Edinburgh Genome Foundry

Compendium of overhangs

There are **136** overhangs in this report. The restriction enzyme used in this compendium is **BsaI**.

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

☑ AAAG CTTT

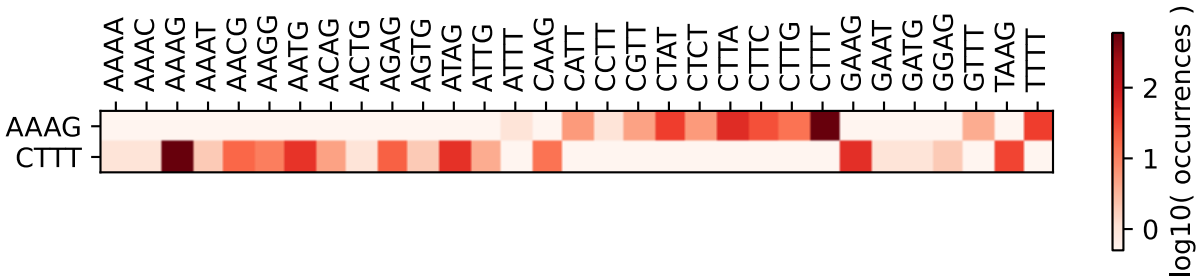
GC content: **25 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

K[EAVGD]
[IESAV*KQGPLRT]K
[*EKQ][RS]
L[SFW*CLY]
[DINSFAVRCGPLYHT]F
[APST][FL]

Misannealing overhangs:



☑ AAAT ATTT

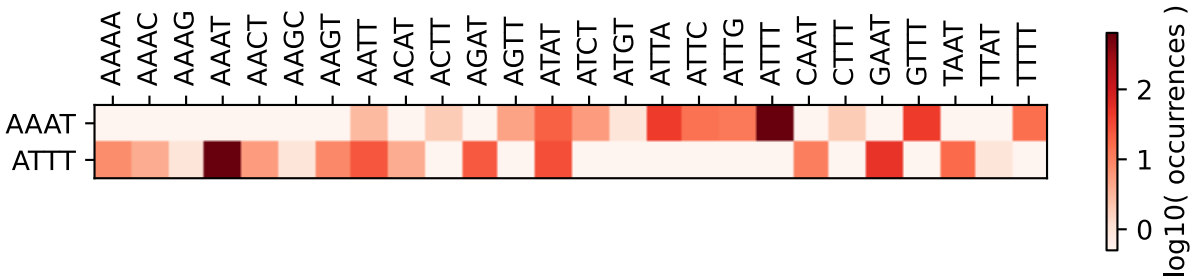
Extreme GC content: 0 %.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

K[SFW*CLY]
[IESAV*KQGPLRT]N
[*EKQ][MI]
I[SFW*CLY]
[IESAV*KQGPLRT]F
[NDYH][FL]

Misannealing overhangs:



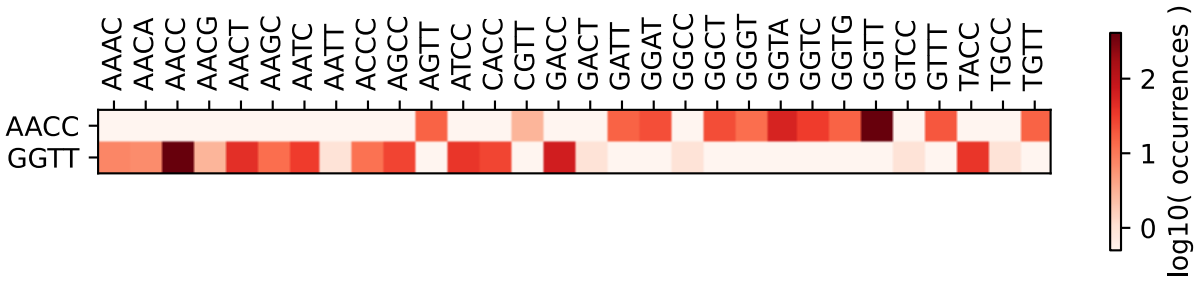
☑ AACC GGTT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

N[PLRHQ]
[IESAV*KQGPLRT]T
[*EKQ][P]
G[SFW*CLY]
[GESWAV*KQMPLRT]V
[WGR][FL]

Misannealing overhangs:



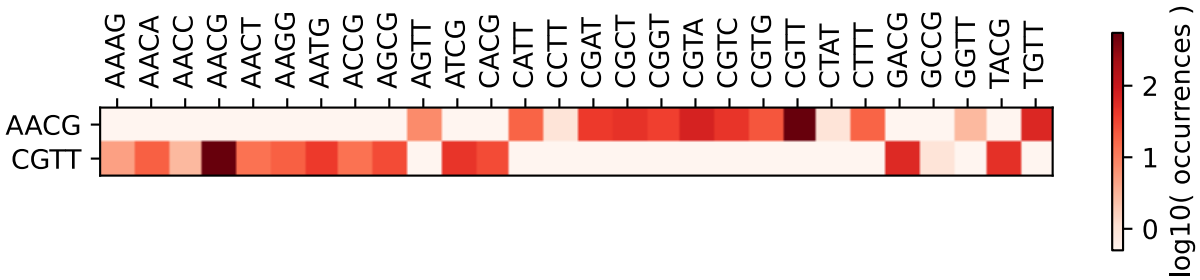
☑ AACG CGTT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

N[EAVGD]
[IESAV*KQGPLRT]T
[*EKQ][R]
R[SFW*CLY]
[DINSFAVRCGPLYHT]V
[APST][FL]

Misannealing overhangs:



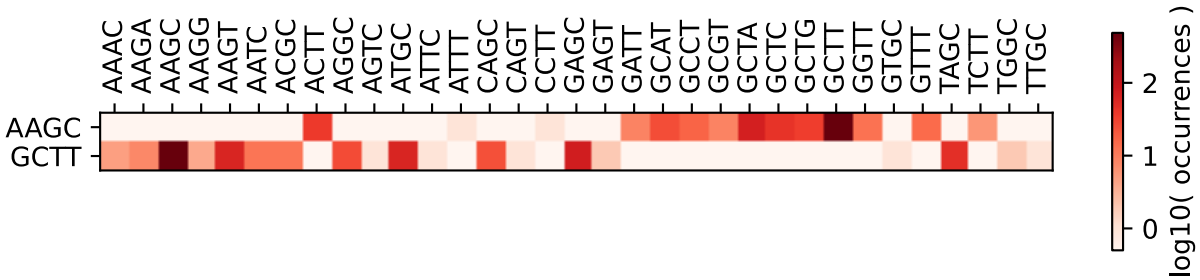
☑ AAGC GCTT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

K[PLRHQ]
[IESAV*KQGPLRT]S
[*EKQ][A]
A[SFW*CLY]
[GESWAV*KQMPLRT]L
[GRCS][FL]

Misannealing overhangs:



☑ AATG CATT

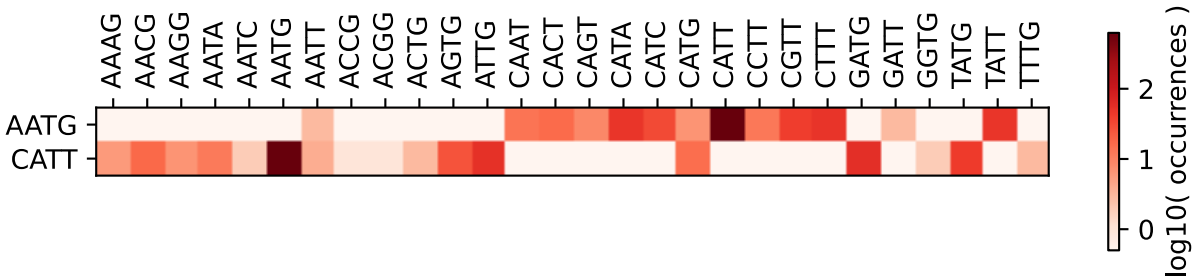
GC content: **25 %**.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

N[EAVGD]
[IESAV*KQGPLRT]M
[*EKQ][W*C]
H[SFW*CLY]
[DINSFAVRCGPLYHT]I
[APST][FL]

Misannealing overhangs:



☒ AATT AATT

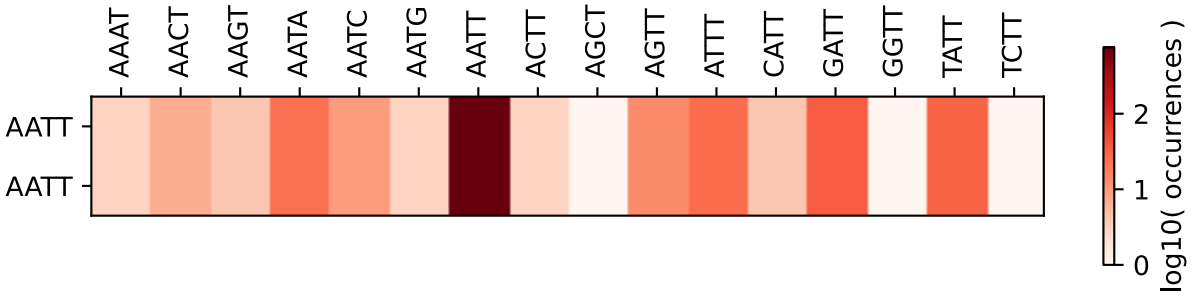
Extreme GC content: 0 %.

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

Can form the following amino acids in 6 translation frames:

N[SFW*CLY]
[IESAV*KQGPLRT]I
[*EKQ][FL]
N[SFW*CLY]
[IESAV*KQGPLRT]I
[*EKQ][FL]

Misannealing overhangs:

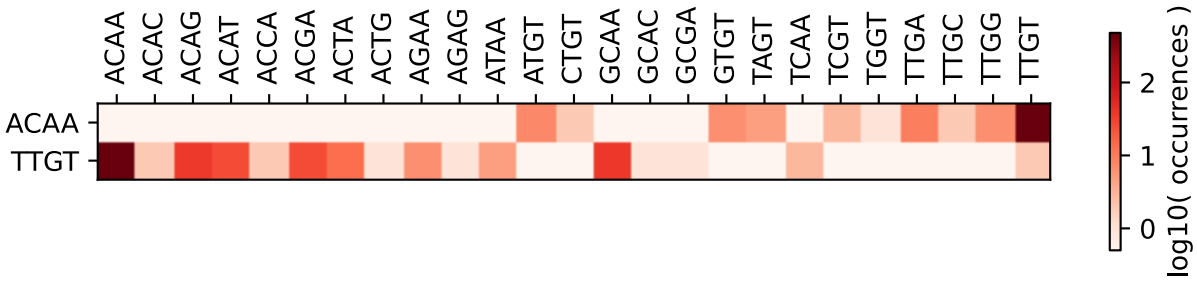


GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

T[INSKMRT]
[IESAV*KQGPLRT]Q
[NDYH][NK]
L[SFW*CLY]
[DINSFAVRCGPLYHT]C
[FVIL][V]

Misannealing overhangs:



☑ ACAT ATGT

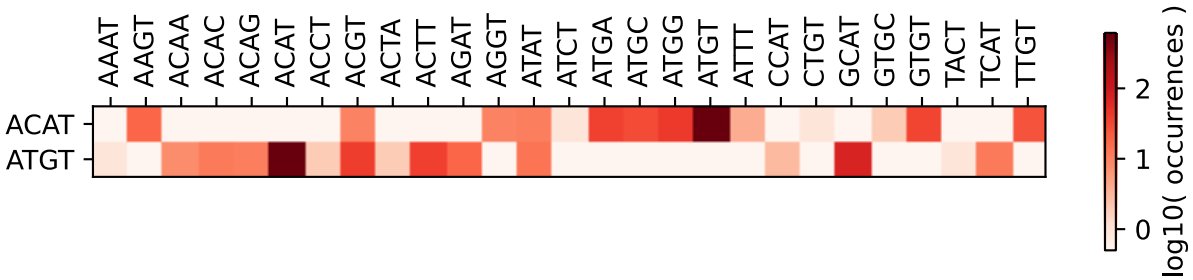
GC content: **25 %**.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

T[SFW*CLY]
[IESAV*KQGPLRT]H
[NDYH][MI]
M[SFW*CLY]
[IESAV*KQGPLRT]C
[NDYH][V]

Misannealing overhangs:



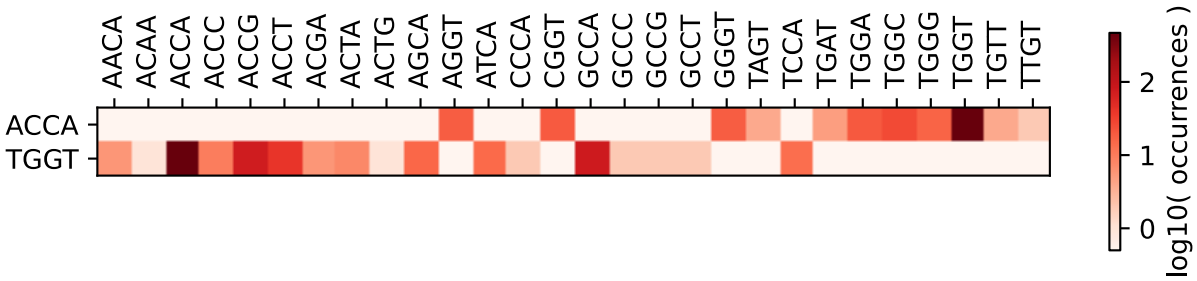
☑ ACCA TGGT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

T[INSKMRT]
[IESAV*KQGPLRT]P
[NDYH][HQ]
W[SFW*CLY]
[DINSFAVRCGPLYHT]G
[MVL][V]

Misannealing overhangs:



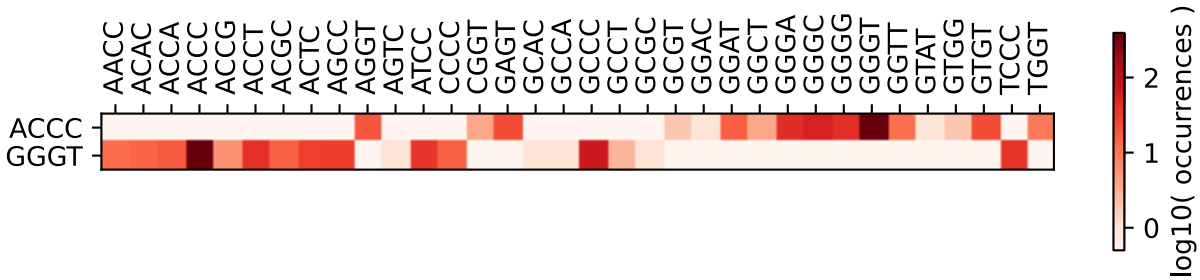
GC content: **75 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

T[PLRHQ]
[IESAV*KQGPLRT]P
[NDYH][P]
G[SFW*CLY]
[GESWAV*KQMPLRT]G
[WGR][V]

Misannealing overhangs:



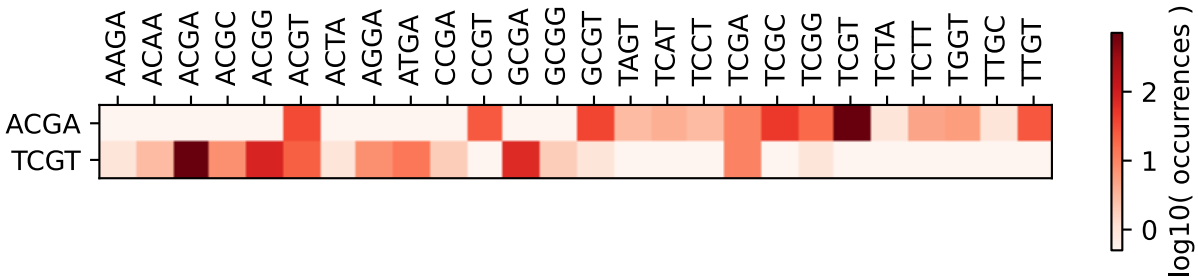
☑ ACGA TCGT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

T[INSKMRT]
[IESAV*KQGPLRT]R
[NDYH][ED]
S[SFW*CLY]
[DINSFAVRCGPLYHT]R
[FVIL][V]

Misannealing overhangs:



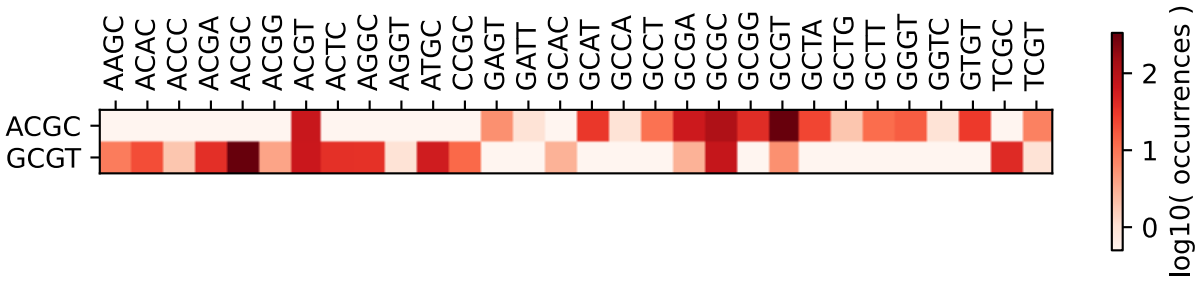
☑ ACGC GCGT

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

T[PLRHQ]
[IESAV*KQGPLRT]R
[NDYH][A]
A[SFW*CLY]
[GESWAV*KQMPLRT]R
[GRCS][V]

Misannealing overhangs:



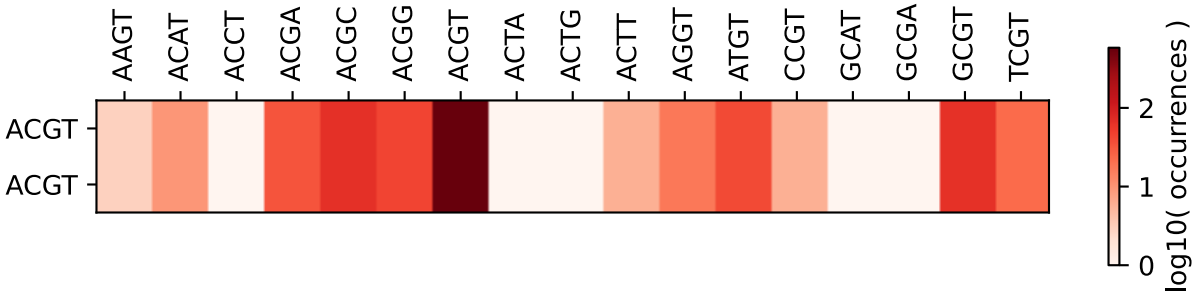
GC content: **50 %**.

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

Can form the following amino acids in 6 translation frames:

T[SFW*CLY]
[IESAV*KQGPLRT]R
[NDYH][V]
T[SFW*CLY]
[IESAV*KQGPLRT]R
[NDYH][V]

Misannealing overhangs:



☑ ACTA TAGT

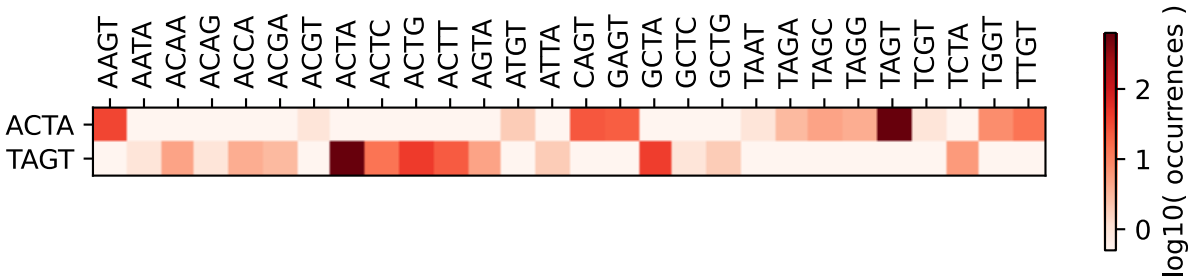
GC content: **25 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

T[INSKMRT]
[IESAV*KQGPLRT]L
[NDYH][Y*]
*[SFW*CLY]
[DINSFAVRCGPLYHT]S
[VIL][V]

Misannealing overhangs:

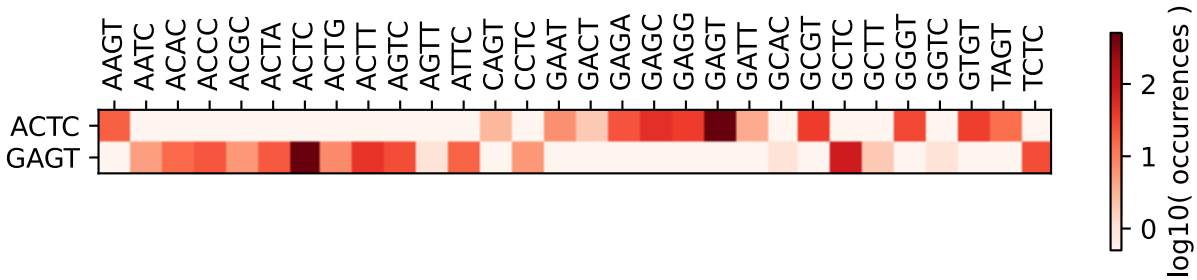


GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

T[PLRHQ]
[IESAV*KQGPLRT]L
[NDYH][S]
E[SFW*CLY]
[GESWAV*KQMPLRT]S
[G*R][V]

Misannealing overhangs:



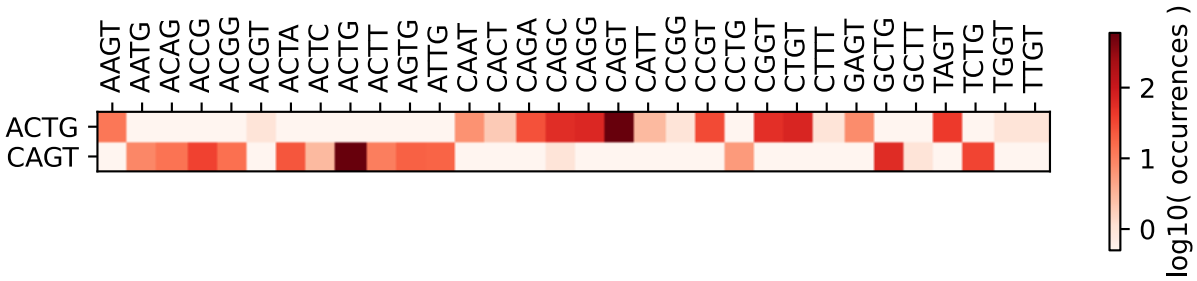
☑ ACTG CAGT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

T[EAVGD]
[IESAV*KQGPLRT]L
[NDYH][W*C]
Q[SFW*CLY]
[DINSFAVRCGPLYHT]S
[APST][V]

Misannealing overhangs:



