

**1,2 | 1,2 | 1,2 | 1,2 | 1,2**

1

2

*(H. pylori)*

1

2

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( PPI )

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7

8- 11

( )

12

13

H

14

15

QPr

2

Pr

<sup>13</sup>C

2

UBT

### 2.3 |

RUT

Warthin- Starry

<sup>18</sup>

Sydney

- 80 °C

-80 °C

### 2.4 | DNA

#### 16SrRNA

DNA

QIAGEN

DNeasy

(341F, 5

DNA® PowerSoil®

( )

( 1) (3.06%) (1.54%)  
 (1.21%) (1.00%) 7(0.96%) (0.96%);  
 9)  
 3.1 | chao1 (P )  
 3.1.1 | - (N ), P N (P  
 2 - D) PCoA P N (P  
 = .001; 2 e)  
 691 OTUs (P) (N)  
 :Proteobacteria (61.96% vs. 5.06%)  
 LefSe N (Firmicutes)  
 Firmicutes (8.53% vs. 9.15%) Bacteroidetes (6.16% vs. 4.54%)  
 (Bacteroidetes) (Actinobacteria)  
 Actinobacteria (0.81% vs. 2.08%) Verrucomicrobia (0.20% vs.  
 (Faecalibacterium) (Lactobacillus) Akkermansia  
 0.56%) P (60.75%) (4.05%) P ( 1)  
 (1.19%) Blautia(1.04%) (0.89%)  
 (0.53%) N :

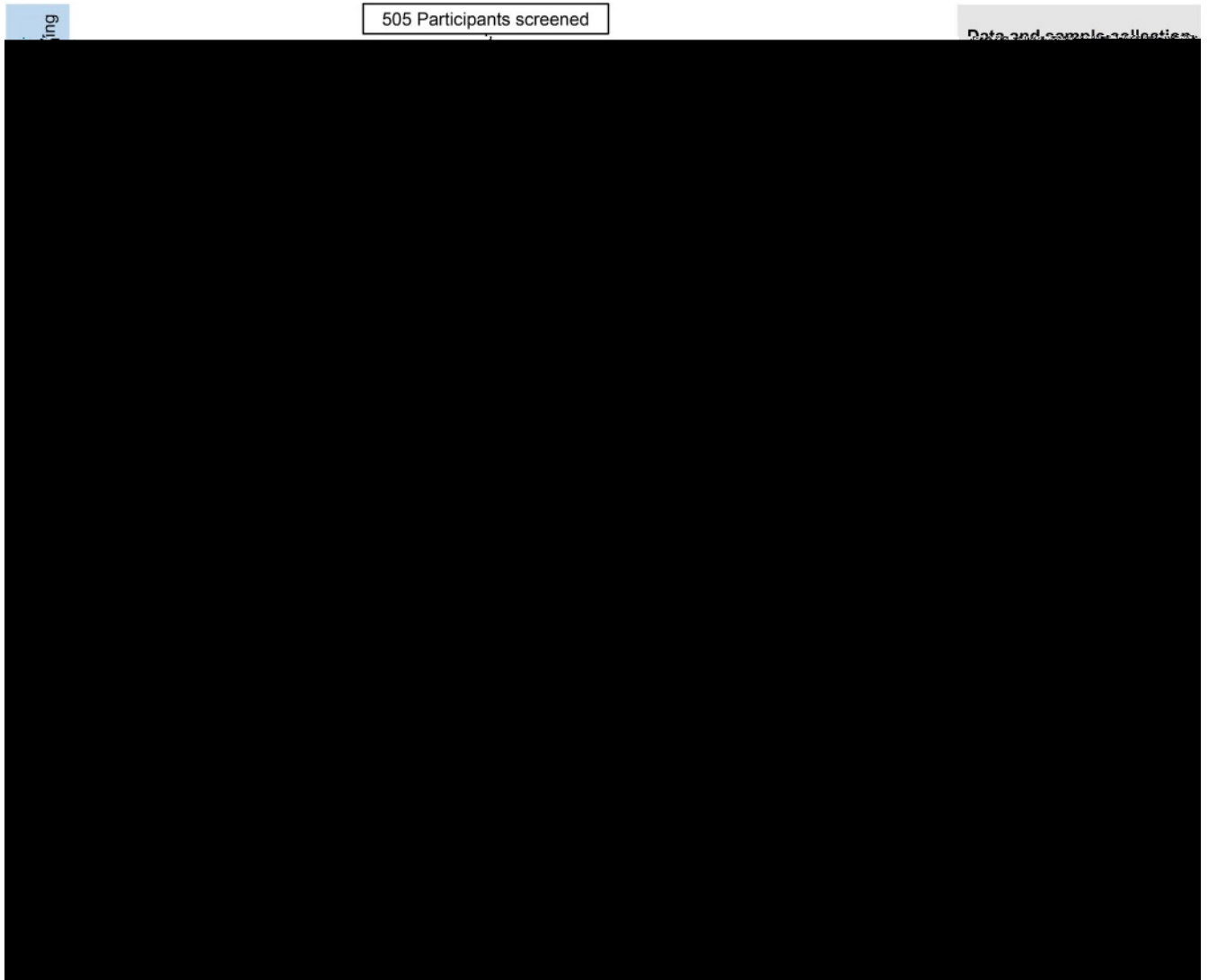


FIGURE 1 <sup>13</sup>C - UBT, <sup>13</sup>C ; Q 14 ; QPr ; Pr ; ; GSRS: ;  
<sup>13</sup>C - UBT, <sup>13</sup>C ; RUT: ; \* COVID- 19

