

Group 1		Group 2	Group 3	Group 4	Group 5
00B028	L2_3	4CB	01B213	C451	C56
00B042	MK01	5CB			C5P
1_1	MK02				
1_2	NY1				
22208	NY2	Group 6	Group 7	Group 8	Group 9
22212	P01_A	FG	G1_1	J1_3a	SP37
22213	P03_A				
22214	P12_A				
22215	P13A	Group 10	Group 11	Group 12	Group 13
22216	PO1	W2P1	Z1S	Z2531	Z651
22217	S07_NCB1	Z7P			
22218	SB04				
22219	SBO1	Group 14	Group 15	Group 16	Group 17
22221	SO1	Z7S21	Z7S3	22211	W11
5_1	SO7		Z9P	J4_1	
5_2	SP11			R35	
6_1	SP17N				
6_2	SP18				
AP02A	W1_1	Group 18	Group 19	Group 20	
AP1	W1_2	R01_A	SER00032	Serratia_ureilytica_T6	
AS2201	W2_4				
COL_1	W3_1				
GP02_2	W3_2				
GP03_A	W4_1				
GP1_1	W4_2				
H3_1	WO1A				
HFP03	Z01_A				
J3_3	Z01				
K1_1	Z03_A				
KRS51	ZO7				
KRS74	00B010				
L1_1					

Fig. 1 Genotypic groups based on average nucleotide identity (ANI). Isolates with 99% similarity were placed in a single group. Explain why some isolate numbers are in red.

Serratia isolates collected across the US

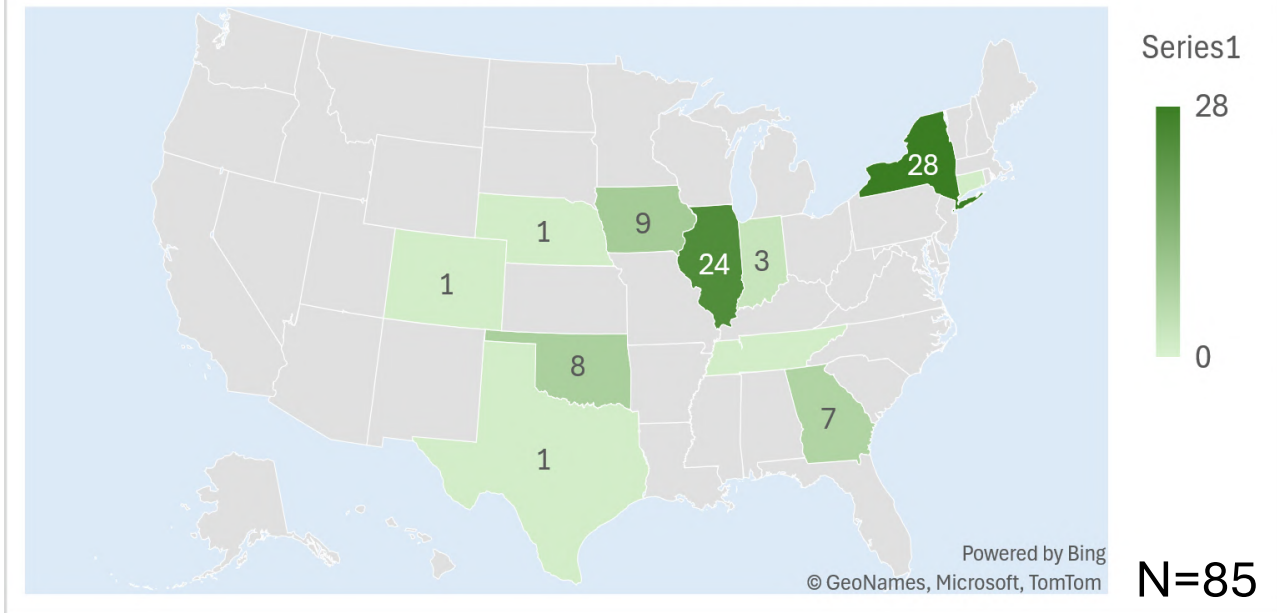


Fig 2. Map of *Serratia* isolates collected from different states for the Whole Genome

