



**Figure S1, Agarose gel electrophoresis of Taq I-digested class 1 integron for *Salmonella enterica* serovar Schwarzengrund.**

Lanes: M, Gene Ruler 100 bp Plus Ladder (Thermo Fisher Scientific K.K., Tokyo); 1, Sal\_G1\* (2017, *aac(6')*-*Iaa-aadA1-tetA-sul1-dfrA14-aphA1*); 2, Sal\_T1 (2008, *aac(6')*-*Iaa-aadA1-tetA-sul1-dfrA14-aphA1*); 3, Sal\_T5 (2008, *aac(6')*-*Iaa-aadA1-tetA-sul1-dfrA14-aphA1*); 4, Sal\_T15 (2008, *aac(6')*-*Iaa-aadA1-tetA-sul1-dfrA14*); 5, Sal\_T22 (2008, *aac(6')*-*Iaa-aadA1-tetA-sul1-dfrA14*); 6, Sal\_G1\* (2017, *aac(6')*-*Iaa-aadA1-tetA-sul1-dfrA14-aphA1*); 7, Sal\_17 (2015, *aac(6')*-*Iaa-aadA1-tetA-sul1-aphA1*); 8, Sal\_100 (2016, *aac(6')*-*Iaa-aadA1-tetA-sul1*); 9, Sal\_112 (2016, *aac(6')*-*Iaa-aadA1-tetA-sul1-dfrA14-aphA1*); 10, Sal\_152 (2016, *aac(6')*-*Iaa-aadA1-tetA-sul1-dfrA14-aphA1*). Taq I-digested PCR products of class 1 integron were resolved in 2% agarose through electrophoresis. Isolation year and the detected antimicrobial resistance genes for each isolate are shown in parentheses.

\* The nucleotide sequence of Class 1 integron of Sal\_G1 was determined via DNA sequence analysis.

All nine isolates shown in this figure were identified as sequence type 241 through multilocus sequence typing.

Table S1. Antimicrobial resistance genes determined by ResFinder

| Antimicrobial<br>resistance gene | Sal_167 <sup>(a)</sup>                             | Sal_249               | Sal_266              | Sal_278               | Sal_291              |
|----------------------------------|--|-----------------------|----------------------|-----------------------|----------------------|
| <i>aac(6')-Iaa</i>               | 438/438 <sup>(b)</sup><br>NC_003197 <sup>(c)</sup> | 438/438<br>NC_003197  | 438/438<br>NC_003197 | 438/438<br>NC_003197  | 438/438<br>NC_003197 |
| <i>ant(3'')-Ia (aadA1)</i>       | 972/972<br>X02340                                  | 972/972<br>X02340     | ND                   | 972/972<br>X02340     | ND                   |
| <i>aph(3'')-Ib (strA)</i>        | ND   | ND                    | ND                   | ND                    | 804/804<br>AF321551  |
| <i>aph(6)-Id (strB)</i>          | ND   | ND                    | ND                   | ND                    | 837/837<br>M28829    |
| <i>aph(3')-Ia (aphA1)</i>        | ND   | 816/816<br>X62115     | 816/816<br>X62115    | 816/816<br>X62115     | 816/816<br>X62115    |
| <i>tetA</i>                      | 1241/1275<br>AF534183                              | 1200/1200<br>AJ517790 | ND                   | 1240/1275<br>AF534183 | ND                   |
| <i>sul1</i>                      | 839/840<br>U12338                                  | 840/840<br>U12338     | ND                   | 837/840<br>U12338     | ND                   |
| <i>sul2</i>                      | ND   | ND                    | ND                   | ND                    | 816/816<br>AY034138  |
| <i>dfrA14</i>                    | 474/474<br>AF393510                                | 474/474<br>AF393510   | ND                   | 474/474<br>AF393510   | 474/474<br>AF393510  |

(a) Isolate code; (b) Alignment Length/Gene Length; (c) Accession no.

