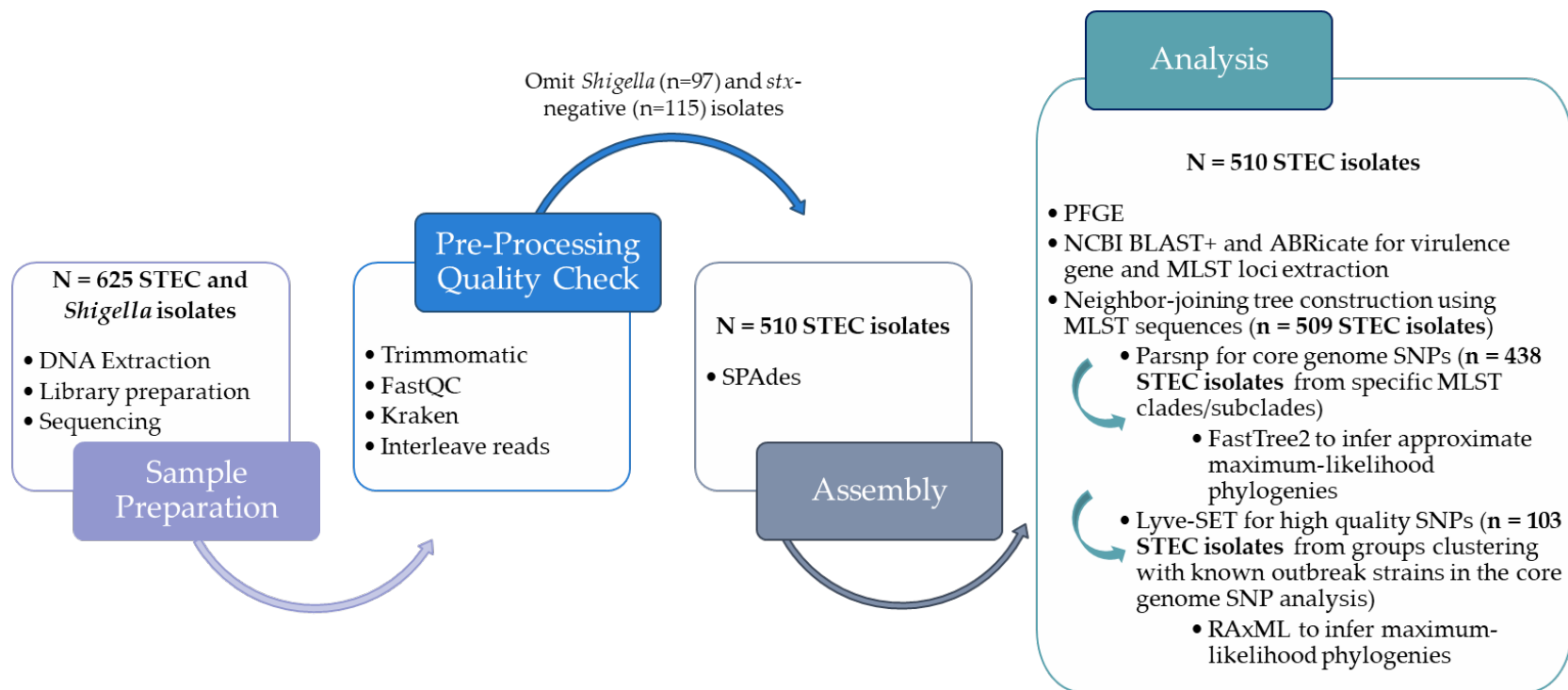


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Figure S1. Flowchart of the bioinformatic tools used to classify 625 Shiga toxin-producing *Escherichia coli* (STEC) isolates or *Shigella* isolates submitted for whole-genome sequencing (WGS) by the Michigan Department of Health and Human Services.



1561 PNUSAE000697.fasta
 1562 PNUSAE003119.fasta
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 1565 PNUSAE006147.fasta
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 1567 PNUSAE014625.fasta
 1568 PNUSAE001003.fasta
 1569 PNUSAE001200.fasta
 1570 PNUSAE012759.fasta

PFGE-XbaI_NonO157

WGS_id
 PNUSAE001586
 PNUSAE001592



Figure S3. cgSNP phylogeny of 186 STEC strains belonging to subclade A within Clade I in the MLST tree. All but two strains were classified as ST-119, while the stars highlight the placement of the two O103:H2 outbreak associated strains, PNUSAE004161 and PNUSAE004654, in the cgSNP phylogeny.

