

Gut Microbiome Report — Human

Patient: Homo sapiens · M5 Age: 32 years Sex: M Sample date: 2026-04-15 Report date: 2026-07-05 Lab: OmicaLabs SL — Pipeline: GenePortal Human Microbiome v2.1 (shotgun metagenomics)

Notice: Clinical support report. It does not constitute a medical diagnosis. Clinical interpretation requires correlation with the complete clinical picture and complementary tests.

1. Main clinical picture (32y, M)

Main verdict: FMT donor: NOT ELIGIBLE — Clostridium perfringens (1607 reads), Clostridioides difficile (7433 reads), Giardia intestinalis (G. duodenalis) (807 reads). Any intestinal pathogen excludes donation or requires clarification before donation.

Profile with mild dysbiosis (mildly altered band).

2. Patient clinical data

Field	Value
Species	human
Age	32
Sex	M
Weight (kg)	76.0
Diet	mediterranean/omni (high in fiber, fruit, vegetables, fish, legumes)
Antibiotics in the last 30 d	False
Antibiotic (drug)	—
Probiotics	False
Sample date	2026-04-15

Field	Value
Storage	—
Geography (ISO)	AU-QLD

2.1 Clinical context

Reason for the test: Healthy control for establishing a personal baseline gut microbiome. Donor screened for a fecal microbiota transplantation (FMT) program.

Main symptoms: - Gastrointestinally asymptomatic. Bristol 3-4 stools, 1-2/day, no abdominal discomfort.

Relevant history: - No history of gastrointestinal disease - FMT screening colonoscopy: endoscopically normal mucosa in all segments - Colonic biopsies: no histopathological findings (no inflammation, no dysplasia) - Negative serologies: HIV, HBV, HCV, syphilis, Strongyloides, CMV, EBV - Stool culture + parasites: negative (including microsporidia, Cyclospora, Cystoisospora) - C. difficile toxin A/B PCR: negative - C. difficile toxin A/B in stool: negative - Fecal calprotectin < 50 µg/g - No travel to tropical areas in the last 12 months - No tattoos or piercings in the last 6 months - Regular exercise: running 3-4 times/week + swimming

Current medication: - None

Family history: - No family history of IBD, colorectal cancer or celiac disease

3. Sample quality (QC)

Metric	Value	Status
Total reads	42,015,912	—
Host reads	0.0%	OK
Post-filter reads	42,011,710	—
Classified reads	12,633,594	—
NTC	—	—
Mock community	—	—

Metric	Value	Status
Batch QC	Not evaluated	—

4. Taxonomic composition

4.1 Top 5 phyla

Phylum	Abundance %
Bacillota (Firmicutes)	58.33
Bacteroidota (Bacteroidetes)	36.06
Pseudomonadota (Proteobacteria)	2.29
Actinomycetota (Actinobacteria)	1.97
Thermodesulfobacteriota	0.75

4.2 Top 10 genera

Genus	Abundance %
Bacteroides	29.18
Phocaeicola (GTDB reclassification of Bacteroides (vulgatus, distasonis, etc.))	16.70
Alistipes	5.67
Parabacteroides	3.23
Odoribacter	0.90
Butyricimonas	0.06
Muribaculum (Muribaculaceae)	0.04
Paramuribaculum	0.04
Duncaniella	0.02
Sodaliphilus	0.00

4.3 Genera of clinical interest

- Phocaeicola (16.70%): Reclassified from Bacteroides (GTDB). Implicated in bile acid metabolism. Common genus in the human gut microbiota.
- Mediterraneibacter (1.83%): Reclassified from Ruminococcus (GTDB). Acetate producer. Part of the Lachnospiraceae group, common in a healthy microbiota.

4.4 Alpha diversity

Index	Value	Healthy range
Shannon	2.538	2.5 - 4.5 (healthy)
Simpson	0.852	0.8 - 0.98 (healthy)
Chao1	799.1	—
Observed ASVs	—	—
Pielou evenness	0.436	—

5. Dysbiosis Index (iHMP HMP2 proxy)

- Dysbiosis Index (z-score sum): 0.602 (mildly altered)
- Bacillota / Bacteroidota ratio: 1.618 (normal)
- β distance (Bray-Curtis vs healthy centroid): 0.7643
- β distance (Euclidean, log10): 0.5974
- Method: iHMP_HMP2_zscore_proxy_human_v2
- Reference: iHMP_HMP2_2019 + Gevers2014_CellHostMicrobe + Gupta2020_NatureComms + Toto2024_PedIBD

Notice: not equivalent to the clinical DI by qPCR.