ND, not determined

Coverage, 97.25-100

Table S2. Sequence types obtained by multilocus sequence typing for representative *Salmonella enterica* serovar Schwarzengrund isolates from retail chicken meat in Japan

|            | Year    | Isolate no.                     | Antimicrobial resistance gene                   | MLST analysis       |                       |
|------------|---------|---------------------------------|---|---------------------|-----------------------|
|            |         |                                 |   | ST                  | Allelic profile       |
| West Japan | 2008    | Sal_T1                          | <i>aac(6')-Iaa-aadA1-tetA-sul1-dfrA14-aphA1</i> | 241                 | 43-47-49-16-41-15-3   |
|            |         | Sal_T5                          | <i>aac(6')-Iaa-aadA1-tetA-sul1-dfrA14-aphA1</i> | 241                 | 43-47-49-16-41-15-3   |
|            |         | Sal_T15                         | <i>aac(6')-Iaa-aadA1-tetA-sul1-dfrA14</i>       | 241                 | 43-47-49-16-41-15-3   |
|            |         | Sal_T22                         | <i>aac(6')-Iaa-aadA1-tetA-sul1-dfrA14</i>       | 241                 | 43-47-49-16-41-15-3   |
|            |         | Sal_T29                         | <i>aac(6')-Iaa-aadA1-tetA-sul1-dfrA14</i>       | 241                 | 43-47-49-16-41-15-3   |
|            |         | Sal_T30                         | <i>aac(6')-Iaa-aadA1-tetA-sul1-aphA1</i>        | 241                 | 43-47-49-16-41-15-3   |
|            | 2016    | Sal_247                         | <i>aac(6')-Iaa-aadA1-tetA-sul1-dfrA14-aphA1</i> | 241                 | 43-47-49-16-41-15-3   |
|            | 2017    | Sal_276                         | <i>aac(6')-Iaa-aadA1-tetA-sul1-dfrA14-aphA1</i> | 241                 | 43-47-49-16-41-15-3   |
| Sal_G4     |         | <i>aac(6')-Iaa-dfrA14-aphA1</i> | 241   | 43-47-49-16-41-15-3 |                       |
| East Japan | 2015    | Sal_17                          | <i>aac(6')-Iaa-aadA1-tetA-sul1-aphA1</i>        | 241                 | 43-47-49-16-41-15-3   |
|            | 2016    | Sal_100                         | <i>aac(6')-Iaa-aadA1-tetA-sul1</i>              | 241                 | 43-47-49-16-41-15-3   |
|            |         | Sal_112                         | <i>aac(6')-Iaa-aadA1-tetA-sul1-dfrA14-aphA1</i> | 241                 | 43-47-49-16-41-15-3   |
|            |         | Sal_145                         | <i>aac(6')-Iaa-aphA1</i>                        | 241                 | 43-47-49-16-41-15-3   |
|            |         | Sal_152                         | <i>aac(6')-Iaa-aadA1-tetA-sul1-dfrA14-aphA1</i> | 241                 | 43-47-49-16-41-15-3   |
|            |         | Sal_167                         | <i>aac(6')-Iaa-aadA1-tetA-sul1-dfrA14</i>       | 241                 | * 43-47-49-16-41-15-3 |
|            |         | Sal_249                         | <i>aac(6')-Iaa-aadA1-tetA-sul1-dfrA14-aphA1</i> | 241                 | * 43-47-49-16-41-15-3 |
|            | 2017    | Sal_270                         | <i>aac(6')-Iaa-strA/B-sul2-dfrA14-aphA1</i>     | 241                 | 43-47-49-16-41-15-3   |
|            |         | Sal_G27                         | <i>aac(6')-Iaa-aphA1</i>                        | 241                 | 43-47-49-16-41-15-3   |
|            |         | Sal_266                         | <i>aac(6')-Iaa-aphA1</i>                        | 241                 | * 43-47-49-16-41-15-3 |
|            |         | Sal_278                         | <i>aac(6')-Iaa-aadA1-tetA-sul1-dfrA14-aphA1</i> | 241                 | * 43-47-49-16-41-15-3 |
|            |         | 2019                            | Sal_301   | <i>aac(6')-Iaa</i>  | 241                   |
|            | Sal_291 |                                 | <i>aac(6')-Iaa-strA/B-sul2-dfrA14-aphA1</i>     | 241                 | * 43-47-49-16-41-15-3 |
| Domestic** | 2015    | Sal_63                          | <i>aac(6')-Iaa-aadA1-tetA-sul1-dfrA14-aphA1</i> | 241                 | 43-47-49-16-41-15-3   |
|            | 2017    | Sal_G1                          | <i>aac(6')-Iaa-aadA1-tetA-sul1-dfrA14-aphA1</i> | 241                 | 43-47-49-16-41-15-3   |
|            |         | Sal_G31                         | <i>aac(6')-Iaa-aphA1</i>                        | 241                 | 43-47-49-16-41-15-3   |

\* ST was determined by WGS.

