

Strain	Serotype	Total number of ORFs	Strain-specific ORFs		Serotype-specific ORFs		ORFs with atypical composition (Chi <sup>2</sup> cutoff : 500)					
			Number	% (a)	Number	% (a)	Total number	% (b)	Strain-specific ORFs		Serotype-specific ORFs	
									Number	% (c)	Number	% (d)
F2365	4b	2847	51	1.79	51	1.79	392	13.77	43	84.31	28	54.90
H7858	4b	3117	69	2.21	50	1.60	273	8.76	36	52.17	18	36.00
F6854	1/2a	2973	97	3.26	83	2.79	198	6.66	42	43.30	2	2.41
EGD-e	1/2a	3058	61	1.99	83	2.71	199	6.51	12	19.67	4	4.82

(a) percentage of strain/serotype specific ORFs out of the total number of ORFs in the genome.

(b) percentage of ORFs with atypical composition out of the total number of ORFs in the genome.

(c) percentage of strain-specific ORFs with atypical composition, out of the number of strain-specific ORFs.

(d) percentage of serotype-specific ORFs with atypical composition, out of the number of serotype-specific ORFs.

**Supplemental Table 3. Genes with atypical G+C composition in *L. monocytogenes* strains F2365, H7858, F6854 and EGD-e.**

The Chi<sup>2</sup> values were calculated as previously described (windows size, 2000 bp; windows shift, 1000 bp) (12). A Chi<sup>2</sup> cutoff of 500 was chosen for identifying ORFs with atypical composition.