5.1 Contribution per taxon

Taxon	Abundance %	z-score	Direction	Contribution
Faecalibacterium	16.06	0.01	health	-0.01
Roseburia	1.43	-0.25	health	+0.25
Alistipes	5.67	0.12	health	-0.12

Taxon	Abundance %	z-score	Direction	Contribution
Prevotella	0.010	0.37	health	-0.37
Ruminococcus	1.40	0.49	health	-0.49
Coprococcus	0.41	0.59	health	-0.59
Subdoligranulum	0.07	-2.31	health	+2.31
Akkermansia	0.21	0.65	health	-0.65
Escherichia coli	0.03	0.28	dysbiosis	+0.28
Clostridium (sensu stricto)	0.00 (not detected)	0.00	dysbiosis	0.00

- 1/10 panel taxa not detected — the DI should be interpreted with caution.
- $\triangle$ Centroid calibrated against a European population reference (European DMP (Gacesa 2022, n=8.208)); local Spanish cohort pending. The β distance and the derived DI have reduced accuracy for non-European populations; interpret as a guide.

6. Indicator species (SCFA producers)

Genus	Detected %	Healthy range	Status
Faecalibacterium	16.06	—	normal
Roseburia	1.43	—	normal
Alistipes	5.67	—	normal
Prevotella	0.01	—	normal
Ruminococcus	1.40	—	normal
Coprococcus	0.41	—	normal
Subdoligranulum	0.07	—	low
Akkermansia	0.21	—	normal
Escherichia coli	0.03	—	normal

Genus	Detected %	Healthy range	Status
Clostridium (sensu stricto)	0.00 (not detected)	—	low

SCFA producers total: 60.96 % (healthy > 12 %)

7. Species-specific biomarkers (clinical enrichment)

Human clinical biomarkers (SoTA 2020-2025 — Gupta 2020 + Frioux 2023 + Zheng 2024)

- Enterosignatures (NMF soft): ES-B=66%, ES-P=0%, ES-F=31%, ES-Bf=2%, ES-Ec=0%
- EDS (Enterotype Dysbiosis Score): 0.34 (mixed enterotype)
- GMHI (Gut Microbiome Health Index): 0.36 (healthy (predicted))
- GMW12 (Chang/Gupta 2024): -0.740 (strongly not healthy) [43S/31NS taxa detected]
- ICB = 12.1% (optimal). Derived from the weighted sum of producer genera (Faecalibacterium, Agathobacter, Roseburia, Eubacterium, Anaerobutyricum, Anaerostipes, Coprococcus, Butyricicoccus, Subdoligranulum). It is NOT a fecal SCFA concentration; qualitative correlation with butyrogenic production.
- C. difficile risk: low
- Disease signatures:
 - Ulcerative Colitis (Zheng 2024 panel): 1 enriched spp, AUC=0.9 — 2 depleted detected. SCREENING ONLY — NOT a diagnosis.

CRC / IBD — Screening (NOT a diagnosis)

- IBD Panel Zheng 2024: UC score=-6.19 | CD score=N/D | Continuous score, no validated diagnostic threshold.
 - UC Panel: 1 enriched spp + 2 depleted spp detected
 - CD Panel: 0 enriched spp + 0 depleted spp detected
 - Note: 2 species in the panel not detectable with MetaPhlAn 4
 - Ref: Zheng et al. 2024, Nature Medicine 30:3555-3567, PMID: 39367251
 - LIMITATION: validated m-ddPCR panel (AUC=0.88 UC, 0.87 CD). The metagenomic approach is NOT externally validated for clinical diagnosis.

Quality Control

- Batch QC status: Not evaluated
- Beneficial genera: detected

- Prevotella altered (0.01%) — Fiber fermenter, healthy in non-Western diets (P. copri)
- Lactobacillus altered (0.00%) — Probiotic, lactate producer; intestinal barrier support

MODERATE ALERTS (2 alerts)

- Dysbiosis index=0.6 — mildly altered
- DI mildly altered
- Estimated age: 32 years (declared) (based on patient data)

Clinical interpretation

Enterotype ES-B (Bacteroides-dominant) with strong membership (0.66). Profile compatible with Bacteroides-dominant. Enterotypes represent continuous trends, not discrete categories (Bulygin 2023).