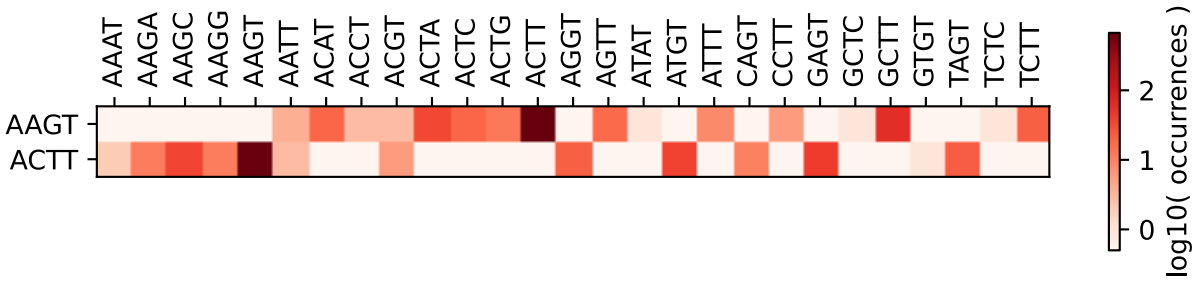
☑ AAGT ACTT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

K[SFW*CLY]
[IESAV*KQGPLRT]S
[*EKQ][V]
T[SFW*CLY]
[IESAV*KQGPLRT]L
[NDYH][FL]

Misannealing overhangs:



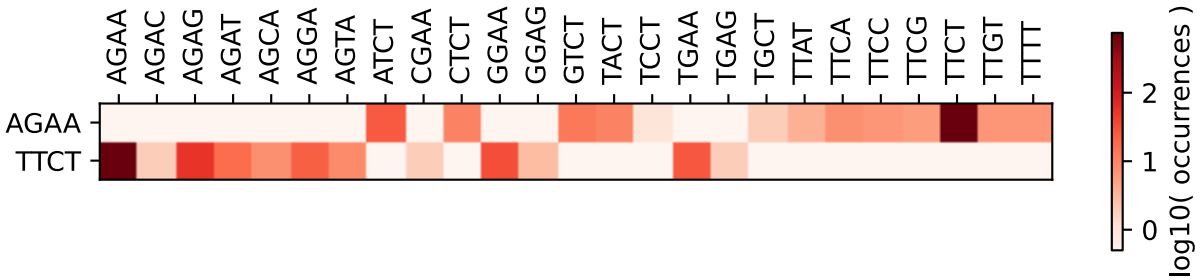
☑ AGAA TTCT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

R[INSKMRT]
[IESAV*KQGPLRT]E
[*EKQ][NK]
F[SFW*CLY]
[DINSFAVRCGPLYHT]S
[FVIL][L]

Misannealing overhangs:

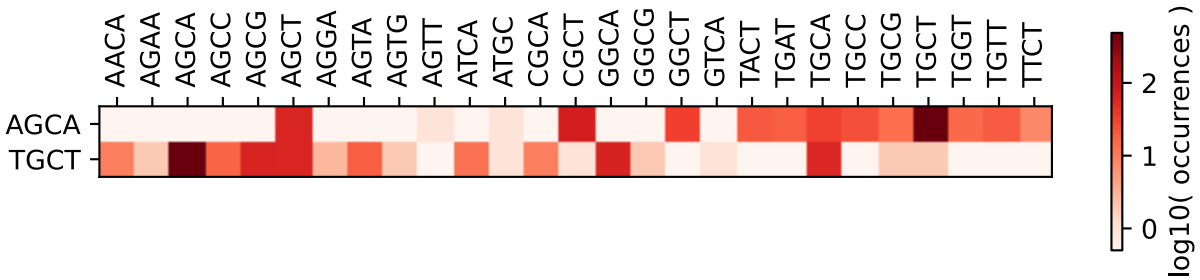


GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

S[INSKMRT]
[IESAV*KQGPLRT]A
[*EKQ][HQ]
C[SFW*CLY]
[DINSFAVRCGPLYHT]A
[MVL][L]

Misannealing overhangs:



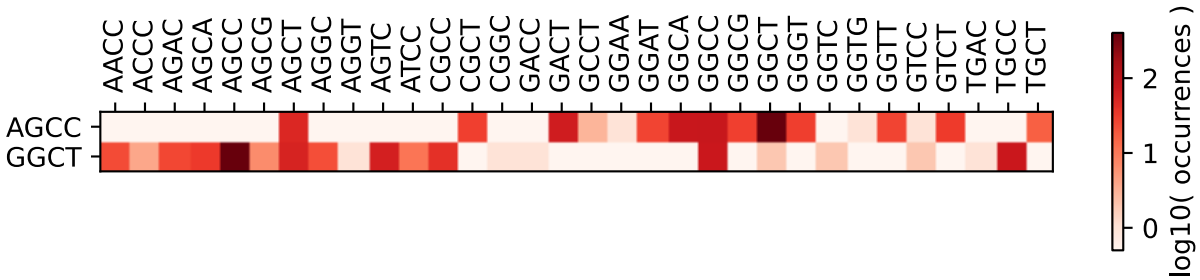
☑ AGCC GGCT

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

S[PLRHQ]
[IESAV*KQGPLRT]A
[*EKQ][P]
G[SFW*CLY]
[GESWAV*KQMPLRT]A
[WGR][L]

Misannealing overhangs:



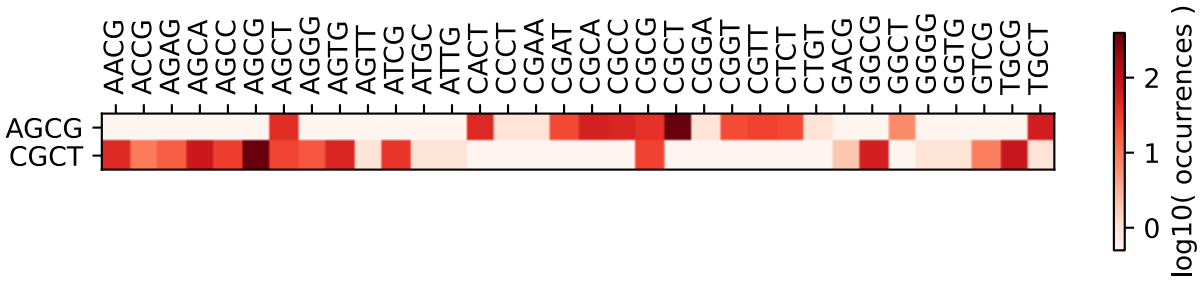
☑ AGCG CGCT

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

S[EAVGD]
[IESAV*KQGPLRT]A
[*EKQ][R]
R[SFW*CLY]
[DINSFAVRCGPLYHT]A
[APST][L]

Misannealing overhangs:



☒ AGCT AGCT

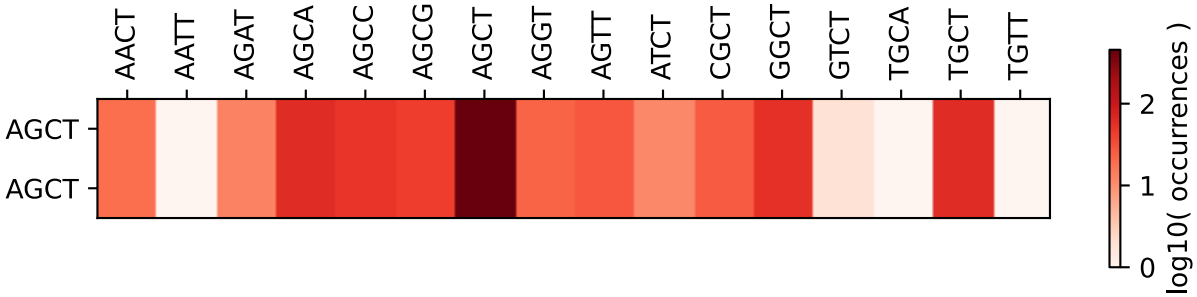
GC content: **50 %**.

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

Can form the following amino acids in 6 translation frames:

S[SFW*CLY]
[IESAV*KQGPLRT]A
[*EKQ][L]
S[SFW*CLY]
[IESAV*KQGPLRT]A
[*EKQ][L]

Misannealing overhangs:



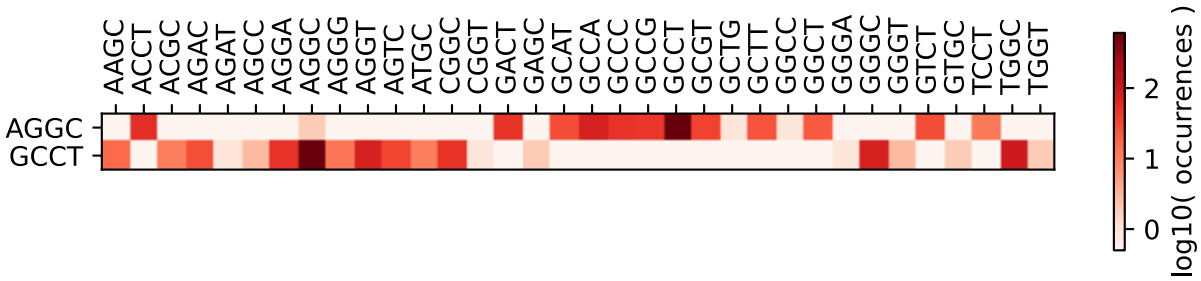
☑ AGGC GCCT

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

R[PLRHQ]
[IESAV*KQGPLRT]G
[*EKQ][A]
A[SFW*CLY]
[GESWAV*KQMPLRT]P
[GRCS][L]

Misannealing overhangs:

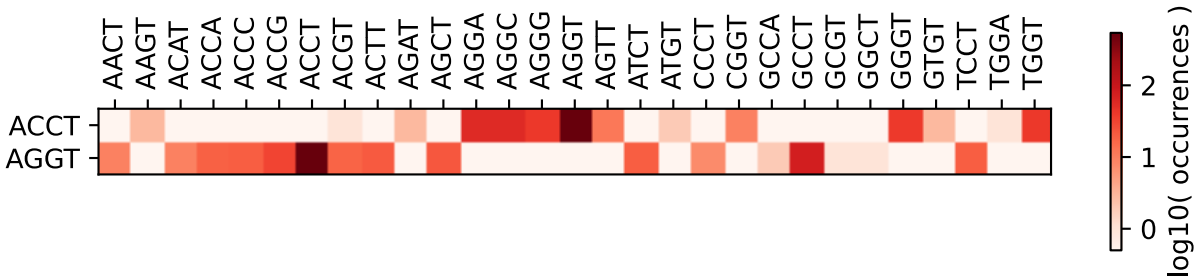


GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

T[SFW*CLY]
[IESAV*KQGPLRT]P
[NDYH][L]
R[SFW*CLY]
[IESAV*KQGPLRT]G
[*EKQ][V]

Misannealing overhangs:



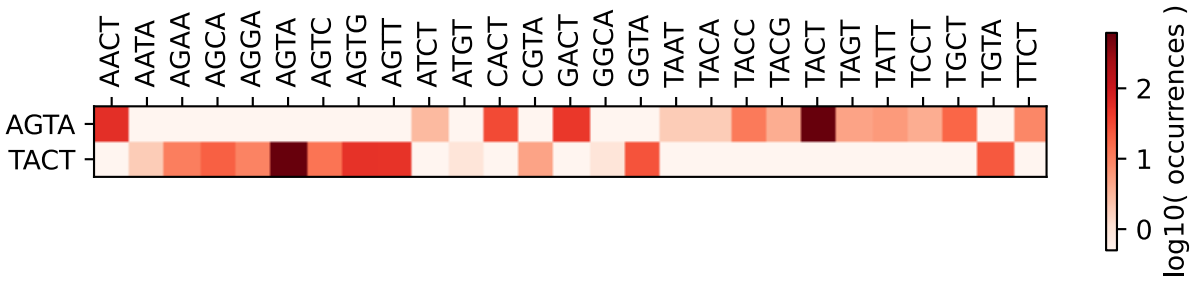
☑ AGTA TACT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

S[INSKMRT]
[IESAV*KQGPLRT]V
[*EKQ][Y*]
Y[SFW*CLY]
[DINSFAVRCGPLYHT]T
[VIL][L]

Misannealing overhangs:



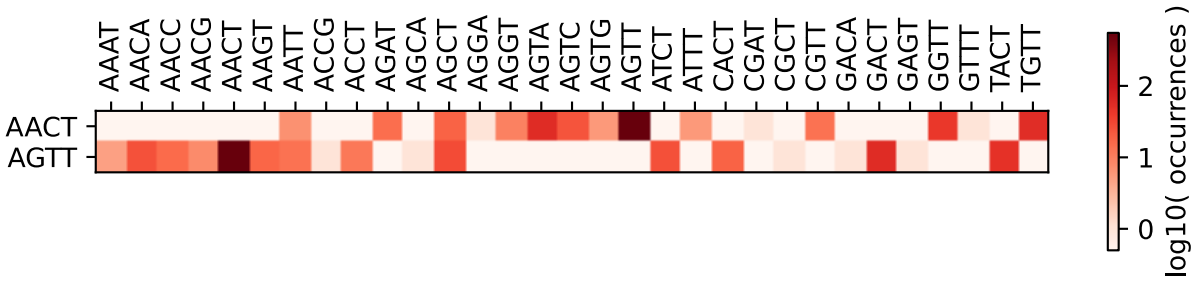
☑ AACT AGTT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

N[SFW*CLY]
[IESAV*KQGPLRT]T
[*EKQ][L]
S[SFW*CLY]
[IESAV*KQGPLRT]V
[*EKQ][FL]

Misannealing overhangs:



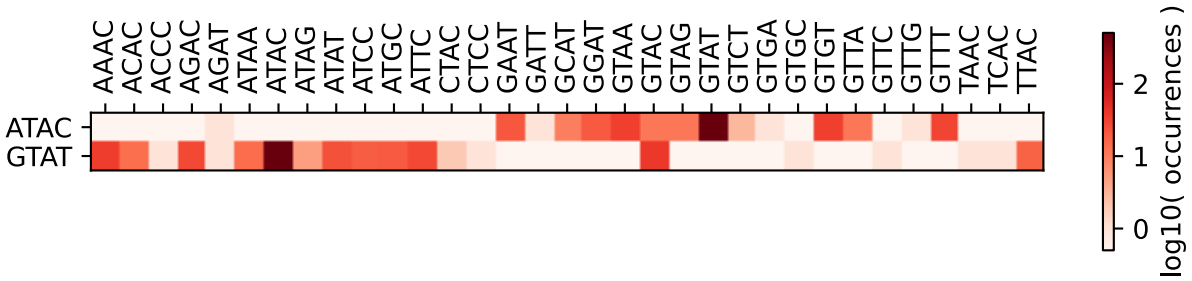
☑ ATAC GTAT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

I[PLRHQ]
[IESAV*KQGPLRT]Y
[NDYH][T]
V[SFW*CLY]
[GESWAV*KQMPLRT]Y
[GRCS][MI]

Misannealing overhangs:



☒ ATAT ATAT

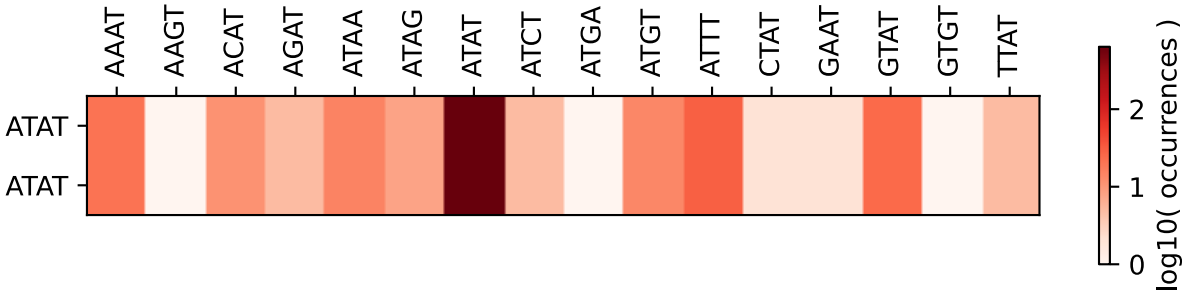
Extreme GC content: 0 %.

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

Can form the following amino acids in 6 translation frames:

I[SFW*CLY]
[IESAV*KQGPLRT]Y
[NDYH][MI]
I[SFW*CLY]
[IESAV*KQGPLRT]Y
[NDYH][MI]

Misannealing overhangs:



☑ ATCA TGAT

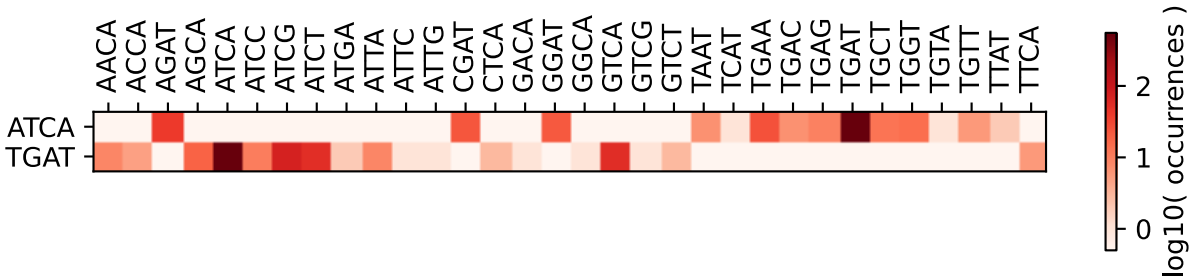
GC content: **25 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

I[INSKMRT]
[IESAV*KQGPLRT]S
[NDYH][HQ]
*[SFW*CLY]
[DINSFAVRCGPLYHT]D
[MVL][MI]

Misannealing overhangs:



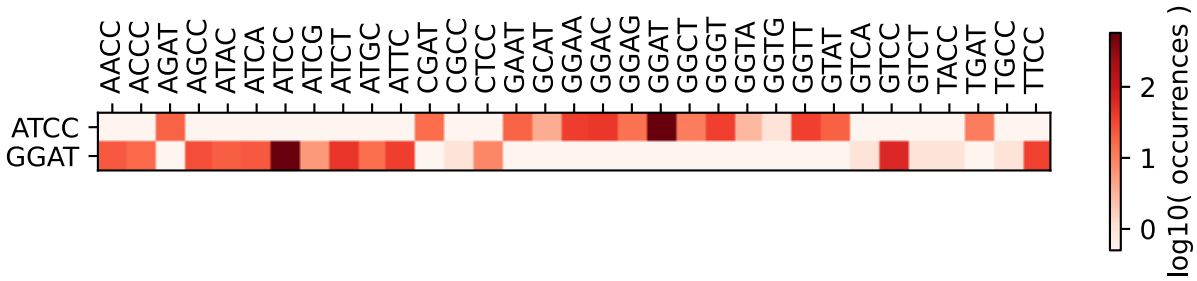
☑ ATCC GGAT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

I[PLRHQ]
[IESAV*KQGPLRT]S
[NDYH][P]
G[SFW*CLY]
[GESWAV*KQMPLRT]D
[WGR][MI]

Misannealing overhangs:



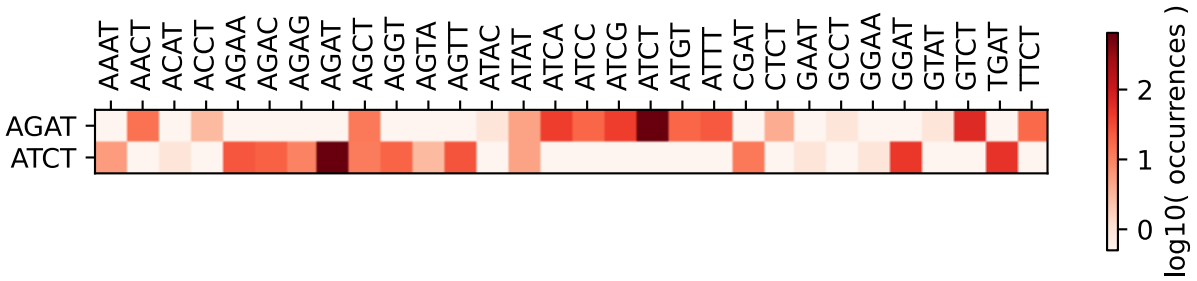
☑ AGAT ATCT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

R[SFW*CLY]
[IESAV*KQGPLRT]D
[*EKQ][MI]
I[SFW*CLY]
[IESAV*KQGPLRT]S
[NDYH][L]

Misannealing overhangs:



☑ ATGG CCAT

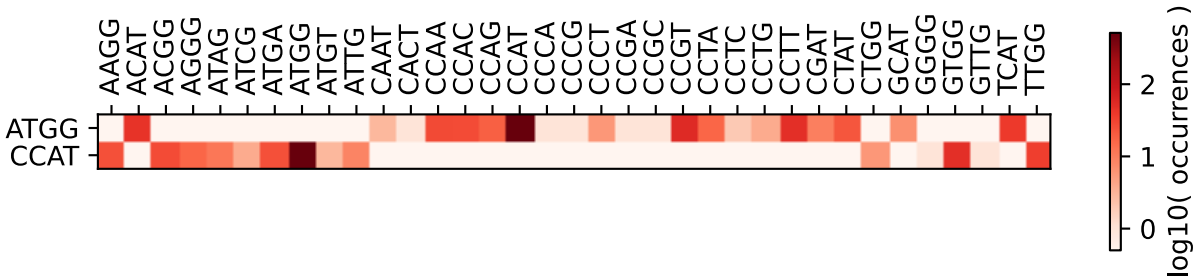
GC content: **50 %**.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

M[EAVGD]
[IESAV*KQGPLRT]W
[NDYH][G]
P[SFW*CLY]
[DINSFAVRCGPLYHT]H
[APST][MI]

Misannealing overhangs:



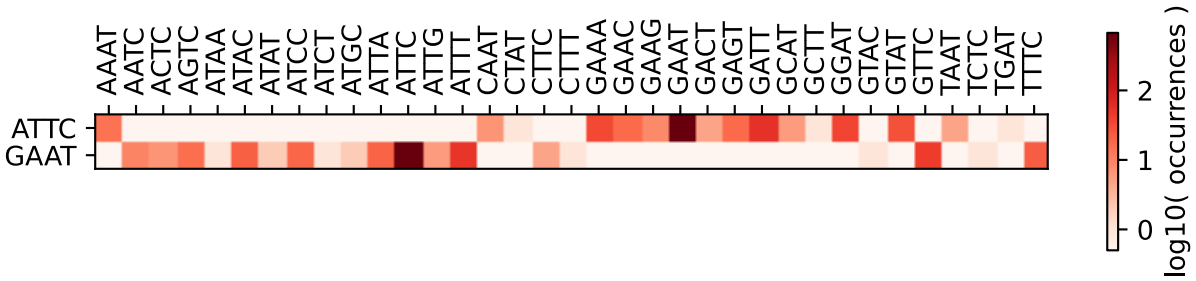
☑ ATTC GAAT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

I[PLRHQ]
[IESAV*KQGPLRT]F
[NDYH][S]
E[SFW*CLY]
[GESWAV*KQMPLRT]N
[G*R][MI]

Misannealing overhangs:



