

## **SUPPLEMENTARY FIGURE LEGEND**

### **Supplementary Figure 1**

**Quantile-quantile plots for the GWAS of (a) EOC and (b) HGSOC.**

Data are shown as observed and expected negative-log p-values.

### **Supplementary Figure 2**

**Manhattan plots for the GWAS of (a) EOC and (b) HGSOC.**

Data are shown as negative-log p-values.

### **Supplementary Figure 3**

**Local association plots for genetic loci reported for EOC in Table 2 near the genes: (a) *AKR1C3*, (b) *LOC101927394*, (c) *UGT2A2*, (d) *WWC1*.**

Data are shown as negative-log p-values.

### **Supplementary Figure 4**

**Local association plots for genetic loci reported for HGSOC in Table 2 near the genes: (a) *FST*, (b) *MAGEC1*, (c) *LOC105376360*, (d) *PRPSAP1*, (e) *GABRG3*, (f) *LOC105377300 / GK2*.**

Data are shown as negative-log p-values.

### **Supplementary Figure 5**

**Results of eQTL analysis in 260 ovarian tissues from AACES participants for selected SNPs from the GWAS of EOC and HGSOC\***

Listed below the figure: \*Boxplots represent the distribution of measured expression versus genotype (rounded to the nearest whole number for imputed dosage variables). P-values are reported from linear models with covariate adjustment for age and two principal components of ancestry.

**Supplementary Table 1: Descriptive statistics for study participants**

Study Sites	EOC			HGSOC		
	Cases	Controls	Total	Cases	Controls	Total
	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)
AAS – African American Cancer Epidemiology Study	467 (61.9)	563 (45.6)	1030 (51.8)	349 (65.0)	563 (45.6)	912 (51.5)
BEL – Belgium Ovarian Cancer Study	0 (0.0)	2 (0.2)	2 (0.1)	0 (0.0)	2 (0.2)	2 (0.1)
BVU – The BioVU DNA Repository	8 (1.1)	98 (7.9)	106 (5.3)	4 (0.7)	98 (7.9)	102 (5.8)
CAM – Cancer Research UK, Cambridge Research Institute	1 (0.1)	0 (0.0)	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)
DKE – Duke University Clinic	7 (0.9)	0 (0.0)	7 (0.4)	3 (0.6)	0 (0.0)	3 (0.2)
DOV – Diseases of the Ovary and their Evaluation	7 (0.9)	27 (2.2)	34 (1.7)	4 (0.7)	27 (2.2)	31 (1.8)
HAW – Hawaii Ovarian Cancer Study	0 (0.0)	3 (0.2)	3 (0.2)	0 (0.0)	3 (0.2)	3 (0.2)
HOP – Hormones and Ovarian Cancer Prediction	16 (2.1)	21 (1.7)	37 (1.9)	10 (1.9)	21 (1.7)	31 (1.8)
LAX – Women's Cancer Program at the Samuel Oschin Comprehensive Cancer Institute	18 (2.4)	0 (0.0)	18 (0.9)	15 (2.8)	0 (0.0)	15 (0.9)
MAY – Mayo Clinic Ovarian Cancer Case-Control Study	3 (0.4)	5 (0.4)	8 (0.4)	2 (0.4)	5 (0.4)	7 (0.4)
MEC – Multiethnic Cohort Study	10 (1.3)	13 (1.1)	23 (1.2)	6 (1.1)	13 (1.1)	19 (1.1)
MOF – Moffitt Cancer Center Ovarian Cancer Study	16 (2.1)	14 (1.1)	30 (1.5)	13 (2.4)	14 (1.1)	27 (1.5)
MSK – Memorial Sloan Kettering Cancer Center	8 (1.1)	20 (1.6)	28 (1.4)	8 (1.5)	20 (1.6)	28 (1.6)
NCO – North Carolina Ovarian Cancer Study	108 (14.3)	160 (13.0)	268 (13.5)	76 (14.2)	160 (13.0)	236 (13.3)
NEC – New England Case-Control Study of Ovarian Cancer	6 (0.8)	5 (0.4)	11 (0.6)	6 (1.1)	5 (0.4)	11 (0.6)
NHS – Nurses' Health Study I and II	3 (0.4)	0 (0.0)	3 (0.2)	3 (0.6)	0 (0.0)	3 (0.2)
NOR – University of Bergen, Haukeland University Hospital, Norway	1 (0.1)	0 (0.0)	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)
NTH – Nijmegen Ovarian Cancer Study	1 (0.1)	0 (0.0)	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)
ORE – Oregon Ovarian Cancer Registry	1 (0.1)	0 (0.0)	1 (0.1)	1 (0.2)	0 (0.0)	1 (0.1)
OVA – Ovarian Cancer in Alberta and British Columbia	1 (0.1)	0 (0.0)	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)
PLC –Prostate-Lung-Colorectal and Ovarian Cancer Screening Trial	5 (0.7)	85 (6.9)	90 (4.6)	2 (0.4)	85 (6.9)	87 (4.9)
RMH – Royal Marsden Hospital Ovarian Cancer Study	1 (0.1)	0 (0.0)	1 (0.1)	1 (0.2)	0 (0.0)	1 (0.1)
RPC – Roswell Park Cancer Institute Ovarian Cancer Cohort	4 (0.5)	0 (0.0)	4 (0.2)	3 (0.6)	0 (0.0)	3 (0.2)
SEA – UK Studies of Epidemiology and Risk Factors in Cancer Heredity (SEARCH) Ovarian Cancer Study	2 (0.3)	1 (0.1)	3 (0.2)	1 (0.2)	1 (0.1)	2 (0.1)
SIS – The Sister Study	8 (1.1)	131 (10.6)	139 (7.0)	3 (0.6)	131 (10.6)	134 (7.6)
SOC – Southampton Ovarian Cancer Study	1 (0.1)	0 (0.0)	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)
STA – Genetic Epidemiology of Ovarian Cancer	12 (1.6)	45 (3.6)	57 (2.9)	4 (0.7)	45 (3.6)	49 (2.8)
UCI – UC Irvine Ovarian Cancer Study	0 (0.0)	2 (0.2)	2 (0.1)	0 (0.0)	2 (0.2)	2 (0.1)
UHN – Princess Margaret Cancer Centre	4 (0.5)	0 (0.0)	4 (0.2)	2 (0.4)	0 (0.0)	2 (0.1)
UKO – UK Ovarian Cancer Population Study	4 (0.5)	10 (0.8)	14 (0.7)	2 (0.4)	10 (0.8)	12 (0.7)
USC – Los Angeles County Case-Control Studies of Ovarian Cancer	31 (4.1)	30 (2.4)	61 (3.1)	18 (3.4)	30 (2.4)	48 (2.7)
WMH – Westmead Institute for Cancer Research – Westmead Hospital	1 (0.1)	0 (0.0)	1 (0.1)	1 (0.1)	0 (0.0)	1 (0.1)
<b>TOTAL</b>	<b>755</b>	<b>1235</b>	<b>1990</b>	<b>537</b>	<b>1235</b>	<b>1772</b>

