



Draft Genome Sequences of 158 *Listeria monocytogenes* Strains Isolated from Black Bears (*Ursus americanus*) in the United States

Phillip Brown,^a Yi Chen,^b Mirena Ivanova,^c Pimplapas Leekitcharoenphon,^c Cameron Parsons,^d Jeffrey Niedermeyer,^d Nicholas Gould,^e Jennifer Strules,^e J. Bernardo Mesa-Cruz,^{f,g} Marcella J. Kelly,^f Michael J Hooker,^{h,†} Michael J. Chamberlain,^h Colleen Olfenbittel,ⁱ Christopher DePerno,^e Driss Elhanafi,^j Sophia Kathariou^{a,d}

^aDepartment of Plant and Microbial Biology, North Carolina State University, Raleigh, North Carolina, USA

^bDivision of Microbiology, Center for Food Safety and Applied Nutrition, Food and Drug Administration, College Park, Maryland, USA

^cResearch Group for Genomic Epidemiology, National Food Institute, Technical University of Denmark, Lyngby, Denmark

^dDepartment of Food, Bioprocessing and Nutrition Sciences, North Carolina State University, Raleigh, North Carolina, USA

^eFisheries, Wildlife, and Conservation Biology, Department of Forestry and Environmental Resources, North Carolina State University, Raleigh, North Carolina, USA

^fDepartment of Fish and Wildlife Conservation, Virginia Tech, Blacksburg, Virginia, USA

^gIntegrative Sciences, Harrisburg University, Harrisburg, Pennsylvania, USA

^hWarnell School of Forestry and Natural Resources, University of Georgia, Athens, Georgia, USA

ⁱNorth Carolina Wildlife Resources Commission, Raleigh, North Carolina, USA

^jBiomufacturing Training and Education Center, North Carolina State University, Raleigh, North Carolina, USA

ABSTRACT *Listeria monocytogenes* is responsible for severe foodborne disease and major economic losses, but its potential reservoirs in natural ecosystems remain poorly understood. Here, we report the draft genome sequences of 158 *L. monocytogenes* strains isolated from black bears (*Ursus americanus*) in the southeastern United States between 2014 and 2017.

Listeria monocytogenes is a facultative intracellular Gram-positive bacterial pathogen responsible for the severe foodborne disease listeriosis (1). Three serotypes (i.e., 1/2a, 1/2b, and 4b) predominate in human listeriosis, with 4b being the leading contributor and including all major hypervirulent clones (1, 2). *L. monocytogenes* is notorious for its persistence in food processing environments (FPEs), but the actual sources of the strains that colonize FPEs remain poorly understood (3). Food animals and agricultural environments have been extensively investigated, while potential reservoirs in natural ecosystems such as wildlife remain underexplored.

We found that wild black bears (*Ursus americanus*) in the southeastern United States were frequently colonized by *L. monocytogenes* without apparent disease symptoms, with 12% of the samples yielding serotype 4b (4). A significant portion of 4b strains exhibited the multiplex PCR profile IVb-vI encountered in emerging clones such as ST382 and 554 (3, 4). Here, we report the whole-genome sequence (WGS) data of 158 *L. monocytogenes* strains from these black bears, including 84 and 57 of serotype 1/2a and 4b, respectively (Table 1). WGS analysis revealed 68 sequence types (STs) based on the multilocus sequence typing (MLST) scheme. Surprisingly, the generally-ubiquitous STs 1, 2, 4, and 6 (5) were markedly uncommon, with only four strains of ST1 and none of ST2, ST4, or ST6. Lineage III, frequently encountered in nonhuman animals (6), was encountered in only nine strains. Dominant groups were clonal complex 554 (CC554) (serotype 4b; $n = 28$), CC388 (serotype 4b; $n = 11$), and CC20 (serotype 1/2a; $n = 9$). The majority of the STs (42/68, ca. 62%) were novel (Table 1).

Fecal samples and rectal and nasal swabs were enriched for *Listeria* using the ISO method with a Half Fraser primary enrichment at 30°C for 24 to 48 h followed by a Full Fraser

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Address correspondence to Phillip Brown, pebrown4@ncsu.edu, or Sophia Kathariou, skathar@ncsu.edu.

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†Deceased.

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TABLE 1 Characteristics of the 158 *Listeria monocytogenes* strains from black bears (*Ursus americanus*) described in this report

