Supplementary Materials

TABLE S1: Goodness of fit test results

Alternative Hypothesis	p-value
GLM-NB > Poisson	0.000
ZIP > Poisson	0.000
ZINB > GLM-NB	0.660
GLM-NB > HNB	0.046

GLM-NB = generalized linear model with negative binomial distribution
Poisson = generalized linear model with Poisson distribution
ZIP = zero-inflated poisson model
ZINB = zero-inflated negative binomial model
HNB = negative binomial hurdle model

TABLE S2: Complete adjusted negative binomial model with interaction terms

	Coefficient	Standard Error	Z Value	p-value	CR (95% CI)
HDP	0.208	0.345	0.604	0.546	1.231 (0.627, 2.419)
T Alleles = 1	-0.027	0.268	-0.102	0.918	0.973 (0.575, 1.645)
T Alleles = 2	0.099	0.307	0.322	0.747	1.104 (0.605, 2.016)
AFB	0.008	0.017	0.498	0.619	1.008 (0.975, 1.043)
Age	-0.041	0.008	-5.232	0.000	0.96 (0.945, 0.975)
Family History	0.372	0.185	2.008	0.045	1.451 (1.009, 2.086)
BMI	-0.022	0.011	-1.918	0.055	0.979 (0.957, 1.000)
Parity	0.334	0.107	3.132	0.002	1.396 (1.133, 1.720)
Menarche	-0.102	0.058	-1.763	0.078	0.903 (0.806, 1.011)
HDP×T alleles = 1	-0.310	0.417	-0.743	0.457	0.734 (0.324, 1.661)
HDP×T alleles = 2	-0.740	0.482	-1.536	0.124	0.477 (0.185, 1.227)

T alleles are treated as factor variables. HDP compares HDP+ to HDP- women. The reference for T alleles is no T alleles (T alleles = 0). The reference for family history is no family history.

TABLE S3: Complete adjusted negative binomial models stratified by HDP status

| | **For HDP+ women only** | | | | |
	Coefficient	Standard Error	Z Value	p-value	CR (95% CI)
T Alleles = 1	-0.500	0.326	-1.536	0.124	0.606 (0.320, 1.148)
T Alleles = 2	-0.760	0.386	-1.967	0.049	0.468 (0.219, 0.997)
AFB	-0.045	0.028	-1.628	0.104	0.956 (0.905, 1.009)
Age	-0.023	0.013	-1.793	0.073	0.978 (0.954, 1.002)
Family History	0.071	0.303	0.235	0.814	1.074 (0.593, 1.946)
BMI	-0.027	0.018	-1.522	0.128	0.973 (0.940, 1.008)
Parity	-0.048	0.179	-0.267	0.790	0.953 (0.671, 1.354)
Menarche	-0.224	0.095	-2.360	0.018	0.799 (0.663, 0.963)

| | **For HDP- women only** | | | | |
	Coefficient	Standard Error	Z Value	p-value	CR (95% CI)
T Alleles = 1	0.013	0.260	0.052	0.959	1.014 (0.608, 1.689)
T Alleles = 2	0.080	0.302	0.264	0.792	1.083 (0.600, 1.955)
AFB	0.022	0.021	1.022	0.307	1.022 (0.980, 1.065)
Age	-0.043	0.010	-4.302	0.000	0.958 (0.940, 0.977)
Family History	0.441	0.229	1.924	0.054	1.554 (0.992, 2.435)
BMI	-0.020	0.014	-1.369	0.171	0.98 (0.953, 1.009)
Parity	0.398	0.131	3.028	0.002	1.489 (1.151, 1.927)
Menarche	-0.041	0.073	-0.556	0.578	0.96 (0.831, 1.109)

T alleles are treated as factor variables. The reference for T alleles is no T alleles. The reference for family history is no family history.

TABLE S4: Complete adjusted negative binomial models stratified by HDP status with alleles treated linearly for trend

	For HDP+ women only				
	Coefficient	Standard Error	Z Value	p-value	CR (95% CI)
T Alleles	-0.380	0.194	-1.960	0.050	0.684 (0.468, 1.000)
AFB	-0.046	0.028	-1.645	0.100	0.955 (0.904, 1.009)
Age	-0.022	0.013	-1.767	0.077	0.978 (0.954, 1.002)
Family History	0.103	0.300	0.342	0.733	1.108 (0.615, 1.996)
BMI	-0.028	0.018	-1.560	0.119	0.973 (0.939, 1.007)
Parity	-0.032	0.178	-0.182	0.856	0.968 (0.684, 1.371)
Menarche	-0.220	0.093	-2.375	0.018	0.802 (0.669, 0.962)

	For HDP- women only				
	Coefficient	Standard Error	Z Value	p-value	CR (95% CI)
T Alleles	0.041	0.151	0.270	0.787	1.042 (0.775, 1.400)
AFB	0.022	0.021	1.031	0.303	1.022 (0.981, 1.065)
Age	-0.043	0.010	-4.308	0.000	0.958 (0.940, 0.977)
Family History	0.436	0.228	1.911	0.056	1.547 (0.989, 2.419)
BMI	-0.020	0.014	-1.348	0.178	0.981 (0.953, 1.009)
Parity	0.402	0.131	3.071	0.002	1.495 (1.157, 1.933)
Menarche	-0.039	0.072	-0.550	0.582	0.961 (0.836, 1.106)

T alleles are treated linearly. The reference for T alleles is no T alleles. The reference for family history is no family history.