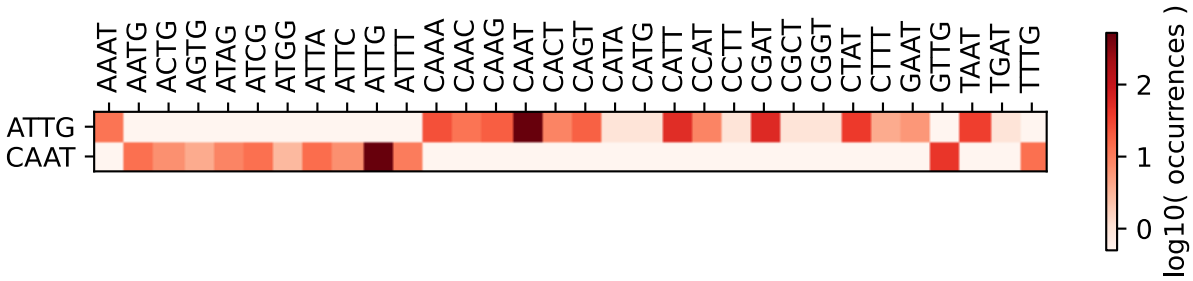
☑ ATTG CAAT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

I[EAVGD]
[IESAV*KQGPLRT]L
[NDYH][W*C]
Q[SFW*CLY]
[DINSFAVRCGPLYHT]N
[APST][MI]

Misannealing overhangs:



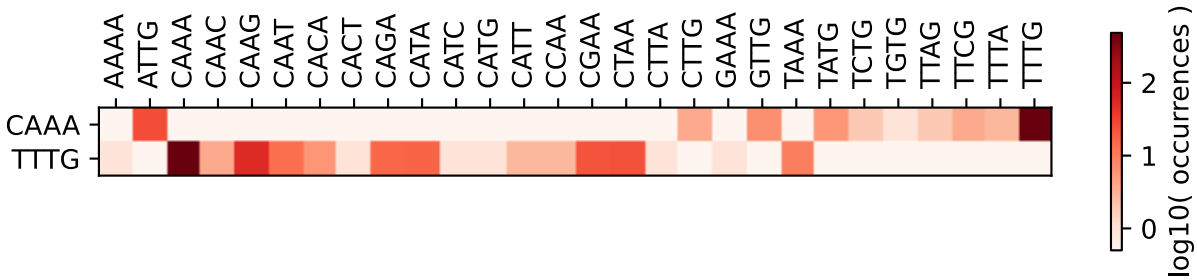
GC content: **25 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

Q[INSKMRT]
[DINSFAVRCGPLYHT]K
[APST][NK]
F[EAVGD]
[DINSFAVRCGPLYHT]L
[FVIL][W*C]

Misannealing overhangs:

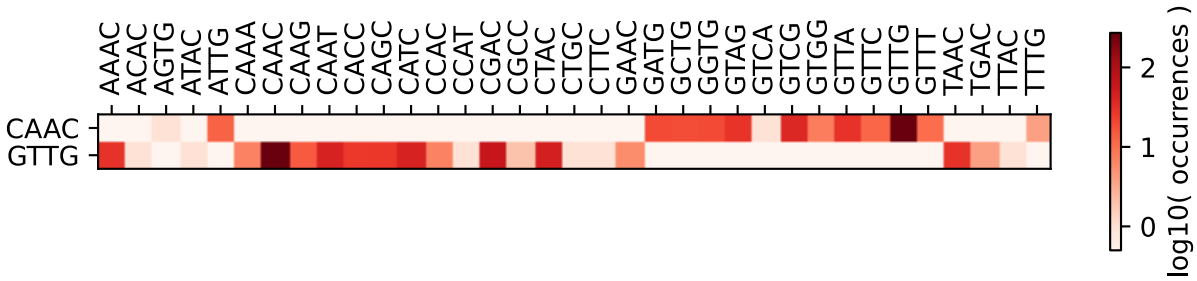


GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

Q[PLRHQ]
[DINSFAVRCGPLYHT]N
[APST][T]
V[EAVGD]
[GESWAV*KQMPLRT]L
[GRCS][W*C]

Misannealing overhangs:



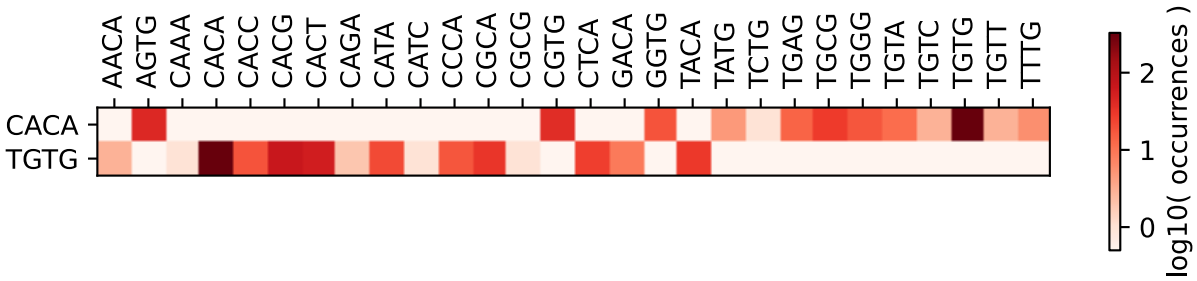
☑ CACA TGTG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

H[INSKMRT]
[DINSFAVRCGPLYHT]T
[APST][HQ]
C[EAVGD]
[DINSFAVRCGPLYHT]V
[MVL][W*C]

Misannealing overhangs:



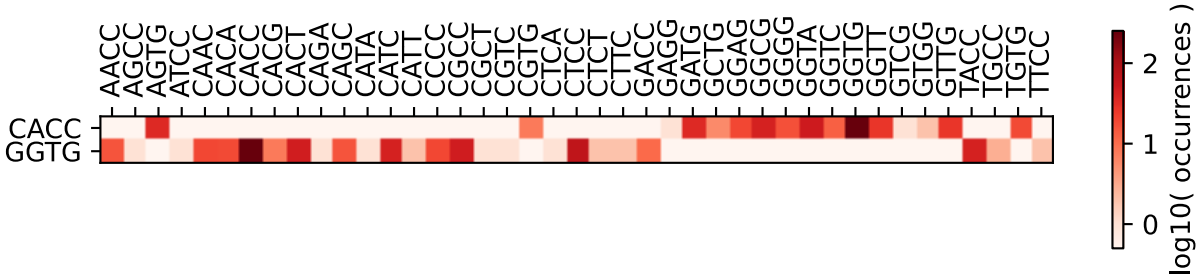
☑ CACC GGTG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

H[PLRHQ]
[DINSFAVRCGPLYHT]T
[APST][P]
G[EAVGD]
[GESWAV*KQMPLRT]V
[WGR][W*C]

Misannealing overhangs:



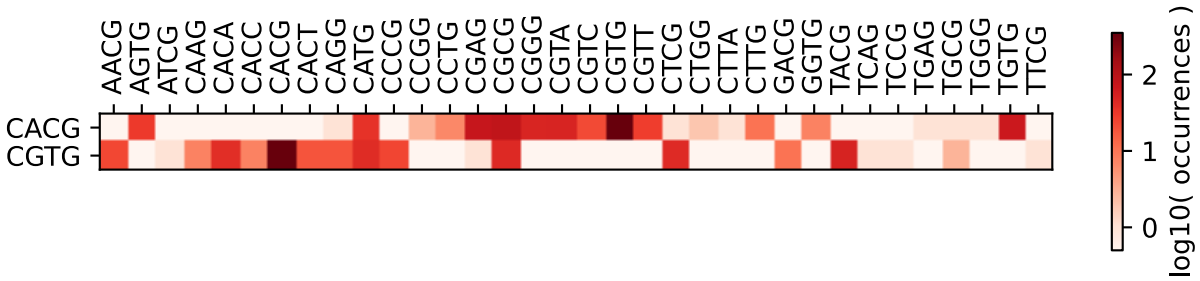
☑ CACG CGTG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

H[EAVGD]
[DINSFAVRCGPLYHT]T
[APST][R]
R[EAVGD]
[DINSFAVRCGPLYHT]V
[APST][W*C]

Misannealing overhangs:



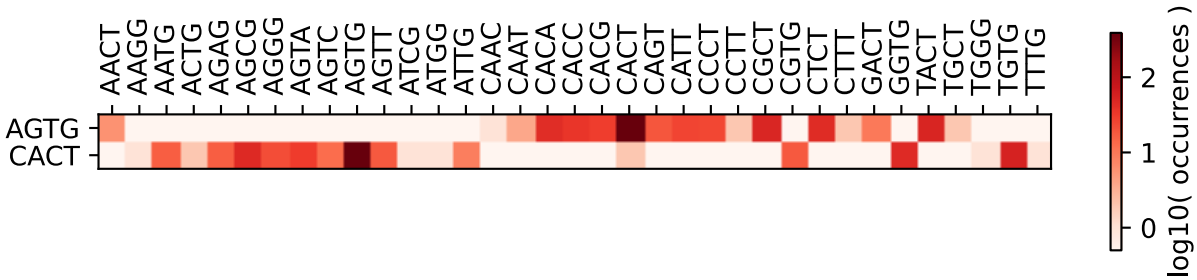
☑ AGTG CACT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

S[EAVGD]
[IESAV*KQGPLRT]V
[*EKQ][W*C]
H[SFW*CLY]
[DINSFAVRCGPLYHT]T
[APST][L]

Misannealing overhangs:



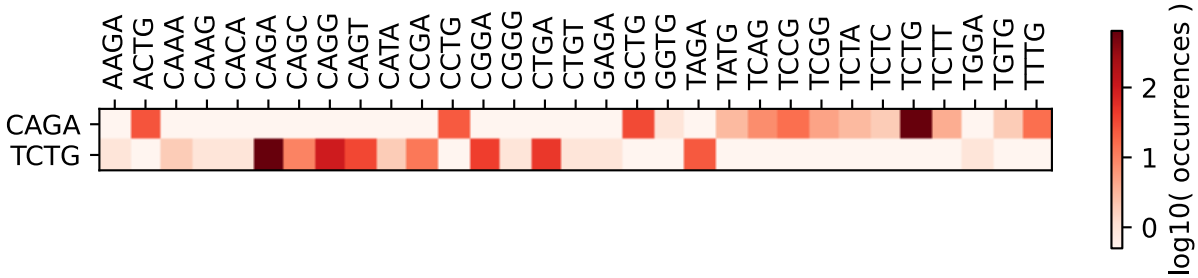
☑ CAGA TCTG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

Q[INSKMRT]
[DINSFAVRCGPLYHT]R
[APST][ED]
S[EAVGD]
[DINSFAVRCGPLYHT]L
[FVIL][W*C]

Misannealing overhangs:



☒ CATG CATG

GC content: **50 %**.

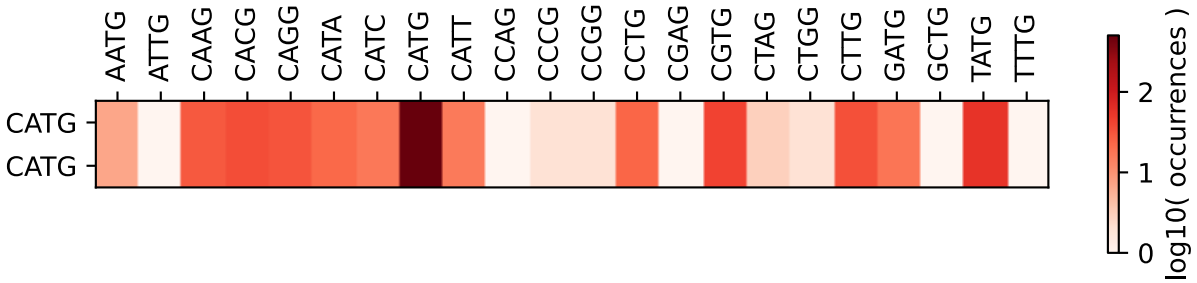
The overhang is palindromic, cannot be used for DNA assembly.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

H[EAVGD]
[DINSFAVRCGPLYHT]M
[APST][W*C]
H[EAVGD]
[DINSFAVRCGPLYHT]M
[APST][W*C]

Misannealing overhangs:



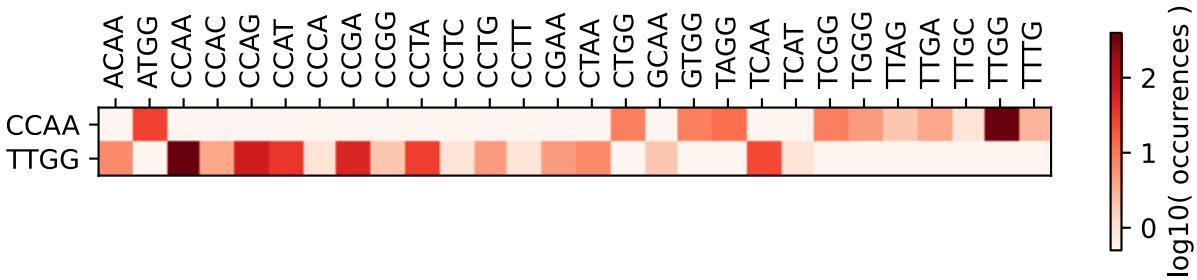
☑ CCAA TTGG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

P[INSKMRT]
[DINSFAVRCGPLYHT]Q
[APST][NK]
L[EAVGD]
[DINSFAVRCGPLYHT]W
[FVIL][G]

Misannealing overhangs:



☑ CCCA TGGG

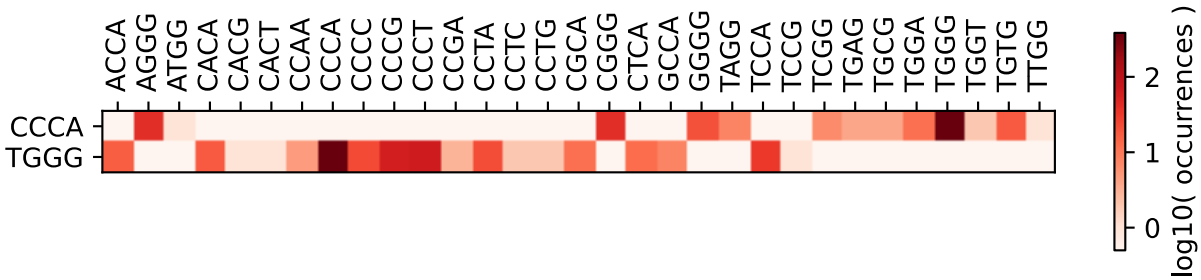
GC content: **75 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

P[INSKMRT]
[DINSFAVRCGPLYHT]P
[APST][HQ]
W[EAVGD]
[DINSFAVRCGPLYHT]G
[MVL][G]

Misannealing overhangs:



☑ AGGG CCCT

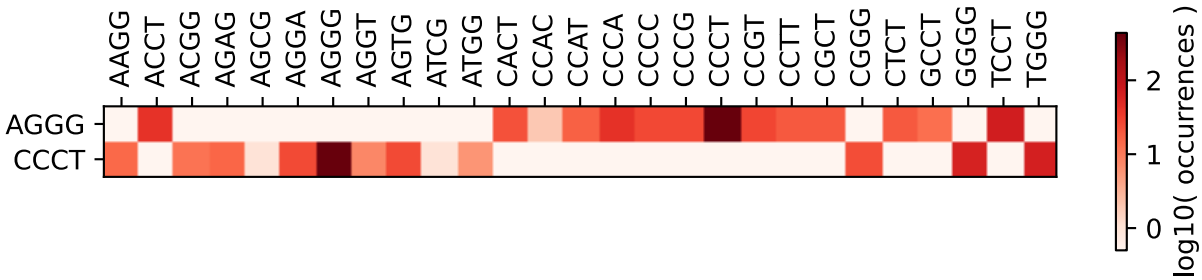
GC content: **75 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

R[EAVGD]
[IESAV*KQGPLRT]G
[*EKQ][G]
P[SFW*CLY]
[DINSFAVRCGPLYHT]P
[APST][L]

Misannealing overhangs:



☒ CCGG CCGG

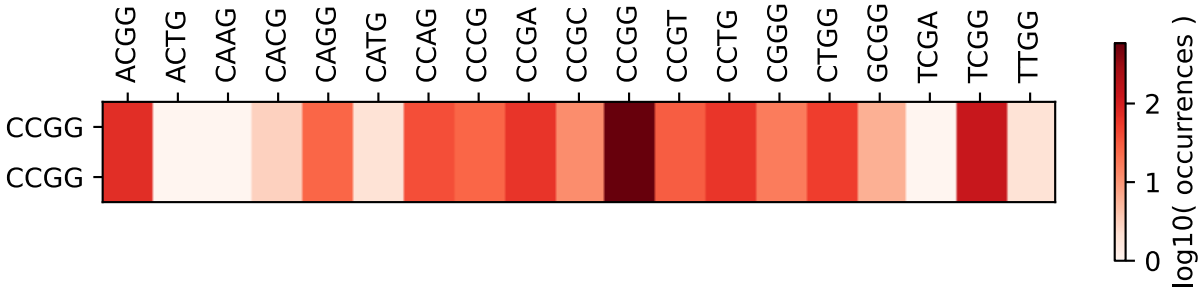
Extreme GC content: 100 %.

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

Can form the following amino acids in 6 translation frames:

P[EAVGD]
[DINSFAVRCGPLYHT]R
[APST][G]
P[EAVGD]
[DINSFAVRCGPLYHT]R
[APST][G]

Misannealing overhangs:



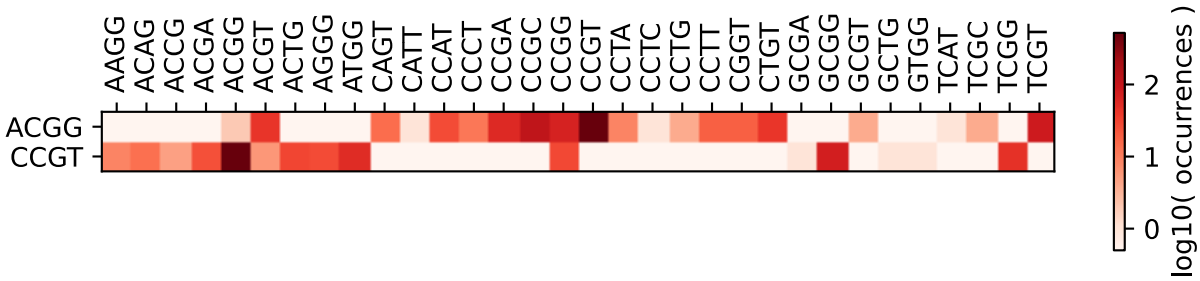
☑ ACGG CCGT

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

T[EAVGD]
[IESAV*KQGPLRT]R
[NDYH][G]
P[SFW*CLY]
[DINSFAVRCGPLYHT]R
[APST][V]

Misannealing overhangs:



☑ CCTA TAGG

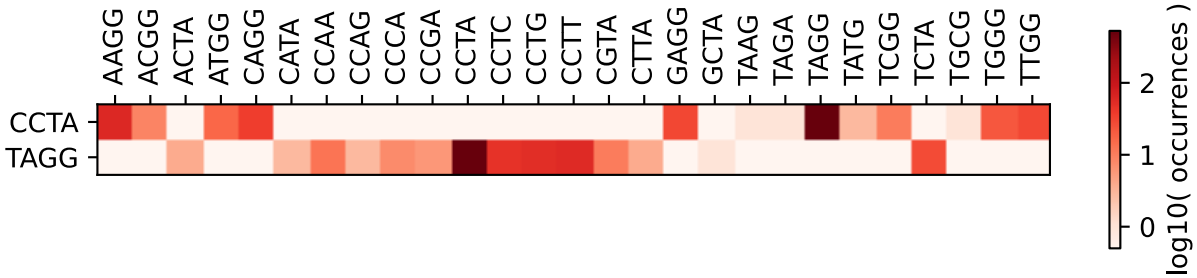
GC content: **50 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

P[INSKMRT]
[DINSFAVRCGPLYHT]L
[APST][Y*]
*[EAVGD]
[DINSFAVRCGPLYHT]R
[VIL][G]

Misannealing overhangs:

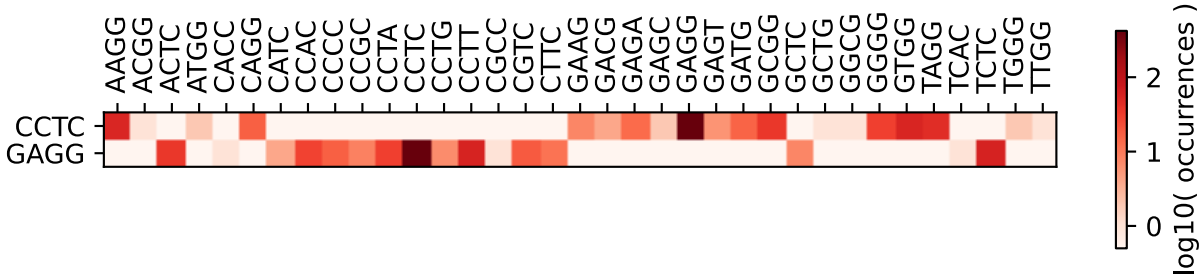


GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

P[PLRHQ]
[DINSFAVRCGPLYHT]L
[APST][S]
E[EAVGD]
[GESWAV*KQMPLRT]R
[G*R][G]

Misannealing overhangs:



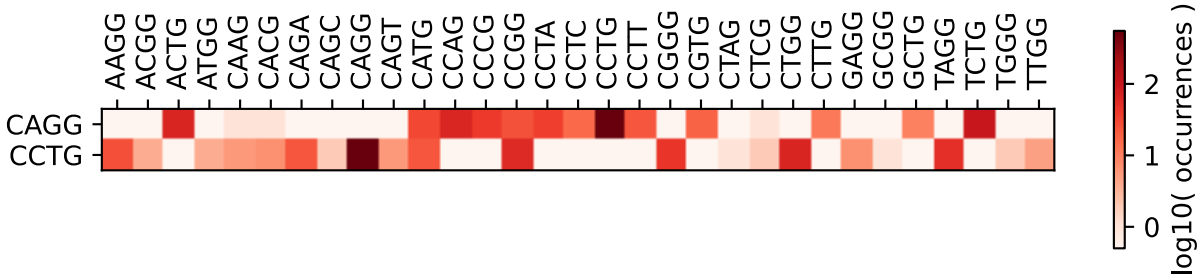
☑ CAGG CCTG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

Q[EAVGD]
[DINSFAVRCGPLYHT]R
[APST][G]
P[EAVGD]
[DINSFAVRCGPLYHT]L
[APST][W*C]

Misannealing overhangs:



