1 Association Of Vitamin D Levels And Risk Of Ovarian Cancer:

2 A Mendelian Randomization Study

3 Word Count (paper+abstract): 3583

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186 Abstract

187 Background

- 188 In vitro and observational epidemiological studies suggest that vitamin D may play a role in
- 189 cancer prevention. However, the relationship between vitamin D and ovarian cancer is
- 190 uncertain, with observational studies generating conflicting findings. A potential limitation
- 191 of observational studies is inadequate control of confounding. To overcome this problem,
- 192 we used Mendelian randomization (MR) to evaluate the association between single
- 193 nucleotide polymorphisms (SNPs) associated with circulating 25-hydroxyvitamin D
- 194 (25(OH)D) concentration and risk of ovarian cancer.

195 Methods

- 196 We employed SNPs with well-established associations with 25(OH)D concentration as
- 197 instrumental variables for MR: rs7944926 (DHCR7), rs12794714 (CYP2R1) and rs2282679
- 198 (GC). We included 31 719 women of European ancestry (10 065 cases, 21 654 controls) from
- 199 the Ovarian Cancer Association Consortium, who were genotyped using customized Illumina
- 200 Infinium iSelect (iCOGS) arrays. A two-sample (summary data) Mendelian randomization
- 201 approach was used, and analyses were performed separately for all ovarian cancer (10 065
- 202 cases) and for high-grade serous ovarian cancer (4 121 cases).
- 203 Results

2 3 4	204	The odds ratio for epithelial ovarian cancer risk (10 065 cases) estimated by combining the
5 6 7	205	individual SNP associations using inverse variance weighting was 1.27 (95% confidence
8 9 10	206	interval: 1.06 to 1.51) per 20nmol/L decrease in 25(OH)D concentration. The estimated odds
11 12 13	207	ratio for high-grade serous epithelial ovarian cancer (4 121 cases) was 1.54 (1.19, 2.01).
14 15 16	208	Conclusions
17 18 19	209	Genetically lowered 25-hydroxyvitamin D concentrations were associated with higher
20 21 22	210	ovarian cancer susceptibility in Europeans. These findings suggest that increasing plasma
23 24 25	211	vitamin D levels may reduce risk of ovarian cancer.
26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44	212	 Key Messages Previous observational studies have reported conflicting findings on the association between serum 25(OH)D concentration and ovarian cancer. Results from this study suggest that lower 25(OH)D concentration associates with higher susceptibility to ovarian cancer. Among different ovarian cancer subtypes, the magnitude of association was the highest for high-grade serous ovarian cancer.

Introduction

214	Ovarian cancer is one of the most fatal cancers among women [1]. Survival following	
215	diagnosis is poor (less than 50% at 5 years post-diagnosis) with a mortality rate of 152 000)
216	per year worldwide [2, 3]. The most common histological subtype is serous carcinoma	
217	(further classified into high grade serous and low grade serous); other subtypes include	
218	mucinous, clear cell and endometrioid carcinomas [4]. Higher parity and oral contraceptiv	e
219	use reduce risk while established risk factors include a history of endometriosis, obesity ar	nd
220	family history of ovarian or breast cancer [5]. Several recent studies have examined wheth	ıer
221	or not serum 25-hydroxyvitamin D (25(OH)D) concentrations are associated with ovarian	
222	cancer risk or mortality [6-12].	
223		
224	Vitamin D is produced in the skin when 7-dehydrocholesterol is exposed to UVB. It	is
225	transported to the liver where it is hydroxylated to become 25(OH)D. It then undergoes a	
226	second hydroxylation step, primarily in the liver, to become the active form, 1,25-	
227	dihydroxyvitaminD (calcitriol). While 25(OH)D is relatively inactive, it has a long half-life ar	۱d
228	its production is loosely regulated, making it a useful indicator of vitamin D status. In vitro	
229	and animal studies suggest that calcitriol has a variety of anti-cancer effects, including the	
230	prevention of cell disjunction [13-16], preventing overgrowth and exerting multiple anti-	
231	proliferative and anti-inflammatory effects [17].	13
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2	233	The association between vitamin D and ovarian cancer is controversial. Most recent
2	234	observational studies found no strong evidence for an association between circulating
2	235	25(OH)D and risk for this cancer [7, 8, 10, 18-20]. One limitation of these studies is that their
2	236	findings may only be generalized for specific populations because of the latitudes in which
2	237	they were conducted. Furthermore, the variety of different 25(OH)D measurement
2	238	techniques as well as the different subtype distribution of ovarian cancers used in the
2	239	various studies might have also affected the results [8]. More fundamentally, a limitation of
2	240	observational studies is that confounding and reverse causation can make it difficult to
2	241	interpret the results. For example, affected individuals may have altered vitamin D levels
2	242	due to their disease status. Randomized clinical trials (RCT) are an attractive alternative to
2	243	observational studies as these remove biases from confounding and reverse causation.
2	244	However, RCTs are costly and logistically cumbersome, and there are no published RCTs
2	245	assessing the relationship between 25(OH)D levels and risk of epithelial ovarian cancer.
2	246	
2	247	Mendelian randomization (MR) is an approach for evaluating associations of an
2	248	exposure with a disease [21, 22]. This technique utilises the fact that allelic variants are
2	249	assigned at random during meiosis, making them potentially robust and unbiased (free from
2	250	confounding effects) instruments to gauge the effect of an exposure (e.g., low vitamin D) on

