

Transposons Currently in Use in Genetic Analysis of *Salmonella* Species

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INTRODUCTION

This chapter discusses the uses of transposons in genetic analysis, with emphasis on work done in *Salmonella typhimurium* (official designation, *Salmonella enterica* serovar Typhimurium) and on the methods available for use in *Salmonella* spp. Many of these methods, however, can be applied to other genera as well.

TYPES OF TRANSPOSONS

The values of transposable elements for genetic analysis have been amply described elsewhere (2, 10, 15, 16). As these elements have become more widely used, the array of variants developed for specific purposes has increased. Below, we list and describe some of the attributes of the transposons that we have found most useful. We then describe current methods for making insertion mutations with these elements.

Derivatives of Tn10

Although the Tn10 element has been widely used in its original, unmodified form, it is being increasingly superseded by a variety of elements that have the advantages of smaller size and the stability that is achieved by removal of transposase activity. The original Tn10 element (9.3 kb) includes flanking copies of IS10 that are capable of independent transposition. Although transposition of the entire transposon is not a problem for genetic analysis, the insertion sequence (IS) elements transpose extremely frequently and cause a significant elevation of mutation frequencies (21, 24). A second disadvantage of the original Tn10 is seen when deletions are sought using the Bochner selection (3). The large terminal repeats are prone to “imprecise excision,” which leads to loss of tetracycline resistance but leaves small segments of the element at the insertion sites. These “imprecise excisants” must be screened through when one is searching for deletions that extend outside of the element into adjacent chromosomal sequences. The smaller element Tn10d-Tet (see below) is not subject to this imprecise excision, and thus, a much higher fraction of clones surviving the Bochner selection are true deletions which extend into the adjacent chromosome. Below, we describe a series of Tn10 derivatives that are in current use.

Tn10d-Tet. Tn10d-Tet is 2.9 kb in size. It differs from the original element by two deletion mutations, each of which removes the bulk of one of the IS10 elements and extends into the central, single-copy region (9). The modified element does not make transposase but has 70 bp of inverse-order IS10 sequence repeated at each end, thus providing sites at which transposase can act (9, 25). Although transposase must be provided to achieve transposition, insertion mutations are completely stable in the absence of an external source of transposase.

Recently, it was observed that the divergent promoters of the tetracycline resistance determinants direct regulated transcripts from both ends of the inserted element into the adjacent chromosomal region (23). This fact has not yet been routinely exploited but shows promise of being widely applicable.

Tn10d-Kan, Tn10d-Cam, Tn10d-Gen. The Tn10d-Kan, Tn10d-Cam, and Tn10d-Gen elements are similar to Tn10d-Tet and contain the terminal 70-bp ends of the original Tn10 element. Each has a different drug resistance determinant placed between these flanking repeats. While Tn10d-Kan (1.8 kb, kanamycin resistance) and Tn10d-Cam (1.5 kb, chloramphenicol resistance) have been used for some time (8, 25), the last element, Tn10d-Gen (2.0 kb, gentamicin resistance), was constructed only recently by Higgins et al. (P. Higgins, X. Yang, Q. Fu, and J. Roth, submitted for publication) and adds a new resistance to the list of available drug markers.

Tn10d-Cam/Gen. Tn10d-Cam/Gen, which also was constructed by Higgins (Higgins et al., submitted for publication), is identical to the Tn10d-Cam described above except that a gentamicin resistance determinant has been inserted in the middle of the coding sequence of the chloramphenicol resistance gene. This element, which is 3.4 kb in size, confers only gentamicin resistance. Its value is that it can be used as a donor to convert the resistance of any existing Tn10d-Cam insertion mutation from Cam^r to Gen^r.

Generating Mutations with Tn10 Derivatives. We found that the new low-specificity transposase mutant of Kleckner and coworkers, which is carried on pNK2881, provides an excellent way of isolating new insertion mutations with less tendency to populate the “hot spots” favored by the original Tn10 (15). We make mutations by a transduction cross (using P22) in which the donor carries the defective element on an F' *pro lac* plasmid derived from *Escherichia coli*. The recipient carries plasmid pNK2881, which expresses the low-specificity transposase. Selection is for the relevant drug resistance. Since the donor element is inserted in material that has no homolog in the recipient, there is no inheritance by recombination. Each transductant requires an act of transposition of the defective element from the transduced fragment into the recipient chromosome. We generally pool these resistant transductants, grow P22 on the pool, and use this pool to transduce individual insertion mutations into a clean genetic background before screening for mutations of interest. Donor strains useful for these procedures are TT10423 *proAB47/F' pro⁺ lac⁺ zzf-1831::Tn10d-Tet*, TT17394 *proAB47/F' pro⁺ lac⁺ zzf-3734::Tn10d-Kan*, TT10605 *proAB47/F' pro⁺ lac⁺ zzf-1837::Tn10d-Cam*, NH2048 *proA36 strA1/F' pro⁺ lac⁺ Tn10d-Gen*, and NH2030 *metA22 metE551 trpD2 ilv-452 galE leu pro strA120 hsdLT6 hsdSA29 hsdB/pPH620* (this strain contains Tn10d-Cam/Gen on an Amp^r plasmid instead of on the F' *pro⁺ lac⁺* plasmid). A useful recipient strain is TT17437 (LT2)/pNK2881 (Amp^r).

In order to avoid lysogenization, it is important to use a high-transducing, low-integrating mutant of P22 (such as P22HT105/int-1) when lysates are being formed.

Use of Tn10 Elements for PCR Priming Sites. The elements described above are extremely useful in conjunction with PCR amplification. This technique can be used to clone the region between inserted elements and to physically map the elements in a known sequence. Listed below are oligonucleotide primers we have found to work well with Tn10 derivatives (P. Chen, M. Ailion, T. Bobik, G. Stormo, and J. Roth, submitted for publication).

Universal (outward directed). The universal primer sequence is just within the inverse (70-bp) repeats found at both ends of all of the Tn10 derivatives described above. It is directed outward, so PCR reactions primed by this oligonucleotide proceed out of the element into adjacent chromosomal sequences. The sequence is 5' GACAAGATGTGTATCCACCTTAAC 3'.

Unique (left end). The unique (left-end) primer is unique to the left end of the Tn10d-Tet element. It primes replication that extends out of the end of the element where the *tetA* gene (tetracycline resistance) is located. Replication proceeds in the same direction as transcription of *tetA*. The sequence is 5' ACCTTTGGTCACCAACGCTTTTCC 3'.

Unique (right end). The unique (right-end) primer is unique to the right end of the Tn10d-Tet element. It primes replication that extends out of the end of the element where the *tetR* gene (repressor of *tetA*) is located. Replication proceeds in the same direction as transcription of *tetR*. The sequence is 5' TCCATTGCTGTTGACAAAGGGAAT 3'.

Derivatives of Phage Mu.

Most of the derivatives of Mu elements were constructed by Malcolm Casadaban and coworkers. The elements were designed to be delivered by Mu virions using wild-type Mu helper phages. Most include a *lac* operon without a promoter and are designed to form fusions of the included *lac* operon to a promoter located near the target site in the bacterial chromosome. As described below, some elements lack both a promoter and a translation start site, so they express *lac* only if they fuse the *lacZ* gene to an expressed chromosomal open reading frame.

MudI (37.2 kb, Operon Fusions) and MudII (35.6 kb, Gene Fusions). MudI and MudII are Casadaban's original constructions; they form operon fusions and gene fusions, respectively (4, 5). The elements are transposition proficient and are induced by high temperature to form complete phages.

MudA (37.2 kb, Operon Fusions) and MudB (35.6 kb, Gene Fusions). MudA and MudB are derivatives of the original Amp^r constructions which have been made transposition defective by the addition of two amber mutations (12). Both are stable in strains lacking an amber suppressor but are made transposition proficient by the presence of a suppressor. Each element is 36 to 37 kb and thus can be transduced only rarely by a P22 virion (44 kb). At high transducing phage multiplicities, these elements can be transduced by two cooperating P22 phages (13).

MudJ (11.3 kb, Operon Fusions) and MudK (9.7 kb, Gene Fusions). MudJ and MudK are the original Kan^r mini-Mud constructions of Casadaban and coworkers (6). They contain deletions of the transposase functions and thus are incapable of transposing without an outside source of transposase.

MudF (14.0 kb, Lac⁺ without Fusions). MudF confers Kan^r and contains a complete *lac* operon, including the *lacI* gene (22). It gives a Lac⁺ phenotype no matter where it inserts. This element provides a useful way of making any *Salmonella* strain Lac⁺ with a wild-type, inducible *lac* operon.

MudCam (2.9 kb, a Simple Drug Resistance Element). MudCam includes no *lac* sequences and contains only a simple drug resistance determinant placed between the ends of phage Mu (7). It can be used as an independent transposable element for making mutations and has special value as a vector for placing a simple drug resistance insertion at the site of a known *lac* fusion insertion. Because this element shares sufficient homology with the ends of MudA, MudB, MudF, MudJ, and MudK, it can be used as a donor in transduction crosses in which the selected Cam^r marker replaces the *lac* and Kan^r (or Amp^r) sequences of the other elements. It should be possible, in principle, to use this element as an intermediate in converting a gene fusion insertion to an operon fusion insertion (to our knowledge, this has not yet been done).

MudSac (5.4 kb, a Counterselectable Kan^r Mini-Mud). MudSac was constructed by M. Lawes and S. Maloy (submitted for publication) for use with the Mud-P22 chromosome mapping method of Benson and Goldman (1). The element is transposition defective and includes the *Bacillus subtilis sacB* (secretory levansucrase) gene, which makes cells sensitive to sucrose. Transpositions of this element are generated via standard techniques (see below) by selecting for insertion mutations that inherit Kan^r. Because MudSac insertions can be counterselected on sucrose, their map positions can be easily determined using Mud-P22 mapping techniques. The MudSac element should also prove to be useful for generating deletions near the

insertion site since one can select for spontaneous sucrose-resistant derivatives of the insertion mutation.

Isolating Insertions of Transposition-Defective Mud Elements. We have found that “transitory *cis* complementation” is a convenient way of providing transposase to the defective elements described above (14). This procedure involves the use of strains that contain the defective element inserted in the bacterial chromosome adjacent to a transposition-proficient MudI prophage. The insertions are placed so that the end of the MudI prophage including the transposition functions is closest to the defective element. When P22 phage is grown on such a strain, the transducing virions that happen to package the defective element frequently include the transposition functions of the adjacent proficient prophage. Because of the sizes of the Mu phages, it is not possible for a single P22 particle (44 kb) to include both the defective prophage and the complete helper genome (37 kb).

The lysate is used to transduce a recipient strain selecting for inheritance of the drug resistance encoded by the defective element. The transduced fragment expresses transposition functions (from the proficient element) which allow the defective element to transpose to the recipient chromosome. This method is particularly effective because the Mu transposase functions tend to act preferentially in *cis*. The appropriate strains for this procedure are TT10288 *hisA9944::MudI hisD9953::MudJ*, TT10381 *hisA9944::MudI hsiD1284::MudK*, TT16528 *hisA9944::MudI hisD9953::MudCam*, TT18310 *hisA9944::MudI hisC10081::MudF*, and MST3281 *hisA9944::MudI his::MudSacI*.

PCR Primers for Mu Ends. The following primers were designed for stimulating PCR reactions from the ends of all Mu-derived elements described above (Chen et al., submitted): for the left end, 5' ATCCCGAATAATCCAATGTCC 3'; for the right end, 5' GAAACGCTTTCGCGTTTTTCGTGC 3'.

TnPhoA

TnPhoA, a derivative of transposon Tn5, was constructed by C. Manoil and J. Beckwith to detect insertions into genes which code for exported proteins (18). The element is transposition proficient and includes at one end a gene for alkaline phosphatase which lacks a promoter, translation start, and signal sequence. Alkaline phosphatase is normally active only if it can be exported to the periplasm. Thus, in order for the protein encoded by the element to be expressed, the element must insert, in the proper orientation and reading frame, into a gene that has a signal sequence. Such insertion mutants are identified on medium including the chromogenic phosphatase substrate 5-bromo-4-chloro-3-indolyl phosphate (X-P). Use of this element in *Salmonella* spp. requires elimination of the normal acid phosphatase, which can also hydrolyze X-P. Finding insertions of TnPhoA into the chromosome requires screening a large number of insertions, since only rare insertions meet all of the criteria for activity listed above. We have done this screening by using the P22 “locked-in” phages of Youdarian et al. (27). This locked-in prophage is placed near a TnPhoA insertion in the *his* operon. When induced, this prophage packages the adjacent material preferentially, and the lysate includes a high titer of particles that include the TnPhoA element; the donor strain carries a plasmid which overproduces the P22 tail protein, which is normally produced at a low level during induced phage growth. This lysate is used to transduce a recipient lacking acid phosphatase (a *phoN* mutant). Selection for His⁺ is maintained to avoid the high level of recombinants that inherit the donor *his::TnPhoA* element by recombination. Most transductant colonies are white on X-P medium, but rare blue insertions in which the element has inserted into a gene with a signal sequence can be identified (28). The necessary donor strain for this procedure is TT15088 *hisD10088::TnPhoA hisHA9556::MudP/pPB13*. The recipient strain is any strain with a *phoN* mutation; the insertion *phoN51::Tn10d-Tet* (e.g., TT13216) can be transduced into the desired strains.

MudP and MudQ (Transposable Locked-In P22 Prophages)

MudP and MudQ permit one to place a “P22 prophage” at virtually any site in the chromosome. Since the prophage lacks P22 attachment sites, induction stimulates the phage to replicate and package DNA processively out of the prophage and into the adjacent bacterial chromosome in a unidirectional manner. This results in a lysate that is very highly enriched for transducing particles that include DNA from a very small region of the chromosome (27). These lysates provide a rich source of DNA which is useful for both cloning and high-frequency transduction of markers in that region. These phages have been used to create a new method for mapping mutations in the *Salmonella* chromosome (1).

MudP and MudQ elements are essentially P22 prophages lacking the attachment site and flanked by the ends of phage Mu; a chloramphenicol resistance determinant is included between the Mu ends. The two phages differ in the orientation of the P22 sequences between the Mu ends. The element transposes as a unit when Mu transposition functions are provided; thus, the entire element can be inserted at any site into which Mu transposition is possible. Alternatively, the MudP and MudQ elements can be transduced into a recipient strain carrying a known Mud element (either the original MudI element or any of the standard mini-Mu elements). The MudP or MudQ element then recombines with the recipient element by using the flanking Mu sequences as regions of homology. This results in the replacement of the recipient element with MudP or MudQ.

The chromosomal mapping method based on these phages employs a set of strains that contain mapped MudP or MudQ prophages. Lysates of these strains are used in spot transduction tests to repair the mutation that is to be mapped. If the unknown mutation is not counterselectable, a *Tn10* insertion in or near the mutant gene can be used in conjunction with the Bochner method of counterselecting tetracycline-resistant strains to permit selective repair by the donor locked-in lysates (3). Since the donor lysates are enriched for only several minutes of chromosome, high-frequency (about 200 kb according to some estimates [17]) repair of the recipient mutation by one or more of the donor mapping strains allows one to determine the chromosomal position of the unknown mutation to within a few map minutes.

