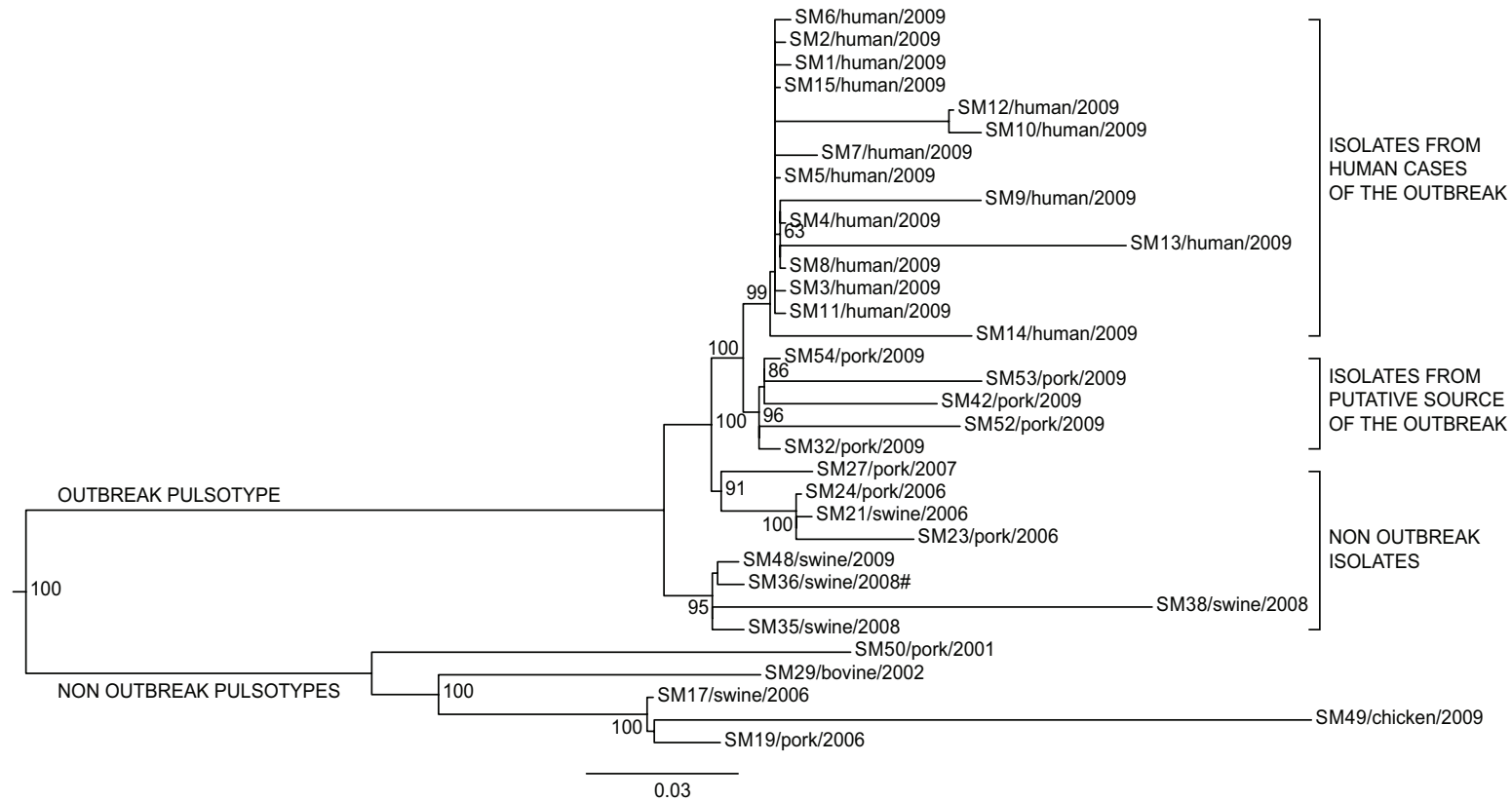


Table S1. Assembly data of *Salmonella* Manhattan isolates sequenced in this study

