

# GGA Method

with pClone Red

by

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# Eco RI

GAATTC

CTTAAG

palindrome

type II

# Eco RI

**G**AATTC

CTTAAG

palindrome

type II

# Eco RI



type II

# Eco RI

G

AATTC

CTTAA

G

type II

# Bsa I

GAGACC

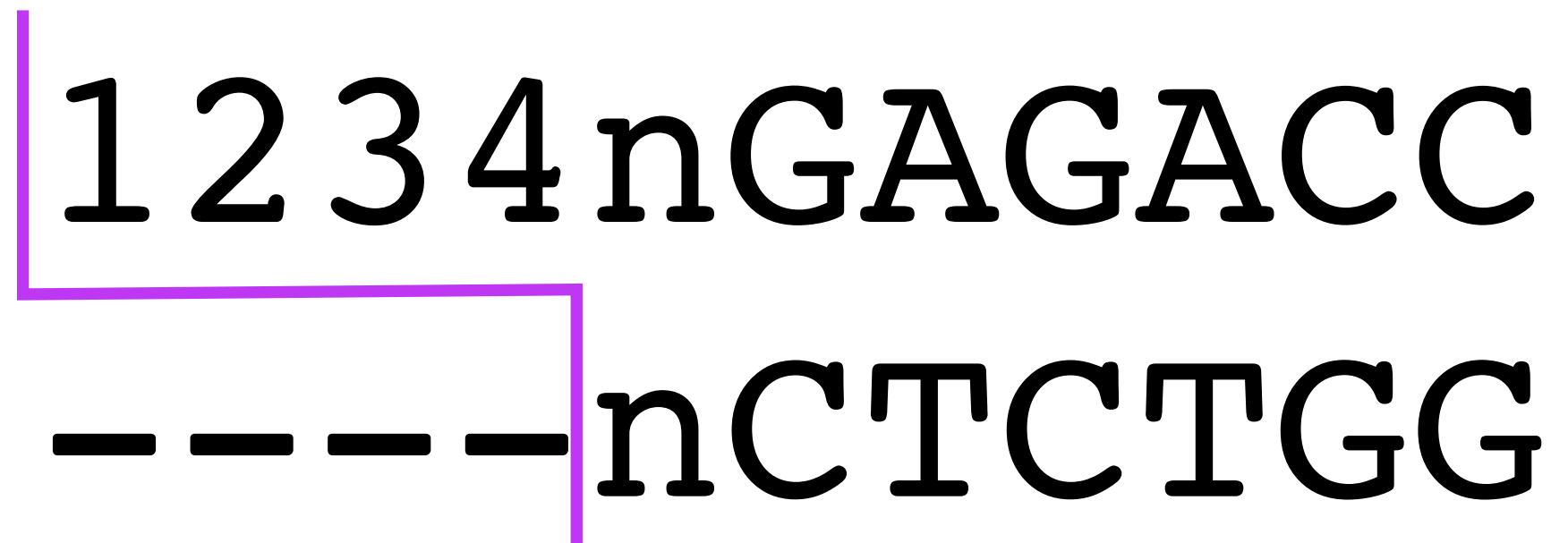
CTCTGG

not a  
palindrome

type II

# Bsa I

1 2 3 4 n G A G A C C  
- - - - n C T C T G G



type II

# Bsa I

1 2 3 4 n G A G A C C

n C T C T G G

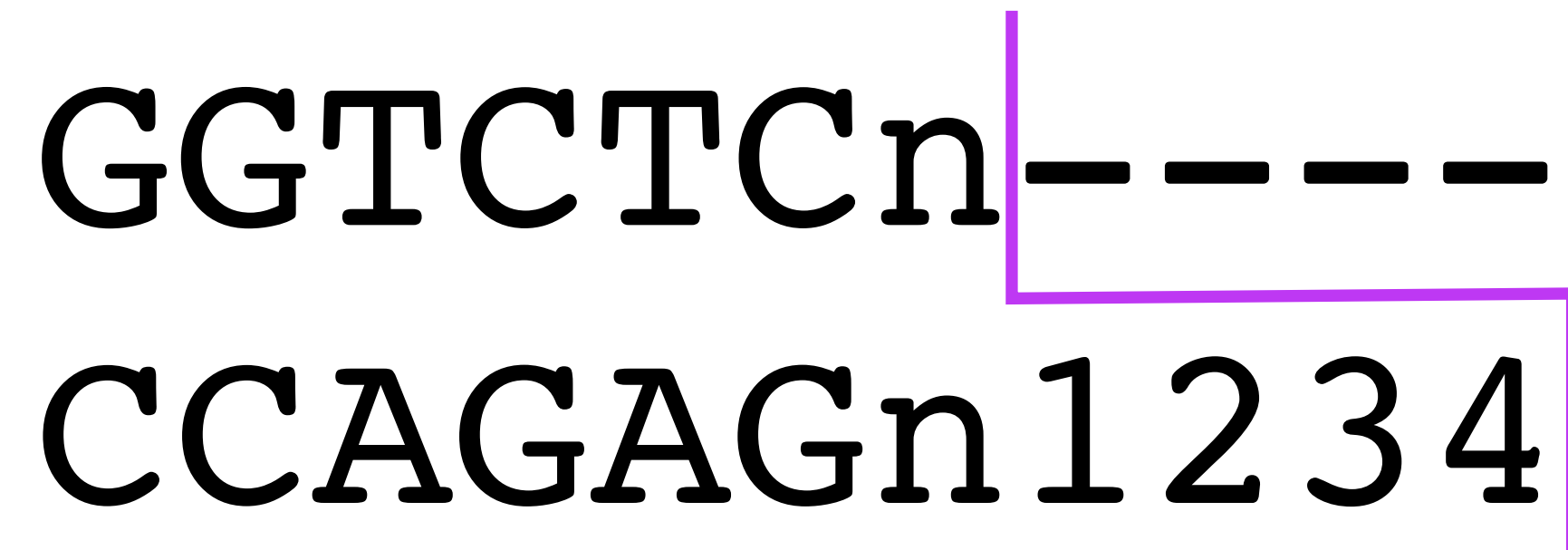
— — — —

type II



# Bsa I

GGTCTCn-----  
CCAGAGn1234

A diagram showing the recognition sequence for the Bsa I restriction enzyme. The top strand is 5'-GGTCTCn-----3' and the bottom strand is 3'-CCAGAGn1234-5'. A purple line highlights the recognition sequence: a vertical line at the end of the top strand, a horizontal line connecting to the start of the bottom strand, and a vertical line at the end of the bottom strand. The 'n' in both strands indicates a variable length of nucleotides between the two recognition sites.