Donor strains useful in transductional conversion of a recipient Mud element to a MudP or a MudQ prophage are the following: TT12915 (=PY13518) *leuA414*(Am) r^-m^+ (Fels2⁻)/F'114*ts lac*⁺ *zzf-20::Tn10 zzf-3551::MudP* and TT12916 (=PY13757) *leuA414*(Am) r^-m^+ (Fels2⁻)/F'114*ts lac*⁺ *zzf-20::Tn10 zzf-3553::MudQ*.

A set of 30 strains in current use for mapping (known affectionately as the “First String Mud-P22 Collection” [N. Benson, personal communication]) is listed in Table 1.

TRANSPOSON-INDUCED MUTATIONS IN *S. TYPHIMURIUM*

Transposon-induced mutations have been isolated in *S. typhimurium* by many investigators as part of a wide range of studies. Most have been isolated by the techniques described above. We present a list of strains of *S. typhimurium* which carry insertions of transposons of several different types (Table 2). The strains of *S. typhimurium* which carry these transposon insertions along with linkage data as to the exact chromosomal locations of the insertions were generously provided to the Salmonella Genetic Stock Center (SGSC) by many different investigators. Table 2 is an update of a previously published table (19). Many of these strains were also listed by Berg and Berg (2).

These strains are listed in the order of the map location of the transposon insertion, with *thr* used as the starting point. These locations have been determined by several techniques. Most have been located next to specific genes by P22 transduction; the distance (in kilobases) from the transposon insertion to the known gene or the distance between two different transposons can be calculated from transduction data with the formula of Wu (26) as modified to take account of the size of the transposon (19). Some *Tn10* insertions have been located on the chromosome by using the rapid mapping method developed by Benson and Goldman with MudP22

(1). *Tn10* has sites for the rarely cutting endonucleases *XbaI* and *BlnI*; locations of *Tn10* insertions on the chromosomal genomic cleavage maps for these enzymes were determined by using pulsed-field gel electrophoresis (17, 20).

TABLE 1 "First String Mud-P22 Collection"^{aa}

TT no.	Strain no. in kit	Point of insertion (min)	Genotype of Mud-P22 insertion	Direction of packaging from insertion site ^b
15226	2	3.5	<i>nadC218::MudP</i>	A
15230	3	8.5	<i>proC693::MudP</i>	A
15232	4	12.0	<i>purE2154::MudQ</i>	A
15238	5	17.0	<i>nadA219::MudP</i>	A
15239	6	21.5	<i>putA1019::MudQ</i>	A
15243	7	28.5	<i>aroD561::MudQ</i>	B
15246	8	33.0	<i>pyrF2690::MudP</i>	B
15630	9	35.9	<i>tre-152::MudP</i>	A
15250	10	40.5	<i>zea-3666::MudP</i>	B
15249	11	40.5	<i>zea-3666::MudQ</i>	A
15258	12	50.0	<i>cysA1585::MudP</i>	B
15632	13	52.0	<i>guaAB5641::MudQ</i>	A
15255	14	52.0	<i>guaAB5641::MudP</i>	B
15261	15	57.0	<i>proU1884::MudP</i>	A
15628	16	57.0	<i>proU1884::MudQ</i>	B
15263	17	60.0	<i>cysHI1574::MudP</i>	B
16707	18	62.7	<i>zgc-3715::Mud Q</i>	B
16709	19	65.0	<i>zgf-3716::MudQ</i>	B
17191	20	68.5	<i>zgi-3717::MudQ</i>	B
17190	21	68.5	<i>zgi-3717::MudP</i>	A
17165	22	73.6	<i>envZ1005::MudQ</i>	A
15265	23	73.6	<i>envZ1005::MudP</i>	B
15267	24	79.7	<i>pyrE2419::MudP</i>	A
15269	25	83.0	<i>ilvA2648::MudP</i>	A
15273	26	86.7	<i>pnuE41::MudQ</i>	A
15272	27	86.7	<i>pnuE41::MudP</i>	B
15276	28	93.0	<i>melAB396::MudP</i>	A
15638	29	97.0	<i>zjh-3725::MudP</i>	A
15633	30	97.0	<i>zjh-3725::MudQ</i>	B

^aSee references 1 and 27.

^bPackaging of DNA into phage heads is clockwise (A) or counterclockwise (B) from the prophage insertion site.

These strains are available to any researcher. Table 2 gives only a limited amount of information on each strain; the complete genotype for any strain can be obtained from the SGSC or from the laboratory in which the strain originated. Requests for information and for strains can be made to the SGSC by telephone (403-220-6792), fax (403-289-9311), or e-mail (kesander@acs.ucalgary.ca). In addition, electronic versions of the strain list can be obtained as follows. A delimited text file and FileMaker Pro (Version 2) database containing complete descriptions of the strains listed in Table 2 are available directly via the University of Calgary Gopher server or by contacting the SGSC. Further details about the structure of the database are described in chapter 136 of this volume. The files can be obtained through Internet as follows: access the University of Calgary Gopher, and then select the following in order: "Faculty and Department information," "Department of Biological Sciences," "Salmonella Genetic Stock Centre." On-line files are updated at regular intervals.

TABLE 2 Strains of *S. typhimurium* LT2 with transposons inserted into the genome^a

CS ^b	Allele no. and linkage ^c	Strain no. ^d
0	<i>thr-447</i> ::Tn5(Kan)	TT2384
0	<i>thr-449</i> ::Tn5(Kan)	TT2752
0	<i>thr-457</i> ::Tn5(Kan)	TT3982
0	<i>thr-458</i> ::MudI1734(Kan)	TL888
0	<i>thr-458</i> ::MudQ(Cam)	TT15222
0	<i>thr-469</i> ::MudA(Amp)	TT8371
0	<i>thr-469</i> ::MudI1734(Kan)	TL886
0	<i>thr-469</i> ::MudJ(Kan)	TT12896
0	<i>thr-469</i> ::MudP(Cam)	TT15223
0	<i>thr-469</i> ::MudQ(Cam)	TT15224
0	<i>thr-471</i> ::Tn10d(Cam)	TT11675
0	<i>thr-472</i> ::MudJ(Kan)	TT12102
0	<i>thr-473</i> ::MudJ(Kan)	TT12103
0	<i>thr-484</i> ::MudA(Amp)	TT13479
0	<i>thr-557</i> ::Tn10(Tet)	TT191
0	<i>thr-557</i> ::Tn10d(Tet) (<i>arcA</i> [93%])	DA3740
0	<i>zaa-1868</i> ::Tn10(Tet) (<i>thr</i> [%ND])	TT11433
1	<i>car-234</i> ::Tn10(Tet)	TT1198
1	<i>car-2413</i> ::Mud1-8(Amp)	TT7901
1	<i>car-2413</i> ::Mud1-8(Amp)	TT12897
1	<i>car-2413</i> ::MudP(Cam)	TT15225
1	<i>car-2705</i> ::MudJ(Kan)	TT12090
1	<i>car-685</i> ::Tn10(Tet)	TT136
1	<i>zab-2011</i> ::Tn10(Tet) (<i>tctIII</i> [44%])	KS1169
1	<i>zab-2012</i> ::Tn10(Tet) (<i>tctIII</i> [58%], <i>car</i> [49%])	KS1170
2	<i>ara-652</i> ::Tn10d(Tet)	TT11556
2	<i>ara-661</i> ::MudJ(Kan)	TT12919
2	<i>ara-669</i> ::MudK(Kan) (<i>ara</i> [89%])	TT16697
2	<i>araB</i> ::Mud1X(Amp)	TN3356
2	<i>araC672</i> ::MudJ(Kan)	TT13479
2	<i>araE660</i> ::Tn10(Tet) (<i>lys</i> [%ND])	TT3698
2	<i>leu-1151</i> ::Tn10(Tet)	TT206
2	<i>leu-1173</i> ::Tn5(Kan)	TT2383
2	<i>leu-1174</i> ::Tn5(Kan)	TT2378
2	<i>leu-1175</i> ::Tn5(Kan)	TT3281
2	<i>leu-1177</i> ::Mud1-8(Amp)	TT8268
2	<i>leu-1179</i> ::Mud1-8(Amp)	TT8269
2	<i>leu-1589</i> ::Tn10d(Cam)	TT11657
2	<i>leu-1590</i> ::MudJ(Kan)	TT14011
2	<i>leuA1179</i> ::MudJ(Kan)	TT12898
2	<i>leuB1196</i> or <i>leuC1196</i> ::Mud1-8(Amp)	TT9634
2	<i>leuB1197</i> or <i>leuC1197</i> ::Mud1-8(Amp)	TT9635
2	<i>leuC1184</i> ::Mud1-8 (Amp)	TT9623
2	<i>leuC1186</i> ::Mud1-8(Amp)	TT9625
2	<i>zac-1090</i> ::Tn5(Kan) (<i>leu</i> [96%])	TT8948
2	<i>zac-1090</i> ::Tn5(Kan) (<i>leu</i> [96%])	TT8949
2	<i>zac-1091</i> ::Tn10(Tet) (<i>leu</i> [91%])	TT8951
2	<i>zac-3696</i> ::Tn10d(Tet) (<i>pnuF178</i> [71%])	TT16300
2	<i>zac-3701</i> ::Tn10(Tet) (<i>leu</i> [41%])	TT14281
3	<i>aroP578</i> ::MudA(Amp)	TT10705
3	<i>aroP579</i> ::MudA(Amp)	TT10706
3	<i>guaC568</i> ::Tn10d(Tet)	TT10546
3	<i>nadC1004</i> ::Mud1(Amp)	JF467
3	<i>nadC218</i> ::MudP(Cam)	TT15226
3	<i>nadC218</i> ::MudQ(Cam)	TT15227
3	<i>nadC220</i> ::MudJ(Kan)	TT12899
3	<i>nadC220</i> ::MudP(Cam)	TT15228
3	<i>nadC367</i> ::MudJ(Kan)	TT10492
3	<i>nadC368</i> ::MudJ(Kan)	TT10493
3	<i>nadC369</i> ::MudJ(Kan)	TT10494
3	<i>nadC370</i> ::MudJ(Kan)	TT10495
3	<i>nadC380</i> ::Tn10(Tet)	TT10541
3	<i>zad-1022</i> ::Tn10(Tet) (<i>nadC</i> [67%])	TT7170
3	<i>zad-1022</i> ::Tn10(Tet) (<i>nadC</i> [67%])	TT7171
3	<i>zad-3131</i> ::Tn10(Tet) (<i>leuBCD</i> [24%])	AK3131
3	<i>zad-3137</i> ::Tn10(Tet) (<i>leuBCD</i> [9%])	AD3137
3	<i>zad-803</i> ::Tn10(Tet) (<i>leu</i> [30%])	TN745

CS ^b	Allele no. and linkage ^c	Strain no. ^d
3	<i>zad-804::Tn10(Tet) (leu [75%])</i>	TN1004
4	<i>pan-540::Tn10(Tet)</i>	TT421
4	<i>pan-564::Tn10d(Cam)</i>	TT11666
4	<i>zae-1614::Tn10(Kan) (pepM [68%])</i>	TN2500
4	<i>zae-1633::Tn10(Cam) (pepM [75%])</i>	TN2852
4	<i>zae-1856::Tn10(Tet) (hemL [%ND])</i>	TT13021
4	<i>zae-1863::Tn10d(Tet) (hemL [>90%])</i>	TT12008
4	<i>zae-1863::Tn10d(Tet) (hemL [95%])</i>	TE274
4	<i>zae-1864::Tn10(Cam) (hemL [>95%])</i>	TT12012
4	<i>zae-1864::Tn10d(Cam) (hemL [>95%])</i>	TT120114
4	<i>zae-3149::Tn10(Tet) (pepM [42%])</i>	AK3149
5	<i>hemL331::MudA(Amp)</i>	TT12117
5	<i>hemL331::MudJ(Kan)</i>	TT12122
5	<i>hemL331::MudJ(Kan)</i>	TT11997
5	<i>hemL332::MudA(Amp)</i>	TT12118
5	<i>hemL332::MudJ(Kan)</i>	TT12123
5	<i>hemL333::MudA(Amp)</i>	TT12119
5	<i>hemL334::MudA(Amp)</i>	TT12120
5	<i>hemL335::MudA(Amp)</i>	TT12121
5	<i>hemL335::MudJ(Kan)</i>	TT12124
5	<i>hemL336::MudJ(Kan)</i>	TT12125
5	<i>hemL336::MudJ(Kan)</i>	TT1200
5	<i>hemL337::MudJ(Kan)</i>	TT12126
5	<i>hemL337::MudJ(Kan)</i>	TT12001
5	<i>hemL416::MudJ(Kan)</i>	TT12131
5	<i>hemL417::MudJ(Kan)</i>	TT12132
5	<i>hemL520::MudJ(Kan)</i>	TT13110
5	<i>zaf-1351::Tn10(Tet) (metP [38%])</i>	HU521
5	<i>zag-1254::Tn10(Tet) (dnaE [50%])</i>	RM268
5	<i>zag-2016::Tn10d(Kan) (dnaE [60%])</i>	TT9772
5	<i>zag-208::Tn10(Tet) (glnD [90%])</i>	SK2314
5	<i>zag-305::Tn10(Tet) (dnaE [50%])</i>	DB9069
5	<i>zag-3262::Tn10(Tet) (dnaE [54%])</i>	AK3262
7	<i>proA1656::Tn10(Tet)</i>	JL2690
7	<i>proA692::Mud1-8(Amp)</i>	TT7882
7	<i>proA692::MudQ(Cam)</i>	TT15229
7	<i>proA692::MudQ(Cam)</i>	TT15231
7	<i>proB1657::Tn10(Tet)</i>	JL2520
7	<i>proB1661::Tn5(Kan)</i>	JL3804
7	<i>proB690::MudJ(Kan)</i>	TT12900
7	<i>proBA662::Tn10(Tet)</i>	TT184
7	<i>zah-3139::Tn10(Tet) (proAB [6%], pepD [%ND])</i>	AK3139
7	<i>zah-806::Tn10(Tet) (pepD [75%])</i>	TN801
8	<i>hemB485::MudJ(Kan)</i>	TT13075
8	<i>proC691::Mud1-8(Amp)</i>	TT9670
8	<i>proC691::MudJ(Kan)</i>	TT12901
8	<i>proC693::Mud1-8(Amp)</i>	TT9667
8	<i>proC693::MudP(Cam)</i>	TT15230
8	<i>zah-3150::Tn10(Tet) (proAB [82%])</i>	AK3150
8	<i>zah-3214::Tn10(Tet) (proAB [5%], pepD [4%])</i>	AK3214
8	<i>zah-3215::Tn10(Tet) (proAB [7%], pepD [2%])</i>	AK3215
8	<i>zah-807::Tn10(Tet) (proAB [40%])</i>	TN986
8	<i>zai-3029::Tn10(Tet) (proC [12%])</i>	AK3029
8	<i>zai-3030::Tn10(Tet) (proC [28%])</i>	AK3030
8	<i>zai-3059::Tn10(Tet) (clmB [35%])</i>	AK3059
8	<i>zai-3170::Tn10(Tet) (proC [26%])</i>	AK3170
9	<i>zai-808::Tn10(Tet) (proC [30%], hemB [10%])</i>	TN789
9	<i>zaj-1034::Tn10(Tet) (lon [50%])</i>	TT8024
10	<i>psiC17::Mud1(Amp)</i>	JF515
10	<i>zba-284::Tn10(Tet) (thil [90%])</i>	TN924
10	<i>zba-6034::Tn10(Tet) (psiC [94%])</i>	JF562
10	<i>zba-883::Tn10(Tet) (apeB21 [50%])</i>	TN1785
12	<i>hemH467::MudJ(Kan)</i>	TT13057
12	<i>hemH468::MudJ(Kan)</i>	TT13058
12	<i>oxiA1049::MudA(Amp)</i>	JF897
12	<i>purE884::Tn10(Tet) (clmG [68%])</i>	TT289
13	<i>apeE1::Tn5(Kan)</i>	TN964
13	<i>apeE2::Tn10(Tet)</i>	TN966
13	<i>purE2154::MudJ(Kan)</i>	TT12313

