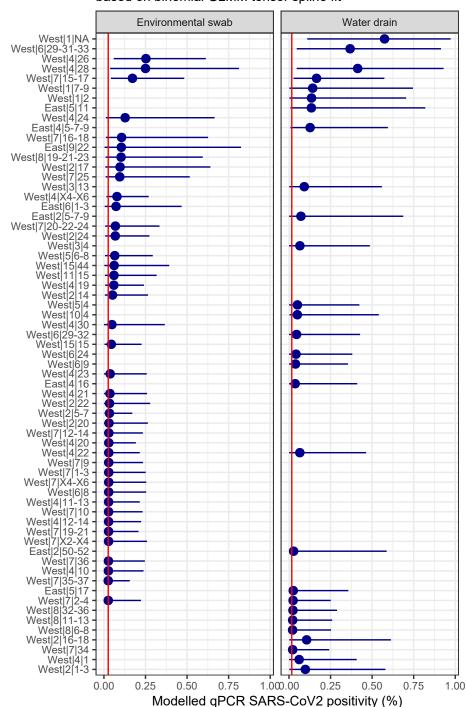
Modelled qPCR SARS-CoV2 positivity (%)

based on binomial GLMM tensor spline fit



(mean plus 95% Cls)