

Supplementary materials

Prenatal PM_{2.5} exposure associated with neonatal gut bacterial colonization and early children's cognitive development

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Table S1. Demographic characteristics of the study subjects for 16sRNA sequencing.

Variable	Total subjects (N = 361)	High exposure (N = 180)	Low exposure (N = 181)	P value*
Prenatal personal PM _{2.5} exposure during pregnancy, µg/m ³				
Entire pregnancy	43.37 ± 3.66	46.3 ± 2.68	40.4 ± 1.51	<0.001
Prenatal personal temperature exposure during pregnancy, °C				
Entire pregnancy	18.0 ± 0.91	17.7 ± 0.80	18.3 ± 0.92	<0.001
Prenatal personal humidity exposure during pregnancy, %rh				
Entire pregnancy	73.2 ± 2.37	72.9 ± 1.72	73.6 ± 2.83	0.004
Prenatal personal O ₃ exposure during pregnancy, µg/m ³				
Entire pregnancy	93.7 ± 6.29	96.3 ± 3.81	91.1 ± 7.16	<0.001
Prenatal personal CO exposure during pregnancy, µg/m ³				
Entire pregnancy	0.75 ± 0.05	0.74 ± 0.04	0.76 ± 0.06	<0.001
Prenatal personal NO ₂ exposure during pregnancy, µg/m ³				
Entire pregnancy	36.0 ± 6.55	34.4 ± 4.33	37.7 ± 7.85	<0.001
Prenatal personal PM ₁₀ exposure during pregnancy, µg/m ³				
Entire pregnancy	50.9 ± 6.49	51.1 ± 4.97	50.7 ± 7.70	0.524
Prenatal personal SO ₂ exposure during pregnancy, µg/m ³				
Entire pregnancy	9.52 ± 1.68	9.48 ± 1.20	9.55 ± 2.05	0.697
Basic demographic characteristic				
Maternal Age, years	29.2 ± 4.20	28.8 ± 4.07	29.5 ± 4.31	0.152
Maternal pregnancy BMI, kg/m ²	21.6 ± 3.06	21.3 ± 3.16	21.9 ± 2.94	0.055
Gestation weight gain (GWG), kg	13.5 ± 5.67	13.2 ± 5.82	13.8 ± 5.51	0.330
Maternal educational level				0.198
Junior high school or below	24 (6.65%)	8 (4.44%)	16 (8.84%)	
Senior high school or Junior college	190 (52.6%)	94 (52.2%)	96 (53.0%)	
College degree or above	147 (40.7%)	78 (43.3%)	69 (38.1%)	
Annual family income, yuan				0.590
<100,000	95 (26.3%)	46 (25.6%)	49 (27.1%)	
100,000-300,000	239 (66.2%)	118 (65.6%)	121 (66.9%)	
>300,000	27 (7.48%)	16 (8.89%)	11 (6.08%)	
Energy intake in pregnancy, kcal	2236 ± 1080	2263 ± 1151	2210 ± 1007	0.643
Gestational age, weeks	39.3 (1.26)	39.4 (1.27)	39.3 (1.26)	0.308
Child sex (%)				0.372
Male	196 (54.3%)	93 (51.7%)	103 (56.9%)	
Female	165 (45.7%)	87 (48.3%)	78 (43.1%)	
Mode of delivery (%)				0.999
Vaginal	159 (44.0%)	79 (43.9%)	80 (44.2%)	
Caesarean	202 (56.0%)	101 (56.1%)	101 (55.8%)	
Parity (%)				0.796
Primipara	202 (56.0%)	99 (55.0%)	103 (56.9%)	
Multipara	159 (44.0%)	81 (45.0%)	78 (43.1%)	

Note: Mean \pm SD for continuous variables and N (%) for categorical variables; SD: Standard deviation; BMI, body mass index calculated as weight in kilograms divided by height in meters squared; preterm birth: gestational age < 37 weeks. P value calculated using the Fisher's exact test and t-test.

Table S2. Results of child neurodevelopmental assessments by Ages and Stages Questionnaire (ASQ®-3)

