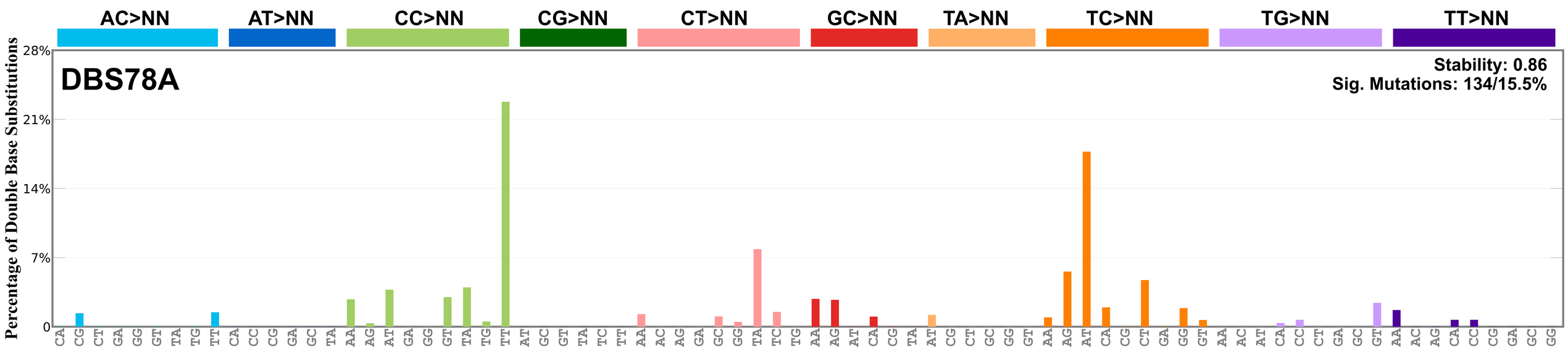
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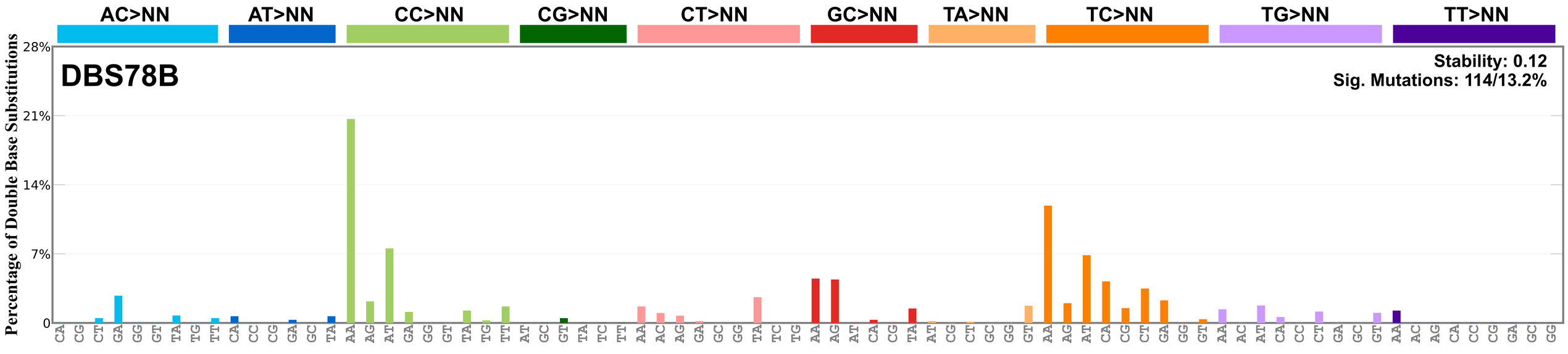
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78A
Stability: 0.86
Sig. Mutations: 134/15.5%
Percentage of Double Base Substitutions
28%
21%
14%
7%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC 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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CG>NN
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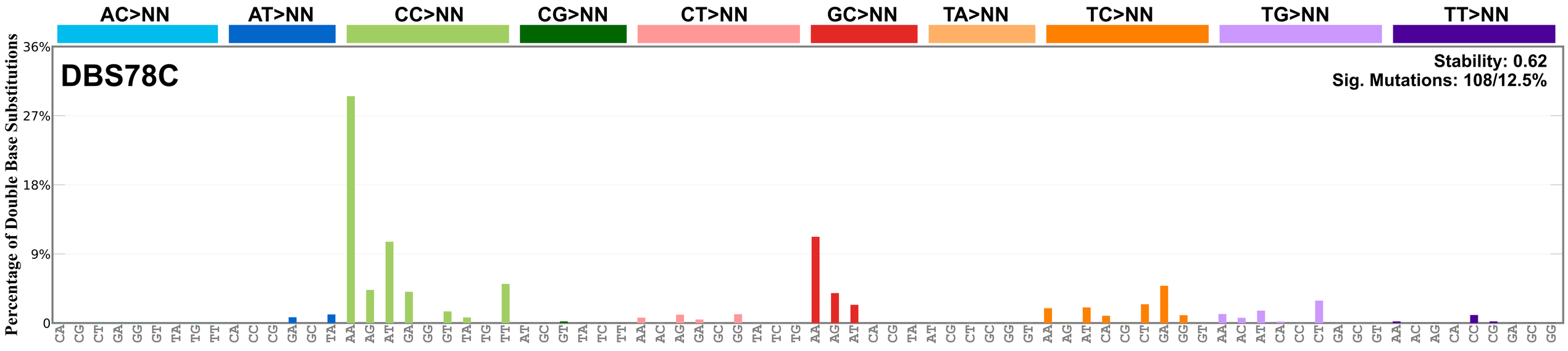
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78B
Stability: 0.12
Sig. Mutations: 114/13.2%
Percentage of Double Base Substitutions
28%
21%
14%