**Supplementary Table 2: Bayesian False-Discovery Probabilities for Ovarian Cancer GWAS SNPs in women of African ancestry**

Subtype	Nearest Gene	SNP ID (Effect / other allele)	OR (95% CI)	P-value	BFDP <sub>1/1K</sub>	BFDP <sub>1/10K</sub>
EOC	<i>AKR1C3</i>	rs4525119 (T/C)	0.70 (0.61-0.81)	4.9 x 10 <sup>-7</sup>	0.08	0.49
	<i>LOC101927394</i>	rs7643459* (T/G)	1.40 (1.22-1.60)	8.4 x 10 <sup>-7</sup>	0.05	0.33
	<i>UGT2A2</i>	rs4286604 (A/G)	0.69 (0.59-0.80)	8.5 x 10 <sup>-7</sup>	0.05	0.34
	<i>WWC1</i>	rs142091544 (T/C)	3.22 (2.02-5.13)	9.4 x 10 <sup>-7</sup>	0.08	0.47
HGSOC	<i>FST</i>	rs37792 (G/A)	0.65 (0.55-0.76)	6.0 x 10 <sup>-8</sup>	0.004	0.04
	<i>MAGEC1</i>	rs57403204 (G/A)	2.62 (1.83-3.76)	1.7 x 10 <sup>-7</sup>	0.01	0.13
	<i>LOC105376360</i>	rs79079890 (G/T)	3.20 (2.05-4.99)	3.0 x 10 <sup>-7</sup>	0.03	0.25
	<i>PRPSAP1</i>	rs66459581 (A/AC)	1.63 (1.35-1.97)	5.1 x 10 <sup>-7</sup>	0.02	0.19
	<i>GABRG3</i>	rs116046250 (G/T)	2.95 (1.92-4.54)	8.7 x 10 <sup>-7</sup>	0.07	0.44
	<i>LOC105377300 / GK2</i>	rs192876988 (C/T)	3.01 (1.94-4.68)	9.2 x 10 <sup>-7</sup>	0.08	0.47

BFDP=Bayesian false-discovery probability; the subscripted number is the level of prior probability

**Supplementary Table 3:** Genes targeted for eQTL analysis within the region of ten EOC- and HGSOC-associated SNPs

<b>Subtype</b>	<b>SNP ID</b>	<b>Build 37 Chr:Pos</b>	<b>Nearest gene</b>	<b>Genes within 100kb</b>	<b>Genes at 100-500kb<sup>a</sup></b>
<b>EOC</b>	rs4525119	10:5091954	<i>AKR1C3</i>	<i>AKR1C3, AKR1C1, AKR1C2</i>	
	rs7643459	3:8004828	<i>LOC101927394</i>	<i>LOC101927394</i>	
	rs4286604	4:70442165	<i>UGT2A2</i>	<i>UGT2B4, UGT2A2, UGT2A1</i>	
	rs142091544	5,167714000	<i>WWC1</i>	<i>WWC1, TENM2</i>	
<b>HGSOC</b>	rs37792	5:52644647	<i>FST</i>		<i>ITGA1, ITGA2, FST, NDUFS4</i>
	rs57403204	X:141078552	<i>MAGEC1</i>	<i>MAGEC1, MAGEC3</i>	
	rs79079890	10:3684148	<i>LOC105376360</i>	<i>LOC105376360</i>	
	rs66459581	17:74355264	<i>PRPSAP1</i>	<i>PRPSAP1, UBALD2, QRICH2, U6, SPHK1, UBE2D, AANAT</i>	
	rs116046250	15:27231950	<i>GABRG3</i>	<i>GABRG3, GABRB3, GABRA6, AK124673</i>	
	rs192876988	4:80297251	<i>GK2</i>	<i>GK2, NAA11, LOC100505875</i>	

<sup>a</sup>Genes in the 100-500kb range are reported and considered in eQTL analysis only for variants with no genes within 100kb.

**Supplementary Table 4:** Summary of genetic association for selected SNPs identified in GWAS of EOC and HGSOC with breast cancer in African American individuals from the AABC study

Nearest Gene	SNP ID (Effect / Other allele)	Build 37 Chr:Pos	EAF	Breast cancer - all		ER positive		ER negative	
				OR ( 95% CI)	P-value	OR (95% CI)	P-value	OR (95% CI)	P-value
<i>AKR1C3</i>	rs4525119 (T/C)	10:5091954	0.328	1.07 (0.99,1.16)	0.098	1.02 (0.93,1.13)	0.621	1.11 (1.00,1.24)	0.058
<i>LOC101927394</i>	rs7643459 (T/G)	3:8004828	0.377	1.05 (0.97,1.13)	0.232	1.02 (0.93,1.12)	0.622	1.13 (1.01,1.26)	0.029
<i>UGT2A2</i>	rs4286604 (A/G)	4:70442165	0.279	0.94 (0.86,1.02)	0.142	0.93 (0.84, 1.04)	0.205	0.96 (0.85,1.09)	0.551
<i>WWC1</i>	rs142091544 (T/C)	5:167714000	0.040	1.07 (0.87, 1.31)	0.530	0.87 (0.67, 1.14)	0.314	1.55 (1.19, 2.02)	0.001
<i>FST</i>	rs37792 (G/A)	5:52644647	0.341	0.96 (0.89, 1.04)	0.424	0.97 (0.88,1.07)	0.578	0.97 (0.87, 1.09)	0.621
<i>MAGEC1</i>	rs57403204 (G/A)	X:141078552	0.051	0.93 (0.77, 1.12)	0.424	0.89 (0.71, 1.12)	0.329	0.97 (0.74, 1.25)	0.813
<i>LOC105376360</i>	rs79079890 (G/T)	10:3684148	0.035	1.22 (0.99,1.50)	0.066	1.21 (0.95,1.55)	0.125	1.12 (0.83,1.52)	0.449
<i>PRPSAP1</i>	rs66459581 (A/AC)	17:74355264	0.228	1.01 (0.92,1.10)	0.890	0.89 (0.80,1.00)	0.054	1.12 (0.99,1.28)	0.081
<i>GABRG3</i>	rs116046250 (G/T)	15:27231950	0.045	0.87 (0.71,1.06)	0.176	0.88 (0.69,1.12)	0.306	0.83 (0.62,1.10)	0.195
<i>LOC105377300</i> <i>/GK2</i>	rs192876988 (C/T)	4:80297251	0.040	1.19 (0.96,1.47)	0.105	1.32 (1.03,1.69)	0.027	1.02 (0.75,1.39)	0.883