Limitations (12)

- There is NO ACMG equivalent for microbiome interpretation. These metrics are orientative and must be integrated with the complete clinical picture.
- Enterotypes: they are NOT discrete categories (Costea 2018, Bulygin 2023). They represent continuous trends on a non-linear manifold.
- GMHI requires species-level data. MetaPhlAn 4 uses GTDB taxonomy (SGBs) while GMHI uses NCBI. The SGB→NCBI mapping is approximate.
- DI V2 panel (10 genera): asymmetric 8:2, AUC=0.745, external validation: independent cohort ongoing.
- The F/B ratio is NOT a reliable standalone biomarker (Finucane 2014 PLOS ONE; Magne 2020 Nutrients). Interpret with DI, diversity and clinical context.
- Detection of ARGs from a metagenome does NOT equate to phenotypic resistance. EUCAST 2024: VME < 5% in only 44% of antibiotics.
- Disease signatures (IBD/CRC/T2D/obesity) are SCREENING TOOLS — NOT diagnostic.
- Reference ranges come mainly from the Dutch Microbiome Project (n=8,208, European population). Their applicability to other populations requires validation.
- Alpha diversity (Shannon) is a coarse ecological measure that does NOT predict clinical outcomes by itself.
- Q2PD (Zielinska et al. 2025, GigaScience 14:giaf015) is a functional index based on MetaCyc metabolic pathways. Currently NOT AVAILABLE.
- Drugs that alter intestinal transit (loperamide, opioids) or gastric pH (PPI) can modify the microbiome composition by changes in residence time and luminal acidity. Interpret with

caution if the patient received them in the 2 weeks before sample collection.

- This report is for research use and clinical context. It does not constitute a medical diagnosis. ISO/TS 24420:2023 covers metagenomic data processing.

References (25)

- Frioux et al. 2023, Cell Host & Microbe 31:1111-1125 (5 ES, 5,230 metagenomes)
- Keller et al. 2024, bioRxiv 2024.08.13.607711 (fuzzy enterotyping, EDS, 16,772 metagenomes)
- Bulygin et al. 2023, PeerJ 11:e15764 (no discrete clusters — manifold learning)
- Gupta et al. 2020, Nature Comms 11:4635 (GMHI, 50 species, AUC=0.73)
- Sun et al. 2024, npj Biofilms 10:96 (GMHI validation, 6,314 metagenomes, AUC=0.825)
- Gevers et al. 2014, Cell Host Microbe 15:382-392 (MD-index)
- Zheng et al. 2024, Nature Medicine 30:3555-3567 (IBD panels, 5,979 metagenomes)
- Piccinno/Segata/Huttenhower 2025, Nature Medicine (CRC pooled 3,741, AUC=0.85)
- Mei/Huttenhower et al. 2024, Nature Medicine 30:2265-2276 (T2D, 8,117 metagenomes)
- Chanda & De 2024, Gut Microbes 16:2304900 (obesity 25 spp, AUC=0.85)
- Gacesa et al. 2022, Nature 604:732-739 (DMP, n=8,208, 9 core species)
- Asnicar et al. 2021, Nature Medicine 27:321-332 (PREDICT 1, n=1,098)
- Andreu-Sanchez/Segata/Fu et al. 2025, Cell (32,152 metagenomes, 42 countries)
- Mancabelli et al. 2024, mSystems (6,653 samples, 5 life stages)
- Shao et al. 2024, Nature Microbiology (1,288 UK neonates, 3 community states)
- Vaiserman et al. 2020, BMC Microbiol 20:114 (F/B age-stratified, n=1,550)
- Finucane et al. 2014, PLOS ONE 9:e84689 (F/B NOT reliable standalone biomarker)
- Magne et al. 2020, Nutrients 12:1474 (F/B critical review)
- Vital et al. 2017, mBio 8:e01492-17 (butyrate producers)
- Dong et al. 2024, Nature Comms (VFDB 2.0 + MetaVF, 62,332 VFGs)
- Lessa et al. 2015, NEJM 372:825-834 (C. difficile epidemiology)
- EUCAST 2024: metagenomic ARG ≠ phenotypic AST
- Zielinska et al. 2025, GigaScience 14:giaf015 (Q2PD, PMID: 40117176, pathway-based dysbiosis, >8,000 samples, outperforms GMHI/hiPCA for IBD)
- ISO/TS 24420:2023 — shotgun metagenomic data processing
- STROBE-Metagenomics, Lancet Infect Dis, Oct 2025