7%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA AG AT CA 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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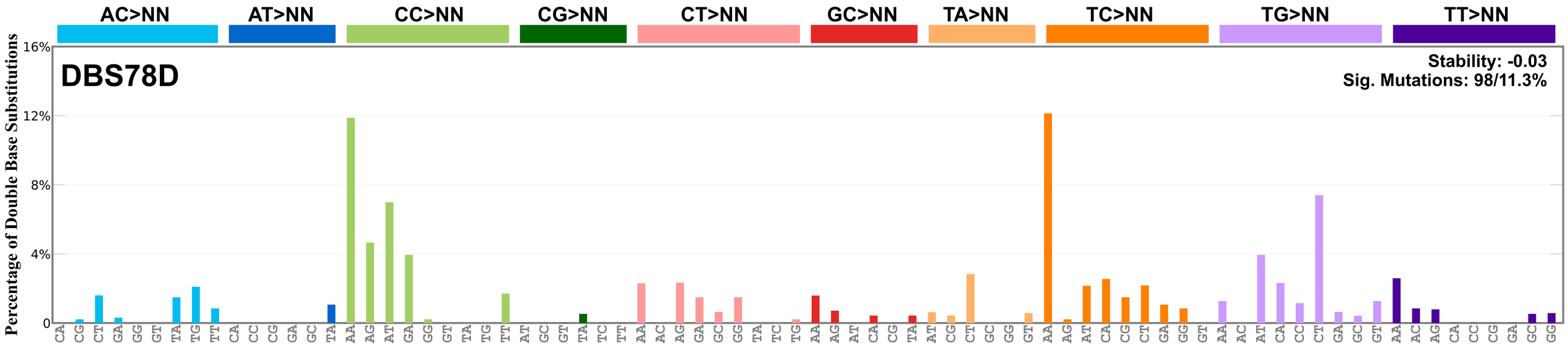
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78C
Stability: 0.62
Sig. Mutations: 108/12.5%
Percentage of Double Base Substitutions
36%
27%
18%
9%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC 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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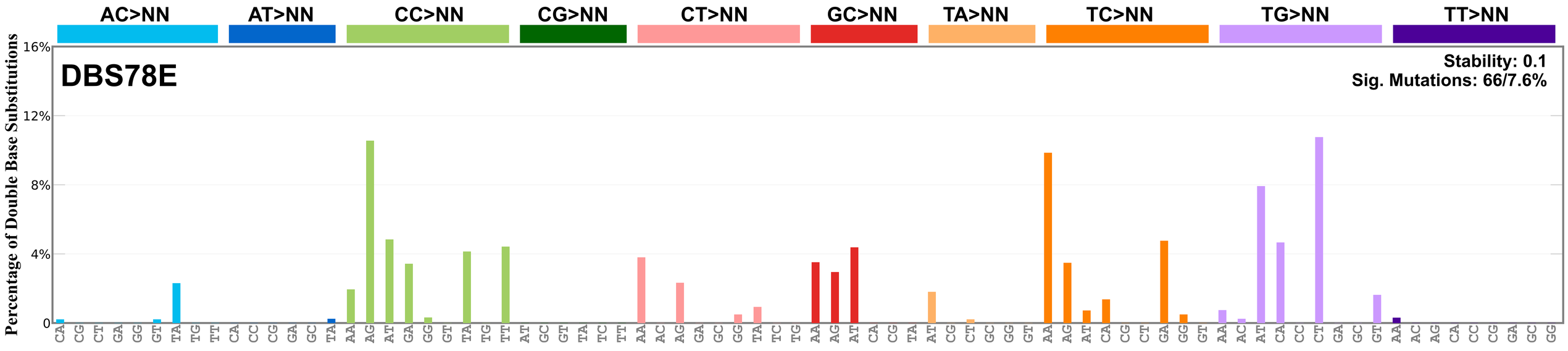
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78D
Stability: -0.03
Sig. Mutations: 98/11.3%
Percentage of Double Base Substitutions
16%
12%
8%
4%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG 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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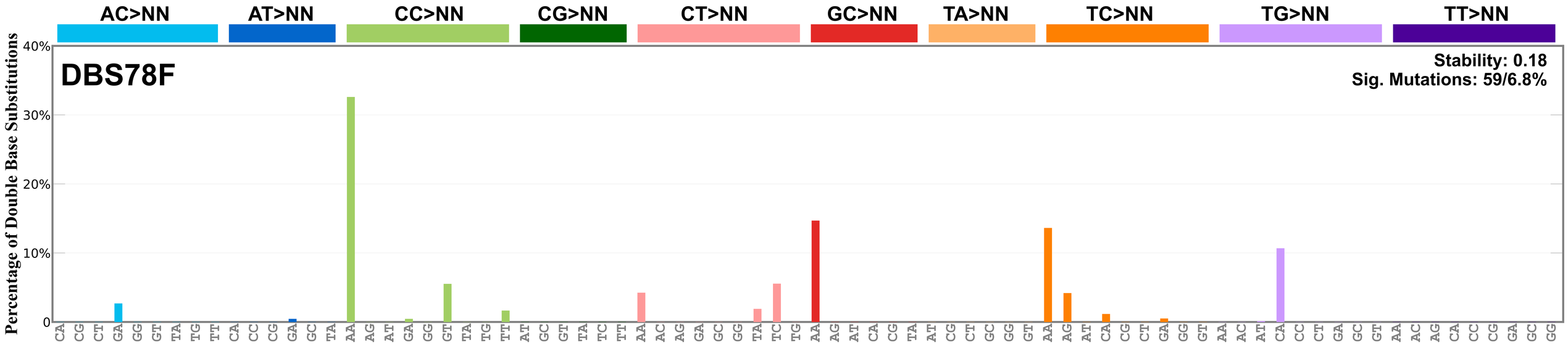
