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Name : XXXXXXXX XXXXXXXXXXXX

Date : XX XX XXXX

Test Asked : Welg1

Report Status : Complete Report



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Patient Name	:	XXXXXXXXXXXXXX	Tests Done	:	WELG1
Referred By	:	XXXXXXXXXXXXXX			
Address	:	XXXXXXXXXXXXXX			

Report Availability Summary

Note: Please refer to the table below for status of your tests.

1 Ready | **0** Ready with Cancellation | **0** Processing | **0** Cancelled in Lab

TEST DETAILS	REPORT STATUS
Gut Microbiome	Ready

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Your **Gut Wellness** Report

Microbiome screening report built from species abundance and pathway profile outputs.

Sample ID: XXXXXXXX

Species sample: XXXXX

Sample ID: XXXXXXXX

Pathway sample: XXXXX

Generated: XXXXX

Service version: XXXXXXXXXXX









Just for you

This report summarizes how your uploaded microbiome species and pathway profiles align with internal reference patterns. It combines abundance-based interpretation with pathway-based functional context so the output is easier to read in one place.

The species section highlights the closest reference pattern and the bacterial signals that support or weaken that alignment. The pathway section adds a functional layer by showing the validated pathway call, its support, and the pathway features driving that decision.

This is a screening-oriented interpretation. It is meant to guide review, discussion, and follow-up. It should be read together with symptoms, history, diet, medications, and clinical context rather than used as a standalone diagnostic conclusion.

Your uploaded data is used here only to render this microbiome report view. The output belongs to the user or organization controlling the report workflow. The report content below describes pattern similarity and functional context; it does not by itself confirm or exclude disease.

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Definitions

Primary species pattern

The dominant microbiome classification based on species-level signals from the model.

Primary pathway pattern

The top predicted functional profile based on pathway probabilities.

Support-adjusted top call

A refined pathway prediction that combines model probability with pathway overlap (Jaccard similarity).

Alternate pattern

The second-highest predicted class from the model, representing a nearby functional or species state.

Support

The product of model probability and pathway overlap, used to validate predictions.

Margin

The difference between top and second support scores, indicating confidence.

Jaccard overlap

A similarity metric measuring overlap between sample pathways and reference pathways: intersection / union.

End of Definitions

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02 **How to Read This Report**
A short introduction to how this microbiome screening report should be interpreted.

05 **Results Summary**
Headline microbiome metrics including species wellness, pathway wellness, diversity, and pathway decision.

06 **Nutritionist Recommendations**
Personalized food and lifestyle suggestions aligned with your microbiome screening profile.

07 **Sample Gut-Friendly Day**
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08 **Species Interpretation**
A narrative explanation of the abundance-pattern call and the species driving and opposing that pattern.

09 **Pathway Summary**
A functional overview of the pathway call, its support, and the pathways that reinforce or weaken it.

12 **Screening use note**
How to interpret screening-oriented outputs and when to seek qualified clinical or nutrition follow-up.

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Your Gut Wellness Report

Sample ID
XXXXXXXXX

Age
XX

Gender
XX

Location
Mumbai

Collection Date
10-6-2026

Overall Status
Moderate

Gut Snapshot

Microbial Diversity — GOOD

Microbial Balance — EXCELLENT

Functional Activity — LIMITED

Wellness Profile — MODERATE

Good variety, but the gut is more skewed than typical healthy patterns

Your gut shows diversity that is broadly in range and even a bit higher than expected, which is a strength. The main issue is balance: the major gut groups are not as balanced as typical healthy patterns, and a few bacteria appear to be carrying more influence than usual. That means this gut may have decent variety but still be less steady and less resilient than it looks at first glance. The activity pattern in the microbiome also leans toward more fermentation and protein breakdown than ideal, which can go along with gas, bloating, uneven digestion, or gut irritation in some people, especially around harder-to-tolerate foods. This kind of pattern may reflect lower fiber intake, lower diet variety, or a more refined or processed-food heavy pattern, although diet cannot be confirmed from this test alone. The food IgG panel also flagged immune exposure signals to foods such as almond, almond milk, and chickpea; these are not allergy results, but they may help guide cautious food rotation alongside symptoms.

- Diversity is a relative strength here, but balance between the main gut groups is reduced, which matters more than variety alone.
- A few less favorable microbes seem to have more influence than usual, making the overall pattern more constrained and in need of attention rather than fully steady.
- The gut activity pattern may fit with gas, bloating, uneven digestion, or food sensitivity in real life, especially if meals are low in fiber or heavily refined.

