

**Supplementary Table 1:** Selection of CP Patients and their status related to Human Papiloma Virus (HPV+/HPV-) used in present study.

	Age	Sex	HPV status
CP1	26	F	positive
CP2	22	M	negative
CP3	30	F	negative
CP4	22	F	negative
CP5	26	F	positive
CP6	50	F	negative
CP7	60	M	negative
CP8	60	F	negative
CP9	50	M	negative
CP10	37	M	negative
CP11	39	M	negative
CP12	34	M	negative
CP13	39	M	negative
CP14	22	F	negative
CP15	55	F	positive
CP16	44	F	negative
CP17	37	M	negative
CP18	40	F	negative
CP19	32	F	positive
CP20	66	F	negative
CP21	33	F	positive
CP22	18	F	negative
CP23	40	F	negative
CP24	39	F	positive
CP25	38	F	negative
CP26	48	M	positive
CP27	40	F	negative
CP28	30	M	negative
CP29	48	F	negative
CP30	36	M	negative
CP31	42	M	negative
CP32	32	M	negative
CP33	31	M	negative
CP34	30	F	negative
CP35	27	M	negative
CP36	42	M	negative
CP37	29	M	negative

CP38	49	M	negative
CP39	30	F	negative
CP40	35	F	negative

**Supplementary Table 2:** Multiplexing with PacBio Barcoded Universal Primers in CP samples

S. No	Sample Name	Barcode Primers Pair Used (Forward and Reverse Primers)	Pooling of Barcoded Samples and Library preparation
1	CP-1	F-R	Library 1
2	CP-2	F1-R1	Library 2
3	CP-3	F2-R1	
4	CP-4	F2-R2	
5	CP-6	F2-R3	
6	CP-7	F2-R4	
7	CP-8	F3-R1	
8	CP-9	F3-R2	
9	CP-10	F3-R3	
10	CP-11	F3-R4	
11	CP-13	F4-R1	
12	CP-14	F4-R2	
13	CP-15	F4-R3	
14	CP-16	F4-R4	
15	CP-18	F1-R1	
16	CP-12	F3-R4	
17	CP-5	F4-R3	
18	CP-19	F1-R2	
19	CP-20	F1-R3	
20	CP-17	F1-R3	
21	CP-21	F1-R1	
22	CP-22	F2-R1	
23	CP-23	F3-R1	
24	CP-24	F4-R1	
25	CP-25	F1-R2	
26	CP-26	F2-R3	
27	CP-27	F3-R3	
28	CP-28	F1-R1	
29	CP-29	F1-R2	
30	CP-30	F1-R3	
31	CP-31	F1-R4	
32	CP-32	F2-R1	
33	CP-33	F2-R2	
34	CP-34	F2-R3	

35	CP-35	F2-R4
36	CP-36	F3-R1
37	CP-37	F3-R2
38	CP-38	F3-R3
39	CP-39	F3-R4
40	CP-40	F4-R1

**Supplementary Table 3:** The number of processed full-length 16S rRNA sequences per CP samples ranged from 672 to 28,780 with an average of 7,357 reads/sample.

Sample Name	Number of Raw CCS Reads	Number of CCS Reads after filtering
CP1	9475	4192
CP2	6556	3736
CP3	16309	10405
CP4	9724	5731
CP5	37158	28780
CP6	12727	7802
CP7	18378	11864
CP8	7825	6007
CP9	7613	5792
CP10	11478	8858
CP11	11737	8586
CP12	25108	20363
CP13	15397	13282
CP14	8138	6149
CP15	10887	8885
CP16	11549	9311
CP17	10286	7811
CP18	6707	5403
CP19	9406	7515
CP20	5860	4690
CP21	14434	11687
CP22	6391	4693
CP23	9393	7172
CP24	11301	8993
CP26	7533	5573

CP27	9707	7193
CP30	3457	3148
CP31	772	672
CP32	5528	5172
CP33	1913	1652
CP34	4241	3544
CP35	6622	4767
CP36	6391	5701
CP37	3306	2928
CP38	4925	4399
CP39	4941	4119
CP40	6123	5646
Total Reads	359296	272774
Average No of Reads	9710.70	7357.32
±SD	6656.78	5117.64

**Supplementary Table 5a:** Alpha diversity values of shannon index for individual CP samples

<b>Group</b>	<b>Shannon</b>	<b>Shannon_Ici</b>	<b>Shannon_hci</b>
CP1	6.866257	6.810809	6.921705
CP10	7.614023	7.578461	7.649585
CP11	7.292934	7.252411	7.333456
CP12	7.996757	7.967874	8.025639
CP13	7.557078	7.498929	7.615228
CP14	7.246837	7.194382	7.299292
CP15	7.708749	7.671141	7.746356
CP16	7.778777	7.738416	7.819138
CP17	7.486967	7.44582	7.528114
CP18	7.244874	7.204657	7.285091
CP19	7.604914	7.572032	7.637797
CP2	6.740064	6.692445	6.787683
CP20	7.077464	7.037181	7.117747
CP21	7.510457	7.456783	7.564131
CP22	7.005247	6.953505	7.056988
CP23	7.217533	7.17357	7.261496
CP24	7.600276	7.5583	7.642252
CP26	7.079197	7.027381	7.131013
CP27	7.38128	7.331073	7.431487
CP3	7.707934	7.666318	7.74955
CP30	6.8497	6.801366	6.898034
CP31	5.60211	5.517967	5.686252
CP32	6.105019	5.995159	6.21488
CP33	5.974474	5.901364	6.047585
CP34	6.665454	6.604803	6.726104
CP35	5.514053	5.420546	5.607561
CP36	6.901879	6.852621	6.951137
CP37	6.587557	6.534557	6.640557
CP38	6.967821	6.921932	7.013711
CP39	6.992089	6.942125	7.042052
CP4	7.102627	7.047715	7.157538
CP40	6.785265	6.728457	6.842072
CP5	8.058471	8.017507	8.099434
CP6	7.799119	7.764647	7.833591
CP7	7.628564	7.596682	7.660446
CP8	7.111301	7.054793	7.16781
CP9	6.787735	6.730904	6.844566

**Supplementary Table 5b:** Alpha diversity analysis tests ANNOVA (Repeated Measures ANNOVA) equal means

	Sum of sqrs	df	Mean square	F	p (same)
Between groups	7.19713E <sup>09</sup>	5	1.43943E <sup>09</sup>	0.8979	<b>0.4837</b>
Within groups	-	222	1.59909E <sup>09</sup>	-	-
Error	-	185	1.60316E <sup>09</sup>	-	-
Between subjects	-	37	1.57878E <sup>09</sup>	-	-
Total	-	227	-	-	-

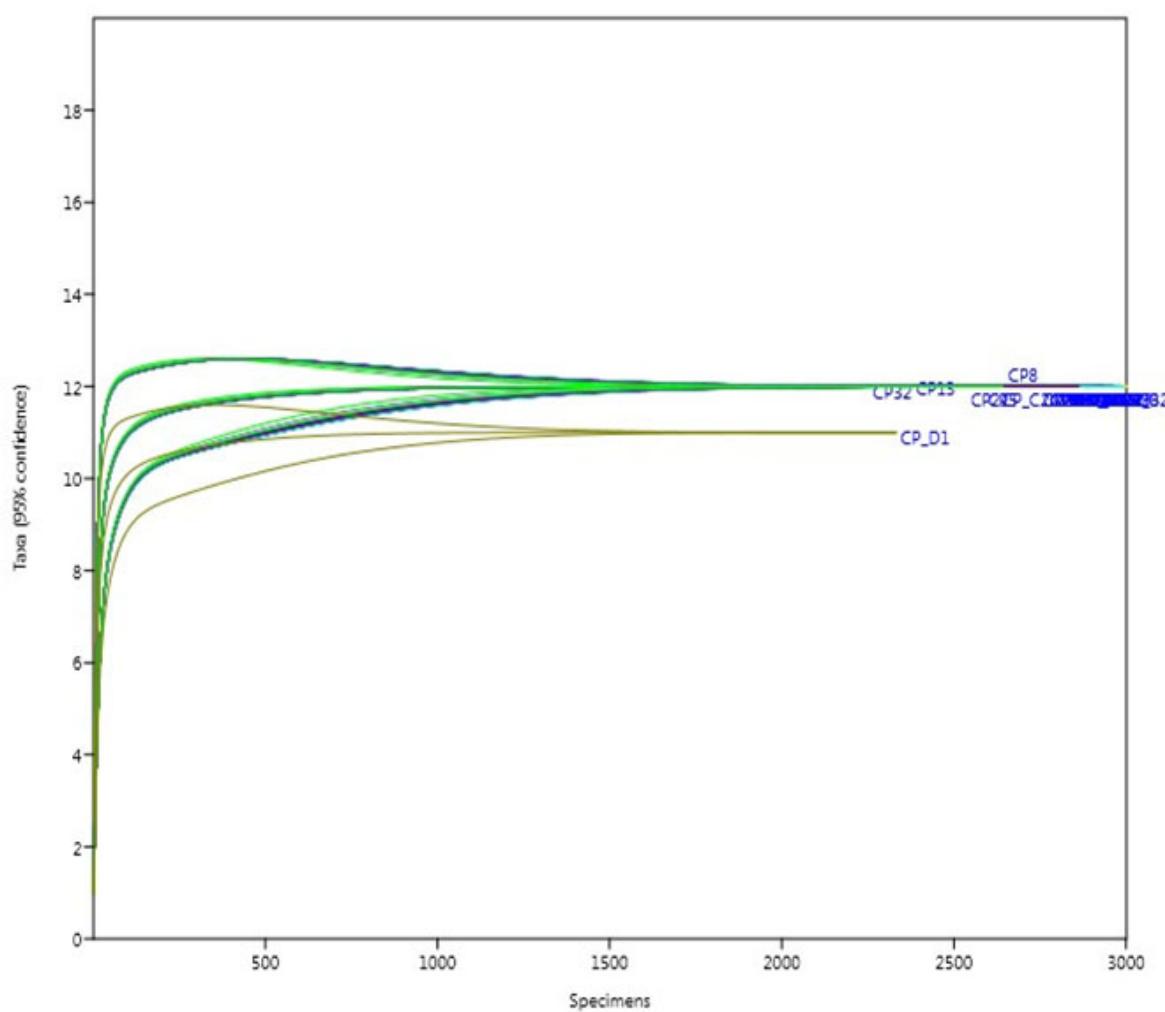
**Supplementary Table 5c:** Tukey's pairwise test showing no significant difference between sampled species in each sample.

nseqs	coverage	sobs	invsimpson	invsimpson_lci	invsimpson_hci
nseqs	0.9999	1	0.7584	0.999	0.8509
coverage	0.3461	0.9999	0.6038	0.9892	0.7176
sobs	0.04313	0.303	0.7404	0.9985	0.8365
invsimpson	1.906	2.252	1.949	0.9286	1
invsimpson_hci	0.5389	0.885	0.582	1.367	0.9694
invsimpson_hci	1.656	2.002	1.699	0.2498	1.117

