Supplemental Table 1. Association between selected miRNA processing and miRNA binding site SNPs and epithelial ovarian cancer risk in a pooled analysis of the US-CAN, UK, and POL studies

Gene (locus) SNP (maj/min allele[a])	Location (putative miRs) [b]	OR (95% CI) reported by Liang et al (Ref. 3)	MAF [c]	Pooled OR (95% CI), adjusted for study [d]	*P*	Pooled OR (95% CI), adjusted for study and ancestry [e]	*P*
miRNA processing							
DDX20 (1p21,1-p13.2)							
rs197414 (C/A) [f]	Missense	0.69 (0.48-0.99)	0.13	1.02 (0.92,1.12)	0.70	1.04 (0.94,1.15)	0.49
DROSHA (5p13.3)							
rs9292427 (C/T) [g]	Intron	0.71 (0.51-0.99)	0.46	1.01 (0.95,1.08)	0.72	1.01 (0.94,1.08)	0.79
rs492176 (T/C)	Intron	-	0.29	1.08 (1.00,1.17)	**0.04**	1.05 (0.97,1.13)	0.16
rs607613 (C/T) [h]	flanks 3'UTR (-12.5 kb)	-	0.13 [c]	1.11 (1.00,1.22)	**0.04**	1.08 (0.98,1.20)	0.11
rs615435 (T/C) [h]	Intron	-	0.15 [c]	1.10 (1.01,1.20)	**0.04**	1.06 (0.97,1.16)	0.22
GEMIN4 (17p13)							
rs2740349 (A/C) [h]	exon 1, ns	0.70 (0.51-0.96)	0.18	0.99 (0.92,1.09)	0.97	1.02 (0.93,1.11)	0.71
rs2740351 (T/C) [i]	flanks 5'UTR	0.71 (0.57-0.87)	0.45	0.98 (0.91,1.04)	0.46	1.00 (0.94,1.07)	0.98
rs7813 (T/G) [i]	exon 1, ns	0.71 (0.57-0.88)	0.46	0.97 (0.91,1.04)	0.38	1.00 (0.93,1.07)	0.91
XPO5 (6p21.1)							
rs2257082 (C/A)	exon 1, ss	0.73 (0.54-0.99)	0.27	0.99 (0.92,1.07)	0.87	1.00 (0.93,1.08)	0.95
miRNA binding sites							
CAV1 (7q31.1)							
rs9920 (G/A)	3'UTR (miR 630)	1.50 (1.04-2.17)	0.10	1.13 (1.10,1.26)	**0.03**	1.06 (0.95,1.19)	0.29
rs1049314 (C/A)	3'UTR (miR-453,196a)	-	0.17 [c]	1.11 (1.02,1.21)	**0.02**	1.08 (0.99,1.19)	0.08
rs1049334 (G/A)	3'UTR (miR-1225-3p)	-	0.08 [c]	0.92 (0.81,1.04)	0.18	0.90 (0.79,1.02)	0.10
rs1049337 (C/T)	3'UTR (miR 612)	-	0.31	0.94 (0.88,1.01)	0.11	0.95 (0.88,1.02)	0.16
rs8713 (A/C)	3'UTR (miR 648)	-	0.17 [c]	1.11 (1.02,1.21)	**0.02**	1.08 (0.99,1.19)	0.08
COL18A1 (21q22.3)							
rs7499 (G/A)	3'UTR (miR-594)	1.47 (1.07-2.02)	0.42 [c]	0.98 (0.92,1.05)	0.57	0.98 (0.92,1.05)	0.50
rs17004785 (G/C)	3'UTR (miR-432, 539)	-	0.11 [c]	0.94 (0.85,1.05)	0.30	0.96 (0.86,1.07)	0.45
E2F2 (1p36)							
rs2075993 (A/C) [j]	3'UTR (miR-663,486-3p)	1.24 (1.00-1.54)	0.48	1.01 (0.95,1.08)	0.67	1.01 (0.94,1.08)	0.87
rs3820028 (T/C) [j]	3'UTR (miR-455-3p)	-	0.49	1.01 (0.94,1.08)	0.78	1.00 (0.94,1.07)	0.78
ILIR1 (2q12)							
rs3917328 (C/T)	3'UTR (miR-335,31)	1.65 (1.03-2.64)	0.05 [c]	1.06 (0.91,1.23)	0.49	1.00 (0.86,1.17)	0.99
rs2110726 (C/T)	3'UTR (miR-658,768-5p)	-	0.38	0.99 (0.92,1.05)	0.66	0.99 (0.92,1.06)	0.77
rs3732133 (G/A) [h]	3'UTR (miR-483-5p)	-	0.01	1.01 (0.95,1.08)	0.85	0.88 (0.57,1.34)	0.55
rs3917325 (T/G)	3'UTR (miR-959)	-	0.05 [c]	1.06 (0.91,1.24)	0.43	1.01 (0.86,1.18)	0.91
rs3917327 (C/G)	3'UTR (miR-1200,887)	-	0.01 [c]	0.96 (0.67,1.38)	0.82	0.88 (0.61,1.28)	0.50