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Headline Interpretation

SPECIES PREDICTION

Healthy

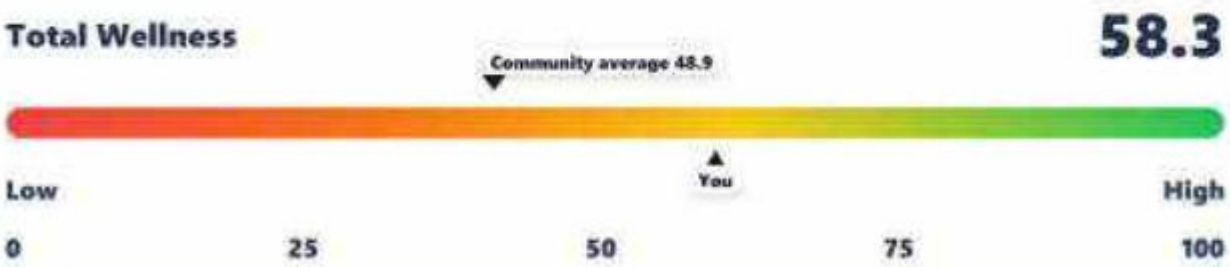
The microbial abundance profile is more closely aligned with the healthy reference pattern in this screening model. This output should be interpreted as a screening-oriented pattern similarity result rather than a diagnosis.

PATHWAY PREDICTION

Mixed functional signals

Functional pathway interpretation: **Mixed functional signals**.

Total Wellness



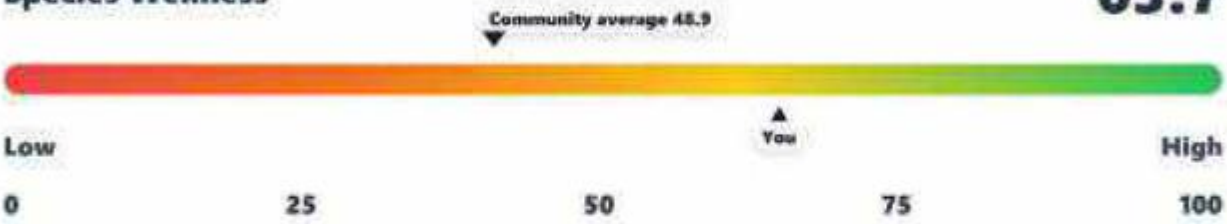
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Species Wellness

Healthy

Species Wellness **63.7**



Pathway Wellness

Mixed functional signals

Pathway Wellness **42.1**



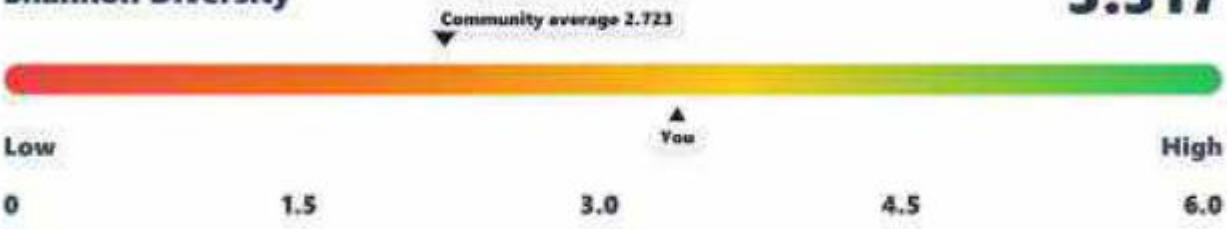
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Microbiome Diversity

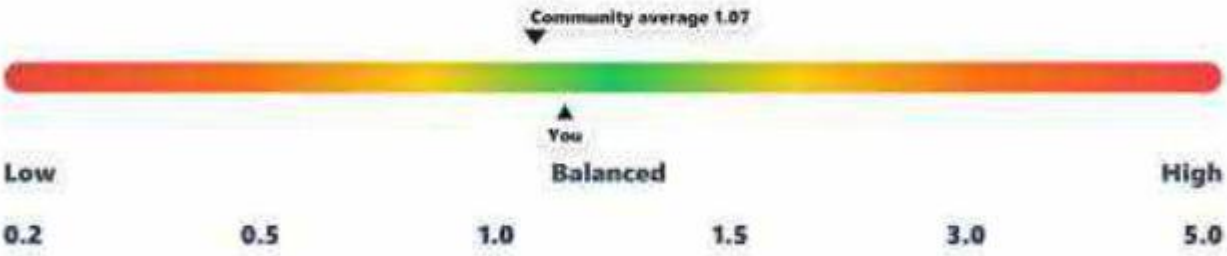
Moderate Diversity

Shannon Diversity **3.317**



Gut Balance (Firmicutes vs Bacteroidetes)

F/B Ratio **0.88**



AGE USED

45

Years included during inference.

