

## Supplementary Note

### Detailed Description of the Case and Control Sample Sets

Subjects were drawn from 11 studies, comprising 6,054 endometrial cancer cases and 14,125 controls. A summary of the studies included in stage1 and stage 2 is shown in Supplementary Table 2, with additional details provided below. All studies were predominantly of women of European ancestry, with the exception of SECS, which included women of Asian ancestry from China. All studies have the relevant IRB approval in each country in accordance with the principles embodied in the Declaration of Helsinki, and informed consent was obtained from all participants.

#### **Australian Studies, incorporating ANECS/ARCBS and NECS**

The Australian National Endometrial Cancer Study (ANECS) is an Australian population-based case-control-family study of cancer of the uterine corpus (1). Women aged 18-79, newly diagnosed with histologically confirmed primary cancer of the endometrium between July 2005 and December 2007 were identified through major hospitals nationally, and also from state-based cancer registries. Excluding women who could not be contacted (mostly due to death, illness or failure to contact), case participation rate was 63%. Cases who reported a family history of cancer were also asked to invite their relatives (with and without cancer) to participate in the family component of the study. Relatives were not genotyped for this SNP study. Female controls, with no personal history of endometrial cancer or hysterectomy were recruited using two sources: A population-based control group comprised women randomly selected using the Australian Electoral Roll (voting is compulsory in Australia) and matched to the age and geographic distribution of the cases (53% participation among those contacted); and a control group of female blood donors recruited with the aid of the Australian Red Cross Blood Service in Queensland (>99% participation rate) (2). Participants completed a detailed questionnaire providing clinical and epidemiological information, including ethnicity of all four grandparents. Information on tumor pathology characteristics was abstracted in standardized format from clinical pathology reports for all patients.

The Newcastle Endometrial Cancer Study (NECS) includes histologically confirmed endometrial cancer cases consecutively recruited from 1992 up to 2005 at the Hunter Centre for Gynaecological Cancer, John Hunter Hospital, Newcastle, New South Wales, Australia (3). The final analysis included 194 endometrial cancer patients. Data on reproductive and environmental risk factors including ethnicity, was collected using self reported questionnaires. Information regarding recurrence, stage, grade and histology of endometrial cancer was collected from medical records. Patients presenting at this hospital-based site were captured by ANECS recruitment from 2005 onwards.

#### **SEARCH**

The Studies of Epidemiology and Risk factors in Cancer Heredity (SEARCH) is an ongoing population-based study with cases ascertained through the Eastern Cancer Registration and Information Centre (<http://www.ecric.org.uk>). All women diagnosed with endometrial cancer between the ages of 18-69 years (average age diagnosis 58 years) from 31 July 2001 to 1<sup>st</sup> September 2007 were eligible for inclusion. Approximately 54% of eligible patients have enrolled in the study. Women taking part in the study were asked to provide a 20ml blood sample for DNA analysis, and to complete a comprehensive epidemiological questionnaire. Controls were also drawn from SEARCH (<http://www.srl.cam.ac.uk/search/Homepage.htm>), but had no prior history of cancer at the time of recruitment. They were female, also between the ages of 18-69 at the time of recruitment and matched to cases in geographical profile. Approximately 35% of eligible controls enrolled in the study. All participants reported Caucasian ethnicity. Information on tumor pathology characteristics was provided by the Eastern Cancer Registration and Information Centre and was derived from clinical pathology reports for all patients.

### **WTCCC**

Controls utilized for stage 1 analysis were genotyped as part of the Wellcome Trust Case Control Consortium (WTCCC2) (4). These controls are drawn from two sources: 2,922 controls from the 1958 Birth Cohort (1958BC), a population-based study in the United Kingdom of individuals born in 1 week in 1958 (5); and 2,737 controls identified through the UK National Blood Service (NBS) (4). The analyses presented here are based on 2,694 1958BC and 2,496 NBS controls for which valid genotype data were available at the time of analysis.

### **BECS**

The Bavarian Endometrial Cancer Cases and Controls Study (BECS) is a single-center case-control study, conducted between 2002 and 2008, with the aim of investigating genetic and epidemiological risk factors for endometrial cancer. Cases were either incident cases referred to the University Hospital Erlangen by surrounding practitioners (66% of the case sample set), or prevalent cases that were outpatients in follow-up care approached within 6.2 ( $\pm 4.6$  SD years after treatment for primary endometrial cancer in the same hospital (34% of the case sample set). Controls were age-matched individuals invited by newspaper advertisement to take part in this case-control study. Epidemiological information for cases and controls was collected by a structured questionnaire, which was completed during an interview and clinical data for the cases was obtained from clinical health records.

### **LES**

The Leuven Endometrial Study (LES) is a hospital based case-control study. Eligible cases, identified by active surveillance of electronic patient files at the Leuven University Hospital, were white women aged 27-80 years diagnosed with endometrial cancer. Clinical data for endometrial cancer patients were recorded during interview at the time of diagnosis, and from pathology reports. All medical records were reviewed by trained abstractors and pathology reports compatible with primary, invasive, epithelial endometrial adenocarcinoma of all stages (I –IV) and all grades were consulted. A control group of healthy female blood donors was recruited with the aid of the Red Cross Blood Service in the University Hospital. Participants completed a detailed questionnaire providing epidemiological information, including self-reported Belgian (Flemish) ethnicity for 3 generations. Participation rates exceeded 95% for both cases and controls.

### **MoMaTEC**

Molecular Markers in Treatment of Endometrial Cancer (MoMaTEC) cases were recruited from an unselected patient population primarily treated for endometrial carcinoma at Haukeland University Hospital, Bergen during 2001-2009. This is the referral hospital for Hordaland county; the area is demographically well defined, with about 450,000 inhabitants, representing approximately 10% of the Norwegian population and with a similar incidence rate and prognosis as the total Norwegian population of endometrial cancers (6-8). Clinical Information for cases regarding age, FIGO stage, histologic subtype, grade and prognosis was extracted from medical records. Controls were healthy female Caucasian blood donors with no known cancer disease, and with known age at sampling. DNA was extracted from peripheral blood samples for cases and controls.

### **NSECG**

National Study of the Genetics of Endometrial Cancer (NSECG) cases were identified from collaborating clinicians throughout the UK from 2008 to present, taking care not to recruit from centres involved in SEARCH. Inclusion criteria were adenocarcinomas of the uterus presenting at 70 years of age or younger. Almost all cases were incident and sampled within 6 months of diagnosis. Peripheral blood was collected from each participant and DNA extracted using standard methods. Tumour histology was confirmed from routine hospital reports and further details of histopathology and other tumor pathology characteristic was abstracted from these clinical pathology reports. Cases were

genotyped for stage 2 SNPs using sequenom iPLEX methodology, as indicated in Supplementary Table 2. Controls (45% males, 55% females) were drawn from the UK1/CORGI colorectal cancer sample set (9), and were spouses or partners of colorectal cancer cases unaffected by cancer and without a personal family history (to 2<sup>nd</sup> degree relative level) of colorectal neoplasia. All cases and controls were of white UK ethnic origin. Control genotype data for stage 2 SNPs were extracted from existing Illumina 550K genome-wide scan data (9), or genotyped using the Kaspar method if the SNP was not present on the Illumina 550K platform.

### **PECS**

The Polish Endometrial Cancer Study (PECS) is a large, population-based, case–control study (10) conducted among women residing in two Polish cities, Warsaw and Lodz, during 2001–2003. Eligible cases were women aged 20–74 newly diagnosed with histologically or cytologically confirmed invasive endometrial cancer, identified through a rapid identification system at participating hospitals and also through the local cancer registries. Eligible controls with no history of endometrial cancer or hysterectomy were identified through the Polish Electronic System (PESEL), a database of all Polish residents, during case accrual. In total, 551 (79.3%) of 695 eligible cases and 1,925 (67.7%) of 2,843 eligible controls agreed to complete an in-person interview, and 88% of participating cases and 94% of participating controls donated blood. Controls with available blood DNA were randomly selected within age and study site strata for genetic studies. All cases and controls were considered to be of Caucasian ethnicity. Medical records of case participants were abstracted for diagnostic parameters. Case and control genotype data for stage 2 SNPs were extracted from existing Illumina 660W-Quad genome-wide scan data.

### **SASBAC**

Details of the population selection process for the Singapore and Sweden Breast/Endometrial Cancer Study (SASBAC) have been published previously (11). Briefly, this population based case-control study was conducted among Swedish women aged 50–74 years, who were residing in Sweden between January 1<sup>st</sup> 1994 and December 31<sup>st</sup> 1995. Endometrial cancer cases were identified through the nationwide cancer registries in Sweden. Controls, frequency-matched for age, were randomly selected from the Swedish Registry of Total Population. The study was restricted to postmenopausal women with an intact uterus and no previous diagnosis of endometrial cancer. All participants provided detailed questionnaire information. For endometrial cancer, histological specimens were reviewed and re-classified by the study pathologist. All participants reported Caucasian ethnicity. Genomic analyses were conducted by the Singapore node of the study.

