Supplementary Figure 1. CLUSTAL Omega multiple sequence alignment of integrase aminoacid sequences of SG11-REs used as a reference.

The meaning of the AA color code is as follows: red (small + hydrophobic), blue (acidic), pink (basic), and green (hydroxy + sulphydryl + amine + G). The following symbols denote the degree of residue conservation. Asterix (*) indicates positions which have a single, fully conserved residue; colon (:) indicates conservation between groups of strongly similar properties; and period(.) indicates conservation between groups of weakly similar properties. The catalytic residue tyrosine (Y) is surrounded by three basic residues at the active site (highlighted in yellow: R-H-RH). The IntG active site is conserved for all 126 SG11-REs in this study.
Supplementary Figures 2. BLAST alignment of the nucleotide sequences of the backbones of SGI1-REs with the reference GI as request.

The colors of the strains correspond to the clusters of SGI1-REs: red (cluster 1: SGI1 cluster), green (cluster 2: PGI1 cluster), blue (cluster 3: PGI2 cluster), purple (cluster 4: AGI1 cluster), brown (cluster 5), black (cluster 6), and grey (cluster 7). The characterized SGI1-REs are underlined. The ORFs of the backbone used as a reference are represented. The following colors are used for ORFs of known function:

- Blue: DNA recombination (int, sit)
- Orange: Transcriptional regulator
- Yellow: Type IV secretion system subunit (tra)
- Light blue: DNA replication (rep)
- Pink: Mobilization gene (mpc)
- Green: Resolvase (res)
- Black: DNA replication, recombination, and repair (helicase-monomoduclease (ybjD))
- Magenta: DNA restriction/modification
- Grey: Toxin-antitoxin system (subtilisin-ATPase)
- Red: Unknown function

The green angled arrows indicate AcaCD binding sites, the red arrow indicates oriT and the black arrow indicates the MDR region. Black vertical lines represent attL and attR attachment sites and the chromosomal trmE gene is shown in black. Backbone variations are described for each SGI1-RE.

(2A) Alignment of SGI1-REs of the SGI1 cluster (cluster 1) with the SGI1 backbone.

SGI1 Salmonella enterica Typhimurium 96-5227 (AF261825) (as a reference); ORFs and genes encoding proteins of known function: S001 (intG) (integrate), S002 (xis) (excisionase), S003 (rep) (replication protein), S004 (helix-turn-helix domain-containing protein), S005 (traN) (conjugal transfer protein), S006 (sycC) (flagellar transcriptional activator subunit C), S007 (sgaD) (flagellar transcriptional activator subunit D), S011 (traG) (conjugal transfer protein), S012 (traH) (conjugal transfer protein), S019 (mpsB) (mobilization protein MpsB), S020 (mpxA) (mobilization protein MpxA), S023 (uvrD) (ATP-dependent helicase), S024 (ybjD) (ATP-dependent endonuclease), S025 (sgiT) (toxin: subtilisin pro tease), S026 (sgiA) (antitoxin: AAA-ATPase), S027 (res) (resolvase).

SGI1-D Salmonella enterica Infantis SRC46 (KU854986): complete backbone.
Salmonella enterica Enteritidis 92-0392 (CP018657): complete backbone.

Salmonella enterica Dublin OSF018603 (AAQBBLO10000010): complete backbone.

Salmonella enterica Panama BCW_2754 (MYAK01000099/4/781/962): complete backbone.

Salmonella enterica Java PNCS013484 (AAXPUJ010000014): complete backbone.

SGI1-PmJN40 Proteus mirabilis JN40 (MF576128): complete backbone. (SGI1-RE followed by another GI in tandem).

Salmonella enterica Derby FDA196946 (AAIUNV010000014): complete backbone.

Vibrio cholerae 2011EL-1271 (CP046839): complete backbone.

SGI1-B2 Proteus mirabilis PmSC17 (KP116299): complete backbone; additional MDR region in S021.

Salmonella enterica Agona 89991 (AAJPHB010000015): complete backbone.

SGI1-F Salmonella enterica Cerro SRC5 (KU847976): complete backbone.

Salmonella enterica Albany R15.2267 (CP065564): complete backbone.

Salmonella enterica Senftenberg SAMEA5552168 (DAAHPW010000016): complete backbone.

Vibrio cholerae 555448 (AAXNYA010000016): complete backbone. (SGI1-RE followed by another GI in tandem).

SGI1-Vc2CHAMA Vibrio cholerae 59-se-2011-11-25T13 (MN708014): deletion of part of S044 due to insertion of the MDR region.

Salmonella enterica Saintpaul FNE0134 (AAQALN010000014/15): deletion of part of S044 due to insertion of the MDR region.

SGI1-Pm2CHAMA Proteus mirabilis Pm2CHAMA (MF372716): deletion of part of S044 due to insertion of the MDR region.

SGI1-PmCA11 Proteus mirabilis CA121511 (MH990673): complete backbone.

SGI1-NDM-1 Vibrio cholerae BRV8 (CTBD01000091): complete backbone; SGI1-RE carrying blaNDM1 and armA.

SGI2 Salmonella enterica Emek SRC19 (AY963803): complete backbone; MDR region in S023.

Salmonella enterica Virchow 129420 (AALLNJ010000009): deletion of part of res and part of the right end of the backbone upstream of S044 due to the insertion of an IS element of the MDR region.

SGI1-Z Proteus mirabilis PmSC42 (KP057606): deletion of part of S025 and S026-res due to the insertion of an IS element of the MDR region.

