

Gut Microbiome Report — Human

Patient: Homo sapiens · M4 Age: 12 years Sex: M Sample date: 2026-05-20 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 (12y, M)

Pre-intervention assessment in a metabolic context: microbiome profile with mild dysbiosis; interpret together with metabolic parameters and a history of recent antibiotic therapy if applicable. No bacterial or eukaryotic pathogens of high clinical priority detected. Profile with mild dysbiosis (mildly altered band).

2. Patient clinical data

Field	Value
Species	human
Age	12
Sex	M
Weight (kg)	87.0
Diet	omnivorous (Kazakh family diet, high in meat/fat, low in fiber)
Antibiotics in the last 30 d	True
Antibiotic (drug)	amoxicillin-clavulanate (7 days, completed 10 days before the sample)
Probiotics	False
Sample date	2026-05-20

Field	Value
Storage	—
Geography (ISO)	KZ

2.1 Clinical context

Reason for the test: Evaluation of gut dysbiosis in severe childhood obesity as part of a comprehensive metabolic study. Assessment before structured dietary intervention and possible referral to a childhood obesity unit.

Main symptoms: - Progressive obesity since age 6 (current BMI 37.7, >p99 for age and sex) - Cervical acanthosis nigricans (marker of insulin resistance) - Nocturnal snoring (suspected obstructive sleep apnea) - Nonspecific recurrent abdominal pain - Chronic constipation (Bristol 1-2, 3 stools/week)

Relevant history: - Early-onset childhood obesity (age 6), acceleration after COVID lockdown - Weight gain of 12 kg in the last 12 months - Confirmed insulin resistance (HOMA-IR 5.2, fasting glucose 102 mg/dL) - Elevated ALT 68 U/L (hepatic steatosis on ultrasound, grade I-II) - Normal TSH (hypothyroidism ruled out) - Sleep apnea test: AHI 6.2/hour (mild obstructive apnea) - Recent antibiotic therapy: amoxicillin-clavulanate for streptococcal pharyngotonsillitis (10 days ago) - Low physical activity (<2 h/week of exercise)

Current medication: - None chronically

Comorbidities: - Severe childhood obesity (BMI >p99) - Insulin resistance (pre-diabetes) - Non-alcoholic hepatic steatosis (pediatric NAFLD) - Mild obstructive sleep apnea - Chronic functional constipation

Family history: - Mother: obesity (BMI 34), gestational diabetes in the patient's pregnancy - Father: overweight (BMI 28), hypercholesterolemia - Maternal grandmother: type 2 diabetes

3. Sample quality (QC)

Metric	Value	Status
Total reads	12,320,442	—
Host reads	0.2%	OK
Post-filter reads	12,289,640	—
Classified reads	2,991,829	—

Metric	Value	Status
NTC	—	—
Mock community	—	—
Batch QC	Not evaluated	—

4. Taxonomic composition

4.1 Top 5 phyla

Phylum	Abundance %
Bacillota (Firmicutes)	43.47
Bacteroidota (Bacteroidetes)	36.35
Candidatus Melainabacteria	8.26
Pseudomonadota (Proteobacteria)	6.05
Actinomycetota (Actinobacteria)	5.17

4.2 Top 10 genera

Genus	Abundance %
Bacteroides	35.36
Phocaeicola (GTDB reclassification of Bacteroides (vulgatus, distasonis, etc.))	4.66
Parabacteroides	12.78
Alistipes	4.32
Butyricimonas	0.61
Odoribacter	0.45
Segatella (GTDB reclassification of Prevotella copri)	0.29

Genus	Abundance %
Prevotella	0.11
Paraprevotella	0.03
Hoylesella (Bacteroidaceae)	0.01

4.3 Genera of clinical interest

- Phocaeicola (4.66%): Reclassified from Bacteroides (GTDB). Implicated in bile acid metabolism. Common genus in the human gut microbiota.
- Mediterraneibacter (0.36%): 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	2.499	2.5 - 4.5 (healthy)
Simpson	0.835	0.8 - 0.98 (healthy)
Chao1	1449.1	—
Observed ASVs	—	—
Pielou evenness	0.404	—

