

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

1

2

(H. pylori)

1

2

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3

(

(PPI)

4

5

6

7

8- 11

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12

13

H

14

15

QPr

2

Pr

¹³C

2

UBT

2.3 |

RUT

Warthin- Starry

¹⁸

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%)
 Firmicutes (8.53% vs. 9.15%) Bacteroidetes (6.16% vs. 4.54%)
 Actinobacteria (0.81% vs. 2.08%) Verrucomicrobia (0.20% vs.
 0.56%) P (60.75%) (4.05%)
 (1.19%) Blautia(1.04%) (0.89%)
 (0.53%) N :



FIGURE 1 ¹³C - UBT, ¹³C ;RUT: ;* COVID-19 ;Pr ; GSRS: ;

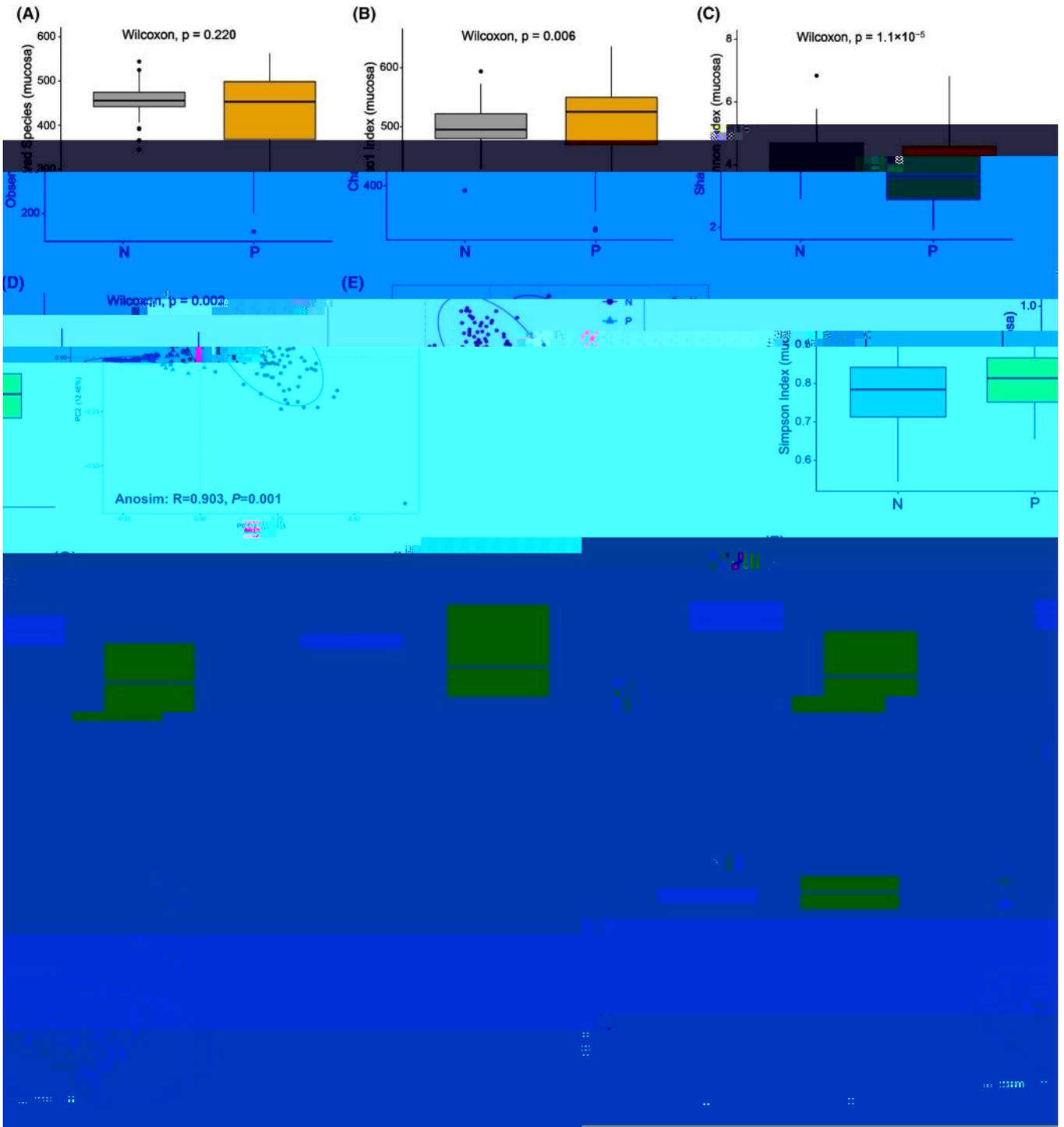
TABLE 1

Q (n = 34)	QPr (n = 31)	Pr (n = 30)	n (n = 56 ¹)	()	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																
¹																
	Pearson	Fisher's exact			(one-way ANOVA)											Kruskal- Wallis