Salmonella enterica Senftenberg 199836 (AAIEYO010000017): deletion of part of S024 and S025-res due to the insertion of an IS element of the MDR region.

SGI1-B-Ec1 Escherichia coli AVC96 (MK599281): insertion of ISe43 in S023.
**SG11-PmSC1111 Proteus mirabilis PmSC1111 (MH998665):** insertion of an IS element of the IS3 family in S007; insertion of part of the MDR region in S010; part of S010-res in inverse orientation due to the presence of IS26 elements in the MDR region.

**Klebsiella pneumoniae 2018C01-046 (CP044368):** deletion of part of S023, S024-res and part of S044 due to insertion of the MDR region.

**Salmonella enterica Newport 193307 (AALJQG010000018):** deletion of part of traN, S006-S008 and part of S009 due to insertion of ISVch4.

**SG11-PmMAT Proteus mirabilis PmMAT (JX089583):** deletion of part of traN, S006-S008 and part of S009.

**SG11-L Morganella morganii Pr5 (LT630458):** deletion of part of traN, S006-S008 and part of S009 due to insertion of ISVch4.

**SG11-K variant Salmonella enterica Kentucky 201001922 (CP028357):** deletion of part of traN, S006-S008 and part of S009 due to insertion of ISVch4; insertion of part of the MDR region in S024; deletion of part of S044 due to insertion of the MDR region.

**SG11-K1 Salmonella enterica Kentucky SRC73 (AY463797):** deletion of part of traN, S006-S008 and part of S009 due to insertion of ISVch4; deletion of part of S044 due to insertion of the MDR region.

**Salmonella enterica Typhimurium FSIS11815820 (AAHSTR010000012):** deletion of S023-res due to the insertion of an IS element of the MDR region.

**Salmonella enterica Weltevreden S4-5182 (MZGE01000033/781):** deletion of part of traN, S006-S008 and part of S009 due to insertion of ISVch4; deletion of part of res and part of S044 due to insertion of the MDR region.

**Salmonella enterica Kentucky K13SK002 (CP037917):** deletion of part of traN, S006-S008 and part of S009 due to insertion of ISVch4; deletion of part of res and part of S044 due to insertion of the MDR region.

**Salmonella enterica Kentucky PU131 (CP026327):** deletion of part of traN, S006-S008 and part of S009 due to insertion of ISVch4; deletion of part of res and part of S044 due to insertion of an IS26 element.

**Vibrio cholerae N2786 (VSHP01000003):** S023-res region composed of 5 ORFs: 2 ORFs share nt identity with the Sputw3181_4077 and Sputw3181_4076 loci of Shewanella sp. W3-18-1 (CP000503) and 3 ORFs encoding an Xcyl family restrictionendonuclease, a site-specific DNA-methyltransferase and a resolvase; absence of MDR region.

**SG11-XJ9S Salmonella enterica Kentucky XJ9S (MN640065):** deletion of part of S025, S026-res and S044 due to insertion of the MDR region.

**Salmonella enterica Typhimurium NCTR350 (NQVV01000039/27):** deletion of part of traN, S006-S008 and part of S009 due to insertion of ISVch4; deletion of part of S025, S026-res and part of S044 due to insertion of the MDR region.

**Providencia stuartii FDAARGOS_294 (NJYE02000002):** insertion of 3 ORFs in S014 including an ORF encoding a hydrolase; deletion of S023-S024; deletion of part of S044; SG11-RE carrying blavEB6 and qnrA1.

**SGI-V (SG11-V) Proteus mirabilis VB1248 (HQ888851):** insertion of 3 ORFs in S014 including an ORF encoding a hydrolase; deletion of S023-S024; deletion of part of S044; SG11-RE carrying blavEB6 and qnrA1.

**SGI0 Proteus mirabilis Pm1LENAR (MH734355):** lower nt identity for the different regions: S014, S021-S022 and S023-S024; absence of MDR region.

**Vibrio cholerae N2726 (VSFX01000005):** insertion of 2 ORFs coding for an MBL fold metallo-hydrolase and an AraC family transcriptional regulator in S014; deletion of S023-S024; absence of MDR region.
Salmonella enterica Kentucky BCW_2895 (MXXV010000018): deletion of part of traN, S006-S008 and part of S009 due to insertion of ISVch4; deletion of part of S024, S025-res and part of S044 due to insertion of the MDR region.

Salmonella enterica Hadar FNE0129 (AANCMD010000013): deletion of the traN-traH region.

Salmonella enterica Typhimurium 806209 (AALNAT010000020): deletion of the traN-traH region.

Vibrio parahaemolyticus 20140829008 (CP034294): 2751 bp insertion between traH and S013 including 2 ORFs, one of which encodes an immunity 49 family protein; deletion of S023-S024; absence of MDR region.

SGI1-LK1 Proteus mirabilis Pm294MATL1 (MH734354): deletion of part of traN, S006-S012 and part of S013 due to insertion of ISVch4.

Vibrio cholerae N2757 (VSGQ01000007): deletion of part of S006, S007-S013 and part of S014; lower nt identity for the S015-S018 region, but better nt identity with P013-P015; insertion of 2 ORFs sharing nt identity with locus A6033_05025 and a region encoding an ImmA/ImmE family metallo-endopeptidase from Aeromonas veronii CB51 (CP015448) between S018 and S019; lower nt identity for the S021-S022 region; the S023-res region shares nt identity with the Sputw3181_4076 locus of Shewanella sp. W3-18-1 (CP0000503), and 3 ORFs encoding an Xyl family restriction endonuclease, a site-specific DNA-methyltransferase and a recombinase; absence of MDR region.