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251	a trait (e.g., cancer) [22]. An instrumental variable (SNP) used in a MR study also has to
252	satisfy the following assumptions [21, 22]: 1) the instrumental variable is associated with
253	the exposure of interest; 2) the instrumental variable is independent of confounding factors
254	that might confound the association of the exposure with the outcome; and 3) the
255	instrumental variable is only associated with the outcome through the exposure (Fig 1). Two
256	key determinants of the power of an MR study are the variance in the modifiable exposure
257	explained by the genetic variants (SNPs) and the sample size of the study associating the
258	relevant SNPs with the trait of interest. To date, SNPs associated with vitamin D level
259	explain only a very small proportion (approximately 1-4%) of the trait variance. Therefore,
260	for MR to be informative for vitamin D concentrations, large sample sizes are needed. Here
261	we use large-scale data from the Ovarian Cancer Association Consortium (OCAC) in an MR
262	framework to assess whether or not SNPs associated with 25(OH)D concentration are
263	related to risk of ovarian cancer.
264	(Fig 1 here: title - Schematic of the Mendelian randomization framework in our study using
265	vitamin D SNPs as instrumental variables.)
266	

267 Methods

268 Data sources

269	Individual level genetic data from the Ovarian Cancer Association Consortium (OCAC) were
270	used in this study. Participants from 43 studies from around the world were genotyped
271	using the Illumina Infinium iSelect (iCOGS) array [23]. Quality control was as per previous
272	work, with related individuals and ancestry outliers removed [4]. We excluded 13 studies of
273	individuals of non-European ancestry [4], the remaining studies that contributed to our
274	analysis were listed in Supplementary Table 4. For examination of all histotypes of ovarian
275	cancer combined, we had 10 065 cases and 21 654 controls for analysis. The distribution of
276	histological subtypes is shown in Table 1. For high-grade serous ovarian cancer, 4 121 cases
277	were available. We also performed MR analysis on the other subtypes individually, although
278	sample sizes were much smaller than for high grade serous cancer.
279	(Table 1 here)
280	
281	SNP selection criteria
282	Several SNPs have been observed in association with 25(OH)D concentrations: rs6013897 in
283	the Cytochrome P450, family 24, subfamily A, polypeptide 1 (CYP24A1) gene; rs2282679 and
284	rs7041 in the Group-Specific Component (GC) gene ; rs12800438 and rs7944926 near the 7-