Group 1 ANI *Serratia ureilytica* distribution

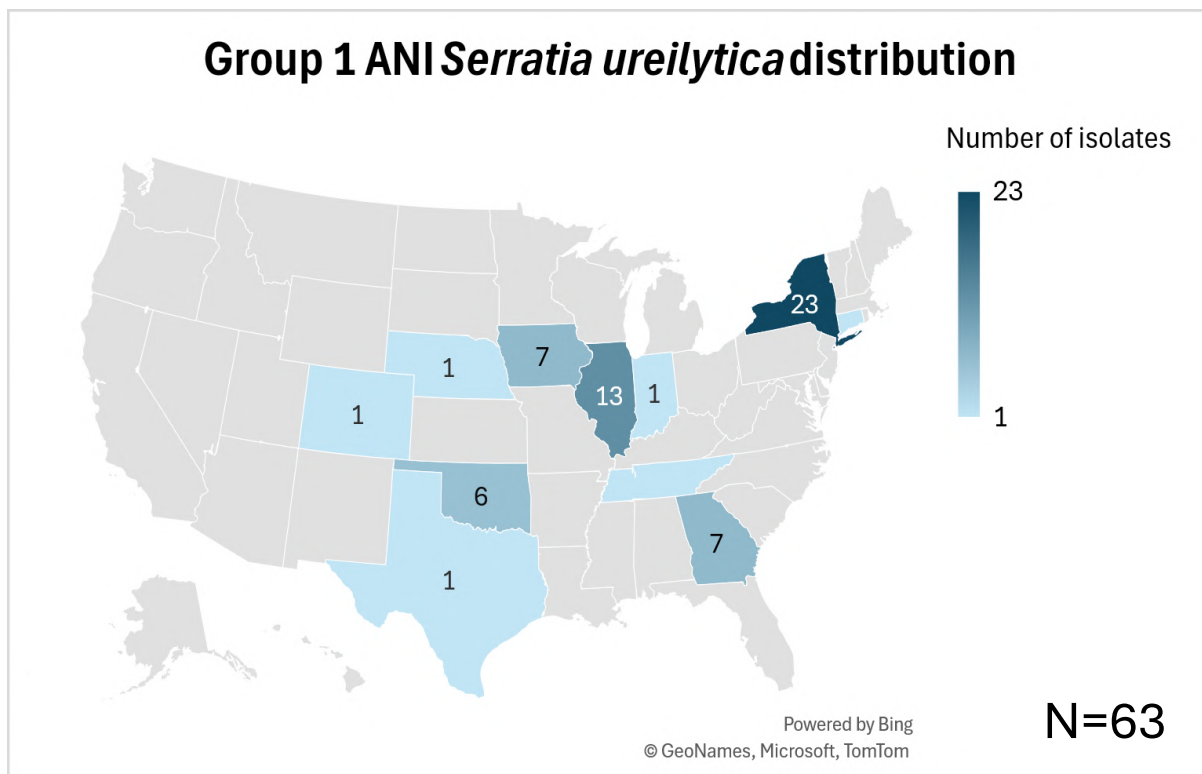


Fig 3. Map of Distribution of *Serratia ureilytica* genotypic group one (ANI >99%)