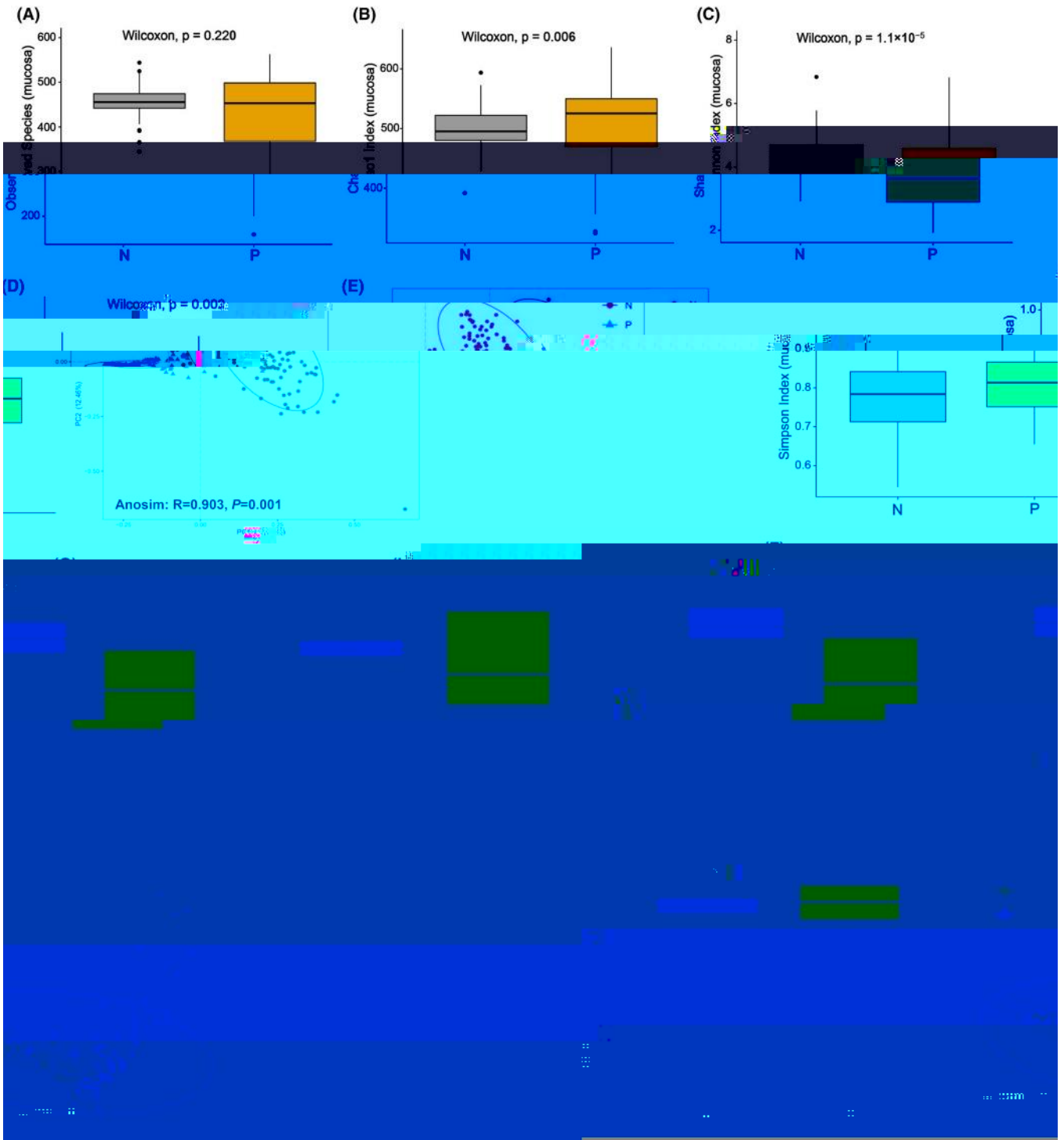
TABLE 1

Q (n = 34)	QPr (n = 31)	Pr (n = 30)	n (n = 56 <sup>1</sup> )	( )	26.32	2.53	26.00	2.46	26.50	2.62	25.86	2.62	0.677			
(%)15 (44.1%)	15 (48.4%)	10 (33.3%)	27 (48.2%)	0.568	BMI	22.36	4.07	22.41	3.57	21.45	3.60	22.09	3.20	0.699		
30 (88.2%)	27 (87.1%)	24 (80.0%)	53 (94.6%)	0.206												
n(%)	3(8.8%)	1(3.2%)	5(16.7%)	2(3.6%)	0.132		n(%)	1(2.9%)	2(6.5%)	1(3.3%)	1(1.8%)	0.735		4  0.44 0.56		
0.64	0.80	0.83	0.99	0.36	0.65	0.075	GSRs	6.03	4.00	4.68	3.65	4.70	3.66	5.14	4.51	0.497
:N	H. pylori	:Pr	:Q	14	:QPr											
BMI																
<sup>1</sup>																
	Pearson	Fisher's exact			(one-way ANOVA)											Kruskal- Wallis

N TCA ADP L D TCA <sup>19</sup>P ( S1A)

3.1.2 |

	1128	OTUs		P	N
			:		(33.06%
vs. 36.87%)	(24.80%	vs. 10.25%)			(22.46%
16.25%)	(10.37%	vs. 29.61%)			(5.57%
	P	(9.7%)			(7.9%)
(6.44%)	(5.47%)				7(5.40%)
	N	(20.8%)			(4.57%)
	(5.29%)				(7.3%)
					(6.1%)
					7(3.61%)
					(3.50%)
					P(1.98%)
					N(0.0057%)
( 10)					
H. pylori	(P )				



