

**Verification of the chromosome region 9q21 association with pelvic organ prolapse using RegulomeDB annotations**

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**Supplementary Materials**

SupplementaryTable 1. Summary on primer sequences<sup>a</sup>, amplicons, and PCR cycling conditions for individual SNPs analyzed in the study

rs# of SNP	Primer sequences 5'-3', external forward/reverse, internal allele-specific forward/reverse	PCR <sup>b</sup>	Amplicon length (bp)
rs1455311	F aagtccatccatcgaggt  R ccggtaataatggatgtgg  F(t) ccatttctgaattacagagggt  R(c) caggaaccctaattaaaaatcaatag	95°C (15s)  62°C (15s)  72 °C (20s)  32 ×	303  150  200
rs1036819	F aaagccccatgtctgaccta  Rtttagtctctggagagaatgtc  F(c)cacttttgctgtctgtacataaac  R(a) ggttctgttttaattgaatgcctt	95°C (15s)  60°C (15s)  72°C (20s)  31 ×	404  288  165
rs4077632	F ggctagctccctggaaacaac  R tgcaagctgtcatcagcata  F(a) gagcaaggtaaccttgcgtga  R(g) cgataagaatttagagaatcgc	95 °C (15s)  60.6°C(14s)  72°C(15s)  31 ×	560  369  232
rs2807303	F cgtcccactccaaactttt  R gtgggttcgcagagttga	95 °C (15s)  60 °C (20s)	344

	F(c) ctttaccacatctcatttcatttc	72 °C (20s)	153
	R(t)gacaagaaaacaggaaggaagaa	31×	241
rs2777781	F tgacctaaagggtataaatgaggaa	94 °C (15s)	343
	R tccctttcaccttgtcagaa	62.3 °C (20s)	
	F(a) ggcatttgcacaaaggctccta	72 °C (22s)	227
	R(t) ctccatttgttatcttgtcctgtta	32 ×	159
rs11139451	F aaggaccattctaaagtggtgac	95 °C (15s)	341
	R actgtgcataaggggacatgagata	61 °C (20s)	
	F(t) agggaaagaagctgtct	72 °C (20s)	151
	R(c) caagagttctgtgtttctg	15 ×	226
		95 °C (15s)	
		50.8 °C (20s)	
		72 °C (15s)	
		16 ×	
rs12237222	Fggatttaaccaggggccgtt	95 °C(15s)	370
	Rgcatccaagctccgcttcct	66°C(15s)	
	F(g)cttttgtgggtttcccactgg	72 °C (15s)	149
	R(t)aaggacgaggctgctcca	30 ×	260
rs12551710	F aggactccagcccccttagact	95 °C(15s)	334
	R cttggagttacttgtgggaaa	63°C(15s)	
	F(t) tccagtcctccactcacat	72 °C (30s)	150
	R(c)cacagaacctgctgtgaaagg	31 ×	225
rs430794	F ggtagtaaggcctgcactctgc	95 °C (15s)	332
	R caactgagtggggagcattt	65.3°C (14s)	
	F(c) catcagcttcagtgccacc	72 °C (14s)	216

	R(a) gcagaacatcaagcaagttacagt	29 ×	159
rs8027714	F ccagcatttctctttcttagc	95 °C (15s)	277
	R acacatatggcaaattgcag	61.2 °C (15s)	
	F(g) tcaaggaatcctaatttttatttag	72 °C (25s)	191
	R(a) ccagaacttgtccctatactattaat	32 ×	140
rs1810636	F ggtgacagatcagcaaccac	95 °C (15s)	557
	R cttcaacccaggaggaagag	59 °C (15s)	
	F(g) cctctaaacaatttttaagcg	72 °C (25s)	236
	R(t) gacacactcaccaaggcacata	30 ×	365
rs2236479	F gggctcttagagggAACAGTG	95 °C (15s)	379
	R cctctgacctccctgtcg	59.6 °C (20s)	
	F(a) cgtgtccttcagaacgaa	72 °C (30s)	168
	R(g) ctgtcctgcatgtcatcc	31 ×	246

<sup>a</sup>The Primer3 algorithm was used to design external primer sequences.

