

# First Descriptive Analysis of the Faecal Microbiota of Wild and Anthropized Barbary Macaques (*Macaca sylvanus*) in the Region of Bejaia, Northeast Algeria

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**Table S1: A measure of sampling effort for each sample using Good's coverage estimator (rarefied table at 10,000 sequences per sample).**

Samples label	Good's coverage (%)
TPG 01	99.79%
TPG 02	99.70%
TPG 03	99.71%
TPG 04	99.82%
TPG 05	99.82%
TPG 06	99.78%
WFG 01	99.83%
WFG 02	99.85%
WFG 03	99.69%
WFG 04	99.75%
WFG 05	99.74%
WFG 06	99.77%



Table S3: The average proportions of Barbary macaque fecal microbiota at phylum level between the TP and WF groups.

Phylum	TPG		WFG	
	Average proportions (%)	S.D (%)	Average proportions (%)	S.D (%)
Firmicutes	94.84135765	71.79498625	93.2697723	69.08536031
Bacteroidetes	<b>0.826921863</b>	0.986793702	<b>4.297393312</b>	5.468066568
Tenericutes	0.318547131	0.203765701	0.52564215	0.724610482
Actinobacteria	0.216688215	0.250110694	0.428547018	0.535452457
Proteobacteria	0.380860213	0.466759419	0.297148029	0.299609051
Bacteria_ph	0.101327325	0.09848449	0.261430321	0.308472218
Cyanobacteria	0.057117246	0.042546163	0.108038838	0.05544829
Verrucomicrobia	<b>2.088066581</b>	2.159629286	<b>0.07798574</b>	0.104098689
Epsilonbacteraeota	0.028560695	0.031495675	0.001783294	0.003987567
Patescibacteria	0.010080253	0.011656221	0.001685204	0.00376823
Spirochaetes	0.663707193	0.934527339	0	0
WPS-2	0.060361654	0.081889499	0	0

**Table S4: The average proportions of Barbary macaque fecal microbiota at genus level between the TP and WF groups.**

Genus	TPG		WFG		p-values	
	Average	S.D	Average	S.D	p-values	corrected
	proportions (%)	(%)	proportions (%)	(%)		
Ruminococcaceae_UCG-002	8.22096752	7.0761071	28.0225812	16.9302915	0.04813761	0.67713577
Ruminococcaceae_ge	4.077813668	2.89077892	20.6580866	15.1114187	0.05747591	0.71337743
Ruminococcus_2	21.09481273	10.4449885	0.62848252	0.61090222	0.00708275	0.37361491
Ruminococcaceae_UCG-005	4.116826587	2.38856974	12.229966	1.54294056	0.00016015	0.03379235
Faecalibacterium	15.90466835	12.96292	0.53312671	0.39644314	0.04532514	0.73566188
Christensenellaceae_R-7_group	6.630294098	2.74685809	1.0837972	0.36402852	0.00602445	0.42371994
Subdoligranulum	6.460949457	4.68995541	1.38162776	1.34721996	0.06015603	0.70516236
Ruminococcaceae_UCG-010	0.875854029	1.38892077	7.31382	5.14795669	0.03729085	0.78683684
Dorea	4.72331511	2.3782348	0.26436299	0.32859089	0.00819821	0.34596426
Lachnospiraceae_ge	3.152472345	1.82190392	2.67551564	1.6315939	0.67215572	0.72359621
Blautia	2.796397509	1.66430774	0.82936693	1.26619486	0.06367894	0.70717136
Ruminococcaceae_UCG-013	0.453843344	0.2030036	3.06293237	2.6735486	0.080913	0.74228883
Ruminococcaceae_NK4A214_group	0.352747653	0.1322385	2.36610889	1.50649851	0.03032927	0.79993457
Erysipelotrichaceae_UCG-003	3.285285733	3.78399277	0.46114911	0.37676798	0.15653782	0.76812744
Prevotella_9	0.104123456	0.06725261	2.11391167	2.19176007	0.09560356	0.80689402
Clostridiales_Family_XIII_AD3011_group	1.134299192	0.77431504	0.67798938	0.36542613	0.27157572	0.68217235
Ruminococcaceae_UCG-014	1.677586276	1.43836958	0.8706717	1.09163328	0.34290509	0.75367682
Akkermansia	2.088066581	2.15962929	0.07798574	0.10409869	0.091942	0.80832339
Clostridiales_Family_XIII_ge	1.286141769	1.72363984	1.0472682	1.50005778	0.81997501	0.86942074
Dialister	0.402175796	0.54161521	0.78299369	0.92463679	0.44955517	0.54830139
Lachnospiraceae_NK4A136_group	0.444445032	0.31284128	0.04110999	0.03647437	0.0341909	0.80158658
Marvinbryantia	0.613767399	0.69400072	0.02128221	0.03437064	0.11459658	0.83378892

