Supplementary Tables

Supplementary Table 1. Candidate outcome variants at the 19p12 locus significantly associated (q<0.05) with greater *ZNF100* expression in normal ovarian tissue (GTEx, n=85).

SNP	PRE* location	p-value
rs10469371	-	2.201E-06
rs4547465	2	2.188E-06
rs8111464	-	2.190E-06
rs8105002	-	2.209E-06
rs4613201	-	2.201E-06
rs10421113	1	2.201E-06
rs10421342	1	2.201E-06
rs4808295	1	2.201E-06
rs10423041	-	2.201E-06
rs4809175	-	2.201E-06
rs7258859	-	1.360E-06
rs10412225	-	2.319E-06
rs11085492	-	2.201E-06

*PRE: putative regulatory element

Supplementary Table 2. Alteration of transcription factor binding position weight matrices (PWMs) by alleles of candidate variants.

Candidate variant (reference/ alternative allele)	Location	PWM*	Reference allele score*	Alternative allele score*
rs4467196 (C/A)	*ZNF100* promoter	-	-	-
rs10421113 (G/A)	*ZNF100* PRE1	GATA_disc3	14.8	2.9
		NRSF_disc8	11	10.8
		PRDM1_known1	-5	7
rs10421342 (G/A)	*ZNF100* PRE1	CTCF_disc1	3.6	9.5
		CTCF_disc3	4.7	16.6
		CTCF_disc8	-0.1	11.6
		CTCF_known1	2.5	9.9
		Roaz_1	-9.1	-20.6
		SMC3_disc1	2.5	10.3
		Zec	5.5	-6.1
rs4808295 (A/G)	*ZNF100* PRE1	Egr-1_known4	1.3	13.3
		Egr-1_known5	3.7	10.9
		FXR_2	11.4	9.1
		GLI	1	11.4
		Hbp1	12	4
		Hoxb3	9.9	11.9
		Nr2f2	8.9	11.2
		Pax-8_1	10.1	8.9
rs78985149 (T/C)	*ZNF100* PRE1	Myc_known1	4.2	12.2
		Myc_known7	1.6	13.5
rs11879157 (C/T)	*ZNF100* PRE2	GR_disc4	1	12.9
		TATA_disc1	-0.5	11.5
		THAP1_disc2	-5.4	6.5
		YY1_known2	6.4	11.7
		YY1_known3	7.9	12.3
		YY1_known4	4.9	16.8
rs4547465 (G/A)	*ZNF100* PRE2	Arid5b	11.9	13.1
		CDP_1	-0.7	11.2
		Foxp1	-10.2	-9.2
		HDAC2_disc3	11.3	9.5
rs942964 (G/A)	*MEF2D* PRE1	GR_known3	1.4	11
rs11264489 (A/G)	*MEF2D* PRE1	Hic1_2	8.5	11.6
		Mxi1_disc1	12.7	13.6
		RFX5_disc1	9.6	12.1
		SREBP_disc1	11.1	13.2
		STAT_known4	8.2	14.4
		STAT_known6	-8.7	3.3
		STAT_known7	8.2	11.9

Candidate variant (reference/ alternative allele)	Location	PWM*	Reference allele score*	Alternative allele score*
rs10159180 (T/C)	*MEF2D* PRE1	E2F_disc6	12.7	9.7
rs11264488 (C/G)	*MEF2D* PRE1	Cdx2_2	10.5	11.6
		Foxp1	5.1	10.5
		HDAC2_disc6	17	10.6
		HNF1_7	9.3	12.3
		Sox_19	10.2	11.3
		Sox_2	16.1	16.5
		p300_disc5	14.1	14.3
rs7550381 (G/A)	*MEF2D* PRE2	AP-2_disc2	12	13
		AP-2_known4	14	14.6
		BDP1_disc1	3.6	3
		CTCF_disc7	10.6	13.8
		CTCF_known1	4.8	9.5
		EBF_disc1	10.7	13.4
		EBF_disc2	12.1	12.6
		EBF_known1	10.8	13.5
		EBF_known2	4	15.2
		GR_disc6	12.7	1.9
		PU.1_disc3	12.4	12.5
		PU.1_known2	-13	-2.5
		VDR_2	13	9.5
		Zic_4	13	11
rs947661 (G/A)	*MEF2D* PRE2	Evi-1_2	-5	-1.6
		Irf_known6	0.8	4.4
		KAP1_disc2	-20.2	-8.4
		Nkx2_11	12.5	7.9
		Pax-4_4	11	12
rs11264494 (C/T)	-	Crx_1	10.9	11.3
		Pitx2	16.2	15.6

*Accessed from Haploreg v4.1 (http://archive.broadinstitute.org/mammals/haploreg)

Supplementary Table 3. Super-enhancers predicted to target *MEF2D* and coincident with candidate variants at 1q22.