type II

# Bsa I

GGTCTCn

CCAGAGn 1 2 3 4

----

type II

# Bsa I

cuts  
left

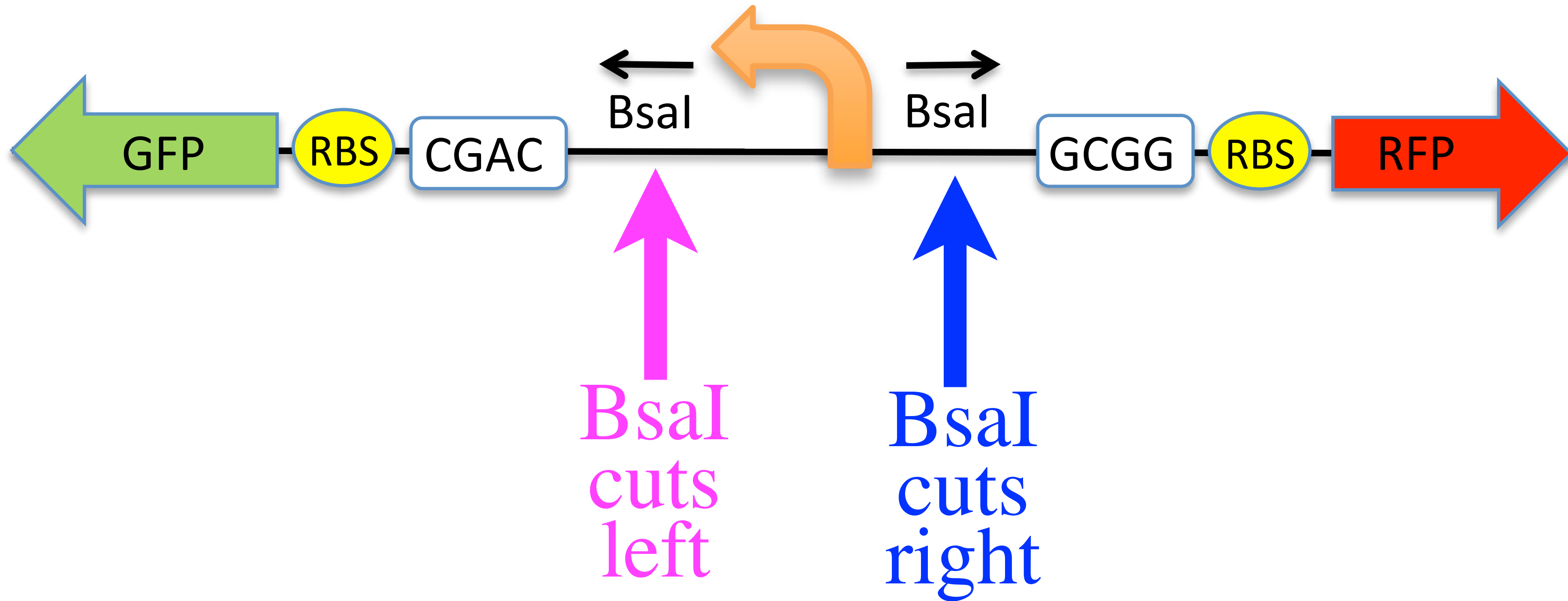
1 2 3 4 n GAGACC  
-----n CTCTGG

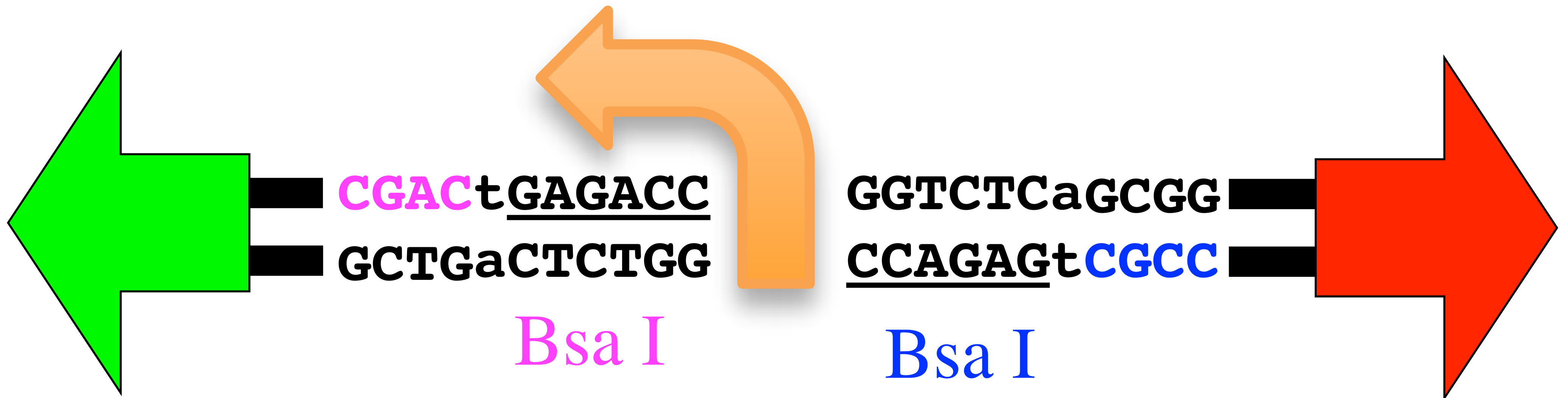