PATHWAY SUPPORT

0.028

Support score for the selected pathway call. Healthy median: 0.142

Mixed functional signals

SPECIES MARGIN

2.389

Raw margin from the species wellness model. Healthy median: 2.067

Healthy

Higher pathway support and species margin are favourable for healthy profiles; lower values are favourable for non-healthy profiles.

SHARED ENRICHED PATHWAYS ACROSS TOP PREDICTIONS

- L-lysine fermentation to acetate and butanoate
- formaldehyde assimilation III (dihydroxyacetone cycle)
- methanogenesis from acetate
- superpathway of adenosine nucleotides de novo biosynthesis I

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Nutritionist Recommendations

Personalized food and lifestyle suggestions based on your microbiome profile.

01 Use cooled rice or millet more often: Try meals built around cooled rice, lemon rice made from previously cooked rice, or curd rice only if tolerated; on other days rotate with ragi dosa, kambu koozh, or little millet upma.

02 Choose gentler dals first: Prefer soaked and well-cooked moong dal, masoor dal, or thin dal in sambar-style meals before using heavier mixed-legume dishes; add jeera, ginger, hing, or ajwain during cooking.

03 Keep one simple fermented food daily if tolerated: Use plain homemade dahi, unsweetened curd, idli, or dosa batter-based foods in simple meals rather than very spicy, oily, or heavily stuffed fermented foods.

04 Build lunches around cooked vegetables and sabzi variety: Include two cooked plant foods at lunch such as beans poriyal with pumpkin, bhindi with carrot, or cabbage with peas, using simple tempering with mustard, curry leaves, jeera, and minimal frying.

05 Reduce frequent fried and ultra-processed snacks: Cut back on bakery biscuits, chips, mixtures, deep-fried snacks, instant noodles, and repeated take-away meals; replace with roasted makhana, fruit with pumpkin seeds, or plain sundal only if tolerated.

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06 Use protein foods in simpler combinations: Keep heavier protein meals simpler, such as fish curry with rice and cooked vegetable, egg with dosa and chutney, or dal-rice with one sabzi, instead of combining multiple rich proteins in one meal.

07 Be cautious with almond and chickpea exposure: Because almond, almond milk, and chickpea were flagged in the wider report, avoid making them daily staples for now; if you use them, watch tolerance, rotate them, and discuss with a clinician or dietitian if symptoms are consistent.

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Sample Gut-Friendly Day

A microbiome-informed preview of how your daily meals could look, based on your current gut patterns.

BREAKFAST

Idli with gentle sides

VEG	Idli with vegetable sambar and coconut chutney with ginger
NON-VEG	Idli with egg white masala on the side and light sambar
VEGAN	Idli with vegetable sambar and coconut-mint chutney

WHY THIS WORKS

This is a familiar, softer, fermented breakfast that may feel lighter than oily breakfast choices and may be easier to tolerate when digestion feels uneven.

- fermentation burden
- sensitivity or uncertainty

MORNING SNACK

Fruit and seed snack

VEG	Guava or papaya with a small sprinkle of pumpkin or sunflower seeds
NON-VEG	Guava or papaya with a side of plain unsweetened curd if tolerated
VEGAN	Guava or papaya with pumpkin or sunflower seeds

WHY THIS WORKS

A simple snack like this adds plant variety without relying on fried or bakery foods and may be easier on the gut than heavy snack mixes.

- dysbiosis

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LUNCH

Rice, dal, fish or sabzi plate

VEG	Cooked rice with moong dal, pumpkin poriyal, and cucumber pachadi only if tolerated
NON-VEG	Cooked rice with simple fish curry, snake gourd poriyal, and thin rasam
VEGAN	Cooked rice with moong dal, pumpkin poriyal, and jeera rasam

WHY THIS WORKS

A simple lunch pattern may lower meal complexity, support starch-based fermentation, and avoid the heaviness of rich mixed dishes.

