

Supplementary Table S2.

Biomarkers	Groups	LDA	p
D1__Bacteria.D2__Proteobacteria.D3__Gammaproteobacteria.	No-	4.3553	0.0001
D4__Enterobacteriales	POAF	36	59
D1__Bacteria.D2__Proteobacteria.D3__Gammaproteobacteria.	No-	4.3553	0.0001
D4__Enterobacteriales.D5__Enterobacteriaceae	POAF	36	59
D1__Bacteria.D2__Proteobacteria.D3__Gammaproteobacteria	No-	4.2403	0.0015
	POAF	85	77
D1__Bacteria.D2__Proteobacteria.D3__Gammaproteobacteria.	No-	4.1069	0.0012
D4__Enterobacteriales.D5__Enterobacteriaceae.D6__ <i>Escherichia Shigella</i>	POAF	85	74
D1__Bacteria.D2__Proteobacteria	No-	3.9950	0.0229
	POAF	73	58
D1__Bacteria.D2__Actinobacteria	POAF	3.9180	7.18 × 10 <sup>-5</sup>
D1__Bacteria.D2__Proteobacteria.D3__Gammaproteobacteria.	No-	3.8750	0.0005
D4__Enterobacteriales.D5__Enterobacteriaceae.D6__ <i>Klebsiella</i>	POAF	9	15
D1__Bacteria.D2__Actinobacteria.D3__Actinobacteria	POAF	3.8063	0.0013
		72	39
D1__Bacteria.D2__Proteobacteria.D3__Alphaproteobacteria.D4__Caulobacteriales	POAF	3.7392	0.0270
		17	78
D1__Bacteria.D2__Proteobacteria.D3__Alphaproteobacteria.D4__Caulobacteriales.D5__Caulobacteraceae	POAF	3.7384	0.0274
		13	32
D1__Bacteria.D2__Proteobacteria.D3__Alphaproteobacteria.D4__Caulobacteriales.D5__Caulobacteraceae.D6__ <i>Brevundimonas</i>	POAF	3.6909	0.0083
		53	09
D1__Bacteria.D2__Proteobacteria.D3__Gammaproteobacteria.	POAF	3.6323	0.0257
D4__ <i>Pseudomonadales</i> .D5__Moraxellaceae		91	98
D1__Bacteria.D2__Proteobacteria.D3__Gammaproteobacteria.	POAF	3.6051	0.0205
D4__Pseudomonadales.D5__Moraxellaceae.D6__ <i>Acinetobacter</i>		87	19
D1__Bacteria.D2__Proteobacteria.D3__Alphaproteobacteria.D4__Rhizobiales	POAF	3.5574	0.0078
		77	93
D1__Bacteria.D2__Bacteroidetes.D3__Bacteroidia.D4__Bacteroidales.D5__ <i>Prevotellaceae</i> .D6__ <i>Alloprevotella</i>	No-	3.4248	7.66 × 10 <sup>-7</sup>
	POAF	63	
D1__Bacteria.D2__Actinobacteria.D3__Actinobacteria.D4__Micrococcales	POAF	3.3779	0.0181
		31	87
D1__Bacteria.D2__Firmicutes.D3__Clostridia.D4__Clostridiales.D5__Lachnospiraceae.D6__ <i>Ruminococcus gnavus</i> group	No-	3.3471	0.0008
	POAF	46	37
D1__Bacteria.D2__Proteobacteria.D3__Gammaproteobacteria.	No-	3.3309	0.0095
D4__Enterobacteriales.D5__Enterobacteriaceae.D6__ <i>Citrobacter</i>	POAF	02	54
D1__Bacteria.D2__Firmicutes.D3__Clostridia.D4__Clostridiales.D5__Ruminococcaceae.D6__ <i>Ruminococcus</i> 2	No-	3.3215	0.0078
	POAF	32	63
D1__Bacteria.D2__Actinobacteria.D3__Thermoleophilia	POAF	3.3123	0.0101
		96	72