Chr	Start*	End*	PRE	Tissue
chr1	156425476	156481717	1	BI Hippocampus Middle
chr1	156425489	156481358	1	BI Brain Hippocampus Middle 150
chr1	156425489	156481358	1	BI Brain Hippocampus Middle 302
chr1	156425572	156481357	1	BI Brain Cingulate Gyrus
chr1	156425594	156481720	1	BI Brain Inferior Temporal Lobe
chr1	156425720	156498527	1	CD14
chr1	156425814	156482547	1	UCSD Psoas Muscle
chr1	156425839	156481284	1	UCSD Sigmoid Colon
chr1	156425855	156481316	1	UCSD Left Ventricle
chr1	156425857	156481259	1	BI Brain Angular Gyrus
chr1	156425860	156481289	1	UCSD Right Atrium
chr1	156425916	156481291	1	UCSD Lung
chr1	156425930	156481272	1	UCSD Esophagus
chr1	156425939	156480889	1	UCSD Gastric
chr1	156425948	156481289	1	UCSD Aorta
chr1	156426421	156481207	1	UCSD Ovary
chr1	156441114	156481261	1	UCSD Small Intestine
chr1	156444182	156481638	1	HSMMtube
chr1	156444667	156481327	1	NHLF
chr1	156444845	156481322	1	Fetal muscle
chr1	156449690	156481292	1	UCSD Spleen
chr1	156458712	156496436	1	Colon Crypt 1
chr1	156467034	156482747	1	HeLa
chr1	156477294	156481293	1	BI Brain Anterior Caudate
chr1	156493382	156495361	2	BI CD8 Memory 7pool
chr1	156493408	156495402	2	BI CD4 Memory Primary 7pool
chr1	156493423	156495629	2	Fetal Thymus
chr1	156493457	156496301	2	MM1S
chr1	156493513	156495490	2	GM12878
chr1	156493519	156495441	2	CD8 primary
chr1	156493523	156495333	2	Jurkat
chr1	156493524	156495393	2	BI CD34 Primary RO01536
chr1	156493536	156495527	2	CD56
chr1	156493728	156495520	2	RPMI-8402
chr1	156493800	156495310	2	UCSD Thymus
chr1	156493904	156494955	2	K562
chr1	156493935	156495434	2	UCSD Small Intestine
chr1	156494146	156495432	2	UCSD Sigmoid Colon
chr1	156494364	156495415	2	UCSD Spleen
chr1	156494455	156495519	2	BI CD34 Primary RO01549

*GRCh37/hg19

Supplementary Table 4. Associations of candidate outcome variants at the 1q22 locus with *MEF2D* and *IQGAP3* expression in normal ovarian tissue (GTEx, n=85).

SNP	PRE location	Gene	p-value	Gene	p-value
rs11264488	1	*MEF2D*	0.180	*IQGAP3*	0.78
rs10159180	1	*MEF2D*	0.180	*IQGAP3*	0.98
rs11264489	1	*MEF2D*	**0.032**	*IQGAP3*	0.57
rs942964	1	*MEF2D*	0.078	*IQGAP3*	0.93
rs35425686	-	*MEF2D*	N/A	*IQGAP3*	N/A
rs6427312	-	*MEF2D*	0.064	*IQGAP3*	0.91
rs6674079	-	*MEF2D*	**0.028**	*IQGAP3*	0.56
rs61813464	-	*MEF2D*	0.084	*IQGAP3*	0.78
rs61813465	-	*MEF2D*	0.084	*IQGAP3*	0.78
rs12084217	-	*MEF2D*	0.084	*IQGAP3*	0.78
rs1750306	-	*MEF2D*	0.028	*IQGAP3*	0.56
rs1778832	-	*MEF2D*	**0.028**	*IQGAP3*	0.56
rs1750307	-	*MEF2D*	**0.028**	*IQGAP3*	0.56
rs1750308	-	*MEF2D*	**0.025**	*IQGAP3*	0.60
rs1778830	-	*MEF2D*	**0.026**	*IQGAP3*	0.57
rs60711781	-	*MEF2D*	N/A*	*IQGAP3*	N/A
rs200223591	-	*MEF2D*	N/A	*IQGAP3*	N/A
rs35361354	-	*MEF2D*	N/A	*IQGAP3*	N/A
rs10908506	-	*MEF2D*	0.080	*IQGAP3*	0.80
rs10908507	-	*MEF2D*	0.080	*IQGAP3*	0.81
rs11264491	-	*MEF2D*	0.079	*IQGAP3*	0.88
rs11264492	-	*MEF2D*	0.090	*IQGAP3*	0.81
rs7533916	-	*MEF2D*	**0.012**	*IQGAP3*	0.74
rs60322795	-	*MEF2D*	**0.012**	*IQGAP3*	0.74
rs11264493	-	*MEF2D*	**0.018**	*IQGAP3*	0.67
rs7544205	-	*MEF2D*	**0.012**	*IQGAP3*	0.74
rs4661177	-	*MEF2D*	**0.013**	*IQGAP3*	0.75
rs947661	2	*MEF2D*	**0.018**	*IQGAP3*	0.67
rs7550381	2	*MEF2D*	**0.014**	*IQGAP3*	0.76
rs12732658	-	*MEF2D*	**0.046**	*IQGAP3*	0.55
rs12747719	-	*MEF2D*	0.180	*IQGAP3*	0.87