- metabolic weakness
- fermentation burden

EVENING SNACK

Light savory tiffin snack

VEG	Roasted makhana or aval upma with ginger and curry leaves
NON-VEG	Roasted makhana with spiced buttermilk if tolerated
VEGAN	Aval upma with ginger, curry leaves, and grated coconut

WHY THIS WORKS

This may be gentler than fried snacks and may help reduce exposure to refined, oily foods that can aggravate an imbalanced gut pattern.

- dysbiosis

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DINNER

Ragi dosa with cooked vegetable side

VEG	Ragi dosa with lauki or chow chow kootu and mint chutney
NON-VEG	Ragi dosa with a simple egg bhurji and cooked spinach
VEGAN	Ragi dosa with lauki kootu made without dairy and mint chutney

WHY THIS WORKS

A lighter dinner with millet and cooked sides may suit a gut showing mixed robustness, especially if late heavy meals trigger gas or bloating.

- bloating tendency
- mixed gut robustness

This preview is suggestive and designed to translate your microbiome insights into practical meal ideas. It is not a medical or therapeutic meal plan.

This sample day is suggestive and intended as a general microbiome-informed food guide. It is not a medical or therapeutic nutrition plan. If you have known food allergies, intolerances, digestive conditions, or other medical concerns, consult a qualified nutritionist or healthcare professional before making significant dietary changes.

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Species Interpretation

Reference Healthy Pattern **Healthy**

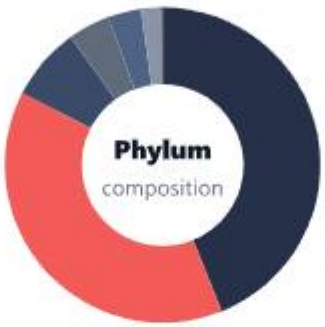
The microbial abundance profile is more closely aligned with the healthy reference pattern in this screening model. This output should be interpreted as a screening-oriented pattern similarity result rather than a diagnosis.

MICROBIAL INTERPRETATION

The species-level evidence indicates mixed signals supporting health but also meaningful opposing contributions. Two highly abundant opposing species, *Bacteroides coprocola* and *Firmicutes bacterium CAG 555*, counterbalance several supportive species including *Ruminococcus lactaris* and Roseburia sp CAG 182. While most supportive species have moderate evidence strength, *Firmicutes bacterium CAG 555* has limited evidence but notable abundance. The opposing burden rivals the supportive burden, signaling a guarded concern overall.

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Phylum-Level Composition



This sample's phylum-level profile is dominated by Bacteroidetes (43.9%), Firmicutes (38.7%), Proteobacteria (7.5%). The chart is computed directly from **phylum_relative_abundance** in `sample_species_predictions.json`.

Bacteroidetes	43.9%
Firmicutes	38.7%
Proteobacteria	7.5%
Lentisphaerae	4.3%
Actinobacteria	3.4%
Verrucomicrobia	2.1%
Euryarchaeota	0.1%
Viruses Unclassified	0.0%

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Evidence-Backed Species Interpretation

Primary species call: Healthy

Supporting species shown: 9

Opposing species shown: 5

Most credible supportive signals

Supportive

- *Ruminococcus lactaris*
- Roseburia sp. CAG 182
- *Bilophila wadsworthia*

Roseburia sp CAG 182

Limited evidence | Unclear

EVIDENCE NOTES

Evidence limited to associations with healthy dietary and microbiome patterns in humans

GUT-RELATED FUNCTIONS

- short-chain fatty acid production
- fermentation

REPORTED ASSOCIATIONS

Not specified

CITATIONS

- Tarallo et al., 2022
- Jacky et al., 2023

Ruminococcus lactaris

Moderate evidence | Unclear

EVIDENCE NOTES

Moderate evidence including human genetic and microbiome association studies

GUT-RELATED FUNCTIONS

- fermentation
- possible gut barrier involvement

REPORTED ASSOCIATIONS

Not specified

CITATIONS

- Fu et al., 2024
- Togo et al., 2018
- Li et al., 2025
- Doumatey et al., 2020

Bifidobacterium catenulatum

Moderate evidence | Unclear

EVIDENCE NOTES

Moderate evidence primarily from immunological and allergy studies

GUT-RELATED FUNCTIONS

- fermentation
- immune modulation

REPORTED ASSOCIATIONS

Not specified

CITATIONS

- Melli et al., 2016
- Zha et al., 2022
- Huang et al., 2025
- Ismail et al., 2016