Neurodevelopmental assessments	Total subjects (<i>N</i> = 361)	Boys (<i>N</i> = 196)	Girls (<i>N</i> = 165)	<i>P</i> value*
Ages and Stages Questionnaire, 3rd edition (ASQ®-3)				
2 months of age				
ASQ-T ^a	236 ± 38.2	233 ± 38.4	238 ± 37.8	0.205
Communication	44.0 ± 12.2	43.2 ± 12.7	45.0 ± 11.6	0.178
Gross motor	52.9 ± 8.95	52.2 ± 9.24	53.6 ± 8.56	0.140
Fine motor	49.1 ± 8.68	48.8 ± 8.73	49.5 ± 8.62	0.386
Problem solving	44.1 ± 13.4	44.4 ± 13.7	43.8 ± 13.0	0.658
Personal-social	45.4 ± 10.0	44.6 ± 9.92	46.4 ± 10.1	0.084
6 months of age				
ASQ-T ^a	221 ± 46.8	218 ± 50.7	224 ± 41.7	0.345
Communication	48.7 ± 9.78	48.5 ± 10.3	48.9 ± 9.14	0.754
Gross motor	37.1 ± 12.0	37.4 ± 12.5	36.8 ± 11.3	0.693
Fine motor	46.7 ± 12.5	45.6 ± 13.0	47.9 ± 11.9	0.166
Problem solving	47.2 ± 12.8	47.1 ± 14.1	47.2 ± 11.1	0.953
Personal-social	41.1 ± 14.3	39.4 ± 14.9	43.0 ± 13.5	0.055
12 months of age				
ASQ-T ^a	241 ± 41.5	237 ± 42.3	245 ± 40.2	0.099
Communication	50.8 ± 10.2	49.8 ± 10.3	52.0 ± 9.87	0.078
Gross motor	46.6 ± 13.3	46.1 ± 12.8	47.2 ± 13.9	0.500
Fine motor	49.4 ± 10.5	49.0 ± 10.8	50.0 ± 10.2	0.472
Problem solving	48.6 ± 11.1	48.3 ± 11.3	49.0 ± 10.9	0.624
Personal-social	44.2 ± 13.2	42.7 ± 13.4	46.2 ± 12.7	0.029*
24 months of age				
ASQ-T ^a	247 ± 41.4	246 ± 40.4	45.2 ± 12.2	0.731
Communication	52.2 ± 11.1	51.0 ± 12.1	45.2 ± 12.2	0.051
Gross motor	52.4 ± 9.13	52.5 ± 8.34	45.2 ± 12.2	0.945
Fine motor	49.7 ± 9.27	50.1 ± 9.23	45.2 ± 12.2	0.457
Problem solving	47.9 ± 11.1	48.4 ± 10.9	45.2 ± 12.2	0.474
Personal-social	44.6 ± 12.0	44.1 ± 11.9	45.2 ± 12.2	0.466

Note: *, *P* value calculated using the t-test; a, ASQ-T, total ASQ score.

Table S3. Results of child suspected neurodevelopment delay (SDD) by Ages and Stages Questionnaire (ASQ®-3)

Neurodevelopmental assessments	Total subjects (<i>N</i> = 361)	Boys (<i>N</i> = 196)	Girls (<i>N</i> = 165)	<i>P</i> value*
Ages and Stages Questionnaire, 3rd edition (ASQ®-3)				
2 months of age				
SDD				0.232
Yes	63 (17.5%)	39 (19.9%)	24 (14.5%)	
No	298 (82.5%)	157 (80.1%)	141 (85.5%)	
SDD-ASQ-T ^a				0.473
Yes	15 (4.16%)	10 (5.10%)	5 (3.03%)	
No	346 (95.8%)	186 (94.9%)	160 (97.0%)	
SDD-Communication				0.223
Yes	20 (5.54%)	14 (7.14%)	6 (3.64%)	
No	341 (94.5%)	182 (92.9%)	159 (96.4%)	
SDD-Gross motor				0.103
Yes	17 (4.71%)	13 (6.63%)	4 (2.42%)	
No	344 (95.3%)	183 (93.4%)	161 (97.6%)	
SDD-Fine motor				0.999
Yes	18 (4.99%)	10 (5.10%)	8 (4.85%)	
No	343 (95.0%)	186 (94.9%)	157 (95.2%)	
SDD-Problem solving				0.851
Yes	15 (4.16%)	9 (4.59%)	6 (3.64%)	
No	346 (95.8%)	187 (95.4%)	159 (96.4%)	
6 months of age				
SDD				0.254
Yes	34 (15.2%)	22 (18.2%)	12 (11.8%)	
No	189 (84.8%)	99 (81.8%)	90 (88.2%)	
SDD-ASQ-T ^a				0.351
Yes	10 (4.48%)	7 (5.79%)	3 (2.94%)	
No	213 (95.5%)	114 (94.2%)	99 (97.1%)	
SDD-Communication				0.889

