



Figure S3

The relationship between MiSeq sequence reads and DNA copy numbers quantified by qPCR. Correlations for the total fish eDNA (all data, **a**; enlarged figure, **b**), Japanese anchovy (*Engraulis japonicus*; all data, **c**; enlarged figure, **d**), and Japanese jack mackerel (*Trachurus japonicus*; all data, **e**; enlarged figure, **f**). Dashed and solid lines indicate 1:1 line and linear regression line, respectively. Regression lines in the enlarged figures were drawn by excluding outliers. All regression lines, except for the lines for total fish eDNA, were significant ($P < 0.05$). Dotted boxed regions in **a**, **c**, and **e** correspond to the range of the graphs in **b**, **d**, and **f**, respectively. The intensity of red colour indicates the slope of the regression line used to convert sequence reads to the copy numbers.