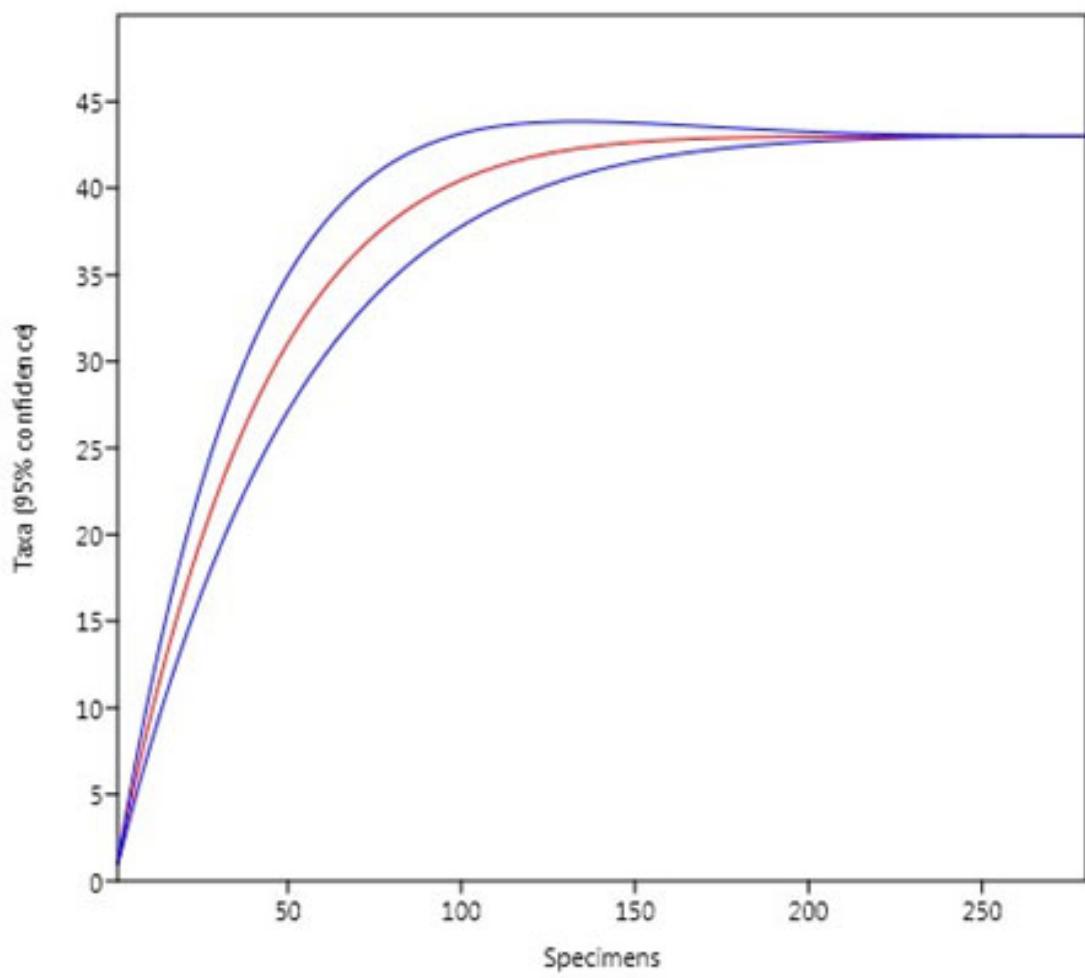
**Supplementary Table 6:** Different Indexes reporting Beta Diversity between HPV+ and HPV- CP dataset.

Whittaker:	2.1392
Harrison:	0.30561
Cody:	36.5
Routledge:	0.32126
Wilson-Shmida	3.6962
Mourelle:	0.52803
Harrison 2:	0.10317
Williams:	0.41935

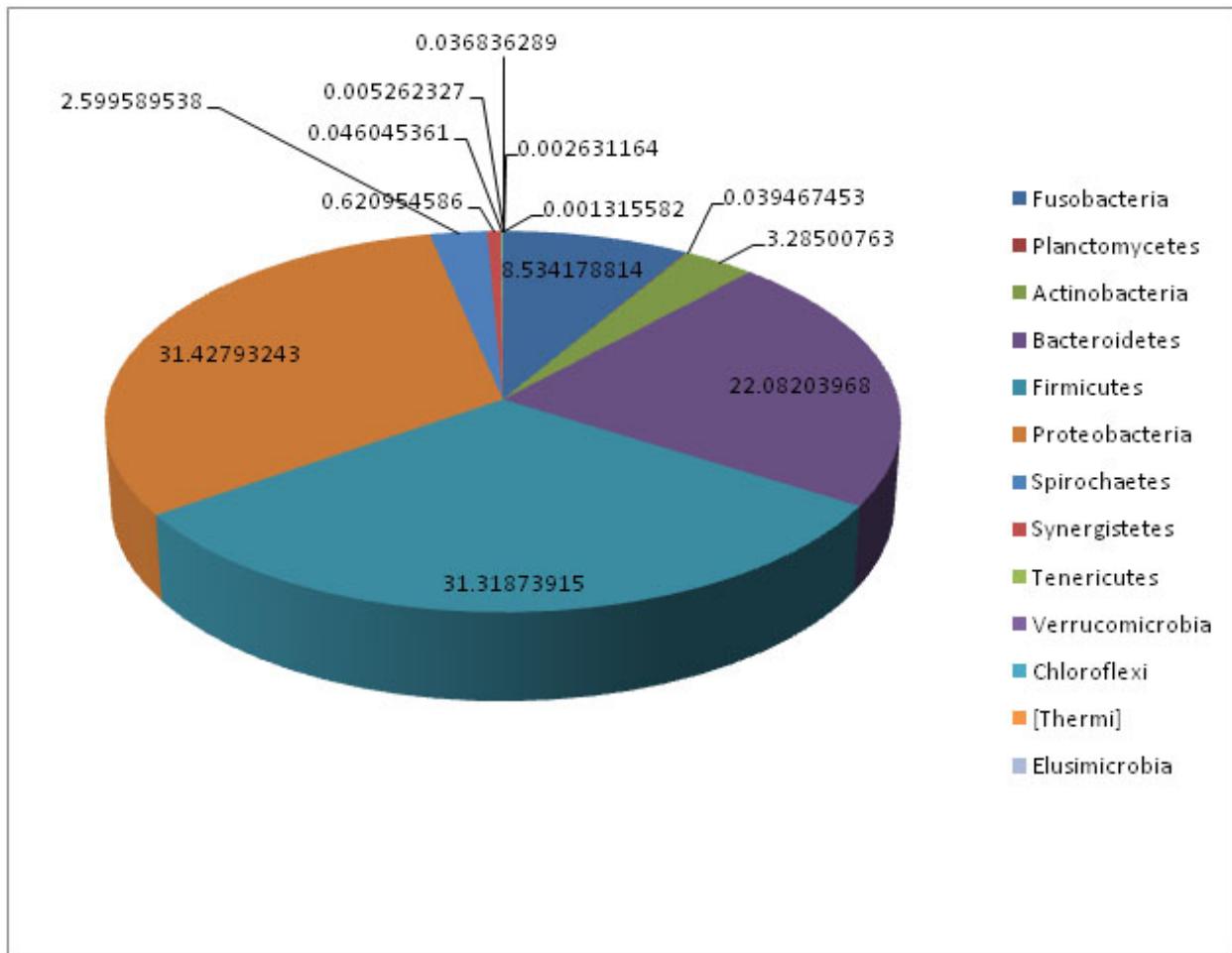
**Supplementary Figure 1a:** Rarefaction Curves calculated at 3% dissimilarity, compare the number of reads with the number of operational taxonomic units (OTUs) found in the DNA from the 40 CP samples. The curves for individual samples which nearly plateaued off for the majority of the samples.



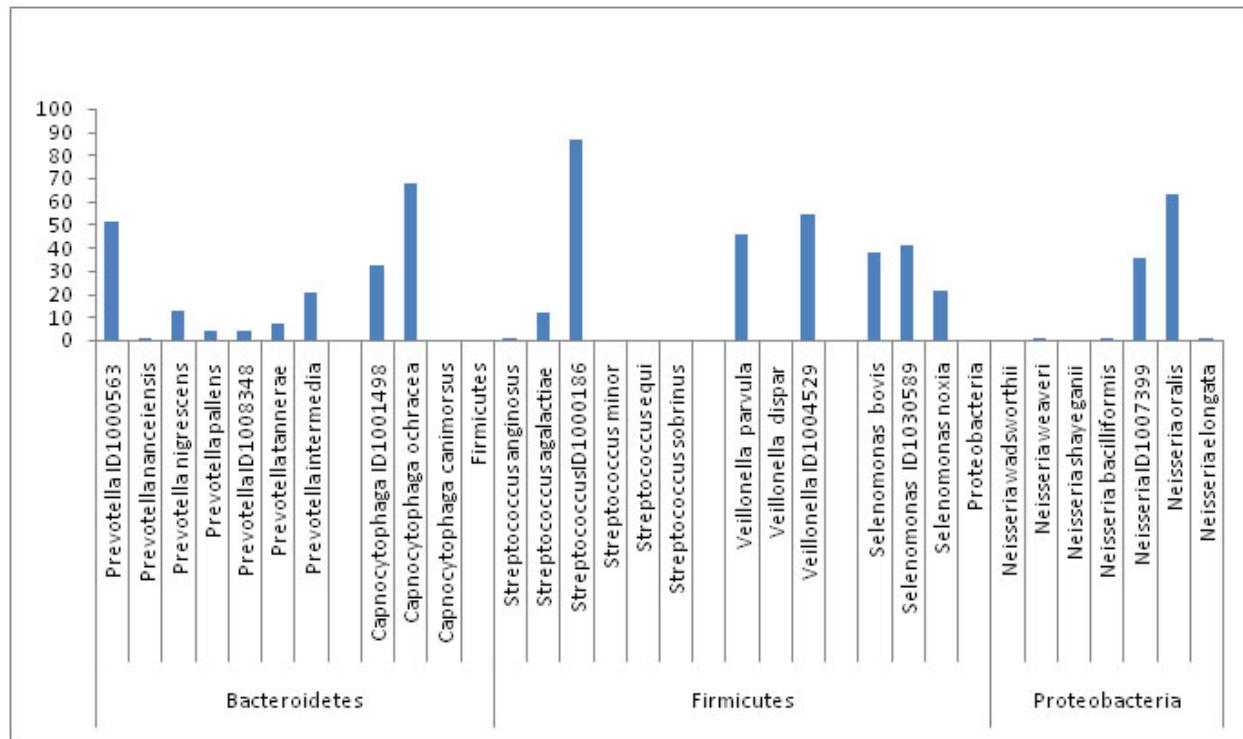
**Supplementary Figure 1b:** Sample rarefaction (Mao tau) curve of alpha diversity for species richness estimation ( $p < 0.05$ ) as a function of number of samples derived from Shanon index values of individual samples.



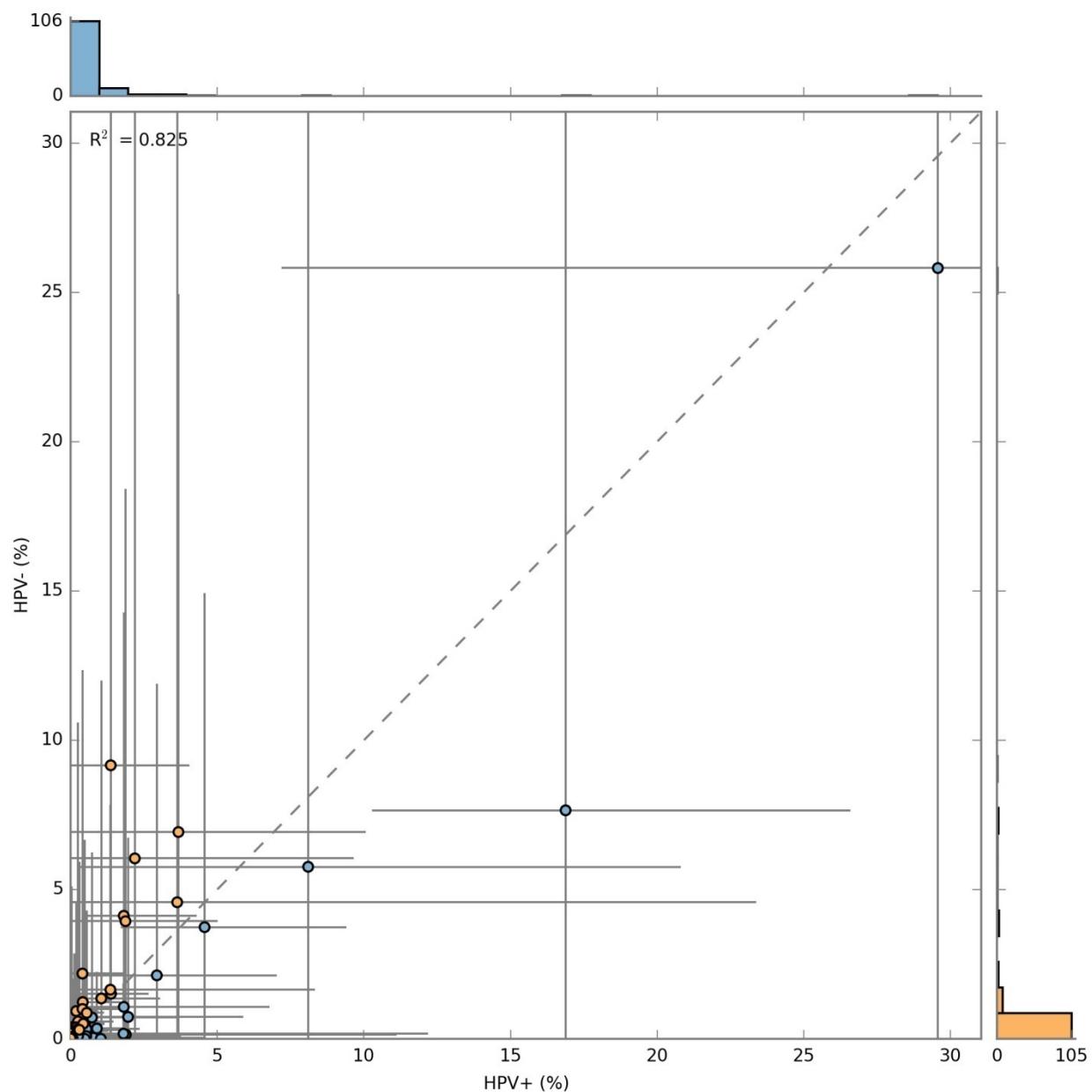
**Supplementary Figure 2a:** Diversity of bacterial phyla identified in granulations tissue of CP samples.