### **SECGS**

The Shanghai Endometrial Cancer Genetic Study (SECGS) includes 832 endometrial cancer cases who were recruited to the Shanghai Endometrial Cancer Study (SECS) and 2,049 controls who were recruited to the Shanghai Breast Cancer Study (SBCS). As described in detail elsewhere, both SECS and SBCS are two population-based case-control studies that were conducted in parallel in Shanghai during same period using an identical study protocol (12, 13). Briefly, 1,199 women aged between 30 and 69 with newly diagnosed with EC 1997 and 2003 were identified through the population-based tumor registry and recruited to the SECS (response rate 83%). The SBCS controls were randomly selected from the general population using the Shanghai Resident Registry with response rate of 74%. Women with prior hysterectomies were not eligible for inclusion in this study. Participants completed a detailed in-person interview at the time of enrollment and provided a blood or buccal cell sample. Case and control genotype data for stage 2 SNPs, or for correlated SNPs with  $R^2 > 0.8$ , were extracted from existing Affymetrix 6.0 genome-wide scan data.

1. Spurdle A, Webb P. Re: Excess of early onset multiple myeloma in endometrial cancer probands and their relatives suggests common susceptibility. *Gynecol Oncol* 2008; 109:153; author reply 4.
2. Marsh A, Healey S, Lewis A, et al. Mutation analysis of five candidate genes in familial breast cancer. *Breast Cancer Res Treat* 2007; 105:377-89.
3. Ashton KA, Proietto A, Otton G, et al. The influence of the Cyclin D1 870 G>A polymorphism as an endometrial cancer risk factor. *BMC Cancer* 2008; 8:272.
4. Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature* 2007; 447:661-78.
5. Power C, Elliott J. Cohort profile: 1958 British birth cohort (National Child Development Study). *Int J Epidemiol* 2006; 35:34-41.
6. Wik E, Trovik J, Iversen OE, et al. Deoxyribonucleic acid ploidy in endometrial carcinoma: a reproducible and valid prognostic marker in a routine diagnostic setting. *Am J Obstet Gynecol* 2009; 201:603 e1-7.
7. Salvesen HB, Iversen OE, Akslen LA. Prognostic significance of angiogenesis and Ki-67, p53, and p21 expression: a population-based endometrial carcinoma study. *J Clin Oncol* 1999; 17:1382-90.
8. Salvesen HB, Carter SL, Mannelqvist M, et al. Integrated genomic profiling of endometrial carcinoma associates aggressive tumors with indicators of PI3 kinase activation. *Proc Natl Acad Sci U S A* 2009; 106:4834-9.
9. Houlston RS, Cheadle J, Dobbins SE, et al. Meta-analysis of three genome-wide association studies identifies susceptibility loci for colorectal cancer at 1q41, 3q26.2, 12q13.13 and 20q13.33. *Nat Genet* 2010; 42:973-7.
10. Brinton LA, Sakoda LC, Lissowska J, et al. Reproductive risk factors for endometrial cancer among Polish women. *Br J Cancer* 2007; 96:1450-6.
11. Weiderpass E, Adami HO, Baron JA, et al. Risk of endometrial cancer following estrogen replacement with and without progestins. *J Natl Cancer Inst* 1999; 91:1131-7.
12. Xu WH, Long JR, Zheng W, et al. Association of thymidylate synthase gene with endometrial cancer risk in a Chinese population. *Cancer Epidemiol Biomarkers Prev* 2009; 18:579-84.
13. Zheng W, Long J, Gao YT, et al. Genome-wide association study identifies a new breast cancer susceptibility locus at 6q25.1. *Nat Genet* 2009; 41:324-8.

## **Study Collaborators**

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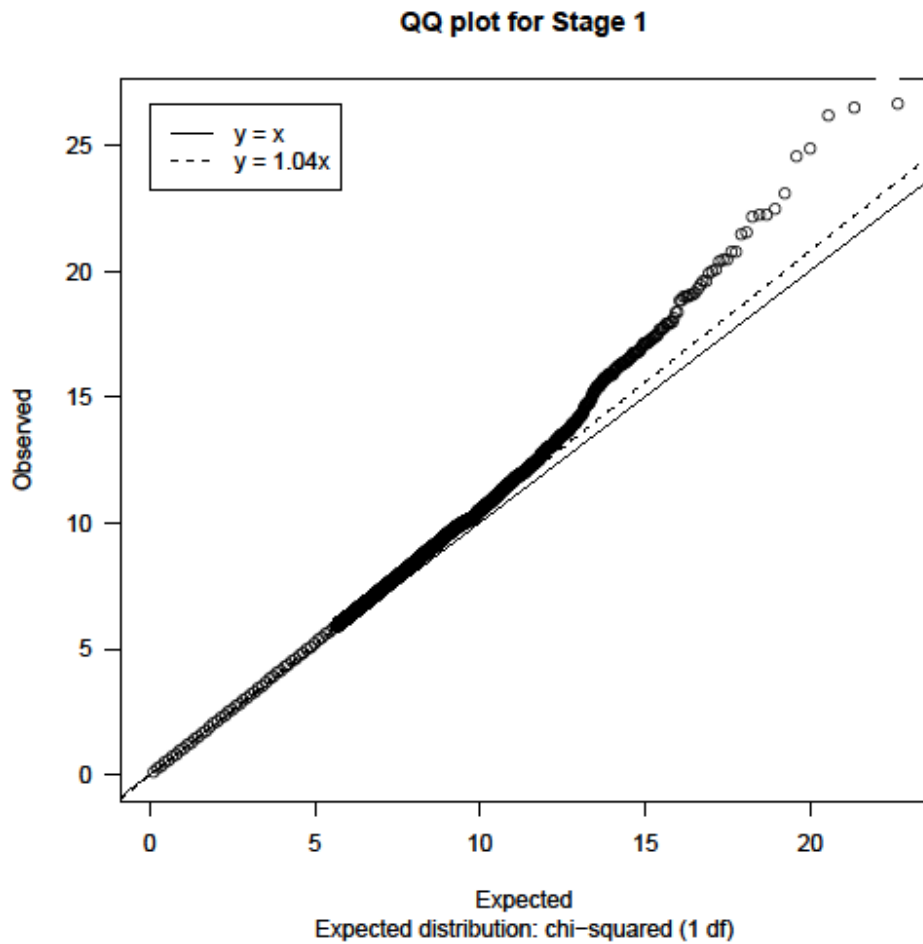
**Supplementary Figure 1: Quantile-quantile plot of the ranked trend test statistics.**

Y-value: observed test statistic (adjusted for the first three principal components – see methods).

X-value: expected statistic under the global null hypothesis of no association.

Markers denote the test statistics for each SNP. Line denotes the expectation under no association.

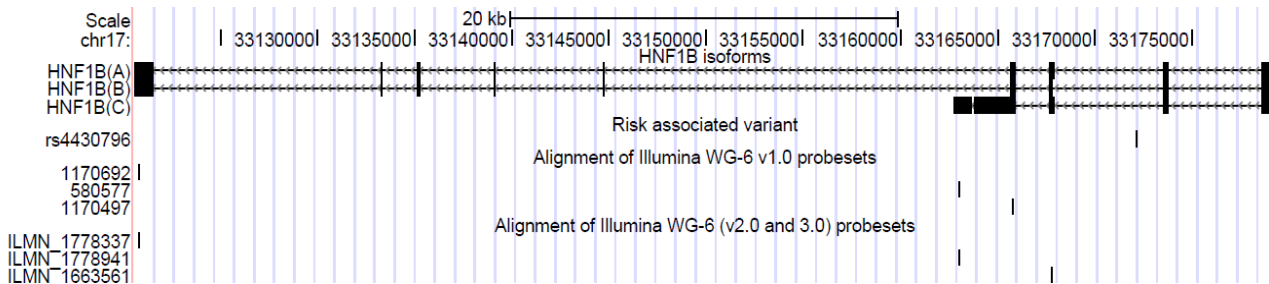
SNPs which showed poor clustering or poor concordance between stages 1 and 2 are excluded from this plot (see methods).



## Supplementary Figure 2: Association of rs4430796 genotype with *HNF1B* gene expression.

### A. Location of Illumina expression probe sequences in relation to *HNF1B* isoforms.

Screenshot of UCSC Genome Browser showing *HNF1B* isoform A (NM\_000458), isoform B (NM\_001165923) and isoform C (NM\_006481), the location of rs4430796, and the location of the Illumina expression probe sequences for *HNF1B* on 3 versions of the Human WG-6 array.



### B. Association of rs4430796 genotype with *HNF1B* expression assessed by Spearman rank analysis across three studies\*

Reference	Tissue source	Population group	Cohort size	Platform	Probe	rho	P-value
Stranger et al <sup>1</sup>	LCLs from peripheral blood	CEU	60	Illumina WG-6 v1	1170692	0.166	0.20
					580577	0.260	<b>0.04</b>
					1170497	0.179	0.18
Dimas et al <sup>2</sup>	LCLs from umbilical cord blood	Western European	75	Illumina WG-6 v3	ILMN_1778337	-0.247	<b>0.03<sup>a</sup></b>
					ILMN_1778941	ND	ND
					ILMN_1663561	-0.291	0.11
Dermitzakis et al <sup>3</sup>	LCLs from peripheral blood	CEU	109	Illumina WG-6 v2	ILMN_1778337	0.218	<b>0.02</b>
					ILMN_1778941	ND	ND
					ILMN_1663561	0.051	0.60
		YRI	108	Illumina WG-6 v2	ILMN_1778337	0.073	0.46
					ILMN_1778941	ND	ND
					ILMN_1663561	0.036	0.71

\* There was known overlap of individuals between the studies of Stranger et al, and Dermitzakis et al: 56/60 CEU individuals assayed by Stranger et al were included in the analysis of 109 CEU individuals by Dermitzakis et al.

