**Table S2.** GBS Not Reported Studies (n=32)

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Study** | **Study purpose** | **Analysis level****-Species level** | **Streptococcus genus identified****(Y/N)** | **DNA extraction kit** | **Sequencing method** | **16S rRNA region** | **Taxonomy assignment/classification database** | **N****-vaginal specimen/pregnant women** | **Population****-participants’ age****-country****-multi-ethnicity (Y/N)** | **trimesters** | **Raw data sharing platform (accession number)** |
| Dominguez-Bello et al. (2010)22 | Delivery mode and newborn initial microbiome (=mother-to-newborn bacterial transmission occurs during birth) | N | Y | PowerSoil® DNA isolation kit (MO BIO laboratories, Carlsbad, CA, USA) | 16S rRNA gene sequencing | V2 | RDP classifier (minimum support threshold: 60%), RDP taxonomic nomenclature    | 4/9 | -Age: 21-33-Venezuela  | **○○●**(sampled 1 hr before delivery) | **N/A** |
| Hernández-Rodríguez et al. (2011)23 | Vaginal microbiome composition variation (across pregnancy, among Mexican women) | Species | N | DNAzol reagent (Invitrogen, Carlsbad, Calif, USA) | PCR-denaturing gradientgel electrophoresis (PCR-DGGE) of 16S rRNA | V3 | BLAST version 2.2.3 search | 64/64 | -Age: 13-43-Mexico | **●●●** | **N/A** |
| Aagaard et al. (2012)24 | Vaginal microbiome composition variation (across pregnancy) | Genus, Species level for Lactobacillus | Y (mentioned Streptococcaceae) | PowerSoil DNA Isolation Kit (MoBio) | 16S rRNA pyrosequencing | V1V3,V3V5 | RDP with Greengenes database and BLAST | 68/24 | -Age: 18-40-USA-Multi-ethnicity: Y | **○●●**(18-40 wks) | **N/A** |
| Frank et al. (2012)25 | Vaginal microbiome composition variation (perinatal MTCT, among HIV-infected pre women) | Y | N | Custom method | 16S rRNA pyrosequencing | Broad-range amplification | BLAST database (All-Species Living Tree Project, ver. LTP\_S95) + RDP Naïve Bayesian classifier | 64/64 | -Age: 21-27-West Africa: Bobo-Dioulasso (Burkina Faso)  | **○○●**(36-38 wks)  | GenBank (accession no. JF461543-JF487783) |
| Hyman et al. (2012)26 | Vaginal microbiome composition variation (during IVF-ET therapy across different hormonal environments) | Genus, Species level for Lactobacillus | Y | DNeasy kit (Qiagen, Valencia, CA) | 16S rRNA | whole 16S region | RDP database | 99/30 | -Age: 28-45-USA-Multi-ethnicity: Y  | **●○○**(6-8 wks) | GenBank (accession no. HQ293151-HQ293203) |
| Hyman et al. (2014)27 | Vaginal microbiota and preterm birth | Yes (mostly Genus, Species level only for Lactobacillus) | Y | DNeasy Tissue and Blood Kit (Qiagen,Valencia, California) with some modifications | 16S rRNA gene(Chain-Terminator (Sanger) Sequencing) | whole 16S region | RDP database | 143/88 | -Age: > 18-USA-Multi-ethnicity: Y | **●●●**  | GenBank (accession no. JX871219 to JX871316) |
| Walther-António et al. (2014)28 | Stable Lactobacillus community during pregnancy | Species level  | Y (Supplemental OTU table includes Streptococcus genus, further identified as Streptococcus anginosus and Streptococcus oralis)  | MoBio Ultraclean Soil Kit (MoBio Laboratories, Inc., Carlsbad, CA) with some modifications | 16S rRNA | V3V5 | Illinois-Mayo Taxon Operations for RNA Dataset Organization (IM-TORNADO) | 95/12 | -Age: 24-36-USA  | **●●●**(8–12, 17–21, 27–31, and 36–38 wks) | MG-RAST (sequence IDs: 4563804.3–4563899.3) |
| Baldwin et al. (2015)29 | Vaginal/amniotic fluid microbiome composition variation (associate with PPROM) | Genus | N | MoBio Ultraclean Soil Kit with MP Fast Prep | 16S rRNA | V3V5 | BLAST and custom IM-TORNADO | 61/15 | -Age: 19-37-USA-Multi-ethnicity: Y | **○●○**(23-24 wks) | NCBI SRA (study accession no. SRP061714) |