CS ^b	Allele no. and linkage ^c	Strain no. ^d
13	<i>purE2154::MudP</i> (Cam)	TT15235
13	<i>purE2154::MudQ</i> (Cam)	TT15232
13	<i>purE2155::MudQ</i> (Cam)	TT15234
13	<i>zbb-121::Tn10</i> (Tet)	TA4326
13	<i>zbb-3089::Tn10</i> (Tet) (<i>clmG</i> [19%])	AK3089
13	<i>zbb-3217::Tn10</i> (Tet) (<i>purE</i> [14%])	AK3217
13	<i>zbb-3260::Tn10</i> (Tet) (<i>purE</i> [7%])	AK3260
13	<i>zbb-3296::Tn10</i> (Tet) (<i>clmG</i> [10%])	AK3296
13	<i>zbb-6809::Tn10d</i> (Tet)	TE2033
13	<i>zbb-6811::Tn10d</i> (Cam) (<i>hemH</i> [40%])	TE3682
13	<i>zbb-876::Tn10</i> (Tet) (<i>apeA</i> [75%], <i>hemH</i> [3%])	TN1781
13	<i>zbc-809::Tn10</i> (Tet) (<i>purE</i> [40%])	TN780
13	<i>zbc-854::Tn10</i> (Tet) (<i>apeE</i> [25%])	TN1338
13	<i>zbc-873::Tn10</i> (Tet) (<i>apeE</i> [60%])	TN1744
14	<i>ahp-11::Tn10</i> (Tet)	TA4190
15	<i>cobD498::MudP</i> (Cam)	TT15237
15	<i>cobD498::MudQ</i> (Cam)	TT15236
15	<i>lip-22::Mud1-8</i> (Amp)	TT10219
15	<i>lip-24::Mud1-8</i> (Amp)	TT10221
15	<i>nadD357::Mud1-8</i> (Amp)	TT10227
15	<i>nadD364::Mud1-8</i> (Amp)	TT10234
15	<i>rodA14::Tn10d</i> (Tet)	DA1356
15	<i>zbe-1023::Tn10</i> (Tet) (<i>nadD</i> [55%], <i>lip</i> [90%])	TT7247
15	<i>zbe-1028::Tn10</i> (Tet) (<i>nadD</i> [74%], <i>lip</i> [14%])	TT7252
15	<i>zbe-1028::Tn10</i> (Tet) (<i>nadD</i> [74%], <i>lip</i> [14%])	TT7255
15	<i>zbe-1029::Tn10</i> (Tet) (<i>nadD</i> [46%], <i>lip</i> [90%])	TT7253
15	<i>zbe-1030::Tn10</i> (Tet) (<i>nadD</i> [50%], <i>lip</i> [10%])	TT7254
16	<i>nag-111::Mud1-8</i> (Amp)	TT10257
16	<i>nag-112::Mud1-8</i> (Amp)	TT10258
16	<i>nag-112::MudJ</i> (Kan)	TT12911
16	<i>zbe-621::Tn10</i> (Tet) (<i>supE</i> [4%])	TT2065
16	<i>zbf-57::Tn10</i> (Tet) (<i>sufG</i> [75%])	DB4289
16	<i>zbf-903::Tn10</i> (Tet)	SL2444
16	<i>zbf-904::Tn10</i> (Tet)	SL2439
16	<i>zbf-99::Tn10</i> (Tet) (<i>supE</i> [74%])	TT2342
17	<i>aroG5823::Tn10d</i> (Tet)	TT13794
17	<i>aroG583::MudJ</i> (Kan)	TT14507
17	<i>nadA1011::MudJ</i> (Kan)	JF1522
17	<i>nadA213::Tn10</i> (Tet)	TT398
17	<i>nadA216::Mud1-8</i> (Amp)	TT8782
17	<i>nadA216::MudI1734</i> (Kan)	TL1182
17	<i>nadA218::Mud1-8</i> (Amp)	TT8784
17	<i>nadA219::Mud1-8</i> (Amp)	TT8785
17	<i>nadA219::MudI1734</i> (Kan)	TL1184
17	<i>nadA219::MudJ</i> (Kan)	TT11334
17	<i>nadA219::MudP</i> (Cam)	TT15238
17	<i>nadA219::MudQ</i> (Cam)	TT15629
17	<i>nadA227::Mud1-8</i> (Amp)	TT8793
17	<i>nadA379::Tn10d</i> (Tet)	TT10540
17	<i>nadB224::Mud1-8</i> (Amp)	TT8790
17	<i>nadC220::Mud1-8</i> (Amp)	TT8786
17	<i>pnuC131::MudK</i> (Kan)	TT15523
17	<i>zbh-3652::Tn10d</i> (Tet)	TT14968
17	<i>zbh-799::Tn10</i> (Tet) (<i>nadA</i> [9.5%])	TT6570
17	<i>zbh-800::Tn10</i> (Tet) (<i>nadA</i> [10%])	TT6571
18	<i>bio-102::Tn10</i> (Tet)	TT403
18	<i>bio-129::Mud1-8</i> (Amp)	TT7800
18	<i>bio-130::Mud1-8</i> (Amp)	TT7801
18	<i>bio-131::MudJ</i> (Kan)	TT12057
18	<i>bio-135::Tn10d</i> (Cam)	TT11670
18	<i>bio-203::Tn10</i> (Tet)	JL2688
18	<i>gal-2661::Mud1-8</i> (Amp)	TT10188
18	<i>gal-2661::MudJ</i> (Kan) (<i>supS501</i>)	TT10496
18	<i>gal-2661::MudJ</i> (Kan)	TT10498
18	<i>gal-2662::MudJ</i> (Kan) (<i>supS501</i>)	TT10497
18	<i>gal-2662::MudJ</i> (Kan)	TT10499
18	<i>gal-2665::Mud1-8</i> (Amp)	TT10192
18	<i>zbi-3020::Tn10</i> (Tet) (<i>oxd-8</i> [6%], <i>galE</i> [10%])	AK3020
18	<i>zbi-812::Tn10</i> (Tet) (<i>galE</i> [90%])	TN1117

CS ^b	Allele no. and linkage ^c	Strain no. ^d
18	<i>zib-3714</i> ::Tn10d(Tet) (<i>chlA</i> [90%])	TT16597
20	<i>aroA554</i> ::Tn10(Tet)	SL1346
20	<i>aroA557</i> ::MudA(Amp)	TT10768
20	<i>aroA557</i> ::MudP(Cam)	TT15627a
20	<i>pfl-101</i> ::Mud1-8(Amp)	HSK21
20	<i>serB1465</i> ::MudJ(Kan)	TT14559
20	<i>serB1466</i> ::Tn10d(Tet)	TT12991
20	<i>serB1469</i> ::Tn10d(Cam)	TT14940
22	<i>zbj-1021</i> ::Tn10(Tet) (<i>IS200VI</i> [%ND])	TT6940
23	<i>asp-544</i> ::Tn10(Tet)	TT176
23	<i>aspC409</i> ::Tn10(Tet)	SMS409
23	<i>pncB150</i> ::Tn10(Tet)	TT6197
23	<i>pncB213</i> ::Mud(Amp)	TT7233
23	<i>zbj-1048</i> ::Tn10(Tet) (<i>pncB</i> [94%])	TT7445
23	<i>zbj-3142</i> ::Tn10(Tet) (<i>oxd-12</i> [23%], <i>aroA</i> [2%])	AK3142
23	<i>zca-6001</i> ::Tn10(Tet) (<i>pncB</i> [80%])	JF188
23	<i>zca-6008</i> ::Tn10(Tet) (<i>pncB</i> [65%])	JF330
23	<i>zca-6009</i> ::Tn10(Tet) (<i>pncB</i> [65%])	JF331
23	<i>zca-6010</i> ::Tn10(Tet) (<i>pncB</i> [96%])	JF332
23	<i>zca-6011</i> ::Tn10(Tet) (<i>pncB</i> [70%])	JF333
24	<i>pyrD2266</i> ::Tn10(Tet)	TT468
24	<i>pyrD2286</i> ::Tn5(Kan)	TT2289
24	<i>zcb-332</i> ::Tn10(Tet) (<i>pyrD</i> [32%], <i>pepN</i> [20%])	AK3232
25	<i>pepN103</i> ::MudJ(Kan)	TN2557
25	<i>pepN88</i> ::Tn10(Tet)	TN770
25	<i>zca-843</i> ::Tn10(Tet) (<i>pepN</i> [30%])	TN799
26	<i>oxiB1056</i> ::MudA(Amp)	JF928
26	<i>put-834</i> ::Tn5(Kan)	TT2292
26	<i>put-835</i> ::Tn5(Kan)	TT2000
26	<i>putA1018</i> ::Mud1-8(Amp)	TT9660
26	<i>putA1019</i> ::MudA(Amp)	TT9661
26	<i>putA1019</i> ::MudP(Cam)	TT15240
26	<i>putA1019</i> ::MudQ(Cam)	TT15239
26	<i>putA810</i> ::Tn10(Tet)	TT946
26	<i>putA854</i> ::Tn5(Kan)	TT2613
26	<i>putP1022</i> ::Mud1-8(Amp)	TT9664
26	<i>putP1023</i> ::MudA(Amp)	TT9665
26	<i>putP1669</i> ::Mud1(Amp)	CH496
26	<i>putP201</i> ::Mud1(Amp)	CH321
26	<i>putP214</i> ::Tn5(Kan)	CH378
26	<i>putP851</i> ::Tn5(Kan)	TT2787
26	<i>zcc-5</i> ::Tn10(Tet) (<i>put</i> [50%])	TT1791
26	<i>zcc-622</i> ::Tn10(Tet) (<i>putP</i> [%ND])	TT2766
26	<i>zcc-623</i> ::Tn10(Tet) (<i>putB</i> [%ND])	TT2767
26	<i>zcc-624</i> ::Tn5(Kan) (<i>put</i> [60%])	TT2651
26	<i>zcc-625</i> ::Tn5(Kan) (<i>put</i> [85%])	TT2653
26	<i>zcc-628</i> ::Tn5(Kan) (<i>put</i> [65%])	TT2659
27	<i>flgL</i> ::Tn10(Tet)	KK2087
27	<i>pyrC1655</i> ::Mud2-8 (Amp)	KP1581
27	<i>pyrC2688</i> ::Mud1-8(Amp)	TT9531
27	<i>pyrC2688</i> ::MudJ(Kan)	TT12903
27	<i>pyrC691</i> ::Tn10(Tet)	TT459
27	<i>zcd-1429</i> ::Tn10(Tet) (<i>pyrC</i> [50%])	DB4672
27	<i>zcd-3176</i> ::Tn10(Tet) (<i>pyrC</i> [30%])	AK3176
27	<i>zce-850</i> ::Tn10(Tet) (<i>purB</i> [50%])	TT6850
27	<i>zce-862</i> ::Tn10(Tet) (<i>purB</i> [20%])	TT6852
27	<i>zcf-850</i> ::Tn10(Tet) (<i>purB</i> [50%])	TN1358
28	<i>pepT7</i> ::Mud1(Amp)	TN1909
28	<i>phoN51</i> ::Tn10d(Tet)	TT13206
28	<i>phoP53</i> ::Tn10d (Tet)	TT13220
28	<i>purB1879</i> ::Mud1-8(Amp)	TT10213
28	<i>purB1879</i> ::MudJ(Kan)	TT12904
28	<i>purB1879</i> ::MudJ(Kan)	TT12316
28	<i>purB1879</i> ::MudP(Cam)	TT15242
28	<i>purB1879</i> ::MudQ(Cam)	TT15241
28	<i>purB1883</i> ::Mud1-8(Amp)	TT10217
28	<i>purB877</i> ::Tn10(Tet)	TT282
28	<i>zcf-3032</i> ::Tn10(Tet) (<i>oxd-6</i> [75%])	AK3032
28	<i>zcf-3041</i> ::Tn10(Tet) (<i>pepT</i> [41%], <i>oxd-18</i> [46%], <i>oxd-6</i> [not linked])	AK3041