*Data were not available (N/A) from GTEx

Supplementary Table 5. PCR primers.

Primer	Primer sequence
Real-time PCR	
ZNF100 5' qPCR	TAGCCTGTGTGGCCCTCTG
ZNF100 3' qPCR	GGCCACATCCCTAAACGTCA
MEF2D 5' qPCR	TTAGATCTGAACAATGCCCAGC
MEF2D 3' qPCR	AGGCTGGTAAGGAGGAGAGC
ACTB 5' qPCR	GGAAATCGTGCGTGACATTAAGG
ACTB 3' qPCR	AGTACTTGCGCTCAGGAGGAGC
ZNF100 3C	
3C Bait	GCCATTCCTAACTCCCAGTTCCAACAATAGG
3C Fragment 1	GTTCATATCACCTTCTATCATTAGGGCCCAGTTCC
3C Fragment 2	AACCTCAGGTGTGCACCACCACACC
3C Fragment 3	TGCTATTTGTGATTGGTGGCCATTTAAGACC
3C Fragment 4	TGTTGTGTCTTCTGAGGTTATCACCTGAAGGG
3C Fragment 5	GCAAGACTCCAAAGTGGGCCAGACC
3C Fragment 6	TCCACCCACAACAATAAACAGAAGCTGTGG
3C Fragment 7	AAATGATAAGGACAGCCAACCGGAAGGC
3C Fragment 8	CCAATTTGTCTGATGTTCTGGCACTTTGC
3C Fragment 9	GGCAAAGCCTTCAACTGGTTCTCAACC
3CFragment 10	ATTGAACAAAGTTTGAGCAACTGCTTCAGAGG
3C Fragment 11	TGAGTGTCTTTCATACCATTACCATCAGCACC
3C Fragment 12	CCTTCCCACCAAAGCAAGCCATGG
3C Fragment 13	TGGAGGACTAATTAACGCAGACTCCATCATAAGG
3C Fragment 14	AGGCAGTTTAAGTGGGTAAAAGAGTTCTCACTGG
3C Fragment 15	CCAGATGAAATGGCTGCACTGTCTGG
3C Fragment 16	TAACAGAGAGAGAGAAAGCTCCTCATGC
3C Fragment 17	ACCAGCCAGGTAAAGCCACGTGAGC
3C Fragment 18	TCCAGTGGCCTTCATCACATGCTGG
3C Fragment 19	GCTGTCACCATGACATCTGCACTCATGG
3C Fragment 20	TTGTAGCCTTGCACCACATAAAGAGAAACTGC
Allele-specific 3C	
Reverse primer	GGTAAGAAGGTGGTGCTGACACATT
Sequencing	GCTTCTCATTAAGATCACATGACCAGTTGG
MEF2D cloning and sequencing	
MEF2D promoter 5'	GGTACCACAGGTAGAGGGAGCAACTGAGC
MEF2D promoter 3'	AAGCTTAGCAAAGAGGGACACAGGATCC
MEF2D prom seqfwd1	TACTTAGACTCCCACCTCCCAA
MEF2D prom seqfwd2	AAGCTAGGCTGAGCTGTGCCTA
MEF2D prom seqfwd3	GGGATTACCTAGGGGACTGTTT
MEF2D PRE1 5'	ACCGGTCTTGAGAGAGAGCCTTTTGCTATCC
MEF2D PRE1 3'	GTCGACATCAATCTTGGAGGAAGGTCGAG
rs942964 T 5'	GTAATTTTGGCAGCAC**T**TCATGAACATTGCTG
rs942964 T 3'	CAGCAATGTTCATGA**A**GTGCTGCCAAAATTAC

