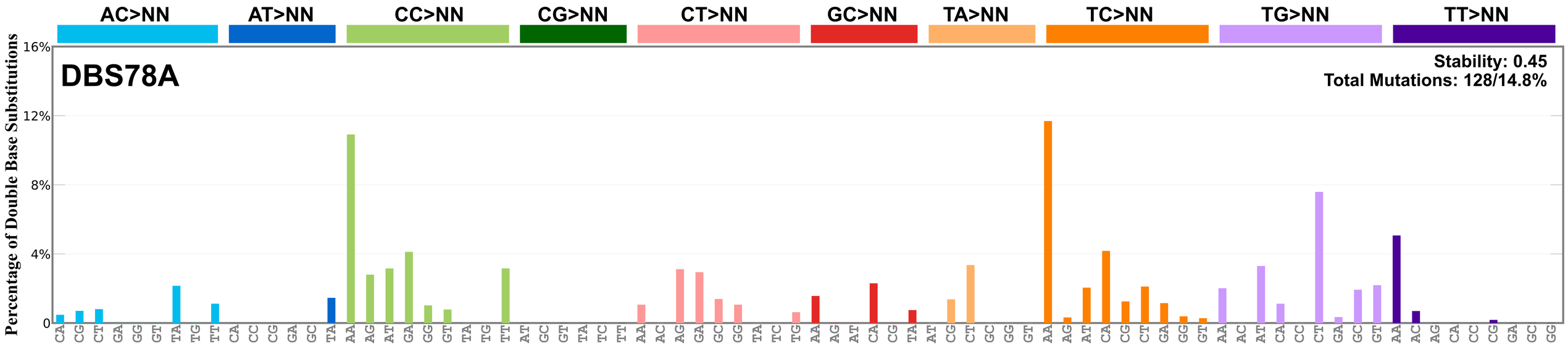
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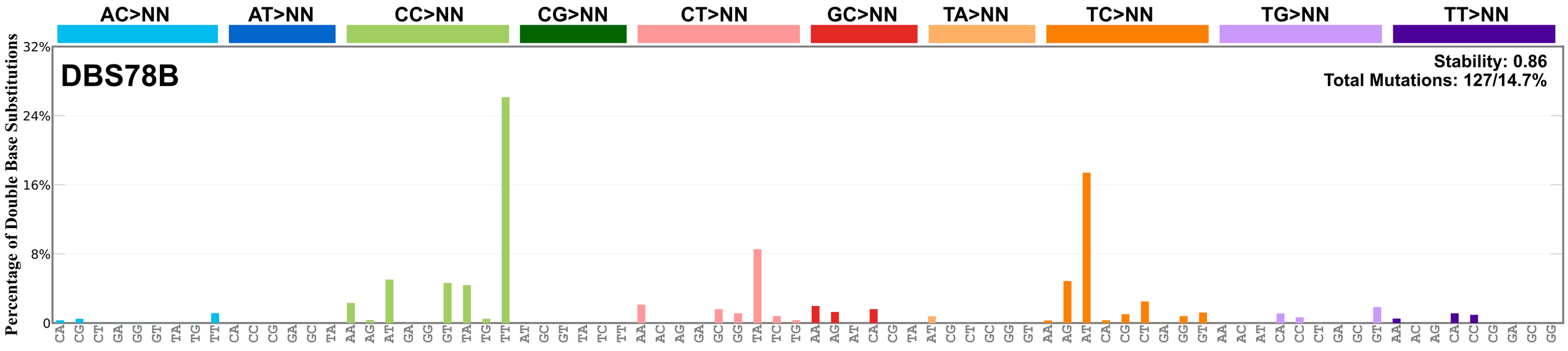
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78A
Stability: 0.45
Total Mutations: 128/14.8%
Percentage of Double Base Substitutions
16%
12%
8%
4%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC 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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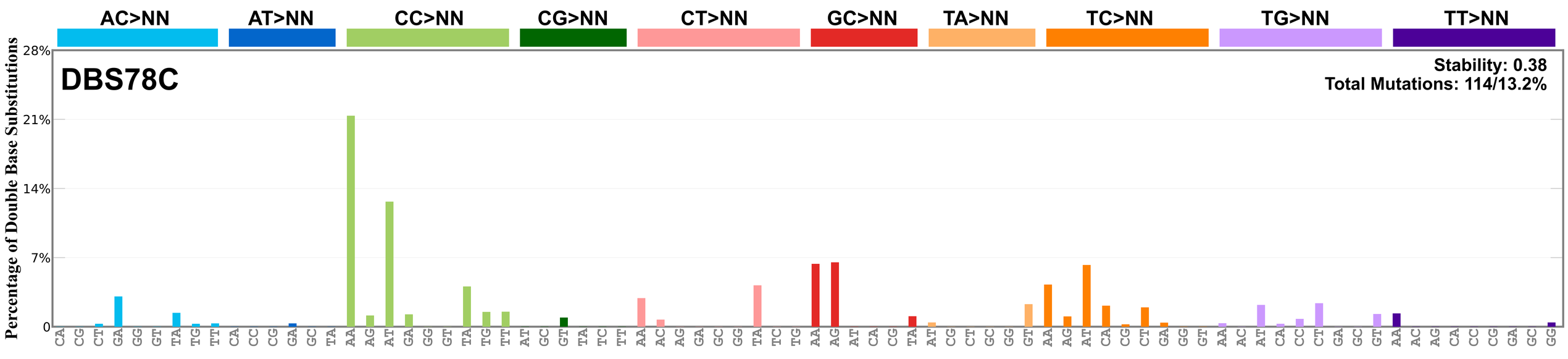
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78B
Stability: 0.86
Total Mutations: 127/14.7%
Percentage of Double Base Substitutions
32%
24%
16%
8%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC 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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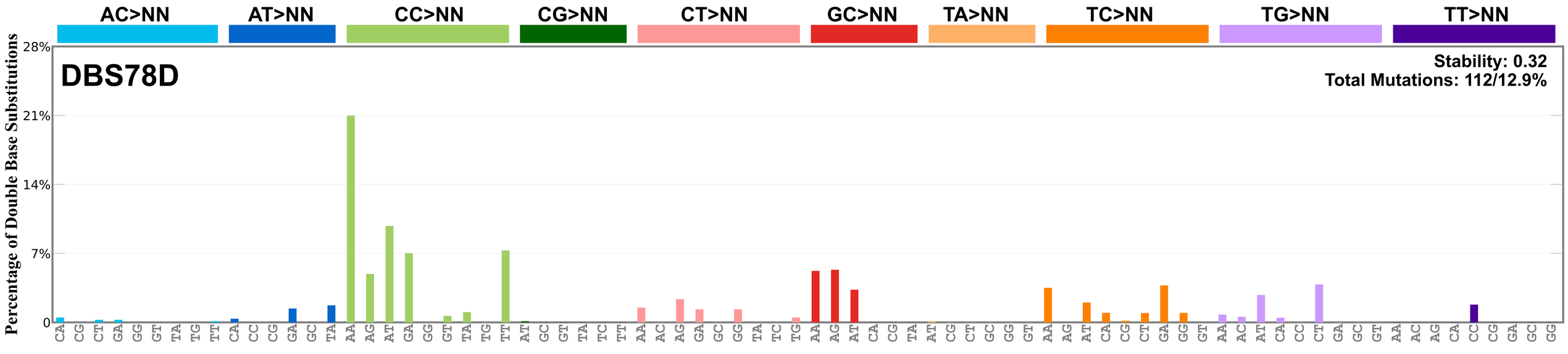
