

Supplemental Material

TABLE S1 Codon usage bias indicated by \hat{N}_c values for each allelic type

AT	\hat{N}_c value	AT	\hat{N}_c value	AT	\hat{N}_c value
<i>L. innocua</i> AT 125	45.94	<i>L. monocytogenes</i> AT 102	47.19	<i>L. seeligeri</i> AT 24	46.17
<i>L. innocua</i> AT 108	46.87	<i>L. monocytogenes</i> AT 103	49.76	<i>L. seeligeri</i> AT 25	49.56
<i>L. innocua</i> AT 109	47.26	<i>L. monocytogenes</i> AT 104	48.28	<i>L. seeligeri</i> AT 28	49.42
<i>L. innocua</i> AT 10	43.64	<i>L. monocytogenes</i> AT 105	48.66	<i>L. seeligeri</i> AT 2	49.02
<i>L. innocua</i> AT 110	45.89	<i>L. monocytogenes</i> AT 106	48.46	<i>L. seeligeri</i> AT 34	46.43
<i>L. innocua</i> AT 116	47.06	<i>L. monocytogenes</i> AT 107	47.70	<i>L. seeligeri</i> AT 35	49.03
<i>L. innocua</i> AT 11	46.35	<i>L. monocytogenes</i> AT 112	49.35	<i>L. seeligeri</i> AT 3	48.89
<i>L. innocua</i> AT 124	46.68	<i>L. monocytogenes</i> AT 113	48.85	<i>L. seeligeri</i> AT 40	49.93
<i>L. innocua</i> AT 128	44.87	<i>L. monocytogenes</i> AT 114	48.14	<i>L. seeligeri</i> AT 49	49.61
<i>L. innocua</i> AT 132	45.69	<i>L. monocytogenes</i> AT 118	46.07	<i>L. seeligeri</i> AT 4	49.61
<i>L. innocua</i> AT 135	47.23	<i>L. monocytogenes</i> AT 119	46.42	<i>L. seeligeri</i> AT 52	46.53
<i>L. innocua</i> AT 139	45.11	<i>L. monocytogenes</i> AT 137	47.98	<i>L. seeligeri</i> AT 68	46.61
<i>L. innocua</i> AT 140	47.04	<i>L. monocytogenes</i> AT 138	48.59	<i>L. seeligeri</i> AT 72	46.48
<i>L. innocua</i> AT 141	44.76	<i>L. monocytogenes</i> AT 144	45.44	<i>L. seeligeri</i> AT 7	49.16
<i>L. innocua</i> AT 142	46.79	<i>L. monocytogenes</i> AT 149	47.92	<i>L. seeligeri</i> AT 8	48.97
<i>L. innocua</i> AT 145	45.94	<i>L. monocytogenes</i> AT 151	46.91	<i>L. seeligeri</i> AT 92	49.30
<i>L. innocua</i> AT 150	45.32	<i>L. monocytogenes</i> AT 152	47.64	<i>L. seeligeri</i> AT 9	46.77
<i>L. innocua</i> AT 161	45.88	<i>L. monocytogenes</i> AT 158	44.80	<i>L. welshimeri</i> AT 111	46.34
<i>L. innocua</i> AT 162	45.98	<i>L. monocytogenes</i> AT 159	46.21	<i>L. welshimeri</i> AT 117	47.28
<i>L. innocua</i> AT 164	46.79	<i>L. monocytogenes</i> AT 160	46.19	<i>L. welshimeri</i> AT 120	47.07
<i>L. innocua</i> AT 22	46.33	<i>L. monocytogenes</i> AT 57	46.11	<i>L. welshimeri</i> AT 123	46.21
<i>L. innocua</i> AT 23	44.94	<i>L. monocytogenes</i> AT 58	46.96	<i>L. welshimeri</i> AT 126	45.69
<i>L. innocua</i> AT 26	46.33	<i>L. monocytogenes</i> AT 59	45.22	<i>L. welshimeri</i> AT 127	45.69
<i>L. innocua</i> AT 30	45.80	<i>L. monocytogenes</i> AT 60	47.22	<i>L. welshimeri</i> AT 129	45.53
<i>L. innocua</i> AT 31	46.00	<i>L. monocytogenes</i> AT 61	48.03	<i>L. welshimeri</i> AT 130	46.52
<i>L. innocua</i> AT 33	45.68	<i>L. monocytogenes</i> AT 62	48.26	<i>L. welshimeri</i> AT 131	45.26

