

Supplementary Figure 1. Manhattan plots for genome-wide associations of genotyped SNPs and genotyped plus imputed SNPs with PTB outcomes in 1,733 African-American mothers from the Boston Birth Cohort, with adjustment for genotyping batch, genetic ancestry, maternal age at delivery, parity and infant's gender. Fig 1a, 1b and 1c are Manhattan plots for overall PTB, spontaneous PTB, and gestational age at delivery (GA), respectively. In each plot, the upper panel and the lower panel represent the genotyped SNPs and the genotyped plus imputed SNPs, respectively. The dashed line represents the genome-wide significance level with  $p=5 \times 10^{-8}$ .



Supplementary Figure 2. The Manhattan plot for genome-wide associations by the 2 degree-offreedom approach to combine signals of SNP main effects and interaction effects with prepregnancy BMI category on overall PTB in 1,586 African-American mothers from the Boston Birth Cohort, adjusted for genotyping batch, genetic ancestry, maternal age at delivery, parity, and infant's gender.



Supplementary Figure 3. The Manhattan plot for genome-wide meta-analyses of SNP× prepregnancy BMI interaction on overall PTB in 1,886 African-American mothers from the Boston Birth Cohort and from the GPN study.

Variable	GEN	EVA <sup>a</sup>	G	PN <sup>a</sup>	<b>GPN</b> <sup>b</sup>						
	African A	American	African	American	Caucasian						
	ТВ	РТВ	ТВ	РТВ	ТВ	РТВ					
N	306	130	169	177	365	318					
Maternal age (year), Mean±SD	$25.7 \pm 5.8$	$26.4 \pm 6.3$	$23.9 \pm 5.4$	$24.4 \pm 5.8$	$25.9\pm5.5$	25.6 ± 5.5					
Pre-pregnancy BMI (kg m <sup>-2</sup> )	Pre-pregnancy BMI (kg m <sup>-2</sup> )										
< 18.5	NA	NA	10 (5.9)	10 (5.7)	0	0					
18.5-24.9	NA	NA	67 (39.6)	61 (34.5)	247(67.7)	192 (60.4)					
25-29.9	NA	NA	33 (19.5)	42 (23.7)	74 (20.3)	73 (23.0)					
$\geq$ 30	NA	NA	49 (29.0)	48 (27.1)	44 (12.0)	53 (16.6)					
Unknown	306	130	10 (5.9)	16 (9.0)	0	0					
Infant's gender: Male	149 (48.7)	65 (50.0)	98 (58.0)	89 (50.3)	186 (51.0)	181 (56.9)					
Nulliparity	NA	NA	67 (39.6)	70 (39.5)	197 (54.0)	172 (54.1)					

Supplementary Table 1. The population characteristics of the two replication cohorts

TB: Term birth; PTB: preterm birth; SD: standard deviation; BMI: body mass index; NA: not available.

<sup>a</sup> The replication samples are African American mothers from the GWAS of Prematurity and Its

Complication (African Americans) (the GENEVA study, dbGaP entry # phs000353.v1.p1), and from the NICHD Genomic and Proteomic Network for Preterm Birth Research (the GPN study, dbGaP entry # phs000714.v1.p1), respectively.

<sup>b</sup> These Caucasian mothers were from the GPN study, all with pre-pregnancy  $BMI > 18.5 \text{ kg m}^{-2}$ .

Supplementary Table 2. Heritability estimates of PTB outcomes and pre-pregnancy BMI in 1,733

Phenotype	V <sub>G</sub> (SE) <sup>b</sup>	Vp (SE) <sup>c</sup>	$h^2 (SE)^d$	Transformed h <sup>2</sup> (SE) <sup>e</sup>	Р
Overall PTB	0.05 (0.05)	0.24 (0.01)	0.21 (0.22)	0.25 (0.27)	0.18
Spontaneous PTB	0.05 (0.05)	0.21 (0.01)	0.22 (0.25)	0.26 (0.29)	0.23
BMI	21.5 (11.4)	43.3 (1.5)	0.50 (0.26)		0.03
Height	17.0 (10.7)	46.6 (1.6)	0.37 (0.23)		0.002

unrelated African-American women using genome-wide SNP data<sup>a</sup>

PTB: Preterm birth; BMI: Body mass index; SE: standard error

<sup>a</sup> Genotyped SNPs with minor allele frequency (MAF) > 0.02 were included.