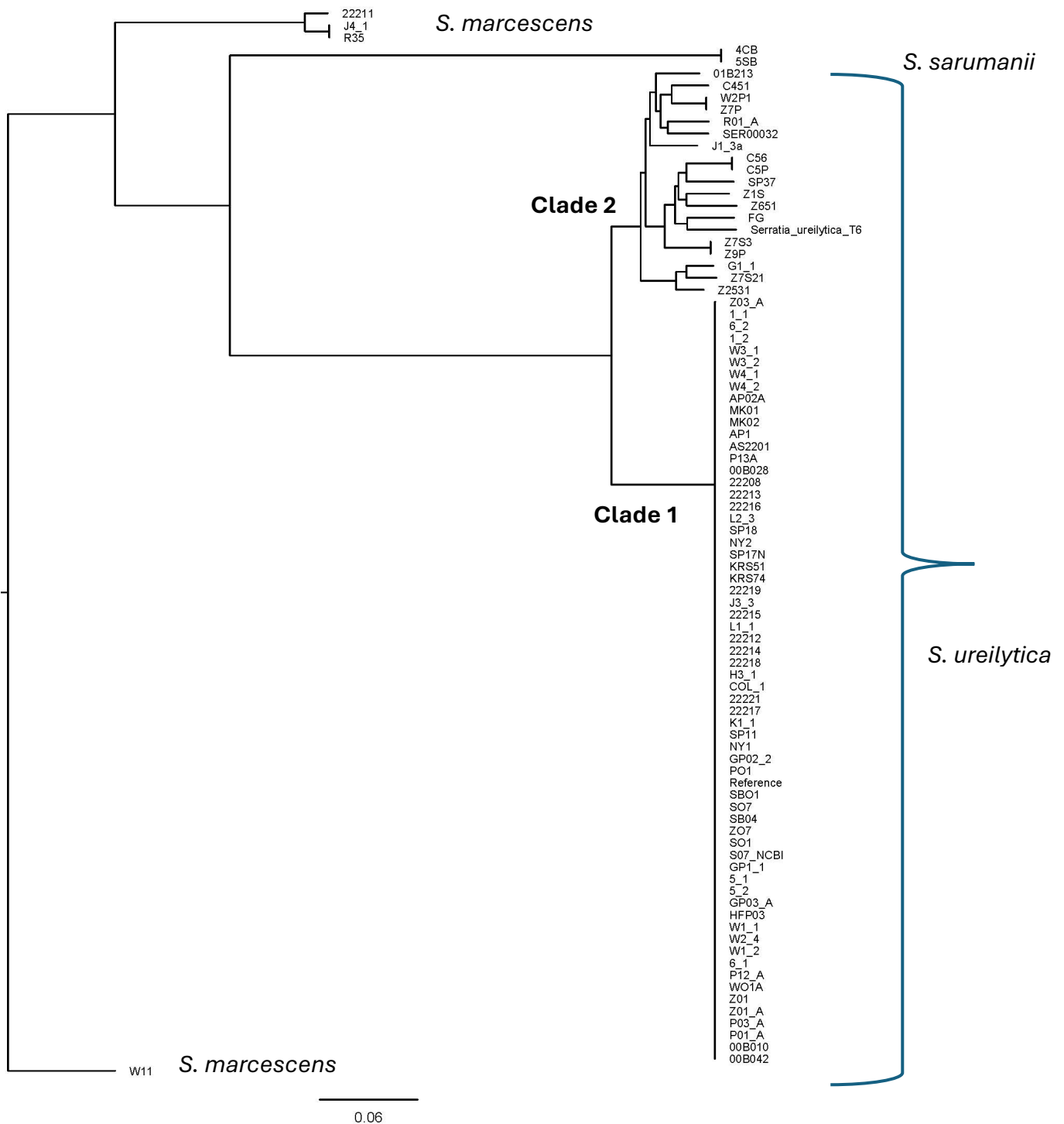


Fig. 4 Single nucleotide polymorphism (SNP) based phylogenetic relationship between 85 *Serratia* isolates from this study and 3 from the RefSeq database, NCBI (SER00032, *Serratia_ureilytica_T6*, S07_NCBI). The query genomes were compared with the reference genome to identify the SNPs. S07_NCBI was chosen as the reference genome in the SNP analysis. Bootstrap values were calculated from 1,000 replications of UFBoot2 bootstrapping. The length of the scale bar indicates 0.006 change per nucleotide site.

