

Table S1. Susceptibility loci identified through 28 published genome-wide association studies in ovarian cancer cohorts.

Subtype	SNP	Locus	Position ^a	EA ^b	EAF ^c	OR	CI ₉₅	P-value	Gene ^d	eQTL ^e	Notes	Reference	DOI
BC-OC	rs200182588	09q31	104094410	insGC	0.56	0.93	(1.14-1.25)	2.80x10 ⁻⁶	SMC2			Kar 2016	10.1158/2159-8290.CD-15-1227
BC-OC	rs8037137	15q26	90963407	T	0.86	1.09	(1.04-1.14)	2.10x10 ⁻⁴	RCCD1	RCCD1		Kar 2016	10.1158/2159-8290.CD-15-1227
BC-PC-OC	rs17041869	02q13	111138666	A	0.88	0.93	(0.88-0.97)	5.30x10 ⁻⁴	BCL2L1			Kar 2016	10.1158/2159-8290.CD-15-1227
BC-PC-OC	rs7937840	11q12	62126500	T	0.26	1.05	(1.01-1.09)	5.80x10 ⁻³	INCENP			Kar 2016	10.1158/2159-8290.CD-15-1227
BC-PC-OC	rs1469713	19p13	19417997	A	0.64	0.96	(0.93-0.99)	6.30x10 ⁻³	GATAD2A	GATAD2A		Kar 2016	10.1158/2159-8290.CD-15-1227
EnOC	rs138031468	01p36.33	1041648	T	0.005	0.08	(0.01-0.56)	3.80x10 ⁻⁵	AGRN			Permeth 2016	10.1093/hmg/ddw196
EnOC	rs61757604	02p22.2	38868261	T	0.02	0.26	(0.12-0.56)	2.20x10 ⁻⁵	DHX57			Permeth 2016	10.1093/hmg/ddw196
EnOC	rs1619379	06p22.1	29817458	T	0.42	1.37	(1.19-1.56)	5.20x10 ⁻⁶	HLA-G, MICG		rs114979098 in reference	Permeth 2016	10.1093/hmg/ddw196
EnOC	rs2638653	08p22	18808700	G	0.41	1.23	(1.11-1.37)	1.30x10 ⁻⁴	PSD3			Earp 2016	10.18632/oncotarget.7121
EnOC	rs1052587	17q21.31	46025238	C	0.22	1.11	(1.04-1.19)	5.20x10 ⁻³	MAPT			Permeth-Wey 2013	10.1038/ncomms2613
EnOC	rs34051361	22q12.1	29186569	A	0.03	1.57	(1.24-1.98)	1.00x10 ⁻⁴	KREMEN1			Lawrenson 2015b	10.1093/carcin/bgv138
EOC	rs56318008	01p36.12	22143914	T	0.15	1.11	(1.07-1.16)	3.90x10 ⁻⁷	WNT4	CDC42		Kuchenbaecker 2015	10.1038/ng.3185
EOC	rs200337373	03p25.1	15644520	A	0.001	NE		8.60x10 ⁻⁶	BTD	BTD		Permeth 2016	10.1093/hmg/ddw196
EOC	rs73757391	05q11.2	57482386	T	0.001	NE		6.40x10 ⁻⁶	ACTBL2	ACTBL2	eQTL reported in Permeth 2016	Permeth 2016	10.1093/hmg/ddw196
EOC	rs9264042	06p21.33	31229024	A	0.13	1.17	(1.07-1.28)	4.70x10 ⁻⁴	HCG27, AL662844.2			Earp 2016	10.18632/oncotarget.7121
EOC	rs199761238	06q25.2	152330917	C	0.001	0.15	(0.03-0.63)	1.10x10 ⁻³	SYNE1			Permeth 2016	10.1093/hmg/ddw196
EOC	rs10808556	08q24	127400902	G	0.41	1.13	(1.04-1.22)	1.70x10 ⁻⁴	CASC8, CCAT2			Ghoussemi 2008	10.1093/jnci/djn190
EOC	rs10505477	08q24	127395198	A	0.5	1.14	(1.04-1.23)	2.00x10 ⁻³	MYC, FAM84B	MYC		Ghoussemi 2008	10.1093/jnci/djn190