D1__Bacteria.D2__Firmicutes.D3__Clostridia.D4__Clostridiales.D5__Lachnospiraceae.D6__ <b>Lachnospira</b>	POAF	3.2797	0.0086
		77	72
D1__Bacteria.D2__Actinobacteria.D3__Coriobacteriia.D4__Coriobacteriales.D5__Atopobiaceae.D6__ <b>Olsenella</b>	No- POAF	3.2534	0.0166
		76	56
D1__Bacteria.D2__Firmicutes.D3__Erysipelotrichia.D4__Erysipelotrichales	No- POAF	3.2244	0.0269
		11	29
D1__Bacteria.D2__Firmicutes.D3__Erysipelotrichia	No- POAF	3.2244	0.0269
		11	29
D1__Bacteria.D2__Firmicutes.D3__Erysipelotrichia.D4__Erysipelotrichales.D5__Erysipelotrichaceae	No- POAF	3.2244	0.0269
		11	29
D1__Bacteria.D2__Verrucomicrobia.D3__Verrucomicrobiae	POAF	3.2201	0.0024
		05	66
D1__Bacteria.D2__Verrucomicrobia	POAF	3.2201	0.0024
		05	66
D1__Bacteria.D2__Actinobacteria.D3__Thermoleophilia.D4__Gaiellales	POAF	3.2064	0.0158
		38	82
D1__Bacteria.D2__Proteobacteria.D3__Gammaproteobacteria.D4__Aeromonadales	POAF	3.2038	2.05 ×
		35	10 <sup>-12</sup>
D1__Bacteria.D2__Proteobacteria.D3__Gammaproteobacteria.D4__Aeromonadales.D5__Aeromonadaceae	POAF	3.1808	3.64 ×
		08	10 <sup>-12</sup>
D1__Bacteria.D2__Proteobacteria.D3__Gammaproteobacteria.D4__Aeromonadales.D5__Aeromonadaceae.D6__ <b>Aeromonas</b>	POAF	3.1808	3.64 ×
		08	10 <sup>-12</sup>
D1__Bacteria.D2__Acidobacteria	POAF	3.1792	0.0252
		49	04
D1__Bacteria.D2__Proteobacteria.D3__Alphaproteobacteria.D4__Rhizobiales.D5__Rhizobiaceae	POAF	3.1713	0.0253
		25	12
D1__Bacteria.D2__Proteobacteria.D3__Alphaproteobacteria.D4__Rhizobiales.D5__Rhizobiaceae.D6__Allorhizobium_Neorhizobium_Pararhizobium_ <b>Rhizobium</b>	POAF	3.1648	0.0261
		91	3
D1__Bacteria.D2__Firmicutes.D3__Bacilli.D4__Bacillales	POAF	3.1465	0.0318
		62	55
D1__Bacteria.D2__Verrucomicrobia.D3__Verrucomicrobiae.D4__Verrucomicrobiales	POAF	3.1399	0.0139
		19	35
D1__Bacteria.D2__Verrucomicrobia.D3__Verrucomicrobiae.D4__Verrucomicrobiales.D5__Akkermansiaceae	POAF	3.1399	0.0105
		16	14
D1__Bacteria.D2__Verrucomicrobia.D3__Verrucomicrobiae.D4__Verrucomicrobiales.D5__Akkermansiaceae.D6__Akkermansi	POAF	3.1399	0.0105
a		16	14
D1__Bacteria.D2__Proteobacteria.D3__Alphaproteobacteria.D4__Rhizobiales.D5__Xanthobacteraceae	POAF	3.1112	0.0045
		56	47
D1__Bacteria.D2__Proteobacteria.D3__Gammaproteobacteria.D4__Pasteurellales.D5__Pasteurellaceae	No- POAF	3.0557	7.77 ×
		87	10 <sup>-5</sup>
D1__Bacteria.D2__Proteobacteria.D3__Gammaproteobacteria.D4__Pasteurellales	No- POAF	3.0557	7.77 ×
		87	10 <sup>-5</sup>

D1__Bacteria.D2__Proteobacteria.D3__Gammaproteobacteria.	No-	3.0229	9.46 ×
D4__Pasteurellales.D5__Pasteurellaceae.D6__ <b>Haemophilus</b>	POAF	02	10 <sup>-5</sup>

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