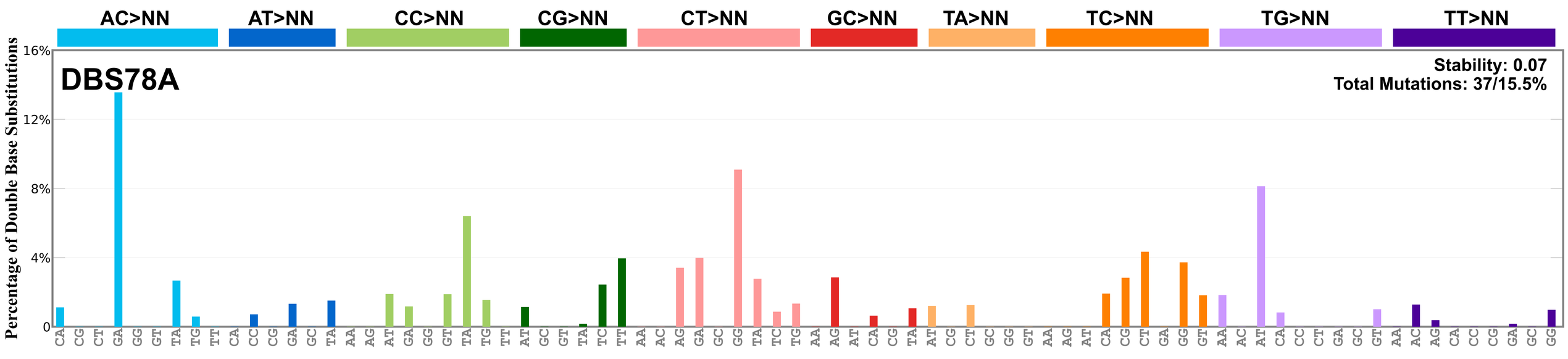
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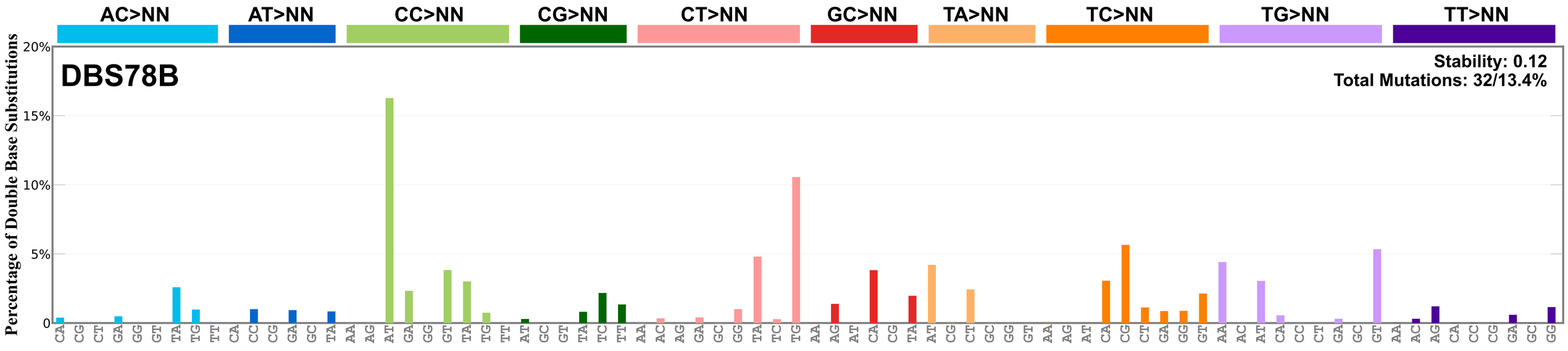
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78A
Stability: 0.07
Total Mutations: 37/15.5%
Percentage of Double Base Substitutions
16%
12%
8%
4%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA AG AT CA CG CT GA GG GT AA AC AT CA CC CT GA GC GT AA AC AG CA CC CG GA GC GG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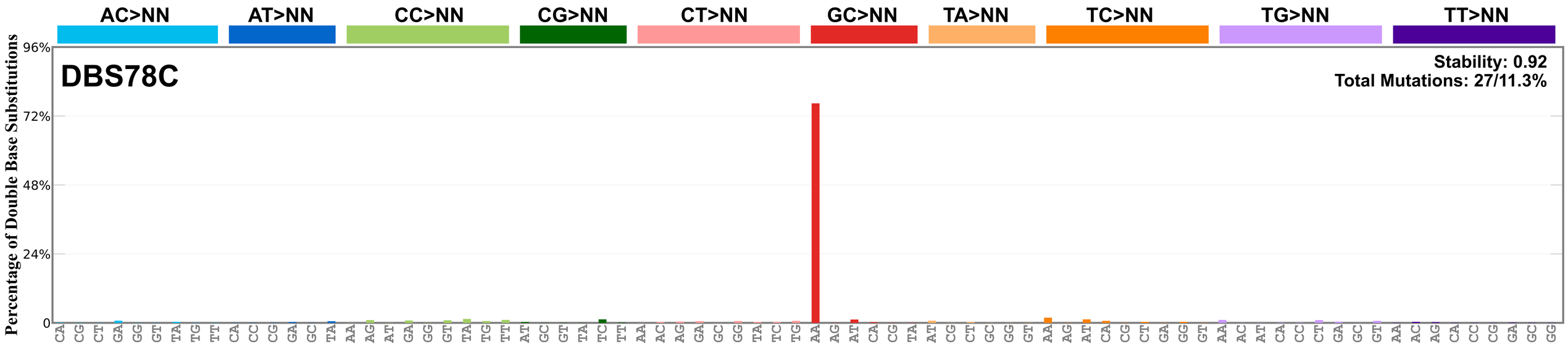
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78B
Stability: 0.12
Total Mutations: 32/13.4%
Percentage of Double Base Substitutions
20%
15%
10%