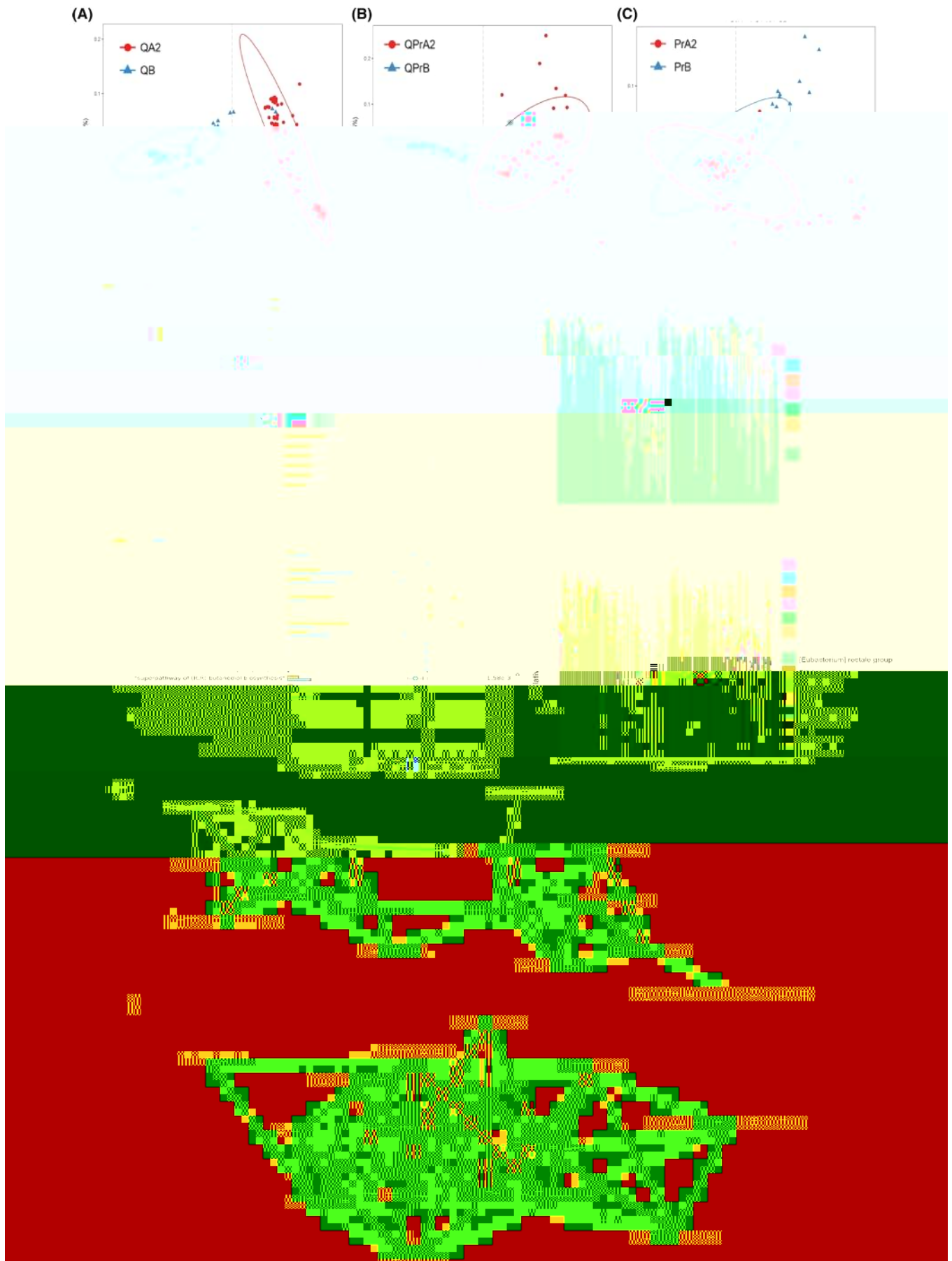
chao1 (P) (N) ;(C) P Shannon (D) P Simpson (A) P N ;(B) P  
 ;(I) P N Simpson (F) P ;(G) P N Chao1 ;(H) P N  
 LEfSe ( 3 4) QPrA2 qqa2 2  
 Akkermansia Faecalibacterium

QA2 , Erysipelatoclostridium Ralstonia  
 ( 3 4) Lachnospiraceae QPrA2 006  
 hydroxypropanoate superpathway Doudoroff ,  
 ), QPrA2  
 QA2 ( 3D)

### 3.2.2 |

(PrB ) (pr2 ) ( S1) PCoA PrB  
 pr2 (P = .004; 3 c)  
 : (60.32% vs. 61.39%)  
 (10.05% vs. 8.89%) (6.94% vs. 3.47%)  
 (0.95% vs. 1.08%) (58.97% vs. 59.2%) ( 3F G)

LEfSe  
 , Parvimonas ( 5) ,  
 ,Faecalibacterium, Roseburia rectalegroup  
 PrA2 PrA2  
 N- 20





