Supplementary Table 1. Numbers of cases and controls from each study that were part of this GWAS.

Study Name	Study abbreviation	Study population	Study type	Number of Subjects[1]	
				cases	controls
STAGE1					
SEARCH Cambridge UK	SEA	UK	Population based	1156 (36)	-
UKOPS (United Kingdom Ovarian Cancer Population Study)	UKO	UK	Population based	522 (16)	-
Cancer Research UK familial ovarian Cancer Register	FOCR	UK	Familial cancer register	47 (3)	-
Royal Marsden Hospital study	RMH	UK	Hospital based	165 (18)	-
UK 58 Birth cohort	58 BC	UK	Cohort	-	1436
UK Colorectal control	NSCR	UK	Population based	-	917
	Subtotal			**1890 (73)**	**2353**
STAGE 2					
Australian Cancer Study (ovarian cancer); Australian Ovarian Cancer Study	AUS	Australia	Population based	1139 (5)	1166 (5)
Diseases of the Ovary and their Evaluation Study	DOVE	Washington State, USA	Population based	794 (1)	799 (1)
Polish Ovarian Cancer Study (1)	POL1	Poland	Population based	555 (35)	517 (10)
Los Angeles County Case-Control Studies of Ovarian Cancer	USC	Los Angeles, USA	Population based	541 (4)	600 (79)
Malignant Ovarian Cancer study	MAL	Copenhagen, Denmark	Population based	446 (1)	556 (5)
Gilda Radner familial ovarian cancer register	GR	Buffalo, USA	Familial cancer register	121	-
Hormones and ovarian cancer prediction study	HOP	Pittsburgh, USA	Population based	392 (1)	396 (1)
Genetic Epidemiology of Ovarian Cancer	STA	Stanford, USA	Population based	297 (2)	417 (1)
UKOPS (United Kingdom Ovarian Cancer Population Study)	UKO	UK	Population based	212	466
Polish Ovarian Cancer Study (2)	POL2	Warsaw & Lodz Poland	Population based	238	228
Bavarian ovarian cancer study	BAV	Germany	Population based	229 (82)	234 (40)
	Subtotal			**4964 (131)**	**5379 (142)**
STAGE 3					
New England case-control study of ovarian cancer	NEC	New Hampshire and eastern Massachusetts, USA	Population based	717	1049
UC Irvine Ovarian Cancer Study, California	UCI	California, USA	Population based	329	528
Mayo Clinic Ovarian Canver Study	MAY	Upper Midwest, USA	Clinic based	376	533
North Carolina Ovarian Cancer Study	NCO	North Carolina, USA	Population based	279	353
Hawaii Ovarian Cancer Study	HAW	Hawaii, USA	Population based	355	650
Hannover-Jena Ovarian Cancer Study	HJOCS	Germany	Hospital based	271	1012
Familial ovarian tumour study	TOR	Canada	Population based	301	294
German Ovarian Cancer Study	GER	Germany	Population based	219	433
Nurses' Health Study, Boston	NHS	USA	Population based	115	380
Melbourne Collaborative Cohort Study	MCCS	Australia	Cohort	127	108
	Subtotal			**3089**	**5340**
	TOTAL			**9943 (204)**	**13072 (142)**

[1] The numbers of subjects that were excluded in analysis because of not passing genotyping quality control criteria are presented in brackets.

Supplementary Table 2. Summary results for the 12 genome wide significant SNPs at 9p22.2 based on stage 1 and stage 2 data for subjects of European ancestry.

Id	SNPs	Base change[1]	Chr9 position[2]	SNP relative to *BNC2* Gene	MAF[3]	LD[4]	Per-allele OR 95%CI [5]	P-trend
1	rs3814113	T/C	16905021	~44kb upsteam	0.31	1.0	0.79 (0.75-0.84)	$2.47x10^{-17}$
2	rs4445329	G/A	16901757	~41kb upstream	0.31	1.0	0.79 (0.75-0.84)	$2.67x10^{-17}$
3	rs10810666	C/T	16901666	40.9kb upstream	0.19	0.74	0.80 (0.75-0.85)	$1.24x10^{-12}$
4	rs10962656	G/A	16867788	7kb upstream	0.14	0.59	0.81 (0.76-0.87)	$5.88x10^{-9}$
5	rs12379183	A/G	16855699	Intron 2	0.22	0.71	0.82 (0.78-0.87)	$1.36x10^{-10}$
6	rs2153271	A/G	16854521	Intron 2	0.41	0.77	0.85 (0.81-0.90)	$4.66x10^{-10}$
7	rs7861573	G/A	16852280	Intron 2	0.22	0.70	0.83 (0.78-0.88)	$3.61x10^{-10}$
8	rs10756819	A/G	16848084	Intron 2	0.33	0.83	0.83 (0.79-0.88)	$4.85x10^{-12}$
9	rs1416742	T/C	16846883	Intron 2	0.4	0.74	0.86 (0.82-0.90)	$1.74x10^{-9}$
10	rs12379687	G/T	16844367	Intron 2	0.15	0.57	0.82 (0.77-0.88)	$1.27x10^{-8}$
11	rs4961501	G/T	16841678	Intron 2	0.23	0.72	0.82 (0.77-0.87)	$8.49x10^{-12}$
12	rs1339552	G/A	16838790	Intron 2	0.41	0.76	0.85 (0.81-0.89)	$1.28x10^{-10}$

