

Online Supplement: Genetic variants associated with preeclampsia and maternal serum sFLT1 levels

Short Title: Genetics of soluble fms-like tyrosine kinase 1

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Expanded Methods

Data Availability

Restrictions apply to availability of these data. Given the sensitive nature of the research, and to preserve patient confidentiality, the data supporting the findings of this study are available from the corresponding author upon reasonable request.

Genotyping and quality control

DNA was extracted from maternal blood and umbilical cord. Genotyping was carried out by the University College London (UCL) Genomics Facility using the Illumina Infinium Global Screening Array Kit (GSA v3). 7,890 samples (4,048 maternal DNA samples and 3,854 cord DNA samples) were analyzed. A total of 654,027 variants were directly genotyped. Twelve samples of the original 7,902 sent to UCL returned an application failure upon processing. We converted the raw Illumina IDAT files to variant call format (VCF) for downstream analyses using bcftools¹ and gtc2vcf² to identify the appropriate BPM manifest file and EGT cluster file. After identifying the appropriate files, we used Illumina's proprietary GenCall algorithm implemented in IAAP Genotyping Command Line Interface to convert the Illumina-specific IDAT files to GTC (Illumina, Inc. San Diego, CA, USA). Finally, we used bcftools +gtc2vcf to convert the GTC files to VCF files.^{1,2} More information on the process can be found at <https://github.com/freeseek/gtc2vcf>.

Of the received 7,890 genotyped samples, we excluded 258 due to genotyping call rates < 95% and 197 due to high/low heterozygosity rate given a threshold of three standard deviations from the mean method-of-moments F coefficient estimator (determined using PLINK2, --het flag).³ We used KING to estimate kinship based on 636,695 directly genotyped SNPs⁴, and excluded 10 confirmed genetic duplicates. After these quality control procedures, 7,425 samples remained for imputation (**Figure S1**).

Genotype imputation

We utilized the freely available NHLBI TOPMed Imputation Server to perform imputation of the POPs data.⁵ To prepare data for imputation, we conducted quality control for 635,691 bi-allelic variants. We used the McCarthy Group Tool version 4.3.0 to check the PLINK .bim file against the TOPMed reference panel (<https://www.well.ox.ac.uk/~wrayner/tools/>) by strand, ref/alt assignment positions, and alleles (CreateTOPMed.pl script). We excluded mitochondrial variants, variants with no match in the TOPMed reference panel (in genome build hg 38), variants with non-matching alleles in POPs and TOPMed, palindromic SNPs with minor allele frequency (MAF)>0.4, and variants with allele frequency difference > 0.2 between POPs and TOPMed. After these procedures, 501,778 variants across the 22 autosomes and the X chromosome remained for imputation.

We took additional quality control steps and excluded 11,498 variants due to liftover failure, monomorphic sites, invalid alleles, mismatched alleles, and variant call rate < 90% after liftover. There were an additional 43,977 variants that were not imputed, where 446,303 directly genotyped variants remained for the imputation process. Phasing was performed with Eagle v2.4⁶ and imputation was performed with Minimac4.⁷ We uploaded 23 per-chromosome VCF files to the TOPMed Imputation Server for processing. Each imputed per-chromosome file was merged and filtered for imputation quality control score (R^2) >0.3 and MAF>0.001, for a total of 16,251,792 variants.

Kinship and sex discordance

Based on kinship estimation from KING⁴, 48 reported parent/offspring pairs did not have a first-degree relationship (kinship estimation < 0.177) and were excluded ($n = 96$). Full siblings and/or participants with a second-degree or closer relationship with another participant outside of their mother-child pairs were also excluded ($n = 154$; kinship estimation > 0.0884). When choosing which relative to exclude, we prioritized complete mother-child pairs. We randomly excluded a sister or second-degree relative if both pairs were present. We performed a sex check using PLINK1 (--check-sex flag)⁸, and identified 11 instances of sex discordance. Of the 11 cases, four samples were estimated as ambiguous (two mothers and two children) and were excluded. We imputed sex for two children with missing sex information. The other five cases were children, and we corrected the recorded sex in the analytical sample based on genotype. This yielded 7,171 samples (3,685 mothers and 3,486 children).

Outcome and covariates

The outcome of interest is standardized soluble fms-like kinase 1 (sFLT1) levels at 12, 20, 28, and, the primary outcome, 36 wkGA. These circulating placental protein levels were adjusted for the exact gestational age, maternal weight at the time of measurement, and sample storage time at the time of sample processing. They were expressed as multiples of the median (MoM) with log transformation scaled to a mean of 0 and variance of 1 (z-score of log10-transformed adjusted MoM). Other phenotypes of interest are longitudinal measurements of sFLT1 and the change in standard deviation (Delta) from 28 to 36 wkGA ($\Delta 36-28 = 36\text{wkGA} - 28\text{wkGA}$). We include participants if they have at least one sFLT1 measurement, and we allowed the sample to vary across the four timepoints for complete case analysis. All four sFLT1 measurements were missing for two children, who were excluded, yielding the final analytical sample of 7,169 individuals (3,685 mothers and 3,484 children; **Figure S1**).

Covariates of interest included fetal sex, maternal age at enrollment, and maternal race/ethnicity. We classified participants into four self-identified maternal race/ethnicity groups based on multiple choice and free-text responses: Asian, Black, White, and other/unknown. The other/unknown group included participants who self-reported as mixed-race, Middle Eastern, South American, and Hispanic/Latino. Other variables of interest included maternal age at when discontinuing full-time education, BMI at 12 wkGA, Index of Multiple Deprivation 2007⁹, small for gestational age defined by the 1990 UK population-based reference¹⁰, smoking use, alcohol use, and preeclampsia status, as defined by guidelines issued by the American College of Obstetricians and Gynecologists in 2013.¹¹ To preserve the size of the sample, we performed simple imputation to account for covariate missingness. For continuous variables, we imputed the median value. We imputed a deprivation index of 9.06 for 161 participants and maternal age of 21 years when discontinuing full-time education for 119 participants. We imputed a BMI of 24.09 at 12 wkGA for one participant. For alcohol use, we imputed that two participants were non-users of alcohol during pregnancy, which was the most prevalent group. For PE status, we imputed five participants as PE cases given record review. We also report relevant perinatal characteristics related to each pregnancy such as birth outcome and gestational age at delivery.

Principal components analysis and genetic similarity

Within the final sample, we separately computed PCs for maternal and fetal genotype data. We calculated PCs with the same directly genotyped, pruned dataset derived for each analysis ($n = 80,396$ variants). This pruned dataset was created using the "snpgdsLDpruning" function in the SNPRelate R package.¹² Among the directly genotyped variants ($n = 636,763$), we included autosomal variants if they were non-monomorphic and had an $\text{MAF} > 5\%$, $\text{call rate} > 95\%$, and $\text{LD } r^2 < \text{sqrt}(0.1)$. We used the PCAir function in the GENESIS Bioconductor R package¹³ to calculate

PCs, accounting for relatedness by including kinship matrices in the computation. We used the default kinship threshold of 0.0221 in the PCAir function.