SNP: single nucleotide polymorphism; EAF: effect allele frequency; OR: odds ratio; CI: confidence interval

**Supplementary Table 5:** Summary of genetic association for selected SNPs identified in GWAS of EOC and HGSOC with prostate cancer in African American individuals from the AAPC study

Nearest Gene	SNP ID (Effect / Other allele)	Build 37 Chr:Pos	EAF	OR (95% CI)	P-value
<i>AKR1C3</i>	rs4525119 (T/C)	10:5091954	0.328	1.03 (0.97, 1.10)	0.304
<i>LOC101927394</i>	rs7643459 (T/G)	3:8004828	0.371	1.07 (1.01, 1.13)	0.034
<i>UGT2A2</i>	rs4286604 (A/G)	4:70442165	0.264	1.08 (1.01, 1.15)	0.025
<i>WWC1</i>	rs142091544 (T/C)	5:167714000	0.036	1.11 (0.94, 1.32)	0.197
<i>FST</i>	rs37792 (G/A)	5:52644647	0.325	0.99 (0.93, 1.03)	0.685
<i>MAGEC1</i>	rs57403204 (G/A)	X:141078552	0.056	0.98 (0.89, 1.09)	0.754
<i>LOC105376360</i>	rs79079890 (G/T)	10:3684148	0.037	0.96 (0.82, 1.13)	0.646
<i>PRPSAP1</i>	rs66459581 (A/AC)	17:74355264	0.230	1.03 (0.96, 1.11)	0.363
<i>GABRG3</i>	rs116046250 (G/T)	15:27231950	0.042	0.93 (0.80, 1.08)	0.365
<i>LOC105377300</i> <i>/ GK2</i>	rs192876988 (C/T)	4:80297251	0.043	0.95 (0.81, 1.12)	0.567

SNP: single nucleotide polymorphism; EAF: effect allele frequency; OR: odds ratio; CI: confidence interval

**Supplementary Table 6:** Summary of results for fine mapping in African ancestry women of loci previously identified in GWAS of European ancestry women

Locus	SNP ID	Build 37 Chr:Pos	Nearest Gene	Phenotype	EOC			HGSC <sup>a</sup>		
					Number of SNPs Plotted	Minimum SNP position in region	Minimum SNP P-value	Number of SNPs Plotted	Minimum SNP position in region	Minimum SNP P-value
<b>Confirmed SNPs in European ancestry OncoArray meta-analysis</b>										
1p34.3	rs58722170	1:38096421	<i>RSP01</i>	Serous	3078	chr1:37917469	2.91E-04	2685	chr1:37917469	3.38E-04
2q14.1	rs752590	2:113972945	<i>PAX8</i>	Mucinous	3615	chr2:114298849	2.31E-03	--	--	--
2q31.1	rs711830	2:177037311	<i>HOXD3</i>	Mucinous	3171	chr2:1177037311	2.23E-03	--	--	--
2q31.1	rs6755777	2:177043226	<i>HAGLR</i>	Serous	3175	chr2:177326682	2.23E-03	2775	chr2:177442640	2.49E-03
3q25.31	rs62274041	3:156435640	<i>TIPARP</i>	HGSC	3204	chr3:156252180	2.01E-03	2863	chr3:156204177	2.37E-03
5p15.33	rs10069690	5:1279790	<i>TERT</i>	Serous	5037	chr5:949207	9.57E-04	4497	chr5:892204	7.97E-04
5p15.33	rs7705526	5:1285974	<i>TERT</i>	Serous borderline	5005	chr5:949207	9.57E-04	4464	chr5:892204	7.97E-04
8q21.13	rs76837345	8:82668818	<i>CHMP4C</i>	HGSC	4045	chr8:82866267	1.44E-05 <sup>c</sup>	3523	chr8:82866267	3.98E-06 <sup>b</sup>
8q24.21	rs1400482	8:128529685	<i>LINC00824</i>	Serous	4414	chr8:128619531	3.51E-04	3897	chr8:128762529	1.86E-03
9p22.2	rs10962692	9:16915874	<i>BNC2</i>	HGSC	5248	chr9:16978052	2.67E-05 <sup>c</sup>	4746	chr9:16986321	5.57E-05
9q34.2	rs8176685	9:136138766	<i>ABO</i>	HGSC	3968	chr9:136075407	5.07E-04	3472	chr9:136267149	3.17E-04
10p12.31	rs144962376	10:21878832	<i>MLLT10</i>	Serous	2514	chr10:21978590	4.13E-03	2162	chr10:22035324	7.73E-03
17q12	rs7405776	17:36093022	<i>HNF1B</i>	Serous	2787	chr17:36195231	5.44E-03	2324	chr17:36113300	7.82E-04
17q12	rs11651755	17:36099840	<i>HNF1B</i>	Clear cell	2778	chr17:36195231	5.44E-03	--	--	--
17q21.31	rs7207826	17:46500673	<i>SKAP1</i>	Serous	2827	chr17:46807761	6.43E-04	2572	chr17:46215732	8.18E-04
17q21.32	rs1879586	17:43567337	<i>PLEKHM1</i>	HGSC	3735	chr17:43954416	1.31E-04	3370	chr17:43945726	1.44E-04
19p13.11	rs4808075	19:17390291	<i>BABAM1</i>	HGSC	9100	chr19:17395213	1.77E-04	4077	chr19:17088458	3.07E-04
19q11.21	rs688187	19:39732752	<i>IFNL3</i>	Mucinous	8360	chr19:39684764	1.21E-04	--	--	--
<b>Newly identified SNPs in European ancestry OncoArray meta-analysis</b>										
2q13	rs2165109	2:111818658	<i>ACOXL</i>	HGSC	2172	chr2:111595642	6.87E-03	1951	chr2:111832215	1.47E-02
3q22.3	rs112071820	3:138849110	<i>BPESC1</i>	Mucinous	2922	chr3:138839642	3.34E-05 <sup>c</sup>	--	--	--
3q28	rs9870207	3:190525516	<i>GMNC</i>	Serous borderline, LGSC	4647	chr3:190657915	3.73E-03	4081	chr3:190839089	3.34E-03
4q32.2	rs13113999	4:167187046	<i>TLL1</i>	Serous borderline	4879	chr4:167492545	4.71E-03	4252	chr4:166876033	8.01E-04
5q12.3	rs555025179	5:66121089	<i>MAST4</i>	Endometrioid	3720	chr5:65907851	5.91E-03	--	--	--
8q21.11	rs150293538	8:77320354	<i>LINC01111</i>	Serous borderline, LGSC	3305	chr8:77354021	1.17E-04	2883	chr8:77320354	2.01E-04
8q24.21	rs9886651	8:128817883	<i>PVT1</i>	HGSC	4449	chr8:129036159	2.67E-04	3962	chr8:129093793	1.52E-03
9q31.1	rs320203	9:104943226	<i>LOC105376188</i>	Mucinous	4927	chr9:105237170	1.49E-03	--	--	--
10q24.33	rs7902587	10:105694301	<i>LOC102724351</i>	Serous borderline, LGSC	3192	chr10:105375295	3.40E-05 <sup>c</sup>	2852	chr10:105300054	1.03E-03
12q24.31	rs7953249	12:121403724	<i>HNF1A-AS1</i>	HGSC	3680	chr12:121113096	6.90E-05	3272	chr12:121113096	2.51E-05 <sup>c</sup>
18q11.2	rs8098244	18:21405553	<i>LAMA3</i>	Serous borderline, LGSC	2685	chr18:21555816	1.84E-05 <sup>b</sup>	2431	chr18:21555816	6.19E-05
22q12.1	rs6005807	22:28934313	<i>TTC28/ LOC101929594</i>	HGSC	2513	chr22:29126617	1.27E-02	2066	chr22:29073209	1.56E-02