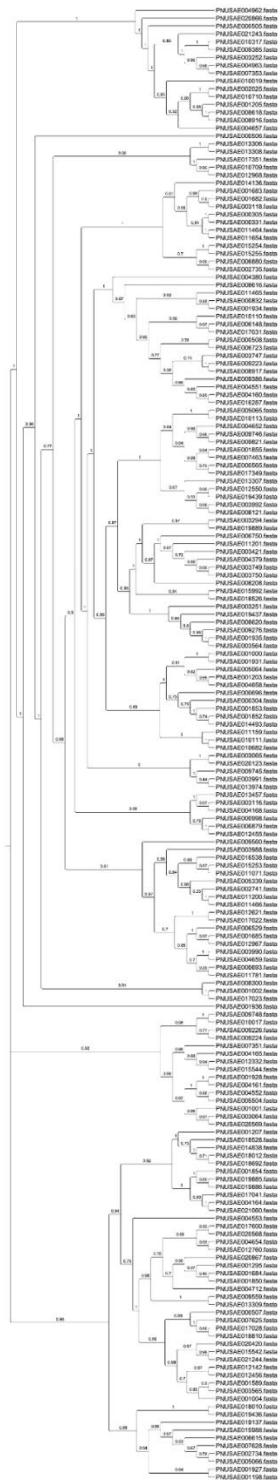


Figure S4. cgSNP analysis of 98 STEC O157:H7 strains classified as ST-66. Sixteen strains from three outbreaks, denoted as ST-66-O1 (open star), ST-66-O2 (black star), and ST-66-O3 (open triangle), were included in the analysis.

