

YOUR PERSONALIZED REPORT

PATHOGENS

The GI-MAP® includes pathogens (bacterial, parasitic and viral) commonly known to cause gastroenteritis. Note that not all individuals with positive findings will present with symptoms. Many factors, including the health of the individual (such as immune health, digestive function, and microbiome balance), the transient nature of most pathogens, and the presence and expression of virulence factors, all contribute to pathogen virulence and individual symptoms.

| BACTERIAL PATHOGENS | Result | Reference |
|---|----------------------|-----------|
| <i>Campylobacter</i> | < dl | < 1.00e3 |
| <i>C. difficile</i> Toxin A | 1.21e5 High ↑ | < 1.00e3 |
| <i>C. difficile</i> Toxin B | 2.27e5 High ↑ | < 1.00e3 |
| <i>Enterohemorrhagic E. coli</i> | < dl | < 1.00e3 |
| <i>E. coli</i> O157 | < dl | < 1.00e3 |
| Enteroinvasive <i>E. coli</i> / <i>Shigella</i> | < dl | < 1.00e2 |
| Enterotoxigenic <i>E. coli</i> LT/ST | < dl | < 1.00e3 |
| Shiga-like Toxin <i>E. coli</i> stx1 | < dl | < 1.00e3 |
| Shiga-like Toxin <i>E. coli</i> stx2 | < dl | < 1.00e3 |
| <i>Salmonella</i> | < dl | < 1.00e4 |
| <i>Vibrio cholerae</i> | < dl | < 1.00e5 |
| <i>Yersinia enterocolitica</i> | 4.46e3 | < 1.00e5 |
| PARASITIC PATHOGENS | | |
| <i>Cryptosporidium</i> | < dl | < 1.00e6 |
| <i>Entamoeba histolytica</i> | < dl | < 1.00e4 |
| <i>Giardia</i> | < dl | < 5.00e3 |
| VIRAL PATHOGENS | | |
| Adenovirus 40/41 | < dl | < 1.00e10 |
| Norovirus GI/II | < dl | < 1.00e7 |

KEY: Results are reported as genome equivalents per gram of stool, which is a standard method for estimating the number of microbes measured per gram of stool, based on qPCR analysis of DNA samples.

Results are expressed in standard scientific notation. For example, a reported result of 3.5e7 is equivalent to 3.5 x 10⁷ microbes per gram, which equals 35,000,000 (35 million) microbes per gram of stool.

< dl represents results below detectable limit.

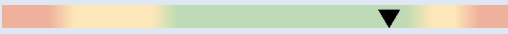





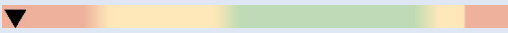


HELICOBACTER PYLORI

H. PYLORI & VIRULENCE FACTORS


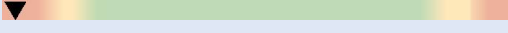

| | Result | Reference |
|-----------------------------------|----------------------|-----------|
| <i>Helicobacter pylori</i> | 2.90e3 High ↑ | < 1.00e3 |
| Virulence Factor, babA | Positive | Negative |
| Virulence Factor, cagA | Positive | Negative |
| Virulence Factor, dupA | Negative | Negative |
| Virulence Factor, iceA | Negative | Negative |
| Virulence Factor, oipA | Negative | Negative |
| Virulence Factor, vacA | Negative | Negative |
| Virulence Factor, virB | Positive | Negative |
| Virulence Factor, virD | Positive | Negative |

COMMENSAL/KEYSTONE BACTERIA

COMMENSAL BACTERIA

| | Result | Reference |
|-------------------------------------|--|----------------|
| <i>Bacteroides fragilis</i> | 8.98e10  | 1.6e9 - 2.5e11 |
| <i>Bifidobacterium</i> spp. | 1.89e10  | > 6.7e7 |
| <i>Enterococcus</i> spp. | 2.45e7  | 1.9e5 - 2.0e8 |
| <i>Escherichia</i> spp. | 2.14e8  | 3.7e6 - 3.8e9 |
| <i>Lactobacillus</i> spp. | 6.55e6  | 8.6e5 - 6.2e8 |
| <i>Enterobacter</i> spp. | 2.07e6  | 1.0e6 - 5.0e7 |
| <i>Akkermansia muciniphila</i> | <dl L  | 1.0e1 - 8.2e6 |
| <i>Faecalibacterium prausnitzii</i> | 5.66e5  | 1.0e3 - 5.0e8 |
| <i>Roseburia</i> spp. | 7.91e5 L  | 5.0e7 - 2.0e10 |

BACTERIAL PHYLA

| | | |
|---------------------------------------|---|-----------------|
| <i>Bacteroidetes</i> | 1.21e12  | 8.6e11 - 3.3e12 |
| <i>Firmicutes</i> | 4.70e10 L  | 5.7e10 - 3.0e11 |
| <i>Firmicutes:Bacteroidetes Ratio</i> | 0.04  | < 1.0 |

OPPORTUNISTIC/OVERGROWTH MICROBES

DYSBIOTIC & OVERGROWTH BACTERIA

| DYSBIOTIC & OVERGROWTH BACTERIA | Result | Reference |
|---------------------------------|--------|-----------|
| <i>Bacillus</i> spp. | 2.56e5 | < 1.76e6 |
| <i>Enterococcus faecalis</i> | 1.81e3 | < 1.00e4 |
| <i>Enterococcus faecium</i> | < dl | < 1.00e4 |
| <i>Morganella</i> spp. | < dl | < 1.00e3 |
| <i>Pseudomonas</i> spp. | < dl | < 1.00e4 |
| <i>Pseudomonas aeruginosa</i> | < dl | < 5.00e2 |
| <i>Staphylococcus</i> spp. | < dl | < 1.00e4 |
| <i>Staphylococcus aureus</i> | 3.83e2 | < 5.00e2 |
| <i>Streptococcus</i> spp. | < dl | < 1.00e3 |

