

Microbial source tracking of human and animal fecal contamination in household settings in northern Ecuador

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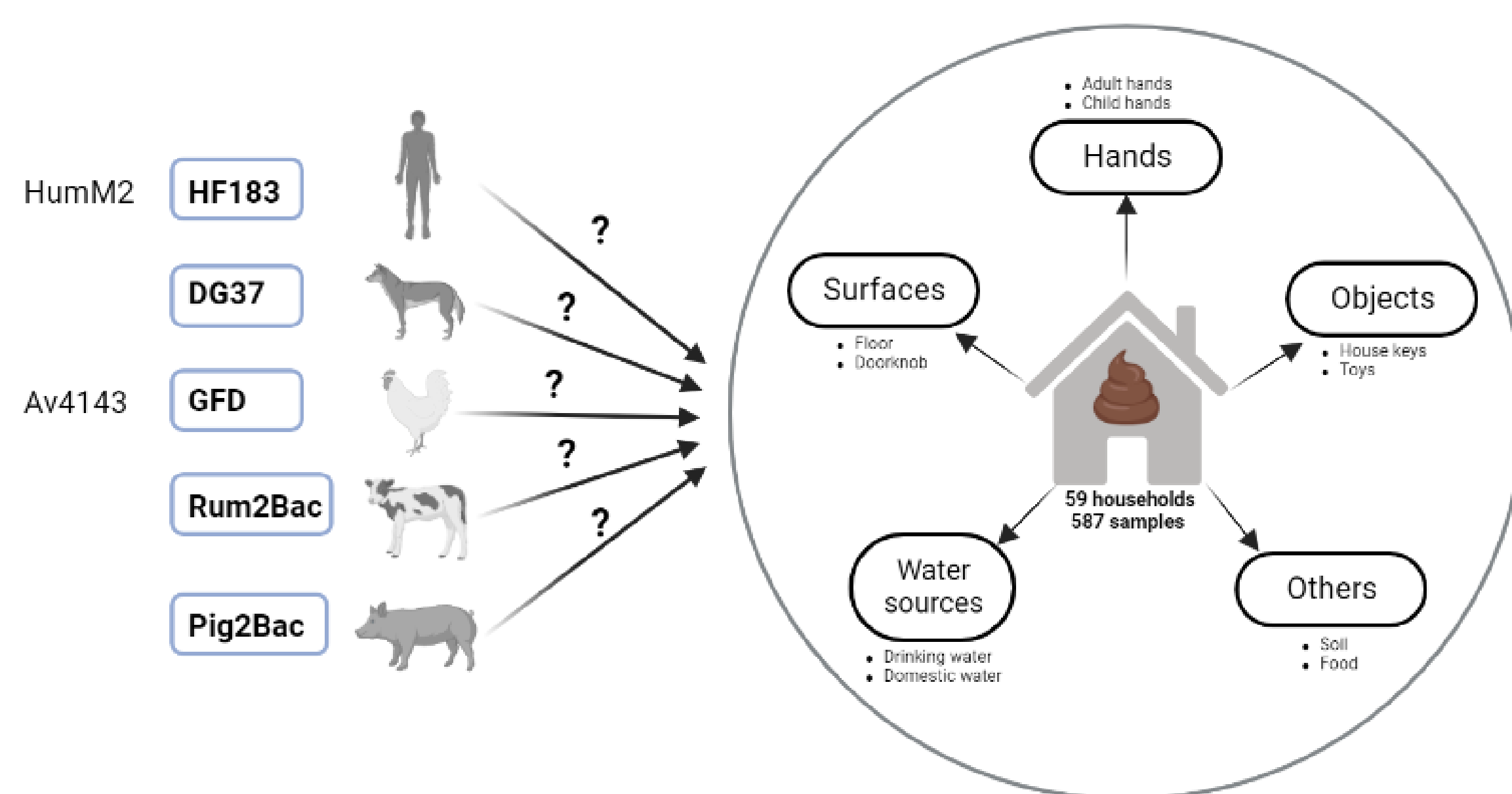
BACKGROUND

- > Environmental exposures to feces represent an important transmission pathway for enteric pathogens¹.
- > Health risks associated with enteric infections disproportionately fall on children in settings where domestic animals are common, hygiene is poor, and enteric pathogen transmission is high.²
- > qPCR analysis of microbial source tracking (MST) markers can be used to quantitatively measure environmental fecal contamination and discriminate between human and animal sources.^{1,3}

The goal of this study was to use MST markers to characterize the **sources** and **intensity** of fecal contamination in households that own animals in northern Ecuador.