EOC: epithelial ovarian cancer; HGSC: high-grade serous ovarian cancer; SNP: single nucleotide polymorphism; Chr: chromosome; Pos: position; LGSC: low-grade serous ovarian cancer.

<sup>a</sup>Fine mapping among HGSC was completed only for those SNPs associated with serous ovarian cancer.

<sup>b</sup>Significant at the Bonferroni threshold (0.05/number of SNPs plotted).

<sup>c</sup>Significant at the suggestive threshold (0.05/(number of SNPs plotted/3)).

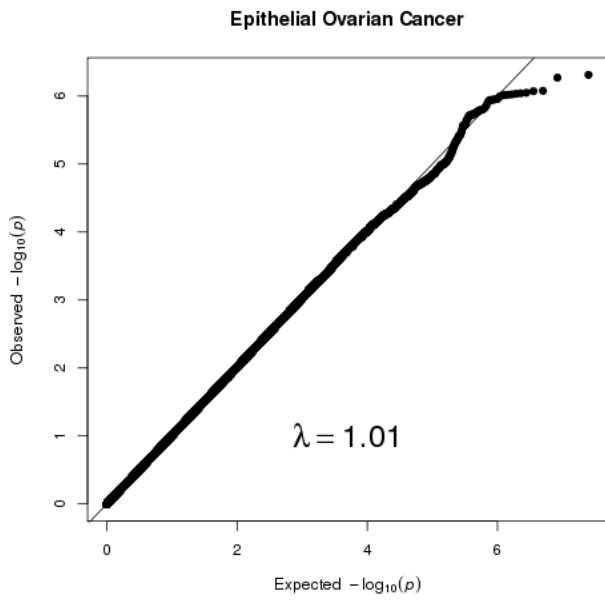
**Supplementary Table 7:** Summary of results for fine mapping in European ancestry women of loci identified in our GWAS of African ancestry women

Gene	SNP ID	Build 37 Chr:Pos	EOC			HGSOC		
			Number of SNPs plotted	Minimum SNP position in region	Min SNP p-value	Number of SNPs plotted	Minimum SNP position in region	Min SNP p-value
<i>AKR1C3</i>	rs4525119	10:5091954	6105	chr10:5341275	2.44E-03	--	--	--
<i>LOC101927394</i>	rs7643459	3:8004828	5466	chr3:8268351	1.12E-03	--	--	--
<i>UGT2A2</i>	rs4286604	4:70442165	5542	chr4:70592790	1.14E-05 <sup>a</sup>	--	--	--
<i>WWC1</i>	rs142091544	5:167714000	3761	chr5:167857657	1.74E-04	--	--	--
<i>FST</i>	rs37792	5:52644647	--	--	--	4416	chr5:52332701	3.94E-05
<i>MAGEC1</i>	rs57403204	X:141078552	--	--	--	3389	chrX:141078552	1.78E-04
<i>LOC105376360</i>	rs79079890	10:3684148	--	--	--	4899	chr10:3463140	2.24E-04
<i>PRPSAP1</i>	rs66459581	17:74355264	--	--	--	4025	chr17:74420211	3.74E-04
<i>GABRG3</i>	rs116046250	15:27231950	--	--	--	3885	chr15:27240688	5.16E-04
<i>LOC105377300/GK2</i>	rs192876988	4:80297251	--	--	--	3443	chr4:80297251	5.76E-04

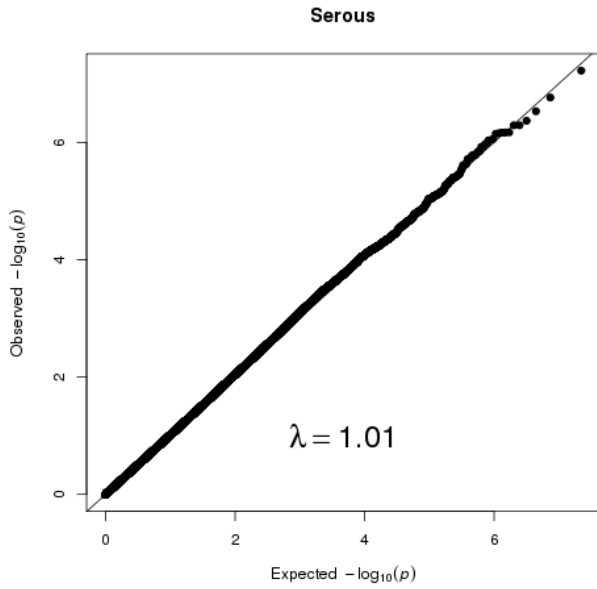
<sup>a</sup>Significant at the suggestive threshold (0.05/(number of SNPs plotted/3)).