To estimate genetic similarity between the POPs cohort and 1000 Genomes, we compute joint principal components of directly genotyped variants in POPs ($n = 7,425$) and the reference panel 1000 Genomes phase 3 ($n = 2,490$).¹⁴ We used the PLINK2 hg19-provided files for independent (i.e., no 1st/2nd degree relationships) 1000 Genomes participants (https://www.cog-genomics.org/plink/2.0/resources#phase3_1kg). In the POPs set, we removed high-LD regions, rare variants ($MAF > 0.05$), and pruned the directly genotyped variants in LD with an $r^2 > \sqrt{0.1}$ using a 50kB window and a step size of 5 (in PLINK2, `--indep-pairwise` flag).³ We filtered to the intersection of pruned variants present in both POPs and 1000 Genomes. QC measures included checking for chromosome mismatch, positional errors, and allele flip issues. Further, POPs and 1000 genomes was merged to compute PCs based on 102,334 variants (`--pca` flag in PLINK2).³ Given that most POPs participants self-identified as White, we used 1000 Genomes to determine the genetic similarity group for European descent. Our estimation is based on the `check_ancestry` function in the PlinkQC R package¹⁵ (https://meyer-lab-cshl.github.io/plinkQC/reference/evaluate_check_ancestry.html).

Using the top two joint computed PCs (PC1 and PC2), we calculated the means for each to determine the center for the similarity group based on the 1000 Genomes cluster. The center is used to compute the Euclidean distance, where the maximum Euclidean distance is determined from the center for the similarity group. All study samples whose Euclidean distance from the centre is within the genetic similarity circle described by the radius, which is the scaling factor (1.5) multiplied by the maximum Euclidean distance, are grouped together. For the European similarity group, we used GBR, British in England and Scotland, to define the ellipsoid for the group ($n = 91$). There were 6,403 participants most similar to GBR ancestry (3,303 mothers and 3,100 children). We harmonized the GBR similarity group with self-identified race/ethnicity, where those who identified as White in the group were included.

Genetic association analyses

Variants associated with PE. Based on the results of previous studies, we selected four variants upstream of the *FLT1* gene found to be strongly associated with PE, which is described in **Supplementary Table 1**. As referenced in Ensembl release 110, these include three regulatory region variants within an enhancer (ENSR00001195603: rs4769612, rs4769613, rs7318880), and an intergenic variant that is more distal, rs12050029.¹⁶ To determine if these proximal *FLT1* SNPs are also associated with standardized sFLT1 levels, PLINK2³ was used to perform the sFLT1-genotype linear regression analyses for the four timepoints across pregnancy, and $\Delta 36-28$. These analyses were performed separately for the fetal and maternal genotype data in addition to with and without PE. Each linear regression included fetal sex, maternal age, maternal race/ethnicity, and the top 10 genetic PCs as covariates.

These analyses were encompassed in a regional analysis of the *FLT1* gene within a 175kb window downstream and upstream. The following base command was used for the regression modeling: `'plink2 --pfile ${pfile} --glm --chr 13 --from-bp 28125346 --to-bp 28670145 --covar ${covar_list} --covar-name ${covar} --require-covar --pheno ${pheno} --pheno-name ${outcomes} --require-pheno --no-input-missing-phenotype --covar-variance-standardize'`. We report effect sizes (Beta) with upper and lower confidence intervals (CIs) with corresponding P-values.

Application of polygenic score of PE. Based on maternal multi-ancestral meta-analysis of PE in Honigberg et al¹⁷, we applied the maternal PE polygenic score (PE-PGS) in our sample to

determine its association with sFLT1 levels among mothers in the POPs cohort. We used the PE-PGS found in the PGS Catalog under PGS003586.^{17,18} This PGS was based on using 1,087,033 genetic variants. To calculate the PE-PGS in the POPs cohort, we used the pgsc_calc pipeline version 2.0.0-alpha.4¹⁹, where the PGS was calculated as a linear combination of each variant's coefficient multiplied by the number of effect alleles contributing to the PGS. Using Nextflow^{20,21}, the PGS was adjusted by genetic ancestry, using the combined Human Genome Diversity Project²² and 1000 Genomes¹⁴ reference panel. Samples in the POPs cohort were projected into the reference PCA space using the online augmentation, decomposition and Procrustes method of the FRAPOSA package.²³ Based on PCA loadings, a Random Forest classifier was used to predict genetic similarity assignment. For these groupings, the scores are adjusted by normalizing the mean distribution and standard deviation, or the distance from the mean score based on ancestry. Further details of the methodology are stated in pgsc_calc documentation. We conducted linear regression analyses for each sFLT1 level as the outcome, using the lm function in R version 4.3.2 with fetal sex, standardized maternal age, maternal race/ethnicity, and top 10 standardized genetic PCs as covariates. For the model estimations for maternal scores with and without PE, we report effect size per standard deviation of the PE-PGS with upper and lower CIs, and P-values.

Variant on chromosome 6 associated with first-trimester sFLT1 levels. Based on the Yan et al²⁴ association found between maternal rs4349809 on chromosome 6 and first-trimester sFLT1 levels, we sought to validate this finding in the POPs cohort across the whole of gestation. Similar to the *FLT1* SNPs, we used PLINK2³ for the single genetic variant linear regression analyses in the maternal and fetal genomes, adjusting for fetal sex, standardized maternal age, maternal race/ethnicity, and the top 10 standardized genetic PCs.