COMMENSAL OVERGROWTH MICROBES

| | | |
|-------------------------------------|--------|----------|
| <i>Desulfovibrio</i> spp. | 1.84e3 | < 7.98e8 |
| <i>Methanobacteriaceae</i> (family) | 1.24e8 | < 3.38e8 |

INFLAMMATORY & AUTOIMMUNE-RELATED BACTERIA

| | | |
|--|------|----------|
| <i>Citrobacter</i> spp. | < dl | < 5.00e6 |
| <i>Citrobacter freundii</i> | < dl | < 5.00e5 |
| <i>Klebsiella</i> spp. | < dl | < 5.00e3 |
| <i>Klebsiella pneumoniae</i> | < dl | < 5.00e4 |
| <i>M. avium</i> subsp. <i>paratuberculosis</i> | < dl | < 5.00e3 |
| <i>Proteus</i> spp. | < dl | < 5.00e4 |
| <i>Proteus mirabilis</i> | < dl | < 1.00e3 |

COMMENSAL INFLAMMATORY & AUTOIMMUNE-RELATED BACTERIA

| | | |
|---------------------------|--------|----------|
| <i>Enterobacter</i> spp. | 2.07e6 | < 5.00e7 |
| <i>Escherichia</i> spp. | 2.14e8 | < 3.80e9 |
| <i>Fusobacterium</i> spp. | 2.56e7 | < 1.00e8 |
| <i>Prevotella</i> spp. | 3.86e7 | < 1.00e8 |

FUNGI/YEAST

FUNGI/YEAST

| FUNGI/YEAST | Result | Reference |
|----------------------------|----------------------|-----------|
| <i>Candida</i> spp. | 4.53e4 High ↑ | < 5.00e3 |
| <i>Candida albicans</i> | < dl | < 5.00e2 |
| <i>Geotrichum</i> spp. | < dl | < 3.00e2 |
| <i>Microsporidium</i> spp. | < dl | < 5.00e3 |
| <i>Rhodotorula</i> spp. | < dl | < 1.00e3 |

VIRUSES

VIRUSES

| VIRUSES | Result | Reference |
|--------------------|--------|-----------|
| Cytomegalovirus | < dl | < 1.00e5 |
| Epstein-Barr Virus | < dl | < 1.00e7 |

PARASITES

| PROTOZOA | Result | Reference |
|---------------------------------|--------------|--------------|
| <i>Blastocystis hominis</i> | < dl | < 2.00e3 |
| <i>Chilomastix mesnili</i> | < dl | < 1.00e5 |
| <i>Cyclospora</i> spp. | < dl | < 5.00e4 |
| <i>Dientamoeba fragilis</i> | < dl | < 1.00e5 |
| <i>Endolimax nana</i> | < dl | < 1.00e4 |
| <i>Entamoeba coli</i> | < dl | < 5.00e6 |
| <i>Pentatrichomonas hominis</i> | < dl | < 1.00e2 |
| WORMS | | |
| <i>Ancylostoma duodenale</i> | Not Detected | Not Detected |
| <i>Ascaris lumbricoides</i> | Not Detected | Not Detected |
| <i>Necator americanus</i> | Not Detected | Not Detected |
| <i>Trichuris trichiura</i> | Not Detected | Not Detected |
| <i>Taenia</i> spp. | Not Detected | Not Detected |

INTESTINAL HEALTH MARKERS

| DIGESTION | Result | Reference |
|---|---|-----------------|
| Steatocrit | <dl  | < 15 % |
| Elastase-1 | >750  | > 200 ug/g |
| GI MARKERS | | |
| β-Glucuronidase | 2584 H  | < 2486 U/mL |
| Occult Blood - FIT | 0  | < 10 ug/g |
| IMMUNE RESPONSE | | |
| Secretory IgA | 552  | 510 - 2010 ug/g |
| Anti-gliadin IgA | 157  | < 175 U/g |
| Eosinophil Activation Protein (EDN, EPX) | 1.40  | < 2.34 ug/g |
| INFLAMMATION | | |
| Calprotectin | 116  | < 173 ug/g |

H. PYLORI ANTIBIOTIC RESISTANCE GENES

| | Result | Reference |
|---|-----------------|-----------------|
| Amoxicillin | Positive | Negative |
| <i>Genes associated with amoxicillin resistance</i> | | |
| PBP1A S414R | Present | |
| PBP1A T556S | Absent | |
| PBP1A N562Y | Absent | |

| | Result | Reference |
|--|-----------------|-----------------|
| Clarithromycin | Positive | Negative |
| <i>Genes associated with clarithromycin resistance</i> | | |
| A2142C | Absent | |
| A2142G | Absent | |
| A2143G | Present | |

| | Result | Reference |
|---|-----------------|-----------------|
| Fluoroquinolones | Negative | Negative |
| <i>Genes associated with fluoroquinolone resistance</i> | | |
| gyrA N87K | Absent | |
| gyrA D91N | Absent | |
| gyrA D91G | Absent | |
| gyrB S479N | Absent | |
| gyrB R484K | Absent | |

| | Result | Reference |
|--|-----------------|-----------------|
| Tetracycline | Negative | Negative |
| <i>Genes associated with tetracycline resistance</i> | | |
| A926G | Absent | |
| AGA926-928TTC | Absent | |