<sup>1</sup> Stranger BE, et al. Relative impact of nucleotide and copy number variation on gene expression phenotypes. *Science*. 2007;315:848–853.

<sup>2</sup> Dimas AS, et al. Common regulatory variation impacts gene expression in a cell type-dependent manner. *Science*. 2009;325:1246–1250.

<sup>3</sup> Dermitzakis, Montgomery, personal communication.

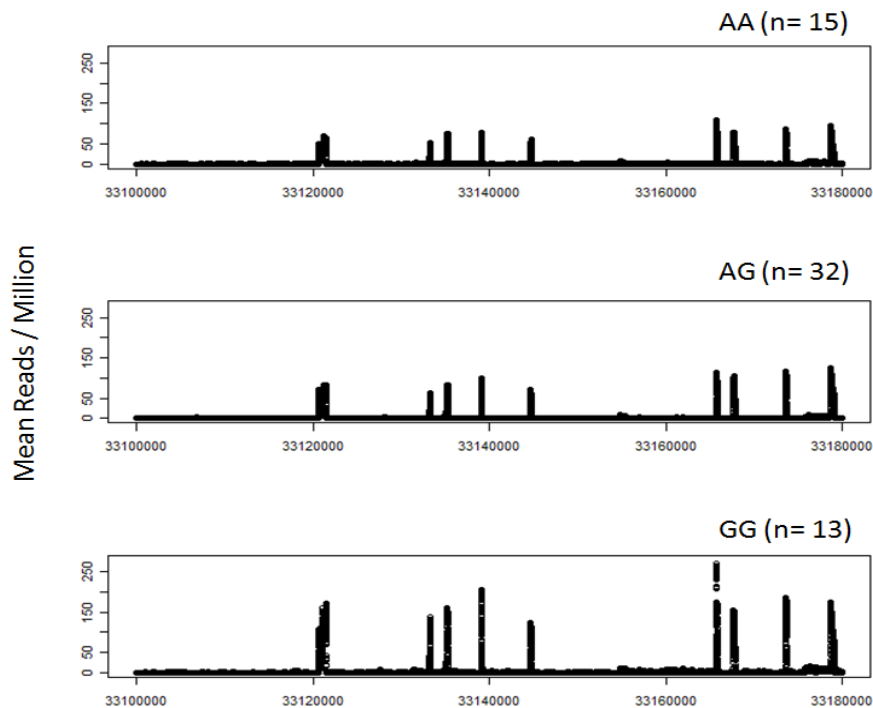
<sup>a</sup> This eQTL was not present in Fibroblasts or T-cells interrogated in the same study likely because the gene was lowly or not-expressed, with mean expression at background detection level in T-cells (6.55) and fibroblasts (6.70), compared to LCLs (8.24).

Abbreviations: LCL, lymphoblastoid cell lines; CEU, Utah residents with Northern and Western European ancestry from the Centre de'Etude du Polymorphisme Humain (CEPH) collection; YRI, Yoruban in Ibadan, Nigeria; ND, no data.

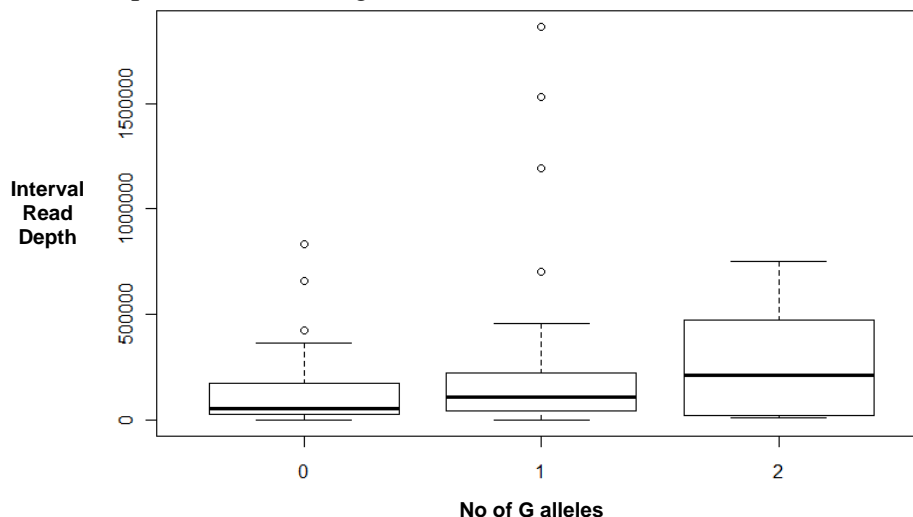


### C. Association of rs4430796 genotype with *HNF1B* expression as assessed by RNA sequencing.

Expression of *HNF1B* was collected using RNA-Sequencing data from 60 CEU HapMap individuals, Caucasians of northern and western European ancestry living in Utah USA<sup>1</sup>. (Note, a large subset of this sample of 60 individuals was assayed previously using Illumina expression array platforms: 43 individuals overlapped with the study by Stranger *et al*<sup>2</sup>, and 55 individuals with the study by Dermitzakis *et al*<sup>3</sup>.) None of the three *HNF1B* isoforms or well-quantified exons (annotated using Gencode v3b) were significantly associated with rs4430796, however all 8 exon quantification of *HNF1B* expression by rs4430796 using Spearman rank tests showed some evidence of association (mean p-value 0.22, sd 0.11). Reduced power and increased difficulty in dissecting the relative contributions of individual transcripts may have prevented detection of a significant association. To further investigate possible associations, the mean reads/million across the interval containing *HNF1B* were stratified by genotypic class for the 60 individuals. There was a non-significant increase in read abundance in the interval of *HNF1B* conditioned on the G-allele ( $P=0.3$ ).



Suggestion of a trend was also seen by analysis of a plot of interval read depth by genotype, with an increase in read depth with increasing number of G alleles.



1. Montgomery, S.B. et al. Transcriptome genetics using second generation sequencing in a Caucasian population. *Nature* 464, 773-7 (2010).
2. Stranger BE, et al. Relative impact of nucleotide and copy number variation on gene expression phenotypes. *Science*. 2007;315:848–853.
3. Dermitzakis, Montgomery, personal communication.

