

Gut Retest + 100 New Bacteria Launch September 2023

Background

Our science team have been busy working hard on a new, groundbreaking way of identifying gut bacteria.

Thanks to more ZOE members (and more microbiome samples) we've discovered more bacteria linked to health.

This new science has discovered thousands of microbes that have never been identified before, hundreds of which are linked with food and with health outcomes like heart disease.

This has allowed us to increase the top bacteria reported in the ZOE Test from 30 to 100.

This means we'll be able to provide the most comprehensive and precise microbiome score together up-to-date food scores based on gut composition.

Key messages

• Discovery of new bacteria (new science)

Our latest scientific breakthrough reveals more about your microbiome. A world-first discovery of novel gut bacteria.

ZOE launches gut health retesting

Retest your microbiome to discover how eating the ZOE way has improved your gut health.

Recalculated microbiome scores for retesters*

We've updated your microbiome score to reflect our new discoveries – from 30 bacteria to a *groundbreaking* 100. All based on our new science with a much bigger dataset thanks to our members.

Proof that the ZOE program works (efficacy)

Already, retesting has shown that 82% of our members have improved their gut health by following the ZOE program.

*this is coming soon for non-retesters and will not have launched in September

The science

Microbiome species associated with cardio-metabolic risk

19 most strongly associated markers from ML results

To represent all 4 metadata categories

Average	Positive								Negative											Prevalence (%)	
142.5	149	168	158	172		162				-	170	163		154		-				99.1 Ruthenibact	erium lactatiformans
167.9		174	165	173	167	175	165		176	173		173	170	173	175	170	171	169	174	92.9 Flavonifract	or plautii
142.3	173	161	168	176		159					175									91.7 Clostridium	leptum
152.9	162	169		154		154	163							166						67.1 Escherichia	coli
152.3		154		153		152													161	66.5 Collinsella ir	itestinalis
154.4	159			151		160						169				167			167	64.3 Clostridium	sp CAG 58
154.6	145	163				171					167			170					166	61.7 Eggerthella	lenta
164.9	169	176	152	171	170	173	170												173	50.5 Anaerotrunc	ius colihominis
167.0	166	170		158	168	176	169												176	50.1 Clostridium	bolteae
160.3	154	152	174	155	169	165	167												170	43.7 Clostridium	spiroforme
159.8	139	165		147	174	170	168												175	43.3 Ruminococc	us gnavus
163.6	168	173		167	175	172	176												172	41.2 Clostridium	innocuum
153.5	138	157		139		145													165	28.6 Blautia hydr	ogenotrophica
165.8	175	172		165	173	174	173									176			171	27.6 Clostridium	symbiosum
161.0	160	164		141	176	169	175		168		164	170	172	172	168	162	170	175	169	26.7 Clostridium	<i>bolteae</i> CAG 59
27.7									22		14	14		13		8		7	31	99.5 Faecalibacte	rium prausnitzii
20.9									19	16	6	20	10	5				5	26	92.5 Eubacterium	i eligens
12.2									2		11	4	7	7		15	6	6	3	89.3 Oscillibacter	sp 57 20
31.5												32		10	1	14		11	29	82.9 Romboutsia	ilealis
10.1			1	12					4		23	3	6	1	5	5	19	1	5	54.6 Haemophilu	s parainfluenzae
9.7								_	3	4	3	1	1	2	2	6	5	4	1	51.3 Firmicutes b	<i>acterium</i> CAG 95
20.5									28		5	10	5	11	11	27		10	9	50.0 Oscillibacter	sp PC13
25.0									18		19	28		14	8	3	21	18	34	46.8 Veillonella d	ispar
14.6								2	14	11	8	5	11	4		23		2	15	41.3 Roseburia s	CAG 182
32.9									25					42		2	20	46	20	40.5 Veillonella a	typica
20.0		4							7		24	19	28	6		13		8	28	40.1 Clostridium	sp CAG 167
27.3									11			33		17	19	1	28	14	19	38.5 Veillonella ir	ifantium
28.9				2					23		1	29	25			10			16	38.2 Bifidobacter	ium _. animalis
24.4									9		22	6	22	9	6	35		13	38	36.0 Prevotella co	opri
14.0	8	23	_	_	8	5	8	1	6	2	28	2	3	3	7	22		3	17	34.3 Firmicutes b	acterium CAG 170
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Improving associations considering unknown species

-0.2 -0.1 0 0.1 0.2

MetaPhlAn 4 db Jan21



45.96 lostridia SGB6367 54 44 uminococcaceae SGB15180 seudoflavonifractor SGB15156 308.97 lostridia SGB14844 311.49 Clostridia SGB14891 315.35 Firmicutes SGB14999 318.76 Instridia SGB4121 336.14 rmicutes SGB3962 338.0 339 57 uminococcaceae SGB15076 341 9 Ruminococcaceae SGB14909 344.73 Firmicutes SGB63163 achnospiraceae SGB4727 Spearman's correlation



Input/Output Genomic database MetaPhlAn 4

Unknown species-level genome bins (SGBs) improves:

1. machine learning based on whole-microbiome composition show stronger associations

2. partial correlations against cardiometabolic health markers

Pasolli E, et al., Cell (2019) Blanco-Miguez A, et al., Nat Biotechnol (2023)

Expanding to 5 PREDICT cohorts

C T 1

- •~35,000 microbiome samples
- Include previously unknown species
- Account for geography
- •Stratify based on dietary patterns
- •ML show strong associations both with cardiometabolic markers and single foods







Cardiometabolic ranks across geography and BMI

Consistent associations between UK and US ranks



SGB ranked w.r.t. cardiometabolic markers vs. their partial correlations against BMI





Cardiometabolic ranks across geography and BMI

Consistent associations between UK and US ranks



SGB ranked w.r.t. cardiometabolic markers vs. their partial correlations against BMI

favorable' SGBs negatively correlates with BMI

'unfavorable' SGBs positively correlates with BMI

Bottom and top 50 ranked SGBs show more consistent correlations with BMI

