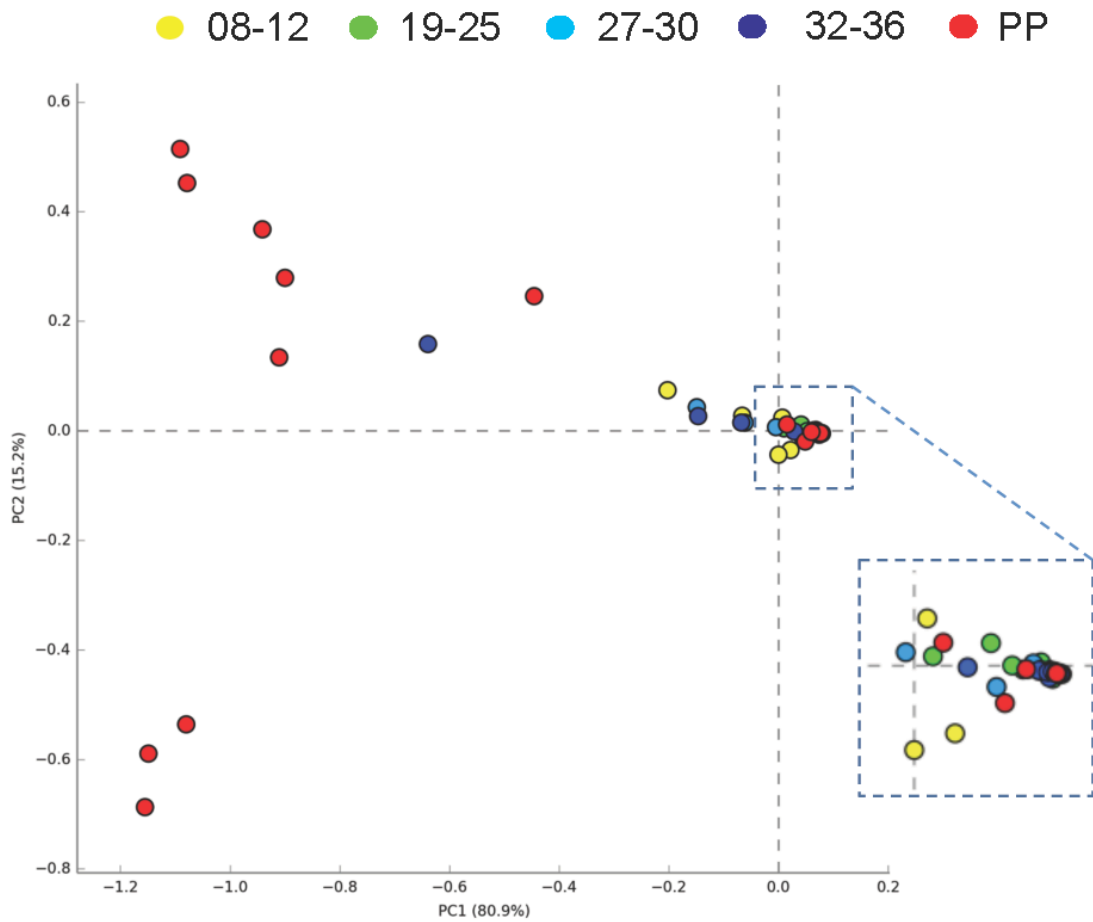


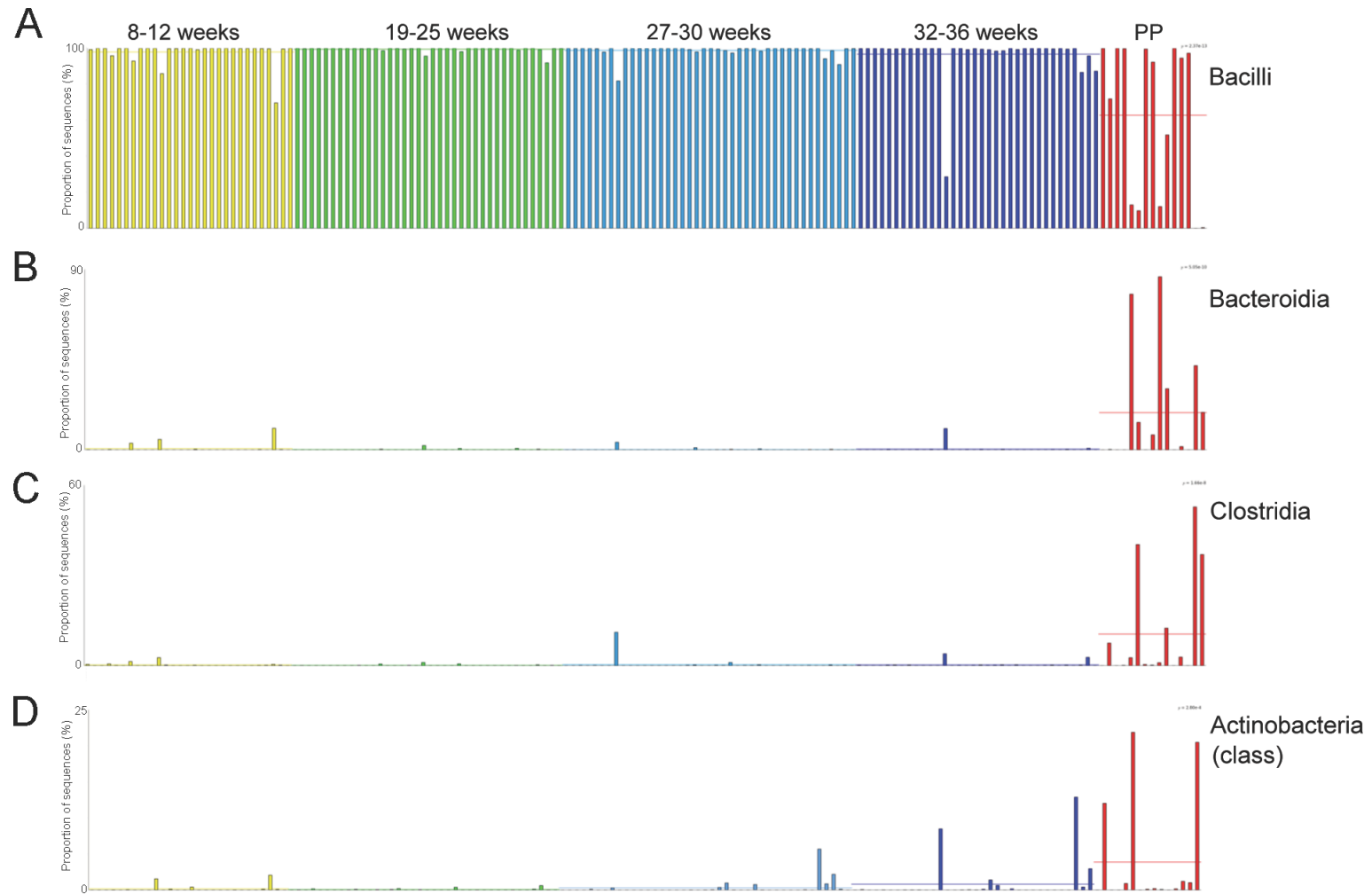
**The vaginal microbiome during pregnancy and the postpartum period in a
European population.**