\*\*The product district could not be identified

MLST, multilocus sequence typing; ST, sequence type.

Table S3. Sequence types of *Salmonella enterica* serovar Schwarzengrund obtained by multilocus sequence typing analysis and their geographical distribution.

| MLST analysis       |                                       | No. of strains | Distribution  |                |        |        |        |                   |
|---------------------|---------------------------------------|----------------|---------------|----------------|--------|--------|--------|-------------------|
| ST                  | Allelic profile                       |                | United States | United Kingdom | Taiwan | Brazil | Canada | Other countries   |
| 96 <sup>(c)</sup>   | 43-47-49-49-41-15-3                   | 1,609          | 1,383         | 129            | 16     | 16     | 12     | 53 <sup>(a)</sup> |
| 241 <sup>(c)</sup>  | 43-47-49- <u>16</u> -41-15-3          | 30             | 3             | 16             | 1      | 0      | 0      | 10 <sup>(b)</sup> |
| 322 <sup>(c)</sup>  | 43-47-49-49-41-15- <u>114</u>         | 12             | 0             | 1              | 5      | 0      | 0      | 6                 |
| 5010 <sup>(c)</sup> | 43-47-49-49-41-15- <u>908</u>         | 3              | 3             | 0              | 0      | 0      | 0      | 0                 |
| 2114 <sup>(c)</sup> | 43-47-49- <u>149</u> -41-15- <u>4</u> | 2              | 0             | 1              | 0      | 0      | 0      | 1                 |
| 7288 <sup>(c)</sup> | 43-47-49-49- <u>1147</u> -15-3        | 2              | 0             | 0              | 2      | 0      | 0      | 0                 |
| 848 <sup>(c)</sup>  | 43-47- <u>25</u> -49-41-15-3          | 1              | 0             | 0              | 0      | 0      | 0      | 1                 |
| 5405 <sup>(c)</sup> | 43- <u>810</u> -49-49-41-15-3         | 1              | 1             | 0              | 0      | 0      | 0      | 0                 |
| 6132 <sup>(c)</sup> | 43-47-49-49-41-15- <u>1035</u>        | 1              | 1             | 0              | 0      | 0      | 0      | 0                 |
| 7884 <sup>(c)</sup> | 43-47-49-49-41-15- <u>1257</u>        | 1              | 1             | 0              | 0      | 0      | 0      | 0                 |
| 2250 <sup>(d)</sup> | <u>516-13-401-131-522-2-531</u>       | 14             | 2             | 12             | 0      | 0      | 0      | 0                 |
| 5815 <sup>(d)</sup> | <u>516-13-401-131-522-2-989</u>       | 1              | 0             | 1              | 0      | 0      | 0      | 0                 |
| 213 <sup>(e)</sup>  | <u>10-7-12-9-70-9-2</u>               | 2              | 0             | 0              | 0      | 0      | 0      | 2                 |
| 19 <sup>(e)</sup>   | <u>10-7-12-9-5-9-2</u>                | 1              | 1             | 0              | 0      | 0      | 0      | 0                 |
| 2488                | <u>516-4-15-131-522-518-531</u>       | 3              | 0             | 2              | 0      | 0      | 0      | 1                 |
| 64                  | <u>10-14-15-31-25-20-33</u>           | 2              | 1             | 0              | 0      | 0      | 0      | 1                 |
| 152                 | <u>62-53-54-60-5-53-54</u>            | 2              | 2             | 0              | 0      | 0      | 0      | 0                 |
| 239                 | <u>50-80-25-85-40-58-4</u>            | 2              | 0             | 2              | 0      | 0      | 0      | 0                 |
| 2885                | <u>480-450-8-204-491-103-303</u>      | 2              | 0             | 0              | 0      | 0      | 0      | 2                 |
| 11                  | <u>5-2-3-7-6-6-11</u>                 | 1              | 1             | 0              | 0      | 0      | 0      | 0                 |
| 13                  | <u>3-3-7-4-3-3-7</u>                  | 1              | 1             | 0              | 0      | 0      | 0      | 0                 |
| 14                  | <u>7-6-8-8-7-8-13</u>                 | 1              | 1             | 0              | 0      | 0      | 0      | 0                 |
| 45                  | <u>10-7-21-14-15-12-12</u>            | 1              | 0             | 0              | 0      | 1      | 0      | 0                 |
| 226                 | <u>84-76-38-16-12-13-4</u>            | 1              | 1             | 0              | 0      | 0      | 0      | 0                 |
| 279                 | <u>62-95-54-96-100-9-100</u>          | 1              | 0             | 1              | 0      | 0      | 0      | 0                 |
| 319                 | <u>118-107-8-51-2-117-16</u>          | 1              | 1             | 0              | 0      | 0      | 0      | 0                 |