 ${}^{b}V_{G}$ : The variance explained by genome-wide SNPs with MAF > 0.02

<sup>c</sup>Vp: The total phenotypic variance

 ${}^{d}h^{2}$ : Estimate of genetic variance (V<sub>G</sub>) proportional to the total phenotypic variance (Vp) on the observed scale, using the GCTA software.

<sup>e</sup>Transformed  $h^2$ : genetic variance proportional to the total phenotypic variance on the liability scale under the assumption that population prevalence is 12% and 8% for overall PTB and spontaneous PTB, respectively.

**Supplementary Table 3a.** The genome-wide significant loci ( $p < 5.0 \times 10^{-8}$ ) associated with PTB outcomes in 1,733 African-American women from the Boston Birth Cohort

SNP	CHR	Position	Gene	Allele <sup>b</sup>	MAF <sup>c</sup>	Overall PTB		Spontaneou	ıs PTB	GA	
						OR (95%CI) <sup>d</sup>	P <sup>d</sup>	OR (95%CI) <sup>d</sup>	$\mathbf{P}^{\mathrm{d}}$	Beta±Se <sup>d</sup>	P <sup>d</sup>
rs1558001	7	81407080	HGF    CACNA2D1	C/T	0.21	1.5 (1.3-1.8)	1.3×10 <sup>-7</sup>	1.7 (1.4-2.0)	3.0×10 <sup>-8</sup>	-0.81±0.15	9.8×10 <sup>-8</sup>
rs149014416 <sup>a</sup>	8	29669769	DUSP4    LOC101929470	AG/A	0.03	2.3 (1.7-3.2)	1.1×10 <sup>-8</sup>	2.4 (1.7-3.5)	1.7×10 <sup>-8</sup>	-0.42±0.09	1.8×10 <sup>-6</sup>
rs8029754	15	99979159	LRRC28    MEF2A	A/G	0.21	1.4 (1.2-1.6)	9.7×10 <sup>-5</sup>	1.5 (1.2-1.7)	7.0×10 <sup>-5</sup>	-0.87±0.15	1.9×10 <sup>-8</sup>

MAF: minor allele frequency; PTB: preterm birth; GA: gestational age. OR: odds ratio; CI: confidence interval.

<sup>a</sup>Imputation score info: 0.98.

<sup>b</sup>Major/minor allele.

<sup>c</sup>Minor allele frequency (MAF) calculated in TB controls.

<sup>d</sup>For each SNP, the allelic dosage of the minor allele was analyzed for its association with each outcome using the frequentist association tests included in SNPTEST, with adjustment for genotyping batch, genetic ancestry, maternal age at delivery, parity, and infant's gender.

Supplementary Table 3b. Replication of the identified genome-wide significant SNPs for their associations with overall PTB in African-

<b>SNP</b> <sup>a</sup>	CHR	Position <sup>b</sup>	Allele		The GENEVA study African American	The GPN study African American			
				MAF <sup>c</sup>	OR (95%CI) <sup>d</sup>	Р	MAF <sup>c</sup>	<b>OR</b> (95%CI) <sup>d</sup>	Р
rs1558001	7	81407080	C/T	0.31	0.7 (0.5-1.0)	0.07	0.22	0.8 (0.6-1.2)	0.37
rs8029754	15	99979159	A/G	0.22	1.0 (0.70-1.42)	0.99	0.21	0.8 (0.5-1.1)	0.19

American mothers from the two replication cohorts.

SNP: single nucleotide polymorphism; CHR: chromosome; MAF; minor allele frequency; OR: odds ratio; CI: conference interval.

<sup>a</sup> The imputed SNP rs149014416 was not available in the two replication samples.

