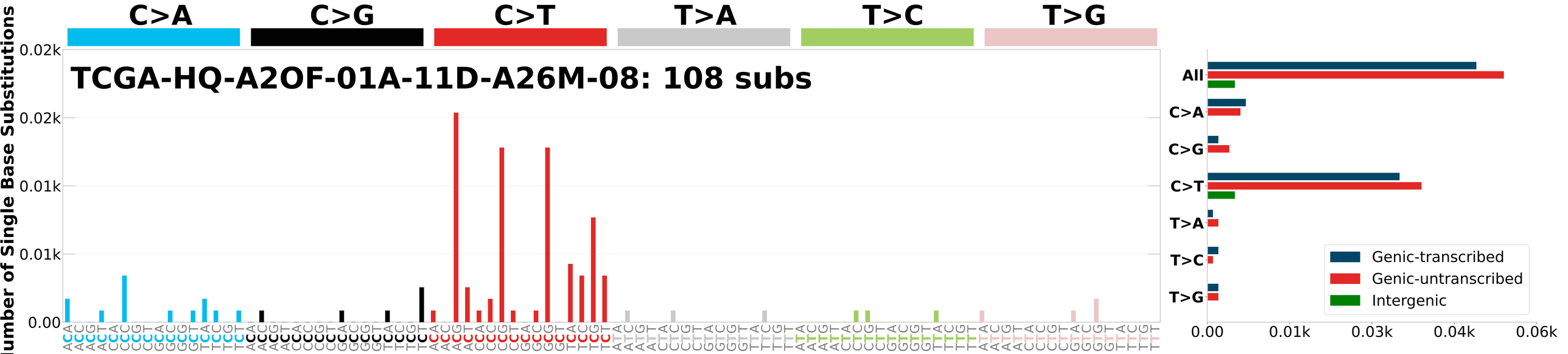

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GV-A40G-01A-11D-A23M-08: 150 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.10k

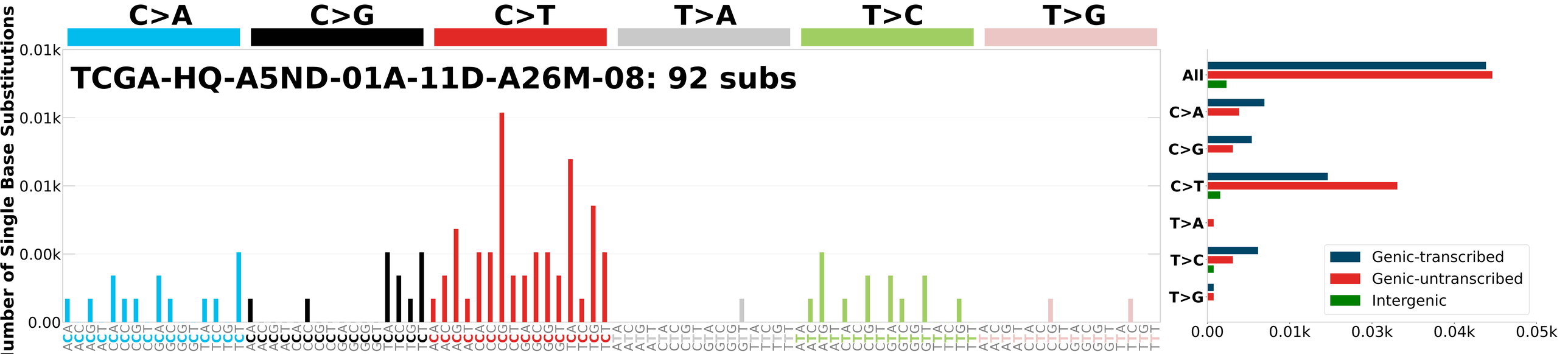

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-GV-A6ZA-01A-12D-A339-08: 289 subs
Number of Single Base Substitutions
0.07k
0.05k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.09k
0.13k
0.18k

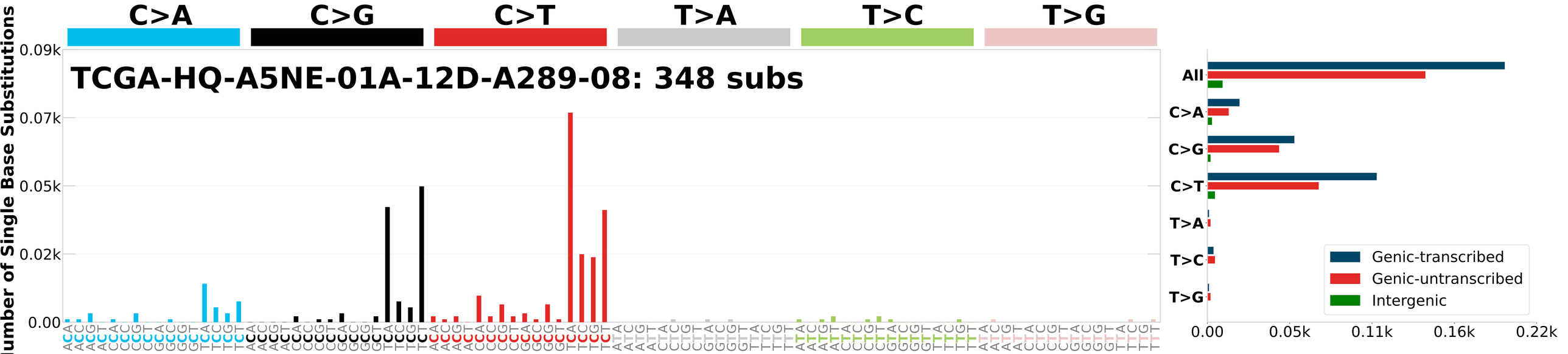

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-H4-A2HO-01A-11D-A17V-08: 77 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

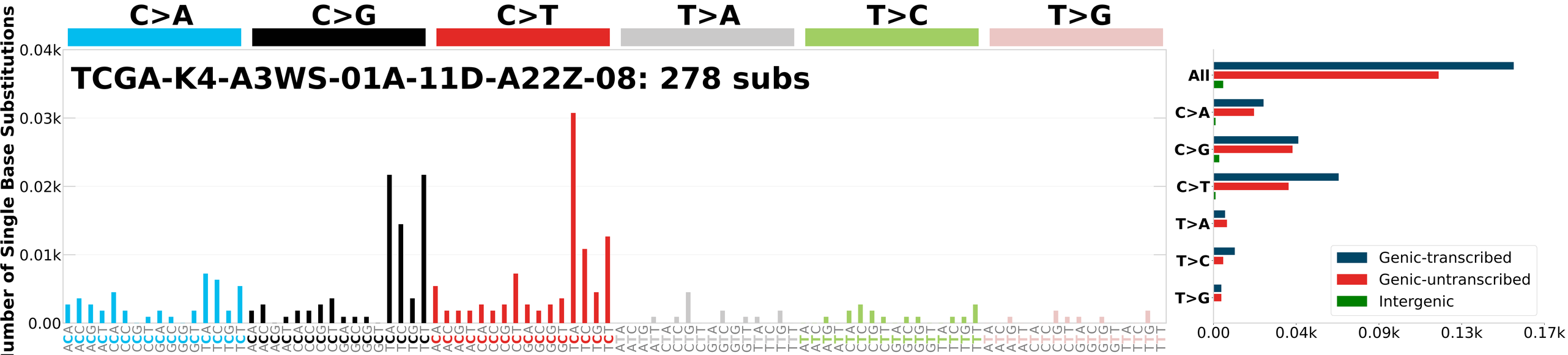

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-H4-A2HQ-01A-11D-A17V-08: 425 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.13k
0.19k
0.25k

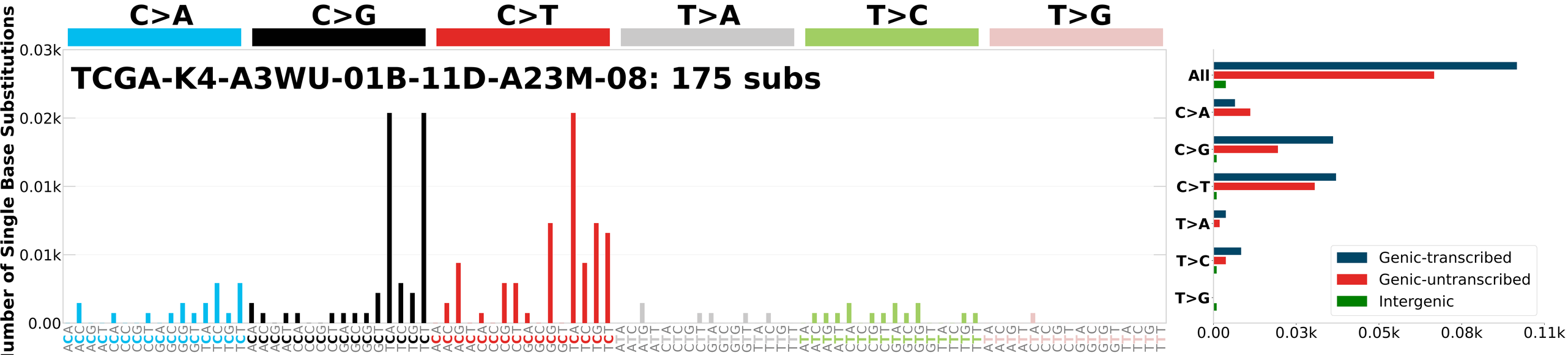

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-HQ-A2OE-01A-11D-A202-08: 142 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

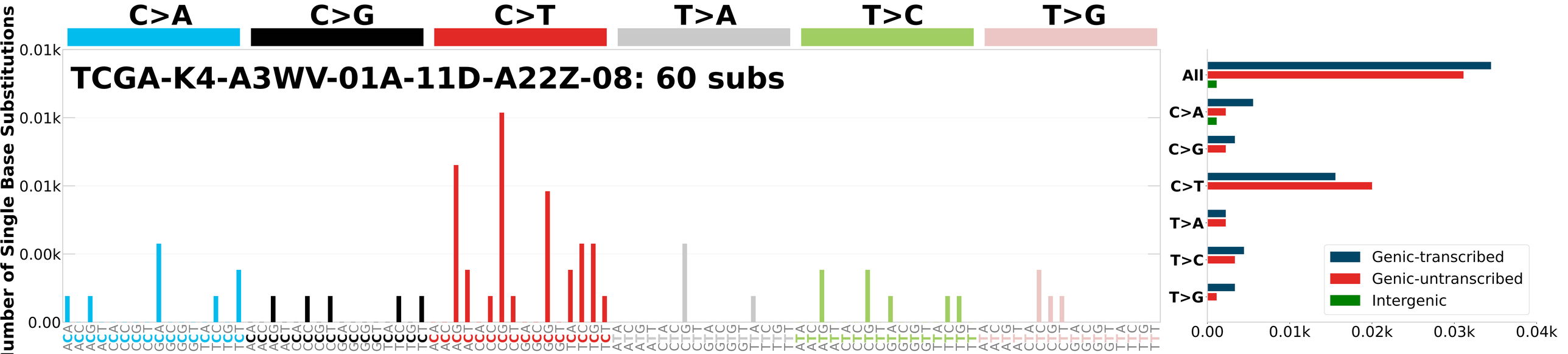

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-HQ-A2OF-01A-11D-A26M-08: 108 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

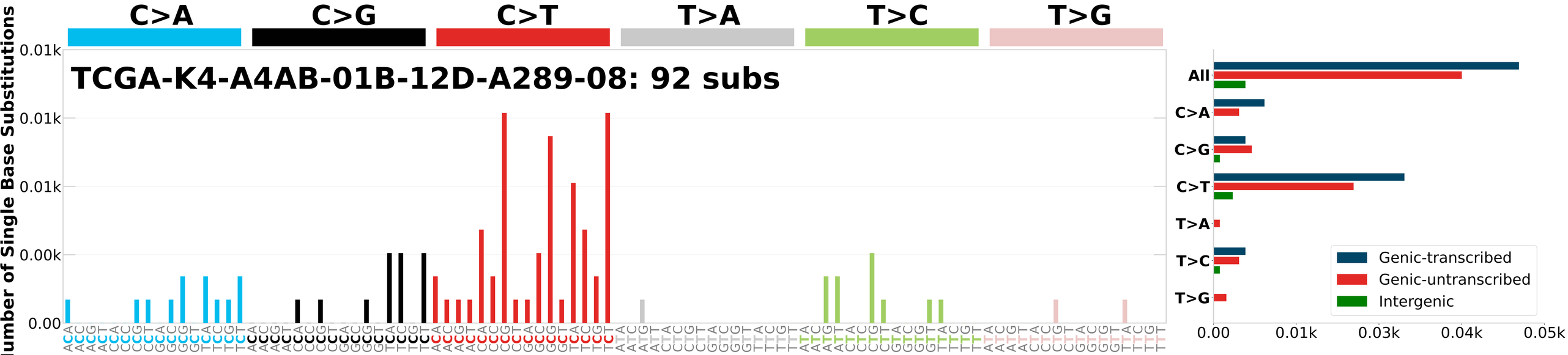

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-HQ-A5ND-01A-11D-A26M-08: 92 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

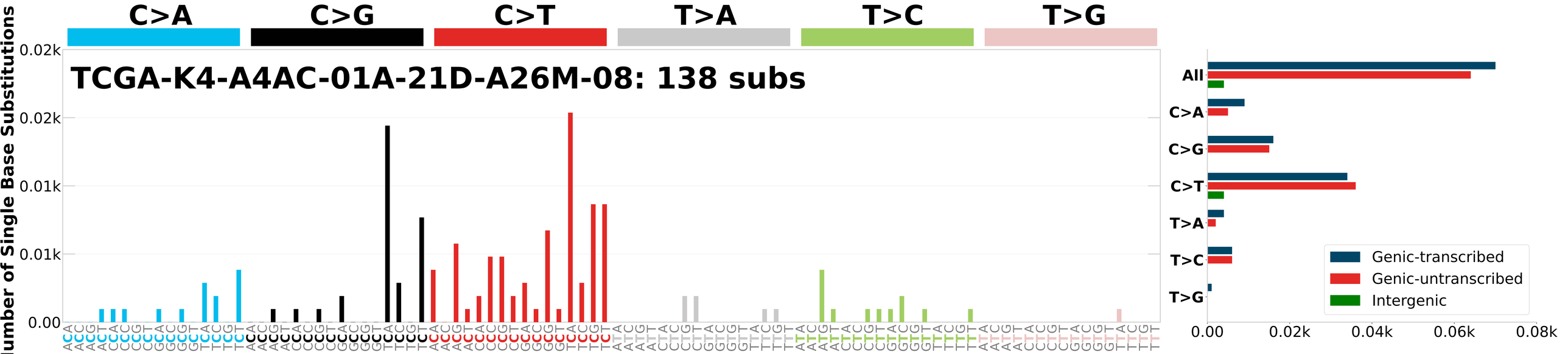

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-HQ-A5NE-01A-12D-A289-08: 348 subs
Number of Single Base Substitutions
0.09k
0.07k
0.05k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.11k
0.16k
0.22k

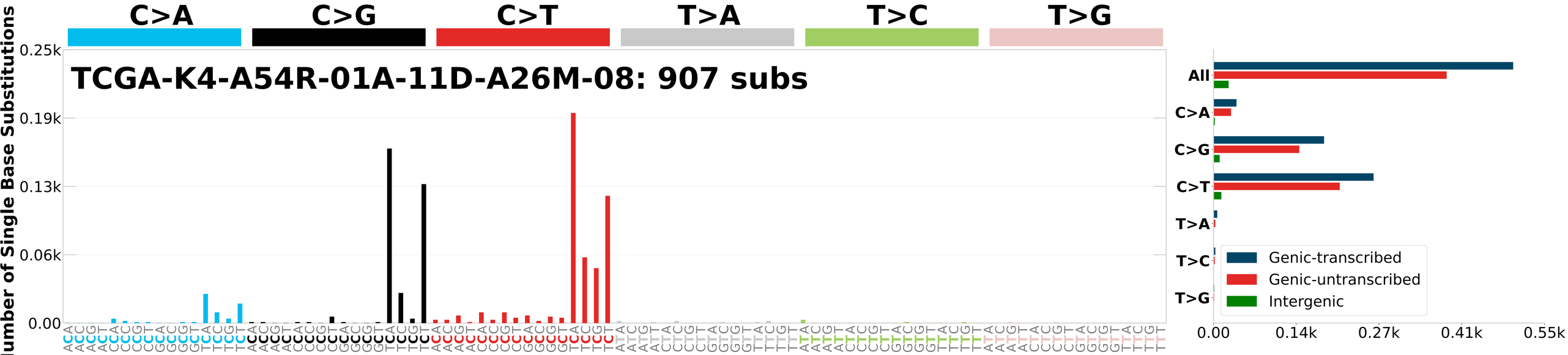

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-K4-A3WS-01A-11D-A22Z-08: 278 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.09k
0.13k
0.17k

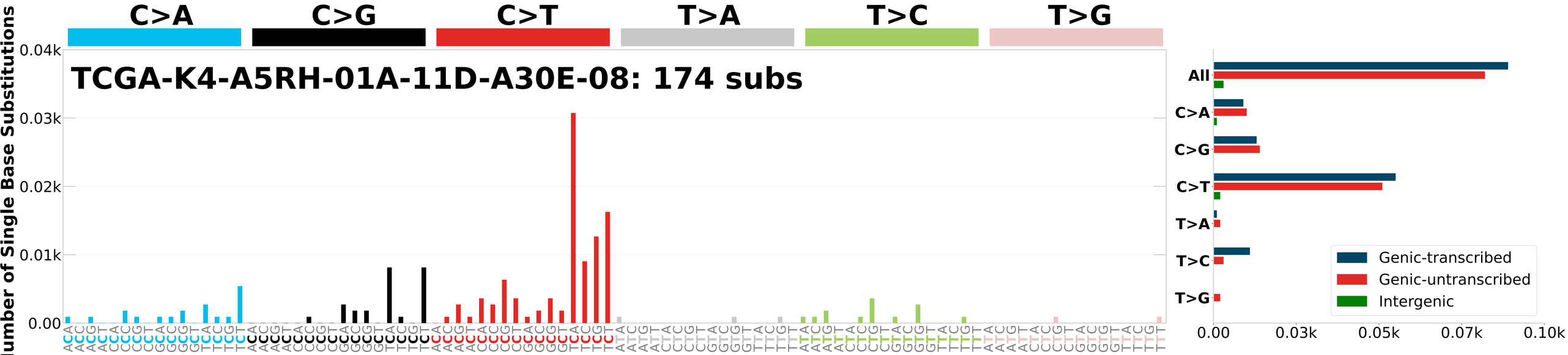

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-K4-A3WU-01B-11D-A23M-08: 175 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.11k

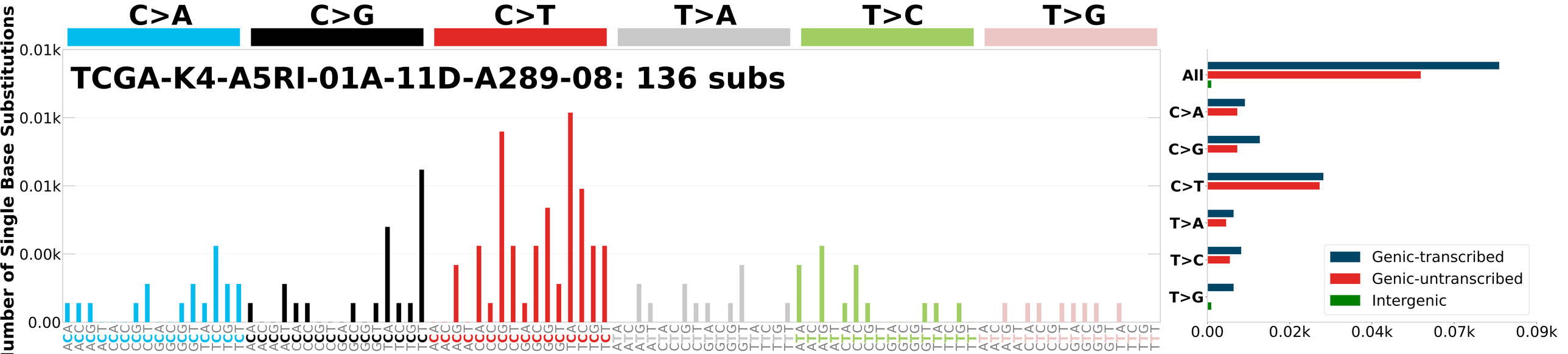

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-K4-A3WV-01A-11D-A22Z-08: 60 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

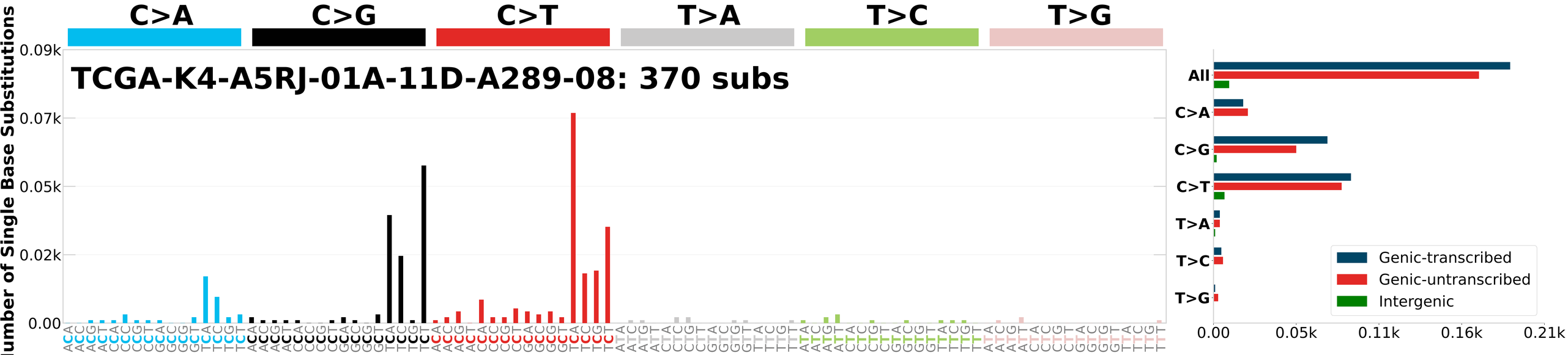

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-K4-A4AB-01B-12D-A289-08: 92 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

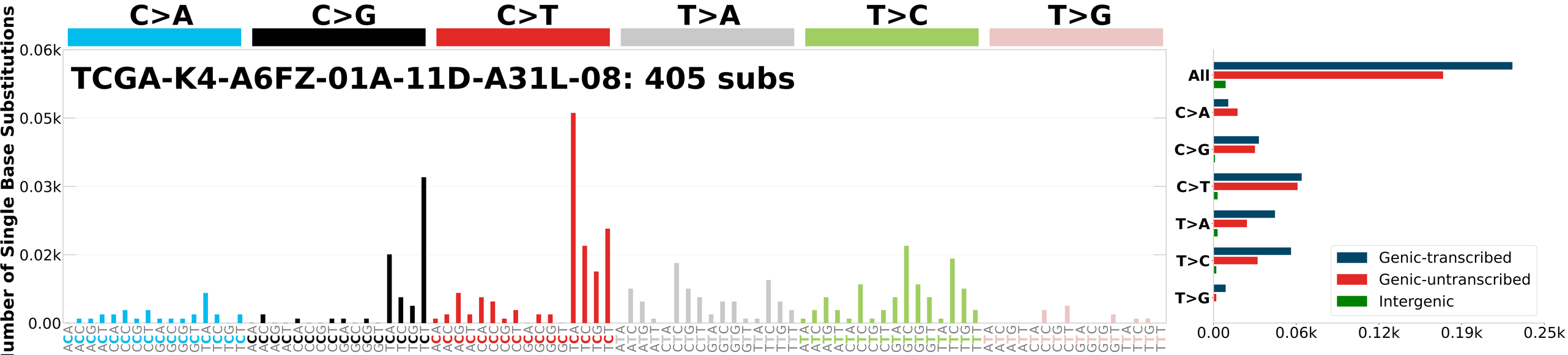

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-K4-A4AC-01A-21D-A26M-08: 138 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

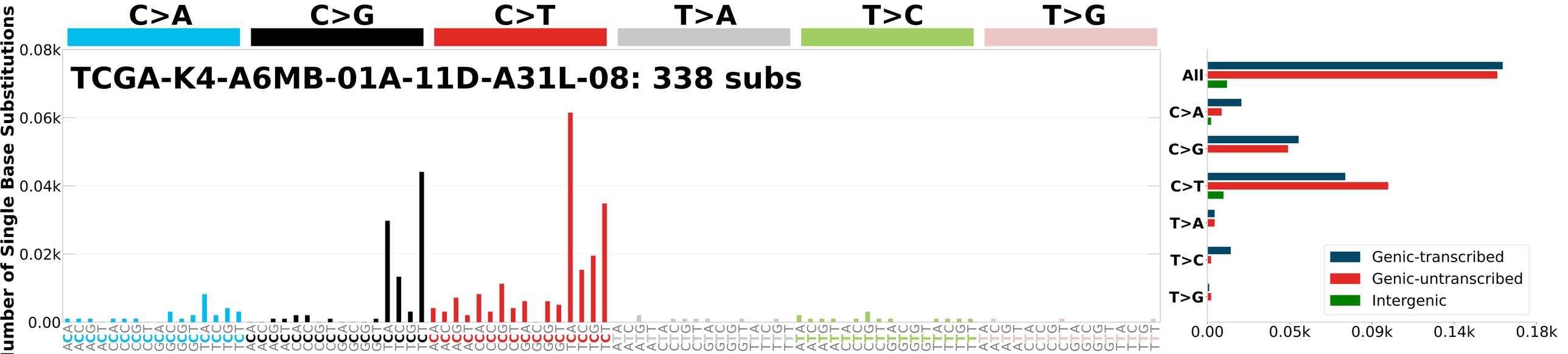

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-K4-A54R-01A-11D-A26M-08: 907 subs
Number of Single Base Substitutions
0.25k
0.19k
0.13k
0.06k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.14k
0.27k
0.41k
0.55k

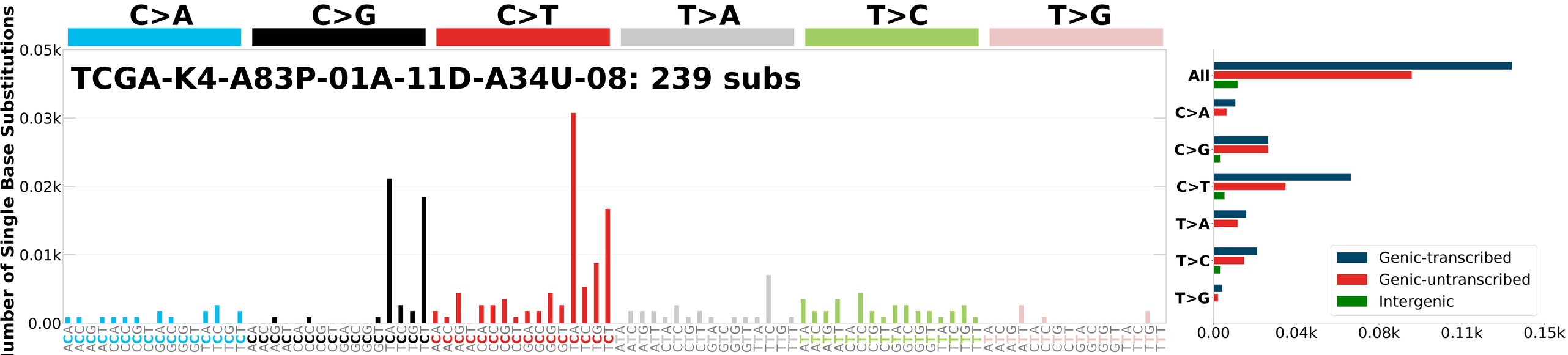

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-K4-A5RH-01A-11D-A30E-08: 174 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.07k
0.10k

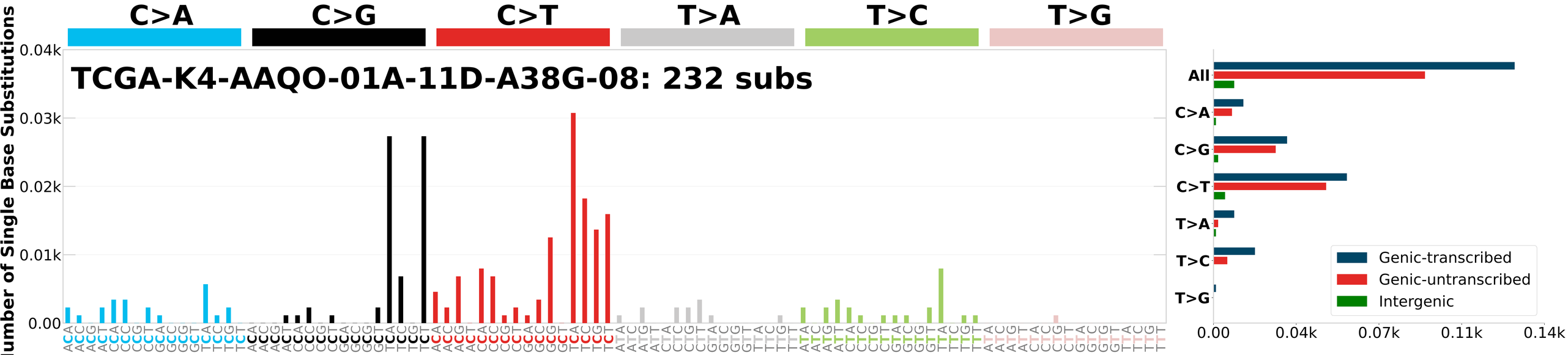

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-K4-A5RI-01A-11D-A289-08: 136 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.07k
0.09k

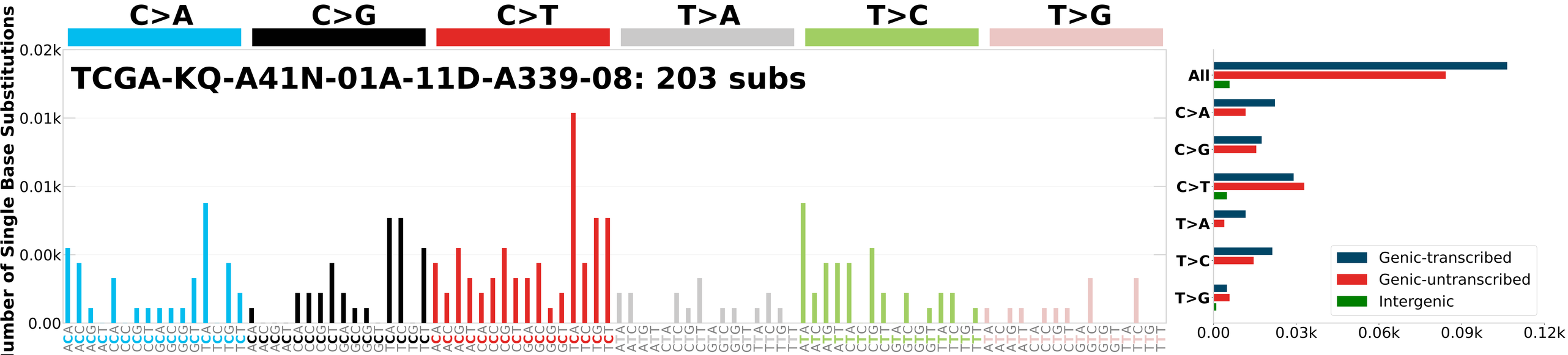

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-K4-A5RJ-01A-11D-A289-08: 370 subs
Number of Single Base Substitutions
0.09k
0.07k
0.05k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.11k
0.16k
0.21k