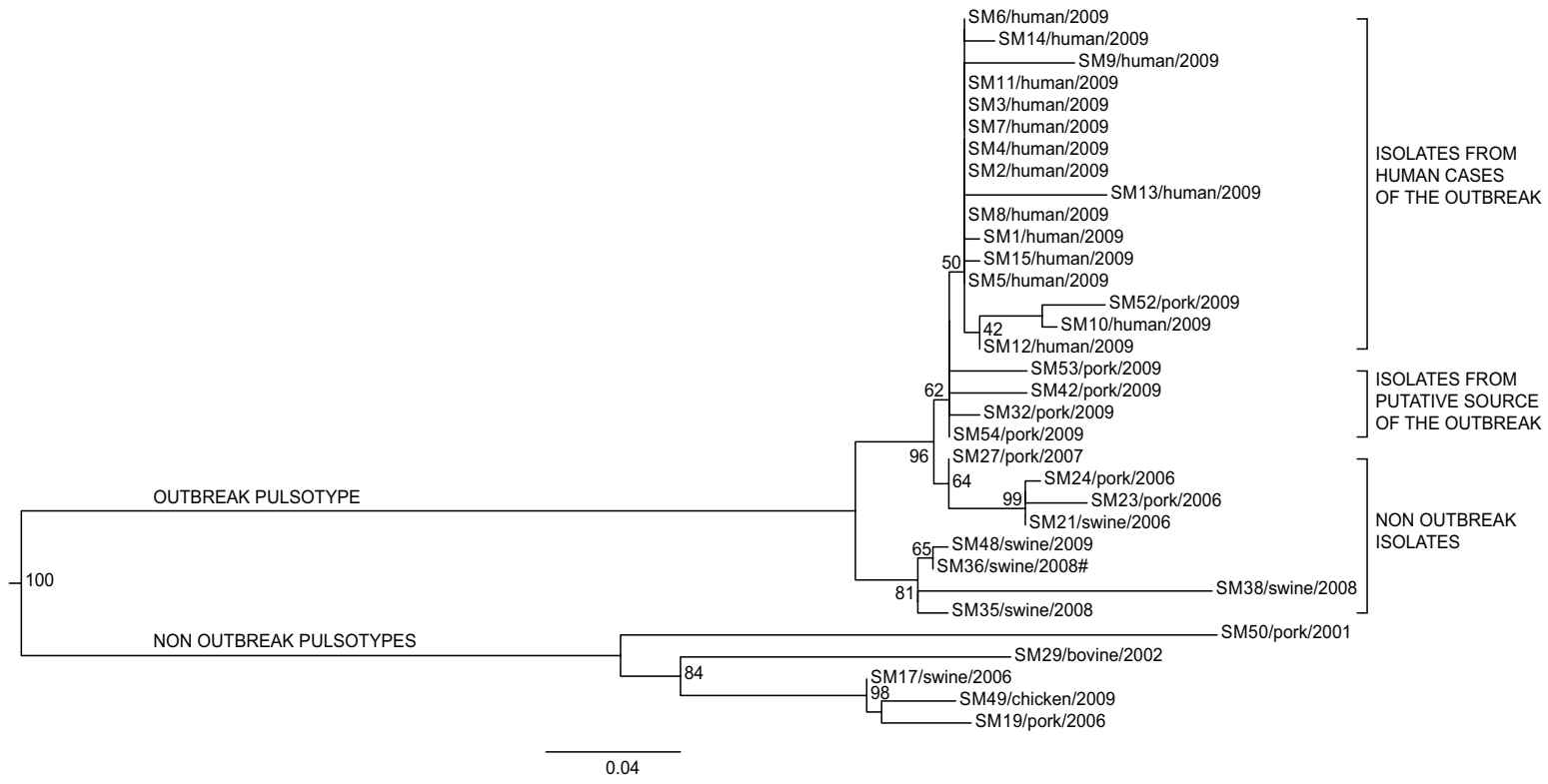
Lab. N.	Assembly Name	N. of Reads assembled	Avg. Coverage	N. of Contigs	N50	Consensus Sequence (bp)
160969_3	SM1	1710982	68.74	156	141280	4719245
160969_5	SM2	2535189	93.97	61	276557	4691989
160969_6	SM3	2521184	95.83	47	550676	4687862
165051_2	SM4	1146836	46.38	141	122404	4721098
165051_3	SM5	2819494	104.36	54	432406	4695440
165051_5	SM6	830776	32.23	151	76537	4716655
165051_7	SM7	2513260	87.78	73	426283	4700219
111113	SM8	7263890	237.97	52	653456	4696541
165051_11	SM9	705833	22.13	377	22555	4690025
165051_12	SM10	4464240	152.62	51	447907	4695242
180073_1	SM11	2139784	71.96	70	220086	4695118
180073_2	SM12	6155851	228.73	65	502439	4701365
180073_3	SM13	550660	19.19	532	15189	4691653
180073_4	SM14	635849	20.68	547	17783	4668733
180073_6	SM15	1718689	67.07	119	206519	4707922
226963	SM17	1115555	45.53	135	94514	4678408
226972	SM19	3647977	136.8	132	612314	4692088
226979	SM21	2113563	81.76	161	186243	4701558
226985	SM23	743857	24.78	370	26335	4647025
226987	SM24	8101538	245.95	101	401695	4680260
226998	SM27	1083529	43.12	1342	28467	4977060
227009	SM29	2745872	115.51	124	239046	4725171
227021	SM32	1534324	55.28	135	109153	4703213
227033	SM35	4401622	170.21	73	398381	4708271
227039	SM36	5195701	198.34	60	441398	4670782
227052	SM38	463509	18.26	560	16977	4659968