GGTCTCn-----

CCAGAGn 1 2 3 4

cuts  
right

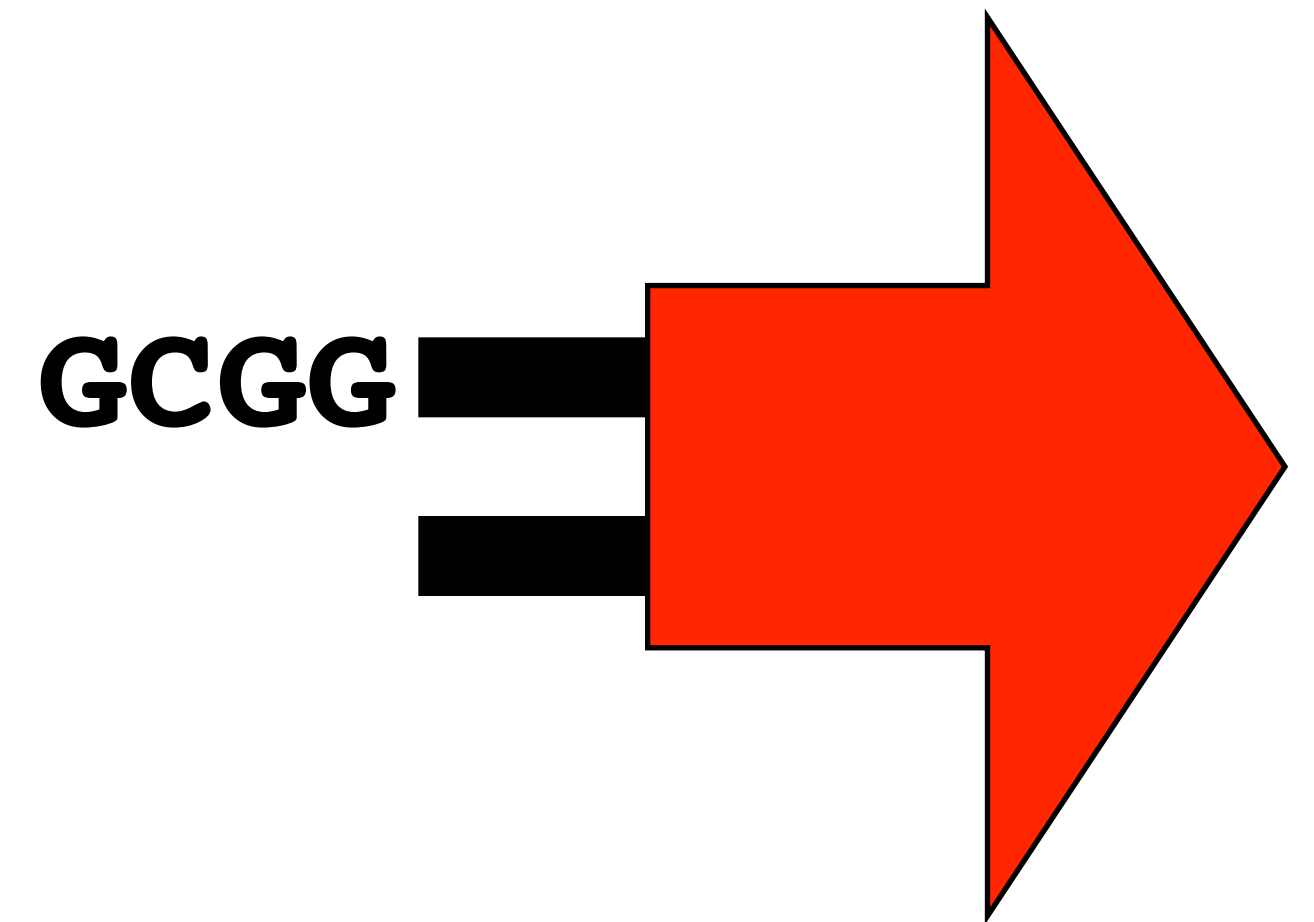
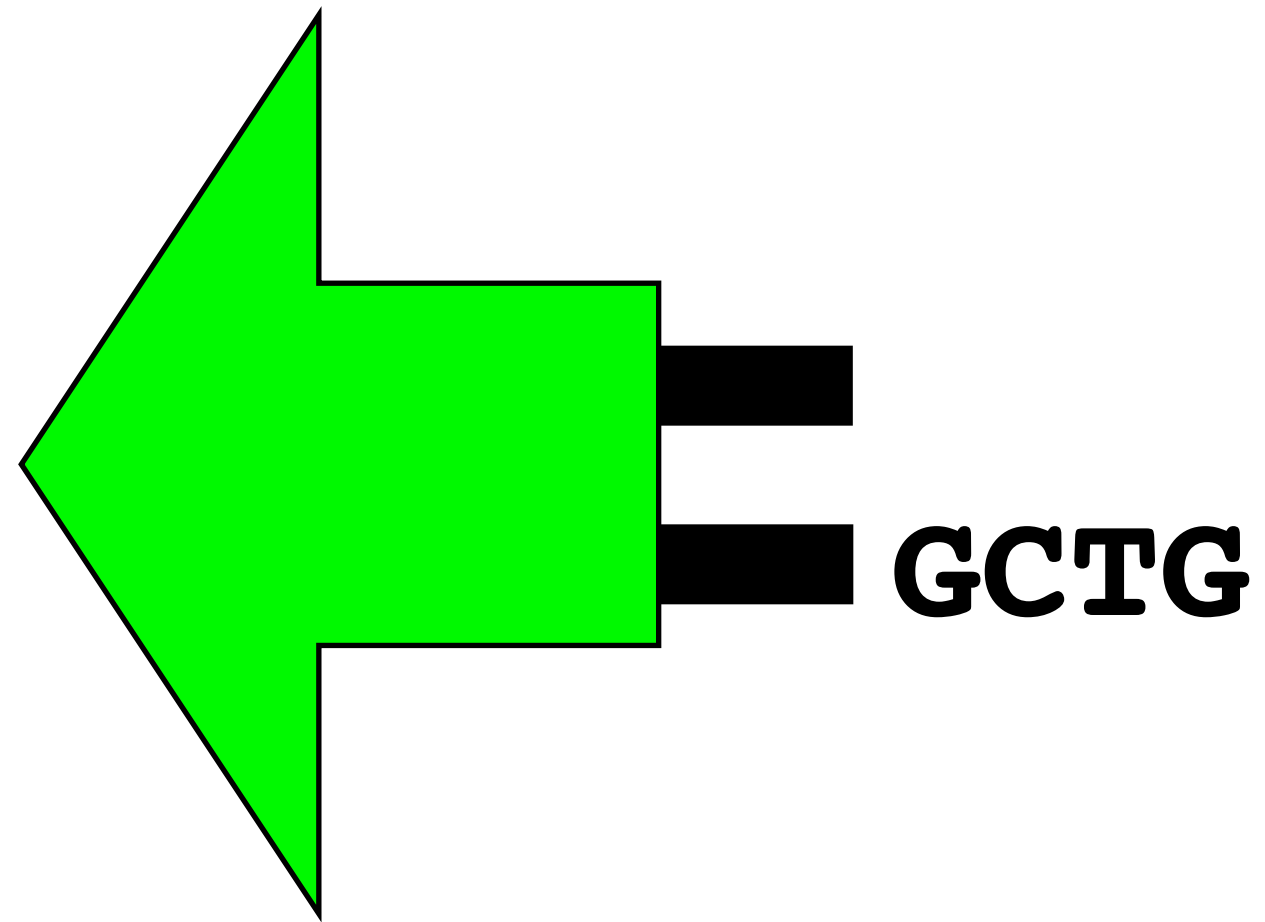
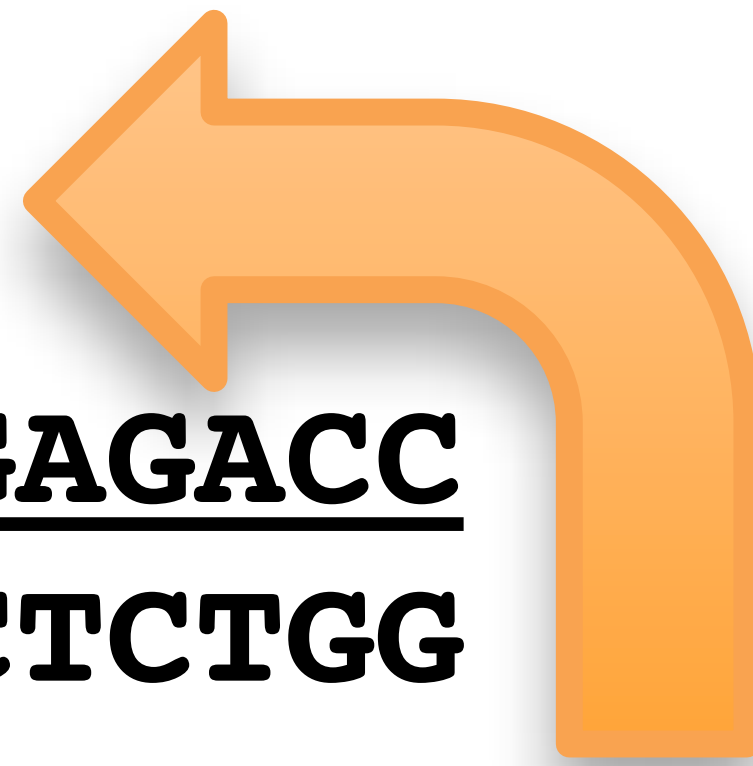
# Part J119137