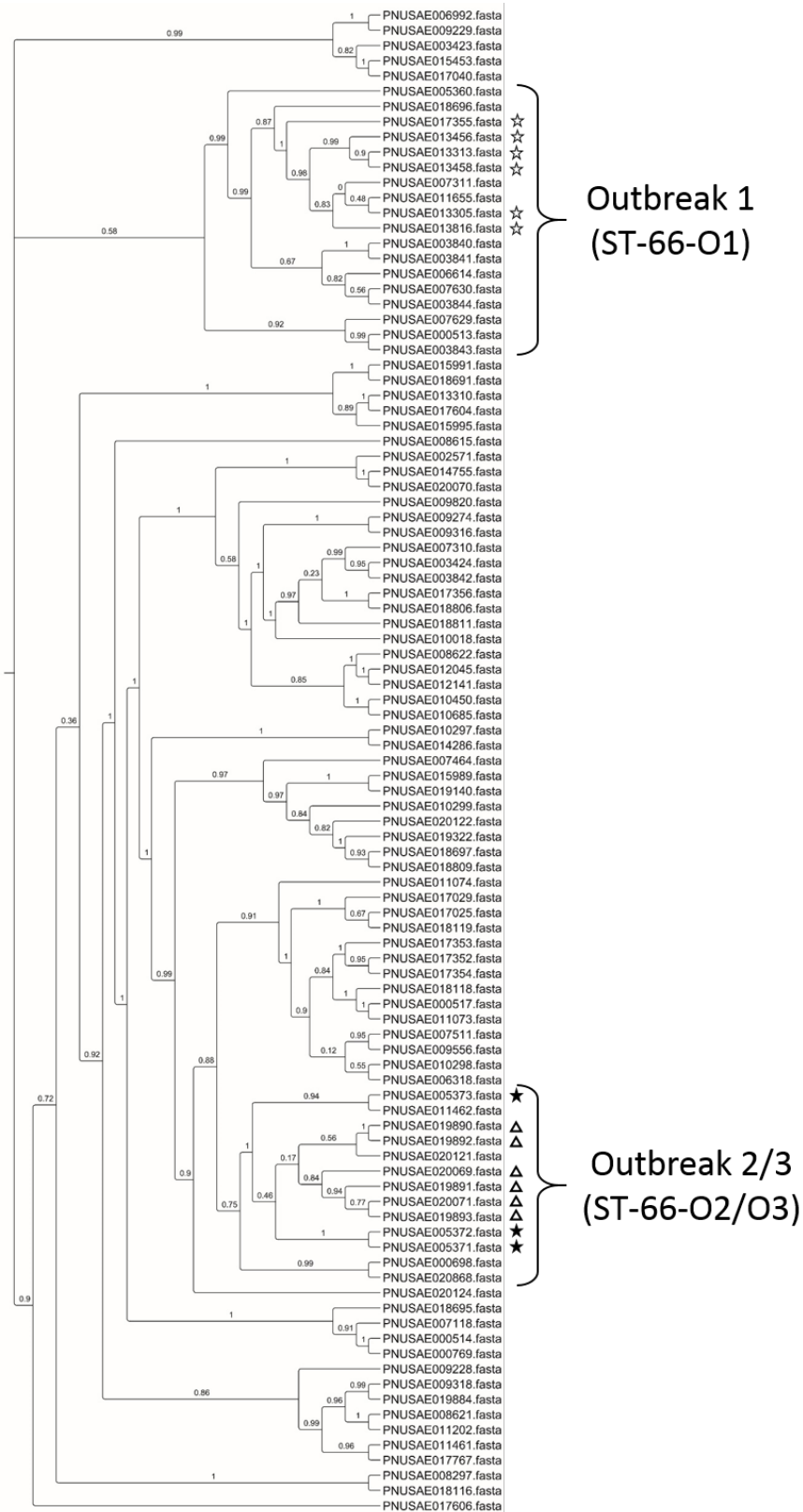


Figure S5. cgSNP analysis of 17 STEC strains belonging to subclade G within Clade I in the MLST tree. Outbreak-associated strains belonging to serogroup O5:H9 are indicated with black stars.

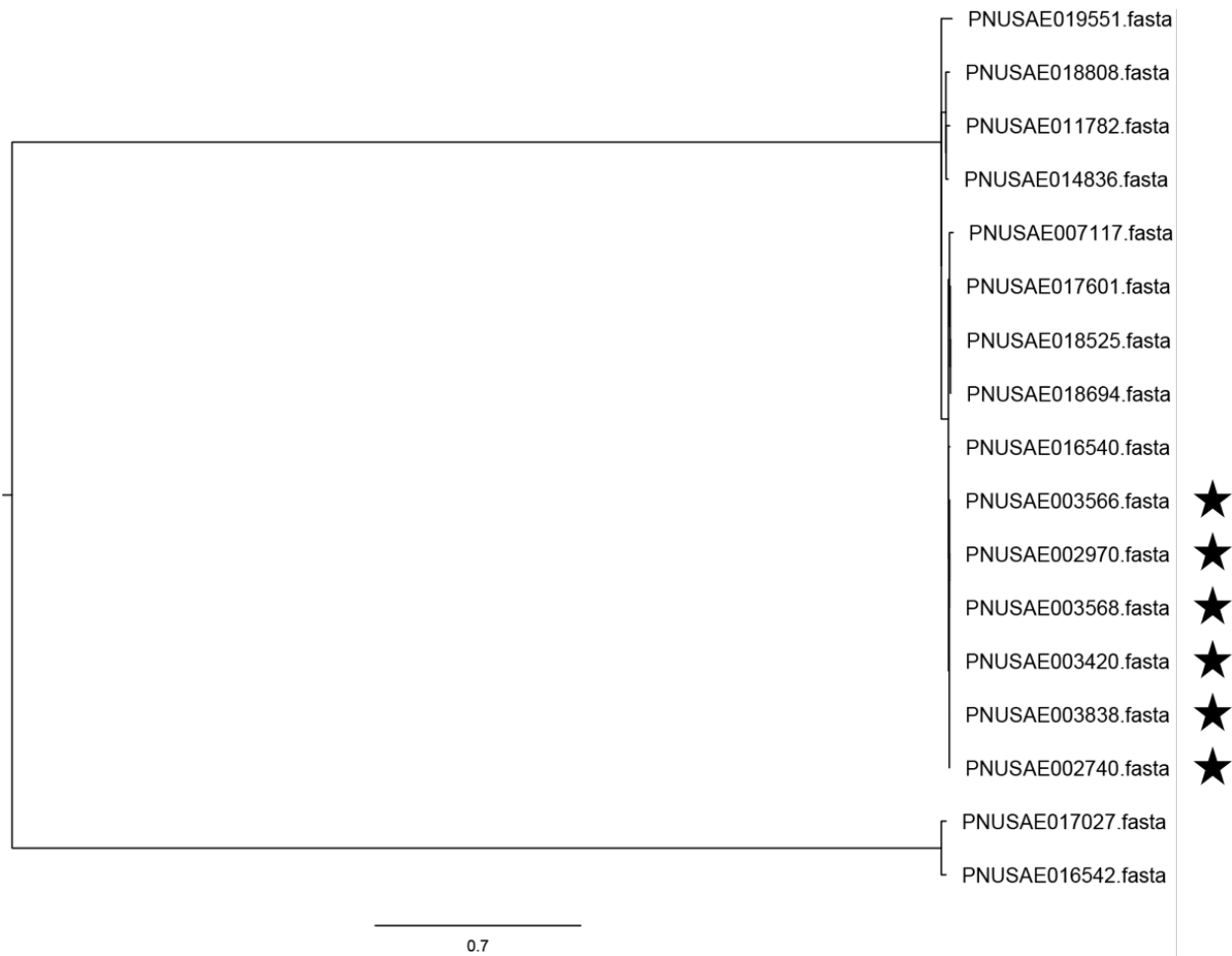


Table S1: Number of STEC serogroups detected in Michigan between 2015 and 2018 for WGS.

