

GI ECOLOGIX™ REPORT

REPORT ID: S000634

TEST REPORTED: 30/12/2019
 TEST RECEIVED: 01/12/2019
 PATIENT NAME:
 PATIENT DOB:
 GENDER: MALE

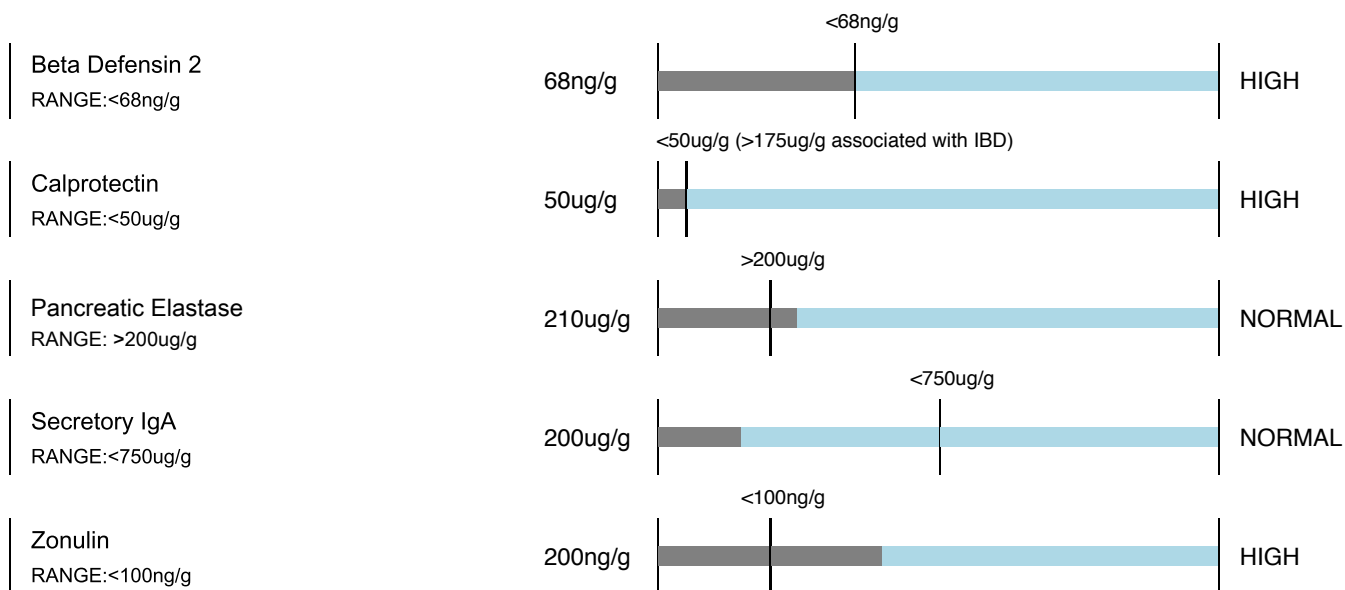
REPORT STATUS: COMPLETED
 CLINICIAN NAME:
 ACCESSION NO: 123456
 SAMPLE TYPE: STOOL

The Phylobioscience GI EcologiX™ profile utilises quantitative real-time PCR (qRT-PCR) for analysis of gastrointestinal microbiota. qRT-PCR results are reported as quantification of microbial gene of interest copies in a community sample relative to endogenous gene control (i.e. gut, vaginal). qRT-PCR reactions are performed using Taqman technology. The results show representative numbers proportional to normalised qRT-PCR value.