Supplementary References

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Supplemental Figures

Figure S1. Study Inclusion Flowchart

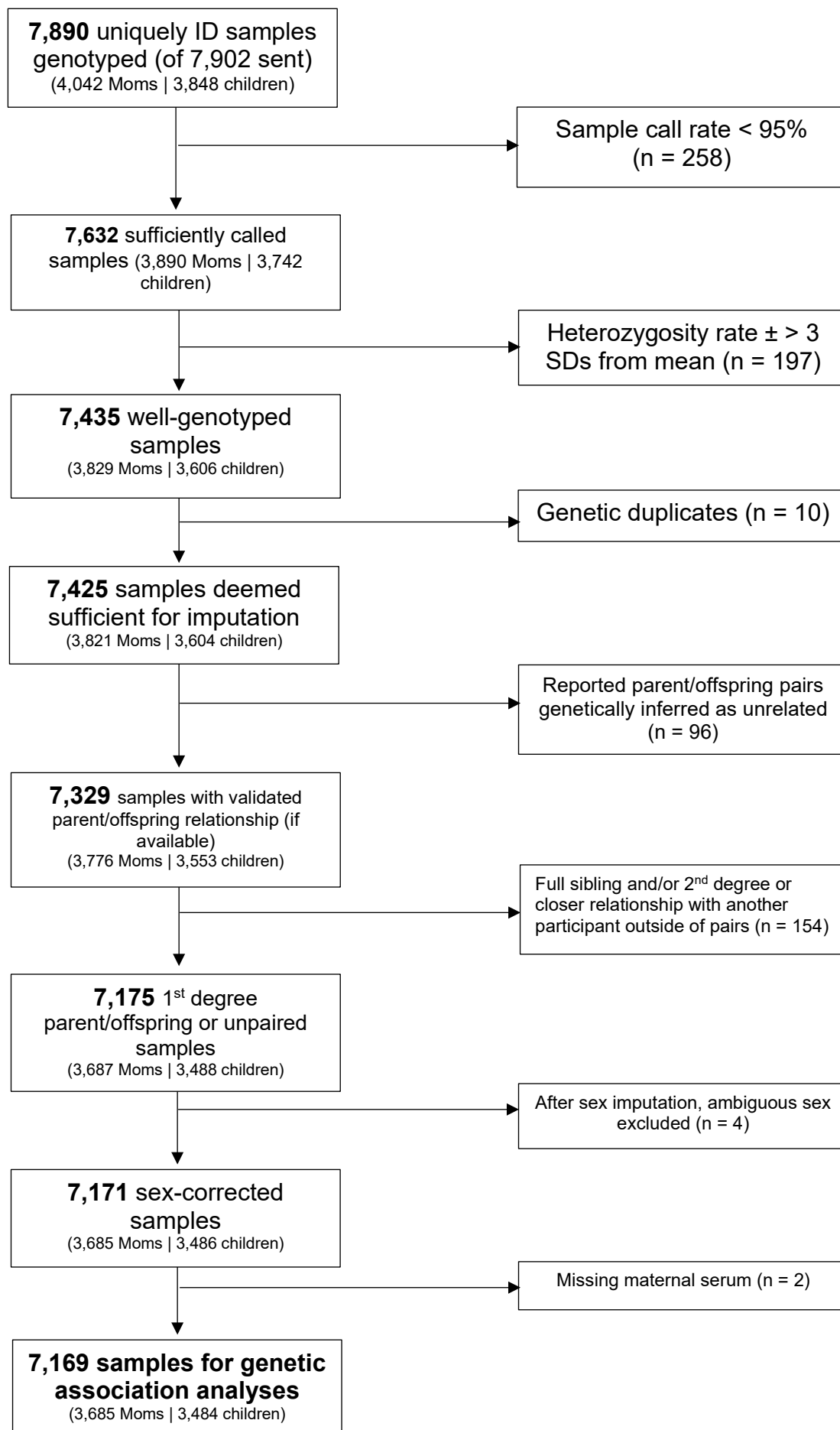
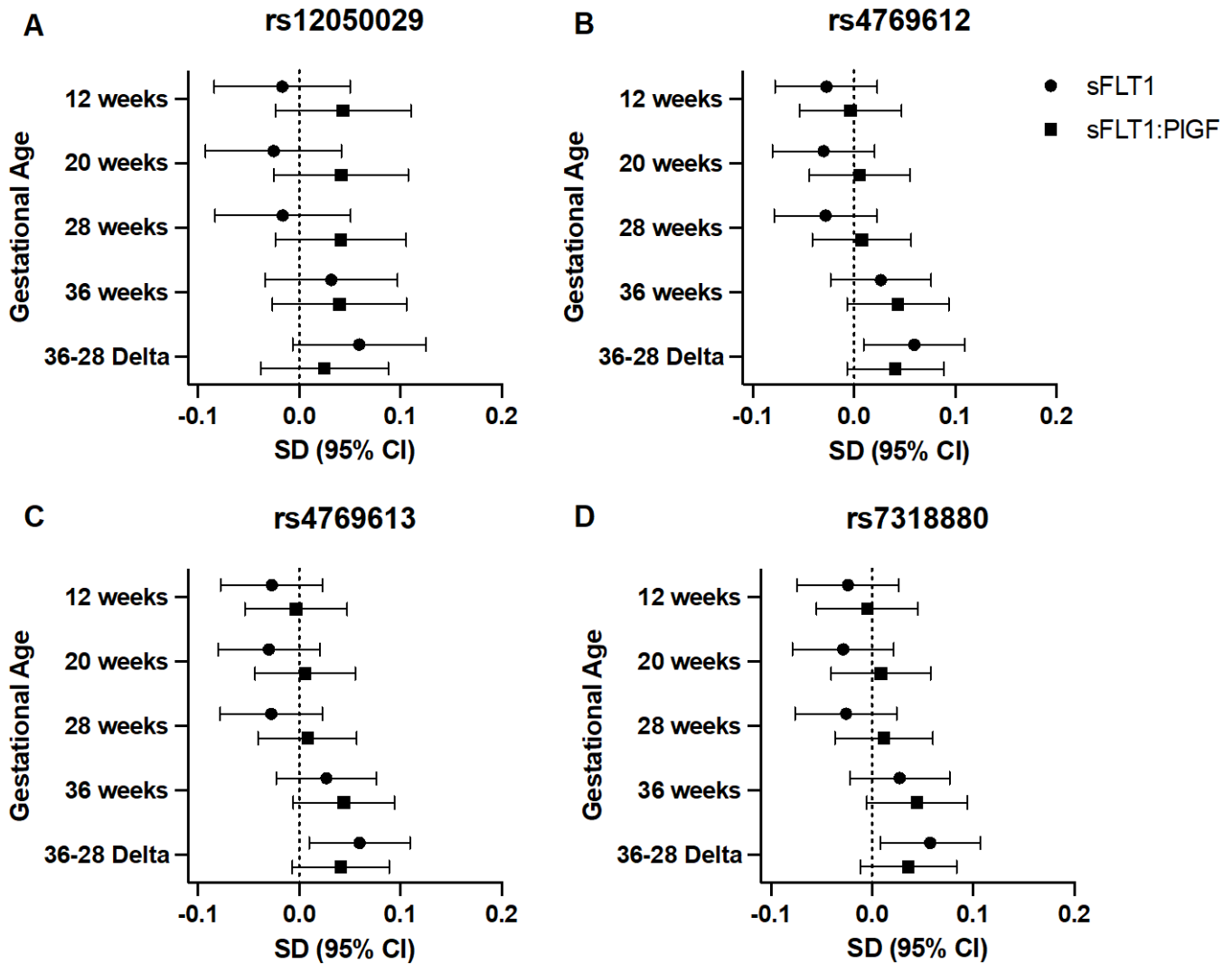


Figure S2. Forest Plots of summary statistics from sFLT1 z-score and sFLT1:PIGF z-score and maternal genotype association study across gestation for the Pregnancy Outcome Prediction study (POPs) participants without preeclampsia.



Four genetic variants near the *FLT1* gene previously found to be associated with preeclampsia (SNP_Effect Allele): **A.** rs12050029_G; **B.** rs4769612_C; **C.** rs4769613_C; **D.** rs7318880_T. SD = Standard Deviation; CI = Confidence Interval; 36-28 Delta refers to the change in standard deviation of sFLT1 between 28 and 36 weeks' gestation.

Supplementary Tables

Table S1. Previous studies reporting significant genetic variants associated with preeclampsia in maternal and fetal genome.

PMID	Author	Genotype	Cases	Controls	SNP (rsid)	POS (hg38)	Effect /Other Allele	OR (95% CI)	P-Value
28628106	McGinnis et al	Fetal	4,380	310,238	rs4769613	13:28564472	C/T	1.21 (1.14-1.28)	5.4×10^{-11}
28628106	McGinnis et al	Fetal	4,380	310,238	rs12050029	13:28653382	G/A	1.19 (1.11-1.28)	3.0×10^{-6}
33239696	Steinthorsdottir et al	Fetal + Maternal	9,515 maternal cases	157,719 maternal controls	rs4769612	13:28564361	C/T	Fetal: 1.17 (1.12-1.23)	Fetal: 3.0×10^{-11}
			6,775 offspring cases	375,372 offspring controls				Maternal: 1.10 (1.06-1.14)	Maternal: 8.9×10^{-7}
37248299	Honigberg et al	Maternal	20,064	703,117	rs7318880	13:28564148	T/C	1.09 (CI not reported)	1.6×10^{-12}
37285119	Tyrmi et al	Maternal	16,743	280,081	rs7318880	13:28564148	T/C	1.10 (1.07-1.13)	5.04×10^{-12}

Rsid = SNP number based on dbSNP155; POS (hg38): position on chromosome based on genome build 38; OR = odds ratio; CI = Confidence Interval

Table S2. Demographic Characteristics in the maternal POPs genomic cohort.