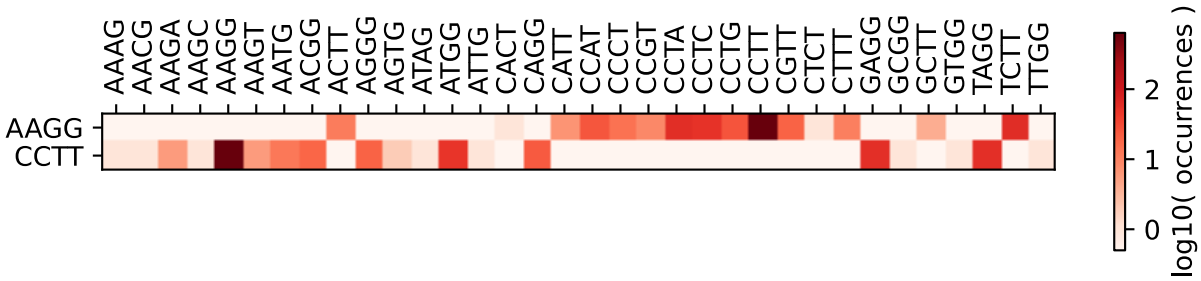
☑ AAGG CCTT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

K[EAVGD]
[IESAV*KQGPLRT]R
[*EKQ][G]
P[SFW*CLY]
[DINSFAVRCGPLYHT]L
[APST][FL]

Misannealing overhangs:



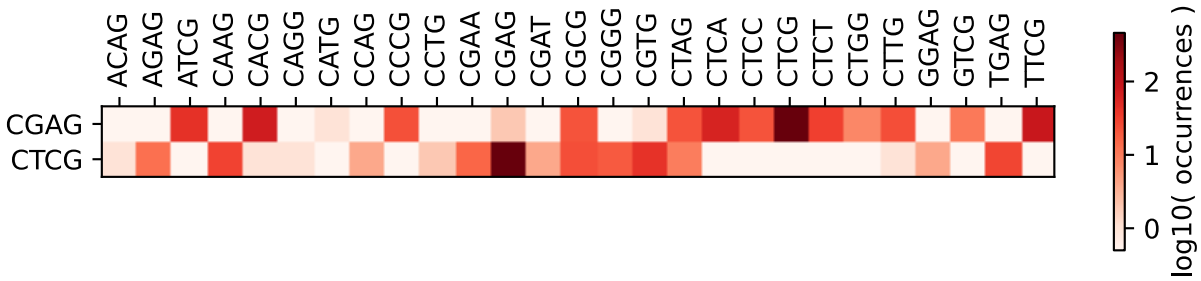
☑ CGAG CTCG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

R[EAVGD]
[DINSFAVRCGPLYHT]E
[APST][RS]
L[EAVGD]
[DINSFAVRCGPLYHT]S
[APST][R]

Misannealing overhangs:



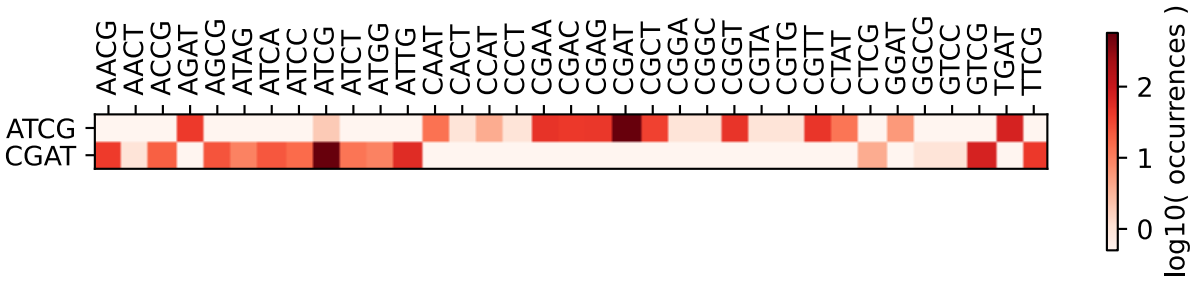
☑ ATCG CGAT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

I[EAVGD]
[IESAV*KQGPLRT]S
[NDYH][R]
R[SFW*CLY]
[DINSFAVRCGPLYHT]D
[APST][MI]

Misannealing overhangs:



☒ CGCG CGCG

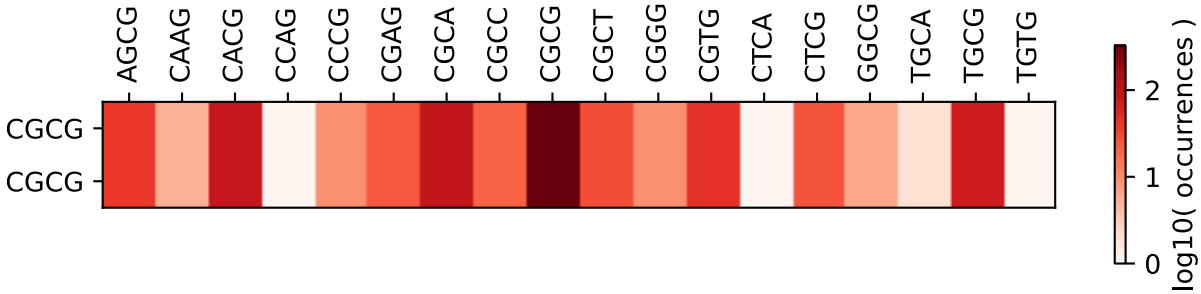
Extreme GC content: 100 %.

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

Can form the following amino acids in 6 translation frames:

R[EAVGD]
[DINSFAVRCGPLYHT]A
[APST][R]
R[EAVGD]
[DINSFAVRCGPLYHT]A
[APST][R]

Misannealing overhangs:



☑ CCCG CGGG

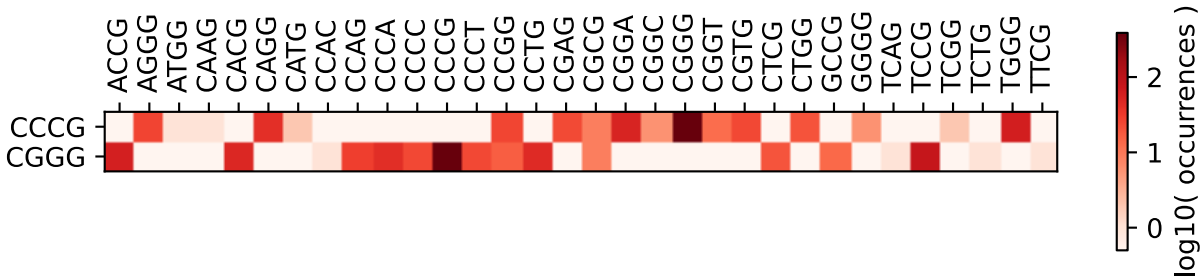
Extreme GC content: 100 %.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

P[EAVGD]
[DINSFAVRCGPLYHT]P
[APST][R]
R[EAVGD]
[DINSFAVRCGPLYHT]G
[APST][G]

Misannealing overhangs:

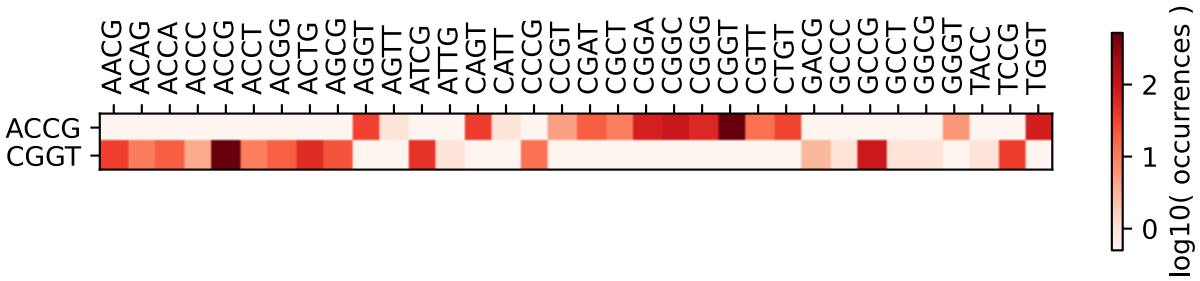


GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

T[EAVGD]
[IESAV*KQGPLRT]P
[NDYH][R]
R[SFW*CLY]
[DINSFAVRCGPLYHT]G
[APST][V]

Misannealing overhangs:



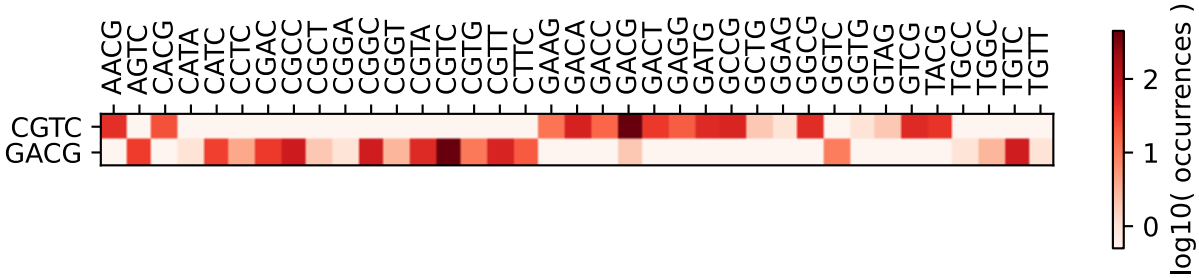
☑ CGTC GACG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

R[PLRHQ]
[DINSFAVRCGPLYHT]V
[APST][S]
D[EAVGD]
[GESWAV*KQMPLRT]T
[G*R][R]

Misannealing overhangs:



☑ CTAA TTAG

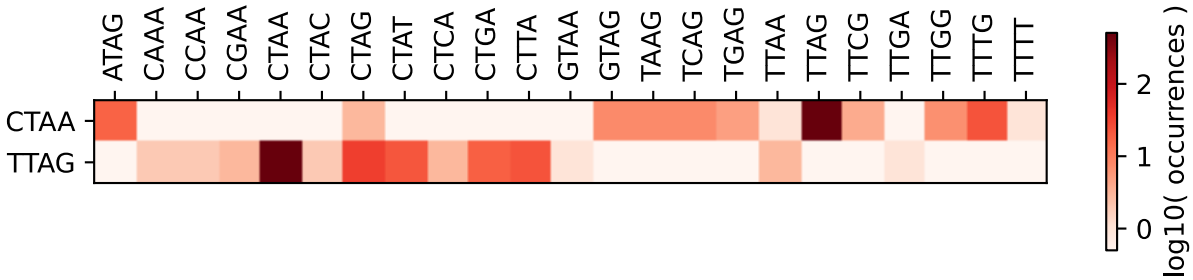
GC content: **25 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

L[INSKMRT]
[DINSFAVRCGPLYHT]*
[APST][NK]
L[EAVGD]
[DINSFAVRCGPLYHT]*
[FVIL][RS]

Misannealing overhangs:



☒ CTAG CTAG

GC content: **50 %**.

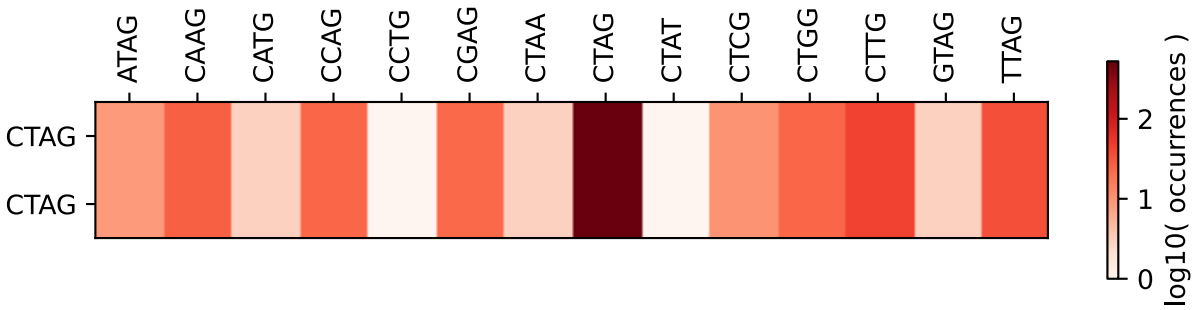
The overhang is palindromic, cannot be used for DNA assembly.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

L[EAVGD]
[DINSFAVRCGPLYHT]*
[APST][RS]
L[EAVGD]
[DINSFAVRCGPLYHT]*
[APST][RS]

Misannealing overhangs:



☑ ATAG CTAT

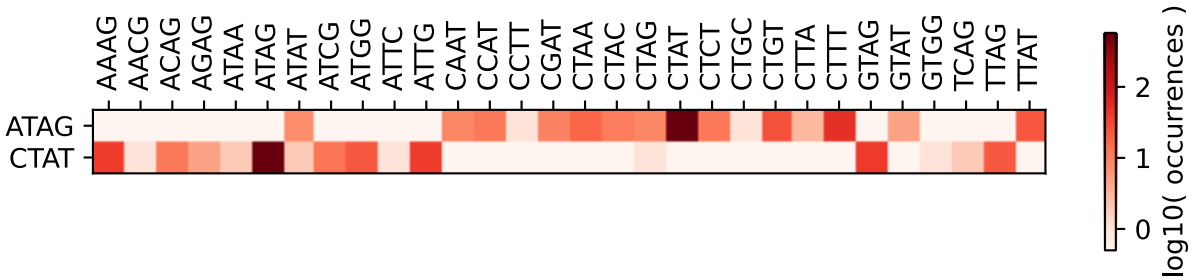
GC content: **25 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

I[EAVGD]
[IESAV*KQGPLRT]*
[NDYH][RS]
L[SFW*CLY]
[DINSFAVRCGPLYHT]Y
[APST][MI]

Misannealing overhangs:

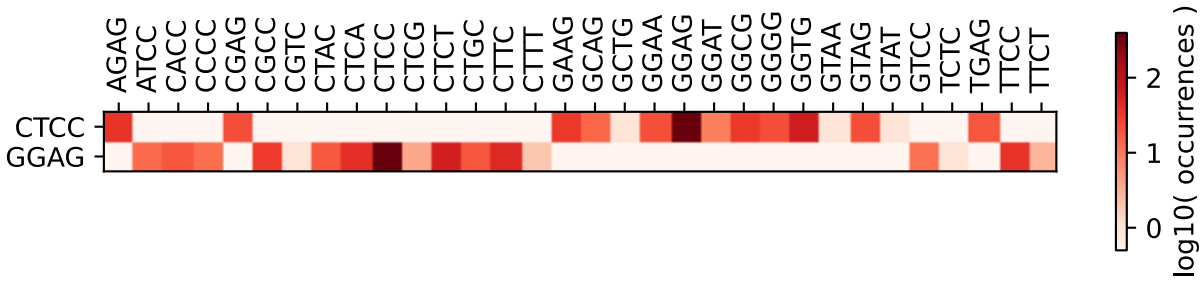


GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

L[PLRHQ]
[DINSFAVRCGPLYHT]S
[APST][P]
G[EAVGD]
[GESWAV*KQMPLRT]E
[WGR][RS]

Misannealing overhangs:



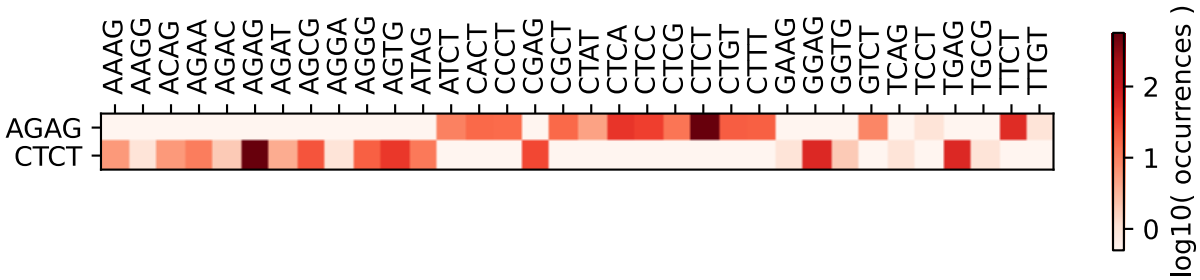
☑ AGAG CTCT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

R[EAVGD]
[IESAV*KQGPLRT]E
[*EKQ][RS]
L[SFW*CLY]
[DINSFAVRCGPLYHT]S
[APST][L]

Misannealing overhangs:



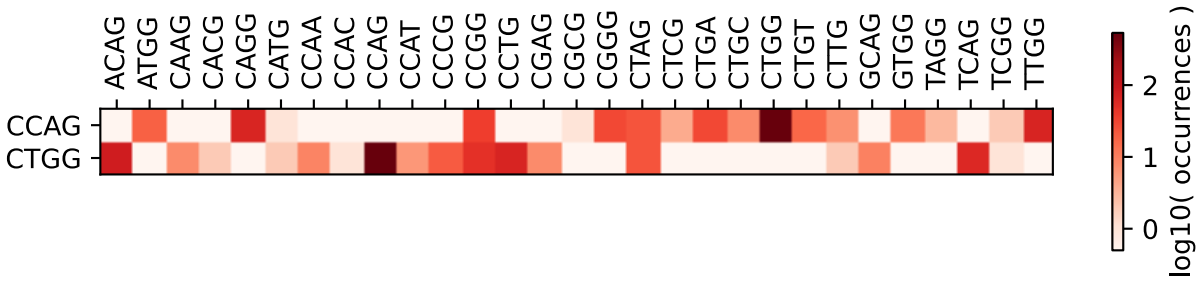
☑ CCAG CTGG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

P[EAVGD]
[DINSFAVRCGPLYHT]Q
[APST][RS]
L[EAVGD]
[DINSFAVRCGPLYHT]W
[APST][G]

Misannealing overhangs:



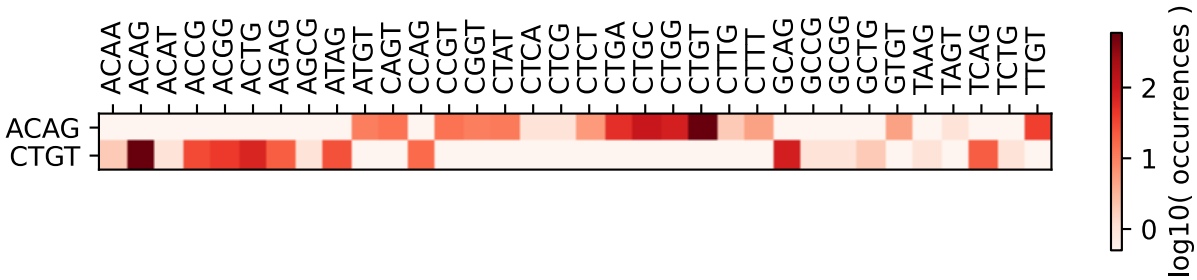
☑ ACAG CTGT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

T[EAVGD]
[IESAV*KQGPLRT]Q
[NDYH][RS]
L[SFW*CLY]
[DINSFAVRCGPLYHT]C
[APST][V]

Misannealing overhangs:



☑ CTTA TAAG

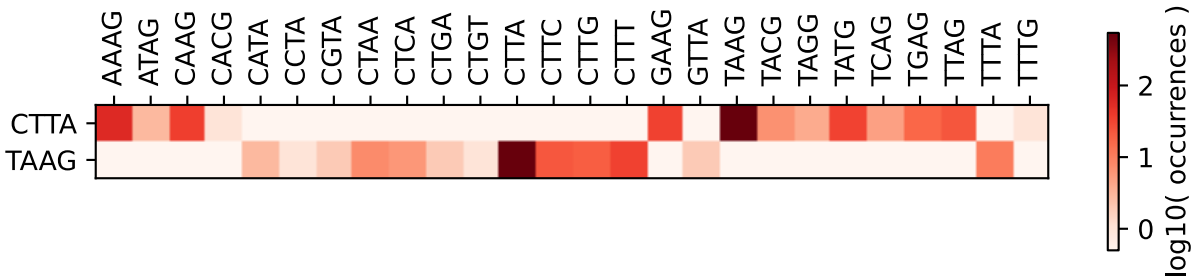
GC content: **25 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

L[INSKMRT]
[DINSFAVRCGPLYHT]L
[APST][Y*]
*[EAVGD]
[DINSFAVRCGPLYHT]K
[VIL][RS]

Misannealing overhangs:

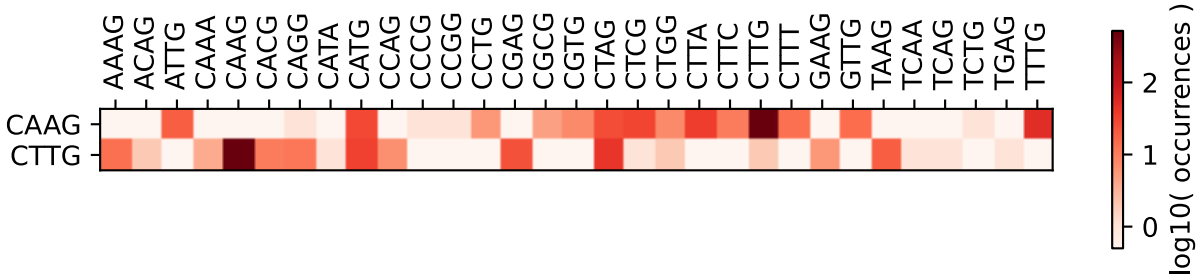


GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

Q[EAVGD]
[DINSFAVRCGPLYHT]K
[APST][RS]
L[EAVGD]
[DINSFAVRCGPLYHT]L
[APST][W*C]

Misannealing overhangs:

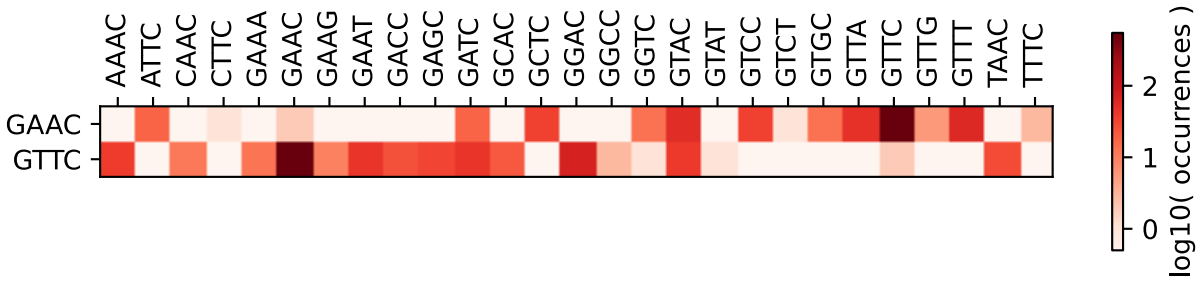


GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

E[PLRHQ]
[GESWAV*KQMPLRT]N
[G*R][T]
V[PLRHQ]
[GESWAV*KQMPLRT]F
[GRCS][S]

Misannealing overhangs:



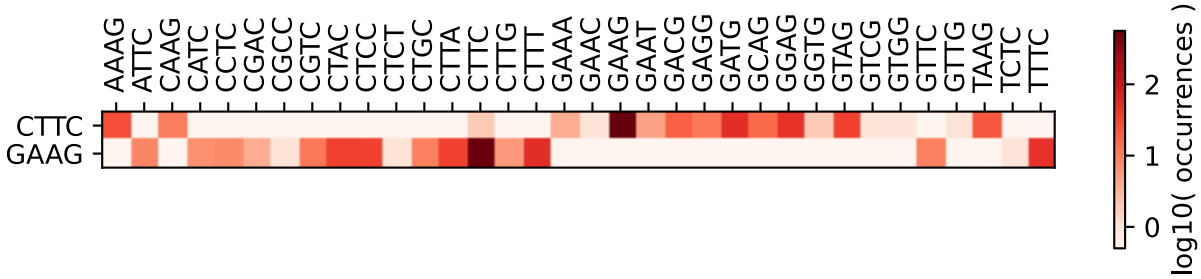
☑ CTTC GAAG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

L[PLRHQ]
[DINSFAVRCGPLYHT]F
[APST][S]
E[EAVGD]
[GESWAV*KQMPLRT]K
[G*R][RS]

Misannealing overhangs:



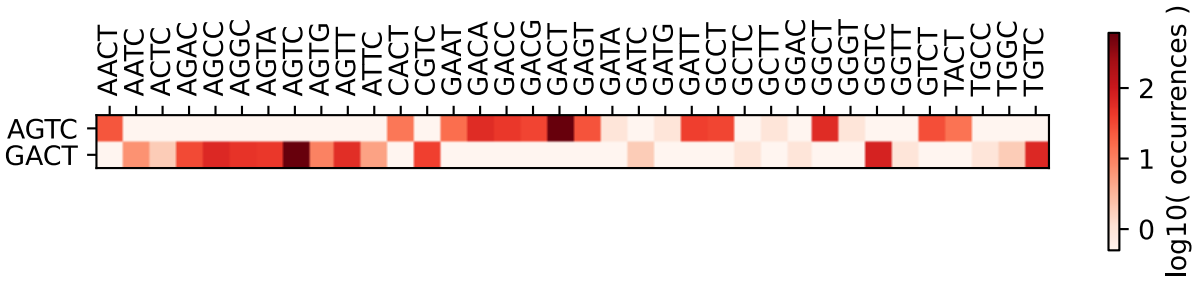
☑ AGTC GACT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

S[PLRHQ]
[IESAV*KQGPLRT]V
[*EKQ][S]
D[SFW*CLY]
[GESWAV*KQMPLRT]T
[G*R][L]

Misannealing overhangs:



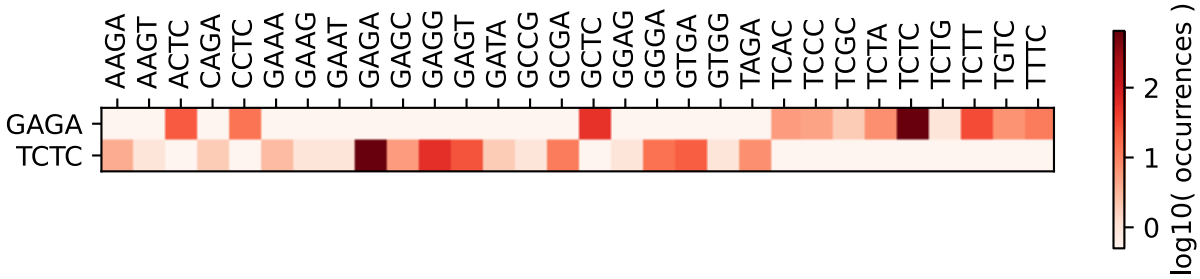
☑ GAGA TCTC

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

E[INSKMRT]
[GESWAV*KQMPLRT]R
[G*R][ED]
S[PLRHQ]
[DINSFAVRCGPLYHT]L
[FVIL][S]

Misannealing overhangs:

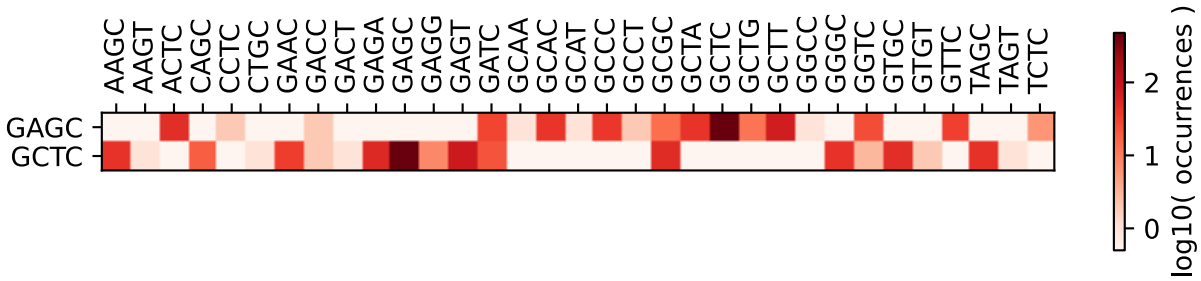


GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

E[PLRHQ]
[GESWAV*KQMPLRT]S
[G*R][A]
A[PLRHQ]
[GESWAV*KQMPLRT]L
[GRCS][S]

Misannealing overhangs:



☒ GATC GATC

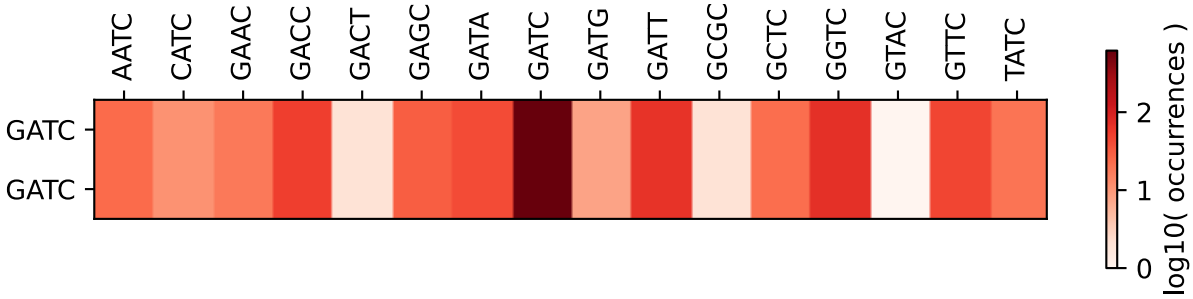
GC content: **50 %**.

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

Can form the following amino acids in 6 translation frames:

D[PLRHQ]
[GESWAV*KQMPLRT]I
[G*R][S]
D[PLRHQ]
[GESWAV*KQMPLRT]I
[G*R][S]

Misannealing overhangs:



☑ CATC GATG

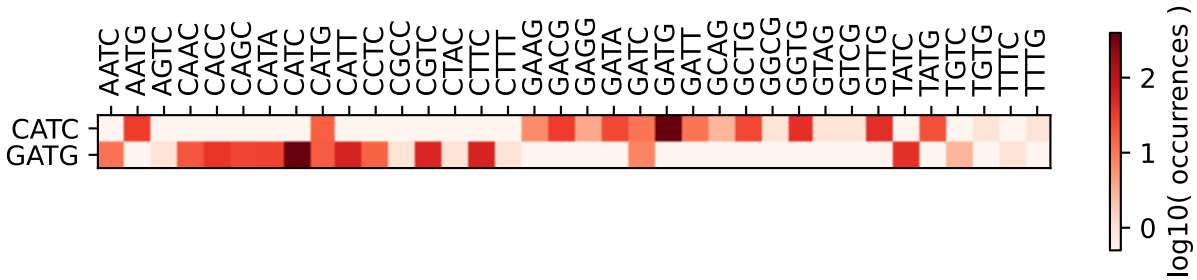
GC content: **50 %**.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

H[PLRHQ]
[DINSFAVRCGPLYHT]I
[APST][S]
D[EAVGD]
[GESWAV*KQMPLRT]M
[G*R][W*C]

Misannealing overhangs:



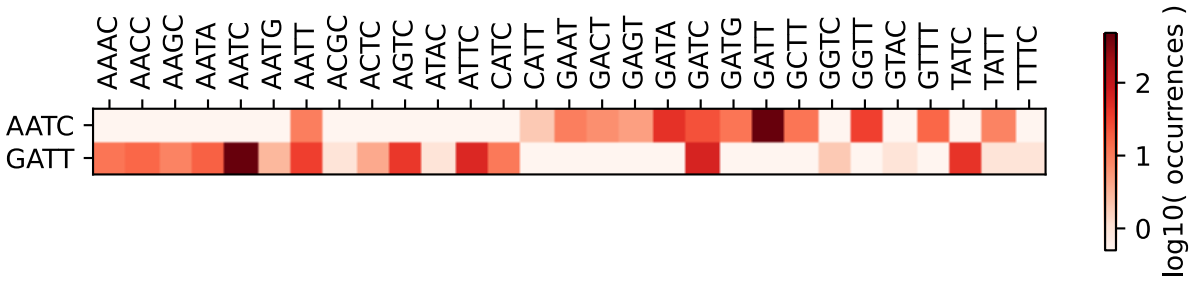
☑ AATC GATT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

N[PLRHQ]
[IESAV*KQGPLRT]I
[*EKQ][S]
D[SFW*CLY]
[GESWAV*KQMPLRT]I
[G*R][FL]

Misannealing overhangs:



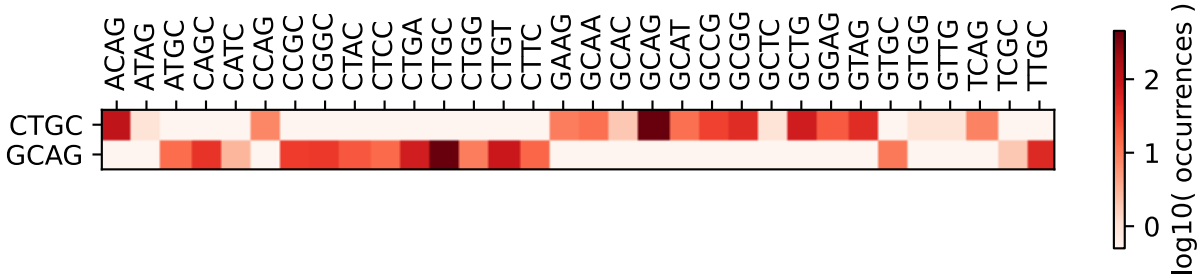
☑ CTGC GCAG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

L[PLRHQ]
[DINSFAVRCGPLYHT]C
[APST][A]
A[EAVGD]
[GESWAV*KQMPLRT]Q
[GRCS][RS]

Misannealing overhangs:



☑ ATGC GCAT

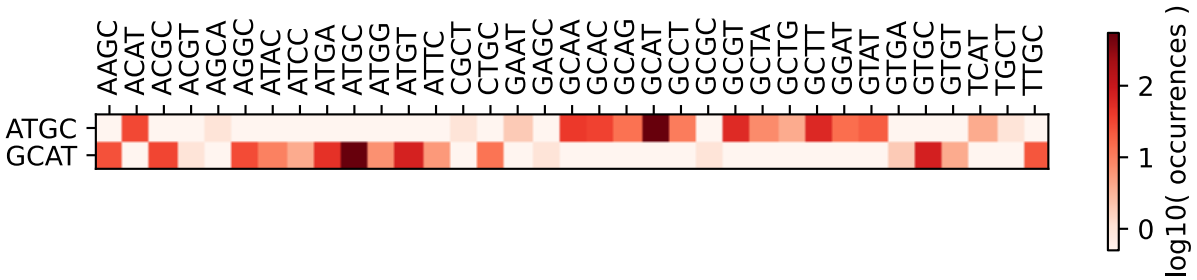
GC content: **50 %**.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

M[PLRHQ]
[IESAV*KQGPLRT]C
[NDYH][A]
A[SFW*CLY]
[GESWAV*KQMPLRT]H
[GRCS][MI]

Misannealing overhangs:



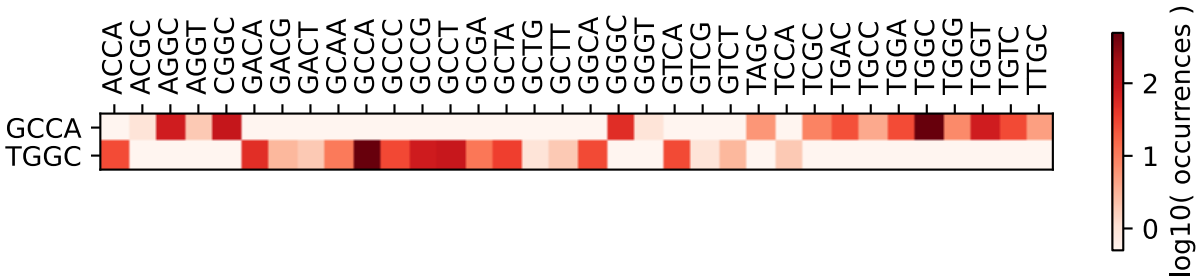
☑ GCCA TGGC

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

A[INSKMRT]
[GESWAV*KQMPLRT]P
[GRCS][HQ]
W[PLRHQ]
[DINSFAVRCGPLYHT]G
[MVL][A]

Misannealing overhangs:



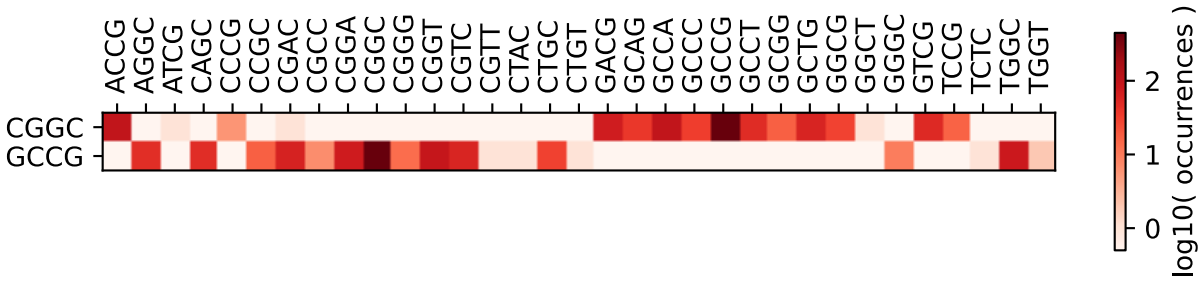
☑ CGGC GCCG

Extreme GC content: 100 %.

Can form the following amino acids in 6 translation frames:

R[PLRHQ]
[DINSFAVRCGPLYHT]G
[APST][A]
A[EAVGD]
[GESWAV*KQMPLRT]P
[GRCS][R]

Misannealing overhangs:



☒ GCGC GCGC

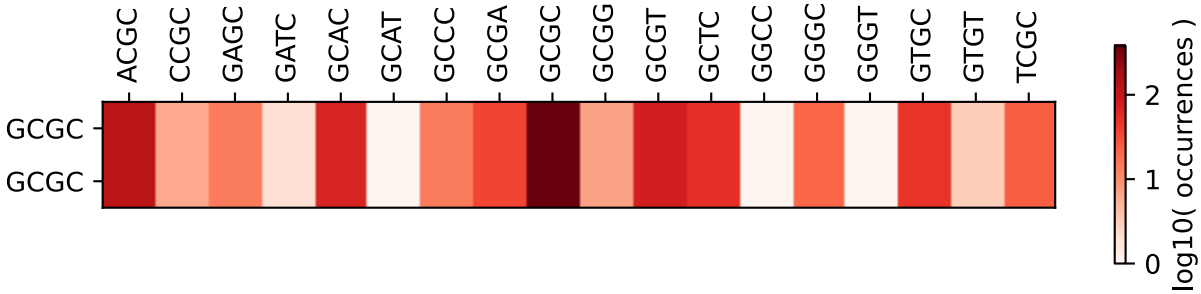
Extreme GC content: 100 %.

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

Can form the following amino acids in 6 translation frames:

A[PLRHQ]
[GESWAV*KQMPLRT]R
[GRCS][A]
A[PLRHQ]
[GESWAV*KQMPLRT]R
[GRCS][A]

Misannealing overhangs:



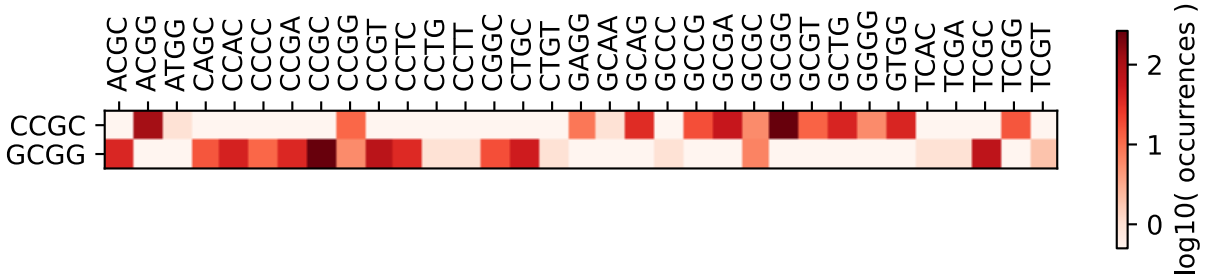
☑ CCGC GCGG

Extreme GC content: 100 %.

Can form the following amino acids in 6 translation frames:

P[PLRHQ]
[DINSFAVRCGPLYHT]R
[APST][A]
A[EAVGD]
[GESWAV*KQMPLRT]R
[GRCS][G]

Misannealing overhangs:



☑ GCTA TAGC

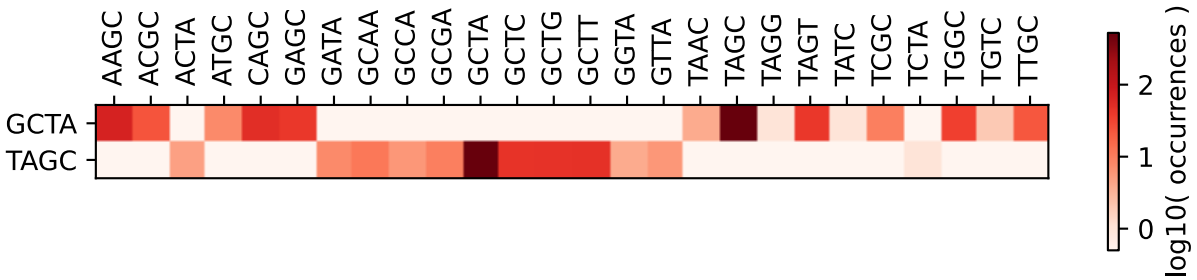
GC content: **50 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

A[INSKMRT]
[GESWAV*KQMPLRT]L
[GRCS][Y*]
*[PLRHQ]
[DINSFAVRCGPLYHT]S
[VIL][A]

Misannealing overhangs:

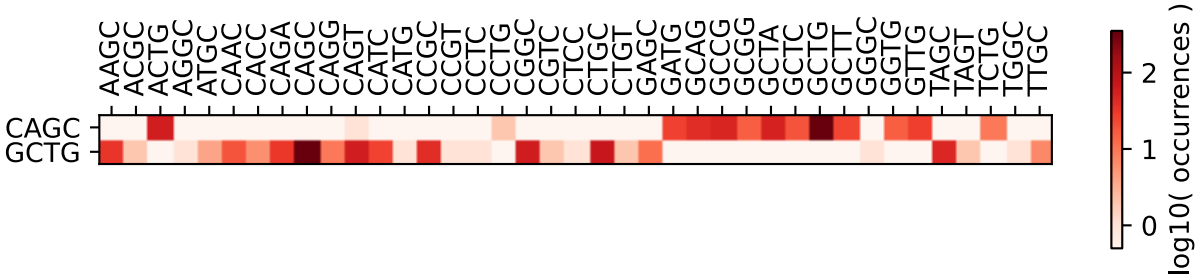


GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

Q[PLRHQ]
[DINSFAVRCGPLYHT]S
[APST][A]
A[EAVGD]
[GESWAV*KQMPLRT]L
[GRCS][W*C]

Misannealing overhangs:



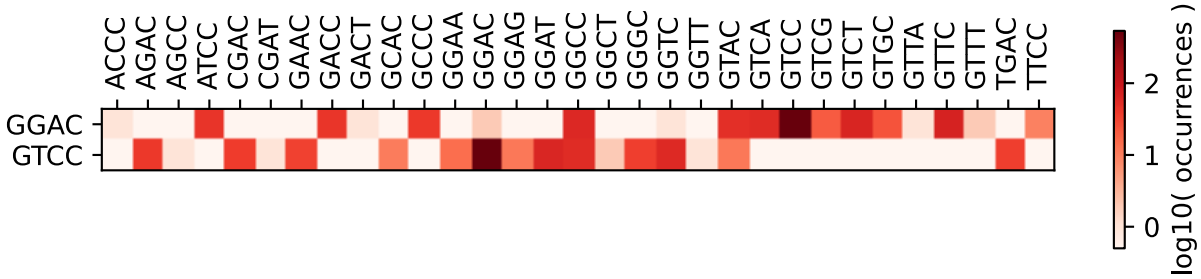
☑ GGAC GTCC

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

G[PLRHQ]
[GESWAV*KQMPLRT]D
[WGR][T]
V[PLRHQ]
[GESWAV*KQMPLRT]S
[GRCS][P]

Misannealing overhangs:

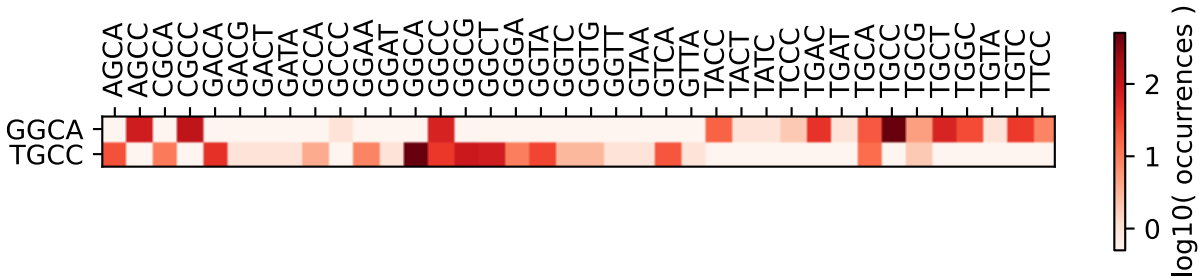


GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

G[INSKMRT]
[GESWAV*KQMPLRT]A
[WGR][HQ]
C[PLRHQ]
[DINSFAVRCGPLYHT]A
[MVL][P]

Misannealing overhangs:



☒ GGCC GGCC

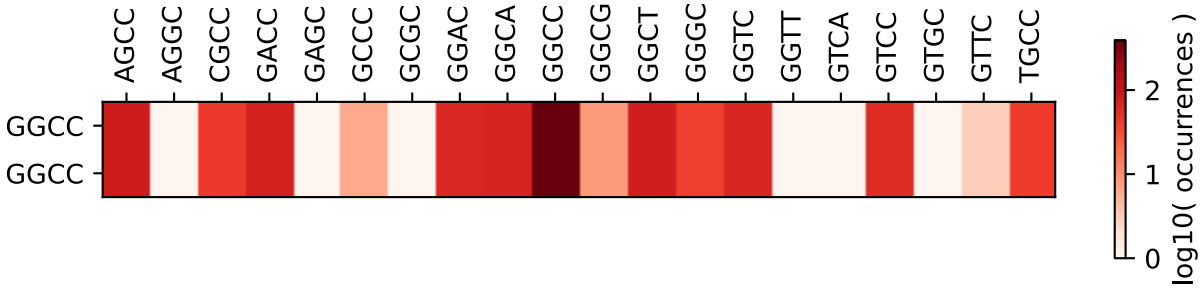
Extreme GC content: 100 %.