EOC	rs6983267	08q24	127401060	G	0.51	1.11	(1.03-1.20)	9.90x10 ⁻³	CASC8, CCAT2 POU5F1B	SRRM1P1,	Variant reported in PC	Ghoussemi 2008	10.1093/jnci/djn190
EOC	rs635634	09q34.2	133279427	T	0.19	1.11	(1.07-1.16)	1.10x10 ⁻⁷	ABO			Kuchenbaecker 2015	10.1038/ng.3185
EOC	rs2228026	14q11.2	20395890	C	0.06	3.28	(1.72-6.29)	1.00x10 ⁻⁴	TEPI			Sun 2017	10.1111/jcmm.12995
EOC	rs10143322	14q32.11	91090233	G	0.22	0.87	(0.82-0.93)	3.00x10 ⁻⁵	DGLUCY			Earp 2016	10.18632/oncotarget.7121
EOC	rs147432497	15q12	25694912	A	0.001	0.16	(0.04-0.67)	1.60x10 ⁻³	ATP10A			Permeth 2016	10.1093/hmg/ddw196
EOC	rs13181	19q13.32	45351661	C	0.36	2.12	(1.14-3.97)	2.00x10 ⁻²	ERCC2			Li 2017	10.1007/s00404-017-4443-4
EOC	rs117841616	20q13.32	59280156	T	0.01	1.93	(1.36-2.74)	2.10x10 ⁻⁴	EDN3, ZNF831			Earp 2016	10.18632/oncotarget.7121
EOC	rs141200301	22q11.2	23781334	T	0.001	NE		7.50x10 ⁻⁵	MMP11			Permeth 2016	10.1093/hmg/ddw196
EOC	rs5752754	22q12.1	28529554	T	0.11	1.11	(1.06-1.16)	2.40x10 ⁻⁶	TTC28			Lawrenson 2015b	10.1093/carcin/bgv138
EOC	rs2853676	5p15.33	1288432	A	0.25	1.10	(1.01-1.18)	2.10x10 ⁻²	TERT	TERT		Beesley 2011	10.1371/journal.pone.0024987
EOC-BRCA1	rs67397200	19p13.11	17290595	G	0.17	1.16	(1.05-1.29)	3.80x10 ⁻⁴	ANKLE1, ABHD8	ANKLE1		Couch 2012	10.1158/1055-9965.EPI-11-0888
HGSC	rs4353340	01p34	37632363	G	0.25	0.90		1.40x10 ⁻⁷	CDC48, RSPO1	CDCA8		Lawrenson 2015a	10.1038/ncomms9234
HGSC	rs58722170	01p34.3	37630749	C	0.23	1.12	(1.08-1.18)	1.10x10 ⁻⁷	RSPO1			Kuchenbaecker 2015	10.1038/ng.3185
HGSC	rs72665317	01p36	22040580	G	0.16	0.89		6.90x10 ⁻⁷	LINC00339, CDC42			Lawrenson 2015a	10.1038/ncomms9234
HGSC	rs1374325	02q31.1	176179243	T	0.32	0.89	(0.83-0.96)	1.40x10 ⁻³	HAGLR, HOXD1			Earp 2016	10.18632/oncotarget.7121
HGSC	rs4679621	03p14.2	59339007	T	0.47	1.10	(1.05-1.15)	4.00x10 ⁻⁵	intergenic			Permeth 2016	10.1093/hmg/ddw196
HGSC	rs2665390	03q25	156679960	C	0.08	1.24	(1.15-1.34)	7.10x10 ⁻⁸	TIPARP	TIPARP		Goode 2010	10.1038/ng.668
HGSC	rs62275810	03q25.31	156930062	G	0.05	1.46	(1.27-1.68)	1.60x10 ⁻⁷	LEKRI		In LD with rs2665390	Earp 2016	10.18632/oncotarget.7121
HGSC	rs17329882	04q26	119028805	C	0.24	1.11	(1.07-1.16)	6.40x10 ⁻⁷	SYNPO2	SYNPO2		Kuchenbaecker 2015	10.1038/ng.3185
HGSC	rs2736109	05p15.33	1296644	A	0.41	0.86	(0.77-0.96)	5.00x10 ⁻³	TERT	TERT		Cao 2015	10.1371/journal.pone.0128829
HGSC	rs381852	05q11.2	55164133	A	0.21	1.14	(1.08-1.21)	9.10x10 ⁻⁶	CDC20B, GPX8			Permeth 2016	10.1093/hmg/ddw196

Table S1. Continued.