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78C
Stability: 0.38
Total Mutations: 114/13.2%
Percentage of Double Base Substitutions
28%
21%
14%
7%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC 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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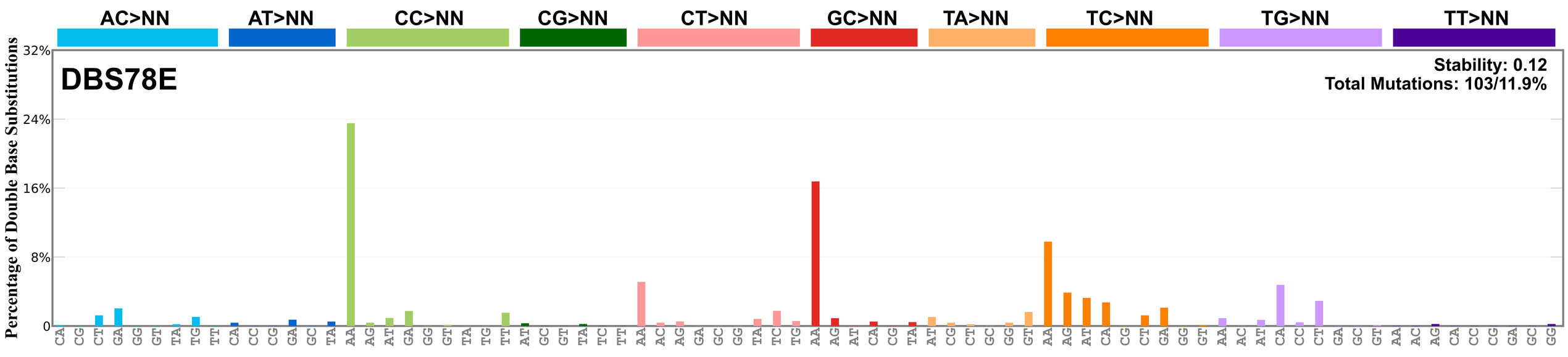
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78D
Stability: 0.32
Total Mutations: 112/12.9%
Percentage of Double Base Substitutions
28%
21%
14%
7%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC 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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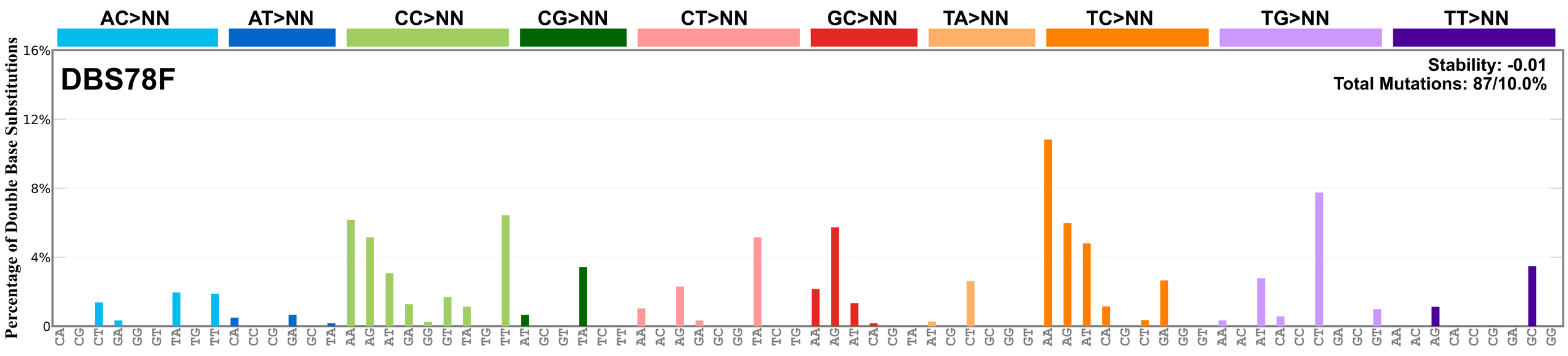