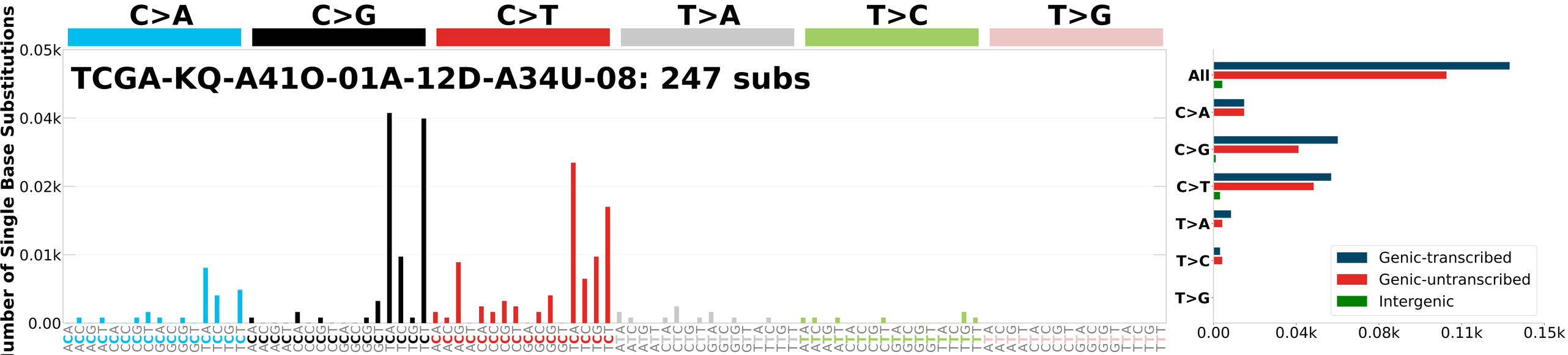

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-K4-A6FZ-01A-11D-A31L-08: 405 subs
Number of Single Base Substitutions
0.06k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.06k
0.12k
0.19k
0.25k

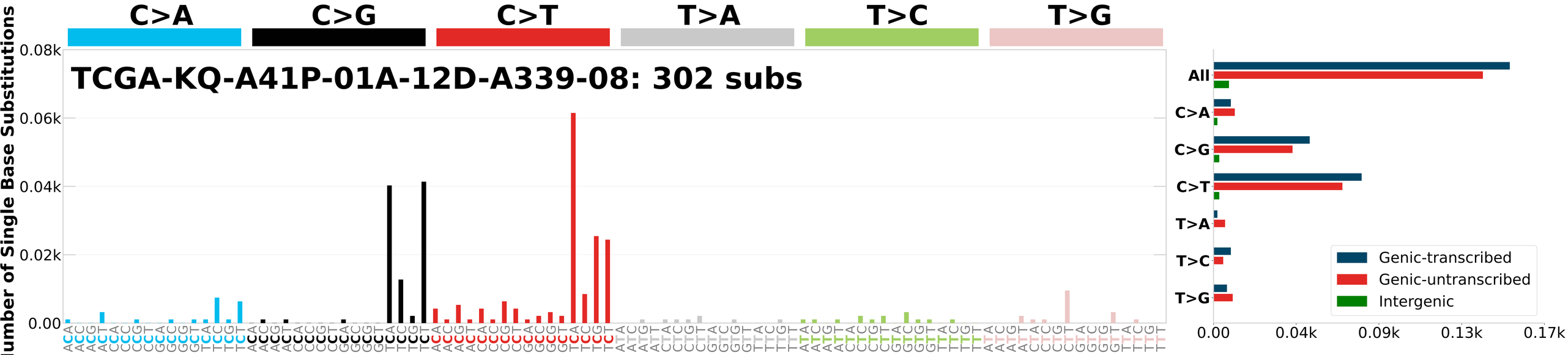

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-K4-A6MB-01A-11D-A31L-08: 338 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.09k
0.14k
0.18k

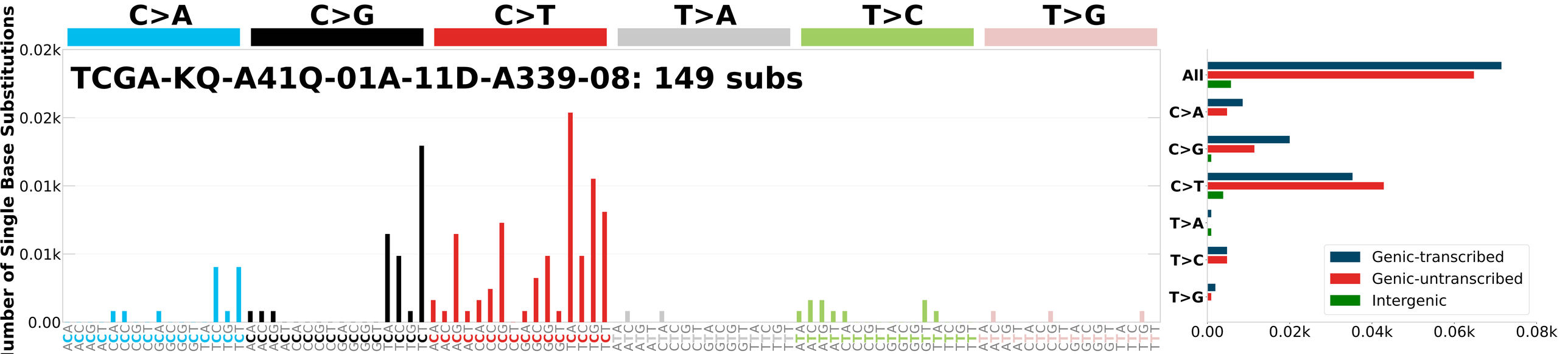

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-K4-A83P-01A-11D-A34U-08: 239 subs
Number of Single Base Substitutions
0.05k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.11k
0.15k

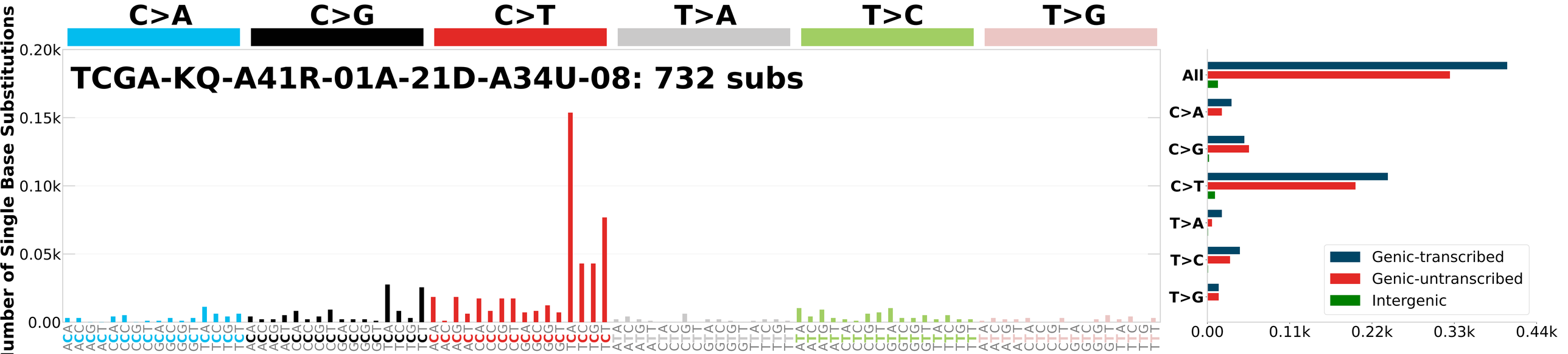

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-K4-AAQO-01A-11D-A38G-08: 232 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.07k
0.11k
0.14k

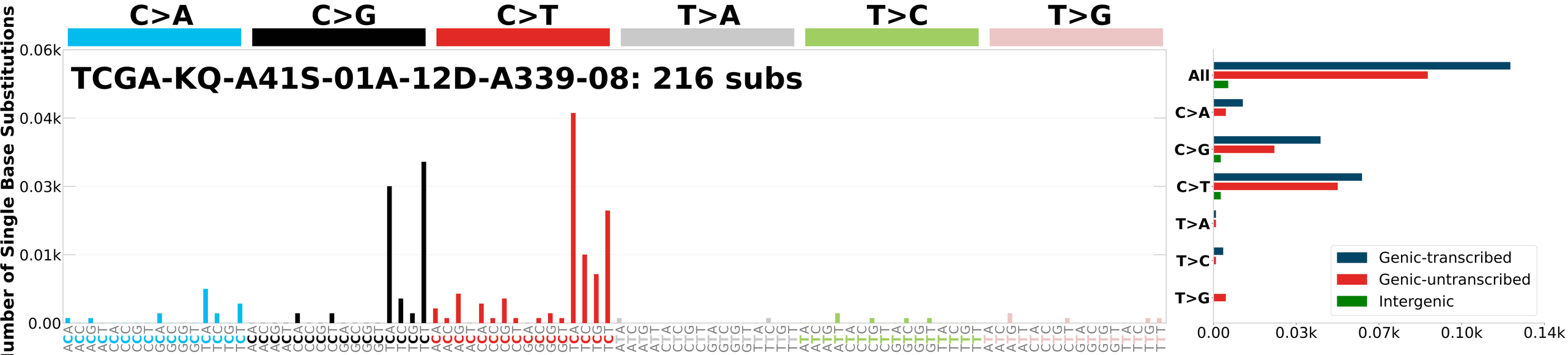

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-KQ-A41N-01A-11D-A339-08: 203 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

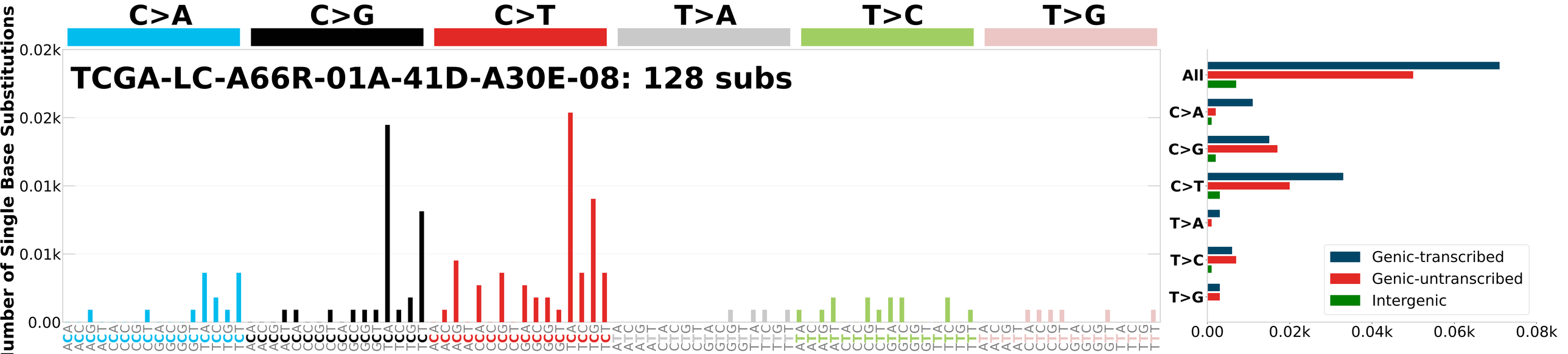

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-KQ-A41O-01A-12D-A34U-08: 247 subs
Number of Single Base Substitutions
0.05k
0.04k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.11k
0.15k

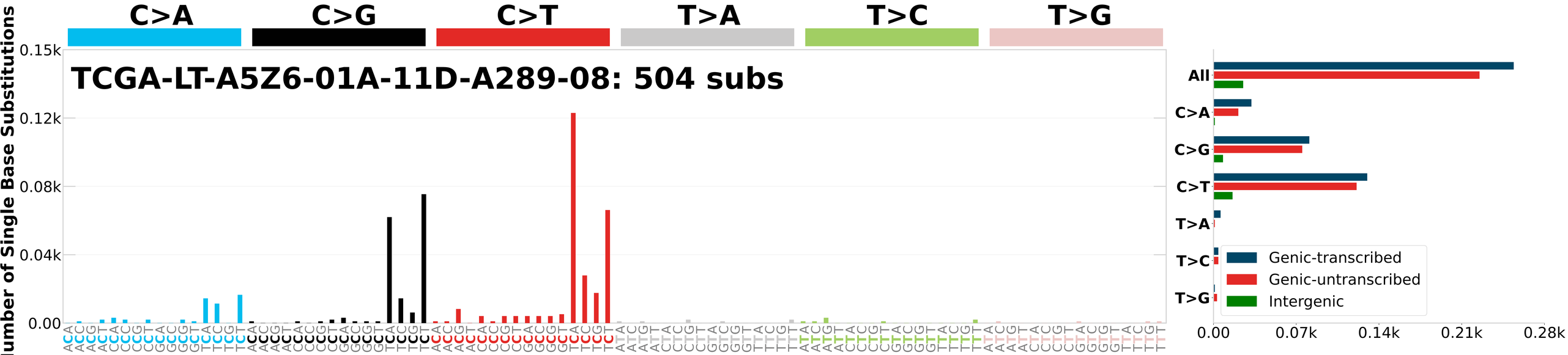

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-KQ-A41P-01A-12D-A339-08: 302 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.09k
0.13k
0.17k

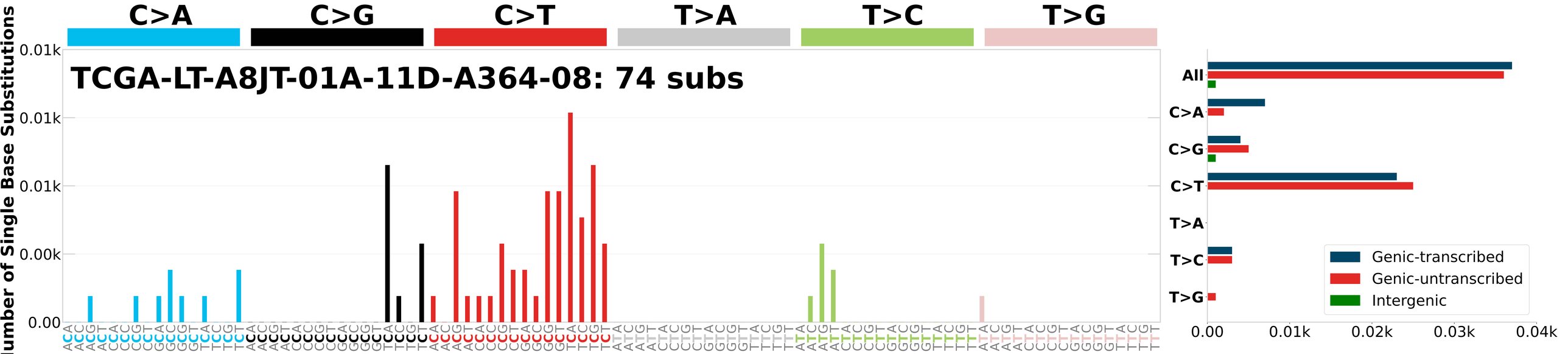

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-KQ-A41Q-01A-11D-A339-08: 149 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

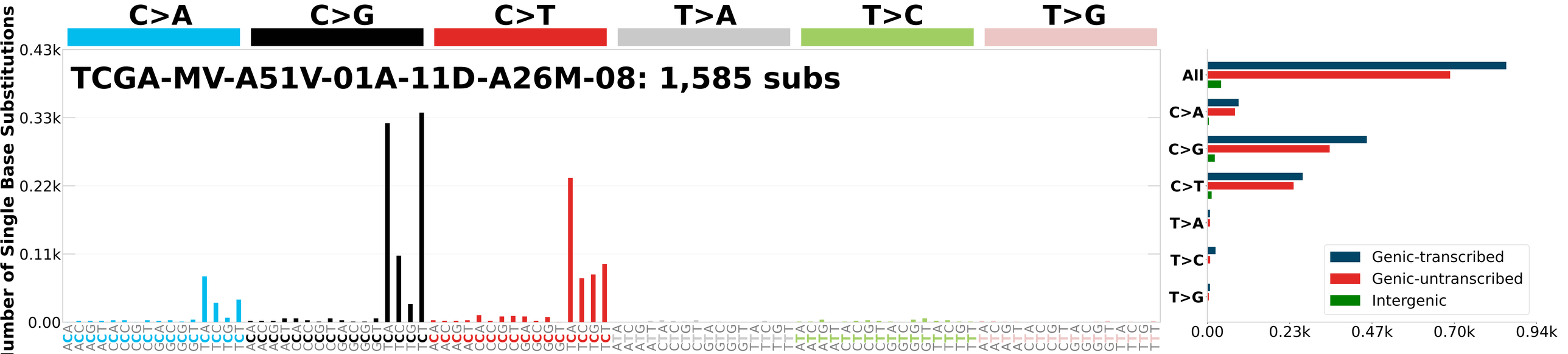

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-KQ-A41R-01A-21D-A34U-08: 732 subs
Number of Single Base Substitutions
0.20k
0.15k
0.10k
0.05k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.11k
0.22k
0.33k
0.44k

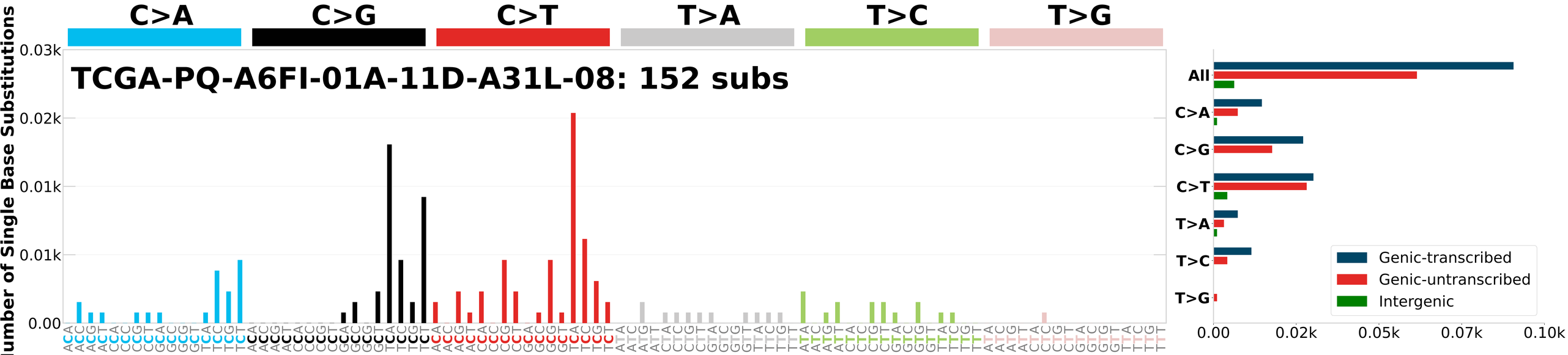

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-KQ-A41S-01A-12D-A339-08: 216 subs
Number of Single Base Substitutions
0.06k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.14k

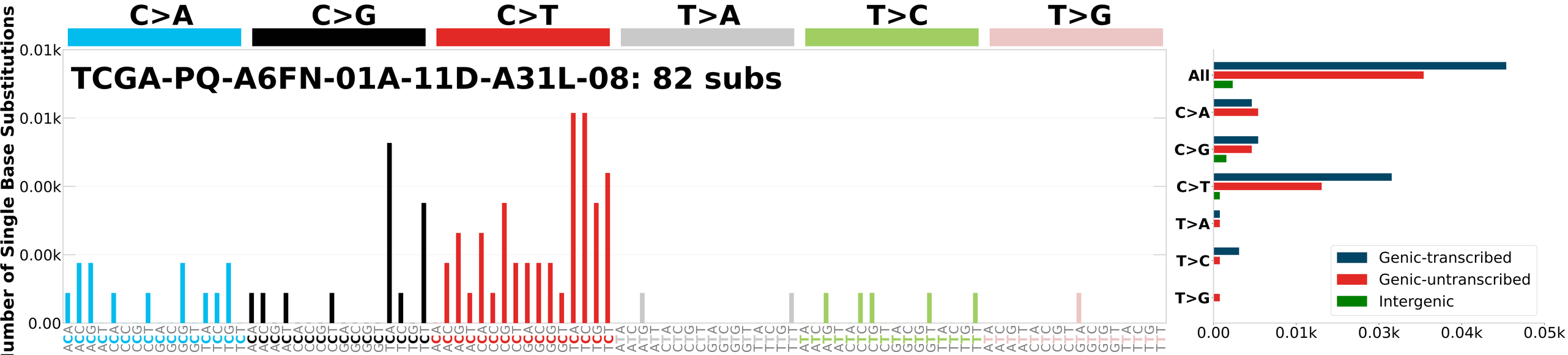

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-LC-A66R-01A-41D-A30E-08: 128 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

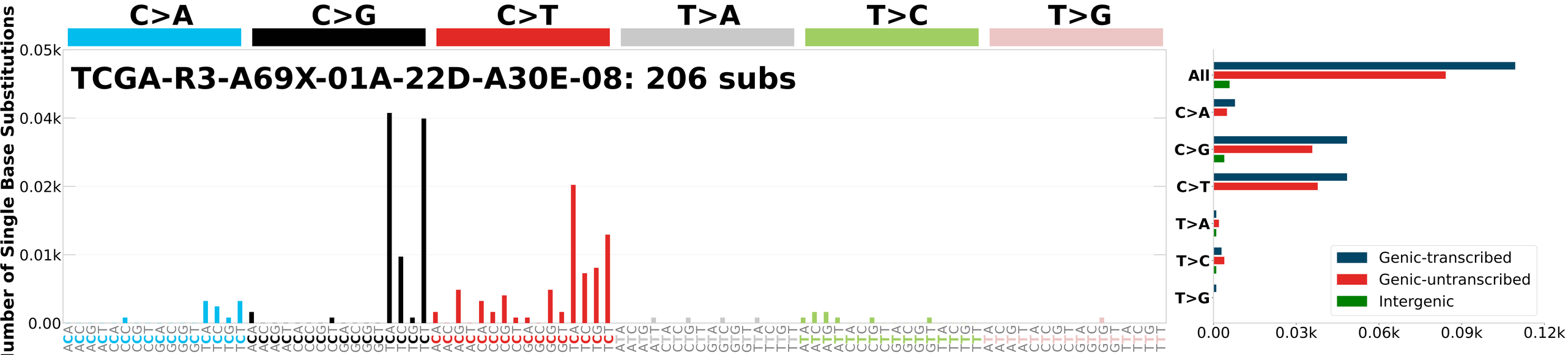

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-LT-A5Z6-01A-11D-A289-08: 504 subs
Number of Single Base Substitutions
0.15k
0.12k
0.08k
0.04k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.14k
0.21k
0.28k

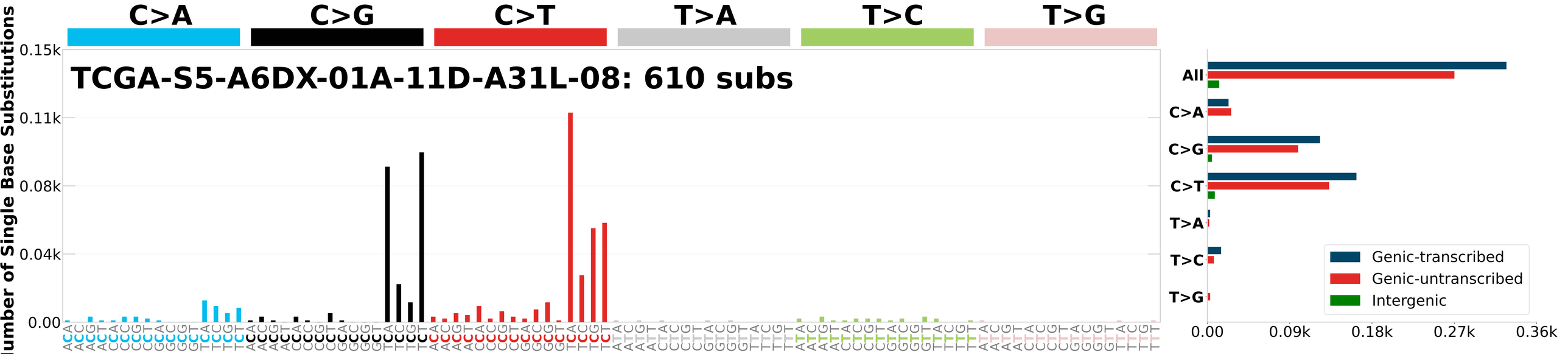

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-LT-A8JT-01A-11D-A364-08: 74 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

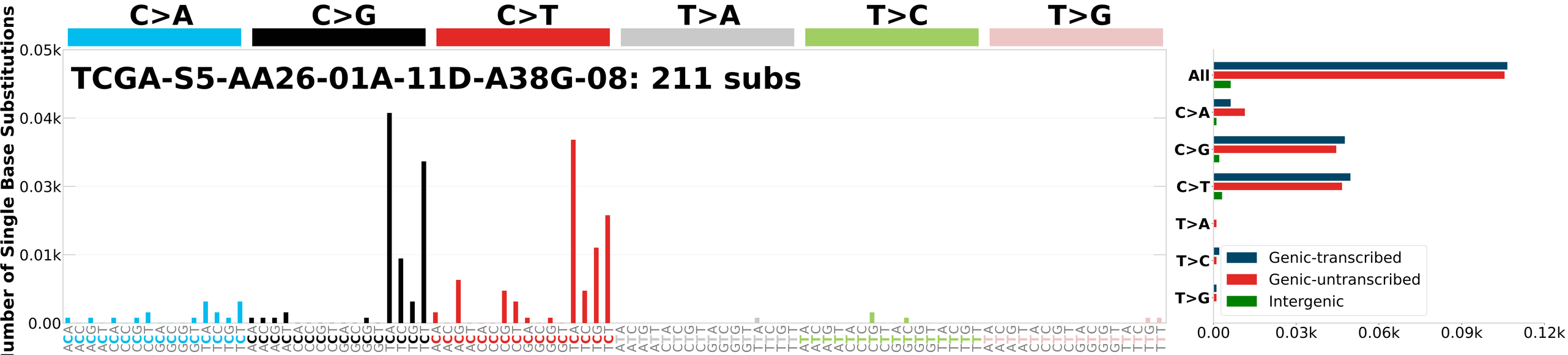

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-MV-A51V-01A-11D-A26M-08: 1,585 subs
Number of Single Base Substitutions
0.43k
0.33k
0.22k
0.11k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.23k
0.47k
0.70k
0.94k

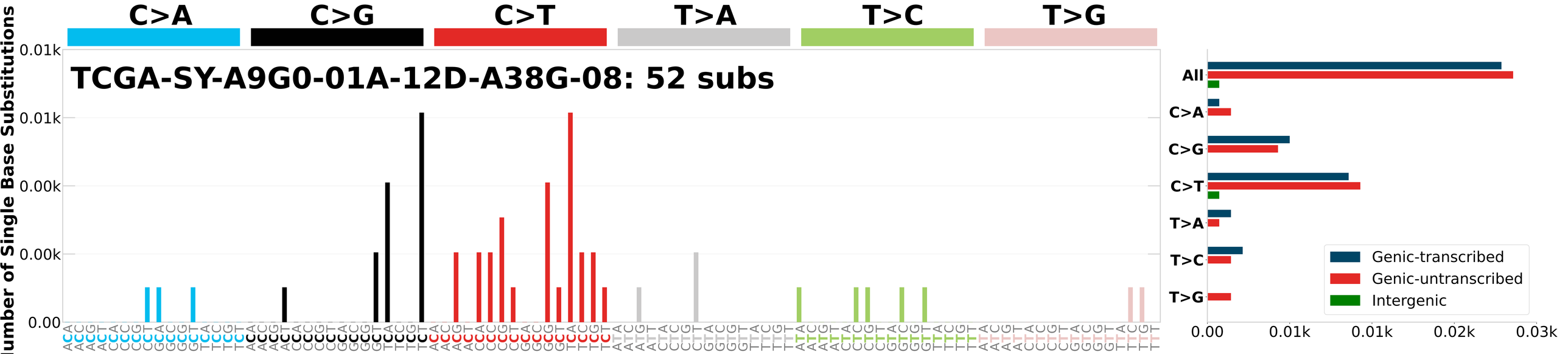

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-PQ-A6FI-01A-11D-A31L-08: 152 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.10k

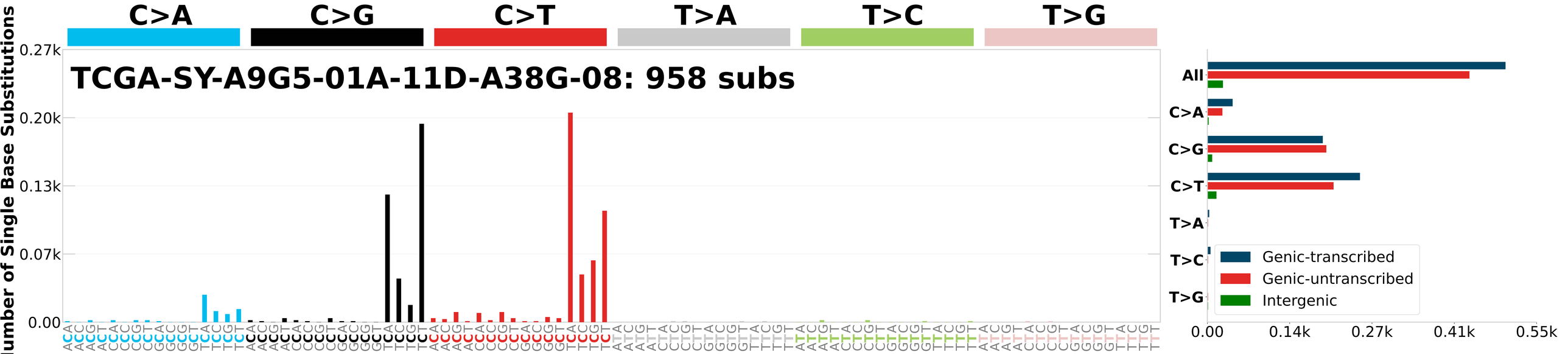

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-PQ-A6FN-01A-11D-A31L-08: 82 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

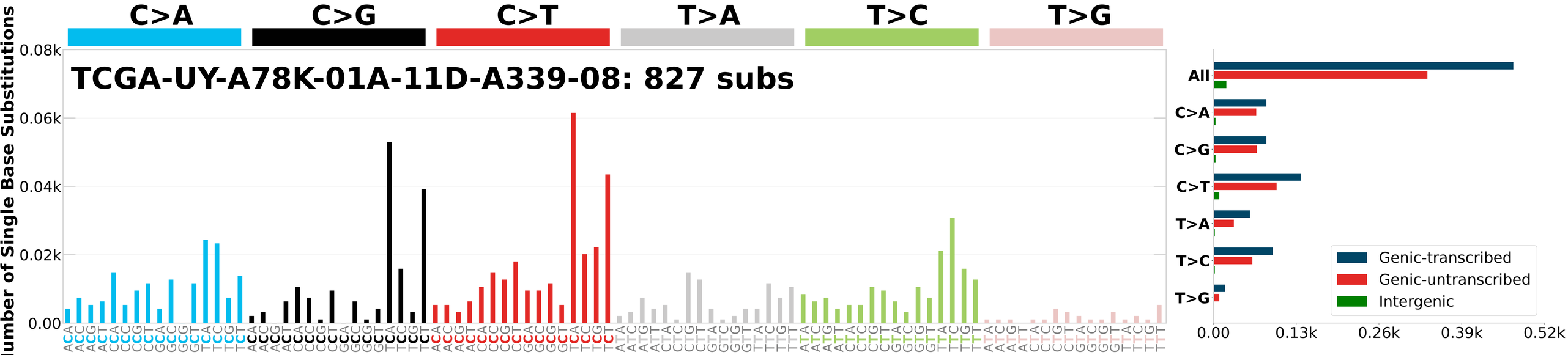

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-R3-A69X-01A-22D-A30E-08: 206 subs
Number of Single Base Substitutions
0.05k
0.04k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