CS ^b	Allele no. and linkage ^c	Strain no. ^d
28	<i>zcf-3140::Tn10</i> (Tet) (<i>oxd-6</i> [85%], <i>oxd-18</i> [2%], <i>pepT</i> [1%])	AK3140
28	<i>zcf-3233::Tn10</i> (Tet) (<i>pepT</i> [20%], <i>oxd-6</i> [17%], <i>oxd-18</i> [23%])	AK3233
28	<i>zcf-778::Tn10</i> (Tet) (<i>purB</i> [98%])	TT6067
28	<i>zcg-3806::Tn10d</i> (Tet) (<i>tppB</i> [%ND])	TT10609
29	<i>gdhA601::Tn10d</i> (Tet)	TT12148
29	<i>pncA148::Tn10</i> (Tet)	TT6195
29	<i>pncA212::Mud1-8</i> (Amp)	TT7674
29	<i>pncA226::Mud1-8</i> (Amp)	TT9847
29	<i>pncA229::Mud1-8</i> (Amp)	TT9850
29	<i>pncA229::MudJ</i> (Kan)	TT11911
29	<i>pncA247::MudJ</i> (Kan)	TT11912
29	<i>pncA251::MudJ</i> (Kan)	TT11913
29	<i>pncA278::Tn10d</i> (Cam)	TT14926
29	<i>pncA278::Tn10d</i> (Cam)	TT10759
29	<i>pncA286::Tn10d</i> (Tet)	TT10757
29	<i>pncX149::Tn10</i> (Tet)	TT6196
29	<i>pncX232::Mud1-8</i> (Amp)	TT9853
29	<i>pncX238::MudJ</i> (Kan)	TT11187
29	<i>pncX242::Mud1-8</i> (Amp)	TT9863
29	<i>pncX287::Tn10d</i> (Tet)	TT11933
29	<i>pncX335::Tn10d</i> (Tet)	TT10758
29	<i>pncX336::Tn10d</i> (Cam)	TT10760
29	<i>ptsG4152::Tn10</i> (Tet)	PP1139
29	<i>zcg-1819::(pncA,X</i> [%ND], <i>xthR</i> [%ND])	TT10281
29	<i>zcg-1819::Tn10d</i> (Tet) (<i>pncA,X</i> [%ND], <i>xthR</i> [%ND])	TT10281
29	<i>zcg-1876::Tn10</i> (Tet) (<i>pncA</i> [60%])	TT11931
29	<i>zch-1436::Tn10</i> (Tet) (<i>gdh</i> [95%], <i>nit</i> [26%])	SK741
29	<i>zch-1838::Tn10</i> (Tet) (<i>nadE</i> [30%])	TT10741
29	<i>zch-1839::Tn10</i> (Tet) (<i>nadE</i> [75%])	TT10744
30	<i>btuCED2::MudJ</i> (Kan)	TT14424
30	<i>btuCED9::Tn10d</i> (Cam)	TT14396
30	<i>zci-3314::Tn10</i> (Tet) (<i>dcp</i> [6%])	AK3314
30	<i>zci-847::Tn5</i> (Kan) (<i>dcp</i> [40%], <i>zci-3314</i> [16%])	TN1162
32	<i>tppB16::Tn10</i> (Tet)	CH695
32	<i>tppB9::Tn5</i> (Kan)	CH345
34	<i>pmi-51::Mud1-8</i> (Amp)	TT10251
34	<i>pmi-51::MudJ</i> (Kan)	TT12912
35	<i>ompD156::Tn10</i> (Tet)	CH338
35	<i>ompD159::Tn10</i> (Tet)	SH7235
35	<i>oxiC1048::MudJ</i> (Kan) (<i>zda-888</i> [98%])	JF1423
35	<i>zda-3127::Tn10</i> (Tet) (<i>oxrA</i> [2%])	AK3127
35	<i>zda-3258::Tn10</i> (Tet) (<i>oxrA</i> [20%])	AK3258
35	<i>zda-3261::Tn10</i> (Tet) (<i>oxrA</i> [2%])	AK3261
35	<i>zda-6751::Tn10</i> (Tet) (<i>oxrA</i> [80%])	PH415
35	<i>zda-888::Tn10</i> (Tet) (<i>oxiC</i> [98%])	TN1909
35	<i>zda-888::Tn10</i> (Tet) (<i>oxrA</i> [15%])	TN1910
36	<i>stiA1::MudJ</i> (Kan)	JF1222
36	<i>zdc-6052::Tn10</i> (Tet) (<i>stiA</i> [83%])	JF428
37	<i>oxrA2::Tn10</i> (Tet)	TN2336
38	<i>cysB::Tn10d</i> (Tet)	TT15052
38	<i>cysB3305::Tn10d</i> (Tet)	TT15115
38	<i>cysB3318::MudJ</i> (Kan)	TT12851
38	<i>oppA305::Mud1</i> (Amp)	CH272
38	<i>oppB255::Tn10</i> (Tet)	CH50
38	<i>oppB303::Mud1</i> (Amp)	CH270
38	<i>oppC304::Mud1</i> (Amp)	CH271
38	<i>oppD302::Mud2</i> (Amp)	CH269
38	<i>oppF326::cat</i> (Cam)	CH1460
38	<i>pyrF2482::MudJ</i> (Kan)	TT12907
38	<i>pyrF2690::Mud1-8</i> (Amp)	TT9533
38	<i>pyrF2690::MudJ</i> (Kan)	TT12906
38	<i>pyrF2690::MudP</i> (Cam)	TT15246
38	<i>pyrF2690::MudQ</i> (Cam)	TT15245
38	<i>pyrF696::Tn10</i> (Tet)	TT464
38	<i>tlp-71::Tn5</i> (Kan)	TN921
38	<i>trp-2451::Tn10</i> (Tet)	TT1333
38	<i>trp-2475::Tn5</i> (Kan)	TT4700
38	<i>trp-2475::Tn5</i> (Kan)	TT2377

CS ^b	Allele no. and linkage ^c	Strain no. ^d
38	<i>trp-2477</i> ::Tn5(Kan)	TT2757
38	<i>trp-2481</i> ::Tn5(Kan)	TT4045
38	<i>trp-2482</i> ::Mud1-8(Amp)	TT10186
38	<i>trp-2490</i> ::Mud1-8(Amp)	TT9782
38	<i>trp-3477</i> ::MudI1734 (Kan)	TT10270
38	<i>trp-3478</i> ::MudJ(Kan)	TT12105
38	<i>trp-3479</i> ::MudJ(Kan)	TT12106
38	<i>trp-3482</i> ::Tn10d(Cam)	TT11682
38	<i>trp-3483</i> ::Tn10d(Tet)	TT13579
38	<i>trp-3484</i> ::Tn10d(Tet)	TT13580
38	<i>zde-1858</i> ::Tn10d (Tet) (<i>hemA</i> [70%])	TT13023
38	<i>zde-6752</i> ::Tn10(Tet) (<i>chlC</i> [%ND])	PM225
38	<i>zde-815</i> ::Tn10(Tet) (<i>trp</i> [50%])	TN817
38	<i>zde-94</i> ::Tn10(Tet) (<i>supF</i> [50%])	TT2337
39	<i>chlC1130</i> ::Tn10(Tet)	TT10269
39	<i>chlC1701</i> ::Mud1-8(Amp)	HSK1001
39	<i>chlC1702</i> ::Mud1-8(Amp)	HSK1002
39	<i>chlC1703</i> ::Mud1-8(Amp)	HSK1003
39	<i>chlC1704</i> ::Mud1-8(Amp)	HSK1004
39	<i>chlC1706</i> ::Mud1-8(Amp)	HSK1006
39	<i>chlC1707</i> ::Mud1-8(Amp)	HSK1007
39	<i>chlC1710</i> ::Mud1-8(Amp)	HSK1010
39	<i>chlC1711</i> ::MudJ(Kan)	TT12187
39	<i>chlC1715</i> ::MudJ(Kan)	TT12191
39	<i>chlC1761</i> ::Mud1-8(Amp)	HSK1011
39	<i>zdf-1857</i> ::Tn10d (Tet) (<i>hemA</i> [%ND])	TT13022
39	<i>zdf-3026</i> ::Tn10(Tet) (<i>chlC</i> ::Mud1-8 [41%], <i>divF</i> [5%])	AK3026
39	<i>zdf-3211</i> ::Tn10(Tet) (<i>chlC</i> ::Mud1-8 [48%], <i>divF</i> [50%])	AK3211
39	<i>zdf-3218</i> ::Tn10(Tet) (<i>chlC</i> ::Mud1-8 [11%])	AK3218
39	<i>zdf-3219</i> ::Tn10(Tet) (<i>chlC</i> ::Mud1-8 [6%])	AK3219
39	<i>zdf-605</i> ::Tn10(Tet) (<i>supC</i> [54%])	TT2345
40	<i>aniI1052</i> ::MudA(Amp)	JF1509
40	<i>dadB101</i> ::MudJ(Kan)	TT1185
40	<i>dadB102</i> ::MudJ(Kan)	TT11186
40	<i>dadB5</i> ::Tn10(Tet)	DB7818
40	<i>dadB6</i> ::Tn10(Tet)	DB7819
40	<i>dadB7</i> ::Tn10(Tet)	DB7820
40	<i>tre-151</i> ::MudJ(Kan)	TT11321
40	<i>tre-152</i> ::MudJ(Kan)	TT11457
40	<i>tre-152</i> ::MudP(Cam)	TT15630
40	<i>tre-152</i> ::MudQ(Cam)	TT15625
40	<i>tre-159</i> ::MudJ(Kan)	TT11322
40	<i>tre-160</i> ::MudJ(Kan)	TT11323
40	<i>tre-57</i> ::Tn10(Tet)	TT1518
40	<i>zdg-1201</i> ::Tn10(Tet) (<i>dadA/B</i> [%ND])	DB7913
40	<i>zdg-1201</i> ::Tn10(Tet) (<i>dadA/B</i> [%ND])	DB7812
40	<i>zdg-3036</i> ::Tn10(Tet) (<i>dadB</i> [90%])	AK3063
40	<i>zdg-3037</i> ::Tn10(Tet) (<i>dadB</i> [90%])	AK3037
40	<i>zdg-3234</i> ::Tn10(Tet) (<i>dadB</i> [40%], <i>divF</i> [5%])	AK3234
41	<i>aroD1141</i> ::Tn10d (Tet)	RT900
41	<i>aroD553</i> ::Tn10(Tet)	TT1454
41	<i>aroD558</i> ::MudP(Cam)	TT15247
41	<i>aroD558</i> ::MudQ(Cam)	TT15248
41	<i>aroD561</i> ::MudP(Cam)	TT15244
41	<i>aroD561</i> ::MudQ(Cam)	TT15243
43	<i>cheA501</i> ::Tn10(Tet)	KK2051
43	<i>cheB502</i> ::Tn10(Tet)	KK2078
43	<i>cheY503</i> ::Tn10(Tet)	KK2014
43	<i>cob-10</i> ::Tn10(Tet)	TT9815
43	<i>cob-11</i> ::Tn10(Tet)	TT9816
43	<i>cob-13</i> ::Tn10(Tet)	TT10441
43	<i>cob-2</i> ::Tn10(Tet)	TT10880
43	<i>cob-21</i> ::MudA(Amp)	RT116
43	<i>cob-21</i> ::MudA(Amp)	TT10324
43	<i>cob-21</i> ::MudJ(Kan)	RT785
43	<i>cob-26</i> ::MudA(Amp)	TT10329
43	<i>cob-27</i> ::MudA(Amp)	TT10330
43	<i>cob-28</i> ::MudA(Amp)	TT10331
43	<i>cob-30</i> ::MudA(Amp)	TT10333

CS ^b	Allele no. and linkage ^c	Strain no. ^d
43	<i>cob-4</i> ::Tn10(Tet)	TT9814
43	<i>cob-5</i> ::Tn5(Kan)	TT7744
43	<i>cob-62</i> ::MudA(Amp)	TT10365
43	<i>cob-62</i> ::MudJ(Kan) (<i>blue cobII</i>)	TT10857
43	<i>cob-66</i> ::MudJ(Kan) (<i>blue cobIII</i>)	TT10858
43	<i>fli-8017</i> ::Tn10(Tet) (IS200IV [%ND])	TT6941
43	<i>fliC</i> ::Tn10(Tet)	KK2503
43	<i>zea-1434</i> ::Tn10(Tet) (<i>flaR</i> [33%], <i>cheR</i> [46%])	ST322
43	<i>zea-1437</i> ::Tn10(Tet) (<i>cheR</i> [66%], <i>flaC</i> [84%])	ST314
43	<i>zea-3666</i> ::MudP(Cam) (<i>cob</i> [%ND])	TT15250
43	<i>zea-3666</i> ::MudQ(Cam) (<i>cob</i> [%ND])	TT15249
43	<i>zea-4</i> ::Tn10(Tet) (<i>HI</i> [1%], <i>flaK</i> [44%], <i>cheA</i> [44%], <i>cheW</i> [40%], <i>cheR</i> [33%], <i>cheB</i> [27%], <i>cheY</i> [33%])	ST316
43	<i>zea-609</i> ::Tn10(Tet) (<i>supD</i> [60%])	TT8388
43	<i>zea-618</i> ::Tn10(Tet) (<i>supD</i> [90%])	TT2070
43	<i>zea-81</i> ::Tn10(Tet) (<i>HI</i> [74%])	TT1952
43	<i>zeb-609</i> ::Tn10(Tet) (<i>supD</i> [%ND])	TT7610
44	<i>cob-24</i> ::MudJ(Kan) (<i>blue cobI</i>)	TT10852
44	<i>cobA28</i> ::MudJ(Kan)	TT14282
44	<i>cobA343</i> ::MudJ(Kan)	TT12895
44	<i>cobA367</i> ::Tn10d(Tet)	TT13584
44	<i>cobA374</i> ::MudJ(Kan)	TT14265
44	<i>cobD498</i> ::MudJ(Kan)	TT15660
44	<i>phs-2101</i> ::MudI(Amp) (<i>zec-2</i> ::Tn10 [20%], <i>hisD</i> ::Tn10 [76%])	EB222
45	<i>gnd-161</i> ::Tn10(Tet)	NK114
45	<i>his(OG)1278</i> ::MudK(Kan)	TT10379
45	<i>hisA8676</i> ::Tn10(Tet)	NK1255
45	<i>hisA9649</i> ::Tn5(Kan)	TT2617
45	<i>hisA9944</i> ::MudI(Amp)	TT10288
45	<i>hisB9442</i> ::Tn10(Tet)	TT7242
45	<i>hisB9643</i> ::Tn5(Kan)	TT2714
45	<i>hisB9646</i> ::Tn5(Kan)	TT2614
45	<i>hisB9650</i> ::Tn5(Kan)	TT2618
45	<i>hisC10082</i> ::Tn10d(Cam)	TT14081
45	<i>hisC10171</i> ::Tn5(Kan)	TT2663
45	<i>hisC8667</i> ::Tn10(Tet)	TT1127
45	<i>hisC9642</i> ::Tn5(Kan)	TT2713
45	<i>hisC9900</i> ::Tn5(Kan)	TT4458
45	<i>hisC9900</i> ::Tn5(Kan)	TT4035
45	<i>hisC9955</i> ::MudI-8(Amp)	TT7694
45	<i>hisD10173</i> ::MudJ(Kan)	TT13426
45	<i>hisD5408</i> ::Tn10(Tet)	TT34
45	<i>hisD9639</i> ::Tn5(Kan)	TT2710
45	<i>hisD9644</i> ::Tn5(Kan)	TT2715
45	<i>hisD9652</i> ::Tn5(Kan)	TT2620
45	<i>hisD9903</i> ::Tn5(Kan)	TT4038
45	<i>hisD9950</i> ::MudI-8(Amp)	TT7689
45	<i>hisD9950</i> ::MudI1734 (Kan)	TL1153
45	<i>hisD9950</i> ::MudP(Cam)	TT15251
45	<i>hisD9952</i> ::MudA(Amp)	TT7691
45	<i>hisD9953</i> ::MudI-8(Amp)	TT7692
45	<i>hisD9953</i> ::MudJ(Kan)	TT10268
45	<i>hisD9953</i> ::MudJ(Kan)	TT10288
45	<i>hisD9953</i> ::MudJ(Kan)	TT10289
45	<i>hisD9967</i> ::MudI-8(Amp)	TT7758
45	<i>hisE9446</i> ::Tn10(Tet)	NK1146
45	<i>hisE9557</i> ::MudI-8(Amp)	TT7696
45	<i>hisE9907</i> ::Tn5(Kan)	TT4474
45	<i>hisF8672</i> ::Tn10(Tet)	NK1256
45	<i>hisF9551</i> ::MudJ(Kan)	RT766
45	<i>hisF9912</i> ::Tn5(Kan)	TT4479
45	<i>hisF9951</i> ::MudI-8(Amp)	TT2690
45	<i>hisF9954</i> ::MudI-8(Amp)	TT7693
45	<i>hisF9954</i> ::MudJ(Kan)	RT767
45	<i>hisG10085</i> ::Tn10d(Cam)	TT11593
45	<i>hisG10172</i> ::Tn10d(Cam)	TT11600
45	<i>hisG1102</i> ::Tn5(Kan) (<i>hisT</i> [45%])	TT2810
45	<i>hisG9424</i> ::Tn10(Tet)	NK1158
45	<i>hisG9631</i> ::Tn5(Kan)	TT2673