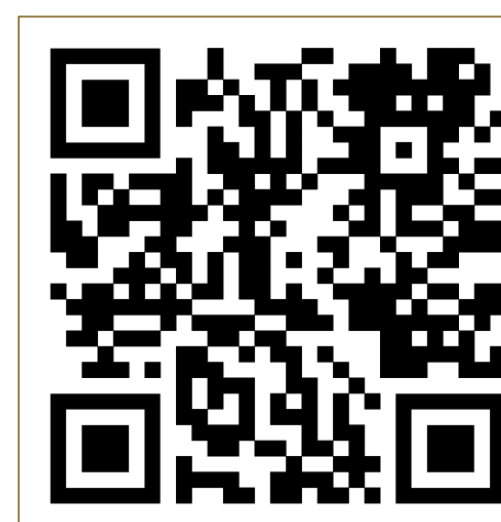
METHODS

- > Validation of MST markers for use in Ecuador
- > Collection of multiple sample types per household
- > qPCR for general and host-associated MST markers



General and human-associated fecal contamination were common in Ecuadorian households. Detection of animal-associated MST markers was less frequent, but animal markers were present at high concentrations when detected. Host-associated fecal contamination was most frequently found in child and adult hand rinses and in floor swab samples.

This research demonstrates that MST is appropriate for characterizing sources of household fecal contamination and will inform a larger analysis of child exposure to animals and their feces in northern Ecuador.



Scan to see additional results!

REFERENCES

¹Fuhrmeister et al. (2019). Predictors of enteric pathogens in the domestic environment from human and animal sources in rural Bangladesh. *Environ. Sci. Technol.* 54(4): 2560.

²McCormick & Lang. (2014). Diarrheal disease and enteric infections in LMIC communities: how big is the problem? *Trop. Dis. Trav. Med. Vaccines* 2(1):1-7.

³Harwood et al. (2014). Microbial source tracking for detection of fecal contamination in environmental waters: relationships between pathogens and human health outcomes. *FEMS Microbiol. Rev.* 38: 1-40.



Fig 1: Animals are ubiquitous in and around study households.