8. Functional profiling (HUMAN 3 + dbCAN 3)

Most represented metabolic pathways (top 10)

Metabolic pathway	Abundance (RPKM)	Clinical interpretation
PWY-7238: sucrose biosynthesis II	27,840	Carbohydrate metabolism — Sucrose biosynthesis. Indicates active bacterial glycolytic activity.
PWY-1042: glycolysis IV	23,237	Glycolysis — Glycolysis (EMP glycolysis). Central pathway of bacterial energy metabolism.
VALSYN-PWY: L-valine biosynthesis	21,461	Amino acid synthesis — Valine biosynthesis. Basal metabolic activity.
DTDPRHAMSYN-PWY: dTDP- β -L-rhamnose biosynthesis	21,021	Cell wall synthesis — dTDP-L-rhamnose biosynthesis (LPS and wall component).
PWY-5686: UMP biosynthesis I	20,900	Nucleotide synthesis — UMP biosynthesis (uridine). Basal bacterial proliferative activity.
PWY-7790: UMP biosynthesis II	20,900	Nucleotide synthesis — UMP biosynthesis (alternative route). Bacterial proliferative activity.
PWY-7791: UMP biosynthesis III	20,900	Nucleotide synthesis — UMP biosynthesis (alternative route). Bacterial proliferative activity.
PWY66-429: fatty acid biosynthesis initiation (mitochondria)	20,593	Bacterial metabolic activity — Bacterial metabolic pathway — part of the basal metabolism of the gut microbiome.
PWY-6163: chorismate biosynthesis from 3-dehydroquinate	20,541	Amino acid synthesis — Chorismate biosynthesis (precursor of aromatic amino acids).
GLYCOGENSYNTH-PWY: glycogen biosynthesis I (from ADP-D-Glucose)	10,256	Glycogen metabolism — Bacterial glycogen biosynthesis. Energy storage.

601 pathways detected in total by HUMAnN 3. The 10 with the highest abundance (RPKM) are shown, excluding unclassified reads.

Note: The most represented pathways correspond mainly to basal (housekeeping) metabolic activity of the commensal microbiota — glycolysis, amino acid synthesis, nucleotides and cell wall. Their clinical relevance is global (it indicates metabolic activity of the microbiome), not individual. Alterations in the relative abundance of specific pathways (butyrate, bile acids, LPS) are more informative than the presence of housekeeping pathways.

8.1 Overall functional assessment

Of the 10 most abundant pathways, 8 are housekeeping pathways (basal metabolism: glycolysis, amino acids, nucleotides, cell wall) and 2 are specialized-metabolism pathways (fermentation, energy storage, isoprenoids).

Interpretation: The diversity of active metabolic pathways indicates a metabolically competent microbiota. The presence of multiple housekeeping pathways at high abundance is expected in a metabolically active microbiome — it means the bacteria are alive, reproducing and processing nutrients.

Clinical relevance of the functional pathways: the presence of housekeeping pathways is necessary but not sufficient for a healthy microbiome. What is clinically relevant is the depletion of butyrate-specific production pathways (butyryl-CoA acetate CoA-transferase pathway) and the elevation of pro-inflammatory pathways (LPS synthesis, flagella). These functional alterations are already reflected in the biomarkers of section 7 (butyrogenic capacity, *C. difficile* risk) and are more clinically actionable than the individual abundance of each housekeeping pathway.

9. Pathogens detected (bacterial + eukaryotic + fungi)

9.1 Bacterial pathogens

[MODERATE] *Clostridium perfringens* — MODERATE - Abundance: 0.00% | Reads: 1,607 - Clinical significance: *cpe/cpa/netE/netF* genes NOT detected by metagenomics. *cpe* encodes the enterotoxin responsible for food poisoning (type A) and necrotizing enteritis (type C). *cpa* (alpha toxin) is the marker of gas gangrene. If the patient is asymptomatic, this isolate probably represents commensal colonization.

[MODERATE] *Clostridioides difficile* — MODERATE - Abundance: 0.00% | Reads: 7,433 - Clinical significance: *tcdA/tcdB* NOT detected by metagenomics — NON-toxigenic strain. Asymptomatic colonization, does not require treatment with oral vancomycin or fidaxomicin. Confirm with toxin A/B PCR if there is compatible clinical presentation (diarrhea, fever, leukocytosis). McDonald 2018 IDSA/SHEA Clin Infect Dis 66:e1.

