Text S1: Manure sampling method

Farm 1: Manure was scraped from the alleys into a holding pit at the end of the barn, where it was then processed through a primary and then a secondary digester. The digestate from the secondary digester entered a holding pit as “digestate with solids”, where it was fed through a screw press to remove most of the liquid in the sample. This material was considered a “solid” in the waste stream, and was typically used as bedding in the barn. The liquid was pumped into an outdoor manure pit, for application to the fields. This was know as “digestate without solids”. Sampling points on farm one were as follows: raw manure sample was taken at the barn pit; and digestate with solids was taken at the holding pit after exiting the secondary digester.

Farm 2: Manure was scraped from the alleys into a holding pit at the end of the barn, where it was then processed through a primary and then a secondary digester. The digestate from the secondary digester entered a holding pit as “digestate with solids”. The liquid was pumped into an outdoor manure pit, for application to the fields. Sampling points on farm two were as follows: raw manure sample was taken at the barn pit; and digestate with solids was taken at the sampling port on the secondary digester.

Farm 3: Manure was scraped from the alleys into a holding pit at the end of the barn, where it was then processed through a primary and then a secondary digester. The digestate from the secondary digester entered a holding pit as “digestate with solids”, where it was fed through a screw press to remove most of the liquid in the sample. This material was considered a “solid” in the waste stream, and was typically used as bedding in the barn. The liquid now was pumped into an outdoor manure pit, for application to the fields. This was know as “digestate without solids”. Sampling

points on farm three were as follows: raw manure sample was taken at the barn pit; and digestate with solids was taken at the sampling port on the secondary digester.

Farm 4: Manure was scraped from the alleys into a holding pit at the end of the barn, where it was then processed through a primary and then a secondary digester. The digestate from the secondary digester entered a holding pit as “digestate with solids”. The liquid was pumped into an outdoor manure pit, for application to the fields. Sampling points on farm four were as follows: raw manure sample was taken at the barn pit; and digestate with solids was taken at the sampling port on the secondary digester.

Farm 5: This large dairy farm had two barns as well as two mesophilic (primary and secondary) digesters and one thermophilic digester, known as digester three. Manure was scraped from the alleys into a holding pit at the end of the barn, and transferred to a larger secondary holding pit where it was then processed through a primary and secondary digester, and then finally through the thermophilic digester. The digestate from digester three entered a holding pit as “digestate with solids”, where it was fed through a screw press to remove most of the liquid in the sample. This material was considered a “solid” in the waste stream, and is typically used as bedding in the barn. The liquid now is pumped into an outdoor manure pit, for application to the fields. This was known as “digestate without solids”. Sampling points on farm five were as follows: raw manure sample was taken at the barn pit; and digestate with solids was taken at two points (the sampling port on the secondary digester as well as at the holding pit after exiting the thermophilic digester).

Farm 6: This farm was not sampled for this present study.

Farm 7: This large dairy farm had multiple barns and only one large scale digester. Manure was scraped from the alleys into a holding pit at the end of the barns, where it was then pumped into a

large indoor mixing/holding pit. Manure was then fed through the digester. The digestate from the digester entered a digestate holding pit as “digestate with solids”, where it was fed through a screw press to remove most of the liquid in the sample and further treated with heat. This material was considered a “solid” in the waste stream, and was typically used as bedding in the barn. The liquid was pumped into an outdoor manure pit, for application to the fields. This was know as “digestate without solids”. Sampling points on farm seven were as follows: raw manure sample was taken at the indoor holding pit; and digestate with solids was taken at the digestate holding pit after exiting the digester.

Table S1: Distribution of restriction enzyme profiles of captured plasmids in raw and digested samples.

Profile designation	Farm	Representative sequenced plasmid	Raw		Digested	
			By sample	By plasmid	By sample	By plasmid
1	1	pT156A	0	0	1	10
2	2	pT295A	0	0	1	10
3	1, 2, 3, 4, 5, 7	pT267A	30	176	31	202
4	1	pT145A	1	10	0	0
5	2	pT247A	2	20	0	0
6	5	pT413A	1	2	1	10
7	3	pT308A	1	3	0	0
8	7	pT476A	0	0	1	5
9	7	pT224A	0	0	1	2
10	1	pT277A	1	9	0	0
Total			36	220	36	239

