



Overhang set report



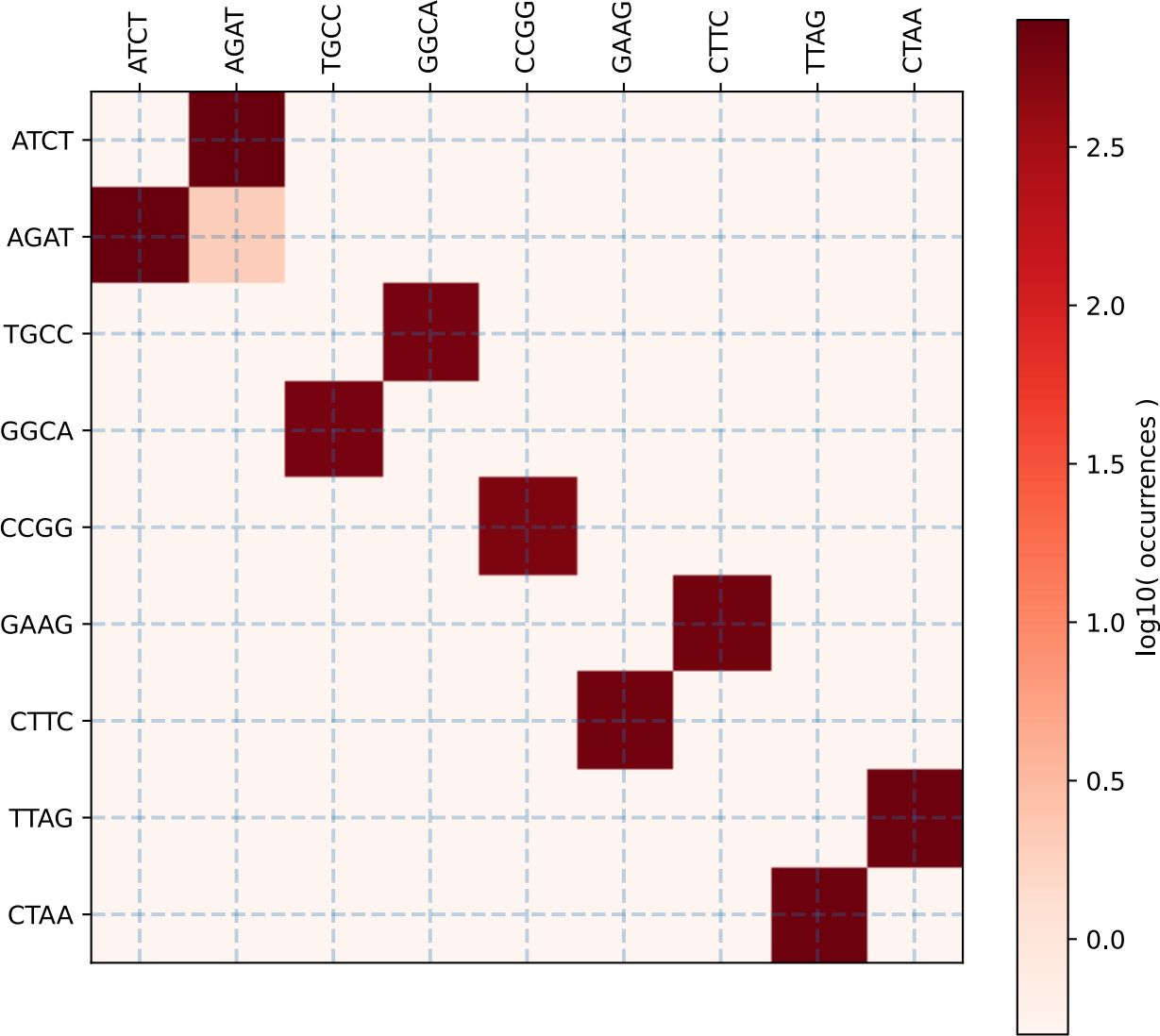
EcoFlex level 1

There are **6** overhangs in this set. The restriction enzyme used for this set is **Esp3I**.