<sup>b</sup>PCR conditions are provided as temperature (duration) of denaturation, annealing and extension phase, respectively, followed by the number of cycles for a given SNP. Each PCR reaction was finished by a final extension phase lasting 5 min.

Supplementary Table 2. Characteristics of the POP and control groups involved in the study

Characteristics	Control	POP	<i>P</i> <sup>e</sup>
	N (%)	N (%)	
	Mean ± SD	Mean ± SD	
Total number	292	210	
POP-Q stage			
Without POP	292 (100)	0 (0.00)	
Stage I	0 (0.00)	0 (0.00)	
Stage II	0 (0.00)	0 (0.00)	
Stage III	0 (0.00)	194 (92.38)	
Stage IV	0 (0.00)	16 (7.62)	
Age <sup>a</sup>	57.25 ± 12.70	57.65 ± 10.80	0.68
BMI (kg/m <sup>2</sup> ) <sup>b</sup>	27.46 ± 6.56	29.17 ± 5.85	<b>5.6 × 10<sup>-4</sup></b>
Vaginal parity <sup>c</sup>			
0	57 (20.73)	4 (1.96)	<b>0.014<sup>f</sup></b>
1	112 (40.73)	79 (38.73)	
2	100 (36.36)	96 (47.06)	
≥3	6 (2.18)	25 (12.25)	
Perineal trauma in childbirth (episiotomy and spontaneous perineal laceration) <sup>d</sup>	93 (32.75)	107 (52.45)	<b>1.7 × 10<sup>-5</sup></b>

Data are missing for: <sup>a</sup>8 controls, 6 POP patients; <sup>b</sup>11 controls, 12 POP patients; <sup>c</sup>17 controls, 6 POP patients; <sup>d</sup>91 controls, 51 POP patients.

<sup>e</sup>Significant results are in bold.

<sup>f</sup>We compared two groups: 0-1 vaginal birth vs. ≥ 2 vaginal birth.

Supplementary Table 3. The distribution of genotypes among cases and controls

SNPs and genotypes	Control		POP		Crude P-value, OR, (95% CI)	Adjusted P-value <sup>a</sup> , OR, (95% CI)
	Number (%)	HWP	Number (%)	HWP		
rs1455311	n=287		n=210			
	T/T	187 (65.2)		146 (69.5)	0.24 (add)	0.10 (add)
	T/C	91 (31.7)	0.70	60 (28.6)	0.61	0.82
rs1036819	n=290		n=211			
	A/A	232 (80.0)		156 (74.3)	0.13 (dom)	0.11 (dom)
	A/C	54 (18.6)	0.55	50 (23.8)	1.00	1.38
rs4077632	n=291		n=209			
	A/A	128 (44.0)		79 (37.8)	0.094 (add)	0.22 (add)
	A/G	134 (46.0)	0.51	101 (48.3)	0.77	1.26

	G/G	29 (10.0)		29 (13.9)		(0.96 – 1.64)	(0.89 – 1.62)	
rs2807303		n=285		n=210				
	C/C	102 (35.8)		80 (38.1)		0.19 (rec)	0.38 (rec)	
	C/T	142 (49.8)	0.53	108 (51.4)	0.13	0.79	0.76	
	T/T	41 (14.4)		22 (10.5)		(0.40 – 1.21)	(0.41 – 1.40)	
rs2777781		n=292		n=210				
	A/A	154 (52.7)		111 (52.9)		0.25 (rec)	0.56 (rec)	
	A/T	122 (41.8)	0.23	82 (39.0)	0.73	1.52	1.25	
	T/T	16 (5.5)		17 (8.1)		(0.75 – 3.08)	(0.59 – 2.67)	
rs11139451		n=291		n=210				
	T/T	185 (63.6)		131 (62.4)		0.78 (dom)	0.74 (dom)	
	T/C	88 (30.2)	0.11	70 (33.3)	1.00	1.05	1.07	
	C/C	18 (6.2)		9 (4.3)		(0.73 – 1.52)	(0.71 – 1.62)	
rs12551710		n=291		n=210				
	C/C	233 (80.1)		171 (81.4)		0.58 (add)	0.70 (add)	
	C/T	56 (19.2)	0.75	39 (18.6)	0.23	0.88	0.91	