250920	SM42	690442	24.49	353	27141	4693959
188806	SM48	2189455	84.38	247	54375	4705944
188795	SM49	1110088	38.44	1162	11195	4727662
188781	SM50	1887637	61.78	320	51793	4764060
188801	SM52	1047164	31.64	166	57534	4690524
216630/1	SM53	599806	21.47	464	20152	4696208
216630/2	SM54	7964395	244.2	67	472508	4700846

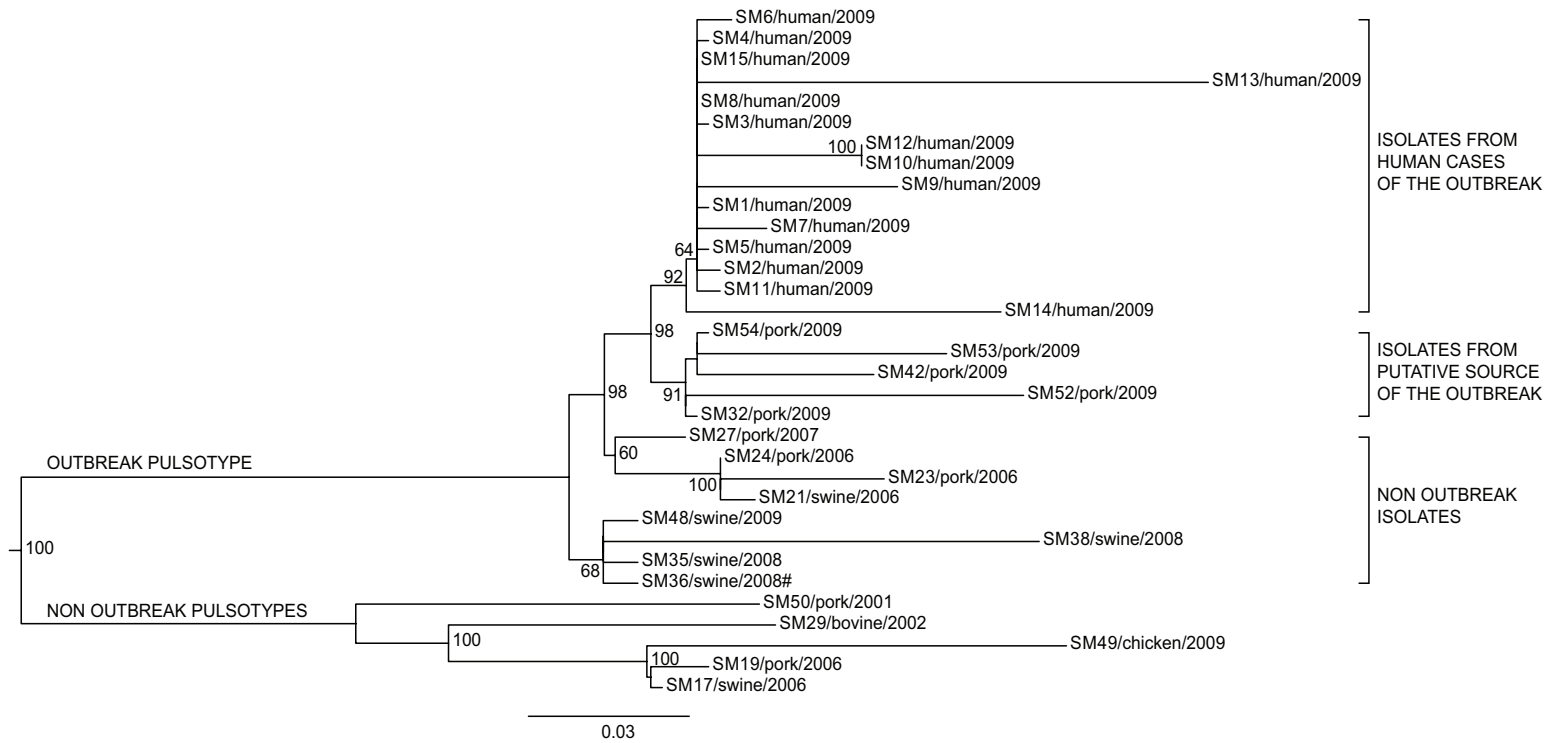
Figure S1. Phylogenetic reconstruction of the 33 *Salmonella* Manhattan isolates based on core (panel A), synonymous (panel B) and non-synonymous (panel C) SNPs datasets, analyzed with Maximum Likelihood method. Bootstrap values are indicated in each principal node of the trees. The scale bar units are nucleotide substitutions per site. # WGS analyses clustered isolate SM36 (pulsotype SXB_PR.0752) together with the isolates of the outbreak pulsotype (SXB_BS0003).