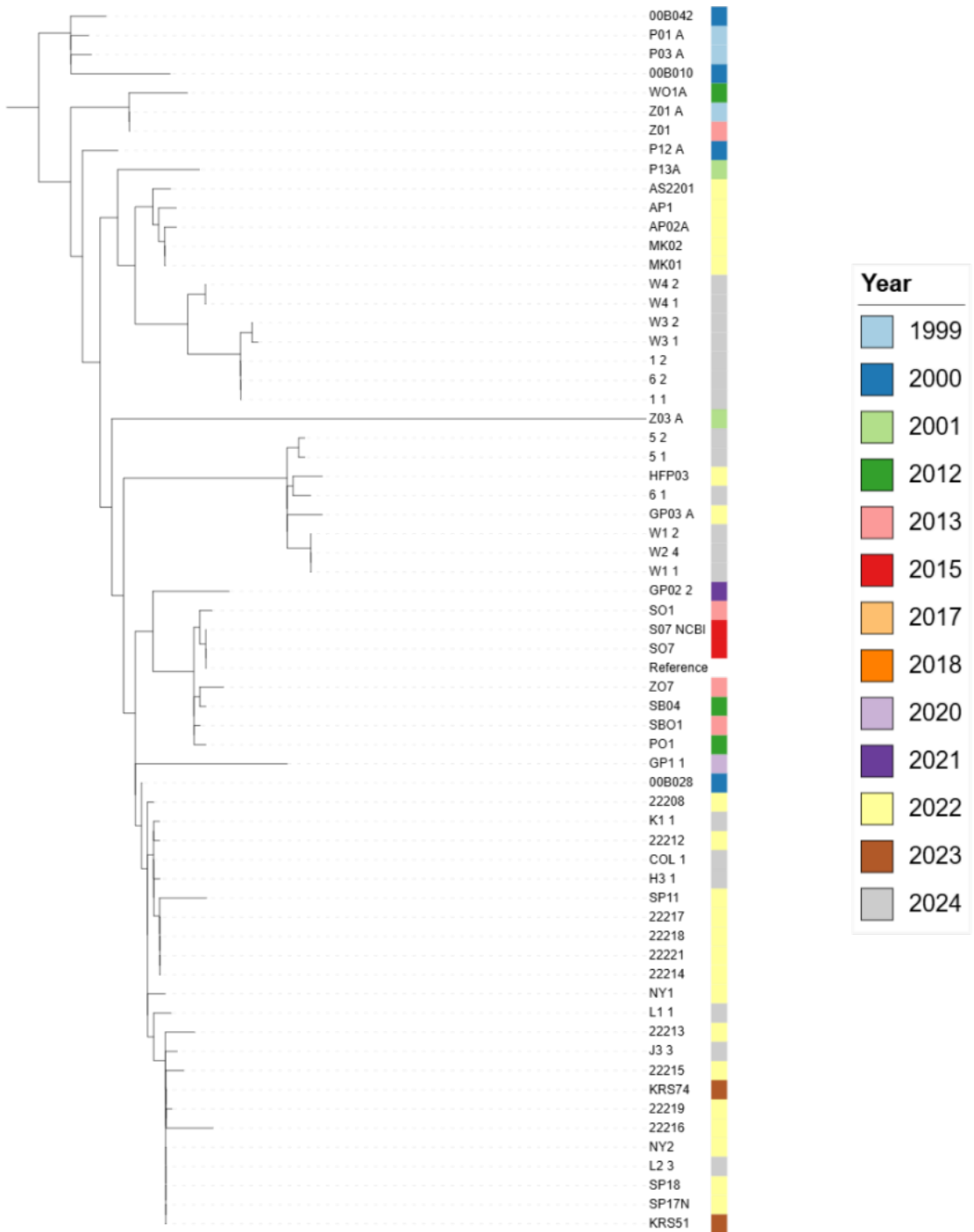


Fig. 5 Single nucleotide polymorphism (SNP) based phylogenetic relationship between 63 *Serratia ureilytica* isolates from this study. The query genomes were compared with the reference genome to identify the SNPs. S07_NCBI was selected as the reference genome for SNP analysis. Bootstrap values were calculated from 1,000 replications of UFBoot2 bootstrapping. The length of the scale bar indicates 0.001 change per nucleotide site.

