1   SUPPLEMENTARY TABLES

2   TABLE S1. Terminal restriction fragments (TRF) of heat-sensitive bacteria associated with *E.*
3   *coli* O157:H7 suppression in the August 2008 experiment (n=4)[a]

		Frequency of 31 candidate TRF[b]			
Dpi[c]	Bedding source[d]	Fluorescence NH > HT (A)[e]	Negative Regression (B)[f]	Fluorescence and Regression (A + B)[g]	TRF[h]
1	Fresh	10	8	4	99, 466, 480, 488
1	In-use[i]	6	2	0	--
1	Washed[i]	6	0	0	--
1	Recycled[i]	0	17	0	--
15	Fresh	5	18	4	75, **130**, **139**, **156**
15	In-use[i]	11	23	10	66, **130**, 136, **139**, 142, 153, **156**, 490, 492, 495
15	Washed[i]	6	0	0	--
15	Recycled	3	10	0	--

4   [a] Farm-derived livestock bedding samples each split into a non-heated (NH) and a heated (HT) sample were used for
5   a TRF analysis: TRFs <300 nt were at an accuracy of ± 1 nt; TRFs >300 nt were binned at ± 2 nt. Fragments that
6   occurred in more than one context are in bold.
7   [b] Thirty-one candidate TRFs with higher fluorescence in NH than the corresponding HT of a particular bedding
8   source were identified by visual inspection of interval plots.
9   [c] After cooling, samples were inoculated with a suspension of *E. coli* O157:H7, and incubated at 21 °C in the dark in
10   the laboratory. One and 15 dpi, colony forming units (CFU) of *E. coli* O157:H7 were determined, and DNA was
11   extracted.
12   [d] Livestock bedding from a sand recycling system at four independent strata: (i) Fresh, front of the cow box; (ii) In-
13   use, back of the cow box; (iii) Washed, used material from the pile following the sand manure separation; and (iv)
14   Recycled, rested (≥ 2 days) in a pile of washed material.
15   [e] The frequency of NH with stronger fluorescence than HT equivalents was determined by Mood's Median test at *P*
16   = 0.05; parameter (A).
17   [f] The frequency of the thirty-one candidate fragments that had a negative regression with CFUs of *E. coli*; parameter
18   (B).
19   [g] The frequency of TRFs that fulfilled both requirement (A) and (B).
20   [h] Identification of TRFs that fulfilled both requirements (A) and (B).
21   [i] CFU of *E. coli* O157:H7 were only numerically higher in HT than NT bedding material.

TABLE S2. Terminal restriction fragments (TRF) of heat-sensitive bacteria associated with *E. coli* O157:H7 suppression in the November 2008 experiment, n=8[a]

Dpi[c]	Bedding source[d]	Frequency of 67 candidate TRF[b]			TRF[h]
		Fluorescence NH > HT (A)[e]	Negative Regression (B)[f]	Fluorescence and Regression (A + B)[g]	
1	Fresh	18	2	0	--
1	In-use[i]	17	16	7	**96**, **145**, **151**, **299**, **488**, 545, **548**
1	Washed[i]	13	12	4	**96**, **99**, **299**, 556
1	Recycled	11	5	1	**118**
7	Fresh	31	16	11	**87**, **89**, **94**, **112**, **115**, **142**, 149, **151**, **299**, 496, 541
7	In-use[i]	28	44	26	**87**, **89**, 92, **94**, **96**, **99**, **112**, **115**, **130**, **136**, 139, **142**, **145**, 147, 149, **297**, **299**, 456, 466, 469, **483**, 486, **488**, 496, 541, 550
7	Washed	35	0	0	--
7	Recycled	32	24	19	**94**, **99**, **118**, 122, **130**, **136**, 156, 202, 272, 275, 278, 280. 282, **297**, **299**, **483**, 546, **548**, 551

[a] Farm-derived livestock bedding samples each split into non-heated (NH) and heated (HT), and used for TRF analysis; TRFs <300 nt were at an accuracy of ± 1 nt; TRFs >300 nt were binned at ± 2 nt. Fragments that occurred in more than one context are in bold.

[b] Sixty-seven candidate TRFs with higher fluorescence in NH than the corresponding HT of a particular source were determined by visual inspection of interval plots.

[c] After cooling, samples were inoculated with a suspension of *E. coli* O157:H7, and incubated in the dark at 21 °C in the laboratory. One and seven dpi, colony forming units (CFU) of *E. coli* O157:H7 were determined and DNA extracted.