Characteristic	All (N = 3,685)	No Preeclamptic Cases (N = 3,450)
Maternal race/ethnicity, n (%)		
Asian	161 (4.4)	156 (4.5)
Black	24 (0.7)	22 (0.6)
White	3,452 (93.7)	3,225 (93.5)
Other/Unknown	48 (1.3)	47 (1.4)
Fetal Sex, Female, n (%)	1,819 (49.4)	1,714 (49.7)
Maternal age, mean [SD]	30.0 [5.0]	30.0 [5.0]
Maternal age at discontinuing full-time education, mean [SD]	21.0 [3.8]	21.1 [3.8]
Maternal BMI, mean [SD]	25.1 [4.7]	24.9 [4.5]
Indices of multiple deprivation (2007) score, mean [SD]	10.3 [6.4]	10.3 [6.4]
Maternal smoker, n (%)	178 (4.8)	169 (4.9)
Maternal alcohol use, n (%)	168 (4.6)	162 (4.7)
Gestational age at delivery, mean [SD]	40.0 [1.9]	40.0 [1.8]
Livebirth, n (%)	3,668 (99.5)	3,433 (99.5)
Small for gestational age, n (%)	334 (9.1)	303 (8.8)
Preterm birth, n (%)	171 (4.6)	146 (4.2)

Small for gestational age was defined as birth weight < 10th percentile based on the 1990 UK population-based reference¹⁰.

Table S3. Sample distribution of mother-child pairs.

Mother	Child		Total
	Absent	Present	
Absent	0	283	283
Present	484	3201	3685
Total	484	3484	3968

Table S4. Summary Statistics from sFLT1 z-score and multi-ethnic and GBR fetal genotype association study across gestation for the Pregnancy Outcome Prediction study (POPs) in non-preeclamptic cases.

SNP	sFLT1 measurement	Effect Allele	Other Allele	EAF	N	Effect	Lower CI	Upper CI	P-Value	GBR P-Value
rs12050029	12 weeks	G	A	0.15	3161	0.00	-0.07	0.07	0.908	0.687
	20 weeks			0.15	3136	0.04	-0.03	0.11	0.310	0.680
	28 weeks			0.15	3134	0.06	-0.01	0.13	0.091	0.301
	36 weeks			0.15	2996	0.09	0.03	0.16	0.006	0.015
	36-28 Delta			0.15	2917	0.05	-0.02	0.11	0.178	0.205
rs4769612	12 weeks	C	T	0.54	3161	0.00	-0.05	0.05	0.978	0.905
	20 weeks			0.54	3136	-0.04	-0.09	0.01	0.123	0.217
	28 weeks			0.54	3134	-0.04	-0.09	0.01	0.135	0.243
	36 weeks			0.54	2996	0.06	0.01	0.11	0.029	0.016
	36-28 Delta			0.54	2917	0.11	0.06	0.16	1.50×10 ⁻⁵	4.26×10 ⁻⁵
rs4769613	12 weeks	C	T	0.54	3161	0.00	-0.05	0.05	0.926	0.907
	20 weeks			0.54	3136	-0.04	-0.10	0.01	0.105	0.215
	28 weeks			0.54	3134	-0.04	-0.09	0.01	0.120	0.243
	36 weeks			0.54	2996	0.06	0.01	0.11	0.030	0.016
	36-28 Delta			0.54	2917	0.11	0.06	0.16	1.23×10 ⁻⁵	4.26×10 ⁻⁵
rs7318880	12 weeks	T	C	0.50	3161	0.00	-0.05	0.05	0.912	0.894
	20 weeks			0.50	3136	-0.04	-0.09	0.01	0.133	0.285
	28 weeks			0.50	3134	-0.04	-0.09	0.01	0.160	0.347
	36 weeks			0.50	2996	0.06	0.01	0.11	0.030	0.013
	36-28 Delta			0.50	2917	0.11	0.06	0.16	2.68×10 ⁻⁵	7.63×10 ⁻⁵

Analyses of fetal participants without preeclampsia. Four genetic variants near the *FLT1* gene previously found to be associated with preeclampsia (SNP_Effect Allele): rs12050029_G; rs4769612_C; rs4769613_C; rs7318880_T; EAF = Effect Allele Frequency; CI = 95% Confidence Interval; GBR = White British Ancestry

Table S5. Summary Statistics from sFLT1 z-score and multi-ethnic and GBR fetal genotype association study across gestation for the Pregnancy Outcome Prediction study (POPs) in overall fetal sample.

SNP	sFLT1 measurement	Effect Allele	Other Allele	EAF	N	Effect	Lower CI	Upper CI	P-Value	GBR P-Value
rs12050029	12 weeks	G	A	0.15	3375	0.01	-0.06	0.08	0.773	0.883
	20 weeks			0.15	3348	0.02	-0.05	0.09	0.532	0.979
	28 weeks			0.15	3346	0.05	-0.02	0.11	0.192	0.611
	36 weeks			0.15	3182	0.07	0.01	0.14	0.028	0.069
	36-28 Delta			0.15	3096	0.05	-0.02	0.11	0.158	0.174
rs4769612	12 weeks	C	T	0.54	3375	-0.01	-0.06	0.04	0.798	0.860
	20 weeks			0.55	3348	-0.05	-0.10	0.00	0.060	0.117
	28 weeks			0.54	3346	-0.04	-0.09	0.01	0.160	0.324
	36 weeks			0.55	3182	0.07	0.02	0.12	0.008	0.003
	36-28 Delta			0.55	3096	0.12	0.07	0.17	2.62×10 ⁻⁶	5.55×10 ⁻⁶
rs4769613	12 weeks	C	T	0.54	3375	-0.01	-0.06	0.04	0.747	0.858
	20 weeks			0.55	3348	-0.05	-0.10	0.00	0.050	0.116
	28 weeks			0.54	3346	-0.04	-0.09	0.01	0.143	0.323
	36 weeks			0.55	3182	0.07	0.02	0.12	0.009	0.003
	36-28 Delta			0.55	3096	0.12	0.07	0.17	2.14×10 ⁻⁶	5.55×10 ⁻⁶
rs7318880	12 weeks	T	C	0.50	3375	-0.01	-0.06	0.04	0.769	0.882
	20 weeks			0.51	3348	-0.05	-0.10	0.00	0.059	0.148
	28 weeks			0.50	3346	-0.03	-0.08	0.02	0.198	0.440
	36 weeks			0.51	3182	0.07	0.02	0.12	0.008	0.002
	36-28 Delta			0.51	3096	0.11	0.07	0.16	4.92×10 ⁻⁶	9.58×10 ⁻⁶

Analyses of fetal participants, with and without preeclampsia. Four genetic variants near the *FLT1* gene previously found to be associated with preeclampsia (SNP_Effect Allele): rs12050029_G; rs4769612_C; rs4769613_C; rs7318880_T; EAF = Effect Allele Frequency; CI = 95% Confidence Interval; GBR = White British Ancestry

Table S6. Summary Statistics from sFLT1 z-score and multi-ethnic and GBR maternal genotype association study across gestation for the Pregnancy Outcome Prediction study (POPs) in non-preeclamptic cases.