285	Dehydrocholesterol Reductase (DHCR7) gene; and rs10741657 and rs12794714 in the
286	Cytochrome P450, family 2, subfamily R, polypeptide 1 (CYP2R1) gene [24-30]. The iCOGs
287	array directly genotyped rs12794714 and rs2282679; rs7944926 was the best imputed
288	DHCR7 SNPs (imputation quality score of 0.92) described by previous study [31]. We were
289	unable to include rs6013897 in CYP24A1 as there were no SNPs in adequate linkage
290	disequilibrium (r^2 >0.3) genotyped on our arrays. These SNPs are potential instrumental
291	variables with respect to 25(OH)D concentrations. To ensure that these SNPs instruments
292	can be applied to the MR via summary statistics approach, we first required accurate
293	25(OH)D association estimates for each of the SNP – the most accurate estimates available
294	were those from Afzal et al. [31] for the SNPs within/near DHCR7 and CYP2R1, whereas the
295	estimates for the GC SNP is only available in Mokry et al. [26]. (the effect of the GC SNP on
296	25(OH)D was only estimated based on 2 347 individuals [26] whereas the estimates for
297	DHCR7 and CYP2R1 were derived based on 30 792 individuals [31]). We then examined their
298	associations with various potential confounders using publicly available GWAS datasets (The
299	complete list of potential confounders that were investigated is available in Supplementary
300	Table 1).

2 3 : 4	302	Statistical analyses
5 6 : 7	303	MR operates by comparing the estimated magnitude of the association of the SNPs on the
8 9 : 10	304	modifiable risk factor (25(OH)D concentration) with the magnitude of the association of the
11 12 13	305	SNP on the outcome of interest (ovarian cancer). Estimates of the association of the
14 15 16	306	relevant SNPs with ovarian cancer status were derived using logistic regressions using
17 18 19	307	SNPTEST [32]. We adjusted for intra-ethnic (i.e. within Europeans) population differences by
20 21 22	308	incorporating the first six principal components and indicators for study number as
23 24 25	309	covariates in the SNP-outcome regressions. To check for evidence of residual population
26 27 28	310	stratification, we computed the genomic control lambda value from 195,183 directly
29 30	311	genotyped autosomal SNPs genome-wide. Additional confounding variables such as time
32 33	312	spent outdoors, socio-economic status and BMI were not adjusted in our model as these
34 35 36	313	information were not available on all individuals in our dataset. Instead, samples with
37 38 39	314	available confounder data (n < 26 000) were retained for subsequent sensitivity analysis
40 41 42	315	(See Discussion).
43 44 45	316	
46 47 48	317	In the absence of information on 25(OH)D concentration levels in the OCAC dataset,
49 50 51	318	we applied a two-sample approach that uses only summary data to assess indirect
52 53 54	319	associations [33] where estimates for the SNP-outcome associations are from a different
55 56 57	320	sample than the SNP-exposure associations. Here we obtain 25(OH)D association estimates
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321	from GWAS summary statistics for SNP instruments that passed the selection criteria
322	mentioned above. Combining these magnitudes of association, the association of 25(OH)D
323	concentration levels on ovarian cancer, the weighted estimate can be computed using the
324	Wald-type ratio estimator [21]. The weighted model that was used to obtain the
325	instrumental variable estimates are shown in the supplementary section. Analyses were
326	performed for all epithelial ovarian cancers irrespective of histological subtype and
327	separately for high-grade serous epithelial ovarian cancer. To be compatible with previous
328	studies [31, 34], estimates were scaled to a 20nmol/Liter change in 25(OH)D level;
329	20nmol/Liter is approximately the inter-tertile range (66 th percentile to 33 rd percentile)
330	observed in a large European study [31].
331	
331 332	Results
331 332 333	Results Validation of instrument strength
331 332 333 334	Results Validation of instrument strength We examined each of the MR assumptions in turn. To satisfy the 1 st MR assumption our
331 332 333 334 335	Results Validation of instrument strength We examined each of the MR assumptions in turn. To satisfy the 1 st MR assumption our SNPs must be clearly associated with 25(OH)D concentrations; typically an F-statistic >10 is a
 331 332 333 334 335 336 	Results Validation of instrument strength We examined each of the MR assumptions in turn. To satisfy the 1 st MR assumption our SNPs must be clearly associated with 25(OH)D concentrations; typically an F-statistic >10 is a commonly used threshold for a strong instrument. We specifically chose SNPs from DHCR7,
 331 332 333 334 335 336 337 	Results Validation of instrument strength We examined each of the MR assumptions in turn. To satisfy the 1 st MR assumption our SNPs must be clearly associated with 25(OH)D concentrations; typically an F-statistic >10 is a commonly used threshold for a strong instrument. We specifically chose SNPs from DHCR7, CYP2R1 and GC which have been clearly shown to be associated with 25(OH)D