Yes	17 (7.62%)	10 (8.26%)	7 (6.86%)	
No	206 (92.4%)	111 (91.7%)	95 (93.1%)	
SDD-Gross motor				0.458
Yes	7 (3.14%)	5 (4.13%)	2 (1.96%)	
No	216 (96.9%)	116 (95.9%)	100 (98.0%)	
SDD-Fine motor				0.236
Yes	12 (5.38%)	9 (7.44%)	3 (2.94%)	
No	211 (94.6%)	112 (92.6%)	99 (97.1%)	
SDD-Problem solving				0.161
Yes	13 (5.83%)	10 (8.26%)	3 (2.94%)	
No	210 (94.2%)	111 (91.7%)	99 (97.1%)	
12 months of age				
SDD				0.474
Yes	43 (15.9%)	27 (17.6%)	16 (13.7%)	
No	227 (84.1%)	126 (82.4%)	101 (86.3%)	
SDD-ASQ-Ta				0.192
Yes	10 (3.94%)	8 (5.67%)	2 (1.77%)	
No	244 (96.1%)	133 (94.3%)	111 (98.2%)	
SDD-Communication				0.314
Yes	20 (7.52%)	14 (9.27%)	6 (5.22%)	
No	246 (92.5%)	137 (90.7%)	109 (94.8%)	
SDD-Gross motor				0.999
Yes	10 (3.77%)	6 (4.03%)	4 (3.45%)	
No	255 (96.2%)	143 (96.0%)	112 (96.6%)	
SDD-Fine motor				0.999
Yes	8 (3.02%)	5 (3.36%)	3 (2.59%)	
No	257 (97.0%)	144 (96.6%)	113 (97.4%)	
SDD-Problem solving				0.891
Yes	13 (4.91%)	8 (5.41%)	5 (4.27%)	
No	252 (95.1%)	140 (94.6%)	112 (95.7%)	
24 months of age				
SDD				0.302
Yes	30 (13.0%)	20 (15.4%)	10 (9.90%)	
No	201 (87.0%)	110 (84.6%)	91 (90.1%)	
SDD-ASQ-Ta				0.999
Yes	12 (5.19%)	7 (5.38%)	5 (4.95%)	
No	219 (94.8%)	123 (94.6%)	96 (95.0%)	
SDD-Communication				0.760
Yes	11 (4.76%)	7 (5.38%)	4 (3.96%)	
No	220 (95.2%)	123 (94.6%)	97 (96.0%)	
SDD-Gross motor				0.218
Yes	11 (4.76%)	4 (3.08%)	7 (6.93%)	

No	220 (95.2%)	126 (96.9%)	94 (93.1%)	
SDD-Fine motor				0.760
Yes	11 (4.76%)	7 (5.38%)	4 (3.96%)	
No	220 (95.2%)	123 (94.6%)	97 (96.0%)	
SDD-Problem solving				0.519
Yes	10 (4.33%)	7 (5.38%)	3 (2.97%)	
No	221 (95.7%)	123 (94.6%)	98 (97.0%)	

Note: *, *P* value calculated using the t-test; a, ASQ-T, total ASQ score.

Table S4. LEFSe analysis on GM between low and high PM_{2.5} exposure groups during pregnancy

genus	group	LDA	<i>P</i> value
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacteriales f__Enterobacteriaceae g__Cronobacter	high	2.866	0.013
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__NA f__NA	high	2.649	0.044
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Pseudomonadales f__Pseudomonadaceae	high	3.844	0.022
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Peptostreptococcaceae g__Paraclostridium	high	2.606	0.044
k__Bacteria p__Fusobacteria c__Fusobacteriia o__Fusobacteriales f__Leptotrichiaceae	high	2.661	0.014
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacteriales f__Enterobacteriaceae g__Rahnella	high	2.753	0.001
k__Bacteria p__Fusobacteria c__Fusobacteriia	high	2.700	0.044
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacteriales f__Enterobacteriaceae g__Enterobacter	high	3.916	0.031
k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Paludibacteraceae g__F0058	high	2.252	0.020
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacteriales	high	4.673	0.040
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__NA	high	2.540	0.044
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacteriales f__Enterobacteriaceae g__Serratia	high	3.460	0.029
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Pseudomonadales f__Pseudomonadaceae g__Pseudomonas	high	3.844	0.022
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacteriales f__Enterobacteriaceae	high	4.673	0.040
k__Bacteria p__Fusobacteria c__Fusobacteriia o__Fusobacteriales	high	2.728	0.044
k__Bacteria p__Actinobacteria c__Actinobacteria o__Corynebacteriales f__Corynebacteriaceae g__Corynebacterium	high	2.468	0.018

k__Bacteria p__Fusobacteria	high	2.688	0.044
k__Bacteria p__Fusobacteria c__Fusobacteriia o__Fusobacteriales f__Leptotrichiaceae g__Leptotrichia	high	2.659	0.006
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__NA f__NA g__NA	high	2.676	0.044
k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Paludibacteraceae	high	2.216	0.020
k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Prevotellaceae g__Prevotellaceae_Ga6A1_group	low	2.173	0.009
k__Bacteria p__Actinobacteria c__Rubrobacteria o__Rubrobacterales f__Rubrobacteriaceae	low	2.174	0.019
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Betaproteobacteriales f__Burkholderiaceae g__Burkholderia_Caballero nia_Paraburkholderia	low	2.184	0.007
k__Bacteria p__Patescibacteria	low	2.657	0.041
k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Tannerellaceae g__Parabacteroides	low	2.248	0.020
k__Bacteria p__Firmicutes c__Erysipelotrichia o__Erysipelotrichales f__Erysipelotrichaceae	low	3.034	0.000
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Ruminococcaceae g__Ruminococcus_2	low	2.138	0.006
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae	low	3.654	0.000
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacteriales f__Enterobacteriaceae g__Citrobacter	low	2.812	0.045
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Betaproteobacteriales	low	3.564	0.000
k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Lactobacillaceae g__Lactobacillus	low	3.847	0.001
k__Bacteria p__Firmicutes c__Erysipelotrichia o__Erysipelotrichales	low	3.042	0.000
k__Bacteria p__Actinobacteria c__Rubrobacteria	low	2.323	0.019
k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Rikenellaceae g__Alistipes	low	2.952	0.010