CS ^b	Allele no. and linkage ^c	Strain no. ^d
45	<i>hisG9632</i> ::Tn5(Kan)	TT2674
45	<i>hisG9648</i> ::Tn5(Kan)	TT2616
45	<i>hisG9958</i> ::Mud1-8(Amp)	TT7697
z45	<i>hisH9430</i> ::Tn10(Tet)	NK1220
45	<i>hisH9528</i> ::Tn5(Kan)	TT2106
45	<i>hisH9962</i> ::Mud1-8(Amp)	TT7701
45	<i>hisH9962</i> ::MudP(Cam)	TT17163
45	<i>hisH9962</i> ::MudQ(Cam)	TT17164
45	<i>hisHA9556</i> ::Mud1-8(Amp)	TT7695
45	<i>hisI9960</i> ::Mud1-8(Amp)	TT7699
45	<i>hisI9965</i> ::Mud1-8(Amp)	TT7756
45	<i>zeb-1845</i> ::Tn10(Tet) (<i>cobR</i> [%ND])	TT14705
45	<i>zeb-3809</i> ::Tn10d(Tet) (<i>cobH</i> [15%])	TT16838
45	<i>zeb-609</i> ::Tn10(Tet) (<i>supD</i> [%ND])	TT7611
45	<i>zeb-6154</i> ::Tn10d(Cam) (<i>cob</i> [%ND], <i>pdu</i> [%ND])	TT16564
45	<i>zeb-6156</i> ::Tn10d(Tet) (<i>phs</i> [%ND])	TT15128
45	<i>zeb-7303</i> ::Tn10d(Cam) (<i>cobH</i> [95%])	TT16839
45	<i>zec-1</i> ::Tn10(Tet) (<i>his</i> [50%], at <i>hisE</i> end)	NK397
45	<i>zec-1</i> ::Tn10(Tet) (<i>his</i> [%ND] at <i>hisE</i> end)	TT781
45	<i>zec-2</i> ::Tn10(Tet) (<i>his</i> [50%], at <i>hisO</i> end)	TT513
45	<i>zec-2</i> ::Tn10(Tet) (<i>his</i> [50%], at <i>hisO</i> end)	NR5294
45	<i>zec-2</i> ::Tn10(Tet) (<i>dam-1</i> [25%])	NR5293
45	<i>zec-3255</i> ::Tn10(Tet) (<i>his</i> [59%])	AK3255
47	<i>zee-3061</i> ::Tn10(Tet) (<i>metG</i> [6%])	AK3061
47	<i>zee-3628</i> ::Tn10d(Cam) (<i>his</i> [%ND])	TT16747
47	<i>zee-3632</i> ::Tn10d(Kan) (<i>his</i> [%ND])	TT16749
47	<i>zee-629</i> ::Tn5(Kan) (<i>hisE</i> [56%], <i>hisE</i> side)	TT2665
47	<i>zee-631</i> ::Tn5(Kan) (<i>hisO</i> [73%], <i>hisO</i> side)	TT2667
47	<i>zee-78</i> ::Tn10(Tet) (<i>metG</i> [80%])	TT2242
49	<i>zef-4</i> ::Tn10(Tet) (<i>gyrA</i> [95%])	DB9031
49	<i>zef-754</i> ::Tn10(Tet) (<i>hisW</i> [90%])	TT5371
50	<i>ompC396</i> ::Tn10(Tet)	SH7241
51	<i>ack-408</i> ::Tn10(Tet)	SMS408
51	<i>hisJ8908</i> ::Tn10(Tet)	TA3178
51	<i>hisM6643</i> ::Tn10(Tet)	TA3195
51	<i>hisP5049</i> ::Tn10(Tet)	TA3090
51	<i>hisP6641</i> ::Tn10(Tet)	TA3193
51	<i>hisQ6642</i> ::Tn10(Tet)	TA3194
51	<i>menB101</i> ::Mud1(Amp)	EB139
51	<i>pta-406</i> ::Tn10(Tet)	SMS406
51	<i>zeg-102</i> ::Tn10(Tet) (<i>dhuA</i> [80%])	TA3088
51	<i>zeg-3118</i> ::Tn10(Tet) (<i>oxd-3</i> [100%], <i>oxd-9</i> [100%], <i>oxd-10</i> [100%], <i>oxd-13</i> [100%], <i>oxd-14</i> [100%], <i>oxd-16</i> [100%])	AK3118
51	<i>zeg-3198</i> ::Tn10(Tet) (<i>oxd-3</i> [50%], <i>oxd-9</i> [48%], <i>oxd-10</i> [41%], <i>oxd-13</i> [37%], <i>oxd-14</i> [40%], <i>oxd-16</i> [24%])	AK3198
51	<i>zeg-3291</i> ::Tn10(Tet) (<i>oxd-3</i> [68%], <i>oxd-9</i> [67%], <i>oxd-10</i> [65%], <i>oxd-13</i> [57%], <i>oxd-14</i> [64%], <i>oxd-16</i> [60%])	AK3291
52	<i>aroC566</i> ::MudP(Cam)	TT15252
52	<i>hisT290</i> ::Tn5(Kan)	TT5866
52	<i>pdx-542</i> ::Tn5(Kan)	TT2758
52	<i>pdx-544</i> ::MudJ(Kan)	TT14029
52	<i>purF1714</i> ::Tn10(Tet)	TT317
52	<i>purF2054</i> ::MudP(Cam)	TT17401
52	<i>purF2144</i> ::MudJ(Kan)	TT4547
52	<i>purF2144</i> ::MudJ(Kan)	TT12305
52	<i>zeh-1888</i> ::Tn10d(Tet) (<i>purF</i> [68%])	TT12233
52	<i>zeh-1893</i> ::MudJ(Kan) (<i>purF</i> [40%])	TT12694
53	<i>crr-307</i> ::Tn10(Tet)	PP994
53	<i>cysA1367</i> ::Tn10(Tet)	NK186
53	<i>cysA1545</i> ::Tn5(Kan)	TT2373
53	<i>cysA1585</i> ::MudJ(Kan)	TT14528
53	<i>cysA1586</i> ::MudJ(Kan)	TT14529
53	<i>cysA3319</i> ::MudJ(Kan)	TT12862
53	<i>cysA3321</i> ::MudJ(Kan)	TT12872
53	<i>cysKAM1585</i> ::Mud1-8(Amp)	TT10508
53	<i>cysKAM1585</i> ::MudP(Cam)	TT15258
53	<i>cysKAM1586</i> ::Mud1-8(Amp)	TT10509
53	<i>cysKAM1586</i> ::MudP(Cam)	TT15254
53	<i>cysKAM1586</i> ::MudQ(Cam)	TT15253

CS ^b	Allele no. and linkage ^c	Strain no. ^d
53	<i>ptsI421::Tn10</i> (Tet)	PP1228
53	<i>zeh-3138::Tn10</i> (Tet) (<i>purF</i> [14%])	AK3138
53	<i>zeh-608::Tn10</i> (Tet) (<i>aroC</i> [40%], <i>hisT</i> [27%])	TA3092
53	<i>zeh-636::Tn5</i> (Kan) (<i>hisT</i> [45%])	TT4279
53	<i>zej-1031::Tn10</i> (Tet) (<i>ptsI</i> [90%])	TT7293
53	<i>zej-3271::Tn10</i> (Tet) (<i>cysA</i> [99%])	AK3271
54	<i>eut-153::MudJ</i> (Kan)	TT13736
54	<i>eut-18::MudJ</i> (Kan)	TT14835
54	<i>eut-206::Tn10d</i> (Tet)	TT14883
54	<i>eut-208::Tn10d</i> (Tet)	TT14769
54	<i>eutR156::MudJ</i> (Kan)	TT13738
54	<i>eutR205::Tn10</i> (Tet) (on F'606)	TT14835
54	<i>purC2156::MudJ</i> (Kan)	TT12315
54	<i>purC882::Tn10</i> (Tet)	TT287
54	<i>purI1757::Tn10</i> (Tet)	TT11
54	<i>purI2152::MudJ</i> (Kan)	TT12311
54	<i>zfa-3644::Tn10</i> (Tet) (<i>eut-18::MudA</i> [95%])	TT11567
54	<i>zfa-3646::Tn10</i> (Tet) (<i>purC</i> side of <i>eut</i>)	TT13438
54	<i>zfa-3647::Tn10</i> (Tet) (<i>cysA</i> side of <i>eut</i> ; B orientation)	TT13439
54	<i>zfa-3648::Tn10</i> (Tet) (<i>cysA</i> side of <i>eut</i> ; A orientation)	TT13440
54	<i>zfa-3649::Tn10</i> (Tet) (<i>purC</i> side of <i>eut</i>)	TT13441
55	<i>guaA554::Tn10</i> (Tet)	TT278
55	<i>guaAB2159::MudJ</i> (Kan)	TT12320
55	<i>guaAB563::MudA</i> (Amp)	TT10766
55	<i>guaAB564::MudA</i> (Amp)	TT10767
55	<i>guaAB564::MudJ</i> (Kan)	TT12321
55	<i>guaAB564I::MudP</i> (Cam)	TT15255
55	<i>guaAB564I::MudQ</i> (Cam)	TT15632
55	<i>guaB544::Tn10</i> (Tet)	TT275
56	<i>glyA540::Tn10</i> (Tet)	TT418
56	<i>glyA971::Tn5</i> (Kan)	SK2292
56	<i>pepB22::MudJ</i> (Kan)	TN2727
56	<i>Zdf-801::Tn10</i> (Tet) (<i>strB</i> [33%], <i>pepB</i> [65%], <i>glyA</i> [!0%])	TN858
56	<i>zfd-1019::Tn10</i> (Tet) (<i>IS200V</i> [%ND])	TT6938
56	<i>zfd-1617::Tn10</i> (Kan) (<i>pepB</i> [99%])	TN2560
57	<i>nadB1017::MudJ</i> (Kan)	JF1521
57	<i>nadB214::Tn10</i> (Tet)	TT399
57	<i>nadB226::MudP</i> (Cam)	TT15259
57	<i>nadB226::MudQ</i> (Cam)	TT15260
57	<i>nadB227::MudJ</i> (Kan)	TT12908
57	<i>nadB499::MudI</i> 1734(Kan)	TT1114
57	<i>nadB499::MudJ</i> (Kan)	TT10738
57	<i>nadB502::MudJ</i> (Kan)	TT11326
57	<i>nadB901::MudI</i> (Amp)	JF153
57	<i>purG1739::Tn10</i> (Tet)	TT315
57	<i>purG1837::Tn5</i> (Kan)	TT2800
57	<i>purG2149::MudP</i> (Cam)	TT15256
57	<i>purG2150::MudP</i> (Cam)	TT15257
57	<i>purG2151::MudJ</i> (Kan)	TT12310
57	<i>purG2324::MudJ</i> (Kan)	TT13609
58	<i>phe-564::MudI</i> -8(Amp)	TT9273
58	<i>phe-566::MudI</i> -8(Amp)	TT9275
58	<i>phe-573::MudJ</i> (Kan)	TT14030
58	<i>phe-574::MudJ</i> (Kan)	TT14031
58	<i>phe571::Tn10d</i> (Tet)	TT13795
58	<i>pheA534::Tn10</i> (Tet)	TT1339
58	<i>tyrA555::Tn10</i> (Tet)	TT126
58	<i>tyrA572::MudI</i> -8(Amp)	TT9864
58	<i>tyrA573::MudI</i> -8(Amp)	TT9865
58	<i>tyrA573::MudJ</i> (Kan)	TT12909
58	<i>zff-3028::Tn10</i> (Tet) (<i>tyrA</i> [6%])	AK3028
58	<i>zff-3055::Tn10</i> (Tet) (<i>tyrA</i> [2%], <i>phe</i> [0%])	AK3055
58	<i>zff-3181::Tn10</i> (Tet) (<i>pheA</i> [38%], <i>tyrA</i> [42%])	AK3181
58	<i>zff-3222::Tn10</i> (Tet) (<i>tyrA</i> [44%], <i>pheA</i> [54%])	AK3222
58	<i>zff-6029::Tn10</i> (Tet) (<i>nadB</i> [30%])	JF509
58	<i>zff-6030::Tn10</i> (Tet) (<i>nadB</i> [60%])	JF516
58	<i>zff-788::Tn10</i> (Tet) (<i>nadB</i> [82.9%])	TT6559

CS ^b	Allele no. and linkage ^c	Strain no. ^d
58	<i>zff-789::Tn10(Tet) (nadB [88%])</i>	TT6560
58	<i>zff-789::Tn10(Tet) (nadB [88%])</i>	TT6581
58	<i>zff-790::Tn10(Tet) (nadB [82%])</i>	TT6561
58	<i>zff-791::Tn10(Tet) (nadB [74%])</i>	TT6562
58	<i>zff-792::Tn10(Tet) (nadB [40%])</i>	TT6563
58	<i>zff-793::Tn10(Tet) (nadB [36%])</i>	TT6564
58	<i>zff-798::Tn10(Tet) (nadB [76%])</i>	TT6569
59	<i>zfg-82::Tn10(Tet) (H2 [95%])</i>	TT1896
60	<i>tctI1511::Tn10(Tet) (into tctI [=tctABCD])</i>	KS204
60	<i>tctI1512::Tn10(Tet) (into tctI [=tctABCD])</i>	KS205
60	<i>tctI1513::Tn10(Tet) (into tctI [=tctABCD])</i>	KS202
60	<i>tctI1514::Tn10(Tet) (into tctI [=tctABCD])</i>	KS203
61	<i>proU1655::Tn10(Tet)</i>	TL188
61	<i>proU1697::Tn10(Tet)</i>	CH710
61	<i>proU1702::Mud1-8(Amp)</i>	CH946
61	<i>proU1705::MudJ(Kan)</i>	CH1301
61	<i>proU1844::Mud1(Amp)</i>	TL346
61	<i>proU1844::Mud1-8(Amp)</i>	TL1311
61	<i>proU1844::MudI1734(Kan)</i>	TL671
61	<i>proU1873::Mud1(Amp)</i>	TL335
61	<i>proU1873::Mud1-8(Amp)</i>	TL1310
61	<i>proU1873::MudI1734(Kan)</i>	TL1150
61	<i>proU1884::MudQ(Cam)</i>	TT15261
61	<i>proU1884::MudQ(Cam)</i>	TT15628
62	<i>aniA(hyd)1088::MudJ(Kan) (srl::Tn10 [45%])</i>	JF1534
62	<i>hyd-101::Mud1(Amp) (srl::Tn10 [20%])</i>	EB138
62	<i>srl-202::Tn10(Tet) (recA [50%])</i>	TT520
62	<i>srl-202::Tn10(Tet)</i>	TT10923
62	<i>srl-203::Tn10d (Cam)</i>	TT14835
62	<i>srl-203::Tn10d(Cam)</i>	TT11183
62	<i>srl-211::Tn5(Kan) (recA [%ND])</i>	TT2979
62	<i>srl-212::Tn5(Kan)</i>	TT2980
62	<i>zfi-2001::Tn10(Tet) (H2 [90%], tct [22%], zfi-2002 [2%])</i>	KS177
62	<i>zfi-2002::Tn10(Tet) (H2 [2%], tct [16%], zfi-2001 [2%])</i>	KS182
62	<i>zfi-2001::Tn10(Tet) (tct [9%], srl [0.1%], nalB [60%])</i>	KS178
62	<i>zfi-2006::Tn10(Tet) (tct [9%], srl [0.2%], nalB [60%])</i>	KS179
62	<i>zfi-2007::Tn10(Tet) (tct, srl, nalB [%ND])</i>	KS184
62	<i>zfi-2009::Tn10(Tet) (tct [3%], srl[0.6%], nalB [74%])</i>	KS180
63	<i>zff-1623::Tn10(Cam) (recA [88%])</i>	TN2700
64	<i>cys(C,D,H,I, or J)1567::Mud1-8(Amp)</i>	TT9636
64	<i>cys(C,D,H,I, or J)1570::Mud1-8(Amp)</i>	TT9639
64	<i>cys(C,D,H,I, or J)1571::Mud1-8(Amp)</i>	TT9640
64	<i>cys(C,D,H,I, or J)1574::Mud1-8(Amp)</i>	TT9643
64	<i>cys(C,D,H,I, or J)1580::Mud1-8(Amp)</i>	TT9648
64	<i>cysC1511::Tn10(Tet)</i>	TT173
64	<i>cysHDC3317::MudJ(Kan)</i>	TT12849
64	<i>cysHIJ1574::MudP(Cam)</i>	TT15263
64	<i>cysHIJ1574::MudQ(Cam)</i>	TT15262
64	<i>cysI1569::MudJ(Kan)</i>	TT14834
64	<i>cysJ13316::MudJ(Kan)</i>	TT12847
64	<i>mutS121::Tn10(Tet)</i>	GW1702
64	<i>mutS121::Tn10(Tet)</i>	GW1704
64	<i>zfi-3727::Tn10d(Tet) (cysH [95%])</i>	TT12288
64	<i>zfi-3728::Tn10d(Tet) (cysJ [95%])</i>	TT12289
64	<i>zfi-3807::Tn10d(Tet)</i>	TT12280
65	<i>argA1832::Tn10(Tet)</i>	TT146
65	<i>argA1936::Tn10d(Cam)</i>	TT11587
65	<i>lys-578::Mud1-8(Amp)</i>	TT7847
65	<i>lys-582::Tn10d(Cam)</i>	TT11662
65	<i>lys-583::MudJ(Kan)</i>	TT14016
65	<i>lysA565::Tn10(Tet)</i>	TT215
65	<i>lysA577::Tn5(Kan)</i>	TT2376
65	<i>mutH101::Tn5(Kan)</i>	GW1810
65	<i>mutH101::Tn5(Kan)</i>	GW1824
65	<i>recB497::MudJ(Kan)</i>	TT13229
65	<i>recB546::Tn10d(Cam)</i>	TT17223
65	<i>recBC::Tn10(Tet)</i>	TT14559
65	<i>recBC531::Tn10(Tet)</i>	DB4659
65	<i>recC498::MudJ(Kan)</i>	TT13230