5%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA AG AT CA CG CT GA GG GT AA AC AT CA CC CT GA GC GT AA AC AG CA CC CG GA GC GG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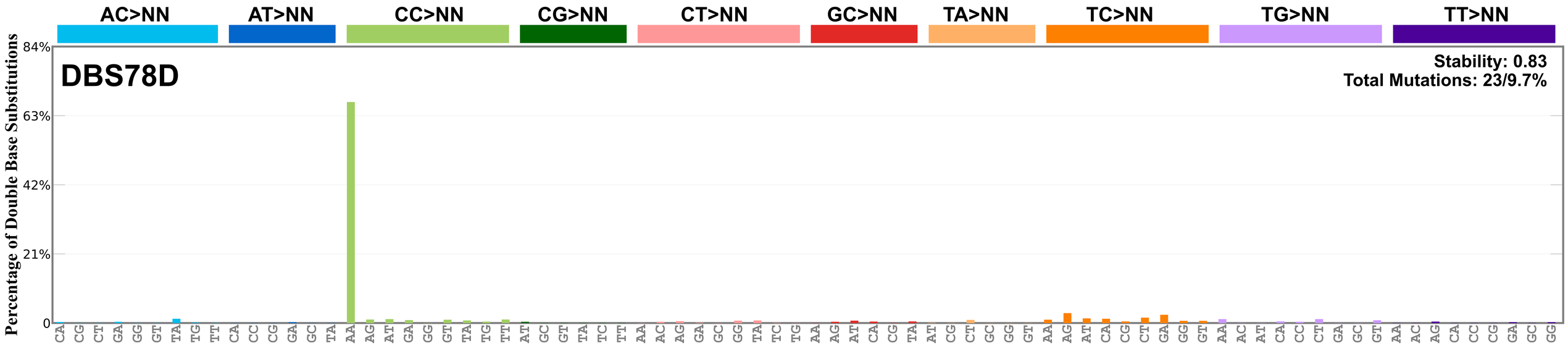
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78C
Stability: 0.92
Total Mutations: 27/11.3%
Percentage of Double Base Substitutions
96%
72%
48%
24%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA AG AT CA CG CT GA GG GT AA AC AT CA CC CT GA GC GT AA AC AG CA CC CG GA GC GG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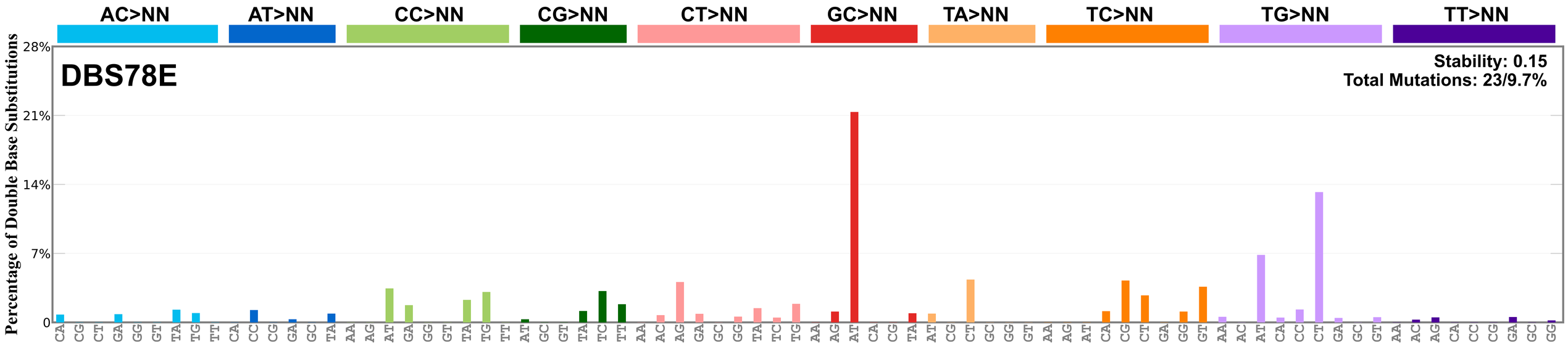
AT>NN
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78D
Stability: 0.83
Total Mutations: 23/9.7%
Percentage of Double Base Substitutions