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2 3 4	339	statistics for each SNP is >90. For the GC SNP, the association of this variant with log-	
5 6 7	340	transformed 25(OH)D were adequate with a F-statistic of 13.38. The SNPs combined expla	ain
8 9 10	341	about 1.3% of the variance in 25(OH)D concentration. It is important to note that these	
11 12 13	342	studies were among few of the many studies linking these SNPs to 25(OH)D concentration	ns
14 15 16	343	[24, 26, 28, 29, 34]. This evidence combined suggests that the SNPs we used are valid	
17 18 19	344	instruments (i.e. weak instrument bias is not a problem in our study).	
20 21 22	345		
23 24			
25 26	346	Assessment for pleiotropy	
27 28 29	347	Next we assessed possible pleiotropy. Of the known ovarian cancer risk factors, some hav	/e
30 31 32	348	an established genetic component, with large GWASs conducted. Examining these GWAS	
33 34 35	349	findings, we found no evidence for association between the SNPs in DHCR7 and CYP2R1 a	nd
36 37	350	potential confounders such as smoking behaviour (Supplementary Table 1), hence satisfyi	ing
38 39 40	351	the 2 nd MR assumption. We found that neither the lead SNPs, nor any SNPs correlated wit	th
41 42 43	352	them, were associated with the possible confounders after Bonferroni corrections. For the	e
44 45 46	353	other ovarian cancer risk factors (OC use, parity), large scale GWASs have not been	
47 48 49	354	conducted because inherited genetic factors are unlikely to play a major role. The 3 rd MR	
50 51 52	355	assumption can be difficult to test directly although the vitamin D metabolism pathway is	
53 54 55	356	well understood and there is substantial evidence that DHCR7 and CYP2R1 play roles in	
56 57 58 59	357	determining or modulating 25(OH)D concentration [24, 25, 34].	20

358	
359	Population stratification
360	MR analyses are unbiased when they reflect the true relationship between genotype and
361	phenotype (rather than for example artifactual associations from unmodeled population
362	structure). Our estimated genomic control lambda value (rescaled to 1 000 cases and
363	controls) was λ_{1000} = 1.005, implying no major effects of population structure. Principal
364	component analysis showed that the OCAC cases and controls were well matched for
365	ancestry (Supplementary Figure 2 and 3 in Supplementary material).
366	
367	Association of SNPs to 25(OH)D concentration
368	To estimate the association of the chosen SNPs on 25(OH)D concentrations, we used SNP-
369	25(OH)D association estimates from both published study [26, 31] that were corrected for
370	seasonal variation. It was shown that the variant rs7944926 near DHCR7 reduced 25(OH)D
371	concentration levels by 2.0 nmol/Liter per risk allele (A) and the variant rs12794714 in
372	CYP2R1 reduced 25(OH)D concentration levels by 3.0 nmol/Liter per risk allele (A). Upon
373	performing conversion of the 25(OH)D estimates from the natural logarithm scale [26], the
374	variant rs2282679 near GC was shown to reduce 25(OH)D levels by approximately 2.5
375	nmol/Liter per 25(OH)D decreasing allele (C).

