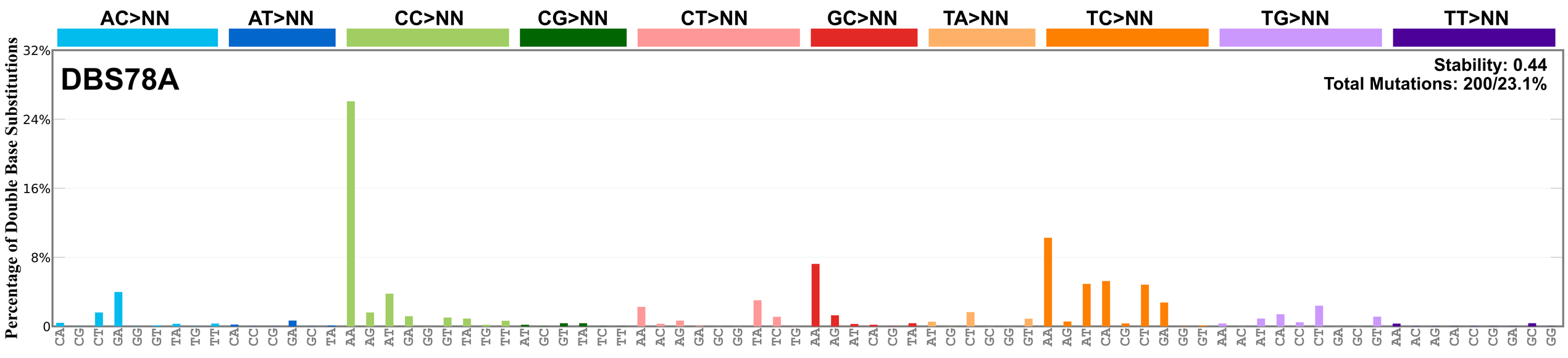
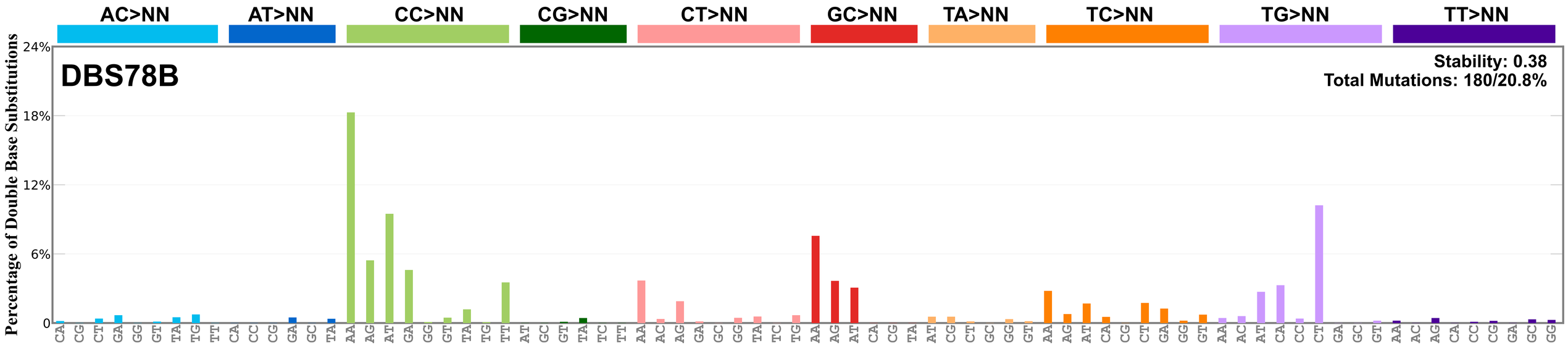

AC>NN
AT>NN
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78A
Stability: 0.44
Total Mutations: 200/23.1%
Percentage of Double Base Substitutions
32%
24%
16%
8%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA 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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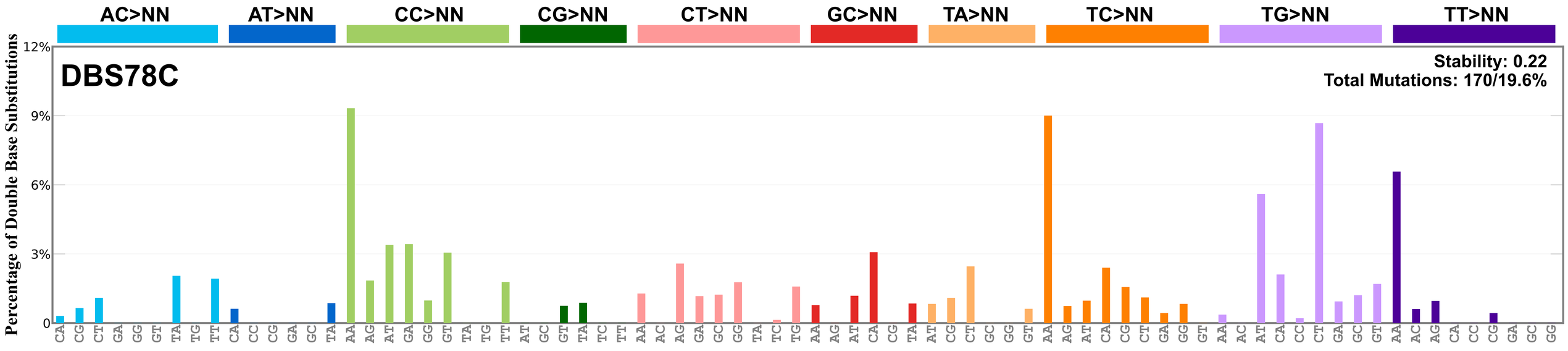
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78B
Stability: 0.38
Total Mutations: 180/20.8%
Percentage of Double Base Substitutions
24%
18%
12%
6%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC 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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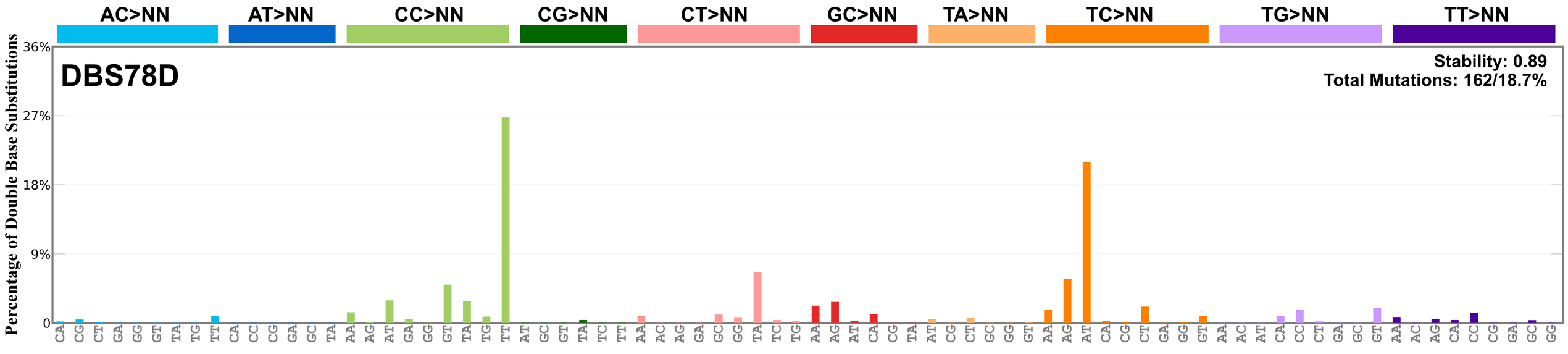