SNP	sFLT1 measurement	Effect Allele	Other Allele	EAF	N	Effect	Lower CI	Upper CI	P-Value	GBR P-Value
rs12050029	12 weeks	G	A	0.15	3348	-0.02	-0.08	0.05	0.623	0.517
	20 weeks			0.15	3385	-0.03	-0.09	0.04	0.459	0.241
	28 weeks			0.16	3312	-0.02	-0.08	0.05	0.634	0.283
	36 weeks			0.15	3156	0.03	-0.03	0.10	0.342	0.382
	36-28 Delta			0.16	3067	0.06	-0.01	0.13	0.077	0.033
rs4769612	12 weeks	C	T	0.53	3348	-0.03	-0.08	0.02	0.291	0.267
	20 weeks			0.54	3385	-0.03	-0.08	0.02	0.246	0.407
	28 weeks			0.54	3312	-0.03	-0.08	0.02	0.280	0.352
	36 weeks			0.54	3156	0.03	-0.02	0.08	0.295	0.201
	36-28 Delta			0.54	3067	0.06	0.01	0.11	0.020	0.010
rs4769613	12 weeks	C	T	0.53	3348	-0.03	-0.08	0.02	0.290	0.267
	20 weeks			0.54	3385	-0.03	-0.08	0.02	0.245	0.407
	28 weeks			0.54	3312	-0.03	-0.08	0.02	0.283	0.357
	36 weeks			0.54	3156	0.03	-0.02	0.08	0.290	0.198
	36-28 Delta			0.54	3067	0.06	0.01	0.11	0.019	0.010
rs7318880	12 weeks	T	C	0.50	3348	-0.02	-0.07	0.03	0.351	0.273
	20 weeks			0.50	3385	-0.03	-0.08	0.02	0.263	0.458
	28 weeks			0.50	3312	-0.03	-0.08	0.02	0.317	0.415
	36 weeks			0.50	3156	0.03	-0.02	0.08	0.275	0.194
	36-28 Delta			0.50	3067	0.06	0.01	0.11	0.023	0.015

Analyses of maternal participants without preeclampsia. Four genetic variants near the *FLT1* gene previously found to be associated with preeclampsia (SNP_Effect Allele): rs12050029_G; rs4769612_C; rs4769613_C; rs7318880_T; EAF = Effect Allele Frequency; CI = 95% Confidence Interval; GBR = White British Ancestry

Table S7. Summary Statistics from sFLT1 z-score and multi-ethnic and GBR maternal genotype association study across gestation for the Pregnancy Outcome Prediction study (POPs) in overall maternal sample.

SNP	sFLT1 measurement	Effect Allele	Other Allele	EA	N	Effect	Lower CI	Upper CI	P-Value	GBR P-Value
rs12050029	12 weeks	G	A	0.16	3573	-0.02	-0.08	0.05	0.598	0.584
	20 weeks			0.15	3612	-0.03	-0.09	0.04	0.413	0.287
	28 weeks			0.16	3535	-0.02	-0.09	0.04	0.522	0.243
	36 weeks			0.16	3351	0.02	-0.05	0.08	0.635	0.726
	36-28 Delta			0.16	3256	0.05	-0.02	0.11	0.166	0.094
rs4769612	12 weeks	C	T	0.54	3573	-0.03	-0.08	0.02	0.207	0.214
	20 weeks			0.54	3612	-0.03	-0.08	0.02	0.219	0.340
	28 weeks			0.54	3535	-0.02	-0.07	0.03	0.372	0.489
	36 weeks			0.54	3351	0.03	-0.02	0.08	0.222	0.109
	36-28 Delta			0.54	3256	0.06	0.01	0.11	0.012	0.005
rs4769613	12 weeks	C	T	0.54	3573	-0.03	-0.08	0.02	0.207	0.214
	20 weeks			0.54	3612	-0.03	-0.08	0.02	0.219	0.339
	28 weeks			0.54	3535	-0.02	-0.07	0.03	0.376	0.494
	36 weeks			0.54	3351	0.03	-0.02	0.08	0.218	0.107
	36-28 Delta			0.54	3256	0.06	0.01	0.11	0.012	0.005
rs7318880	12 weeks	T	C	0.50	3573	-0.03	-0.08	0.02	0.240	0.201
	20 weeks			0.50	3612	-0.03	-0.08	0.02	0.243	0.406
	28 weeks			0.50	3535	-0.02	-0.07	0.03	0.451	0.585
	36 weeks			0.50	3351	0.03	-0.02	0.08	0.185	0.094
	36-28 Delta			0.50	3256	0.06	0.01	0.11	0.015	0.008

Analyses of all maternal participants, with and without preeclampsia. Four genetic variants near the *FLT1* gene previously found to be associated with preeclampsia (SNP_Effect Allele): rs12050029_G; rs4769612_C; rs4769613_C; rs7318880_T; EAF = Effect Allele Frequency; CI = 95% Confidence Interval; GBR = White British Ancestry

Table S8. Summary Statistics from sFLT1:PIGF ratio z-score and multi-ethnic and GBR fetal genotype association study across gestation for the Pregnancy Outcome Prediction study (POPs) in non-preeclamptic cases.

SNP	sFLT1: PIGF measurement	Effect Allele	Other Allele	EAF	N	Effect	Lower CI	Upper CI	P-Value	GBR P-Value
rs12050029	12 weeks	G	A	0.15	3161	0.08	0.01	0.15	0.025	0.156
	20 weeks			0.15	3136	0.07	0.00	0.14	0.041	0.304
	28 weeks			0.15	3134	0.11	0.04	0.17	0.001	0.015
	36 weeks			0.15	2996	0.11	0.04	0.17	0.002	0.006
	36-28 Delta			0.15	2917	0.02	-0.05	0.08	0.635	0.519
rs4769612	12 weeks	C	T	0.54	3161	0.04	-0.02	0.09	0.181	0.297
	20 weeks			0.54	3136	0.03	-0.02	0.08	0.253	0.393
	28 weeks			0.54	3134	0.03	-0.02	0.08	0.207	0.337
	36 weeks			0.54	2996	0.10	0.05	0.15	1.21×10 ⁻⁴	2.91×10 ⁻⁴
	36-28 Delta			0.54	2917	0.08	0.03	0.13	0.002	0.001
rs4769613	12 weeks	C	T	0.54	3161	0.03	-0.02	0.09	0.191	0.299
	20 weeks			0.54	3136	0.03	-0.02	0.08	0.257	0.395
	28 weeks			0.54	3134	0.03	-0.02	0.08	0.214	0.341
	36 weeks			0.54	2996	0.10	0.05	0.15	9.76×10 ⁻⁵	2.96×10 ⁻⁴
	36-28 Delta			0.54	2917	0.08	0.03	0.13	0.001	0.001
rs7318880	12 weeks	T	C	0.50	3161	0.03	-0.02	0.08	0.269	0.394
	20 weeks			0.50	3136	0.03	-0.02	0.08	0.290	0.426
	28 weeks			0.50	3134	0.03	-0.02	0.08	0.231	0.338
	36 weeks			0.50	2996	0.10	0.05	0.15	1.18×10 ⁻⁴	3.00×10 ⁻⁴
	36-28 Delta			0.50	2917	0.08	0.03	0.13	0.001	0.001

Analyses of fetal participants without preeclampsia. Four genetic variants near the *FLT1* gene previously found to be associated with preeclampsia (SNP_Effect Allele): rs12050029_G; rs4769612_C; rs4769613_C; rs7318880_T; EAF = Effect Allele Frequency; CI = 95% Confidence Interval; GBR = White British Ancestry

Table S9. Summary Statistics from sFLT1:PIGF ratio z-score and multi-ethnic and GBR fetal genotype association study across gestation for the Pregnancy Outcome Prediction study (POPs) in overall fetal sample.