5. Dysbiosis Index (iHMP HMP2 proxy)

- Dysbiosis Index (z-score sum): 1.281 (mildly altered)
- Bacillota / Bacteroidota ratio: 1.196 (normal)
- β distance (Bray-Curtis vs healthy centroid): 0.8726
- β distance (Euclidean, log10): 0.6965
- 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	7.13	-0.34	health	+0.34
Roseburia	0.74	-0.53	health	+0.53
Alistipes	4.32	0.07	health	-0.07
Prevotella	0.11	0.69	health	-0.69
Ruminococcus	0.11	0.07	health	-0.07
Coprococcus	0.16	0.44	health	-0.44
Subdoligranulum	0.38	-1.36	health	+1.36
Akkermansia	1.08	0.87	health	-0.87
Escherichia coli	7.43	1.19	dysbiosis	+1.19
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.
- Δ 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	7.13	—	normal
Roseburia	0.74	—	normal
Alistipes	4.32	—	normal
Prevotella	0.11	—	normal
Ruminococcus	0.11	—	normal
Coprococcus	0.16	—	normal

Genus	Detected %	Healthy range	Status
Subdoligranulum	0.38	—	normal
Akkermansia	1.08	—	normal
Escherichia coli	7.43	—	normal
Clostridium (sensu stricto)	0.00 (not detected)	—	low

SCFA producers total: 57.35 % (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=71%, ES-P=0%, ES-F=10%, ES-Bf=9%, ES-Ec=10%
- EDS (Enterotype Dysbiosis Score): 0.29 (defined enterotype)
- GMHI (Gut Microbiome Health Index): -0.46 (not healthy (predicted))
- GMWI2 (Chang/Gupta 2024): -0.123 (not healthy) [43S/29NS taxa detected]
- ICB = 7.5% (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: moderate
- 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=-4.28 | 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
 - Roseburia altered (0.74%) — Butyrate producer (*R. intestinalis*), depleted in IBD
 - Ruminococcus altered (0.11%) — Resistant starch degrader (*R. bromii*), key for fiber
 - Prevotella altered (0.11%) — Fiber fermenter, healthy in non-Western diets (*P. copri*)
 - Lactobacillus altered (0.00%) — Probiotic, lactate producer; intestinal barrier support
- Pathogenic alerts (2):
 - [MODERATE] Clostridioides elevated (0.10% > 0.1%) — *C. difficile* detected — clinical significance depends on toxins (tcdA/tcdB), not on abundance; toxinotyping required
 - [MODERATE] Escherichia coli elevated (7.43% > 3.0%) — Commensal overgrowth with no virulence genes detected (STEC/EPEC/EIEC pathotypes only if stx1/stx2/eae/ipaH present in VFDB)
 - ⚠ Shigella detected (0.33%) is probably cross-mapping of enteroinvasive *E. coli* (EIEC, ipaH+). *E. coli* is 22.7x more abundant. Confirm with specific ipaH PCR + MLST if there is compatible clinical presentation.

MODERATE ALERTS (5 alerts)

- Low alpha diversity (Shannon=2.50, lower limit of the healthy range 2.5) — correlate with diet, recent antibiotic therapy or low-grade chronic inflammation
- Dysbiosis index=1.3 — mildly altered
- [MODERATE] Clostridioides elevated (0.10% > 0.1%) — *C. difficile* detected — clinical significance depends on toxins (tcdA/tcdB), not on abundance; toxinotyping required
- [MODERATE] Escherichia coli elevated (7.43% > 3.0%) — Commensal overgrowth with no virulence genes detected (STEC/EPEC/EIEC pathotypes only if stx1/stx2/eae/ipaH present in VFDB)
- DI mildly altered

- Estimated age: 12 years (declared) (based on patient data)

Clinical interpretation

Enterotype ES-B (*Bacteroides*-dominant) with strong membership (0.71). Profile compatible with *Bacteroides*-dominant. Enterotypes represent continuous trends, not discrete categories (Bulygin 2023). Moderate *C. difficile* risk. Monitor clinical course.

