

**Gill Na⁺/K⁺-ATPase in the threespine stickleback (*Gasterosteus aculeatus*):
changes in transcript levels and sites of expression during acclimation to
seawater**

APPENDIX

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Running heads

Left = Kusakabe *et al.*

Right = Gill Na⁺/K⁺-ATPase in the threespine stickleback

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Appendix Figure 1. mRNA levels of the gill sodium-potassium ATPase α -subunit (*atp1a1a.4-201*, *atp1a1a.4-204*, *atp1a2*, *atp1a3a*, and *atp1a3b*) of the (a–e) Ono and (f–j) Gifu threespine stickleback populations during the seawater acclimation process. The crossing point (Cp) values obtained from the real-time quantitative PCR were plotted without any corrections with internal controls to see the differences in overall expression levels among different transcripts. Cp values indicate how rapidly the PCR products are detected and represent an approximation of the overall transcript levels. Smaller Cp values indicate higher expression levels.

Appendix Figure 2. Boxplots of Reads Per Kilobase Million (RPKM) of four genes encoding ATP1A. RPKM data were obtained from Artemov et al. (2017). RNA-sequencing was conducted in the gills of Russian freshwater and marine threespine stickleback ecotypes exposed either to freshwater or seawater.