|       |  |      |      |     |    |    |    |    |
|-------|--|------|------|-----|----|----|----|----|
| 404   | <b><u>46-122-3-18-6-138-133</u></b>    | 1    | 1    | 0   | 0  | 0  | 0  | 0  |
| 419   | <b><u>13-11-25-72-10-23-23</u></b>     | 1    | 1    | 0   | 0  | 0  | 0  | 0  |
| 548   | <b><u>13-11-25-197-12-71-4</u></b>     | 1    | 0    | 0   | 0  | 1  | 0  | 0  |
| 2045  | <b><u>16-16-26-18-478-12-18</u></b>    | 1    | 0    | 0   | 0  | 0  | 0  | 1  |
| 2046  | <b><u>47-64-108-96-491-455-303</u></b> | 1    | 0    | 1   | 0  | 0  | 0  | 0  |
| 3752  | <b><u>111-11-577-74-388-71-4</u></b>   | 1    | 0    | 1   | 0  | 0  | 0  | 0  |
| 5226  | <b><u>346-64-25-86-76-22-41</u></b>    | 1    | 0    | 1   | 0  | 0  | 0  | 0  |
| 5927  | <b><u>22-11-25-21-224-892-1007</u></b> | 1    | 0    | 1   | 0  | 0  | 0  | 0  |
| 6221  | <b><u>39-86-108-204-76-42-86</u></b>   | 1    | 0    | 0   | 0  | 0  | 0  | 1  |
| Total |  | 1707 | 1405 | 169 | 24 | 18 | 12 | 79 |

These data were obtained from the *Salmonella* Genome Databases [22] and EnteroBase [23].

Allele types that differ from ST96 are underlined and in bold.

MLST, multilocus sequence typing; ST, sequence type.

(a) Ireland (7), Austria (6), Germany (4), Trinidad and Tobago (4), Scotland (3), Vietnam (3), Denmark (2), Ecuador (2), Northern Ireland (2), Thailand (2), South Africa (2), Indonesia (1), Italy (1), Netherlands (1), Poland (1), Puerto Rico (1), Tunisia (1), Unknown (10).

(b) India (4), Ireland (1), Northern Ireland (1), Poland (1), Zimbabwe (1), Unknown (2).

(c), (d), (e) Each group consists of related STs that differed in one or two loci only.

Table S4. Number of bases different among the seven genes from ST96.