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78E
Stability: 0.12
Total Mutations: 103/11.9%
Percentage of Double Base Substitutions
32%
24%
16%
8%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC 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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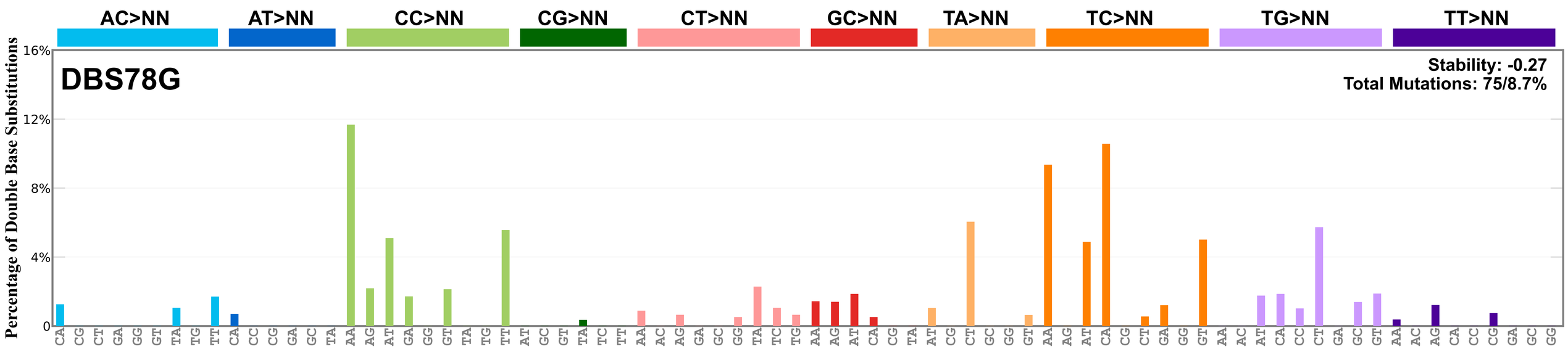
AT>NN
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78F
Stability: -0.01
Total Mutations: 87/10.0%
Percentage of Double Base Substitutions
16%
12%
8%
4%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG 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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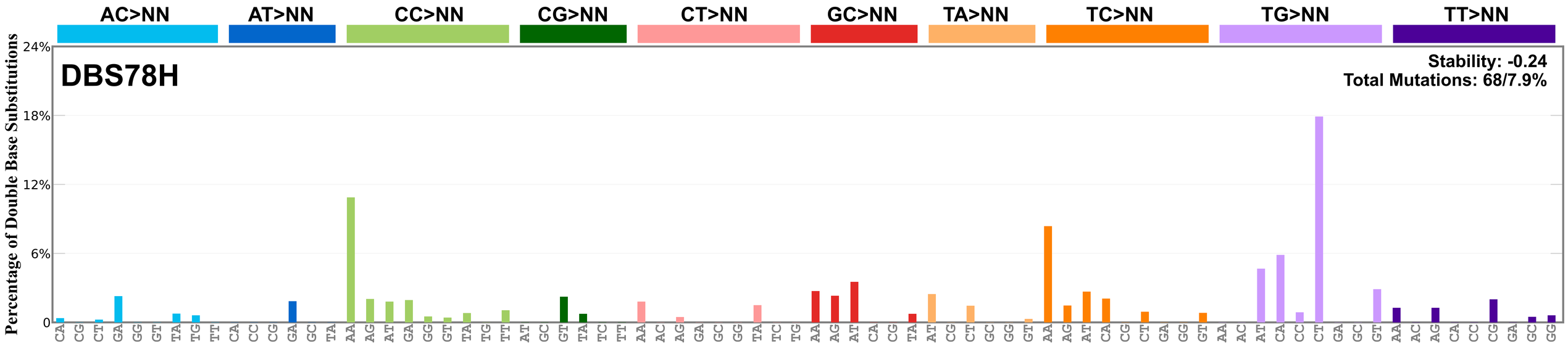