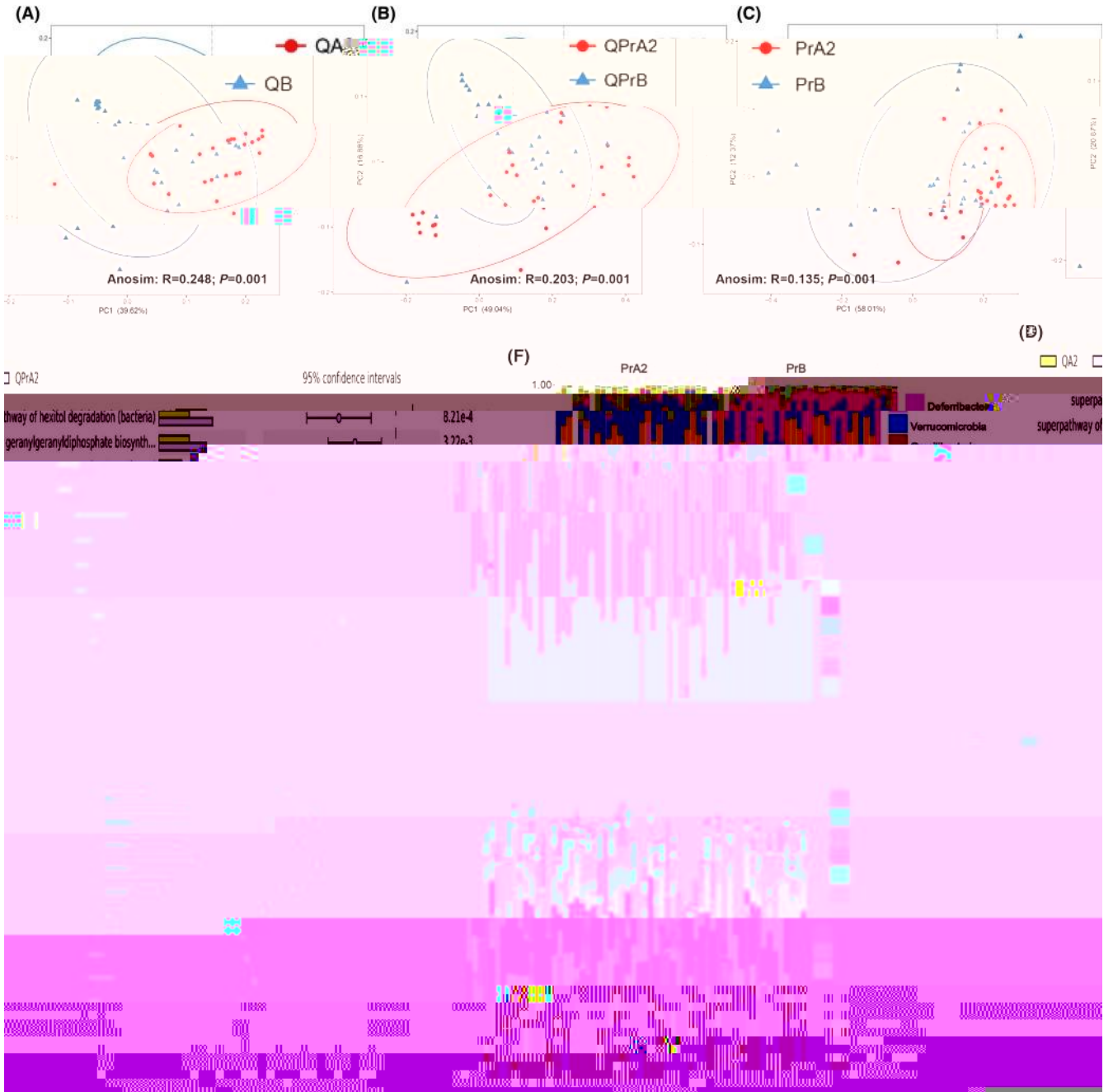
(F) (G) (QPrB) (qpr2);(C) (PrB) PCoA (pr2) (D) QA2 (QB) (QPrA2) (q2) ;(E) PrB pr2 ;(B)  
(PrB) (PrB) (pr2) 15 2 (I)  
(H)

Hp Hp  
Hp 22%  
(2)

77.92%

32

33



(F) (QPrB) (qpr2):(C) (PrB) PCoA (QB) (q2) : (B)  
(G) (PrB) (pr2) (pr2) (D) QA2 QPrA2 (E) PrB pr2  
(F) (G) (PrB) (pr2) 15



Fusobacteria) ( ,Porphyromonas,

N

2

14,15,34,35

35

1.54%

(2.03%)

(0.0082%)

35

(Fusobacterium,

Fusobacteria) <sup>36</sup> P

N

)<sup>37</sup>

)<sup>38</sup> N

lwofii anitratu

39

40

lwofii

<sup>41</sup> lwofii

- 8

42

lwofii

43

lwofii

48 , 49 , 50  
 51 *ventriosum*,<sup>52</sup>  
 Bifidobacterium QPrA2  
 53,54  
 (Bacillus) (Lactobacillus) QPrA2  
 QPrA2 Hp qqa2

#### 4.4 |

55,56 pH ( )  
 57 ( )

H

LYZ, ZYY SYX

ZYY, SYX, SZL, BJS, YW, LMM, ZJL, ZHY, YX  
ZYY SYX

, , ( , , )

**ORCID**

(h.p ylori )

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*VacA*

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*2021;00:e12848*

<https://doi.org/10.1111/hel.12848>

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1

- p ( p )	- n ( n )	t a x a	LDA
D_0__Bacteria.D_1__Firmicutes			N 4.515470022
D_0__Bacteria.D_1__Bacteroidetes			N 4.096019614
D_0__Bacteria.D_1__Actinobacteria			N 3.921596415
D_0__Bacteria.D_1__Verrucomicrobia			N 3.298286853
D_0__Bacteria.D_1__Firmicutes.D_2__Bacilli.D_3__Lactobacillales.D_4__Streptococcaceae D_5__			N 4.073636909
D_0__Bacteria.D_1__Proteobacteria.D_2__Betaproteobacteria.D_3__Neisseriales.D_4__Neisseriaceae D_5__			N 3.67784489
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Peptostreptococcaceae D_5__			N 2.914469694
D_0__Bacteria.D_1__Actinobacteria.D_2__Actinobacteria.D_3__Actinomycetales.D_4__ Actinomycetaceae.D_5__Actinomyces			N 3.557949615
D_0__Bacteria.D_1__Proteobacteria.D_2__Gammaproteobacteria.D_3__Pasteurellales D_4__ Pasteurellaceae.D_5__Haemophilus			N 3.299343748
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Ruminococcaceae D_5__Faecalibacterium			N 3.343526871
D_0__Bacteria.D_1__Firmicutes.D_2__Bacilli.D_3__Lactobacillales.D_4__Lactobacillaceae.D_5__Lactobacillus			N 3.54532777
D_0__Bacteria.D_1__Firmicutes.D_2__Negativicutes.D_3__Selenomonadales.D_4__Veillonellaceae D_5__ Megamonas			N 2.37095116
D_0__Bacteria.D_1__Verrucomicrobia.D_2__Verrucomicrobiae.D_3__Verrucomicrobiales D_4__ Verrucomicrobiaceae.D_5__Akkermansia			P 3.323582255
D_0__Bacteria.D_1__Proteobacteria			P 4.76160696
D_0__Bacteria.D_1__Cyanobacteria			P 2.72004186
D_0__Bacteria.D_1__Proteobacteria.D_2__Epsilonproteobacteria.D_3__Campylobacterales D_4__Helicobacteraceae.D_5__Helicobacter			P 4.855220878
D_0__Bacteria.D_1__Bacteroidetes.D_2__Bacteroidia.D_3__Bacteroidales.D_4__Bacteroidaceae D_5__			P 3.233495559
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Lachnospiraceae D_5__Fusicatenibacter			P 2.387107415
D_0__Bacteria.D_1__Cyanobacteria.D_2__Chloroplast.D_3__Golenkinialongispicula.D_4__ Golenkinialongispicula.D_5__Golenkinialongispicula			P 2.908905146
D_0__Bacteria.D_1__Actinobacteria.D_2__Actinobacteria.D_3__Micrococcales.D_4__ MicrococcalesIncertaeSedis.D_5__Timonella			P 2.882966768