CS ^b	Allele no. and linkage ^c	Strain no. ^d
65	<i>recC499</i> ::MudJ(Kan)	TT13231
65	<i>RecC500</i> ::MudJ(Kan)	TT13232
65	<i>recC501</i> ::MudJ(Kan)	TT13233
65	<i>relA21</i> ::Tn10(Tet)	TT7542
65	<i>serA1472</i> ::Tn10d(Cam)	TT11671
65	<i>zga-1041</i> ::Tn5(Kan) (<i>relA</i> [70%])	TT8039
65	<i>zgb-1042</i> ::Tn5(Kan) (<i>relA</i> [36%])	TT8956
65	<i>zgb-12</i> ::Tn10(Tet) (<i>recBC</i> , <i>thy</i> [100%])	TT1710
65	<i>zgb-18</i> ::Tn10(Tet) (<i>recBC</i> [67%], <i>thy</i> [84%], <i>argA</i> [3%])	TT1711
65	<i>zgb-18</i> ::Tn10(Tet) (<i>thyA</i> [84%], <i>recBC</i> [67%], <i>argA</i> [3%])	TT1712
65	<i>zgb-3669</i> ::MudJ(Kan) (<i>recB</i> [89%])	TT13872
65	<i>zgb-607</i> ::Tn10(Tet) (<i>relA</i> [13%])	TA2437
65	<i>zgc-1010</i> ::Tn10(Tet) (<i>IS200I</i> [%ND])	TT6929
65	<i>zgc-3121</i> ::Tn10(Tet) (<i>thyA</i> [12%])	AK3121
65	<i>zgc-3122</i> ::Tn10(Tet) (<i>thyA</i> [15%])	AK3122
65	<i>zgc-3132</i> ::Tn10(Tet) (<i>lysA</i> [20%])	AK3132
65	<i>zgc-3143</i> ::Tn10(Tet) (<i>lysA</i> [3%])	AK3143
65	<i>zgc-3146</i> ::Tn10(Tet) (<i>thyA</i> [18%])	AK3146
65	<i>zgc-3179</i> ::Tn10(Tet) (<i>lysA</i> [6%])	AK3179
65	<i>zgc-3231</i> ::Tn10(Tet) (<i>lysA</i> [12%])	AK3231
65	<i>zgc-3715</i> ::MudP(Cam)	TT16706
65	<i>zgc-3715</i> ::MudQ(Cam)	TT16707
65	<i>zgc-3716</i> ::MudP(Cam)	TT16708
65	<i>zgc-3716</i> ::MudQ(Cam)	TT16709
65	<i>zgc-732</i> ::Tn10(Tet) (<i>sufD</i> [90%], <i>recBC</i> [67%], <i>argA</i> [3%])	TT3680
66	<i>pepP6</i> ::Tn10(Tet)	TN853
66	<i>serA977</i> ::Tn10(Tet)	TT169
66	<i>zgd-3085</i> ::Tn10(Tet) (<i>serA</i> [36%], <i>pepP</i> [78%])	AK3085
66	<i>zgd-3159</i> ::Tn10(Tet) (<i>serA</i> [64%])	AK3159
66	<i>zgd-3209</i> ::Tn10(Tet) (<i>serA</i> [16%], <i>pepP</i> [10%])	AK3209
66	<i>zgd-866</i> ::Tn5(Kan) (<i>serA</i> [60%])	TN1655
67	<i>mutB131</i> ::Tn5(Kan)	GW1809
68	<i>aniF1068</i> ::MudA(Amp) (<i>metC</i> ::Tn10 [20%])	JF1101
68	<i>aniG1072</i> ::MudJ(Kan) (<i>metC</i> ::Tn10 [5%])	JF1295
68	<i>zge-3012</i> ::Tn10(Tet) (<i>oxd-2</i> [59%])	AK3012
68	<i>zge-3076</i> ::Tn10(Tet) (<i>oxd-5</i> [10%], <i>metC</i> [0%], <i>clmF</i> [0%])	AK3076
68	<i>zge-3084</i> ::Tn10(Tet) (<i>oxd-2</i> [71%])	AK3084
68	<i>zge-3134</i> ::Tn10(Tet) (<i>oxd-5</i> [7%], <i>metC</i> [0%])	AK3134
68	<i>zge-3189</i> ::Tn10(Tet) (<i>oxd-5</i> [20%], <i>metC</i> [0%], <i>clmF</i> [0%])	AK3189
68?	<i>zgi-3642</i> ::Tn10(Tet) (<i>pnuE</i> [96%])	TT13267
68?	<i>zgi-3650</i> ::Tn10d(Tet) (<i>pnuE</i> [50%])	TT15147
68?	<i>zgi-3651</i> ::Tn10d(Tet) (<i>pnuE</i> [16%]; <i>glp</i> , <i>rha</i> [8%])	TT13500
69	<i>metC1975</i> ::Tn10(Tet)	TT14
69	<i>zgf-2010</i> ::Tn10(Tet) (<i>metC</i> [30%], <i>cpd</i> [30%])	KS1086
69	<i>zgf-3017</i> ::Tn10(Tet) (<i>metC</i> [60%], <i>oxd-5</i> [2%], <i>clmF</i> [50%])	AK3017
69	<i>zgf-3213</i> ::Tn10(Tet) (<i>metC</i> [82%], <i>oxd-5</i> [30%])	AK3213
69	<i>zgf-3246</i> ::Tn10(Tet) (<i>metC</i> [30%], <i>oxd-5</i> [2%], <i>clmF</i> [25%])	AK3246
72	<i>argG1822</i> ::Tn10(Tet)	TT142
72	<i>ntrA209</i> ::Tn10(Tet)	SK284
72	<i>zgi-3163</i> ::Tn10(Tet) (<i>argG</i> [49%], <i>dna-610</i> [85%])	AK3163
72	<i>zgi-3177</i> ::Tn10(Tet) (<i>argG</i> [34%], <i>dna-169</i> [88%])	AK3177
72	<i>zgi-3717</i> ::MudP(Cam)	TT17190
72	<i>zgi-3717</i> ::MudQ(Cam)	TT17191
72	<i>zgj-201</i> ::Tn10(Tet) (<i>ntrA</i> [90%], <i>glbB</i> [7%])	SK195
72	<i>zgj-3265</i> ::Tn10(Tet) (<i>clmC</i> [6%])	AK3265
72	<i>zgj-7301</i> ::Tn10d(Tet) (<i>arcB</i> [15%])	DA2654
73	<i>argR</i> ::Tn10d(Tet)	TT16712
73	<i>argR372</i> ::Tn10(Tet)	KR1400
73	<i>aroE568</i> ::MudA(Amp)	TT10786
73	<i>aroE568</i> ::MudJ(Kan)	TT14750
73	<i>aroE568</i> ::MudQ(Cam)	TT15626
73	<i>aroE568</i> ::MudQ(Cam)	TT15634
73	<i>envB13</i> ::Tn10d(Tet)	DA1352
73	<i>zhh-3124</i> ::Tn10(Tet) (<i>aroE</i> [69%], <i>oxrB</i> [2%])	AK3124
73	<i>zhh-3195</i> ::Tn10(Tet) (<i>aroE</i> [84%], <i>oxrB</i> [5%], <i>clmE</i> [30%], <i>rpsL</i> [1%])	AK3195
73	<i>zhh-3301</i> ::Tn10(Tet) (<i>aroE</i> [20%], <i>oxrB</i> [2%])	AK3301
73	<i>zhh-736</i> ::Tn5(Kan) (<i>supU</i> [10%])	TT4030
74	<i>crp-773</i> ::Tn10(Tet)	PP1037

CS ^b	Allele no. and linkage ^c	Strain no. ^d
74	<i>cysG</i> ::Tn10(Tet)	NR5500
74	<i>cysG1510</i> ::Tn10(Tet)	TT172
74	<i>cysG1542</i> ::Tn5(Kan)	TT2290
74	<i>cysG1542</i> ::Tn5(Kan)	TT1971
74	<i>cysG1573</i> ::Mud1-8(Amp)	TT9642
74	<i>cysG1573</i> ::MudJ(Kan) (<i>cysG</i> [95%])	TT13041
74	<i>cysG1573</i> ::MudP(Cam)	TT15264
74	<i>cysG1573</i> ::MudQ(Cam)	TT15631
74	<i>cysG3169</i> ::Tn10d(Tet)	TT13505
74	<i>cysG3170</i> ::MudA(Amp)	TT13506
74	<i>cysG3171</i> ::MudJ(Kan)	TT13507
74	<i>cysG3315</i> ::MudJ(Kan)	TT12819
74	<i>cysG3320</i> ::MudJ(Kan)	TT12864
74	<i>zhc-1431</i> ::Tn10(Tet) (<i>crp</i> [50%])	DU8802
74	<i>zhc-3665</i> ::Tn10d(Tet) (<i>cysG</i> [95%])	TT15028
74	<i>zhd-117</i> ::Tn10(Tet) (<i>malA</i> region [including <i>malT</i> , <i>Q</i>] [46%])	TA3947
75	<i>aroB542</i> ::Tn5(Kan)	TT2742
75	<i>envZ1005</i> ::MudJ(Kan)	CH1118
75	<i>envZ1005</i> ::MudP(Cam)	TT15265
75	<i>envZ1009</i> ::MudQ(Cam)	TT17165
75	<i>malQ210</i> ::MudI (Amp)	TA3999
75	<i>ompR1001</i> ::Tn5(Kan)	CH511
75	<i>ompR1009</i> ::Tn10(Tet)	CH1351
75	<i>ompR1009</i> ::Tn10(Tet)	CJD359
75	<i>zhd-3081</i> ::Tn10(Tet) (<i>aroB</i> [70%])	AK3081
75	<i>zhd-3173</i> ::Tn10(Tet) (<i>aroB</i> [86%])	AK3173
75?	<i>zhf-105</i> ::Tn10(Tet) (<i>aroD</i> [41%], <i>purF</i> [4%], <i>hisT</i> [27%])	TT1720
77	<i>optA10</i> ::MudJ(Kan)	TN3101
77	<i>zhg-1635</i> ::Tn10(Cam) (<i>opt</i> [20%])	TN3061
77	<i>zhh-1013</i> ::Tn10(Tet) (<i>IS200II</i> [%ND])	TT6932
77	<i>zhh-3073</i> ::Tn10(Tet) (<i>opt-10</i> ::MudJ [40%])	AK3073
77	<i>zhh-3082</i> ::Tn10(Tet) (<i>opt-10</i> ::MudJ [40%])	AK3082
77	<i>zhh-3108</i> ::Tn10(Tet) (<i>opt-10</i> ::MudJ [50%])	AK3108
77	<i>zhh-3109</i> ::Tn10(Tet) (<i>opt-10</i> ::MudJ [78%])	AK3109
77	<i>zhh-3147</i> ::Tn10(Tet) (<i>opt-10</i> ::MudJ [55%])	AK3147
77	<i>zhh-3228</i> ::Tn10(Tet) (<i>opt-10</i> ::MudJ [20%])	AK3228
77	<i>zhh-3287</i> ::Tn10(Tet) (<i>opt-10</i> ::MudJ [60%])	AK3287
79	<i>fdhA13277</i> ::MudJ(Kan)	TT13277
79	<i>xyl-183</i> ::Tn10(Tet)	SA1982
79	<i>zhi-1426</i> ::Tn10(Tet) (<i>xyl</i> [50%])	SA1980
79	<i>zhi-3040</i> ::Tn10(Tet) (<i>xyl</i> [4%])	AK3040
80	<i>zhj-1024</i> ::Tn5(Kan) (<i>pyrE</i> [75%])	TT7244
80	<i>zhj-1025</i> ::Tn10(Tet) (<i>pyrE</i> [70%])	TT7245
80	<i>zhj-1039</i> ::Tn5(Kan) (<i>pyrE</i> [9%ND])	TT8935
80	<i>zhj-1080</i> ::Tn5(Kan) (<i>pyrE</i> [10%], <i>glc</i> side)	TT10038
80	<i>zhj-118</i> ::Tn10(Tet) (<i>pyrE</i> [64%], <i>rfa</i> [93%])	TA4217
80	<i>zhj-1404</i> ::Tn10(Tet) (<i>pyrE</i> [67%], <i>cysE</i> [2%])	SA2703
80	<i>zhj-1404</i> ::Tn10(Tet) (<i>pyrE</i> [67%], <i>cysE</i> [2%])	SA3053
80	<i>zhj-1405</i> ::Tn10(Tet) (<i>pyrE</i> [78%], <i>cysE</i> [9%])	SA2704
80	<i>zhj-1405</i> ::Tn10(Tet) (<i>pyrE</i> [78%], <i>cysE</i> [9%])	SA3056
80	<i>zhj-1405</i> ::Tn10(Tet) (<i>pyrE</i> [78%], <i>cysE</i> [9%])	SA3058
80	<i>zhj-1416</i> ::Tn10(Tet) (<i>pyrE</i> [4%], <i>cysE</i> [87%])	SA2715
80	<i>zhj-1416</i> ::Tn10(Tet) (<i>pyrE</i> [4%], <i>cysE</i> [87%])	SA3054
80	? <i>zhj-3312</i> ::Tn10(Tet) (<i>oxrE</i> [40%], <i>pyrE</i> [0%], <i>apeR</i> [0%])	AK3312
80	<i>zhj-3699</i> ::Tn10d(Tet) (<i>cysE</i> [93%], <i>rfa</i> [15%], <i>pyrE</i> [0%])	SA3915
80	<i>zhj-3700</i> ::Tn10d(Tet) (<i>cysE</i> [70%], <i>rfa</i> [50%], <i>pyrE</i> [0%])	SA3916
80	<i>zhj-3705</i> ::Tn10d(Tet) (<i>cysE</i> [100%], <i>rfa</i> [15%], <i>pyrE</i> [0%])	SA3918
80	<i>zhj-3708</i> ::Tn10d(Tet) (<i>cysE</i> [56%], <i>rfa</i> [100%], <i>pyrE</i> [44] [insertion may be in <i>rfa</i>])	SA4030
80	<i>zhj-3710</i> ::Tn10d(Tet) (located between <i>cysE</i> [%ND] and <i>rfa</i>)	SA4031
80	<i>zhj-3712</i> ::Tn10d(Tet) (<i>cysE</i> [21%], <i>rfa</i> [36%], <i>pyrE</i> [1%])	SA3919
80	<i>zhj-3713</i> ::Tn10d(Cam) (<i>cysE</i> [%ND])	TT15716
80	<i>zhj-3713</i> ::Tn10d(Tet) (<i>cysE</i> [45%], <i>rfa</i> [27%], <i>pyrE</i> [12%])	SA3920
80	<i>zhj-3808</i> ::Tn10d(Cam) (<i>cysE</i> [%ND])	TT15717
80	<i>zhj-901</i> ::Tn10(Tet) (<i>cysE</i> [%ND])	SL1432
81	<i>pyrE2149</i> ::MudP(Cam)	TT15267
81	<i>pyrE2149</i> ::MudQ(Cam)	TT15266
81	<i>pyrE2155</i> ::MudP(Cam)	TT15233
81	<i>pyrE2678</i> ::Mud1-8(Amp)	TT9521