<i>L. innocua</i> AT 36	44.47	<i>L. monocytogenes</i> AT 63	46.96	<i>L. welshimeri</i> AT 133	44.77
<i>L. innocua</i> AT 37	46.13	<i>L. monocytogenes</i> AT 64	47.95	<i>L. welshimeri</i> AT 134	45.38
<i>L. innocua</i> AT 38	45.72	<i>L. monocytogenes</i> AT 65	46.11	<i>L. welshimeri</i> AT 13	46.90
<i>L. innocua</i> AT 39	44.62	<i>L. monocytogenes</i> AT 66	48.59	<i>L. welshimeri</i> AT 146	45.87
<i>L. innocua</i> AT 44	46.60	<i>L. monocytogenes</i> AT 67	47.62	<i>L. welshimeri</i> AT 147	46.63
<i>L. innocua</i> AT 45	45.60	<i>L. monocytogenes</i> AT 74	45.64	<i>L. welshimeri</i> AT 148	46.71
<i>L. innocua</i> AT 53	43.88	<i>L. monocytogenes</i> AT 75	45.52	<i>L. welshimeri</i> AT 14	45.89
<i>L. innocua</i> AT 56	44.78	<i>L. monocytogenes</i> AT 76	45.01	<i>L. welshimeri</i> AT 157	45.76
<i>L. innocua</i> AT 6	47.23	<i>L. monocytogenes</i> AT 77	45.14	<i>L. welshimeri</i> AT 15	45.90
<i>L. innocua</i> AT 70	44.94	<i>L. monocytogenes</i> AT 78	46.75	<i>L. welshimeri</i> AT 16	46.17
<i>L. innocua</i> AT 71	44.74	<i>L. monocytogenes</i> AT 79	48.63	<i>L. welshimeri</i> AT 17	44.78
<i>L. innocua</i> AT 87	45.83	<i>L. monocytogenes</i> AT 80	49.61	<i>L. welshimeri</i> AT 19	45.59
<i>L. innocua</i> AT 88	45.82	<i>L. monocytogenes</i> AT 81	47.05	<i>L. welshimeri</i> AT 21	46.82
<i>L. innocua</i> AT 91	46.19	<i>L. monocytogenes</i> AT 82	48.51	<i>L. welshimeri</i> AT 27	46.34
<i>L. innocua</i> AT 94	47.14	<i>L. monocytogenes</i> AT 83	50.36	<i>L. welshimeri</i> AT 29	45.96
<i>L. ivanovii</i> AT 153	51.97	<i>L. monocytogenes</i> AT 84	50.12	<i>L. welshimeri</i> AT 32	45.96
<i>L. ivanovii</i> AT 154	51.96	<i>L. monocytogenes</i> AT 85	48.96	<i>L. welshimeri</i> AT 41	45.41
<i>L. ivanovii</i> AT 155	51.82	<i>L. monocytogenes</i> AT 86	48.68	<i>L. welshimeri</i> AT 43	46.10
<i>L. ivanovii</i> AT 156	51.87	<i>L. monocytogenes</i> AT 90	48.04	<i>L. welshimeri</i> AT 46	45.90
<i>L. ivanovii</i> AT 165	52.33	<i>L. monocytogenes</i> AT 96	50.04	<i>L. welshimeri</i> AT 47	45.50
<i>L. ivanovii</i> AT 73	52.30	<i>L. monocytogenes</i> AT 97	48.02	<i>L. welshimeri</i> AT 48	46.53
<i>L. marthii</i> AT 136	49.04	<i>L. monocytogenes</i> AT 98	46.34	<i>L. welshimeri</i> AT 51	46.51
<i>L. marthii</i> AT 143	48.70	<i>L. monocytogenes</i> AT 99	48.90	<i>L. welshimeri</i> AT 54	46.23
<i>L. marthii</i> AT 18	50.17	<i>L. seeligeri</i> AT 121	46.60	<i>L. welshimeri</i> AT 55	45.23
<i>L. marthii</i> AT 42	49.31	<i>L. seeligeri</i> AT 122	46.60	<i>L. welshimeri</i> AT 5	45.56
<i>L. marthii</i> AT 50	48.65	<i>L. seeligeri</i> AT 12	46.17	<i>L. welshimeri</i> AT 69	46.41
<i>L. marthii</i> AT 95	48.70	<i>L. seeligeri</i> AT 163	44.75	<i>L. welshimeri</i> AT 89	46.70
<i>L. monocytogenes</i> AT 100	50.28	<i>L. seeligeri</i> AT 1	49.02	<i>L. welshimeri</i> AT 93	45.97
<i>L. monocytogenes</i> AT 101	47.49	<i>L. seeligeri</i> AT 20	45.89		