k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Peptostreptococcaceae	low	2.629	0.012
k__Bacteria p__Firmicutes c__Bacilli o__Bacillales f__Sporolactobacillaceae	low	2.013	0.006
k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales	low	3.508	0.041
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Ruminococcaceae	low	3.265	0.004
k__Bacteria p__Actinobacteria c__Coriobacteriia o__Coriobacteriales f__Eggerthellaceae	low	2.146	0.001
k__Bacteria p__Firmicutes c__Negativicutes o__Selenomonadales	low	2.293	0.037
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Ruminococcaceae g__Eubacterium_coprostanoligenes_group	low	2.007	0.002
k__Bacteria p__Actinobacteria c__Rubrobacteria o__Rubrobacterales	low	2.486	0.019
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__Eubacterium_hallii_group	low	2.263	0.025
k__Bacteria p__Patescibacteria c__Saccharimonadia o__Saccharimonadales f__Saccharimonadaceae g__Candidatus_Saccharimonas	low	2.662	0.016
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__NA	low	2.512	0.004
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Pasteurellales f__Pasteurellaceae g__Haemophilus	low	2.363	0.002
k__Bacteria p__Firmicutes c__Bacilli o__Bacillales f__Sporolactobacillaceae g__uncultured	low	2.006	0.006
k__Bacteria p__Actinobacteria c__Actinobacteria o__Corynebacteriales f__Nocardiaceae	low	3.064	0.002
k__Bacteria p__Verrucomicrobia c__Verrucomicrobiae	low	2.568	0.015
k__Bacteria p__Firmicutes c__Erysipelotrichia o__Erysipelotrichales f__Erysipelotrichaceae g__Dubosiella	low	2.493	0.000
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Eubacteriaceae	low	2.183	0.019
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Betaproteobacteriales f__Burkholderiaceae	low	3.565	0.000
k__Bacteria p__Firmicutes c__Clostridia	low	3.938	0.000

k__Bacteria p__Acidobacteria c__Acidobacteriia o__Subgroup_2 f__uncultured_Acidobacteria_bacterium g__uncultured_Acidobact eria_bacterium	low	2.356	0.004
k__Bacteria p__Proteobacteria c__Deltaproteobacteria o__Desulfovibrionales	low	2.453	0.010
k__Bacteria p__Acidobacteria c__Acidobacteriia o__Subgroup_2 f__uncultured_Acidobacteria_bacterium	low	2.429	0.004
k__Bacteria p__Proteobacteria c__Alphaproteobacteria o__Rhizobiales f__Rhizobiaceae g__Mesorhizobium	low	3.136	0.004
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Betaproteobacteriales f__Burkholderiaceae g__Noviherbaspirillum	low	2.658	0.032
k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Rikenellaceae	low	2.985	0.013
k__Bacteria p__Actinobacteria c__Coriobacteriia o__Coriobacteriales	low	3.037	0.000
k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Bacteroidaceae g__Bacteroides	low	3.064	0.017
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Betaproteobacteriales f__Burkholderiaceae g__Parasutterella	low	2.194	0.010
k__Bacteria p__Proteobacteria c__Alphaproteobacteria o__Azospirillales	low	2.597	0.025
k__Bacteria p__Actinobacteria c__Coriobacteriia	low	3.028	0.000
k__Bacteria p__Bacteroidetes c__Bacteroidia	low	3.499	0.032
k__Bacteria p__Firmicutes c__Negativicutes	low	2.289	0.037
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Clostridiaceae_1 g__Clostridium_sensu_stricto_1	low	3.393	0.008
k__Bacteria p__Acidobacteria c__Acidobacteriia o__Subgroup_2	low	2.027	0.019
k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Bacteroidaceae	low	3.040	0.017
k__Bacteria p__Patescibacteria c__Saccharimonadia	low	2.657	0.024
k__Bacteria p__Firmicutes c__Erysipelotrichia o__Erysipelotrichales f__Erysipelotrichaceae g__Erysipelatoclostridium	low	2.373	0.000
k__Bacteria p__Actinobacteria c__Coriobacteriia o__Coriobacteriales f__Coriobacteriaceae g__Collinsella	low	2.973	0.000