(2B) Alignment of SGI1-REs of the PGI1 cluster (cluster 2) with the PGI1-PmESC backbone.
**PGI1-PmPEL Proteus mirabilis PEL (KF856624):** 21-bp deletion in *int*; complete SGI1-RE carrying *bla*\textsubscript{VEB-3}, *bla*\textsubscript{NDM1} and *bla*\textsubscript{DHA-1}).

**Salmonella enterica Senftenberg CVM 34514 (CP051329):** P025 truncated by an IS element of the MDR region.

**Salmonella enterica Heidelberg AZ-TG74856 (AAFUZP010000001):** SGI1-RE inserted in the intergenic region between *sodB* and *purR*; P025 truncated by an IS element of the MDR region.

**Shewanella algae A3/19 (JACDTT010000025/49):** insertion of an IS26 element in *res*; absence of MDR region.

**Salmonella enterica Heidelberg BCW_3410 (MXSU01000026/6):** SGI1-RE inserted in the intergenic region between *sodB* and *purR*; *res* truncated by an IS element of the MDR region.

**Salmonella enterica Montevideo FSIS11706644 (AANGCS010000016):** P011-P014 region shares nt identity with the A6033_05010 and A6033_05015 loci of *Aeromonas veronii* CB51 (CP015448); region between P016 and P017 shares nt identity with a region of *Aeromonas veronii* CB51 containing 2 ORFs, one of which encodes an ImmA/IrrE family metallo-endopeptidase; P021-*res* region shares nt identity with A023 and A024; absence of MDR region.

**Salmonella enterica Infantis 355107 (AAMIAE010000014):** P011 region shares nt identity with the A6033_05005 and A6033_05010 loci of *Aeromonas veronii* CB51 (CP015448); longer intergenic region between P016 and P017; P021-*res* region corresponds to an 8.5 kb segment with 7 ORFs showing no significant identity to known gene sequences, including ORFs encoding a DNA helicase, a macro domain-containing protein, 2 DUF4433 domain-containing proteins, and a resolvase; absence of MDR region.

**Vibrio cholerae 9760 (RHMB01000014):** very low nt identity with PGI1 for *traN*; *traH* found upstream of *traG*; P011 region shares nt identity with the A6033_05010 locus of *Aeromonas veronii* CB51 (CP015448); longer intergenic region between P016 and P017; absence of MDR region.

**Salmonella enterica Montevideo FSIS11814837 (ROHT01000031):** very low nt identity with PGI1 for *traN*; *traH* found upstream of *traG*; P011 region shares nt identity with the A6033_05010 locus of *Aeromonas veronii* CB51 (CP015448); longer intergenic region between P016 and P017; absence of MDR region.

**Vibrio cholerae BD21 (QEEE01000038):** *rep-traN* region shares nt identity with the FE240_17910, FE240_17915 and FE240_17920 loci encoding a TrfA protein, a DNA-binding protein and TraN in *Aeromonas simiae* A6 (CP040449); region between P007 and P008 shares nt identity with the A6033_04990 locus of *Aeromonas veronii* CB51 (CP015448); P011-P012 region shares nt identity with the FE240_17960 and FE240_17965 loci of *Aeromonas simiae* A6; longer intergenic region between P016 and P017; absence of MDR region.

**Vibrio cholerae 01-8_S93 (QZUV01000027):** *rep-traN* region shares nt identity with the FE240_17910, FE240_17915 and FE240_17920 loci encoding a TrfA protein, a DNA-binding protein and TraN in *Aeromonas simiae* A6 (CP040449); region between P007 and P008 shares nt identity with the A6033_04990 locus of *Aeromonas veronii* CB51 (CP015448); P011-P012 region shares nt identity with the FE240_17960 and FE240_17965 loci of *Aeromonas simiae* A6; longer intergenic region between P016 and P017; absence of MDR region.

**Vibrio navarresis VN-0515 (MPKK01000014):** region between P007 and P008 shares nt identity with the A6033_04990 locus of *Aeromonas veronii* CB51 (CP015448); *traH* found upstream of *traG*; P011-P014 region shares nt identity with the A6033_05010 and A6033_05015 loci of *Aeromonas veronii* CB51; longer intergenic region between P016 and P017; P021-*res* region corresponds to an 8.5 kb segment with 7 ORFs showing no significant identity to known gene sequences, including ORFs encoding a DNA helicase, a macro domain-containing protein, 2 DUF4433 domain-containing proteins, and a resolvase; absence of MDR region.

**Vibrio cholerae PNUSA000839 (AAXNBC010000015/39):** very low nt identity with PGI1 for *traN*; *traH* found upstream of *traG*; P011 region shares nt identity with the A6033_05010 locus of *Aeromonas veronii* CB51 (CP015448); longer intergenic region between P016 and P017; absence of MDR region.

**Shewanella algae Sh392 (QFDC01000022/74/49):** very low nt identity with PGI1 for *traN*; *traH* found upstream of *traG*; P011 region shares nt identity with the A6033_05010 locus of *Aeromonas veronii* CB51 (CP015448);
longer intergenic region between P016 and P017; region between P020 and P022 shares nt identity with A023 and A024; absence of MDR region.