Strain name	Serotype	ST*	CC	Yr	Isolation		City, state, country	Identifier	Capture coordinates	Sample type	No. of contigs	Total length (bp)	GC content (%)	N ₅₀ (bp)	Coverage (x)	No. of reads	Sequencing method	Read quality control and trimming tools	GenBank	BioSample	Assembly	Sequence Read Archive
					Year	Location																
SK839	1/2a	788	7	2014	NC, USA	UNK-1	Unknown	Unknown	Feces	14	2,886,019	37.9	1,493,457	78	534,583	illumina M5Seq	CLC Genomics	AZACD0000000000	SAMN17815015	GCA_017121895.1	SRR13642977	
SK8109	1/2a	900	7	2014	NC, USA	UNK Caswell	Unknown	Unknown	Feces	18	2,909,257	37.9	1,481,159	93	665,817	illumina M5Seq	Workbench 7.5.1	AZACD0000000000	SAMN17815130	GCA_017120345.1	SRR13643217	
SK8403	1/2a	365	14	2016	Ashville, NC, USA	N056	35-584589 N, 82-6231004 W	Orphan	Nasal swab	67	2,932,209	37.9	428,130	1,170	13,346,689	illumina NextSeq 500	CLC Genomics	AZACD0000000000	SAMN08183176	GCA_004626455.1	SRR6394897	
SK8557	1/2a	1388	14	2016	Ashville, NC, USA	N131	35-648864 N, 82-470895 W	Orphan	Feces	30	2,902,022	37.9	339,136	484	4,857,222	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXD0000000000	SAMN08183184	GCA_004625815.1	SRR6392039	
SK8560	1/2a	1388	14	2016	Ashville, NC, USA	N131	35-648864 N, 82-470895 W	Orphan	Rectal swab	23	2,953,489	37.8	1,504,505	60	461,506	illumina M5Seq	CLC Genomics	AZACD0000000000	SAMN17814197	GCA_017123355.1	SRR13642676	
SK8165	1/2a	20	20	2015	Ashville, NC, USA	N061	35-581700 N, 82-518469 W	Orphan	Rectal swab	18	2,970,085	37.9	525,811	424	4,304,067	illumina M5Seq	Workbench 7.5.1	AZAS4000000000	SAMN17815064	GCA_017069151.1	SRR13643076	
SK823	1/2a	20	20	2014	Ashville, NC, USA	N024	35-581683 N, 82-518469 W	Orphan	Feces	18	2,858,149	37.9	583,919	65	397,990	illumina M5Seq	CLC Genomics	AZACD0000000000	SAMN17814492	GCA_017122155.1	SRR13642860	
SK847	1/2a	20	20	2014	Marion, GA, USA	UGA169	Unknown	Orphan	Rectal swab	23	3,028,268	37.8	299,142	48	303,351	illumina M5Seq	Workbench 7.5.1	AZACD0000000000	SAMN17815018	GCA_017121245.1	SRR13642885	
SK8612	1/2a	20	20	2016	Ashville, NC, USA	N087	35-603350 N, 82-527849 W	Orphan	Feces	18	3,039,614	37.8	562,688	183	1,915,619	illumina M5Seq	CLC Genomics	AZACD0000000000	SAMN17814371	GCA_017059255.1	SRR13642909	
SK8217	1/2a	1384	20	2015	Ashville, NC, USA	N043	35-499100 N, 82-530667 W	Orphan	Rectal swab	15	2,972,380	37.9	525,813	119	1,215,566	illumina M5Seq	Workbench 7.5.1	AZACD0000000000	SAMN17815039	GCA_017069215.1	SRR13643125	
SK8362	1/2a	1384	20	2015	Ashville, NC, USA	N095	35-517192 N, 82-573830 W	Orphan	Rectal swab	19	2,973,852	37.9	525,813	247	2,582,252	illumina M5Seq	CLC Genomics	AZACD0000000000	SAMN17815131	GCA_017068775.1	SRR13643229	
SK8455	1/2a	1384	20	2016	Ashville, NC, USA	N116	35-517192 N, 82-573830 W	Orphan	Nasal swab	21	2,892,383	37.9	583,956	1,170	12,258,689	illumina NextSeq 500	Workbench 7.5.1	AAAXE0000000000	SAMN08183153	GCA_004623875.1	SRR6395536	
SK8528	1/2a	1384	20	2016	Ashville, NC, USA	N125	35-648864 N, 82-470895 W	Orphan	Feces	22	2,848,312	37.9	583,887	1,027	10,377,382	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXE0000000000	SAMN08183182	GCA_004622345.1	SRR6397281	
SK8740	1/2a	1484	20	2017	Ashville, NC, USA	N151	35-591109 N, 82-493996 W	Orphan	Rectal swab	16	2,936,976	37.9	573,660	105	1,049,569	illumina M5Seq	Workbench 7.5.1	AZACD0000000000	SAMN17814274	GCA_017059075.1	SRR13642884	
SK8690	1/2a	321	321	2016	Ashville, NC, USA	N145	35-684397 N, 82-576257 W	Orphan	Feces	18	3,000,799	37.8	489,037	190	1,938,787	illumina M5Seq	CLC Genomics	AZACD0000000000	SAMN17814134	GCA_017059375.1	SRR13642851	
SK8197	1/2a	1370	570	2015	Ashville, NC, USA	N059	35-646382 N, 82-492551 W	Orphan	Nasal swab	27	2,848,964	37.9	570,292	456	4,617,926	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXD0000000000	SAMN08183171	GCA_004625055.1	SRR6395184	
SK8116	1/2a	1362	787	2014	Ashville, NC, USA	N049	35-520216 N, 82-477618 W	Orphan	Rectal swab	12	2,976,860	37.9	544,553	102	721,551	illumina M5Seq	Workbench 7.5.1	AZACD0000000000	SAMN17814358	GCA_017122695.1	SRR13642907	