| ST   | Allelic profile                       | <i>aroC</i> | <i>dnaN</i> | <i>hemD</i> | <i>hisD</i> | <i>purE</i> | <i>sucA</i> | <i>thrA</i> | total |
|------|---------------------------------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------|
| 96   | 43-47-49-49-41-15-3                   | -           | -           | -           | -           | -           | -           | -           | -     |
| 241  | 43-47-49- <u>16</u> -41-15-3          | 0           | 0           | 0           | 7           | 0           | 0           | 0           | 7     |
| 322  | 43-47-49-49-41-15- <u>114</u>         | 0           | 0           | 0           | 0           | 0           | 0           | 1           | 1     |
| 5010 | 43-47-49-49-41-15- <u>908</u>         | 0           | 0           | 0           | 0           | 0           | 0           | 1           | 1     |
| 2114 | 43-47-49- <u>149</u> -41-15- <u>4</u> | 0           | 0           | 0           | 1           | 0           | 0           | 3           | 4     |
| 7288 | 43-47-49-49- <u>1147</u> -15-3        | 0           | 0           | 0           | 0           | 1           | 0           | 0           | 1     |
| 848  | 43-47- <u>25</u> -49-41-15-3          | 0           | 0           | 1           | 0           | 0           | 0           | 0           | 1     |
| 5405 | 43- <u>810</u> -49-49-41-15-3         | 0           | 1           | 0           | 0           | 0           | 0           | 0           | 1     |
| 6132 | 43-47-49-49-41-15- <u>1035</u>        | 0           | 0           | 0           | 0           | 0           | 0           | 1           | 1     |
| 7884 | 43-47-49-49-41-15- <u>1257</u>        | 0           | 0           | 0           | 0           | 0           | 0           | 1           | 1     |
| 2250 | <u>516-13-401-131-522-2-531</u>       | 4           | 7           | 2           | 6           | 7           | 8           | 11          | 45    |
| 5815 | <u>516-13-401-131-522-2-989</u>       | 4           | 7           | 2           | 6           | 7           | 8           | 12          | 46    |
| 213  | <u>10-7-12-9-70-9-2</u>               | 3           | 8           | 6           | 9           | 8           | 6           | 6           | 46    |
| 19   | <u>10-7-12-9-5-9-2</u>                | 3           | 8           | 6           | 9           | 7           | 6           | 6           | 45    |
| 2488 | <u>516-4-15-131-522-518-531</u>       | 4           | 8           | 5           | 6           | 7           | 8           | 11          | 49    |
| 64   | <u>10-14-15-31-25-20-33</u>           | 3           | 8           | 5           | 9           | 8           | 7           | 4           | 44    |
| 152  | <u>62-53-54-60-5-53-54</u>            | 4           | 8           | 6           | 9           | 7           | 9           | 5           | 48    |
| 239  | <u>50-80-25-85-40-58-4</u>            | 1           | 13          | 1           | 7           | 4           | 4           | 3           | 33    |
| 2885 | <u>480-450-8-204-491-103-303</u>      | 6           | 11          | 3           | 6           | 6           | 7           | 7           | 46    |
| 11   | <u>5-2-3-7-6-6-11</u>                 | 3           | 9           | 3           | 8           | 7           | 5           | 6           | 41    |
| 13   | <u>3-3-7-4-3-3-7</u>                  | 5           | 8           | 4           | 5           | 8           | 8           | 6           | 44    |
| 14   | <u>7-6-8-8-7-8-13</u>                 | 3           | 9           | 3           | 6           | 8           | 4           | 11          | 44    |
| 45   | <u>10-7-21-14-15-12-12</u>            | 3           | 8           | 5           | 8           | 4           | 9           | 10          | 47    |
| 226  | <u>84-76-38-16-12-13-4</u>            | 3           | 3           | 5           | 7           | 2           | 7           | 3           | 30    |
| 279  | <u>62-95-54-96-100-9-100</u>          | 4           | 11          | 6           | 6           | 9           | 6           | 5           | 47    |
| 319  | <u>118-107-8-51-2-117-16</u>          | 4           | 5           | 3           | 6           | 7           | 6           | 8           | 39    |
| 404  | <u>46-122-3-18-6-138-133</u>          | 2           | 9           | 3           | 8           | 7           | 13          | 4           | 46    |
| 419  | <u>13-11-25-72-10-23-23</u>           | 2           | 8           | 1           | 4           | 14          | 6           | 4           | 39    |
| 548  | <u>13-11-25-197-12-71-4</u>           | 2           | 8           | 1           | 8           | 2           | 7           | 3           | 31    |
| 2045 | <u>16-16-26-18-478-12-18</u>          | 4           | 11          | 4           | 8           | 9           | 9           | 8           | 53    |

|      |  |   |    |   |   |    |    |   |    |
|------|--|---|----|---|---|----|----|---|----|
| 2046 | <b><u>47-64-108-96-491-455-303</u></b> | 3 | 10 | 4 | 6 | 6  | 5  | 7 | 41 |
| 3752 | <b><u>111-11-577-74-388-71-4</u></b>   | 4 | 8  | 2 | 5 | 4  | 7  | 3 | 33 |
| 5226 | <b><u>346-64-25-86-76-22-41</u></b>    | 4 | 10 | 1 | 5 | 6  | 10 | 4 | 40 |
| 5927 | <b><u>22-11-25-21-224-892-1007</u></b> | 3 | 8  | 1 | 2 | 13 | 3  | 3 | 33 |
| 6221 | <b><u>39-86-108-204-76-42-86</u></b>   | 4 | 7  | 4 | 6 | 6  | 8  | 6 | 41 |

The DNA sequences for 7 genes obtained from the Salmonella Genome Databases [22] and EnteroBase [23] were compared to determine different numbers of bases.

Allele types that differ from ST96 are underlined and in bold.

