

CORRECTION

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# Correction to: De novo transcriptome assembly, annotation and comparison of four ecological and evolutionary model salmonid fish species

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## Correction

Following the publication of this article [1], the authors found that they incorrectly reported the BUSCO completeness for the PhyloFish brown trout and European whitefish transcriptomes. This was due to an error in their TransDecoder pipeline and restricted to those two datasets and their interpretation. Carruthers et al. apologise for this misreported result and thank the authors of the PhyloFish database for bringing it to their attention.

The correct version of Table 3 has been included in this correction.

**Table 3** Summary of the complete, duplicated, fragmented and missing orthologs inferred from Benchmarking Universal Single-Copy Orthologs (BUSCO) search against the 4584 single-copy orthologs for Actinopterygii

BUSCO statistic	Atlantic salmon	Brown trout	Arctic char	European whitefish	PhyloFish brown trout	PhyloFish European whitefish	NCBI Atlantic salmon RefSeq Proteins
Complete BUSCOs	3461 (79%)	3596 (78%)	3589 (78%)	3512 (76%)	4254 (92%)	4202 (91%)	4476 (97%)
Complete -single-copy BUSCOs	1900 (42%)	1897 (41%)	1988 (44%)	1938 (42%)	2327 (50%)	2444 (53%)	1398 (30%)
Complete - duplicated BUSCOs	1741 (37%)	1699 (37%)	1601 (34%)	1574 (34%)	1927 (43%)	1758 (38%)	3078 (67%)
Fragmented BUSCOs	439 (10%)	424 (10%)	431 (10%)	452 (11%)	83 (1.8%)	113 (2.4%)	80 (1.7%)
Missing BUSCOs	504 (10%)	564 (12%)	564 (12%)	620 (13%)	247 (5.3%)	269 (5.8%)	28 (0.6%)

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1. Carruthers M, et al. De novo transcriptome assembly, annotation and comparison of four ecological and evolutionary model salmonid fish species. *BMC Genomics*. 2018;19:32. <https://doi.org/10.1186/s12864-017-4379-x>.