SK8117	1/2a	1362	787	2014	Ashville, NC, USA	N049	35-520216 N, 82-477618 W	Orphan	Rectal swab	11	2,939,966	37.9	526,146	124	860,770	illumina M5Seq	Workbench 7.5.1	AZACD0000000000	SAMN17814323	GCA_017123095.1	SRR13642767	
SK8100	1/2a	838	838	2014	Ashville, NC, USA	N040	35-496205 N, 82-503329 W	Orphan	Swab	126	2,870,294	37.9	43,622	60	596,869	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	DAKHH0000000000	SAMN31891312	GCA_056470765.1	SRR22428071	
SK8137	1/2a	838	838	2014	Ashville, NC, USA	N058	35-625244 N, 82-535214 W	Orphan	Feces	24	2,891,928	37.9	436,201	70	497,362	illumina M5Seq	CLC Genomics	AZACD0000000000	SAMN17814481	GCA_017122395.1	SRR13642946	
SK8140	1/2a	838	838	2014	Ashville, NC, USA	N059	35-627214 N, 82-498245 W	Orphan	Feces	42	2,875,338	37.9	292,529	35	348,942	illumina M5Seq	Workbench 7.5.1	AZACD0000000000	SAMN17815088	GCA_017069155.1	SRR13643175	
SK8144	1/2a	1368	906	2014	VA, USA	VT BBRC 119	Unknown	Orphan	Rectal swab	16	2,917,963	37.9	525,325	139	957,279	illumina M5Seq	CLC Genomics	AZACD0000000000	SAMN17814324	GCA_017123075.1	SRR13642766	
SK8187	1/2a	1368	906	2015	VA, USA	VT BBRC 119	Unknown	Orphan	Nasal swab	22	2,871,959	37.9	524,454	929	10,194,404	illumina NextSeq 500	Workbench 7.5.1	AAAXD0000000000	SAMN08183180	GCA_004627565.1	SRR6392095	
SK8190	1/2a	1368	906	2015	VA, USA	VT BBRC 119	Unknown	Orphan	Nasal swab	26	2,867,340	37.9	517,587	487	4,564,458	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXD0000000000	SAMN08183173	GCA_004625795.1	SRR6396393	
SK8427	1/2a	912	912	2016	Ashville, NC, USA	N110	35-584093 N, 82-531423 W	Orphan	Rectal swab	25	2,933,152	37.8	299,475	1,265	13,648,343	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXD0000000000	SAMN08183175	GCA_004626415.1	SRR6394294	
SK8429	1/2a	912	912	2016	Ashville, NC, USA	N110	35-584093 N, 82-531423 W	Orphan	Swab	56	2,951,097	37.9	147,691	71	718,963	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	DAKCD0000000000	SAMN31788316	GCA_026352655.1	SRR22336611	
SK8397	1/2a	1383	912	2016	Ashville, NC, USA	N095	35-517192 N, 82-573830 W	Orphan	Nasal swab	26	2,961,311	37.8	271,119	772	8,477,955	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXD0000000000	SAMN08183169	GCA_004623015.1	SRR6394323	
SK8398	1/2a	1383	912	2016	Ashville, NC, USA	N095	35-517192 N, 82-573830 W	Orphan	Nasal swab	34	2,967,471	37.8	186,234	76	774,220	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	DAKCD0000000000	SAMN31788315	GCA_026352635.1	SRR22336613	
SK8593	1/2a	913	913	2016	Ashville, NC, USA	N136	35-635396 N, 82-595204 W	Orphan	Rectal swab	18	3,054,992	37.8	439,804	245	2,573,081	illumina M5Seq	Workbench 7.5.1	AZAAH0000000000	SAMN17814125	GCA_017059535.1	SRR13642643	
SK8599	1/2a	920	920	2016	Ashville, NC, USA	N137	35-526433 N, 82-595204 W	Orphan	Feces	17	3,011,733	37.9	437,579	253	2,627,535	illumina M5Seq	Workbench 7.5.1	AZACD0000000000	SAMN17814127	GCA_017059395.1	SRR13642645	
SK8632	1/2a	920	920	2016	Ashville, NC, USA	N061	35-517192 N, 82-573830 W	Orphan	Nasal swab	19	2,925,003	37.9	1,478,054	81	637,413	illumina M5Seq	CLC Genomics	AZACD0000000000	SAMN17814180	GCA_017123395.1	SRR13642670	
SK8719	1/2a	920	920	2016	Ashville, NC, USA	N138	35-517192 N, 82-573830 W	Orphan	Nasal swab	18	3,050,966	37.8	437,585	193	2,017,452	illumina M5Seq	Workbench 7.5.1	AZARF0000000000	SAMN17815012	GCA_017069475.1	SRR13642975	
SK8285	1/2a	935	935	2015	Ashville, NC, USA	N084	35-625251 N, 82-535369 W	Orphan	Rectal swab	18	2,943,324	37.8	433,614	59	598,692	illumina M5Seq	Workbench 7.5.1	AZARD0000000000	SAMN17815069	GCA_017069195.1	SRR13643130	
SK8333	1/2a	935	935	2015	Ashville, NC, USA	N015	35-511962 N, 82-529787 W	Orphan	Rectal swab	17	3,102,371	37.8	498,362	375	3,990,037	illumina M5Seq	Workbench 7.5.1	AZAAO0000000000	SAMN17815091	GCA_017068535.1	SRR13643193	
SK8339	1/2a	935	935	2015	Ashville, NC, USA	N093	35-619101 N, 82-507734 W	Orphan	Rectal swab	23	2,967,758	37.9	297,084	716	7,488,147	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXE0000000000	SAMN08183158	GCA_004626155.1	SRR6395469	
SK8343	1/2a	935	935	2015	Ashville, NC, USA	N093	35-619101 N, 82-507734 W	Orphan	Nasal swab	14	3,052,216	37.8	526,690	410	4,276,797	illumina M5Seq	Workbench 7.5.1	AZAAO0000000000	SAMN17815093	GCA_017068555.1	SRR13643188	