<sup>b</sup> Major/minor allele

<sup>c</sup> Minor allele frequency (MAF) calculated in TB controls

<sup>d</sup> The association between each SNP (additive genetic model) and PTB was analyzed using the logistic regression model, with adjustment for genetic ancestry, parity (only in the GPN study) and infant's gender.

rs11161721		N (%PTB)		pre-pregnancy BMI category-PTB association <sup>a</sup>						
	NW	OW	OB	OR	95%CI	<i>P</i> -value				
	Ear	ly PTB (<32	weeks of gesta	tion)						
CC	323 (9.3)	209 (19.6)	161 (21.1)	1.6	1.2-2.1	7.3×10 <sup>-4</sup>				
СА	164 (16.5)	99 (21.2)	105 (11.4)	0.9	0.6-1.3	0.44				
AA	19 (10.5)	19 (10.5)	15 (0.0)	0.7	0.1-5.1	0.70				
Interaction test <sup>b</sup>										
G×E				0.6	0.4-0.8	0.003				
Late PTB (32 to 36 and 6/7 weeks of gestation)										
CC	399 (26.6)	267 (37.1)	210 (39.5)	1.4	1.2-1.7	4.3×10 <sup>-4</sup>				
СА	217 (36.9)	119 (34.5)	122 (23.8)	0.7	0.6-1.0	0.02				
AA	40 (57.5)	24 (29.2)	19 (21.1)	0.4	0.2-0.8	0.01				
Interaction test <sup>b</sup>										
G×E				0.5	0.4-0.7	1.3×10 <sup>-7</sup>				
Spontaneous PTB										
CC	391 (25.1)	249 (32.5)	188 (32.4)	1.2	1.0-1.5	0.03				
СА	214 (36.0)	129 (39.5)	116 (19.8)	0.7	0.6-0.9	0.02				
AA	35 (51.4)	23 (26.1)	17 (11.8)	0.3	0.1-0.8	0.009				
Interaction test <sup>b</sup>										
G×E				0.6	0.4-0.7	1.2×10 <sup>-5</sup>				
		Medically-in	ndicated PTB							
CC	331 (11.5)	227 (26.0)	183 (30.6)	1.9	1.5-2.4	1.8×10 <sup>-7</sup>				
CA	167 (18.0)	89 (12.4)	111 (16.2)	0.9	0.6-1.2	0.41				
AA	24 (29.2)	20 (15.0)	17 (11.8)	0.6	0.2-1.9	0.42				
Interaction test <sup>b</sup>										
G×E				0.5	0.3-0.7	1.7×10 <sup>-5</sup>				
		РТВ у	with IUI							
CC	324 (9.6)	205 (18.0)	162 (21.6)	1.6	1.2-2.1	6.2×10 <sup>-4</sup>				
CA	165 (17.0)	99 (21.2)	101 (7.9)	0.7	0.5-1.1	0.09				
AA	23 (26.1)	19 (10.5)	16 (6.3)	0.5	0.1-1.8	0.27				
Interaction test <sup>b</sup>										
G×E				0.5	0.3-0.7	3.0×10 <sup>-4</sup>				
	-	PTB wi	thout IUI							
CC	398 (26.4)	271 (38.0)	209 (39.2)	1.4	1.1-1.7	5.8×10 <sup>-4</sup>				
CA	216 (36.6)	119 (34.4)	126 (26.2)	0.8	0.6-1.0	0.07				
AA	36 (52.8)	24 (29.2)	18 (16.7)	0.4	0.2-0.8	0.01				
Interaction test <sup>b</sup>										
G×E				0.5	0.4-0.7	7.4×10 <sup>-7</sup>				

**Supplementary Table 4.** Consistency of the rs11161721 × pre-pregnancy BMI interaction effect across different PTB subtypes in 1,586 African American mothers from the Boston Birth Cohort

NW: normal weight (pre-pregnancy BMI:  $18.5 - 24.9 \text{ kg m}^2$ ); OW: overweight (pre-pregnancy BMI:  $25.0 - 29.9 \text{ kg m}^2$ ); OB: obesity (pre-pregnancy BMI  $\geq 30 \text{ kg m}^2$ ); PTB: preterm birth; IUI: Intra-uterine inflammation; OR: odds ratio; CI: confidence interval.

