Table S1. Primers for fimbrial genes used in this study.

Fimbrial gene	Forward primer (5'→3') Reverse primer (5'→3')	Amplicon size (bp)	Reference or Gene accession #
bcfD	GACAACATGCGGAGTGTCAT	572	*Yue et al*
	GACATCTGTCAGCGGATCG		(2012)
csgA	GGATTCCACGTTGAGCATTT	312	*Smith et al*
	GTTGTTGCCAAAACCAACCT		(2010)
fimA	ACTATTGCGAGTCTGATGTTTG	508	*Wu et al*
	CGTATTTCATGATAAAGGTGGC		(2012)
lpfD	ATCCGTTTGTGGGTGAAAGT	597	*Yue et al*
	GGCATCAAAGCATGAAGGTT		(2012)
pefA	ACACGCTGCCAATGAAGTGA	450	*Smith et al*
	ACTGCGAAAGATGCCACAGA		(2010)
pegD	TATGTGGCAAAGACAGGAA	524	AM933172.1*
	GCAAAGAATCAATGGAGCA		(2246402-2246925)
safC	TGTTCTGGCTCCTTGTTTGACG	612	*Townsend et al*
	TTCTGTTTGACCTCCACCCGAG		(2001)
sefA	GATACTGCTGAACGTAGAAGG	488	*Oliveira et al*
	GCGTAAATCAGCATCTGCAGTAGC		(2003)
staA	TTTAGAAGCATCGGCACG	501	AL513382.1*
	ATGGTTATGGCTATGGGTT		(216884-217384)
stbD	CAGATTATCCTGCGATCGTG	554	*Yue et al*
	CATCCCGTCAACCCAAGTAG		(2012)
stcA	GCTGCTATTTGGATCTAGTGTC	355	CP002614.1*
	TGAGTATGATTCAGGCGTTC		(2246947-2247301)
stdB	GCCACATCAACCGAAAT	477	AM933172.1*
	CCAGAACCAGGTCTACGC		(3077526-3078002)
steB	CGCACTCCATCGCCCACAT	549	AM933172.1*
	GCTGCCAGTTATCGCCGTTCT		(2986399-2986947)
stfH	CTTCGCAAGCGCACTAGTTA	555	*Yue et al*
	CGCATCCCAGGAGATATCAA		(2012)
stgA	CGCTCTGGTTCTGTCTTCT	443	AL513382.1*
	CTGTGGTATCAATCGTGCT		(3780619-3781061)
sthE	GTTATATCTGGCGCTTATTCTGC	572	*Yue et al*
	CCAAATACAGATGGGTCAGGA		(2012)
stiH	TCCGCAGGGAATAAGGGTA	600	*Yue et al*
	TCAGCGAATCTGAATCTCCA		(2012)
stjA	TATGAAACGGCAAAGGGAGT	593	*Yue et al*
	CGTCAGCACTTCCCACTGTA		(2012)
stkA	TGCCTGTACGGTTCCTGC	482	CP003416.1*
	TTTCCACGGTCTGGTTTCT		(952532-953013)
tcfA	TCGCTATGTTTGCATGTGGT	316	*Suez et al*
	TTCAGGAACAGCCTCGAAGT		(2013)

* The PCR system was established in this study with the in 2 cluded gene accession # and the location of target gene.

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Table S2. Poultry *Salmonella* isolated from 51 farms.

Number positive / number tested (%)				
Chicken	Duck	Goose	Pigeon	Turkey
11/87 (12.6)	3/87 (3.4)	5/31 (16.1)	0/33 (0)	8/93 (8.6)
21/193 (10.9)	7/70 (10.0)	7/95 (7.4)	6/89 (6.7)	8/64 (12.5)
5/82 (6.1)	7/66 (10.6)	10/79 (12.6)	4/50 (8.0)	9/52 (17.3)
16/143 (11.2)	2/52 (3.8)	6/30 (20.0)	1/54 (1.9)	5/47 (10.6)
20/180 (11.1)	5/88 (5.7)	7/65 (10.8)	3/55 (5.5)	2/53 (3.8)
6/39 (15.4)	4/49 (8.2)	4/29 (13.8)	0/16 (0)	
3/35 (8.6)	5/67 (7.5)	4/38 (10.5)	2/57 (3.5)	
14/169 (8.3)	5/73 (6.8)	11/42 (26.2)	1/63 (1.6)	
3/93 (3.2)	3/49 (6.1)	5/42 (11.9)		
6/68 (8.8)		3/35 (8.6)		
3/58 (5.2)		4/47 (8.5)		
9/123 (7.3)				
4/55 (7.3)				
8/64 (12.5)				
20/137 (14.6)				
7/59 (11.9)				
9/82 (11.0)				
2/39 (5.1)				

Table S3. Poultry *Salmonella* serovars in 12 provinces of China.

Serovars	Number of isolates											
	Jiangsu	Anhui	Zhejiang	Shandong	Shanghai	Hebei	Beijing	Sichuan	Henan	Xinjiang	Guangdong	Heilongjiang
S. Pullorum	20	2	3	8	0	4	3	0	3	10	0	2
S. Typhimurium	24	1	5	4	1	3	0	2	4	6	0	0
S. Enteritidis	20	5	6	0	0	0	0	3	2	3	0	0
S. Indiana	11	3	2	4	0	0	0	0	2	3	0	0
S. Heidelberg	4	7	8	0	0	0	0	0	1	0	0	2
S. Potsdam	5	3	2	4	0	0	0	0	2	7	0	0
S. Kentucky	9	0	0	4	0	3	0	0	0	2	1	0
S. Thompson	4	1	0	0	0	1	1	0	0	2	0	0
S. Saintpaul	6	0	1	0	3	0	0	0	0	1	5	0
S. Kottbus	1	2	0	1	0	0	0	0	0	0	0	0
S. Agona	0	0	0	0	0	0	0	0	3	0	0	0
S. Gallinarum	6	0	3	0	0	0	0	1	0	0	0	2
S. Blockley	1	9	0	0	0	0	0	0	1	2	0	0
S. Bazenheid	2	6	0	2	0	0	0	0	0	0	0	0
S. Anatum	3	0	2	0	0	0	0	0	0	0	0	0
S. Montevideo	0	0	0	4	0	1	0	0	0	0	0	0
S. Derby	3	0	0	0	0	0	0	4	0	0	0	0
S. Reading	0	0	1	2	0	0	0	0	0	0	0	0
S. Senftenberg	0	0	0	1	0	0	0	0	0	0	0	0
S. Meleagridis	0	2	0	0	0	0	0	0	0	0	0	0
Total	119	41	33	34	4	12	4	10	18	36	6	6

Fig. S1. Map of the poultry *Salmonella* spp. detection regions. For this study, 3,566 rectal swab samples were obtained from 7 regions of 12 provinces in China. Below each region label is the total number of *Salmonella*-positive samples over the total number of samples received from poultry farms in that region.