2

- p ( p )	- n ( n )	t a x a	LDA
D_0__Bacteria.D_1__Actinobacteria			N 4.25784569
D_0__Bacteria.D_1__Actinobacteria.D_2__Actinobacteria.D_3__Corynebacteriales D_4__Mycobacteriaceae.D_5__Mycobacterium			N 4.19527242
D_0__Bacteria.D_1__Proteobacteria.D_2__Alphaproteobacteria.D_3__Rhodospirillales D_4__Rhodospirillaceae.D_5__Skermanella			N 3.64673657

D_0_Bacteria	D_1_Plantomycetes N	LDA
D_0_Bacteria.D_1_Actinobacteria.D_2_Actinobacteria.D_3_Corynebacteriales.D_4_Nocardiaceae	D_5_N	3.4232614
Gordonia		2.95217119
D_0_Bacteria.D_1_Proteobacteria.D_2_Alphaproteobacteria.D_3_Rhizobiales	D_4_Methylobacteriaceae.D_5_Methylobacterium	N
		2.91909344
D_0_Bacteria.D_1_Plantomycetes.D_2_Plantomycetacia.D_3_Plantomycetales	D_4_Plantomycetaceae.D_5_Gemmata	N
		2.91711111
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae	D_5_Eubacterium_rectalegroup	N
		2.29693209
D_0_Bacteria D_1_Firmicutes P		
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Streptococcaceae	D_5_Streptococcus P	4.16815777
D_0_Bacteria D_1_Bacteroidetes P D_0_Bacteria D_1_Fusobacteria P		3.8104557
D_0_Bacteria.D_1_Fusobacteria.D_2_Fusobacteriia.D_3_Fusobacteriales.D_4_Fusobacteriaceae	D_5_P	3.72915656
		3.51824737
D_0_Bacteria.D_1_Proteobacteria.D_2_Betaproteobacteria.D_3_Neisseriales.D_4_Neisseriaceae	D_5_P	3.42371271
		3.38083865
D_0_Bacteria.D_1_Proteobacteria.D_2_Epsilonproteobacteria.D_3_Campylobacterales	D_4_Helicobacteraceae.D_5_Helicobacter	P
		3.31405553
D_0_Bacteria.D_1_Actinobacteria.D_2_Actinobacteria.D_3_Actinomycetales	D_4_Actinomycetaceae.D_5_Actinomyces	P
		3.11133216
D_0_Bacteria.D_1_Proteobacteria.D_2_Epsilonproteobacteria.D_3_Campylobacterales	D_4_Campylobacteraceae.D_5_Campylobacter	P
		2.96317977
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Porphyrimonadaceae	D_5_Porphyrimonas	P
		2.87332037
D_0_Bacteria.D_1_Firmicutes.D_2_Negativicutes.D_3_Selenomonadales.D_4_Veillonellaceae	D_5_P	2.87002323
		2.85705228
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Peptostreptococcaceae	D_5_P	2.80222108
		2.79100979
D_0_Bacteria.D_1_Actinobacteria.D_2_Actinobacteria.D_3_Micrococcales.D_4_Micrococcaceae	D_5_P	2.72295299
		2.67501231
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Carnobacteriaceae	D_5_Granulicatella P	2.64684346
D_0_Bacteria.D_1_Proteobacteria.D_2_Gammaproteobacteria.D_3_Pseudomonadales	D_4_Moraxellaceae.D_5_Acinetobacter	P

3

- c (qb ) (q2 ) taxa

	LDA
D_0_Bacteria.D_1_Proteobacteria.D_2_Epsilonproteobacteria.D_3_Campylobacterales	QB 4.88622722
D_4_Helicobacteraceae.D_5_Helicobacter	
D_0_Bacteria.D_1_Proteobacteria	QB 4.82846948
D_0_Bacteria.D_1_Firmicutes	QA2 4.62660629
D_0_Bacteria.D_1_Bacteroidetes	QA2 4.2998718