SNP	sFLT1: PIGF measurement	Effect Allele	Other Allele	EAF	N	Effect	Lower CI	Upper CI	P-Value	GBR P-Value
rs12050029	12 weeks	G	A	0.15	3375	0.08	0.01	0.14	0.029	0.174
	20 weeks			0.15	3348	0.05	-0.02	0.12	0.147	0.691
	28 weeks			0.15	3346	0.09	0.02	0.15	0.013	0.097
	36 weeks			0.15	3182	0.09	0.03	0.16	0.007	0.015
	36-28 Delta			0.15	3096	0.03	-0.04	0.09	0.423	0.288
rs4769612	12 weeks	C	T	0.54	3375	0.04	-0.02	0.09	0.171	0.264
	20 weeks			0.55	3348	0.02	-0.03	0.07	0.426	0.635
	28 weeks			0.54	3346	0.04	-0.01	0.09	0.112	0.146
	36 weeks			0.55	3182	0.11	0.06	0.16	2.71×10 ⁻⁵	4.86×10 ⁻⁵
	36-28 Delta			0.55	3096	0.08	0.03	0.12	0.002	0.002
rs4769613	12 weeks	C	T	0.54	3375	0.03	-0.02	0.09	0.180	0.266
	20 weeks			0.55	3348	0.02	-0.03	0.07	0.431	0.637
	28 weeks			0.54	3346	0.04	-0.01	0.09	0.116	0.148
	36 weeks			0.55	3182	0.11	0.06	0.16	2.17×10 ⁻⁵	4.96×10 ⁻⁵
	36-28 Delta			0.55	3096	0.08	0.03	0.13	0.001	0.002
rs7318880	12 weeks	T	C	0.50	3375	0.03	-0.02	0.08	0.244	0.328
	20 weeks			0.51	3348	0.02	-0.03	0.07	0.529	0.719
	28 weeks			0.50	3346	0.04	-0.01	0.09	0.130	0.146
	36 weeks			0.51	3182	0.11	0.06	0.15	2.48×10 ⁻⁵	4.57×10 ⁻⁵
	36-28 Delta			0.51	3096	0.08	0.03	0.12	0.001	0.002

Analyses of all fetal participants, with and without preeclampsia. Four genetic variants near the *FLT1* gene previously found to be associated with preeclampsia (SNP_Effect Allele): rs12050029_G; rs4769612_C; rs4769613_C; rs7318880_T; EAF = Effect Allele Frequency; CI = 95% Confidence Interval; GBR = White British Ancestry

Table S10. Summary Statistics from sFLT1:PIGF ratio z-score and multi-ethnic and GBR maternal genotype association study across gestation for the Pregnancy Outcome Prediction study (POPs) in non-preeclamptic cases.

SNP	sFLT1:PIGF measurement	Effect Allele	Other Allele	EAF	N	Effect	Lower CI	Upper CI	P-Value	GBR P-Value
rs12050029	12 weeks	G	A	0.15	3348	0.04	-0.02	0.11	0.204	0.276
	20 weeks			0.15	3385	0.04	-0.02	0.11	0.220	0.561
	28 weeks			0.16	3312	0.04	-0.02	0.11	0.213	0.366
	36 weeks			0.15	3156	0.04	-0.03	0.11	0.238	0.199
	36-28 Delta			0.16	3067	0.02	-0.04	0.09	0.438	0.278
rs4769612	12 weeks	C	T	0.53	3348	0.00	-0.05	0.05	0.897	0.914
	20 weeks			0.54	3385	0.01	-0.04	0.06	0.821	0.595
	28 weeks			0.54	3312	0.01	-0.04	0.06	0.759	0.509
	36 weeks			0.54	3156	0.04	-0.01	0.09	0.088	0.066
	36-28 Delta			0.54	3067	0.04	-0.01	0.09	0.094	0.132
rs4769613	12 weeks	C	T	0.53	3348	0.00	-0.05	0.05	0.905	0.923
	20 weeks			0.54	3385	0.01	-0.04	0.06	0.817	0.591
	28 weeks			0.54	3312	0.01	-0.04	0.06	0.744	0.495
	36 weeks			0.54	3156	0.04	-0.01	0.09	0.084	0.063
	36-28 Delta			0.54	3067	0.04	-0.01	0.09	0.094	0.133
rs7318880	12 weeks	T	C	0.50	3348	0.00	-0.05	0.05	0.850	0.881
	20 weeks			0.50	3385	0.01	-0.04	0.06	0.726	0.504
	28 weeks			0.50	3312	0.01	-0.04	0.06	0.631	0.457
	36 weeks			0.50	3156	0.04	-0.01	0.09	0.079	0.064
	36-28 Delta			0.50	3067	0.04	-0.01	0.08	0.137	0.169

Analyses of maternal participants without preeclampsia. Four genetic variants near the *FLT1* gene previously found to be associated with preeclampsia (SNP_Effect Allele): rs12050029_G; rs4769612_C; rs4769613_C; rs7318880_T; EAF = Effect Allele Frequency; CI = 95% Confidence Interval; GBR = White British Ancestry

Table S11. Summary Statistics from sFLT1:PIGF ratio z-score and multi-ethnic and GBR maternal genotype association study across gestation for the Pregnancy Outcome Prediction study (POPs) in overall maternal sample.

SNP	sFLT1:PIGF measurement	Effect Allele	Other Allele	EAF	N	Effect	Lower CI	Upper CI	P-Value	GBR P-Value
rs12050029	12 weeks	G	A	0.16	3573	0.04	-0.03	0.10	0.243	0.257
	20 weeks			0.15	3612	0.03	-0.03	0.10	0.294	0.492
	28 weeks			0.16	3535	0.03	-0.03	0.10	0.337	0.463
	36 weeks			0.16	3351	0.04	-0.03	0.10	0.279	0.227
	36-28 Delta			0.16	3256	0.02	-0.04	0.08	0.468	0.316
rs4769612	12 weeks	C	T	0.54	3573	0.00	-0.05	0.05	0.986	0.846
	20 weeks			0.54	3612	0.01	-0.04	0.05	0.786	0.574
	28 weeks			0.54	3535	0.02	-0.03	0.07	0.429	0.216
	36 weeks			0.54	3351	0.05	0.00	0.10	0.050	0.026
	36-28 Delta			0.54	3256	0.04	-0.01	0.09	0.081	0.115
rs4769613	12 weeks	C	T	0.54	3573	0.00	-0.05	0.05	0.979	0.837
	20 weeks			0.54	3612	0.01	-0.04	0.05	0.782	0.569
	28 weeks			0.54	3535	0.02	-0.03	0.07	0.419	0.209
	36 weeks			0.54	3351	0.05	0.00	0.10	0.048	0.025
	36-28 Delta			0.54	3256	0.04	-0.01	0.09	0.081	0.116
rs7318880	12 weeks	T	C	0.50	3573	0.00	-0.05	0.05	0.947	0.870
	20 weeks			0.50	3612	0.01	-0.04	0.06	0.653	0.436
	28 weeks			0.50	3535	0.03	-0.02	0.07	0.298	0.163
	36 weeks			0.50	3351	0.05	0.00	0.10	0.036	0.019
	36-28 Delta			0.50	3256	0.04	-0.01	0.08	0.122	0.145

Analyses of all maternal participants, with and without preeclampsia. Four genetic variants near the *FLT1* gene previously found to be associated with preeclampsia (SNP_Effect Allele): rs12050029_G; rs4769612_C; rs4769613_C; rs7318880_T; EAF = Effect Allele Frequency; CI = 95% Confidence Interval; GBR = White British Ancestry

Table S12. Variants scored and missing in the POPs cohort, based on application of the polygenic score of preeclampsia in Honigberg et al^{17,18}.