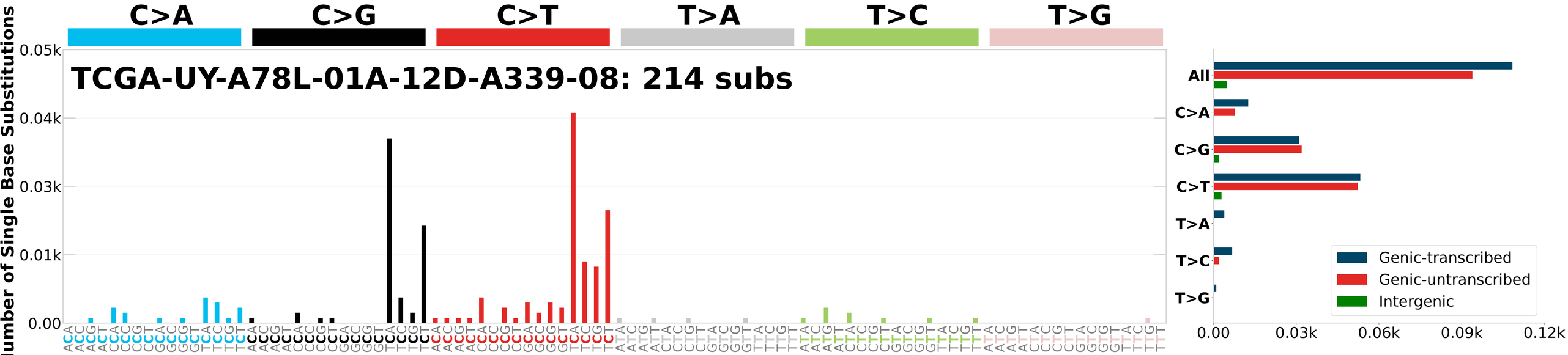

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-S5-A6DX-01A-11D-A31L-08: 610 subs
Number of Single Base Substitutions
0.15k
0.11k
0.08k
0.04k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.09k
0.18k
0.27k
0.36k

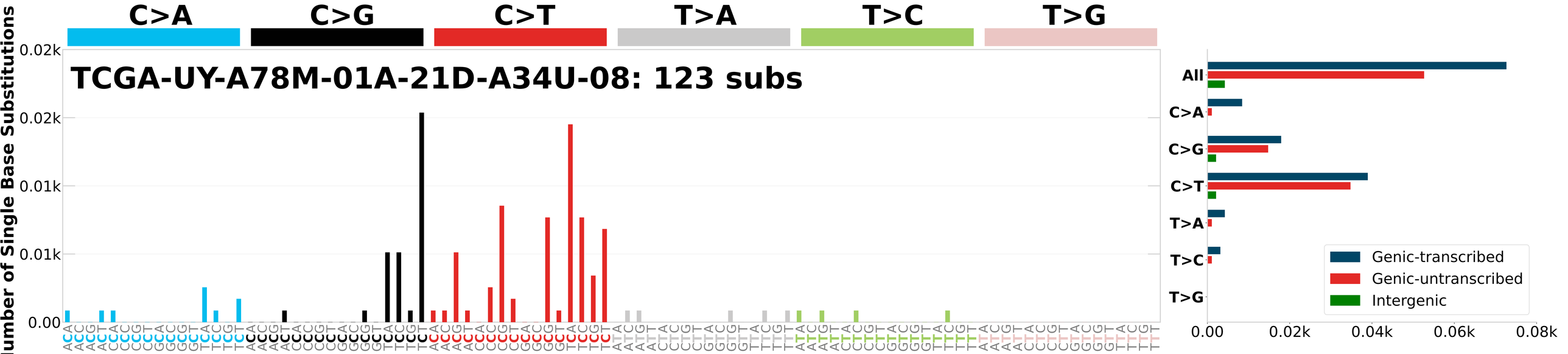

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-S5-AA26-01A-11D-A38G-08: 211 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

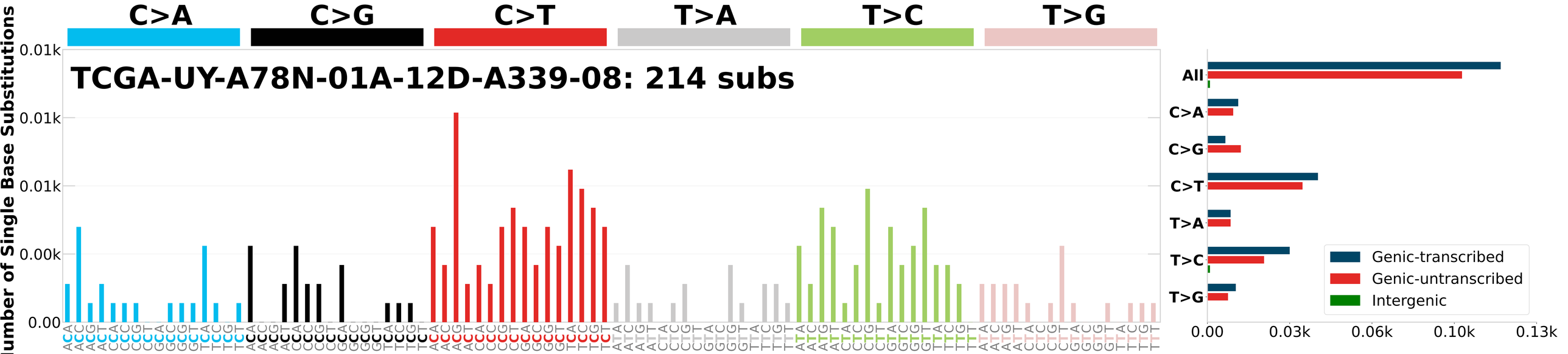

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-SY-A9G0-01A-12D-A38G-08: 52 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.02k
0.03k

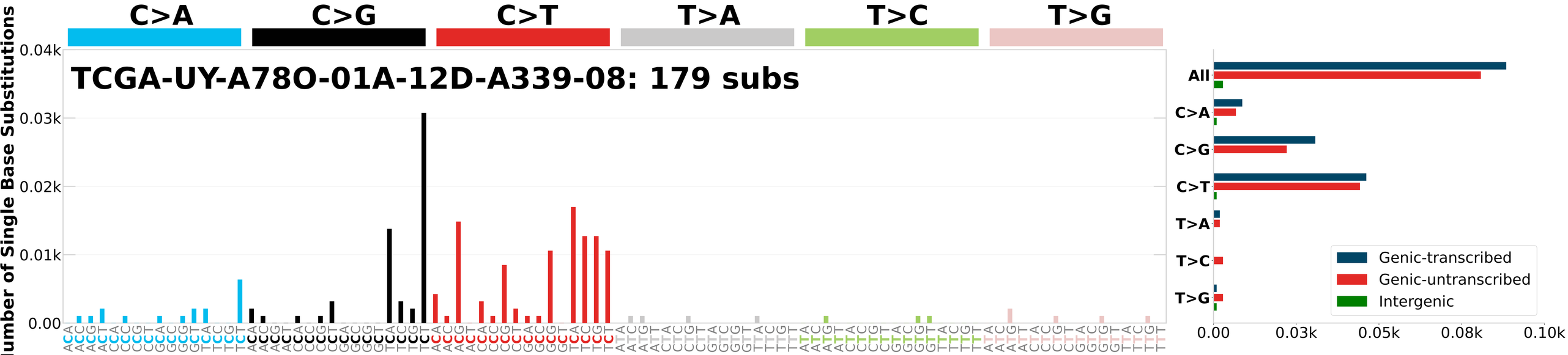

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-SY-A9G5-01A-11D-A38G-08: 958 subs
Number of Single Base Substitutions
0.27k
0.20k
0.13k
0.07k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.14k
0.27k
0.41k
0.55k

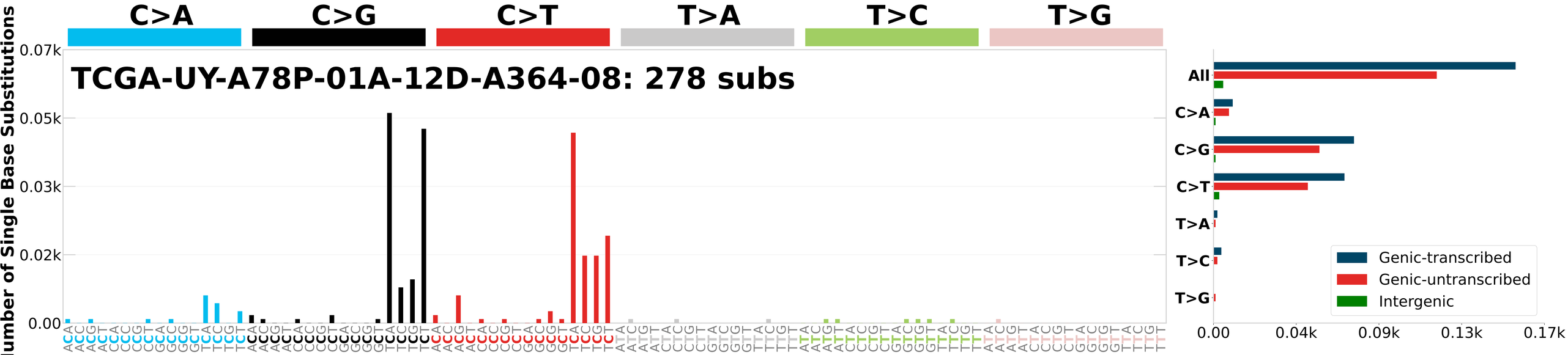

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A78K-01A-11D-A339-08: 827 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.13k
0.26k
0.39k
0.52k

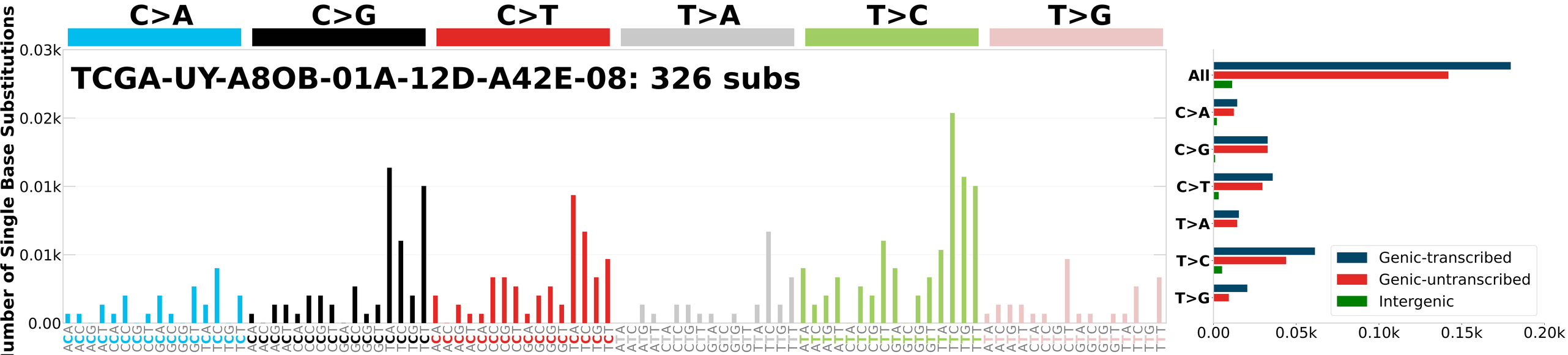

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A78L-01A-12D-A339-08: 214 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

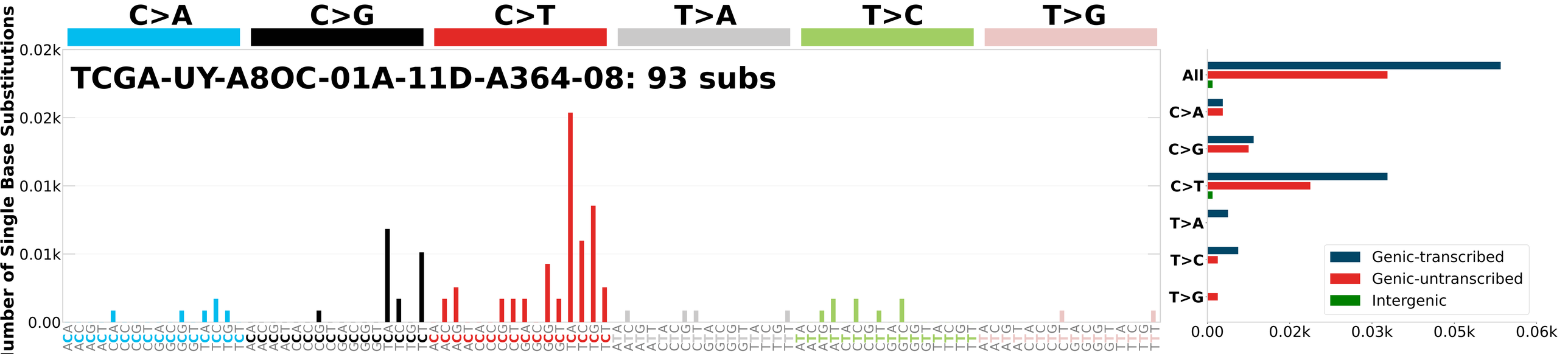

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A78M-01A-21D-A34U-08: 123 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

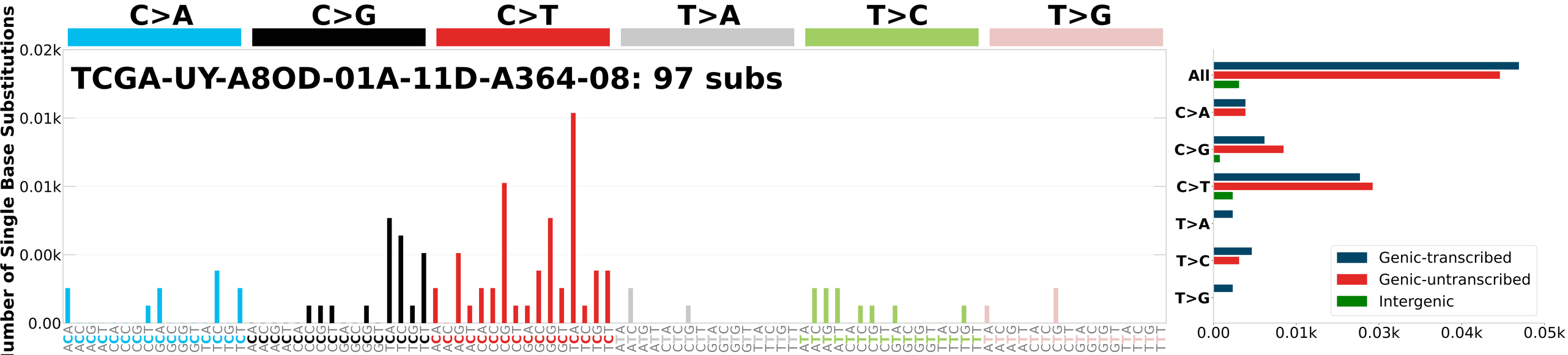

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A78N-01A-12D-A339-08: 214 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.10k
0.13k

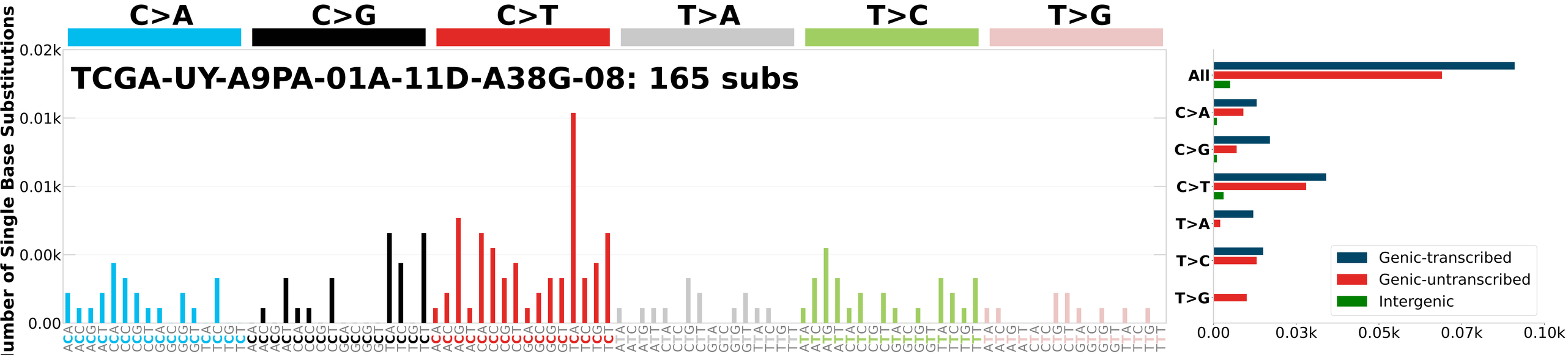

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A78O-01A-12D-A339-08: 179 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.10k

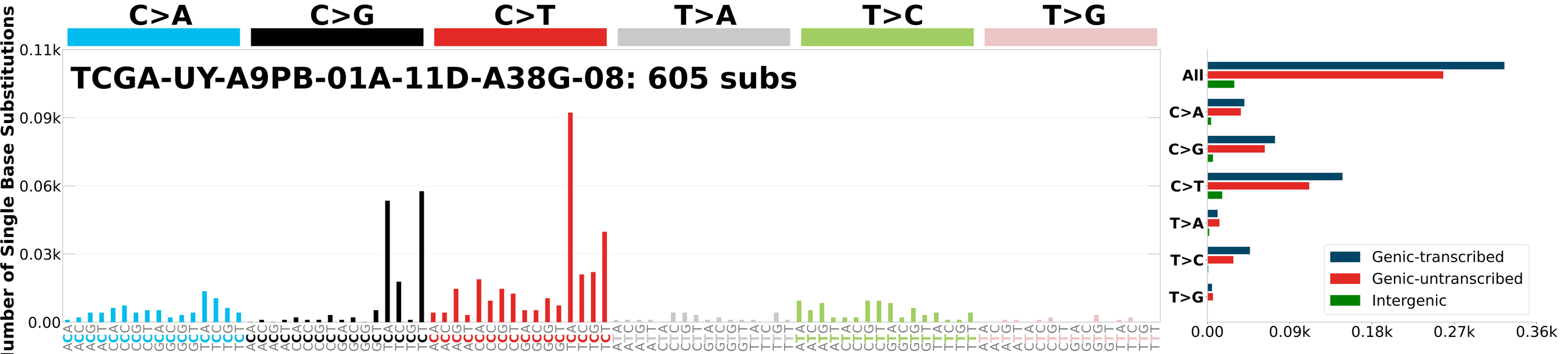

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A78P-01A-12D-A364-08: 278 subs
Number of Single Base Substitutions
0.07k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.09k
0.13k
0.17k

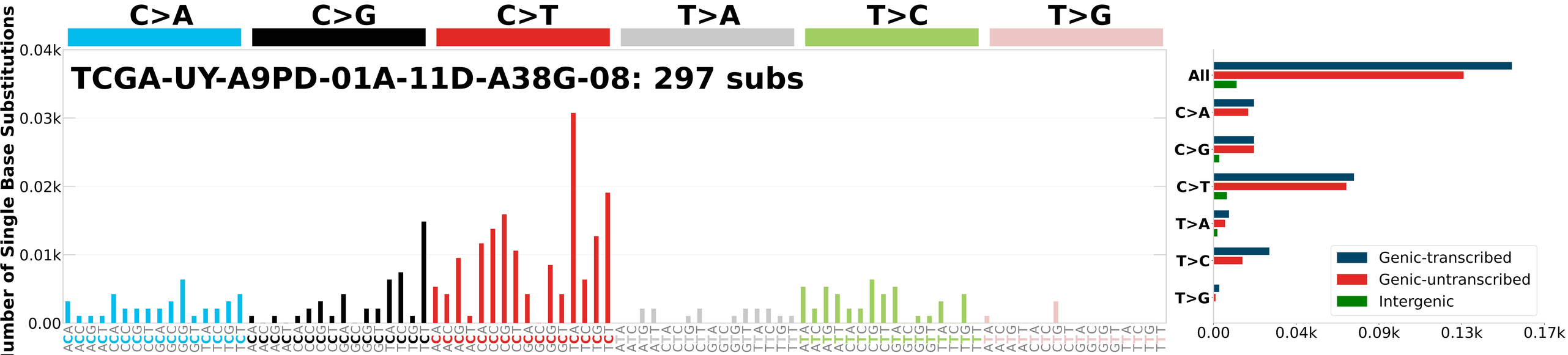

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A8OB-01A-12D-A42E-08: 326 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.10k
0.15k
0.20k

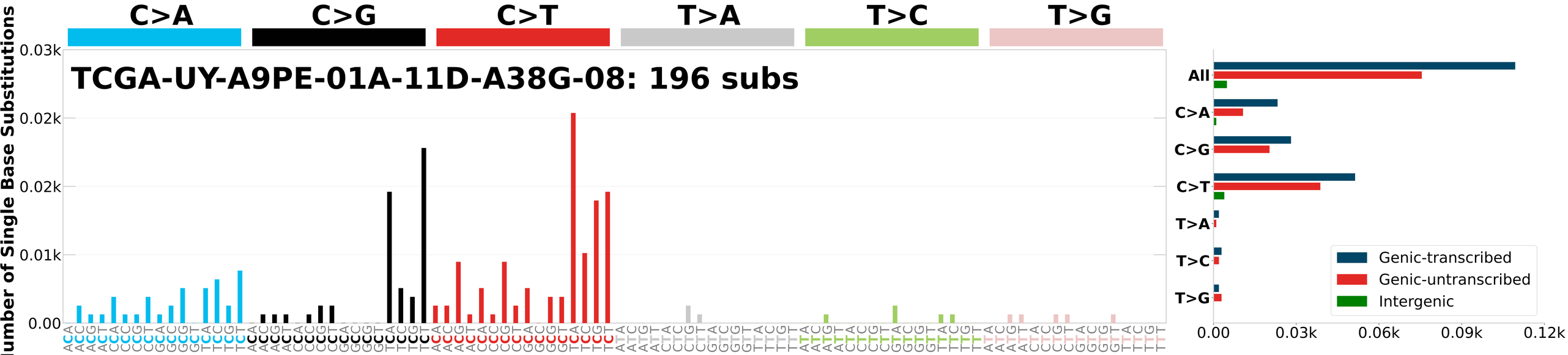

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A8OC-01A-11D-A364-08: 93 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.06k

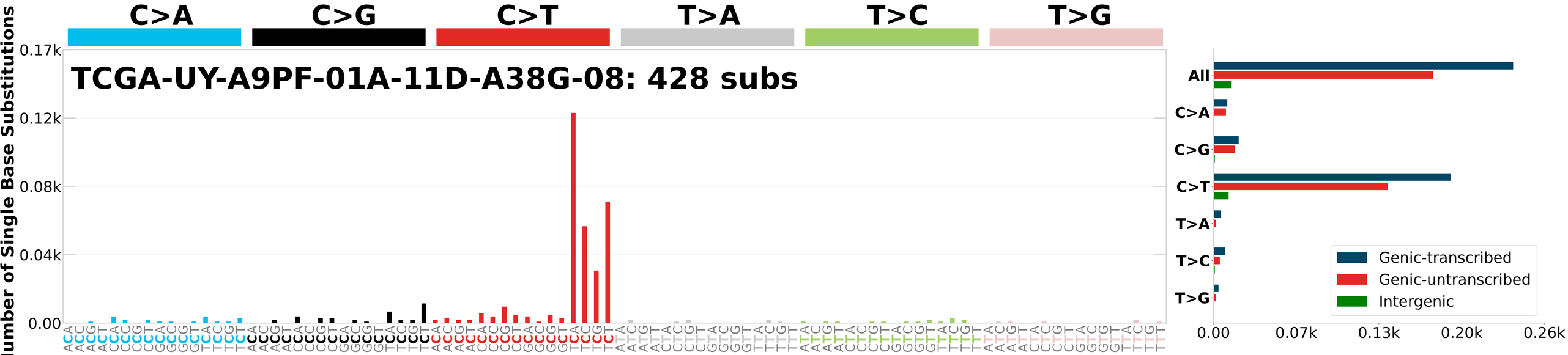

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A8OD-01A-11D-A364-08: 97 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

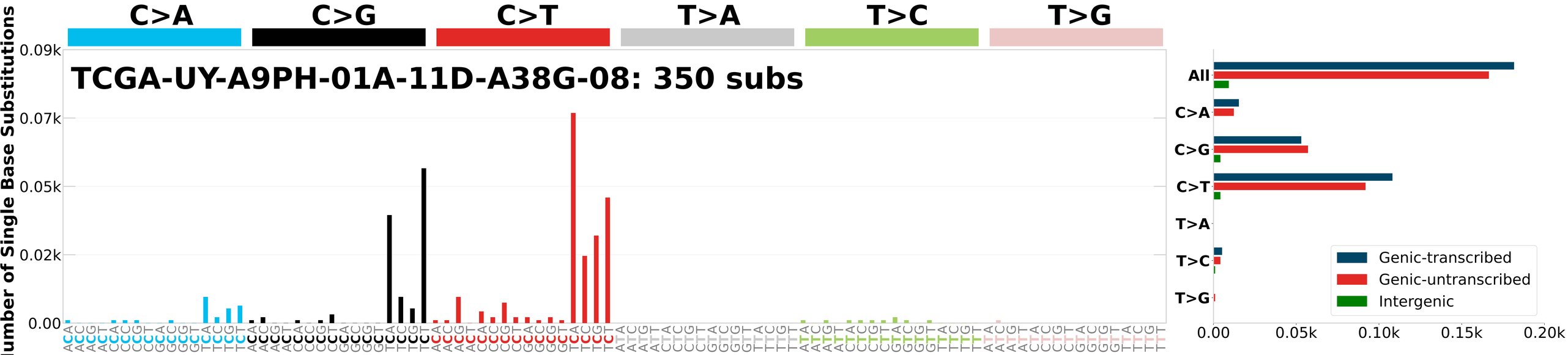

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A9PA-01A-11D-A38G-08: 165 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.07k
0.10k

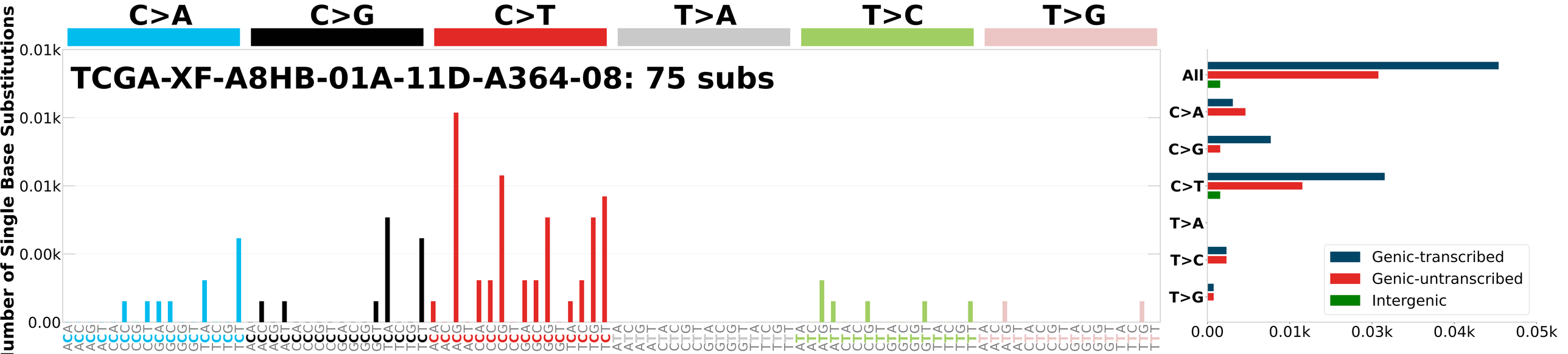

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A9PB-01A-11D-A38G-08: 605 subs
Number of Single Base Substitutions
0.11k
0.09k
0.06k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.09k
0.18k
0.27k
0.36k

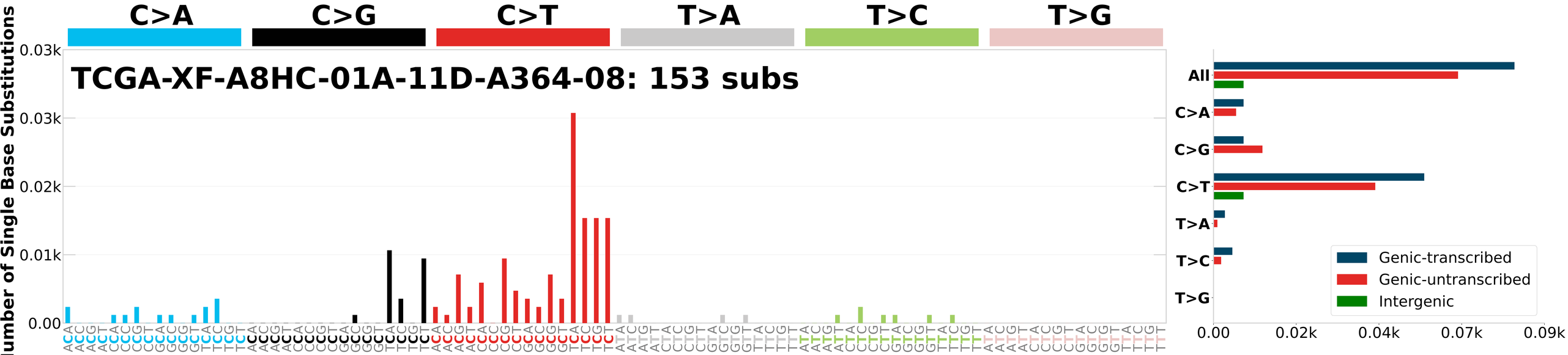

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A9PD-01A-11D-A38G-08: 297 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.09k
0.13k
0.17k

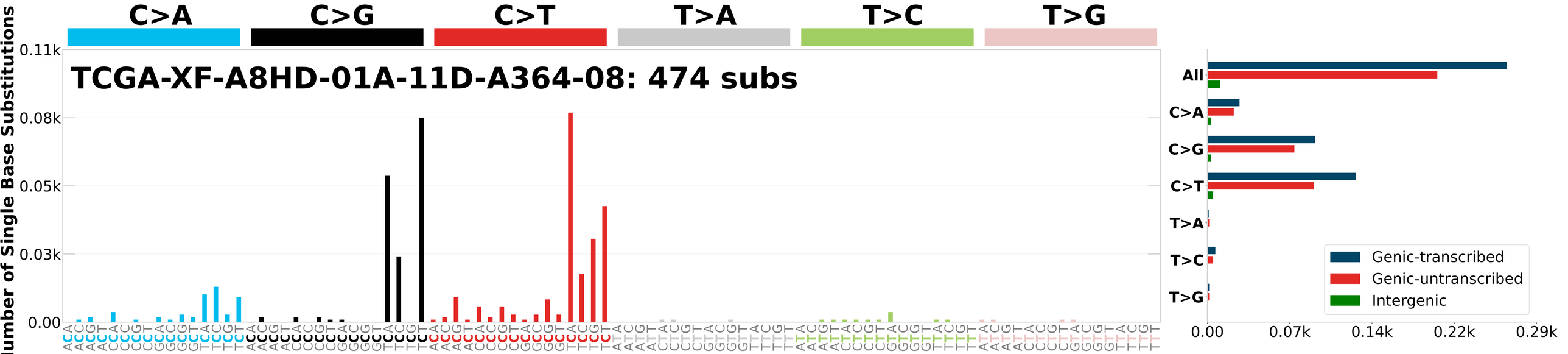

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A9PE-01A-11D-A38G-08: 196 subs
Number of Single Base Substitutions
0.03k
0.02k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

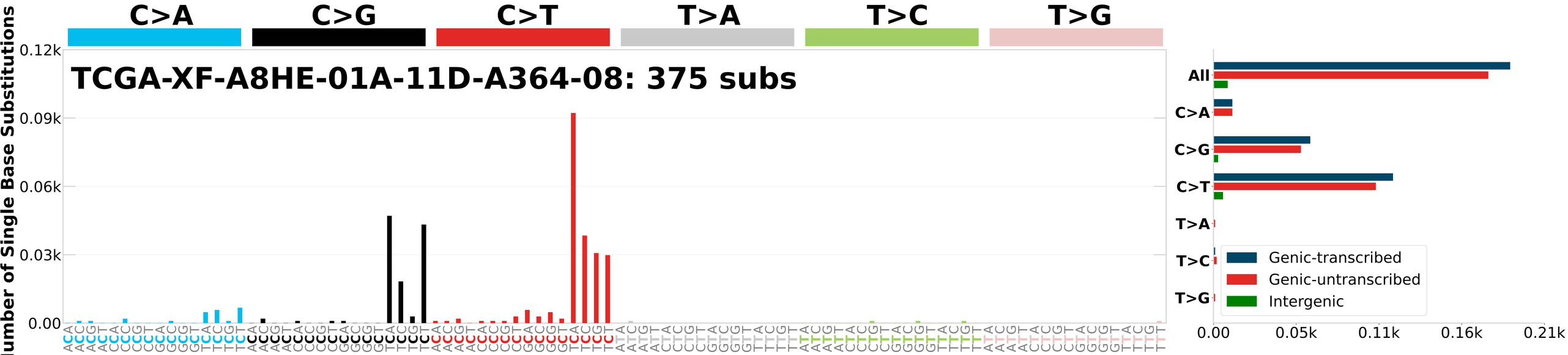

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A9PF-01A-11D-A38G-08: 428 subs
Number of Single Base Substitutions
0.17k
0.12k
0.08k
0.04k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.13k
0.20k
0.26k

