

Table S1. *Salmonella* isolates from poultry.

Strains	serovar	H2S	Year of isolate	Diagnosis center	Poultry	MLST	short read sequencing	
							Number of short reads	average coverage
GSI-1	S. Infantis	+	2010	A institute	breast meat	32	6,941,126	120
GSI-9	S. Infantis	-	2010	A institute	leg	32	5,384,204	93
GST-92	S. Typhimurium	+	2010	B center	breast meat	328	2,431,972	42
GST-106	S. Typhimurium	-	2010	A institute	leg	328	4,120,728	71
GST-108	S. Typhimurium	-	2010	A institute	minched meat	328	3,679,422	63
GST-204	S. Typhimurium	-	2010	B center	breast meat	328	4,024,782	69

Table S2. Identified nonsynonymous SNVs between H2S-producing and non-producing isolates among *S. enterica* Infantis.

Genome position in SIN*	SIN (H2S+)	GSI-1 (H2S+)	GSI-9 (H2S-)	Nonsynonymous mutation in GSI-9	strand	product
23428	G	G	A	(32A->T)	+	Putative cytoplasmic protein
157729	A	A	G	(52N->S)	+	putative LysR-family transcriptional regulator
1017933	G	G	T	(414R->L)	+	DNA internalization-related competence protein ComEC/Rec2
1082826	C	C	T	(219R->H)	-	Inositol phosphate phosphatase sopB
1182769	C	C	T	(127P->S)	+	3-oxoacyl-[acyl-carrier-protein] synthase, KASII
1186293	G	G	C	(26A->P)	+	DNA polymerase III delta prime subunit
1693731	G	G	A	(30S->L)	-	FIG01046477: hypothetical protein
1988432	G	G	A	(225Q->stop)	-	Cystine ABC transporter, ATP-binding protein
1999721	A	A	C	(344E->D)	+	Cytoplasmic alpha-amylase
2086936	G	G	A	(120Q->stop)	-	Thiosulfate reductase precursor
2303924	C	C	A	(87D->Y)	-	DNA gyrase subunit A
2490455	G	G	A	(57A->T)	+	putative inner membrane protein
2788654	C	C	T	(27E->K)	-	Putative glycoporin
3979687	A	A	T	(168T->S)	+	Threonine dehydratase biosynthetic
4299833	A	A	G	(1050K->E)	+	5-methyltetrahydrofolate--homocysteine methyltransferase
4422523	G	G	T	(132L->M)	-	Transcriptional regulatory protein basR/pmrA

* Reference genome sequence was used with *S. infantis* SIN genome sequence.

Table S3. Identified nonsynonymous SNVs between H₂S-producing and non-producing isolates among *S. enterica* Typhimurium.

Genome position in T000240*	T000240 (H ₂ S+)	GST-92 (H ₂ S+)	GST-106 (H ₂ S-)	GST-108 (H ₂ S-)	GST-204 (H ₂ S-)	Nonsynonymous mutation in GST-92	Nonsynonymous mutation in GST-106, GST108 and GST204	Strand	Product
206563	G	G	A	A	A	-	(355R->C)	-	putative fimbrial usher protein
235302	C	C	T	T	T	-	(15A->V)	+	fimbrial subunit
696064	G	G	A	A	A	-	(191G->D)	+	enterobactin synthase subunit E
755192	G	G	T	T	T	-	(312P->H)	-	hypothetical protein
783801	A	A	G	G	G	-	(164E->G)	+	N-acetyl glucosamine-specific PTS system IABC protein
887326	G	G	A	A	A	-	(174H->Y)	-	phosphotransferase
1486813	G	G	T	T	T	-	(125A->S)	+	secreted effector protein
1592651	G	G	A	A	A	-	(214S->L)	-	putative major facilitator family transporter YdeE
2135053	G	G	T	T	T	-	(480C->stop)	-	thiosulfate reductase
2335986	C	C	A	A	A	-	(40E->D)	-	putative cytoplasmic protein
2371632	T	A	C	C	C	(87N->Y)	(87N->D)	-	DNA gyrase subunit A
2426912	T	T	C	C	C	-	(157T->A)	-	NADH dehydrogenase subunit H
2520050	G	G	T	T	T	-	(131P->T)	-	manganese transport protein MntH
3268636	G	G	T	T	T	-	(156P->T)	-	putative mannitol dehydrogenase
3295526	A	A	C	C	C	-	(270T->P)	+	nucleoside permease NupG
3604976	G	G	T	T	T	-	(66L->I)	-	putative cytoplasmic protein
4775729	G	G	T	T	T	-	(122G->W)	+	putative permease
4834481	C	C	T	T	T	-	(555A->T)	-	putative ATP-dependent Lon protease

* Reference genome sequence was used with *S. Typhimurium* T000240 genome sequence.