TABLE S2 Results of tree topology tests for topology of optimal *sigB* tree (Figure S1) and re-arranged tree (Figure S2)

Tree 1	Tree 2	Diff - Ln L	<i>p</i> -KH	<i>p</i> -SH	<i>p</i> -AU
Optimal tree ^a	Re-arranged tree ^b	73.715	0.0001*	0.0006*	0.0000*

KH: Kishino-Hasegawa test using normal approximation, two-tailed test

SH: Shimodaira-Hasegawa test using RELL bootstrap, one-tailed test

AU: Shimodaira Approximately Unbiased test

^a Ln L of tree 1 is -4197.422

^b Ln L of tree 1 is -4271.137

* $p < 0.05$

TABLE S3 Putative recombination events inferred by RDP4 and PHI test*

	Recombination determined by RDP4			<i>p</i> -value for recombination determined by PHI test
	Recombinant Sequence(s)	Putative parental sequence (Minor × Major donors)	Detection methods(s)	
<i>L. monocytogenes</i> & <i>L.innocua</i>	<i>L. monocytogenes</i> AT 75			
	<i>L. monocytogenes</i> AT 74	<i>L. innocua</i> AT 139 (AT 135) × <i>L. monocytogenes</i> AT 83 (AT 62, 66, 79, 81, 82, 84, 85, 86, 90, 97, 99, 101, 103, 104, 105, 107, 113, 138, 149, 152)	SiScan 3Seq	0.0002
	<i>L. monocytogenes</i> AT 76			
	<i>L. monocytogenes</i> AT 77			

*Recco did not detect any significant recombination events.

TABLE S4 21 whole genome sequences (WGS) of *Listeria* downloaded from the NCBI database

Isolates	Accession number	Features
<i>Listeria monocytogenes</i> SLCC2378 (lineage I)	NC_018585.1	scaffolds: 1, contigs: 1, N50: 2,941,360, L50: 1
<i>Listeria monocytogenes</i> WSLC1042 (lineage I)	NZ_CP007210.1	scaffolds: 1, contigs: 1, N50: 2,942,168, L50: 1
<i>Listeria monocytogenes</i> ATCC 19117 (lineage I)	NC_018584.1	scaffolds: 1, contigs: 1, N50: 2,951,805, L50: 1
<i>Listeria monocytogenes</i> WSLC1001 (lineage II)	NZ_CP007160.1	scaffolds: 1, contigs: 1, N50: 2,951,235, L50: 1
<i>Listeria monocytogenes</i> FSL R2-0561 (lineage II)	NC_017546.1	scaffolds: 1, contigs: 1, N50: 2,973,801, L50: 1
<i>Listeria monocytogenes</i> SLCC2479 (lineage II)	NC_018589.1	scaffolds: 1, contigs: 1, N50: 2,972,172, L50: 1
<i>Listeria monocytogenes</i> L99 (lineage III)	NC_017529.1	scaffolds: 1, contigs: 1, N50: 2,979,198, L50: 1
<i>Listeria monocytogenes</i> HCC23 (lineage III)	NC_011660.1	scaffolds: 1, contigs: 1, N50: 2,976,212, L50: 1
<i>Listeria monocytogenes</i> SLCC2376 (lineage III)	NC_018590.1	scaffolds: 1, contigs: 1, N50: 2,840,185, L50: 1
<i>Listeria monocytogenes</i> FSL J1-0208 (lineage IV)	NZ_CM001469.1	scaffolds: 2, contigs: 9, N50: 527,857, L50: 2
<i>Listeria innocua</i> FSL J1-0023	NZ_CM001049.1	scaffolds: 1, contigs: 1,177, N50: 5,329, L50: 152
<i>Listeria innocua</i> FSL S4-0378	CM001048.1	scaffolds: 1, contigs: 2,291, N50: 2,883, L50: 290
<i>Listeria innocua</i> Clip11262	NC_003212.1	scaffolds: 2, contigs: 2, N50: 3,011,208, L50: 1
<i>Listeria ivanovii</i> FSL F6-0596	CM001050.1	scaffolds: 1, contigs: 1,919, N50: 3,514, L50: 243
<i>Listeria ivanovii</i> WSLC3009	NZ_CP007172.1	scaffolds: 1, contigs: 1, N50: 2,919,538, L50: 1
<i>Listeria ivanovii</i> PAM 55	NC_016011.1	scaffolds: 1, contigs: 1, N50: 2,928,879, L50: 1
<i>Listeria seeligeri</i> FSL N1-0067	NZ_CM001051.1	scaffolds: 1, contigs: 1,476, N50: 5,270, L50: 168
<i>Listeria seeligeri</i> FSL S4-0171	CM001052.1	scaffolds: 1, contigs: 1,625, N50: 3,692, L50: 235
<i>Listeria seeligeri</i> SLCC3954	NC_013891.1	scaffolds: 1, contigs: 1, N50: 2,797,636, L50: 1
<i>Listeria marthii</i> FSL S4-0120	CM001047.1	scaffolds: 1, contigs: 1,378, N50: 4,723, L50: 166
<i>Listeria welshimeri</i> SLCC5334	NC_008555.1	scaffolds: 1 contigs: 1; N50: 2,814,130, L50: 1