84%
63%
42%
21%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA AG AT CA CG CT GA GG GT AA AC AT CA CC CT GA GC GT AA AC AG CA CC CG GA GC GG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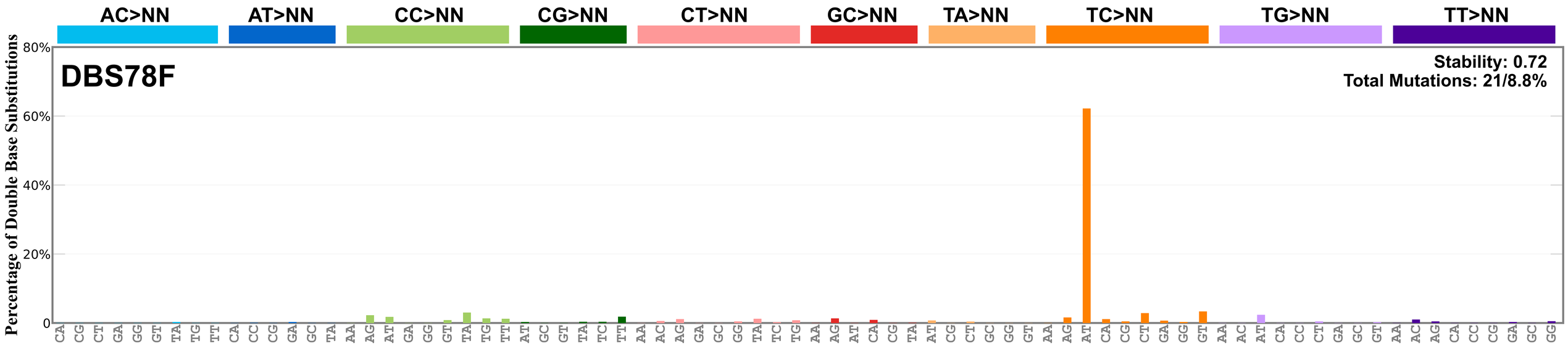
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78E
Stability: 0.15
Total Mutations: 23/9.7%
Percentage of Double Base Substitutions
28%
21%
14%
7%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA AG AT CA CG CT GA GG GT AA AC AT CA CC CT GA GC GT AA AC AG CA CC CG GA GC GG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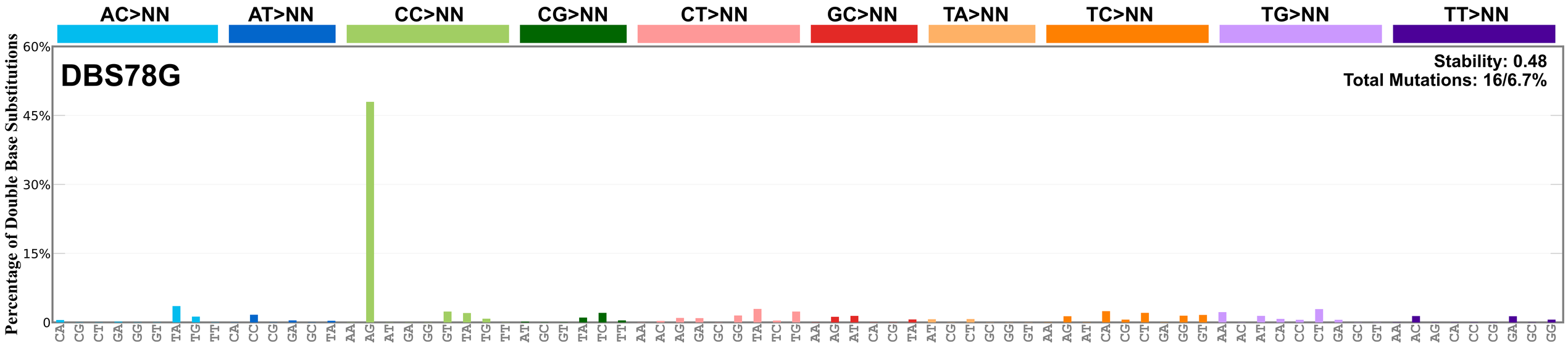
AT>NN
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78F