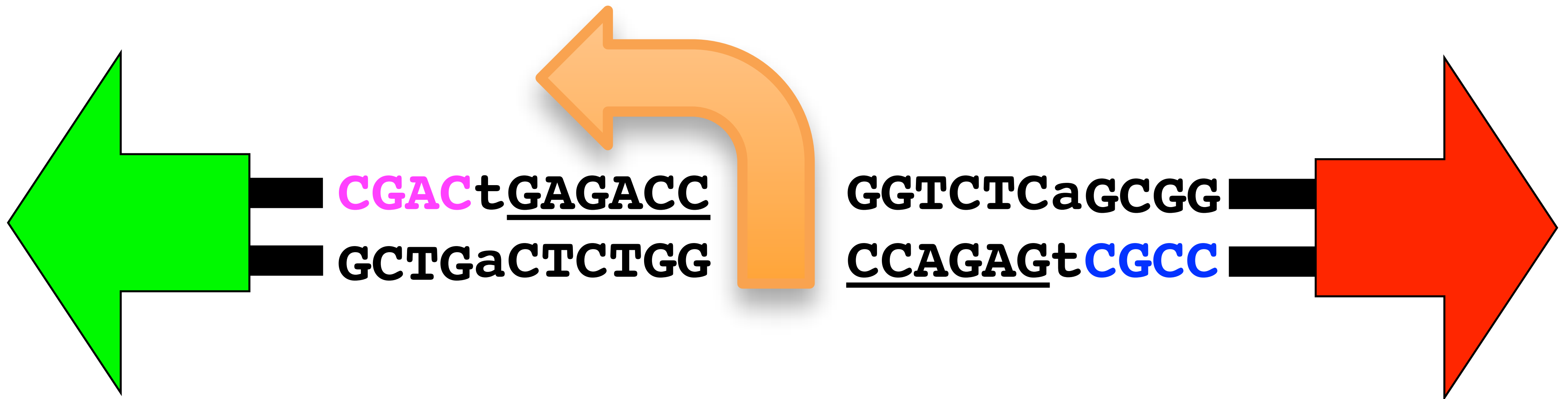




**CGAC** t **GAGACC**  
**aCTCTGG**

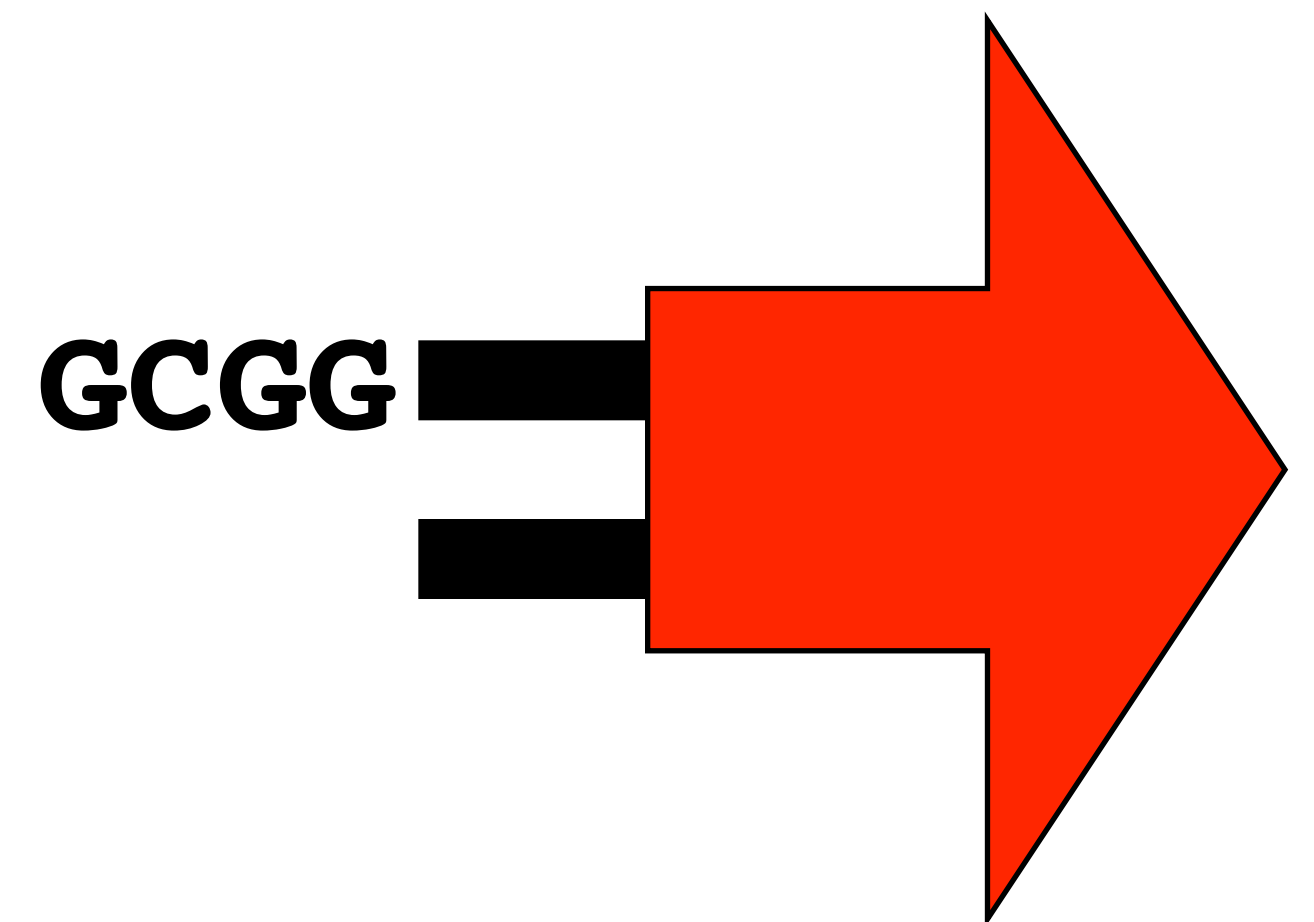
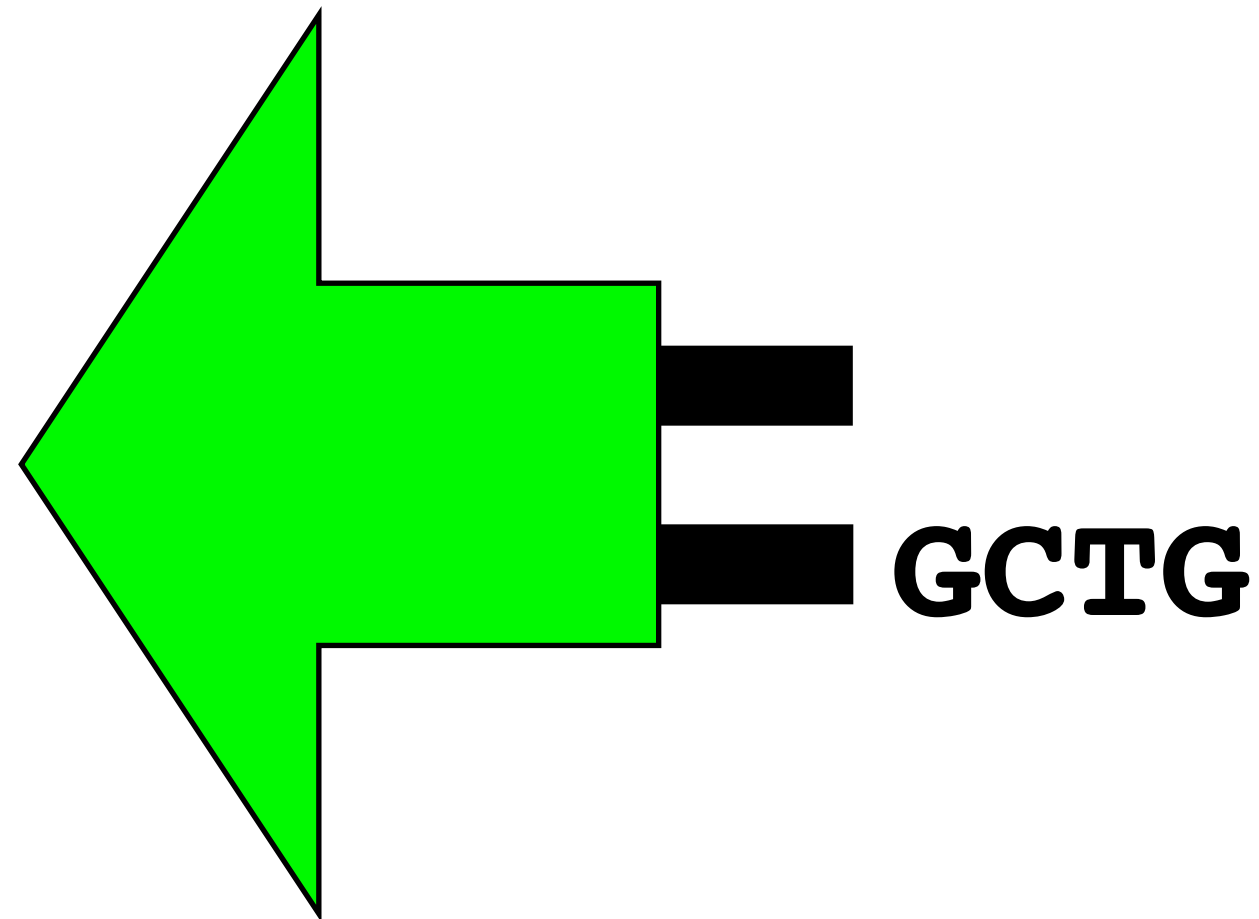
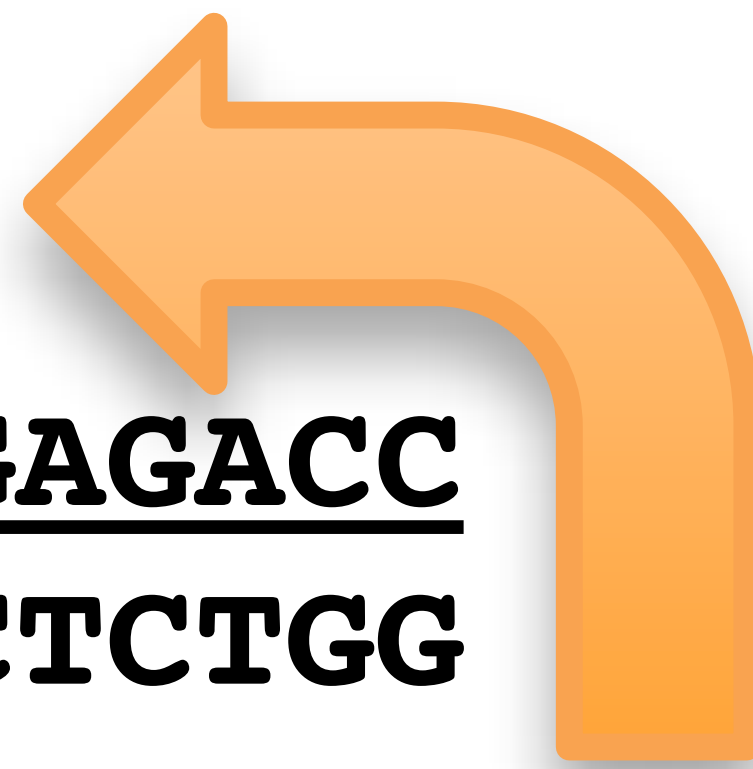
**GGTCTCa**  
**CCAGAGt** **CGCC**



