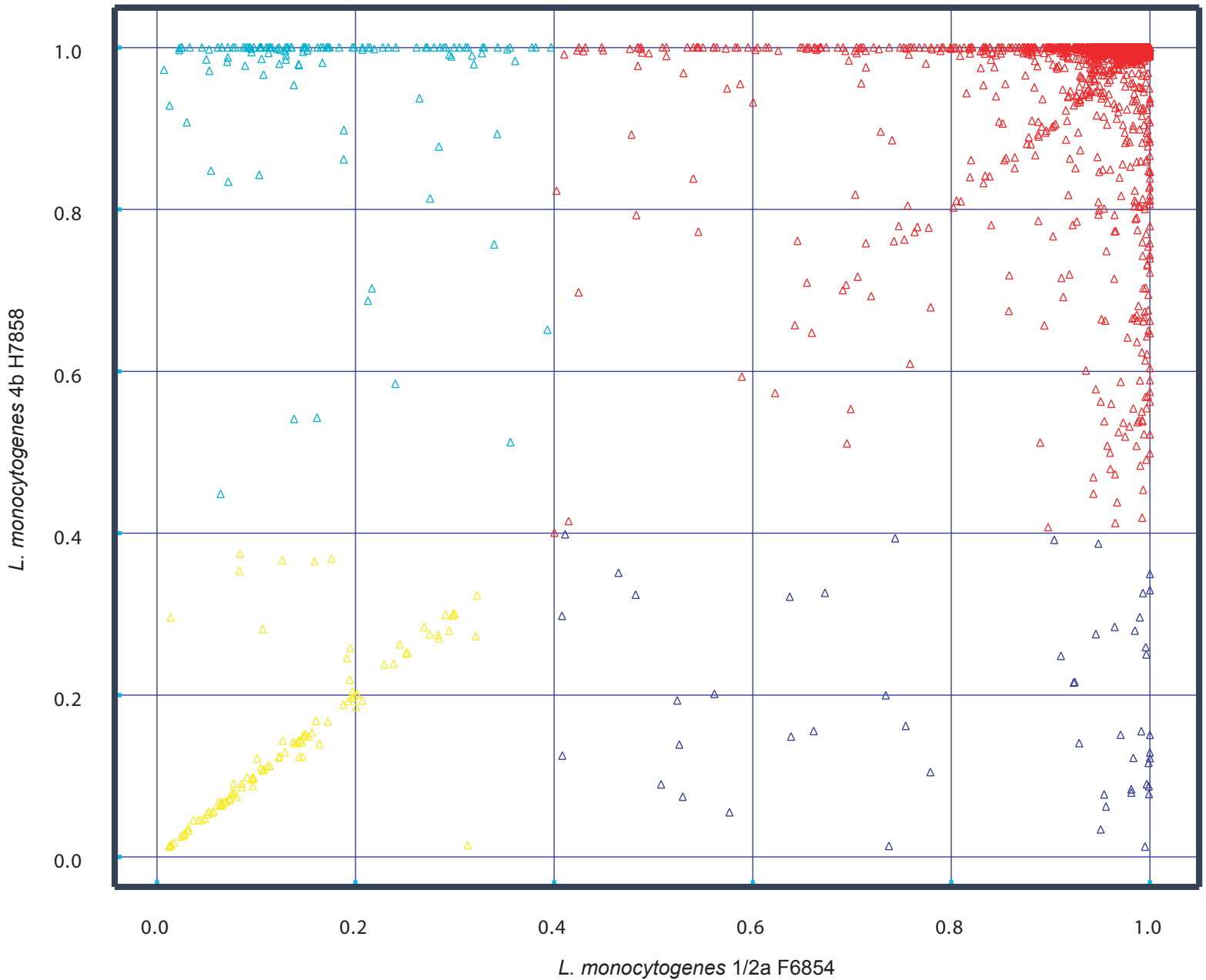


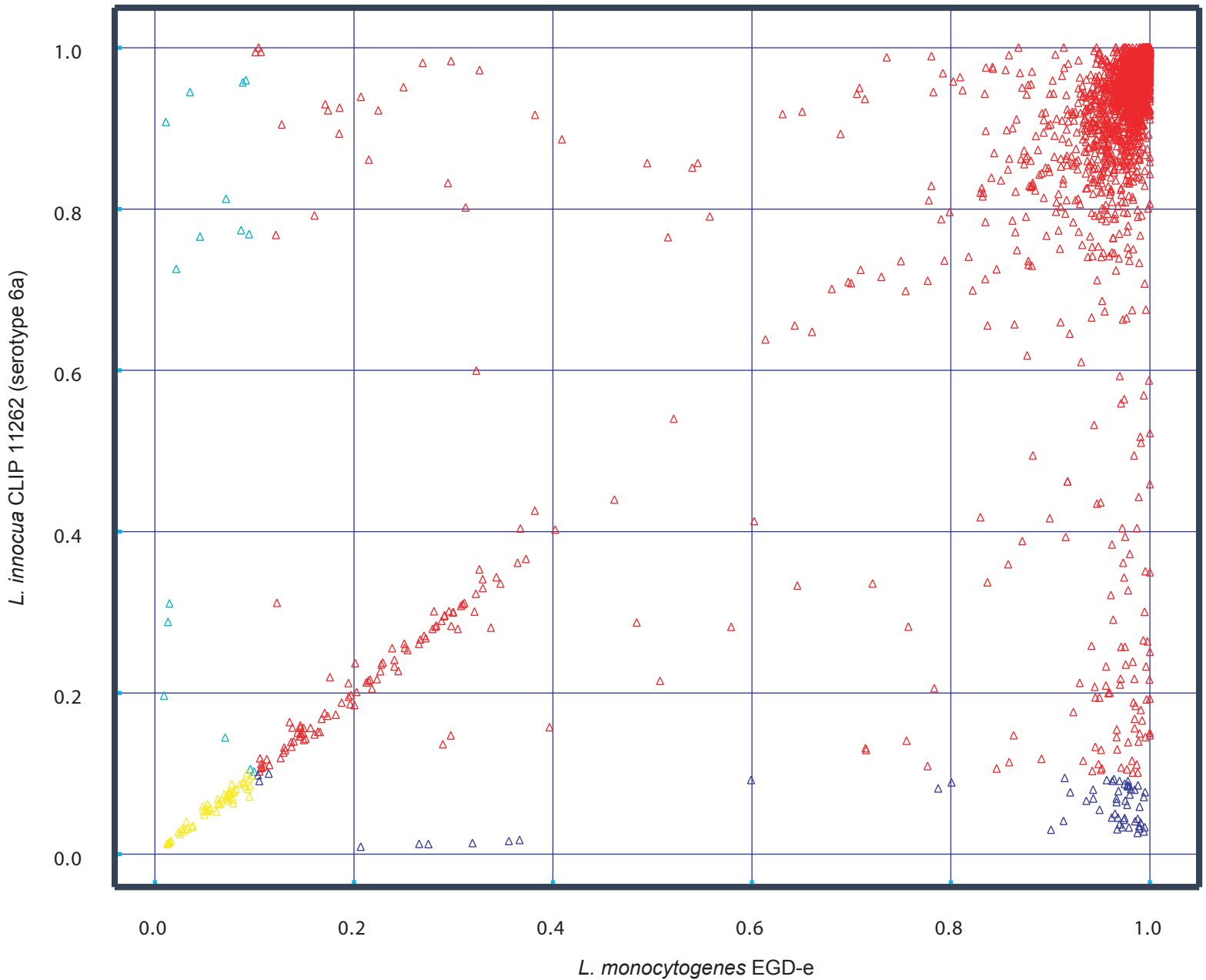
Blast Score Ratio Analysis with *L. monocytogenes* 4b F2365



Supplemental Figure 1A. BLAST score ratio analysis of *L. monocytogenes* strains H7858 and F6854.