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

Can form the following amino acids in 6 translation frames:

G[PLRHQ]
[GESWAV*KQMPLRT]A
[WGR][P]
G[PLRHQ]
[GESWAV*KQMPLRT]A
[WGR][P]

Misannealing overhangs:



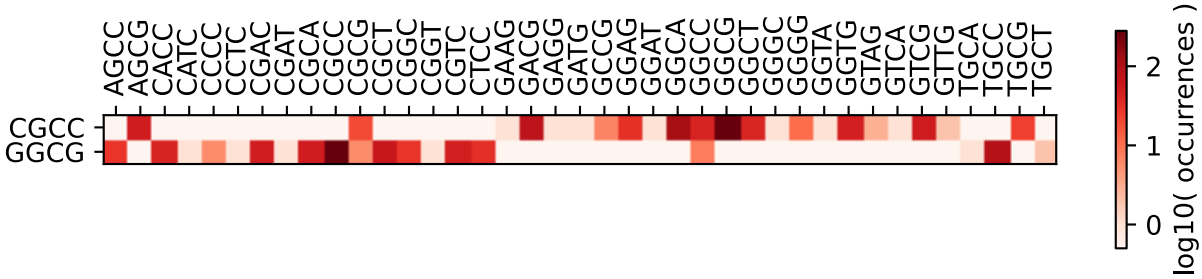
CGCC GGCG

Extreme GC content: 100 %.

Can form the following amino acids in 6 translation frames:

R[PLRHQ]
[DINSFAVRCGPLYHT]A
[APST][P]
G[EAVGD]
[GESWAV*KQMPLRT]A
[WGR][R]

Misannealing overhangs:



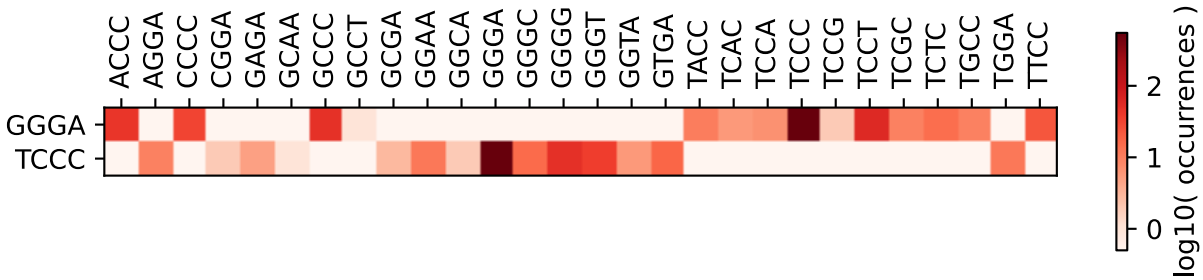
GC content: **75 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

G[INSKMRT]
[GESWAV*KQMPLRT]G
[WGR][ED]
S[PLRHQ]
[DINSFAVRCGPLYHT]P
[FVIL][P]

Misannealing overhangs:



GCCC GGGC

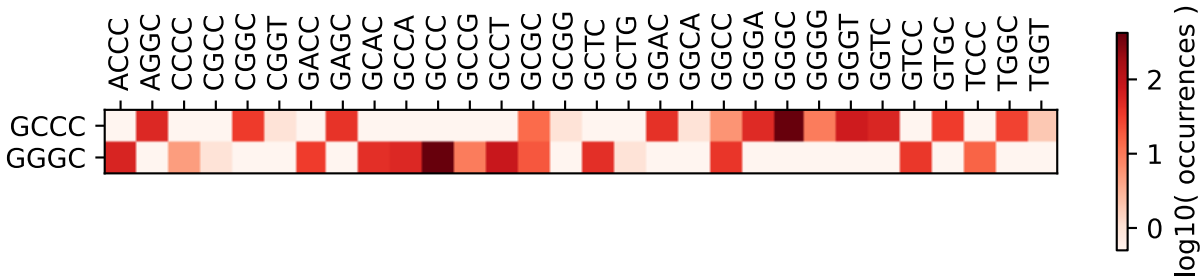
Extreme GC content: 100 %.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

A[PLRHQ]
[GESWAV*KQMPLRT]P
[GRCS][P]
G[PLRHQ]
[GESWAV*KQMPLRT]G
[WGR][A]

Misannealing overhangs:



☑ CCCC GGGG

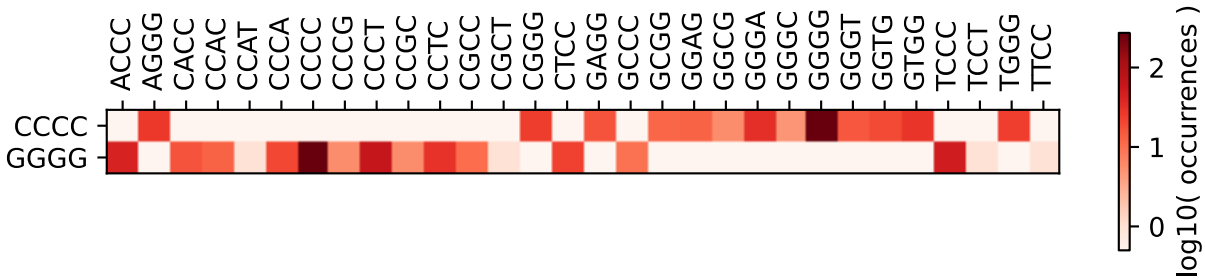
Extreme GC content: 100 %.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

P[PLRHQ]
[DINSFAVRCGPLYHT]P
[APST][P]
G[EAVGD]
[GESWAV*KQMPLRT]G
[WGR][G]

Misannealing overhangs:



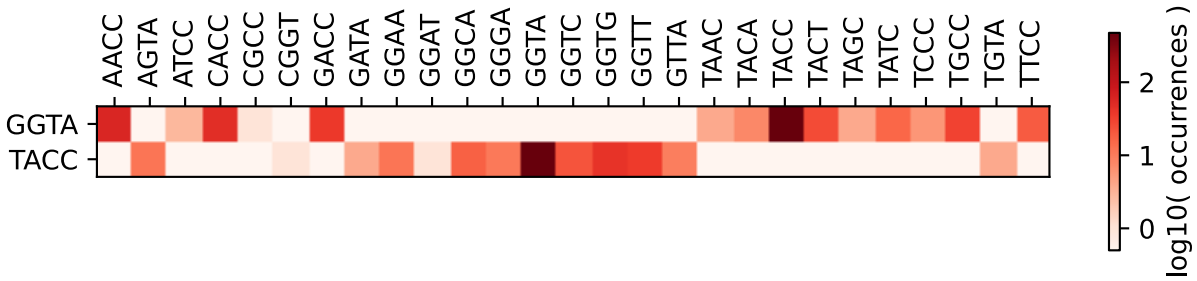
☑ GGTA TACC

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

G[INSKMRT]
[GESWAV*KQMPLRT]V
[WGR][Y*]
Y[PLRHQ]
[DINSFAVRCGPLYHT]T
[VIL][P]

Misannealing overhangs:



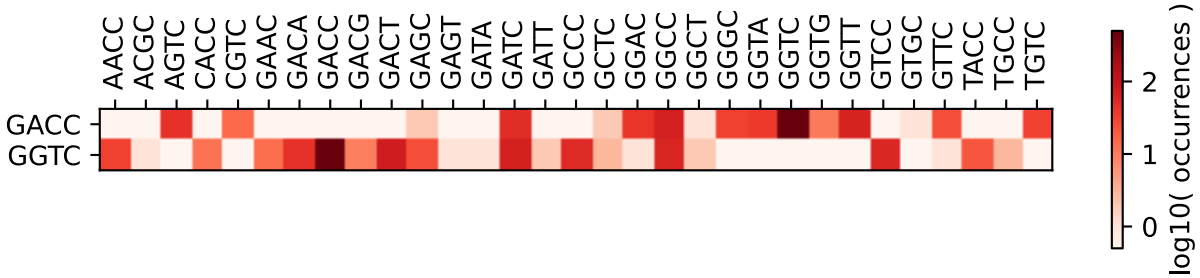
☑ GACC GGTC

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

D[PLRHQ]
[GESWAV*KQMPLRT]T
[G*R][P]
G[PLRHQ]
[GESWAV*KQMPLRT]V
[WGR][S]

Misannealing overhangs:



☒ GTAC GTAC

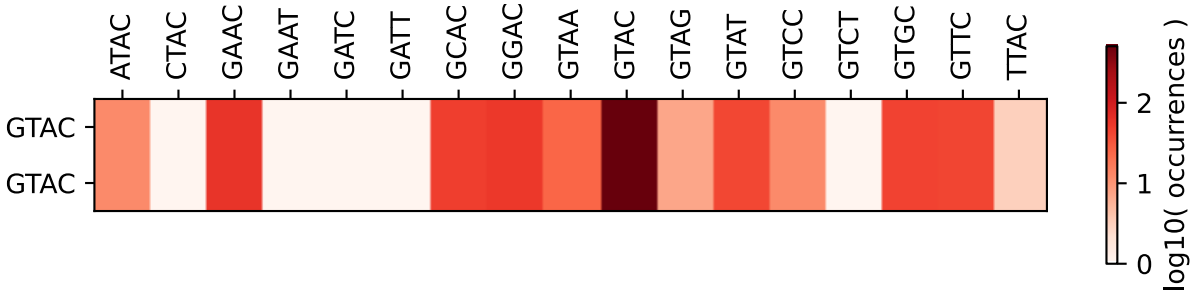
GC content: **50 %**.

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

Can form the following amino acids in 6 translation frames:

V[PLRHQ]
[GESWAV*KQMPLRT]Y
[GRCS][T]
V[PLRHQ]
[GESWAV*KQMPLRT]Y
[GRCS][T]

Misannealing overhangs:



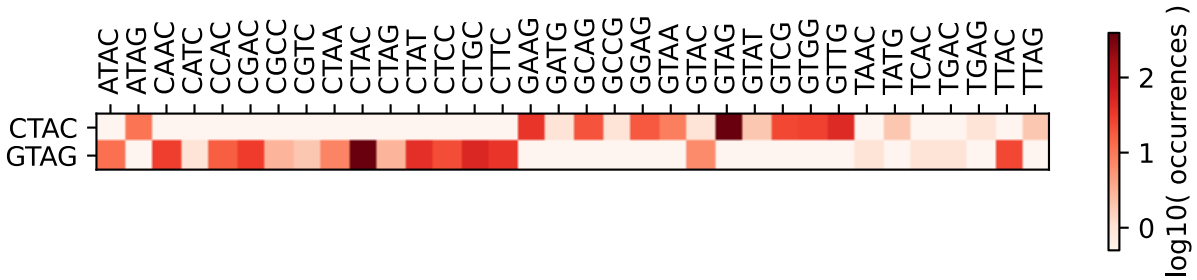
GC content: **50 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

L[PLRHQ]
[DINSFAVRCGPLYHT]Y
[APST][T]
V[EAVGD]
[GESWAV*KQMPLRT]*
[GRCS][RS]

Misannealing overhangs:

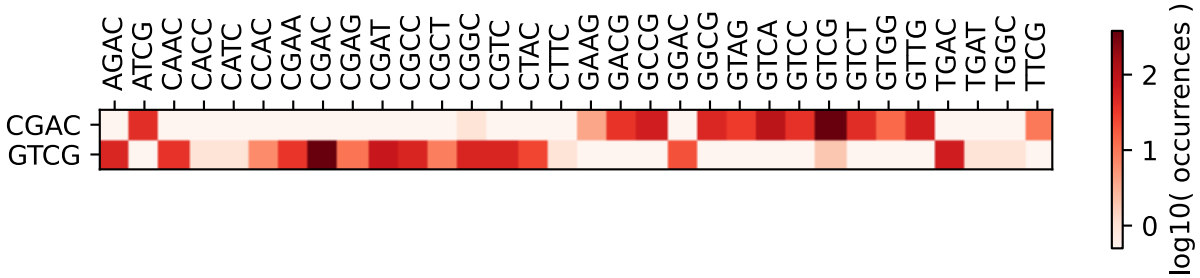


GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

R[PLRHQ]
[DINSFAVRCGPLYHT]D
[APST][T]
V[EAVGD]
[GESWAV*KQMPLRT]S
[GRCS][R]

Misannealing overhangs:



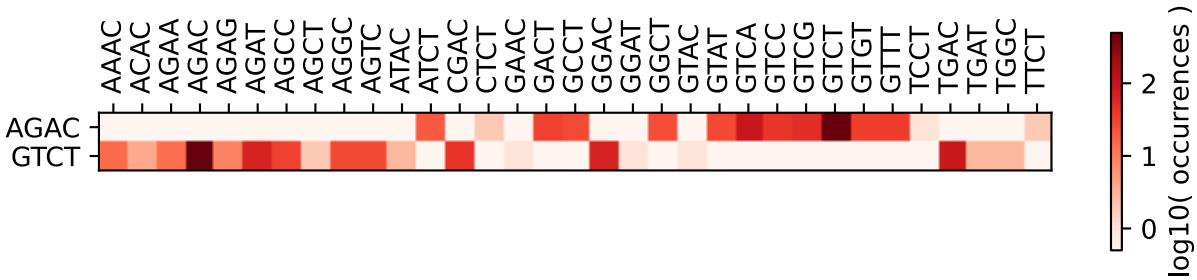
☑ AGAC GTCT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

R[PLRHQ]
[IESAV*KQGPLRT]D
[*EKQ][T]
V[SFW*CLY]
[GESWAV*KQMPLRT]S
[GRCS][L]

Misannealing overhangs:



☑ GTGA TCAC

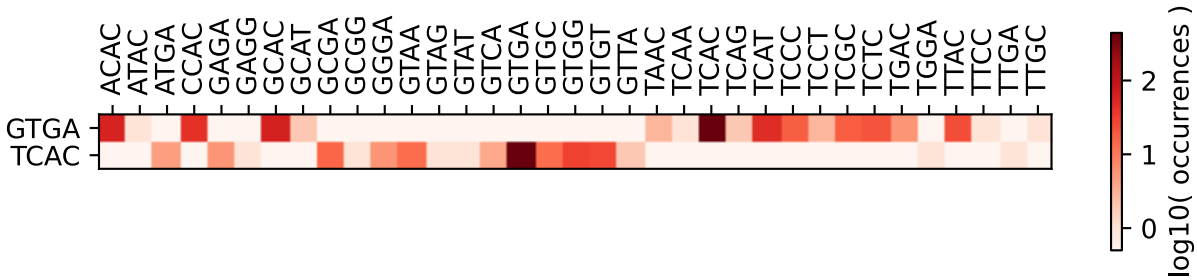
GC content: **50 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

V[INSKMRT]
[GESWAV*KQMPLRT]*
[GRCS][ED]
S[PLRHQ]
[DINSFAVRCGPLYHT]H
[FVIL][T]

Misannealing overhangs:



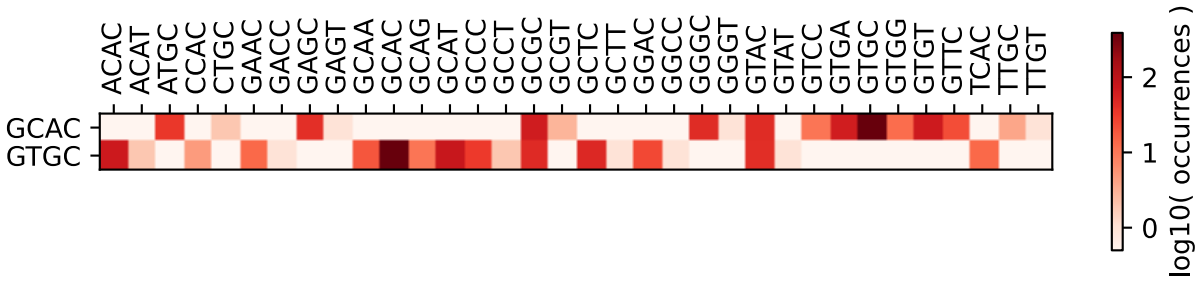
☑ GCAC GTGC

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

A[PLRHQ]
[GESWAV*KQMPLRT]H
[GRCS][T]
V[PLRHQ]
[GESWAV*KQMPLRT]C
[GRCS][A]

Misannealing overhangs:



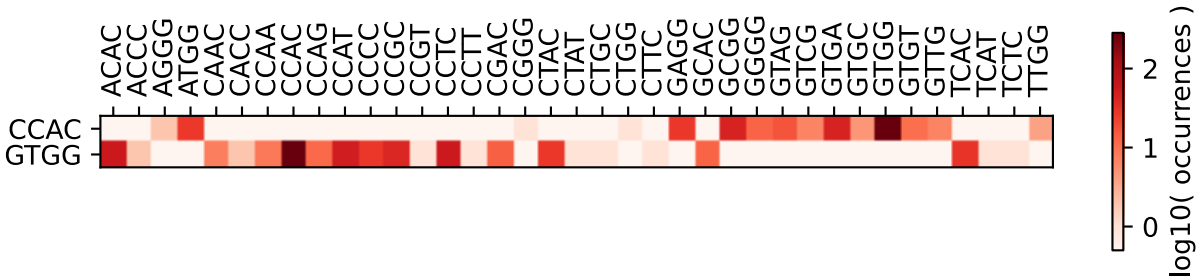
☑ CCAC GTGG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

P[PLRHQ]
[DINSFAVRCGPLYHT]H
[APST][T]
V[EAVGD]
[GESWAV*KQMPLRT]W
[GRCS][G]

Misannealing overhangs:



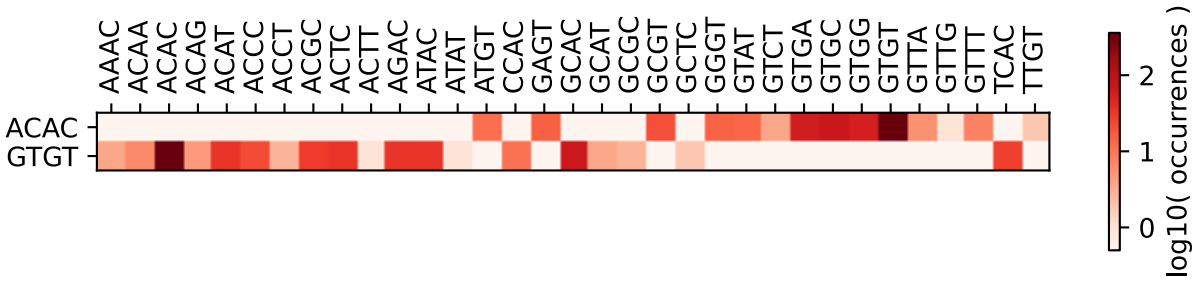
☑ ACAC GTGT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

T[PLRHQ]
[IESAV*KQGPLRT]H
[NDYH][T]
V[SFW*CLY]
[GESWAV*KQMPLRT]C
[GRCS][V]

Misannealing overhangs:



☑ AAAC GTTT

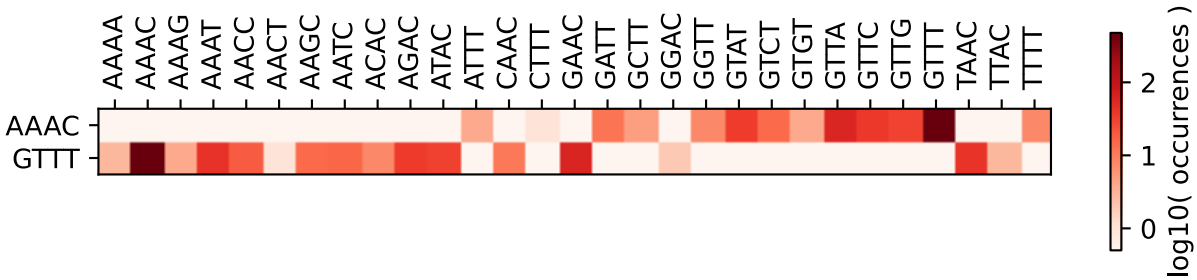
GC content: **25 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

K[PLRHQ]
[IESAV*KQGPLRT]N
[*EKQ][T]
V[SFW*CLY]
[GESWAV*KQMPLRT]F
[GRCS][FL]

Misannealing overhangs:



☑ GTTA TAAC

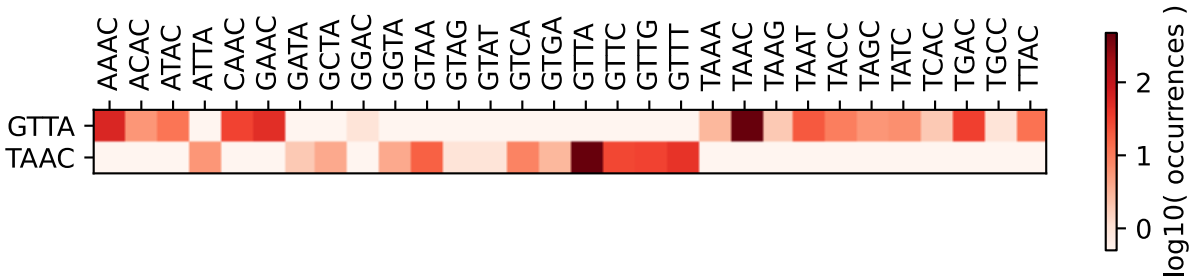
GC content: **25 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

V[INSKMRT]
[GESWAV*KQMPLRT]L
[GRCS][Y*]
*[PLRHQ]
[DINSFAVRCGPLYHT]N
[VIL][T]

Misannealing overhangs:



☑ ATTA TAAT

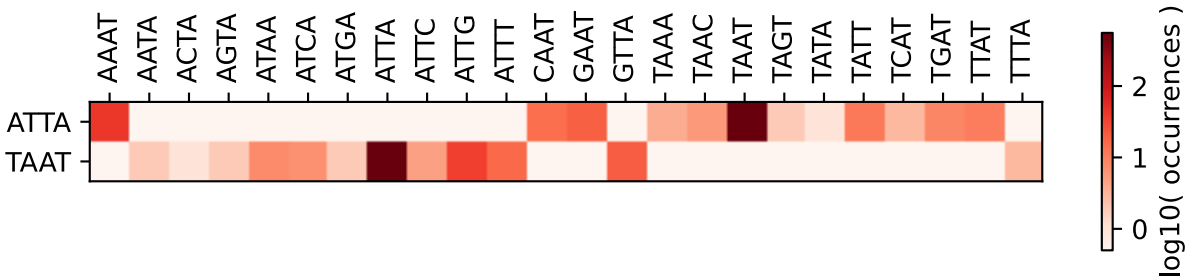
Extreme GC content: 0 %.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

