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CORRIGENDUM

Fish gut microbiota analysis differentiates physiology and behavior of invasive Asian carp and indigenous American fish

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Correction to: *The ISME Journal* (2014) **8**, 541–551; doi:10.1038/ismej.2013.181

Sequencing information was missing from the published article. The data can be found here: http://www.ncbi.nlm.nih.gov/sra/SRX245252[accn. The description of the data is linked to this corrigendum as Supplementary Information.

The fasta file (GZSD-SVCP.fasta) contains all sequences obtained from the foregut and hindgut samples of gizzard shad (GZSD) and silver carp (SVCP). These sequences have been denoised together with the sequences of other samples in the same 454 pyrosequencing runs using QIIME (v 1.5.0). The sequence ID format in the fasta file was shown as follows:

```
>19_24186
ATACGGGAGGGGCA...
```

The red number represents the sample ID, which corresponds to the ID in Supplementary Table S1. This table can also be found at the end of this document.

The blue number represents the sequence ID, which was generated by the 'split_libraries.py' command of QIIME.