(Continued on next page)

TABLE 1 (Continued)

Strain name	Serotype	ST ^a	CC	Yr	Isolation		City, state, country	Identifier	Capture coordinates	Sample type	No. of contigs	Total length (bp)	GC content (%)	N ₅₀ (bp)	Coverage (x)	No. of reads	Sequencing method	Read quality control and trimming tools	GenBank	BioSample	Assembly	Sequence Read Archive
					Bear	Bear																
S48473	1/2a	935	935	2016	Ashville, NC, USA	N119	35.5925983 N, -82.525923 W	Feces	23	2,972,025	37.9	297,080	914	9,509,848	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXDU000000000	SAMN08183151	GCA_004622335.1	SRR6394749		
S48751	1/2a	935	935	2017	Ashville, NC, USA	N156	35.609041 N, -82.537208 W	Feces	15	2,993,701	37.8	511,924	155	1,575,853	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAHCO000000000	SAMN17814275	GCA_017059025.1	SRR13642691		
S48114	1/2a	1361	940	2014	Ashville, NC, USA	N049	35.522016 N, -82.477618 W	Feces	16	2,900,601	37.8	547,356	118	844,171	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCOA000000000	SAMN17814345	GCA_017122785.1	SRR13642816		
S48305	1/2a	1361	940	2015	Ashville, NC, USA	N057	35.620224 N, -82.519569 W	Feces	28	2,863,544	37.9	321,631	880	8,882,622	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXEE000000000	SAMN08183164	GCA_004622535.1	SRR6395258		
S48357	1/2a	1361	940	2015	Ashville, NC, USA	N014	35.618094 N, -82.497380 W	Rectal swab	18	2,991,420	37.9	505,271	332	3,444,938	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAOH000000000	SAMN17815144	GCA_017068715.1	SRR13643240		
S48369	1/2a	1361	940	2015	Ashville, NC, USA	N099	35.646548 N, -82.560473 W	Feces	14	2,877,928	37.9	547,099	78	546,293	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZACNR000000000	SAMN17815041	GCA_017068895.1	SRR13643069		
S48430	1/2a	955	955	2016	Ashville, NC, USA	N079	35.5925983 N, -82.525923 W	Feces	14	2,877,928	37.9	585,180	149	1,546,959	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAOH000000000	SAMN17815085	GCA_017068475.1	SRR13643191		
S48345	1/2a	956	956	2015	Ashville, NC, USA	N016	35.511962 N, -82.529787 W	Rectal swab	18	3,035,456	37.8	502,994	566	6,107,663	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAOH000000000	SAMN17815195	GCA_017067795.1	SRR13643293		
S48409	1/2a	956	956	2016	Ashville, NC, USA	N108	35.590995 N, -82.537394 W	Feces	17	2,955,677	37.8	1,488,778	251	2,535,356	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAOH000000000	SAMN17815043	GCA_017068995.1	SRR13643123		
S48313	1/2a	983	983	2015	Ashville, NC, USA	RK CLUB 91014	Unknown	Rectal swab	14	2,908,278	37.9	564,970	78	788,984	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAOZ000000000	SAMN17815020	GCA_017121305.1	SRR13642986		
S48357	1/2a	1055	1055	2014	Macon, GA, USA	UGA170	32.519241 N, -83.425799 W	Rectal swab	16	2,956,658	37.8	428,541	90	550,570	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZACNR000000000	SAMN17815020	GCA_017121305.1	SRR13642986		
S48363	1/2a	1357	1357	2014	Ashville, NC, USA	N034	35.468036 N, -82.489578 W	Feces	53	2,883,063	37.9	115,587	28	167,582	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZACP000000000	SAMN17814452	GCA_017122455.1	SRR13642935		
S48390	1/2a	1359	1359	2014	Macon, GA, USA	UGA177	32.547886 N, -83.521293 W	Rectal swab	14	2,976,506	37.8	528,722	79	497,075	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZACP000000000	SAMN17814433	GCA_017122615.1	SRR13642927		
S48113	1/2a	1360	1360	2014	Ashville, NC, USA	N046	35.499100 N, -82.550667 W	Feces	22	2,937,965	37.9	296,518	97	687,659	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZACT000000000	SAMN17814356	GCA_017122955.1	SRR13642905		
S48125	1/2a	1364	1364	2014	Ashville, NC, USA	N052	35.623417 N, -82.545153 W	Feces	15	2,897,294	37.9	528,714	74	518,894	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZACR000000000	SAMN17814132	GCA_017123775.1	SRR13642648		
S48350	1/2a	1386	1364	2016	Ashville, NC, USA	N124	35.566479 N, -82.545153 W	Rectal swab	29	2,862,908	37.9	423,828	779	7,828,376	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXER000000000	SAMN08183146	GCA_004627135.1	SRR6396634		
S48102	1/2a	1365	1365	2014	Ashville, NC, USA	N041	35.618657 N, -82.377747 W	Rectal swab	12	3,067,177	37.9	542,982	101	654,669	illumina MiSeq	CLC Genomics Workbench 7.5.1	AB1HH000000000	SAMN31921597	GCA_026273155.1	SRR23625246		
S48128	1/2a	1365	1365	2014	Ashville, NC, USA	N052	35.623417 N, -82.545153 W	Feces	17	2,982,947	37.8	1,497,612	84	622,685	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZACT000000000	SAMN17814507	GCA_017122135.1	SRR13642959		
S48183	1/2a	1367	1367	2015	Ashville, NC, USA	N003	35.632554 N, -82.504740 W	Nasal swab	16	2,849,327	37.9	525,049	46	461,453	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAAOF000000000	SAMN17815103	GCA_017068505.1	SRR13643201		
S48185	1/2a	1367	1367	2015	Ashville, NC, USA	N003	35.632554 N, -82.504740 W	Nasal swab	18	2,845,633	37.9	1,467,872	722	7,357,255	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXDP000000000	SAMN08183179	GCA_004625115.1	SRR6395220		
S48191	1/2a	1369	1369	2015	Ashville, NC, USA	N006	35.634546 N, -82.496066 W	Nasal swab	25	2,875,347	37.9	321,632	829	8,680,965	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXA000000000	SAMN08183170	GCA_004624215.1	SRR6395220		
S48193	1/2a	1369	1369	2015	Ashville, NC, USA	N006	35.634546 N, -82.496066 W	Nasal swab	15	2,998,969	37.9	523,428	447	4,587,351	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAAOC000000000	SAMN17815120	GCA_017068695.1	SRR13643231		
S48309	1/2a	1369	1369	2015	Ashville, NC, USA	N057	35.620224 N, -82.499686 W	Rectal swab	26	2,905,958	37.9	321,634	1,043	10,679,862	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXE000000000	SAMN08183163	GCA_004625365.1	SRR6395508		
S48391	1/2a	1369	1369	2015	Ashville, NC, USA	N057	35.620224 N, -82.519569 W	Nasal swab	16	2,995,234	37.9	523,399	251	2,612,940	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAP000000000	SAMN17815136	GCA_017068795.1	SRR13643218		
S48275	1/2a	1369	1369	2016	Ashville, NC, USA	N150	35.630332 N, -82.469195 W	Feces	15	3,087,202	37.8	523,409	205	2,172,841	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAAHD000000000	SAMN17814284	GCA_017059015.1	SRR13642694		
S48198	1/2a	1371	1371	2015	Ashville, NC, USA	N059	35.646932 N, -82.469195 W	Nasal swab	20	2,872,274	37.9	570,428	1,110	11,166,016	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXDG000000000	SAMN08183188	GCA_004623375.1	SRR6391874		
S48235	1/2a	1371	1371	2015	Ashville, NC, USA	N072	35.600941 N, -82.492351 W	Rectal swab	19	2,870,816	37.9	570,428	1,226	12,372,196	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXE000000000	SAMN08183172	GCA_004626435.1	SRR6396903		
S48199	1/2a	1372	1372	2015	Ashville, NC, USA	N063	35.648012 N, -82.504740 W	Nasal swab	51	3,078,012	37.9	425,383	1,063	11,470,077	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXE000000000	SAMN08183161	GCA_004625905.1	SRR6395334		
S48265	1/2a	1372	1372	2015	Ashville, NC, USA	N080	35.620224 N, -82.499686 W	Rectal swab	16	2,996,697	37.9	529,306	442	4,615,515	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAAFF000000000	SAMN17814439	GCA_017058255.1	SRR13642933		
S48266	1/2a	1372	1372	2015	Ashville, NC, USA	N080	35.620224 N, -82.519569 W	Rectal swab	20	2,879,254	37.9	529,167	69	700,714	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAARE000000000	SAMN17814477	GCA_017069015.1	SRR13642936		
S48325	1/2a	1372	1372	2015	Ashville, NC, USA	N089	35.619101 N, -82.50734 W	Nasal swab	24	2,898,432	37.9	423,961	1,263	12,864,737	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXE000000000	SAMN08183143	GCA_004626655.1	SRR6396650		
S48428	1/2a	1372	1372	2016	Ashville, NC, USA	N110	35.584093 N, -82.551423 W	Rectal swab	58	2,916,174	37.9	114,851	138	1,439,357	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXE000000000	SAMN08183168	GCA_004626235.1	SRR6395235		
S48512	1/2a	1372	1372	2016	Ashville, NC, USA	N124	35.566479 N, -82.537394 W	Feces	24	2,899,986	37.8	329,882	1,021	10,282,021	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXDR000000000	SAMN08183148	GCA_004626165.1	SRR6394746		
S48580	1/2a	1372	1372	2016	Ashville, NC, USA	N109	35.590995 N, -82.537394 W	Feces	18	2,905,866	37.8	527,444	53	407,517	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCX000000000	SAMN17814192	GCA_017123375.1	SRR13642674		
S48274	1/2a	1374	1374	2015	Ashville, NC, USA	N081	35.605348 N, -82.560473 W	Rectal swab	17	2,949,710	37.9	337,428	127	890,234	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZACT000000000	SAMN17814269	GCA_017123235.1	SRR13642683		
S48295	1/2a	1376	1376	2015	Ashville, NC, USA	N085	35.605348 N, -82.560473 W	Rectal swab	27	2,857,929	37.9	291,362	1,038	10,357,963	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXE000000000	SAMN08183166	GCA_004627515.1	SRR6395254		
S48330	1/2a	1381	1381	2015	Ashville, NC, USA	N091	35.620224 N, -82.560473 W	Rectal swab	25	2,895,064	37.8	431,535	946	9,675,234	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXD000000000	SAMN08183177	GCA_004623995.1	SRR6394855		

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TABLE 1 (Continued)