Supplementary Table 1: Stage 1, stage 2 and combined results for 47 SNPs selected for replication.													
SNP	Alleles	Chromosome	Position	Stage 1				Stage 2				Combined	
				cases/controls	MAF*	P (1df)	OR (95% CI)	cases/controls	MAF*	P (1df)	OR (95% CI)	P (1df)	OR (95% CI)
rs673604	A/G	1	35460402	1265/5188	0.08	6.11E-07	1.45 (1.25-1.67)	3741/6151	0.09	4.10E-02	1.11 (1.00-1.23)	5.88E-06	1.21 (1.12-1.32)
rs12117146	G/A	1	227871836	1264/5186	0.13	1.11E-05	1.32 (1.17-1.49)	3743/6065	0.13	6.98E-01	1.02 (0.93-1.11)	4.77E-03	1.11 (1.03-1.19)
rs1453194	A/C	2	19736284	1265/5187	0.12	2.26E-05	0.72 (0.61-0.84)	3804/5864	0.12	7.85E-01	0.99 (0.90-1.08)	1.93E-02	0.91 (0.84-0.99)
rs990270	C/A	2	40435853	1265/5189	0.39	7.13E-07	1.25 (1.15-1.37)	3816/6217	0.43	2.31E-01	1.04 (0.98-1.10)	1.80E-04	1.10 (1.05-1.15)
rs6544324	G/A	2	40436562	1265/5185	0.38	3.24E-05	1.21 (1.11-1.32)	3798/5897	0.41	3.12E-01	1.03 (0.97-1.09)	1.90E-03	1.08 (1.03-1.14)
rs1477004	G/A	2	40465576	1265/5187	0.31	4.63E-05	1.21 (1.10-1.33)	3806/6255	0.34	7.05E-01	1.01 (0.95-1.08)	1.11E-02	1.07 (1.02-1.12)
rs1124787	A/C	2	46168439	1264/5185	0.40	1.63E-04	0.84 (0.77-0.92)	3815/6220	0.38	1.40E-02	1.08 (1.02-1.14)	9.57E-01	1.00 (0.95-1.05)
rs10167555	C/A	2	46174610	1263/5177	0.20	5.39E-05	0.78 (0.70-0.88)	3699/5900	0.18	1.50E-02	1.10 (1.02-1.18)	8.93E-01	1.00 (0.93-1.06)
rs4954564	A/G	2	136611978	1265/5190	0.26	5.79E-03	1.15 (1.04-1.26)	3778/6159	0.30	6.56E-01	1.02 (0.95-1.08)	5.58E-02	1.05 (1.00-1.11)
rs4663132	A/G	2	234970071	1264/5189	0.45	1.25E-04	1.19 (1.09-1.30)	3727/6121	0.55	6.22E-01	1.02 (0.96-1.08)	1.12E-02	1.06 (1.01-1.12)
rs12489038	A/C	3	12986140	1265/5189	0.17	5.52E-04	1.22 (1.09-1.36)	3799/6205	0.19	2.21E-01	1.05 (0.97-1.13)	3.59E-03	1.10 (1.03-1.16)
rs720625	A/G	3	45785098	1264/5188	0.36	2.54E-05	1.21 (1.11-1.33)	3757/6196	0.38	9.31E-01	1.00 (0.94-1.06)	1.63E-02	1.06 (1.01-1.12)
rs798741	G/A	4	1682211	1265/5188	0.19	9.68E-06	1.27 (1.14-1.41)	3755/6192	0.21	6.56E-01	1.02 (0.95-1.09)	4.66E-03	1.09 (1.03-1.16)
rs1320071	A/G	4	7979091	1265/5179	0.39	1.56E-04	0.84 (0.76-0.92)	3749/6161	0.38	4.42E-01	1.02 (0.96-1.09)	1.53E-01	0.96 (0.92-1.01)
rs10008860	G/A	4	8020494	1265/5190	0.43	1.25E-05	1.22 (1.11-1.33)	3812/6216	0.44	6.65E-01	1.01 (0.96-1.07)	5.47E-03	1.07 (1.02-1.12)
rs6537310	G/A	4	145856182	1265/5187	0.44	7.67E-06	0.81 (0.74-0.89)	3772/6129	0.42	2.76E-01	0.97 (0.91-1.03)	8.05E-04	0.92 (0.88-0.97)
rs1425542	A/G	5	113902191	1264/5188	0.21	4.29E-05	1.24 (1.12-1.38)	3119/4622	0.21	2.95E-01	0.96 (0.89-1.04)	9.34E-02	1.06 (0.99-1.12)
rs2548975	G/A	5	133438999	1264/5189	0.19	2.07E-05	1.26 (1.13-1.40)	3810/6211	0.20	9.81E-01	1.00 (0.93-1.08)	1.80E-02	1.07 (1.01-1.14)
rs986359	A/C	5	136675003	1264/5183	0.36	4.59E-05	1.20 (1.10-1.32)	3811/6211	0.37	9.38E-01	1.00 (0.94-1.06)	2.46E-02	1.06 (1.01-1.11)
rs10515787	G/A	5	158407789	1265/5187	0.01	9.58E-04	1.75 (1.25-2.44)	3774/6218	0.02	4.15E-01	1.10 (0.87-1.39)	1.04E-02	1.28 (1.06-1.55)
rs2493046	G/A	6	488134	1264/5184	0.11	6.78E-05	1.31 (1.15-1.49)	3816/6223	0.12	4.38E-01	1.04 (0.95-1.13)	4.67E-03	1.11 (1.03-1.20)
rs4149366	G/A	6	2960488	1265/5189	0.07	4.29E-05	0.66 (0.55-0.81)	2312/3779	0.07	1.20E-01	1.12 (0.97-1.30)	2.28E-01	0.93 (0.83-1.05)
rs559901	G/A	6	153899629	1264/5187	0.28	6.97E-05	1.21 (1.10-1.33)	3767/5902	0.30	5.28E-01	1.02 (0.96-1.09)	6.56E-03	1.08 (1.02-1.14)
rs2049449	A/C	7	14665378	1265/5188	0.14	6.63E-05	1.28 (1.13-1.44)	3810/6225	0.15	2.06E-01	1.05 (0.97-1.14)	1.09E-03	1.12 (1.04-1.19)
rs9969635	A/C	8	10369046	1265/5188	0.10	3.06E-05	1.33 (1.17-1.53)	3288/5295	0.11	3.83E-01	1.05 (0.95-1.15)	1.59E-03	1.14 (1.05-1.23)
rs11784168	A/G	8	28083277	1264/5187	0.13	4.38E-04	1.25 (1.10-1.41)	3811/6218	0.15	6.30E-02	0.92 (0.85-1.00)	6.66E-01	1.02 (0.95-1.09)
rs17589981	A/G	9	9109229	1265/5184	0.32	1.32E-04	1.20 (1.09-1.31)	3805/6187	0.33	5.65E-01	0.98 (0.92-1.04)	1.04E-01	1.04 (0.99-1.10)
rs4295736	G/A	9	81072159	1263/5188	0.06	6.27E-05	1.42 (1.19-1.68)	3816/6189	0.07	7.31E-01	0.98 (0.87-1.10)	4.61E-02	1.10 (1.00-1.22)
rs11138152	G/A	9	81156461	1265/5188	0.08	7.38E-06	1.40 (1.21-1.62)	3762/6204	0.09	1.39E-01	0.93 (0.84-1.03)	1.84E-01	1.06 (0.97-1.15)
rs1932658	A/G	9	86005570	1258/5167	0.26	8.54E-05	1.22 (1.10-1.34)	3775/6089	0.28	7.45E-01	0.99 (0.93-1.06)	6.04E-02	1.05 (1.00-1.11)
rs7358426	A/G	11	22079689	1265/5189	0.31	4.09E-05	0.81 (0.74-0.90)	3766/6197	0.31	1.35E-01	0.95 (0.89-1.02)	5.65E-04	0.91 (0.86-0.96)
rs521319	G/A	11	63928607	1265/5188	0.30	2.92E-04	1.19 (1.08-1.30)	3805/6216	0.32	2.13E-01	0.96 (0.90-1.02)	3.38E-01	1.03 (0.97-1.08)
rs2238136	G/A	12	46563980	1265/5188	0.25	6.01E-06	1.25 (1.14-1.38)	3814/6224	0.27	7.91E-01	0.99 (0.93-1.06)	2.25E-02	1.07 (1.01-1.12)
rs7132324	G/A	12	46593576	1264/5187	0.33	5.90E-05	1.21 (1.10-1.33)	3744/6186	0.34	4.87E-01	1.02 (0.96-1.09)	5.06E-03	1.08 (1.02-1.13)
rs10870680	G/A	13	19638681	1265/5186	0.20	2.68E-04	0.81 (0.72-0.90)	3815/6221	0.19	2.15E-01	0.95 (0.89-1.03)	2.50E-03	0.91 (0.85-0.97)
rs11846930	G/A	14	61627081	1264/5187	0.07	8.25E-05	1.38 (1.18-1.63)	3801/6229	0.07	7.50E-01	1.02 (0.91-1.14)	1.25E-02	1.13 (1.03-1.23)
rs2123458	A/G	14	64128910	1265/5178	0.29	8.54E-05	1.21 (1.10-1.33)	3516/5519	0.30	6.07E-01	1.02 (0.95-1.09)	7.41E-03	1.08 (1.02-1.14)
rs1568221	G/A	15	34434869	1265/5187	0.33	3.01E-05	1.21 (1.11-1.33)	3811/6220	0.35	1.07E-01	1.05 (0.99-1.12)	2.36E-04	1.10 (1.04-1.15)
rs7191629	A/G	16	5689444	1265/5185	0.27	5.88E-05	1.22 (1.11-1.34)	3641/6074	0.28	5.18E-01	1.02 (0.96-1.09)	4.88E-03	1.08 (1.02-1.14)
rs4782024	G/A	16	17166439	1265/5185	0.04	1.18E-04	0.55 (0.41-0.75)	3770/5848	0.03	2.02E-01	1.11 (0.95-1.31)	4.80E-01	0.95 (0.82-1.10)
rs4430796	A/G	17	33172153	1262/5179	0.48	3.06E-07	0.79 (0.73-0.87)	2332/4349	0.48	2.00E-04	0.87 (0.81-0.94)	7.11E-10	0.84 (0.79-0.89)
rs4239217	A/G	17	33173100	1265/5190	0.41	2.48E-07	0.79 (0.72-0.86)	2342/4307	0.40	2.00E-03	0.89 (0.82-0.96)	1.19E-08	0.84 (0.80-0.90)
rs7501939	G/A	17	33175269	1263/5187	0.40	2.17E-06	0.80 (0.73-0.88)	3337/5234	0.40	1.00E-03	0.90 (0.84-0.96)	5.35E-08	0.86 (0.82-0.91)
rs1212721	G/A	18	5245109	1264/5183	0.21	1.27E-04	0.80 (0.72-0.90)	3760/6195	0.20	9.73E-01	1.00 (0.93-1.08)	4.23E-02	0.94 (0.88-1.00)
rs364418	G/A	18	7803239	1264/5190	0.39	4.61E-05	1.20 (1.10-1.32)	3770/6207	0.43	5.03E-01	1.02 (0.96-1.08)	5.51E-03	1.07 (1.02-1.13)
rs918171	G/A	19	3287539	1265/5188	0.07	1.41E-04	1.36 (1.16-1.59)	3769/6208	0.07	1.70E-02	1.14 (1.03-1.28)	3.70E-05	1.21 (1.11-1.32)
rs1557203	A/G	20	33627877	1265/5187	0.07	1.53E-04	1.36 (1.16-1.60)	3817/6224	0.08	2.86E-01	1.06 (0.95-1.17)	2.92E-03	1.14 (1.05-1.24)

\* MAF=minor allele frequency in controls

NB: Not all of the p-values for Stage 1 are less than 1E-04. This is because Stage 2 SNP selection was based on a slightly earlier version of the dataset and was not corrected by PCA.