N TCA ADP L D TCA ¹⁹P (S1A)

3.1.2 |

	1128	OTUs		P	N
			:		(33.06%
vs. 36.87%)		(24.80% vs. 10.25%)			(22.46% vs.
16.25%)		(10.37% vs. 29.61%)			(5.57% vs. 2.25%)
	P	(9.7%)		(7.9%)	
(6.44%)		(5.47%)		7(5.40%)	(4.57%)
	N	(20.8%)		(7.3%)	(6.1%)
		(5.29%)		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

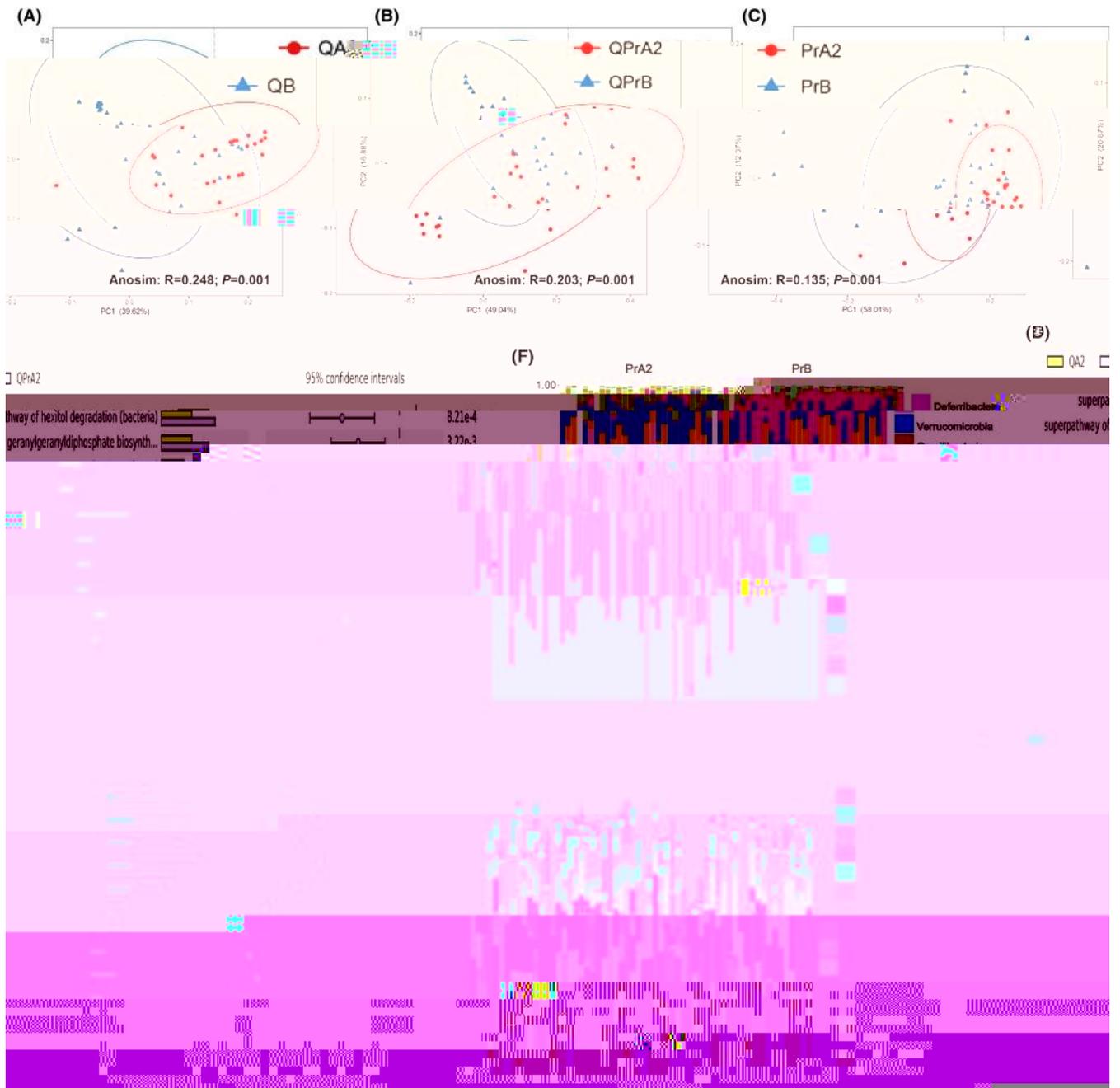
(F) (QPrB) (GPrB);(C) (PrB) PCoA (QB) (q2) ;(B)
(G) (PrB) (pr2) (pr2) (pr2) (D) QA2 QPrA2 ;(E) PrB pr2
(H) (PrB) (pr2) (pr2) 15 2 (I)