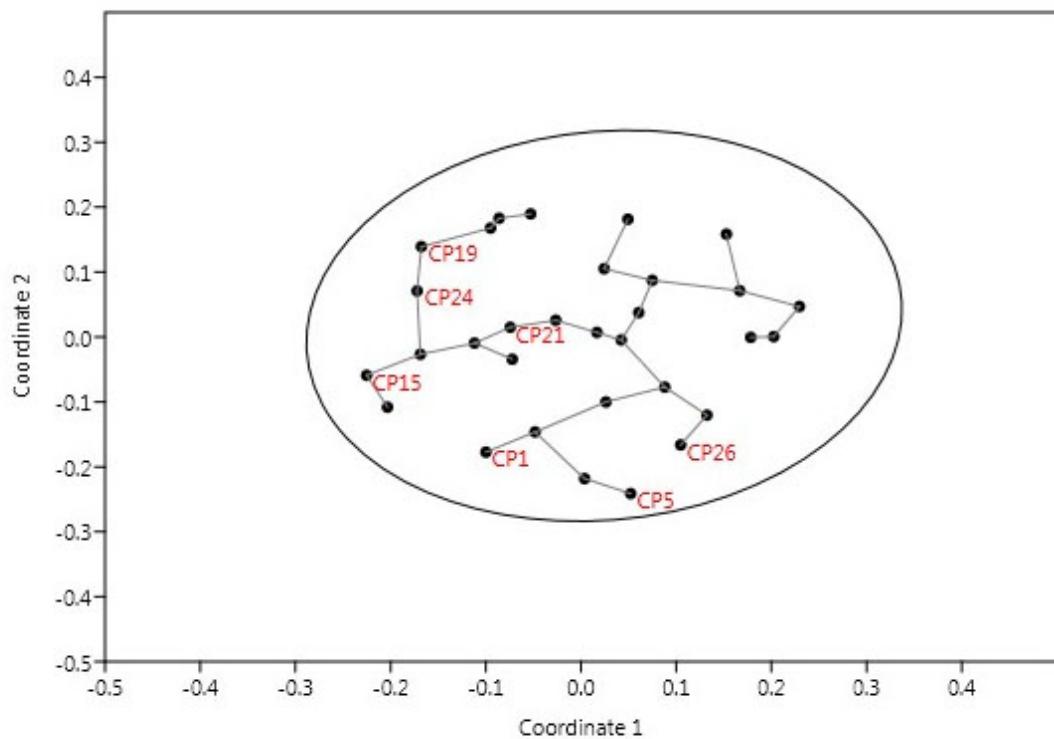
**Supplementary Figure 2b:** Diversity of bacterial species in CP samples identified in granulation tissue.



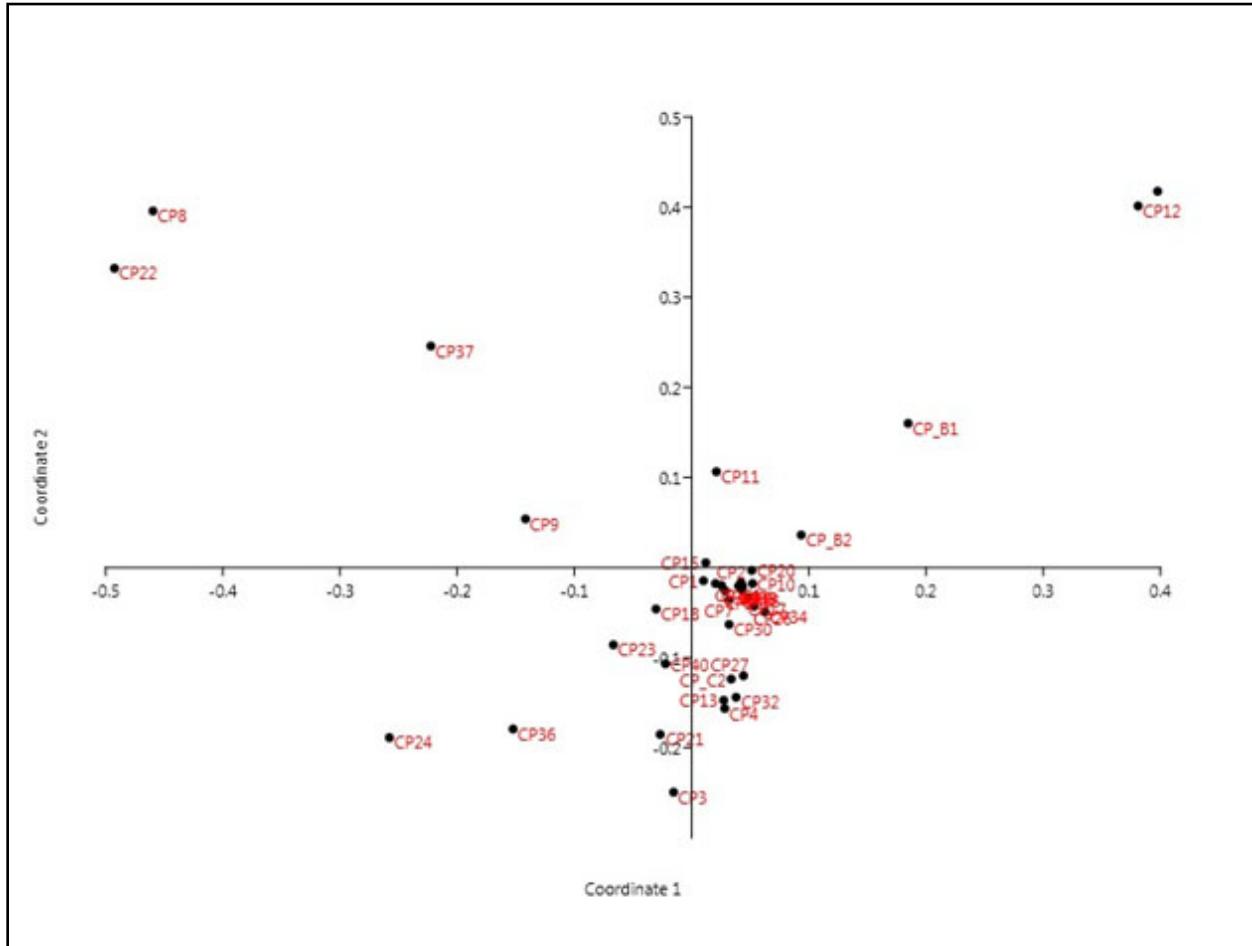
**Supplementary Figure 3a:** Scatter plot and correlation estimates of bacterial species abundance between HPV+ and HPV- samples in CP samples.



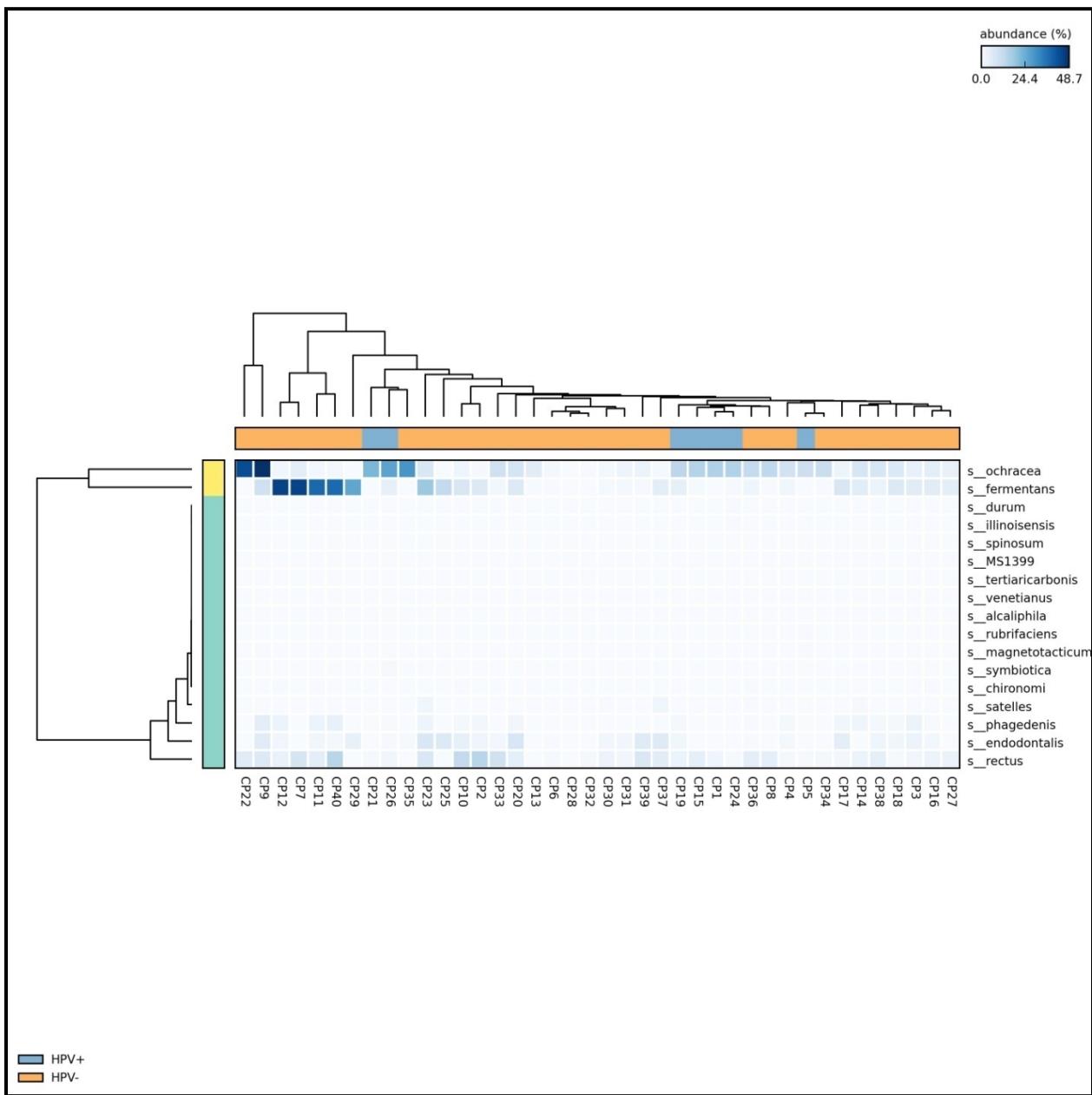
**Supplementary Figure 3b:** Beta diversity non-metric multidimensional scaling plot based on Theta YC two axis coordinate values obtained through mothur using Weighted UniFrac algorithm, showing distance or dissimilarity between each sample pair.