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78G
Stability: -0.27
Total Mutations: 75/8.7%
Percentage of Double Base Substitutions
16%
12%
8%
4%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG 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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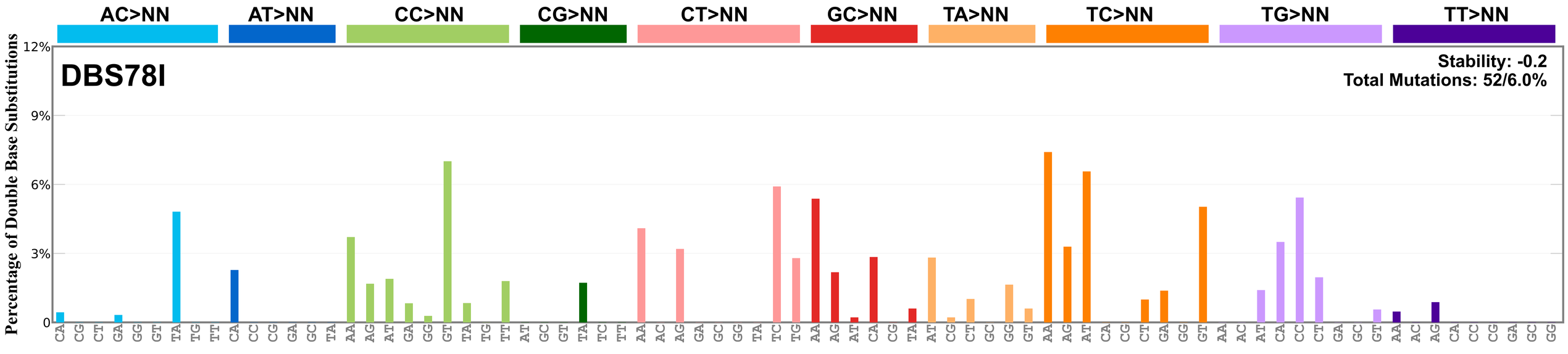
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78H
Stability: -0.24
Total Mutations: 68/7.9%
Percentage of Double Base Substitutions
24%
18%
12%
6%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC 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
DBS78I
Stability: -0.2
Total Mutations: 52/6.0%
Percentage of Double Base Substitutions
12%
9%
6%
3%
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