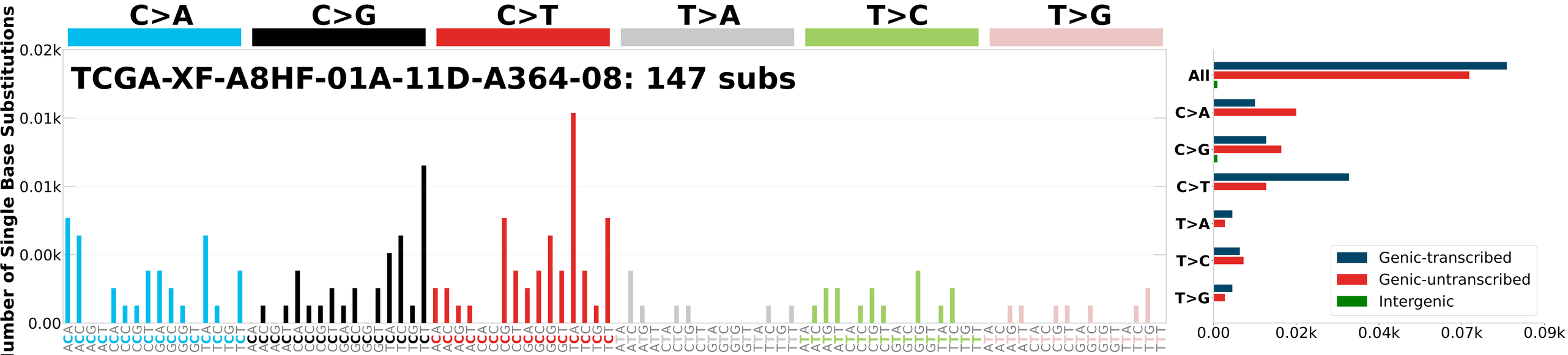

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-UY-A9PH-01A-11D-A38G-08: 350 subs
Number of Single Base Substitutions
0.09k
0.07k
0.05k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.10k
0.15k
0.20k

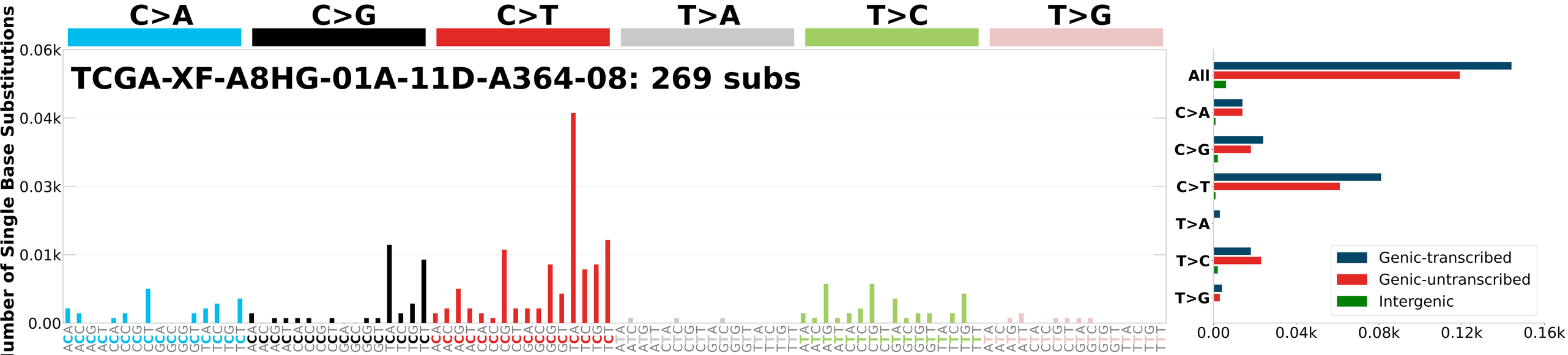

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A8HB-01A-11D-A364-08: 75 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

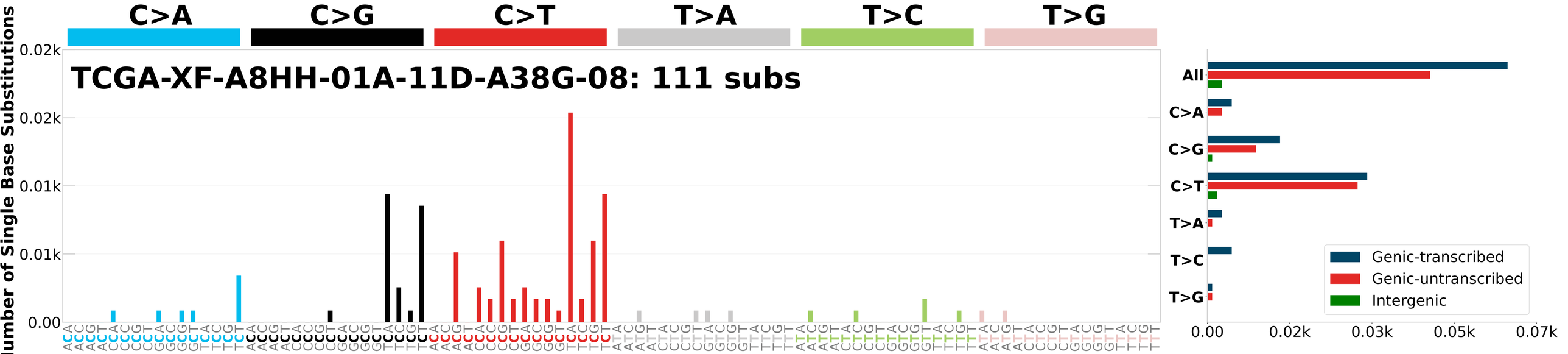

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A8HC-01A-11D-A364-08: 153 subs
Number of Single Base Substitutions
0.03k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.07k
0.09k

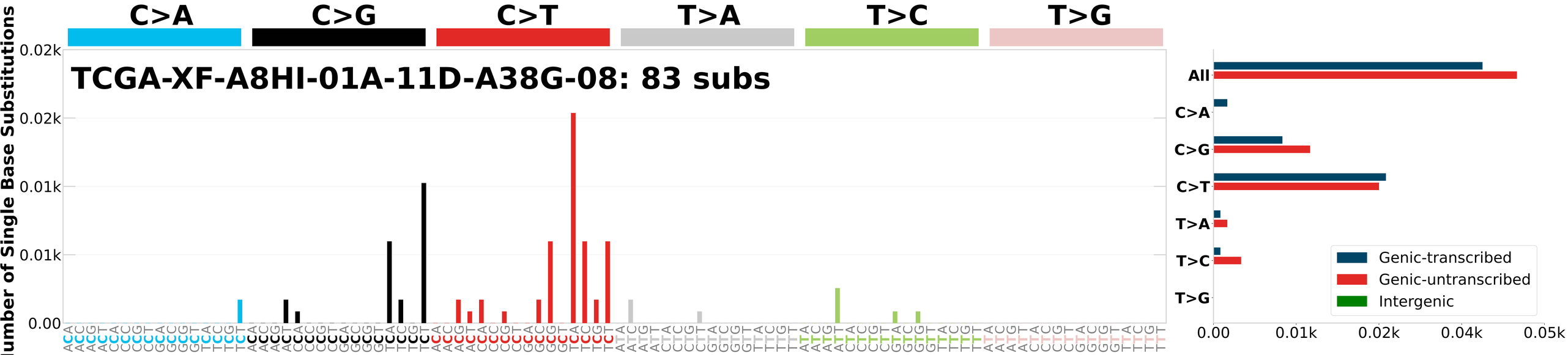

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A8HD-01A-11D-A364-08: 474 subs
Number of Single Base Substitutions
0.11k
0.08k
0.05k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.14k
0.22k
0.29k

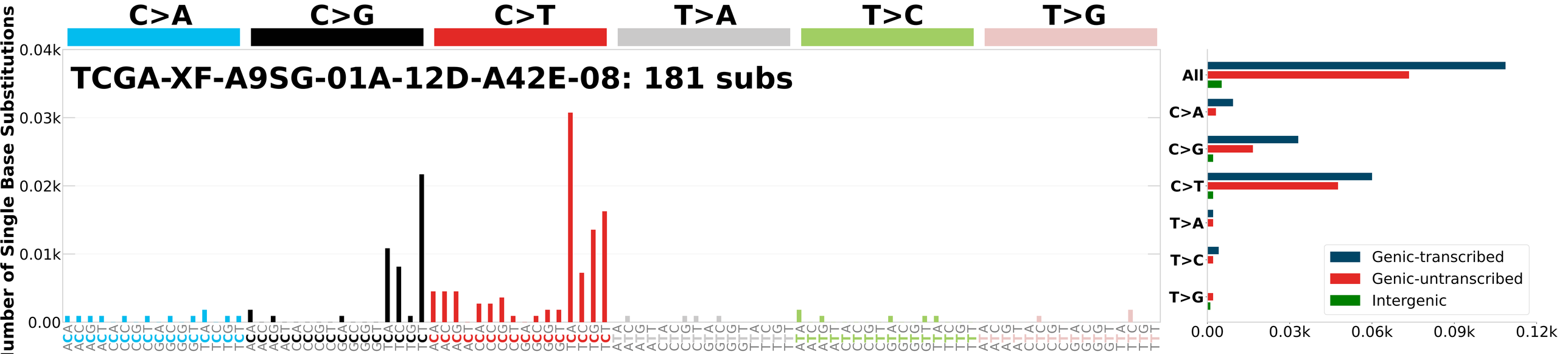

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A8HE-01A-11D-A364-08: 375 subs
Number of Single Base Substitutions
0.12k
0.09k
0.06k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.11k
0.16k
0.21k

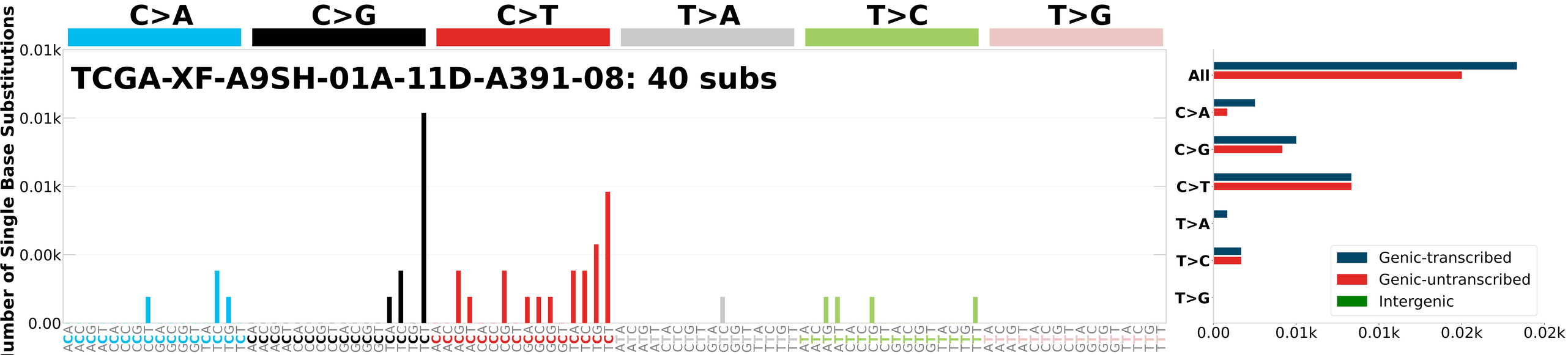

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A8HF-01A-11D-A364-08: 147 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.07k
0.09k

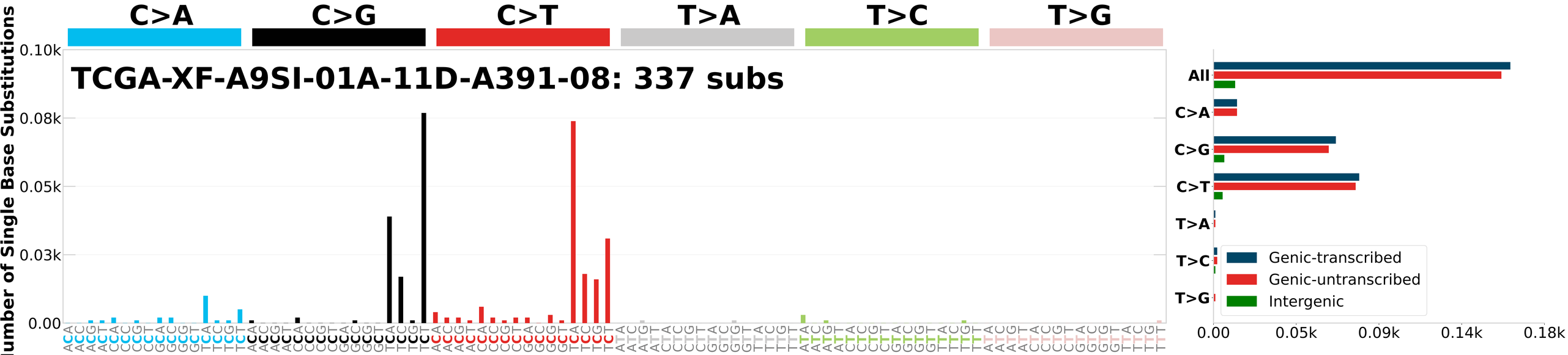

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A8HG-01A-11D-A364-08: 269 subs
Number of Single Base Substitutions
0.06k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.12k
0.16k

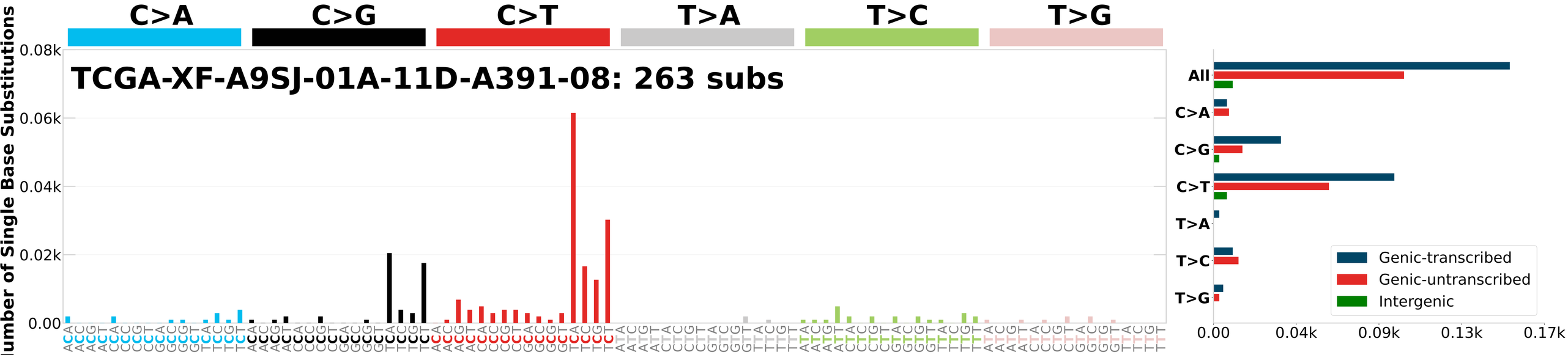

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A8HH-01A-11D-A38G-08: 111 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.07k

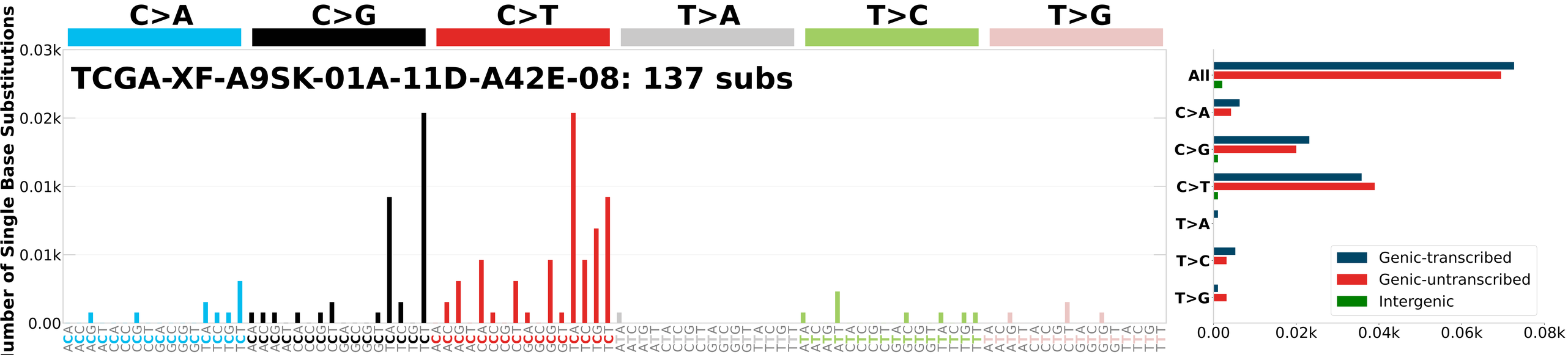

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A8HI-01A-11D-A38G-08: 83 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

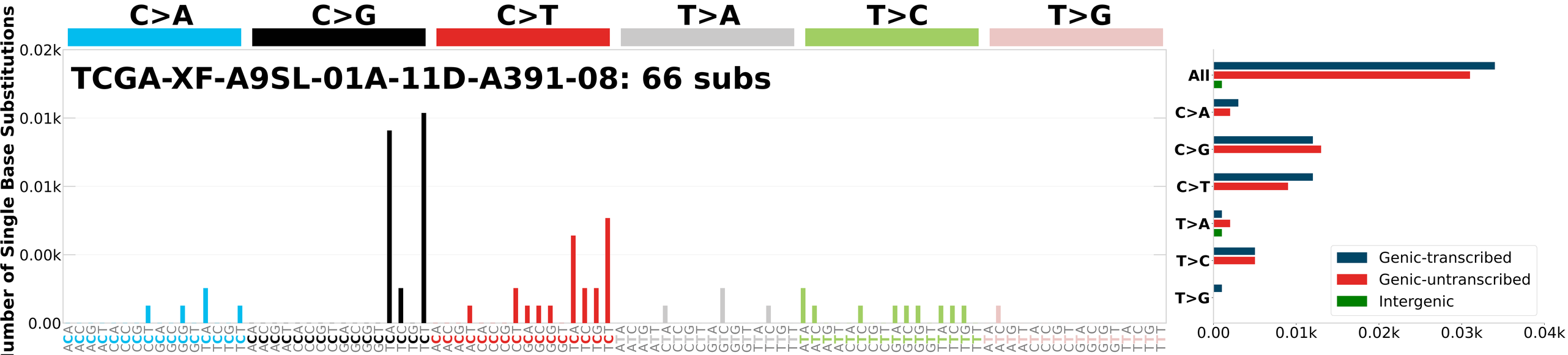

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9SG-01A-12D-A42E-08: 181 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

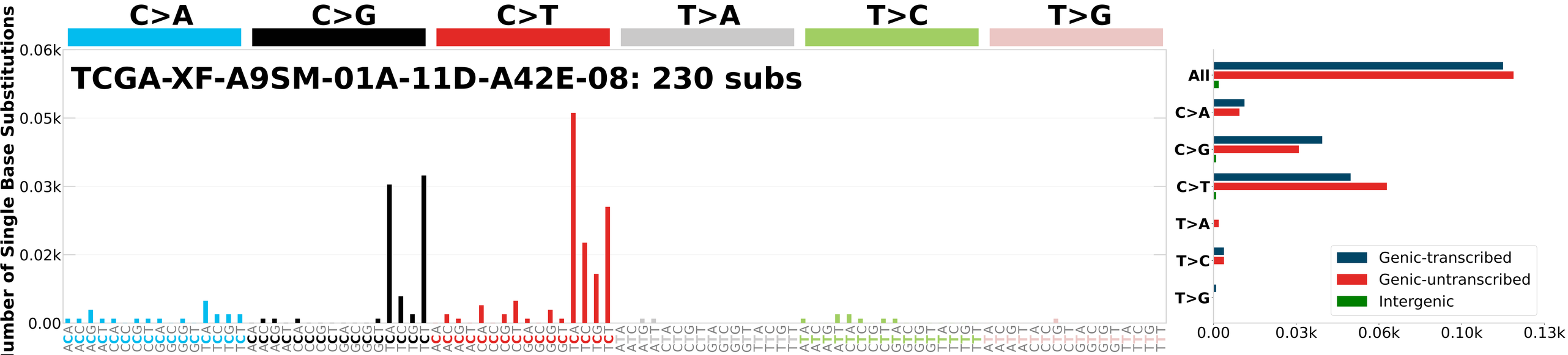

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9SH-01A-11D-A391-08: 40 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.02k
0.02k

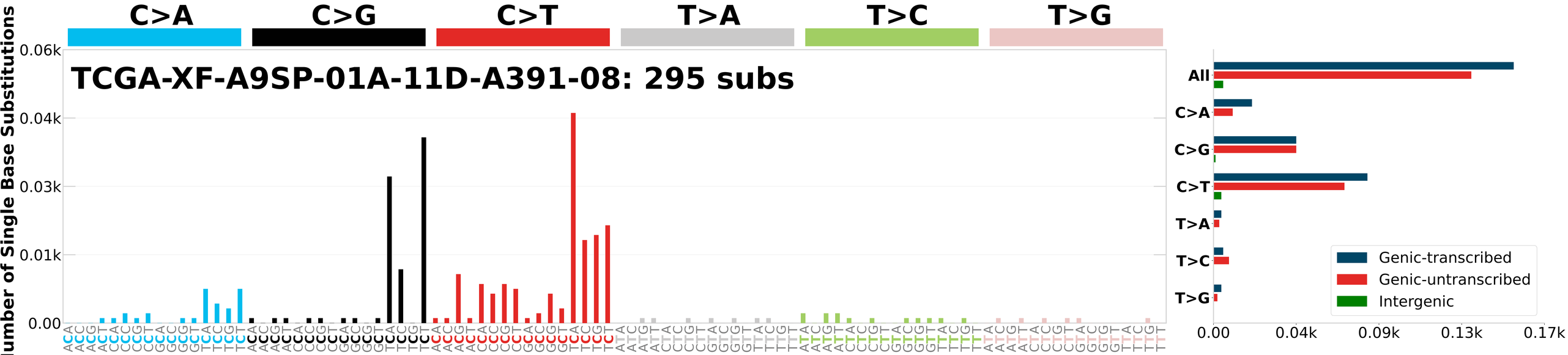

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9SI-01A-11D-A391-08: 337 subs
Number of Single Base Substitutions
0.10k
0.08k
0.05k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.09k
0.14k
0.18k

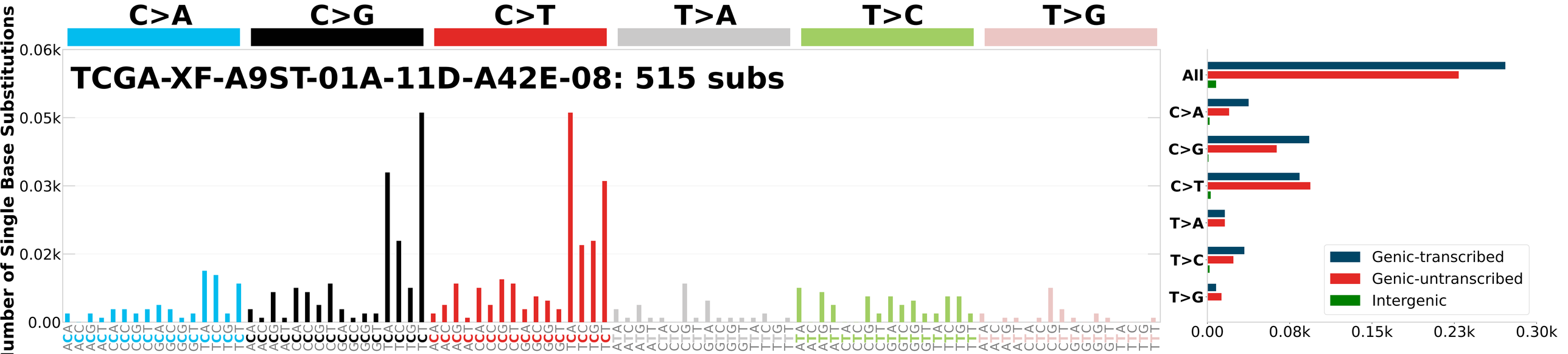

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9SJ-01A-11D-A391-08: 263 subs
Number of Single Base Substitutions
0.08k
0.06k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.09k
0.13k
0.17k

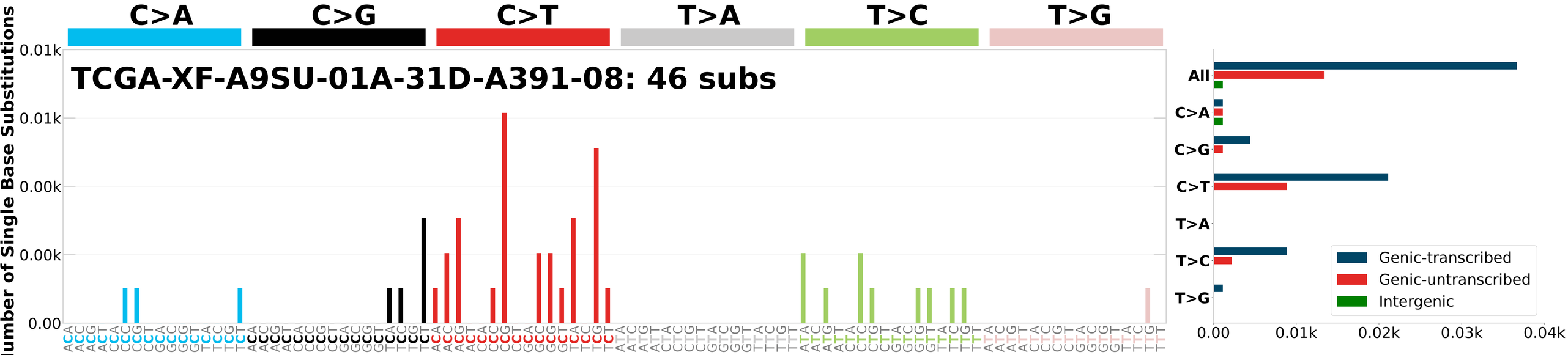

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9SK-01A-11D-A42E-08: 137 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

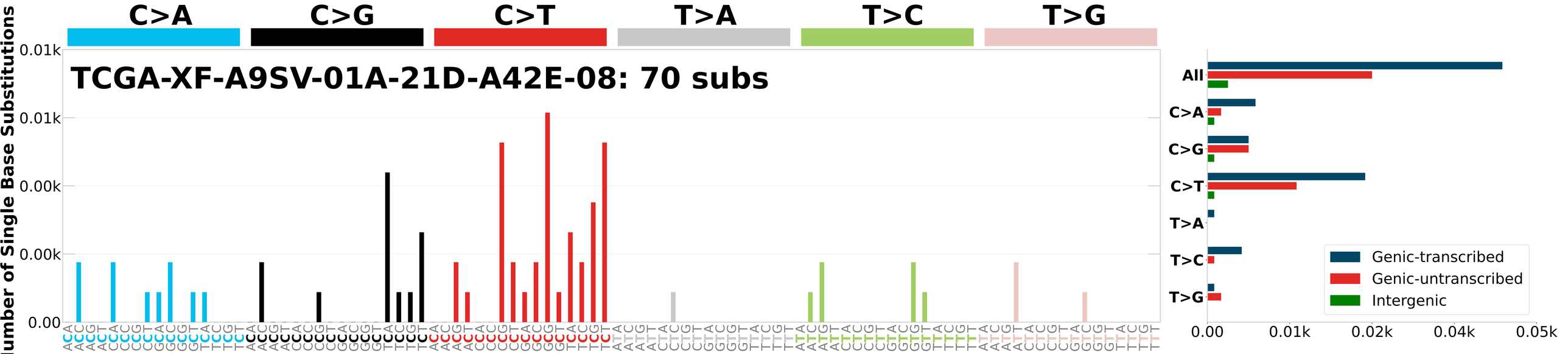

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9SL-01A-11D-A391-08: 66 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

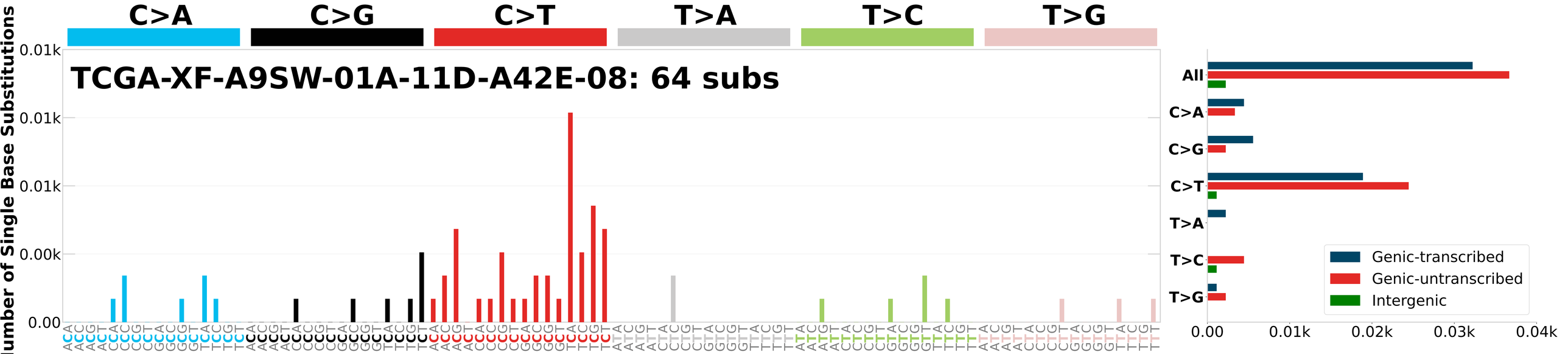

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9SM-01A-11D-A42E-08: 230 subs
Number of Single Base Substitutions
0.06k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.10k
0.13k

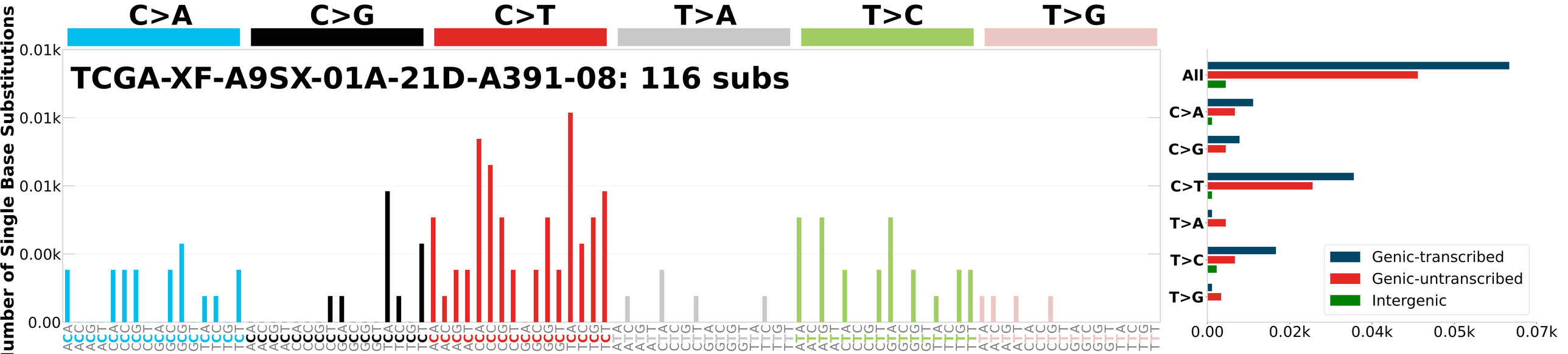

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9SP-01A-11D-A391-08: 295 subs
Number of Single Base Substitutions
0.06k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.09k
0.13k
0.17k

