Supplemental Fig. 1. Alignment of recombinases:

E. coli	XerD	AAC75932; 1A0P
B. anthracis	IntXO	GBAA_RS29165; GBAA_pXO1_182
B. anthracis	XerD	GBAA_RS20945; GBAA_4311
B. anthracis	XerC	GBAA_RS19275; GBAA_3969
B. anthracis	XerS	GBAA_RS29235; GBAA_pXO1_200
P1 phage	Cre	YP_006472.1
S. cerevisiae	Flp	AKA10108.1

The sequences of the proteins listed above are aligned below in the same order as listed. The active site residues identified for IntXO recombinase (second line below) in Fig.3D are highlighted below in red, where the stars (*) mark these as 4 of the 6 fully conserved residues: IntXO R-186, H-292, R-295 and Y-327

```
XerD      --------------------------------QD----------LARIEQFL-DALWLEK      17
IntXO     -MNIINYEHNNQLVKSKSDFFDSSHFEKIMGMGIRNIDYSQLSEGSLVYLFLHDEPSLTK      59
XerD      ---------------------------------M----------EDQLKDFI-HYMVVEK      16
XerC      -------------------------------MNV----------KKLLQLFV-GYLQIER      18
XerS      ------------MSN-----QEKEKFKILIDKHK----------SKMPWYII-EYAEMKT      32
Cre       MSNLLTVHQNL--PALPVDATSDEVRKNLMDMF-----------------------RDRQ      35
Flp       ------------MPQ----------FDILCKTP----------PKVLVRQFVERF----E      24


XerD      NLAENTLNAYRRDLSMMVEWLHHRGLTLATA-Q-----------------SDDLQA--LL      57
IntXO     KRSERTKKLYLHDLSHFLRYIKETIGI------------------IKELSHNEMEI--YF      99
XerD      GLAKNTVVSYERDLKSYVKYLQKVEQAKSFH-E---------------VTRLHIVN--FL      58
XerC      NYSKYTIASYQNDLEHFVQFMEREGIS-SFL-D---------------ITYADVRL--YL      59
XerS      ALSPATLYAYITEFEKFLKWLISNRLAVENG-KVVTNICDVPISTLENLPLNEART--FQ      89
Cre       AFSEHTWKMLLSVCRSWAAWC------------------KLNNRKWFPAEPEDVRD--YL      75
Flp       RPSGE-KIALCAAELTYLCWMITHNGTAIKRATFMSYNTIISN----SLSLDIVNKSLQF      79
            :                :

XerD      AERLEGG-YKATSSAR-------------------LLSAVRRLFQYLYREKFREDDPSAH      97
IntXO     -YQLSKK-YAATTLRR-------------------KKTVVQQFLKYVYDNNGLSDNFSSR      138
XerD      QHLKENG-KSSKTLAR-------------------HIASIRSFHQFLLRERAVEHDPSVH      98
XerC      TTLHDEK-LARKSVAR-------------------KVSSLRSLYRFLMREGYRKDNPFAL      99
XerS      RYLQGEG-IETRAINR-------------------TFSALKSLFKYLAQNTENEQGENYI      129
Cre       LYLQARG-LAVKTIQQ-------------------HLGQLNMLHRRSGLPRPSDSNAVSL      115
Flp       KYKTQKATILEASLKKLIPAWEFTIIPYYGQKHQSDITDIVSSLQLQFESSEEADKGNSH      139
                      :  :                       :    :

XerD      -------L--------------------ASPKLPQRLPKDLSEAQVERLLQAPLID----      126
IntXO     LKK----V---------------------SVKKEELVNRDLFPEEVNEILDTLKKTNF--      171
XerD      -------I--------------------ETPQGERKLPKVLSVDEVEALLQTPKMT----      127
XerC      -------A--------------------SLPKKELSIPKFLYAEELEELFEVSDTE----      128
XerS      SRNVMDKIELHKEKVDAAARADDVANMIFNEKDDVAFLQFLANDYGEMLKDISPKKYS--      187
Cre       ---VMRRI--RKENVDAGERAK----------QALAFERT-DFDQVRSLMENSD------      153
Flp       SKKMLKAL----------------------------------LSEGESIWEITEKILNSF      165
                                                        . : :

XerD      ---QPLELRDKAMLEVLYATG---LRVSELVGLTMSDISLR----QGVVR----------      166
IntXO     --------FMYSLFFLLTTTG---LRIEEVANAKWADLVFHPSLNVYLLR----------      210
XerD      ---SAFGVRDKAMLELLYATG---LRVSELIALNLEDVHLT----MGFVR----------      167
XerC      ---TPLGQRNQALLELMYATG---IRVSECVNLQLTDIDFA----VGTIL----------      168
XerS      -FFQRDKERDIAIISLILGTG---LRVSEVASLTISSINFR----QGKVK----------      229
Cre       ---RCQDIRNLAFLGIAYNTL---LRIAEIARIRVKDISRT----DGGRM----------      193
Flp       EYTSRFTKTKTLYQFLFLATFINCGRFSDIKNVDPKSFKLVQNKYLGVIIQCLVTETKTS      225
                         :   *     *. :       ..