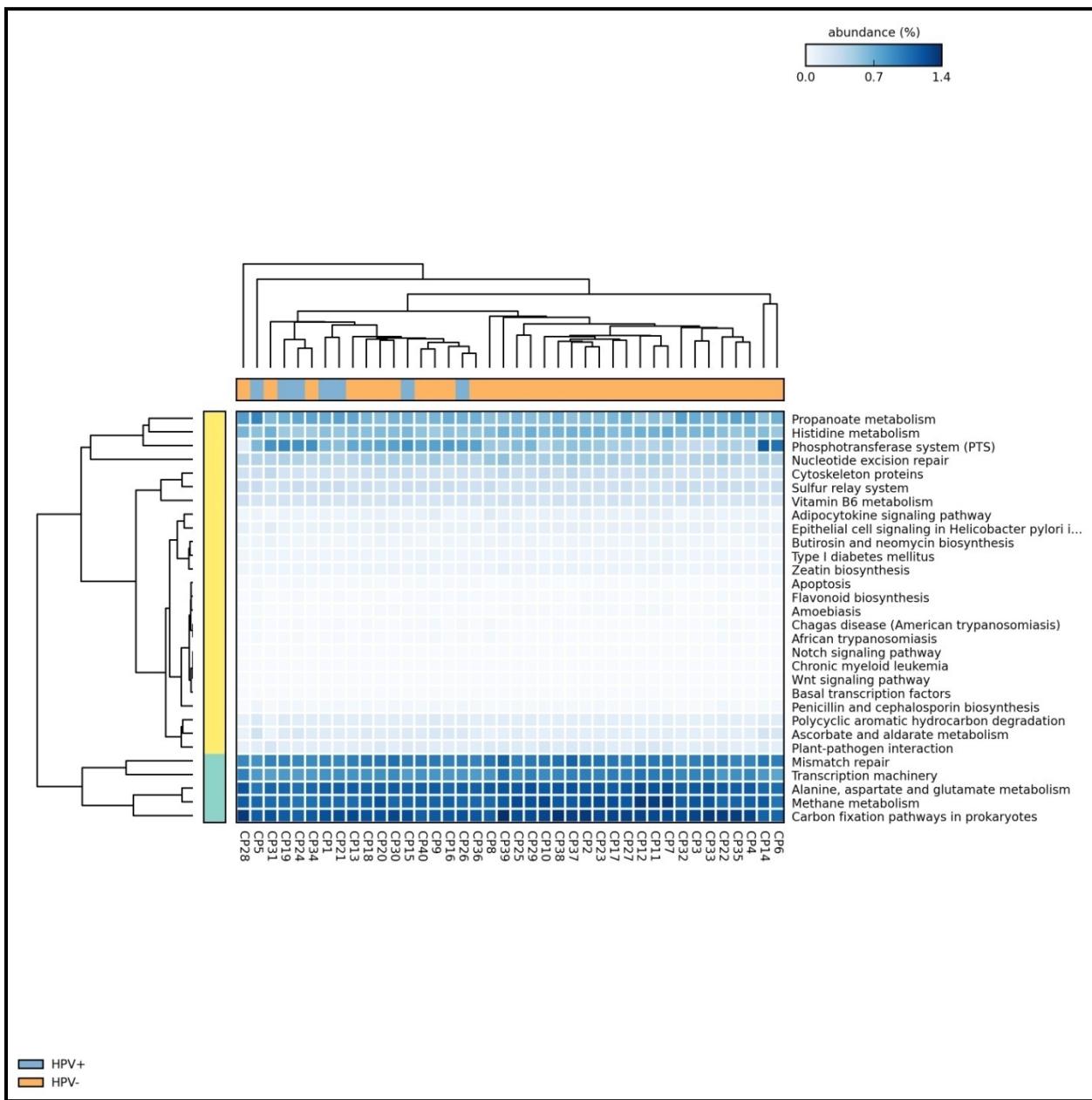
**Supplementary Figure 3c:** Principal coordinates analysis (PCoA) plot from ThetaYC values of beta diversity distance matrix. Where, coordinate 1 (X-axis) shows the maximum amount of variation present in the samples, with respect to coordinate 2 (Y-axis). Representation of OTU's between HPV+ and HPV - samples is randomly distributed.



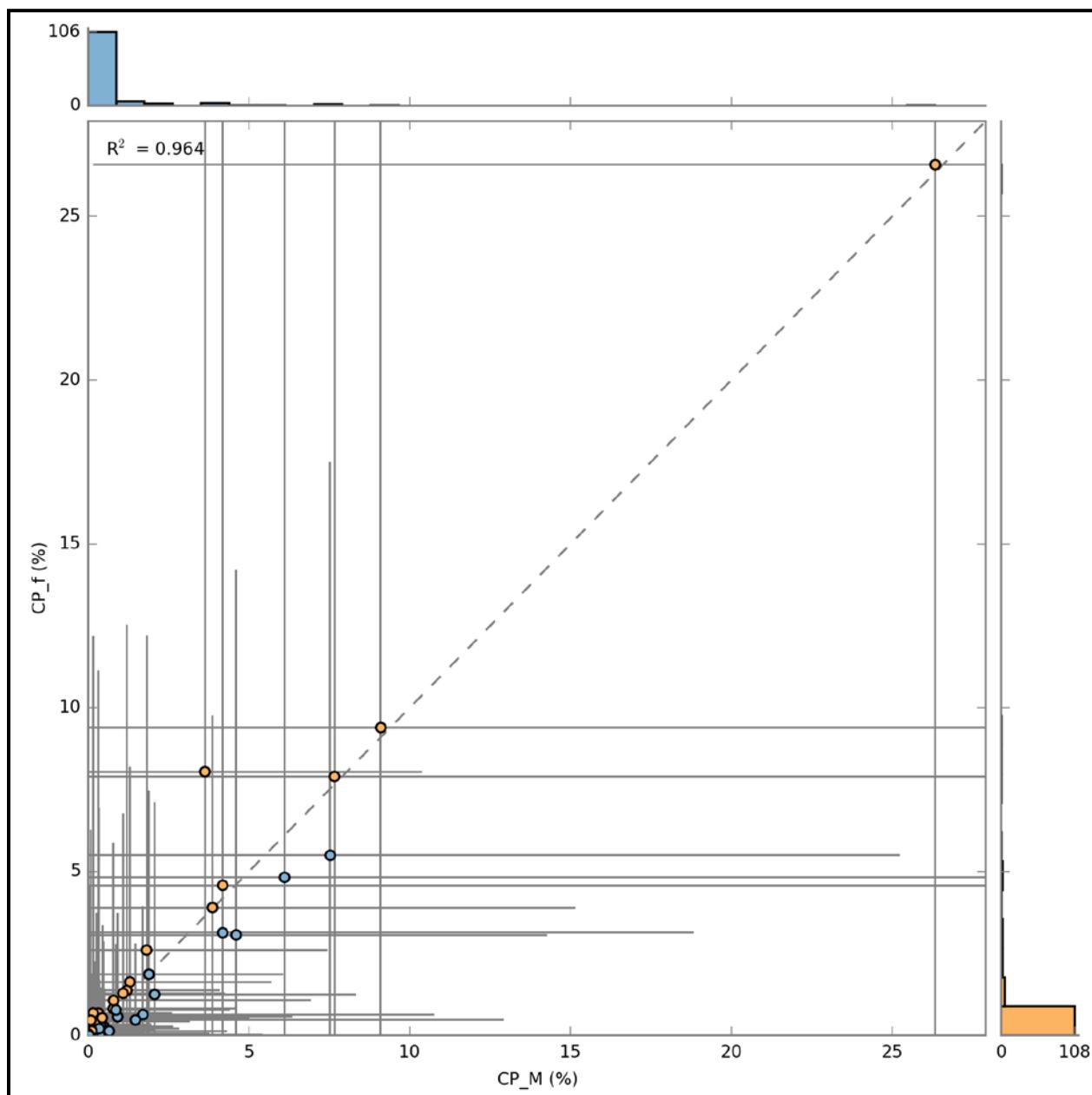
**Supplementary Figure 4:** Heat-map profile of abundance distribution of identified species in CP samples.



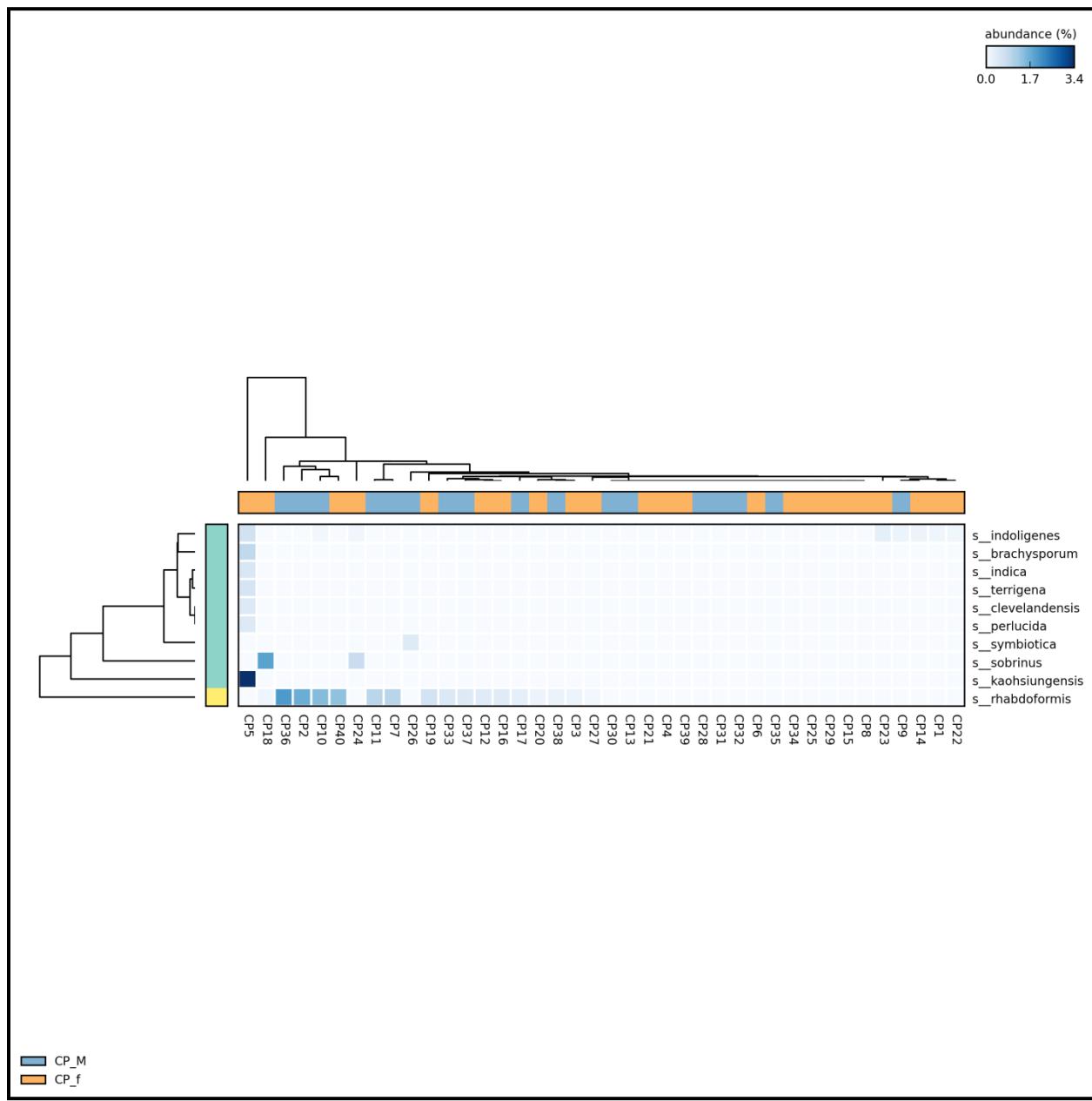
**Supplementary Figure 5a:** Scatter plot and correlation estimates of bacterial species functional predictions between HPV+ and HPV- samples in CP samples.



