Supplementary information 1. Query search terms, dates, and results for each database.

Search parameter	**Items found/included**
Pubmed Query search on 01-02-2022	
((("meconium"[MeSH Terms] OR "meconium"[All Fields] OR "meconiums"[All Fields]) AND ("microbiome s"[All Fields] OR "microbiomic"[All Fields] OR "microbiomics"[All Fields] OR "microbiota"[MeSH Terms] OR "microbiota"[All Fields] OR "microbiome"[All Fields] OR "microbiomes"[All Fields])) OR (("meconium"[MeSH Terms] OR "meconium"[All Fields] OR "meconiums"[All Fields]) AND ("microbiota"[MeSH Terms] OR "microbiota"[All Fields] OR "microbiotas"[All Fields] OR "microbiota s"[All Fields] OR "microbiotae"[All Fields]))) AND ((humans[Filter]) AND (english[Filter]))	121
Language filter	English
Population filter	Human
Scopus Query search on 01-02-2022	
TITLE-ABS-KEY(meconium microbiome OR meconium microbiota) AND (LIMIT-TO (LANGUAGE,"English")) AND (LIMIT-TO (EXACTKEYWORD,"Human"))	110
Language filter	English
Population filter	Human
Duplicates	83
Web of Science Query search on 02-02-2022	
(ALL=(meconium microbiome OR meconium microbiota)) AND (LA==("ENGLISH"))	178
Language filter	English
Duplicates	114
Total screened after duplicate removal	212
Total articles after exclusion	69

Supplementary information 2. A list of TruSeq adapter sequences used as truncated overhangs during the 2-step PCR protocols first round of PCR

Adapter name	Adapter sequence
F1	ATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT
F2	ATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTgt
F3	ATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTagag
F4	ATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTtagtgt
R1	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT
R2	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTa
R3	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTtct
R4	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTctgagtg

Supplementary information 4. Relative frequencies of bacterial composition of meconium samples based on the delivery mode and the usage of intrapartum antibiotics. Top ten most frequent taxa are shown, and the rest are collapsed in the “other” category.

Vaginal delivery			
Phyla (%)		**Genera (%)**	
Firmicutes	54	*Staphylococcus*	25
Proteobacteria	31	*Escherichia-Shigella*	19
Actinobacteriota	11	*Streptococcus*	8.1
Bacteroidota	2.5	*Enterococcus*	7.1
Fusobacteriota	0.57	*Lactobacillus*	6.2
d__Bacteria	0.14	*Cutibacterium*	5.2
Verrucomicrobiota	0.11	*Bradyrhizobium*	3.9
Deinococcota	0.096	*Corynebacterium*	2.9
Patescibacteria	0.019	*Clostridium_sensu_stricto_1*	1.7
Unassigned	0.0035	*Bacillus*	0.95
other	0.00025	other	19

Vaginal delivery with intrapartum antibiotics			
Phyla (%)		**Genera (%)**	
Firmicutes	40	*Staphylococcus*	23
Proteobacteria	31	*Escherichia-Shigella*	13
Actinobacteriota	25	*Cutibacterium*	12
Bacteroidota	2.7	*Lactobacillus*	5.1
Deinococcota	0.38	*Bradyrhizobium*	5.1
Fusobacteriota	0.36	*Streptococcus*	4.7
Chloroflexi	0.32	*Corynebacterium*	3.8
d__Bacteria	0.18	*Enhydrobacter*	3.0
Fibrobacterota	0.017	*Anaerococcus*	2.1
Planctomycetota	0.010	*Lawsonella*	1.7
other	0.016	other	26

C-section delivery			
Phyla (%)		**Genera (%)**	
Proteobacteria	35	*Cutibacterium*	22
Actinobacteriota	33	*Staphylococcus*	15
Firmicutes	26	*Bradyrhizobium*	12
Bacteroidota	3.6	*Corynebacterium*	4.0
d__Bacteria	1.2	*Streptococcus*	3.0
Deinococcota	0.70	*Enhydrobacter*	2.4
Acidobacteriota	0.37	*Acinetobacter*	1.9
Fusobacteriota	0.20	*Pseudomonas*	1.4
Patescibacteria	0.16	*Lactococcus*	1.3
Chloroflexi	0.11	*Bacillus*	1.3
other	0.27	other	35

Supplementary information 5. Kruskal-Wallis H pairwise comparisons between each sample group of alpha diversity metrices Shannon Index and observed features as well as beta diversity using PCoA with Bray-Curtis dissimilarity. Each group's sample size n is included. The table includes Kruskal-Wallis H and the corrected p-value using Benjamini-Hochberg correction method as well as p-value of the PERMANOVA test. Significant values have been marked in bold.