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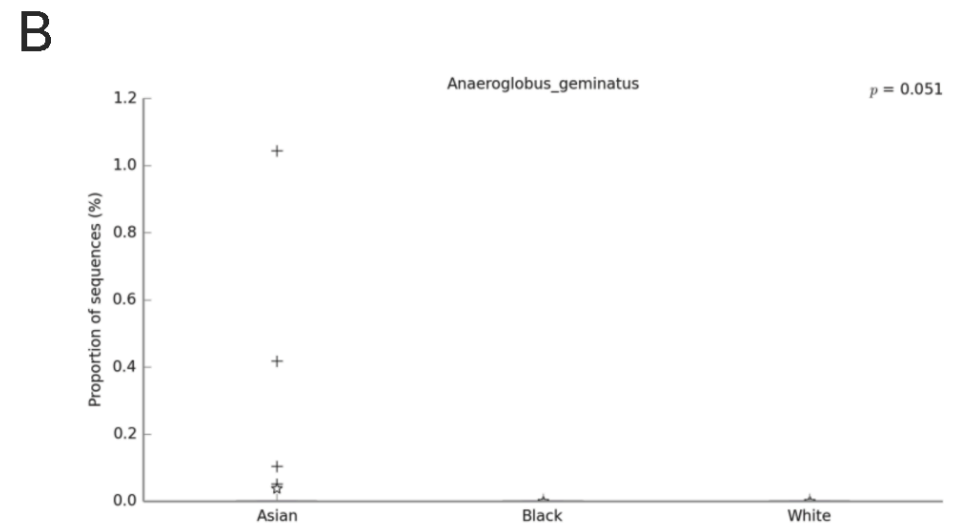
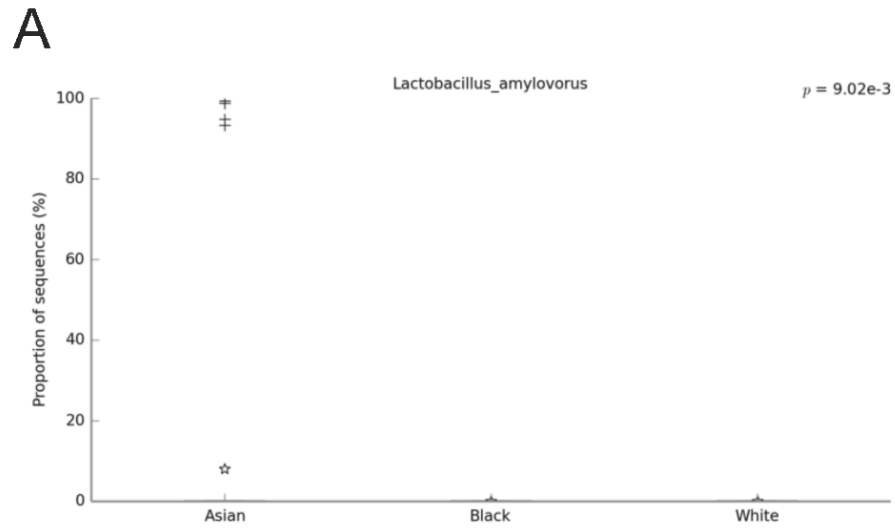
SUPPLEMENTARY INFORMATION



Supplementary Figure 1. PCA of bacterial genera data collected from patients at 8-12 (yellow), 19-25 (green), 27-30 (light blue) and 32-36 (dark blue) weeks gestation or 6 weeks post partum (PP; red).



Supplementary Figure 2. Relative abundance of bacterial classes in cross sectional data collected from patients at 8-12 (yellow), 19-25 (green), 27-30 (light blue) and 32-36 (dark blue) weeks gestation or 6 weeks post partum (PP; red). Data is presented to as proportion of sequences assigned to bacterial classes (A) Bacilli, (B) Bacteroidia, (C) Clostridia or (D) Actinobacteria.



Supplementary Figure 3. Bacterial species detected predominately in Asian samples. Box plot describing proportion of sequences derived from **(A)** *Lactobacillus amylovorus* and **(B)** *Anaeroglobus germinatus*. Star indicates mean proportion of group.

Supplementary Table 1. Linear mixed model regression analysis for examining bacterial species abundance across pregnancy time points. To test if bacterial species abundance changes significantly over the course of pregnancy we excluded postpartum measurements and performed a linear regression for each microorganism. Abundances were log-transformed and regressed against time and adjusted for ethnicity and patient ID, whereby patient ID is modelled as a random effect to account for the correlation between samples of the same individual. “NA” indicates a lack of convergence in the model because of too few data-points. Fold changes are reported as NAs if values in one of the two groups are 0 or if the corresponding regression-metrics are non-zero.