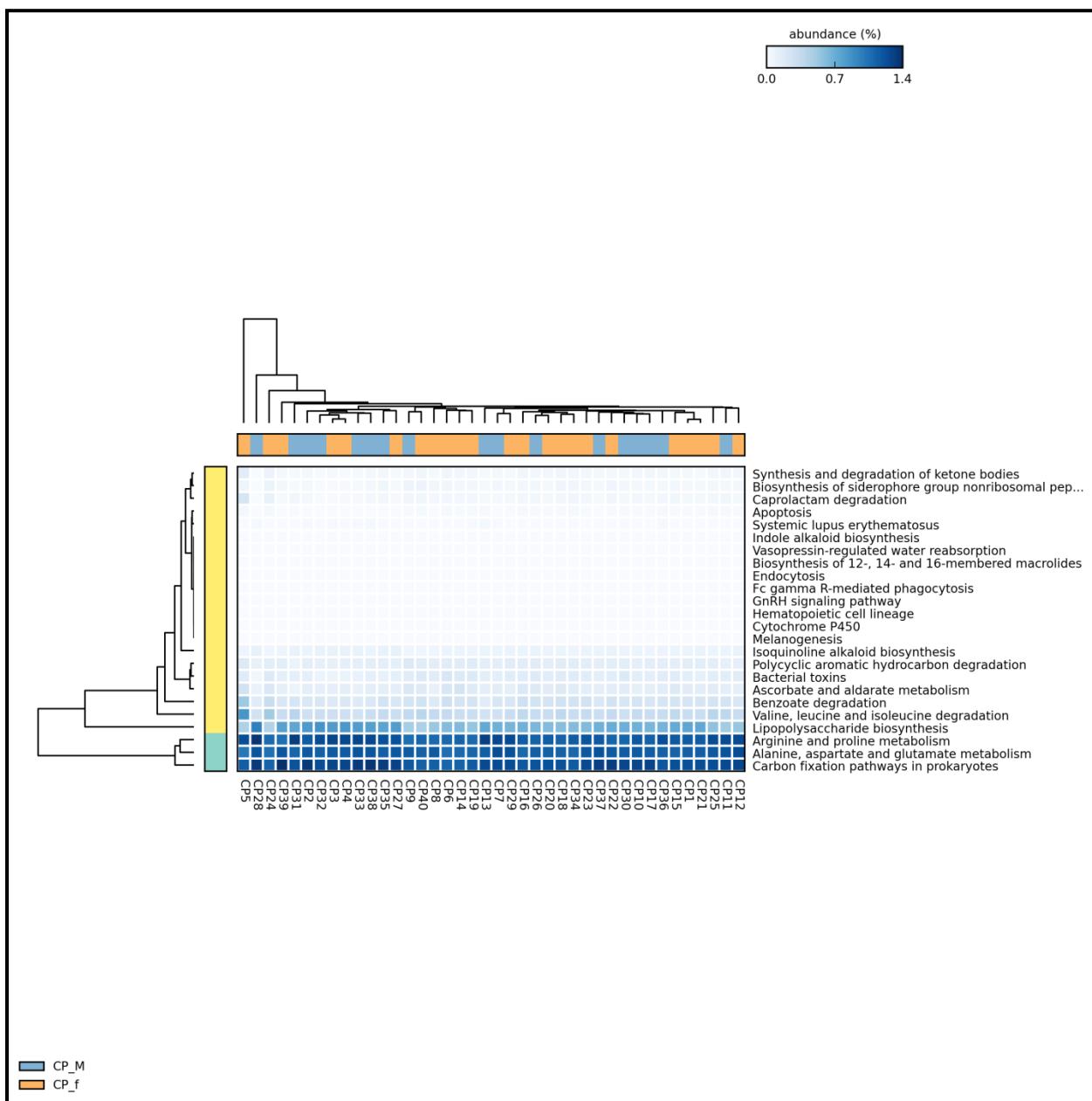
**Supplementary Figure 6a:** Scatter plot and correlation estimates of bacterial species abundance between Male and Female samples in CP samples.



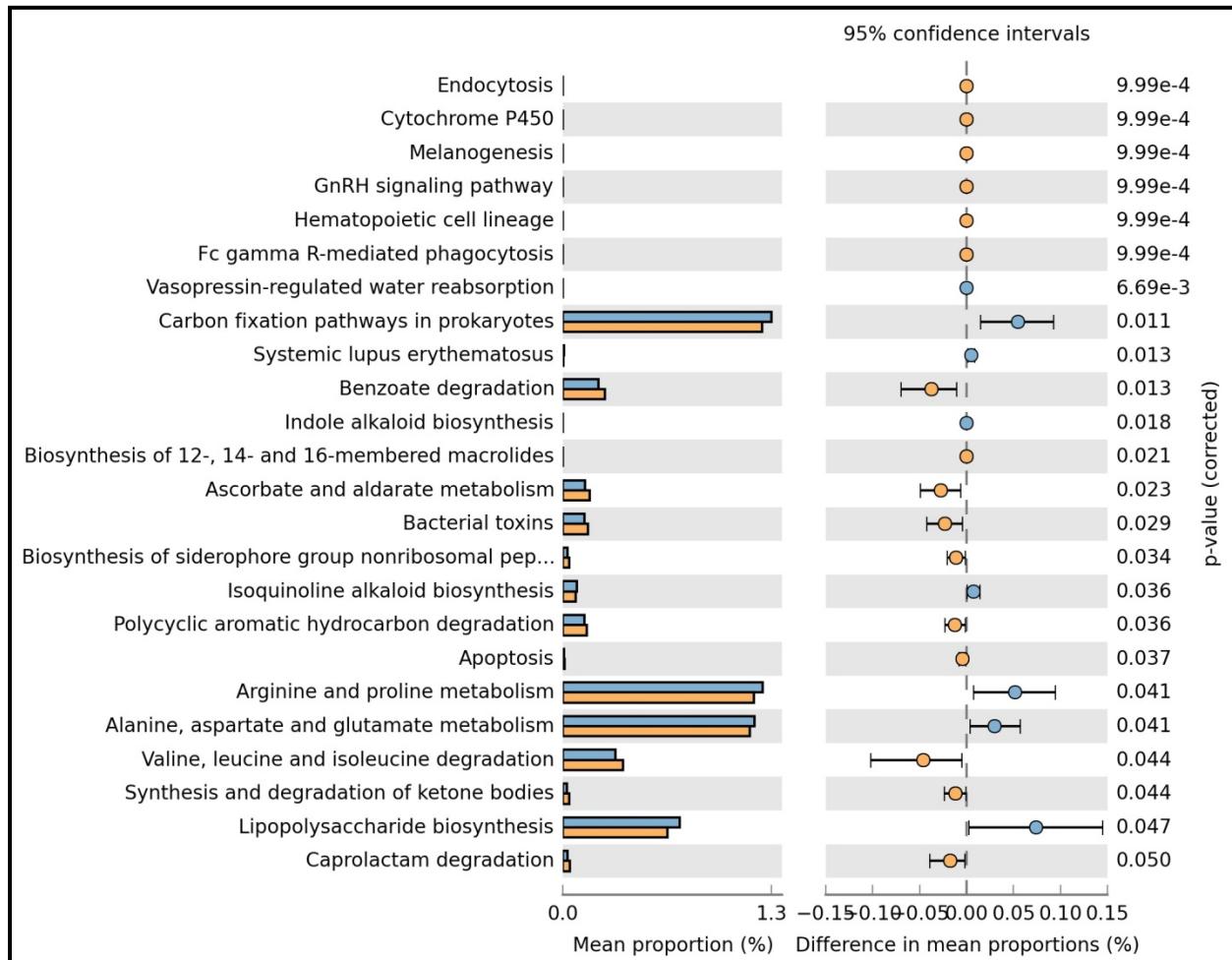
**Supplementary Figure 6b:** Heat-map profile of abundance distribution of identified species in Male and Female samples in CP samples.



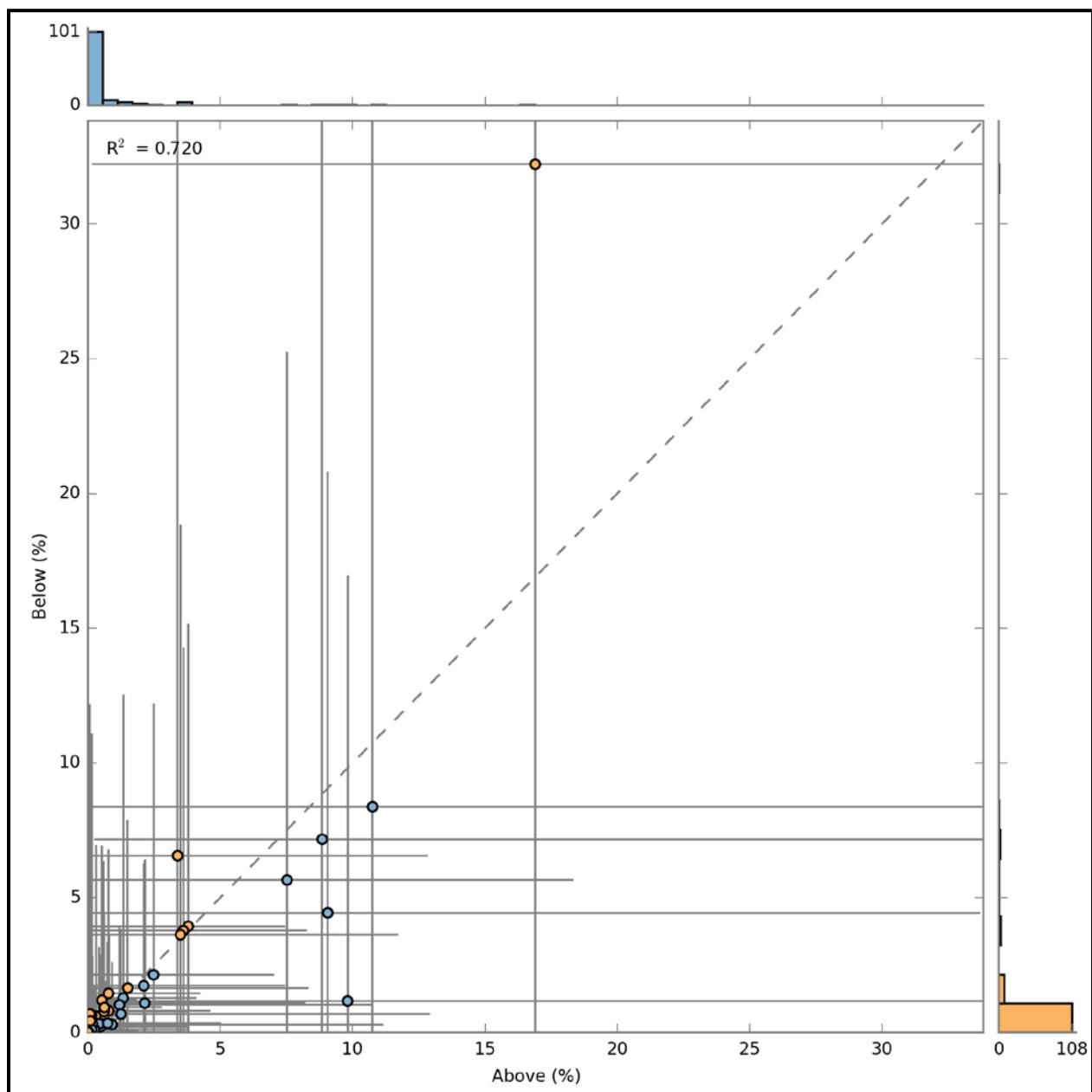
**Supplementary Figure 7a:** Heat-map profile of functional predictions of identified species in Male and Female samples in CP samples.