Error! Palindromic overhang(s): CCGG

Error! Nonpalindromic overhang(s) with reverse complement: GAAG; CTTC

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





AGAT

ATCT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

R[LF*SWYC]

[EVQLRPGT*ISAK]D

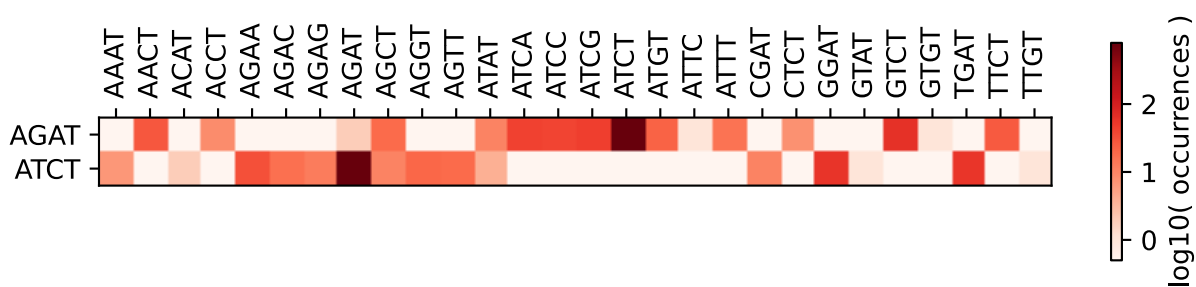
[QKE*][IM]

I[LF*SWYC]

[EVQLRPGT*ISAK]S

[NDYH][L]

Misannealing overhangs:





GGCA

TGCC

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

G[NRTIMSK]

[EVQLRPGT*MSWAK]A

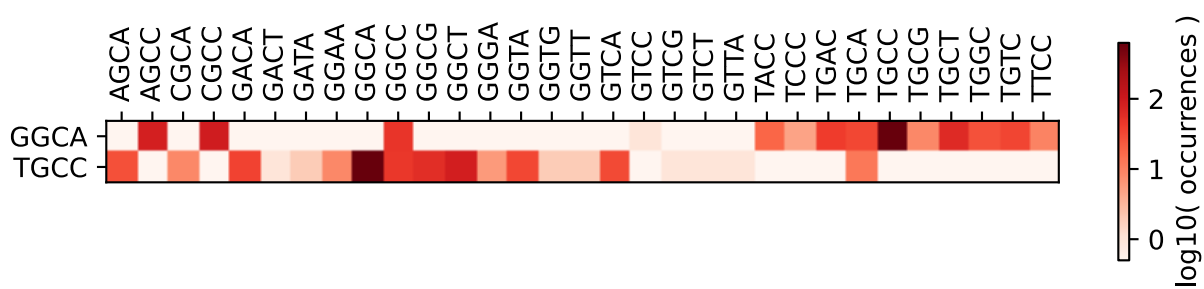
[WRG][QH]

C[PQLRH]

[VNPLRDGFTISHAYC]A

[LVM][P]

Misannealing overhangs:





CCGG

CCGG

Extreme GC content: 100 %.

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

Can form the following amino acids in 6 translation frames:

P[EVDGA]

[VNPLRDGFTISHAYC]R

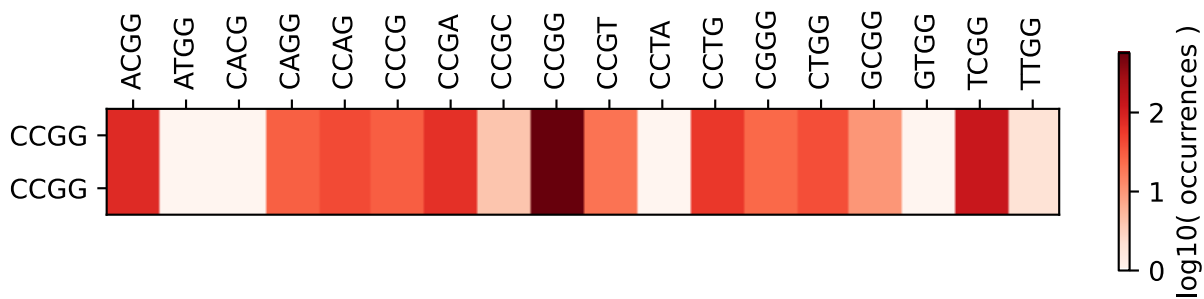
[PTAS][G]

P[EVDGA]

[VNPLRDGFTISHAYC]R

[PTAS][G]

Misannealing overhangs:





CTTC

GAAG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

L[PQLRH]

[VNPLRDGFTISHAYC]F

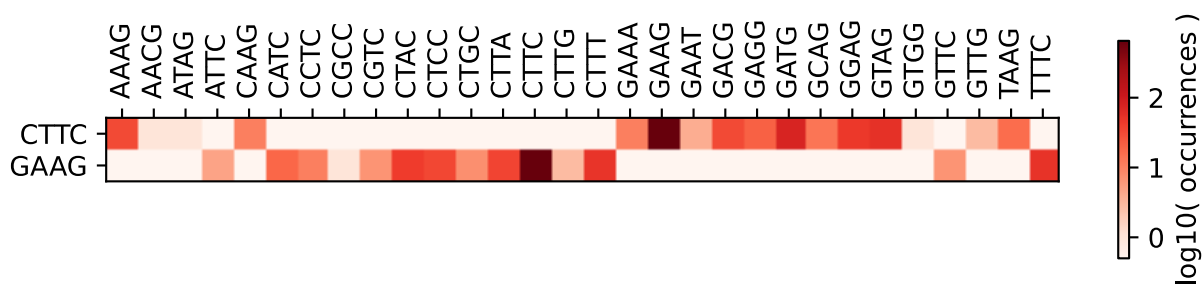
[PTAS][S]

E[EVDGA]

[EVQLRPGT*MSWAK]K

[R*G][RS]

Misannealing overhangs:





CTTC

GAAG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

L[PQLRH]

[VNPLRDGFTISHAYC]F

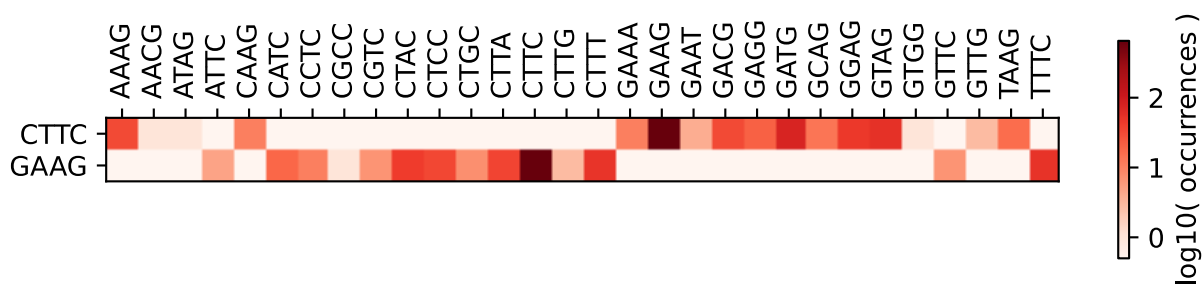
[PTAS][S]

E[EVDGA]

[EVQLRPGT*MSWAK]K

[R*G][RS]

Misannealing overhangs:





CTAA

TTAG

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

L[NRTIMSK]

[VNPLRDGFTISHAYC]*

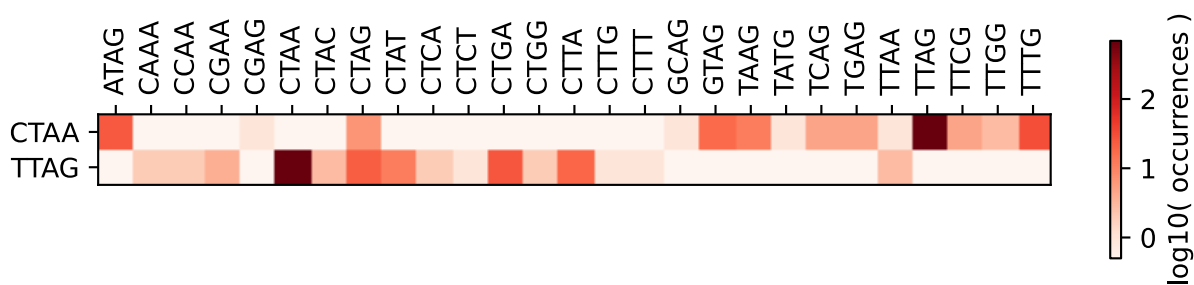
[PTAS][NK]

L[EVDGA]

[VNPLRDGFTISHAYC]*

[FLVI][RS]

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.