IMEVe10432-62 *Vibrio cholerae* 10432-62 (CP010812): very low nt identity with PGII for *traN*; *traH* found upstream of *traG*; P011 region shares nt identity with the A6033_05010 locus of *Aeromonas veronii* CB51 (CP015448); longer intergenic region between P016 and P017; region between P020 and P022 shares nt identity with A023-A024; absence of MDR region.

*Shewanella foddinae* 74A (SLWF01000006): very low nt identity with PGII for *traN*; *traH* found upstream of *traG*; P011 region shares nt identity with the A6033_05010 locus of *Aeromonas veronii* CB51 (CP015448); longer intergenic region between P016 and P017; P022-*res* region shares nt identity with S023-S024 followed by 3 ORFs encoding a *BsuBI/PstI* restriction endonuclease, an N-6 DNA methylase and a resolvase; P025 region corresponds to an ORF encoding a DUF4365 domain-containing protein.

*Rheinheimera nanhaiensis* E407-8 (BAFK01000015): very low nt identity with PGII for *traN*; *traH* found upstream of *traG*; P011-P016 region shares nt identity with the A6033_05010 locus of *Aeromonas veronii* CB51 (CP015448) and PGI2-015-PGI2-018; region between P020 and P022 shares nt identity with S023-S024; absence of MDR region.

*Vibrio cholerae* SAMEA4057619 (DACPGR010000009): *rep-traN* region shares nt identity with the FE240_17910, FE240_17915 and FE240_17920 loci encoding a TrfA protein, a DNA-binding protein and TraN in *Aeromonas simiae* A6 (CP040449); *traI* found upstream of *traG*; P011-P012 region shares nt identity with the FE240_17960 and FE240_17965 loci of *Aeromonas simiae* A6; longer intergenic region between P016 and P017; P021-*res* region corresponds to an 8.5 kb segment with 7 ORFs showing no significant identity to known gene sequences, including ORFs encoding a DNA helicase, a macro-domain-containing protein, 2 DUF4433 domain-containing proteins, and a resolvase; absence of MDR region.

*Shewanella sp.* KCT (LVDJ01000007): very low nt identity with PGII for *traN*; region between P007 and P008 shares nt identity with the A6033_04990 locus of *Aeromonas veronii* CB51 (CP015448); region between P010 and P015 shares nt identity with the A6033_05010 and A6033_05015 loci of *Aeromonas veronii* CB51; longer intergenic region between P016 and P017; P022-*res* region shares nt identity with S023-S024 followed by 3 ORFs encoding a *BsuBI/PstI* restriction endonuclease, an N-6 DNA methylase and a resolvase; P025 region corresponds to an ORF encoding a DUF4365 domain-containing protein; absence of MDR region.

*Escherichia coli* N63148 (NTM01000010): very low nt identity with PGII for *traN*; low nt identity with PGII for *traG*; *traH* found upstream of *traG*; region between P010 and P015 shares nt identity with the A6033_05010 and A6033_05015 loci of *Aeromonas veronii* CB51 (CP015448); longer intergenic region between P016 and P017; P022-*res* region shares nt identity with S023-S024 followed by 3 ORFs encoding a *BsuBI/PstI* restriction endonuclease, an N-6 DNA methylase and a resolvase; P025 region followed by 3 ORFs encoding proteins of unknown function; absence of MDR region.

IMEVmSCCF01 *Vibrio mimicus* SCCF01 (CP016383): very low nt identity with PGII for *traN*; low nt identity with PGII for *traG*; *traH* found upstream of *traG*; region between P010 and P015 shares nt identity with the A6033_05010 and A6033_05015 loci of *Aeromonas veronii* CB51 (CP015448); longer intergenic region between P016 and P017; P022-*res* region shares nt identity with S023-S024 followed by 3 ORFs encoding a *BsuBI/PstI* restriction endonuclease, an N-6 DNA methylase and a resolvase; P025 region corresponds to an ORF encoding a DUF4365 domain-containing protein; absence of MDR region.
(2C) Alignment of SGII-REs of the PGII2 cluster (cluster 3) with the PGII2 backbone.

PGII2 Proteus mirabilis BC11-24 (MG201402) (as a reference); ORFs and genes encoding proteins of known function: PGII2-001 (intA) (integrate), PGII2-002 (xis) (excisionase), PGII2-003 (rep) (replication protein), PGII2-004 (helix-turn-helix domain-containing protein), PGII2-005 (traN) (conjugal transfer protein), PGII2-006 (sgaC) (flagellar transcriptional activator subunit C), PGII2-007 (sgaD) (flagellar transcriptional activator subunit D), PGII2-011 (traG) (conjugal transfer protein), PGII2-012 (traH) (conjugal transfer protein), PGII2-019 (mpsB) (mobilization protein MpsB), PGII2-020 (mpsA) (mobilization protein MpsA); absence of res (resolvase) probably due to insertion of the MDR region.

PGII2-zym28 Morganella morganii zy_m28 (MW080367): complete backbone; absence of res probably due to insertion of the MDR region. SGII-RE carrying blactXm-3, fosaA3 and aac(6')-Ib-cr.

PGII2-Ec2 Escherichia coli SCP17-71-2 (MN708013): complete backbone; absence of res probably due to insertion of the MDR region.

Pseudomonas aeruginosa MRSN1906 (RXVB01000034/21): complete backbone; absence of res probably due to insertion of the MDR region.