Group comparisons		Shannon Index		Observed features		Bray-Curtis dissimilarity
		H	p-value	H	p-value	PERMANOVA p-value
VD (n=109)	VD+AB (n=35)	0.034	0.855	0.795	0.373	**0.001**
VD (n=109)	CS (n=171)	**14.148**	**<0.001**	0.027	0.870	**0.001**
VD+AB (n=35)	CS (n=171)	**5.850**	**0.016**	0.499	0.480	**0.003**

Supplementary information 7. ANCOM results of the newborn, maternal, and environmental factors. Differentially abundant features have been analyzed in Phyla and Genera level.

Prenatal (maternal) factors	**Phyla**	**W**	**Genera**	**W**
Age of the mother during pregnancy (<30 or ≥30 years)	no	no	no	no
Weight of the mother at the beginning of the pregnancy (<65 or ≥65 kg)	no	no	*Pelomonas*	411
Weight of the mother at the end of the pregnancy (<80 or ≥80 kg)	no	no	*Pelomonas*	414
Weight gain of the mother during pregnancy (<15 or ≥15 kg)	no	no	Pelomonas	423
Maternal GDM	Acidobacteriota	7	c__Bacilli	321
Maternal lactic acid bacteria usage during pregnancy	no	no	*Corynebacteriaceae* f__Beijerinckiaceae	155 115
Maternal antibiotics during pregnancy	no	no	no	no
Maternal medicine during pregnancy	no	no	*Acidovorax*	445
Maternal smoking during pregnancy	no	no	*Acidovorax*	444
Maternal fish consumption (<1, 1, or >1 per week)	Acidobacteriota	11	*Acidiphilium*	347
Maternal meat consumption (<5, 5-6, or 6> per week)	Acidobacteriota	14	*Acidiphilium*	363
Prenatal (environmental) factors	**Phyla**	**W**	**Genera**	**W**
Forest exposure of the mother during pregnancy (<2 or ≥2 hours)	no	no	no	no
Owning a summer cottage	no	no	no	no
Presence of furry pets in the household during pregnancy	no	no	no	no
Presence of older siblings in the household during pregnancy	no	no	no	no
Postnatal factors	**Phyla**	**W**	**Genera**	**W**
Sex of the newborn	no	no	no	no
Newborn’s weight (<3500 or ≥3500 g)	no	no	no	no
Newborn’s height (<50 or ≥50 cm)	Acidobacteriota	14	*Rahnella1* *Bryocella*	394 354
Head circumference of the newborn at birth (<35 or ≥35 cm)	Acidobacteriota	13	*Rahnella1* *Bryocella*	364 327

Supplementary information 8. Regression analysis using linear mixed model on the most abundant phyla. We analyzed seven different delivery and maternal factors. Factors with p-values of ≤0.05 have been marked in bold.

