Overhang set report

☒ Disastandard

There are **9** overhangs in this set. The restriction enzyme used for this set is **Esp3I**.

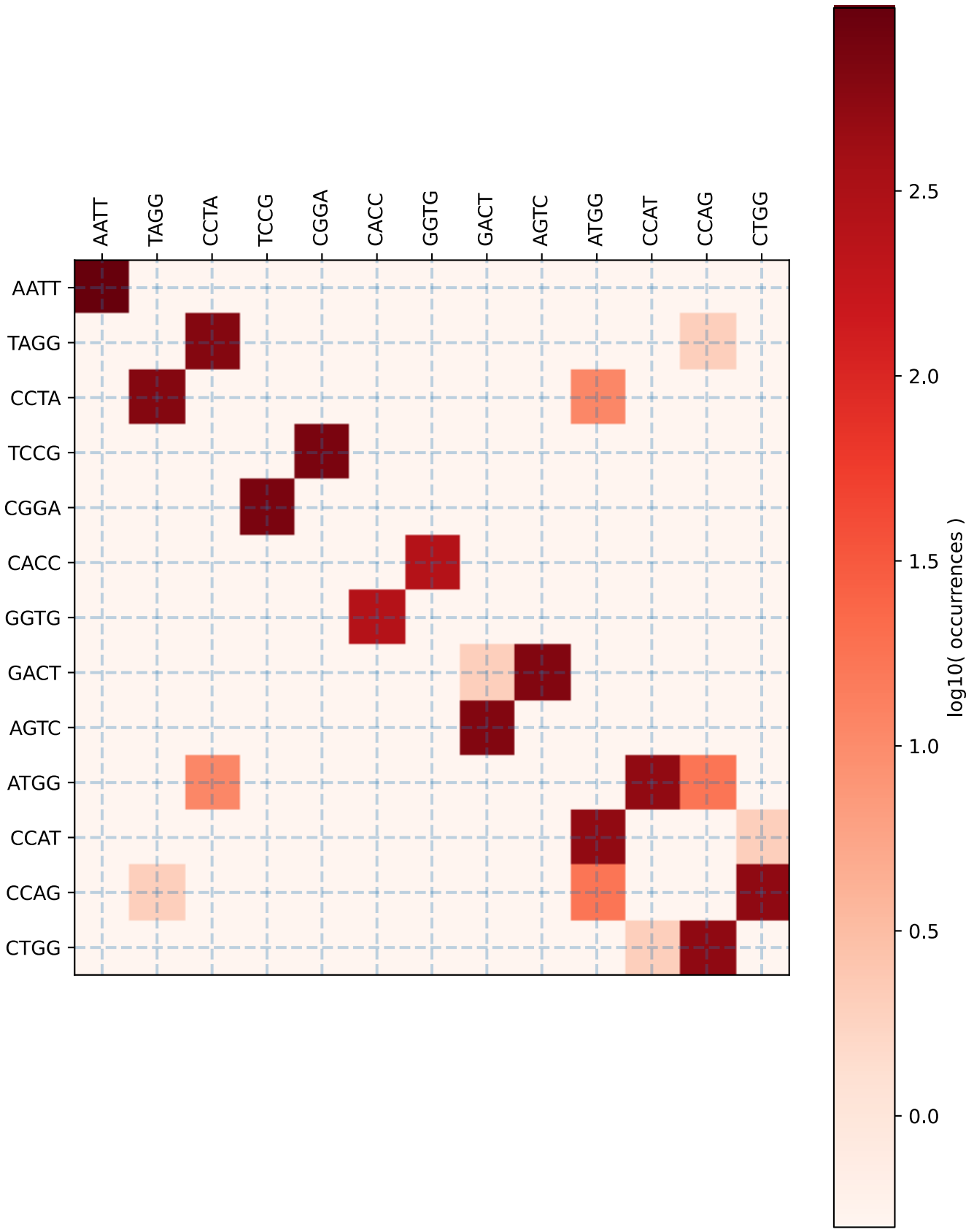
Error! **Duplicate overhangs in set.**

Error! **Palindromic overhang(s): AATT**

Error! **Nonpalindromic overhang(s) with reverse complement: TAGG; CCTA**

Please see the Appendix on the last page for an explanation of details.