Cronobacter sakazakii CFSAN019572 (AAXWFR010000026/21): region between PGII2-024 and PGII2-066 shares nt identity with A025-res encoding a BsaBl/PsaI restriction endonuclease, an N-6 DNA methylase and a resolvase; PGII2-066 truncated by insertion of the MDR region.

Vibrio cholerae SA10G (CP053820): very low nt identity with PGII2 for the PGII2-021-PGII2-022 region and the region is longer; region between PGII2-024 and PGII2-066 shares nt identity with A025-res, genes encoding a BsaBl/PsaI restriction endonuclease, an N-6 DNA methylase and a recombinase; P2-066-P2-068 region shares nt identity with P025; absence of MDR region.

Vibrio parahaemolyticus V67 (JACBDZ010000015): region between PGII2-014 and PGII2-015 shares nt identity with P012 and P013; PGII2-023-PGII2-068 region corresponds to 5 ORFs encoding a mechanosensitive ion channel family protein, a magnesium and cobalt transport protein CorA, a FAD-protein FMN transference, a calcium/sodium antiporter and an undecaprenyl-diphosphate phosphatase; absence of res; absence of MDR region.

Vibrio mimicus 08-2414 (JACGMF010000003): region between PGII2-014 and PGII2-019 shares nt identity with the FE240_17965 locus of Aeromonas simiae A6 (CP040449), P013-P016 which shares nt identity with the FE240_17970, FE240_17975, FE240_17980 and FE240_17985 loci of Aeromonas simiae A6, and the FE240_17990 locus of Aeromonas simiae A6 encoding a permease; region between PGII2-022 and PGII2-066 shares nt identity with S023-S024, followed by 3 ORFs encoding a BsaBl/PsaI restriction endonuclease, an N-6 DNA methylase and a resolvase; P2-066-P2-068 region shares nt identity with P025; absence of MDR region.

Vibrio mimicus 1011-1073 (CP035682): region between PGII2-014 and PGII2-019 shares nt identity with the FE240_17965 locus of Aeromonas simiae A6 (CP040449), P013-P016 which shares nt identity with the FE240_17970, FE240_17975, FE240_17980 and FE240_17985 loci of Aeromonas simiae A6, and the FE240_17990 locus of Aeromonas simiae A6 encoding a permease; region between PGII2-022 and PGII2-066 shares nt identity with S023-S024, followed by 3 ORFs encoding a BsaBl/PsaI restriction endonuclease, an N-6 DNA methylase and a resolvase; P2-066-P2-068 region shares nt identity with P025; absence of MDR region.
**K Salmonella enterica** KpST48_NDM (VCE01000001): deletion between PG12-002 and rep; central region of traN shares nt identity with PG12-004 (traN); PG12-023-PG12-024 region shares nt identity with S023-res; PG12-066-PG12-068 region shares nt identity with P025; absence of MDR region.

**K Klebsiella pneumoniae** AGI1: methylase (protein), activator helix domain between P016 and P017 shares nt identity with Escherichia coli DNA methylase and a resolvase; PG12-066-PG12-068 region shares nt identity with P025; absence of MDR region.

**Vibrio cholerae** N2775 (VSHF01000011/12): central region of traN shares nt identity with P004 (traN); PG12-015 region shares nt identity with P012-P014; longer intergenic region between PG12-018 and PG12-019; longer region PG12-020-PG12-021; PG12-023-PG12-024 region shares nt identity with the Sputw3181_4076 locus of Shewanella sp. W3-18-1 (CP000503), and with A025-res encoding a BsaBI/PsrI restriction endonuclease, an N-6 DNA methylase and a resolvase; PG12-066-PG12-068 region shares nt identity with P025. (SG1-RE followed by another GI in tandem).

**Vibrio cholerae** 984-81 (JMBM01000001): central region of traN shares nt identity with P004 (traN); PG12-015 region shares nt identity with P012-P014; longer intergenic region between PG12-018 and PG12-019; longer region PG12-020-PG12-021; PG12-023-PG12-024 region shares nt identity with the Sputw3181_4076 locus of Shewanella sp. W3-18-1 (CP000503), and with A025-res encoding a BsaBI/PsrI restriction endonuclease, an N-6 DNA methylase and a resolvase; PG12-066-PG12-068 region shares nt identity with P025.

**Escherichia coli** KK-NP016 (BFWH01000021): most of the backbone (PG12-002-PG12-024 region) shares nt identity with PG11 regions: P002-P010 region; followed by P011-P014 region that shares nt identity with the A6033_05010 and A6033_05015 loci of Aeromonas veronii CB51 (CP015448); P015-P016 region; region between P016 and P017 shares nt identity with a region of Aeromonas veronii CB51 between the A6033_05020 and A6033_05025 loci, containing an ORF encoding an ImmA/IrrE family metallo-endopeptidase; P017-P021 region followed by a region sharing nt identity with S023-S024 and 3 ORFs encoding a BsaBI/PsrI restriction endonuclease, an N-6 DNA methylase and a resolvase; PG12-066-PG12-068 region shares nt identity with Shewanella lothica PV-4 (CP000606) from bases 4593806 to 4593138; absence of MDR region.

(2D) Alignment of SG1-REs of the AG11 cluster (cluster 4) with the AG11 backbone.