rs3917329 (G/T)	3'UTR (miR-505)	-	0.07	0.95 (0.83,1.09)	0.49	0.93 (0.81,1.07)	0.32
KRAS (12p12.1)							
rs13096 (A/G) [k]	3'UTR (miR-1244)	1.26 (1.01-1.57)	0.45	1.00 (0.94,1.07)	0.94	0.99 (0.93,1.06)	0.85
rs712 (C/A)	3'UTR (miR-200b,c, 330-5p)	-	0.45 [c]	1.00 (0.94,1.07)	0.95	0.99 (0.93,1.06)	0.84
rs7960917 (T/C)	3'UTR (miR-152)	-	0.21 [c]	0.98 (0.90,1.06)	0.63	0.97 (0.89,1.05)	0.40
rs7973623 (G/A)	3'UTR (miR-519a-c,380-3p,410)	-	0.21 [c]	0.98 (0.90,1.06)	0.63	0.97 (0.89,1.05)	0.40
UGT2A3 (4q13.2)							
rs17147016 (T/A) [h]	3'UTR (miR-224, 1279)	1.47 (1.08-2.01)	0.19 [c]	1.02 (0.93,1.11)	0.70	1.01 (0.93,1.10)	0.88
rs3749514 (T/G)	3'UTR (miR-641)	-	0.15	0.99 (0.87,1.13)	0.91	0.99 (0.87,1.13)	0.90

Abbreviations: US-CAN=United States-Canada; UK=United Kingdom; POL=Poland; maj=major; min=minor; miR=miRNA; UTR= untranslated region; ns=non-synonymous SNP; ss=synonymous SNP; OR (CI) =odds ratio (confidence interval); MAF=minor allele frequency among all controls;

[a] The major allele represents the most frequently-occurring allele and serves as the reference allele during modeling.

[b] SNP location derived from Illumina annotation files, HapMap2 data (http://hapmap.ncbi.nlm.nih.gov/), and dbSNP (http://www.ncbi.nlm.nih.gov/projects/SNP/). SNPinfo http://snpinfo.niehs.nih.gov/ and the PolymiRTS database (http://compbio.uthsc.edu/miRSNP) were used to predict miRNAs whose binding activity may be altered due to the SNP location.

[c] Genotype data was imputed for all participants using MACH version 1.0.16 using phased data from HapMap release 22 (genome build 36) derived from individuals with European ancestry (CEU).

[d] Pooled OR and 95% CI estimated using a log-additive model adjusted for study (US-CAN, UK, POL)

[e] Pooled OR and 95% CI estimated using a log-additive model adjusted for study and the first two principal components representing European ancestry

[f] *DDX20* rs19714 is in linkage disequilibrium (LD) (r^2 =0.90) with rs197383 identified by Liang et al.

[g] *DROSHA* rs9292427 is in LD (r^2 =0.98) with rs4867329 identified by Liang et al.

[h] SNP deviates from Hardy Weinberg Equilibrium among all controls with P_{HWE} values of 0.020 for rs607613, 0.040 for rs615435, 0.013 for rs2740349, 0.004 for rs3732133, and 0.034 for rs17147016, respectively.

[i] *GEMIN4* SNP pair in LD (r^2 =1)

[j] *E2F2* SNP pair in LD (r^2 =0.97)

[k] *KRAS* rs13096 is in LD (r^2 =1) with rs10771184 identified by Liang et al.

Statistically significant *P* values (<0.05) are in bold type. All *P*-values are two-sided.