Correction to: Characterization and genome sequencing of three *Aeromonas hydrophila*-specific phages, CF8, PS1, and PS2

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Authors would like to correct the incorrect version of Fig. 2 in the online publication. Correct version of Fig. 2 is updated here.

The original article can be found online at <https://doi.org/10.1007/s00705-020-04644-0>.

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Fig. 2 Genome-based phylogenetic analysis of CF8, PS1, and PS2 phages from this study with other *Aeromonas* phages genome sequences available in the NCBI database. The branches are coloured based on bootstrap values. Bootstrap values are shown at the nodes. Based on nucleotide sequence similarities, the phages have been clus-

tered at the species (S), genus (G) and family (F) level. The scale bar represents 0.2 substitutions per nucleotide. The last two letters (in red) of the branch tip labels indicate the country code. More details about the accession numbers, host, and country of isolation of these phages can be found in Supplementary Table S1

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