**AG11 Acinetobacter baumannii** D4 (KP054476) (as a reference); ORFs and genes encoding proteins of known function: A001 (intA) (integrase), A002 (xis) (excisionase), A003 (rep) (replication protein), A004 (helix-turn-helix domain-containing protein), A005 (traN) (conjugal transfer protein), A006 (agaD) (flagellar transcriptional activator subunit C), A007 (agaD) (flagellar transcriptional activator subunit D), A011 (traG) (conjugal transfer protein), A012 (traH) (conjugal transfer protein), A019 (mpsB) (mobilization protein MpsB), A020 (mpsA) (mobilization protein MpsA), A025 (BsaBI-PsrI restriction endonuclease family protein), A026 (N-6 DNA methylase), A027 (res) (resolvase). SG11-RE carrying blhteg1.

**AG14 Klebsiella pneumoniae** K1781 (FLIQ01000020/22); shorter intergenic region between A018 and A019; A023-A024 region corresponds to the Sputw3181_4076 locus of Shewanella sp. W3-18-1 (CP000503).
*Salmonella enterica* Infantis H124280339 (AAFGGL010000026/29): shorter intergenic region between A018 and A019; A023-A024 region corresponds to the Sputw3181_4076 locus of *Shewanella* sp. W3-18-1 (CP000503).

*Vibrio fluvialis* GCCln30 (JACNEY010000015): shorter intergenic region between A018 and A019; A023-res region corresponds to part of the Sputw3181_4076 locus of *Shewanella* sp. W3-18-1 (CP000503).

AGH4 *Salmonella enterica* Agona 24.H.04 (CASR01000049/44): shorter intergenic region between A018 and A019; A023-A024 region corresponds to the Sputw3181_4076 locus of *Shewanella* sp. W3-18-1 (CP000503).

AGH11 variant *Proteus mirabilis* (MK422178): shorter intergenic region between A018 and A019; A023-res region corresponds to part of the Sputw3181_4076 locus of *Shewanella* sp. W3-18-1 (CP000503).

AGH11 variant *Salmonella enterica* Stanley DMS 1112 (MXLM01000016): shorter intergenic region between A018 and A019; A023-res region corresponds to part of the Sputw3181_4076 locus of *Shewanella* sp. W3-18-1 (CP000503).

AGH11 variant *Escherichia coli* MOD1-EC6520 (NLVVY01000018/47/28): shorter intergenic region between A018 and A019; A023-res region corresponds to part of the Sputw3181_4076 locus of *Shewanella* sp. W3-18-1 (CP000503).

*Vibrio cholerae* 495747 (AAXOLK010000011): insertion of a transposon into A015; shorter intergenic region between A018 and A019; absence of MDR region.

AG13 (AGII-C) *Salmonella enterica* Derby 2014LSAL02547 (CP029486): shorter intergenic region between A017 and A018; A023-A024 region corresponds to the Sputw3181_4076 locus of *Shewanella* sp. W3-18-1 (CP000503).

AG1 *Vibrio sp*. 2017V-1124 (OKKN010000025/42): shorter intergenic region between A018 and A019; shorter intergenic region between A020 and A021; A023-A024 region corresponds to the Sputw3181_4076 locus of *Shewanella* sp. W3-18-1 (CP000503); absence of MDR region.

AG15 *Salmonella enterica* Cubana 76814 (AYUE01000008/66): A015 region shares nt identity with P012-P014; shorter intergenic region between A018 and A019; A023-A024 region corresponds to the Sputw3181_4076 locus of *Shewanella* sp. W3-18-1 (CP000503).

*Vibrio cholerae* Vc3017 (JAEMFW010000021): A015-A018 region shares nt identity with the FE240_17965 locus of *Aeromonas simiae* A6 CP040449), P013-P016 region that shares nt identity with the FE240_17970, FE240_17975, FE240_17980 and FE240_17985 loci of *Aeromonas simiae* A6, followed by the FE240_17990 locus of *Aeromonas simiae* A6 encoding a permease; A023-A024 region shares nt identity with the Sputw3181_4076 locus of *Shewanella* sp. W3-18-1 (CP000503).

*Vibrio cholerae* N2769 (VSHA010000173): A014-A018 region shares nt identity with the FE240_17965 locus of *Aeromonas simiae* A6 CP040449), P013-P016 region that shares nt identity with the FE240_17970, FE240_17975, FE240_17980 and FE240_17985 loci of *Aeromonas simiae* A6, followed by the FE240_17990 locus of *Aeromonas simiae* A6 encoding a permease; A023-A024 region shares nt identity with the Sputw3181_4076 locus of *Shewanella* sp. W3-18-1 (CP000503); insertion of an ISVcb4-like element in A026.

AG11 (AGII-B) *Vibrio cholerae* V060002 (AP018677): deletion between A007 and A009 leading to the loss of A008; deletion of part of A025, and A026-res due to insertion of the MDR region.

AG12 (AGII-A) *Enterobacter hormaechei* EelC2185 (MI545561): deletion between A007 and A009 leading to the loss of A008; deletion of part of A025, and A026-res due to insertion of the MDR region.

AG12 *Vibrio cholerae* 133-73 (JDKK01000013): deletion between A007 and A009 leading to the loss of A008; deletion of part of A025, and A026-res due to insertion of the MDR region.

AG13 *Vibrio cholerae* 4874 (NOJL01000025/29/33): A015-A018 region shares nt identity with the FE240_17965 locus of *Aeromonas simiae* A6 CP040449), P013-P016 region that shares nt identity with the FE240_17970, FE240_17975, FE240_17980 and FE240_17985 loci of *Aeromonas simiae* A6, followed by the FE240_17990}
locus of *Aeromonas simiae* A6 encoding a permease; **A023-A024** region shares nt identity with the Sputw3181_4076 locus of *Shewanella* sp. W3-18-1 (CP000503).