k__Bacteria p__Verrucomicrobia	low	2.550	0.015
k__Bacteria p__Verrucomicrobia c__Verrucomicrobiae o__Verrucomicrobiales f__Akkermansiaceae g__Akkermansia	low	2.573	0.008
k__Bacteria p__Actinobacteria c__Actinobacteria o__Corynebacteriales f__Nocardiaceae g__Rhodococcus	low	3.067	0.004
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales	low	3.938	0.000
k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Lactobacillaceae	low	3.847	0.001
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Clostridiaceae_1	low	3.375	0.010
k__Bacteria p__Actinobacteria c__Coriobacteriia o__Coriobacteriales f__Coriobacteriaceae	low	2.973	0.000
k__Bacteria p__Verrucomicrobia c__Verrucomicrobiae o__Verrucomicrobiales f__Akkermansiaceae	low	2.575	0.008
k__Bacteria p__Actinobacteria c__Rubrobacteria o__Rubrobacterales f__Rubrobacteriaceae g__Rubrobacter	low	2.280	0.019
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__Fusicatenibacter	low	2.385	0.002
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Eubacteriaceae g__Eubacterium	low	2.170	0.019
k__Bacteria p__Proteobacteria c__Deltaproteobacteria	low	2.414	0.007
k__Bacteria p__Bacteroidetes	low	3.499	0.032
k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Tannerellaceae	low	2.225	0.036
k__Bacteria p__Patescibacteria c__Saccharimonadia o__Saccharimonadales	low	2.648	0.024
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__Anaerostipes	low	2.127	0.000
k__Bacteria p__Proteobacteria c__Alphaproteobacteria o__Rhizobiales f__Rhizobiaceae	low	3.157	0.001
k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Muribaculaceae g__uncultured_bacterium	low	2.907	0.045
k__Bacteria p__Epsilonbacteraeota c__Campylobacteria o__Campylobacterales f__Sulfurospirillaceae g__Sulfurospirillum	low	2.486	0.045

k__Bacteria p__Epsilonbacteraeota c__Campylobacteria o__Campylobacterales f__Sulfurospirillaceae	low	2.596	0.045
k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Betaproteobacteriales f__Burkholderiaceae g__Ralstonia	low	3.496	0.000
k__Bacteria p__Firmicutes c__Erysipelotrichia	low	3.039	0.000
k__Bacteria p__Verrucomicrobia c__Verrucomicrobiae o__Verrucomicrobiales	low	2.566	0.012
k__Bacteria p__Proteobacteria c__Alphaproteobacteria	low	3.177	0.044
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__Blautia	low	3.226	0.000
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__Ruminococcus gnavus group	low	3.121	0.000
k__Bacteria p__Proteobacteria c__Deltaproteobacteria o__Desulfovibrionales f__Desulfovibrionaceae	low	2.451	0.010
k__Bacteria p__Proteobacteria c__Alphaproteobacteria o__Azospirillales f__Azospirillaceae	low	2.811	0.025
k__Bacteria p__Proteobacteria c__Alphaproteobacteria o__Azospirillales f__Azospirillaceae g__Skermanella	low	2.856	0.025
k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Peptostreptococcaceae g__Romboutsia	low	2.705	0.008

In this analysis, it was found that a total of 102 bacterial taxa differential abundant between low and high PM_{2.5} exposure groups (linear discriminant analysis LDA score >2, $P < 0.05$). There were 82 feature taxa in the low exposure group and 20 feature taxa in the high group, except for 3 unannotated taxa in the low exposure group and 3 in the high group, particularly, a total of 45 bacterial genera were differential abundant between the study groups at the genus level.

Table S5. Association of KEGG functional pathways with prenatal PM_{2.5} exposure was analyzed using MaAsLin2(FDR q-value < 0.25).