| DiGiulio et al. (2015)30 | pregnancy-associated microbiome variation (before and after pregnancy) | Yes | N(not in top 20) | PowerSoil® DNA isolation kit (MO BIO laboratories, Carlsbad, CA, USA) | 16S rRNA gene sequencing | V3-V5 | RDP classifier version 2.2 | 1188/49 | -Age: 19-45-USA-Multi-ethnicity: Y | **●●●**(weekly sampling) | NCBI SRA (SRP no. 288562) |
| Huang et al. (2015)31 | Vaginal microbiome composition variation (sampling sites) | Y (Species level only for Lactobacillus)  | Y | DNA MAGNETICS and EXTRACT kit (Shenzhen BioEAsy Biotechnologies. Co., Ltd., China) | 16S rRNA | V4V6 | RDP classifier (default database) | 216/24 | -Age: 19.4-39.2-China  | **●●●**  | European Bioinformatics Institute (accession no. from ERS371314 to ERS371619) |
| Brumbaugh et al. (2016)32 | Delivery mode and newborn initial microbiome (=mother-to-newborn bacterial transmission occurs during birth) | Genus level | N\*GBS clinical test (+) during prenatal screening | Powerfecal DNA Isolation Kit (Mo Bio, Carlsbad, CA) | 16S rRNA | V1V2 | SINA (1.2.11), Used Silva 115NR99 as reference | 23/23 | -Age: 29-33-Not specified  | **○○●**(sampled immediately before delivery) | NCBI SRA under (project no. PRJNA278085) |
| Jayaprakash et al. (2016)33 | Vaginal microbiome composition variation (following PPROM, to predicts latency duration and perinatal outcomes) | Species level | Y - Streptococcus pseudopneumoniaeidentified\*GBS clinical test (+) | magnetic bead-based kit (MagMAX, Life Technologies, Burlington, ON) | Pyrosequencing | cpn60 universal target | cpnDB\_nr reference database (downloaded from www.cpndb.ca) | 70/36 | -Age: 22-40-Canada-Multi-ethnicity: Y | **○●●**(24-33 wks) | NCBI SRA (Accession SRP077099, BioProject PRJNA326844) |
| Lauder et al. (2016)34 | To examine if bacterial DNA in placenta samples are derive from contamination in dust or commercial reagents | Genus level | Y | PSP Stool DNA Plus kit (STRATEC Biomedical, Berlin-Buch, Germany) | 16S rRNA | V1V2 | UCLUST consensus method of QIIME 1.8, using the GreenGenes 16S rRNA gene database v. 13\_8 | 6/6 | -Age: 22-40-USA-Multi-ethnicity: Y | **○○●**(during spontaneous Labor/following ROM) | NCBI SRA (bio project PRJNA309332) |
| Nelson et al. (2016)35 | Vaginal microbiome composition variation/profile (high risk for SPTB) | Genus level | Y - also included participants’ BV state | MoBio (Carlsbad, CA) PowerSoilhtp96 well Soil DNA Isolation plates | 16S rRNA | V4 | Greengenes database (v13\_8)+ (BLAST only for Lactobacillus at species level) | 40/40 | -Age: mean 18.74 (sd 2.61)-USA-AA women | **●●○**(<16 wks or 20-24 wks) | **N/A** |
| Subramaniam et al. (2016)36 | Vaginal microbiome composition variation (by BV, birth timing & race) | Genus | Y | fecal DNA isolation kit from Zymo Research | 16S rRNA | V4 | RDP classifier with Greengenes database (v13\_8) | 39/40 | -Age: mean 21.4 (sd 2.3)-USA-Multi-ethnicity: Y | **○●○**(25-26 wks) | **N/A** |
| Callahan et al. (2017)37 | Vaginal microbiota and preterm birth (Caucasian cf. AA) | Yes (only for Lactobacillus and Gardnerella genus) | Y(in Fig. S5-S6.) | PowerSoil® DNA isolation kit (MO BIO laboratories, Carlsbad, CA, USA) | 16S rRNA gene sequencing | V4 | Silva v123 database using implementation of the RDP naive Bayesian classifier | 2179/135 | -Age: 18-45-USA-Multi-ethnicity: Y | **●●●**(weekly sampling) | NCBI SRA (accession no. SRP115697) |