## LDA

D_0__Bacteria.D_1__Bacteroidetes.D_2__Bacteroidia.D_3__Bacteroidales.D_4__Bacteroidaceae	D_5__	QA2	4.03401871
D_0__Bacteria.D_1__Firmicutes.D_2__Bacilli.D_3__Lactobacillales.D_4__Streptococcaceae	D_5__Streptococcus	QA2	3.92602829
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Ruminococcaceae	D_5__	QA2	3.75358047
Faecalibacterium			3.62432951
D_0__Bacteria	D_1__Actinobacteria	QA2	3.48139128
D_0__Bacteria.D_1__Bacteroidetes.D_2__Bacteroidia.D_3__Bacteroidales.D_4__Prevotellaceae	D_5__Prevotella9	QA2	3.46456961
D_0__Bacteria.D_1__Proteobacteria.D_2__Gammaproteobacteria.D_3__Enterobacteriales	D_4__	QA2	3.4424591
Enterobacteriaceae.D_5__Klebsiella			3.34025246
D_0__Bacteria.D_1__Firmicutes.D_2__Erysipelotrichia.D_3__Erysipelotrichales.D_4__Erysipelotrichaceae	D_5__	QA2	3.28397117
Erysipelatoclostridium			3.26511808
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Lachnospiraceae	D_5__Blautia	QA2	3.23098578
D_0__Bacteria.D_1__Proteobacteria.D_2__Gammaproteobacteria.D_3__Enterobacteriales	D_4__	QA2	3.18595421
Enterobacteriaceae.D_5__Escherichia_Shigella			3.18365486
D_0__Bacteria.D_1__Actinobacteria.D_2__Actinobacteria.D_3__Bifidobacteriales.D_4__Bifidobacteriaceae	D_5__	QA2	3.14355733
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Ruminococcaceae			3.05232679
			3.03587575
			3.0090912
			2.9957898
			2.97462037
			2.96675244
			2.95762604
			2.86700172
			2.85786547
			2.77321386
			2.7626834
			2.74701739
			2.67789918
			2.64723903

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(qprb ) (qpra2 ) ta x a

		LDA
D_0__Bacteria.D_1__Proteobacteria.D_2__Epsilonproteobacteria.D_3__Campylobacteriales.D_4__Helicobacteraceae.D_5__Helicobacter	QPrB	4.88756938
D_0__Bacteria.D_1__Proteobacteria	QPrB	4.80192236
D_0__Bacteria.D_1__Firmicutes	QPrA2	4.59350171
D_0__Bacteria.D_1__Bacteroidetes	QPrA2	4.24845203
D_0__Bacteria.D_1__Firmicutes.D_2__Bacilli.D_3__Lactobacillales.D_4__Streptococcaceae D_5__Streptococcus	QPrA2	4.01123217
D_0__Bacteria.D_1__Bacteroidetes.D_2__Bacteroidia.D_3__Bacteroidales.D_4__Bacteroidaceae D_5__Bacteroides	QPrA2	3.90001517
D_0__Bacteria.D_1__Actinobacteria	QPrA2	3.69279781
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Ruminococcaceae D_5__Faecalibacterium	QPrA2	3.62768201
D_0__Bacteria.D_1__Bacteroidetes.D_2__Bacteroidia.D_3__Bacteroidales.D_4__Prevotellaceae D_5__Prevotella9	QPrA2	3.41624392
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Lachnospiraceae D_5__Blautia	QPrA2	3.39930329
D_0__Bacteria.D_1__Actinobacteria.D_2__Actinobacteria.D_3__Bifidobacteriales.D_4__Bifidobacteriaceae D_5__	QPrA2	3.26730164
D_0__Bacteria.D_1__Fusobacteria	QPrA2	3.25407621
D_0__Bacteria.D_1__Proteobacteria.D_2__Gammaproteobacteria.D_3__Enterobacteriales.D_4__Enterobacteriaceae.D_5__Escherichia_Shigella	QPrA2	3.22113933
D_0__Bacteria.D_1__Proteobacteria.D_2__Gammaproteobacteria.D_3__Enterobacteriales.D_4__Enterobacteriaceae.D_5__Klebsiella	QPrA2	3.22005068
D_0__Bacteria.D_1__Proteobacteria.D_2__Betaproteobacteria.D_3__Neisseriales.D_4__Neisseriaceae D_5__	QPrA2	3.19719411
D_0__Bacteria.D_1__Firmicutes.D_2__Negativicutes.D_3__Selenomonadales.D_4__Veillonellaceae D_5__Veillonella	QPrA2	3.17306135
D_0__Bacteria.D_1__Fusobacteria.D_2__Fusobacteriia.D_3__Fusobacteriales.D_4__Fusobacteriaceae D_5__	QPrA2	3.1503736
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Ruminococcaceae	QPrA2	3.07429675
D_5__Subdoligranulum D_0__Bacteria.D_1__Firmicutes.D_2__Bacilli.D_3__Lactobacillales.D_4__Lactobacillaceae	QPrA2	3.05005098
D_5__Lactobacillus D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Lachnospiraceae	QPrA2	2.9701391
D_5__Eubacterium_rectalegroup	QPrA2	2.94485025
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Lachnospiraceae D_5__Lachnospira	QPrA2	2.93288073
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Lachnospiraceae D_5__Fusicatenibacter	QPrA2	2.85361267
D_0__Bacteria.D_1__Firmicutes.D_2__Bacilli.D_3__Lactobacillales.D_4__Enterococcaceae D_5__Enterococcus	QPrA2	2.78480148
D_0__Bacteria.D_1__Bacteroidetes.D_2__Bacteroidia.D_3__Bacteroidales.D_4__Rikenellaceae D_5__Alistipes	QPrA2	2.66130808
D_0__Bacteria.D_1__Firmicutes.D_2__Negativicutes.D_3__Selenomonadales.D_4__Veillonellaceae D_5__Dialister	QPrA2	2.61565704
D_0__Bacteria.D_1__Verrucomicrobia.D_2__Verrucomicrobiae.D_3__Verrucomicrobiales.D_4__Verrucomicrobiaceae.D_5__Akkermansia	QPrA2	2.55583573
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Lachnospiraceae	QPrA2	2.5333569
D_5__Roseburia	QPrA2	2.48856104
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Christensenellaceae	QPrA2	2.43964914
D_0__Bacteria.D_1__Firmicutes.D_2__Bacilli.D_3__Bacillales.D_4__Bacillaceae.D_5__Bacillus	QPrA2	2.32644233
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Lachnospiraceae.D_5__LachnospiraceaeUCG_006		
D_0__Bacteria.D_1__Verrucomicrobia		