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78E
Stability: 0.1
Sig. Mutations: 66/7.6%
Percentage of Double Base Substitutions
16%
12%
8%
4%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT 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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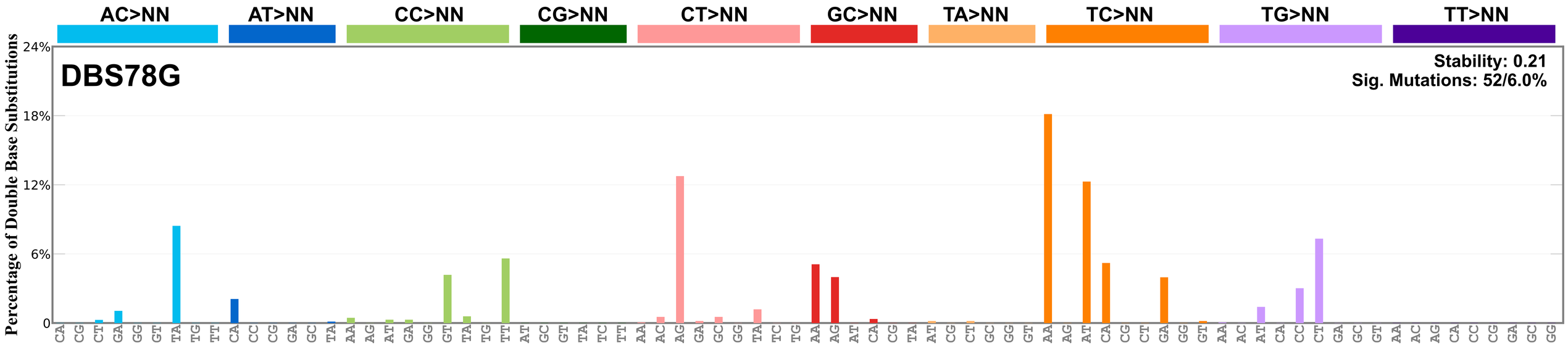
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78F
Stability: 0.18
Sig. Mutations: 59/6.8%
Percentage of Double Base Substitutions
40%
30%
20%
10%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG 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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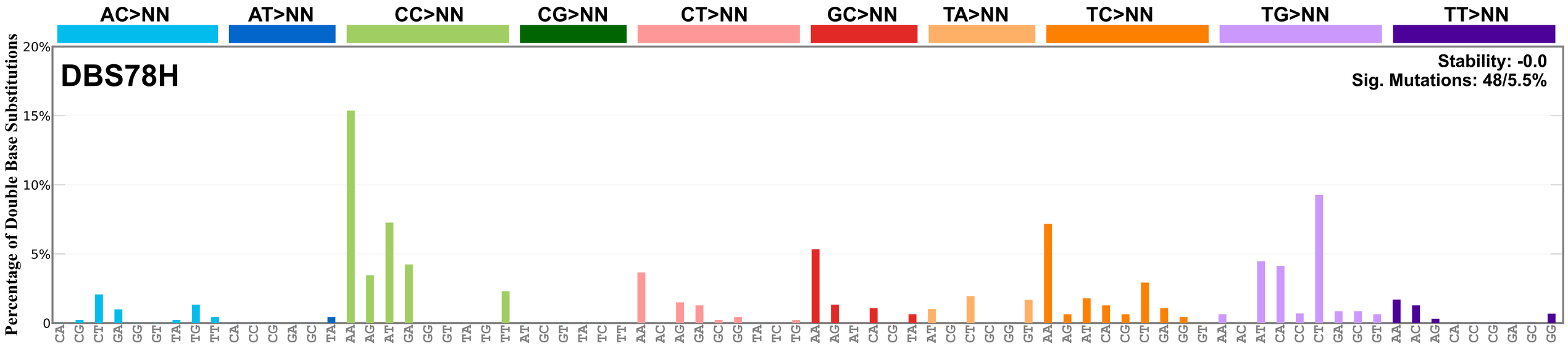