Supplementary Table 2: Endometrial cancer sample sets included in Stage 1 and Stage 2 analyses.*					
Study	Abbreviation	General Setting	Cases	Controls	Genotyping platform**
<b>Stage 1 Sample Sets</b>					
Australian National Endometrial Cancer Study	ANECs	Australia; population based case-control study	599	-	Illumina 610K
Study of Epidemiology and Risk Factors in Cancer Heredity	SEARCH	England; population based case-control study	666	-	Illumina 610K
Wellcome Trust Case-Control Consortium	WTCCC	UK: sample from 1958 Birth Cohort and UK Blood Donors from NBS	-	5,190	Illumina 1.2M
<b>Stage 2 Sample Sets</b>					
Australian National Endometrial Cancer Study***	ANECs	Australia; population based case-control study	607	587	Sequenom iPLEX
Australian Red Cross Blood Service***	ARCBS	Brisbane, Australia; female donor controls		577	Sequenom iPLEX
Newcastle Endometrial Cancer Study***	NECS	Newcastle, Australia; hospital-based cases	194	-	Sequenom iPLEX
Study of Epidemiology and Risk Factors in Cancer Heredity	SEARCH	England; population based case-control study	688	1,600	ABI Fluidigm
Bavarian Endometrial Cancer Study	BECS	Germany; population based case-control study	222	396	Sequenom iPLEX
Leuven Endometrial Cancer Study	LES	Belgium; hospital based case-control study	238	671	Sequenom iPLEX
Molecular Markers in Treatment of Endometrial Cancer	MoMaTEC	Norway; population based case-control study	213	138	Sequenom iPLEX
National Study of the Genetics of Endometrial Cancer	NSECG	United Kingdom; population based case-control study	829	998	Sequenom iPLEX (cases); Illumina 550K or Kaspar for selected SNPs (controls)
Polish Endometrial Cancer Study	PECS	Poland, Warsaw and Lodz; population based case-control study	466	897	Illumina 660W-Quad
Singapore and Swedish Breast/Endometrial Cancer Study	SASBAC	Sweden; population based cohort study	500	1,022	Sequenom iPLEX
Shanghai Endometrial Cancer Genetic Study	SECS	Shanghai, China; population based case-control studies	832	2,049	Affymetrix 6.0
<b>Total</b>			<b>6,054</b>	<b>14,125</b>	
*The number of cases and controls represents the maximum number of genotypes from cases and controls of reported Caucasian ethnicity, with the exception of SECS samples of Chinese ancestry.					
**Fluidigm genotyping was performed in Cambridge using primers and probes supplied by Applied Biosystems as Assays-By-Design. Sequenom's MassARRAY system and iPLEX technology (Sequenom Inc, San Diego, CA) was used for genotyping for most other studies, using matrix-assisted laser desorption/ionization time of flight mass spectrometry for the determination of allele-specific primer extension products. Oligonucleotides were designed using MassARRAY Assay Design software (version 3.1, Sequenom Inc) in Brisbane for use at other sites undertaking iPLEX genotyping (Leuven – LES, Singapore Genome Institute – SASBAC), and results were analysed using TYPER software (version 3.4, Sequenom Inc).					
***Australian stage 2 samples considered as a single group for statistical analysis					

Supplementary Table 3: Stage 1, stage 2 (endometrioid histology cases only) and combined results for 47 SNPs selected for replication.													
SNP	Alleles	Chromosome	Position	Stage 1				Stage 2: endometrioid histology only				Combined: endometrioid histology only	
				cases/controls	MAF*	P (1df)	OR (95% CI)	cases/controls	MAF*	P (1df)	OR (95% CI)	P (1df)	OR (95% CI)
rs673604	A/G	1	35460402	1265/5188	0.08	6.11E-07	1.45 (1.25-1.67)	2948/6151	0.09	4.90E-02	1.12 (1.00-1.25)	4.58E-06	1.23 (1.12-1.34)
rs12117146	G/A	1	227871836	1264/5186	0.13	1.11E-05	1.32 (1.17-1.49)	2951/6065	0.13	6.93E-01	1.02 (0.93-1.12)	3.17E-03	1.12 (1.04-1.20)
rs1453194	A/C	2	19736284	1265/5187	0.12	2.26E-05	0.72 (0.61-0.84)	2977/5864	0.12	5.93E-01	0.97 (0.89-1.07)	3.19E-03	0.89 (0.82-0.97)
rs990270	C/A	2	40435853	1265/5189	0.39	7.13E-07	1.25 (1.15-1.37)	2989/6217	0.43	2.22E-01	1.04 (0.98-1.11)	9.76E-05	1.11 (1.05-1.17)
rs6544324	G/A	2	40436562	1263/5185	0.38	3.24E-05	1.21 (1.11-1.32)	2975/5897	0.42	3.30E-01	1.03 (0.97-1.10)	1.46E-03	1.09 (1.03-1.15)
rs1477004	G/A	2	40465576	1265/5187	0.31	4.63E-05	1.21 (1.10-1.33)	2977/6255	0.34	6.70E-01	1.01 (0.95-1.08)	6.95E-03	1.08 (1.02-1.14)
rs1124787	A/C	2	46168439	1264/5185	0.40	1.63E-04	0.84 (0.77-0.92)	2985/6220	0.38	2.70E-02	1.08 (1.01-1.15)	6.72E-01	0.99 (0.94-1.04)
rs10167555	C/A	2	46174610	1263/5177	0.20	5.39E-05	0.78 (0.70-0.88)	2907/5900	0.19	5.90E-02	1.08 (1.00-1.17)	4.53E-01	0.97 (0.91-1.04)
rs4954564	A/G	2	136611978	1265/5190	0.26	5.79E-03	1.15 (1.04-1.26)	2955/6159	0.30	6.79E-01	1.02 (0.95-1.09)	4.93E-02	1.06 (1.00-1.12)
rs4663132	A/G	2	234970071	1264/5189	0.45	1.25E-04	1.19 (1.09-1.30)	2927/6121	0.55	7.89E-01	1.01 (0.95-1.07)	1.39E-02	1.07 (1.01-1.12)
rs12489038	A/C	3	12986140	1265/5189	0.17	5.52E-04	1.22 (1.09-1.36)	2970/6205	0.19	3.62E-01	1.04 (0.96-1.12)	6.21E-03	1.09 (1.03-1.17)