| Freitas et al. (2017)38 | Vaginal microbiome composition variation (healthy preg women) | Species level | Y - other species of Streptococcus identified  | MagMAX™ Total Nucleic Acid Isolation Kit (Life Technologies, Burlington, ON, Canada) | Pyrosequencing | cpn60 universal target | manually curated reference set of 1,561 OTU sequences representing human vaginal microbiota - generated originally by de novo assembly of cpn60 sequence reads from each of 546 vaginal microbiomes | 182/182 | -Age: 18-49-USA-Multi-ethnicity: Y | **●●○**(11-16 wks) | NCBI SRA (Accession SRP073152, BioProject PRJNA317763) |
| Nasioudis et al. (2017)39 | Vaginal microbiome composition variation (first cf. subsequent conception) | Yes (only for Lactobacillus) | Y | QIAamp DNA Mini Kit (Qiagen, Hilden, GER) | 16S rRNA | V1V3 | BLAST | 155/155 | -Age:first conception 32.3 (3.8); prior termination 33.3 (4.7); spont. abortion 36.0 (5.5); prior delivery 34.6 (3.7)-USA-Multi-ethnicity: Y | **●○○**(8-12 wks) | N/A |
| Nasioudis et al. (2017)40 | Vaginal microbiome composition variation (of 1st trimester, stress and autophagy in vaginal epithelial cell) | Yes (Species level for Lactobacillus), Genus level for Gardnerella, Bifidobacterium, andStreptococcus | Y | Custom protocol | 16S rRNA | V1V3 | RDP Bayesian classifier (Ver. 2.5) | 154/154 | -Age: mean 33.8-USA-Multi-ethnicity: Y | **●○○**(8-12 wks) | N/A |
| Roesch et al. (2017)41 | Vaginal microbiome composition variation (impact of intrapartum Penicillin prophylaxis for GBS infection among pregnant women with PTB) | Genus level |  N\*GBS clinical test (+) Streptococcus detected in 74% of samples during sequencing (in addition to clinical screening) | QIAamp Fast DNA Stool Mini Kit (Qiagen, Valencia, CA, USA) | 16S rRNA | V4 | QIIME(12) based on the UCLUST method against the Greengenes 13.5 database | 27/27 | -Age: Group 1 (26.2 ± 6.6), Group 2 (25.0 ± 7.0), Group 3 (24.5±4.6), Group 4 (25.7±8.7)-Brazil | **●●●**(<32 wks) | NCBI SRA (BioProject ID PRJNA354838, study number SRP093885) |
| Stout et al. (2017)42 | Vaginal microbiota and preterm birth (among AA) | Yes (only for Lactobacillus) | Y | PowerSoil® DNA isolation kit (MO BIO laboratories, Carlsbad, CA, USA) | 16S rRNA gene sequencing | V1V3, V3V5 | RDP Naive Bayesian Classifier (ver.2.5, training set 9)+NCBI database only for Lactobacillus species (BLAST) | 149/77 | -Age: not specified-USA-Multi-ethnicity: Y | **●●●**  | NCBI Bioproject (no. PRJNA294119) |
| Goltsman et al. (2018)43 | pregnancy-associated microbiome (Shotgun metagenomics) | Yes(strain-level) | N(not in top 15 Fig.1A/S-Fig.2C) | PowerSoil® DNA isolation kit (MO BIO laboratories, Carlsbad, CA, USA) | Shotgun metagenomics | N/A | EMIRGE | 101/10 | -Age: 20-38-USA-Multi-ethnicity: Y | **●●●**  | NCBI BioProject database (accession no. PRJNA288562, details in Table S5) |
| Leizer et al. (2018)44 | Pregnancy vaginal environments when Lactobacillus are dominant | Y (might be only for Lactobacillus)  | N\*GBS clinical test (+) | QIAamp DNA Mini Kit (Qiagen, Hilden, Germany) with some modifications | 16S rRNA   | V1-V3 | SILVA bacterial sequence database + RDP Bayesian classifier (2.5) | 157/157 | -Age: 26-44-Japan | **●○○**(<12 wks) | **N/A** |
| Matsumoto et al. (2018)45 | Vaginal microbiome composition variation (preg cf. non-preg cf. sex workers) | Y(but not reported, except for Lactobacillus genus) | Y | Custom protocol | 16S rRNA gene sequencing | V3-V4 | RDP Classifier | 24/24 | -Age: non-specified-Japan  | ???Non-specified | N/A |
| Wylie et al. (2018)46 | Vaginal microbiome composition variation (patient vs. provider collected specimen) | Y(but not reported) | N(not reported within top 21 genus) | PowerSoil® DNA isolation kit (MO BIO laboratories, Carlsbad, CA, USA) | 16S rRNA | V1V3, V3V5 | RDP naïve bayesian classifier (ver. 2.5) | 94/47 | -Age: not specified-USA-Multi-ethnicity: Y | **●●●**(5-33 wks) | NCBI SRA under Bioproject PRJNA294119, details of the SRA accession no. in article) |