I[INSKMRT]
[IESAV*KQGPLRT]L
[NDYH][Y*]
*[SFW*CLY]
[DINSFAVRCGPLYHT]N
[VIL][MI]

Misannealing overhangs:



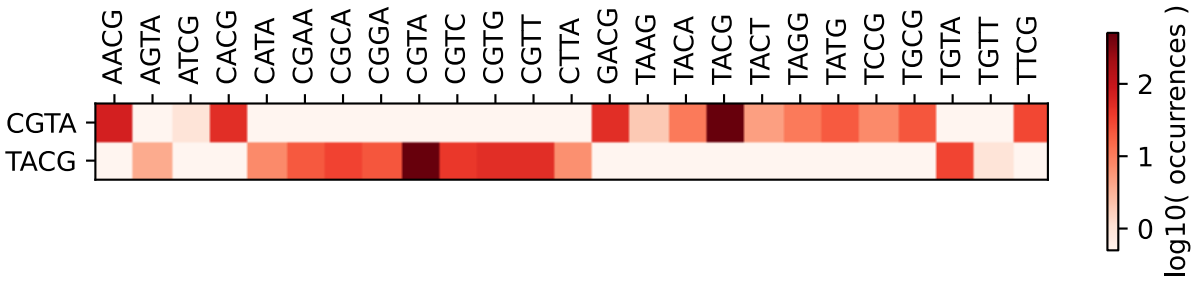
☑ CGTA TACG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

R[INSKMRT]
[DINSFAVRCGPLYHT]V
[APST][Y*]
Y[EAVGD]
[DINSFAVRCGPLYHT]T
[VIL][R]

Misannealing overhangs:



☑ TAGA TCTA

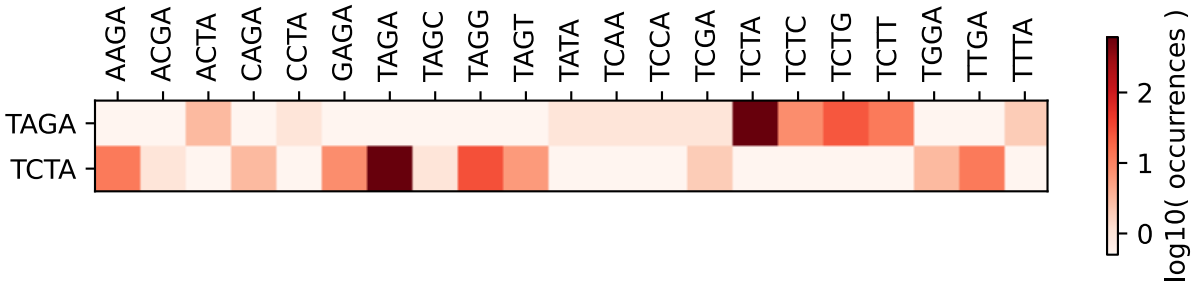
GC content: **25 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

*[INSKMRT]
[DINSFAVRCGPLYHT]R
[VIL][ED]
S[INSKMRT]
[DINSFAVRCGPLYHT]L
[FVIL][Y*]

Misannealing overhangs:



☒ TATA TATA

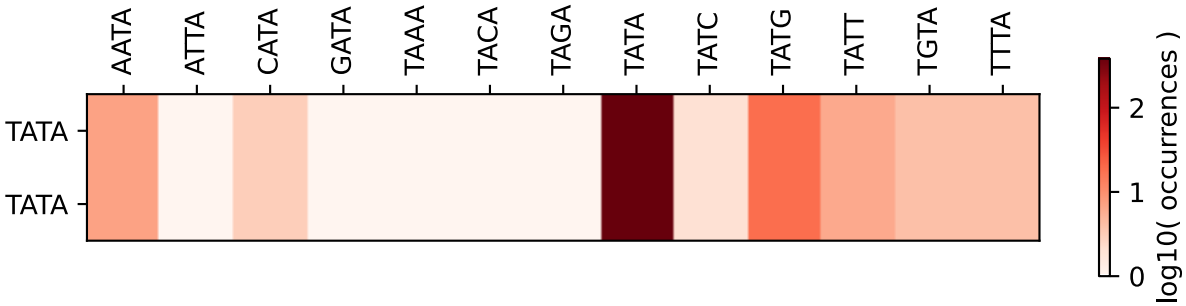
Extreme GC content: 0 %.

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

Can form the following amino acids in 6 translation frames:

Y[INSKMRT]
[DINSFAVRCGPLYHT]I
[VIL][Y*]
Y[INSKMRT]
[DINSFAVRCGPLYHT]I
[VIL][Y*]

Misannealing overhangs:

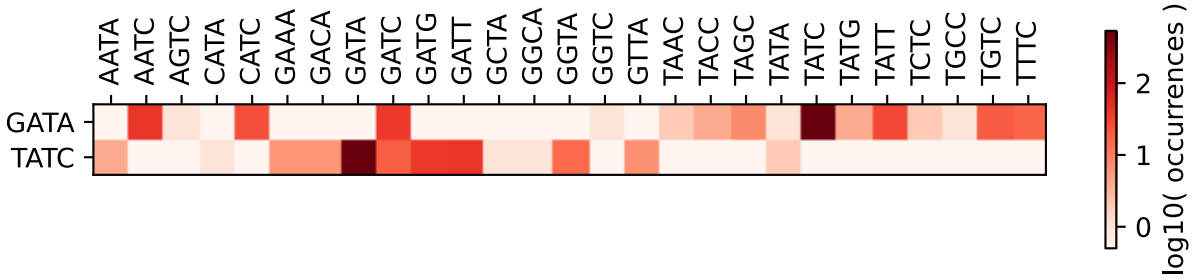


GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

D[INSKMRT]
[GESWAV*KQMPLRT]I
[G*R][Y*]
Y[PLRHQ]
[DINSFAVRCGPLYHT]I
[VIL][S]

Misannealing overhangs:



☑ CATA TATG

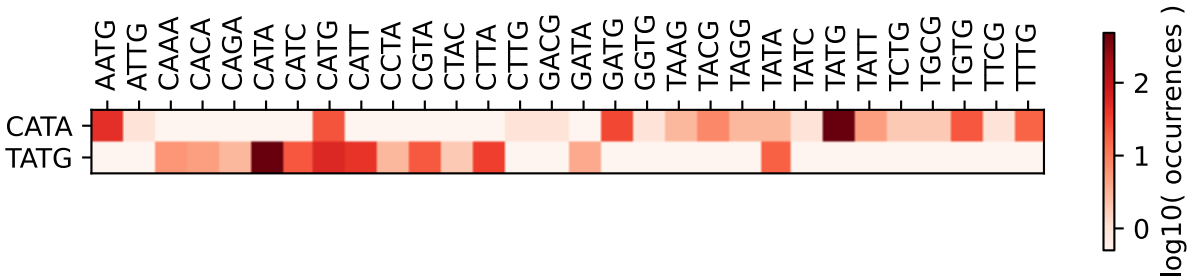
GC content: **25 %**.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

H[INSKMRT]
[DINSFAVRCGPLYHT]I
[APST][Y*]
Y[EAVGD]
[DINSFAVRCGPLYHT]M
[VIL][W*C]

Misannealing overhangs:



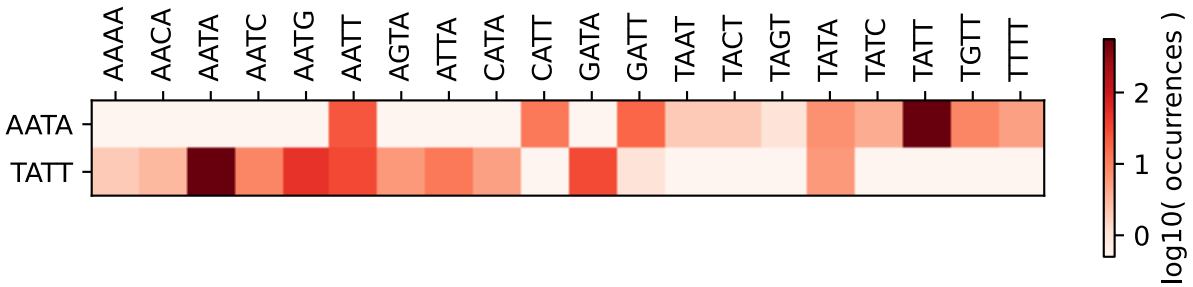
☑ AATA TATT

Extreme GC content: 0 %.

Can form the following amino acids in 6 translation frames:

N[INSKMRT]
[IESAV*KQGPLRT]I
[*EKQ][Y*]
Y[SFW*CLY]
[DINSFAVRCGPLYHT]I
[VIL][FL]

Misannealing overhangs:



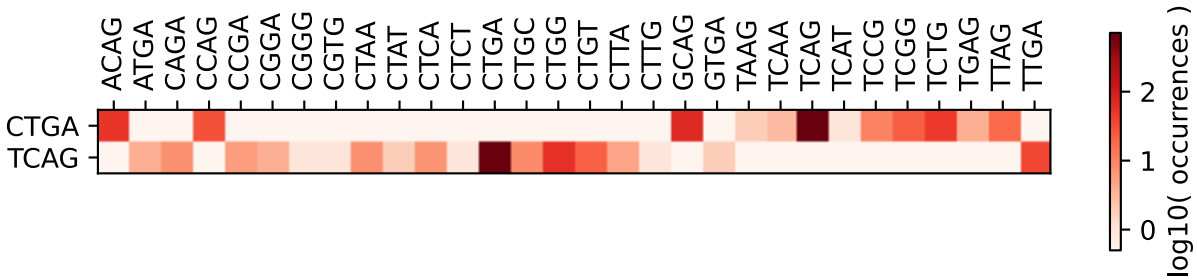
GC content: **50 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

L[INSKMRT]
[DINSFAVRCGPLYHT]*
[APST][ED]
S[EAVGD]
[DINSFAVRCGPLYHT]Q
[FVIL][RS]

Misannealing overhangs:



☑ ATGA TCAT

GC content: **25 %**.

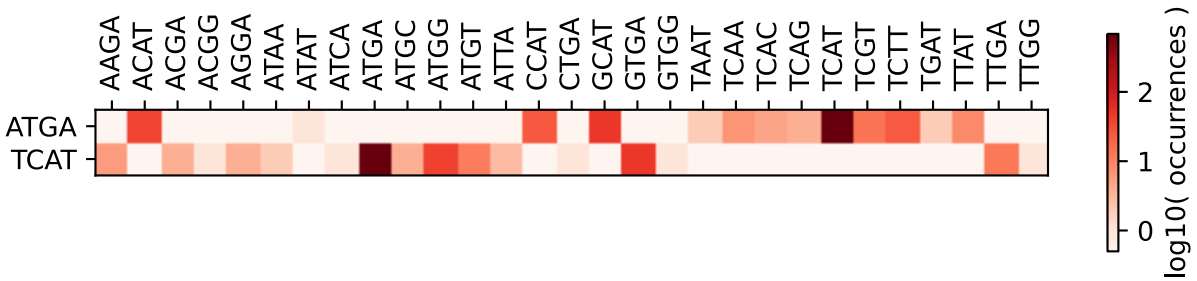
The overhang contains the start codon ATG.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

M[INSKMRT]
[IESAV*KQGPLRT]*
[NDYH][ED]
S[SFW*CLY]
[DINSFAVRCGPLYHT]H
[FVIL][MI]

Misannealing overhangs:

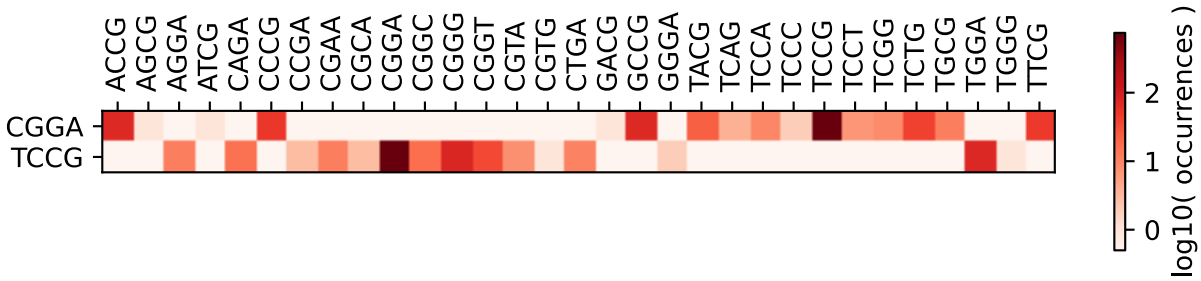


GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

R[INSKMRT]
[DINSFAVRCGPLYHT]G
[APST][ED]
S[EAVGD]
[DINSFAVRCGPLYHT]P
[FVIL][R]

Misannealing overhangs:



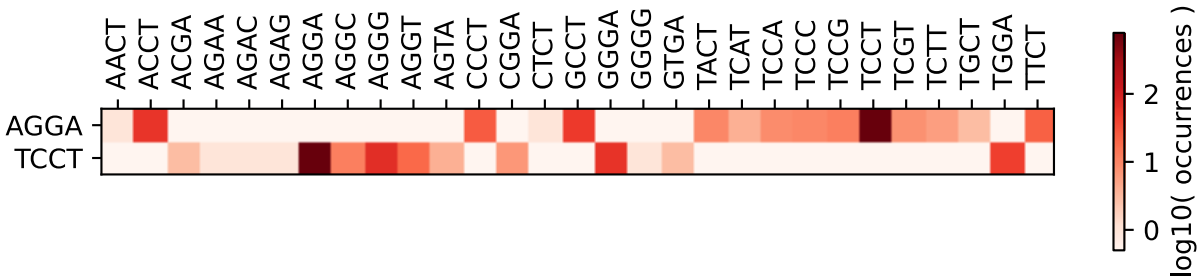
☑ AGGA TCCT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

R[INSKMRT]
[IESAV*KQGPLRT]G
[*EKQ][ED]
S[SFW*CLY]
[DINSFAVRCGPLYHT]P
[FVIL][L]

Misannealing overhangs:



☒ TCGA TCGA

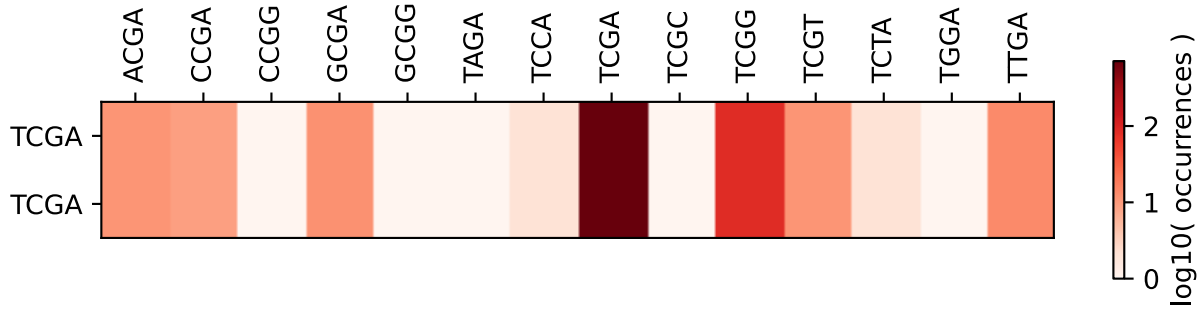
GC content: **50 %**.

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

Can form the following amino acids in 6 translation frames:

S[INSKMRT]
[DINSFAVRCGPLYHT]R
[FVIL][ED]
S[INSKMRT]
[DINSFAVRCGPLYHT]R
[FVIL][ED]

Misannealing overhangs:



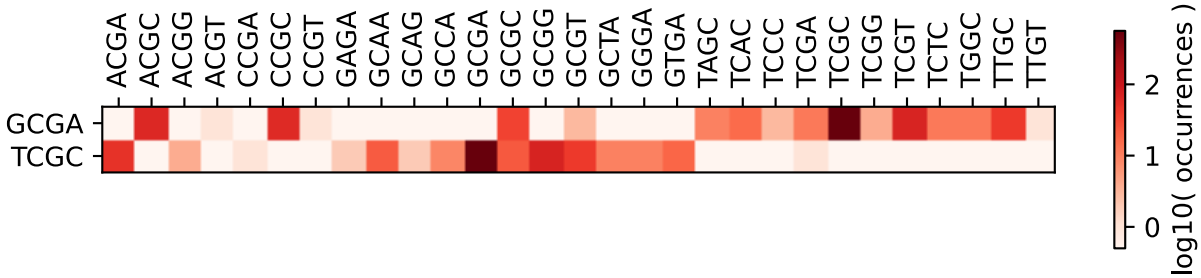
☑ GCGA TCGC

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

A[INSKMRT]
[GESWAV*KQMPLRT]R
[GRCS][ED]
S[PLRHQ]
[DINSFAVRCGPLYHT]R
[FVIL][A]

Misannealing overhangs:

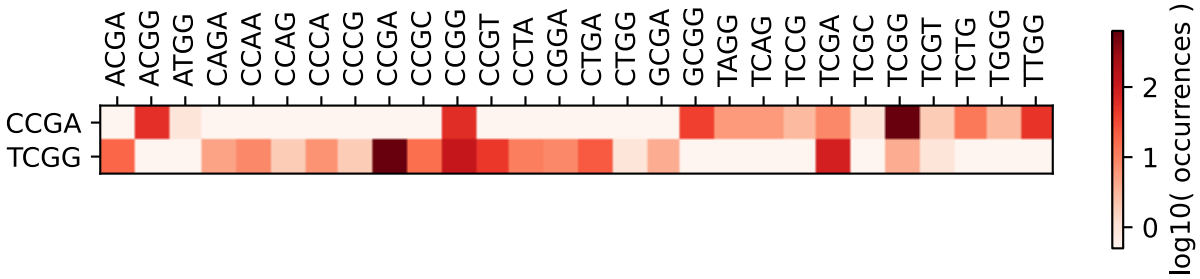


GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

P[INSKMRT]
[DINSFAVRCGPLYHT]R
[APST][ED]
S[EAVGD]
[DINSFAVRCGPLYHT]R
[FVIL][G]

Misannealing overhangs:



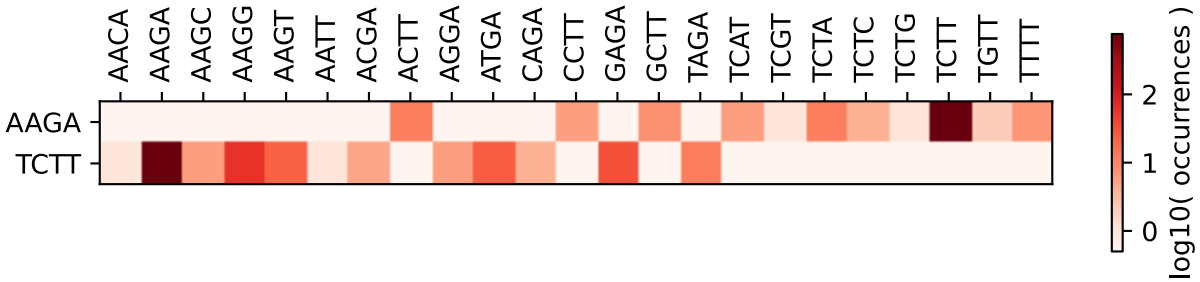
☑ AAGA TCTT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

K[INSKMRT]
[IESAV*KQGPLRT]R
[*EKQ][ED]
S[SFW*CLY]
[DINSFAVRCGPLYHT]L
[FVIL][FL]

Misannealing overhangs:



☑ GTCA TGAC

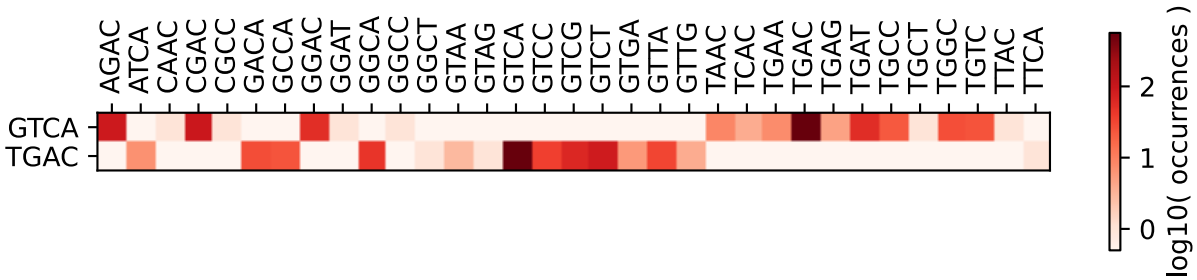
GC content: **50 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

V[INSKMRT]
[GESWAV*KQMPLRT]S
[GRCS][HQ]
*[PLRHQ]
[DINSFAVRCGPLYHT]D
[MVL][T]

Misannealing overhangs:



☑ CTCA TGAG

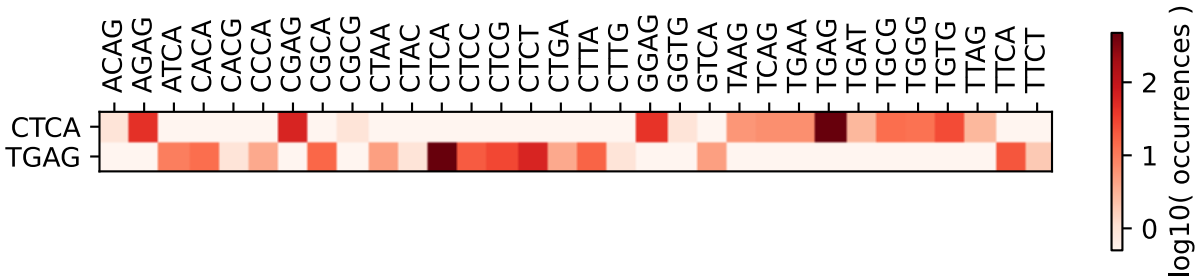
GC content: **50 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

L[INSKMRT]
[DINSFAVRCGPLYHT]S
[APST][HQ]
*[EAVGD]
[DINSFAVRCGPLYHT]E
[MVL][RS]

Misannealing overhangs:



☒ TGCA TGCA

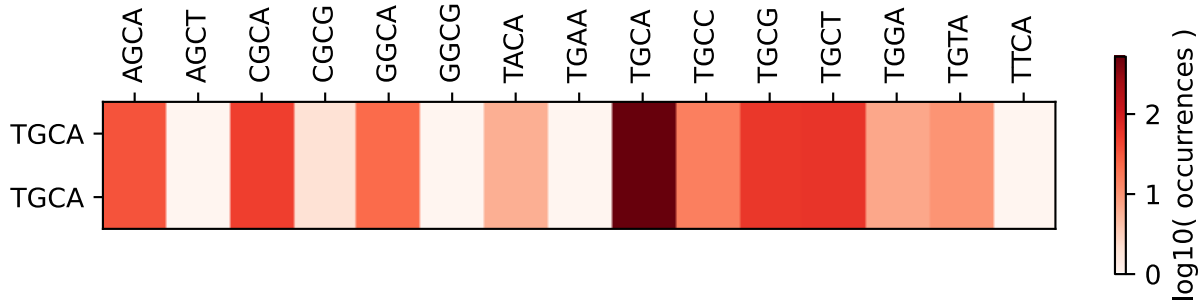
GC content: **50 %**.