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78G
Stability: 0.21
Sig. Mutations: 52/6.0%
Percentage of Double Base Substitutions
24%
18%
12%
6%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG 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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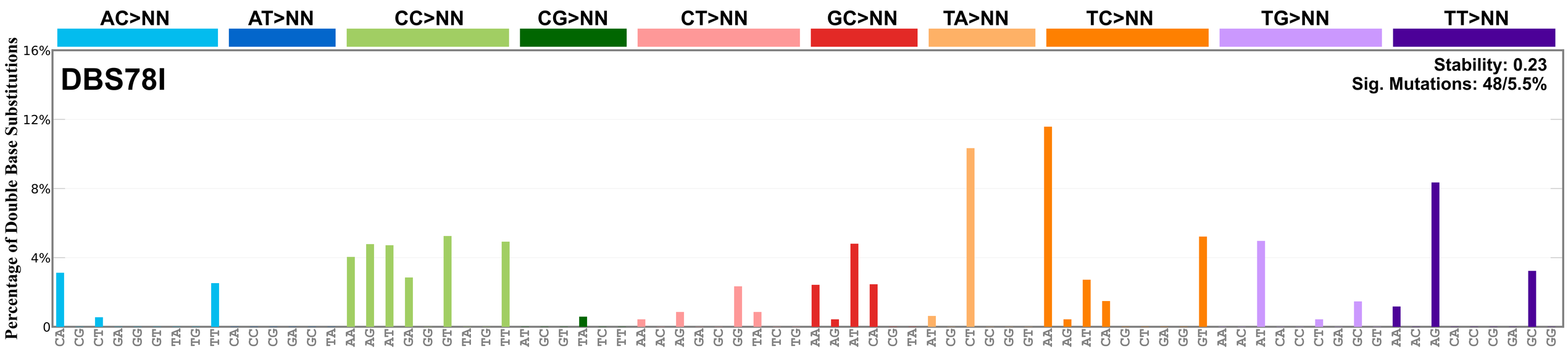
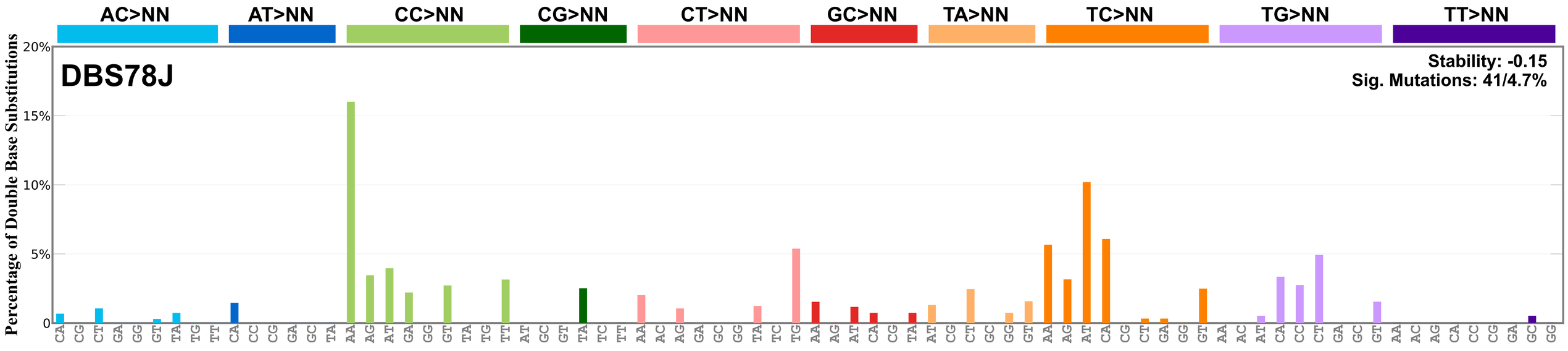
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78H
Stability: -0.0
Sig. Mutations: 48/5.5%
Percentage of Double Base Substitutions
20%
15%
10%
5%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG 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


AC>NN
AT>NN
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78I