[LOW] *Giardia intestinalis* (*G. duodenalis*) — LOW - Abundance: 0.00% | Reads: 807 - Clinical

significance: Giardiasis — the main intestinal parasitosis with notifiable potential (assemblages A and B). Chronic diarrhea.

9.3 Fungi (mycobiome)

Note on fungal detection by shotgun metagenomics: Fungal biomass in stool is typically <0.1% of the total metagenome (Nash et al. 2017, Microbiome). The sensitivity of shotgun for fungi is lower than for bacteria due to low abundance, a cell wall resistant to lysis (chitin/glucans), and large genomes with lower coverage per sequencing depth. A negative result does NOT rule out a clinically relevant fungal infection. Always interpret in the clinical and dietary context of the patient.

Classification methodology: Fungi are classified according to the BugID/BugSeq matrix (2026): clinical classification of the species (according to WHO/ECDC priority lists) × universal signal threshold. The threshold has been calibrated against the natural distribution of fungal abundance in the human fecal metagenome: the breakpoint at 10 RPM separates the normal mycobiotic background from elevated signal, consistent with the MetaMIC minimum reporting. An absolute floor of 30 reads filters cross-mapping noise. IMPORTANT: There are no species-validated thresholds in the literature for fungi in stool by shotgun — these thresholds are for screening, not diagnostic. Any detection at trace level requires orthogonal confirmation (culture + ITS PCR) before making clinical decisions.

Possible traces

- *Candida auris* (fungus) — Abundance: 0.0000% | Reads: 209 | 5.0 RPM
 - Clinical significance: WHO CRITICAL Priority 1. Emerging MDR nosocomial pathogen. Resistant to azoles, frequently to echinocandins, occasionally to amphotericin B. Intestinal colonization = potential reservoir for ICU outbreaks. Detection in a hospitalized/immunosuppressed patient requires urgent confirmation and consideration of activating the infection control protocol. In an immunocompetent outpatient, low-signal detections (<10 RPM) have a high probability of being Kraken2 cross-mapping — always confirm with culture before acting.
 - Confirmatory gold standard: CHROMagar culture + MALDI-TOF (may be confused with *C. haemulonii* in Vitek2 systems) + *C. auris*-specific PCR + D1/D2 sequencing
 - ⚠ WHO CRITICAL PRIORITY 1 — trace-level detection. Reads compatible with *Candida auris* are detected but below the clinical signal threshold (10 RPM). In an immunocompetent outpatient without recent hospitalization, the probability that it is a false positive due to Kraken2 cross-mapping is high. Do NOT activate the infection control protocol without prior confirmation by CHROMagar culture + MALDI-TOF + specific PCR. If the patient is hospitalized, in the ICU, or immunosuppressed, consider urgent confirmation and activate the protocol if

confirmed.

- *Candida krusei* (fungus) — Abundance: 0.0000% | Reads: 69 | 1.6 RPM
 - Clinical significance: INTRINSICALLY resistant to fluconazole. Emerging in onco-hematology with azole prophylaxis. Detection in stool + neutropenia + fluconazole prophylaxis = HIGH clinical value (selective pressure). Mortality 40-60%.
 - Confirmatory gold standard: CHROMagar culture + MALDI-TOF + ITS PCR (distinctive pale pink colonies on CHROMagar)
- *Cryptococcus neoformans* (fungus) — Abundance: 0.0000% | Reads: 235 | 5.6 RPM
 - Clinical significance: Encapsulated opportunistic yeast. Meningoencephalitis in AIDS (CD4<100). Intestinal colonization documented as a portal of entry. Fecal detection + AIDS/severe cellular immunosuppression → systemic workup (urgent serum CrAg). In immunocompetent: environmental (pigeon/eucalyptus droppings).
 - Confirmatory gold standard: CSF India ink + Sabouraud culture + urease test + latex agglutination (CrAg) + MALDI-TOF