rs11264489 C 5’	CCTGTGTCTTC**C**CGGCAACGCAG
rs11264489 C 3’	CTGCGTTGCCG**G**GAAGACACAGG
rs10159180 G 5’	CTTGATCGTTACCTC**G**TTCAAACTCCAGTCC
rs10159180 G 3’	GGACTGGAGTTTGAA**C**GAGGTAACGATCAAG
rs11264488 C 5’	CAATAATAAAA**C**AGAAGAAAAATAACGGCATACAG
rs11264488 C 3’	CTTCTGTTTTATTATTGTTTTTT**G**GTGGACTGGAG
MEF2D PRE1 seqfwd1	CTGGAGTGCAGTGGCGCAAT
MEF2D PRE1 seqfwd2	CCTGGCATAAAGCAGGAATGAAA
MEF2D PRE1 seqfwd3	GGCAATGGAGGAAGTGACAGAA
MEF2D PRE2 AgeI5’	ACCGGTCTCTTGTCTGTGGTCTGTTTAATATGTGG
MEF2D PRE2 SalI3’	GTCGACAATTGTCCTCCAAAGAGGTTACACTGG
rs7550381 T 5’	CTCTTCCTTCCCC**T**GGGGGACAGAGAG
rs7550381 T 3’	CTCTCTGTCCCCC**A**GGGGAAGGAAGAG
rs947661 T 5’	GC**T**ACTCTAATTTCTACCCCACCCGTTTTACACAC
rs947661 T 3’	GTGGGGTAGAAATTAGAGTAGCTTCTCTTCTC**A**[#]GC
MEF2D PRE2 seqfwd1	TTTCTGTAGAGCCGGCCTTT
MEF2D PRE2 seqfwd2	AGACACCTGCCCTGACATCTGAA
ZNF100 cloning and sequencing primers	
ZNF100 promoter 5’	GGTACCACAATGTGCCTGGTCTGAAATGC
ZNF100 promoter 3’	AAGCTTAGCAGAAGACACAGAGAAGTGAGAGC
rs4467196 T 5’	ATCCACATGTGGCT**T**ACATTCATTTTAGATG
rs4467196 T 3’	CATCTAAAATGAATGT**A**AGCCACATGTGGAT
ZNF100 PRE1 5’	ACCGGTTGCTGGGCCCTTTATCTAAATCC
ZNF100 PRE1 3’	GTCGACAATGTGTCAGCACCACCTTCTTACC
rs10421113 A 5’	GCACCTGAGAC**A**GGAAAGGAGAAAC
rs10421113 A 3’	GTTTCTCCTTTCC**T**GTCTCAGGTGC
rs10421342 A 5’	CACCTTTGCACTA**A**AGGGTGGTTACGATACC
rs10421342 A 3’	GGTATCGTAACCACCCT**T**TAGTGCAAAGGTG
rs4808295 T 5’	GAAACACCCA**T**TCATGAACCCTTTCC
rs4808295 T 3’	GGAAAGGGTTCATG**A**ATGGGTGTTTC
rs78985149 G 5’	CTCTTGAGCACAT**G**GTACCTGCTTAATAATTATTG
rs78985149 G 3’	CAATAATTATTAAGCAGGTAC**C**ATGTGCTCAAGAG
ZNF100 PRE1 seqfwd1	GTGGGACCAACATTACCAAGTGATT
ZNF100 PRE2 5’	ACCGGTGTAGAGACAGGGTTTCG
ZNF100 PRE2 3’	GTCGACGCCCAGTGTTAAGTACG
rs11879157 A 5’	CCTAACGGCC**A**TCTTCATTTACATTCAAACC
rs11879157 A 3’	GGTTTGAATGTAAATGAAGA**T**GGCCGTTAGG
rs4547465 T 5’	CTGTTGATTCTATATTTTGG**T**TATTGTGAAGAGTG
rs4547465 T 3’	CACTCTTCACAATA**A**CCAAAATATAGAATCAACAG

Underlined sequence indicates restriction enzyme site.
Bolded base indicates SNP locus.