*Proteus mirabilis* PmBR607 (CP049753): deletion between **A007 and A009** leading to the loss of **A008; A023-res** region shares nt identity with P021-res including ORFs encoding a subtilisin and an ATPase. **SGI1-RE** carrying **blaCTX-M-2**.

**(2E)** Alignment of SGI1-REs of the cluster 5 with the SGI1-RE5sW3-18-1 backbone.

SGI1-RE5sW3-18-1 *Shewanella* sp W3-18-1 (CP000503): (as a reference); ORFs and genes encoding proteins of known function: **Sh001** (intG) (integrate), **Sh002** (xis) (excisionase), **Sh003** (rep) (replication protein), **Sh004** (helix-turn-helix domain-containing protein), **Sh005** (traN) (conjugal transfer protein), **Sh006** (sgaC) (flagellar transcriptional activator subunit C), **Sh007** (sgaD) (flagellar transcriptional activator subunit D), **Sh011** (traG) (conjugal transfer protein), **Sh012** (traH) (conjugal transfer protein), **Sh019** (mpsB) (mobilization protein MpsB), **Sh020** (mpsA) (mobilization protein MpsA), **Sh024** (BsuB1-Psr1 restriction endonuclease family protein), **Sh025** (N-6 DNA methylase), **Sh026** (resolvase), absence of MDR region.

*Shewanella algae* 150735_CP068229: shorter intergenic region between **Sh018 and Sh019**.

*Shewanella* sp DC2-4 (JABRYR010000002): region between **Sh014 and Sh016** shares nt identity with P012-P014; shorter **Sh021-Sh022** region; **Sh027** region corresponds to an ORF encoding an AAA family ATPase; absence of MDR region.

*Vibrio parahaemolyticus* A1EZ952 (LRTI010000059): shorter intergenic region between **Sh014 and Sh015**; **Sh024-Sh026** region corresponds to 3 ORFs encoding an XcyI family restriction endonuclease, a site-specific DNA-methyltransferase and a resolvase; absence of MDR region.

*Shewanella* sp CG-4-9-14-0-8 (PFTI01000029): (shorter intergenic region between **Sh014 and Sh015**; shorter **Sh021-Sh022** region; absence of MDR region.

*Shewanella vesiculosa* CG_2015-06_42_33 (JAACRN010000013): shorter intergenic region between **Sh014 and Sh015**; shorter **Sh021-Sh022** region; absence of MDR region.

*Shewanella frigidimarina* CG_2015-04_42_94 (JAACRB010000031): shorter intergenic region between **Sh014 and Sh015**; shorter **Sh021-Sh022** region; absence of MDR region.

*Shewanella vesiculosa* CG_2015-09_42_97 (JAACSM010000021/26): shorter **Sh007** region; shorter intergenic region between **Sh014 and Sh015**; shorter **Sh021-Sh022** region; absence of MDR region.

*Vibrio cholerae* VN-2808 (MCBB0100198/211/210/160): insertion of an IS4 element between **Sh002 and rep**; central region of **traN** shares nt identity with P004 (**traN**); insertion of an IS5 element in **Sh009**; region between **Sh013 and Sh015** corresponds to the insertion of an IS66 element and an ORF encoding a restriction endonuclease; shorter region **Sh021-Sh022; Sh023-res** region corresponds to 2 ORFs encoding an YkgJ family cysteine cluster protein and a type II toxin-antitoxin system PemK/MazF family toxin; absence of **res**; absence of MDR region.
(2F) Alignment of SGII-REs of the clusters 6 and 7 with the SGII-RE6tCC-PW-9 backbone.

**SGII-RE6tCC-PW-9** *Idiomarina tyrosinivorans* CC-PW-9 (PIQH01000002): (as a reference); ORFs and genes encoding proteins of known function: **1001** (*intaq*) (integrase), **1002** (*xis*) (excisionase), **1003** (*rep*) (replication protein), **1004** (helix-turn-helix domain-containing protein), **1005** (*traN*) (conjugal transfer protein), **1006** (*sgaC*) (flagellar transcriptional activator subunit C), **1007** (*sgaD*) (flagellar transcriptional activator subunit D), **1011** (*traG*) (conjugal transfer protein), **1019** (*mpsB*) (mobilization protein MpsB), **1020** (*mpsA*) (mobilization protein MpsA), **1024** (*BsuB1-Pst1 restriction endonuclease family protein), **1025** (N-6 DNA methylase), **1026** (res) (resolvase).

*Marinobacter lutaoensis* T5054 (MSCW01000004): 1023-1025 region corresponds to 4 ORFs encoding a magnesium/cobalt transporter CorA, a FAD: protein FMN transferase, a calcium/sodium antiporter, and an undecaprenyl-diphosphate phosphatase; absence of MDR region.

*Idiomarina* sp. REDSEA-S21_B4 (LUNZ01000035/12): 1023 region corresponds to an IS3 element; 1027 region corresponds to 2 ORFs encoding a chromate efflux transporter and a helix-turn-helix transcriptional regulator; absence of MDR region.

*Halomonas meridiana* Eplume2 (AP022869): insertion of an IS1380 element between *traN* and 1006; 1023 region corresponds to an ORF encoding an AAA family ATPase; 1027 region shares nt identity with S044; absence of MDR region.

