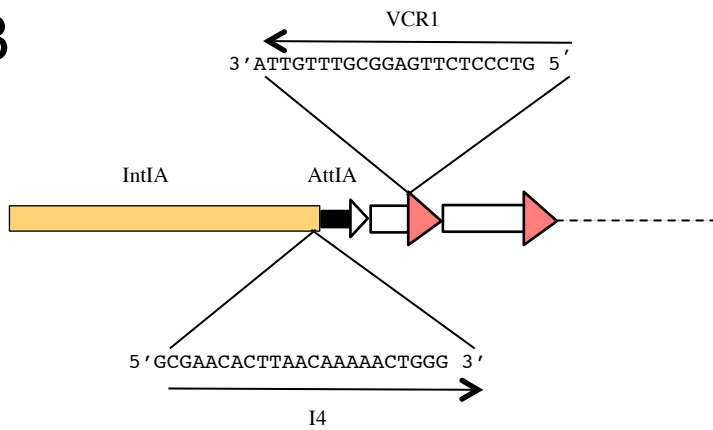


A

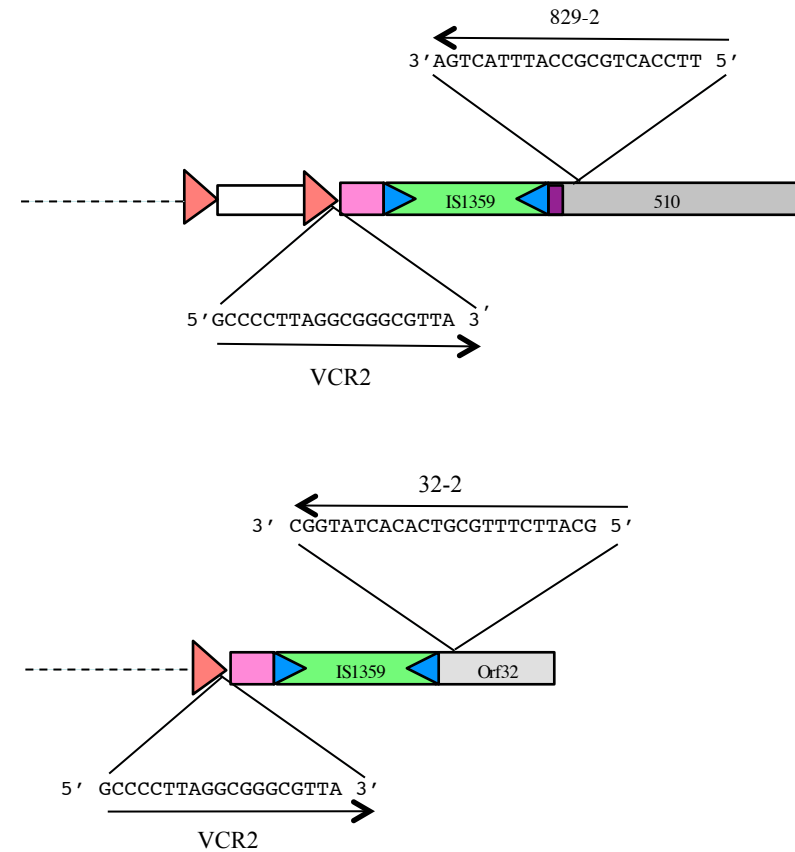
TAACAAACGCGTCAAGAGGGACAGCCAACGCGTGGCATT TTTATTATGCGTTGGTTTTGTGATTATGGTGTATGCGTTAAGTTAGTAGTAGCGTTGGCT **GCCCCCTAGGCGGGCGTTA**
ATTGTTTGGCAGTTCTCCCTGTGGTTGCGCACCGTAAAAATAATACGCAACCAAAACACTAATACCACAATACGCAATTCATCATCATCGCAACCGACGGGGGAATCCGCCCGCAAT

← VCR1 VCR2 →

B



C



Supplemental Figure 1. A, a typical VCR sequence, showing the location of the VCR1 and VCR2 primers used in the SI typing. PCRs. B, Sequence and location of the two primers used for *intIA* proximal cassette characterization. C, Sequence and location of the different primers used for *intIA* distal cassette characterization.



+ -

Supplemental Figure 2. Phd RT-PCR was performed on N16961 total RNA (end exponential time) with PV1 and PV2 primers with (+) or without (-) AMV reverse transcriptase.

Clustal Alignment of PhdSI, PhdPsy, PhdSba, PhdSyr and PhdP1 (see text)

```

Phd_SI      --MNRKVEAYGVDAVERPKIKASKKLDLT--GDAGRQIVKSETKLALR--THQKTFTKLA
Phd_Psy     MMMNKNIELYGVKVVVARPKIKAEKNLNL--GGSGKQIVKSETKLVLR--THRAC-----
Phd_Sba     --MLNETKKYGVNIVERPHVKANKKLDLT--GGCGKQIVHSETKLVLR--THKNTFRKLA
Phd_Syr     --MNHKLNTYGVSIIVERPKVKAIKKLDLG--GDSGKQIVYSETKLVLR--THKKTFFKLA
Phd_P1      MQSINFRTARGNLSEVLNNVEAGEEVEITRRGREPAVIVSKATFEAYKKAALDAEFASLF
           .      *      :::* :::: : *      ** . * . : :
    
```

```

Phd_SI      DM-----
Phd_Psy     -----
Phd_Sba     DM-----
Phd_Syr     DM-----
Phd_P1      DTL DSTN KELVNR
    
```

Identity (%)	Phd VC
Phd VC	100
Phd P ₁	17 (not detected by blastp)

Identity (%)	Doc VC
Doc VC	100
Doc P ₁	32 (E=4e-13)

SUPPLEMENTAL Figure 3

CcdA

```

          10      20      30      40      50      60      70      80
F plasmid  -----MKQRIT----VTVSDSYQLLKAYDVNISGLVSTTMQNEARRLRAERWKAENQEGMAEVARFIEMNGSFADENRDW (82)
V. fischeri MRNQYNTQAVKKATNLTLSNDLLAEAKRLKINLSATMEKALSQEVSKLKRQEWLEQNSEAIDACNELTDKYGLFSDSYRVF (81)
          .* ..   :*: :   :   :*:*. :   :. * :   .* :* *.:   .: : * *:* * :

```

CcdB

```

          10      20      30      40      50      60      70      80      90      100
F plasmid  -MQFKVYTYKRES---RYRLFVDVQSDIIDTPGRRMVIPLASARLLS-DKVSRELYPVVHIGDE-SWRMMTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI (101)
V. fischeri MSQFTLYKNKDKSSAKTYPFVVDVQSDLLDNLNTRLVPLTPIELLD-KKAPSHLCPTIHIDEG-DFIMLTQQMTSVPVKILSEPVNELSTFRNEIIAAIDFLITGI (105)
          **.* : ..   : .:** **::. . *:*:*:. . :. : . * * : : : .: :*: : :***. . . : * .. * *::: **

```

Identity (%)	CcdA _F
CcdA _F	100
CcdA _{Vfi}	22 (E= 0.65)

Identity (%)	CcdB _F
CcdB _F	100
CcdB _{Vfi}	41 (E= 4e-13)

SUPPLEMENTAL Figure 4