GI Health Markers (ELISAS)

RESULTS:

RATING:

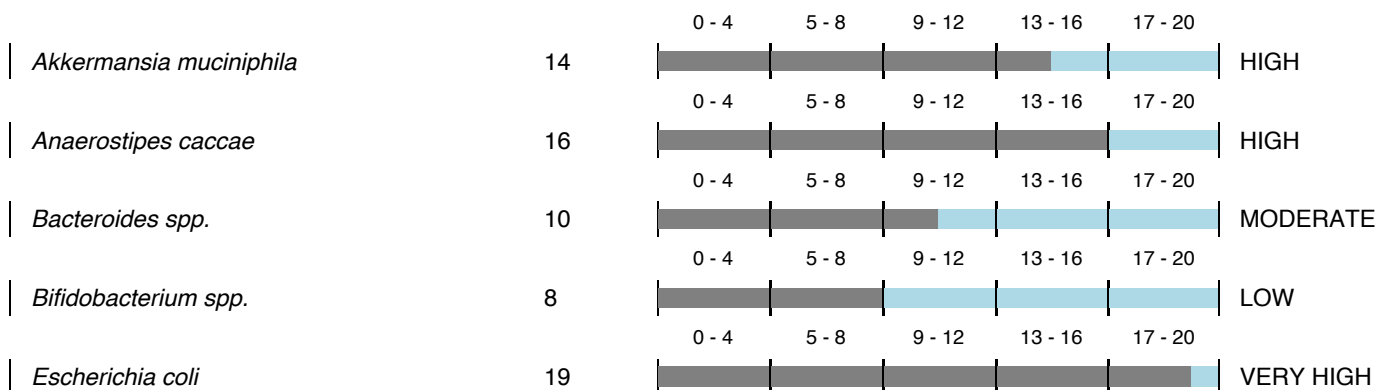


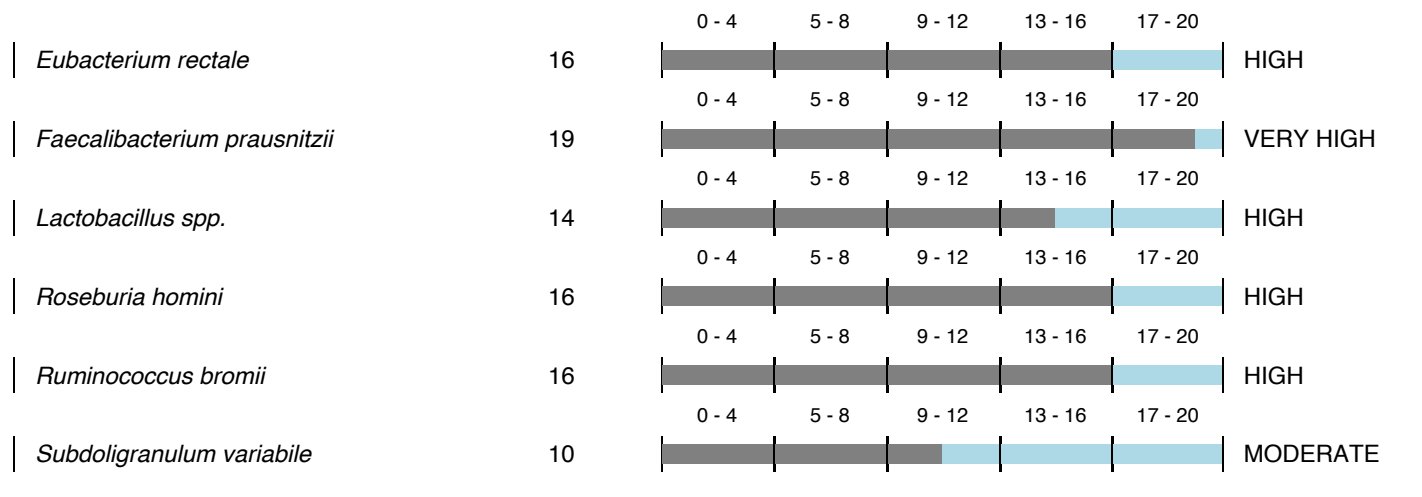
▲ Health immune markers are quantified using enzyme-linked immunosorbent assay (ELISA) which is based on antigen-antibody reactions. Please refer to the Phylobioscience interpretive guide for more details on health markers.