Subtype	SNP	Locus	Position ^a	EA ^b	EAF ^c	OR	CI ₉₅	P-value	Gene ^d	eQTL ^e	Notes	Reference	DOI
HGSC	rs2297980	06p12.1	54308615	G	0.09	0.83	(0.77-0.9)	2.30x10 ⁻⁶	TINAG			Permeth 2016	10.1093/hmg/ddw196
HGSC	rs9380516	06p21.31	35534425	T	0.15	0.83	(0.76-0.91)	6.40x10 ⁻⁵	RP3-340B19.3, AL033519.3			Earp 2016	10.18632/oncotarget.7121
HGSC	rs1265112	06p21.33	31150242	C	0.32	0.88	(0.83-0.94)	9.00x10 ⁻⁵	CCHCR1		rs116151586 in reference	Permeth 2016	10.1093/hmg/ddw196
HGSC	rs2853961	06p21.33	31264212	A	0.36	0.89	(0.84-0.94)	1.10x10 ⁻⁴	HLA-C		rs113935384 in reference	Permeth 2016	10.1093/hmg/ddw196
HGSC	rs2233976	06p21.33	31112217	T	0.07	0.84	(0.77-0.92)	1.30x10 ⁻⁴	C6orf15		rs149771958 in reference	Permeth 2016	10.1093/hmg/ddw196
HGSC	rs72856718	06p21.33	31157480	A	0.07	0.84	(0.77-0.92)	2.80x10 ⁻⁴	CCHCR1		rs114470046 in reference	Permeth 2016	10.1093/hmg/ddw196
HGSC	rs130072	06p21.33	31144707	T	0.07	0.84	(0.77-0.92)	2.90x10 ⁻⁴	CCHCR1		rs116682468 in reference	Permeth 2016	10.1093/hmg/ddw196
HGSC	rs2073724	06p21.33	31161930	T	0.07	0.84	(0.77-0.93)	3.10x10 ⁻⁴	TCF19		rs115538919 in reference	Permeth 2016	10.1093/hmg/ddw196
HGSC	rs6456822	06p22.1	28512858	C	0.31	0.91	(0.87-0.94)	2.60x10 ⁻⁷	GPX6		rs116133110 in the reference	Kuchenbaecker 2015	10.1038/ng.3185
HGSC	rs240783	06q16.3	100520861	T	0.4	0.89	(0.84-0.95)	7.90x10 ⁻⁴	ASCC3			Earp 2016	10.18632/oncotarget.7121
HGSC	rs1400482	08q24.21	128529685	A	0.1	0.80	(0.73-0.89)	1.70x10 ⁻⁵	LINC00824			Earp 2016	10.18632/oncotarget.7121
HGSC	rs1243180	10p12	21626690	A	0.31	1.11	(1.07-1.15)	1.40x10 ⁻⁷	MLLT10	MLLT10		Pharoah 2013	10.1038/ng.2564
HGSC	rs9971210	10p12.31	21590155	G	0.51	1.11	(1.04-1.19)	1.20x10 ⁻³	MLLT10		In LD with rs1243180	Earp 2016	10.18632/oncotarget.7121
HGSC	rs138643956	10q22.3	77608099	A	0.004	3.68	(1.79-7.55)	1.90x10 ⁻⁴	KCNMA1			Earp 2016	10.18632/oncotarget.7121
HGSC	rs145514333	11q13.1	64759717	T	0.004	3.59	(1.91-6.77)	2.70x10 ⁻⁵	PYGM			Permeth 2016	10.1093/hmg/ddw196
HGSC	rs11571833	13q13	32398489	T	0.008	1.57	(1.33-1.85)	6.40x10 ⁻⁸	BRCA2	BRCA2	Gene also present in COSMIC	Kar 2016	10.1158/2159-8290.CD-15-1227
HGSC	rs147445846	16q22.3	72959011	C	0.001	0.34	(0.19-0.61)	7.00x10 ⁻⁵	ZFX3			Permeth 2016	10.1093/hmg/ddw196
HGSC	rs150321809	17q21.2	41501347	T	0.003	2.45	(1.65-3.65)	6.50x10 ⁻⁶	KRT13, AC019349.1	KRT13	eQTL reported in Permeth 2016	Permeth 2016	10.1093/hmg/ddw196
HGSC	rs3785880	17q21.31	45916010	G	0.46	0.87	(0.82-0.93)	5.00x10 ⁻⁵	MAPT		In LD with rs12942666	Earp 2016	10.18632/oncotarget.7121
HGSC	rs9303542	17q21.32	48334138	G	0.27	1.14	(1.09-1.20)	1.40x10 ⁻⁷	SKAP1	SKAP1		Goode 2010	10.1038/ng.668
HGSC	rs104894658	18p11.21	13885298	A	0.002	10.15	(2.86-35.99)	2.80x10 ⁻⁵	MC2R	MC2R		Permeth 2016	10.1093/hmg/ddw196
HGSC	rs56069439	19p13.11	17283116	A	0.26	1.15	(1.15-1.23)	1.80x10 ⁻⁴	ANKLE1	ANKLE1, ABHD8 GNAS	In LD with rs8170	Earp 2016	10.18632/oncotarget.7121
HGSC	rs6026494	20q13	58756836	G	0.11	1.16		5.10x10 ⁻⁷	GNAS			Lawrenson 2015a	10.1038/hcomms9234
HGSC	rs6092485	20q13.31	57469958	G	0.34	1.13	(1.05-1.21)	6.80x10 ⁻⁴	CTCF			Earp 2016	10.18632/oncotarget.7121
HGSC	rs6005807	22q12.1	28538325	C	0.91	1.17	(1.11-1.24)	1.10x10 ⁻⁷	TTC28	CHEK2		Lawrenson 2015b	10.1093/carcin/bgv138
MOC	rs2072590	02q31	176177905	T	0.33	1.30	(1.17-1.44)	7.30x10 ⁻⁷	HOXD1	HOXD1, HOXD3	Goode 2010	10.1038/ng.668	
MOC	rs955276744	22q12.1	28730359	A	NA	1.56	(1.25-1.98)	1.00x10 ⁻⁴	ZNRF3		'chr22: 29126347.D' in reference	Lawrenson 2015b	10.1093/carcin/bgv138

