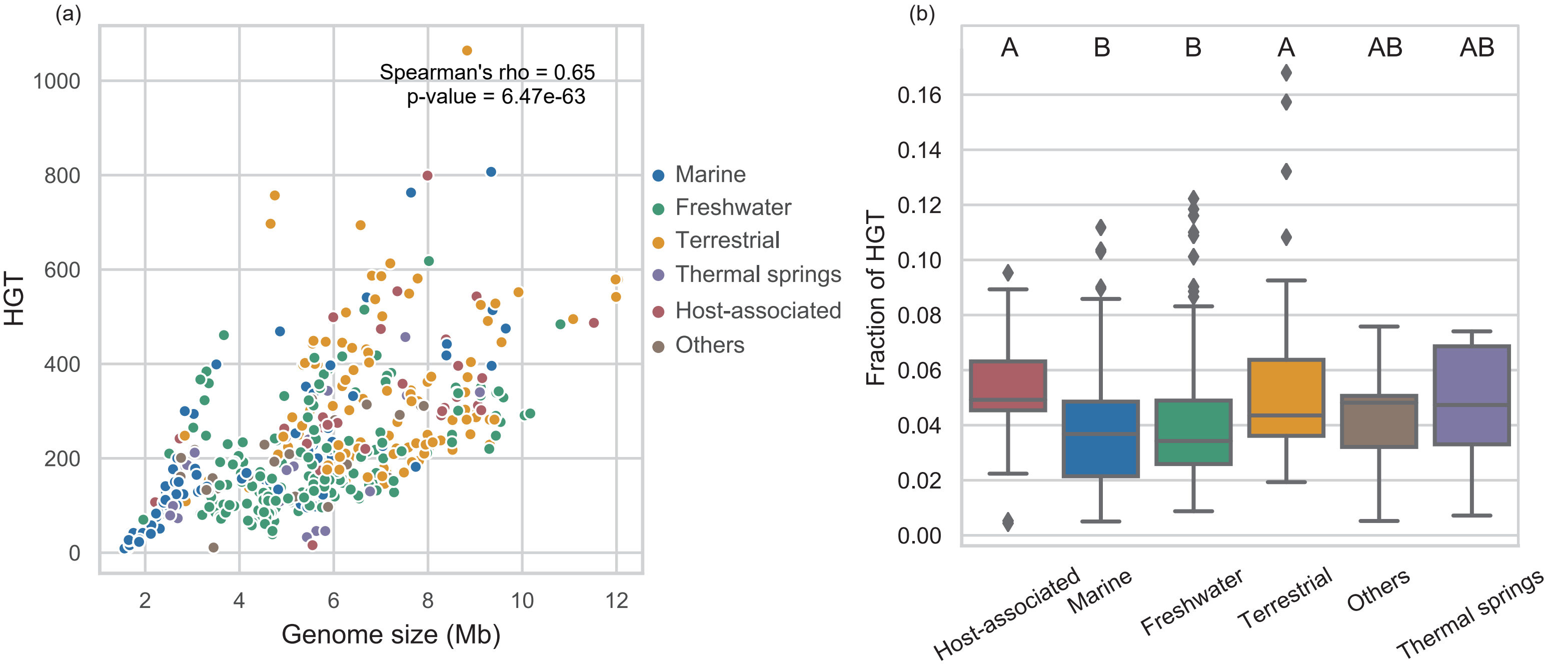

Fig. S12. Analysis of genome sizes and HGT events. a, The relations between the predicted numbers of HGT and genome sizes. b, Distribution of proportion of predicted transferred genes per genome corresponding to marine (n = 99), freshwater (n = 184), terrestrial (n = 125), host-associated (n = 33), thermal springs (n = 26) and others (n = 24) environments. Boxes marked with different letters on top denote its statistically significant differences at the Pvalue <0.01.