Serogroup	Year				Total
	2015	2016	2017	2018	
O5	0	6	2	7	15
O17	0	3	0	3	6
O28ac	0	1	0	1	2
O55	0	2	0	0	2
O69	1	0	1	1	3
O71	1	1	8	7	17
O73 or O17/O77	0	0	1	1	2
O8	0	0	0	3	3
O80	0	0	0	1	1
O84	0	1	2	1	4
O85	0	0	1	0	1
O98	0	0	0	1	1
O109	0	1	0	0	1
O113	0	0	1	0	1
O115	0	1	0	0	1
O117	0	1	0	0	1
O118	0	0	0	1	1
O123	4	3	3	3	13
O130	0	1	0	0	1
O151	2	3	3	2	10
O153/O178	0	0	0	1	1
O156	0	0	0	2	2
O165	0	0	1	1	2
O166	0	1	0	0	1
O172	0	0	0	1	1
O177	0	0	0	3	3
O183	0	0	1	2	3
O26	14	12	10	15	51
O45	13	16	21	11	61
O103	21	23	26	41	111
O111	10	10	11	16	47
O121	8	13	6	1	28
O145	0	2	0	4	6
O157	5	11	33	49	98
NT	5	0	1	3	9
Totals	84	112	132	182	510

Table S2. Accession numbers for STEC strains used in the study. Sequences were submitted to the National Center for Biotechnology Information (NCBI) as part of BioProject PRJNA218110 available at: www.ncbi.nlm.nih.gov/bioproject/218110 (accessed on 1 September 2019).

NCBI BioSample	CDC PulseNet Strain Name
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SAMN03382867	PNUSAE000305
SAMN03382869	PNUSAE000331
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SAMN03492161	PNUSAE000506
SAMN03492162	PNUSAE000507
SAMN03492163	PNUSAE000508
SAMN03492164	PNUSAE000509
SAMN03492165	PNUSAE000510
SAMN03492166	PNUSAE000511
SAMN03492167	PNUSAE000512
SAMN03610070	PNUSAE000563
SAMN03610071	PNUSAE000564
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SAMN03610079	PNUSAE000513
SAMN03610080	PNUSAE000517
SAMN03763865	PNUSAE000692
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NCBI BioSample	CDC PulseNet Strain Name
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SAMN03981628	PNUSAE001199
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SAMN04191665	PNUSAE001588
SAMN04191666	PNUSAE001589
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SAMN04230435	PNUSAE001591
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SAMN04351183	PNUSAE001934
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NCBI BioSample	CDC PulseNet Strain Name
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SAMN04568477	PNUSAE002567
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SAMN05432139	PNUSAE003568
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SAMN10432149	PNUSAE020124
SAMN10432150	PNUSAE020122
SAMN10432151	PNUSAE020121

NCBI BioSample	CDC PulseNet Strain Name
SAMN10432152	PNUSAE019891
SAMN10432153	PNUSAE020120
SAMN10432154	PNUSAE019886
SAMN10432284	PNUSAE020123
SAMN10449172	PNUSAE020349
SAMN10503925	PNUSAE020569
SAMN10503926	PNUSAE020568
SAMN10619093	PNUSAE020420
SAMN10619107	PNUSAE020868
SAMN10619108	PNUSAE020867
SAMN10619110	PNUSAE020866
SAMN10661712	PNUSAE021245
SAMN10661713	PNUSAE021244
SAMN10661714	PNUSAE021060
SAMN10661715	PNUSAE021058
SAMN10661716	PNUSAE021059
SAMN10700124	PNUSAE018009
SAMN10700163	PNUSAE021358
SAMN10700164	PNUSAE018012
SAMN10700165	PNUSAE018011
SAMN10700166	PNUSAE018010
SAMN10774441	PNUSAE021243
SAMN10774615	PNUSAE019893
SAMN10774616	PNUSAE021666
SAMN10774617	PNUSAE021473
SAMN10774618	PNUSAE019885

Note: Sequences belonging to strains PNUSAE009316 and PNUSAE018692 are missing from the NCBI database