Phyla	Factor	Mean Difference	p-value	95% CI	
				Lower	Upper
Actinobacteriota	**intrapartum ab (no, yes)**	**-0.087**	**0.031**	**-0.116**	**-0.008**
	delivery mode (vd, cs)	-0.062	0.118	-0.141	0.016
	forest exposure h (<2, ≥2)	-0.024	0.776	-0.090	0.042
	older siblings (no, yes)	-0.002	0.956	-0.059	0.056
	furry pets (no, yes)	0.007	0.795	-0.046	0.059
	mom weight gain kg (<15, ≥15)	-0.021	0.809	-0.084	0.042
	mom age y (<30, ≥30)	-0.003	0.912	-0.056	0.050
Firmicutes	intrapartum ab (no, yes)	0.087	0.094	-0.015	0.189
	delivery mode (vd, cs)	**0.153**	**0.003**	**0.052**	**0.225**
	forest exposure h (<2, ≥2)	0.053	0.364	-0.033	0.138
	older siblings (no, yes)	0.009	0.809	-0.065	0.084
	furry pets (no, yes)	0.024	0.494	-0.044	0.092
	mom weight gain kg (<15, ≥15)	0.019	0.926	-0.062	0.100
	mom age y (<30, ≥30)	0.016	0.649	-0.053	0.085
Proteobacteria	intrapartum ab (no, yes)	0.012	0.823	-0.090	0.113
	delivery mode (vd, cs)	-0.078	0.129	-0.178	0.023
	forest exposure h (<2, ≥2)	-0.035	0.690	-0.120	0.050
	older siblings (no, yes)	-0.010	0.783	-0.084	0.063
	furry pets (no, yes)	-0.023	0.508	-0.090	0.045
	mom weight gain kg (<15, ≥15)	0.023	0.872	-0.058	0.103
	mom age y (<30, ≥30)	-0.013	0.718	-0.081	0.056
Bacteroidota	intrapartum ab (no, yes)	-0.006	0.751	-0.044	0.032
	delivery mode (vd, cs)	-0.002	0.921	-0.040	0.036
	forest exposure h (<2, ≥2)	0.004	0.986	-0.028	0.036
	older siblings (no, yes)	0.003	0.853	-0.025	0.030
	furry pets (no, yes)	-0.008	0.534	-0.033	0.017
	mom weight gain kg (<15, ≥15)	-0.014	0.586	-0.045	0.016
	mom age y (<30, ≥30)	0.000	0.974	-0.026	0.025

Supplementary information 9. Regression analysis using linear mixed model on the most interesting genera. We analyzed seven different delivery and maternal factors. Factors with p-values of ≤0.05 have been marked in bold.

Genera	Factor	Mean Difference	p-value	95% CI	
				Lower	Upper
Lactobacillus	intrapartum ab (no, yes)	0.011	0.579	-0.027	0.048
	delivery mode (vd, cs)	0.035	0.071	-0.003	0.072
	forest exposure h (<2, ≥2)	0.009	0.856	-0.022	0.041
	older siblings (no, yes)	0.018	0.205	-0.010	0.046
	furry pets (no, yes)	0.003	0.818	-0.022	0.028
	mom weight gain kg (<15, ≥15)	0.014	0.596	-0.016	0.045
	mom age y (<30, ≥30)	0.005	0.682	-0.021	0.031
Streptococcus	intrapartum ab (no, yes)	0.011	0.615	-0.033	0.055
	delivery mode (vd, cs)	0.019	0.397	-0.025	0.063
	forest exposure h (<2, ≥2)	0.003	0.995	-0.034	0.040
	older siblings (no, yes)	0.018	0.267	-0.014	0.051
	furry pets (no, yes)	0.015	0.312	-0.014	0.045
	mom weight gain kg (<15, ≥15)	-0.003	0.994	-0.039	0.032
	mom age y (<30, ≥30)	0.013	0.402	-0.017	0.043
Escherichia-Shigella	intrapartum ab (no, yes)	0.035	0.213	-0.020	0.090
	delivery mode (vd, cs)	**0.065**	**0.020**	**0.010**	**0.120**
	forest exposure h (<2, ≥2)	0.004	0.996	-0.043	0.050
	older siblings (no, yes)	-0.002	0.914	-0.043	0.038
	furry pets (no, yes)	-0.011	0.575	-0.048	0.027
	mom weight gain kg (<15, ≥15)	-0.006	0.985	-0.050	0.039
	mom age y (<30, ≥30)	-0.002	0.930	-0.040	0.036
Staphylococcus	intrapartum ab (no, yes)	0.008	0.833	-0.064	0.079
	delivery mode (vd, cs)	0.041	0.255	-0.030	0.113
	forest exposure h (<2, ≥2)	0.022	0.772	-0.039	0.082
	older siblings (no, yes)	-0.045	0.096	-0.098	0.008
	furry pets (no, yes)	-0.009	0.706	-0.058	0.039
	mom weight gain kg (<15, ≥15)	0.015	0.889	-0.042	0.073
	mom age y (<30, ≥30)	0.024	0.330	-0.025	0.074
Enterococcus	intrapartum ab (no, yes)	0.031	0.084	-0.004	0.065
	delivery mode (vd, cs)	0.003	0.845	-0.031	0.038
	forest exposure h (<2, ≥2)	0.018	0.350	-0.011	0.047
	older siblings (no, yes)	**0.034**	**0.010**	**0.008**	**0.059**
	furry pets (no, yes)	-0.015	0.192	-0.039	0.008
	mom weight gain kg (<15, ≥15)	-0.006	0.931	-0.034	0.022
	mom age y (<30, ≥30)	-0.022	0.074	-0.045	0.002
Cutibacterium	intrapartum ab (no, yes)	-0.053	0.096	-0.115	0.009
	delivery mode (vd, cs)	**-0.074**	**0.020**	**-0.135**	**-0.012**
	forest exposure h (<2, ≥2)	0.014	0.884	-0.038	0.067
	older siblings (no, yes)	-0.009	0.707	-0.055	0.037
	furry pets (no, yes)	0.015	0.479	-0.027	0.057
	mom weight gain kg (<15, ≥15)	-0.036	0.236	-0.086	0.014
	mom age y (<30, ≥30)	-0.001	0.958	-0.044	0.042