Bilophila wadsworthia

Moderate evidence | Unclear

EVIDENCE NOTES

Evidence indicates role in diet-related microbiome changes; potential relevance to inflammation

GUT-RELATED FUNCTIONS

- fermentation
- possible inflammatory modulation

REPORTED ASSOCIATIONS

Not specified

CITATIONS

- David et al., 2014
- Verhaar et al., 2021
- Fackelmann et al., 2025
- Liu et al., 2024

Anaerotruncus colihominis

Moderate evidence | Unclear

EVIDENCE NOTES

Moderate multi-omic and animal model evidence with emerging functional context

GUT-RELATED FUNCTIONS

- fermentation
- glutamate metabolism

REPORTED ASSOCIATIONS

Not specified

CITATIONS

- Yoon et al., 2025
- Deng et al., 2025
- Chang et al., 2025
- Han et al., 2024

Lactobacillus ruminis

Moderate evidence | Unclear

EVIDENCE NOTES

Moderate evidence from human and functional studies including schizophrenia microbiome context

GUT-RELATED FUNCTIONS

- fermentation
- immune modulation

REPORTED ASSOCIATIONS

Not specified

CITATIONS

- Wang et al., 2024
- Wang et al., 2020
- Taweechotipatr et al., 2009
- Rahayu et al., 2019

Holdemanella biformis

Moderate evidence | Context-dependent

EVIDENCE NOTES

Moderate evidence highlighting anti-inflammatory and immune modulation potential

GUT-RELATED FUNCTIONS

- anti-inflammatory
- immune cell modulation

REPORTED ASSOCIATIONS

Not specified

CITATIONS

- Wang et al., 2026
- Pujo et al., 2021
- Yamada et al., 2021
- Huang et al., 2024

Eubacterium sp OM08 24

Limited evidence | Unclear

EVIDENCE NOTES

No supporting literature evidence retrieved

GUT-RELATED FUNCTIONS

- fermentation

REPORTED ASSOCIATIONS

Not specified

Intestinimonas butyriciproducens

Moderate evidence | Unclear

EVIDENCE NOTES

Moderate evidence from cohort and functional animal intervention studies

GUT-RELATED FUNCTIONS

- butyrate production
- metabolic health improvement

REPORTED ASSOCIATIONS

Not specified

CITATIONS

- Rampanelli et al., 2025
- Bui et al., 2016
- Lin et al., 2025
- Kläring et al., 2013

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Most credible opposing signals

Opposing

- *Bacteroides coprocola*
- *Firmicutes bacterium CAG 555*
- *Bacteroides plebeius*

Firmicutes bacterium CAG 555

Limited evidence | Unclear

EVIDENCE NOTES

Limited evidence mostly from pathogenic strain toxin gene studies

GUT-RELATED FUNCTIONS

Not specified

REPORTED ASSOCIATIONS

Not specified

CITATIONS

- O'Reilly et al., 1990
- Ning et al., 2022

Bacteroides coprocola

Moderate evidence | Unclear

EVIDENCE NOTES

Moderate evidence from metabolic and diabetes-related gut microbiome studies

GUT-RELATED FUNCTIONS

- carbohydrate metabolism
- short-chain fatty acid production

REPORTED ASSOCIATIONS

Not specified

CITATIONS

- Vallianou et al., 2023
- Gu et al., 2024
- Kitahara et al., 2005
- Chen et al., 2017

Leuconostoc garlicum

Limited evidence | Unclear

EVIDENCE NOTES

No literature evidence retrieved

GUT-RELATED FUNCTIONS

Not specified

REPORTED ASSOCIATIONS

Not specified

Bacteroides plebeius

Moderate evidence | Context-dependent

EVIDENCE NOTES

Moderate evidence in cancer and immune-related microbiome studies

GUT-RELATED FUNCTIONS

- carbohydrate metabolism

REPORTED ASSOCIATIONS

Not specified

CITATIONS

- Kim et al., 2024
- Chen et al., 2025
- Chen et al., 2025
- Liang et al., 2022

Acidaminococcus sp CAG 542

Limited evidence | Unclear

EVIDENCE NOTES

No supporting literature evidence retrieved

GUT-RELATED FUNCTIONS

Not specified

REPORTED ASSOCIATIONS

Not specified

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Uncertain or weakly characterized signals

- Eubacterium sp. OM08 24
- *Leuconostoc garlicum*
- Acidaminococcus sp. CAG 542

Important caution: The presence at moderate to high abundance of opposing species associated with metabolic and immune disturbances warrants caution. Although some beneficial species are present, the overall balance of species and supporting evidence suggests close monitoring of gut health. The mixed microbial pattern and meaningful opposing burden reduce confidence in a strongly healthy gut microbiome status.