Table S5. *Salmonella enterica* serovar  
Schwarzengrund isolates obtained from chicken  
meat from various production regions.

| District                | No. of isolates |           |
|-------------------------|-----------------|-----------|
|                         | 2008            | 2015-2019 |
| West Japan              | 37              | 10        |
| East Japan              |                 | 49        |
| Domestic <sup>(a)</sup> |                 | 28        |
| Total                   | 37              | 87        |

(a) The product district could not be identified.



Table S6. PCR conditions for detection of antimicrobial resistance genes and class 1 intergron.

| Targeted gene    | F/R* | Primer sequences 5' - 3'   | Expected products size | Final primer conc. | Annealing Temp. | Positive control                                    | Reference or Accession No. |
|------------------|------|----------------------------|------------------------|--------------------|-----------------|---|----------------------------|
| Multiplex PCR 1  |      |                            |                        |                    |                 |   |                            |
| <i>aadA</i>      | F    | GTG GAT GGC GGC CTG AAG CC | 525 bp                 | 0.1 µM             | 63°C            | <i>S. Schwarzengrund</i> Sal_15<br>(in this study)  | 39                         |
|                  | R    | AAT GCC CAG TCG GCA GCG    |                        |                    |                 |   |                            |
| <i>strA/strB</i> | F    | ATG GTG GAC CCT AAA ACT CT | 893 bp                 | 0.4 µM             |                 | <i>S. Schwarzengrund</i> Sal_264<br>(in this study) |                            |
|                  | R    | CGT CTA GGA TCG AGA CAA AG |                        |                    |                 |   |                            |
| Multiplex PCR 2  |      |                            |                        |                    |                 |   |                            |
| <i>aphA1</i>     | F    | ATG GGC TCG CGA TAA TGT C  | 634 bp                 | 0.4 µM             |                 | <i>S. Schwarzengrund</i> Sal_15<br>(in this study)  | 39                         |
|                  | R    | CTC ACC GAG GCA GTT CCA T  |                        |                    |                 |   |                            |
| <i>aphA2</i>     | F    | GAT TGA ACA AGA TGG ATT GC | 347 bp                 | 0.1 µM             |                 | <i>S. Typhimurium</i> Sal_243<br>(unpublished)      |                            |
|                  | R    | CCA TGA TGG ATA CTT TCT CG |                        |                    |                 |   |                            |
| Multiplex PCR 3  |      |                            |                        |                    |                 |   |                            |
| <i>tetA</i>      | F    | GGC GGT CTT CTT CAT CAT GC | 502 bp                 | 0.1 µM             | 63°C            | <i>S. Schwarzengrund</i> Sal_17<br>(in this study)  | 39                         |
|                  | R    | CGG CAG GCA GAG CAA GTA GA |                        |                    |                 |   |                            |
| <i>tetB</i>      | F    | CGC CCA GTG CTG TTG TTG TC | 173 bp                 | 0.2 µM             |                 | <i>Escherichia coli</i> tori13<br>(unpublished)     |                            |
|                  | R    | CGC GTT GAG AAG CTG AGG TG |                        |                    |                 |   |                            |
| Multiplex PCR 4  |      |                            |                        |                    |                 |   |                            |
| <i>sul1</i>      | F    | CGG CGT GGG CTA CCT GAA CG | 433 bp                 | 0.2 µM             | 66°C            | <i>S. Schwarzengrund</i> Sal_167<br>(in this study) | 39                         |
|                  | R    | GCC GAT CGC GTG AAG TTC CG |                        |                    |                 |   |                            |
| <i>sul2</i>      | F    | CGG CAT CGT CAA CAT AAC CT | 721 bp                 | 0.3 µM             |                 | <i>S. Schwarzengrund</i> Sal_291<br>(in this study) |                            |
|                  | R    | TGT GCG GAT GAA GTC AGC TC |                        |                    |                 |   |                            |