Tatapov annealing plot:



☒ AATT AATT

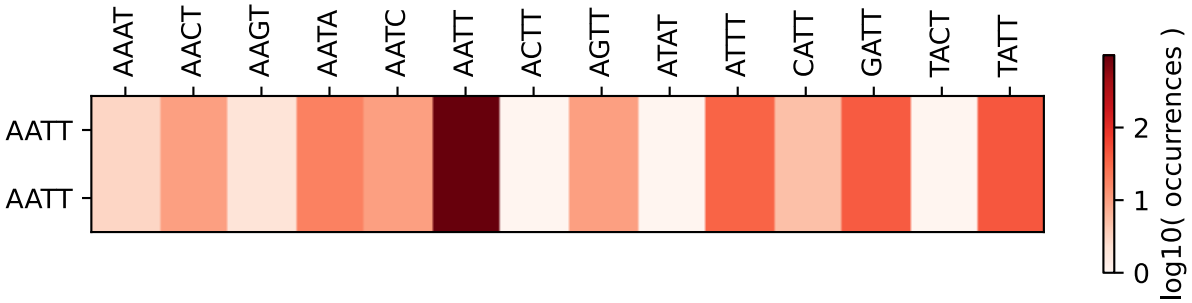
Extreme GC content: 0 %.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

N[LF*SWYC]
[EVQLRPGT*ISAK]I
[QKE*][FL]
N[LF*SWYC]
[EVQLRPGT*ISAK]I
[QKE*][FL]

Misannealing overhangs:



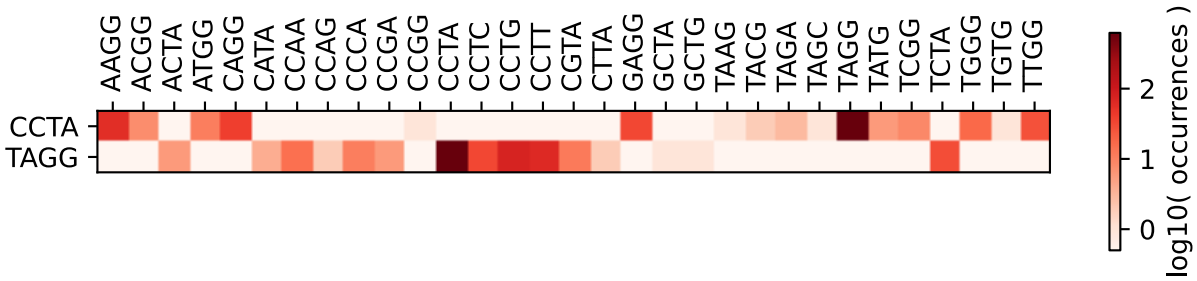
☑ CCTA TAGG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

P[NRTIMSK]
[VNPLRDGFTISHAYC]L
[PTAS][Y*]
*[EVDGA]
[VNPLRDGFTISHAYC]R
[LVI][G]

Misannealing overhangs:



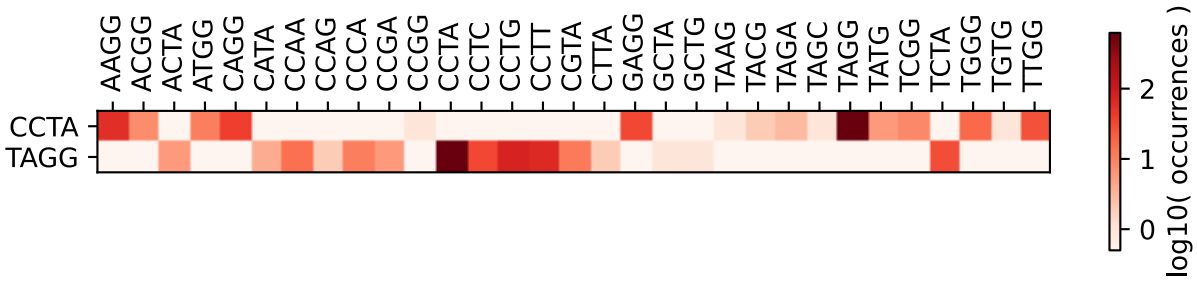
☑ CCTA TAGG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

P[NRTIMSK]
[VNPLRDGFTISHAYC]L
[PTAS][Y*]
*[EVDGA]
[VNPLRDGFTISHAYC]R
[LVI][G]

Misannealing overhangs:



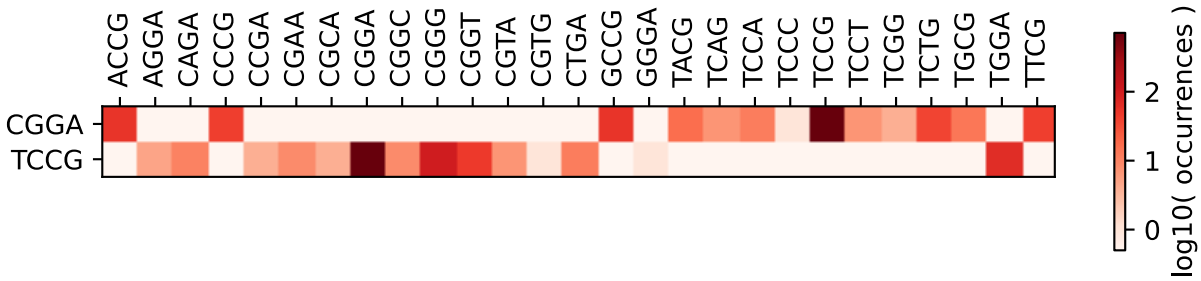
☑ CGGA TCCG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

R[NRTIMSK]
[VNPLRDGFTISHAYC]G
[PTAS][DE]
S[EVDGA]
[VNPLRDGFTISHAYC]P
[FLVI][R]

Misannealing overhangs:



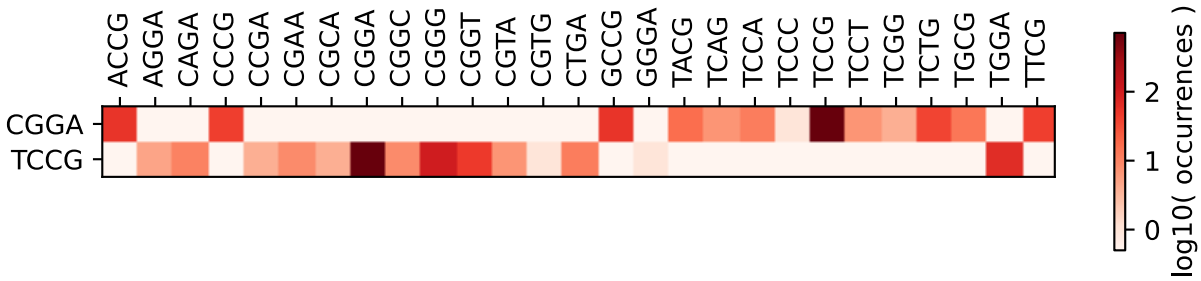
☑ CGGA TCCG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

R[NRTIMSK]
[VNPLRDGFTISHAYC]G
[PTAS][DE]
S[EVDGA]
[VNPLRDGFTISHAYC]P
[FLVI][R]

Misannealing overhangs:



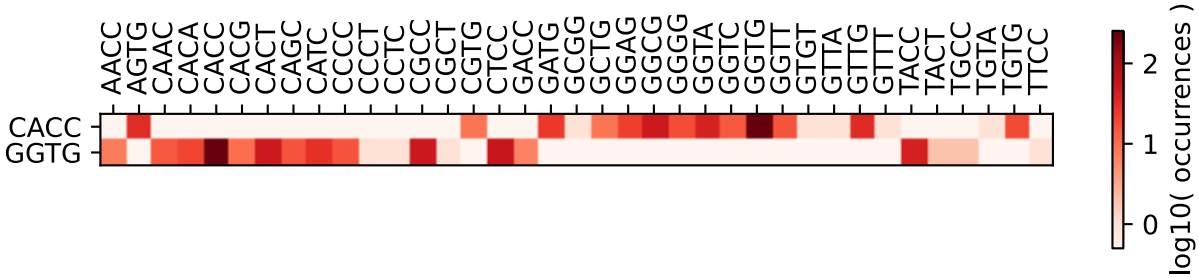
☑ CACC GGTG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

H[PQLRH]
[VNPLRDGFTISHAYC]T
[PTAS][P]
G[EVDGA]
[EVQLRPGT*MSWAK]V
[WRG][W*C]

Misannealing overhangs:



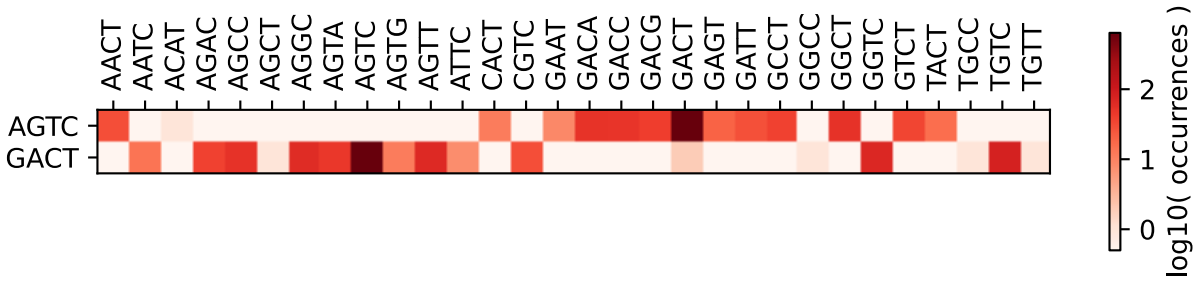
☑ AGTC GACT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

S[PQLRH]
[EVQLRPGT*ISAK]V
[QKE*][S]
D[LF*SWYC]
[EVQLRPGT*MSWAK]T
[R*G][L]

Misannealing overhangs:



☑ ATGG CCAT

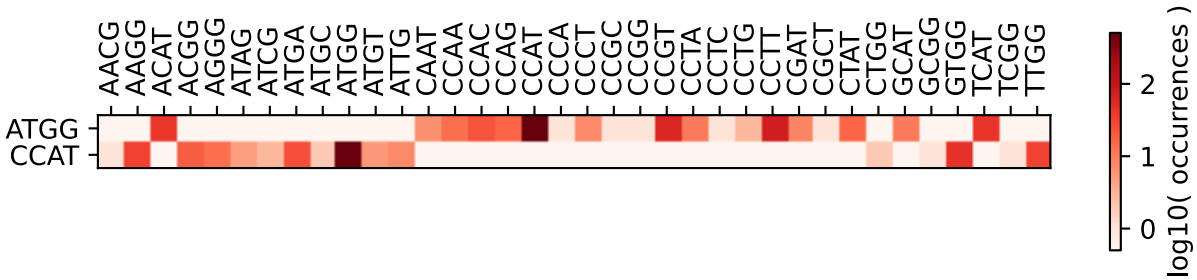
GC content: **50 %**.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

M[EVDGA]
[EVQLRPGT*ISAK]W
[NDYH][G]
P[LF*SWYC]
[VNPLRDGFTISHAYC]H
[PTAS][IM]

Misannealing overhangs:



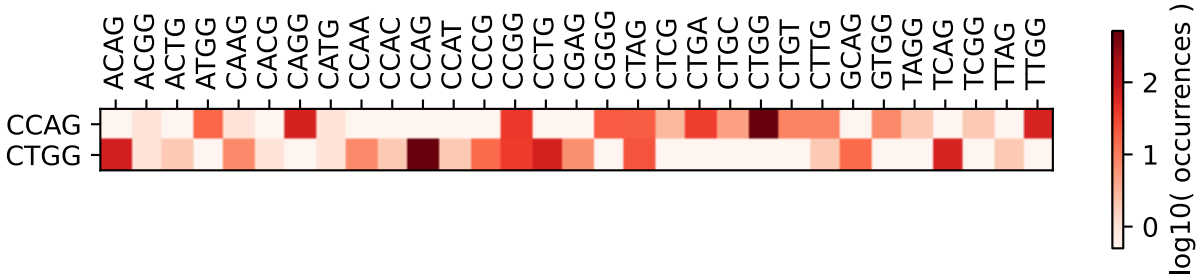
☑ CCAG CTGG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

P[EVDGA]
[VNPLRDGFTISHAYC]Q
[PTAS][RS]
L[EVDGA]
[VNPLRDGFTISHAYC]W
[PTAS][G]

Misannealing overhangs:



Appendix

The report consists of 3 sections: results, overhangs, appendix.

Result page(s)

The first page describes the overhang set. The result is also summarised with a symbol:

☑ : good overhang set

⚠ : warning; there are ways to significantly improve the set

☒ : error: the set cannot be used for DNA assembly

Overhang pages

Each overhang is also analysed separately. The result is summarised with a symbol:

☑ : good overhang

☒ : unusable palindromic sequence

Overhangs are unpaired nucleotides at the end of a double-stranded linear DNA molecule. Overhangs can be on either strand; 5' or 3' overhangs. After DNA ligation with another DNA with a complementary overhang, these remain in the sequence as fusion sites ("scars").

Overhang sets

Use the GoldenHinges Python package to generate a set of mutually compatible overhangs that can be used for DNA assembly.