2 3	376	
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6 7	3//	Nendelian randomization analysis for all ovarian cancer subtypes
8 9 10	378	We determined the associations between the 25(OH)D associated SNPs (rs7944926 and
11 12 13	379	rs12794714) and risk of ovarian cancer in Table 2. rs12794714 and rs2282679 was directly
14 15 16	380	genotyped in our dataset, whereas rs7944926 was well imputed (imputation quality score
17 18 19	381	0.92). For all epithelial ovarian cancer subtypes combined, the estimated magnitude of
20 21 22	382	association for a 1.0 nmol/Liter change in 25(OH)D level was -0.0076 (standard error (S.E.)=
23 24 25	383	0.0109) for the MR analysis performed via rs7944926 in <i>DHCR7</i> . This translates into an odds
26 27 28	384	ratio (OR) of 1.17(0.76-1.78) per 20nmol/Liter decrease in 25(OH)D levels. Similarly, the
29 30 31	385	magnitude of association was -0.0137, S.E.= 0.0063 for rs12794714 in CYP2R1, with
32 33 34	386	corresponding OR of 1.31(1.03-1.69) per 20 nmol/Liter decrease in 25(OH)D and the
35 36 37	387	magnitude of association is -0.0110, S.E.= 0.0082 with OR of 1.25(0.90-1.71) for rs2282679
38 39 40	388	in GC. Since all these SNPs are independent, a more accurate estimate will be obtained from
41 42 43	389	the combined associations of the three SNPs. The combined weighted magnitude of
44 45 46	390	association is -0.0118, with a S.E. of 0.0045. The resultant OR per 20nmol/Liter change in
47 48 49	391	25(OH)D on all epithelial ovarian cancer subtypes combined is 1.27 (1.06-1.51).
50 51 52	392	(Table 2 here)
53 54 55	393	

394	Mendelian Randomization analysis for high grade serous ovarian cancer
395	Similar associations were observed between SNPs for 25(OH)D concentration and high
396	grade serous epithelial ovarian cancer. We obtained a magnitude of association estimate of
397	-0.0209 (S.E.= 0.0154) and -0.0257 (S.E.= 0.0091) and -0.0173 (S.E.= 0.0117) for
398	rs7944926, rs12794714 and rs2282679 respectively. This resulted in an OR of 1.51(0.83-
399	2.78) using rs7944926, 1.67(1.18-2.38) using rs12794714, and 1.41(0.89-2.23) per 20
400	nmol/Liter decrease in 25(OH)D. Weighting across all SNP instruments yielded an estimated
401	magnitude of –0.0218 (S.E.= 0.0067). Hence a 20 nmol/Liter decrease in 25(OH)D
402	corresponds to an OR of 1.54(1.19-2.01) for high grade serous ovarian cancer.
403	(Figure 2 here)
404	(Figure 3 here)
405	Discussion
406	Even though the SNPs chosen in our study only explain a small fraction (~1.3%) of the
407	variance of 25(OH)D concentration, because our case-control sample was so large, we were

- 408 able to demonstrate associations with ovarian cancer risk. A genetically scored decrease of
- 409 20nmol/Liter of serum 25(OH)D concentration levels, increased the risk of epithelial ovarian
- 410 cancer by about 30% in European ancestry women, with a larger association seen in high

411 grade serous disease.
412
413 <u>Comparison with previous findings</u>
414 A recent Danish study [31] used MR to show that low circulating 25(OH)D concentrations
415 were associated with cancer mortality among Europeans. That study did not separate the
416 associations of risk and mortality and was underpowered to draw conclusions on any
417 specific cancer type. Here, for the first time, we demonstrate that for epithelial ovarian
418 cancer, there is a causal effect of low 25(OH)D concentrations on risk.

associations between 25(OH)D and ovarian cancer status. The recent meta-analysis [8] of 10 individual cohort studies (884 cases and 1 605 controls) found no association between 25(OH)D concentration and development of ovarian cancer. Findings from epidemiologic studies may differ from our MR based results because observational studies can be affected

Our results are inconsistent with some previous studies that have reported no

425 by confounding and reverse causation, though cohort studies such as [8] would be expected

to be less affected.