|                                     |        |                               |                         |         |      |                                  |            |  |
|-------------------------------------|--------|-------------------------------|-------------------------|---------|------|----------------------------------|------------|--|
| PCR 1                               |        |                               |                         |         |      |                                  |            |  |
| <i>dfrA14</i>                       | F      | ATR GCT GCG AAA GCG AAA AA    | 455 bp                  | 0.5 µM  | 47°C | <i>S. Schwarzengrund</i> Sal_167 | DQ388123,  |  |
|                                     | R      | CCC TTT TTC CAA ATT TGA TAG C |                         |         |      | (in this study)                  | NG_047699, |  |
|                                     |        |                               |                         |         |      |                                  | MT513102,  |  |
|                                     |        |                               |                         |         |      |                                  | CP062226   |  |
| PCR 2                               |        |                               |                         |         |      |                                  |            |  |
| <i>aac (6')-Iaa</i>                 | F      | TGG CAT CAT TTA TTG CGA TG    | 237 bp                  | 0.5 µM  | 57°C | <i>S. Schwarzengrund</i> Sal_167 | CP053865   |  |
|                                     | R      | TTG TAT TTT CCG GCG AGG TA    |                         |         |      | (in this study)                  |            |  |
| PCR 3                               |        |                               |                         |         |      |                                  |            |  |
| <i>intI1</i>                        | F      | GCC TTG CTG TTC TTC TAC GG    | 558 bp                  | 0.25 µM | 55°C | <i>S. Schwarzengrund</i> Sal_G1  | 40         |  |
|                                     | R      | GAT GCC TGC TTG TTC TAC GG    |                         |         |      | (in this study)                  |            |  |
| PCR 4                               |        |                               |                         |         |      |                                  |            |  |
| Variable region of class 1 integron |        |                               |                         |         |      |                                  |            |  |
|                                     | 5' -CS | GGC ATC CAA GCA GCA AG        | variable <sup>(a)</sup> | 0.25 µM | 55°C | <i>S. Schwarzengrund</i> Sal_G1  | 40         |  |
|                                     | 3' -CS | AAG CAG ACT TGA CCT GA        |                         |         |      | (in this study)                  |            |  |

(a) variable size depending on the inserted gene(s).

\*F, Forward; R, Reverse

Table S7. PCR primers used in the amplification and DNA sequencing for multilocus sequence typing.

| Targeted gene | F/R* | Primer sequences 5' - 3'        | Expected products size | Objective for each primer |
|---------------|------|---------------------------------|------------------------|---------------------------|
| <i>thrA</i>   | F    | GTC ACG GTG ATC GAT CCG GT      | 852 bp                 | PCR and DNA sequencing    |
|               | R    | CAC GAT ATT GAT ATT AGC CCG     |                        | PCR and DNA sequencing    |
| <i>purE</i>   | F    | ATG TCT TCC CGC AAT AAT CC      | 510 bp                 | PCR and DNA sequencing    |
|               | R    | TCA TAG CGT CCC CCG CGG ATC     |                        | PCR and DNA sequencing    |
|               | F    | CGC ATT ATT CCG GCG CGT GT      |                        | DNA Sequencing            |
| <i>sucA</i>   | F    | AGC ACC GAA GAG AAA CGC TG      | 643 bp                 | PCR and DNA sequencing    |
|               | R    | GGT TGT TGA TAA CGA TAC GTA C   |                        | PCR and DNA sequencing    |
| <i>hisD</i>   | F    | GAA ACG TTC CAT TCC GCG CAG AC  | 894 bp                 | PCR and DNA sequencing    |
|               | R    | CTG AAC GGT CAT CCG TTT CTG     |                        | PCR and DNA sequencing    |
|               | F    | GTC GGT CTG TAT ATT CCC GG      |                        | DNA Sequencing            |
| <i>aroC</i>   | F    | CCT GGC ACC TCG CGC TAT AC      | 826 bp                 | PCR and DNA sequencing    |
|               | R    | CCA CAC ACG GAT CGT GGC G       |                        | PCR and DNA sequencing    |
| <i>hemD</i>   | F    | ATG AGT ATT CTG ATC ACC CG      | 666 bp                 | PCR and DNA sequencing    |
|               | R    | ATC AGC GAC CTT AAT ATC TTG CCA |                        | PCR and DNA sequencing    |
|               | F    | GTG GCC TGG AGT TTT CCA CT      |                        | DNA Sequencing            |
|               | R    | GAC CAA TAG CCG ACA GCG TAG     |                        | DNA Sequencing            |
| <i>dnaN</i>   | F    | ATG AAA TTT ACC GTT GAA CGT GA  | 833 bp                 | PCR and DNA sequencing    |
|               | R    | AAT TTC TCA TTC GAG AGG ATT GC  |                        | PCR and DNA sequencing    |
|               | R    | CCA TCC ACC AGC TTC GAG GT      |                        | DNA Sequencing            |

\*F, Forward; R, Reverse

All primers were followed to the description in previous report [41].