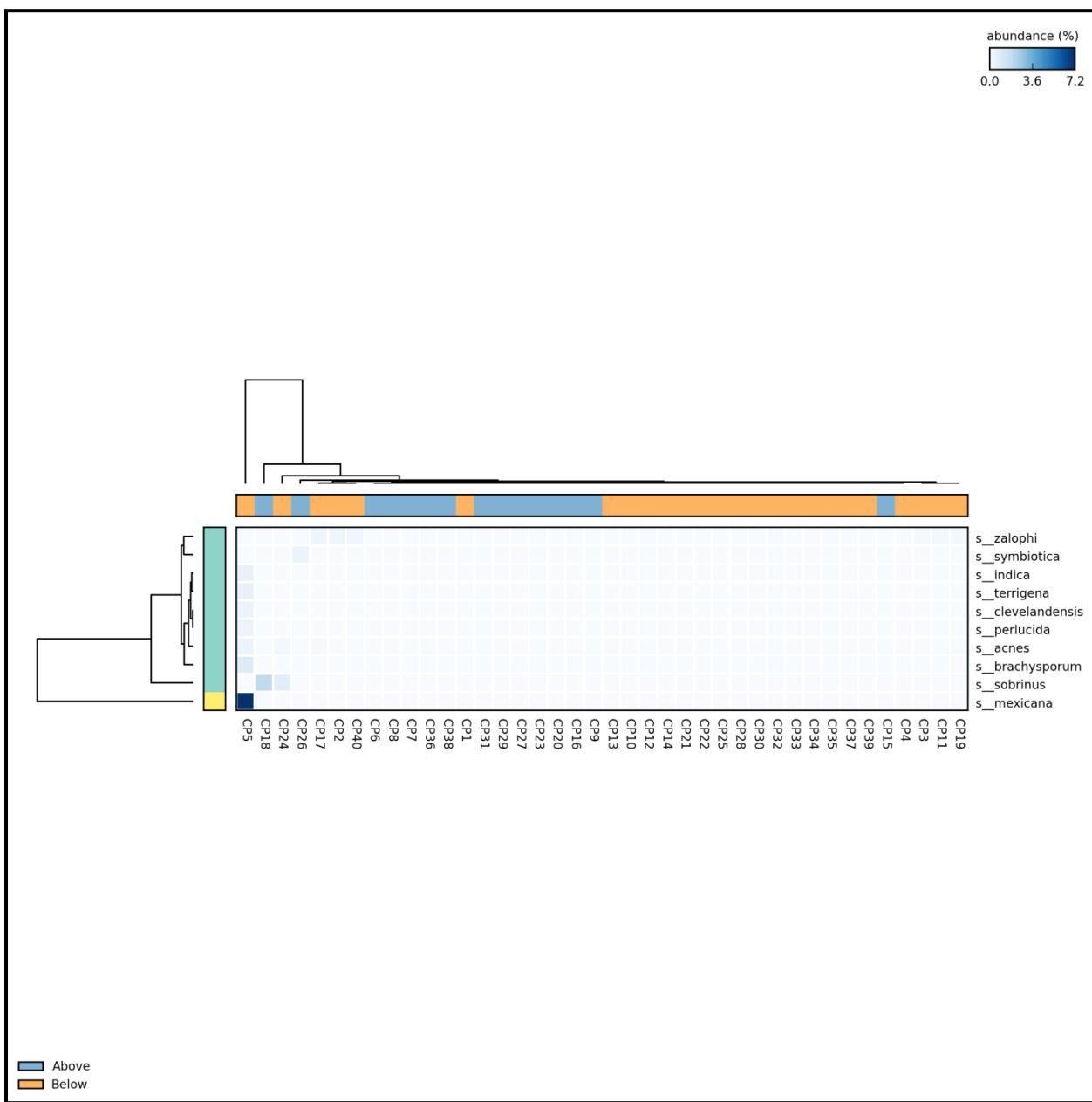
**Supplementary Figure 7b:** Mean proportion of bacterial species abundance between male and female CP samples. The significant difference observed between the two groups at 95% confidence level and p<0.05 are reported.



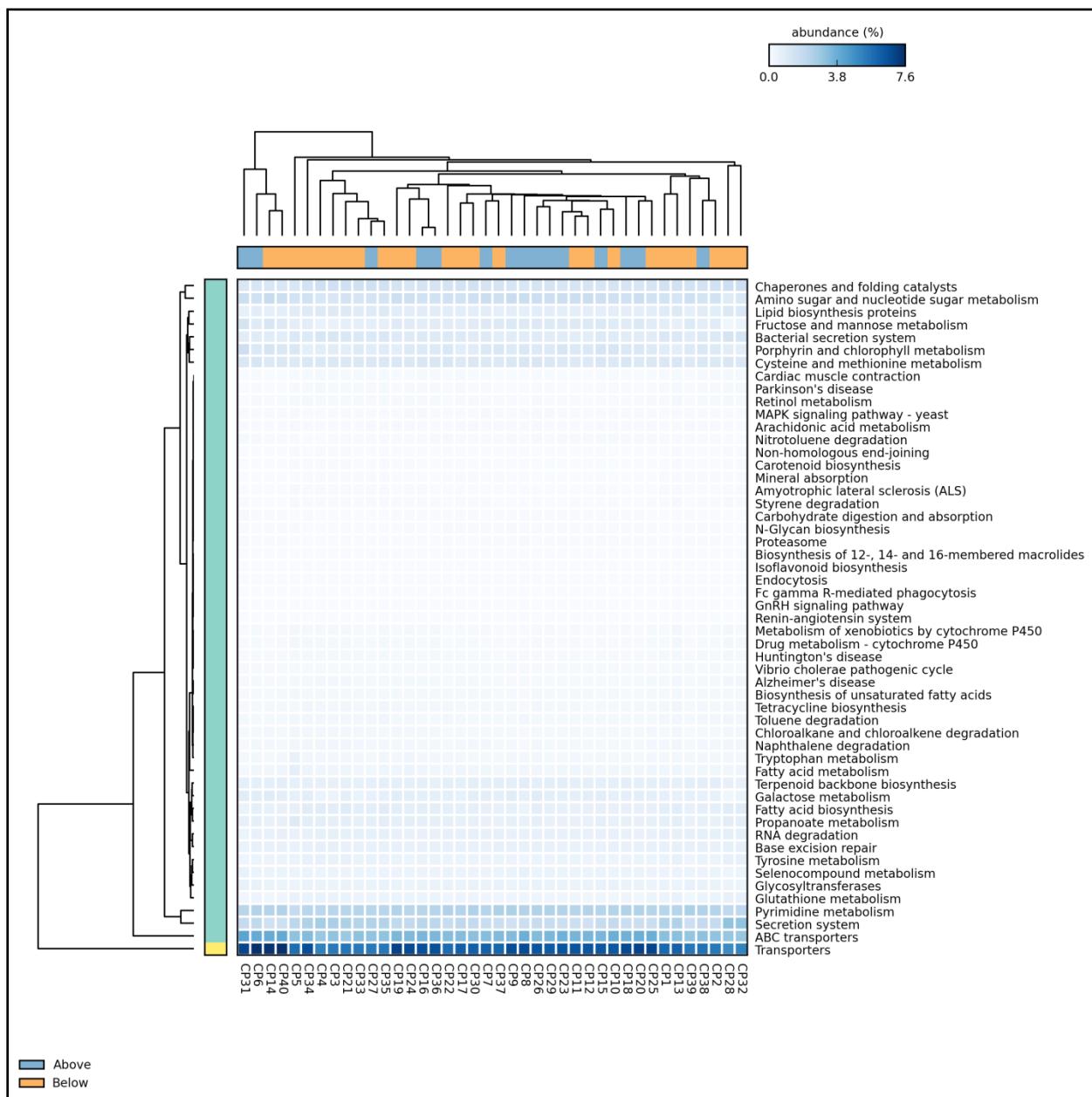
**Supplementary Figure 8a:** Scatter plot and correlation estimates of bacterial species abundance between Age above and below 40 samples in CP samples.



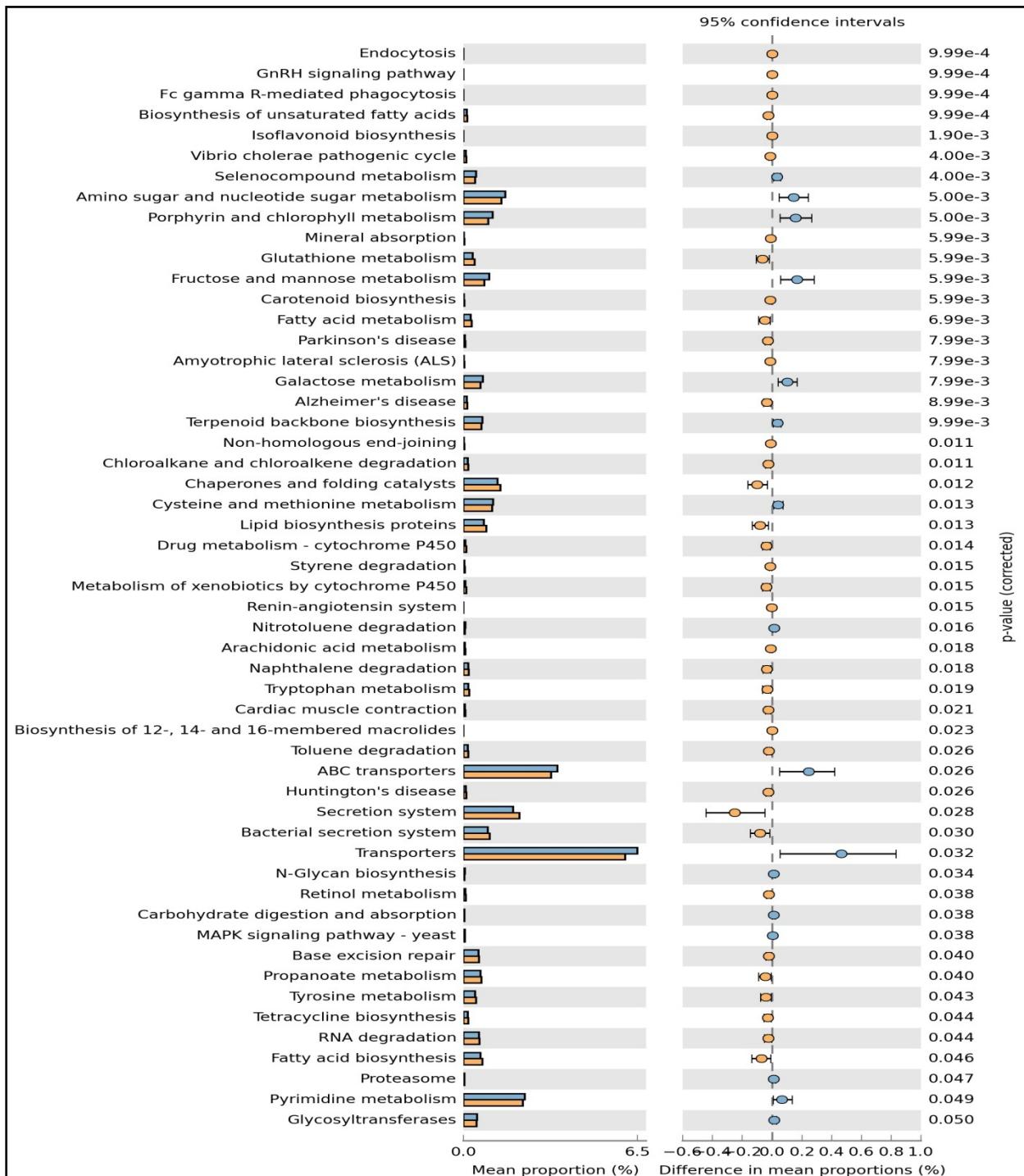
**Supplementary Figure 8b:** Heat-map profile of abundance distribution of identified species in Age above and below 40 samples in CP samples.