RESULTS

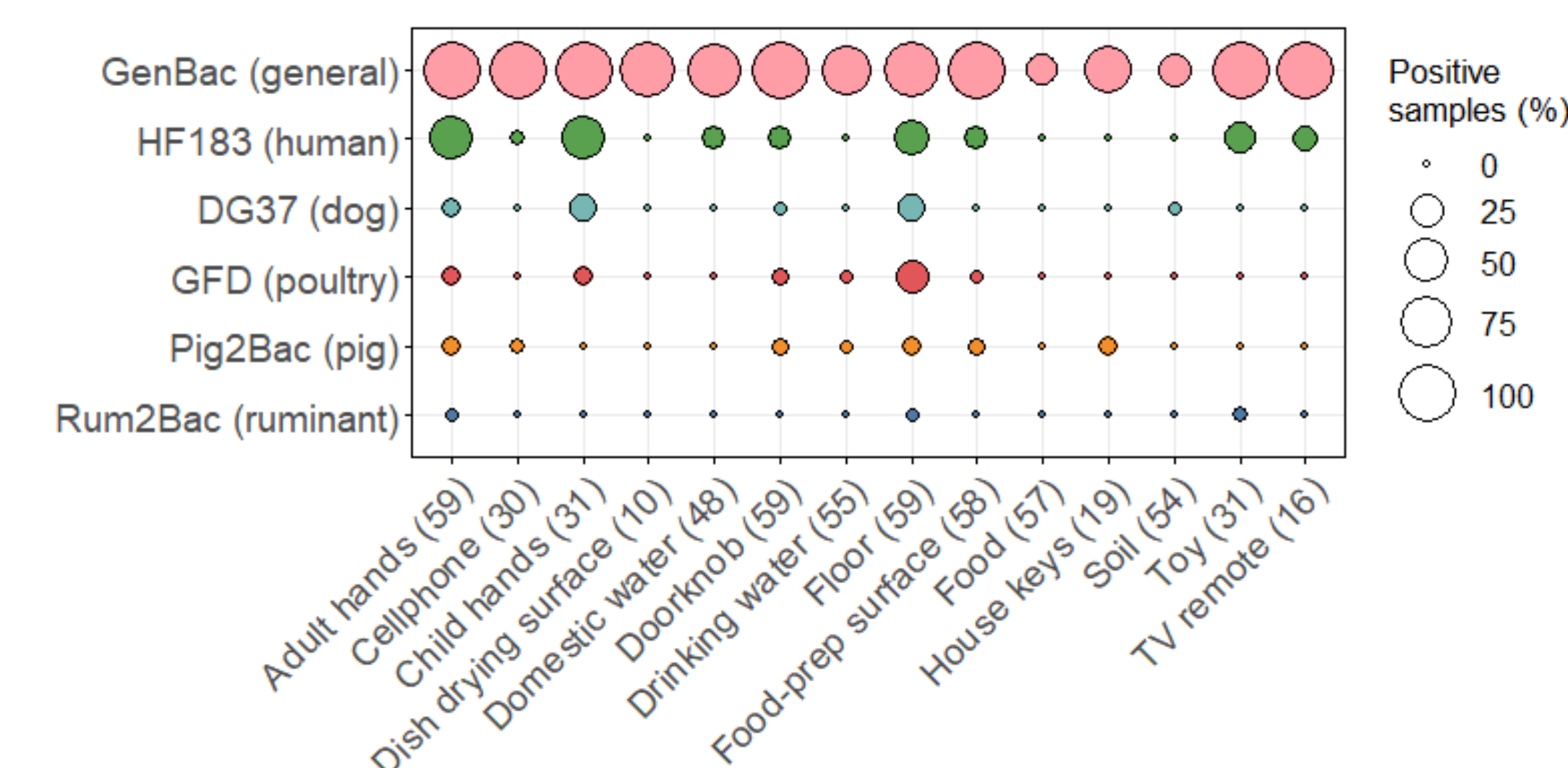


Fig. 2: Prevalence of MST markers by sample type; numbers in parentheses indicate *n* for each sample type.

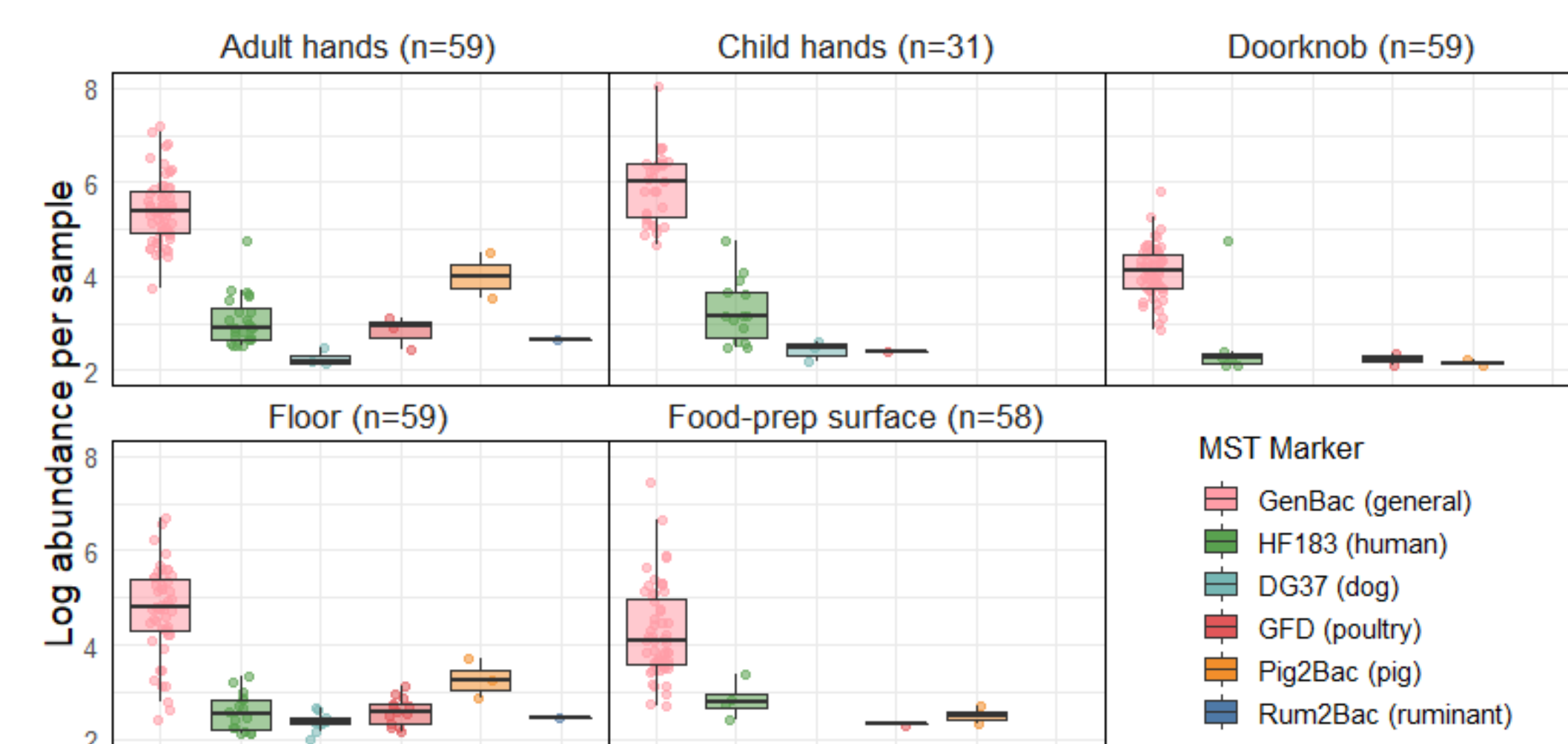


Fig. 3: Abundance of MST markers by sample type; only results with Ct values > LOQ and sample types with detection of ≥3 host-associated markers are shown.