By sample: The number of manure samples where each plasmid profile was found

By plasmid: The number of isolated plasmids likely shared the same plasmid profile

Table S2: SNPs between a reference genome (T159A) and Illumina sequence reads from other transconjugants'genomes using SNIPPY

Strain ID	T221A			T286A			T304A			T306A			T409A			T478A			T496A		
	POS	REF	ALT	POS	REF	ALT	POS	REF	ALT	POS	REF	ALT	POS	REF	ALT	POS	REF	ALT	POS	REF	ALT
	9549	T	C	63985	C	T	4333	G	T	64545	A	C	9549	T	C	79357	T	C	77820	C	A
				77820	C	A	64545	A	C	9549	T	C	1171	A	G	9549	T	C	9549	T	C
				9549	T	C	9549	T	C				342	T	C	336	C	T	1171	A	G
													387	A	G	342	T	C	336	C	T
													519	T	C	387	A	G	342	T	C
																			387	A	G
																			519	T	C
Variant-SNPs	1			3			3			2			5			5			7		

POS: position on the reference genome, REF: a nucleotide on the reference genome, ALT: an alternative nucleotide on a mapping genome.

Table S3: AMR genes detected with the ABRicate tool.

Plasmids	AMR genes
pT247A	*bla*$_{\text{CTX-M-14}}$ (100%)
pT257A	*bla*$_{\text{CTX-M-27}}$ (100%), *catB4* (19.49 %), *catB4* (19.67 %), *ant(3'')-Ia* (17%)
pT156A	*bla*$_{\text{CTX-M-55}}$ (100%), *bla*$_{\text{TEM-141}}$ (86.64%), *catB4* (19.49 %), *catB4* (19.67 %), *ant(3'')-Ia* (17%)
pT224A	*bla*$_{\text{CTX-M-55}}$ (100%), *fosA3* (100%), *bla*$_{\text{TEM-141}}$ (86.64%), *catB4* (19.49 %), *catB4* (19.67 %), *ant(3'')-Ia* (17%)
pT199A	*bla*$_{\text{CTX-M-1}}$ (100%), *catB4* (19.49 %)
pT82A	*lnu(B)* (99.75%), *aadA14* (100%), *catB4* (100%), *bla*$_{\text{OXA-1}}$ (100%), *aac(6')Ib-cr* (100%), *bla*$_{\text{CTX-M-15}}$ (100%), *floR* (99.92%), *aph(6)-Id* (100%), *aph(3'')-Ib* (100%), *sul2* (100%), *dfrA1* (100%), *catB4* (19.49 %)
pT101A	*lnu(B)* (99.75%), *aadA14* (100%), *catB4* (100%), *bla*$_{\text{OXA-1}}$ (100%), *aac(6')Ib-cr* (100%), *bla*$_{\text{CTX-M-15}}$ (100%), *floR* (99.92%), *aph(6)-Id* (100%), *aph(3'')-Ib* (100%), *sul2* (100%), *dfrA1* (100%), *catB4* (19.49 %)
pT159A	*lnu(B)* (99.75%), *aadA14* (100%), *catB4* (100%), *bla*$_{\text{OXA-1}}$ (100%), *aac(6')Ib-cr* (100%), *bla*$_{\text{CTX-M-15}}$ (100%), *floR* (99.92%), *aph(6)-Id* (100%), *aph(3'')-Ib* (100%), *sul2* (100%), *dfrA1* (100%), *catB4* (19.49 %)
pT209A	*lnu(B)* (99.75%), *aadA14* (100%), *catB4* (100%), *bla*$_{\text{OXA-1}}$ (100%), *aac(6')Ib-cr* (100%), *bla*$_{\text{CTX-M-15}}$ (100%), *floR* (99.92%), *aph(6)-Id* (100%), *aph(3'')-Ib* (100%), *sul2* (100%), *dfrA1* (100%), *catB4* (19.49 %)
pT267A	*lnu(B)* (99.75%), *aadA14* (100%), *catB4* (100%), *bla*$_{\text{OXA-1}}$ (100%), *aac(6')Ib-cr* (100%), *bla*$_{\text{CTX-M-15}}$ (100%), *floR* (99.92%), *aph(6)-Id* (100%), *aph(3'')-Ib* (100%), *sul2* (100%), *dfrA1* (100%), *catB4* (19.49 %)
pT270A	*lnu(B)* (99.75%), *aadA14* (100%), *catB4* (100%), *bla*$_{\text{OXA-1}}$ (100%), *aac(6')Ib-cr* (100%), *bla*$_{\text{CTX-M-15}}$ (100%), *floR* (99.92%), *aph(6)-Id* (100%), *aph(3'')-Ib* (100%), *sul2* (100%), *dfrA1* (100%), *catB4* (19.49 %)

The percentages in the brackets above indicate the coverage of sequences detected on these plasmids compared to the reported gene in the database

Table S4: Antimicrobial resistance phenotype of *E. coli* CV601 used as the recipient in patch matings.