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Pathway Summary

Pathway Summary

Primary pathway call: Mixed functional signals

Support-adjusted top call: Healthy

Canonicality: Non Canonical

Pathway wellness: 42.1/100

The support-adjusted call combines probability with Jaccard overlap for more robust classification.

OVERALL INTERPRETATION

Your pathway profile shows some healthy functional signals, but overall it appears more mixed and less balanced than ideal.

PATHWAY INTERPRETATION

Gut health relevance is mixed; while a few supporting pathways indicate moderate to high relevance for microbial growth and energy metabolism, opposing pathways with high gut health relevance suggest elevated protein catabolism and fermentation burdens associated with irritation and inflammation.

Pathway signals related to imbalance show both support and opposition, with opposing pathways indicating notable burden, especially in proteolytic metabolism and fermentation stress, and supporting pathways moderately related to amino acid biosynthesis and energy balance.

Intolerance-related pathways are present on both sides but are more strongly represented among opposing pathways linked to fermentation and protein catabolism, suggesting a potential intolerance risk; supporting pathways generally show limited relevance to intolerance.

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Protein / Amino Acid Metabolism

Leaning less favorable

This category shows more amino-acid breakdown than ideal, which can go with stress or inflammatory pressure.

HELPFUL PATTERNS

- L-isoleucine biosynthesis I (from threonine)
  Amino Acid Biosynthesis | Microbial anabolic capacity
- L-lysine fermentation to acetate and butanoate
  SCFA / Saccharolytic Fermentation | Gut protection

POTENTIAL CONCERNS

- superpathway of L-citrulline metabolism
  Other Functional Metabolism | Mixed or unclear functional significance
- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
  Cell Envelope / Pro-inflammatory Structures | Inflammatory pressure
- tRNA charging
  Growth / Replication Housekeeping | Microbial turnover
- L-glutamate degradation V (via hydroxyglutarate)
  Protein / Nitrogen Catabolism | Protein putrefaction burden

Carbohydrate Metabolism

Leaning less favorable

This category suggests heavier fermentation or less efficient carbohydrate handling.

HELPFUL PATTERNS

- superpathway of fermentation (Chlamydomonas reinhardtii)

POTENTIAL CONCERNS

- starch degradation V

  Carbohydrate Fermentation / Energy Harvest Fermentation load

- pyruvate fermentation to acetate and lactate II

  Carbohydrate Fermentation / Energy Harvest Fermentation load

Energy Metabolism

Leaning favourable

Energy generation looks more efficient overall, with stronger respiration-type activity.

HELPFUL PATTERNS

- nitrate reduction VI (assimilatory)

  Energy Metabolism Microbial energy efficiency

- formaldehyde oxidation I

  Energy Metabolism Microbial energy efficiency

POTENTIAL CONCERNS

- superpathway of sulfur oxidation (Acidianus ambivalens)

  Other Functional Metabolism Mixed or unclear functional significance

Nucleotide / DNA-RNA Metabolism

Less favorable

Higher nucleotide-building or turnover signals can reflect faster microbial turnover in a stressed gut state.

POTENTIAL CONCERNS

- adenosine deoxyribonucleotides de novo biosynthesis II

  Growth / Replication Housekeeping Microbial turnover

- purine nucleobases degradation I (anaerobic)

  Protein / Nitrogen Catabolism Protein putrefaction burden

Cell Structure / Bacterial Growth

Less favorable

Growth and cell-structure signals look less balanced than ideal.

POTENTIAL CONCERNS

- peptidoglycan biosynthesis III (mycobacteria)

  Cell Envelope / Pro-inflammatory Structures Inflammatory pressure

- dTDP-N-acetylthomosamine biosynthesis

  Other Functional Metabolism Mixed or unclear functional significance

Detox / Compound Processing

Favourable

These pathways suggest the microbiome is handling a range of compounds reasonably well.