Hp Hp
Hp 22%
(2)

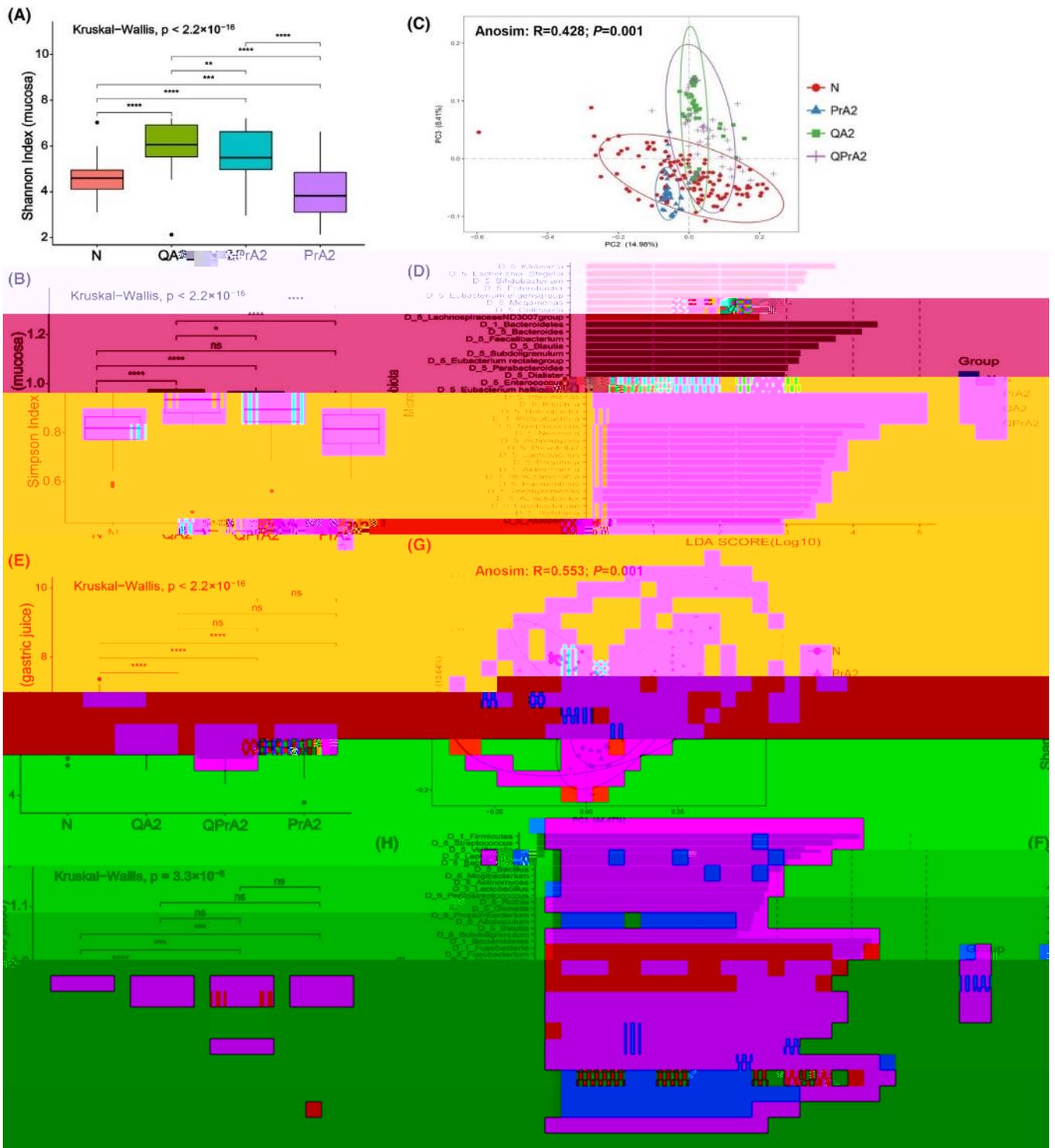
77.92%

32

33



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



(QA2 QPrA2 PrA2) Shannon Simpson 2 (QPrA2) (qqa2)
 H. pylori (N) (G) PCoA N 3
 N QA2 (H) LefSe PrA2 (C) PCoA N 3
 (QA2 QPrA2 PrA2) (E) Shannon (F) Simpson
 H. pylori (N) (G) PCoA N 3
 N QA2 (H) LefSe PrA2 (C) PCoA N 3