CS ^b	Allele no. and linkage ^c	Strain no. ^d
81	<i>pyrE2678</i> ::MudJ(Kan)	TT12910
81	<i>pyrE2681</i> ::Mud1-8(Amp)	TT9524
82	<i>zia-1026</i> ::Tn5(Kan) (<i>glcC</i> [40%])	TT7246
82	<i>zia-1036</i> ::Tn10(Tet) (<i>spoT</i> [90%])	TT7433
82	<i>zia-1438</i> ::Tn10(Tet) (<i>ilvB</i> [50%])	DU2603
82	<i>zia-3104</i> ::Tn10(Tet) (<i>mgtB</i> [11%], <i>pyrE</i> [0%])	AK3104
83	<i>aniH</i> ::MudA(Amp)	JF1410
83?	<i>avtA1</i> ::Tn5(Kan)	CBS514
83	<i>ilvB</i> ::Tn5(Kan)	RL511
83	<i>mgtB10</i> ::MudJ(Kan)	MM281
83	<i>mgtB11</i> ::MudJ(Kan)	MM197
83	<i>zia-1603</i> ::Tn10(Cam) (<i>mgtB</i> [85%], <i>glcC</i> [29%])	MM223
83	<i>zia-2055</i> ::Tn5(Kan) (<i>gyrB</i> [35%])	TT11294
83	<i>zia-3048</i> ::Tn10(Tet) (<i>mgtB</i> [95%], <i>glcC</i> [2%])	AK3048
83	<i>zia-3123</i> ::Tn10(Tet) (<i>mgtB</i> [95%], <i>pyrE</i> [0%], <i>apeR</i> [0%])	AK3123
83	<i>zia-3125</i> ::Tn10(Tet) (<i>mgtB</i> [95%])	AK3125
83	<i>zia-3205</i> ::Tn10(Tet) (<i>mgtB</i> [36%], <i>glcC</i> [0%], <i>dnaA</i> [0%], <i>pyrE</i> [0%], <i>apeR</i> [0%])	AK3205
83	<i>zia-3294</i> ::Tn10(Tet) (<i>glcC</i> [5%], <i>pyrE</i> [0%], <i>mgtB</i> [0%], <i>ilvC</i> [0%])	AK3294
83	<i>zia-3295</i> ::Tn10(Tet) (<i>mgtB</i> [4%], <i>ilvC</i> [0%], <i>pyrE</i> [0%], <i>apeR</i> [0%])	AK3295
83	<i>zia-3306</i> ::Tn10(Tet) (<i>mgtB</i> [10%])	AK3306
84	<i>apeR47</i> ::Tn5(Kan)	TN901
84	<i>atp</i> ::Tn10(Tet)	TT1039
84	<i>psiR1</i> ::Tn10(Tet)	JF753
84	<i>unc-102</i> ::Tn10(Tet)	TT1042
84	<i>uncA</i> ::Tn10(Tet)	TT1044
84	<i>zib-1001</i> ::Tn10(Tet) (<i>dnaA</i> [%ND])	TT7440
84	<i>zib-1001</i> ::Tn10(Tet) (<i>dna</i> [%ND])	TT7441
84?	<i>zib-1040</i> ::Tn5(Kan) (<i>hisU</i> [30%], <i>dnaA</i> [30%])	TT8038
84	<i>zib-3119</i> ::Tn10(Tet) (<i>apeR49</i> ::Tn5 [94%], <i>dnaA</i> [56%], <i>apeR</i> [22%], <i>zia</i> ::Tn7 [1%])	AK3119
84	<i>zib-3120</i> ::Tn10(Tet) (<i>apeR49</i> ::Tn5 [100%], <i>dnaA</i> [68%], <i>apeR</i> [24%], <i>zia</i> ::Tn7 [2%])	AK3120
84	<i>zib-3130</i> ::Tn10(Tet) (<i>apeR49</i> ::Tn5 [36%], <i>dnaA</i> [90%], <i>apeR</i> [7%], <i>zia</i> ::Tn7 [10%])	AK3130
84	<i>zib-3241</i> ::Tn10(Tet) (<i>apeR49</i> ::Tn5 [85%])	AK3241
84	<i>zib-6</i> ::Tn10(Tet) (<i>dnaA</i> [95%])	DB9048
84	<i>zib-748</i> ::Tn10(Tet) (<i>hisU</i> [30%])	TT3920
84	<i>zic-3068</i> ::Tn10(Tet) (<i>apeR49</i> ::Tn5 [4%], <i>apeR</i> [50%])	AK3068
84	<i>zic-851</i> ::Tn10(Tet) (<i>apeR</i> [73%])	TN1239
84	<i>zic-870d</i> ::Tn10(Tet) (<i>apeR</i> [60%])	TN1741
85	<i>cya-1091</i> ::Tn10(Tet) (<i>hemCD</i> [90%])	PP1002
85	<i>cya-1092</i> ::Tn10(Tet)	PP1038
85	<i>ilvA2173</i> ::Tn10(Tet)	TT4
85	<i>ilvA2648</i> ::MudP(Cam)	TT15269
85	<i>ilvA2648</i> ::MudQ(Cam)	TT15268
85	<i>ilvA595</i> ::Tn10(Tet)	TT58
85	<i>ilvD2103</i> ::Tn10(Tet)	TT81
85	<i>ilvD2171</i> ::Tn5(Kan)	TT2288
85	<i>ilvE1005</i> ::Tn10(Tet)	TT48
85	<i>ilvE201</i> ::Tn10(Tet)	CBS514
85	<i>ilvE2093</i> ::Tn10(Tet)	TT71
85	<i>ilvG1006</i> ::Tn10(Tet)	TT61
85	<i>ilvG1007</i> ::Tn10(Tet)	TT66
85	<i>uvrD421</i> ::Tn5(Kan)	GW1808
85	<i>zid-2</i> ::Tn10(Tet) (<i>cya</i> [95%], <i>hisR</i> [40%], <i>hemCD</i> [75%])	TT2104
85	<i>zid-3265</i> ::Tn10(Tet) (<i>ilvC</i> [9%], <i>corA</i> [0%], <i>clmD</i> [70%])	AK3265
85	<i>zid-64</i> ::Tn10(Tet) (<i>ilv</i> [40%])	TT2010
86	<i>corA45</i> ::MudJ(Kan)	MM199
86	<i>metE2092</i> ::Tn5(Kan)	TT2370
86	<i>metE2113</i> ::Mud1-8(Amp)	TT7858
86	<i>metE2113</i> ::MudA(Amp)	TT11460
86	<i>metE2113</i> ::MudJ(Kan)	TT14305
86	<i>metE2119</i> ::Mud1-8 (Amp)	TT7864
86	<i>metE2119</i> ::MudJ(Kan)	TT11461
86	<i>metE2131</i> ::MudP(Cam)	TT15271
86	<i>metE2131</i> ::MudQ(Cam)	TT15270
86	<i>metE2357</i> ::MudJ(Kan)	TT12073
86	<i>metE2362</i> ::MudJ(Kan)	TT12068

CS ^b	Allele no. and linkage ^c	Strain no. ^d
86	<i>metE862::Tn10</i> (Tet)	TT218
86	<i>pepQ8::MudJ</i> (Kan)	TN2712
86	<i>zei-3162::Tn10</i> (Tet) (<i>metE</i> [75%], <i>corA</i> [25%], <i>ilvC</i> [0%], <i>pepQ</i> [0%])	AK3162
86	<i>zie-1634::Tn10</i> (Cam) (<i>polA</i> [3%])	Tn3005
86	<i>zie-1846::Tn5</i> (Kan) (<i>metE</i> [30%])	TT10548
86	<i>zie-1870::Tn10</i> (Cam) (<i>metE</i> [90%])	TT11561
86	<i>zie-3024::Tn10</i> (Tet) (<i>pepQ</i> [65%], <i>metE</i> [2%], <i>polA</i> [6%])	AK3024
86	<i>zie-3145::Tn10</i> (Tet) (<i>pepQ</i> [89%], <i>ilvC</i> [33%], <i>metE</i> [0–1%])	AK3145
86	<i>zie-3161::Tn10</i> (Tet) (<i>pepQ</i> [4%], <i>metE</i> [30%], <i>corA</i> [8%], <i>ilvC</i> [0%])	AK3161
86	<i>zie-3228::Tn10</i> (Tet) (<i>clmA</i> [45%])	AK3228
86	<i>zie-3229::Tn10</i> (Tet) (<i>clmA</i> [50%])	AK3229
86	<i>zie-3235::Tn10</i> (Tet) (<i>metE</i> [7%], <i>corA</i> [37%], <i>pepQ</i> [0%])	AK3235
86	<i>zie-3299::Tn10</i> (Tet) (<i>clmA</i> [70%])	AK3299
86	<i>zie-3305::Tn10</i> (Tet) (<i>clmA</i> [45%])	AK3305
86	<i>zie-6804::Tn10d</i> (Cam) (<i>hemN</i> [65%])	TE3104
86	<i>zie-6805::Tn10d</i> (Tet) (<i>hemG</i> [50%])	TE2727
87	<i>glnA120::Tn10</i> (Tet)	SK389
87	<i>glnA392::Tn5</i> (Kan)	SK1239
87	<i>ntrB137::Tn10</i> (Tet)	SK398
87	<i>ntrC352::Tn10</i> (Tet)	SK835
87	<i>zif-205::Tn10</i> (Tet) (<i>glnA</i> [40%], <i>rha</i> proximal)	SK273
87	<i>zif-214::Tn10</i> (Tet)	SL5388
87	<i>zif-214::Tn10</i> (Tet) (<i>ntrC</i> [75%], <i>polA</i> proximal)	SK811
88	<i>pnuE41::MudJ</i> (Kan)	TT13266
88	<i>pnuE41::MudP</i> (Cam)	TT15272
88	<i>pnuE41::MudQ</i> (Cam)	TT15273
88	<i>pnuE84::MudJ</i> (Kan)	TT13265
88	<i>pnuE84::MudJ</i> (Kan)	TT13270
88	<i>zig-1935::Tn10</i> (Tet)	JF1493
89	<i>argB183::Tn10</i> (Tet)	TT744
89	<i>argE1843::Tn10</i> (Tet)	TT368
89	<i>argH1823::Tn10</i> (Tet)	TT137
89	<i>btuB1::MudJ</i> (Kan)	TT13749
89	<i>btuB10::Tn10d</i> (Cam)	TT14398
89	<i>btuB18::MudJ</i> (Kan)	TT14415
89	<i>btuB19::MudJ</i> (Kan)	TT14416
89	<i>btuB22::Tn10d</i> (Tet)	TT14420
89	<i>btuB23::Tn10d</i> (Tet)	TT14421
89	<i>btuB7::MudJ</i> (Kan)	TT14297
89	<i>hemE464::MudJ</i> (Kan)	TT13054
89	<i>hemE529::MudJ</i> (Kan)	TT13288
89	<i>metB879::Tn10</i> (Tet)	TT225
89	<i>metF2094::Tn5</i> (Kan)	TT2381
89	<i>metF877::Tn10</i> (Tet)	TT233
89	<i>oxiE4::MudJ</i> (Kan) (<i>argH::Tn10</i> [65%])	JF1420
89	<i>oxrG::Tn10</i> (Tet)	JF1509
89	<i>ppc-2::Tn10</i> (Tet)	KS77
89	<i>psiB12::Mud1</i> (Amp)	JF512
89	<i>zii-166::Tn5</i> (Kan)	TA4101
89	<i>zii-614::Tn10</i> (Tet)	TA4267
89	<i>zii-614::Tn10</i> (Tet) (<i>argH</i> [30%], <i>sufJ</i> [40%])	TT2385
90	<i>purD1735::Tn10</i> (Tet)	TT311
90	<i>purD1835::Tn5</i> (Kan)	TT2798
90	<i>purD1874::MudP</i> (Cam)	TT15274
90	<i>purD1874::MudQ</i> (Cam)	TT15635
90	<i>purD1877::MudJ</i> (Kan)	TT13952
90	<i>purH1829::Tn5</i> (Kan)	TT2792
90	<i>purH887::Tn10</i> (Tet)	TT292
90	<i>thiA343::MudJ</i> (Kan)	TT14040
90	<i>thiA541::Tn10</i> (Tet)	TT501
91	<i>aceA1::Tn10</i> (Tet)	TT8027
91	<i>aceA101::Tn10</i> (Tet)	MS226
91	<i>aceA112::MudJ</i> (Kan)	MS1309
91	<i>aceB102::Tn10</i> (Tet)	MS229
91	<i>aceB113::MudJ</i> (Kan)	MS1311
91	<i>malE212::Tn10</i> (Tet)	TA5051
91	<i>malE776::Tn10</i> (Tet)	TS616