<sup>a</sup> The pre-pregnancy BMI category-PTB association was analyzed in women carrying CC, CA and AA genotypes at *rs11161721*, separately, using the logistic regression model with adjustment for genotyping batch, genetic ancestry, maternal age at delivery, parity, and infant's gender.

<sup>b</sup> The interaction effect was analyzed in the total sample by adding pre-pregnancy BMI category, *rs11161721* (under the additive genetic model) and their interaction term into the regression model, with adjustment of the same covariates as mentioned above.

**Supplementary Table 5.** The associations between pre-pregnancy BMI category and overall PTB within each genotype strata at rs11161721, and the rs11161721  $\times$  pre-pregnancy BMI interaction effect on overall PTB in the Boston Birth Cohort, after removing those with obesity-related gestational complications

rs11161721	N (%PTB)				Model	1 <sup>a</sup>	Model 2 <sup>b</sup>				
	NW	OW	OB	OR	95%CI	P	OR	95%CI	Р		
		Mothers	without dia	betes/	gestational	diabetes					
CC	412 (30.6)	272 (42.3)	197 (44.2)	1.3	1.1-1.6	0.001	1.4	1.2-1.7	5.3×10 <sup>-4</sup>		
CA	233 (42.9)	125 (44.8)	110 (29.1)	0.8	0.6-1.0	0.03	0.7	0.6-0.9	0.02		
AA	40 (57.5)	24 (33.3)	17 (17.6)	0.4	0.2-0.8	0.01	0.4	0.2-0.9	0.02		
Interaction te	est										
G×E				0.6	0.4-0.7	1.1×10 <sup>-6</sup>	0.5	0.4-0.7	6.1×10 <sup>-7</sup>		
Mothers without hypertensive disorders during pregnancy											
CC	379 (26.4)	251 (35.9)	174 (39.0)	1.3	1.1-1.6	0.005	1.4	1.1-1.7	0.003		
CA	210 (38.1)	124 (38.7)	102 (23.5)	0.7	0.6-1.0	0.03	0.7	0.5-0.9	0.01		
AA	35 (57.1)	24 (33.3)	17 (17.6)	0.4	0.2-0.8	0.01	0.4	0.2-0.8	0.02		
Interaction te	est										
G×E				0.5	0.4-0.7	2.3×10 <sup>-6</sup>	0.5	0.4-0.7	1.2×10 <sup>-6</sup>		
Μ	others witho	ut diabetes/g	estational d	iabete	es and with	out hyper	tensive	disorders			
CC	367 (25.6)	229 (34.5)	150 (37.3)	1.3	1.0-1.6	0.02	1.3	1.1-1.6	0.02		
CA	203 (37.9)	110 (39.1)	89 (23.6)	0.7	0.6-1.0	0.03	0.7	0.5-0.9	0.02		
AA	34 (55.9)	22 (31.8)	15 (13.3)	0.3	0.1-0.8	0.01	0.3	0.1-0.7	0.01		
Interaction te	est										
G×E				0.5	0.4-0.7	$1.2 \times 10^{-5}$	0.5	0.4-0.7	8.6×10 <sup>-6</sup>		

NW: normal weight (pre-pregnancy BMI:  $18.5 - 24.9 \text{ kg m}^2$ ); OW: overweight (pre-pregnancy BMI:  $25.0 - 29.9 \text{ kg m}^2$ ); OB: obesity (pre-pregnancy BMI  $\geq 30 \text{ kg m}^2$ ); PTB: preterm birth; TB; term birth; OR: odds ratio; CI: confidence interval.