rs720625	A/G	3	45785098	1264/5188	0.36	2.54E-05	1.21 (1.11-1.33)	2951/6196	0.38	7.30E-01	1.01 (0.95-1.08)	6.14E-03	1.08 (1.02-1.13)
rs798741	G/A	4	1682211	1265/5188	0.19	9.68E-06	1.27 (1.14-1.41)	2952/6192	0.21	8.43E-01	0.99 (0.92-1.07)	1.46E-02	1.08 (1.02-1.15)
rs1320071	A/G	4	7979091	1265/5179	0.39	1.56E-04	0.84 (0.76-0.92)	2946/6161	0.38	9.64E-01	1.00 (0.94-1.07)	3.12E-02	0.94 (0.89-0.99)
rs10008860	G/A	4	8020494	1265/5190	0.43	1.25E-05	1.22 (1.11-1.33)	2984/6216	0.44	4.89E-01	1.02 (0.96-1.09)	1.85E-03	1.09 (1.03-1.14)
rs6537310	G/A	4	145856182	1265/5187	0.44	7.67E-06	0.81 (0.74-0.89)	2949/6129	0.42	9.50E-02	0.95 (0.89-1.01)	7.96E-05	0.90 (0.86-0.95)
rs1425542	A/G	5	113902191	1264/5188	0.21	4.29E-05	1.24 (1.12-1.38)	2434/4622	0.21	4.80E-01	0.97 (0.89-1.06)	3.64E-02	1.07 (1.00-1.15)
rs2548975	G/A	5	133438999	1264/5189	0.19	2.07E-05	1.26 (1.13-1.40)	2984/6211	0.20	9.76E-01	1.00 (0.92-1.08)	1.41E-02	1.08 (1.02-1.15)
rs986359	A/C	5	136675003	1264/5183	0.36	4.59E-05	1.20 (1.10-1.32)	2982/6211	0.37	8.63E-01	0.99 (0.93-1.06)	2.11E-02	1.06 (1.01-1.12)
rs10515787	G/A	5	158407789	1265/5187	0.01	9.58E-04	1.75 (1.25-2.44)	2965/6218	0.02	2.42E-01	1.16 (0.91-1.49)	3.53E-03	1.34 (1.10-1.64)
rs2493046	G/A	6	488134	1264/5184	0.11	6.78E-05	1.31 (1.15-1.49)	2988/6223	0.12	3.06E-01	1.05 (0.96-1.16)	1.75E-03	1.13 (1.05-1.22)
rs4149366	G/A	6	2960488	1265/5189	0.07	4.29E-05	0.66 (0.55-0.81)	2435/3779	0.07	2.18E-01	1.11 (0.94-1.30)	1.00E-01	0.90 (0.80-1.02)
rs559901	G/A	6	153899629	1264/5187	0.28	6.97E-05	1.21 (1.10-1.33)	2963/5902	0.30	4.62E-01	1.03 (0.96-1.10)	3.65E-03	1.09 (1.03-1.15)
rs2049449	A/C	7	14665378	1265/5188	0.14	6.63E-05	1.28 (1.13-1.44)	2981/6225	0.16	3.32E-01	1.04 (0.96-1.14)	1.77E-03	1.12 (1.04-1.20)
rs9969635	A/C	8	10369046	1265/5188	0.10	3.06E-05	1.33 (1.17-1.53)	2587/5423	0.11	5.41E-01	1.03 (0.93-1.15)	2.20E-03	1.14 (1.05-1.24)
rs11784168	A/G	8	28083277	1264/5187	0.13	4.38E-04	1.25 (1.10-1.41)	2984/6218	0.14	1.18E-01	0.93 (0.85-1.02)	4.16E-01	1.03 (0.96-1.11)
rs17589981	A/G	9	9109229	1265/5184	0.32	1.32E-04	1.20 (1.09-1.31)	2977/6187	0.33	4.52E-01	0.98 (0.91-1.04)	1.05E-01	1.05 (0.99-1.10)
rs4295736	G/A	9	81072159	1263/5188	0.06	6.27E-05	1.42 (1.19-1.68)	2988/6189	0.07	5.10E-01	0.96 (0.84-1.09)	5.94E-02	1.10 (1.00-1.22)
rs11138152	G/A	9	81156461	1265/5188	0.08	7.38E-06	1.40 (1.21-1.62)	2955/6204	0.09	1.02E-01	0.91 (0.82-1.02)	1.65E-01	1.06 (0.97-1.16)
rs1932658	A/G	9	86005570	1258/5167	0.26	8.54E-05	1.22 (1.10-1.34)	2951/6089	0.28	5.61E-01	1.02 (0.95-1.09)	6.17E-03	1.08 (1.02-1.15)
rs7358426	A/G	11	22079689	1265/5189	0.31	4.09E-05	0.81 (0.74-0.90)	2958/6197	0.30	1.53E-01	0.95 (0.89-1.02)	4.84E-04	0.90 (0.85-0.96)
rs521319	G/A	11	63928607	1265/5188	0.30	2.92E-04	1.19 (1.08-1.30)	2985/6216	0.32	4.89E-01	0.98 (0.91-1.05)	1.23E-01	1.04 (0.99-1.10)
rs2238136	G/A	12	46563980	1265/5188	0.25	6.01E-06	1.25 (1.14-1.38)	2986/6224	0.27	6.45E-01	1.02 (0.95-1.09)	2.55E-03	1.09 (1.03-1.16)
rs7132324	G/A	12	46593576	1264/5187	0.33	5.90E-05	1.21 (1.10-1.33)	2947/6186	0.34	4.19E-01	1.03 (0.96-1.10)	2.66E-03	1.09 (1.03-1.15)
rs10870680	G/A	13	19638681	1265/5186	0.20	2.68E-04	0.81 (0.72-0.90)	2985/6221	0.19	5.99E-01	0.98 (0.90-1.06)	1.17E-02	0.92 (0.86-0.98)
rs11846930	G/A	14	61627081	1264/5187	0.07	8.25E-05	1.38 (1.18-1.63)	2976/6229	0.07	9.03E-01	1.01 (0.89-1.14)	1.39E-02	1.13 (1.03-1.25)
rs2123458	A/G	14	64128910	1265/5178	0.29	8.54E-05	1.21 (1.10-1.33)	2770/5519	0.30	3.74E-01	1.03 (0.96-1.11)	2.07E-03	1.09 (1.03-1.16)
rs1568221	G/A	15	34434869	1265/5187	0.33	3.01E-05	1.21 (1.11-1.33)	2984/6220	0.35	1.01E-01	1.06 (0.99-1.13)	1.47E-04	1.11 (1.05-1.17)
rs7191629	A/G	16	5689444	1265/5185	0.27	5.88E-05	1.22 (1.11-1.34)	2880/6074	0.28	7.02E-01	1.01 (0.94-1.09)	6.72E-03	1.08 (1.02-1.15)
rs4782024	G/A	16	17166439	1265/5185	0.04	1.18E-04	0.55 (0.41-0.75)	2962/5848	0.03	3.55E-01	1.09 (0.91-1.30)	2.47E-01	0.91 (0.79-1.06)
rs4430796	A/G	17	33172153	1262/5179	0.48	3.06E-07	0.79 (0.73-0.87)	1786/4349	0.47	2.56E-05	0.84 (0.77-0.91)	4.28E-11	0.82 (0.77-0.87)
rs4239217	A/G	17	33173100	1265/5190	0.41	2.48E-07	0.79 (0.72-0.86)	1753/4307	0.39	5.90E-04	0.86 (0.79-0.94)	1.27E-09	0.83 (0.78-0.88)
rs7501939	G/A	17	33175269	1263/5187	0.40	2.17E-06	0.80 (0.73-0.88)	2562/5234	0.38	3.30E-04	0.88 (0.82-0.94)	7.57E-09	0.85 (0.80-0.90)
rs1212721	G/A	18	5245109	1264/5183	0.21	1.27E-04	0.80 (0.72-0.90)	2953/6195	0.20	8.67E-01	1.01 (0.93-1.09)	4.14E-02	0.93 (0.88-1.00)
rs364418	G/A	18	7803239	1264/5190	0.39	4.61E-05	1.20 (1.10-1.32)	2962/6207	0.43	8.09E-01	0.99 (0.93-1.06)	3.17E-02	1.06 (1.01-1.12)
rs918171	G/A	19	3287539	1265/5188	0.07	1.41E-04	1.36 (1.16-1.59)	2960/6208	0.07	7.10E-02	1.12 (0.99-1.26)	1.94E-04	1.20 (1.09-1.32)
rs1557203	A/G	20	33627877	1265/5187	0.07	1.53E-04	1.36 (1.16-1.60)	2989/6224	0.08	3.24E-01	1.06 (0.95-1.19)	2.62E-03	1.15 (1.05-1.26)