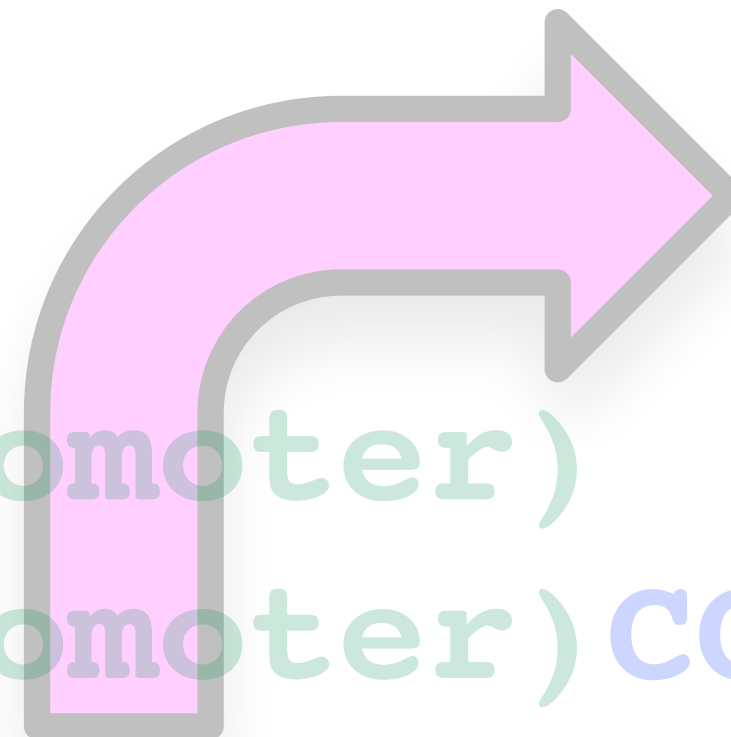


**CGAC** **t** **GAGACC**  
**aCTCTGG**

**GGTCTCa**  
**CCAGAGt** **CGCC**



**CGAC** (promoter)  
(promoter) **CGCC**

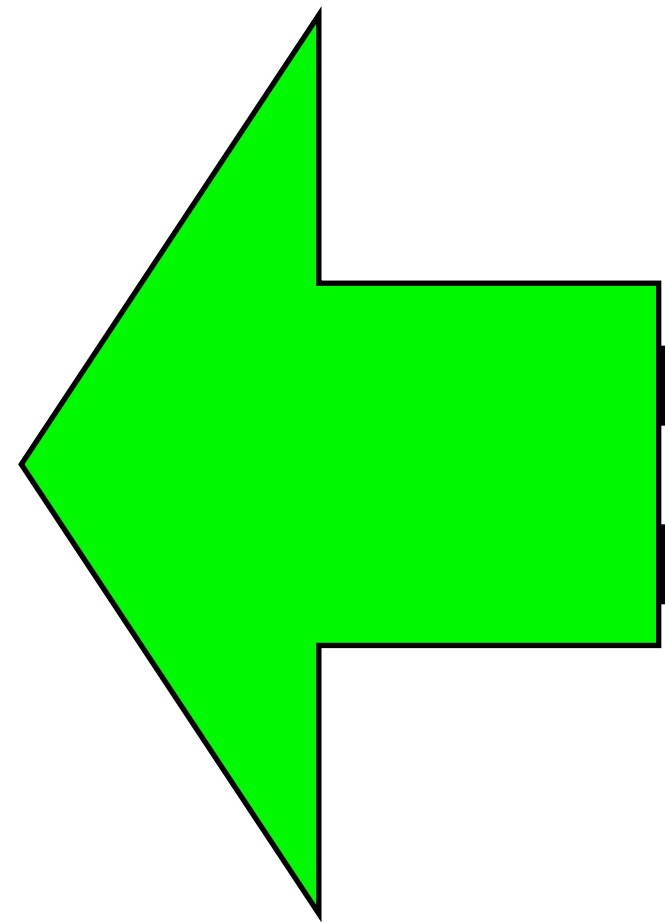