Table S1. Continued.

Subtype	SNP	Locus	Position ^a	EA ^b	EAF ^c	OR	CI ₉₅	P-value	Gene ^d	eQTL ^e	Notes	Reference	DOI
OCCC	rs757210	17q12	37736525	A	0.37	0.80	(0.72-0.88)	3.90x10 ⁻⁶	HNFB1B	HNFB1B		Pharoah 2013	10.1038/ng.2564
OCCC	rs11651755	17q12	37739849	T	0.49	0.80	(0.70-0.91)	7.10x10 ⁻⁴	HNFB1B	HNFB1B		Shen 2013	10.1038/ncomms2629
OCCC	rs78371015	22q12.1	28849623	T	0.04	1.40	(1.17-1.67)	2.00x10 ⁻⁴	ZNRF3			Lawrenson 2015b	10.1093/carcin/bgv138

Susceptibility loci with an OR P>5.0x10⁻⁸ are included. ^aHuman genome reference assembly GRCh38/hg38. ^bEA is not necessarily on the leading strand. Preferably quoted by original publication, otherwise the minor allele, or with frequency corresponding to EAF. ^cEAF, preferably in case cohort, otherwise in the European ancestry population in the 1000 Genomes Project. ^dGene(s) in closest proximity to the most significant ovarian cancer risk variant at each locus. ^eGene with published functional correlation with phenotype and thus the likely gene responsible. Preferably quoted by reference; otherwise Ensembl's Biomart database ('Associated gene with phenotype'). BC-PC-OC and BC-OC, EOC loci from meta-analyses of datasets from breast, prostate and ovarian cancer; CI, confidence interval; DOI, date of issue; EAF, EA frequency; EnOC, endometrioid ovarian cancer; EOC, epithelial ovarian cancer (no subtype specified); EOC-BRCA1, EOC cases including BRCA1 carriers (The Consortium of Investigators of Modifiers of BRCA1/2); eQTL, expression quantitative trait loci; HGSC, high grade serous carcinoma; MOC, mucinous ovarian cancer; NE, not estimable (due to low heterozygosity count); OCC, ovarian clear cell carcinoma; OR, odds ratio; SNP, single nucleotide polymorphism.