

Table 1: Anthropomorphic and clinical characteristics of patients, as means +/- standard deviation. * Statistically different when Wilcoxon P-value <0.05. **O**: Obese; **E**: Extremely Obese; **N**: Non-Obese.

Anthropomorphic and clinical characteristics of patients							
Characteristics	All patients	Extremely Obese	Non obese	Obese	p-value E vs N	p-value O vs N	p-value E vs O
	62	26	16	20	Wilcoxon p-value < 0.05	Wilcoxon p-value < 0.05	Wilcoxon p-value < 0.05
Age (years)	44.48±13.72	41.96±11.8	49.88±12.21	43.45±16.40	0.032*	0.1385	1
Woman (n)	43 (69%)	18 (69%)	8 (50%)	17 (85%)			
Smoker (n)	7 (11.2%)	3 (11.5%)	2 (12.5%)	2 (10%)	ns	ns	ns
Height (m)	1.66±0.069	1.66±0.075	1.67±0.07	1.67±0.064	0.6324	0.6546	0.5626
Weight (kg)	108.75±31.26	136.70±20.74	68.93±7.73	104.27±10	7.565e-08*	3.664e-07*	3.167e-07*
BMI (kg/m2)	39.15±11.15	49.64±6.84	24.67±2.19	37.07±1.53	7.67e- 08****	3.81e-07****	3.57e-13****
Waist (cm)	114.35±23.38	133.34±16.35	86.56±9.45	111.9±13.50	1.156e-08*	1.523e-07*	1.5e-05*
Blood Glucose (mg/dl)	109.41±33.22	115.69±45.97	103.38±10.75	106.06±23.97	0.969	0.7501	0.7063
Total Cholesterol (mmol/L)	181.92±36.64	185.50±35.89	175.49±35.09	182.40±39.89	0.4071	0.514	0.903
HDL Cholesterol (mmol/L)	43.33±12.40	43.55±10.92	43.51±17.52	42.90±9.72	0.4371	0.3476	0.5796
GOT	29.99±30.60	36.98±34.54	26.85±37.13	23.43±15.07	0.02419*	0.5036	0.04855*
GPT	32.72±24.52	44.21±29.79	18.11±8.66	29.46±18.23	0.0005431*	0.02582*	0.07802
GGT	53.31±110	67.61±146	27.83±15.92	55.11±98.85	0.08029	0.3078	0.4379
HCT %	41.09±4.79	42.24±6.21	39.81±3.86	40.63±2.79	0.2597	0.487	0.4378

Table 2: Relative abundances. Phyla (%) in groups of patients and statistical significance between groups. * Statistically different when Wilcoxon P-value <0.05.

Relative abundance of the top 10 bacteria at the Phyla level of taxonomy						
Phyla	Non obese	Obese	Extremely obese	N vs O	O vs E	N vs E
	%	%	%	Wilcoxon P- value <0.05	Wilcoxon P- value <0.05	Wilcoxon P- value <0.05
Proteobacteria	79.34	83.05	82.11	0.77	0.41	0.29
Firmicutes	7.1	7.57	4.98	0.82	0.96	0.83
Actinobacteriota	8.75	5.29	4.74	0.69	0.46	0.73
Bacteroidota	2.32	1.72	2.29	0.43	0.32	0.95
Campilobacterota	1.45	2.03	5.56	1	0.64	0.6
Fusobacteriota	0.45	0.29	0.09	0.041	0.1	0.41
Acidobacteriota	0.21	0.02	0.08	0.87	0.15	0.29
Verrucomicrobiota	0.3	0	0			
Bellovibrionota	0.02	0	0.06			
Spirochaetota	0	0	0.09			
Others	0.07	0.03	0			

Table 3: Relative abundances. Top 10 most abundant families (%) in groups of patients and statistical significance between groups. * Statistically different when Wilcoxon P-value <0.05. **O**: Obese; **E**: Extremely Obese; **N**: Non-Obese.

Relative abundance of the top 10 bacteria at the Family level of taxonomy						
Family	Non obese	Obese	Extremely Obese	N vs O	O vs E	N vs E
	%	%	%	Wilcoxon P-value < 0.05	Wilcoxon P-value < 0.05	Wilcoxon P-value < 0.05
Enterobacteriaceae	15.07	17.24	16.74	0.69	0.96	0.99
Pseudomonadaceae	12.26	15.31	16.41	0.19	0.97	0.27
Yersiniaceae	7.4	18.06	16.53	0.013*	0.78	0.0041**
Burkholderiaceae	21.39	5.71	9.05	0.0012**	0.28	0.0063**
Comamonadaceae	6.37	3.87	5.14	0.3	0.27	0.71
Alcaligenaceae	4.19	5.01	4.49	0.13	0.97	0.025*
Xanthomonadaceae	0.92	5.84	4.82	0.016*	0.96	0.0025**
Helicobacteraceae	1.22	1.98	5.49	0.4	0.095	0.018*
Moraxellaceae	3.96	2.23	1.36	0.26	0.34	0.29
Micrococcaceae	3.01	1.6	1.96	0.11	0.65	0.13

Table 4: Summary of the discriminant taxa identified by multiple multivariate analyses. Network, sPLS, Random Forest analyses were compared.

Bacteria discriminant found by different methods			
Bacteria	Network	sPLS DA	Random Forest
	Alcaligenaceae	Alcaligenaceae	Alcaligenaceae
	Burkholderiaceae	Burkholderiaceae	Burkholderiaceae
	Morganellaceae	Morganellaceae	Morganellaceae
	Xanthomonadaceae	Xanthomonadaceae	Xanthomonadaceae
	Yersiniaceae	Yersiniaceae	

Table 5: Discriminant molecular pathways as a signature of non-obese and obese groups. Are represented the pathways identifications in Metacyc and its equivalent in KEGG. The obese and extremely obese groups were pooled since almost no discriminant pathways were identified between these two groups.

Pathways discriminant found in different BMI groups		
Pathways	Non obese	Obese and Extremely obese
	PWY-6269	PWY-6165
	PWY-5509	PWY-7446
	PWY-6397	GOLPDLCAT-PWY
	P184-PWY	P125-PWY
	PWY-7295	PWY-1361
	GOBALSYN-PWY	PWY-6660
		AEROBACTINSYN-PWY
		PWY-5651
		CHLOROPHYLL-SYN
		PWY-7046
		PWY-7391

Table 6: KEGG Pathways obtained by iPath 3 for BMI group

BMI Group	KEGG Pathways
Non obese	map00052: Galactose metabolism map00520: Amino sugar and nucleotide sugar metabolism map00860: Porphyrin and chlorophyll metabolism
Obese and Extremely obese	map00561: Glycerolipid metabolism map00680: Methane metabolism map00400: Phenylalanine, tyrosine and tryptophan biosynthesis map00290: Valine, leucine and isoleucine biosynthesis map00650: Butanoate metabolism map00660: C5-Branched dibasic acid metabolism map00760: Nicotinate and nicotinamide metabolism map00380: Tryptophane metabolism map00260: Glycine, serine and threonine metabolism map00270: Cysteine and methionine metabolism map00030: Lysine biosynthesis map00860: Porphyrin and chlorophyll metabolism