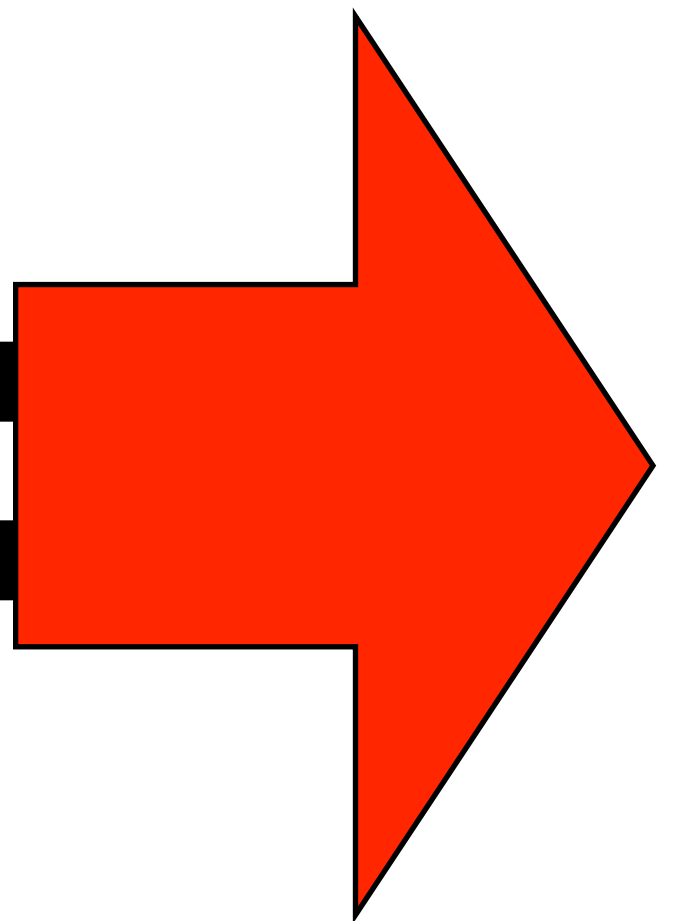
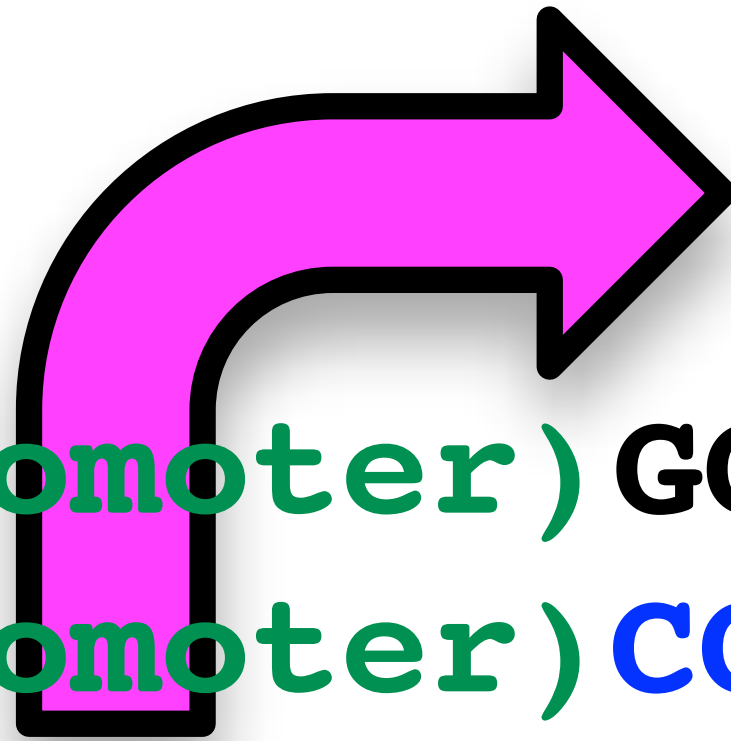
CGAC t GAGACC  
aCTCTGG



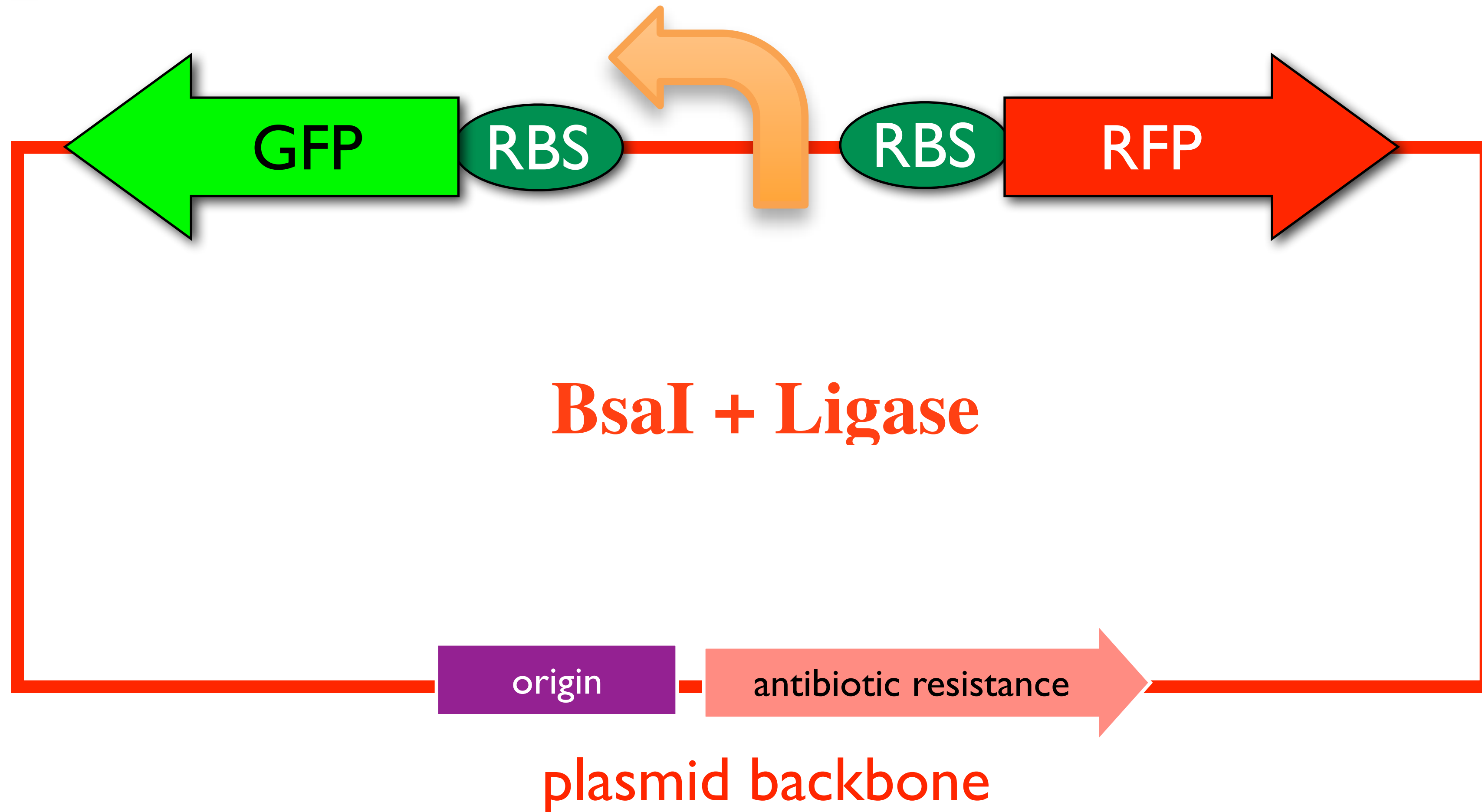
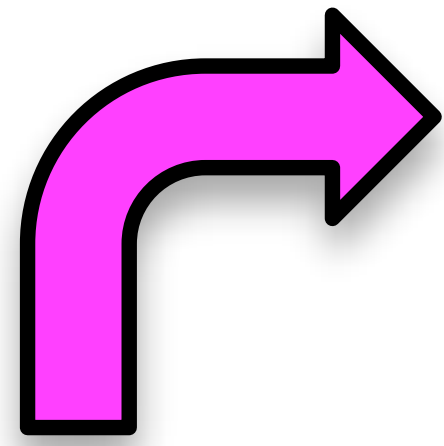
GGTCTCa  
CCAGAG tCGCC