\* MAF=minor allele frequency in controls

NB: All stage 1 cases were chosen on the basis of endometrioid histology

NB: Not all of the p-values for Stage 1 are less than 1E-04. This is because Stage 2 SNP selection was based on a slightly earlier version of the dataset and was not corrected by PCA.

Supplementary Table 4: Stage 2 results for 47 SNPs selected for replication, by histology												
SNP	Alleles	Chromosome	Position	Nctrls	endometrioid only (case control)			non-endometrioid only (case control)			non-endometrioid vs endometrioid (case only)	
					Ncases	P (1df)	OR (95% CI)	Ncases	P (1df)	OR (95% CI)	P (1df)	OR (95% CI)
rs673604	A/G	1	35460402	6151	2948	<b>4.90E-02</b>	1.12 (1.00-1.25)	697	5.04E-01	1.07 (0.88-1.30)	8.57E-01	0.98 (0.80-1.21)
rs12117146	G/A	1	227871836	6065	2951	6.93E-01	1.02 (0.93-1.12)	677	6.44E-01	1.04 (0.88-1.23)	8.07E-01	1.02 (0.86-1.22)
rs1453194	A/C	2	19736284	5864	2977	5.93E-01	0.97 (0.89-1.07)	711	5.25E-01	1.06 (0.89-1.25)	7.71E-01	1.03 (0.86-1.23)
rs990270	C/A	2	40435853	6217	2989	2.22E-01	1.04 (0.98-1.11)	711	2.34E-01	1.07 (0.96-1.20)	8.79E-01	1.01 (0.90-1.14)
rs6544324	G/A	2	40436562	5897	2975	3.30E-01	1.03 (0.97-1.10)	708	2.64E-01	1.07 (0.95-1.19)	9.04E-01	1.01 (0.89-1.14)
rs1477004	G/A	2	40465576	6255	2977	6.70E-01	1.01 (0.95-1.08)	714	5.99E-01	1.03 (0.92-1.16)	6.50E-01	0.97 (0.86-1.10)
rs1124787	A/C	2	46168439	6220	2985	<b>2.70E-02</b>	1.08 (1.01-1.15)	714	2.34E-01	1.07 (0.96-1.20)	7.69E-01	0.98 (0.87-1.11)
rs10167555	C/A	2	46174610	5900	2907	5.90E-02	1.08 (1.00-1.17)	683	<b>7.00E-03</b>	1.22 (1.06-1.40)	1.61E-01	1.11 (0.96-1.29)
rs4954564	A/G	2	136611978	6159	2955	6.79E-01	1.02 (0.95-1.09)	707	5.59E-01	1.04 (0.92-1.17)	6.69E-01	0.97 (0.85-1.11)
rs4663132	A/G	2	234970071	6121	2927	7.89E-01	1.01 (0.95-1.07)	690	4.56E-01	1.04 (0.93-1.17)	3.53E-01	1.06 (0.94-1.20)
rs12489038	A/C	3	12986140	6205	2970	3.62E-01	1.04 (0.96-1.12)	713	5.71E-01	1.04 (0.90-1.20)	6.00E-01	1.04 (0.89-1.22)
rs720625	A/G	3	45785098	6196	2951	7.30E-01	1.01 (0.95-1.08)	695	4.79E-01	0.96 (0.85-1.08)	3.63E-01	0.94 (0.83-1.07)
rs798741	G/A	4	1682211	6192	2952	8.43E-01	0.99 (0.92-1.07)	692	3.59E-01	1.07 (0.93-1.22)	2.74E-01	1.09 (0.94-1.26)
rs1320071	A/G	4	7979091	6161	2946	9.64E-01	1.00 (0.94-1.07)	694	1.11E-01	1.10 (0.98-1.23)	1.21E-01	1.10 (0.97-1.25)
rs10008860	G/A	4	8020494	6216	2984	4.89E-01	1.02 (0.96-1.09)	712	7.71E-01	0.98 (0.88-1.10)	6.68E-01	0.97 (0.86-1.10)
rs6537310	G/A	4	145856182	6129	2949	9.50E-02	0.95 (0.89-1.01)	708	3.37E-01	1.06 (0.95-1.18)	<b>1.30E-02</b>	1.17 (1.03-1.32)
rs1425542	A/G	5	113902191	4622	2434	4.80E-01	0.97 (0.89-1.06)	569	5.30E-01	0.95 (0.81-1.11)	8.10E-01	0.98 (0.83-1.16)
rs2548975	G/A	5	133438999	6211	2984	9.76E-01	1.00 (0.92-1.08)	710	6.51E-01	1.03 (0.90-1.18)	3.98E-01	1.07 (0.92-1.23)
rs986359	A/C	5	136675003	6211	2982	8.63E-01	0.99 (0.93-1.06)	714	9.61E-01	1.00 (0.89-1.12)	8.02E-01	1.02 (0.90-1.15)
rs10515787	G/A	5	158407789	6218	2965	2.42E-01	1.16 (0.91-1.49)	698	8.81E-01	1.04 (0.65-1.64)	2.83E-01	0.77 (0.48-1.24)
rs2493046	G/A	6	488134	6223	2988	3.06E-01	1.05 (0.96-1.16)	712	8.36E-01	1.02 (0.86-1.21)	5.81E-01	0.95 (0.79-1.14)
rs4149366	G/A	6	2960488	3779	2435	2.18E-01	1.11 (0.94-1.30)	566	1.30E-01	1.22 (0.94-1.57)	5.07E-01	1.09 (0.84-1.41)
rs559901	G/A	6	153899629	5902	2963	4.62E-01	1.03 (0.96-1.10)	695	5.04E-01	0.96 (0.84-1.09)	5.14E-01	0.96 (0.84-1.09)
rs2049449	A/C	7	14665378	6225	2981	3.32E-01	1.04 (0.96-1.14)	713	1.08E-01	1.13 (0.97-1.31)	4.13E-01	1.07 (0.91-1.25)
rs9969635	A/C	8	10369046	5423	2587	5.41E-01	1.03 (0.93-1.15)	598	5.78E-01	1.06 (0.87-1.28)	7.48E-01	0.97 (0.79-1.19)
rs11784168	A/G	8	28083277	6218	2984	1.18E-01	0.93 (0.85-1.02)	712	4.60E-01	0.94 (0.80-1.11)	6.71E-01	0.96 (0.81-1.15)
rs17589981	A/G	9	9109229	6187	2977	4.52E-01	0.98 (0.91-1.04)	712	6.27E-01	1.03 (0.92-1.16)	2.96E-01	1.07 (0.94-1.21)
rs4295736	G/A	9	81072159	6189	2988	5.10E-01	0.96 (0.84-1.09)	713	9.28E-01	1.01 (0.80-1.27)	6.04E-01	1.07 (0.84-1.36)
rs11138152	G/A	9	81156461	6204	2955	1.02E-01	0.91 (0.82-1.02)	697	5.37E-01	0.94 (0.77-1.15)	9.77E-01	1.00 (0.81-1.25)
rs1932658	A/G	9	86005570	6089	2951	5.61E-01	1.02 (0.95-1.09)	708	7.50E-02	0.89 (0.79-1.01)	<b>1.50E-02</b>	0.85 (0.74-0.97)
rs7358426	A/G	11	22079689	6197	2958	1.53E-01	0.95 (0.89-1.02)	697	4.26E-01	0.95 (0.84-1.08)	9.73E-01	1.00 (0.87-1.14)
rs521319	G/A	11	63928607	6216	2985	4.89E-01	0.98 (0.91-1.05)	704	1.98E-01	0.92 (0.82-1.04)	3.14E-01	0.94 (0.82-1.07)
rs2238136	G/A	12	46563980	6224	2986	6.45E-01	1.02 (0.95-1.09)	712	2.03E-01	0.92 (0.81-1.05)	1.81E-01	0.91 (0.79-1.05)
rs7132324	G/A	12	46593576	6186	2947	4.19E-01	1.03 (0.96-1.10)	689	6.03E-01	0.97 (0.86-1.09)	3.27E-01	0.94 (0.83-1.07)
rs10870680	G/A	13	19638681	6221	2985	5.99E-01	0.98 (0.90-1.06)	714	5.20E-02	0.86 (0.74-1.00)	5.10E-02	0.85 (0.73-1.00)
rs11846930	G/A	14	61627081	6229	2976	9.03E-01	1.01 (0.89-1.14)	709	7.93E-01	0.97 (0.78-1.21)	7.74E-01	0.97 (0.76-1.23)
rs2123458	A/G	14	64128910	5519	2770	3.74E-01	1.03 (0.96-1.11)	637	7.72E-01	0.98 (0.86-1.12)	5.13E-01	0.95 (0.83-1.10)
rs1568221	G/A	15	34434869	6220	2984	1.01E-01	1.06 (0.99-1.13)	712	4.79E-01	1.04 (0.93-1.17)	8.36E-01	0.99 (0.87-1.12)
rs7191629	A/G	16	5689444	6074	2880	7.02E-01	1.01 (0.94-1.09)	652	5.41E-01	1.04 (0.92-1.18)	5.79E-01	1.04 (0.91-1.19)
rs4782024	G/A	16	17166439	5848	2962	3.55E-01	1.09 (0.91-1.30)	697	3.76E-01	1.15 (0.85-1.55)	6.55E-01	1.08 (0.78-1.49)
rs4430796	A/G	17	33172153	4349	1786	<b>2.56E-05</b>	0.84 (0.77-0.91)	484	3.74E-01	0.94 (0.82-1.08)	2.20E-01	1.10 (0.95-1.28)
rs4239217	A/G	17	33173100	4307	1753	<b>5.90E-04</b>	0.86 (0.79-0.94)	588	6.18E-01	0.97 (0.85-1.10)	7.60E-02	1.14 (0.99-1.31)
rs7501939	G/A	17	33175269	5234	2562	<b>3.30E-04</b>	0.88 (0.82-0.94)	690	4.29E-01	0.95 (0.85-1.07)	1.68E-01	1.09 (0.96-1.24)
rs1212721	G/A	18	5245109	6195	2953	8.67E-01	1.01 (0.93-1.09)	696	4.62E-01	0.95 (0.82-1.09)	6.10E-01	0.96 (0.82-1.12)
rs364418	G/A	18	7803239	6207	2962	8.09E-01	0.99 (0.93-1.06)	698	<b>9.00E-03</b>	1.16 (1.04-1.30)	<b>1.70E-02</b>	1.16 (1.03-1.31)
rs918171	G/A	19	3287539	6208	2960	7.10E-02	1.12 (0.99-1.26)	698	<b>2.40E-02</b>	1.27 (1.03-1.56)	2.35E-01	1.14 (0.92-1.42)
rs1557203	A/G	20	33627877	6224	2989	3.24E-01	1.06 (0.95-1.19)	712	4.13E-01	1.09 (0.89-1.32)	8.05E-01	1.03 (0.83-1.27)

NB: the numbers of cases with and without endometrioid histology do not sum to the total number of Stage 2 cases in Supplementary Table 1, because the main analysis also included a small number of cases for whom we did not have access to histology data.

**Supplementary Table 5: Endometrial cancer case-control analysis using genotypes imputed from 1000 Genomes Project for SNPs within the rs4430796 linkage disequilibrium block**