Fusobacteria) (,Porphyromonas,

N

2

14,15,34,35

35

1.54%

(2.03%)

(0.0082%)

35

(Fusobacterium,

Fusobacteria) ³⁶ P

N

)³⁷

)³⁸ N

lwofii anitratu

39

40

lwofii

⁴¹ lwofii

- 8

42

lwofii

43

lwofii

48 , 49 , 50
 51 *ventriosum*,⁵²
 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)

2

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VacA

MBio 4 (3): 2013; e609-e612

2021;00:e12848

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

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_ N	2.91909344
Methylobacteriaceae.D_5_Methylobacterium			
D_0_Bacteria.D_1_Plantomycetes.D_2_Plantomycetacia.D_3_Plantomycetales		D_4_ N	2.91711111
Plantomycetaceae.D_5_Gemmata			
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Lachnospiraceae		D_5_ N	2.29693209
Eubacterium_rectalegroup			
D_0_Bacteria D_1_Firmicutes P			4.16815777
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Streptococcaceae		D_5_ Streptococcus P	3.8104557
D_0_Bacteria D_1_Bacteroidetes P D_0_Bacteria D_1_Fusobacteria P			3.72915656
D_0_Bacteria.D_1_Fusobacteria.D_2_Fusobacteriia.D_3_Fusobacteriales.D_4_Fusobacteriaceae		D_5_ P	3.51824737
			3.42371271
D_0_Bacteria.D_1_Proteobacteria.D_2_Betaproteobacteria.D_3_Neisseriales.D_4_Neisseriaceae		D_5_ P	3.38083865
			3.31405553
D_0_Bacteria.D_1_Proteobacteria.D_2_Epsilonproteobacteria.D_3_Campylobacterales		D_4_ P	3.11133216
Helicobacteraceae.D_5_Helicobacter			
D_0_Bacteria.D_1_Actinobacteria.D_2_Actinobacteria.D_3_Actinomycetales		D_4_ P	2.96317977
Actinomycetaceae.D_5_Actinomyces			
D_0_Bacteria.D_1_Proteobacteria.D_2_Epsilonproteobacteria.D_3_Campylobacterales		D_4_ P	2.87332037
Campylobacteraceae.D_5_Campylobacter			
D_0_Bacteria.D_1_Bacteroidetes.D_2_Bacteroidia.D_3_Bacteroidales.D_4_Porphyrimonadaceae		D_5_ P	2.85705228
Porphyromonas			
D_0_Bacteria.D_1_Firmicutes.D_2_Negativicutes.D_3_Selenomonadales.D_4_Veillonellaceae		D_5_ P	2.80222108
			2.79100979
D_0_Bacteria.D_1_Firmicutes.D_2_Clostridia.D_3_Clostridiales.D_4_Peptostreptococcaceae		D_5_ P	2.72295299
			2.67501231
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Bacillales.D_4_FamilyXI		D_5_ Gemella P	2.64684346
D_0_Bacteria.D_1_Actinobacteria.D_2_Actinobacteria.D_3_Micrococcales.D_4_Micrococcaceae		D_5_ P	
D_0_Bacteria.D_1_Fusobacteria.D_2_Fusobacteriia.D_3_Fusobacteriales.D_4_Leptotrichiaceae		D_5_ P	
D_0_Bacteria.D_1_Firmicutes.D_2_Bacilli.D_3_Lactobacillales.D_4_Carnobacteriaceae		D_5_ Granulicatella P	
D_0_Bacteria.D_1_Proteobacteria.D_2_Gammaproteobacteria.D_3_Pseudomonadales		D_4_ P	
Moraxellaceae.D_5_Acinetobacter			

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

(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

	QB	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 D_4__Mycobacteriaceae.D_5__Mycobacterium	QB	3.65531265
D_0__Bacteria.D_1__Proteobacteria.D_2__Alphaproteobacteria.D_3__Rhizobiales D_4__Methylobacteriaceae.D_5__Methylobacterium	QB	3.38529279

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

3.
0
7
7
0
8
2
5
4

3.
0
6
8
1
6
7
5
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%)			