Stability: 0.72
Total Mutations: 21/8.8%
Percentage of Double Base Substitutions
80%
60%
40%
20%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA AG AT CA CG CT GA GG GT AA AC AT CA CC CT GA GC GT AA AC AG CA CC CG GA GC GG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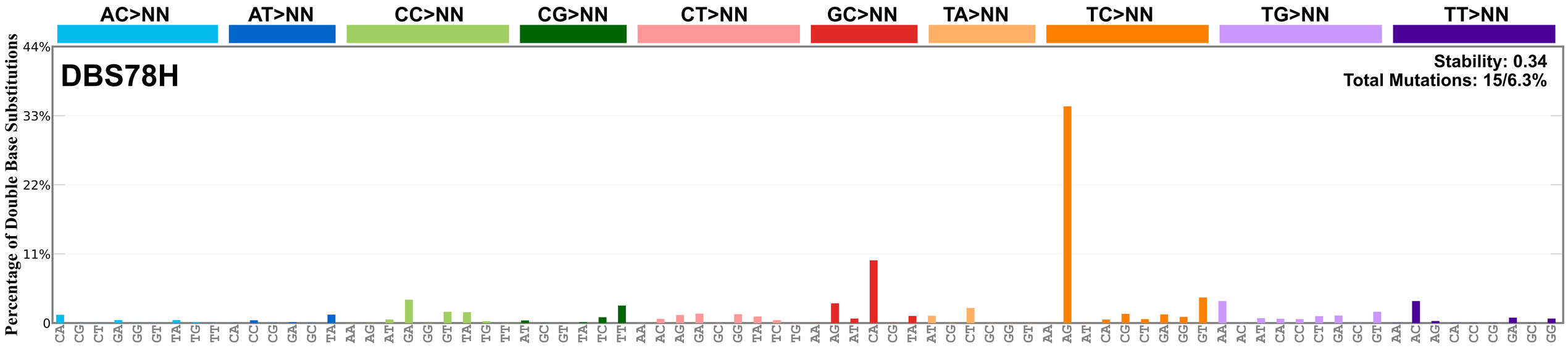
AT>NN
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78G
Stability: 0.48
Total Mutations: 16/6.7%
Percentage of Double Base Substitutions
60%
45%
30%
15%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA AG AT CA CG CT GA GG GT AA AC AT CA CC CT GA GC GT AA AC AG CA CC CG GA GC GG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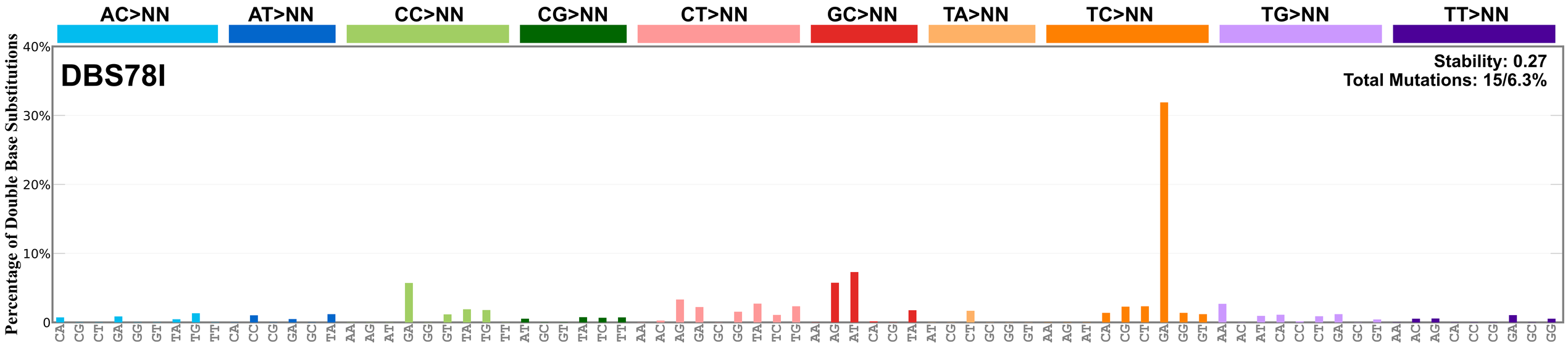