[d] Livestock bedding from a sand recycling system at eight independent strata of each of the following: (i) Fresh, front of the cow box; (ii) In-use, back of the cow box; (iii) Washed, used material from the pile following the sand manure separation; and (iv) Recycled, rested (≥ 2 days) in a pile of washed material.

[e] The frequency of NH with stronger fluorescence than HT equivalents was determined by Mood's Median test at $P = 0.05$; parameter (A).

[f] The frequency of the sixty-seven candidate fragments that had a negative regression with CFUs of *E. coli* O157:H7; parameter (B).

[g] The frequency of TRFs that fulfilled both requirement (A) and (B).

[h] Identification of TRFs that fulfilled both requirements (A) and (B).

TABLE S3. Terminal restriction fragments (TRF) of heat-sensitive bacteria associated with *E. coli* O157:H7 suppression in the March 2009 experiment, n=8[a]

Dpi[c]	Bedding source[d]	Frequency of 78 candidate TRF[b]			TRF[h]
		Fluorescence NH>HT (A)[e]	Negative Regression (B)[f]	Fluorescence and Regression (A + B)[g]	
1	Fresh	33	19	11	**89**, 139, **142, 145, 149, 156, 184**, 465, 486, 533, **537**
1	In-use	27	38	17	66, **85, 89, 96, 142, 149 152, 156, 184, 299, 308, 492, 495, 537**, 548, **550**, 554
1	Washed	21	24	5	**87, 89, 142, 492**, 508
1	Recycled	21	28	17	**89, 96**, 99, **147, 156, 299**, 304, **308**, 488, **492, 495**, 500, 503, 505, **547, 550**, 555
10	Fresh	15	17	2	163, **550**
10	In-use	30	35	15	*85*, **87**, 136, **142, 145, 147, 152**, 163, 202, 222, 304, 488, **492, 495**, 499
10	Washed	24	16	3	92, 94, **547**
10	Recycled	17	15	1	122

[a] Farm-derived livestock bedding samples each split into non-heated (NT) and heated (HT), and used for TRF analysis; TRFs <300 nt were at an accuracy of ± 1 nt; TRFs >300 nt were binned at ± 2 nt. Fragments that occurred in more than one context are in bold.

[b] Seventy-eight candidate TRFs with higher fluorescence in NH than the corresponding HT of a particular source were determined by visual inspection of interval plots.

[c] After cooling, samples were inoculated with a suspension of *E. coli* O157:H7, and incubated at 21 °C in the dark in the laboratory. One and ten dpi, colony forming units (CFU) of *E. coli* O157:H7 were determined and DNA extracted.

[d] Livestock bedding from a sand recycling system at eight independent strata of each of the following: (i) Fresh, front of the cow box; (ii) In-use, back of the cow box; (iii) Washed, used material from the pile following the sand manure separation; and (iv) Recycled, rested (≥ 2 days) in a pile of washed material.

[e] The frequency of NH with stronger fluorescence than HT equivalents was determined by Mood's Median test at *P* = 0.05; parameter (A).

[f] The frequency of the seventy-eight candidate fragments that had a negative regression with CFUs of *E. coli* O157:H7 were noted; parameter (B).

[g] The frequency of TRFs that fulfilled both requirement (A) and (B).

[h] Identification of TRFs that fulfilled both requirements (A) and (B).

1 TABLE S4. Terminal restriction fragments (TRF) of bacteria found to be more abundant
2 in non-heated (NH) recycled or washed bedding samples on 1 dpi or 7 dpi, respectively,
3 associated with *E. coli* O157:H7 suppression in the 10 November Experiment, n=8[a]

Recycled[c] versus Dpi[d]	Frequency of 29 candidate TRF[b]			TRF[h]
	Fluorescence Suppressive > other (A)[e]	Negative regression (B)[f]	Fluorescence and Regression (A + B)[g]	
1 Fresh[c]	13	9	6	**118**, *297*, **299, 302, 306, 508**
1 In-use[c]	9	9	5	*83*, **118**, *299*, **302**, *306*
1 Washed[c]	7	9	4	*83*, **118, 302, 508**
Washed[c] versus	Frequency of 28 candidate TRFs[b]			TRFs[h]
7 Fresh[c]	12	n/a[i]	n/a	**118, 202**, 269, **272, 275, 276, 278, 280, 282**, 297, **543**, 548
7 In-use[c]	10	n/a	n/a	**92, 118, 202, 272, 275, 276, 278, 280, 282, 543**
7 Recycled[ej]	10	n/a	n/a	**92, 118, 202, 272, 275, 276, 278, 280, 282, 543**