PGS	N variants in model	Variants scored	Variants missing (%)	Missing (n)
Preeclampsia PGS, Honigberg et al	1,087,033	1,084,190	0.26	2,843

Table S13. Linear regression of maternal preeclampsia polygenic score (PGS) on sFLT1 levels across gestation

Cohort	sFLT1 measurement	N	Effect per SD	Lower CI	Upper CI	P-value
Maternal – no PE	12 weeks	3348	-0.06	-0.10	-0.03	3.69E-04
	20 weeks	3385	-0.04	-0.07	-0.003	0.030
	28 weeks	3312	-0.03	-0.06	0.01	0.115
	36 weeks	3156	0.01	-0.02	0.05	0.547
	36-28 Delta	3067	0.05	0.01	0.08	0.010
Maternal – All	12 weeks	3573	-0.06	-0.09	-0.02	0.001
	20 weeks	3612	-0.03	-0.07	0.00	0.049
	28 weeks	3535	-0.02	-0.06	0.01	0.210
	36 weeks	3351	0.01	-0.03	0.04	0.631
	36-28 Delta	3256	0.04	0.00	0.07	0.031
Maternal GBR – no PE	12 weeks	2851	-0.07	-0.11	-0.03	4.22E-04
	20 weeks	2887	-0.05	-0.08	-0.01	0.017
	28 weeks	2835	-0.04	-0.08	0.00	0.045
	36 weeks	2709	0.00	-0.03	0.04	0.892
	36-28 Delta	2635	0.05	0.01	0.09	0.013
Maternal GBR - All	12 weeks	3050	-0.06	-0.10	-0.03	0.001
	20 weeks	3089	-0.04	-0.08	0.00	0.030
	28 weeks	3034	-0.03	-0.07	0.01	0.097
	36 weeks	2885	0.00	-0.03	0.04	0.866
	36-28 Delta	2806	0.04	0.00	0.08	0.029

Application of PGS based on maternal PE meta-analyses conducted in Honigberg et al^{17,18}.

Adjusting for fetal sex, standardized maternal age, maternal race/ethnicity, and the top 10 standardized genetic principal components

EAF = Effect Allele Frequency; CI = 95% Confidence Interval; GBR = White British Ancestry

Table S14. Linear regression of maternal preeclampsia polygenic score (PGS) on sFLT1:PIGF levels across gestation

Cohort	sFLT1:PIGF measurement	N	Effect per SD	Lower CI	Upper CI	P-value
Maternal – no PE	12 weeks	3348	-0.05	-0.09	-0.02	0.002
	20 weeks	3385	-0.01	-0.05	0.02	0.429
	28 weeks	3312	0.02	-0.01	0.06	0.192
	36 weeks	3156	0.03	-0.01	0.06	0.143
	36-28 Delta	3067	0.02	-0.01	0.05	0.279
Maternal – All	12 weeks	3573	-0.05	-0.09	-0.02	0.004
	20 weeks	3612	-0.01	-0.04	0.03	0.746
	28 weeks	3535	0.02	-0.01	0.06	0.164
	36 weeks	3351	0.02	-0.01	0.06	0.194
	36-28 Delta	3256	0.01	-0.02	0.04	0.498
Maternal GBR – no PE	12 weeks	2851	-0.06	-0.10	-0.02	0.002
	20 weeks	2887	-0.02	-0.05	0.02	0.406
	28 weeks	2835	0.02	-0.02	0.05	0.382
	36 weeks	2709	0.02	-0.01	0.06	0.220
	36-28 Delta	2635	0.02	-0.02	0.06	0.280
Maternal GBR - All	12 weeks	3050	-0.05	-0.09	-0.02	0.005
	20 weeks	3089	-0.01	-0.04	0.03	0.760
	28 weeks	3034	0.02	-0.02	0.06	0.304
	36 weeks	2885	0.02	-0.01	0.06	0.234
	36-28 Delta	2806	0.01	-0.02	0.05	0.438

Application of PGS based on maternal PE meta-analyses conducted in Honigberg et al.

Adjusting for fetal sex, standardized maternal age, maternal race/ethnicity, and the top 10 standardized genetic principal components

EAF = Effect Allele Frequency; CI = 95% Confidence Interval; GBR = White British Ancestry

Table S15. Fetal validation analysis of rs4349809 with sFLT1, a maternal genetic variant previously found to be associated with sFLT1 levels in early gestation.

Cohort	SNP	sFLT1 measurement	Effect Allele	Other Allele	EAF	N	Effect	Lower CI	Upper CI	P-Value
Fetal – no PE	rs4349809	12 weeks	G	T	0.45	3161	-0.03	-0.08	0.02	0.210
		20 weeks			0.45	3136	0.00	-0.05	0.06	0.853
		28 weeks			0.45	3134	0.02	-0.03	0.07	0.393
		36 weeks			0.45	2996	0.01	-0.04	0.06	0.729
		36-28 Delta			0.46	2917	-0.01	-0.06	0.04	0.822
Fetal - All	rs4349809	12 weeks	G	T	0.46	3375	-0.04	-0.09	0.00	0.077
		20 weeks			0.45	3348	-0.01	-0.06	0.04	0.683
		28 weeks			0.46	3346	0.02	-0.03	0.07	0.461
		36 weeks			0.45	3182	0.00	-0.04	0.05	0.856
		36-28 Delta			0.46	3096	0.00	-0.05	0.05	0.927
Fetal GBR - no PE	rs4349809	12 weeks	G	T	0.46	2683	-0.02	-0.07	0.04	0.530
		20 weeks			0.46	2670	0.01	-0.04	0.07	0.664
		28 weeks			0.46	2677	0.03	-0.02	0.09	0.259
		36 weeks			0.46	2569	0.01	-0.04	0.06	0.687
		36-28 Delta			0.46	2504	-0.01	-0.07	0.04	0.615
Fetal GBR - All	rs4349809	12 weeks	G	T	0.46	2875	-0.03	-0.08	0.02	0.268
		20 weeks			0.46	2861	0.00	-0.06	0.05	0.911
		28 weeks			0.46	2869	0.03	-0.02	0.08	0.288
		36 weeks			0.46	2737	0.01	-0.04	0.06	0.688
		36-28 Delta			0.46	2666	-0.01	-0.06	0.05	0.769

Summary statistics from sFLT1 z-score and multi-ethnic fetal genotype association study across gestation for the Pregnancy Outcome Prediction study (POPs) participants. EAF = Effect Allele Frequency; CI = 95% Confidence Interval; GBR = White British Ancestry

Table S16. Maternal validation analysis of rs4349809 with sFLT1, a maternal genetic variant previously found to be associated with sFLT1 levels in early gestation.