Antibiotics	*E. coli* recipient CV601	
	MIC (mg/L)	Interpretation
Amikacin	32	I
Amoxicillin/Clavulanic Acid	4	S
Ampicillin	4	S
Ampicillin/Sulbactam	≤ 4	S
Azithromycin	2	NI
Aztreonam	≤ 8	I
Cefazolin	≤ 4	I
Cefepime	≤ 4	SD
Cefotaxime	≤ 0.25	S
Cefotetan	≤ 8	S
Cefoxitin	8	S
Cefpodoxime	≤ 2	S
Ceftazidime	≤ 1	S
Ceftiofur	0.5	NI
Ceftriaxone	≤ 1	S
Cefuroxime (sodium)	≤ 4	S
Chloramphenicol	4	S
Ciprofloxacin	≤ 0.5	S
Gatifloxacin	≤ 1	NI
Gentamicin	≤ 2	S
Imipenem	≤ 2	I
Meropenem	≤ 1	S
Nalidixic Acid	8	NI
Nitrofurantoin	≤ 16	S
Piperacillin	≤ 16	S
Piperacillin/Tazobactam	≤ 16	S
Streptomycin	4	NI
Sulfisoxazole	128	NI
Tetracycline	≤ 4	S
Ticarcillin/Clavulanic Acid	≤ 16	S
Trimethoprim/Sulfamethoxazole	≤ 0.5	S

The results were interpreted by the Sensititre™ automated system. R: Resistant, I: Intermediate, S: Susceptible, SD: susceptible-dose dependent, NI: No interpretation

Table S5: A full list of drugs used in participating farms

Farm	Drugs used
1	No drugs/antibiotics were recoded as being used regularly
2	Borgal (Trimethoprim), Depocillin (Procaine Penicillan G), Excede (Ceftiofur), Excentel RT4 (Ceftiofur), Micotil (Tilmicosin), Nuflor (Florfenicol), Polyflex (Ampicillin), Resflor (Florfenicol), Trimidox (Trimethoprim-Sulfadoxine), Zuprevo (Tildipirosin Injection, 180 mg/mL)
3	Trimidox (Trimethoprim-Sulfadoxine), Excede (Ceftiofur), Pennicillin, Polyflex (Ampicillin), Cefa Dry (Cephapirin benzathine), Special Formula 17900 Cefa Lacc (Cephapirin), Spectro mast (Ceftiofur)
4	Nuflor (Florfenicol), Excede 200 (Ceftiofur), Excentel RT4 (Ceftiofur), Dexamethazone 5 (prednisolone), Predef 2X (isoflupredone acetate) , Metacam (Meloxicam), Anafen (Ketoprofen), LP Oxitet (Oxytetracycline), Res4 (IBR)
5	Liquamycin (Oxytetracycline), Trivetrin (Trimethoprim, sulfadoxine), and Penicillin
7	Anafen (Ketoprofen), A180 (Danoflaxacin), Banamine (Flunixin-meglumine), Borgal (Trimethoprim), Cefa Dry (Cephapirin benzathine), Cefa Lak (Cephapirin), Cystorelin (Gonadorelin diacetate tetrahydrate), Depocillin (Procaine Penicillan G), Dexamethasone 5 (Dexamethasone sodium phosphate), Draxxin (tulathromycin), Dupocillin (Procaine Benzathine Penicillan G), Eprine X (Eprinomectin), Erthyo-36 (Erythromycin), Estrumate (Cloprostenol), Excede (Ceftiofur), Excentel RT4 (Ceftiofur), Flucor T (Flumetasone), Inforce 3 (BRSV, IBR, Parainfluenza), Lincomycin