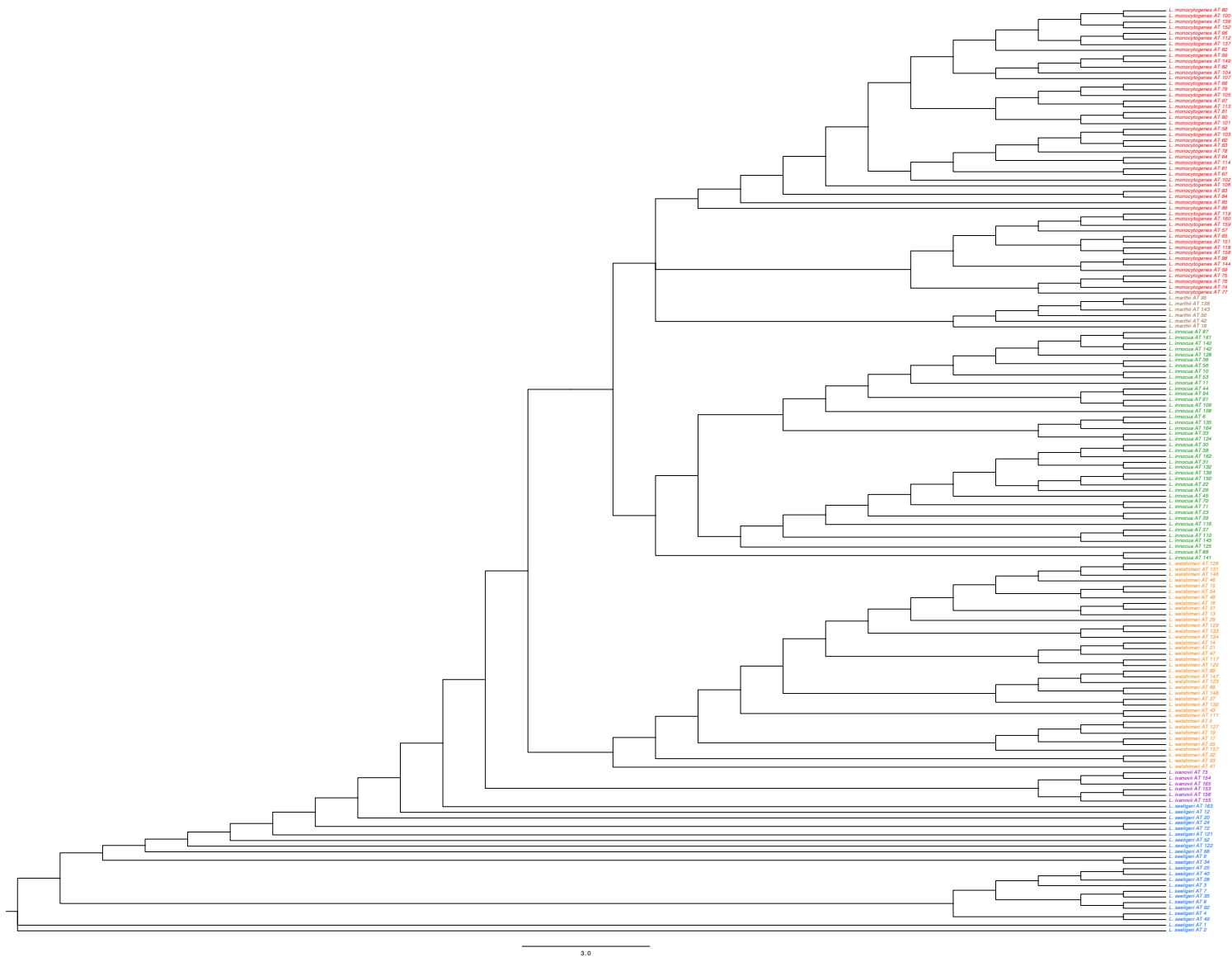


FIGURE S1 Re-arranged tree based on the consensus tree in Fig. S1. *L. monocytogenes* is indicated by red, *L. marthii* by brown, *L. innocua* by green, *L. welshimeri* by yellow, *L. seeligeri* by blue, and *L. ivanovii* by purple.