Strain name	Serotype	ST ^a	CC	Yr	Isolation		Identifier	Capture coordinates	Sample type	No. of contigs	Total length (bp)	GC content (%)	N ₅₀ (bp)	Coverage (x)	No. of reads	Sequencing method	Read quality control and trimming tools	GenBank	BioSample	Assembly	Sequence Read Archive
					City, state, country	Bear															
SK8353	1/2a	1381	1381	2015	Ashville, NC, USA	USA	35.619101 N, -82.507734 W	Rectal swab	25	2,935,652	37.8	356,741	70	716,619	illumina NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	AZADQ000000000	SAMN17815115	GCA_017068835.1	SRRI3643212	
SK8354	1/2a	1387	1387	2016	Ashville, NC, USA	USA	35.619101 N, -82.507734 W	Nasal swab	23	2,828,993	37.9	568,823	572	5,665,666	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAAXE000000000	SAMN08183155	GCA_004627075.1	SRR6395801	
SK8699	1/2a	1389	1389	2016	Ashville, NC, USA	USA	35.517418 N, -82.575864 W	Rectal swab	20	2,963,264	37.8	459,921	86	690,705	illumina NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	AZACR000000000	SAMN17814182	GCA_017123815.1	SRRI3642669	
SK8149	1/2a	1475	1475	2014	VA, USA	USA	35.566479 N, -82.589689 W	Feces	38	2,863,550	37.9	180,571	31	304,540	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZG000000000	SAMN17815125	GCA_017068755.1	SRRI3643233	
SK8150	1/2a	1476	1476	2014	VA, USA	USA	Unknown	Rectal swab	85	2,920,183	37.8	64,528	22	226,959	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZO000000000	SAMN17815194	GCA_017067915.1	SRRI3643294	
SK8209	1/2a	1477	1477	2015	Ashville, NC, USA	USA	35.560815 N, -82.594653 W	Rectal swab	32	2,918,323	37.8	292,789	42	432,109	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZQ000000000	SAMN17815095	GCA_017069175.1	SRRI3643196	
SK8243	1/2a	1478	1478	2015	Ashville, NC, USA	USA	35.618079 N, -82.378587 W	Feces	14	2,966,718	37.9	524,291	565	5,896,291	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZR000000000	SAMN17815036	GCA_017069535.1	SRRI3643070	
SK8293	1/2a	1479	1479	2015	Ashville, NC, USA	USA	35.645548 N, -82.576047 W	Rectal swab	17	2,850,802	37.9	421,556	64	639,119	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZC000000000	SAMN17815042	GCA_017069235.1	SRRI3643080	
SK8278	1/2a	1483	1483	2017	Ashville, NC, USA	USA	35.609941 N, -82.557208 W	Feces	14	3,035,504	37.8	527,573	115	1,184,669	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZH000000000	SAMN17814285	GCA_017058975.1	SRRI3642695	
SK8231	1/2a	1487	1487	2015	Ashville, NC, USA	USA	35.609941 N, -82.557208 W	Feces	19	3,038,326	37.8	295,311	438	4,598,873	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZL000000000	SAMN17815040	GCA_017069435.1	SRRI3643067	
SK8201	1/2a	1487	1487	2016	Ashville, NC, USA	USA	35.566479 N, -82.589689 W	Rectal swab	21	3,039,759	37.8	293,870	197	2,056,553	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZA000000000	SAMN17814162	GCA_017059275.1	SRRI3642663	
SK8269	1/2b	379	379	2015	Ashville, NC, USA	USA	35.620224 N, -82.519569 W	Nasal swab	48	2,904,373	37.9	173,236	33	339,275	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZO000000000	SAMN17815079	GCA_017069035.1	SRRI3643136	
SK8516	1/2b	379	379	2016	Ashville, NC, USA	USA	35.566479 N, -82.519569 W	Feces	31	2,885,571	37.9	345,706	736	7,400,246	illumina NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	AAAF000000000	SAMN08183145	GCA_004626735.1	SRR6397282	
SK8281	1/2b	736	736	2017	Ashville, NC, USA	USA	35.560815 N, -82.537208 W	Nasal swab	23	3,001,405	37.9	256,949	226	2,303,773	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZG000000000	SAMN17814377	GCA_017059055.1	SRRI3642911	
SK858	1/2b	2973	2973	2014	Macon, GA, USA	USA	32.519241 N, -83.435799 W	Swab	87	3,000,949	37.8	60,186	89	910,060	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZQ000000000	SAMN31891309	GCA_026470745.1	SRR22428074	
SK859	1/2b	2973	2973	2014	Macon, GA, USA	USA	32.519241 N, -83.435799 W	Swab	94	3,015,184	37.8	63,864	89	911,078	illumina NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	DAKH000000000	SAMN31891310	GCA_026470745.1	SRR22428073	
SK8106	1/2c	789	789	2014	Ashville, NC, USA	USA	35.499100 N, -82.550667 W	Feces	22	2,928,853	37.8	423,378	78	572,235	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZL000000000	SAMN17815138	GCA_017120365.1	SRRI3643222	
SK815	1/2c	789	789	2014	Ashville, NC, USA	USA	35.619750 N, -82.519523 W	Feces	18	2,925,154	37.8	423,470	56	339,038	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZK000000000	SAMN17814487	GCA_017122035.1	SRRI3642967	
SK8479	1/2c	1385	1385	2016	Ashville, NC, USA	USA	35.592583 N, -82.519523 W	Nasal swab	27	2,851,686	37.9	596,964	716	7,092,281	illumina NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	AAAXE000000000	SAMN08183150	GCA_004626915.1	SRR6396261	
SK8159	4b	1	1	2015	Ashville, NC, USA	USA	35.581200 N, -82.518469 W	Feces	32	2,917,084	37.9	298,032	1,067	11,288,130	illumina NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	AAAXD000000000	SAMN08183189	GCA_004622875.1	SRR6391962	
SK8350	4b	1	1	2015	Ashville, NC, USA	USA	35.619101 N, -82.507734 W	Rectal swab	201	2,966,721	37.8	41,544	98	1,005,851	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZL000000000	SAMN17815135	GCA_017120105.1	SRRI3643223	
SK8581	4b	1	1	2016	Ashville, NC, USA	USA	35.589890 N, -82.514457 W	Rectal swab	18	3,028,114	37.9	476,515	244	2,547,440	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZS000000000	SAMN17814497	GCA_017069395.1	SRRI3642962	
SK8682	4b	1	1	2016	Ashville, NC, USA	USA	35.620987 N, -82.523371 W	Feces	14	2,933,894	37.9	516,971	203	2,033,106	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZG000000000	SAMN17814147	GCA_017059355.1	SRRI3642655	
SK8111	4b	1039	2	2014	Ashville, NC, USA	USA	35.618193 N, -82.537877 W	Rectal swab	19	2,975,332	37.9	323,707	75	600,860	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZL000000000	SAMN17815132	GCA_017120325.1	SRRI3643220	
SK8112	4b	1039	2	2014	Ashville, NC, USA	USA	35.618193 N, -82.537877 W	Rectal swab	17	3,016,345	37.9	477,787	105	806,060	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZP000000000	SAMN17814387	GCA_017122915.1	SRRI3642910	
SK8121	4b	1039	2	2014	Ashville, NC, USA	USA	35.620924 N, -82.537877 W	Rectal swab	19	2,925,293	37.9	477,783	76	509,221	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZR000000000	SAMN17814170	GCA_017123735.1	SRRI3642654	
SK8297	4b	1039	2	2015	Ashville, NC, USA	USA	35.665948 N, -82.523347 W	Nasal swab	30	2,900,303	37.9	307,904	870	8,920,502	illumina NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	AAAXE000000000	SAMN08183165	GCA_004625335.1	SRR6395255	
SK8461	4b	1039	2	2016	Ashville, NC, USA	USA	35.625293 N, -82.597632 W	Rectal swab	30	2,942,750	38.0	307,907	1,104	11,284,292	illumina NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	AAAXE000000000	SAMN08183152	GCA_004622375.1	SRR6395704	
SK8537	4b	1039	2	2016	Ashville, NC, USA	USA	35.625293 N, -82.597632 W	Feces	32	2,939,836	37.9	307,899	565	5,827,138	illumina NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	AAAXE000000000	SAMN08183140	GCA_004625495.1	SRR6397048	
SK8542	4b	1039	2	2016	Ashville, NC, USA	USA	35.625293 N, -82.597632 W	Feces	31	2,901,866	37.9	307,910	506	5,106,444	illumina NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	AAAXE000000000	SAMN08183154	GCA_004627615.1	SRR6395509	
SK8134	4b	631	4	2014	Ashville, NC, USA	USA	35.630684 N, -82.597632 W	Feces	14	2,903,802	38.0	593,005	78	483,920	illumina NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	ABINS000000000	SAMN31821589	GCA_026375595.1	SRR22362539	
SK8444	4b	631	4	2016	Ashville, NC, USA	USA	35.517192 N, -82.509554 W	Feces	37	2,874,823	37.9	244,554	1,342	13,828,113	illumina NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	AAAXD000000000	SAMN08183178	GCA_004625775.1	SRR6394325	
SK8467	4b	631	4	2016	Ashville, NC, USA	USA	35.517192 N, -82.573830 W	Nasal swab	24	3,003,387	37.9	251,638	152	1,556,226	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZQ000000000	SAMN17815082	GCA_017068875.1	SRRI3643182	
SK8634	4b	382	183	2016	Ashville, NC, USA	USA	35.517192 N, -82.573830 W	Nasal swab	17	3,006,694	37.9	309,733	60	481,371	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZR000000000	SAMN17814187	GCA_017123255.1	SRRI3642672	
SK8123	4b	388	388	2014	Ashville, NC, USA	USA	35.508438 N, -82.553691 W	Rectal swab	16	2,932,212	37.9	543,959	83	569,106	illumina MiSeq	CLC Genomics Workbench 7.5.1	AZAZR000000000	SAMN17814135	GCA_017123595.1	SRRI3642652	
SK8282	4b	388	388	2015	Ashville, NC, USA	USA	35.508438 N, -82.553691 W	Nasal swab	30	2,887,474	37.9	498,306	814	8,124,789	illumina NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	AAAXE000000000	SAMN08183160	GCA_004623835.1	SRR6395362	