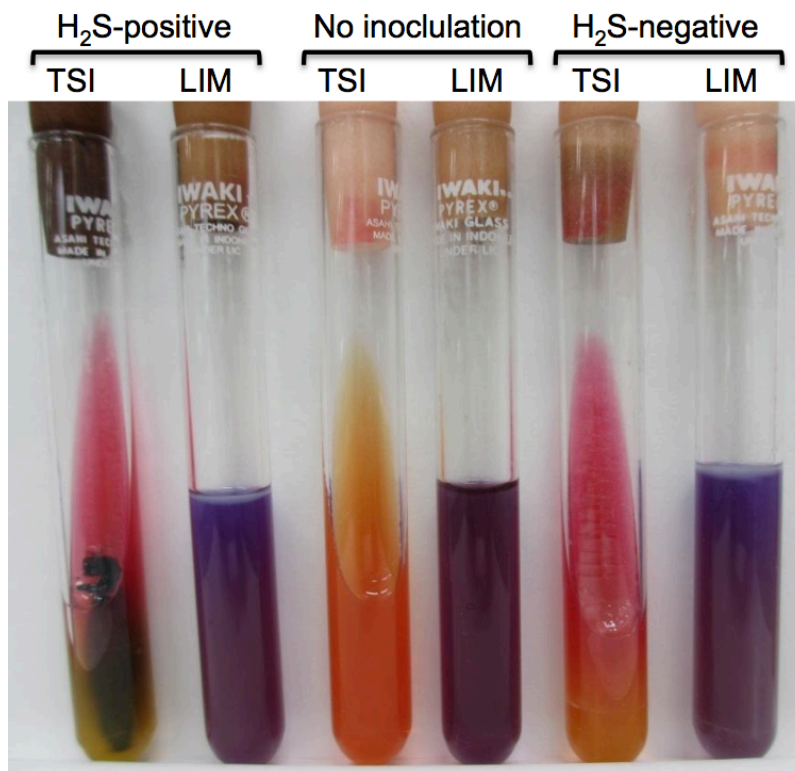


Fig. S1. H₂S production and lysine decarboxylase test of *Salmonella* isolates on TSI and LIM-agar. *Salmonella* metabolise thiosulfate to produce H₂S, reacting with ferrous sulfate to form ferrous sulfide, which is visible as a black precipitate on TSI-slant. *Salmonella* decarboxylate lysine, increasing the pH to alkaline on LIM agar.

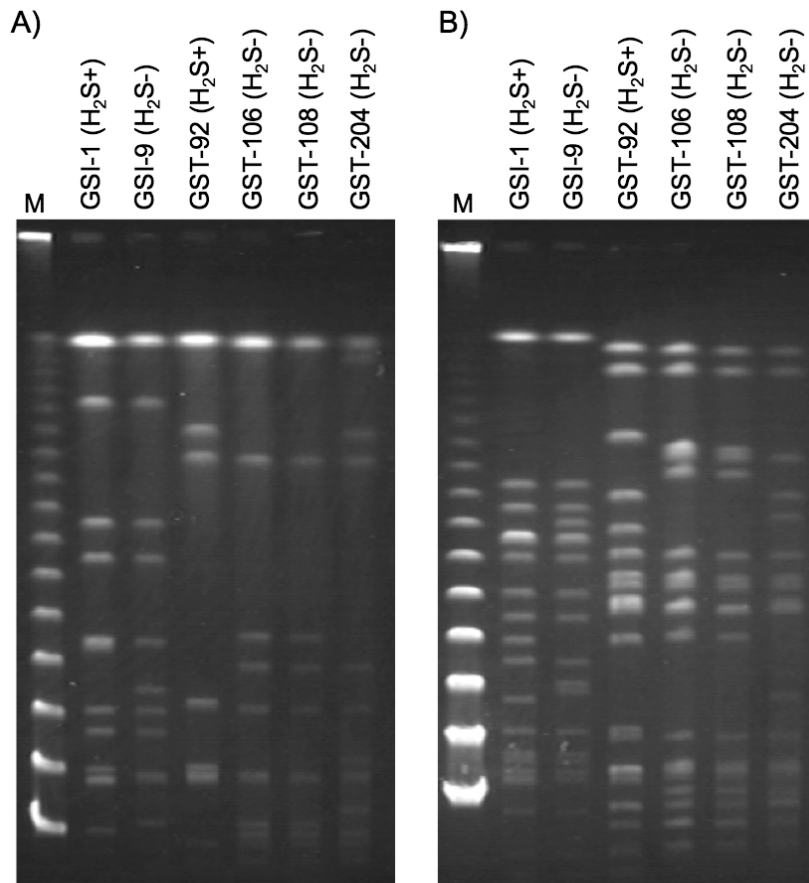


Fig. S2. PFGE analysis of the *Salmonella* isolates. Restriction enzyme A) *BlnI* and B) *XbaI*. M: Lambda ladder marker for PFGE.