**Supplementary Figure 9a:** Heat-map profile of functional predictions of identified species in age above 40 (blue) and below 40 years (yellow) samples in CP samples.



**Supplementary Figure 9b:** Mean proportion of bacterial species abundance between age above 40 (blue bar) and below 40 years (yellow bar) samples in CP samples. The significant difference observed between the two groups at 95% confidence level and p<0.05 are reported.



**Supplementary Table 4: Observed number of OTUs at a 3% dissimilarity level and the diversity estimation database for species richness in forty CP samples.**

Level_1	Level_2	Level_3	Level_4	Level_5	Level_6	Level_7	Observatio	CP1
k_Bacteri	p_Actinob	c_Actinob	o_Actinon	f_Propion	g_Propior	s_acnes	ID1000517	0
k_Bacteri	p_Bacter	c_Clostrid	o_Bacter	f_Prevote	g_Prevote	s_nanceie	ID1001920	1
k_Bacteri	p_Firmicu	c_Clostrid	o_Clostrid	f_Lachnos	g_Lachno	s_orale	ID1009036	1
k_Bacteri	p_Firmicu	c_Clostrid	o_Clostrid	f_Veillone	g_Veillone	s_parvula	ID1009968	37
k_Bacteri	p_Proteo	c_Gamma	o_Pseudo	f_Moraxe	g_Acinetos	s_schindle	ID1012848	0
k_Bacteri	p_Proteo	c_Gamma	o_Pasteur	f_Pasteur	g_Haemo	s_para infl	ID1016422	1
k_Bacteri	p_Actinob	c_Actinob	o_Actinon	f_Coryne	g_Corynel	s_durum	ID1017764	0
k_Bacteri	p_Proteo	c_Gamma	o_Pasteur	f_Pasteur	g_Actinob	s_parahaem	ID1019193	0
k_Bacteri	p_Firmicu	c_Clostrid	o_Clostrid	f_Veillone	g_Veillone	s_dispar	ID1019878	0
k_Bacteri	p_Firmicu	c_Bacilli	o_Lactoba	f_Lactoba	g_Lactoba	s_salivari	ID1021172	0
k_Bacteri	p_Actinob	c_Actinob	o_Actinon	f_Nocardi	g_Rhodoc	s_fascians	ID1021308	0
k_Bacteri	p_Bacter	c_Bacter	o_Bacter	f_Prevote	g_Prevote	s_nigresce	ID1028549	6
k_Bacteri	p_Bacter	c_Flavoba	o_Flavoba	f_Flavoba	g_Capnocc	s_ochrace	ID102901	109
k_Bacteri	p_Proteo	c_Alphapr	o_Sphingo	f_Sphingo	g_Sphingo	s_asaccha	ID102915	0
k_Bacteri	p_Firmicu	c_Bacilli	o_Lactoba	f_Lactoba	g_Lactoba	s_iners	ID1033552	0
k_Bacteri	p_Bacter	c_Bacter	o_Bacter	f_Prevote	g_Prevote	s_pallens	ID1033790	1
k_Bacteri	p_Proteo	c_Gamma	o_Xantho	f_Xanthor	g_Pseudo	s_mexicar	ID104184	0
k_Bacteri	p_Firmicu	c_Bacilli	o_Lactoba	f_Strepto	g_Strepto	s_anginos	ID1047674	1
k_Bacteri	p_Firmicu	c_Bacilli	o_Lactoba	f_Strepto	g_Strepto	s_agalacti	ID1059977	u
k_Bacteri	p_Firmicu	c_Clostrid	o_Clostrid	f_Peptost	g_Peptost	s_anaero	ID105998	0
k_Bacteri	p_Proteo	c_Alphapr	o_Rhizobi	f_Methylc	g_Methyls	s_adhaesi	ID1074248	0
k_Bacteri	p_Proteo	c_Delta	o_Desulfo	f_Desulfo	g_Desulfo	s_rhabdof	ID10829	0
k_Bacteri	p_Firmicu	c_Clostrid	o_Clostrid	f_Veillone	g_Selenor	s_noxia	ID1086250	6
k_Bacteri	p_Proteo	c_Betapr	o_Neisser	f_Neisseri	g_Neisser	s_bacillifo	ID1106060	0
k_Bacteri	p_Bacter	c_Flavoba	o_Flavoba	f_Flavoba	g_Flavoba	s_gelidila	ID1107152	0
k_Bacteri	p_Proteo	c_Gamma	o_Pseudo	f_Pseudor	g_Pseudo	s_alcalige	ID1107697	0
k_Bacteri	p_Synergi	c_Synergi	o_Synergi	f_Dethios	g_Pyramic	s_piscoler	ID1120396	0
k_Bacteri	p_Actinob	c_Actinob	o_Actinon	f_Dermab	g_Devries	s_agamar	ID1126230	0
k_Bacteri	p_Actinob	c_Actinob	o_Actinon	f_Microcc	g_Rothia	s_terrae	ID1128355	2
k_Bacteri	p_Fusoba	c_Fusoba	o_Fusoba	f_Leptotri	g_Strepto	s_monilif	ID11292	0
k_Bacteri	p_Firmicu	c_Bacilli	o_Lactoba	f_Enteroc	g_Enteroc	s_haemo	ID1129461	0
k_Bacteri	p_Firmicu	c_Clostrid	o_Clostrid	f_Clostrid	g_Protein	s_ethanol	ID1133895	0
k_Bacteri	p_Proteo	c_Gamma	o_Xantho	f_Xanthor	g_Pseudo	s_kaohsiu	ID1135553	0
k_Bacteri	p_Bacter	c_Flavoba	o_Flavoba	f_Flavoba	g_Zhouia	s_amyloly	ID1136009	3
k_Bacteri	p_Proteo	c_Betapr	o_Burkho	f_Comam	g_Aquinc	s_tertiarie	ID1137566	0
k_Bacteri	p_Actinob	c_Actinob	o_Actinon	f_Mycoba	g_Mycob	s_vaccae	ID113826	0
k_Bacteri	p_Bacter	c_Flavoba	o_Flavoba	f_Flavoba	g_Lutaone	s_thermo	ID1138276	0
k_Bacteri	p_Proteo	c_Gamma	o_Cardi	f_Cardiob	g_Sutton	s_ornitho	ID1139148	0
k_Bacteri	p_Proteo	c_Alphapr	f_Sphingo	g_Sphingo	s_Sphingo	mali	ID1139751	1
k_Bacteri	p_Actinob	c_Corioba	o_Corioba	f_Corioba	g_Paraegg	s_hongko	ID1140324	0
k_Bacteri	p_Proteo	c_Gamma	o_Alteron	f_[Chrom	g_Rheinh	s_perlucic	ID1141610	0
k_Bacteri	p_Actinob	c_Actinob	o_Actinon	f_Nocardi	g_Marmo	s_aequore	ID1142974	0
k_Bacteri	p_Firmicu	c_Clostrid	o_Clostrid	f_Veillone	g_Selenor	s_bovis	ID1143338	13
k_Bacteri	p_Proteo	c_Gamma	o_Alteron	f_Shewan	g_Shewar	s_algae	ID115224	2
k_Bacteri	p_Actinob	c_Actinob	o_Actinon	f_Actinon	g_Actinon	s_hyovagi	ID12569	7
k_Bacteri	p_Proteo	c_Epsilon	o_Campyl	f_Helicob	g_Wolinell	s_succino	ID128801	0
k_Bacteri	p_Actinob	c_Actinob	o_Actinon	f_Coryne	g_Corynel	s_pilosum	ID13467	0