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78H
Stability: 0.34
Total Mutations: 15/6.3%
Percentage of Double Base Substitutions
44%
33%
22%
11%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA AG AT CA CG CT GA GG GT AA AC AT CA CC CT GA GC GT AA AC AG CA CC CG GA GC GG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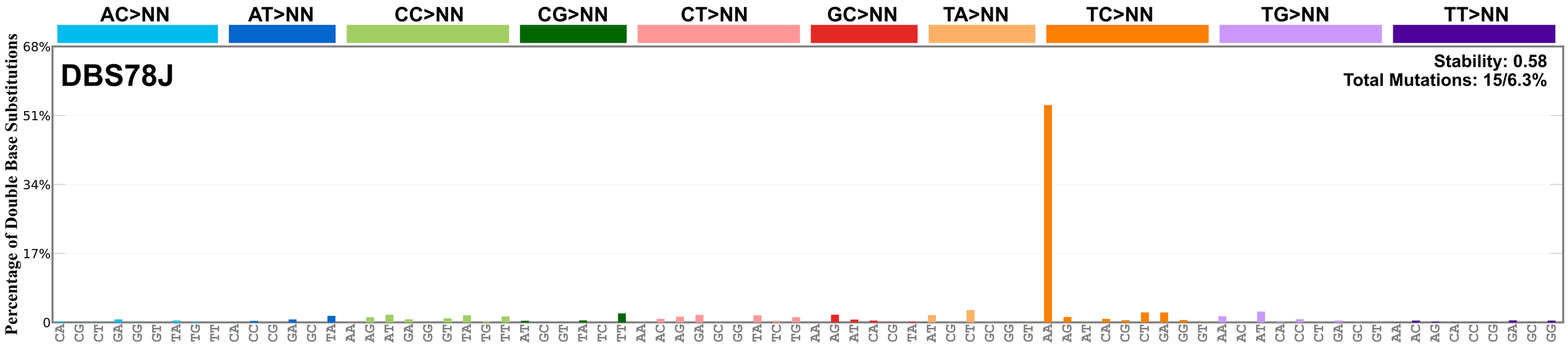
AT>NN
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78I
Stability: 0.27
Total Mutations: 15/6.3%
Percentage of Double Base Substitutions
40%
30%
20%
10%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA AG AT CA CG CT GA GG GT AA AC AT CA CC CT GA GC GT AA AC AG CA CC CG GA GC GG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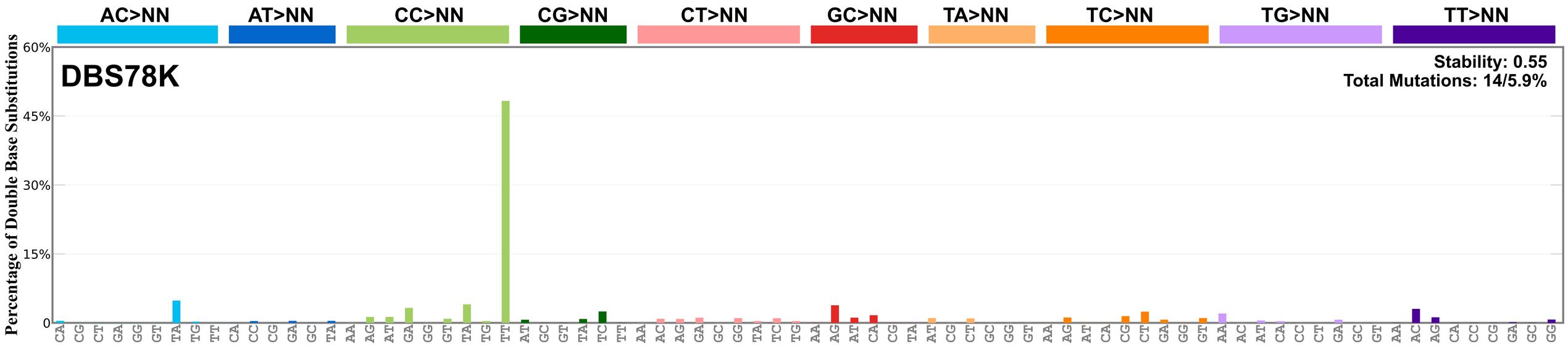
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78J
Stability: 0.58
Total Mutations: 15/6.3%
Percentage of Double Base Substitutions
68%
51%
34%
17%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA AG AT CA CG CT GA GG GT AA AC AT CA CC CT GA GC GT AA AC AG CA CC CG GA GC GG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CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78K
Stability: 0.55
Total Mutations: 14/5.9%
Percentage of Double Base Substitutions
60%
45%
30%
15%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA AG AT CA CG CT GA GG GT AA AC AT CA CC CT GA GC GT AA AC AG CA CC CG GA GC GG