[1] The most common allele in controls is given first, [2] genome build NCBI B36 assembly. [3] MAF: minor allele frequency in ovarian cancer controls, [4] pairwise correlation (r^2) between associated SNPs with rs3814113 in European control subjects. [5] Per rare allele Odds ratios with 95% confidence interval are presented.

Supplementary Table 3: Ovarian cancer risks for the rs3814113 SNP by ancestry group in combined analysis.

Ethnic group	No. cases /controls	Per allele OR 95%CI	P-trend
All	9739/12931	0.82 (0.79-0.86)	**$2.47x10^{-19}$**
European	8761/11831	0.82 (0.79-0.86)	**$5.10x10^{-19}$**
African	52/67	0.54 (0.29-0.99)	0.048
Asian	237/296	0.83 (0.63-1.10)	0.19
Other	378/292	0.87 (0.70-1.07)	0.19

Data highlighted with bold text are GWAS significant ($P<5.0x10^{-8}$)

Supplementary Table 4: Ovarian cancer risks for the rs3814113 SNP after stratification by histological subtype in combined analysis for subjects of European ancestry.

Tumor subtype	No. cases /controls	Per allele OR 95%CI	P-trend
All types	8761/11831	0.83 (0.79-0.86)	**$5.10x10^{-19}$**
Serous	4847/11831	0.77 (0.73-0.81)	**$4.10x10^{-22}$**
Mucinous	626/11831	0.97 (0.86-1.09)	0.60
Endometrioid	1320/11831	0.86 (0.79-0.97)	0.001
Clear cell	628/11831	0.94 (0.83-1.07)	0.34
Other[1]	1226/11831	0.83 (0.76-0.91)	**$6.6x10^{-5}$**

[1] Other: included all the invasive epithelial ovarian cancer cases except serous, mucinous, endometrioid and clear cell ovarian cancer subtypes. Data highlighted with bold text are GWAS significant ($P<5.0x10^{-8}$)

Supplementary Table 5: Ovarian cancer risks for the rs3814113 SNP by age in combined analysis for subjects of European ancestry.

Tumor subtype	<40	40-49	50-59	>60	P-trend[1]
Overall	1.12 (0.93-1.36)	0.83 (0.75-0.91)	0.82 (0.74-0.89)	0.80 (0.73-0.85)	0.006
Serous	1.05 (0.81-1.37)	0.76 (0.67-0.86)	0.81 (0.73-0.91)	0.76 (0.70-0.83)	0.044

[1] Test for trend on the OR by age, fitting a linear interaction term in logistic regression.

Supplementary Table 6: Comparison of the notable results from candidate gene studies with the results from this GWAS

SNP	Gene/locus	Reported[a] OR	Reported[a] P-value	Reference	GWAS[b] OR	GWAS[b] P-value
rs4954956[c]	NXPH2	1.14	0.00017	Song et al, 2009 [20]	0.99	0.84
rs11683487[d]	NMI	0.87	0.032	Quaye et al., 2009 [21]	0.86	0.027
rs2740574	CYP3A4	2.81	0.017	Pearce et al., 2009 [22]	1.19	0.16
rs2287498[c]	TP53	1.30	0.0059	Schildkraut et al., 2009 [23]	1.03	0.78
rs12951053[c]	TP53	1.20	0.056	Schildkraut et al., 2009 [23]	1.05	0.66
rs2854344	RB1	0.88	0.041	Ramus et al., 2008 [24]	0.88	0.15
rs2273535	AURKA	1.10	0.027	Ramus et al., 2008 [24]	1.01	0.84
rs10505477	8q24	1.14	0.002	Ghoussaini et al., 2008 [25]	1.10	0.03
rs10808556	8q24	1.13	0.0017	Ghoussaini et al., 2008 [25]	1.11	0.02
rs6983267	8q24	1.11	0.0099	Ghoussaini et al., 2008 [25]	1.10	0.04
rs2660753	3p12	1.19	0.012	Song et al., 2008 [26]	1.05	0.53
rs3731257	CDKN2A	0.91	0.008	Gayther et al., 2007 [27]	0.97	0.89
rs2066827	CDKN1B	0.93	0.036	Gayther et al., 2007 [27]	1.02	0.76
rs2191249	BRIP1	0.90	0.045	Song et al, 2007 [28]	0.87	0.01
rs4988344	BRIP1	1.15	0.02	Song et al, 2007 [28]	0.95	0.42