HELPFUL PATTERNS

- superpathway of allantoin degradation in yeast

Other Functional Pathways

Leaning less favorable

These pathways matter but do not fit neatly into one major metabolism bucket.

HELPFUL PATTERNS

- taxadiene biosynthesis (engineered)

POTENTIAL CONCERNS

- inosine-5'-phosphate biosynthesis III

  Growth / Replication Housekeeping Microbial turnover

- phosphatidate metabolism, as a signaling molecule

  Neuroactive / Amine Signaling Biogenic amine tendency

In simple terms, this pathway profile is **mixed functional signals**-leaning (support-adjusted: **healthy**), but not perfectly clean. The strongest story comes from the category cards above, which separate functions that look more supportive from those that appear more mixed or less favorable.

Top Functional Predictions

Prediction 1

Class: CRC

Probability: 0.295

Support: 0.000

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Pathway Validation Snapshot

Selected Functional Pattern

Decision: Healthy

Canonicality: Non Canonical

Support: 0.028

Pathway Drivers

Class-Agnostic Top Pathways

#	Pathway	Mean |SHAP|
1	superpathway of sulfur oxidation (Acidianus ambivalens)	0.2607
2	aerobic respiration I (cytochrome c)	0.2246
3	superpathway of L-tyrosine biosynthesis	0.1742
4	pyrimidine deoxyribonucleosides salvage	0.1271
5	L-lysine fermentation to acetate and butanoate	0.1264
6	L-isoleucine biosynthesis II	0.1173
7	nitrate reduction VI (assimilatory)	0.0985
8	L-glutamate degradation V (via hydroxyglutarate)	0.0985
9	6-hydroxymethyl-dihydropterin diphosphate biosynthesis III (Chlamydia)	0.0929
10	phytol degradation	0.0919
11	L-arginine biosynthesis III (via N-acetyl-L-citrulline)	0.0911
12	methanogenesis from acetate	0.0909
13	tRNA charging	0.0886
14	superpathway of adenosine nucleotides de novo biosynthesis I	0.0884
15	biotin biosynthesis II	0.0861
16	Bifidobacterium shunt	0.0854
17	sucrose degradation III (sucrose invertase)	0.0828
18	L-tryptophan biosynthesis	0.0810
19	γ-glutamyl cycle	0.0794
20	flavin biosynthesis I (bacteria and plants)	0.0781

Appendix

The tables below summarize the top 10 species and pathway drivers for and against the selected patterns.

Species Driver Tables

Species Supporting the Selected Pattern

#	Species	Contribution	Direction
1	*Roseburia sp. CAG 182*	0.1249	Supports pattern
2	*Ruminococcus lactaris*	0.0811	Supports pattern
3	*Bifidobacterium catenulatum*	0.0745	Supports pattern
4	*Bilophila wadsworthia*	0.0731	Supports pattern
5	*Anaerotruncus colihominis*	0.0643	Supports pattern
6	*Lactobacillus ruminis*	0.0617	Supports pattern
7	*Holdemanella biformis*	0.0569	Supports pattern
8	*Eubacterium sp. OM08 24*	0.0558	Supports pattern
9	*Flavonifractor plautii*	0.0490	Supports pattern
10	*Intestinimonas butyriciproducens*	0.0436	Supports pattern

Species Acting Against the Selected Pattern

#	Species	Contribution	Direction
1	*Firmicutes bacterium CAG 555*	-0.1441	Acts against pattern
2	*Bacteroides coprocola*	-0.1343	Acts against pattern
3	*Streptococcus salivarius*	-0.0916	Acts against pattern
4	*Leuconostoc garlicum*	-0.0772	Acts against pattern
5	*Bacteroides plebeius*	-0.0605	Acts against pattern
6	*Gordonibacter pamelaeae*	-0.0586	Acts against pattern
7	*Ruminococcus bromii*	-0.0540	Acts against pattern
8	*Eubacterium sp. CAG 38*	-0.0477	Acts against pattern
9	*Acidaminococcus sp. CAG 542*	-0.0403	Acts against pattern
10	*Bifidobacterium breve*	-0.0361	Acts against pattern