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

Can form the following amino acids in 6 translation frames:

C[INSKMRT]
[DINSFAVRCGPLYHT]A
[MVL][HQ]
C[INSKMRT]
[DINSFAVRCGPLYHT]A
[MVL][HQ]

Misannealing overhangs:



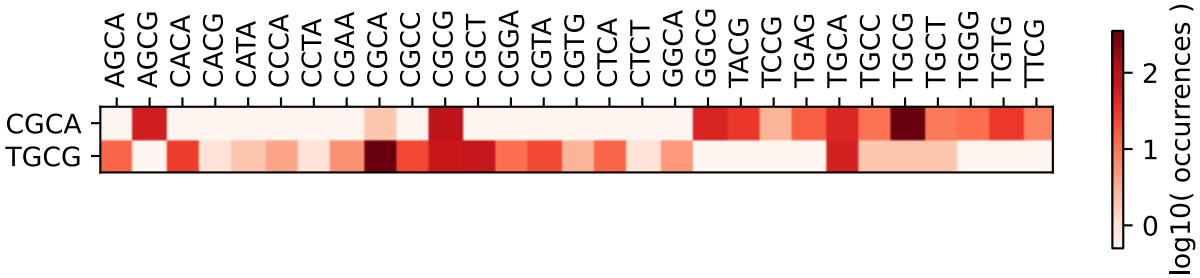
☑ CGCA TGCG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

R[INSKMRT]
[DINSFAVRCGPLYHT]A
[APST][HQ]
C[EAVGD]
[DINSFAVRCGPLYHT]A
[MVL][R]

Misannealing overhangs:



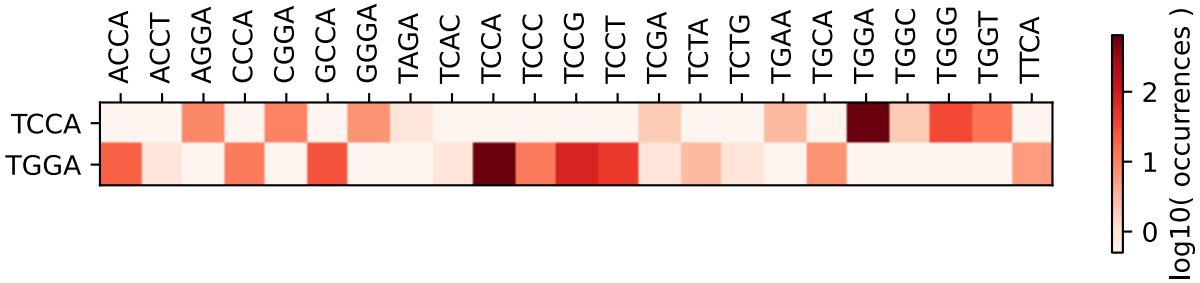
☑ TCCA TGGA

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

S[INSKMRT]
[DINSFAVRCGPLYHT]P
[FVIL][HQ]
W[INSKMRT]
[DINSFAVRCGPLYHT]G
[MVL][ED]

Misannealing overhangs:



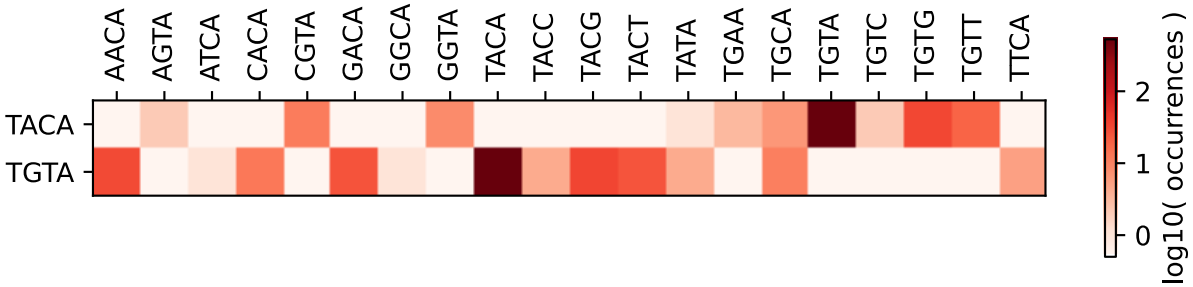
☑ TACA TGTA

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

Y[INSKMRT]
[DINSFAVRCGPLYHT]T
[VIL][HQ]
C[INSKMRT]
[DINSFAVRCGPLYHT]V
[MVL][Y*]

Misannealing overhangs:

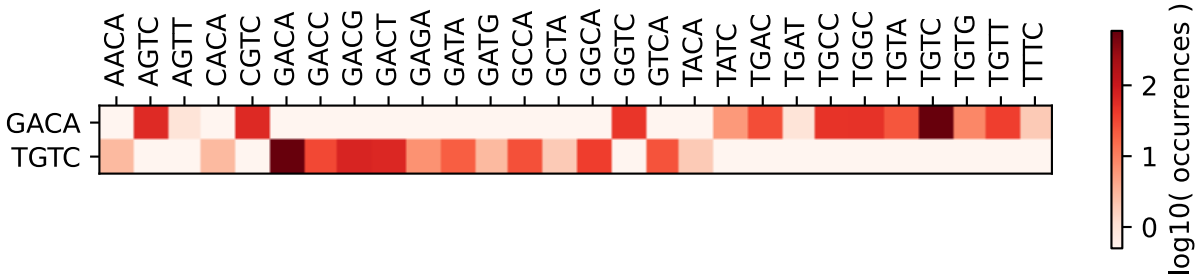


GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

D[INSKMRT]
[GESWAV*KQMPLRT]T
[G*R][HQ]
C[PLRHQ]
[DINSFAVRCGPLYHT]V
[MVL][S]

Misannealing overhangs:



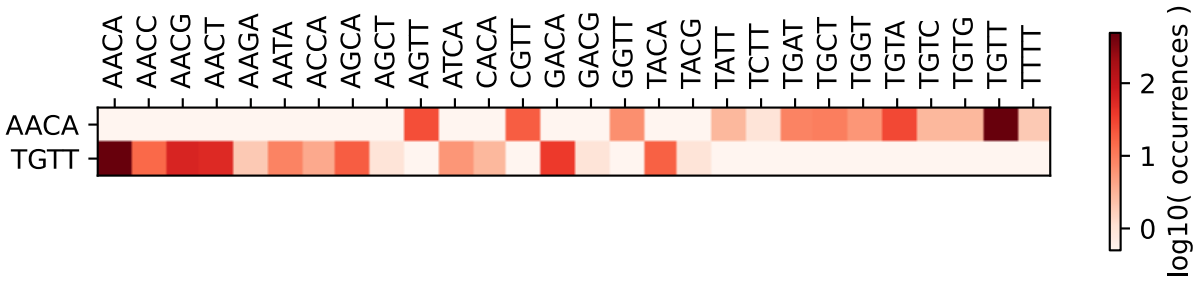
☑ AACA TGTT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

N[INSKMRT]
[IESAV*KQGPLRT]T
[*EKQ][HQ]
C[SFW*CLY]
[DINSFAVRCGPLYHT]V
[MVL][FL]

Misannealing overhangs:



☒ TTAA TTAA

Extreme GC content: 0 %.

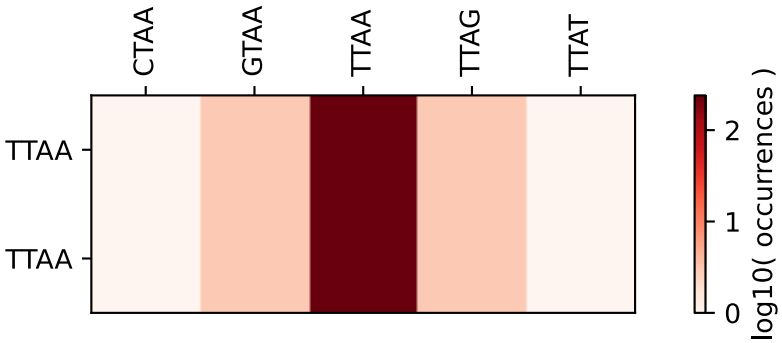
The overhang is palindromic, cannot be used for DNA assembly.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

L[INSKMRT]
[DINSFAVRCGPLYHT]*
[FVIL][NK]
L[INSKMRT]
[DINSFAVRCGPLYHT]*
[FVIL][NK]

Misannealing overhangs:



☑ GTAA TTAC

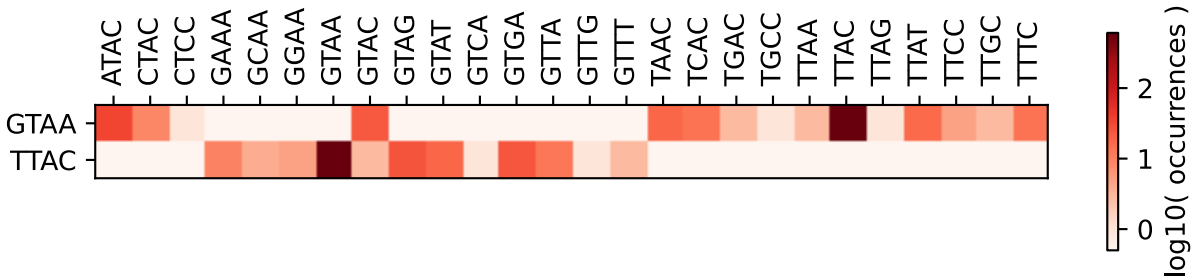
GC content: **25 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

V[INSKMRT]
[GESWAV*KQMPLRT]*
[GRCS][NK]
L[PLRHQ]
[DINSFAVRCGPLYHT]Y
[FVIL][T]

Misannealing overhangs:



☑ ATAA TTAT

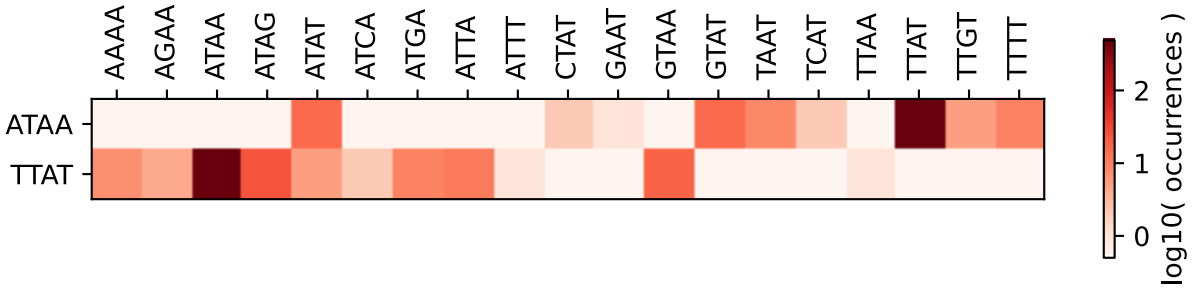
Extreme GC content: 0 %.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

I[INSKMRT]
[IESAV*KQGPLRT]*
[NDYH][NK]
L[SFW*CLY]
[DINSFAVRCGPLYHT]Y
[FVIL][MI]

Misannealing overhangs:



☑ TGAA TTCA

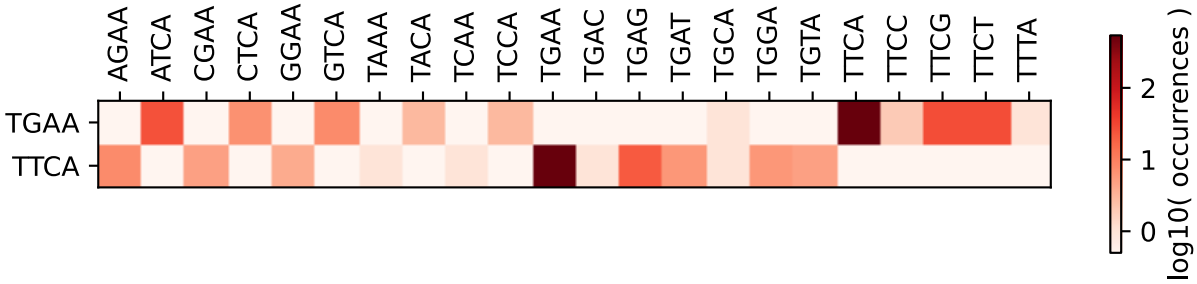
GC content: **25 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

*[INSKMRT]
[DINSFAVRCGPLYHT]E
[MVL][NK]
F[INSKMRT]
[DINSFAVRCGPLYHT]S
[FVIL][HQ]

Misannealing overhangs:



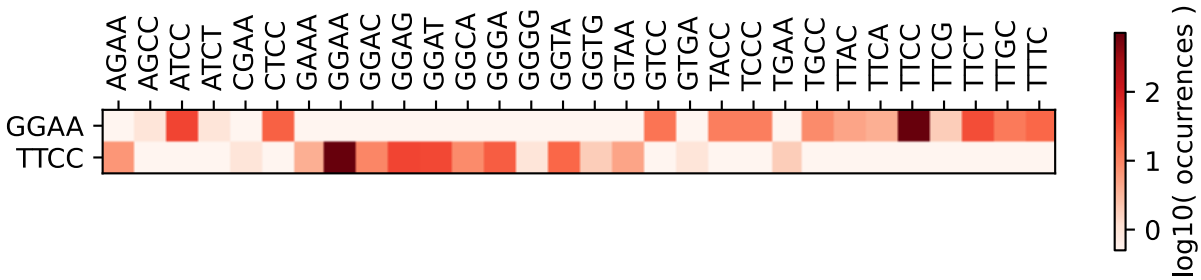
☑ GGAA TTCC

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

G[INSKMRT]
[GESWAV*KQMPLRT]E
[WGR][NK]
F[PLRHQ]
[DINSFAVRCGPLYHT]S
[FVIL][P]

Misannealing overhangs:



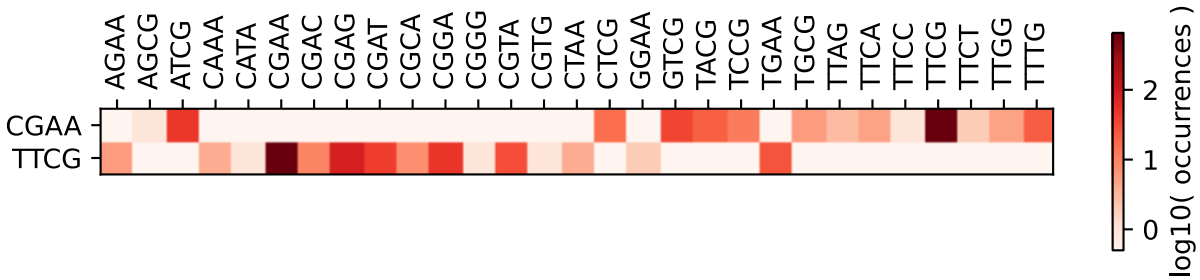
☑ CGAA TTCG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

R[INSKMRT]
[DINSFAVRCGPLYHT]E
[APST][NK]
F[EAVGD]
[DINSFAVRCGPLYHT]S
[FVIL][R]

Misannealing overhangs:



☑ TCAA TTGA

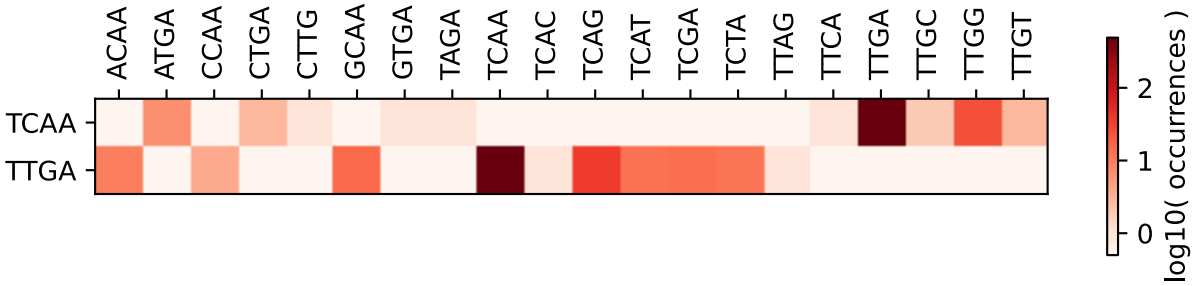
GC content: **25 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

S[INSKMRT]
[DINSFAVRCGPLYHT]Q
[FVIL][NK]
L[INSKMRT]
[DINSFAVRCGPLYHT]*
[FVIL][ED]

Misannealing overhangs:

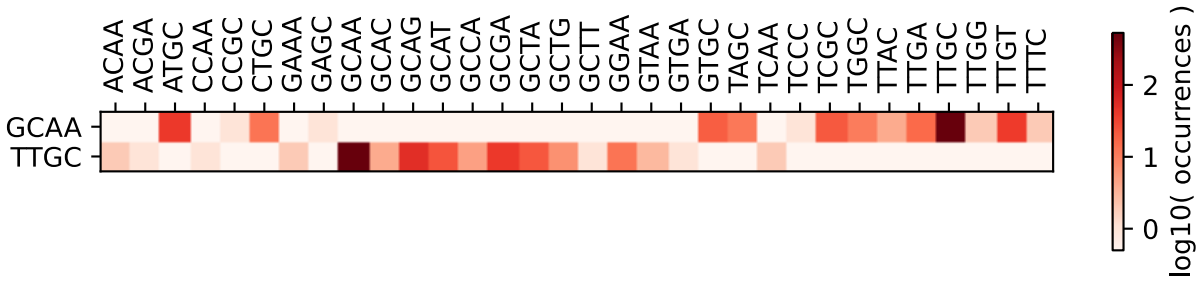


GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

A[INSKMRT]
[GESWAV*KQMPLRT]Q
[GRCS][NK]
L[PLRHQ]
[DINSFAVRCGPLYHT]C
[FVIL][A]

Misannealing overhangs:



☑ TAAA TTTA

Extreme GC content: 0 %.

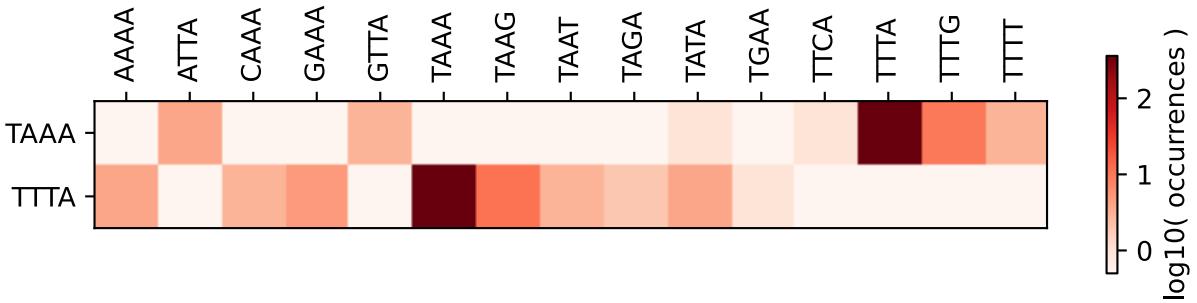
The overhang contains a stop codon (TAA, TAG or TGA).

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

*[INSKMRT]
[DINSFAVRCGPLYHT]K
[VIL][NK]
F[INSKMRT]
[DINSFAVRCGPLYHT]L
[FVIL][Y*]

Misannealing overhangs:



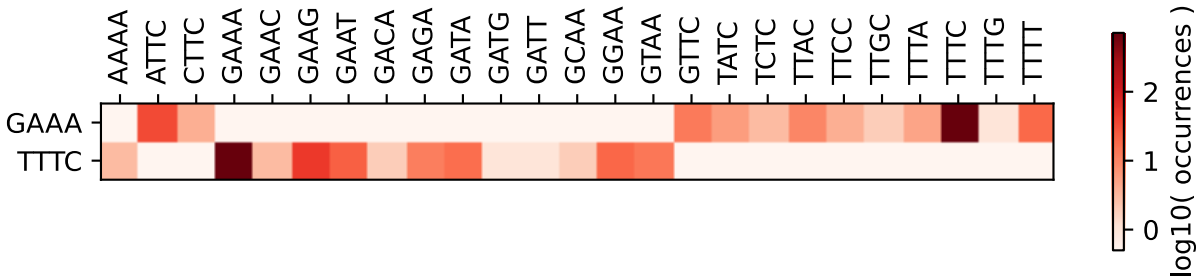
GC content: **25 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

E[INSKMRT]
[GESWAV*KQMPLRT]K
[G*R][NK]
F[PLRHQ]
[DINSFAVRCGPLYHT]F
[FVIL][S]

Misannealing overhangs:



☑ AAAA TTTT

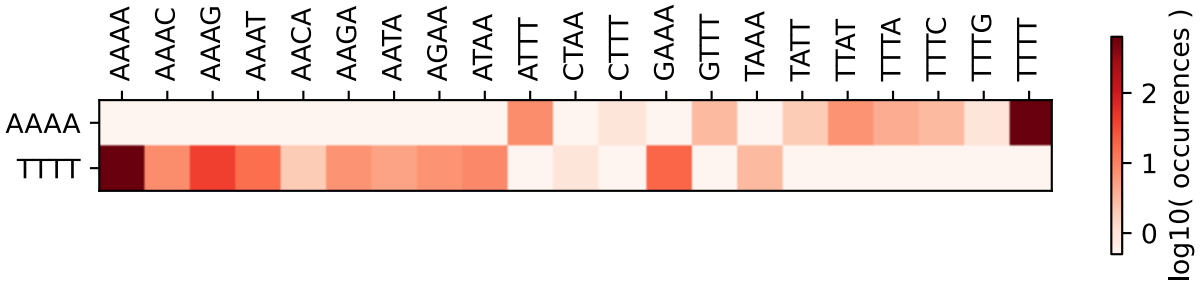
Extreme GC content: 0 %.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

K[INSKMRT]
[IESAV*KQGPLRT]K
[*EKQ][NK]
F[SFW*CLY]
[DINSFAVRCGPLYHT]F
[FVIL][FL]

Misannealing overhangs:



Appendix

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

Summary page(s)

The first page summarises the compendium.

Overhang pages

Each overhang is 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. These overhangs create "sticky" (non-blunt) DNA ends. Overhangs can be on either strand; 5' or 3' overhangs. During DNA assembly, these overhangs are created by type IIS restriction enzymes, and ligated with another DNA with a complementary overhang, by ligases. The type of the restriction enzyme and the ligase influences the misannealing rate, which is displayed in a summary plot. For more details, see the Tatapov package and Pryor et al. (PLoS ONE (2020) 15(9): e0238592).

After the assembly, these overhangs remain in the sequence as fusion sites ("scars"). If this is in a coding sequence (CDS), then addition of nucleotides can ensure that the two joining parts remain in the same translation frame. By carefully choosing which nucleotides we add, we can select suitable amino acids, or start/stop codons. For each overhang, a list of codons is also displayed that shows translation options. The GeneDom package can be used for automating the addition of these nucleotides, the overhangs and the enzyme sites.

Overhang sets

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