(Lincomycin), Metacam (Meloxicam), Micotil (Tilmicosin), Nuflor (Florfenicol), Pen G (Penicillin G procaine), Pirsue (Pirlimycin hydrochloride), Polyflex (Ampicillin), Predef (Isoflupredone acetate), Resflor (Florfenicol), Res4 (IBR), Rumensin (Monensin), Spectro Mast (Ceftiofur), Trivetrin (Trimethoprim, sulfadoxine)

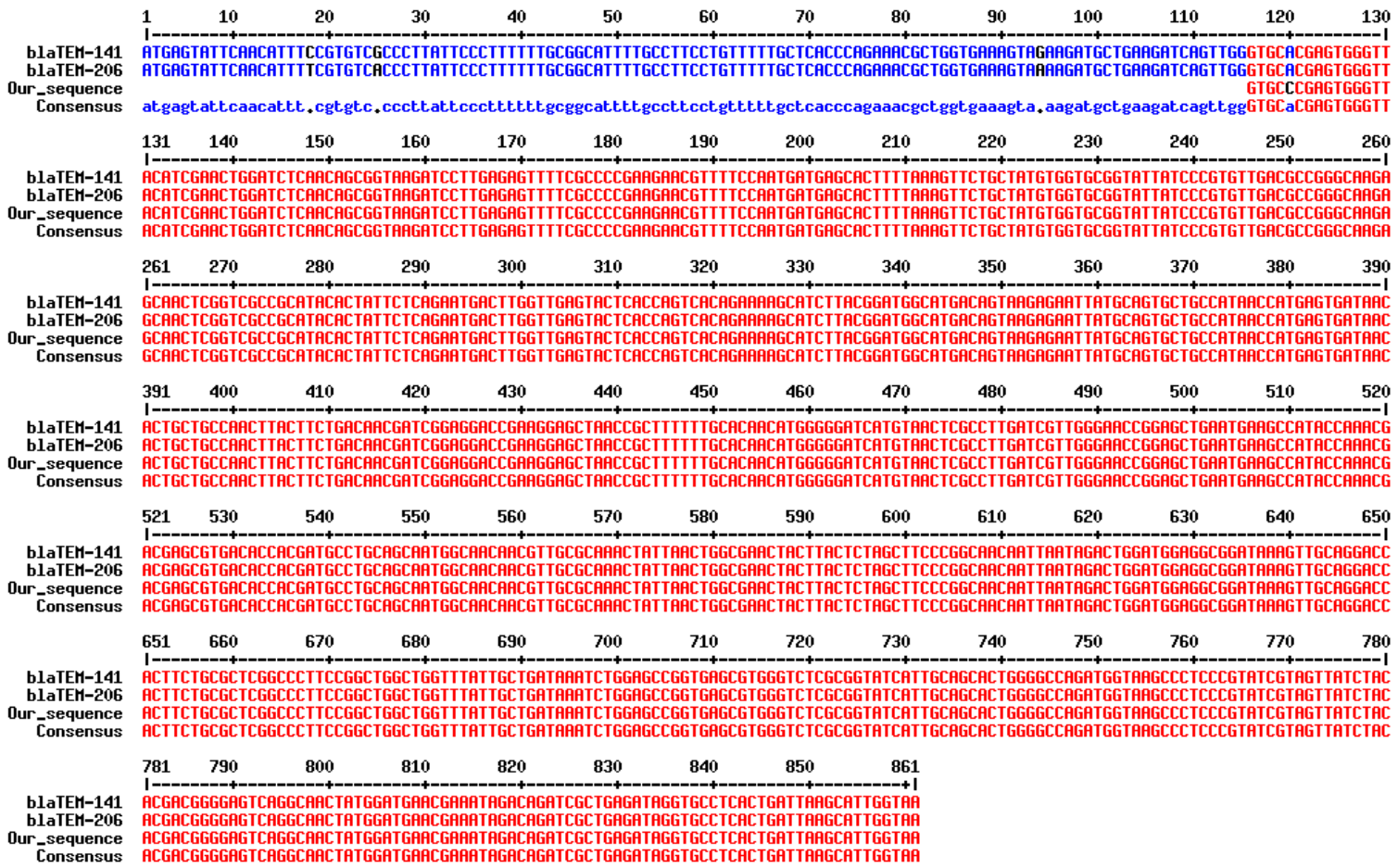

Fig. S1: Multiple sequence alignment of different *bla*$_{\text{TEM}}$ variants (*bla*$_{\text{TEM-141}}$ and *bla*$_{\text{TEM-206}}$) obtained from the Comprehensive Antibiotic Resistance Database (https://card.mcmaster.ca/) with our sequence using online tool (http://multalin.toulouse.inra.fr/multalin/).

