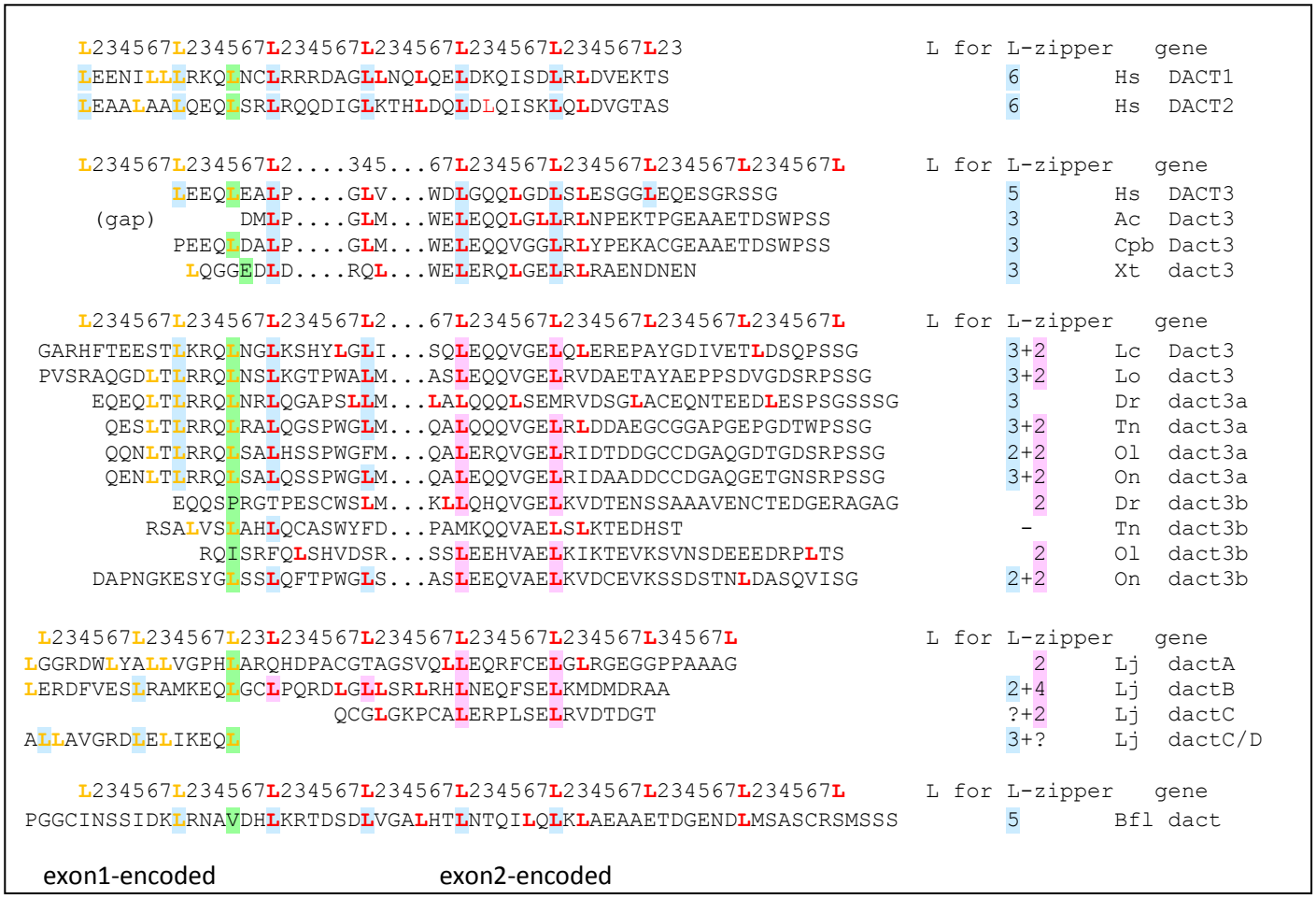
Additional File 12.

Arrangement of the leucine zipper in gnathostome Dact1, 2 and 3, and in cyclostome and *Branchiostoma* dact proteins.



Amino acids are displayed using the 1-letter code. A template with L correctly placed for a L-zipper is shown above each set of sequences. Abbreviations: see Additional File 1.

Green highlighter, end of exon 1 - encoded sequences
orange L, L encoded by 1st exon
red L, L encoded by 2nd exon

L contributing to a continuous or 1st part of a bipartite L zipper are highlighted in blue, L contributing to the 2nd part of a L zipper are highlighted in pink.

In gnathostome Dact1 and Dact2 proteins, the exon1-2 splice generates a continuous 6x leucine (L-) zipper (top).

In coelacanth (Lc) and actinopterygian dact3 proteins, 3 amino acids having been lost, leading to a bipartite motif. In most teleost dact3b sequences, conversion of L into other amino acids further reduced the L-zipper. In tetrapod Dact3 proteins, additional four amino acids have been shed, restoring a reduced but continuous L-zipper.

In cyclostomes, dact A carries a small, exon 2 encoded L-zipper, and dact B a bipartite L-zipper. For dact C and D, exon 1 cannot currently be allocated, hence the state of the L-zipper is unclear.

In Branchiostoma dact, a continuous 5L zipper is found.