Stability: 0.23
Sig. Mutations: 48/5.5%
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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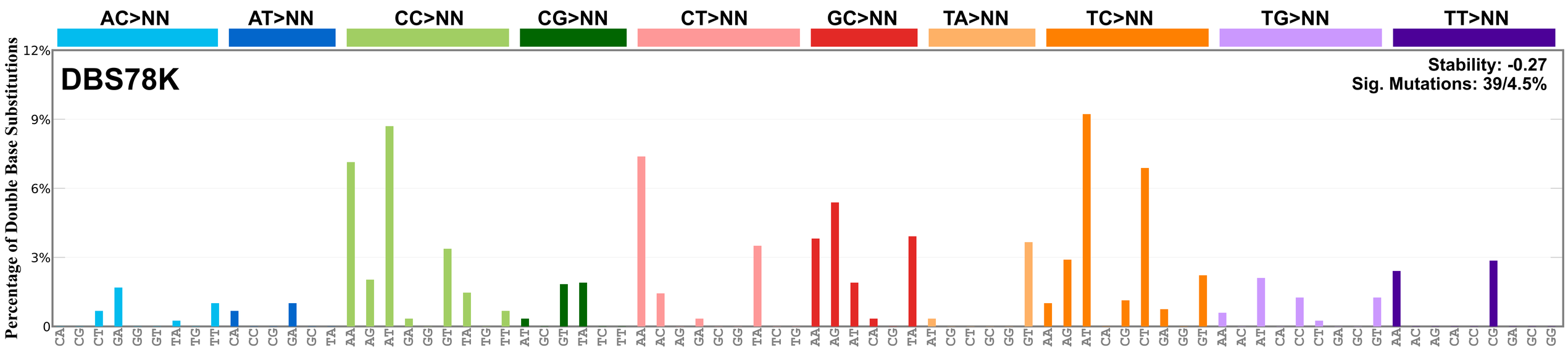
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78J
Stability: -0.15
Sig. Mutations: 41/4.7%
Percentage of Double Base Substitutions
20%
15%
10%
5%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA 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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CG>NN
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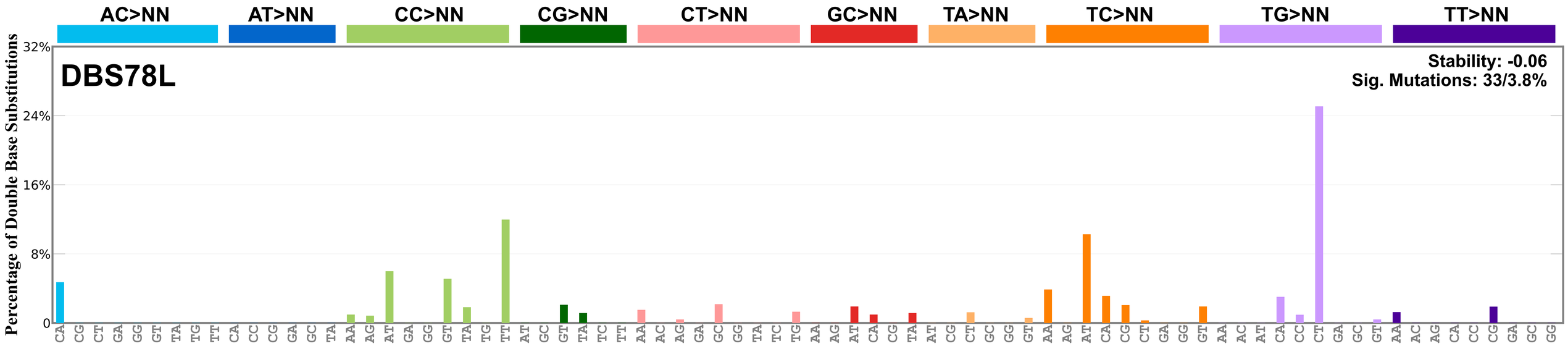
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78K
Stability: -0.27
Sig. Mutations: 39/4.5%
Percentage of Double Base Substitutions
12%
9%
6%