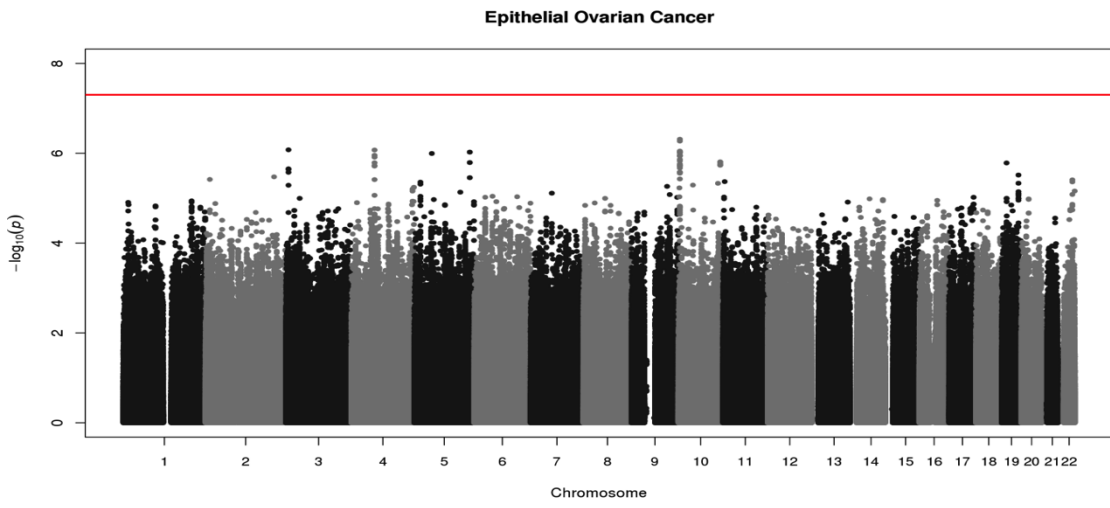
(a)



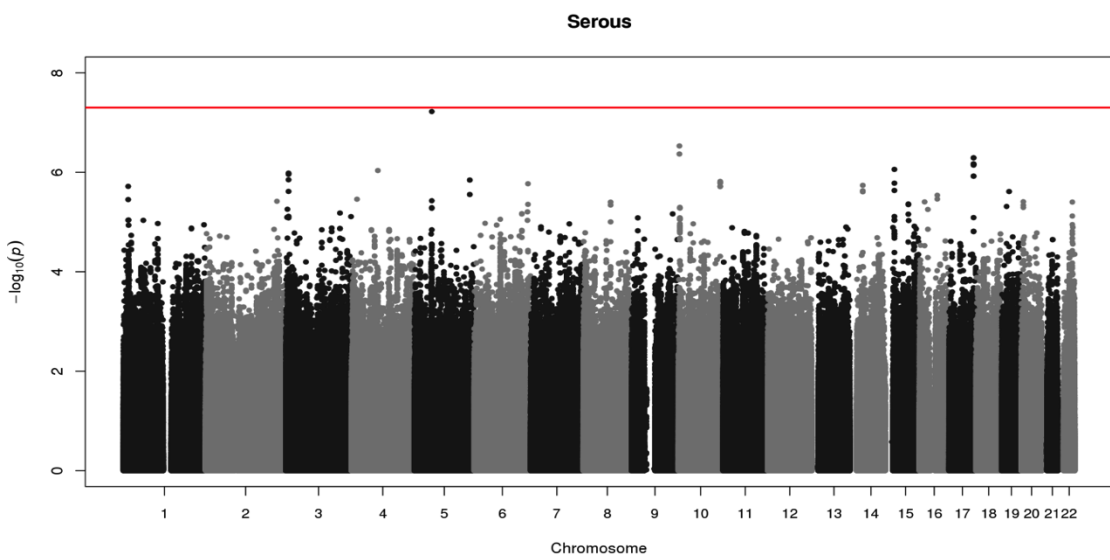
(b)



(a)



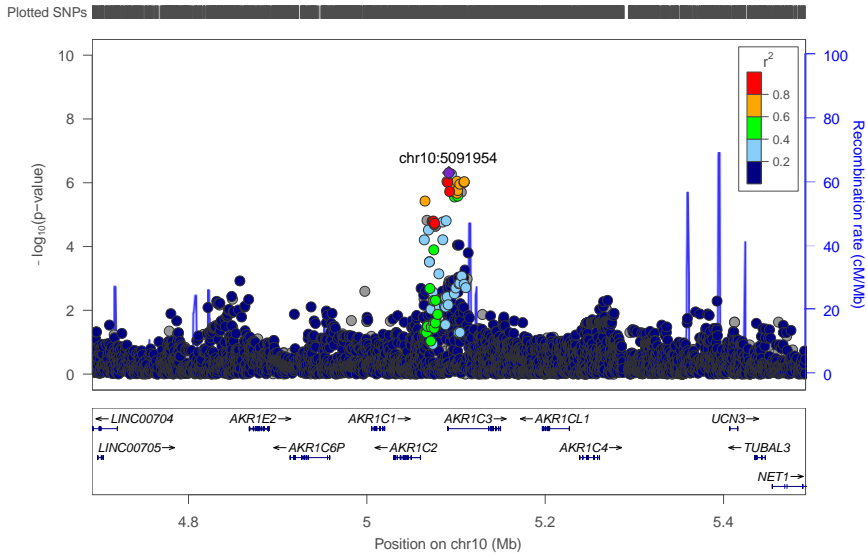
(b)