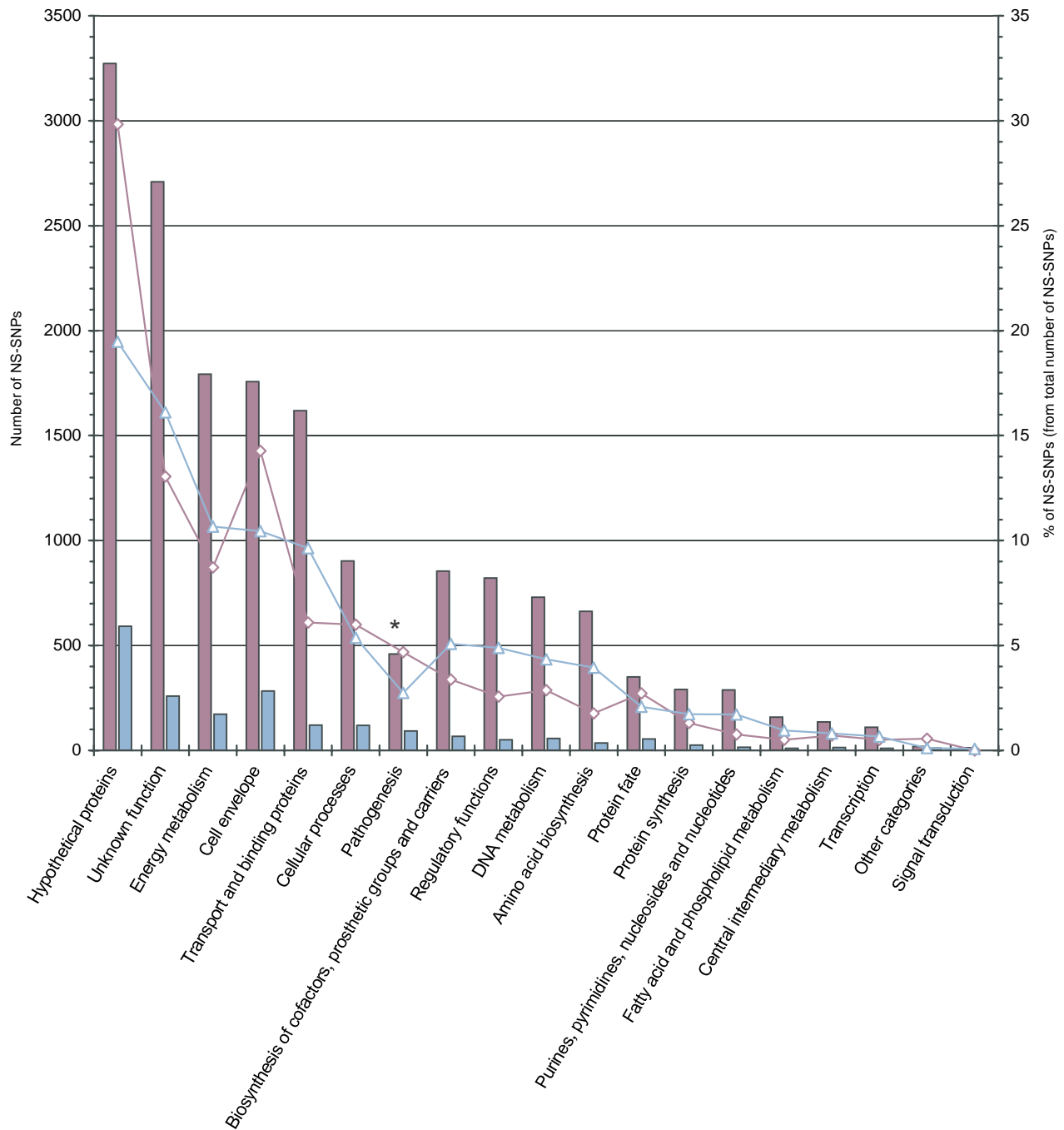
L. monocytogenes strain F2365 was used as reference. Each point represents a single protein. Proteins that cluster in the upper right hand corner are indicative of coding regions that are similar between all three organisms. Proteins in the lower right are those that are conserved among *L. monocytogenes* F2365 and *L. monocytogenes* F6854 but are not shared with *L. monocytogenes* H7858; upper left are similar between *L. monocytogenes* F2365 and *L. monocytogenes* H7858 and lower left are unique to *L. monocytogenes* F2365.