3%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA AG AT CA CG CT GA GG GT AA AC AT CA CC CT GA GC GT AA AC AG CA CC CG GA GC GG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CG>NN
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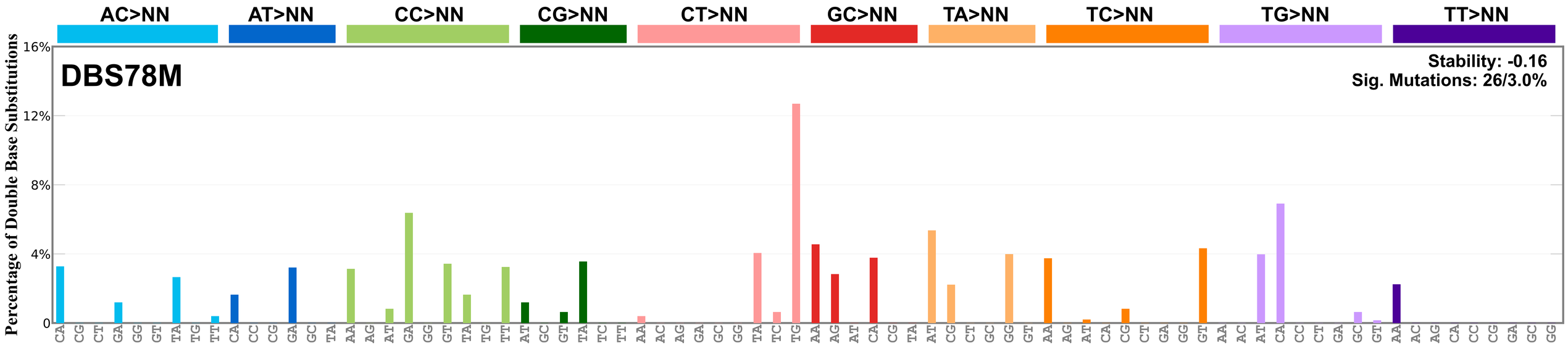
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78L
Stability: -0.06
Sig. Mutations: 33/3.8%
Percentage of Double Base Substitutions
32%
24%
16%
8%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG GT AA AG AT CA CG 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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CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78M
Stability: -0.16
Sig. Mutations: 26/3.0%
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