Supplementary Table 6. All studies included in the meta-analysis according to chemotherapy subset ("Any chemo" & "Standard chemo")

Study (Location)	Ascertainment	Follow-up	[a]Overall Survival		[a]Progression-Free Survival	
			Any Chemo (N)	Std Chemo (N)	Any Chemo (N)	Std Chemo (N)
AUS (Australia)	Patients were diagnosed from 2002-2006; recruited through surgical treatment centers throughout Australia & cancer registries of Queensland, S. Australia, W. Australia, Tasmania, New South Wales & Victoria	Medical records reviewed at 6 - 12 month intervals	976	584	976	584
[b]BAV (Southeast Germany)	Patients recruited through hospitals in Erlangen, Northern Bavaria, Germany from May 2002 to August 2008	Cancer registry, medical records, and patient contact	57	29	0	0
BEL (Belgium)	Patients attending the Gynecologic Oncology Unit at the Leuven University Hospital diagnosed with incident ovarian cancer from 2009 onwards	Patient contact and vital statistics	272	123	272	123
BVU (USA)	Patients diagnosed or treated at Vanderbilt University Medical Center clinics. Includes all ovarian cancer patients included in the Tumor Registry, as well as patients not included in the Tumor Registry but with verified diagnoses.	Data were abstracted from study participants clinical electronic medical record	64	41	64	41
CNI (Spain)	Patients ascertained through CNIO familial cancer consultancy or referrals to CNIO for BRCA1/2 mutation screening or attending hospitals in Madrid in Medical Oncology Divisions;	Data obtained from medical records by research nurses and data managers at centres	25	15	25	15
HAW (USA: Hawaii & Southern CA)	Hawaii Tumor Registry; patients diagnosed between 1993 and 2008	Standard US NCI SEER-registry follow-up methods and review of the medical charts	50	16	50	16
[b]HJO (Germany)	Patients ascertained from the Hannover Medical School or the Friedrich-Schiller University Jena	Clinical and pathology data were drawn from medical records.	78	24	0	0
HOP (USA: OH, PA and NY)	Patients were identified from three catchment areas (western PN, northern OH & western NY) through a variety of sources including physician offices, cancer registries and pathology	Structured interview using detailed questionnaires, and review of medical records from physicians, pathologists, hospitals.	436	197	436	197

Study (Location)	Ascertainment	Follow-up	[a]Overall Survival		[a]Progression-Free Survival	
			Any Chemo (N)	Std Chemo (N)	Any Chemo (N)	Std Chemo (N)
	databases.					
HSK (Germany)	Patients attending the Gynecologic Oncology Unit at the Dr. Horst-Schmidt Kliniken, Wiesbaden, diagnosed with incident ovarian cancer between 2005-2009	Institutional database, medical records and patients contact at least annually	151	86	151	86
ICN (multi-center)	Patients were enrolled in ICON7 between 2006 and 2009 at 263 centers in the United Kingdom, Germany, France, Canada, Australia,New Zealand, Denmark, Finland, Norway,Sweden, and Spain; and were randomly assigned in a 1:1 ratio to receive carboplatin- paclitaxel (standard-chemotherapy group), or to the same regimen plus bevacizumab	Patients were follow-up every 3 months until disease progression was documented. If no evidence of disease progression, follow-up interval was extended to every 6 months during years four and five and yearly thereafter. After documented disease progression, patients were followed every 6 months up to 5 years after study entry, and yearly thereafter to document survival and ovarian cancer therapy	363	162	366	164
LAX (USA: Southern CA)	Patients were identified through the Women's Cancer Research Institute biorepository from 1989 onwards. Patients presenting to the gynecologic cancer service with epithelial ovarian cancer are identified in IRB 901 (Tissue Bank) and IRBs 1080 and 4049 (Gilda Radner Hereditary Cancer).	Annual chart abstraction and cancer registry updates	221	95	221	95
MAC (USA: North Central)	Patients attending Mayo Clinic diagnosed from 2000 onwards identified outside a six state surrounding region or greater than one year from diagnosis.	Patient contact and vital statistics	138	63	138	63
MAL (Denmark)	Incident cases diagnosed 1994 -1999 from municipalities of Copenhagen & Frederiksberg & surrounding counties.	Danish Civil Registration System and Danish Register of Causes of Death	376	112	376	112