Normalized Blast Score with *L. monocytogenes* 4b F2365



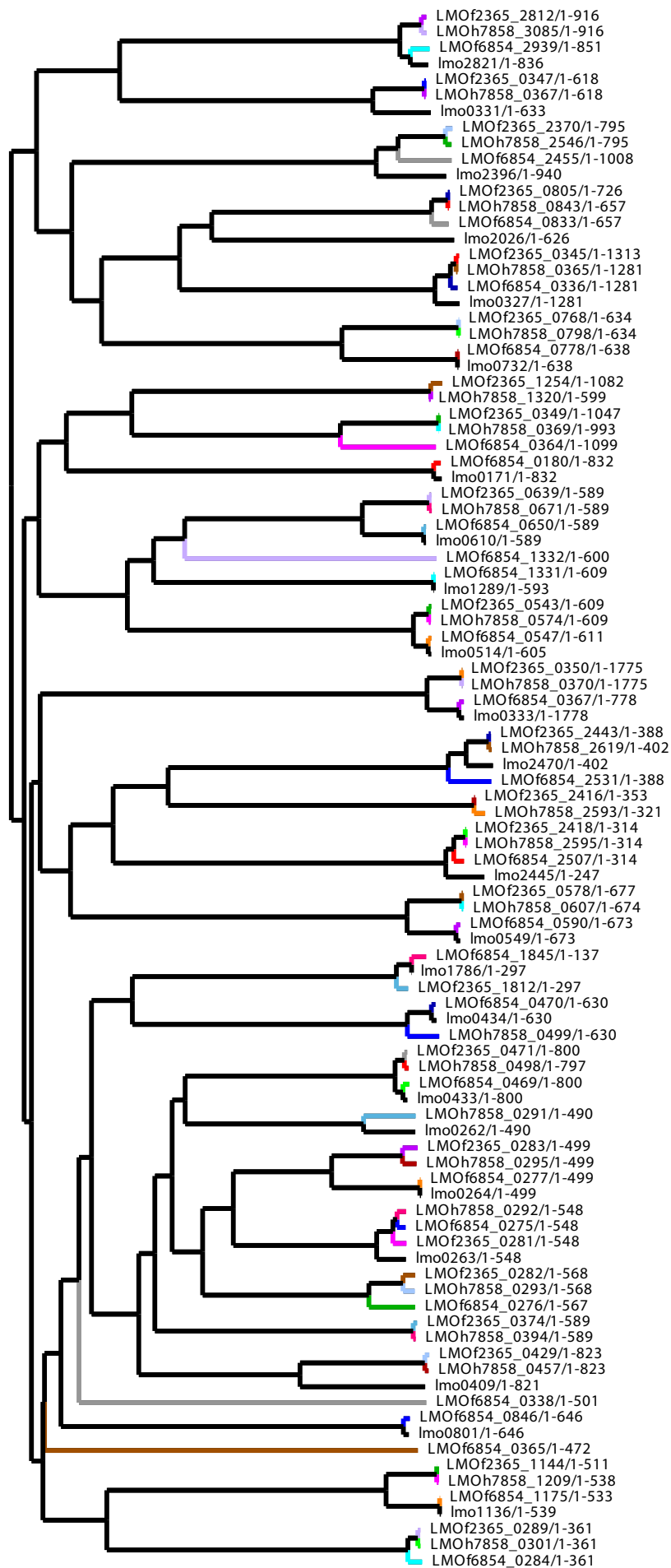
Supplemental Figure 1B. BLAST score ratio analysis of *L. monocytogenes* strain EGD-e and *L. innocua* strain CLIP 11262.

L. monocytogenes strain F2365 was used as reference. Each point represents a single protein. Proteins that cluster in the upper right hand corner are indicative of coding regions that are similar between all three organisms. Proteins in the lower right are those that are conserved among *L. monocytogenes* F2365 and *L. monocytogenes* EGD-e but are not shared with *L. innocua* CLIP 11262; upper left are similar between *L. monocytogenes* F2365 and *L. innocua* CLIP 11262 and lower left are unique to *L. monocytogenes* F2365.



Supplemental Figure 2. Distribution of NS-SNPs grouped by main role category in *L. monocytogenes* strains H7858 and F6854.

On the left Y-axis is displayed the total number of NS-SNPs for each main role category: purple bars, strain F6854; blue bars, strain H7858. On the right Y-axis is displayed the percentage of NS-SNPs for each role category, from the total number of NS-SNPs: purple diamonds, strain F6854; blue triangles, strain H7858. Pathogenesis, which belongs in the role category of cellular processes, has been separated to demonstrate the high levels of mutations that have occurred in the genes in this role category.



0.1 Tree balance = 0.0

Supplemental Figure 3. Phylogenetic analysis of the internalins present in the F2365, H7858, F6854 and EGD-e strains of *L. monocytogenes*.

Internalins were identified by the presence of Leucine Rich Repeat (LRR) motifs, using hidden Markov model (HMM) PF00560 (www.sanger.ac.uk/cgi-bin/Pfam). Internalin sequences were aligned using ClustalW, and the phylogenetic tree was generated with Belvu.