Panel A.

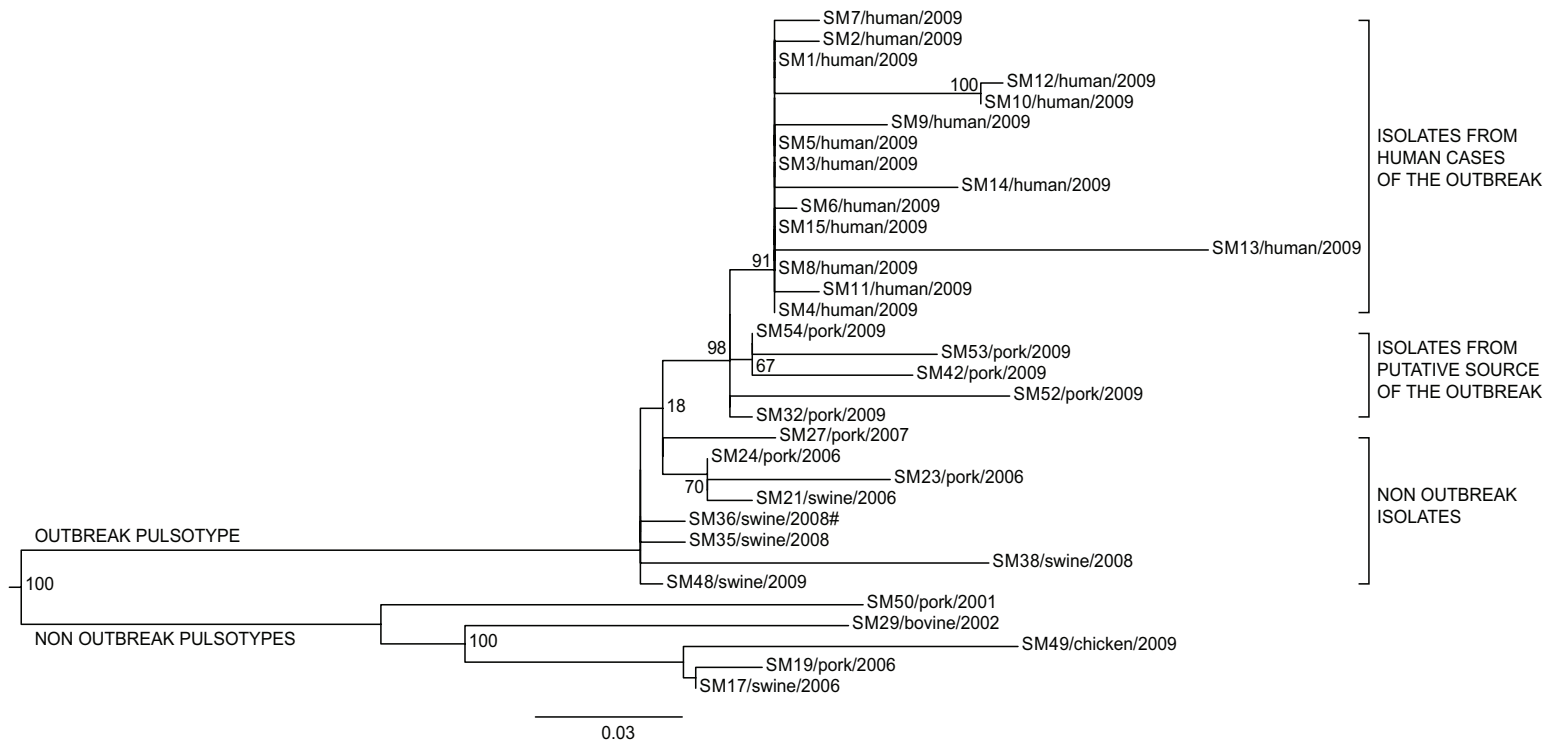