SGI1-RE7MaKG14 *Marinobacter adhaerens* KG14 (JABEVQ010000005/1) (cluster 7): insertion of an IS element of the IS66 family with an ORF encoding a manganese efflux pump in the region between 1002 and rep; no significant similarity for the 1013-1014 region; 1023-1027 region corresponds to 4 ORFs encoding an AAA family ATPase, a DNA mismatch endonuclease Vsr, a DUF4928 family protein, and a DNA (cytosine-5-)methyltransferase; absence of res; absence of MDR region.

*Marinobacter* sp. SAT109 (PAYG01000030/41) (cluster 7): shorter region between 1009 and *traG*; 1023-1027 region corresponds to 4 ORFs encoding an AAA family ATPase truncated by an ISL3 element, a DNA mismatch endonuclease Vsr, a DUF4928 family protein, a DNA (cytosine-5-)methyltransferase; absence of res; absence of MDR region.

*Pseudohongiella nitratireducens* SCS-111 (LWHN01000034/30/29): insertion of an ISL3-like element between 1002 and rep; insertion of an ISL3-like element in 1006; no significant similarity for the 1013-1014 region; 1023 region corresponds to an ORF encoding an AAA family ATPase; 1027 region shares nt identity with S044; absence of MDR region.

*Pseudohongiella nitratireducens* CGMCC 1.15425 (BMIY01000006): insertion of an ISL3-like element between 1002 and rep; insertion of an ISL3-like element in 1006; no significant similarity for the 1013-1014 region; 1023 region corresponds to an ORF encoding an AAA family ATPase; 1027 region shares nt identity with S044; absence of MDR region.
Supplementary Figures 3. BLAST alignment of the first part of the SGI1-RE backbones (attL-oriT segment).

The colors of the strains correspond to the clusters of SGI1-REs: red (cluster 1: SGI1 cluster), green (cluster 2: PGI1 cluster), blue (cluster 3: PGI2 cluster), purple (cluster 4: AGI1 cluster), brown (cluster 5). The characterized SGI1-REs are underlined. The ORFs of the query sequence are represented. The following colors are used for ORFs of known function:

- **DNA recombination (int, xis)**
- **DNA replication (rep)**
- **Transcriptional activator**
- **Mobilization gene (mps)**
- **Transcriptional regulator**
- **DNA replication, recombination, and repair (helicase)**
- **Unknown function**

The green angled arrows indicate AcaCD binding sites, and the red arrow indicates oriT. The black vertical line represents attL or attR attachment sites.

**(3A) Alignment with the alpA-oriT segment of Aeromonas veronii CB51 (CP015448).**

**(3B) Alignment with the alpA-oriT segment of Aeromonas simiae A6 (CP040449).**
(3C) Alignment with the first part of PGI1 backbone.
Supplementary Figures 4. BLAST alignment of the second part of the SGI1-RE backbones (oriT-attrR segment) with the ORFs of known SGI1-REs.

The colors of the strains correspond to the clusters of SGI1-REs: red (cluster1: SGI1 cluster), green (cluster 2: PGI1 cluster), blue (cluster 3: PGI2 cluster), purple (cluster 4: AGI1 cluster), brown (cluster 5), black (cluster 6). The characterized SGI1-REs are underlined. The ORFs of the query sequence are represented. The following colors are used for ORFs of known function:

- **Toxin-antitoxin system (subtilisin-ATPase)**
- **DNA replication, recombination, and repair (helicase-endonuclease (yDJ)**
- **DNA restriction/modification**
- **Unknown function**

**4A** Alignment with the Sputw3181_4076 locus of *Shewanella* sp W3-18-1 (CP000503).

**4B** Alignment with S025-S026 (*sgiT-sgiA*) (encoding a subtilisin and an ATPase: TA).
(4C) Alignment with S023-S024 (uvrD-ybjD) (encoding a helicase and an endonuclease).

(4D) Alignment with A025-A026 (encoding a BstB1-PstI restriction endonuclease and an N-6 DNA methylase).

(4E) Alignment with A023-A024.
Supplementary Figures 5. BLAST alignment of the unusual ORFs of the second part of the SGI1-RE backbones (oriT-attR segment) with all SGI1-REs.

The colors of the strains correspond to the clusters of SGI1-REs: red (cluster1: SGI1 cluster), green (cluster 2: PGI1 cluster), blue (cluster 3: PGI2 cluster), brown (cluster 5). The ORFs of the query sequence are represented. The following colors are used for ORFs of known function:

- Resolvase
- DNA replication, recombination, and repair (helicase)
- DNA restriction/modification
- Unknown function

(5A) Alignment with the ORFs encoding a DNA-helicase, a macro domain-containing protein, two DUF4433 domain-containing proteins and a resolvase of *S. Infantis* 355107 (AAMIAE010000014).

(5B) Alignment with the ORFs encoding a *BsuB1*-Pst1 restriction endonuclease, an *Eco57I* restriction-modification methylase and a resolvase of IMEVmSCCF01 from *Vibrio mimicus* SCCF01 (CP016383).

(5C) Alignment with the ORFs encoding an XcyI restriction endonuclease, a DNA-methyltransferase, and a resolvase of *Vibrio cholerae* N2786 (VSHP01000003).
Supplementary Figure 6. Weblogo of the attL and attR attachment sites.

Supplementary Figure 7. Weblogo of the AcaCD binding sites.