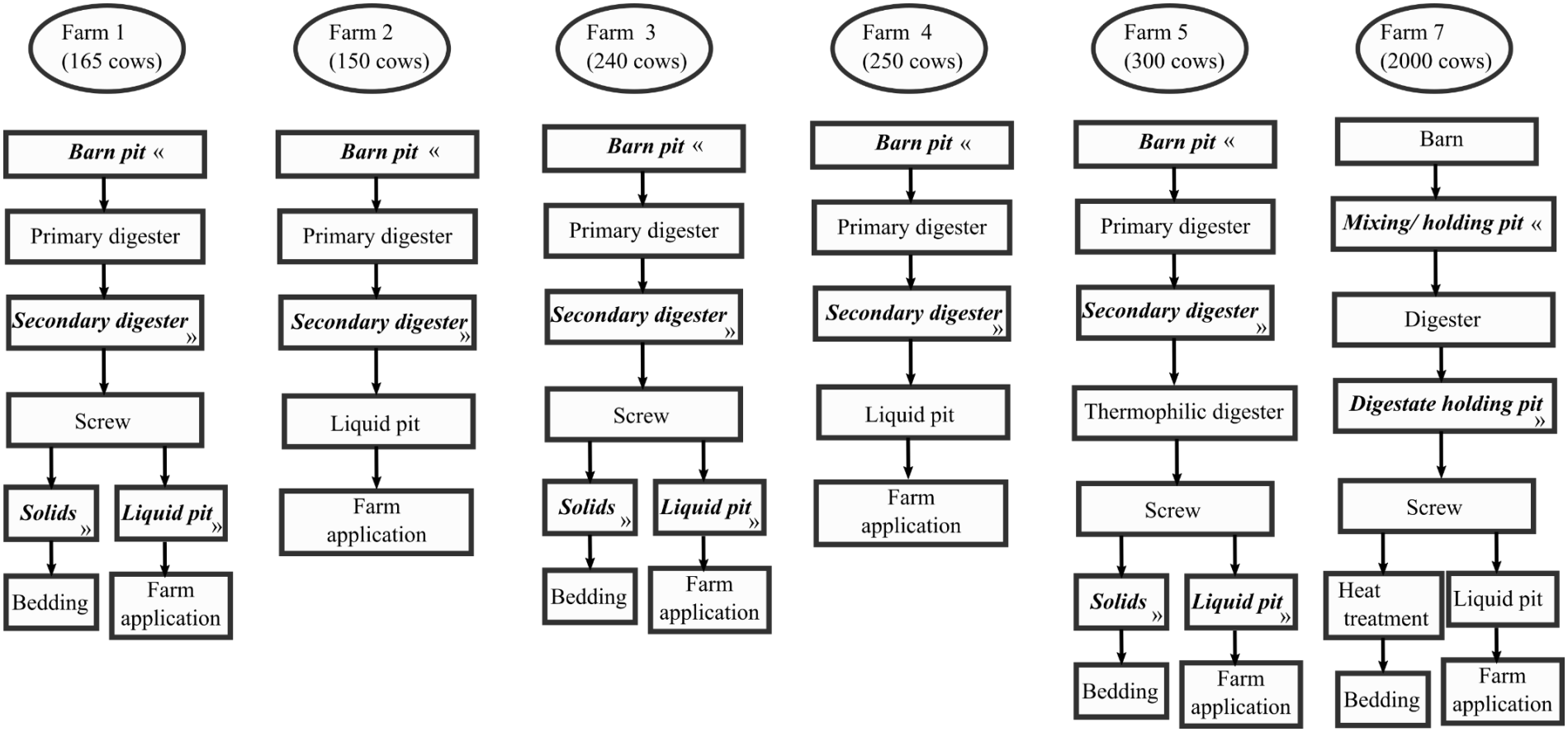

Fig. S2: A flow chart depicting anearobic digestion stages for each farm. Bold italic text indicates where raw («) and digested (») samples were taken.