<sup>a</sup>In model 1, the maternal pre-pregnancy BMI-PTB association was analyzed in women carrying the CC, CA and AA genotype at rs11161721, separately, using the logistic regression model with adjustment for genotyping batch, genetic ancestry, maternal age at delivery, parity, and infant's gender. The interaction effect was analyzed in the total sample by adding the pre-pregnancy BMI category, rs11161721 (under the additive genetic model) and their interaction term into the regression model, with adjustment for the same covariates mentioned above.

<sup>b</sup>In model 2, additional covariates, including smoking during pregnancy, stress during lifetime, stress during pregnancy, and history of illicit drug use, were also adjusted in both the association test and the interaction test.

**Supplementary Table 6.** The associations between pre-pregnancy BMI category and overall PTB within each genotype strata at rs11161721, and the rs11161721 × pre-pregnancy BMI interaction effect on overall PTB in the Boston Birth Cohort, stratified by infant's gender

rs11161721		N (%PTB)		pre-pregnancy BMI category-PTB association <sup>a</sup>						
	NW	OW	OB	OR	95%CI	<i>P</i> -value				
Girls										
CC	208 (32.2)	155 (45.2)	131 (45.8)	1.3	1.1-1.7	0.02				
CA	108 (50.0)	64 (43.8)	70 (30.0)	0.7	0.5-1.0	0.03				
AA	21 (61.9)	15 (26.7)	9 (11.1)	0.3	0.1-1.5	0.13				
G×E <sup>b</sup>				0.5	0.4-0.7	1.7×10 <sup>-5</sup>				
			Boys							
CC	221 (31.2)	153 (45.8)	113 (50.4)	1.6	1.2-2.1	3.2×10 <sup>-4</sup>				
CA	136 (39.0)	76 (44.7)	64 (31.3)	0.9	0.6-1.2	0.34				
AA	21 (57.1)	11 (45.5)	10 (30.0)	0.5	0.2-1.5	0.24				
G×E <sup>b</sup>				0.5	0.4-0.7	1.6×10 <sup>-4</sup>				

NW: normal weight (pre-pregnancy BMI:  $18.5 - 24.9 \text{ kg m}^2$ ); OW: overweight (pre-pregnancy BMI:  $25.0 - 29.9 \text{ kg m}^2$ ); OB: obesity (pre-pregnancy BMI  $\geq 30 \text{ kg m}^2$ ); PTB: preterm birth; OR: odds ratio; CI: confidence interval.

<sup>a</sup>The pre-pregnancy BMI - PTB association was analyzed in women carrying the CC, CA and AA genotype at rs11161721, separately, using the logistic regression model with adjustment for genotyping batch, genetic ancestry, age at delivery, and parity.

<sup>b</sup>The interaction effect was analyzed by adding pre-pregnancy BMI category, rs11161721 (under the additive genetic model) and their interaction term into the logistic regression model, with adjustment for the same covariates as mentioned above.

**Supplementary Table 7.** The interaction effects between rs11161721 and pre-pregnancy BMI category on overall PTB in the infants from the Boston Birth Cohort and from the GPN study

rs11161721 <sup>a</sup>	pre-pregnancy BMI	<b>BBC African-American infants</b>				GPN African-American infants					
		n	PTB,%	OR	95%CI	Pb	n	PTB,%	OR	95%CI	P <sup>b</sup>
CC	NW	42	23.8	ref			66	45.5	ref		
CC	OWO	56	35.7	2.0	0.8-5.1	0.13	98	57.1	1.5	0.8-2.8	0.23
CA	NW	20	50.0	3.9	1.3-11.8	0.01	44	43.2	0.8	0.4-1.8	0.63
CA	OWO	28	39.3	2.6	0.9-7.3	0.07	51	49.0	1.1	0.5-2.3	0.84
AA	NW	4 <sup>c</sup>	75.0	-	-	-	7	71.4	3.0	0.5-1.7	0.21
AA	OWO	3°	66.7	-	-	-	10	20.0	0.3	0.1-1.3	0.10
Interaction test <sup>d</sup>											
G×E				0.4	0.2-1.0	0.05			0.5	0.2-1.1	0.07

BMI: body mass index; NW: normal weight (pre-pregnancy BMI:  $18.5 - 24.9 \text{ kg m}^2$ ); OWO: overweight and/or obesity (pre-pregnancy BMI  $\geq 25 \text{ kg m}^2$ ). BBC: Boston Birth Cohort. PTB: preterm birth; OR: odds ratio; CI: confidence interval.

