

1 **Description of Additional Supplementary Files**
2 **Longitudinal Gut Microbiota Tracking Reveals the Dynamics of Horizontal Gene**
3 **Transfer**

4 **Authors**

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20 File Name: Supplementary Data 1

21 Description: Quality assessment of all metagenome-assembled genomes (MAGs),
22 including completeness, contamination, N50, genome size, taxonomy assignment
23 (GTDBv214 and SGB), MASH clusters, and other QC metrics used to determine high-
24 quality genomes for downstream analyses.

27 File Name: Supplementary Data 2

28 Description: List of all detected recent horizontal gene transfer (HGT) events between
29 genome pairs, including donor and recipient species, genomic coordinates, event length,
30 sequence similarity clusters, supporting evidence, and filtering status.

32 File Name: Supplementary Data 3

33 Description: Detailed annotation of each transferred DNA segment, including MAG
34 information and insertion information.

36 File Name: Supplementary Data 4

37 Description: Results of functional enrichment analyses of genes found in HGT segments,
38 including PFAMs annotation, with p-values, FDR, and FoldChange.

40 File Name: Supplementary Data 5

Description: Species pangenomes annotated with virulence factors, AMR-related genes, and ARGs, alongside species relative abundances and community classifications.

File Name: Supplementary Data 6

Description: Pairwise species data used to test associations between HGT rate, phylogenetic distance, co-abundance patterns, and network centrality metrics.

File Name: Supplementary Data 7

Description: Association results linking HGT segments to host phenotypes, including lifestyle, medication usage, and demographic variables, based on linear mixed models and corrected p-values.

File Name: Supplementary Data 8

Description: Comparison of HDMI with WAAFLE, including simulation settings and recovery rate evaluations.

File Name: Supplementary Data 9

Description: Catalog of long HGT segments (>10 kb), including annotations and genomic context.

File Name: Supplementary Data 10

Description: ARG annotations for all MAGs and all HGT segments, including predicted resistance gene families, confidence levels, and genomic context, based on RGI and CARD databases.

File Name: Supplementary Data 11

Description: Species-level ecological and genomic trait profiles (e.g., oxygen tolerance, motility, habitat range, genome size, GC content) used to analyze biological factors shaping HGT patterns.