Supplementary information 10. Differentially abundant predicted metabolic pathways based on the delivery mode and the usage of intrapartum antibiotics in vaginal delivery samples. Metacyc.org was used to find detailed pathway names.

Delivery mode		
Pathway name	Detailed pathway name	W
FUC-RHAMCAT-PWY	superpathway of fucose and rhamnose degradation	360
PWY-7094	fatty acid salvage	354
GLYCOL-GLYOXDEG-PWY	superpathway of glycol metabolism and degradation	352
GLCMANNANAUT-PWY	superpathway of N-acetylglucosamine, N-acetylmannosamine and N-acetylneuraminate degradation	346
PROTOCATECHUATE-ORTHO-CLEAVAGE-PWY	protocatechuate degradation II (ortho-cleavage pathway)	343
PWY-5920	superpathway of heme b biosynthesis from glycine	336
PWY0-41	allantoin degradation IV (anaerobic)	335
LEU-DEG2-PWY	L-leucine degradation I	332
PWY-6629	superpathway of L-tryptophan biosynthesis	327
PWY-7431	aromatic biogenic amine degradation (bacteria)	327
PWY0-1277	3-phenylpropanoate and 3-(3-hydroxyphenyl) propanoate degradation	325
HCAMHPDEG-PWY	3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation to 2-hydroxypentadienoate	324
PWY-6690	cinnamate and 3-hydroxycinnamate degradation to 2-hydroxypentadienoate	324
PWY-7446	sulfoquinovose degradation I	323
P108-PWY	pyruvate fermentation to propanoate I	320
ECASYN-PWY	enterobacterial common antigen biosynthesis	318
PWY-4984	urea cycle	318
P161-PWY	acetylene degradation (anaerobic)	317
PWY-7315	dTDP-N-acetylthomosamine biosynthesis	317
ORNDEG-PWY	superpathway of ornithine degradation	314
ARGDEG-PWY	superpathway of L-arginine, putrescine, and 4-aminobutanoate degradation	312
ORNARGDEG-PWY	superpathway of L-arginine and L-ornithine degradation	312
PWY-3781	aerobic respiration I (cytochrome c)	302
KDO-NAGLIPASYN-PWY	superpathway of (Kdo)$_2$-lipid A biosynthesis	300
PWYG-321	mycolate biosynthesis	285
Intrapartum antibiotics		
Pathway name	Detailed pathway name	W
PWY-7094	fatty acid salvage	367
P108-PWY	pyruvate fermentation to propanoate I	348
PWY-7431	aromatic biogenic amine degradation (bacteria)	341
PROTOCATECHUATE-ORTHO-CLEAVAGE-PWY	protocatechuate degradation II (ortho-cleavage pathway)	337
PWY-3781	aerobic respiration I (cytochrome c)	335
GLYCOL-GLYOXDEG-PWY	superpathway of glycol metabolism and degradation	331
FUC-RHAMCAT-PWY	superpathway of fucose and rhamnose degradation	330
PWY0-41	allantoin degradation IV (anaerobic)	330