**R packages details**

All analyses were performed using R Studio (RStudio (2021), Integrated Development for R. RStudio, PBC, Boston, MA) (v 1.3.1093) equipped with car ([Fox and Weisberg, 2011](https://elifesciences.org/articles/49452#bib34)), readxl, writexl, lme4 (Bates et al., 2015), lmerTest (Kuznetsova et al., 2017), lmtest, DHARMa, dplyr, tidyverse, Rmisc, knitr and mass ([Venables and Ripley, 2002](https://elifesciences.org/articles/49452#bib91)) packages to perform exploratory analysis, run the main models, perform post-hoc tests and create output tabs. Figures were generated using ggplot2 ([Wickham, 2011](https://elifesciences.org/articles/49452#bib98)), ggpubr, sjPlot, sjmisc, qqplotr, ggpub, magrittr, gridExtra, ggsignif, patchwork, RColorBrewer.