Manichaikul et al., Supplementary Figure 2

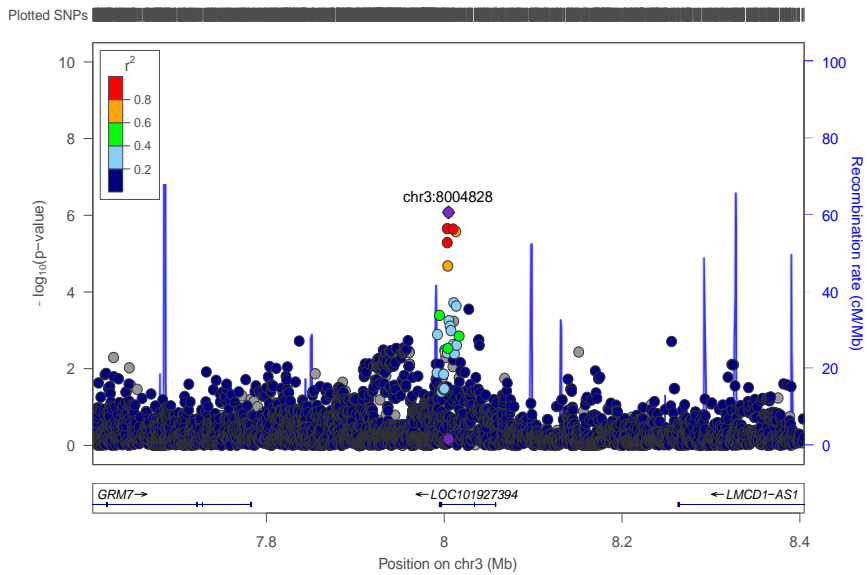
(a)

### Epithelial Ovarian Cancer



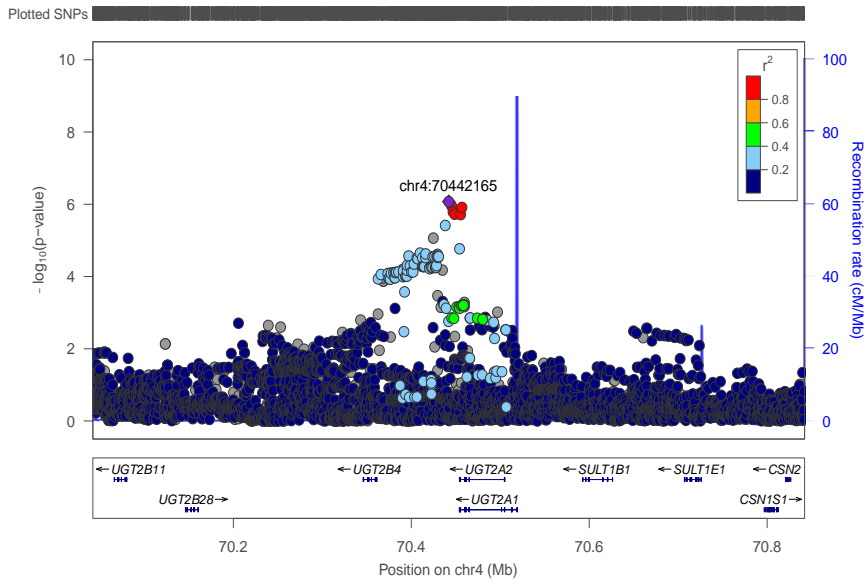
(b)

### Epithelial Ovarian Cancer



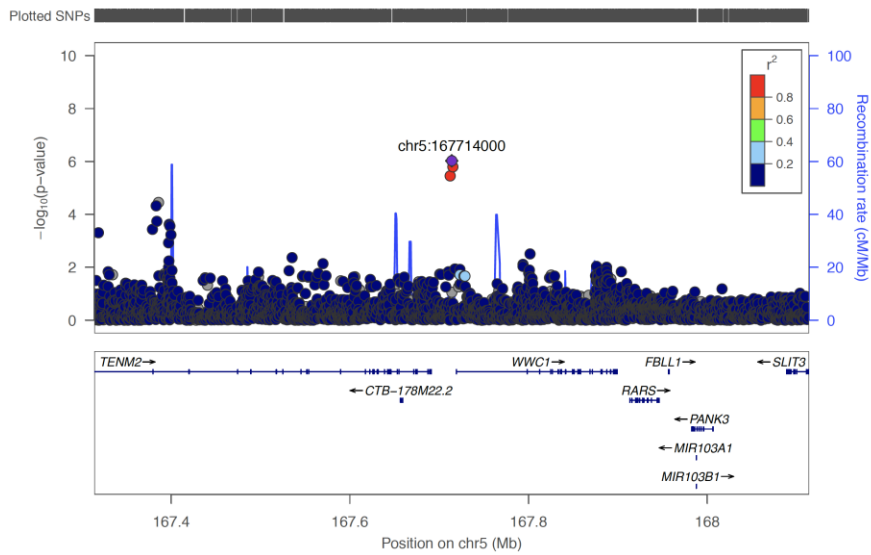
(c)

### Epithelial Ovarian Cancer



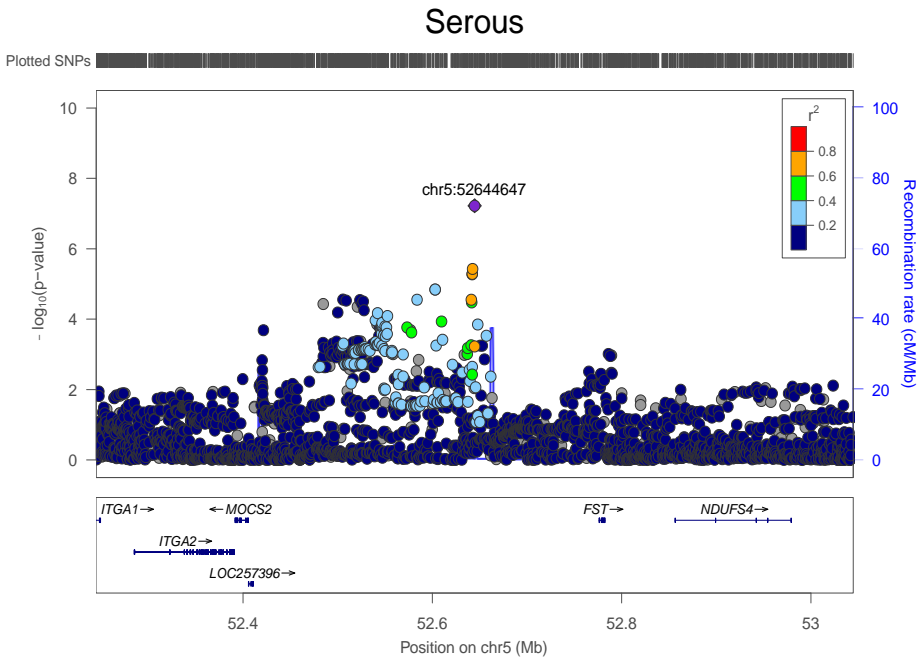
(d)