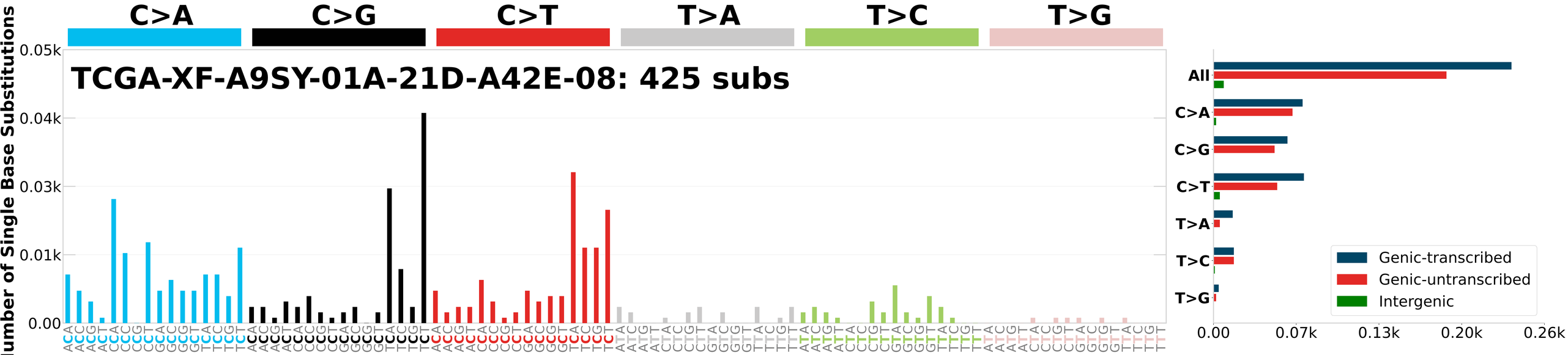

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9ST-01A-11D-A42E-08: 515 subs
Number of Single Base Substitutions
0.06k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.08k
0.15k
0.23k
0.30k

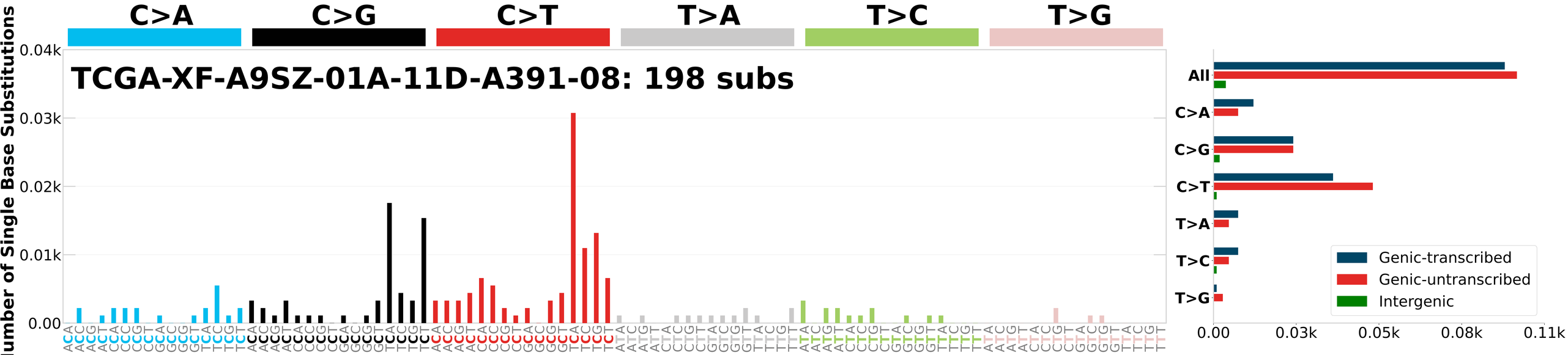

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9SU-01A-31D-A391-08: 46 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

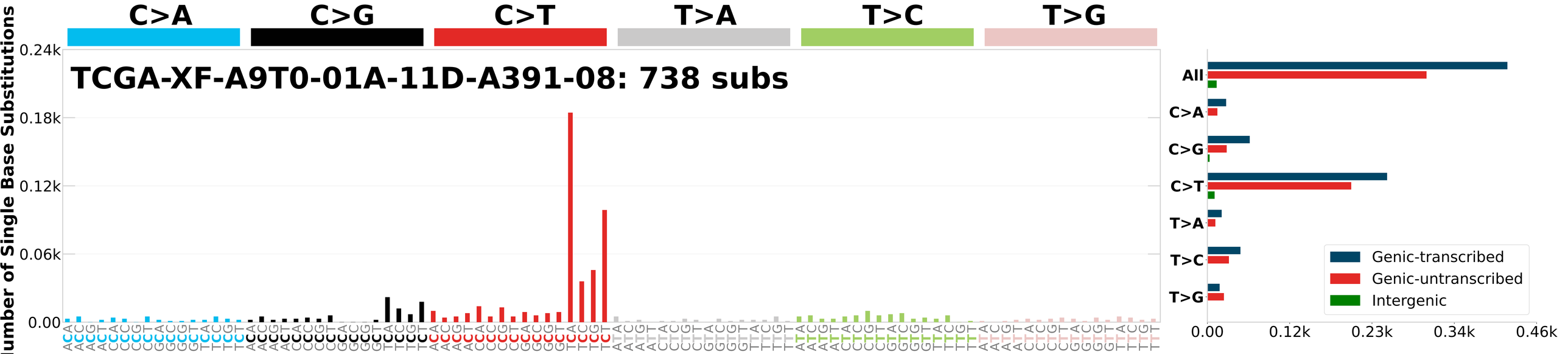

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9SV-01A-21D-A42E-08: 70 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

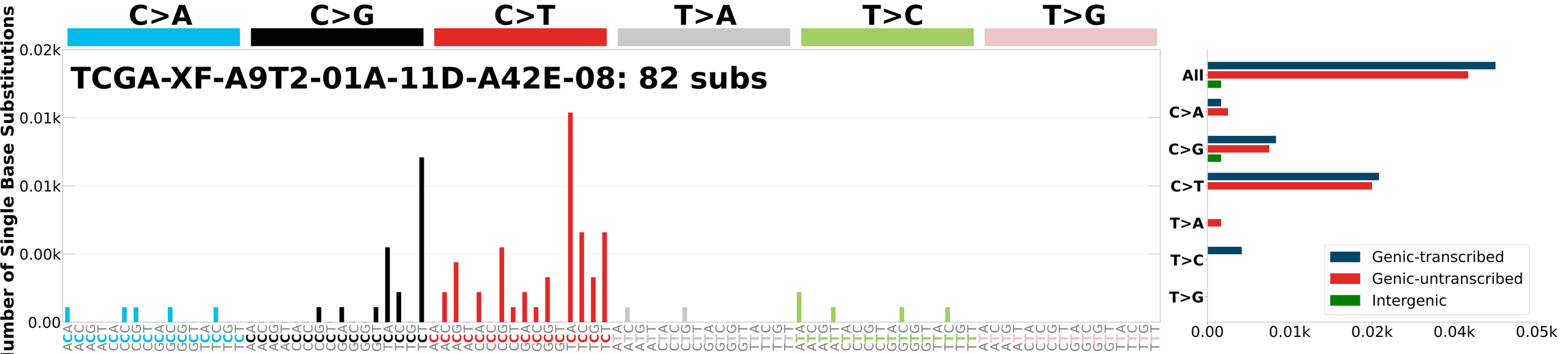

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9SW-01A-11D-A42E-08: 64 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

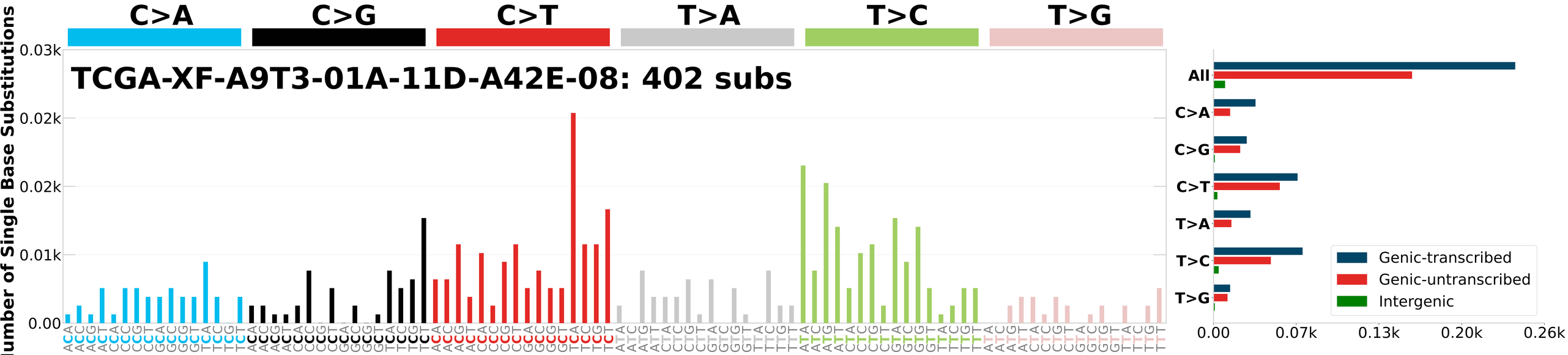

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9SX-01A-21D-A391-08: 116 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.05k
0.07k

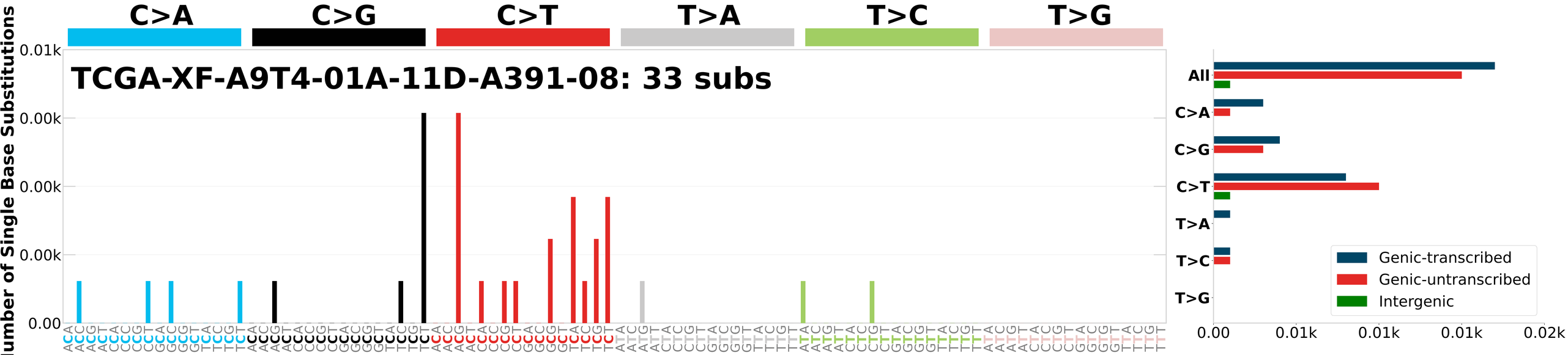

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9SY-01A-21D-A42E-08: 425 subs
Number of Single Base Substitutions
0.05k
0.04k
0.03k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.13k
0.20k
0.26k

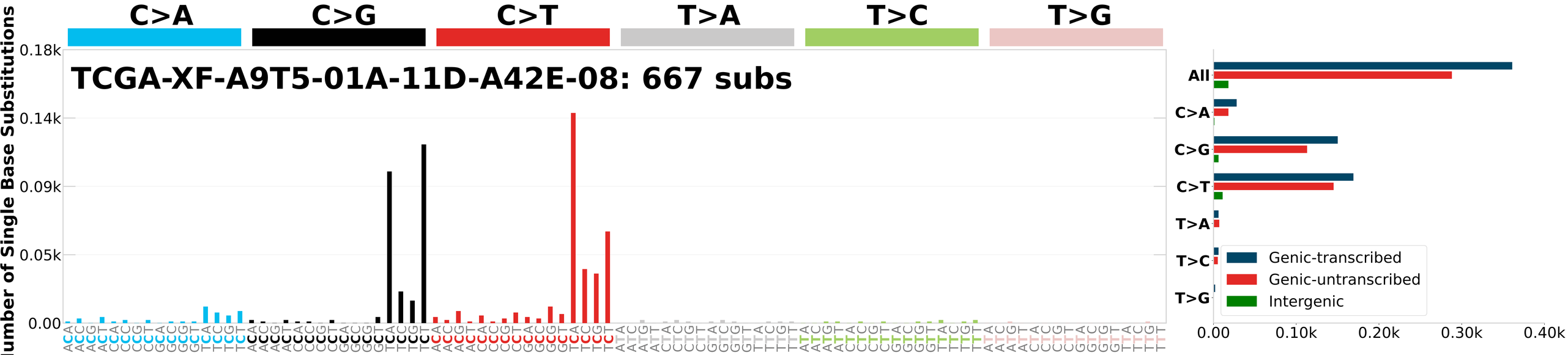

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9SZ-01A-11D-A391-08: 198 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.11k

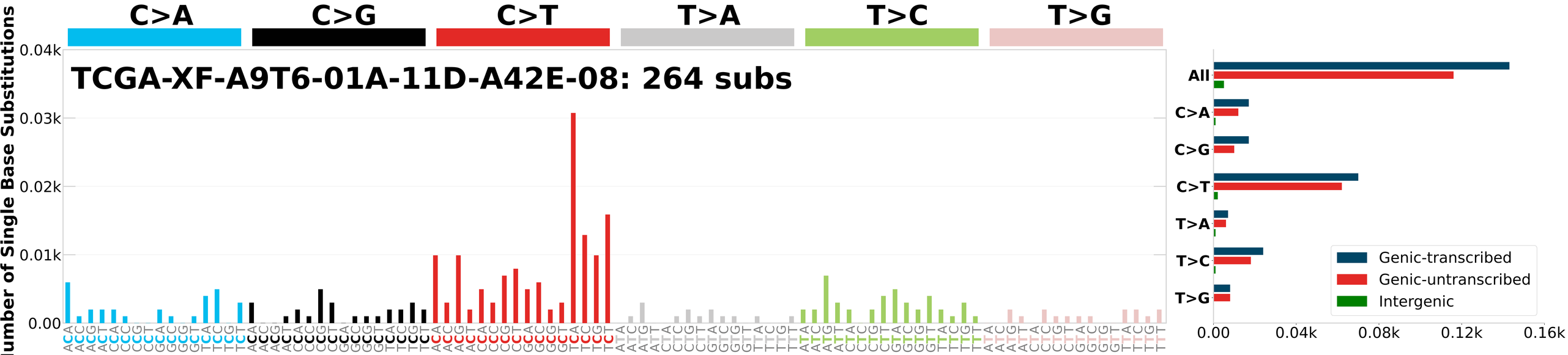

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9T0-01A-11D-A391-08: 738 subs
Number of Single Base Substitutions
0.24k
0.18k
0.12k
0.06k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.12k
0.23k
0.34k
0.46k

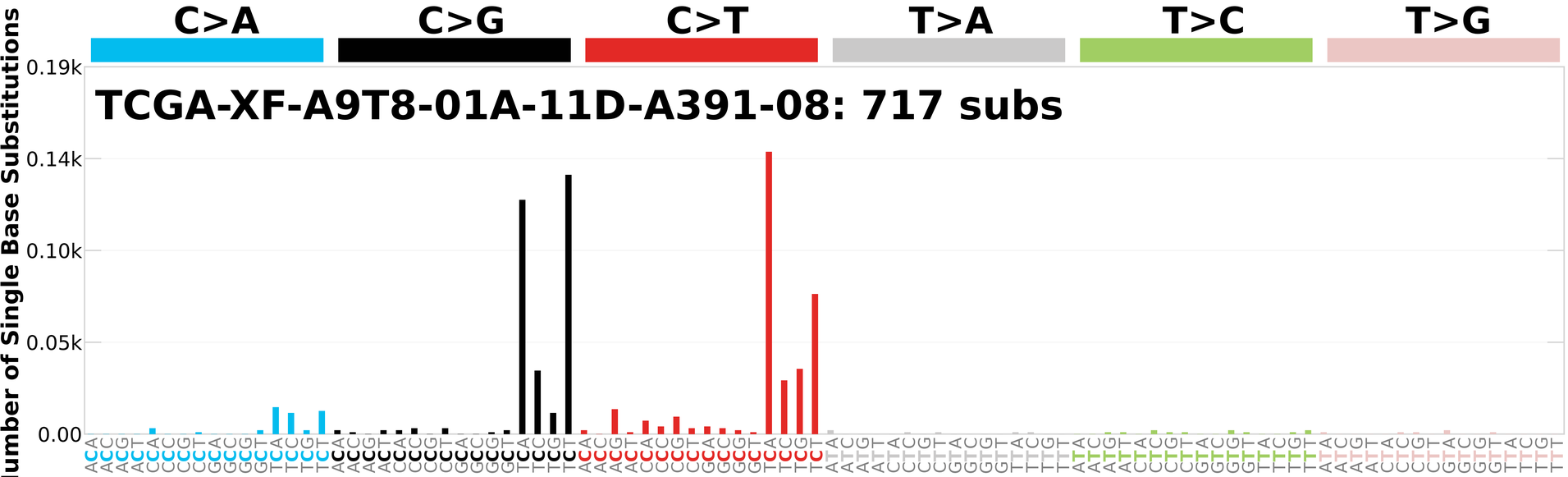

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9T2-01A-11D-A42E-08: 82 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

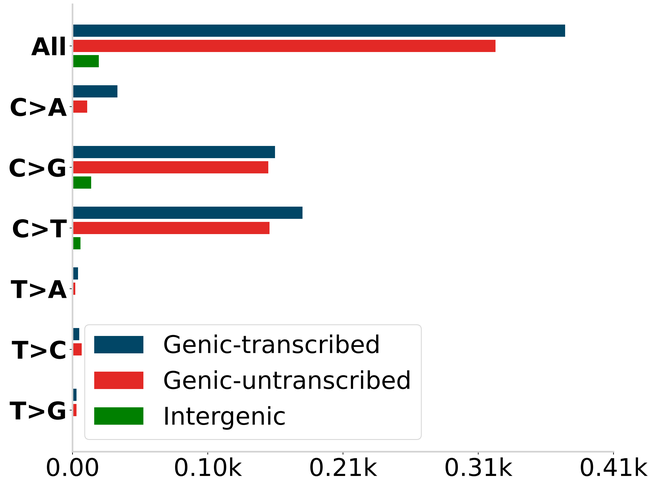

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9T3-01A-11D-A42E-08: 402 subs
Number of Single Base Substitutions
0.03k
0.02k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.13k
0.20k
0.26k

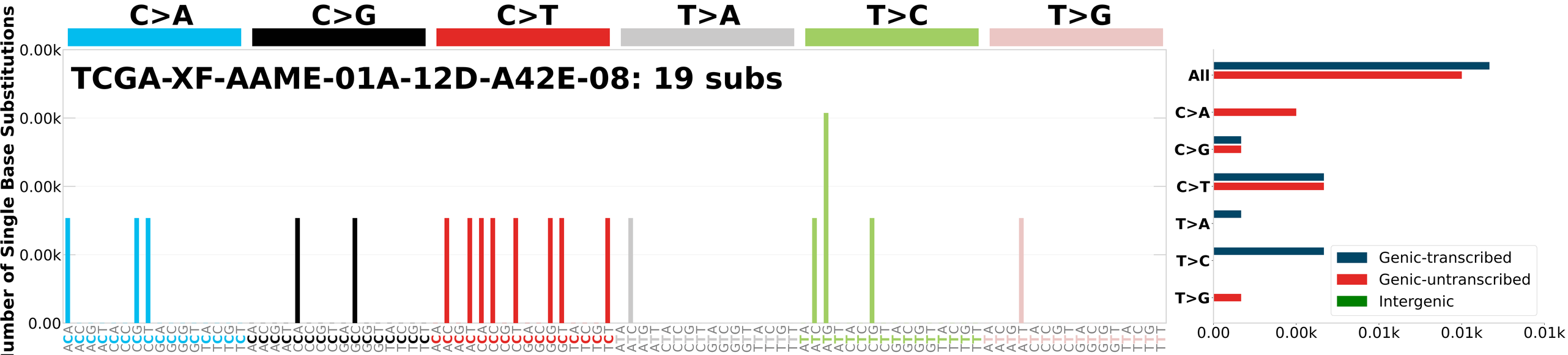

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9T4-01A-11D-A391-08: 33 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.01k
0.02k

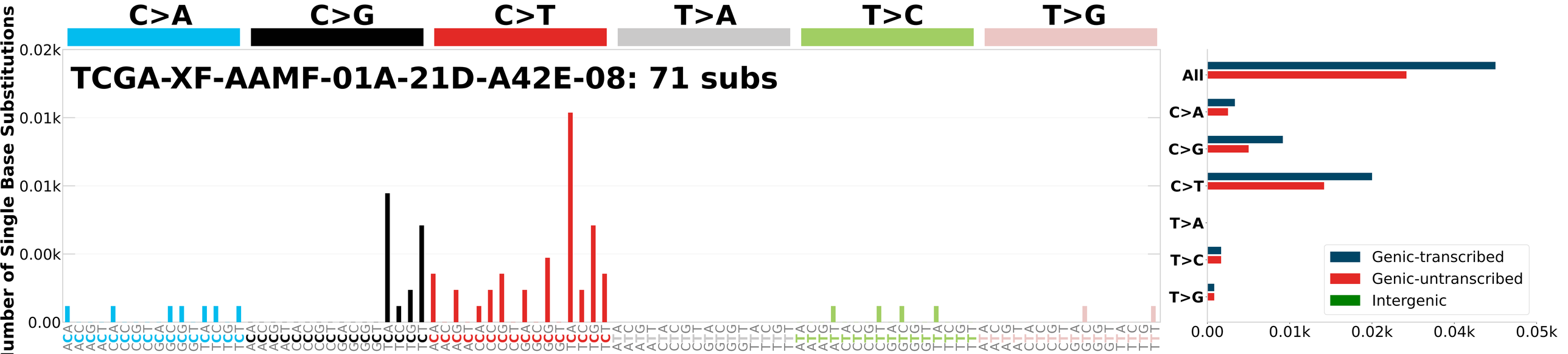

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9T5-01A-11D-A42E-08: 667 subs
Number of Single Base Substitutions
0.18k
0.14k
0.09k
0.05k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.10k
0.20k
0.30k
0.40k

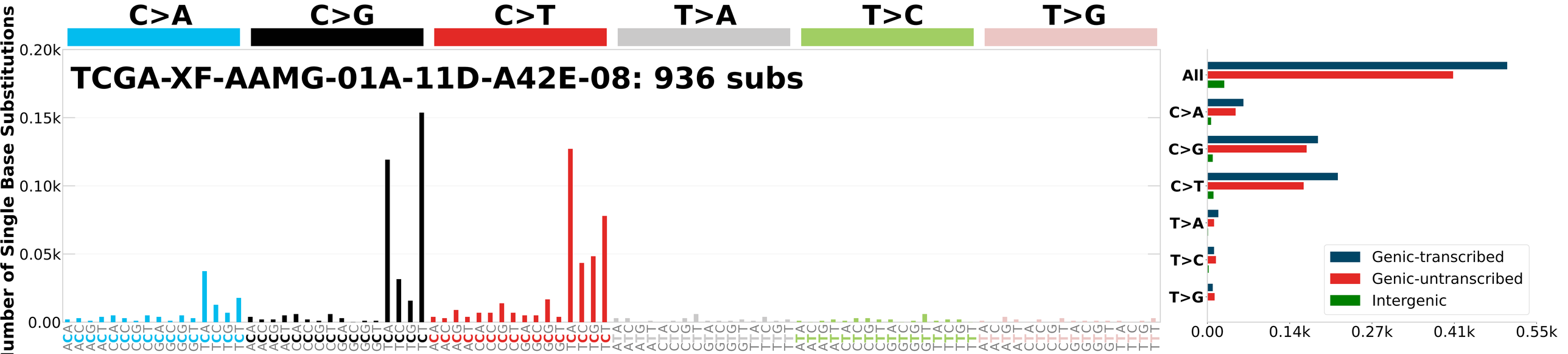

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9T6-01A-11D-A42E-08: 264 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.12k
0.16k

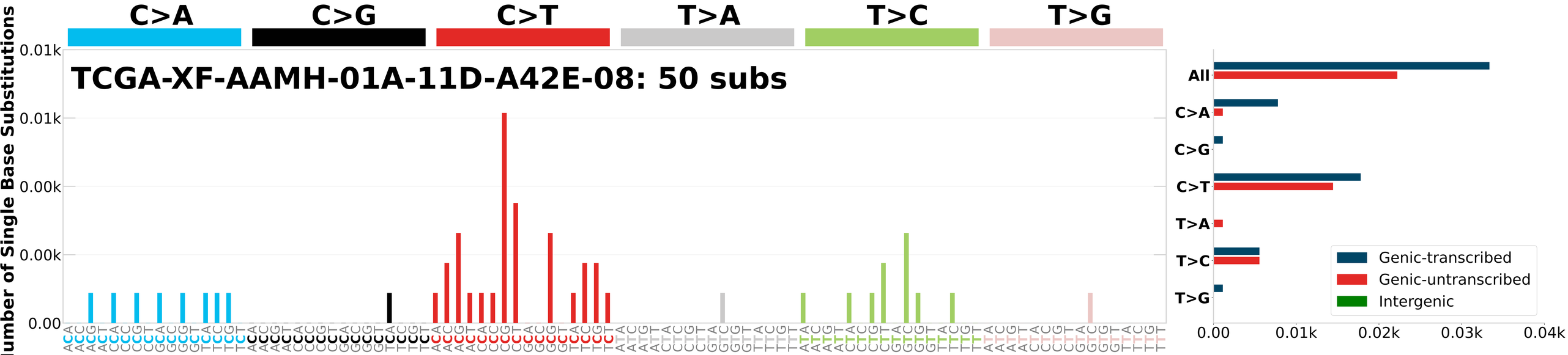

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-A9T8-01A-11D-A391-08: 717 subs
Number of Single Base Substitutions
0.19k
0.14k
0.10k
0.05k
0.00

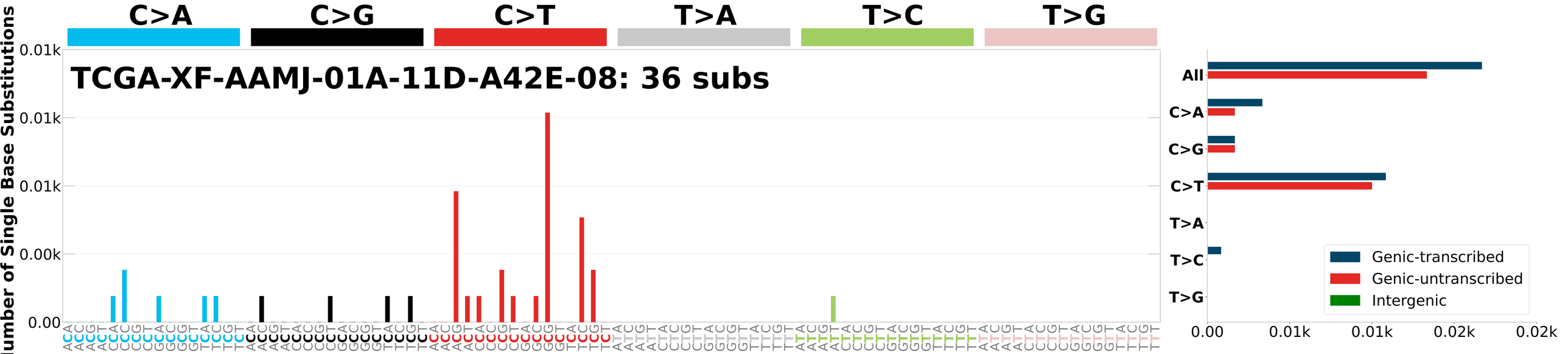

All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.10k
0.21k
0.31k
0.41k

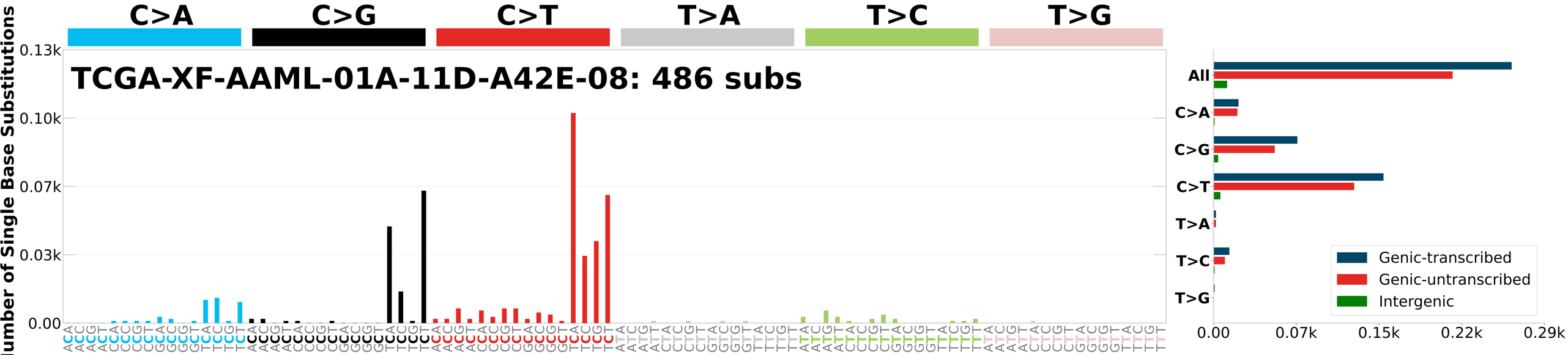

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAME-01A-12D-A42E-08: 19 subs
Number of Single Base Substitutions
0.00k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.00k
0.01k
0.01k
0.01k

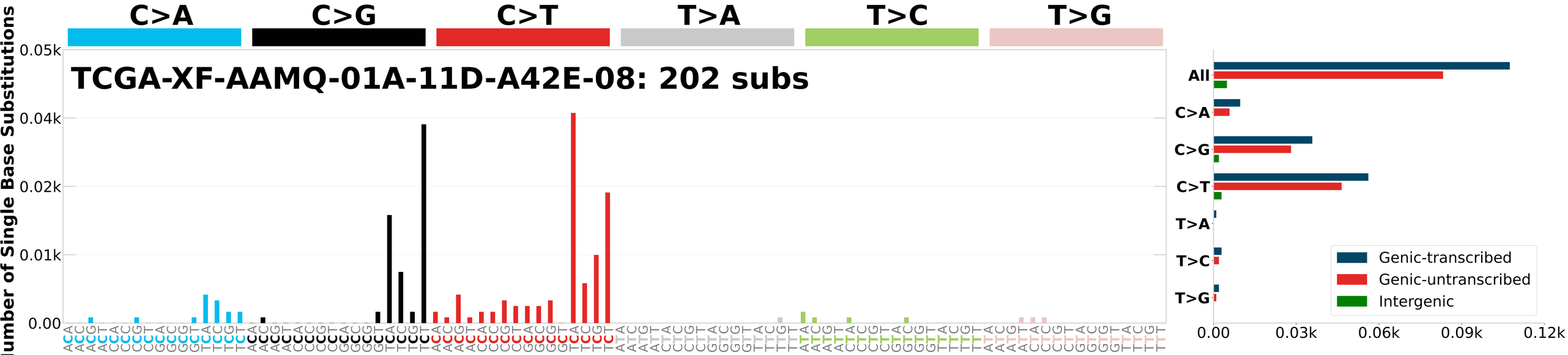

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAMF-01A-21D-A42E-08: 71 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