Clostridiales_vadinBB60_group_ge	0.01847603	0.02422983	0.40004541	0.36596554	0.06706978	0.67389156
Mollicutes_RF39_ge	0.308450654	0.18946336	0.46769848	0.65017413	0.61836646	0.68311687
Rikenellaceae_ge	0.041919881	0.05079602	0.50624908	0.59609794	0.14233517	0.77006974
Coprococcus_3	0.482516245	0.42086207	0.12965872	0.17677867	0.12937606	0.80289262
Bacteroidales_ge	0.082304824	0.12243411	0.42005867	0.41903662	0.13564606	0.81775195
Muribaculaceae_ge	0.391965603	0.5209604	0.12604965	0.07475135	0.30791563	0.70619781
Solobacterium	0.228419124	0.13393793	0.01858528	0.01682345	0.01686735	0.50843025
Candidatus_Stoquefichus	0.193312001	0.18772405	0.17741607	0.29684759	0.9217517	0.95807689
Ruminococcus_1	0.273517981	0.32043287	0.42919689	0.82389918	0.70637924	0.75657878
Bacteria_ge	0.101327325	0.09848449	0.26143032	0.30847222	0.3111969	0.70604888
Ruminiclostridium_6	0.065536105	0.08996252	0.18852079	0.11845272	0.09636694	0.7820548
Gastranaerophilales_ge	0.057117246	0.04254616	0.10803884	0.05544829	0.13637332	0.79929921
Coprococcus_1	0.365552337	0.4072913	0.05444758	0.05833399	0.14936475	0.78789906
Rhodospirillales_ge	0.01011003	0.01166408	0.15487377	0.16165206	0.10170855	0.79483345
Coriobacteriales_ge	0.065567743	0.09943914	0.37138423	0.44717835	0.19056543	0.62827039
Lactobacillus	0.201135341	0.23605452	0.02201995	0.03574008	0.15170099	0.78070509
Christensenellaceae_ge	0.077341493	0.02445028	0.04542072	0.04483099	0.20097713	0.63292799
Ruminiclostridium_5	0.099197271	0.03748149	0.01552093	0.01470373	0.00284992	0.30066673
Fusicatenibacter	0.179433876	0.20118691	0.06454182	0.0982924	0.2876482	0.7057415
Rikenellaceae_RC9_gut_group	0.067399539	0.05795919	0.5864638	1.19579124	0.37663267	0.47873189
Prevotellaceae_ge	0.035276514	0.02160297	0.42177236	0.81455924	0.33732598	0.74921875
Escherichia-Shigella	0.099144736	0.07468659	0.0072193	0.00827121	0.03997709	0.76683335
Clostridiales_ge	0.026850073	0.02439611	0.08617842	0.06679341	0.1089437	0.82096861
Holdemanella	0.132076582	0.21142416	0.0424996	0.03666657	0.39112846	0.49418027
Ruminococcaceae_UCG-003	0.088985924	0.09277447	0.03313923	0.02828822	0.24594366	0.64867639
Ruminococcaceae_UCG-009	0.003352276	0.00474084	0.16481511	0.23161045	0.17980416	0.61191415
Agathobacter	0.001677571	0.00375116	1.21860526	2.39617236	0.30760256	0.71323232
Phascolarctobacterium	3.521397617	7.70806465	0.0018754	0.00419352	0.35409001	0.77023702