### Epithelial Ovarian Cancer

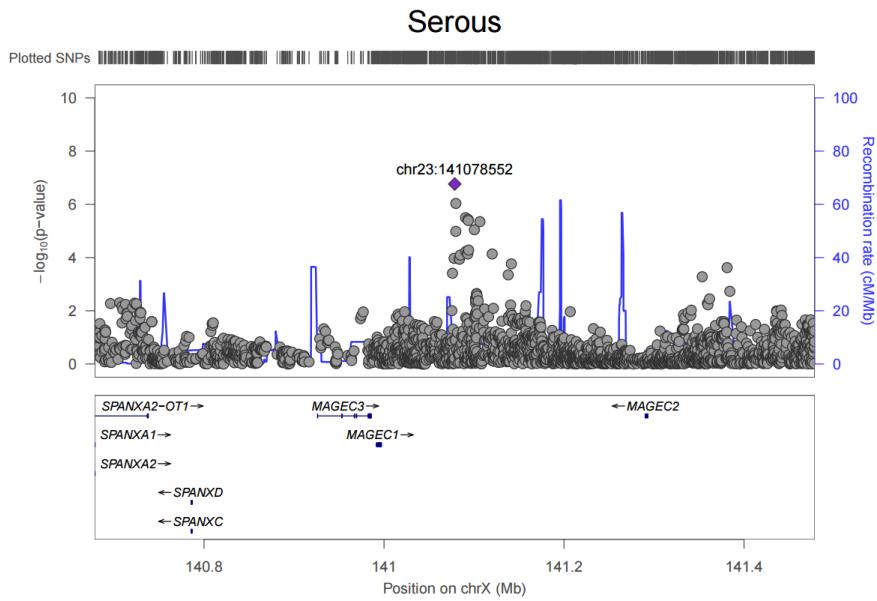


Manichaikul et al., Supplementary Figure 3

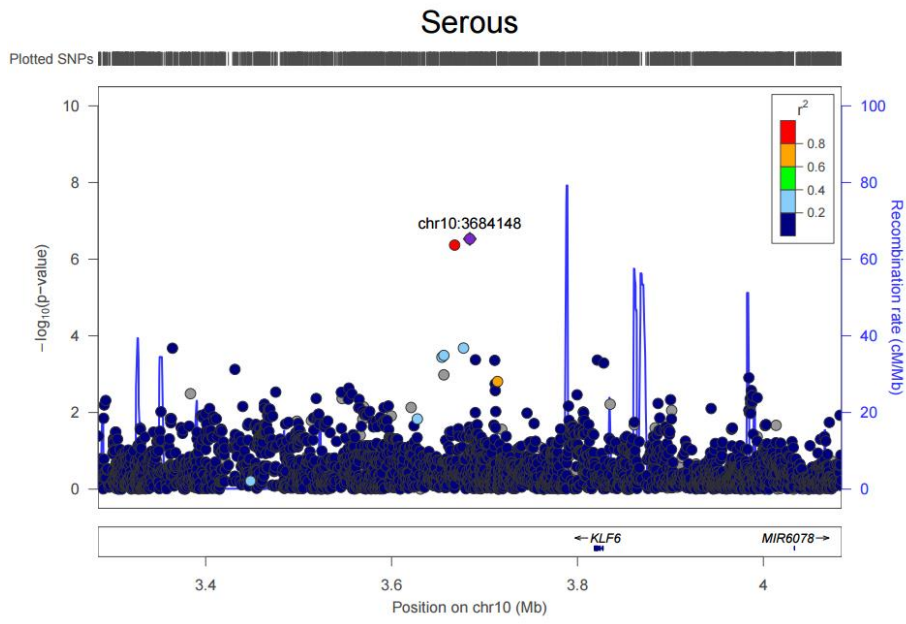
(a)



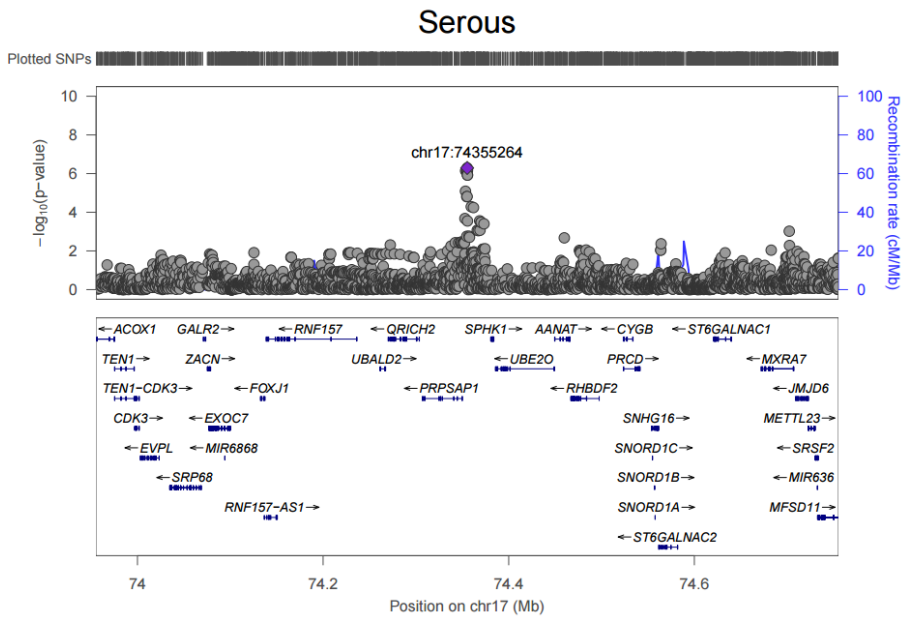
(b)



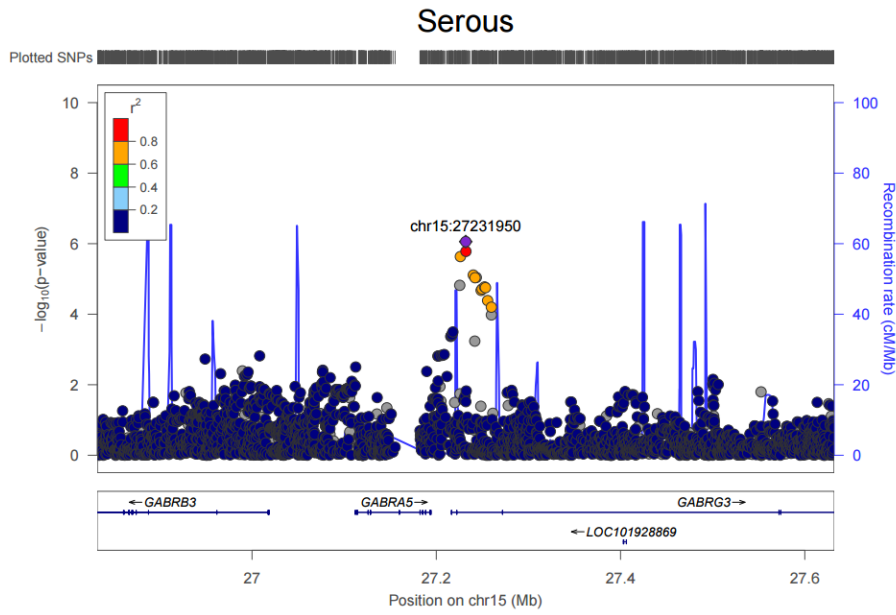
(c)