| Chen et al. (2019)47 | Vaginal microbiome composition variation (HPV infected preg cf. non-preg) | Yes(but at least not in the presented 30 in figure 6) | Y(in most top 20 genus) | QIAamp DNA Mini Kit (Qiagen, Hilden, Germany) | 16S rRNA | V3V4 | RDP classifier script (ver. 2.2), Silva database (Release 128) | 135/86 | -Age: 25-40-China | **○●●**(16-30 wks) | NCBI SRA (accession no. SRP126438) |
| Dobbler et al. (2019)48 | Vaginal microbiome composition variation (3rd trimester) | Species level, including Lactobacillus, Prevotella, and Gardnerella | N | QIAamp Fast DNA Stool Mini Kit | 16S rRNA | V4 | Greengenes database | 27/27 | -Age: Cluster 1: 27.14 ± 7.4; Cluster 2: 24.33 ± 3.6; Cluster 3: 23.71 ± 6.0-Brazil | **○○●**(37-40 wks)  | NCBI SRA (accession SRP093885, Run no. SRR7657414 to SRR7657440) |
| He et al. (2019)49 | Vaginal microbiota and preterm birth/birth outcome (Chinese women) | Species (only for Lactobacillus genus) | Y | Custom method | 16S rRNA | V3V4 | DADA2 with SILVA and BLAST | 113/113 | -Age: 17-34-China | **●●●**(12-27 wks) | NCBI SRA (accession no. SRP216638) |
| Jefferson et al. (2019)50 | Vaginal microbiome composition variation (association with Vitamin D) | Species | N | PowerSoil kit (MoBio) | 16S rRNA | V1V3 | STIRRUPS | 537/236 | -Age: 18-42-USA-Multi-ethnicity: Y  | **●●●**(7-15, 21-28, and 31-40 wks) | N/A |
| Liu et al. (2019)51 | Delivery mode and newborn initial microbiome (=mother-to-newborn bacterial transmission occurs during birth) | Genus | Y | Custom method | 16S rRNA gene  | V4V5 | SILVA SSU database v132 | 78/78 | -Age: mean 28.9 (sd 4.5)-China | **○○●**(sampled one hour from delivery) | NCBI SRA (accession no. PRJNA559967) |
| Price et al. (2019)52 | Vaginal microbiome composition variation (HIV infection & Treatment) | Species level | N | Qiagen ATL buffer (Valencia, CA) with some modifications | Whole genome shotgun (WGS) sequencing | N/A | Alignment using Bowtie2, Taxonomic composition estimated using the HUMAnN2 pipeline | 256/461 | -Age: median 27<20 (n=24), 20-34 (n=194), >=35 (n=29), missing (n=7)-Zambiam   | **○●○**(16–20 wks) | N/A |
| Witkin et al. (2019)53 | Vaginal microbiome composition variation (according to HDAC1 level in vaginal epithelial cell) | Y (might be only for Lactobacillus genus)  | Y | Q"IAamp DNA Mini Kit (Qiagen, Hilden, Germany) with some modifications | 16S rRNA  | V1V3 | SILVA bacterial sequence database (ver. 1.27) | 300/150 | -Age: Not specified | **●○○**(8-12 wks) | N/A |

 **Note.** The symbol **●○○** indicates the first, **○●○** the second, and **○○●** the third trimester respectively;The symbol **\*** indicates GBS was detected and reported from clinical screening test (but not from DNA sequencing); preg = pregnant; AA=African American; RDP=Ribosomal Database Project; ROM=rupture of membranes; PPROM=preterm premature rupture of membranes; SPTB=spontaneous preterm birth; sd=standard deviation; IVF-ET therapy=In Vitro Fertilization & Embryo Transfer therapy; MTCT=mother-to-child transmission; BV=bacterial vaginosis; NCBI = National Center for Biotechnology Information; ENA = European Nucleotide Archive; SRA: Sequence Read Archive/Short Read Archive; no. = number. NCBI BioProject database (<https://www.ncbi.nlm.nih.gov/bioproject>), European Nucleotide Archive (<https://www.ebi.ac.uk/ena/browser>), European Bioinformatics Institute (<http://www.ebi.ac.uk/>), MG-RAST (<http://metagenomics.anl.gov>).

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