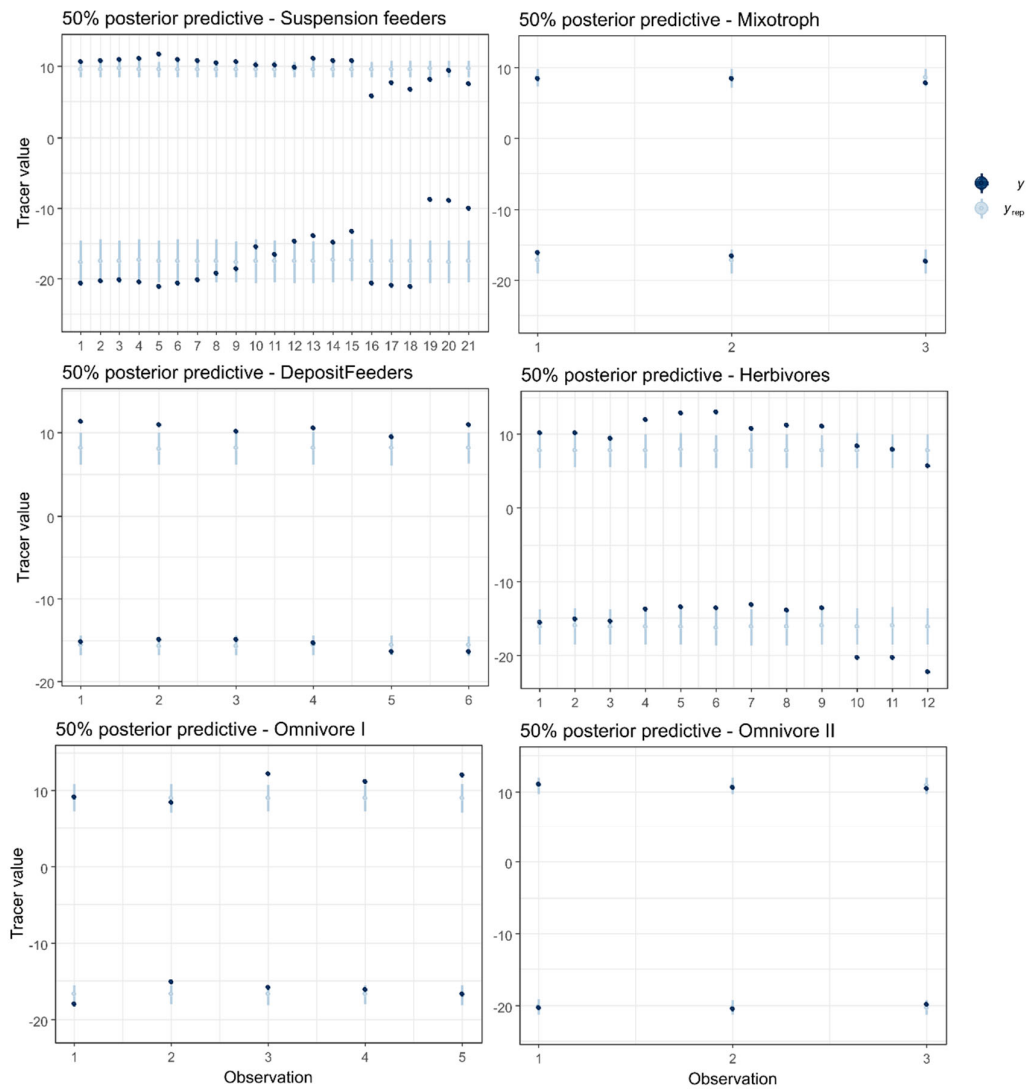


**Figure S1.** Diagnostic plots from the R *simmr* mixing model package with the result of the model fit for each species. Data points (denoted by the graph as  $y$ ) located widely within the ranges of fitted values (denoted  $y_{rep}$ ; the default is a 50% interval) indicate well fit of the model.



**Figure S2.** Diagnostic plots from the R *simmr* mixing model package with the result of the model fit for each trophic group. Data points (denoted by the graph as  $y$ ) located widely within the ranges of fitted values (denoted  $y_{rep}$ ; the default is a 50% interval) indicate well fit of the model.