Cohort	SNP	sFLT1 measurement	Effect Allele	Other Allele	EAF	N	Effect	Lower CI	Upper CI	P-Value
Maternal – no PE	rs4349809	12 weeks	G	T	0.46	3348	-0.09	-0.14	-0.04	1.86×10 ⁻⁴
		20 weeks			0.46	3385	-0.06	-0.11	-0.01	0.021
		28 weeks			0.46	3312	-0.02	-0.07	0.03	0.350
		36 weeks			0.46	3156	-0.01	-0.06	0.03	0.586
		36-28 Delta			0.46	3067	0.02	-0.03	0.06	0.526
Maternal - All	rs4349809	12 weeks	G	T	0.46	3573	-0.10	-0.15	-0.05	4.11×10 ⁻⁵
		20 weeks			0.46	3612	-0.06	-0.11	-0.01	0.013
		28 weeks			0.46	3535	-0.02	-0.07	0.03	0.380
		36 weeks			0.46	3351	-0.01	-0.06	0.04	0.666
		36-28 Delta			0.47	3256	0.02	-0.03	0.07	0.442
Maternal GBR - no PE	rs4349809	12 weeks	G	T	0.47	2851	-0.08	-0.13	-0.03	0.003
		20 weeks			0.47	2887	-0.05	-0.10	0.00	0.065
		28 weeks			0.47	2835	-0.02	-0.07	0.04	0.532
		36 weeks			0.47	2709	-0.01	-0.06	0.05	0.835
		36-28 Delta			0.47	2635	0.02	-0.03	0.07	0.426
Maternal GBR - All	rs4349809	12 weeks	G	T	0.47	3050	-0.09	-0.14	-0.04	0.001
		20 weeks			0.47	3089	-0.05	-0.10	0.00	0.054
		28 weeks			0.47	3034	-0.01	-0.07	0.04	0.610
		36 weeks			0.47	2885	-0.01	-0.06	0.04	0.821
		36-28 Delta			0.48	2806	0.02	-0.03	0.07	0.413

Summary statistics from sFLT1 z-score and multi-ethnic maternal genotype association study across gestation for the Pregnancy Outcome Prediction study (POPs) participants. EAF = Effect Allele Frequency; CI = 95% Confidence Interval; GBR = White British Ancestry

Table S17. Fetal validation analysis of rs4349809 with sFLT1:PIGF, a maternal genetic variant previously found to be associated with sFLT1 levels in early gestation.

Cohort	SNP	sFLT1:PIGF measurement	Effect Allele	Other Allele	EAF	N	Effect	Lower CI	Upper CI	P-Value
Fetal – no PE	rs4349809	12 weeks	G	T	0.45	3161	0.00	-0.05	0.05	0.979
		20 weeks			0.45	3136	0.02	-0.03	0.07	0.465
		28 weeks			0.45	3134	0.01	-0.04	0.05	0.827
		36 weeks			0.45	2996	0.02	-0.03	0.07	0.486
		36-28 Delta			0.46	2917	0.01	-0.04	0.06	0.791
Fetal - All	rs4349809	12 weeks	G	T	0.46	3375	-0.01	-0.06	0.04	0.784
		20 weeks			0.45	3348	0.00	-0.05	0.05	0.938
		28 weeks			0.46	3346	0.00	-0.04	0.05	0.858
		36 weeks			0.45	3182	0.01	-0.04	0.06	0.627
		36-28 Delta			0.46	3096	0.01	-0.04	0.05	0.780
Fetal GBR - no PE	rs4349809	12 weeks	G	T	0.46	2683	0.01	-0.05	0.06	0.821
		20 weeks			0.46	2670	0.00	-0.05	0.06	0.987
		28 weeks			0.46	2677	0.00	-0.06	0.05	0.873
		36 weeks			0.46	2569	0.01	-0.05	0.06	0.810
		36-28 Delta			0.46	2504	0.00	-0.05	0.06	0.921
Fetal GBR - All	rs4349809	12 weeks	G	T	0.46	2875	0.00	-0.05	0.06	0.859
		20 weeks			0.46	2861	-0.01	-0.07	0.04	0.593
		28 weeks			0.46	2869	0.00	-0.05	0.05	0.956
		36 weeks			0.46	2737	0.00	-0.05	0.06	0.868
		36-28 Delta			0.46	2666	0.00	-0.05	0.05	0.912

Summary statistics from sFLT1 z-score and multi-ethnic fetal genotype association study across gestation for the Pregnancy Outcome Prediction study (POPs) participants. EAF = Effect Allele Frequency; CI = 95% Confidence Interval; GBR = White British Ancestry

Table S18. Maternal validation analysis of rs4349809 with sFLT1:PIGF, a maternal genetic variant previously found to be associated with sFLT1 levels in early gestation.

Cohort	SNP	sFLT1:PIGF measurement	Effect Allele	Other Allele	EAF	N	Effect	Lower CI	Upper CI	P-Value
Maternal – no PE	rs4349809	12 weeks	G	T	0.46	3348	-0.04	-0.09	0.01	0.124
		20 weeks			0.46	3385	-0.05	-0.10	0.00	0.037
		28 weeks			0.46	3312	-0.04	-0.09	0.00	0.077
		36 weeks			0.46	3156	-0.01	-0.06	0.04	0.750
		36-28 Delta			0.46	3067	0.03	-0.02	0.07	0.273
Maternal - All	rs4349809	12 weeks	G	T	0.46	3573	-0.04	-0.09	0.00	0.077
		20 weeks			0.46	3612	-0.05	-0.10	0.00	0.041
		28 weeks			0.46	3535	-0.03	-0.08	0.02	0.209
		36 weeks			0.46	3351	0.00	-0.05	0.04	0.854
		36-28 Delta			0.47	3256	0.02	-0.02	0.07	0.364
Maternal GBR - no PE	rs4349809	12 weeks	G	T	0.47	2851	-0.02	-0.08	0.03	0.362
		20 weeks			0.47	2887	-0.06	-0.11	0.00	0.033
		28 weeks			0.47	2835	-0.06	-0.11	-0.01	0.031
		36 weeks			0.47	2709	-0.01	-0.06	0.04	0.633
		36-28 Delta			0.47	2635	0.03	-0.02	0.09	0.173
Maternal GBR - All	rs4349809	12 weeks	G	T	0.47	3050	-0.03	-0.08	0.02	0.248
		20 weeks			0.47	3089	-0.05	-0.10	0.00	0.048
		28 weeks			0.47	3034	-0.04	-0.09	0.01	0.125
		36 weeks			0.47	2885	-0.01	-0.06	0.04	0.654
		36-28 Delta			0.48	2806	0.03	-0.02	0.07	0.305

Summary statistics from sFLT1 z-score and multi-ethnic maternal genotype association study across gestation for the Pregnancy Outcome Prediction study (POPs) participants. EAF = Effect Allele Frequency; CI = 95% Confidence Interval; GBR = White British Ancestry

Data & Code Availability

Description	Source / Repository	Persistent ID / URL
Preeclampsia PGS	PGS Catalog	https://www.pgscatalog.org/score/PGS003586/
Code	Github	https://github.com/jasamack/POPs-sFLT1