Species	Fold Change	Estimate	Std. Error	t value	P value	Q value
<i>Lactobacillus_crispatus</i>	1.2802	0.0056	0.0260	0.2168	8.3E-01	1.0E+00
<i>Lactobacillus_iners</i>	-1.3837	-0.0305	0.0332	-0.9179	3.6E-01	1.0E+00
<i>Lactobacillus_jensenii</i>	-1.0210	-0.0290	0.0397	-0.7314	4.6E-01	1.0E+00
<i>Lactobacillus_gasseri</i>	-1.1092	0.0556	0.0481	1.1555	2.5E-01	1.0E+00
<i>Lactobacillus_amylovorus</i>	1.1531	0.0031	0.0030	1.0304	3.0E-01	1.0E+00
<i>Prevotella_timonensis</i>	-3.8382	0.0086	0.0334	0.2578	8.0E-01	1.0E+00
<i>Prevotella_bivia</i>	4.5640	-0.0134	0.0292	-0.4591	6.5E-01	1.0E+00
<i>Streptococcus_agalactiae</i>	38.8851	-0.0269	0.0195	-1.3787	1.7E-01	1.0E+00
<i>Unclassified</i>	-1.8171	-0.0023	0.0232	-0.1007	9.2E-01	1.0E+00
<i>Atopobium_vaginae</i>	-12.2966	0.0411	0.0314	1.3085	1.9E-01	1.0E+00
<i>Finegoldia_magna</i>	-1.0441	0.0143	0.0251	0.5692	5.7E-01	1.0E+00
<i>Lactobacillus_delbrueckii</i>	42.8582	-0.0147	0.0126	-1.1611	2.5E-01	1.0E+00
<i>Sneathia_sanguinegens</i>	NA	0.0616	0.0628	0.9809	3.3E-01	1.0E+00
<i>Prevotella_disiens</i>	2.3448	-0.0059	0.0083	-0.7096	4.8E-01	1.0E+00
<i>Prevotella_amnii</i>	NA	NA	NA	NA	NA	NA
<i>Streptococcus_anginosus</i>	1.7241	0.0087	0.0184	0.4716	6.4E-01	1.0E+00
<i>Ureaplasma_parvum</i>	5.3038	-0.0083	0.0178	-0.4690	6.4E-01	1.0E+00
<i>Anaerococcus_vaginalis</i>	-7.6765	0.0221	0.0153	1.4481	1.5E-01	1.0E+00
<i>Aerococcus_christensenii</i>	-3.7557	0.0331	0.0308	1.0724	2.8E-01	1.0E+00
<i>Prevotella_buccalis</i>	NA	-0.0278	0.0200	-1.3915	1.6E-01	1.0E+00
<i>Dialister_micraerophilus</i>	-1.5993	0.0061	0.0121	0.5040	6.1E-01	1.0E+00

<i>Prevotella_corporis</i>	NA	-0.0120	0.0117	-1.0274	3.0E-01	1.0E+00
<i>Dialister_propionificiens</i>	4.6897	-0.0092	0.0153	-0.6026	5.5E-01	1.0E+00
<i>Veillonella_montpellierensis</i>	1.1724	0.0035	0.0105	0.3342	7.4E-01	1.0E+00
<i>Peptoniphilus_lacrimalis</i>	NA	0.0056	0.0043	1.3124	1.9E-01	1.0E+00
<i>Lactobacillus_salivarius</i>	NA	NA	NA	NA	NA	NA
<i>Staphylococcus_devriesei</i>	-1.7059	-0.0018	0.0094	-0.1878	8.5E-01	1.0E+00
<i>Anaerococcus_lactolyticus</i>	NA	0.0085	0.0113	0.7513	4.5E-01	1.0E+00
<i>Staphylococcus_capitis</i>	1.1724	-0.0020	0.0064	-0.3216	7.5E-01	1.0E+00
<i>Peptoniphilus_harei</i>	NA	-0.0087	0.0108	-0.8073	4.2E-01	1.0E+00
<i>Peptostreptococcus_anaerobius</i>	NA	NA	NA	NA	NA	NA
<i>Peptoniphilus_gorbachii</i>	NA	NA	NA	NA	NA	NA
<i>Fusobacterium_nucleatum</i>	NA	-0.0070	0.0079	-0.8837	3.8E-01	1.0E+00
<i>Gardnerella_vaginalis</i>	1.3856	0.0000	0.0099	-0.0036	1.0E+00	1.0E+00
<i>Campylobacter_ureolyticus</i>	NA	0.0059	0.0080	0.7415	4.6E-01	1.0E+00
<i>Peptococcus_niger</i>	NA	NA	NA	NA	NA	NA
<i>Corynebacterium_pyruviciproducens</i>	-5.1176	0.0026	0.0093	0.2781	7.8E-01	1.0E+00
<i>Streptococcus_gallolyticus</i>	NA	NA	NA	NA	NA	NA
<i>Porphyromonas_bennonis</i>	NA	0.0008	0.0020	0.4159	6.8E-01	1.0E+00
<i>Prevotella_denticola</i>	NA	NA	NA	NA	NA	NA
<i>Anaeroglobus_geminatus</i>	NA	-0.0122	0.0081	-1.5024	1.3E-01	1.0E+00
<i>Anaerococcus_murdochii</i>	NA	-0.0076	0.0082	-0.9244	3.6E-01	1.0E+00
<i>Propionibacterium_acnes</i>	NA	-0.0004	0.0028	-0.1328	8.9E-01	1.0E+00
<i>Actinomyces_europaeus</i>	NA	NA	NA	NA	NA	NA
<i>Scardovia_wiggisiae</i>	NA	NA	NA	NA	NA	NA
<i>Murdochiella_asaccharolytica</i>	NA	0.0002	0.0037	0.0600	9.5E-01	1.0E+00
<i>Rare OTUs</i>	-1.7059	0.0195	0.0175	1.1147	2.6E-01	1.0E+00