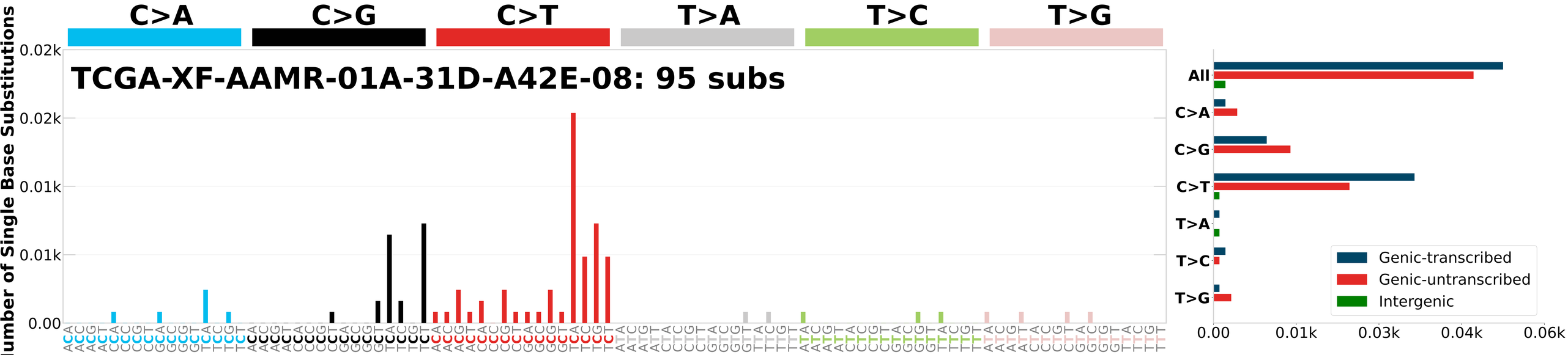

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAMG-01A-11D-A42E-08: 936 subs
Number of Single Base Substitutions
0.20k
0.15k
0.10k
0.05k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.14k
0.27k
0.41k
0.55k

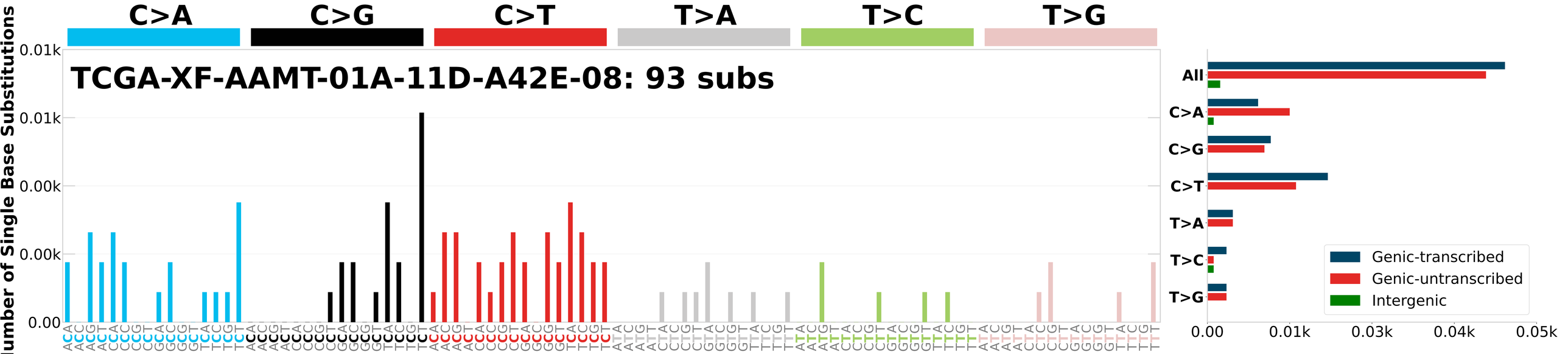

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAMH-01A-11D-A42E-08: 50 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

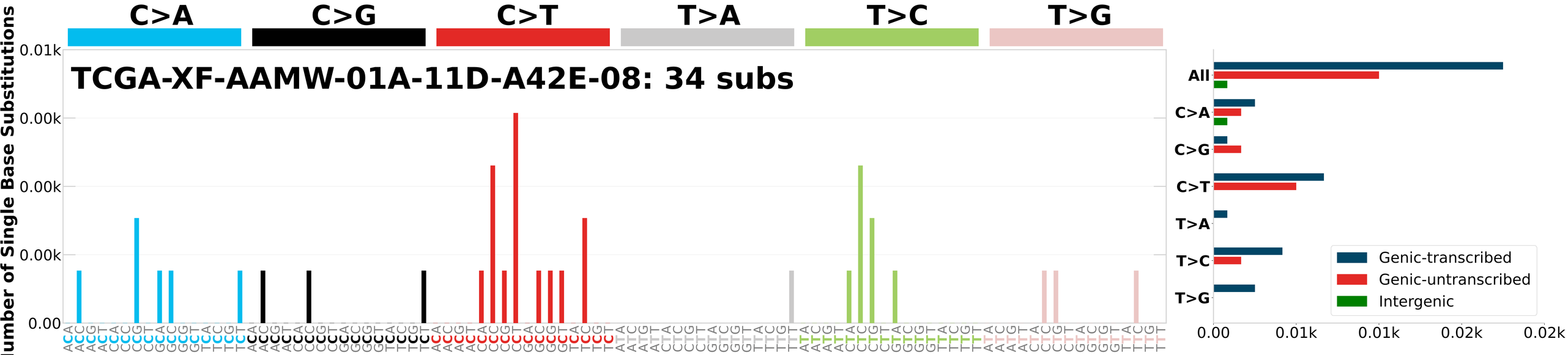

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAMJ-01A-11D-A42E-08: 36 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.02k
0.02k

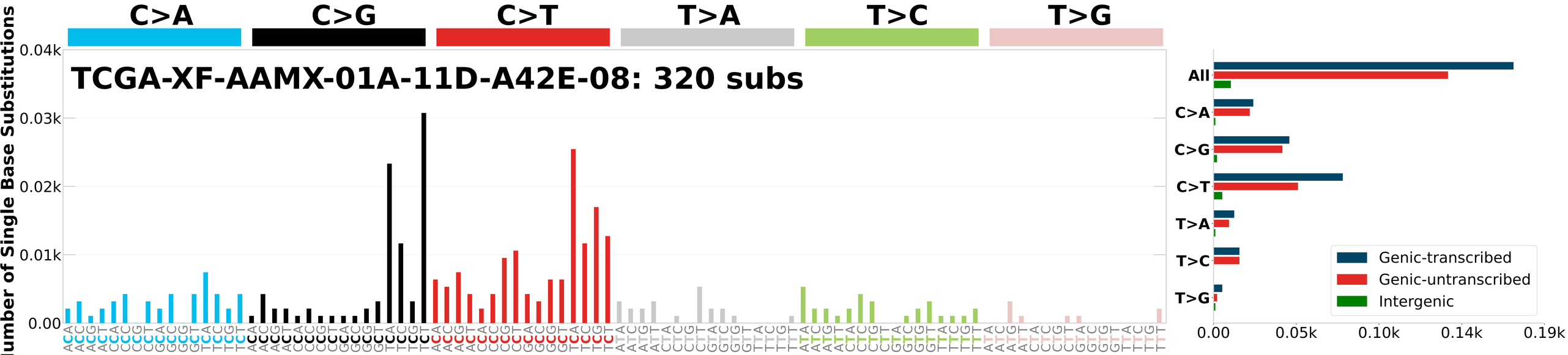

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAML-01A-11D-A42E-08: 486 subs
Number of Single Base Substitutions
0.13k
0.10k
0.07k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.15k
0.22k
0.29k

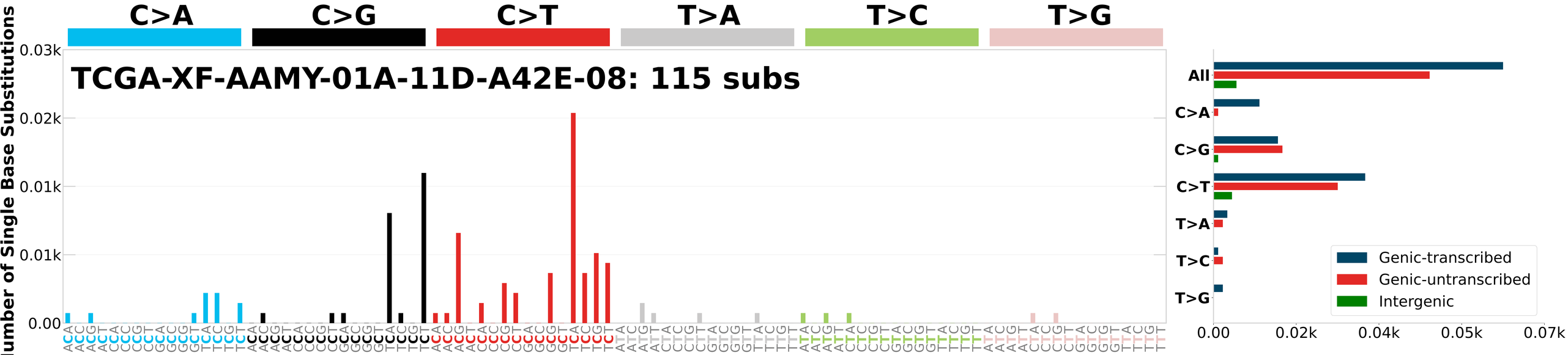

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAMQ-01A-11D-A42E-08: 202 subs
Number of Single Base Substitutions
0.05k
0.04k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

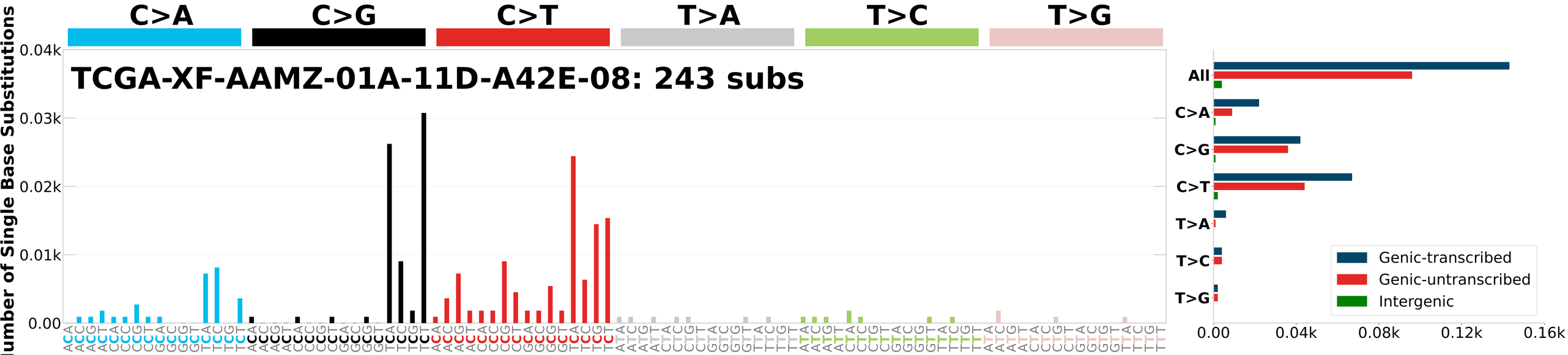

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAMR-01A-31D-A42E-08: 95 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

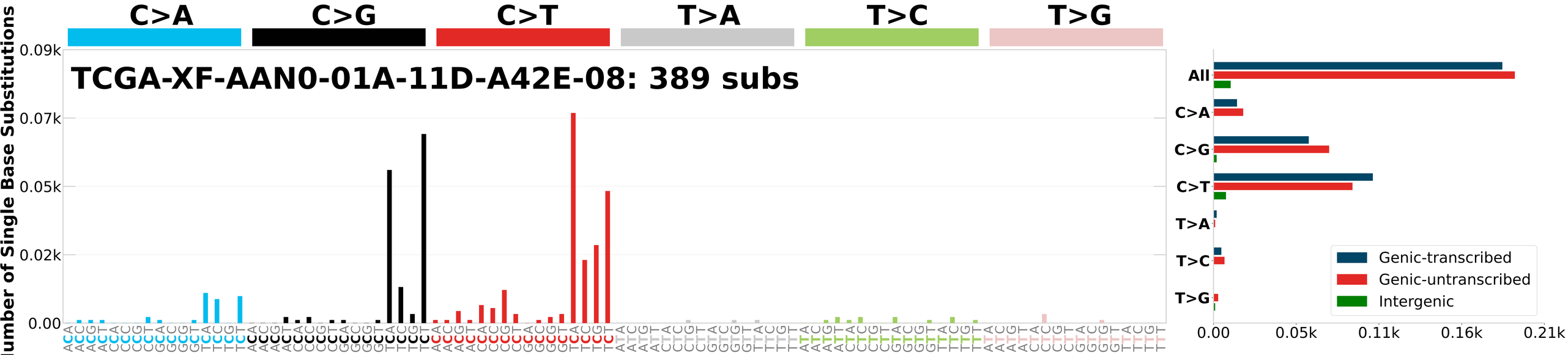

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAMT-01A-11D-A42E-08: 93 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

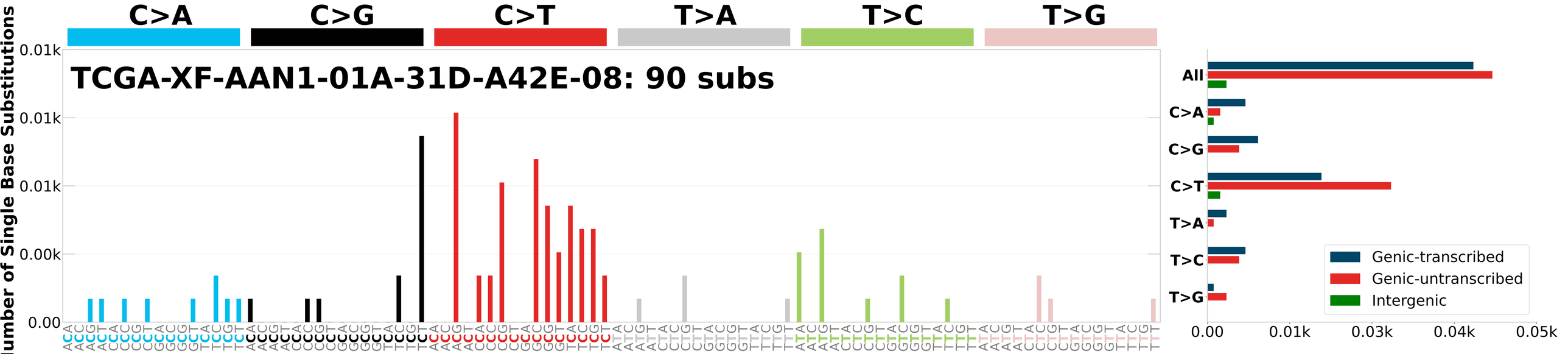

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAMW-01A-11D-A42E-08: 34 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.02k
0.02k

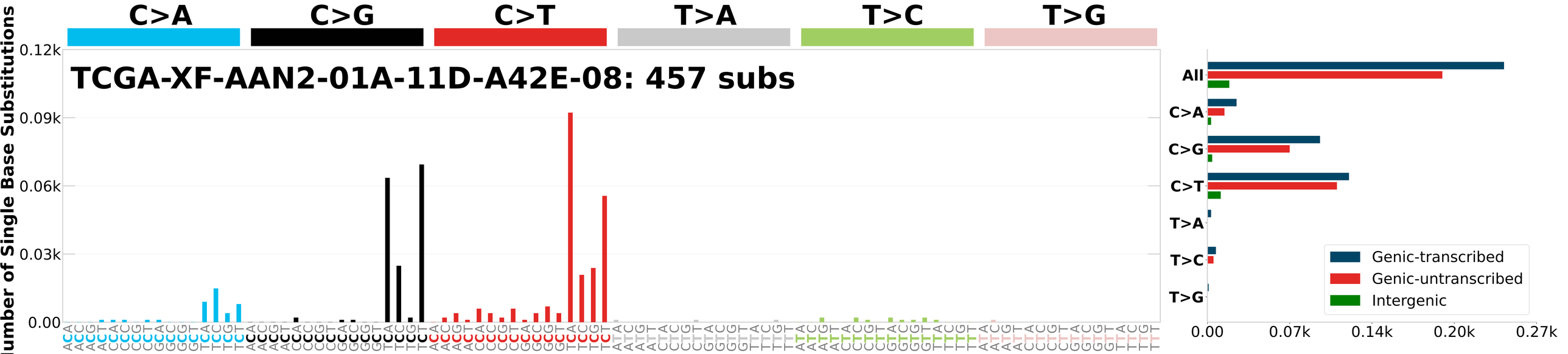

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAMX-01A-11D-A42E-08: 320 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.10k
0.14k
0.19k

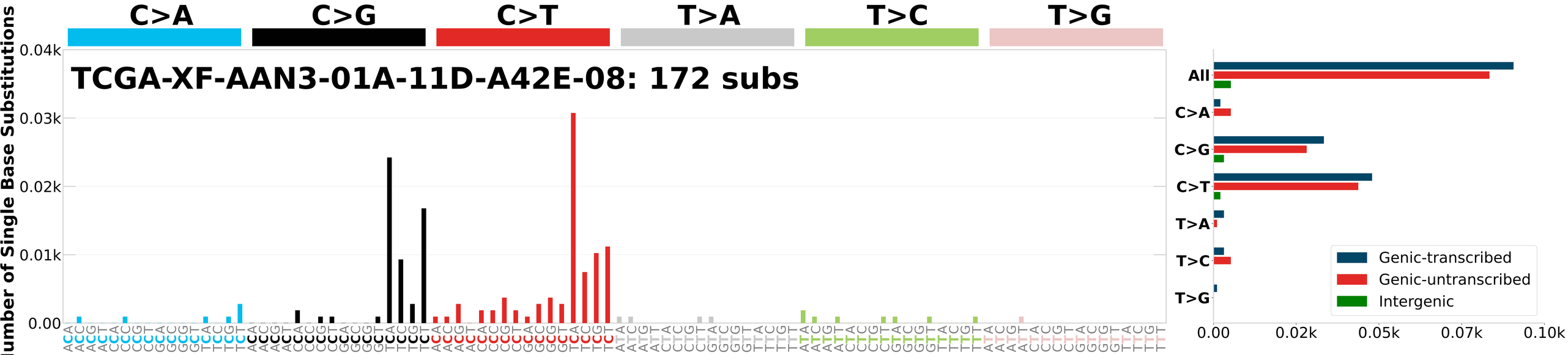

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAMY-01A-11D-A42E-08: 115 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.05k
0.07k

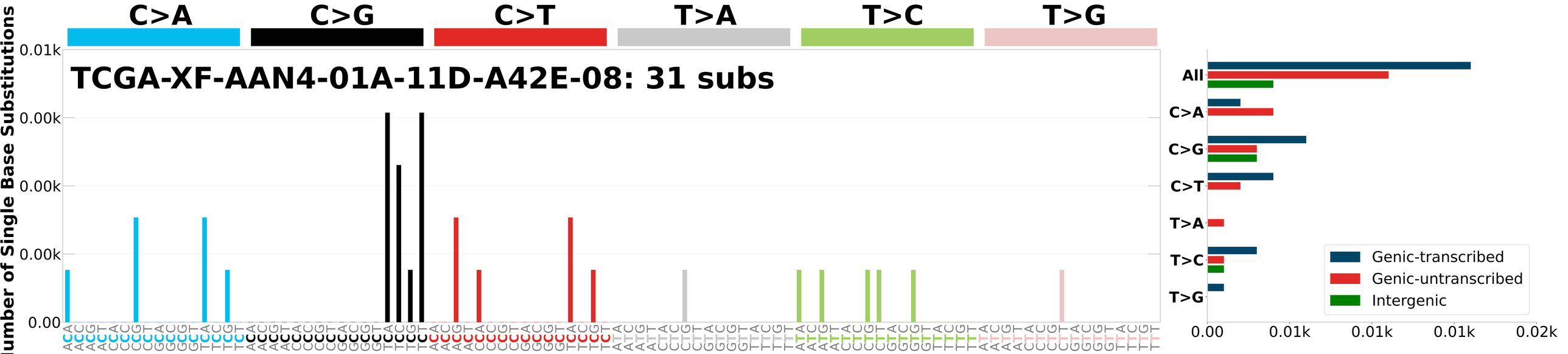

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAMZ-01A-11D-A42E-08: 243 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.08k
0.12k
0.16k

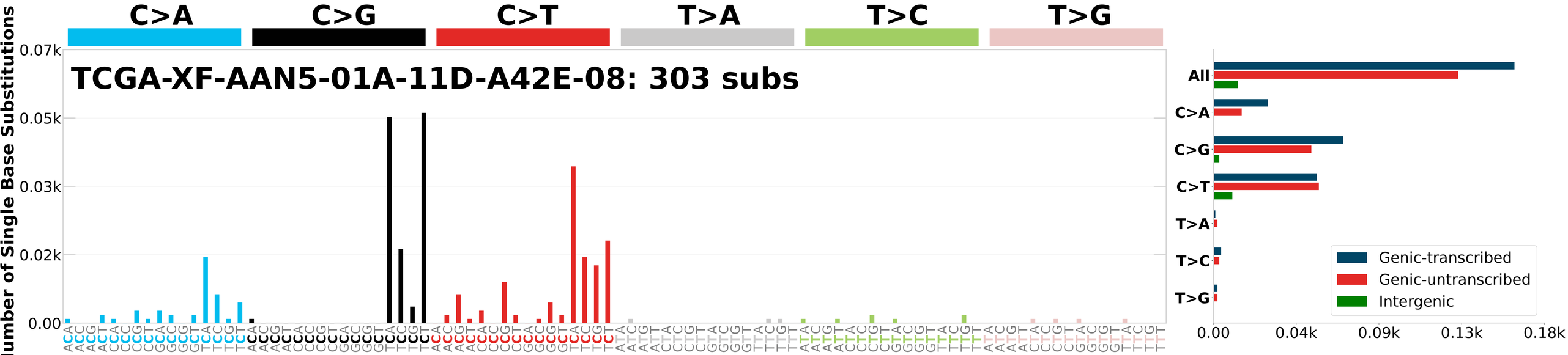

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAN0-01A-11D-A42E-08: 389 subs
Number of Single Base Substitutions
0.09k
0.07k
0.05k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.11k
0.16k
0.21k

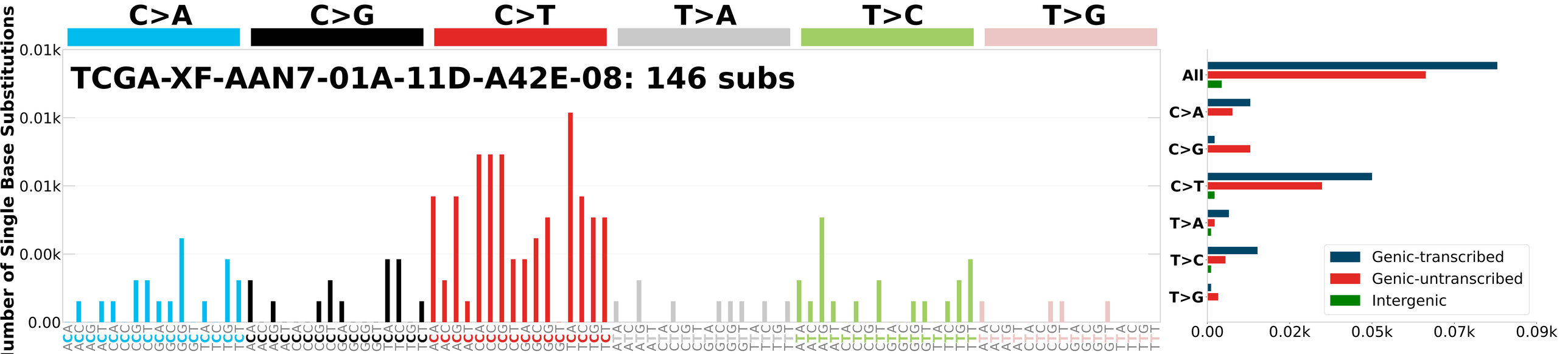

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAN1-01A-31D-A42E-08: 90 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

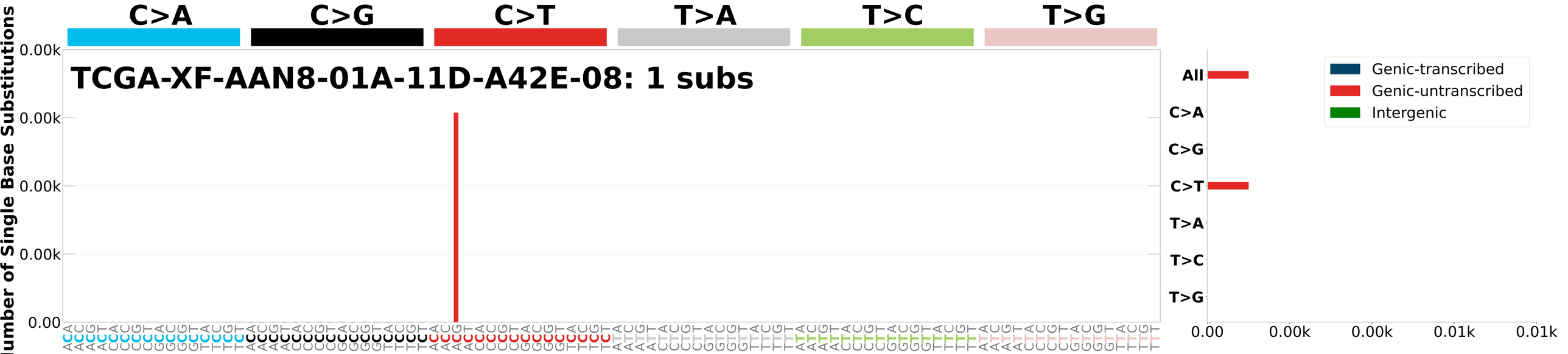

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAN2-01A-11D-A42E-08: 457 subs
Number of Single Base Substitutions
0.12k
0.09k
0.06k
0.03k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.14k
0.20k
0.27k

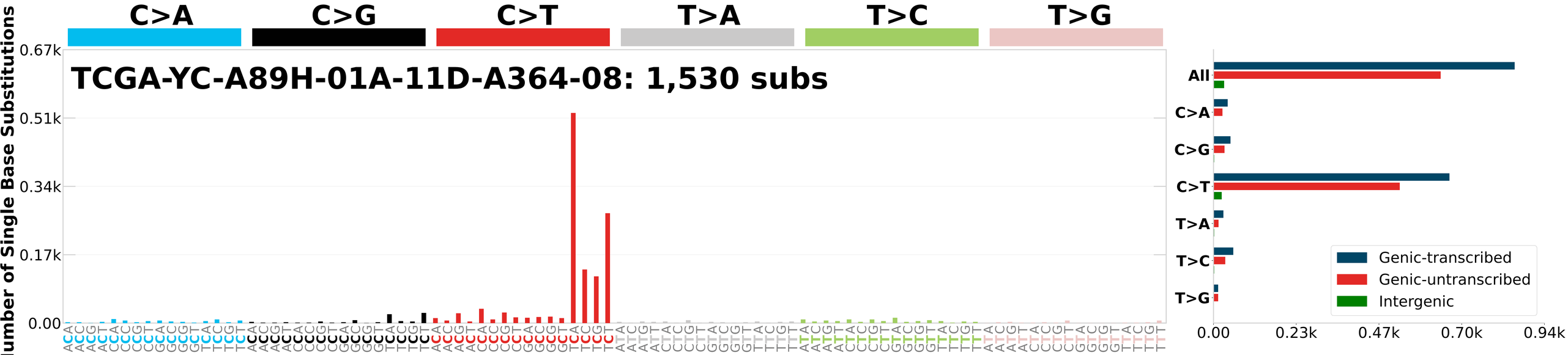

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAN3-01A-11D-A42E-08: 172 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.10k

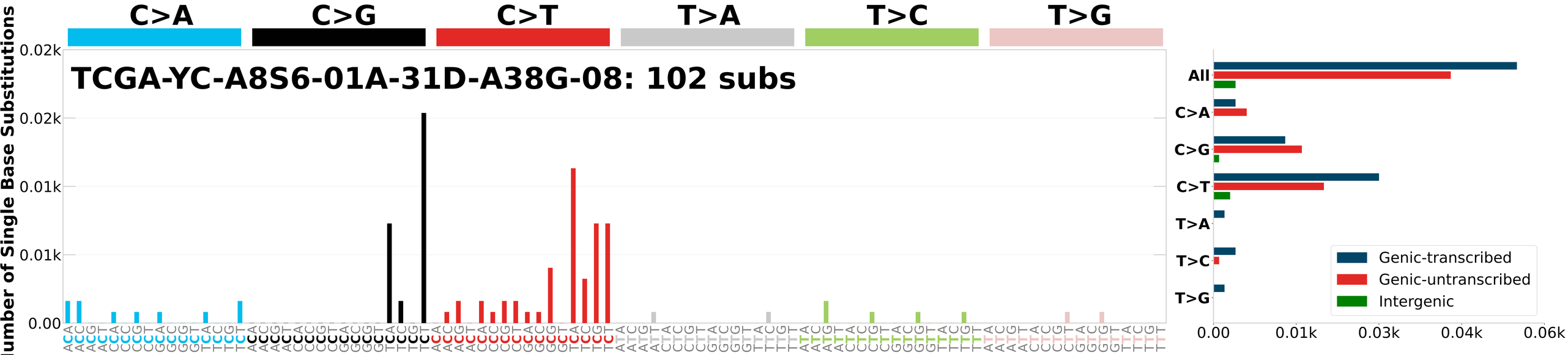

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAN4-01A-11D-A42E-08: 31 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.01k
0.02k

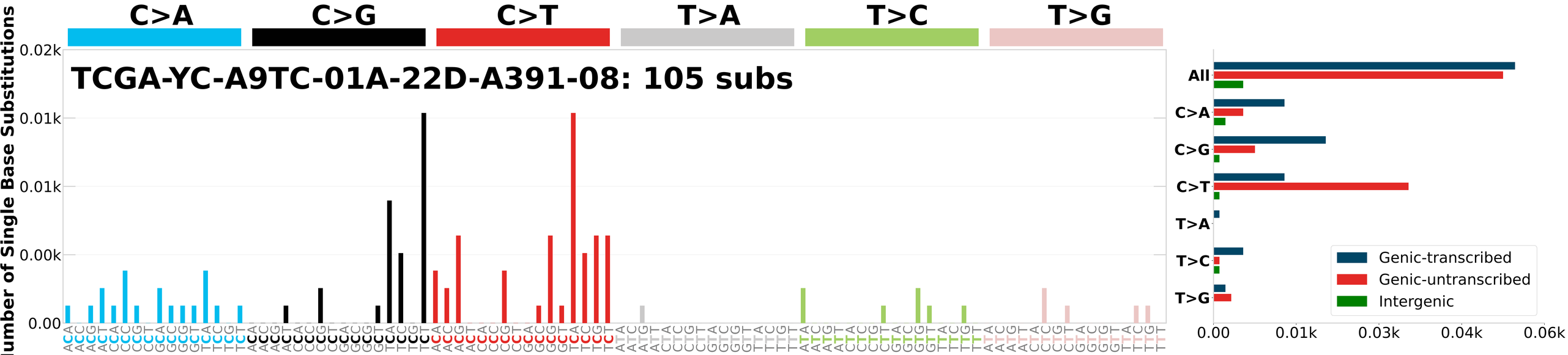

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAN5-01A-11D-A42E-08: 303 subs
Number of Single Base Substitutions
0.07k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.09k
0.13k
0.18k