Pathway Driver Tables

Pathways Supporting the Selected Functional Pattern

#	Pathway	SHAP	Direction
1	superpathway of L-citrulline metabolism	0.1118	Supports pattern
2	inosine-5'-phosphate biosynthesis III	0.1111	Supports pattern
3	nitrate reduction VI (assimilatory)	0.1014	Supports pattern
4	superpathway of allantoin degradation in yeast	0.0872	Supports pattern
5	UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)	0.0752	Supports pattern
6	peptidoglycan biosynthesis III (mycobacteria)	0.0749	Supports pattern
7	L-isoleucine biosynthesis I (from threonine)	0.0746	Supports pattern
8	tRNA charging	0.0662	Supports pattern
9	starch degradation V	0.0611	Supports pattern
10	formaldehyde oxidation I	0.0532	Supports pattern

Pathways Acting Against the Selected Functional Pattern

#	Pathway	SHAP	Direction
1	L-glutamate degradation V (via hydroxyglutarate)	-0.1932	Acts against pattern
2	L-lysine fermentation to acetate and butanoate	-0.1332	Acts against pattern
3	adenosine deoxyribonucleotides de novo biosynthesis II	-0.1315	Acts against pattern
4	superpathway of sulfur oxidation (Acidianus ambivalens)	-0.0932	Acts against pattern
5	dTDP-N-acetylthomosamine biosynthesis	-0.0895	Acts against pattern
6	pyruvate fermentation to acetate and lactate II	-0.0846	Acts against pattern
7	purine nucleobases degradation I (anaerobic)	-0.0833	Acts against pattern
8	phosphatidate metabolism, as a signaling molecule	-0.0790	Acts against pattern
9	superpathway of fermentation (Chlamydomonas reinhardtii)	-0.0789	Acts against pattern

#	Pathway	SHAP	Direction
10	taxadiene biosynthesis (engineered)	-0.0704	Acts against pattern

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Screening Note

Screening Use Note

This output is generated from a microbiome screening model and is intended to describe similarity of bacterial abundance patterns and functional pathway signatures to internal reference groups. It should not be used alone to diagnose, exclude, or confirm a medical condition.

This report presents screening-oriented microbiome pattern interpretation for wellness review and guided follow-up. It is not a standalone diagnostic report.

Evidence

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CUSTOMER DETAILS

As declared in our data base

Name: XXXXXXXXXX **Age:** XX **Sex:** XXXX

Barcodes/Sample_Type	:	XXXXXXXXXXXXXXX
Labcode	:	XXXXXXXXXXXXXXX
Ref By	:	XXXXXXXXXXXXXXX
Sample_Type/Tests	:	STOOL SAMPLE WI:WELG1
Address	:	XXXXXXXXXXXXXXX
Sample Collected on (SCT)	:	XXXXXXXXXXXXXXX
Report Released on (RRT)	:	XXXXXXXXXXXXXXX
Amount Collected	:	-

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CONDITIONS OF REPORTING

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EXPLANATIONS

- Majority of the specimen processed in the laboratory are collected by Pathologists and Hospitals we call them as "Clients".
- **Name** - The name is as declared by the client and recored by the personnel who collected the specimen.
- **Ref.Dr** - The name of the doctor who has recommended testing as declared by the client.
- **Labcode** - This is the accession number in our laboratory and it helps us in archiving and retrieving the data.
- **Barcode** - This is the specimen identity number and it states that the results are for the specimen bearing the barcode (irrespective of the name).
- **SCP** - Specimen Collection Point - This is the location where the blood or specimen was collected as declared by the client.
- **SCT** - Specimen Collection Time - The time when specimen was collected as declared by the client.
- **SRT** - Specimen Receiving Time - This time when the specimen reached our laboratory.
- **RRT** - Report Releasing Time - The time when our pathologist has released the values for Reporting.
- **Reference Range** - Means the range of values in which 95% of the normal population would fall.

SUGGESTIONS

- Values out of reference range requires reconfirmation before starting any medical treatment.
- Retesting is needed if you suspect any quality shortcomings.
- Testing or retesting should be done in accredited laboratories.
- For suggestions, complaints, clinical support or feedback, write to us at **customersupport@thyrocare.com** or call us on **022-3090 0000**





+ *T&C Apply, #As on 5th December 2024 (Applicable for all company owned labs except Bhagalpur & Vijayawada),*

• *As per survey on doctors' perception of laboratory diagnostics (IJARIIT, 2023), -Mumbai Reference Lab is CAP Accredited*