(prb ) (pr a2 ) ta x a

LDA

D_0__Bacteria.D_1__Verrucomicrobia	D_2__Spartobacteria	2.25157052
D_0__Bacteria.D_1__Bacteroidetes.D_2__Bacteroidia.D_3__Bacteroidales.D_4__Prevotellaceae	D_5__PrevotellaceaeNK3B31group	2.24634925
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Ruminococcaceae	D_5__Ruminococcus1	2.22739045
D_0__Bacteria.D_1__Verrucomicrobia.D_2__Spartobacteria.D_3__Chthoniobacterales	D_4__DA101soilgroup.D_5__unculturedbacterium	2.19023489
D_0__Bacteria.D_1__Cyanobacteria.D_2__Cyanobacteria.D_3__SubsectionI.D_4__FamilyI	Ambiguous_taxa	2.04433288
D_0__Bacteria.D_1__Firmicutes.D_2__Negativicutes.D_3__Selenomonadales.D_4__Veillonellaceae	D_5__Megamonas	2.03882681
D_0__Bacteria	D_1__Cyanobacteria	2.00720187
D_0__Bacteria.D_1__Firmicutes.D_2__Bacilli.D_3__Lactobacillales.D_4__Strep159>22 51 364.97 418.06 393.05 reW* nBT/F1 7		3.52503934
		2.84391025
		2.62227403
		2.60265322
		2.56038684
		2.32049361
		2.29823066
		2.28053464
		2.26386778
		2.15333625
		2.15333625
		2.09791937
		2.04009138

- c (qb ) (q2 ) ta x a

LDA

D_0__Bacteria.D_1__Proteobacteria	QB	3.93611726
D_0__Bacteria.D_1__Actinobacteria	QB	3.88361698
D_0__Bacteria.D_1__Firmicutes	QB	3.7963922
D_0__Bacteria.D_1__Actinobacteria.D_2__Actinobacteria.D_3__Corynebacteriales	QB	3.65531265
D_4__Mycobacteriaceae.D_5__Mycobacterium		
D_0__Bacteria.D_1__Proteobacteria.D_2__Alphaproteobacteria.D_3__Rhizobiales	QB	3.38529279
D_4__Methylobacteriaceae.D_5__Methylobacterium		

D\_0\_\_Bacteria.D\_1\_\_Firmicutes.D\_2\_\_Clostridia.D\_3\_\_Clostridiales.D\_4\_\_Ruminococcaceae  
D\_5\_\_Faecalibacterium

D\_0\_\_Bacteria.D\_1\_\_Proteobacteria.D\_2\_\_Gammaproteobacteria.D\_3\_\_Pasteurellales.D\_4\_\_  
Pasteurellaceae.D\_5\_\_Haemophilus

		LDA
D_0__Bacteria.D_1__Proteobacteria.D_2__Betaproteobacteria.D_3__Burkholderiales.D_4__Alcaligenaceae.D_5__Sutterella	QA2	2.59820905
D_0__Bacteria.D_1__Proteobacteria.D_2__Betaproteobacteria.D_3__Neisseriales.D_4__Neisseriaceae D_5__Eikenella	QA2	2.38443367
D_0__Bacteria.D_1__Proteobacteria.D_2__Gammaproteobacteria.D_3__Cardiobacteriales D_4__Cardiobacteriaceae.D_5__Cardiobacterium	QA2	2.30448283
D_0__Bacteria.D_1__Proteobacteria.D_2__Gammaproteobacteria.D_3__Xanthomonadales D_4__Xanthomonadaceae.D_5__Stenotrophomonas	QA2	2.2638945
D_0__Bacteria.D_1__Firmicutes.D_2__Negativicutes.D_3__Selenomonadales.D_4__Veillonellaceae D_5__	QA2	2.25443962
D_0__Bacteria.D_1__Firmicutes.D_2__Negativicutes.D_3__Selenomonadales.D_4__Veillonellaceae D_5__Megasphaera	QA2	2.21289108
D_0__Bacteria.D_1__Bacteroidetes.D_2__Flavobacteriia.D_3__Flavobacteriales.D_4__Flavobacteriaceae D_5__Bergeyella	QA2	2.21200715
D_0__Bacteria.D_1__Tenericutes.D_2__Mollicutes.D_3__Mycoplasmatales.D_4__Mycoplasmataceae D_5__	QA2	2.18511001
D_0__Bacteria.D_1__Tenericutes.D_2__Mollicutes.D_3__Mycoplasmatales.D_4__Mycoplasmataceae D_5__	QA2	2.18094814
D_0__Bacteria.D_1__Bacteroidetes.D_2__Bacteroidia.D_3__Bacteroidales.D_4__Porphyromonadaceae D_5__Tannerella	QA2	2.10578016
D_0__Bacteria.D_1__Tenericutes		