Supplementary Table 2. Linear mixed model regression analysis for exploring the association between microbial species abundance and pregnancy status. To examine if microorganism abundance changes significantly after pregnancy, a binary time variable was created with time=0 for measurements during pregnancy and time=1 for postpartum measurements. Using this binary time variable we performed a linear regression for each microorganism. Abundances were log-transformed and regressed against time adjusted for ethnicity and patient ID, whereby patient ID is modelled as a random effect to account for the correlation between samples of the same individual. Fold changes are reported as NAs if values in one of the two groups are 0 or if the corresponding regression-metrics are non-zero.

Species	Fold Change	Estimate	Std. Error	t value	P value	Q value
<i>Lactobacillus_crispatus</i>	-2.2915	-0.6555	0.2883	-2.2739	2.3E-02	6.7E-01
<i>Lactobacillus_iners</i>	-2.4702	-0.2210	0.1709	-1.2936	2.0E-01	8.9E-01
<i>Lactobacillus_jensenii</i>	-2.2858	-0.4816	0.2539	-1.8971	5.8E-02	8.9E-01
<i>Lactobacillus_gasseri</i>	-1.4661	-0.1517	0.2472	-0.6135	5.4E-01	8.9E-01
<i>Lactobacillus_amylovorus</i>	-260.6690	-0.0418	0.0801	-0.5225	6.0E-01	8.9E-01
<i>Prevotella_timonensis</i>	45.2014	0.9192	0.3169	2.9003	3.7E-03	1.3E-01
<i>Prevotella_bivia</i>	178.2422	0.5947	0.3345	1.7781	7.5E-02	8.9E-01
<i>Streptococcus_agalactiae</i>	141.4718	0.4491	0.2961	1.5167	1.3E-01	8.9E-01
<i>Unclassified</i>	11.4152	1.0624	0.2972	3.5745	3.5E-04	1.4E-02
<i>Atopobium_vaginae</i>	-38.1866	-0.0863	0.0917	-0.9408	3.5E-01	8.9E-01
<i>Fingoldia_magna</i>	21.9414	0.5846	0.1885	3.1007	1.9E-03	6.9E-02
<i>Lactobacillus_delbrueckii</i>	-167.4296	-0.0484	0.0638	-0.7578	4.5E-01	8.9E-01
<i>Sneathia_sanguinegens</i>	NA	-0.0278	0.0526	-0.5286	6.0E-01	8.9E-01
<i>Prevotella_disiens</i>	153.6941	0.4531	0.2028	2.2344	2.5E-02	7.1E-01
<i>Prevotella_amnii</i>	NA	NA	NA	NA	NA	NA
<i>Streptococcus_anginosus</i>	302.9333	0.7621	0.2808	2.7141	6.6E-03	2.1E-01
<i>Ureaplasma_parvum</i>	2.6371	0.0753	0.1074	0.7008	4.8E-01	8.9E-01
<i>Anaerococcus_vaginalis</i>	31.6893	0.6372	0.2194	2.9039	3.7E-03	1.3E-01
<i>Aerococcus_christensenii</i>	-2.7097	-0.0150	0.1089	-0.1375	8.9E-01	8.9E-01
<i>Prevotella_buccalis</i>	3.7013	0.3226	0.1237	2.6074	9.1E-03	2.8E-01
<i>Dialister_micraerophilus</i>	55.0788	0.4407	0.1616	2.7278	6.4E-03	2.1E-01