k_Bacteri:p_Proteobacteriia_Alphaproteobacteria_Rhizobiales_g_Shinellales_s_granuli	ID136134	0
k_Bacteri:p_Proteobacteriia_Gamma proteobacteria_Xanthomonadales_g_Pseudomonas_indica	ID146193	0
k_Bacteri:p_Firmicutes_Bacilli_o_Lactobacillales_f_Streptococcaceae_g_Streptococcus_minor	ID150451	0
k_Bacteri:p_Firmicutes_Bacilli_o_Lactobacillales_f_Aerococcaceae_g_Granulicella_balaensis	ID15059	4
k_Bacteri:p_Proteobacteriia_Gamma proteobacteria_Oceanobacterales_g_Halomonadales_g_Halomicrobium_phoceale	ID153241	1
k_Bacteri:p_Firmicutes_Bacilli_o_Lactobacillales_f_Streptococcaceae_g_Streptococcus_equi	ID15355	0
k_Bacteri:p_Proteobacteriia_Beta proteobacteria_Tremblayales_f_Tremblayellales_g_Carsonellales_s_ruddii	ID1543534	1
k_Bacteri:p_Bacteroidetes_Bacteroidia_Bacteroidales_f_Porphyrinaceae_g_Macellis_fermentans	ID158646	1
k_Bacteri:p_Verrucomicrobia_Verrucomicrobiales_Verrucomicrobium_g_Verrucomicrobium_spinosum	ID1596	0
k_Bacteri:p_Proteobacteriia_Beta proteobacteria_Burkholderiales_f_Comamonadaceae_g_Comamonas_terrigena	ID1639373	0
k_Bacteri:p_Firmicutes_Bacilli_o_Lactobacillales_f_Streptococcaceae_g_Streptococcus_sobrinus	ID167118	0
k_Bacteri:p_Proteobacteriia_Gamma proteobacteria_Enterobacteriales_f_Enterobacteriaceae_g_Shigellas_s Boydii	ID1780074	0
k_Bacteri:p_Proteobacteriia_Beta proteobacteria_Burkholderiales_f_Comamonadaceae_g_Polyangium_brachys	ID181669	0
k_Bacteri:p_Proteobacteriia_Gamma proteobacteria_Pseudomonadales_g_Moraxellaceae_g_Acinetobacter_venetianus	ID181761	0
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k_Bacteri:p_Actinobacteria_Actinobacteria_Actinomycetophyta_Micrococcaceae_g_Rothiella_s_amarae	ID1925093	0
k_Bacteri:p_Bacteroidetes_Bacteroidia_Bacteroidales_f_Porphyrinaceae_g_Porphyrinaceae_endodotis	ID1938	1
k_Bacteri:p_Proteobacteriia_Gamma proteobacteria_Alteromonadales_f_Shewanellaceae_g_Shewanella_shewantis_amazoniensis	ID197265	0
k_Bacteri:p_Bacteroidetes_Bacteroidia_Bacteroidales_f_Paraprevotellaceae_g_Prevotella_tannerae	ID2047	5
k_Bacteri:p_Bacteroidetes_Bacteroidia_Bacteroidales_f_Prevotellaceae_g_Prevotella_intermedia	ID2218	25
k_Bacteri:p_Proteobacteriia_Gamma proteobacteria_Pseudomonadales_g_Moraxellaceae_g_Moraxella_ovis	ID223485	0
k_Bacteri:p_Spirochaetes_Spirochaetes_Spirochaetaceae_g_Spirochete_g_Treponema_socronsense	ID2310825	2
k_Bacteri:p_Actinobacteria_Actinobacteria_Actinomycetophyta_Tsukamurellaceae_g_Gordonella_kropperae	ID236778	0
k_Bacteri:p_Proteobacteriia_Alphaproteobacteria_Rhizobiales_g_Methylomonas_magnetcoccus	ID237209	0
k_Bacteri:p_Actinobacteria_Actinobacteria_Actinomycetophyta_Beutenbergiaceae_g_Beutenbergia_cavernalis	ID2500552	0
k_Bacteri:p_Actinobacteria_Actinobacteria_Coriobacteriales_f_Coriobacteriaceae_g_Coriobacter_atopobiotis_rimae	ID251702	0
k_Bacteri:p_Proteobacteriia_Beta proteobacteria_Burkholderiales_f_Comamonadaceae_g_Brachyspira_chironiae	ID265983	0
k_Bacteri:p_Elusimicrobia_Elusimicrobia_Elusimicrobium_g_Elusimicrobium_minutum	ID278595	0
k_Bacteri:p_Planctomicrobia_Planctomicrobia_Pirellulales_f_Pirellulaceae_g_Planctomicrobium_MS139	ID2905450	0
k_Bacteri:p_Spirochaetes_Spirochaetes_Spirochaetaceae_g_Spirochaete_g_Treponema_amylolyticum	ID29328	0
k_Bacteri:p_Firmicutes_Clostridia_Clostridiaceae_f_Veillonellaceae_g_Acetobacter_longum	ID3107842	0
k_Bacteri:p_Bacteroidetes_Flavobacteriia_Flavobacteriales_f_Flavobacteriaceae_g_Capnophlyctis_canimonis	ID314128	0
k_Bacteri:p_Proteobacteriia_Gamma proteobacteria_Alteromonadales_f_Chromatium_g_Rheinheimera_nanhaiensis	ID325282	0
k_Bacteri:p_Tenericutes_Mollicutes_Mycoplasma_g_Mycoplasma_zalophi	ID336960	0
k_Bacteri:p_Bacteroidetes_Bacteroidia_Bacteroidales_f_Bacteroidaceae_g_Bacteroides_nordii	ID344827	0
k_Bacteri:p_Firmicutes_Bacilli_o_Lactobacillales_f_Leuconostocaceae_g_Weissella_parameciae	ID352468	0
k_Bacteri:p_Firmicutes_Bacilli_o_Bacillales_f_Planoctenaceae_g_Staphylococcus_saprophilus	ID354839	0
k_Bacteri:p_Proteobacteriia_Gamma proteobacteria_Pasteurellales_f_Pasteurellaceae_g_Gallibacter_genomicus	ID359719	0
k_Bacteri:p_Actinobacteria_Actinobacteria_Bifidobacteriales_f_Bifidobacteriaceae_g_Bifidobacterium_bifidum	ID365385	0
k_Bacteri:p_Spirochaetes_Spirochaetes_Spirochaetaceae_g_Spirochaete_g_Treponema_phagedense	ID3928	0
k_Bacteri:p_Proteobacteriia_Gamma proteobacteria_Aeromicrobacteria_Aeromonas_g_Aeromonas_sanarelli	ID4006670	0
k_Bacteri:p_Firmicutes_Erysipelotrichia_Erysipelotrichales_f_Erysipelotrichaceae_g_Bulleidiella_moorei	ID4030370	0
k_Bacteri:p_Proteobacteriia_Gamma proteobacteria_Pseudomonadales_g_Moraxellaceae_g_Enhydrus_aerosaccharinus	ID407441	0
k_Bacteri:p_Proteobacteriia_Epsilonproteobacteria_Campylobacteriales_f_Campylobacteraceae_g_Campylobacter_rectus	ID416537	15
k_Bacteri:p_Proteobacteriia_Beta proteobacteria_Neisseriales_f_Neisseriaceae_g_Neisseria_shayeganii	ID4233669	0
k_Bacteri:p_Proteobacteriia_Gamma proteobacteria_Vibrionales_f_Pseudomonadaceae_g_Vibrios_s_mimicus	ID4270835	0
k_Bacteri:p_Bacteroidetes_Flavobacteriia_Flavobacteriales_f_Weeksellaceae_g_Bergeyellales_zoohelcum	ID4297519	1
k_Bacteri:p_Proteobacteriia_Gamma proteobacteria_Pseudomonadales_f_Pseudomonadaceae_g_Pseudomonas_cuatrecasasii	ID4301996	0
k_Bacteri:p_Proteobacteriia_Gamma proteobacteria_Xanthomonadales_g_Xanthomonas_stenorhizophora	ID4331923	0
k_Bacteri:p_Firmicutes_Clostridia_Clostridiaceae_f_Lachnospiraceae_g_Johnsonia_ignava	ID4332505	0

k_Bacteri:p_Proteo	c_Betaprc	o_Neisser	f_Neisseri	g_Neisser	s_wadswc	ID4335663	0
k_Bacteri:p_Proteo	c_Betaprc	o_Neisser	f_Neisseri	g_Neisser	s_weaveri	ID4337487	1
k_Bacteri:p_Fusoba	c_Fusoba	o_Fusoba	f_Leptotri	g_Sebaldes	s_termitic	ID4358870	15
k_Bacteri:p_Proteo	c_Alphapr	o_Rhizobi	f_Bradyrh	g_Afipia	s_clevelar	ID4367627	0
k_Bacteri:p_Firmicu	c_Clostrid	o_Clostrid	f_Clostrid	g_Clostrid	s_caminiti	ID4368040	0
k_Bacteri:p_Proteo	c_Betaprc	o_Neisser	f_Neisseri	g_Neisser	s_oralis	ID4373910	368
k_Bacteri:p_Proteo	c_Betaprc	o_Burkho	f_Comam	g_Leptothe	s_ginseng	ID4395318	0
k_Bacteri:p_Firmicu	c_Clostrid	o_Clostrid	f_Clostrid	g_Clostrid	s_aciduric	ID4462654	0
k_Bacteri:p_Proteo	c_Betaprc	o_Neisser	f_Neisseri	g_Kingella	s_potus	ID4476050	0
k_Bacteri:p_Synergic	c_Synergi	o_Synergi	f_Dethios	g_Jonque	s_anthrop	ID484439	0
k_Bacteri:p_Firmicu	c_Clostrid	o_Clostrid	f_Lachnos	g_Moryells	s_indolige	ID514200	1
k_Bacteri:p_Plancto	c_Plancto	o_Gemma	f_Isospha	g_Nostoc	s_limicola	ID51778	0
k_Bacteri:p_Proteo	c_Gamma	o_Cardiol	f_Cardiob	g_Cardiob	s_valvarui	ID544152	8
k_Bacteri:p_Proteo	c_Alphapr	o_Rhizobi	f_Beijerin	g_Chelato	s_asaccha	ID548469	0
k_Bacteri:p_Proteo	c_Gamma	o_Pseudo	f_Moraxe	g_Alkanin	s_illinoise	ID552246	0
k_Bacteri:p_Proteo	c_Gamma	o_Enterok	f_Enterob	g_Serratia	s_symbiot	ID576678	0
k_Bacteri:p_Proteo	c_Betaprc	o_Neisser	f_Neisseri	g_Neisser	s_elongat	ID6402	3
k_Bacteri:p_Proteo	c_Gamma	o_Pseudo	f_Pseudor	g_Pseudo	s_compos	ID673640	0
k_Bacteri:p_Firmicu	c_Bacilli	o_Lactob	f_Aerococ	g_Abiotro	s_defectiv	ID678690	0
k_Bacteri:p_Firmicu	c_Clostrid	o_Clostrid	f_Veillone	g_Anaero	s_glycerin	ID731367	6
k_Bacteri:p_Firmicu	c_Erysipel	o_Erysipe	f_Erysipel	g_Anaero	s_furcosa	ID761476	0
k_Bacteri:p_Proteo	c_Alphapr	o_Rhodos	f_Rhodos	g_Reyran	s_massilie	ID801271	0
k_Bacteri:p_Proteo	c_Alphapr	o_Rhodos	f_Acetoba	g_Acidispl	s_rubrifac	ID806916	0
k_Bacteri:p_Proteo	c_Gamma	o_Pseudo	f_Pseudor	g_Pseudo	s_alcaliph	ID83866	0
k_Bacteri:p_Firmicu	c_Clostrid	o_Clostrid	f_Lachnos	g_Shuttle	s_satelles	ID851782	0
k_Bacteri:p_Proteo	c_Betaprc	o_Neisser	f_Neisseri	g_Kingella	s_denitrifi	ID851932	29
k_Bacteri:p_Proteo	c_Gamma	o_Pasteur	f_Pasteur	g_Pasteur	s_aeroger	ID9498	0
k_Bacteri:p_Proteo	c_Gamma	o_Pasteur	f_Pasteur	g_Actinob	s_delphin	ID9510	0

tes. The high quality sequences were processed through Mothur package against gg\_13\_8\_99.gg.tax

CP10	CP11	CP12	CP13	CP14	CP15	CP16	CP17	CP18
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0	0	0	0	0	0	0	0	0
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65	60	150	3	64	29	12	0	11
23	10	23	78	42	194	69	30	46
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62	0	0	0	0	0	2	0	0
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13	19	42	0	0	0	1	5	1
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17	7	6	0	0	0	6	4	1
2	7	10	19	89	307	4	1	0
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0	2	2	0	0	0	3	1	2
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0	1	2	9	5	16	3	0	14
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0	1	0	0	0	3	0	0	0

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2	5	5	63	1	5	5	1	7
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0	0	0	0	0	0	0	0	13
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46	12	25	0	1	1	18	59	13
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48	57	105	0	15	5	13	15	3
82	1	4	0	8	1	5	384	89
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28	28	58	0	11	3	1	18	1
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0	0	0	0	0	0	0	0	0
0	0	3	0	5	1	2	0	0
4	2	4	0	0	0	3	0	0
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0	0	0	0	0	0	0	0	0
11	0	0	0	0	0	1	36	2
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1	0	7	0	0	0	0	3	0
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144	34	48	1	16	56	41	15	4
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0	0	0	0	0	0	0	0	0
10	3	4	1	0	2	1	13	0



CP19	CP2	CP20	CP21	CP22	CP23	CP24	CP26	CP27
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27	66	15	1	17	77	45	12	18
108	2	44	623	332	47	137	192	44
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75	3	28	91	25	18	65	39	30
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5	6	1	0	0	0	0	0	1
0	5	0	0	25	68	5	5	7
2	5	0	40	0	1	1	0	1
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9	0	0	4	6	1	10	0	2
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6	0	5	1	1	0	5	6	0
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33	9	94	0	15	66	3	24	44
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32	22	33	1	0	121	5	29	58
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0	0	0	0	0	0	0	0	0
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15	8	40	2	0	46	1	4	1
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77	35	61	1	3	1	4	2	42
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5	12	13	0	0	6	1	12	1
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3	0	1	0	2	5	2	7	1
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0	0	0	0	0	0	0	0	0
10	5	9	0	0	0	1	2	1
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1	5	1	0	0	3	0	0	2
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7	5	9	0	0	16	1	2	2
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24	50	24	14	43	47	6	12	36
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8	0	1	1	1	1	9	8	13
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13	4	18	135	2	3	451	2	49
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10	45	10	4	0	4	0	0	27
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14	39	0	0	0	1	0	36	6
22	346	6	7	28	6	1	8	4
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3	8	5	4	0	0	108	3	3
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19	55	10	51	10	5	83	34	32
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6	53	1	0	3	0	1	0	1
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**Total OTUs**

11	
41	
329	
2072	
0	
2	
3	
7	
2	
3	
2	
926	
3177	
2	
1	
310	
153	
70	
1224	
121	
0	
86	
967	
87	
1	
8	
63	
0	
132	
1	
3	
1	
72	
94	
3	
1	
1	
1	
46	
1	
9	
1	
1717	
115	
141	
2	
20	

1  
11  
0  
338  
298  
10  
334  
2420  
3  
12  
20  
1  
19  
4  
2  
2  
491  
6  
539  
1491  
3  
357  
2  
6  
1  
56  
16  
1  
3  
86  
0  
11  
0  
10  
36  
1  
3  
1  
4  
264  
1  
35  
0  
1053  
4  
2  
150  
1  
1  
69

1  
74  
760  
9  
24  
10557  
8  
3  
1  
4  
22  
2  
91  
2  
8  
3  
197  
8  
286  
447  
3  
53  
5  
4  
27  
324  
0  
0