CS ^b	Allele no. and linkage ^c	Strain no. ^d
91	<i>met-900 (metA or B)::Tn10(Tet)</i>	TT256
91	<i>meth2355::MudJ(Kan)</i>	TT11202
91	<i>pepE8::MudJ(Kan)</i>	TN2719
91	<i>zij-1816::Tn10(Tet) (metH [73%])</i>	TT10846
91	<i>zij-1818::Tn10(Tet) (metH [54%])</i>	TT10848
91	<i>zij-1819::Tn10(Tet) (metH [83%])</i>	TT10849
91	<i>zij-1821::Tn10(Tet) (metH [12%])</i>	TT10851
91	<i>zij-6032::Tn10d(Cam) (purH [25%])</i>	SV2049
91	<i>zja-1230::Tn10(Tet) (malB [28%], malG [%ND])</i>	TA5053
91	<i>zja-861::Tn5(Kan) (malB [8%])</i>	TA3949
91	<i>zjb-861::Tn5(Kan) (malB [5%], pep [3%])</i>	TN1425
93	<i>aniB1054::MudA(Amp) (zid-27::Tn10 [15%])</i>	JF1427
93	<i>aniC1052::MudJ(Kan) (zid-27::Tn10 [98%])</i>	JF1325
93?	<i>fhl-101::Mud1(Amp) (melA::Tn10 [21%], zdj-27::Tn10 [46%])</i>	EB137
93	<i>mel-351::Tn10(Tet)</i>	TT1662
93	<i>melAB396::MudP(Cam)</i>	TT15276
93	<i>melAB396::MudQ(Cam)</i>	TT15275
93	<i>proP1667::Tn5(Kan)</i>	CH638
93	<i>proP1667::Tn5(Kan)</i>	CH486
93	<i>proP1673::Mud1(Amp)</i>	CH500
93	<i>proP1681::Mud1(Amp)</i>	TL357
93	<i>proP1681::Mud11734(Kan)</i>	TL1278
93	<i>proP1696::Mud1(Amp)</i>	TL372
93	<i>proP1696::Mud11734(Kan)</i>	TL1280
93	<i>psiD19::MudA(Amp) (zid-27::Tn10 [74%])</i>	JF663
93	<i>zjd-27::Tn10(Tet) (proP [60%], mel [30%])</i>	TT1800
94	<i>poxA401::Tn10(Tet)</i>	SMS401
94	<i>zjc-1016::Tn10(Tet) (IS200III [%ND])</i>	TT6935
95	<i>mutL111::Tn10(Tet)</i>	GW1714
95	<i>mutL111::Tn10(Tet)</i>	GW1716
95?	<i>phoN51::Tn10d(Tet)</i>	TT13217
95?	<i>phoP52::Tn10d(Tet)</i>	TT13207
95	<i>purA1881::Mud1-8(Amp)</i>	TT10215
95	<i>purA1881::MudP(Cam)</i>	TT15277
95	<i>purA1882::Mud1-8(Amp)</i>	TT10216
95	<i>purA2158::MudJ(Kan)</i>	TT12319
95	<i>purA874::Tn10(Tet)</i>	TT273
95	<i>zjg-3290::Tn10(Tet) (purA [88%])</i>	AK3290
96	<i>mgtA27::MudJ(Kan)</i>	MM299
96	<i>pepA201::Tn10(Tet)</i>	CH351
96	<i>pyrB2691::Mud1-8(Amp)</i>	TT9534
96	<i>pyrB2694::Mud1-8(Amp)</i>	TT9537
96	<i>pyrB692::Tn10(Tet)</i>	TT460
96	<i>zjh-1628::Tn10(Cam) (pyrB [14%], mtgA [24%])</i>	MM116
97	<i>argI1833::Tn10(Tet)</i>	TT147
97	<i>argI1850::Tn5(Kan)</i>	TT2374
97	<i>zjh-3725::MudP(Cam)</i>	TT15638
97	<i>zji-1072::Tn5(Kan) (hsdSA [20%], argI [7%])</i>	TT8082
97	<i>zji-1073::Tn10(Tet) (argI [15%], hsdSA [%ND])</i>	TT8088
97	<i>zji-3103::Tn10(Tet) (pepA [46%], argI [82%], pyrB [22%], hsdSA [%ND])</i>	AK3103
97	<i>zji-3160::Tn10(Tet) (pepA [46%], argI [88%], pyrB [8%], hsdSA [%ND])</i>	AK3160
97	<i>zji-3196::Tn10(Tet) (pepA [38%], argI [72%], pyrB [22%])</i>	AK3196
97	<i>zji-3200::Tn10(Tet) (pepA [15%], argI [30%], pyrB [21%])</i>	AK3200
97	<i>zji-3252::Tn10(Tet) (pepA [70%], argI [52%], pyrB [12%], hsdSA [%ND])</i>	AK3252
97	<i>zji-3253::Tn10(Tet) (pepA, argI, pyrB, hsdSA [%ND])</i>	AK3253
97	<i>zji-33::Tn10(Tet) (pyrB [83%])</i>	TT563
97	<i>zji-841::Tn10(Tet) (pepA [45%])</i>	TN797
97	<i>zji-842::Tn5(Kan) (argI [88%], pyrB [44%], pepA [28%])</i>	TN1040
99	<i>nadI548::MudK(Kan)</i>	TT13508
99	<i>nadI553::MudK(Kan)</i>	TT13513
99	<i>nadI608(=pnuA176)::Tn10d(Tet)</i>	TT16072
99	<i>nadI609(=pnuA177)::Tn10d(Tet)</i>	TT16073
99	<i>nadIS509::MudJ(Kan)</i>	TT11431
99	<i>pnuA101::MudJ(Kan)</i>	TT13121
99	<i>pnuA113::MudK(Kan)</i>	TT13518

CS ^b	Allele no. and linkage ^c	Strain no. ^d
99	<i>pnuA126(nadI579)::Tn10d(Tet)</i>	TT15340
99	<i>serB965::Tn10(Tet)</i>	TT21
99	<i>zjj-1004::Tn10(Tet)</i> (<i>pnuA</i> [66%], <i>thr</i> [15%] <i>serB</i> [50%])	TT6736
99	<i>zjj-1433::Tn10(Tet)</i> (<i>dnaC</i> [95%])	DB9159
99	<i>zjj-3042::Tn10(Tet)</i> (<i>serB</i> [99%], <i>trpR</i> [44%], <i>thrB</i> [0%])	AK3042
99	<i>zjj-3112::Tn10(Tet)</i> (<i>serB</i> [78%], <i>trpR</i> [46%], <i>thrB</i> [0%])	AK3112
99	<i>zjj-3116::Tn10(Tet)</i> (<i>thrB</i> [8%], <i>serB</i> [25%], <i>trpR</i> [76%])	AK3116
99	<i>zjj-3240::Tn10(Tet)</i> (<i>serB</i> [86%], <i>trpR</i> [27%], <i>thrB</i> [0%])	AK3240
NM	<i>arg-1917::MudJ(Kan)</i>	TT11563
NM	<i>btu-151::MudA(Amp)</i>	RT847
NM	<i>btu-6::Tn10(Tet)</i>	RT128
NM	<i>cob-111::Tn10d(Tet)</i>	TT14112
NM	<i>cob-112::Tn10d(Tet)</i>	TT14104
NM	<i>cob-236::Tn10d(Tet)</i>	TT12747
NM	<i>cob-265::Tn10d(Cam)</i>	TT13707
NM	<i>cob-356::Tn10d(Cam)</i>	TT13409
NM	<i>cob-358::Tn10d(Cam)</i>	TT14732
NM	<i>cob-596::MudK(Kan)</i>	TT16578
NM	<i>cob-8::Tn5(Kan)</i>	TT7747
NM	<i>cysA3314::MudJ(Kan)</i>	TT12878
NM	<i>cysB3306::MudJ(Kan)</i>	TT12818
NM	<i>dam-101::Tn10d(Tet)</i>	TT1691
NM	<i>dam-102::MudJ(Kan)</i>	TT11692
NM	<i>dam-103::MudJ(Kan)</i>	TT11693
NM	<i>dam-104::MudJ(Kan)</i>	TT11694
NM	<i>dam-105::MudJ(Kan)</i>	TT11695
NM	<i>dnaQ200::Tn10(Tet)</i>	RM822
NM	<i>eal-1::Tn5(Kan)</i>	TT8101
NM	<i>hem-466::MudJ(Kan)</i>	TT13056
NM	<i>hisD1284::MudK(Kan)</i>	TT10380
NM	<i>ilv-2170::Tn5(Kan)</i>	TT1962
NM	<i>ilv-2652::MudJ(Kan)</i>	TT12065
NM	<i>ilv-2660::Tn10d(Cam)</i>	TT11637
NM	<i>nirA1::Tn10(Tet)</i>	TT15812
NM	<i>nirB2::Tn10(Tet)</i>	TT15813
NM	<i>nirB3::Tn10(Tet)</i>	TT15814
NM	<i>pdu-1::MudA(Amp)</i>	RT811
NM	<i>pdu-12::MudA(Amp)</i>	TT16566
NM	<i>pdu-17::MudA(Amp)</i>	TT16567
NM	<i>pdu-20::MudA(Amp)</i>	TT16568
NM	<i>pdu-3::MudA(Amp)</i>	RT847
NM	<i>pdu-30::Tn10(Tet)</i>	TT10927
NM	<i>pdu-31::Tn10(Tet)</i>	TT11073
NM	<i>pdu-8::MudA(Amp)</i>	TT16565
NM	<i>pps-85::Tn10d(Tet)</i>	RT910
NM	<i>purK2319::Tn10d(Tet)</i>	TT12890
NM	<i>purK2320::Tn10d(Tet)</i>	TT12891
NM	<i>recB546::Mud(Cam)</i>	TT16817
NM	<i>recD541::Tn10d(Cam)</i>	TT16812
NM	<i>recD542::Tn10d(Cam)</i>	TT16813
NM	<i>recD543::Tn10d(Cam)</i>	TT16814
NM	<i>recD543::Tn10d(Tet)</i>	TT16814
NM	<i>recD544::Tn10d(Tet)</i>	TT16815
NM	<i>recF1::Tn5(Kan)</i>	TT11292
NM	<i>recF2::Tn5(Kan)</i>	TT11293
NM	<i>recF522::Tn5(Kan)</i>	TT11292
NM	<i>recJ504::MudJ(Kan)</i>	TT15278
NM	<i>sbcB2::Tn10d(Cam)</i>	TT17602
NM	<i>thr-485::MudJ(Kan)</i>	TT14041
NM	<i>thr-486::MudJ(Kan)</i>	TT14042
NM	<i>tyr-576::MudJ(Kan)</i>	TT12107
NM	<i>zxx-1891::Tn10d(Tet)</i> (<i>purK</i> [70%])	TT12276
NM	<i>zxx-1891::Tn10d(Tet)</i> (<i>purK</i> [70%])	TT12884
NM	<i>zxx-3780::Tn10d(Cam)</i> (<i>purK</i> [80%])	TT12884

CS ^b	Allele no. and linkage ^c	Strain no. ^d
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^aThese mutant strains of *S. typhimurium* LT2 have been isolated in many different laboratories; the largest number come from the laboratory of J. R. Roth. The strains have been provided to the SGSC, where they are maintained and are available for circulation to any investigator.

^bThe centisome (CS) indicates the location on the map at which the transposon listed for the strain is inserted. This location is based on the genetic map of *S. typhimurium* given the chapter 110 of this volume. Since this map is based on physical distances, the locations of some genes are different from this in earlier versions of the linkage map, which were based on genetic distances indicated in minutes (of transfer time in conjunction) (19). The locations of transposon insertions with the same CS numbers are frequently but not always known with respect to each other. For example, at CS2, the insertion in *araB* is counterclockwise from the insertions in *leu* according to the genetic map (displayed as a circle in chapter 128, but the exact locations of the insertions designated *zac* are not known with respect to each other.

^cThe gene into which the transposon is inserted and its allele number are at the left. Insertions into a gene cause loss of gene function, e.g., insertions in *thr* result in a Thr (threonine-requiring) phenotype. Transposon insertions which cause no detectable change in phenotype are designated zxx followed by an allele number. If these insertions have been located on the genetic map (e.g., through linkage to known genes), this designation is changed according to the system of Hong and Ames (11); thus, insertions at 0 CS are *zaa*, insertions at 1 CS are *zab*, etc. The allele number of the mutation produced by the insertion is never changed even if the map position must be changed as data are refined; the second two letters of the designation may be changed to indicate the new map location, but they are frequently not changed, and thus, though these letters are helpful in locating an insertion on the genetic map, they are not always indicate the exact position.

The transposon inserted in each strain is indicated after the double colon; each transposon type is described in more detail in the text. Strains with insertions at the same CS are listed in the alphabetical order of the transposon type. The antibiotic resistance associated with each transposon is indicated in parentheses after the transposon. Some of the data used to locate the site of the transposon insertion are given after the insertion. The percentage is the joint transduction phage P22 between the transposon and the listed gene (%ND, percentage not determined).

^dStrain number of the strain which carries the transposon insertion. (Other strains may carry the same insertion). The full genotype of this strain is not given here, for the strain may carry many other mutations, including some which are linked to the transposon by P22 transduction. These data and details on source and derivation of the strain will be sent by the SGSC on request; see the text or chapter 136 for electronic and other addresses.

The laboratory of origin of the strain is usually indicated by the strain designation, as follows: AK, A. Kukral c/o R. Maurer, Case Western Reserve University; CBS, C. Berg, University of Connecticut; CH, C. Higgins, Oxford University; CJD, C. Dorman, University of Dundee; DA, D. Anton, Argentina (or D. Andersson, Uppsala); DB, D. Berkowitz, Massachusetts Institute of Technology (MIT); DU, R. Burns, Duke University; EB, E. Barrett, University of California at Davis (UC Davis); GW, G. Walker, MIT; HSK; H.S. Kwan, Chinese University of Hong Kong; HU, P. Ayling, University of Hull; JF, J. W. Foster, University of South Alabama; JL, J. Ingraham, UC Davis; KK, K. Kutsukake, Hiroshima Univ.; KP, J. Neuhard, Copenhagen; KR, R. Kellen, University of Regina; KS, W. W. Kay, University of Victoria; MM, M. Maguire, Case Western Reserve University; MS, S. Maloy, University of Illinois; NK, N. Kleckner, Harvard University; NR, D. Podger, Australia; PH, P. Hallenbach, University of Montreal; PM, P. Margolin, c/o SGSC; PP, P. W. Postma, Netherlands; RL, T. VanDyk, DuPont Co.; RT, R. Jeter, Texas Tech. University; SA, K. Sanderson, University of Calgary; SH, P.H. Makela, Finland; SK, S. Kutsu, UC Berkeley; SL, B.A. D. Stocker, Stanford University; SMS, T. VanDyk, DuPont Co.; ST, D. Koshland, UC Berkeley; SV, J. Casadesu, University of Seville; TA, B. N. Ames, UC Berkeley; TE, T. Elliott, University of Alabama; TL, L. Csonka, Purdue University; TN, C. Miller, University of Illinois; TS, T. Palva, Swedish University of Agricultural Science; TT, J. Roth, University of Utah.

ACKNOWLEDGMENTS

We are greatly indebted to the many investigators who provided the strains listed in Table 2 along with published or unpublished genetic information. We thank Tim Galitsky and Nick Benson for their critical comments regarding the manuscript.

Work in Calgary was supported by an Infrastructure Grant and an Operating grant from the Natural Sciences and Engineering Research Council of Canada and by grant R01AI34829 from the National Institute of Allergy and Infectious Diseases. Work in Utah was supported by grant GM27068 from the National Institutes of Health.

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