<sup>a</sup> The rs11161721variant in the infants, which was genotyped in the BBC and imputed in the GPN study.

<sup>b</sup> The analyses were conducted using the logistic regression model, adjusted for the genetic ancestry, parity and infant's gender.

<sup>c</sup> Due to a small sample size in the BBC, children with the rs11161721-AA genotype were combined with their counterparts carrying the rs11161721-AC genotype in the logistic regression analyses.

<sup>d</sup>The interaction effect was analyzed by adding maternal pre-pregnancy BMI category, infant's rs11161721 (under the additive genetic model) and their interaction term into the logistic regression model, with adjustment for the same covariates as mentioned above.

**Supplementary Table 8.** Analyses of the interaction effects between maternal pre-pregnancy BMI, maternal-origin A allele at rs11161721, and paternal-origin A allele at rs11161721 on overall PTB in 120 African-American mother-infant pairs from the BBC and in 276 African-American mother-infant pairs from the GPN study

rs11161721	<b>Pre-pregnancy</b>	Ν	Aother-infa	nt pairs f	nt pairs from the BBC			Mother-infant pairs from the GPN				
A allele <sup>a</sup>	BMI	n	РТВ, %	OR	95%CI	P <sup>b</sup>	n	<b>PTB</b> , %	OR	95%CI	$P^{\mathrm{b}}$	
Maternal-origin	A allele											
0	NW	42	21.4	ref			92	43.5	ref			
0	OWO	53	33.9	1.9	0.7-5.1	0.19	124	58.9	1.8	1.0-3.1	0.04	
1	NW	14	71.4	8.0	2.0-3.3	0.003	25	56.0	1.6	0.6-4.0	0.31	
1	OWO	11	54.5	4.4	1.0-1.9	0.05	35	28.6	0.5	0.2-1.1	0.09	
Paternal-origin A	A allele											
0	NW	46	32.6	ref			84	46.4	ref			
0	OWO	46	37.0	1.4	0.6-3.5	0.48	123	52.0	1.2	0.7-2.1	0.55	
1	NW	10	40.0	1.6	0.4-6.8	0.55	33	45.4	0.9	0.4-2.1	0.82	
1	OWO	18	38.9	1.2	0.3-3.8	0.82	36	52.8	1.2	0.6-2.7	0.63	
Interaction <sup>c</sup>												
Maternal-origin	A allele $\times$ pre-pres	gnancy O	WO	0.3	0.0-2.1	0.21			0.2	0.1-0.6	0.004	
Paternal-origin A	A allele × pre-preg	nancy OV	VO	0.8	0.1-6.3	0.83			1.2	0.4-3.8	0.72	

BMI: body mass index; NW: normal weight (pre-pregnancy BMI:  $18.5 - 24.9 \text{ kg m}^{-2}$ ); OWO: overweight (pre-pregnancy BMI  $\geq 25 \text{ kg m}^{-2}$ ); PTB: preterm birth. OR: odds ratio; CI: confidence interval.

<sup>a</sup> The number of maternal-origin A allele or paternal-origin A allele at rs11161721 in the infants.

<sup>b</sup> The analyses were conducted using the logistic regression model, adjusted for maternal genetic ancestry, parity and infant's gender.

<sup>c</sup> The interaction effect was analyzed by adding maternal-origin A allele at rs11161721 (coded as 1 vs 0), paternal-origin A allele at rs11161721, maternal pre-pregnancy BMI category (coded as 0=NW, 1=OWO), and the interaction term between maternal pre-pregnancy BMI category and maternal-origin A allele, as well as the interaction term between maternal pre-pregnancy BMI category and paternal-origin A allele into the same logistic regression model, with adjustment for the same covariates as mentioned above.