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78C
Stability: 0.22
Total Mutations: 170/19.6%
Percentage of Double Base Substitutions
12%
9%
6%
3%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC GG 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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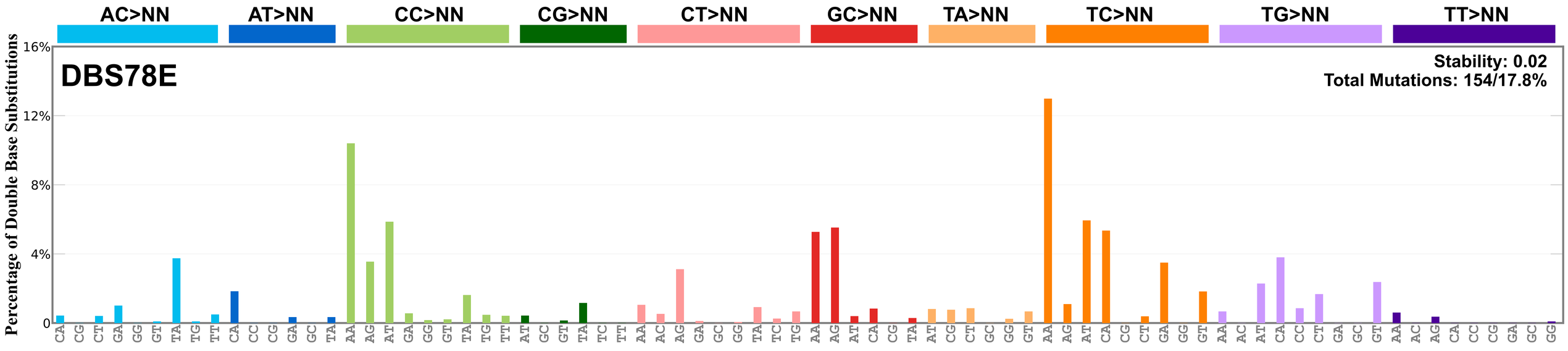
CC>NN
CG>NN
CT>NN
GC>NN
TA>NN
TC>NN
TG>NN
TT>NN
DBS78D
Stability: 0.89
Total Mutations: 162/18.7%
Percentage of Double Base Substitutions
36%
27%
18%
9%
0
CA CG CT GA GG GT TA TG TT CA CC CG GA GC TA AA AG AT GA GG GT TA TG TT AT GC GT TA TC TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG TA AT CG CT GC 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
DBS78E
Stability: 0.02
Total Mutations: 154/17.8%
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