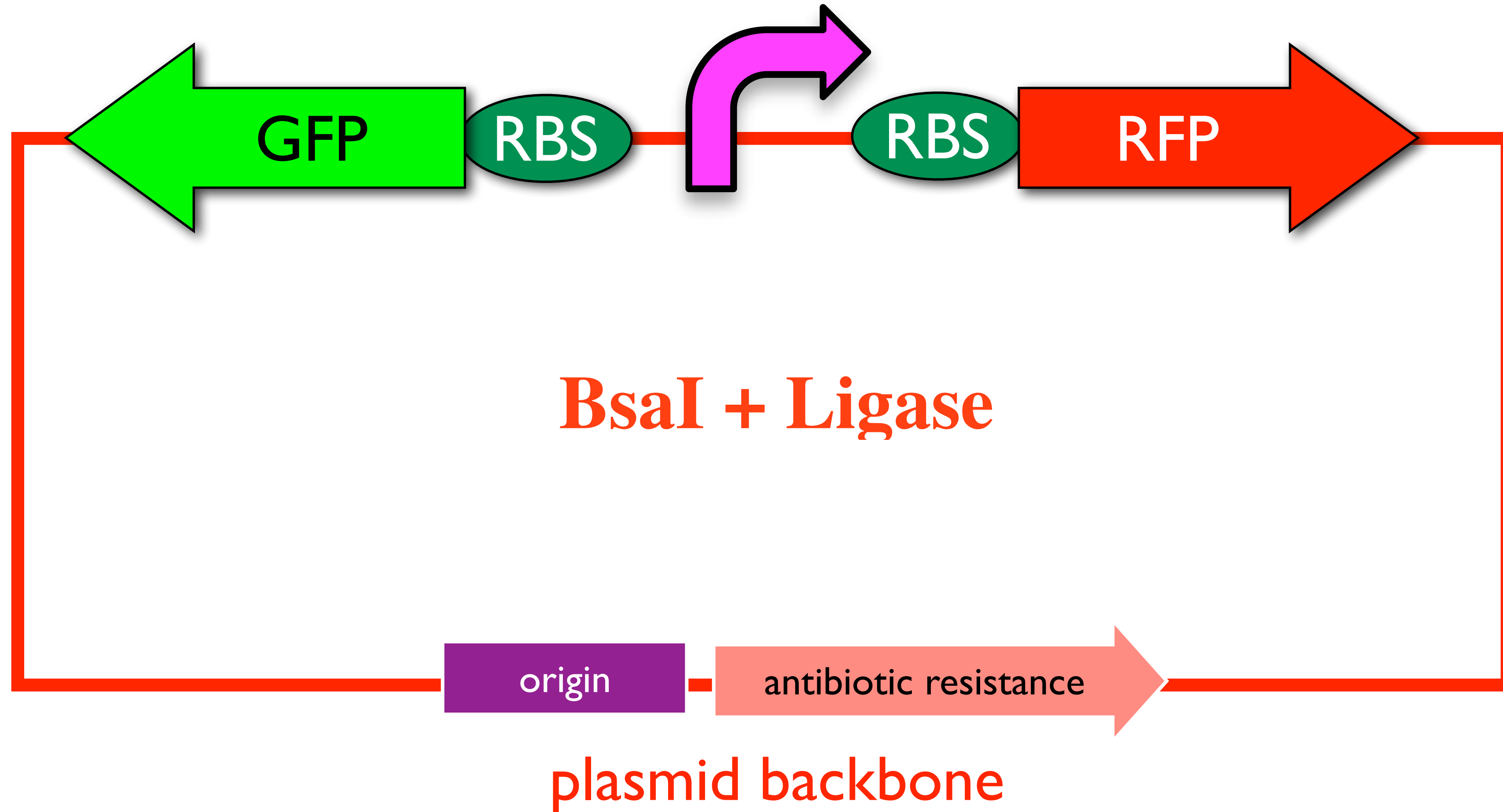
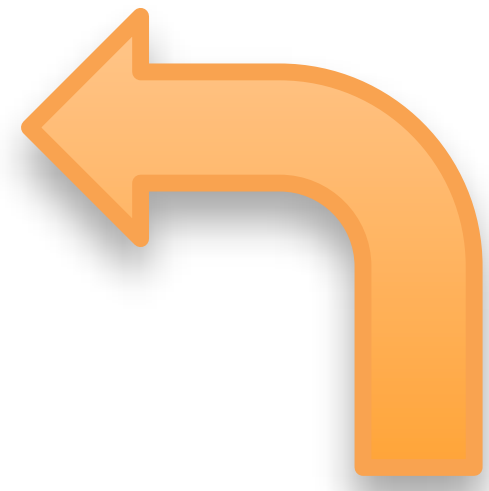
CGAC (promoter) GCGG  
GCTG (promoter) CGCC