Study (Location)	Ascertainment	Follow-up	[a]Overall Survival		[a]Progression-Free Survival	
			Any Chemo (N)	Std Chemo (N)	Any Chemo (N)	Std Chemo (N)
MAY (USA: North Central)	Patients attending Mayo Clinic enrolled within one year of diagnosis from 2000 onwards identified in a six state surrounding region.	Patient contact and vital statistics	1005	394	1005	394
[b]NCO (USA: Central and Eastern NC)	Patients were identified through the North Carolina Central Cancer Registry by using rapid case ascertainment in a 48 county region of NC. Pathology reports for ovarian cancer patients were forwarded to the Central Cancer Registry and then to the study office within 2 months of diagnosis.	National Death Index and North Carolina Central Cancer Registry every 18-24 months	212	121	0	0
NEC (USA: NH & Eastern MA)	Patients were identified through state-wide cancer registries and hospital tumor boards in eastern Massachusetts and New Hampshire.	Annual medical record abstraction and death record database updates	66	30	66	30
NOR (Norway)	All patients treated for suspected gynecologic cancer from one region of Norway	Data was collected by reviewing the medical records in the hospital	168	98	0	0
OPL (Australia)	Women aged 18-79 years with primary invasive epithelial ovarian cancer diagnosed between May 2012 and October 2014 identified through the major treatment centres in each state in Australia.	Medical records reviewed at recruitment and then annually.	384	96	330	96
ORE (USA: OR)	Registry and tissue repository of patients with ovarian cancer (or at risk for ovarian cancer and control case undergoing surgery for benign gynecologic conditions that aren't included in OCAC). Focus of the current research is on Fanconi DNA repair genes and proteins.	Cancer registry and electronic medical record reviews every three months	14	0	14	0

Study (Location)	Ascertainment	Follow-up	[a]Overall Survival		[a]Progression-Free Survival	
			Any Chemo (N)	Std Chemo (N)	Any Chemo (N)	Std Chemo (N)
PVD (Denmark)	All patients admitted with a pelvic mass at Rigshospitalet, University of Copenhagen, are included in the study with a blood sample less than 14 days before surgery/diagnosis of ovarian cancer and with FFPE and fresh frozen tissues if possible	Patient contact, recorded in online database and vital statistics	180	0	180	0
RBH (Australia)	Patients treated at Royal Brisbane Hospital diagnosed from 1985-1996 and recruited to the Biospecimen Bank in the Department of Obstetrics and Gynecology	Medical record abstraction	116	0	116	0
SRO (UK)	Patients randomised into a prospective phase III comparison of paclitaxel-carboplatin versus docetaxel-carboplatin as first line chemotherapy in stage Ic-IV epithelial ovarian cancer (SCOTROC 1) which recruited from 1998 to 2000	Performed every 2 months until progressive disease was documented. If no evidence of progression within 2 years of randomization, follow-up interval extended to 3 months during the 3rd year, and to 4 months for the 4th year. Thereafter (or after progression), patients were followed every 6 months.	124	49	124	49
[c]TCGA (UK & North American)	Patients diagnosed with serous tumours from 2006 at 15 participating UK and North America cancer centers	Patients followed according to site protocol. Clinical data finalized in August 2010. More information can be obtained at http://cancergenome.nih.gov/	335	145	337	147
UHN (Canada)	All women attending the Division of Gynecologic Oncology outpatient clinics at Princess Margaret Hospital who have consented to provide a blood sample to the GYNE Site Biobank, and have a confirmed diagnosis of epithelial ovarian cancer.	Clinical data obtained via medical record	131	53	131	53
VAN (Canada)	Patients attending VGH and/or BC Cancer Agency Division of Gynecologic Oncology	Clinical data obtained via medical record review	143	52	143	52
WMH (Australia)	Patients treated at Westmead Hospital, Sydney, diagnosed from 1992 onwards and recruited to the Gynaecological Oncology	Medical record abstraction	75	35	75	35

Study (Location)	Ascertainment	Follow-up	[a]Overall Survival		[a]Progression-Free Survival	
			Any Chemo (N)	Std Chemo (N)	Any Chemo (N)	Std Chemo (N)
	Biospecimen Bank at Westmead (GynBiobank)					
Total			**6160**	**2620**	**5596**	**2352**

[a]N is the largest dataset with SNP data and complete covariate data for all analyzed SNPs; differences in N for specific SNP analyses may be due to a small number of missing genotypes.
[b]These sites were excluded from PFS analysis due to missing or inconsistent data
[c]Clinical follow-up, chemotherapy and genotype data downloaded from http://cancergenome.nih.gov/