Commensal Bacteria

RESULTS:

ABUNDANCE:



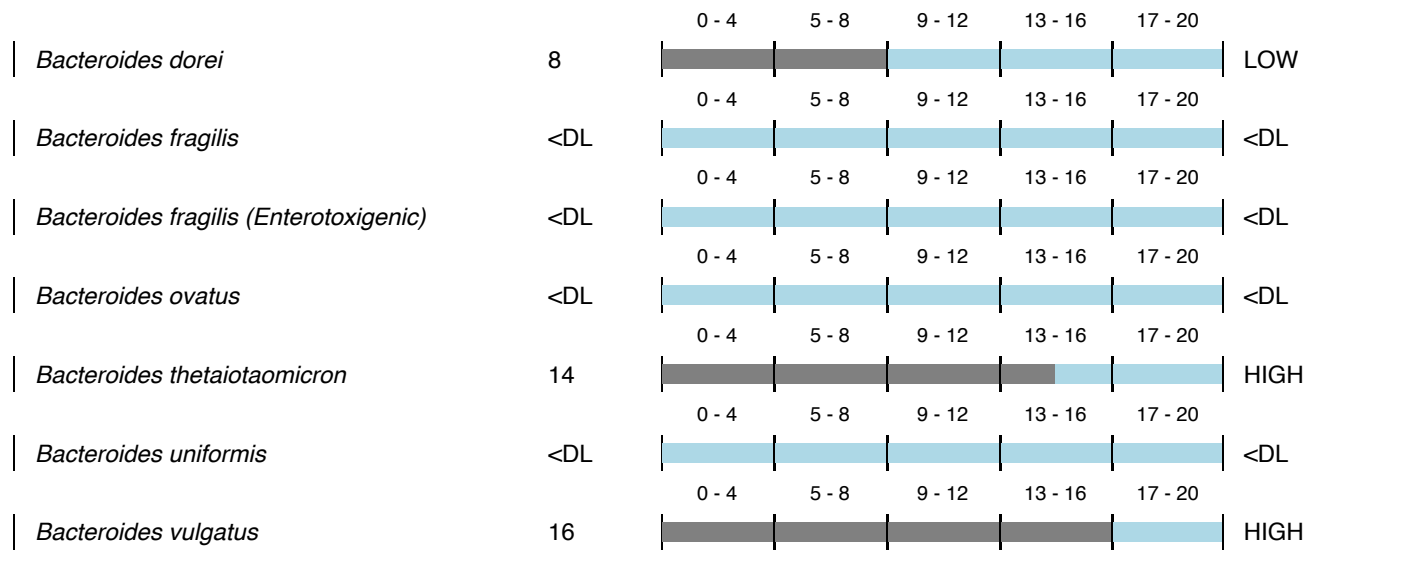


Commensal bacteria live in symbiosis with the host under normal conditions. To learn more about associations between commensal bacteria and clinical conditions, please refer to the Phyllobioscience interpretive guide. <DL: Microorganism is not detected/below detection limit.

Bacteroides Sub Group

RESULTS:

ABUNDANCE:

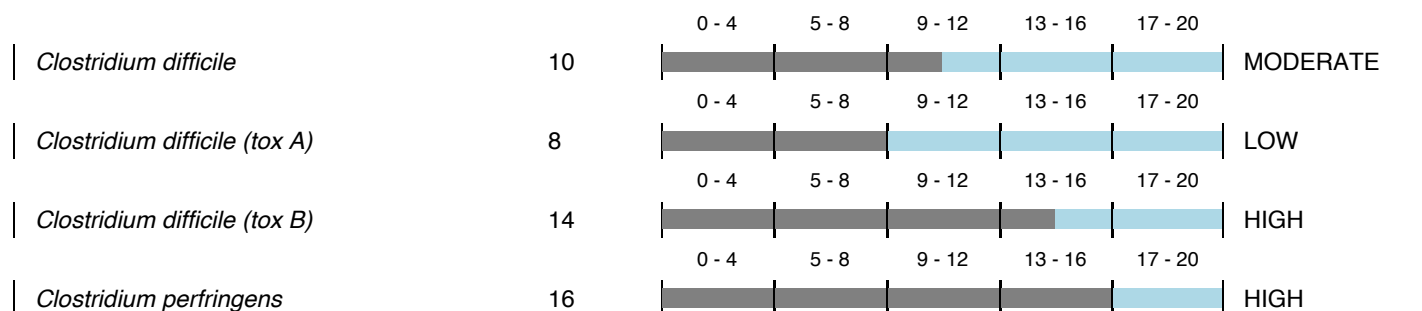


Bacteroides bacteria are gram-negative members of the GI microbiota. Please refer to the Phyllobioscience interpretive guide for information on associations with dysbiosis, clinical conditions and disease. <DL: Microorganism is not detected/below detection limit.

Clostridium Sub Group

RESULTS:

ABUNDANCE:



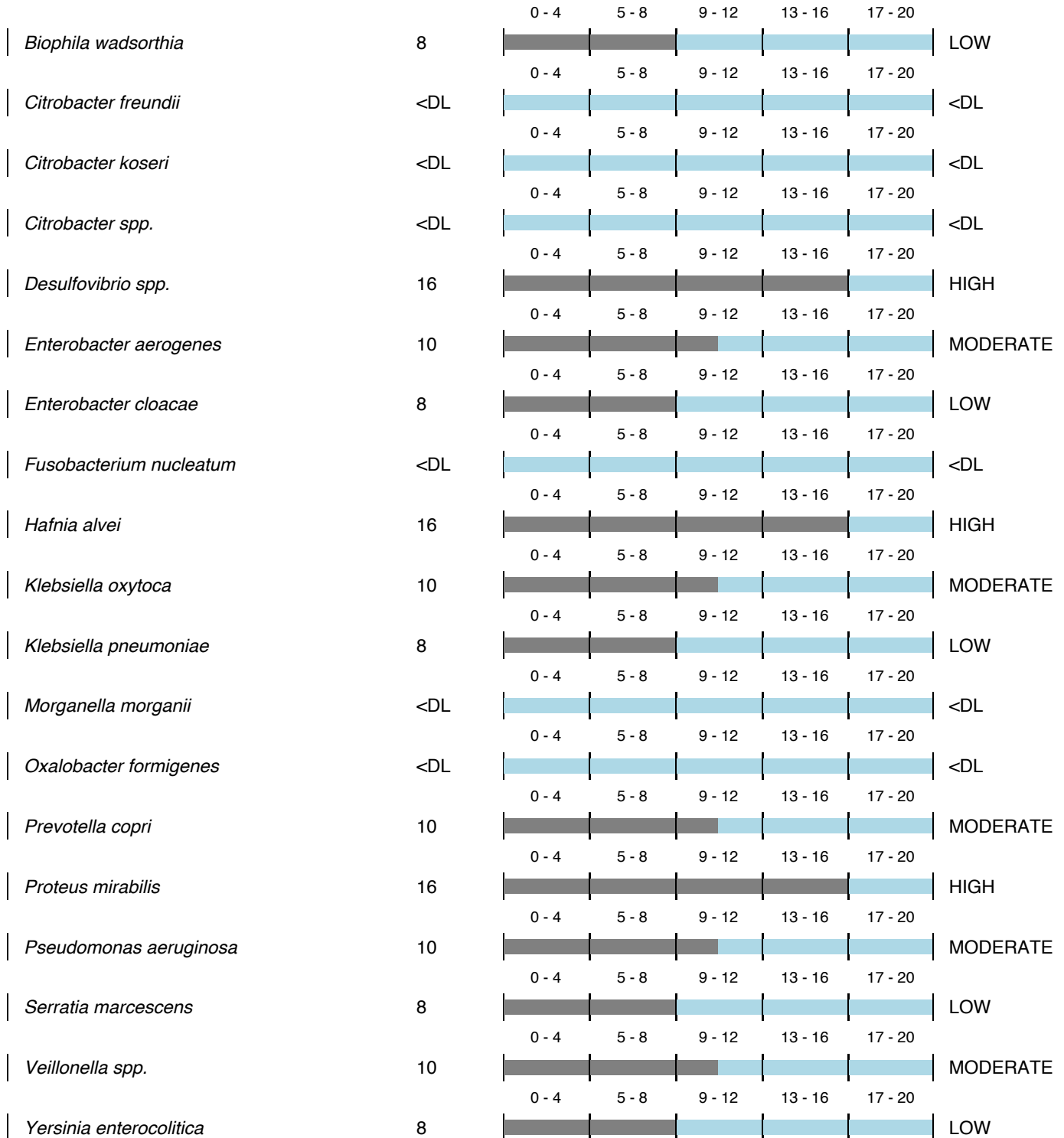


▲ Clostridium bacteria are gram-positive members of the GI microbiota. Please refer to the Phylobioscience interpretive guide for information on associations with dysbiosis, clinical conditions and disease. <DL: Microorganism is not detected/below detection limit.

Gram Negative (-) Bacteria

RESULTS:

ABUNDANCE:

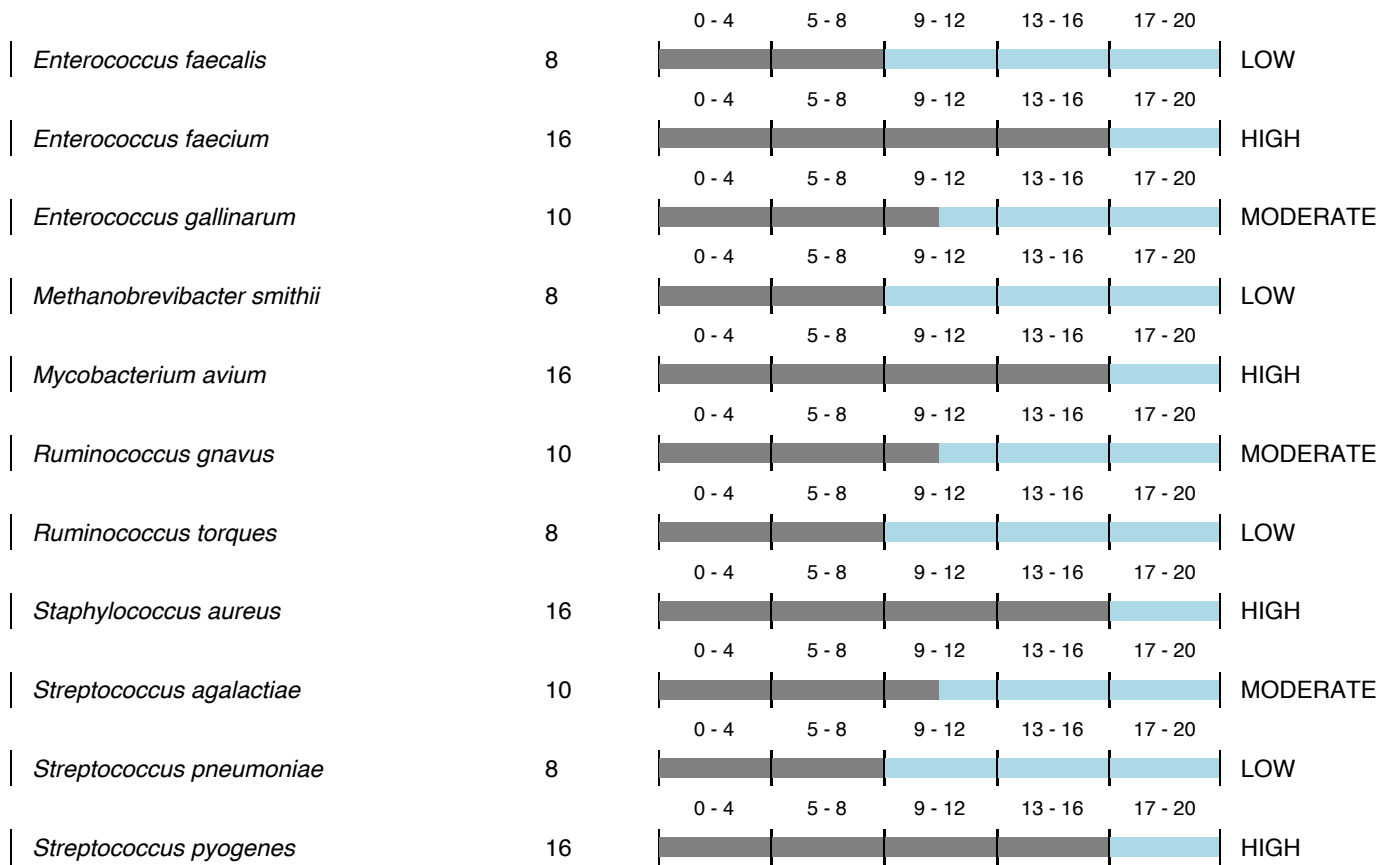


Gram-negative bacteria are members of the healthy GI microbiota. Please refer to the Phylobioscience interpretive guide for information on associations with clinical conditions, LPS endotoxemia and disease. <DL: Microorganism is not detected/below detection limit.

Gram Positive (+) Bacteria

RESULTS:

ABUNDANCE:



Gram-positive bacteria are members of the healthy GI microbiota. Please refer to the Phylobioscience interpretive guide for information on associations with clinical conditions and disease. <DL: Microorganism is not detected/below detection limit.

H Pylori

RESULTS:

ABUNDANCE:

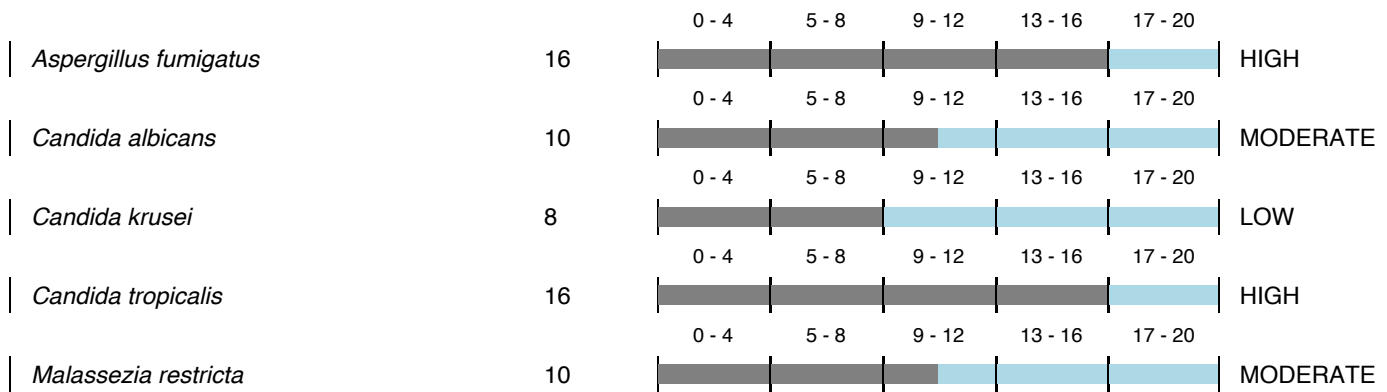


Helicobacter pylori is a gram-negative bacterium usually found in the stomach. It is believed to be a stable member of the human microbiota and it is asymptomatic in 90% of the individuals. H Pylori Stool Antigen is run as a confirmatory test to establish potential pathogenicity to host. Please refer to the Phylobioscience interpretive guide for information on associations with clinical conditions and disease. <DL: Microorganism is not detected/below detection limit.

