This paper is concerned with evaluating the potential virulence of probiotic *Enterococcus faecalis*. I am interested in *Enterococcus* and am currently working on a large HBM project so any information on HBM microbiota is most welcome. I have noticed quite a bit of *E. faecalis* in other HBM studies but I am always skeptical of misdiagnosis in microbiome samples resulting from universal primer choice. This paper does not suffer from this potential setback.
The paper is well written but could benefit from additional information in several places. The authors should investigate the virulence factors and report whether these factors (or functional homologs) are present in other GRAS probiotics.

On L30, the authors state that *E. faecalis* is a promising probiotic candidate in human breast milk; while there are available human-targeted products that use *E. faecalis* fermentation products and autolysate, are there any probiotic uses of *E. faecalis* live cells? I would suggest toning down this statement as the potential virulence associated with probiotics are not yet fully established. I think this is important as the health of neonates is concerned.

On L42, the authors missed the word “in”. The authors should also very briefly describe what a subsystem functions they refer to (e.g. virulence).

On L43, the authors state that common biological functions were observed in all samples, this statement is unnecessary. If the authors wish to say something about ubiquitous function, one that may allude to adaptation could be stated here. For example (and hypothetically), all isolates contained a biofilm forming cassette regardless of source would be more striking. If the authors are including normal metabolism to refer to the metabolic crosstalk between bacterium and host, this needs to be stated. I will leave the decision on up to the authors, however.

On L71, the authors mention observations by Anjum *et al*. Similar findings were observed when HBM *E. faecium* isolates were observed by Leigh *et al.,* 2022. This paper may aid in some later comparisons too even though the species are not identical, their translocation and adaptions seem very simialar.

On L84, the authors mention Jimenez *et al*. 2013. I don’t believe that this study accounted for antibiotic usage in the donor species. As antibiotics are used quite extensively in farms, this may explain the differences in resistance profiles. I would expect the translocation of resistant phenotypes in human samples if recently treated with antibiotics too. The authors are too reliant on this single citation to support their claims. Further reading is required to decipher trends more concretely.

On L89, the authors describe the finding of Chen *et al*., 2016. The only mention of antibiotic usage in this paper is for cephalexin following Caesarian section. There may have been other antibiotics prescribed in the (almost) a year between birth and donation. Other papers on HBM need to be explored for this, other Gram positive species may provide a greater insight into this.

On L96, two studies does not constitute multiple studies. Please strengthen this statement.

On L121, the Vitek protocol was validated with *E. coli*, why was an *Enterococcus* species not used? I am unfamiliar with running this particular protocol so please forgive me if this is a silly question.

On L145, I have always found this phylogeny method to be unreliable. Considering the scope of this study, why didn't the authors do something more stable such as finding all single-copy ubiquitous genes using BLASTN (or something similar), aligning them, trimming them, and then using a robust phylogeny builder like IQTREE-2?

On L175, I wouldn't worry at all about 0.5% contamination. This could be from so many normal sources such as a transposon from a closely related species.

Figure 1 is much too crowded. Each genome should be presented as a separate figure.

Figure 3 is unacceptable. This phylogeny was built without a root and needs to be redone and better displayed. An unrooted phylogeny is largely meaningless.

Figures 4-6 would be much better if submitted as tables.