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TABLE 1 (Continued)

Strain name	Serotype	ST ^a	CC	Yr	Isolation		Identifier	Capture coordinates	Sample type	No. of contigs	Total length (bp)	GC content (%)	N ₅₀ (bp)	Coverage (x)	No. of reads	Sequencing method	Read quality control and trimming tools	GenBank	BioSample	Assembly	Sequence Read Archive
					City, state, country	Bear															
SKB544	4b	388	388	2016	Ashville, NC, USA	VA	35:620224.N -82:519569.W	Feces	26	2,927,480	37.9	538,013	624	6,372,548	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXDF000000000	SAMN08183186	GCA_004627595.1	SRR6391880	
SKB578	4b	388	388	2016	Ashville, NC, USA	VA	35:625263.N -82:597632.W	Feces	18	2,942,399	37.9	303,674	54	422,691	illumina MiSeq	CLC Genomics	AZCR000000000	SAMN17814246	GCA_017123795.1	SRR13642678	
SKB647	4b	388	388	2016	Ashville, NC, USA	VA	35:590995.N -82:537394.W	Feces	20	3,008,530	37.9	538,173	174	1,789,146	illumina MiSeq	CLC Genomics	AZAAHA000000000	SAMN17814124	GCA_017059325.1	SRR13642646	
SKB676	4b	388	388	2016	Ashville, NC, USA	VA	35:6363396.N -82:525301.W	Rectal swab	19	3,055,291	37.9	538,212	180	1,876,916	illumina MiSeq	CLC Genomics	AZAZAGV000000000	SAMN17814142	GCA_017059315.1	SRR13642661	
SKB698	4b	388	388	2016	Ashville, NC, USA	VA	35:495956.N -82:517875.W	Feces	15	2,934,732	37.9	543,712	66	530,090	illumina MiSeq	CLC Genomics	SAMN17815133	GCA_017120065.1	SRR13643213		
SKB769	4b	388	388	2017	Ashville, NC, USA	VA	35:566479.N -82:589689.W	Rectal swab	25	2,946,457	37.9	498,310	135	1,350,967	illumina MiSeq	CLC Genomics	AZAZAGR000000000	SAMN17814282	GCA_017059295.1	SRR13642696	
SKB776	4b	388	388	2017	Ashville, NC, USA	VA	35:5804093.N -82:531423.W	Rectal swab	24	2,941,322	37.9	498,313	194	1,931,148	illumina MiSeq	CLC Genomics	AZAZAGS000000000	SAMN17814426	GCA_017059135.1	SRR13642922	
SKB860	4b	2145	388	2014	Ashville, NC, USA	VA	35:5804093.N -82:531423.W	Nasal swab	15	2,883,400	37.9	515,701	79	470,837	illumina MiSeq	CLC Genomics	AZAZCLO00000000	SAMN17815029	GCA_017121425.1	SRR13643007	
SKB861	4b	2145	388	2014	Ashville, NC, USA	VA	35:468036.N -82:489578.W	Feces	88	2,902,099	37.9	66,824	82	812,998	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	DAKHKF000000000	SAMN31891311	GCA_026647025.1	SRR22428072	
SKB103	4b	554	554	2014	Ashville, NC, USA	VA	35:480248.N -82:489578.W	Feces	14	2,913,078	37.9	408,295	83	598,058	illumina MiSeq	CLC Genomics	AZAZCOY000000000	SAMN17814186	GCA_017123295.1	SRR13642673	
SKB104	4b	554	554	2014	Ashville, NC, USA	VA	35:508438.N -82:553691.W	Rectal swab	16	2,947,880	37.9	408,295	108	787,268	illumina MiSeq	CLC Genomics	AZAZCKY000000000	SAMN17815142	GCA_017120265.1	SRR13643242	
SKB155	4b	554	554	2015	Ashville, NC, USA	VA	35:581291.N -82:553691.W	Rectal swab	34	2,911,678	37.9	307,794	1,000	10,851,154	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXDV000000000	SAMN08183187	GCA_004624655.1	SRR6394375	
SKB361	4b	554	554	2015	Ashville, NC, USA	VA	35:571792.N -82:518469.W	Rectal swab	21	3,029,941	37.9	408,295	181	1,907,733	illumina MiSeq	CLC Genomics	AZAZCOU000000000	SAMN17814247	GCA_017123135.1	SRR13642680	
SKB373	4b	554	554	2015	Ashville, NC, USA	VA	35:645248.N -82:572830.W	Feces	18	2,987,566	37.9	408,295	208	2,161,193	illumina MiSeq	CLC Genomics	AZAZLX000000000	SAMN17815086	GCA_017120615.1	SRR13643192	
SKB379	4b	554	554	2015	VA, USA	VA	Unknown 82:560473.W	Feces	33	2,892,284	37.9	308,144	929	10,067,487	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXDX000000000	SAMN08183174	GCA_004626315.1	SRR6394911	
SKB441	4b	554	554	2016	Ashville, NC, USA	VA	35:491520.N -82:564499.W	Feces	32	2,899,903	37.9	307,794	1,206	12,519,329	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXDT000000000	SAMN08183167	GCA_004624955.1	SRR6394748	
SKB494	4b	554	554	2016	Ashville, NC, USA	VA	35:648864.N -82:490895.W	Feces	30	2,955,636	37.8	303,515	1,267	13,087,194	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXD5000000000	SAMN08183149	GCA_004623955.1	SRR6394738	