7

(qprb ) (qpra2 ) ta x a

		LDA
D_0__Bacteria.D_1__Proteobacteria	QPrB	4.12341231
D_0__Bacteria.D_1__Actinobacteria	QPrB	3.84571752
D_0__Bacteria.D_1__Actinobacteria.D_2__Actinobacteria.D_3__Corynebacteriales.D_4__Mycobacteriaceae D_5__	QPrB	3.77161497
D_0__Bacteria.D_1__Proteobacteria.D_2__Alphaproteobacteria.D_3__Rhizobiales.D_4__Methylobacteriaceae.D_5__Methylobacterium	QPrB	3.39278595
D_0__Bacteria.D_1__Proteobacteria.D_2__Gammaproteobacteria.D_3__Pasteurellales.D_4__Pasteurellaceae.D_5__Haemophilus	QPrB	3.38549213
D_0__Bacteria.D_1__Proteobacteria.D_2__Alphaproteobacteria.D_3__Rhodospirillales.D_4__Rhodospirillaceae.D_5__Skermanella	QPrB	3.24115499
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Ruminococcaceae D_5__Faecalibacterium	QPrB	3.04953456
D_0__Bacteria.D_1__Proteobacteria.D_2__Gammaproteobacteria.D_3__Enterobacteriales.D_4__Enterobacteriaceae.D_5__Escherichia_Shigella	QPrB	2.99829076
D_0__Bacteria.D_1__Actinobacteria.D_2__Actinobacteria.D_3__Pseudonocardiales.D_4__Pseudonocardia.D_5__Actinomycetospora	QPrB	2.80185792
D_0__Bacteria.D_1__Actinobacteria.D_2__Actinobacteria.D_3__Pseudonocardiales.D_4__Pseudonocardia.D_5__Pseudonocardia	QPrB	2.7878197
D_0__Bacteria.D_1__Proteobacteria.D_2__Gammaproteobacteria.D_3__Pseudomonadales.D_4__Moraxellaceae.D_5__Acinetobacter	QPrB	2.76216078
D_0__Bacteria.D_1__Actinobacteria.D_2__Actinobacteria.D_3__Bifidobacteriales.D_4__Bifidobacteriaceae D_5__	QPrB	2.72812873
D_0__Bacteria.D_1__Actinobacteria.D_2__Actinobacteria.D_3__Bifidobacteriales.D_4__Bifidobacteriaceae D_5__	QPrB	2.72812873
D_0__Bacteria.D_1__Proteobacteria.D_2__Gammaproteobacteria.D_3__Xanthomonadales.D_4__Xanthomonadaceae.D_5__Pseudoxanthomonas	QPrB	2.70720634

## LDA

D_0__Bacteria.D_1__Proteobacteria.D_2__Gammaproteobacteria.D_3__Xanthomonadales.D_4__Xanthomonadaceae.D_5__Luteimonas	QPrB	2.70687092
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Lachnospiraceae D_5__Eubacterium_elifensgroup	QPrB	2.65830928
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Lachnospiraceae D_5__Eubacterium_rectalegroup	QPrB	2.17290207
D_0__Bacteria.D_1__Firmicutes.D_2__Bacilli.D_3__Lactobacillales.D_4__Streptococcaceae D_5__Streptococcus	QPrA2	3.7214577
D_0__Bacteria.D_1__Firmicutes.D_2__Negativicutes.D_3__Selenomonadales.D_4__Veillonellaceae.D_5__Veillonella	QPrA2	3.51150476
D_0__Bacteria.D_1__Bacteroidetes.D_2__Flavobacteriia.D_3__Flavobacteriales.D_4__Flavobacteriaceae D_5__Capnocytophaga	QPrA2	2.67140041
D_0__Bacteria.D_1__Actinobacteria.D_2__Actinobacteria.D_3__Actinomycetales.D_4__Actinomycetaceae D_5__	QPrA2	2.6268426
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Ruminococcaceae D_5__RuminococcaceaeUCG_014	QPrA2	2.56166666
D_0__Bacteria.D_1__Bacteroidetes.D_2__Bacteroidia.D_3__Bacteroidales.D_4__Prevotellaceae.D_5__Prevotella6	QPrA2	2.42951702
D_0__Bacteria.D_1__Bacteroidetes.D_2__Bacteroidia.D_3__Bacteroidales.D_4__Prevotellaceae D_5__PrevotellaceaeGa6A1group	QPrA2	2.3404686
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__FamilyXI.D_5__Parvimonas	QPrA2	2.31525167
D_0__Bacteria.D_1__Firmicutes.D_2__Negativicutes.D_3__Selenomonadales.D_4__Veillonellaceae D_5__	QPrA2	2.23308764
D_0__Bacteria.D_1__Proteobacteria.D_2__Betaproteobacteria.D_3__Burkholderiales.D_4__Alcaligenaceae D_5__Sutterella	QPrA2	2.21631005
D_0__Bacteria.D_1__Firmicutes.D_2__Negativicutes.D_3__Selenomonadales.D_4__Veillonellaceae D_5__Megasphaera	QPrA2	2.15456139
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Lachnospiraceae D_5__LachnospiraceaeUCG_001	QPrA2	2.10116293
D_0__Bacteria.D_1__Firmicutes.D_2__Clostridia.D_3__Clostridiales.D_4__Lachnospiraceae D_5__Eubacterium_ventriosumgroup	QPrA2	2.08940656



**LDA**

3.94095768  
3.85600089  
3.73866923  
  
3.43566394  
  
3.40411224  
  
3.18799219  
3.16980817

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9  
2

.98974791



<i>H. pylori</i>	(P	n = 190)	<i>H. pylori-</i>	(N	N = 112)
(61.96%)		(8.53%)			(5.06%)
(6.16%)					(4.54%)
(0.81%)	<i>Verrucomicrobia</i>	(0.20%)	(2.08%)		(0.56%)
	(60.75%)	(4.05%)			(3.06%)
(1.19%)	<i>Blautia</i>	(1.04%)			(1.54%)
	9(0.89%)	(0.53%)			(1.21%)
					(1.00%)
(0.47%)	<i>fusicatenbacter</i>	(0.40%)	7(0.96%)		(0.96%)
-		(0.38%)			(0.75%)
			(0.67%)		(0.60%)

<i>H. pylori</i>	(P	n = 190)	<i>H. pylori-</i>	(N	N = 112)
(33.06%)		(24.80%)			
(22.46%)		(10.37%)			
(5.57%)		(9.7%)			
		(7.9%)			
(6.44%)		(5.47%)			
		7(5.40%)			
		(4.57%)			
(4.30%)		(2.81%)			
		(2.35%)			
		(1.98%)			