genus	Coefficient	P value	q-value
Environmental.Information.Processing__Signal.transduction__Plant.hormone.signal.transduction.	-0.253	0.000	0.003
Metabolism__Amino.acid.metabolism__Alanine..aspartate.and.glutamate.metabolism.	-0.021	0.000	0.003
Not.Included.in.Pathway.or.Brite__Unclassified..signaling.and.cellular.processes__Cell.growth	-0.069	0.000	0.003
Metabolism__Biosynthesis.of.other.secondary.metabolites__Neomycin..kanamycin.and.gentamicin.biosynthesis.	-0.254	0.000	0.008
Metabolism__Metabolism.of.terpenoids.and.polyketides__Nonribosomal.peptide.structures.	-0.253	0.000	0.015
Brite.Hierarchies__Protein.families..signaling.and.cellular.processes__Secretion.system.	0.020	0.000	0.028
Brite.Hierarchies__Protein.families..metabolism__Polyketide.biosynthesis.proteins.	-0.307	0.000	0.028
Metabolism__Glycan.biosynthesis.and.metabolism__N.Glycan.biosynthesis.	-0.275	0.000	0.033
Metabolism__Carbohydrate.metabolism__Ascorbate.and.aldarate.metabolism.	0.052	0.000	0.044
Human.Diseases__Infectious.disease..parasitic__Amoebiasis.	-0.321	0.000	0.051
Metabolism__Biosynthesis.of.other.secondary.metabolites__Penicillin.and.cephalosporin.biosynthesis.	-0.179	0.000	0.079
Brite.Hierarchies__Protein.families..genetic.information.processing__Transcription.machinery.	-0.017	0.000	0.091
Metabolism__Metabolism.of.cofactors.and.vitamins__Nicotinate.and.nicotinamide.metabolism.	-0.019	0.001	0.149
Metabolism__Metabolism.of.cofactors.and.vitamins__Ubiquinone.and.other.terpenoid.quinone.biosynthesis.	0.026	0.001	0.149
Human.Diseases__Neurodegenerative.disease__Parkinson.disease.	-0.106	0.001	0.162
Metabolism__Energy.metabolism__Carbon.fixation.pathways.in.prokaryotes.	-0.037	0.001	0.162
Metabolism__Metabolism.of.terpenoids.and.polyketides__Limonene.and.pinene.degradation.	-0.257	0.001	0.191

Metabolism__Metabolism.of.terpenoids.and.polyketides__Polyketide.sugar.unit.biosynthesis.	-0.229	0.001	0.191
Genetic.Information.Processing__Replication.and.repair__Homologous.recombination.	-0.018	0.001	0.206
Metabolism__Lipid.metabolism__Arachidonic.acid.metabolism.	0.041	0.001	0.206
Metabolism__Lipid.metabolism__Steroid.biosynthesis.	-0.304	0.001	0.206
Metabolism__Lipid.metabolism__Steroid.hormone.biosynthesis.	-0.287	0.001	0.206
Metabolism__Lipid.metabolism__Ether.lipid.metabolism.	-0.317	0.002	0.247
Organismal.Systems__Immune.system__NOD.like.receptor.signaling.pathway.	-0.035	0.002	0.247
Environmental.Information.Processing__Signal.transduction__Plant.hormone.signal.transduction.	-0.253	0.000	0.003

In this analysis, it was found that PM_{2.5} exposure groups associated with a total of 24 KEGG functional pathways ($P < 0.05$ and q-value < 0.25).

Table S6. Spearman's correlation analysis between KEGG functional pathways and prenatal PM_{2.5} exposure.

	Ruminococcus gnavus group	Romboutsia	Parabacteroides	Burkholderia Caballeronia Paraburkholderia	Blautia	Bacteroides	Alistipes
r							
Plant.hormone.signal.transduction.	0.914	0.442	0.307	0.237	0.617	0.121	0.068
Alanine..aspartate.and.glutamate.metabolism.	0.195	0.273	0.398	0.171	0.359	0.472	0.423
Cell.growth	0.327	0.357	0.459	0.066	0.494	0.458	0.370
Neomycin..kanamycin.and.gentamicin.biosynthesis.	0.491	0.378	0.239	0.311	0.476	0.142	0.153
Nonribosomal.peptide.structures.	0.367	0.405	0.446	0.323	0.607	0.455	0.456
Secretion.system.	-0.129	-0.154	-0.367	-0.064	-0.192	-0.363	-0.406
Polyketide.biosynthesis.proteins.	0.226	0.279	0.262	0.242	0.319	0.249	0.267
N.Glycan.biosynthesis.	0.229	0.365	0.520	0.299	0.503	0.604	0.635
Ascorbate.and.aldarate.metabolism.	-0.190	-0.204	-0.404	-0.201	-0.299	-0.395	-0.477
Amoebiasis.	0.361	0.411	0.479	0.199	0.541	0.471	0.399
Penicillin.and.cephalosporin.biosynthesis.	0.400	0.317	0.382	0.396	0.507	0.390	0.450
Transcription.machinery.	0.303	0.257	0.406	0.314	0.437	0.363	0.501
Nicotinate.and.nicotinamide.metabolism.	0.318	0.253	0.306	0.314	0.370	0.335	0.369
Ubiquinone.and.other.terpenoid.quinone.biosynthesis.	-0.389	-0.286	-0.373	-0.303	-0.433	-0.342	-0.381
Parkinson.disease.	0.467	0.357	0.366	0.200	0.532	0.307	0.247
Carbon.fixation.pathways.in.prokaryotes.	0.360	0.238	0.352	0.151	0.379	0.301	0.300