SKB513	4b	554	554	2016	Ashville, NC, USA	VA	35:56479.N -82:580689.W	Feces	30	2,889,359	37.9	308,144	1,007	10,132,309	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXEQ000000000	SAMN08183147	GCA_004624395.1	SRR6396513	
SKB536	4b	554	554	2016	Ashville, NC, USA	VA	35:675463.N -82:580689.W	Feces	30	2,959,942	37.9	295,426	870	9,131,000	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXD0000000000	SAMN08183183	GCA_004625675.1	SRR6392040	
SKB543	4b	554	554	2016	Ashville, NC, USA	VA	35:675463.N -82:580689.W	Feces	28	2,902,028	37.9	303,515	795	8,056,112	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXFD000000000	SAMN08183144	GCA_004627115.1	SRR6397911	
SKB558	4b	554	554	2016	Ashville, NC, USA	VA	35:668949.N -82:597632.W	Feces	27	2,957,295	37.8	308,144	691	7,103,431	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXET000000000	SAMN08183185	GCA_004624435.1	SRR6396649	
SKB614	4b	554	554	2016	Ashville, NC, USA	VA	35:603339.N -82:527849.W	Rectal swab	18	2,933,332	37.9	408,294	65	510,190	illumina MiSeq	CLC Genomics	AZAZCND000000000	SAMN17814196	GCA_017123315.1	SRR13642675	
SKB757	4b	554	554	2017	Ashville, NC, USA	VA	35:570732.N -82:499853.W	Feces	23	2,943,198	37.9	296,833	123	1,228,096	illumina MiSeq	CLC Genomics	AZAZCFM000000000	SAMN17814281	GCA_017123215.1	SRR13642692	
SKB896	4b	554	554	2014	Ashville, NC, USA	VA	35:564102.N -82:469931.W	Feces	12	2,915,645	37.9	540,987	70	438,738	illumina MiSeq	CLC Genomics	AZAZCFX000000000	SAMN17814398	GCA_017122875.1	SRR13642912	
SKB897	4b	554	554	2014	Ashville, NC, USA	VA	35:564102.N -82:469931.W	Feces	14	2,987,892	37.9	540,987	96	606,506	illumina MiSeq	CLC Genomics	AZAZCFU000000000	SAMN17814418	GCA_017122875.1	SRR13642918	
SKB98	4b	554	554	2014	Ashville, NC, USA	VA	35:564102.N -82:469931.W	Rectal swab	15	2,992,035	37.9	408,295	114	822,705	illumina MiSeq	CLC Genomics	AZAZCFV000000000	SAMN17814249	GCA_017123455.1	SRR13642679	
SKB317	4b	999	554	2015	Ashville, NC, USA	VA	35:566807.N -82:564075.W	Rectal swab	27	2,889,958	37.9	308,152	712	7,127,335	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXE5000000000	SAMN08183156	GCA_004626675.1	SRR6395721	
SKB42	4b	999	554	2014	NC, USA	NC	Unknown -82:564075.W	Feces	17	2,935,295	37.9	408,287	87	537,195	illumina MiSeq	CLC Genomics	AZAZCZV000000000	SAMN17815017	GCA_017121285.1	SRR13642978	
SKB43	4b	999	554	2014	Ashville, NC, USA	VA	35:580511.N -82:498622.W	Swab	70	2,895,361	37.9	85,377	58	579,252	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	DAKHKO000000000	SAMN31891307	GCA_0266470685.1	SRR22428076	
SKB45	4b	999	554	2014	Ashville, NC, USA	VA	35:580511.N -82:498622.W	Rectal swab	15	2,910,935	37.9	408,287	74	443,013	illumina MiSeq	CLC Genomics	AZAZCPO000000000	SAMN17814438	GCA_017123435.1	SRR13642934	
SKB46	4b	999	554	2014	Ashville, NC, USA	VA	35:580511.N -82:498622.W	Swab	90	2,907,630	37.9	62,497	82	808,884	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	DAKHMB000000000	SAMN31891308	GCA_026647125.1	SRR22428075	
SKB275	4b	1375	554	2015	Ashville, NC, USA	VA	35:649548.N -82:560473.W	Rectal swab	19	3,073,987	37.9	408,354	126	910,517	illumina MiSeq	CLC Genomics	AZAZCZD000000000	SAMN17814271	GCA_017123465.1	SRR13642682	
SKB321	4b	1378	554	2015	Ashville, NC, USA	VA	35:619101.N -82:507734.W	Feces	31	2,900,741	37.9	307,904	844	8,601,599	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXFA000000000	SAMN08183142	GCA_004627255.1	SRR6399033	
SKB329	4b	1378	554	2015	Ashville, NC, USA	VA	35:619101.N -82:507734.W	Rectal swab	25	2,902,558	37.9	307,919	1,075	10,918,862	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXEH000000000	SAMN08183159	GCA_004623535.1	SRR6395462	
SKB337	4b	1378	554	2015	Ashville, NC, USA	VA	35:619101.N -82:507734.W	Rectal swab	30	2,901,161	37.9	303,526	881	8,951,458	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXEY000000000	SAMN08183157	GCA_004624275.1	SRR6397297	
SKB341	4b	1378	554	2015	USA	VA	Unknown -82:507734.W	Nasal swab	20	3,029,015	37.9	303,526	377	3,880,975	illumina MiSeq	CLC Genomics	AZAZCMI000000000	SAMN17815092	GCA_017120251.1	SRR13643199	