	T/T	2 (0.7)		0 (0.0)		(0.57 – 1.37)	(0.56 – 1.47)
rs430794		n=289		n=210			
	C/C	148 (51.2)		122 (58.1)		0.13 (dom)	0.11 (dom)
	C/A	113 (39.1)	0.39	72 (34.3)	0.27	0.76	0.72
	A/A	28 (9.7)		16 (7.6)		(0.53 – 1.08)	(0.49 – 1.08)
rs8027714		n=290		n=210			
	G/G	278 (95.9)		197 (93.8)		0.30 (dom)	0.27 (dom)
	G/A	12 (4.1)	1.00	13 (6.2)	1.00	1.53	1.66
	A/A	0 (0.0)		0 (0.0)		(0.68 – 3.42)	(0.67 – 4.09)
rs1810636		n=290		n=210			
	G/G	119 (41.0)		101 (48.1)		0.12 (dom)	0.25 (dom)
	G/T	144 (49.7)	0.09	91 (43.3)	0.75	0.75	0.79
	T/T	27 (9.3)		18 (8.6)		(0.53 – 1.07)	(0.53 – 1.18)
rs2236479		n=287		n=207			
	G/G	131 (45.6)		81 (39.1)		0.14 (add)	0.097 (add)
	A/G	120 (41.8)	0.29	94 (45.4)	0.66	1.22	1.28

A/A	36 (12.5)	32 (15.5)	(0.94 – 1.57)	(0.96 – 1.71)
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HWP, Hardy–Weinberg probability; OR, odds ratio; CI, confidence interval; rec, recessive model; dom, dominant model; add, additive model.

<sup>a</sup>Adjusted by age, body mass index (BMI), perineal trauma in childbirth and vaginal parity. In the multivariate analysis, the number of cases and controls may be less than in the crude analysis since some subjects had insufficient data on covariates.

Supplementary Table 4. Linkage disequilibrium analysis of six SNPs in the region 9q21

D'	rs11139451	rs12237222	rs12551710	rs2777781	rs2807303
<i>P</i> – value					
rs4077632	0.149	0.034	0.323	0.009	0.022
	0.073	0.367	$4.17 \times 10^{-6}$	0.895	0.515
rs11139451		0.257	0.129	0.236	0.0007
		$1.45 \times 10^{-6}$	0.009	0.019	0.988
rs12237222			0.266	0.052	0.098
			0.001	0.252	0.035
rs12551710				0.043	0.373
				0.456	0.002
rs2777781					0.177
					0.008

D' and *P* – value for linkage are given for every pair of SNPs.

Supplementary Table 5. Fst pairwise values between populations

Pops	CHD	GIH	JPT	TSI	YRI	RUS	MEX	LWK
CEU	0.1108	0.0324	0.0753	0	0.1574	0	0.0236	0.1654
CHD		0.0492	0.0148	0.1302	0.1951	0.1104	0.0712	0.1822
GIH			0.029	0.0435	0.1548	0.0297	0.0159	0.1341
JPT				0.079	0.1749	0.0689	0.0499	0.1562
TSI					0.1681	0.0017	0.0281	0.1638
YRI						0.1482	0.1148	0.0093
RUS							0.0256	0.1575
MEX								0.101