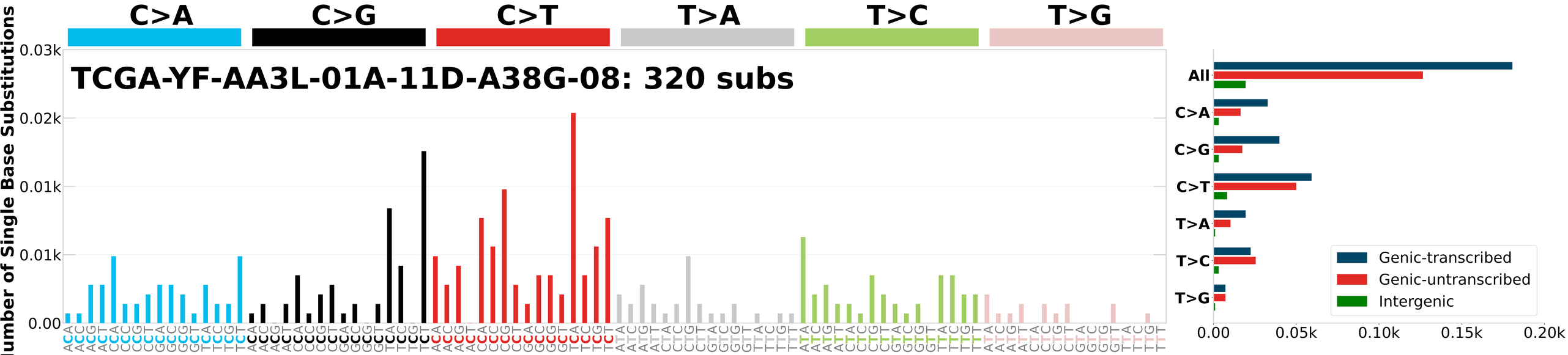

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAN7-01A-11D-A42E-08: 146 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.09k

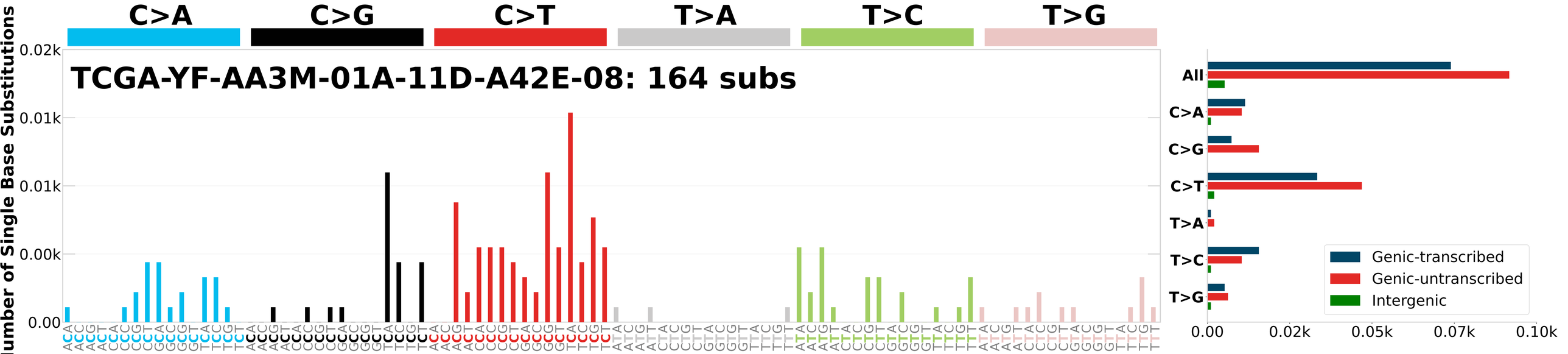

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-XF-AAN8-01A-11D-A42E-08: 1 subs
Number of Single Base Substitutions
0.00k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
0.00
0.00k
0.00k
0.01k
0.01k
Genic-transcribed
Genic-untranscribed
Intergenic

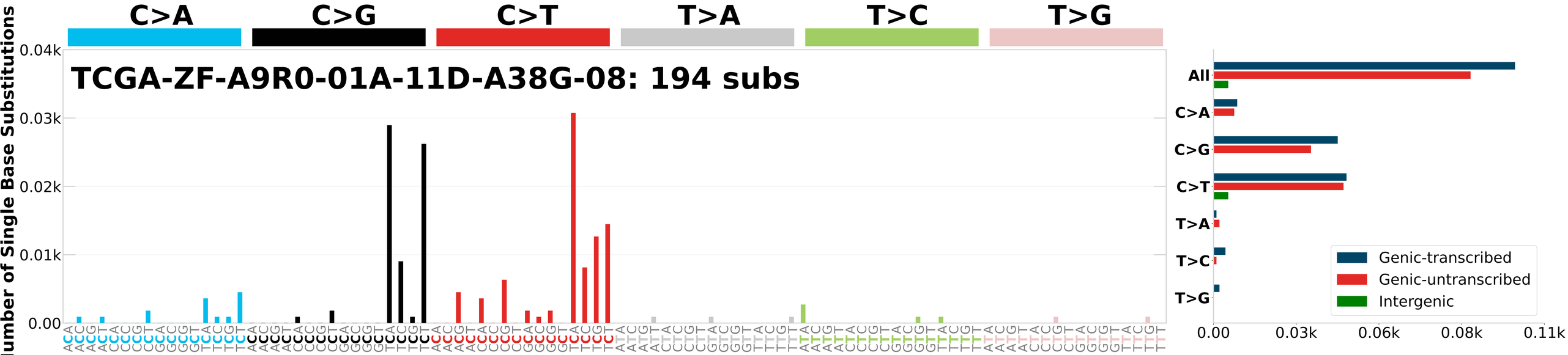

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-YC-A89H-01A-11D-A364-08: 1,530 subs
Number of Single Base Substitutions
0.67k
0.51k
0.34k
0.17k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.23k
0.47k
0.70k
0.94k

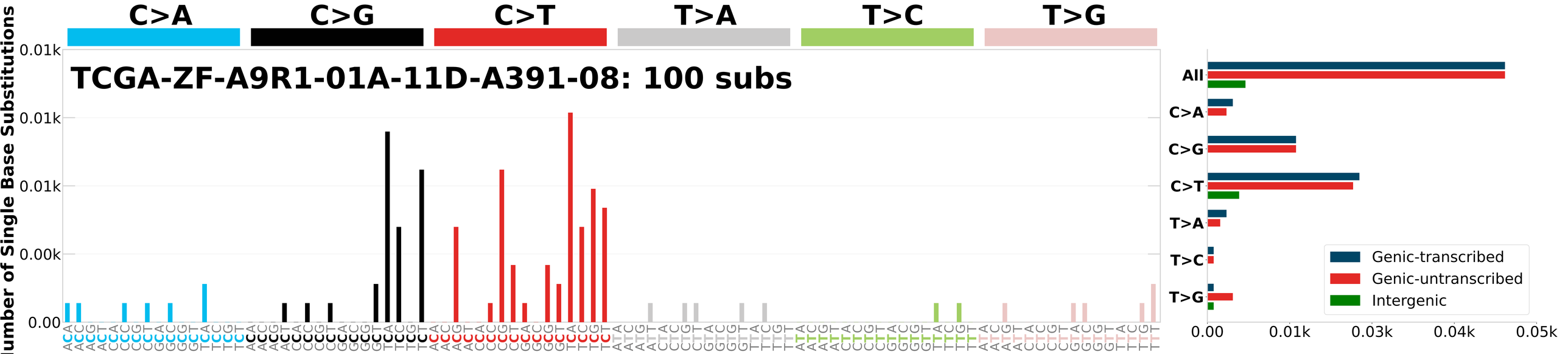

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-YC-A8S6-01A-31D-A38G-08: 102 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

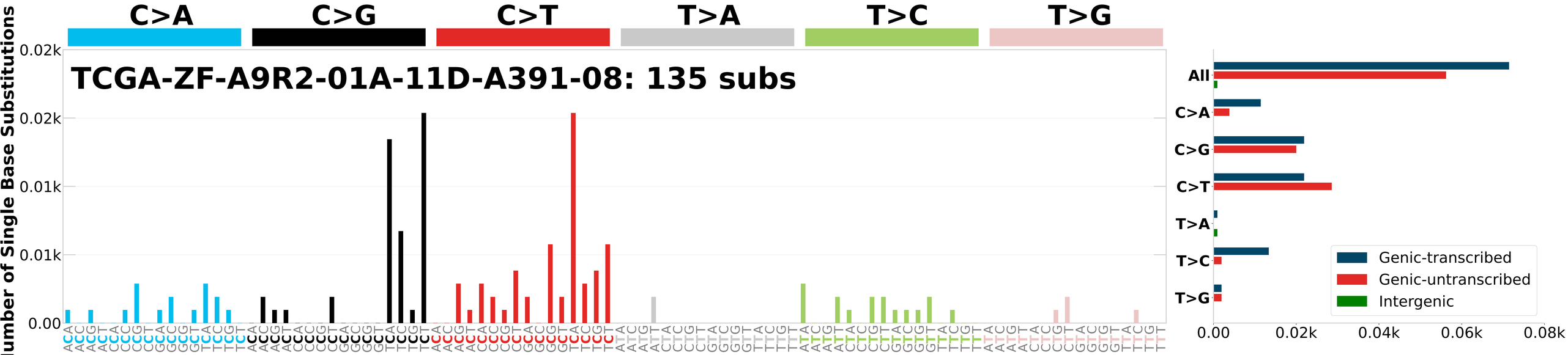

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-YC-A9TC-01A-22D-A391-08: 105 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

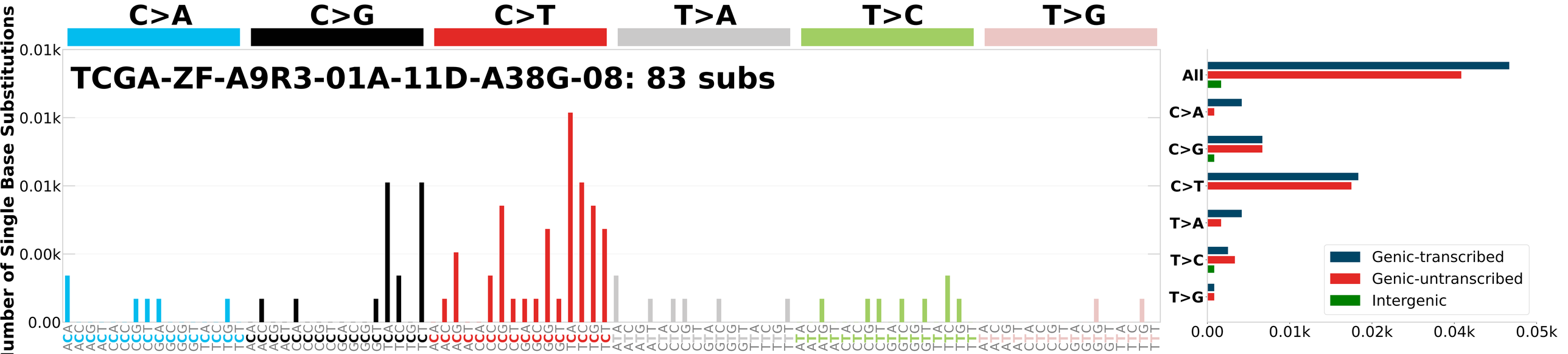

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-YF-AA3L-01A-11D-A38G-08: 320 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.10k
0.15k
0.20k

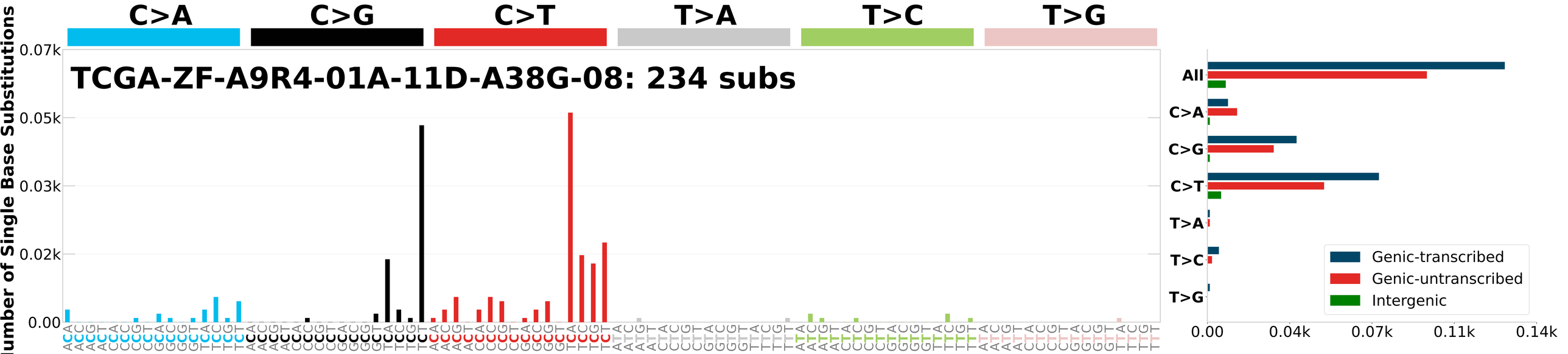

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-YF-AA3M-01A-11D-A42E-08: 164 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.10k

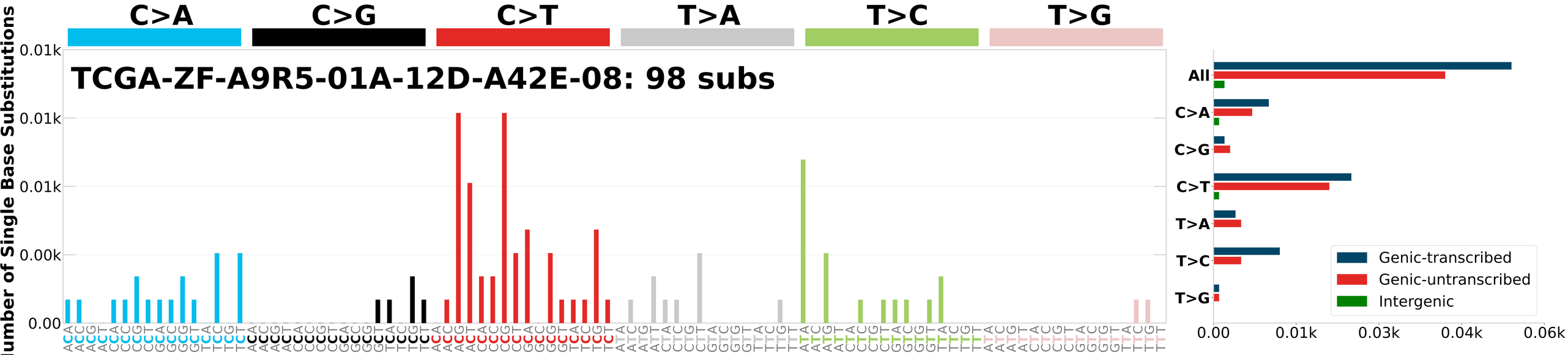

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9R0-01A-11D-A38G-08: 194 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.08k
0.11k

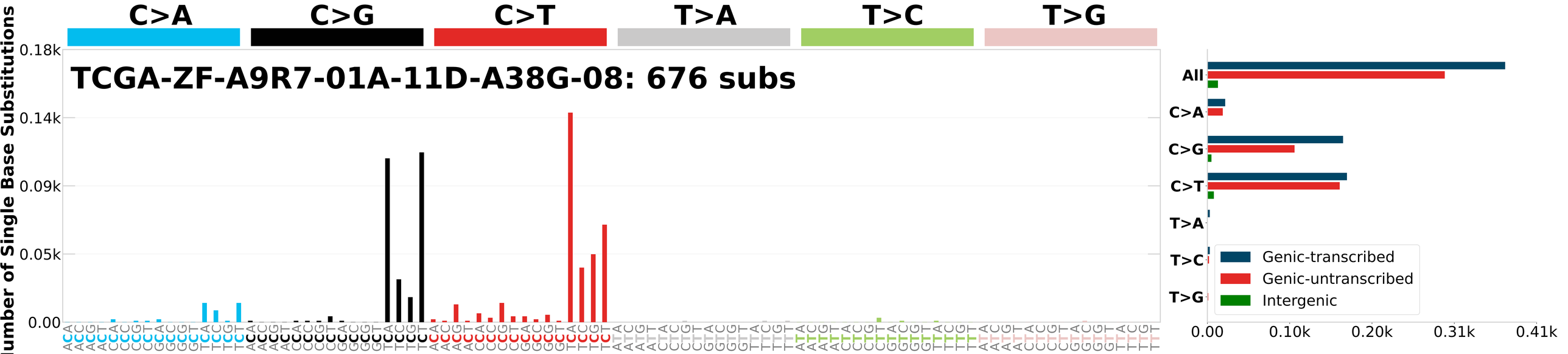

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9R1-01A-11D-A391-08: 100 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

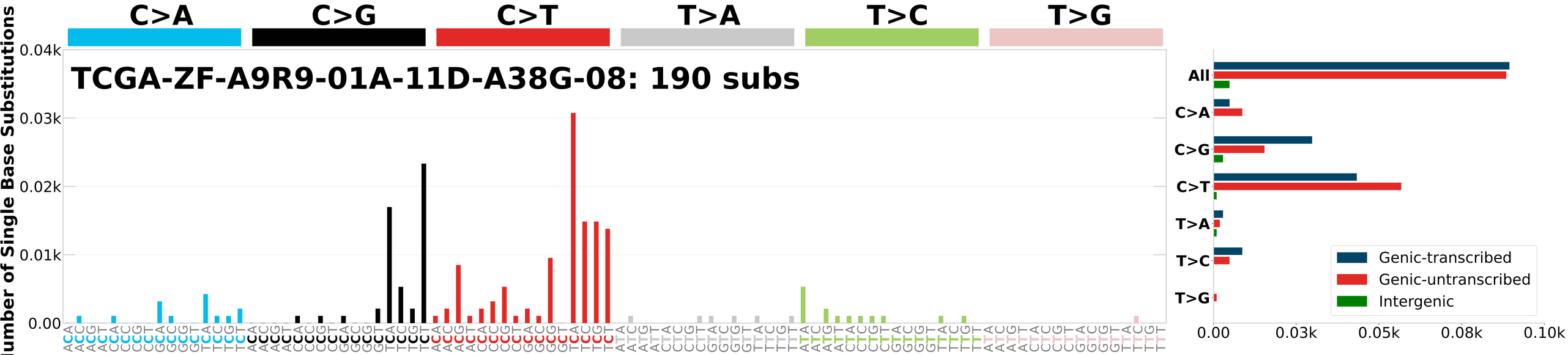

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9R2-01A-11D-A391-08: 135 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

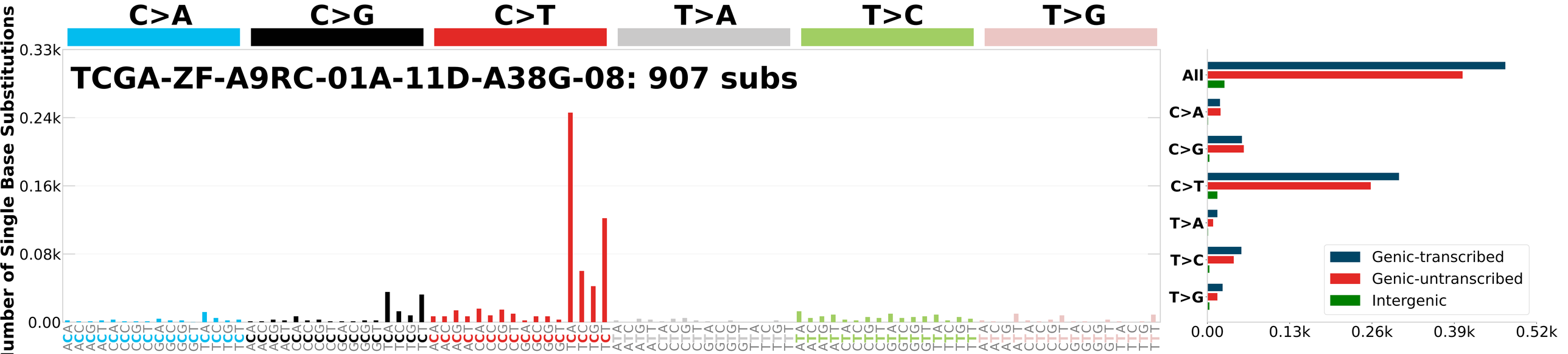

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9R3-01A-11D-A38G-08: 83 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.04k
0.05k

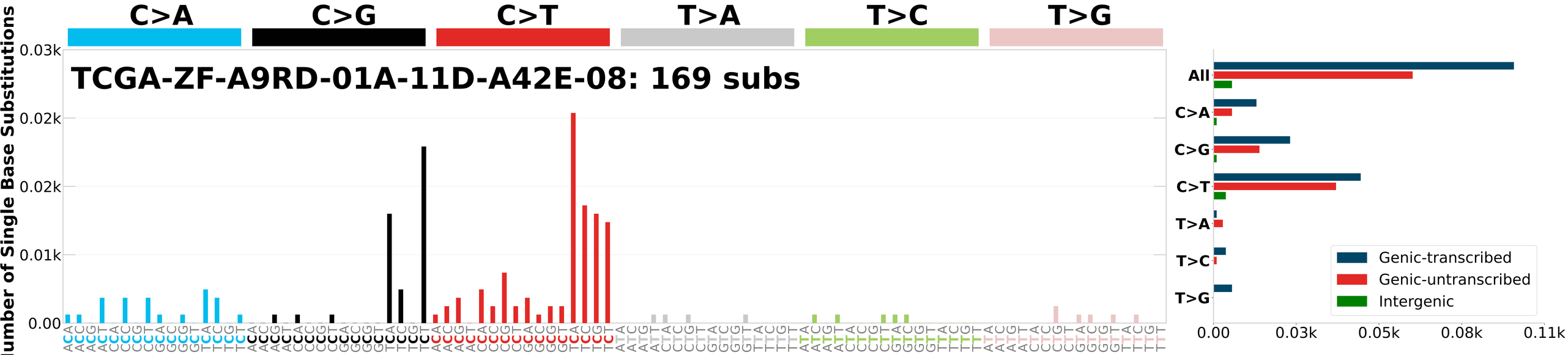

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9R4-01A-11D-A38G-08: 234 subs
Number of Single Base Substitutions
0.07k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.04k
0.07k
0.11k
0.14k

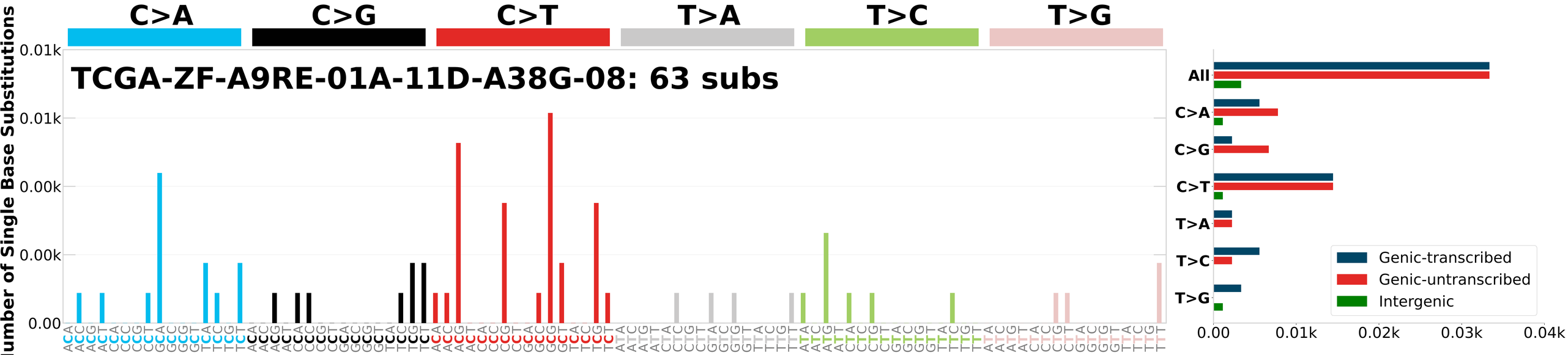

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9R5-01A-12D-A42E-08: 98 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

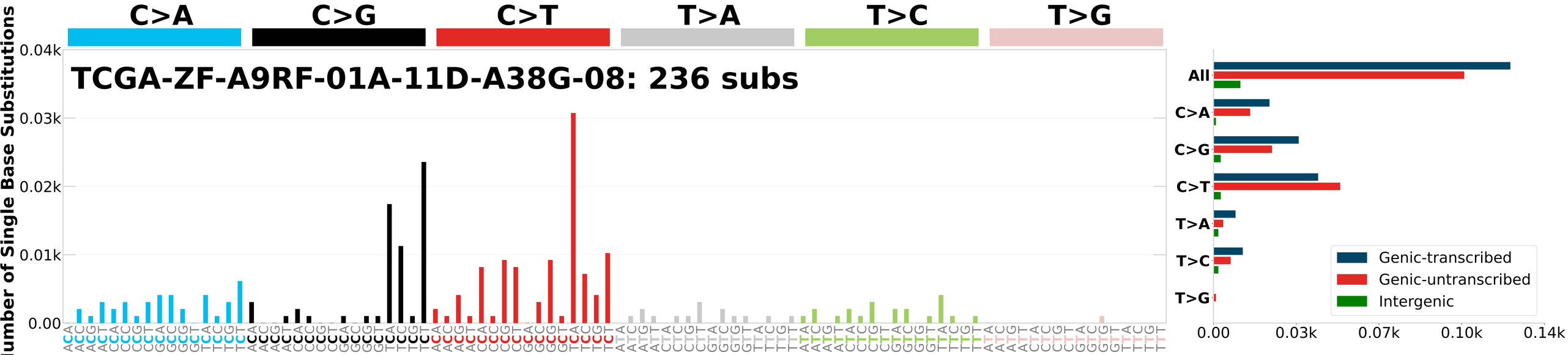

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9R7-01A-11D-A38G-08: 676 subs
Number of Single Base Substitutions
0.18k
0.14k
0.09k
0.05k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.10k
0.20k
0.31k
0.41k

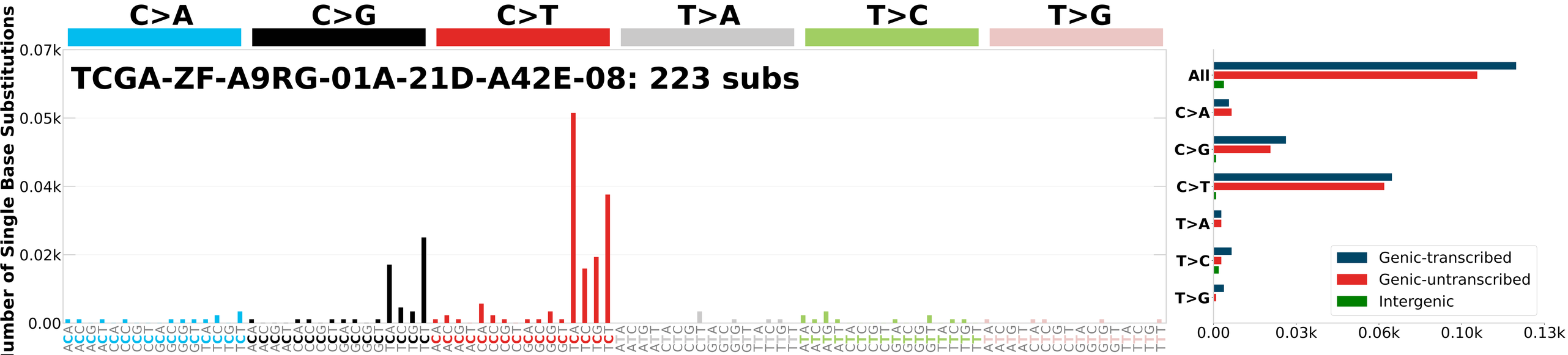

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9R9-01A-11D-A38G-08: 190 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.10k

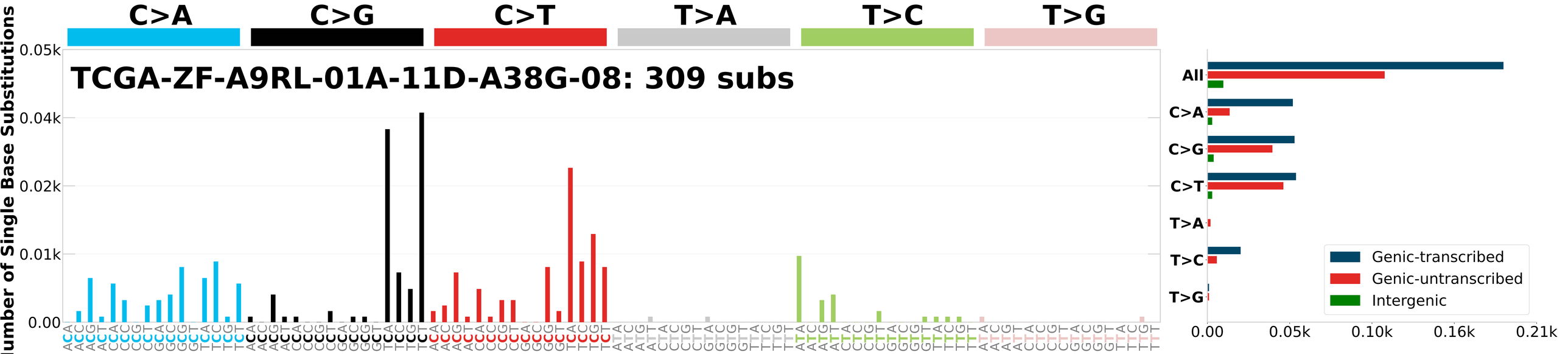

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9RC-01A-11D-A38G-08: 907 subs
Number of Single Base Substitutions
0.33k
0.24k
0.16k
0.08k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.13k
0.26k
0.39k
0.52k

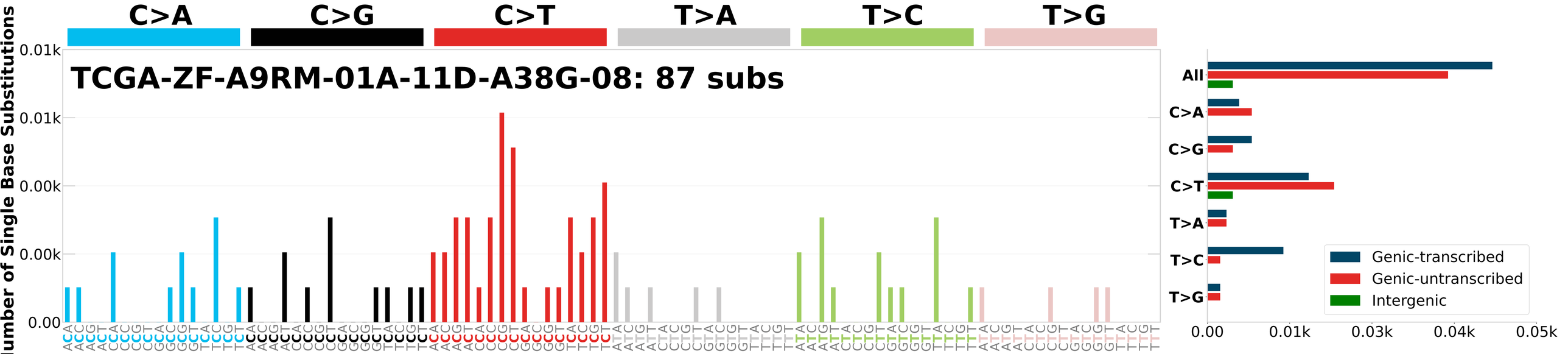

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9RD-01A-11D-A42E-08: 169 subs
Number of Single Base Substitutions
0.03k
0.02k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.05k
0.08k
0.11k

