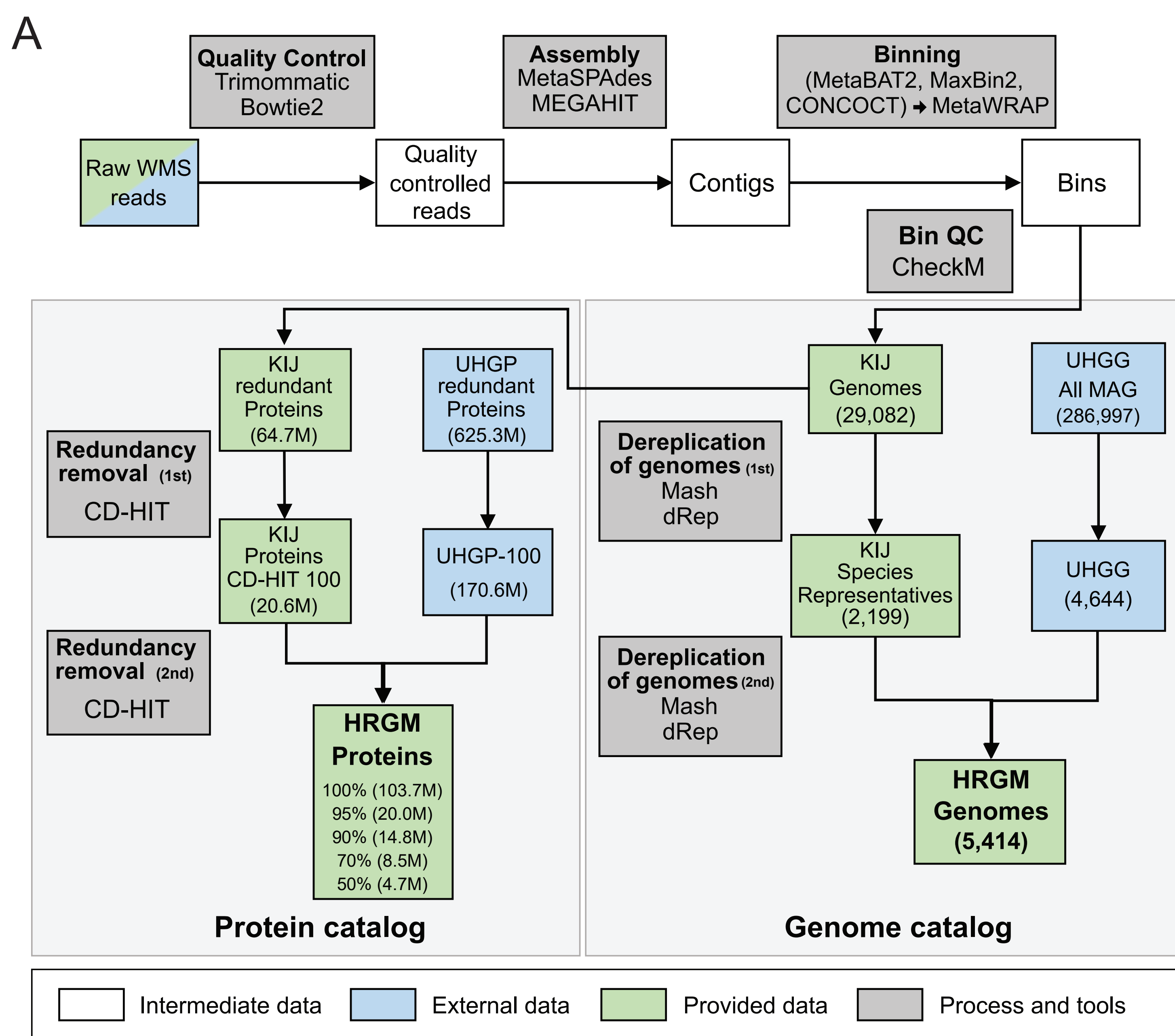


BACKGROUND

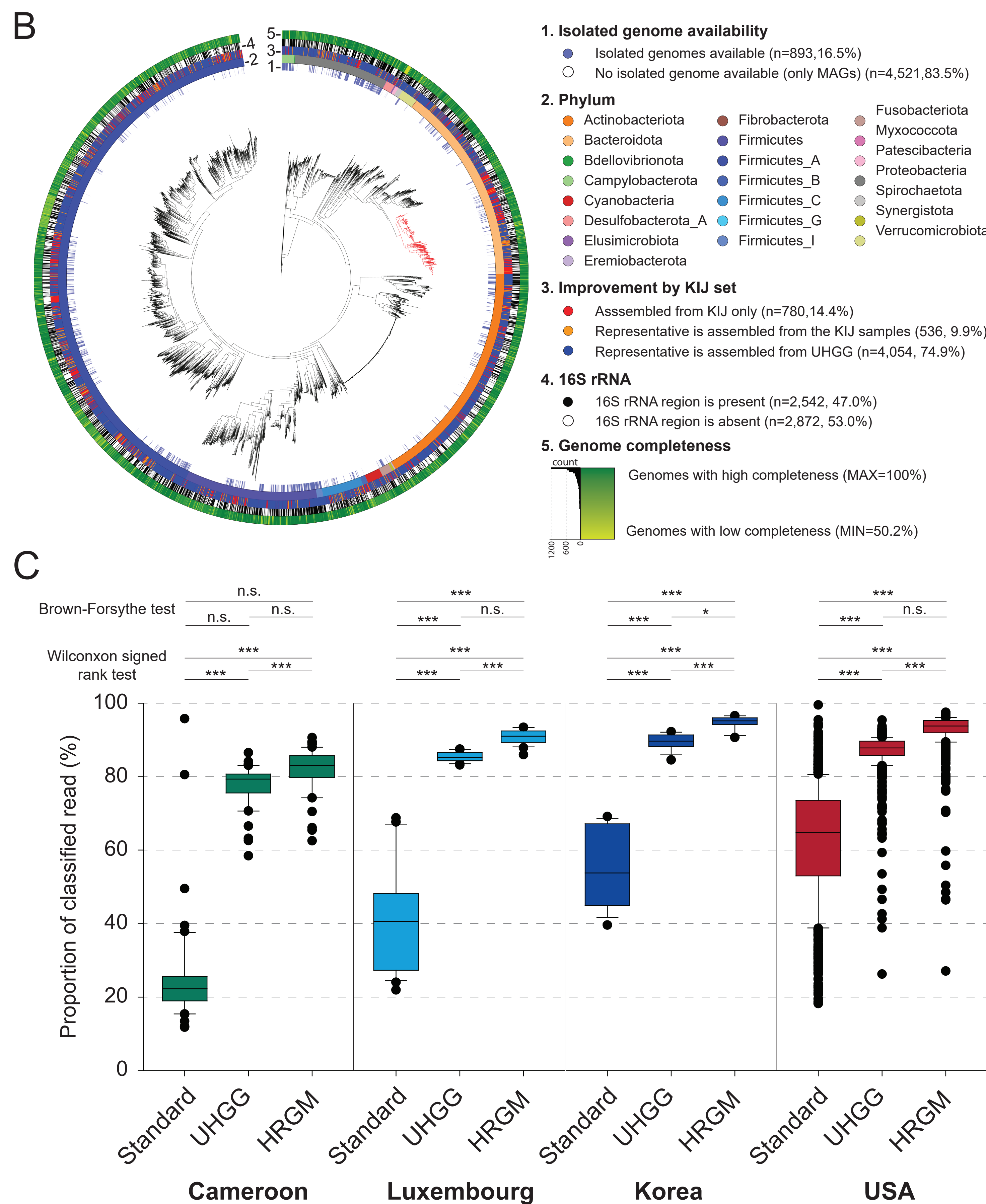
- A large portion of human gut microbiota are un-isolated yet; Therefore, we lack genome sequences of them.
- Recently, metagenome-assembled genomes (MAGs) substantially increase the phylogenetic diversity of uncultured taxa; However, it is biased for geographical location and lifestyle.
- In this study, we constructed comprehensive human gut microbiome genome and protein catalogs by incorporating fecal whole metagenomic shotgun (WMS) sequencing samples from under-represented populations.

METHODS

- We compiled fecal WMS sequencing of 90 Koreans (newly sequenced in this study), 805 Japanese, and 110 Indian (Public dataset) (Figure A).
- For the 90 Korean samples, we performed ultra-deep (25Gbp - 60Gbp, average 30Gbp) WMS sequencing.
- We performed de-novo metagenomic assembly and species-level dereplication with UHGG genomes, and constructed Human Reference Gut Microbiome (HRGM) with 5,414 prokaryotic species (Figure A).



RESULT 1 - The improvement of HRGM



- We obtained 780 novel species and improved the genome quality of 536 species representatives (Figure B).
- We found that 4,521 (83.5%) species are exclusively assembled from metagenomic data (Figure B).
- We observed significant improvement in classification proportion compared to the RefSeq-CG-based standard database and the UHGG-based database, regardless of ethnicity (Figure C).
- Moreover, variance in classification rate across samples is reduced except for the Cameroon cohort (Figure C).

RESULT 2 - Novel Bacteroidaceae are associated to diet-related lifestyle of Asian