Limonene.and.pinene.degradation.	0.535	0.360	0.298	0.609	0.475	0.141	0.218
Polyketide.sugar.unit.biosynthesis.	0.350	0.440	0.485	0.429	0.507	0.442	0.418
Homologous.recombination.	0.243	0.215	0.326	-0.085	0.278	0.295	0.200
Arachidonic.acid.metabolism.	-0.118	-0.312	-0.344	-0.052	-0.284	-0.387	-0.272
Steroid.biosynthesis.	0.215	0.484	0.527	0.525	0.455	0.536	0.608
Steroid.hormone.biosynthesis.	0.177	0.322	0.450	0.412	0.423	0.531	0.708
Ether.lipid.metabolism.	0.248	0.349	0.320	0.491	0.370	0.278	0.479
NOD.like.receptor.signaling.pathway.	0.349	0.290	0.423	0.221	0.428	0.395	0.395
<i>P value</i>							
Plant.hormone.signal.transduction.	0.000	0.000	0.000	0.000	0.000	0.021	0.195
Alanine..aspartate.and.glutamate.metabolism.	0.000	0.000	0.000	0.001	0.000	0.000	0.000
Cell.growth	0.000	0.000	0.000	0.213	0.000	0.000	0.000
Neomycin..kanamycin.and.gentamicin.biosynthesis.	0.000	0.000	0.000	0.000	0.000	0.007	0.004
Nonribosomal.peptide.structures.	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Secretion.system.	0.014	0.003	0.000	0.228	0.000	0.000	0.000
Polyketide.biosynthesis.proteins.	0.000	0.000	0.000	0.000	0.000	0.000	0.000
N.Glycan.biosynthesis.	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Ascorbate.and.aldarate.metabolism.	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Amoebiasis.	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Penicillin.and.cephalosporin.biosynthesis.	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Transcription.machinery.	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Nicotinate.and.nicotinamide.metabolism.	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Ubiquinone.and.other.terpenoid.quinone.biosynthesis.	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Parkinson.disease.	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Carbon.fixation.pathways.in.prokaryotes.	0.000	0.000	0.000	0.004	0.000	0.000	0.000
Limonene.and.pinene.degradation.	0.000	0.000	0.000	0.000	0.000	0.007	0.000
Polyketide.sugar.unit.biosynthesis.	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Homologous.recombination.	0.000	0.000	0.000	0.107	0.000	0.000	0.000
Arachidonic.acid.metabolism.	0.025	0.000	0.000	0.320	0.000	0.000	0.000
Steroid.biosynthesis.	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Steroid.hormone.biosynthesis.	0.001	0.000	0.000	0.000	0.000	0.000	0.000
Ether.lipid.metabolism.	0.000	0.000	0.000	0.000	0.000	0.000	0.000
NOD.like.receptor.signaling.pathway.	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Note: The r value indicates the Spearman correlation of the pathway with the characteristic bacterial genus, while the P value manifests the significance of their correlation.

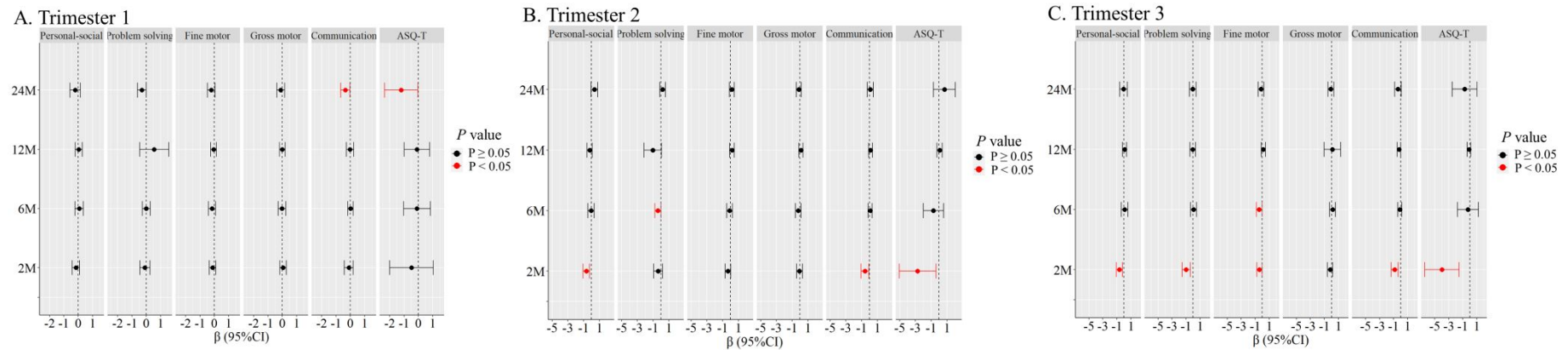


Figure S1. Prenatal individual PM_{2.5} exposure of entire pregnancy and children's ASQ scores

Note: Results were presented as calculated values and 95% confidence intervals (CI) and the highlighted associations in red are at *P* value 0.05. These models adjusted for confounding factors of parents' characteristic (parity, maternal age, maternal pre-gravid BMI, maternal physical activity, maternal educational level, annual family income, pregnancy syndrome, passive smoking status, season of conception, delivery mode, paternal age) and children (child age at ASQ test, feeding patterns and child sex).