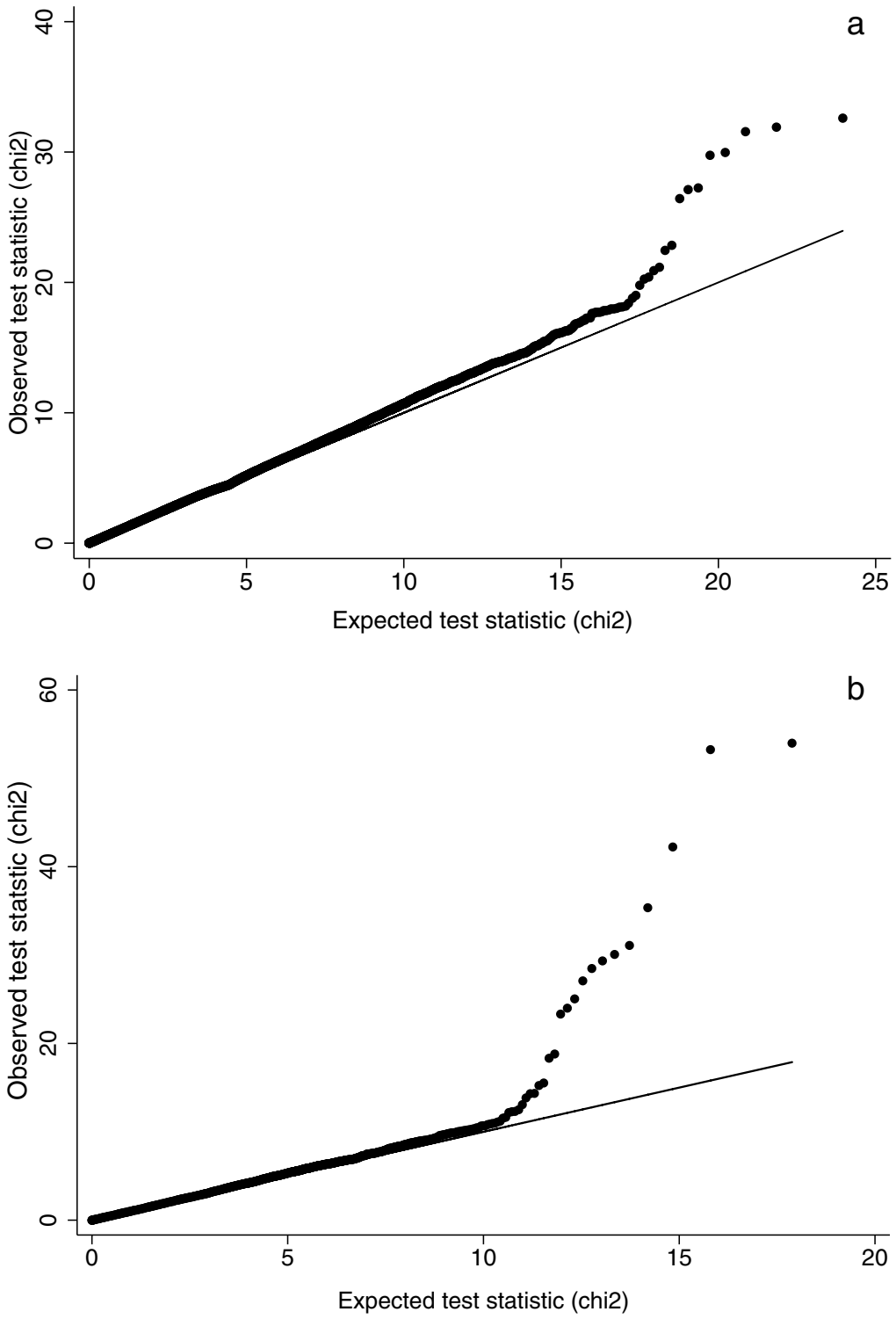
a – reported per-allele OR and trend test unless otherwise indicated

b - results from Stage 1 under same genetic model as published data.

c – serous subtype only

d – dominant model

Supplementary figure 1: Quantile-quantile plots for the test statistics for Stage 1 and Stage 2 analyses



Quantile-quantile plots for the test statistics (Chi squared Cochran-Armitage 1 d.f.) for (a) Stage 1 and (b) Stage 2 restricted to subjects of European ancestry. Under the null hypothesis of no association at any locus, the points would be expected to follow the black line.