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 (HUMAnN 3 + dbCAN 3)

Most represented metabolic pathways (top 10)

Metabolic pathway	Abundance (RPKM)	Clinical interpretation
PWY-7238: sucrose biosynthesis II	6,144	Carbohydrate metabolism — Sucrose biosynthesis. Indicates active bacterial glycolytic activity.
VALSYN-PWY: L-valine biosynthesis	5,506	Amino acid synthesis — Valine

Metabolic pathway	Abundance (RPKM)	Clinical interpretation
		biosynthesis. Basal metabolic activity.
PWY-6386: UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)	5,450	Cell wall synthesis — Peptidoglycan biosynthesis (bacterial cell wall component).
PWY-6385: peptidoglycan biosynthesis III (mycobacteria)	5,406	Cell wall synthesis — Peptidoglycan biosynthesis (mycobacteria).
PWY-6387: UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)	5,373	Cell wall synthesis — Peptidoglycan biosynthesis (bacterial cell wall component).
PEPTIDOGLYCANSYN-PWY: peptidoglycan biosynthesis I (meso-diaminopimelate containing)	5,236	Cell wall synthesis — Peptidoglycan biosynthesis. Fundamental bacterial structure.
PWY-7953: UDP-N-acetylmuramoyl-pentapeptide biosynthesis III (meso-diaminopimelate containing)	5,120	Cell wall synthesis — Peptidoglycan biosynthesis (variant).
DTDPRHAMSYN-PWY: dTDP- β -L-rhamnose biosynthesis	5,103	Cell wall synthesis — dTDP-L-rhamnose biosynthesis (LPS and wall component).
TRNA-CHARGING-PWY: tRNA charging	5,093	Protein synthesis — tRNA charging. Basal translational activity; present in all active bacteria.
NONMEVIPP-PWY: methylerythritol phosphate pathway I	2,528	Bacterial metabolic activity — Bacterial metabolic pathway — part of the basal metabolism of the gut microbiome.

777 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, 9 are housekeeping pathways (basal metabolism: glycolysis, amino acids, nucleotides, cell wall) and 1 is a specialized-metabolism pathway (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] *Escherichia coli* (pathotypes) — MODERATE - Abundance: 0.00% | Reads: 28,426 - Clinical significance: Enteropathogenic *E. coli* virulence genes (stx1/stx2/eae/ipaH/elt/est/aggR/afa) NOT detected by metagenomics. *E. coli* is a ubiquitous commensal of the human gut. Pathogenicity depends on the pathotype determined by specific virulence genes: STEC/STEC (stx1/stx2+eae), EPEC (eae), ETEC (elt/est), EIEC (ipaH), EAEC (aggR/afa). Without these determinants, the detected strain probably represents non-pathogenic commensal colonization. Interpret in clinical context: if there is acute diarrhea or HUS, confirm with multiplex pathotype PCR + Shiga toxin in stool. Mandatory notification (RD 1054/2002) applies only to laboratory-confirmed STEC.

[MODERATE] *Clostridioides difficile* — MODERATE - Abundance: 0.00% | Reads: 2,945 - 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.

9.1.x Taxonomic ambiguities (probable cross-mapping)

△ Note: *Shigella* detected (0.33%) is probably cross-mapping of enteroinvasive *E. coli* (EIEC, ipaH+). *E. coli* is 22.7x more abundant. Confirm with specific ipaH PCR + MLST if there is compatible clinical presentation.

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.

Mycobiome — traces without clinical significance

- Traces of environmental/dietary fungal DNA were detected (12 species: *Aspergillus flavus*, *Candida albicans*, *Candida auris*, *Candida glabrata*, *Candida krusei*...; 1748 total reads) in an immunocompetent outpatient. No clinical significance. Confirm with culture + ITS PCR only if there are risk factors (immunosuppression, hospitalization, TPN, prior antifungals).

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

- Total phage load (325 reads): 0.0050%

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.

9.x Taxonomic ambiguities (probable cross-mapping)

The following findings are flagged as probable cross-mapping with a more abundant taxon. They must not be interpreted as confirmed pathogens; they require specific PCR/MLST before clinical decisions.

- ⚠ Shigella detected (0.33%) is probably cross-mapping of enteroinvasive E. coli (EIEC, ipaH+). E. coli is 22.7x more abundant. Confirm with specific ipaH PCR + MLST if there is compatible clinical presentation.

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
FOLLOW-UP	Routine clinical follow-up. Re-test the microbiome only if symptoms persist or factors change (antibiotherapy, diet, FMT).	Decided by severity — Monitoring	Routine clinical follow-up	Only if symptoms

12. Clinical conclusions

- Dysbiosis index: 1.281 (mildly altered band).
- Enterotype Dysbiosis Score: 0.29 (defined enterotype).
- Reactive commensal expansion of Escherichia coli, Clostridioides difficile without virulence genes (VFDB negative) — does not suggest acute infection. No specific clinical action required.
- 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
- MixS-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), MixS-Human v6.3.0 and ISO/TS 24420:2023 for shotgun metagenomic data processing.