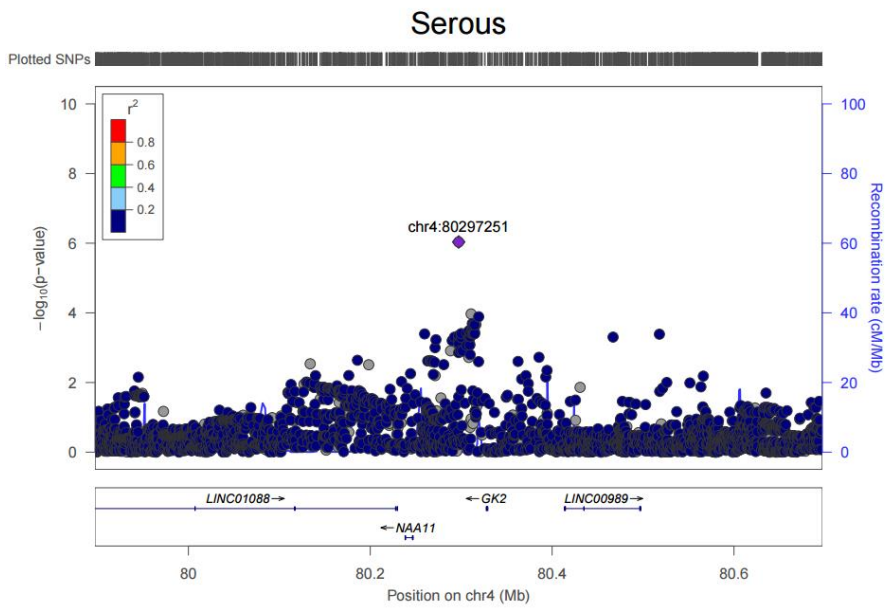
(d)



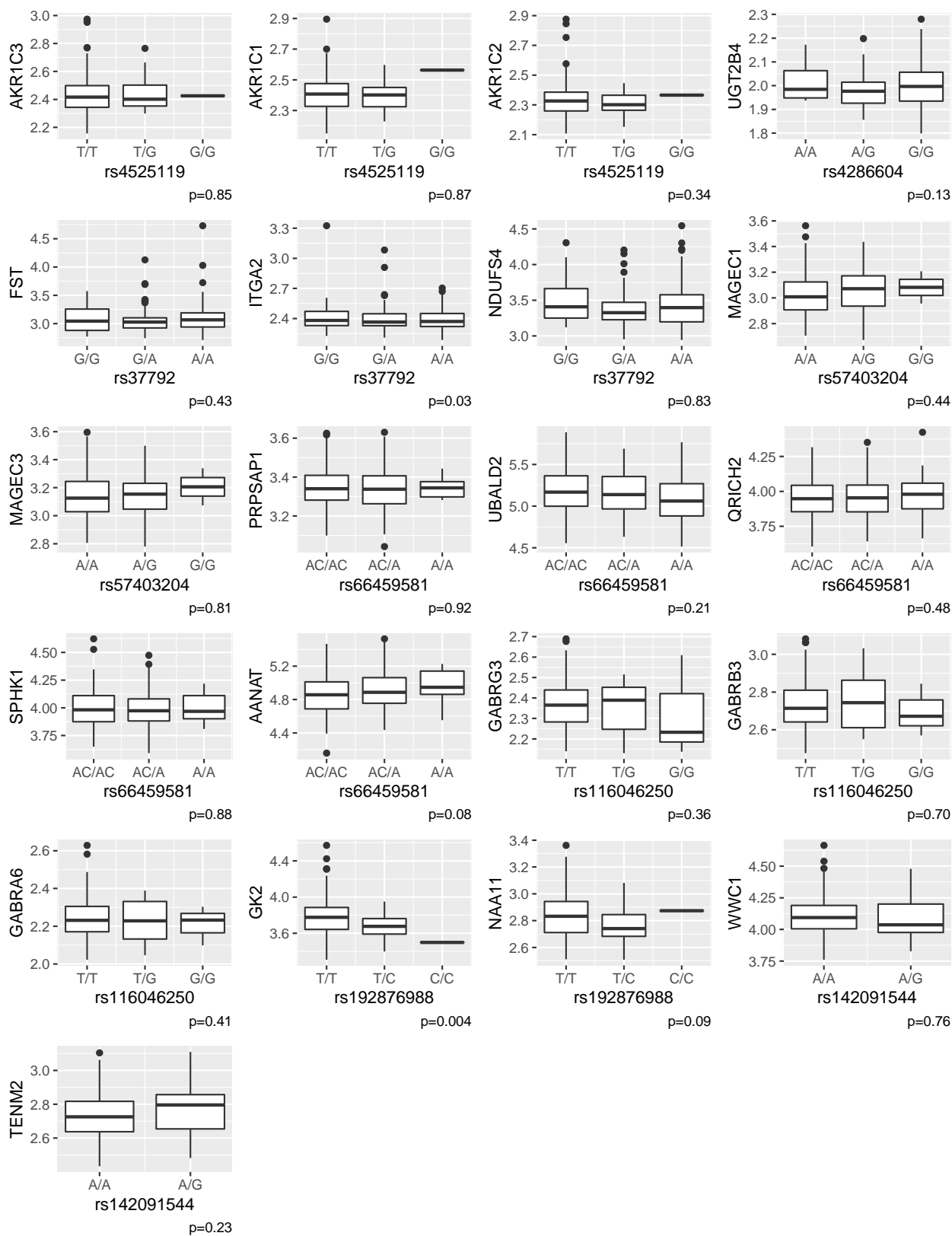
(e)



(f)



Manichaikul et al., Supplementary Figure 4



Manichaikul et al., Supplementary Figure 5