Incidental findings

- *Aspergillus flavus* (fungus) — Abundance: 0.0000% | Reads: 150 | 3.6 RPM
 - Clinical significance: 2nd most common clinical *Aspergillus*. Aflatoxin producer (IARC Group 1 carcinogen). Invasive fungal sinusitis + keratitis. Fecal detection: possible pre-invasive colonization in the immunosuppressed OR dietary exposure to aflatoxins (cereals/nuts).
 - Confirmatory gold standard: Sabouraud culture + MALDI-TOF + ITS/calmodulin PCR + galactomannan
- *Candida parapsilosis* (fungus) — Abundance: 0.0000% | Reads: 188 | 4.5 RPM
 - Clinical significance: 3rd most common clinical *Candida*. Associated with NICU neonates, catheters, TPN. Forms biofilms on devices. Relevant in prolonged hospitalization. Generally susceptible to azoles.
 - Confirmatory gold standard: Culture + MALDI-TOF + ITS PCR
- *Candida tropicalis* (fungus) — Abundance: 0.0000% | Reads: 106 | 2.5 RPM
 - Clinical significance: 4th most common clinical *Candida*. Highly virulent (proteinases, filamentation). Associated with profound onco-hematological neutropenia. Greater tissue invasion than other *Candida* spp. Mortality 30-50% in candidemia.
 - Confirmatory gold standard: CHROMagar culture + MALDI-TOF + ITS PCR
- *Candida albicans* (fungus) — Abundance: 0.0000% | Reads: 79 | 1.9 RPM

- Clinical significance: Most frequent GI commensal yeast. Opportunistic pathogen in the immunosuppressed (neutropenia, transplant, AIDS). Invasive candidiasis from the GI tract. >0.1% in a patient with risk factors = relevant overgrowth.
 - Confirmatory gold standard: CHROMagar culture + MALDI-TOF + ITS1/ITS2 PCR
- *Saccharomyces cerevisiae* (fungus) — Abundance: 0.0000% | Reads: 127 | 3.0 RPM
 - Clinical significance: Baker's/brewer's yeast. Most cases = DIETARY (bread, beer, wine, cheese, *S. boulardii* probiotics). In the ICU/severely immunosuppressed it can cause fungemia by translocation. FP WARNING: a diet rich in bread/beer/cheese → positive reads without real infection. ALWAYS interpret in dietary context.
 - Confirmatory gold standard: Sabouraud culture + MALDI-TOF + ITS PCR
- *Candida glabrata* (fungus) — Abundance: 0.0000% | Reads: 105 | 2.5 RPM
 - Clinical significance: 2nd most common clinical *Candida*. Frequent fluconazole resistance (intrinsically high MIC). Emerging in ICU/onco-hematology/transplant. Fecal detection relevant if prior azole prophylaxis. Candidemia with mortality 40-50%.
 - Confirmatory gold standard: CHROMagar culture + MALDI-TOF + ITS PCR
- *Pneumocystis jirovecii* (fungus) — Abundance: 0.0000% | Reads: 33 | 0.8 RPM
 - Clinical significance: Atypical fungus. PCP pneumonia in severely immunosuppressed patients (AIDS CD4<200, transplant, corticosteroids, anti-TNF). Intestinal colonization documented in HIV+ patients may precede lung infection. ANY fecal detection + PCP risk factors + respiratory symptoms → urgent workup (beta-D-glucan + BAL PCR). In immunocompetent: self-limiting subclinical colonization.
 - Confirmatory gold standard: *P. jirovecii*-specific PCR (mtLSU rRNA or beta-tubulin) in BAL/induced sputum + serum beta-D-glucan + direct immunofluorescence
- *Malassezia restricta* (fungus) — Abundance: 0.0000% | Reads: 79 | 1.9 RPM
 - Clinical significance: Cutaneous lipophilic commensal. Emerging association with Crohn's (Limon 2019 mBio) and UC — possible role in intestinal inflammation via Th17 antifungal immunity. In IBD: biomarker of fungal dysbiosis. In healthy: skin contamination or commensalism without significance.
 - Confirmatory gold standard: ITS PCR + culture on Dixon medium (requires lipids; does not grow on standard Sabouraud)
- *Malassezia globosa* (fungus) — Abundance: 0.0000% | Reads: 60 | 1.4 RPM
 - Clinical significance: Cutaneous lipophilic commensal. Together with *M. restricta*, associated with the IBD gut microbiome (Crohn's, UC). Possible trigger of inflammation via dectin-1/CARD9. In active IBD: marker of a pro-inflammatory

mycobiome. In healthy: no clinical significance.

- Confirmatory gold standard: ITS PCR + culture on modified Dixon medium

Confirmatory gold standard for fungi: Culture on CHROMagar/Sabouraud medium + MALDI-TOF + ITS1/ITS2 PCR. Taxonomic identification by shotgun has screening value; species confirmation and the antifungal susceptibility profile require isolation in culture.