Panel B.

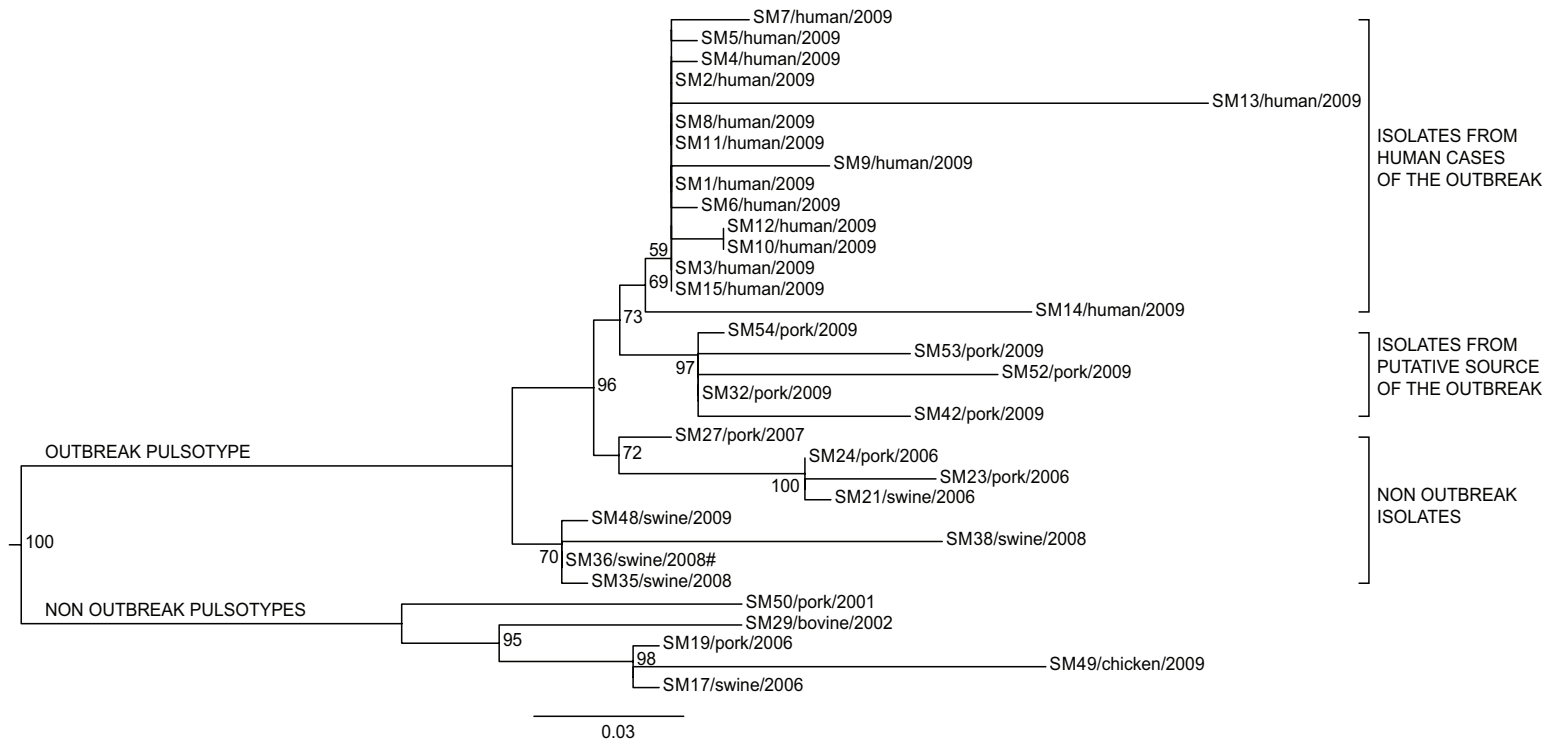


Panel C.