XerD      -------VIGKGNKERLVPLGEEAVYWLETYLEHGR-----PWLLNGV--S--IDVLFPS      210
IntXO     -------VVGKGNKTREVRIFEDVLNDLCHLRQLRK-----QKSELDA--S-SSSAFLPK      255
XerD      -------CVGKGNKERIIPLGSLATEAIQKYIEKGR-----RELMGKK--V--VDALFLN      211
XerC      -------VMGKGKKQRYIPFGSYAQDALITYIENGR-----KQLAEKT--EEQSHMVFLN      214
XerS      -------VTRKGNKRSSVLATRSCLDDVQEYIKVRP-----SKYNCPQ----DEDLLFVT      273
Cre       -------LIHIGRTKTLVSTAG-----VEKALSLGVTKLVERWISVSGVADDPNNYLFCR      241
Flp       VSRHIYFFSARGRIDPLVYLDE--------FLRNSE-------------------PVLKR      258
                     *.    :                                      .:

XerD      QRAQ----------QMTRQTF-----WHRIKHY-------AVLAGID-SEKLSPHVLRHA      247
IntXO     ADGS----------HYRADYLSKYVAEKIEETN-------LPFLRYR-KHRITPHTCRHF      297
XerD      HHGN----------RLSRQGF-----WKILKRL-------AKEANIE--KELTPHTLRHS      247
XerC      AKGT----------PLTSRGV-----RYVLNEL-------IKKASLT--MRISPHILRHT      250
XerS      NYKG----------KYTQLTV-----RAIQKLC-------DKYSSAF-DEKRSPHKLRHT      310
Cre       VRKNGVA-APSATSQLSTRAL-----EGIFEATHRLIYGAKDDSGQR-YLAWSGHSARVG      294
Flp       VNRTGNSSSNKQEYQLLKDNLV----RSYNKAL----KKNAPYSIFAIKNGPKSHIGRHL      310
                              .         :                     . *  *
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XerD      FATHLLNHGADLRVVQMLL-GHSDLST----TQIYTHVATERLRQLHQ------------      290
IntXO     FANHLMGKGVELKKIRDYL-GHESIMT----TERYLRERTRRQNLATIDIGNSLF-----      347
XerD      FATHLLENGADLRAVQEML-GHADIST----TQIYTHVSKTRLKDVYKQFHPRA------      296
XerC      FATHMLDEGADLRTVQELL-GHENLST----TQIYTHVSKERLRSVYMKHHPRA------      299
XerS      YATNHYKENKDLVLLRDQL-GHTSVEV----TSIYTNINNEKKREAVDRLERRQFE----      361
Cre       AARDMARAGVSIPEIMQAG-GWTNVNI----VMNYIRNLDSETGAMVRLLEDGD------      343
Flp       MTSFLSMKGL--TELTNVVGNWSDKRASAVARTTYTHQITAIPDH-YFALVSRYYAYDPI      367
           :            :        .          * .

XerD      -------------------------------------------------------- 290
IntXO     -------------------------------------------------------- 347
XerD      -------------------------------------------------------- 296
XerC      -------------------------------------------------------- 299
XerS      -------------------------------------------------------- 361
Cre       -------------------------------------------------------- 343
Flp       SKEMIALKDETNPIEEWQHIEQLKGSAEGSIRYPAWNGIISQEVLDYLSSYINRRI 423
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Supplementary Table 1. List of genes discussed in this work

Gene					Protein	
Gene name	Description or function	Locus tag	Old or alternative locus tag	Source	Protein size (aa)	Protein sequence, N- and C-termini; protein accession code
Partition system components, etc.						
orf 20	minireplicon	GBAA_RS28535	GBAA_pXO1_0020	*B. anthracis*	564	MEKL…VNLL WP_000413217
orf 23	minireplicon	GBAA_RS28545	GBAA_pXO1_0023	*B. anthracis*	569	MGKS…MEIK WP_000520265
amsP	MSI	GBAA_RS28725	GBAA_pXO1_0069	*B. anthracis*	201	MIDE…FGKK WP_000564672
minP	MSI	GBAA_RS28775	GBAA_pXO1_0082	*B. anthracis*	61	MDIL…SKKK WP_000353184
sojP	MSI (ParA)	GBAA_RS28785	GBAA_pXO1_0084	*B. anthracis*	272	MDRP…GLRN WP_000375827
tubZ	MSII (TubZ/RepX)	GBAA_RS28715	GBAA_pXO1_0067	*B. anthracis*	435	MAGN…KLSF WP_000918302
tubR	MSII (TubR)	GBAA_RS28720	GBAA_pXO1_0068	*B. anthracis*	91	MSNN…EKNN WP_002194758
esat6-like	Unknown	GBAA_RS29195	GBAA_pXO1_0190	*B. anthracis*	410	MSTQ…DSDK WP_000107153
Tyrosine recombinases						
intXO	MSII	GBAA_RS29165	GBAA_pXO1_0182	*B. anthracis*	317	MGIR….NSLF WP_010890022
intXO	MSII	GBAA_RS29165	GBAA_pXO1_0182	*B. anthracis*	347	MNII…NSLF WP_001021546
xerS	Unknown	GBAA_RS29235	GBAA_pXO1_0200	*B. anthracis*	361	MSNQ…RQFE WP_000070475
xerC	Chromosome partition	GBAA_RS19275	GBAA3969	*B. anthracis*	299	MNVK…HPRA WP_001101226
xerD	Chromosome partition	GBAA_RS20945	GBAA4311	*B. anthracis*	296	MEDQ…HPRA WP_000390080
xerD	Chromosome partition	AAC75932	PDB: 1A0P	*E. coli*	298	MKQD…HPRA WP_000806638
cre	Phage replication	P1_gp003		P1 phage	343	MNSL…EDGD YP_006472.1
flp	Plasmid replication	R0010W		*S. cerevisiae*	423	MPQF…NRRI AKA10108.1

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