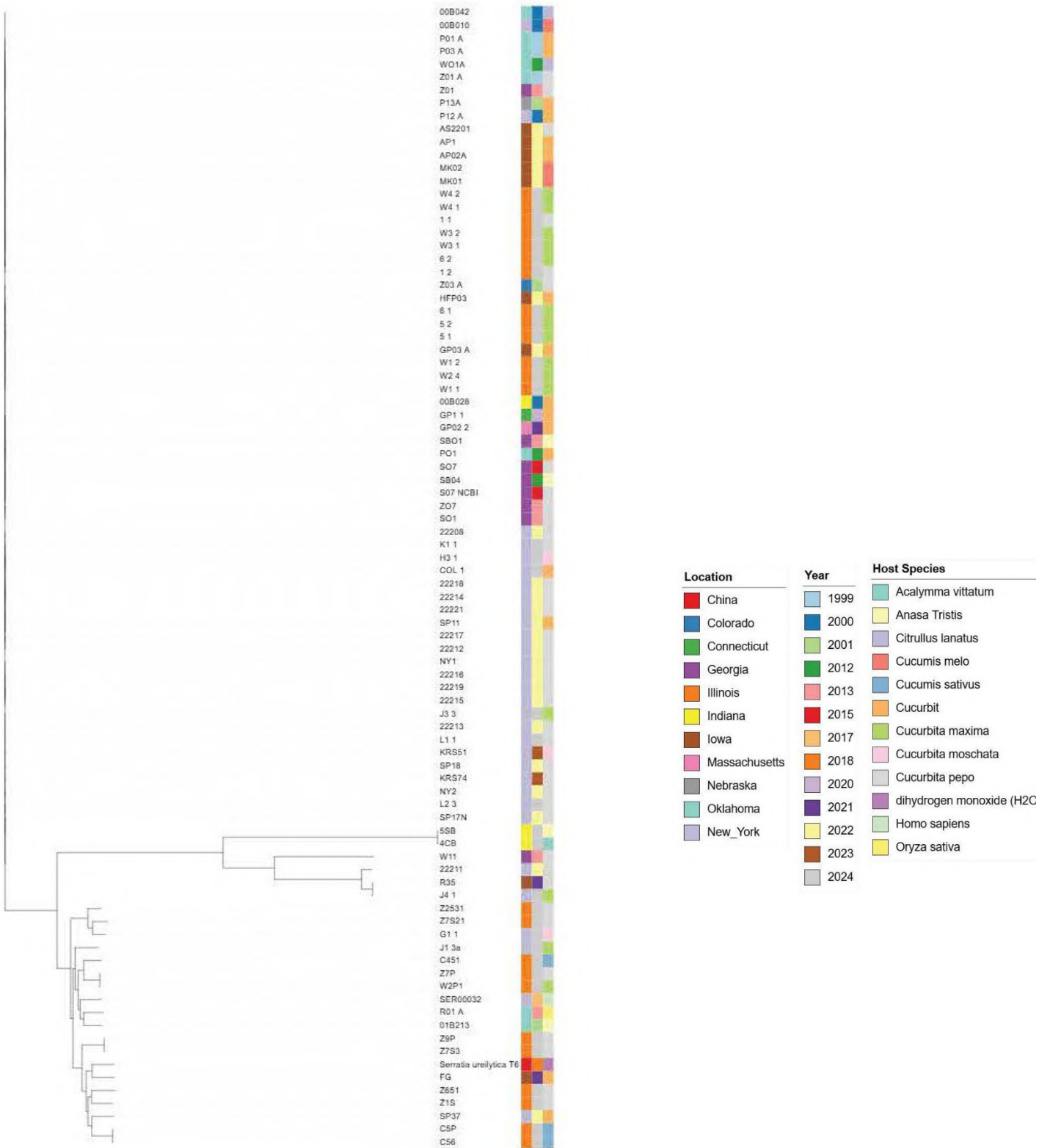


Fig. 6 Core genome-based phylogenetic relationship between 85 *Serratia* isolates from this study and 3 from the RefSeq database, NCBI (SER00032, *Serratia_ureilytica_T6*, S07_NCBI). The query genomes were compared with the reference genome to identify the SNPs. S07_NCBI was chosen as the reference genome. Location, year, and host species are shown in the three colored bars.