# GGA Ligation Method

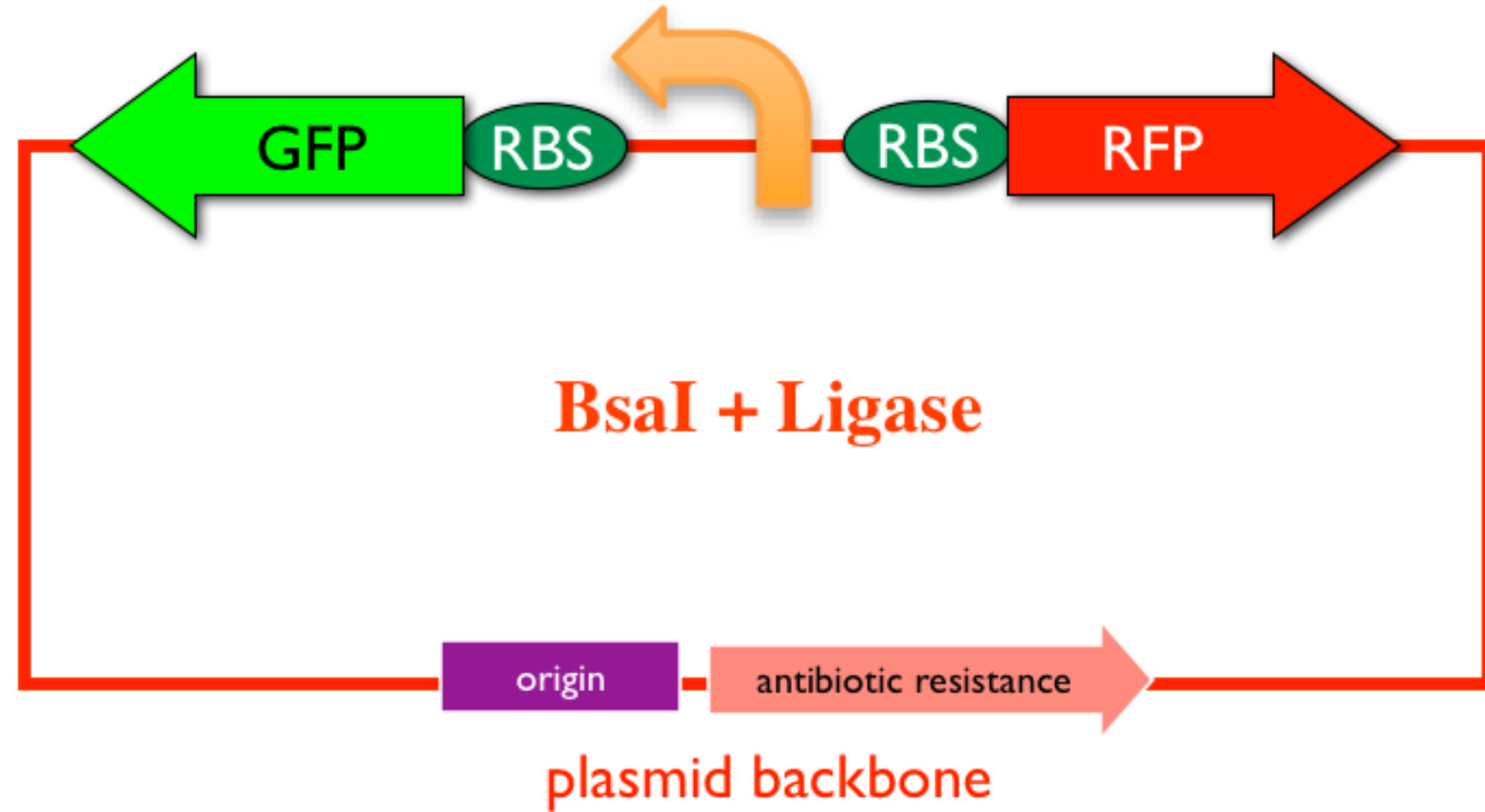


# GGA Ligation Method



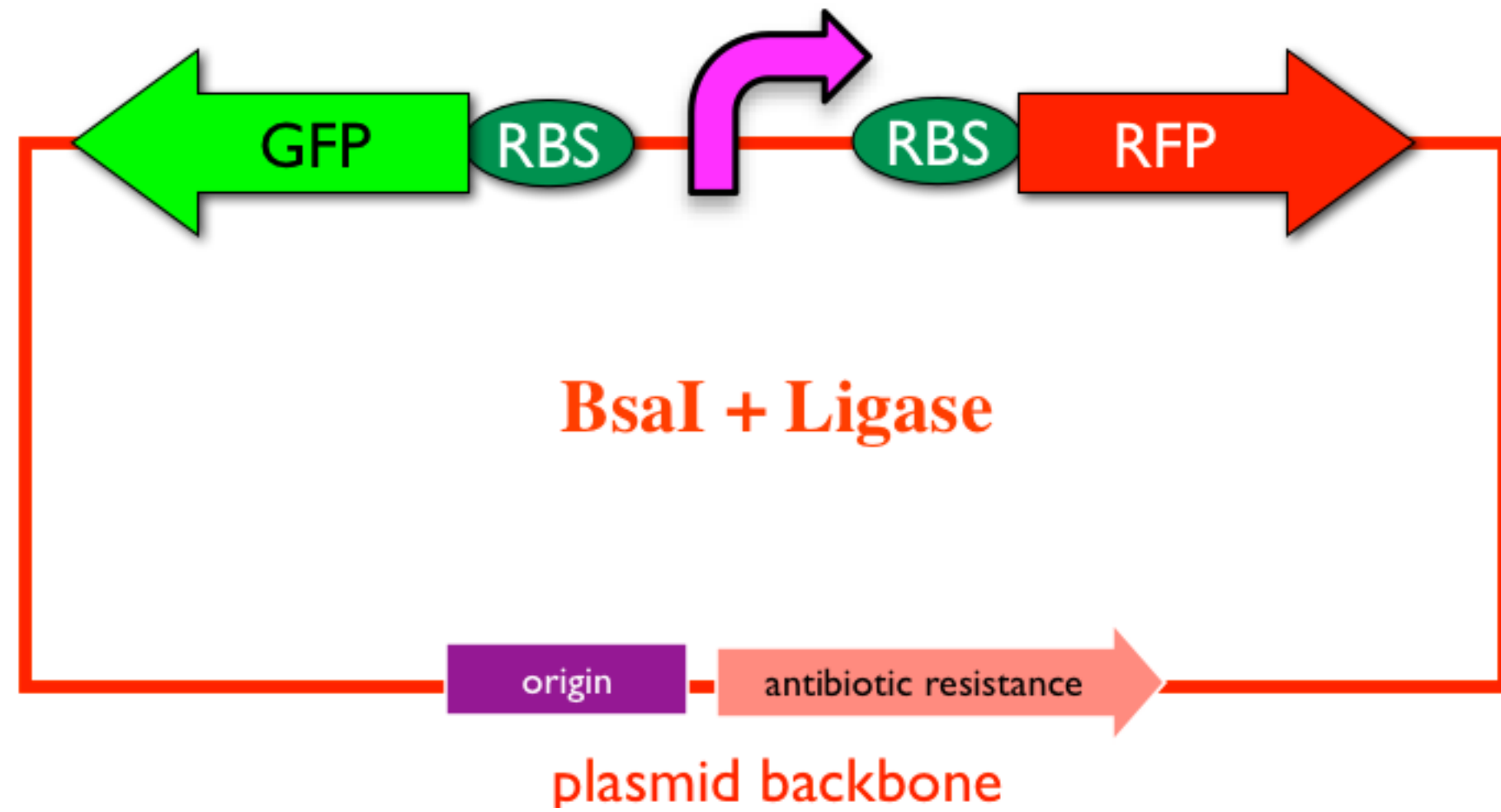


# GGA Ligation Method





# GGA Ligation Method





# GGA Ligation Method