Mycology

RESULTS:

ABUNDANCE:

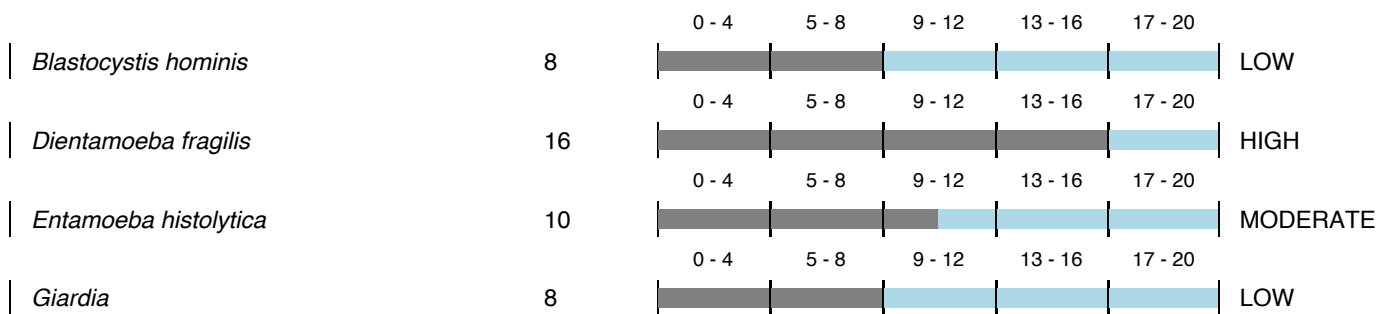


Commensal yeast and fungi live in symbiosis with host under normal conditions. Following dysbiosis or imbalance, overgrowth of fungi can occur causing pathogenic activity. Please refer to the Phylobioscience interpretive guide for further information on commensal fungi. <DL: Microorganism is not detected/below detection limit.

Parasitology

RESULTS:

ABUNDANCE:



Parasites can be non-pathogenic in the human population. In specific circumstances they can become pathogenic. Please refer to the Phylobioscience interpretive guide for information on associations with clinical conditions and disease. ND: Microorganism is not detected/below detection limit.

Short Chain Fatty Acid Production

	Butyrate	Propionate	Acetate	Key
<i>Akkermansia muciniphila</i>		***	**	* Low
<i>Anaerostipes caccae</i>	**			** Moderate
<i>Bacteroides spp.</i>		***		*** High
<i>Bifidobacterium spp.</i>		*	***	
<i>Clostridium spp.</i>	***	*		
<i>Escherichia coli</i>			*	
<i>Eubacterium spp.</i>	**			
<i>Faecalibacterium prausnitzii</i>	***			
<i>Lactobacillus spp.</i>	*	*	***	
<i>Roseburia homini</i>	**			
<i>Subdoligranulum variabile</i>	*			

Pryde, S. E., Duncan, S. H., Hold, G. L., Stewart, C. S., & Flint, H. J. (2002). The microbiology of butyrate formation in the human colon. *FEMS Microbiology Letters*, 217(2), 133–139.

Fernández, J., Redondo-Blanco, S., Gutiérrez-del-Río, I., Miguélez, E. M., Villar, C. J., & Lombó, F. (2016). Colon microbiota fermentation of dietary prebiotics towards short-chain fatty acids and their roles as anti-inflammatory and antitumour agents: A review. *Journal of Functional Foods*, 25, 511–522.

Louis, P., & Flint, H. J. (2016). Formation of propionate and butyrate by the human colonic microbiota. *Environmental Microbiology*, 19(1), 29–41.

Morrison, D.J., Preston, T. (2016). Formation of short chain fatty acids by the gut microbiota and their impact on human metabolism. *Gut Microbes*. 2016; 7(3): 189–200.

Chia LW, Hornung BVH, Aalvink S, Schaap PJ, de Vos WM, Knol J, Belzer C. (2018) Deciphering the trophic interaction between *Akkermansia muciniphila* and the butyrogenic gut commensal *Anaerostipes caccae* using a metatranscriptomic approach. *Antonie Van Leeuwenhoek*. 2018 Jun;111(6):859–873.

Rivière A, Selak M, Lantin D, Leroy F, De Vuyst L (2016) Bifidobacteria and Butyrate-Producing Colon Bacteria: Importance and Strategies for Their Stimulation in the Human Gut. *Front Microbiol*. 2016; 7: 979.