



S11 Fig. Relative genetic diversity of HA genes of influenza B viruses circulating in different regions of the world. Effective population sizes over time inferred by Bayesian skyride analysis for HA of Victoria- (blue) and Yamagata-lineage (red) viruses isolated in (A, E) the USA, (B, F) Europe, (C, G) SC/SEA and (D, H) Oceania. Solid lines represent median values and shaded areas represent 95% highest probability densities (HPD) credible intervals across MCMC samples.