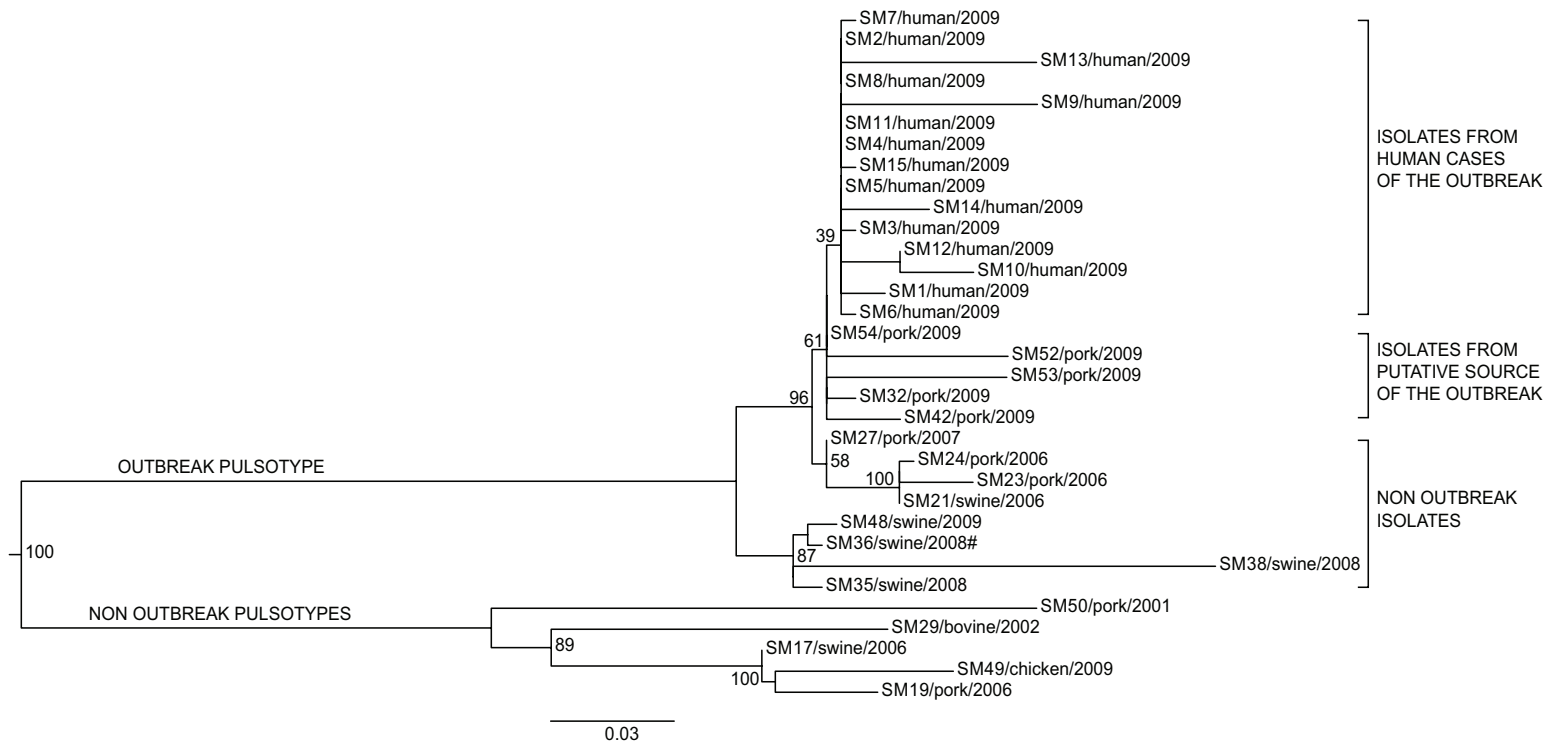
Figure S2: Phylogenetic reconstruction of the 33 *Salmonella* Manhattan isolates analyzed with the Maximum Likelihood algorithm, based on SNPs in first (panel A), second (panel B), third (Panel C) and first+second codon positions (Panel D) datasets. Bootstrap values are indicated in each principal node of the trees. The scale bar units are nucleotide substitutions per site. # WGS analyses clustered isolate SM36 (pulsotype SXB_PR.0752) together with the isolates of the outbreak pulsotype (SXB_BS0003).