Alloscardovia	0.060462834	0.03427715	0	0	0.01091291	0.38377073
Burkholderiaceae_ge	0	0	0.05661436	0.05418336	0.06667877	0.70346103
Ruminiclostridium_9	0.036893871	0.02823094	0.04993038	0.0573658	0.6617152	0.71600978
Coprococcus_2	0.224613721	0.34836854	0.01384807	0.01466189	0.23422572	0.65028457
Succinivibrio	0.224620318	0.31419098	0.03770354	0.02653142	0.24156125	0.64518259
Clostridium_sensu_stricto_1	0.005026138	0.00767579	0.10655054	0.13534949	0.15449892	0.77617314
Lachnospiraceae_ND3007_group	0.003351432	0.00473964	0.09042096	0.12254811	0.17308417	0.77703746
Streptococcus	0.038785695	0.03016069	0.01640609	0.02403699	0.22498987	0.6329715
Coriobacteriales_ge_ge	0.010113922	0.0082694	0.05716279	0.0882741	0.28782209	0.69805128
Anaeroplasma	0.010096477	0.01430234	0.05794367	0.07443636	0.21333647	0.60829724
Anaerosporeobacter	0.04027653	0.03528731	0	0	0.05112766	0.67424604
Alistipes	0	0	0.05613423	0.06624919	0.11665951	0.79403731
Lachnospiraceae_UCG-010	0.015092407	0.02582476	0.02434147	0.01640404	0.51707497	0.59946603
Ruminococcaceae_UCG-008	0.025238426	0.02834956	1.64118005	3.65067231	0.36773963	0.47603105
Butyricicoccus	0.015117267	0.01265576	0.0266144	0.02775872	0.42728353	0.52723289
Sarcina	0.045562246	0.05133229	0.00524581	0.00785762	0.1404553	0.8009748
Anaerostipes	0.067310564	0.08909995	0.01561262	0.02003068	0.2565107	0.66819455
Lachnospira	0.020193524	0.02665597	0.06379742	0.0775523	0.27822522	0.6906532
Oxalobacter	0.015107235	0.0112791	0.01357515	0.02157247	0.89176685	0.93149904
Olsenella	0.075493185	0.10307429	0	0	0.16240405	0.76149453
Prevotellaceae_UCG-001	0.051959674	0.06264869	0	0	0.12282757	0.78535205
Parabacteroides	0.013412304	0.01382776	0.01393962	0.01640156	0.9572807	0.98051567
Ralstonia	0	0	0.01521364	0.01263568	0.043181	0.75926598
Anaerofustis	0.03357577	0.04672558	0.01186915	0.01476386	0.36024355	0.76011388
Campylobacter	0.028560695	0.03149567	0.00178329	0.00398757	0.11615555	0.81696072
Defluviitaleaceae_UCG-011	0.03018414	0.03842536	0.11551469	0.25354372	0.48890708	0.58282143
Roseburia	0.103953267	0.13661921	0.00514742	0.00515142	0.16684645	0.76531739
Lachnospiraceae_UCG-001	0.023495213	0.03320011	0.0471675	0.07606443	0.54436628	0.62424611

Intestinibacter	0.006698821	0.01497902	2.88385589	6.42490919	0.36262983	0.7575732
Anaerovibrio	0.011769538	0.00905917	0.00334504	0.00747974	0.14100078	0.78292539
Cellulosilyticum	0	0	0.0220531	0.02633366	0.12001306	0.79133613
Rickettsiales_fa_ge	0	0	0.00860324	0.00728312	0.04590031	0.69178323
Treponema_2	0.663707193	0.93452734	0	0	0.17313555	0.76107504
WPS-2_ge	0.060361654	0.0818895	0	0	0.16022083	0.7683317
Bacteroides	0.006700843	0.01110935	0.01066891	0.01267946	0.61032414	0.67778102
Alloprevotella	0.031859226	0.05820261	0.04214533	0.08073989	0.82236357	0.86759356
Ruminococcaceae_V9D2013_group	0.001674705	0.00374475	0.01039956	0.01219295	0.177536	0.61409994
Saccharimonadaceae_ge	0.010080253	0.01165622	0.0016852	0.00376823	0.17604243	0.61908254
Fastidiosipila	0.023552091	0.03630382	0	0	0.20657661	0.61391077
Rhodospirillales_fa_ge	0.006709164	0.00748967	0.00334504	0.00747974	0.49353091	0.58502821
Atopobiaceae_ge	0.00505053	0.00505073	0	0	0.07559506	0.72502534
Peptococcaceae_ge	0.010070534	0.01423468	0	0	0.17450775	0.75145174
Lachnospiraceae_FCS020_group	0.39212006	0.58223454	0.00523911	0.00810302	0.19748218	0.63134455
Psychrobacter	0.02516873	0.04744899	0	0	0.28887043	0.6926325
Erysipelotrichaceae_UCG-004	0	0	0.06136537	0.09604684	0.21247827	0.62267937
GCA-900066225	0.00336025	0.00475215	0.00514136	0.00514564	0.58224598	0.65002064