Abbreviations: BMI, body mass index, ASQ, Ages and Stages Questionnaire, SDD, suspected developmental delay at follow up point.

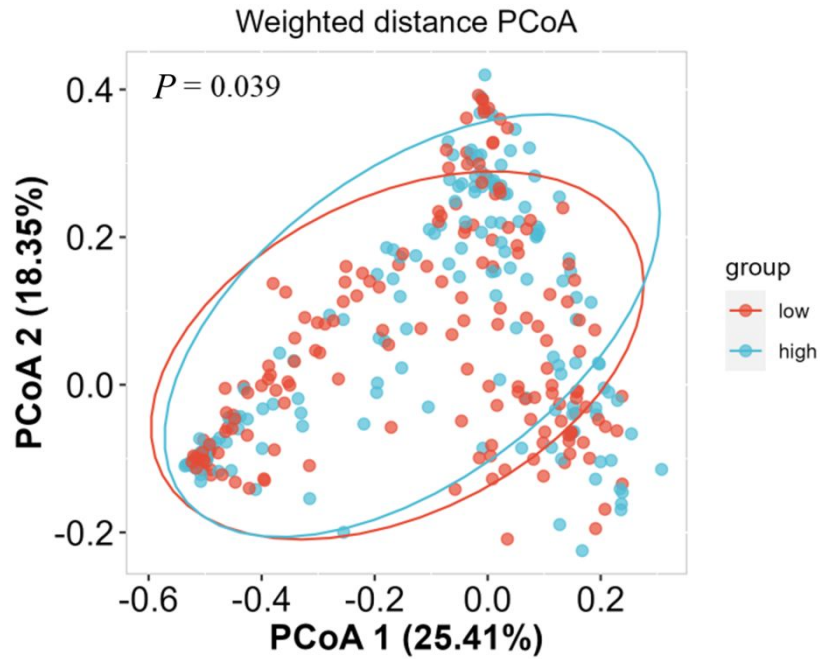


Figure S2. The microbiota structures of neonatal feces samples from the prenatal $PM_{2.5}$ high exposure group and low group.

Note: The PCoA result revealed a significant diverse in gut microbiome structure between the two groups (PERMANOVA, $P = 0.039$). The two principal component scores contribute to 25.41% (PCoA1) and 18.35% (PCoA2) of total variations. Each symbol indicates an individual sample.

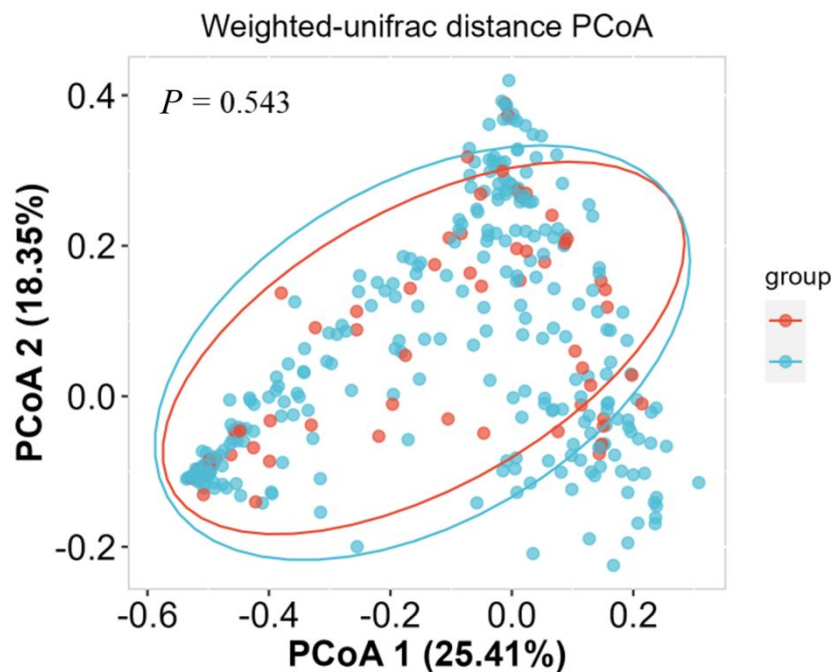


Figure S3. The microbiota structures of neonatal feces samples from the SDD group and control group.

Note: The PCoA result found no significant difference in gut microbiome structure between the two groups (PERMANOVA, $P = 0.543$). The two principal component scores contribute to 25.41% (PCoA1) and 18.35% (PCoA2) of total variations. Each symbol indicates an individual sample.