△ Very low abundance (<0.01%). Detection of fungi at trace level in shotgun metagenomics may reflect: (1) real subclinical colonization, (2) environmental contamination (ubiquitous spores), or (3) dietary origin (bread, beer, cheese, probiotics). The fungal cell wall (chitin/glucans) is resistant to standard DNA extraction lysis, which underestimates the real abundance. Correlate with clinical findings and consider targeted culture if there are risk factors (immunosuppression, prolonged hospitalization, parenteral nutrition, broad-spectrum antibiotic therapy).

WARNING — Dietary false positives: Detection of *Saccharomyces cerevisiae* DNA (baker's/brewer's yeast) is common in fecal shotgun and almost always reflects recent dietary intake (bread, beer, wine, cheese, *S. boulardii* probiotics), NOT infection. ALWAYS interpret in dietary context before attributing clinical significance.

9.4 Viruses / phages

- Phage: uncultured phage cr2_1: 0.0051%
- Phage: uncultured phage cr13_1: 0.0047%
- Phage: Faecalibacterium phage FP_Brigit: 0.0024%
- Phage: Faecalibacterium phage FP_Taranis: 0.0022%
- Phage: Faecalibacterium phage FP_Epona: 0.0006%

Clinical note: The viruses detected are commensal bacteriophages, normal components of the gut microbiome with no known clinical implication. No pathogenic human DNA viruses were detected above reporting thresholds.

10. Antibiotic resistance (AMR genes)

[OK] No acquired resistance genes were detected in the assembled contigs (AMRFinderPlus + VFDB).

Note: The absence of ARGs in a metagenome does NOT guarantee phenotypic susceptibility. EUCAST 2024: VME < 5% in only 44% of antibiotics. Requires culture + antibiogram.

11. Prioritized recommendations

Priority	Action	Justification	Gold standard	Timeframe
COMPLEMENTARY	Confirmatory PCR for Giardia intestinalis (G. duodenalis)	Detected at 0.00%	Specific PCR	1-2 weeks
URGENT	Rule out the candidate for FMT donation	Clostridium perfringens, Clostridioides difficile, Giardia intestinalis (G. duodenalis) detected	FMT donor exclusion protocol	Immediate

12. Clinical conclusions

- Dysbiosis index: 0.602 (mildly altered band).
- Enterotype Dysbiosis Score: 0.34 (mixed enterotype).
- FMT donor: NOT ELIGIBLE due to detection of Clostridium perfringens, Clostridioides difficile, Giardia intestinalis (G. duodenalis). Donation is not appropriate until confirmation/resolution according to protocol.
- No acquired antibiotic resistance genes were detected.
- Notice: report of. It does not constitute a medical diagnosis. Interpretation requires complete clinical correlation.

13. Methodology and limitations — regulatory compliance

- STORMS guidelines, Mirzayi et al. Nat Med 2021
- MlxS-Human v6.3.0 (Genomic Standards Consortium)
-
- EUCAST 2025 + IDSA/SHEA antimicrobial stewardship
- Pipeline: GenePortal Human Microbiome v2.1 (shotgun metagenomics)
- Generated: 2026-07-05 22:57

Limitations:

- Shotgun DNA does not detect RNA viruses (coronavirus, rotavirus, calicivirus, astrovirus); it requires RNA-seq or specific PCR.
- Relative abundance does not equate to viability or an absolute CFU count; the official numerical DI requires quantitative qPCR.
- Shotgun provides AMR genotype but not a phenotypic profile (MIC); it requires targeted

culture + antibiogram.

- Critical eukaryotic pathogens (e.g. Giardia, Cryptosporidium) require specific PCR as the gold standard — shotgun sensitivity at ~3-6M reads is limited.
- Clinical interpretation requires correlation with the clinical picture, diet, previous treatments and other complementary tests.

14. Validation

Role	Name	License number
Analysis lead (bioinformatics)	_____	OmicaLabs SL — Pipeline GenePortal Human Microbiome v2.1
Clinical validation lead	Juan Carlos Barba Carretero	Nº Col. 002395189P

OmicaLabs SL — Clinical decision support report. Processing, analysis and interpretation performed in accordance with STORMS (Mirzayi 2021), MlXS-Human v6.3.0 and ISO/TS 24420:2023 for shotgun metagenomic data processing.