(Continued on next page)

TABLE 1 (Continued)

Strain name	Serotype	ST ^a	CC	Yr	Isolation		Identifier	Capture coordinates	Sample type	No. of contigs	Total length (bp)	GC content (%)	N ₅₀ (bp)	Coverage (x)	No. of reads	Sequencing method	Read quality control and trimming tools	Accession no.		
					City, state, country	Bear												GenBank	BioSample	Assembly
SKB349	4b	1378	554	2015	Asheville, NC, USA	VT BBRC 121	35,619,101 N, -82,507,734 W	Rectal	25	2,911,540	37.9	327,771	589	5,931,561	illumina MiSeq	CLCGenomics Workbench 7.5.1	AAZCLJ000000000	SAMN17815134	GCA_017120385.1	SRR13643211
SKB374	4b	801	651	2015	Asheville, NC, USA	UNKCUB	35,619,101 N, -82,507,734 W	swab	20	3,053,097	37.9	498,503	236	2,561,831	illumina MiSeq	CLCGenomics Workbench 7.5.1	AAZCMB000000000	SAMN17815087	GCA_017120645.1	SRR13643189
SKB770	4b	801	651	2017	Asheville, NC, USA	9415	35,570,500 N, -82,651,075 W	Feces	17	3,041,941	37.9	544,009	125	1,300,339	illumina MiSeq	CLCGenomics Workbench 7.5.1	AAZCPJ000000000	SAMN17814423	GCA_017122895.1	SRR13642915
SKB775	4b	801	651	2017	Asheville, NC, USA	N158	35,580,093 N, -82,551,423 W	Rectal swab	18	2,980,467	37.9	498,505	141	1,432,594	illumina MiSeq	CLCGenomics Workbench 7.5.1	AAZCPK000000000	SAMN17814424	GCA_017122635.1	SRR13642920
SKB142	Lineage III	264	264	2014	VA, USA	VT BBRC 121	Unknown	Feces	25	3,030,315	37.9	386,361	841	9,160,449	illumina NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	AAAXDL000000000	SAMN08183181	GCA_004624105.1	SRR6392089
SKB142	Lineage III	1366	434	2014	VA, USA	VT BBRC 119	Unknown	Feces	14	2,960,623	38.1	489,760	117	851,785	illumina MiSeq	CLCGenomics Workbench 7.5.1	AAZCOE000000000	SAMN17814332	GCA_017123115.1	SRR13642765
SKB75	Lineage III	1358	1358	2014	Macon, GA, USA	UGA175	32,466,313 N, -83,576,571 W	Rectal	26	2,906,536	38.0	234,666	72	439,480	illumina MiSeq	CLCGenomics Workbench 7.5.1	AAZCGO000000000	SAMN17814432	GCA_017122535.1	SRR13642928
SKB118	Lineage III	1363	1363	2014	Macon, GA, USA	UGA179	32,548,795 N, -83,452,115 W	Rectal swab	20	2,974,737	37.8	541,748	71	456,905	illumina MiSeq	CLCGenomics Workbench 7.5.1	AAZCCO000000000	SAMN17814346	GCA_017122275.1	SRR13642815
SKB119	Lineage III	1363	1363	2014	Macon, GA, USA	UGA179	32,548,795 N, -83,452,115 W	Rectal swab	23	2,985,300	37.8	546,918	68	483,223	illumina MiSeq	CLCGenomics Workbench 7.5.1	AAZCRM000000000	SAMN17814157	GCA_017123555.1	SRR13642657
SKB259	Lineage III	1373	1373	2015	Asheville, NC, USA	N079	35,620,224 N, -82,551,956 W	Nasal swab	13	2,934,131	38.0	527,500	119	833,950	illumina MiSeq	CLCGenomics Workbench 7.5.1	AAZCCO000000000	SAMN17814273	GCA_017123175.1	SRR13642688
SKB381	Lineage III	1382	1382	2015	VA, USA	VT BBRC 127	Unknown	Feces	13	2,959,658	38.0	588,980	54	405,818	illumina MiSeq	CLCGenomics Workbench 7.5.1	AAZCRO000000000	SAMN17814248	GCA_017123335.1	SRR13642677
SKB782	Lineage III	1486	1486	2017	Asheville, NC, USA	N037	35,560,815 N, -82,594,653 W	Nasal swab	25	3,119,481	37.8	522,775	171	1,821,171	illumina MiSeq	CLCGenomics Workbench 7.5.1	AAZCPJ000000000	SAMN17814430	GCA_017122575.1	SRR13642923
SKB67	Lineage III	2158	2158	2016	Macon, GA, USA	UGA174	32,481,646 N, -83,578,157 W	Rectal swab	12	2,996,511	37.9	596,909	90	559,546	illumina MiSeq	CLCGenomics Workbench 7.5.1	AAZCPH000000000	SAMN17814467	GCA_017122495.1	SRR13642931

^a Sequence type (ST) designations in bold are novel STs first identified in this study.

secondary enrichment at 37°C for 48 h, as previously described (4). Strains were streaked from frozen stocks (−80°C) on tryptic soy (TS) agar (Becton, Dickinson & Co.) and incubated at 37°C overnight. Genomic DNA was extracted by the DNeasy blood and tissue kit (Qiagen, Valencia, CA) from strains grown overnight at 37°C in brain heart infusion or TS broth. Libraries were prepared using 0.5 to 1 ng of genomic DNA with a Nextera XT DNA library preparation kit (Illumina, San Diego, CA, USA). Genomes were sequenced using either a NextSeq 500 sequencer with the NextSeq 500/550 high-output kit v2.5 (300 cycles, 2 by 150 bp) (Illumina) or a MiSeq desktop sequencer with the MiSeq kit v2 (500 cycles, 2 by 250 bp) (Illumina) according to the manufacturer's instructions (Table 1). Raw sequencing reads were quality controlled by FastQC v0.11.5 (7) and trimmed using BBDuk2 from BBTools v38.89 (<https://sourceforge.net/projects/bbmap/>) or using CLC Genomics Workbench 7.5.1 (CLC Bio, Boston, MA) (Table 1). Reads were deposited into the National Center for Biotechnology Information (<https://www.ncbi.nlm.nih.gov>), and assemblies produced by SKESA v 2.2 (8) were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v 6.3 (9). STs and CCs were identified using BIGSdb-Lm, hosted by the Institut Pasteur (<https://bigsdbs.pasteur.fr/listeria/>) (10). Default parameters were used for all software.

Data availability. This whole-genome shotgun project has been deposited in GenBank under the accession numbers found in Table 1. The versions described in this paper are the first version.

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REFERENCES

- Swaminathan B, Gerner-Smidt P. 2007. The epidemiology of human listeriosis. *Microbes Infect* 9:1236–1243. <https://doi.org/10.1016/j.micinf.2007.05.011>.
- Maury MM, Tsai YH, Charlier C, Touchon M, Chenal-Francois V, Leclercq A, Criscuolo A, Gaultier C, Roussel S, Brisabois A, Disson O, Rocha EPC, Brisse S, Lecuit M. 2016. Uncovering *Listeria monocytogenes* hypervirulence by harnessing its biodiversity. *Nat Genet* 48:308–313. <https://doi.org/10.1038/ng.3501>.
- Lee S, Chen Y, Gorski L, Ward TJ, Osborne J, Kathariou S. 2018. *Listeria monocytogenes* source distribution analysis indicates regional heterogeneity and ecological niche preference among serotype 4b clones. *mBio* 9:e00396-18. <https://doi.org/10.1128/mBio.00396-18>.
- Parsons C, Niedermeyer J, Gould N, Brown P, Strules J, Parsons AW, Bernardo Mesa-Cruz J, Kelly MJ, Hooker MJ, Chamberlain MJ, Olfenbuttel C, DePerno C, Kathariou S. 2020. *Listeria monocytogenes* at the human-wildlife interface: black bears (*Ursus americanus*) as potential vehicles for *Listeria*. *Microb Biotechnol* 13:706–721. <https://doi.org/10.1111/1751-7915.13509>.
- Cantinelli T, Chenal-Francois V, Diancourt L, Frezal L, Leclercq A, Wirth T, Lecuit M, Brisse S. 2013. "Epidemic clones" of *Listeria monocytogenes* are widespread and ancient clonal groups. *J Clin Microbiol* 51:3770–3779. <https://doi.org/10.1128/JCM.01874-13>.
- Roberts A, Nightingale K, Jeffers G, Fortes E, Kongo JM, Wiedmann M. 2006. Genetic and phenotypic characterization of *Listeria monocytogenes* lineage III. *Microbiology (Reading)* 152:685–693. <https://doi.org/10.1099/mic.0.28503-0>.
- Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. <http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>.
- Souvorov A, Agarwala R, Lipman DJ. 2018. SKESA: strategic k-mer extension for scrupulous assemblies. *Genome Biol* 19:153. <https://doi.org/10.1186/s13059-018-1540-z>.
- Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI prokaryotic genome annotation pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>.
- Jolley KA, Maiden MC. 2010. BIGSdb: scalable analysis of bacterial genome variation at the population level. *BMC Bioinformatics* 11:595. <https://doi.org/10.1186/1471-2105-11-595>.