SNP name	Position	Alleles	MAF	Rsq	r <sup>2</sup> with rs4430796	P-value	Genotyped in stage 1?
rs7405776	33167135	G/A	0.38	0.66	0.51	<b>6.07E-07</b>	
c17_pos33169359	33169359	T/G	0.05	0.61	0.04	6.63E-01	
rs2005705	33170413	G/A	0.45	0.89	0.83	<b>2.35E-07</b>	
c17_pos33170534	33170534	T/C	0.14	0.35	0.18	4.29E-03	
rs757211	33170591	C/T	0.49	0.66	0.46	<b>9.31E-07</b>	
rs757210	33170628	C/T	0.37	0.99	0.57	<b>1.27E-06</b>	yes
<b>rs4430796</b>	<b>33172153</b>	<b>A/G</b>	<b>0.47</b>	<b>1.00</b>	-	<b>2.92E-07</b>	<b>yes</b>
rs4239217	33173100	A/G	0.40	1.00	0.80	<b>2.60E-07</b>	yes
rs11651755	33173953	T/C	0.47	0.99	1.00	<b>1.82E-07</b>	
c17_pos33173971	33173971	G/C	0.07	0.96	0.06	7.08E-01	
rs10908278	33174065	A/T	0.47	0.95	0.96	<b>2.25E-07</b>	
rs11657964	33174880	G/A	0.41	0.95	0.77	<b>9.67E-07</b>	
rs7501939	33175269	C/T	0.40	1.00	0.80	<b>1.16E-06</b>	yes
rs8064454	33175699	C/A	0.47	0.98	1.00	<b>4.72E-07</b>	
rs12601991	33175746	G/T	0.45	0.76	0.64	<b>1.38E-06</b>	
rs11263762	33176039	G/A	0.46	0.77	0.67	<b>1.22E-06</b>	
rs7405696	33176148	G/C	0.46	0.77	0.67	<b>1.22E-06</b>	
rs11651052	33176494	G/A	0.47	0.97	1.00	<b>4.63E-07</b>	
rs757209	33176946	G/A	0.49	0.77	0.78	<b>6.15E-07</b>	
rs9901746	33177262	G/A	0.44	0.74	0.62	<b>1.69E-06</b>	
rs11263763	33177678	A/G	0.49	0.87	0.96	<b>3.71E-07</b>	
rs11658063	33177985	G/C	0.39	0.96	0.80	<b>8.59E-07</b>	
rs12453443	33178234	C/G	0.44	0.74	0.60	<b>3.49E-06</b>	
c17_pos33178389	33178389	C/G	0.06	0.77	0.05	6.57E-01	
c17_pos33178417	33178417	C/G	0.07	0.91	0.06	6.55E-01	
rs34443065	33179971	C/T	0.13	0.46	0.11	1.02E-01	
rs9913260	33180010	G/A	0.28	0.55	0.40	1.30E-05	
rs3760511	33180426	T/G	0.32	0.99	0.30	1.45E-03	yes
c17_pos33181982	33181982	T/C	0.06	0.75	0.05	6.60E-01	
c17_pos33182146	33182146	T/G	0.07	0.88	0.06	6.61E-01	
c17_pos33182283	33182283	A/G	0.07	0.86	0.06	6.58E-01	
rs67143603	33182344	T/C	0.33	0.92	0.27	2.19E-03	
rs17626423	33182480	T/C	0.21	0.99	0.21	3.71E-02	yes
<b>Notes:</b>							
Genotypes were imputed for all 1265 endometrial cancer cases and 5190 controls included in stage 1 of the study							
1000 Genomes Project data (CEU population) was used as the reference panel.							
MAF=minor allele frequency (i.e. frequency of the allele listed second)							
Rsq is an estimate of the squared correlation between the imputed and true genotypes for this SNP (SNPs with Rsq<0.3 are not shown)							
P-values <1e-5 are shown in bold.							

Supplementary Table 6: Frequency of common <i>HNF1B</i> locus haplotypes in Stage 1 endometrial cancer cases and controls*							
Haplotype	Frequency	Case Frequency	Control Frequency	p-value			
<b>AGGAAA</b>	<b>0.343</b>	<b>0.304</b>	<b>0.353</b>	<b>5.39E-06</b>			
GAAGCA	0.310	0.333	0.304	5.70E-03			
GAAGAG	0.180	0.192	0.177	8.08E-02			
<b>GGAGAA</b>	<b>0.071</b>	<b>0.068</b>	<b>0.071</b>	<b>5.20E-01</b>			
GAAGAA	0.029	0.036	0.027	2.55E-02			
<b>GGGAAG</b>	<b>0.023</b>	<b>0.025</b>	<b>0.023</b>	<b>6.60E-01</b>			
<b>GGGAAA</b>	<b>0.014</b>	<b>0.011</b>	<b>0.015</b>	<b>2.11E-01</b>			
* Common (>1%) haplotypes defined by tag SNPs rs757210, rs4430796, rs4239217, rs7501939, rs3760511, and rs1762642, respectively							
Rare allele of rs4430796 lies only on haplotypes shown in bold							



**Supplementary Table 7: Stage 1 Endometrial cancer risk estimates for GWAS-identified prostate cancer loci.**

SNP	Region	Chromosome	Build36 Position	Reference*	Endometrial Cancer Stage 1 P-value	Proxy SNP and $r^2$ with prostate SNP (if SNP not typed in endometrial study)	Notes: LD with other prostate cancer SNPs
rs1465618	THADA	2	43407453	Eeles et al 2009	1.00		
rs721048	EHBP1	2	62985235	Gudmundsson et al 2008	0.48	rs2710646; $r^2=1.00$	
rs2710646	EHBP1	2	62988383	Gudmundsson et al 2008	0.48		$r^2=1.00$ with rs721048
rs12621278	ITGA6	2	173019799	Eeles et al 2009	0.26		
rs2660753	3p12.1	3	87193364	Eeles et al 2008	0.16		
rs10934853	3q21.3	3	129521063	Gudmundsson et al 2009	0.27		
rs12500426	PDLIM5	4	95733632	Eeles et al 2009	0.59		
rs17021918	PDLIM5	4	95781900	Eeles et al 2009	0.73		
rs7679673	TET2	4	106280983	Eeles et al 2009	0.83	rs4698932; $r^2=0.69$	
rs9364554	SLC22A3	6	160753654	Eeles et al 2008	0.77		
rs10486567	JAZF1	7	27943088	Thomas et al 2008	0.81		
rs6465657	LMTK2	7	97654263	Eeles et al 2008	0.51		
rs2928679	NKX3-1	8	23494920	Eeles et al 2009	0.90		
rs1512268	NKX3-1	8	23582408	Eeles et al 2009	0.33		
rs10086908	8q24 (1)	8	128081119	Amin Al Olama et al 2009	0.38		
rs1016343	8q24 (2)	8	128162479	Amin Al Olama et al 2009	0.85		
rs13254738	8q24 (2)	8	128173525	Haiman et al 2007	0.48	rs1456315; $r^2=0.68$	
rs6983561	8q24 (2)	8	128176062	Amin Al Olama et al 2009	0.45	rs16901966; $r^2=1.00$	
rs16901979	8q24 (2)	8	128194098	Gudmundsson et al 2007	0.42	rs10505483; $r^2=1.00$	$r^2=0.84$ with rs6983561
rs620861	8q24 (3)	8	128404855	Amin Al Olama et al 2009	0.26		
rs6983267	8q24 (4)	8	128482487	Yeager et al 2007	0.60		
rs1447295	8q24 (5)	8	128554220	Amundadottir et al 2006	0.68		
rs4242382	8q24 (5)	8	128586755	Eeles et al 2008	0.78		$r^2=1.00$ with rs1447295
rs10090154	8q24 (5)	8	128601319	Amin Al Olama et al 2009	0.68	rs1447295; $r^2=1.00$	$r^2=1.00$ with rs1447295
rs10993994	MSMB	10	51219502	Eeles et al 2008	0.19		
rs4962416	CTBP2	10	126686862	Thomas et al 2008	0.43		
rs7127900	11p15	11	2190150	Eeles et al 2009	0.58		
rs7931342	11q13.2	11	68751073	Eeles et al 2008	0.56		
rs10896449	11q13.2	11	68751243	Thomas et al 2008	0.61		$r^2=0.97$ with rs7931342
rs11649743	17q12	17	33149092	Sun et al 2008	0.76		
<b>rs4430796</b>	<b>HNF1B</b>	<b>17</b>	<b>33172153</b>	<b>Gudmundsson et al 2007a</b>	<b>3.06E-07</b>		
rs1859962	17q24.3	17	66620348	Gudmundsson et al 2007a	0.23		
rs8102476	19q13.2	19	43427453	Gudmundsson et al 2009	0.41		
rs2735839	KLK3	19	56056435	Eeles et al 2008	0.51		
rs5759167	22q13.2	22	41830156	Eeles et al 2009	0.20		
rs5945572	NUDT10/11	X	51246423	Gudmundsson et al 2008	0.69		$r^2=0.91$ with rs5945619
rs5945619	NUDT10/11	X	51258412	Eeles et al 2008	0.56		

\*References for Supplementary Table 3 (Caucasian studies only)

Amin Al Olama, A. et al. Multiple loci on 8q24 associated with prostate cancer susceptibility. *Nat Genet* **41**, 1058-1060 (2009).

Amundadottir, L.T. et al. A common variant associated with prostate cancer in European and African populations. *Nat Genet* **38**, 652-658 (2006).

Eeles, R.A. et al. Multiple newly identified loci associated with prostate cancer susceptibility. *Nat Genet* **40**, 316-321 (2008).

Eeles, R.A. et al. Identification of seven new prostate cancer susceptibility loci through a genome-wide association study. *Nat Genet* **41**, 1116-1121 (2009).

Gudmundsson, J. et al. Genome-wide association study identifies a second prostate cancer susceptibility variant at 8q24. *Nat Genet* **39**, 631-637 (2007).

Gudmundsson, J. et al. Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes. *Nat Genet* **39**, 977-983 (2007).

Gudmundsson, J. et al. Common sequence variants on 2p15 and Xp11.22 confer susceptibility to prostate cancer. *Nat Genet* **40**, 281-283 (2008).

Gudmundsson, J. et al. Genome-wide association and replication studies identify four variants associated with prostate cancer susceptibility. *Nat Genet* **41**, 1122-1126 (2009).

Haiman, C.A. et al. Multiple regions within 8q24 independently affect risk for prostate cancer. *Nat Genet* **39**, 638-644 (2007).

Sun, J. et al. Evidence for two independent prostate cancer risk-associated loci in the HNF1B gene at 17q12. *Nat Genet* **40**, 1153-1155 (2008).

Thomas, G. et al. Multiple loci identified in a genome-wide association study of prostate cancer. *Nat Genet* **40**, 310-315 (2008).

Yeager, M. et al. Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. *Nat Genet* **39**, 645-649 (2007).