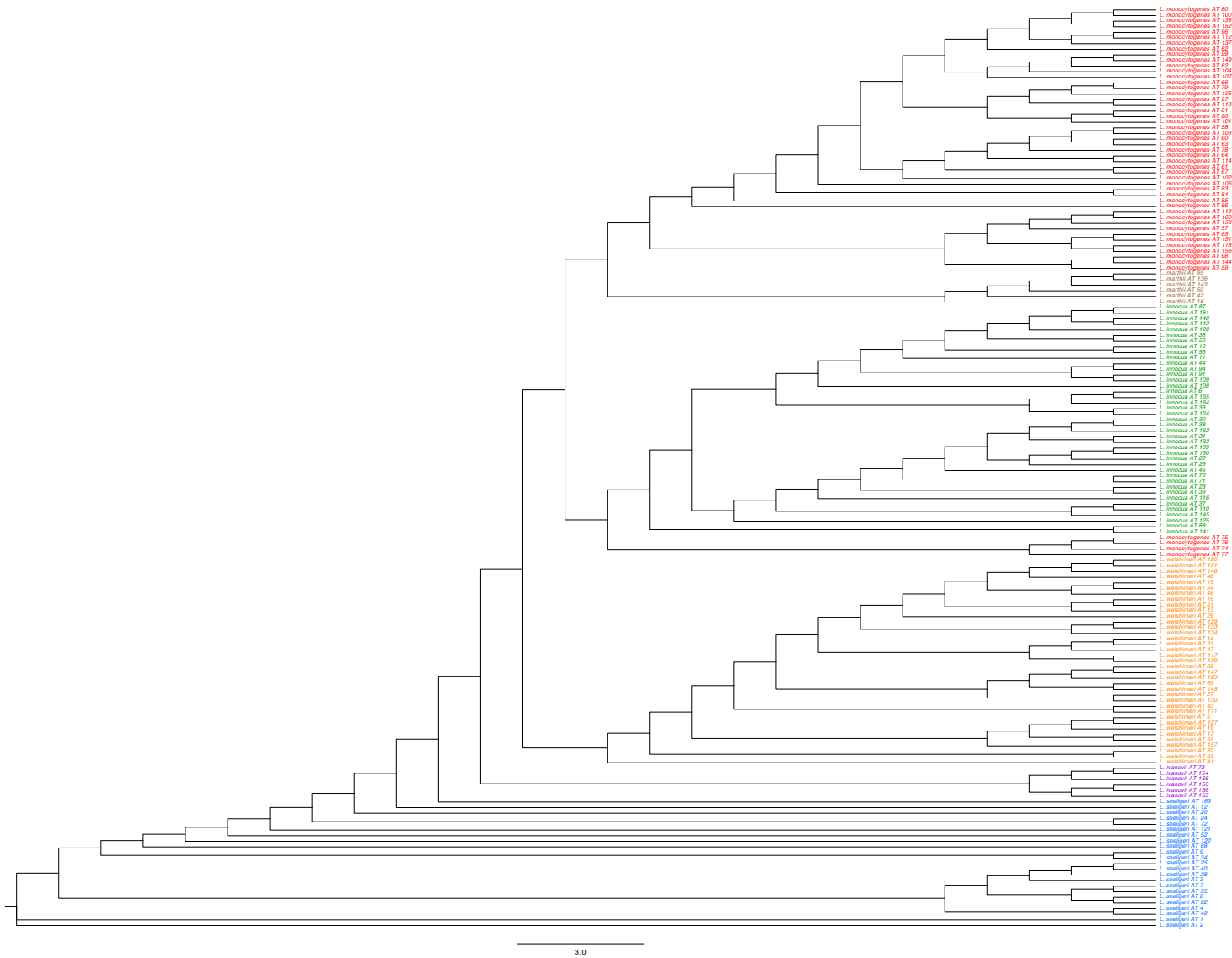


FIGURE S2 Consensus tree inferred by maximum likelihood method using *sigB* of 164 *Listeria* sensu stricto allelic types. *L. monocytogenes* is indicated by red, *L. marthii* by brown, *L. innocua* by green, *L. welshimeri* by yellow, *L. seeligeri* by blue, and *L. ivanovii* by purple.