4 [a] Farm-derived livestock bedding samples each split into a non-heated (NH) and a heated (HT) sample were
5 used for TRF analysis; TRFs <300 nt were at an accuracy of ± 1 nt; TRFs >300 nt were binned at ± 2 nt.
6 TRFs that occurred in more than one context are in bold; values of NH samples were compared.
7 [b] Twenty-nine (or 28) candidate TRFs with higher fluorescence in the most suppressive NH source
8 compared to the other NH sources at 1 dpi or 7 dpi were determined by visual inspection of interval plots.
9 [c] Livestock bedding from a sand recycling system at eight independent strata of each of the following: (i)
10 Fresh, front of the cow box; (ii) In-use, back of the cow box; (iii) Washed, used material from the pile
11 following the sand manure separation; and (iv) Recycled, rested (≥ 2 days) in a pile of washed material.
12 [d] After cooling, samples were inoculated with a suspension of *E. coli* O157:H7, and incubated in the dark at
13 21 °C in the laboratory. One and seven dpi, colony forming units (CFU) of *E. coli* O157:H7 were
14 determined and DNA extracted.
15 [e] The frequency of the more suppressive source with stronger fluorescence than the less suppressive
16 sources was determined by Mood's Median test at $P = 0.05$; parameter (A).
17 [f] The frequency of the 29 candidate fragments that had a negative regression with CFUs of *E. coli*;
18 parameter (B).
19 [g] The frequency of TRFs that fulfilled both requirement (A) and (B).
20 [h] Identification of TRFs that fulfilled both requirements (A) and (B); only (A) for samples from 7 dpi.
21 [i] No CFUs were detected in the Washed bedding material. No test for regression could be conducted. The
22 higher frequency of TRFs is considered an overestimate of those involved in *E. coli* O157:H7
23 suppressiveness.
24 [j] CFU of *E. coli* O157:H7 were only numerically higher in the Recycled than the Washed bedding material.
25

1 TABLE S5. Terminal restriction fragments (TRF) of bacteria found to be more abundant
2 in non-heated (NH) recycled bedding samples and concomitant with *E. coli* O157:H7
3 suppression in a 23 March Experiment, n=8[a]

Dpi[c]	Recycled[d] versus	Frequency of 14 candidate TRF[b]			TRF[h]
		Fluorescence Suppressive > other (A)[e]	Negative regression in Recycled (B)[f]	Fluorescence and Regression (A + B)[g]	
1	Fresh[id]	8	10	7	99, **308**, **500**, **505**, **508**, 555, **623**
1	In-use[d]	5	10	4	**500**, **505**, **508**, **623**
1	Washed[d]	4	10	3	304, **308**, **505**
	Washed[d] versus	Frequency of 11 candidate TRFs			
10	Fresh[d]	3	3	0	--
10	In-use[dj]	2	3	0	--
	Recycled[d] versus	Frequency of 11 candidate TRFs			
10	Fresh[d]	3	0	0	--
10	In-use[dj]	2	0	0	--

4 [a] Farm-derived livestock bedding samples each split into a non-heated (NH) and a heated (HT) sample, and
5 used for TRF analysis; TRFs <300 nt were at an accuracy of ± 1 nt; TRFs >300 nt were binned at ± 2 nt.
6 TRFs that occurred in more than one context are high-lighted in bold; values of NH samples were
7 compared.
8 [b] Fourteen (11, 11) candidate TRFs with higher fluorescence in more suppressive than the less suppressive
9 were determined by visual inspection of interval plots.
10 [c] After cooling, samples were inoculated with a suspension of *E. coli* O157:H7, and incubated at 21 °C in
11 the dark in the laboratory. One and ten dpi, colony forming units (CFU) of *E. coli* O157:H7 were
12 determined and DNA extracted.
13 [d] Livestock bedding from a sand recycling system at eight independent strata of each of the following: (i)
14 Fresh, front of the cow box; (ii) In-use, back of the cow box; (iii) Washed, used material from the pile
15 following the sand manure separation; and (iv) Recycled, rested (≥ 2 days) in a pile of washed material.
16 [e] The frequency of the more suppressive source with stronger fluorescence than the less suppressive
17 sources was determined by Mood's Median test at $P = 0.05$ and recorded; parameter (A).
18 [f] The frequency of the candidate TRFs that had a negative regression with CFUs of *E. coli* O157:H7;
19 parameter (B).
20 [g] The frequency of TRFs that fulfilled both requirement (A) and (B).
21 [h] Identification of TRFs that fulfilled both requirements (A) and (B).
22 [i] The CFU of *E. coli* O157:H7 were not significantly different from the counts in Recycled samples.
23 [j] The CFU of *E. coli* O157:H7 were not significantly different from the counts in Washed, Recycled, or
24 Fresh samples.