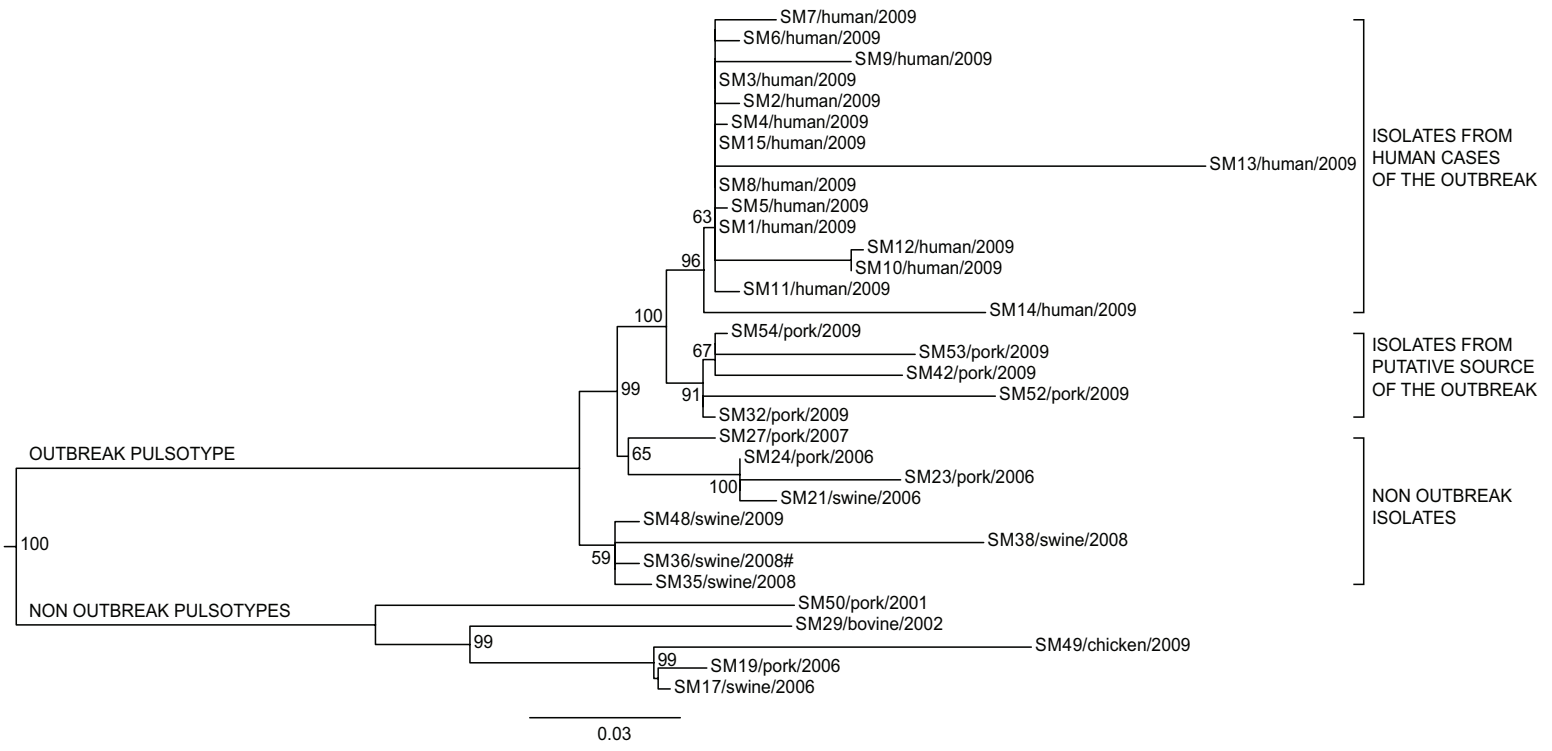
Panel A.



Panel B.



Panel C.



Panel D.