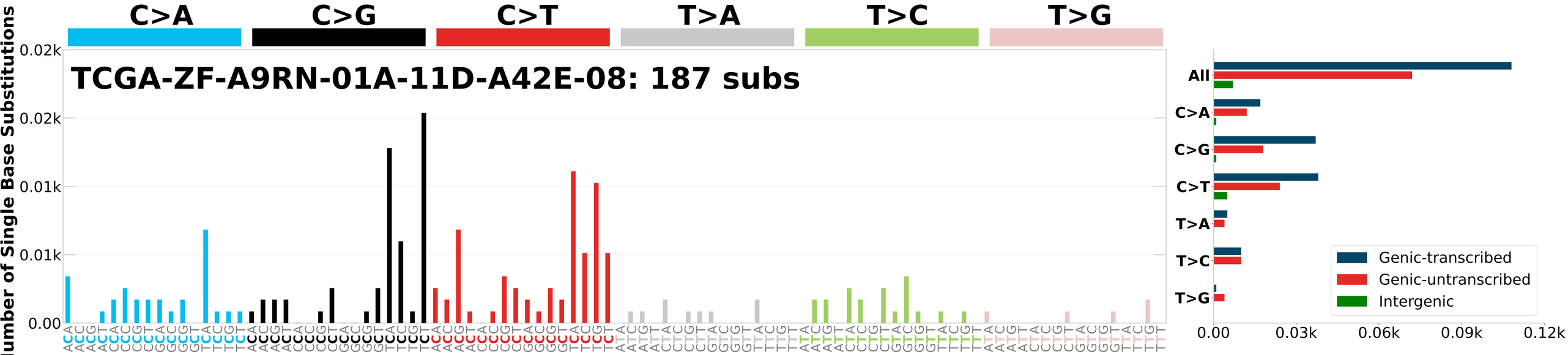

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9RE-01A-11D-A38G-08: 63 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

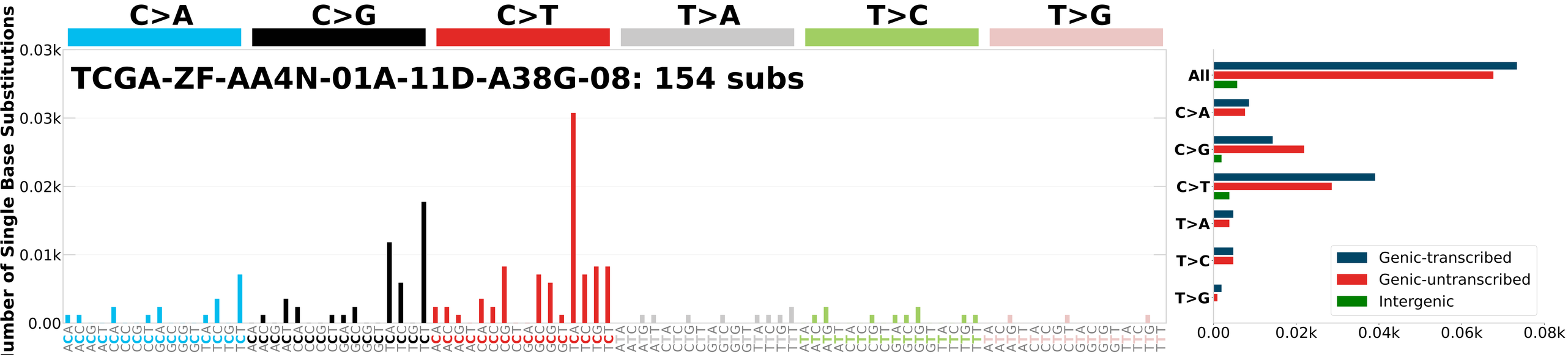

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9RF-01A-11D-A38G-08: 236 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.14k

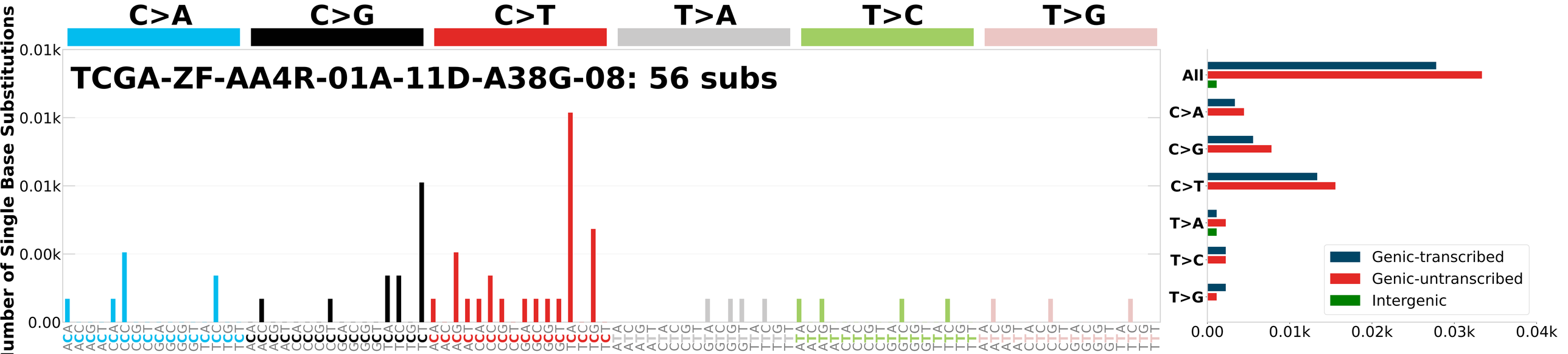

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9RG-01A-21D-A42E-08: 223 subs
Number of Single Base Substitutions
0.07k
0.05k
0.04k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.10k
0.13k

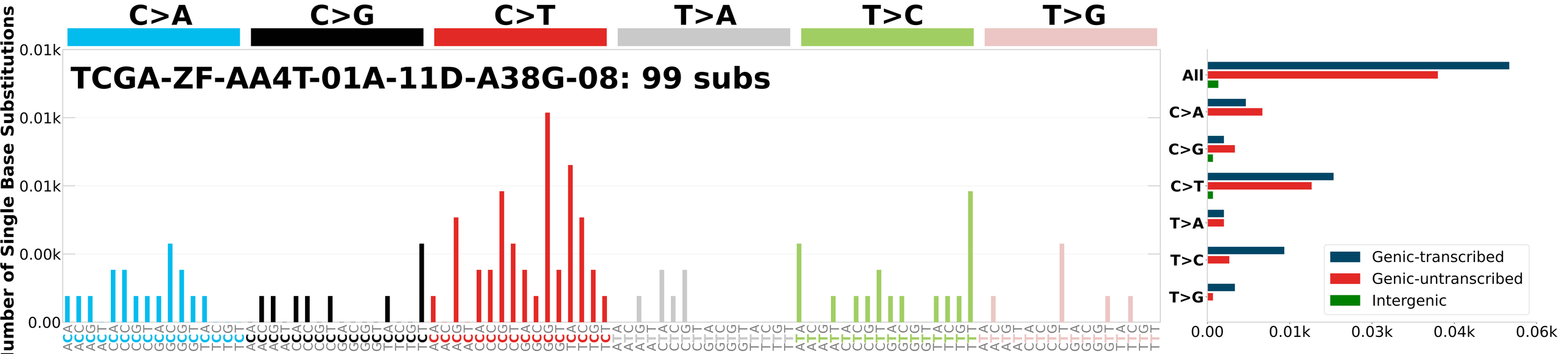

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9RL-01A-11D-A38G-08: 309 subs
Number of Single Base Substitutions
0.05k
0.04k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.05k
0.10k
0.16k
0.21k

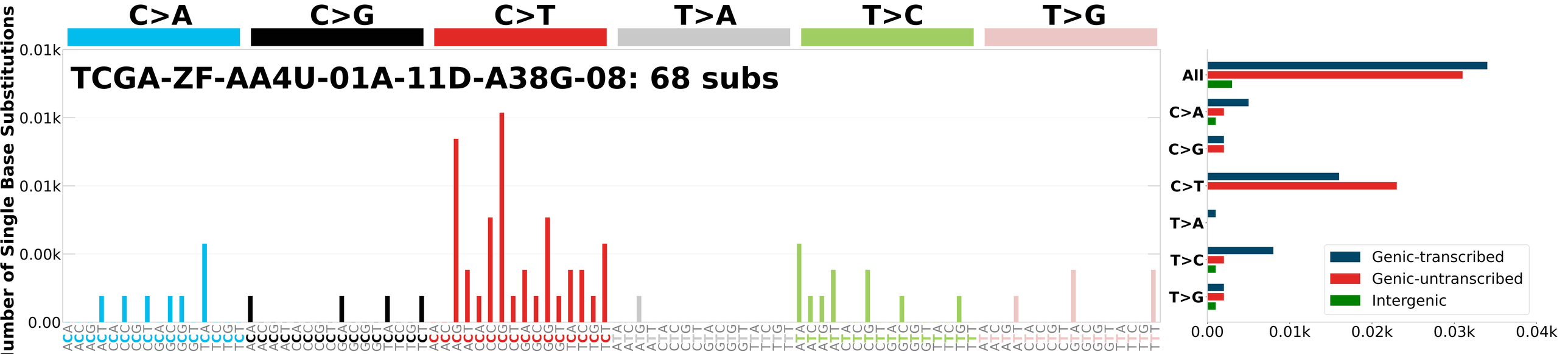

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9RM-01A-11D-A38G-08: 87 subs
Number of Single Base Substitutions
0.01k
0.01k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.05k

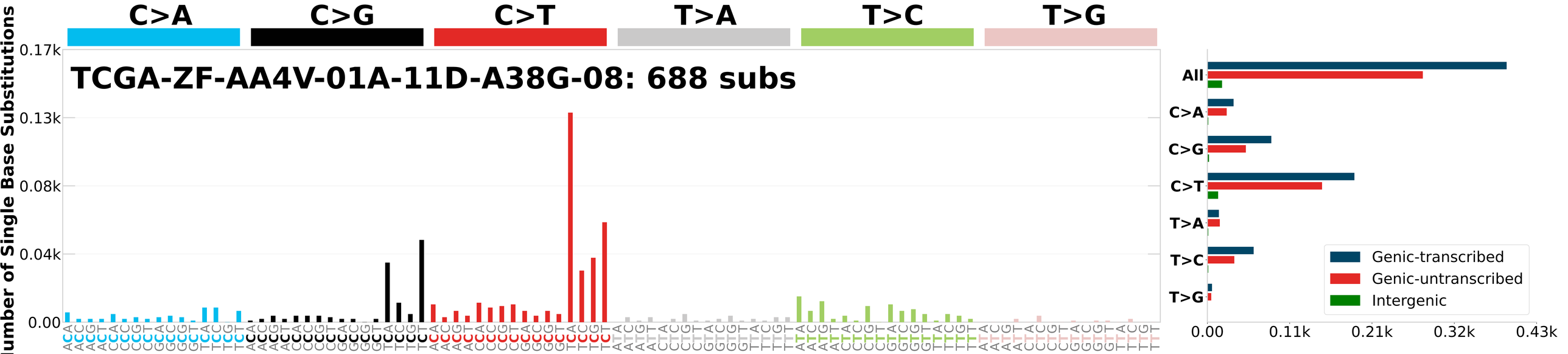

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-A9RN-01A-11D-A42E-08: 187 subs
Number of Single Base Substitutions
0.02k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k

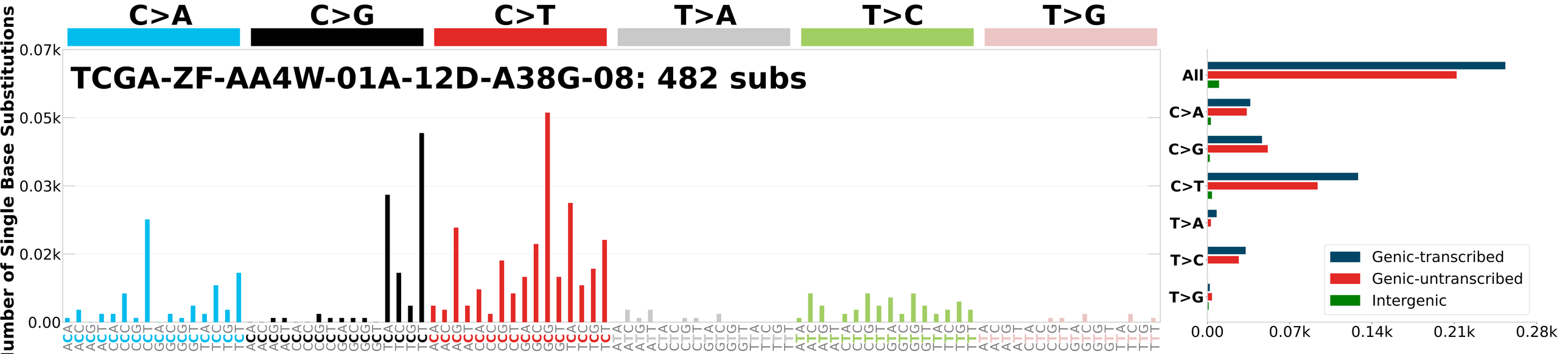

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA4N-01A-11D-A38G-08: 154 subs
Number of Single Base Substitutions
0.03k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.04k
0.06k
0.08k

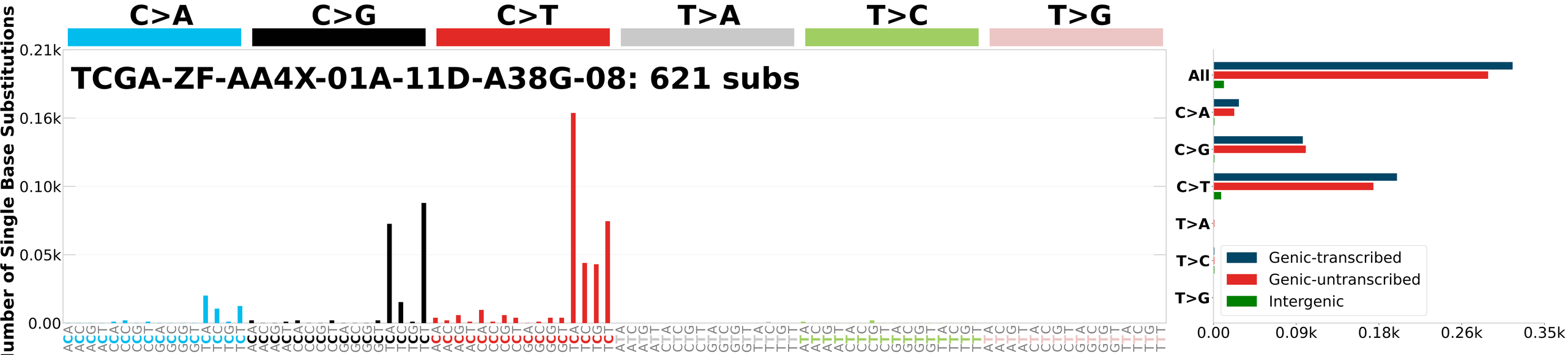

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA4R-01A-11D-A38G-08: 56 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

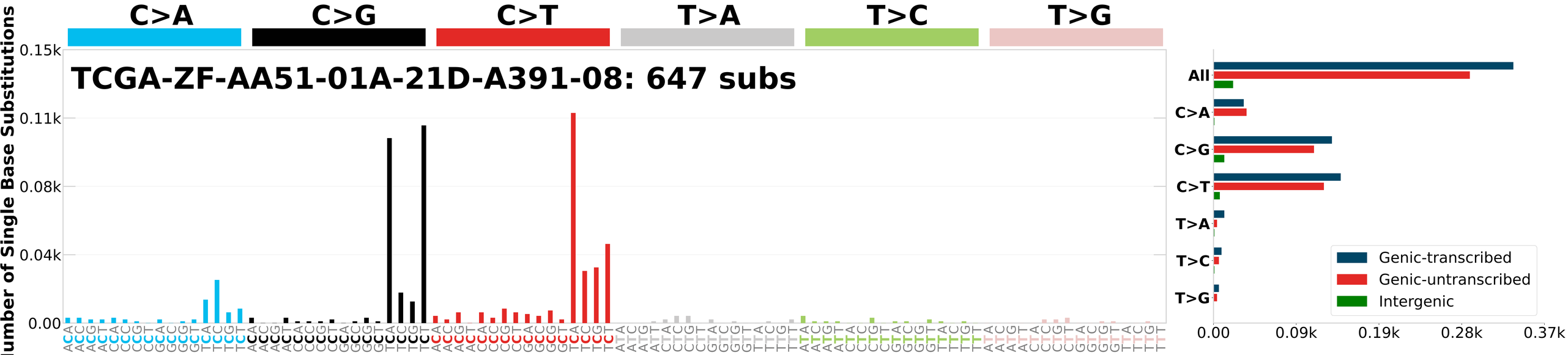

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA4T-01A-11D-A38G-08: 99 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k

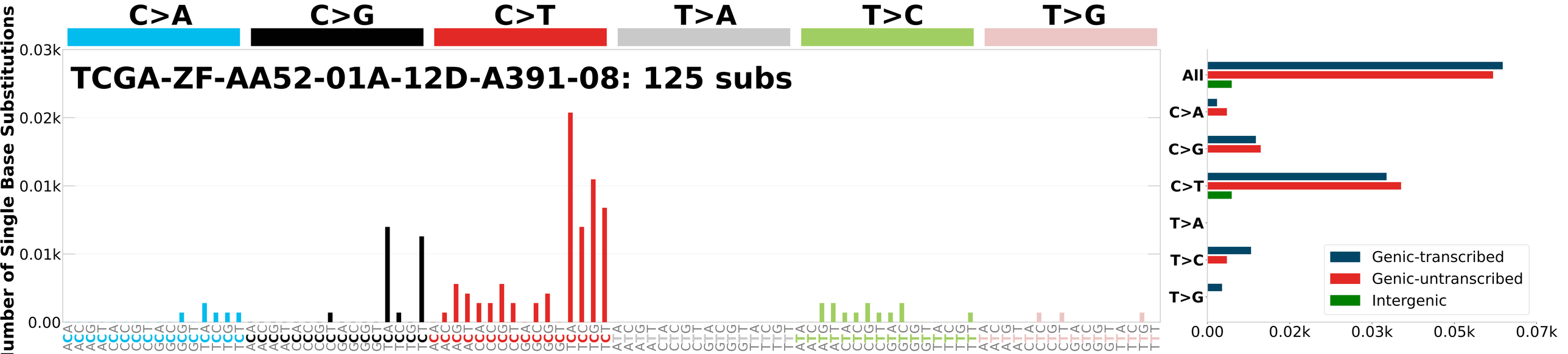

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA4U-01A-11D-A38G-08: 68 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k

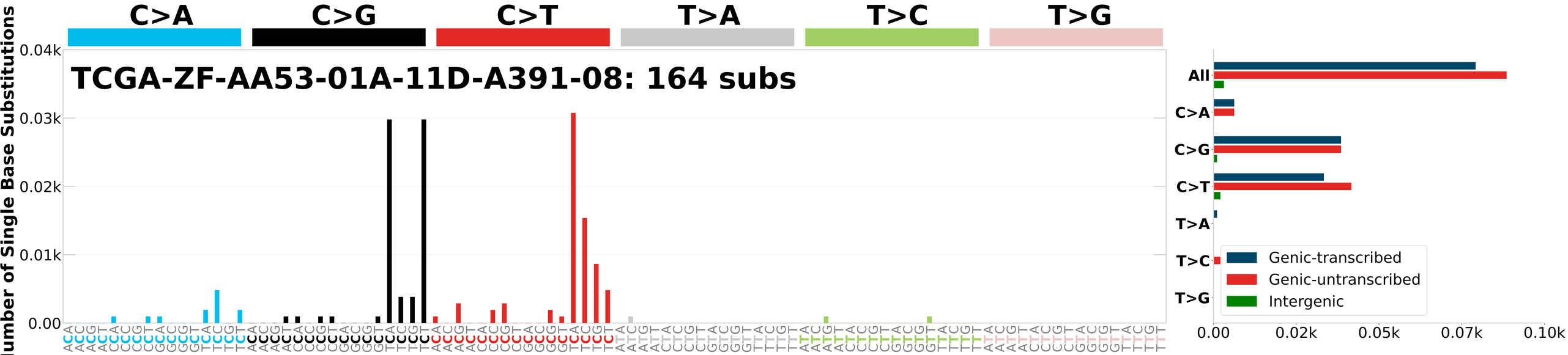

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA4V-01A-11D-A38G-08: 688 subs
Number of Single Base Substitutions
0.17k
0.13k
0.08k
0.04k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.11k
0.21k
0.32k
0.43k

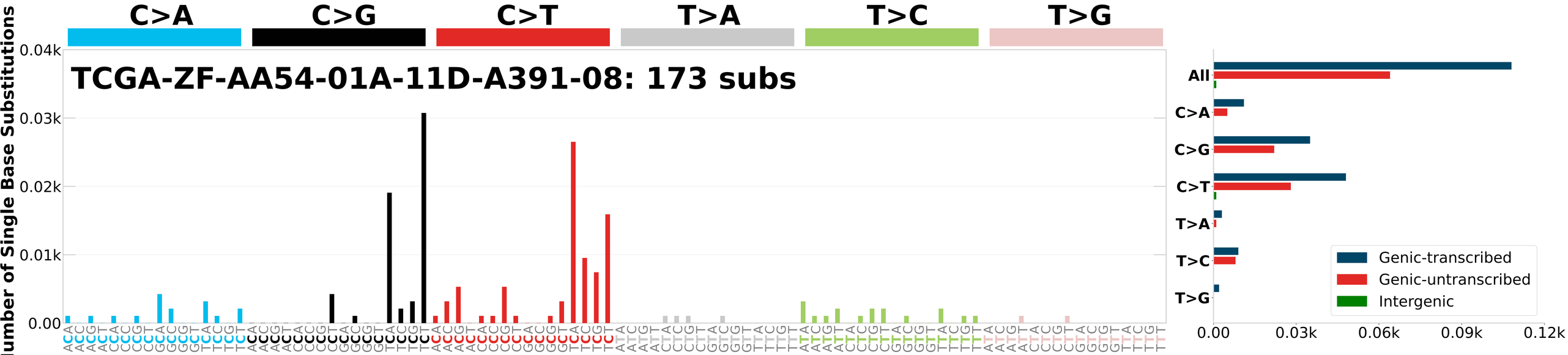

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA4W-01A-12D-A38G-08: 482 subs
Number of Single Base Substitutions
0.07k
0.05k
0.03k
0.02k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.07k
0.14k
0.21k
0.28k

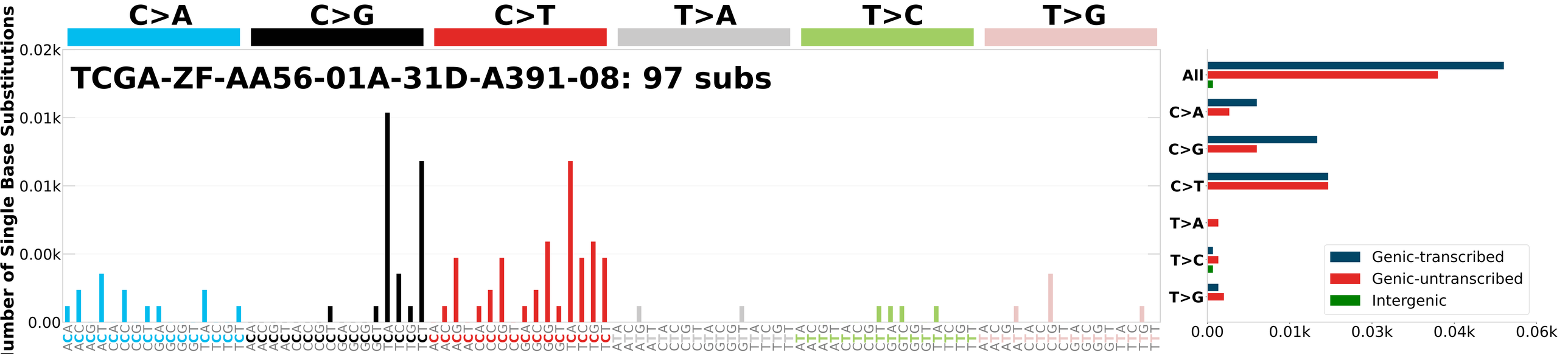

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA4X-01A-11D-A38G-08: 621 subs
Number of Single Base Substitutions
0.21k
0.16k
0.10k
0.05k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.09k
0.18k
0.26k
0.35k

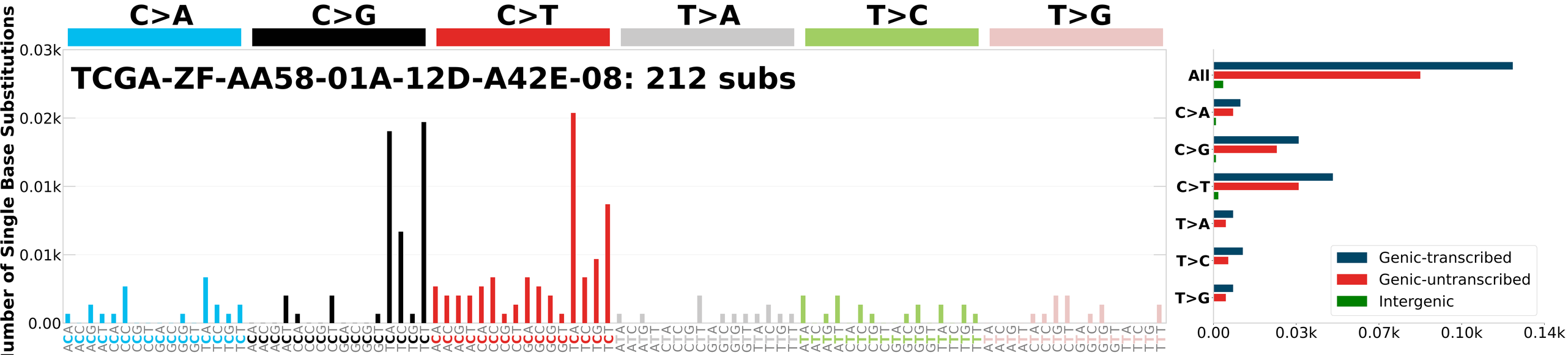

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA51-01A-21D-A391-08: 647 subs
Number of Single Base Substitutions
0.15k
0.11k
0.08k
0.04k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.09k
0.19k
0.28k
0.37k

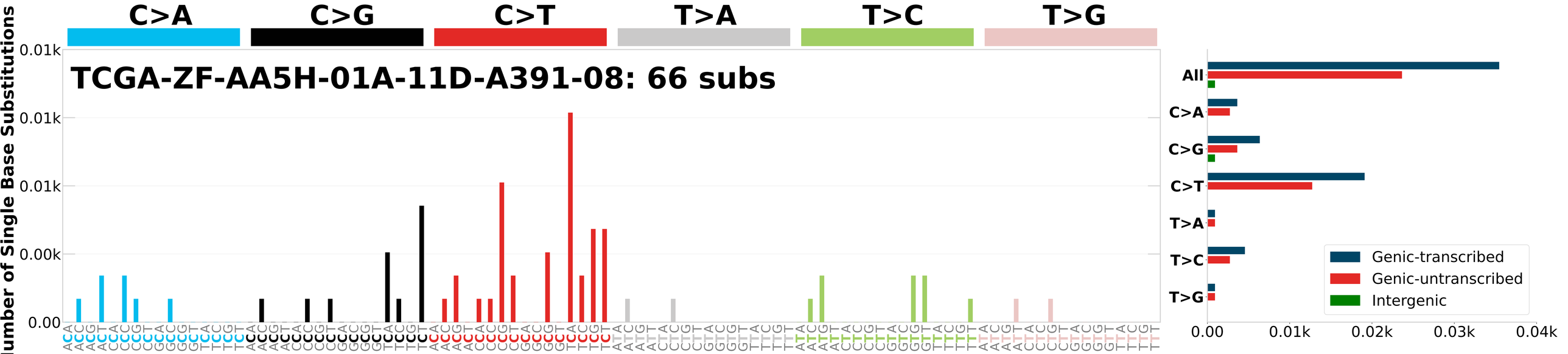

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA52-01A-12D-A391-08: 125 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.03k
0.05k
0.07k

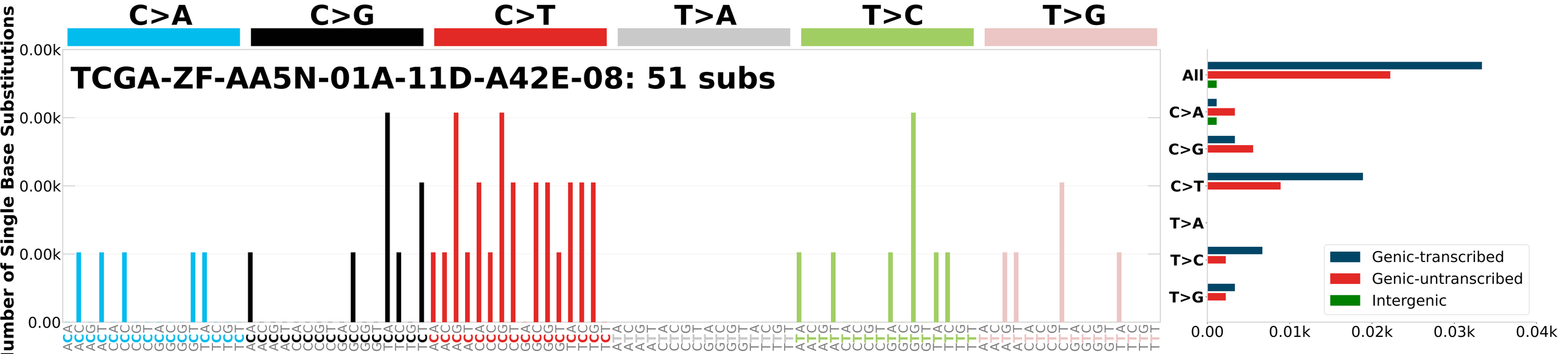

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA53-01A-11D-A391-08: 164 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.02k
0.05k
0.07k
0.10k

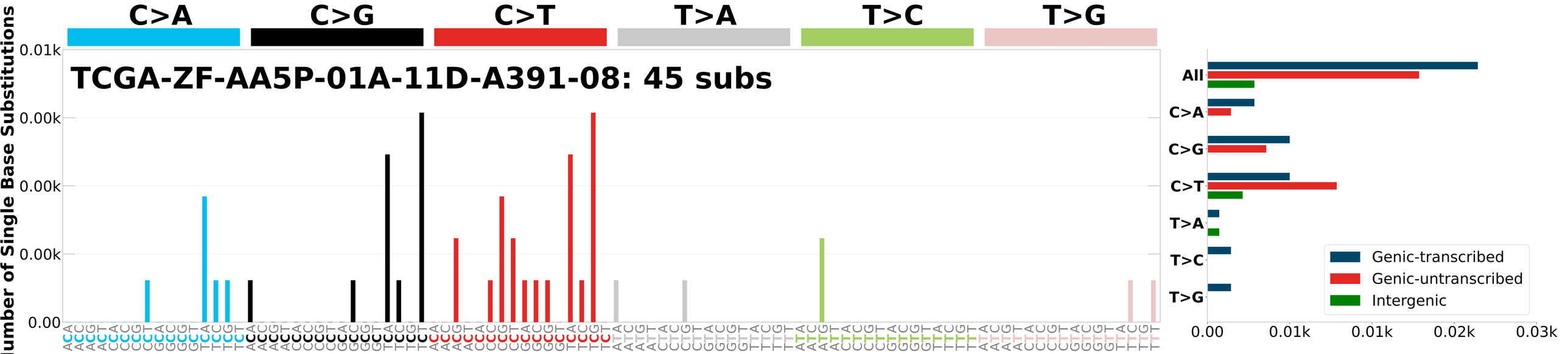

C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA54-01A-11D-A391-08: 173 subs
Number of Single Base Substitutions
0.04k
0.03k
0.02k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.06k
0.09k
0.12k


C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA56-01A-31D-A391-08: 97 subs
Number of Single Base Substitutions
0.02k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.03k
0.04k
0.06k


C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA58-01A-12D-A42E-08: 212 subs
Number of Single Base Substitutions
0.03k
0.02k
0.01k
0.01k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.03k
0.07k
0.10k
0.14k


C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA5H-01A-11D-A391-08: 66 subs
Number of Single Base Substitutions
0.01k
0.01k
0.01k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k


C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA5N-01A-11D-A42E-08: 51 subs
Number of Single Base Substitutions
0.00k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.02k
0.03k
0.04k


C>A
C>G
C>T
T>A
T>C
T>G
TCGA-ZF-AA5P-01A-11D-A391-08: 45 subs
Number of Single Base Substitutions
0.01k
0.00k
0.00k
0.00k
0.00
All
C>A
C>G
C>T
T>A
T>C
T>G
Genic-transcribed
Genic-untranscribed
Intergenic
0.00
0.01k
0.01k
0.02k
0.03k