<i>Prevotella_corporis</i>	59.4701	0.2892	0.2042	1.4166	1.6E-01	8.9E-01
<i>Dialister_propionificaciens</i>	51.6722	0.3942	0.1713	2.3010	2.1E-02	6.4E-01
<i>Veillonella_montpellierensis</i>	NA	-0.0113	0.0330	-0.3419	7.3E-01	8.9E-01
<i>Peptoniphilus_lacrimalis</i>	355.0000	0.3717	0.1782	2.0860	3.7E-02	8.9E-01
<i>Lactobacillus_salivarius</i>	NA	0.0201	0.0061	3.3051	9.5E-04	3.6E-02
<i>Staphylococcus_devriesei</i>	15.7778	0.1133	0.1071	1.0584	2.9E-01	8.9E-01
<i>Anaerococcus_lactolyticus</i>	36.8148	0.3669	0.1932	1.8987	5.8E-02	8.9E-01
<i>Staphylococcus_capitis</i>	11.5704	0.1093	0.0709	1.5415	1.2E-01	8.9E-01
<i>Peptoniphilus_harei</i>	46.5444	0.2067	0.1333	1.5504	1.2E-01	8.9E-01
<i>Peptostreptococcus_anaerobius</i>	NA	0.3284	0.0473	6.9379	4.0E-12	1.8E-10
<i>Peptoniphilus_gorbachii</i>	NA	0.1000	0.0253	3.9524	7.7E-05	3.2E-03
<i>Fusobacterium_nucleatum</i>	27.4533	0.0903	0.1253	0.7208	4.7E-01	8.9E-01
<i>Gardnerella_vaginalis</i>	25.7885	0.1254	0.0937	1.3385	1.8E-01	8.9E-01
<i>Campylobacter_ureolyticus</i>	14.8762	0.1085	0.0908	1.1953	2.3E-01	8.9E-01
<i>Peptococcus_niger</i>	NA	0.1531	0.0287	5.3412	9.2E-08	4.0E-06
<i>Corynebacterium_pyruviciproducens</i>	1.9930	0.0794	0.0406	1.9561	5.0E-02	8.9E-01
<i>Streptococcus_gallolyticus</i>	NA	NA	NA	NA	NA	NA
<i>Porphyromonas_bennonis</i>	757.3333	0.2864	0.1429	2.0044	4.5E-02	8.9E-01
<i>Prevotella_denticola</i>	NA	NA	NA	NA	NA	NA
<i>Anaeroglobus_geminatus</i>	-1.1268	0.0378	0.0353	1.0687	2.9E-01	8.9E-01
<i>Anaerococcus_murdochii</i>	24.6133	0.1225	0.0773	1.5846	1.1E-01	8.9E-01
<i>Propionibacterium_acnes</i>	137.2667	0.1311	0.1008	1.2999	1.9E-01	8.9E-01
<i>Actinomyces_europaeus</i>	NA	0.0795	0.0242	3.2885	1.0E-03	3.7E-02
<i>Scardovia_wiggisiae</i>	NA	0.1006	0.0298	3.3781	7.3E-04	2.8E-02
<i>Murdochiella_asaccharolytica</i>	50.4889	0.1511	0.0832	1.8150	7.0E-02	8.9E-01
<i>Rare OTUs</i>	6.9502	0.4082	0.1079	3.7842	1.5E-04	6.3E-03

Supplementary Table 3. Linear mixed model regression analysis for examining CSTs across pregnancy timepoints. To test if CSTs change significantly over the course of pregnancy we excluded postpartum measurements and performed a linear regression for each CST. A CST indicator variable was created where CST=1 for samples that could be assigned to the given CST and CST=0 for all other samples. Time was regressed against CST adjusted for ethnicity and patient ID, whereby patient ID is modelled as a random effect to account for the correlation between samples of the same individual.

CST	08-12	19-25	27-30	32-36	Estimate	Std. Error	t value	P value	Q value
1	13 (46%)	17 (46%)	17 (43%)	13 (37%)	0.1553	0.1868	0.8312	4.1E-01	9.3E-01
2	2 (7%)	3 (8%)	5 (12%)	3 (9%)	-0.1253	0.3163	-0.3963	6.9E-01	9.3E-01
3	7 (25%)	11 (30%)	12 (30%)	12 (36%)	-0.2094	0.2031	-1.0314	3.0E-01	9.3E-01
4	2 (7%)	0 (0%)	0 (0%)	1 (3%)	0.6234	0.6319	0.9865	3.2E-01	9.3E-01
5	4 (14%)	6 (16%)	5 (12%)	5 (15%)	0.0224	0.2668	0.0841	9.3E-01	9.3E-01