428 Strength and limitations

429	A strength of our study is that the mechanism through which our chosen SNPs influence
430	25(OH)D levels is well understood. DHCR7 encodes the enzyme 7-dehydrocholestrol
431	reductase, which is responsible for the conversion of 7-dehydrocholestrol to cholesterol.
432	Reduced activities of 7-dehydrocholestrol reductase, leading to low cholesterol and
433	accumulation of 7-dehydrocholestrol, are partially attributable to DHCR7 variants [24, 25,
434	29]. Although rs7944926 lies outside DHCR7, this variant modulates expression of DHCR7
435	[35]. <i>CYP2R1</i> is an enzyme which converts vitamin D_3 to 25(OH)D in the liver [36], with
436	rs12794714 unambiguously associated with 25(OH)D concentrations via GWAS [29]. The GC
437	gene has a primary role in vitamin D transport. Previous studies shown that the rs2282679
438	variant in particular were also strongly associated (P=4.0×10 ⁴²) with serum vitamin D
439	binding protein (DBP) based on the study performed on 1 674 individuals in the Twins UK
440	cohort [29]. The GC variants were also hypothesized to affect bioavailability of vitamin D
441	through variation in circulating DBP. In view of evidence for its association towards vitamin
442	D, the rs2282679 SNP is among one of the most associated variant with 25(OH)D (P=1.9×10 $^{-1}$
443	109) in the SUNLIGHT GWAS [29]. These variants (rs7944926, rs12794714 and rs2282679)
444	thus affect 25(OH)D levels through varying vitamin D metabolism, bioavailability or
445	transport, rendering them appropriate instrumental variables for use in MR [26, 27, 31, 34].
446	

2 3 4	447	One limitation is that our two-sample MR analysis assumes that the standard error
5 6 7	448	of the exposure (SNP to 25(OH)D) estimates is negligibly small [33, 37] – given the large
8 9 10	449	sample size in the Danish study [31], this is a reasonable assumption. In addition, the MR
11 12 13	450	framework assumes a linear relationship in the association of the SNP instruments on the
14 15 16	451	underlying exposure. Although our MR estimates indicate that a decrease of 20nmol/Liter in
17 18 19	452	25(OH)D concentration is associated with a 30% increased risk of epithelial ovarian cancer,
20 21 22	453	this estimated effect size is derived from a larger sample size of women with a range of
23 24 25	454	25(OH)D concentrations. Previous studies using MR to examine 25(OH)D concentrations
26 27 28	455	with different outcomes have dealt with this in various ways. For example, the published
29 30 31	456	study that we used [31] assumed linearity of change across raw 25(OH)D values. In contrast,
32 33	457	the study by Mokry et al. [26] on vitamin D and multiple sclerosis (MS) considered the
34 35 36	458	association to be linear on log transformed 25(OH)D.
37 38 39	459	
40 41 42	460	We examined the implications of these approaches by re-computing our findings
43 44 45	461	based on exposure estimates on the original scale (from the Danish study [31]) and on the
46 47 48	462	log scale (from MR study on MS [26]) (see Supplementary Table 2). We note that in addition
49 50 51	463	to the scale differences, the estimates of the magnitude of association of each SNP on
52 53 54	464	25(OH)D differed due to random sampling error (with estimates from the Danish study [31]
55 56 57 58	465	derived from a much larger sample size than those in the MS study [26]). We hence
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66	repeated our analysis by adopting SNP-exposure estimates used by the MS study [26] for
67	the SNP rs12785878 (LD to rs7944926 with r^2 = 1.0) in the DHCR7 gene. Although our result
68	was robust to differences in scaling (log transformed or non-transformed 25(OH)D
69	concentrations, see Supplementary Table 2), in practice a 20nmol/Liter increase is more
70	likely to make an impact on women with low 25(OH)D concentrations than those whose
71	concentration is already high.
72	
73	In our main analysis, there were concerns that the effect of the GC SNP on 25(OH)D
74	was not estimated with high accuracy (GC SNP estimates were based on 2 347 individuals
75	[26] whereas the estimates for DHCR7 and CYP2R1 were derived based on 30 792
76	individuals [31]), as well as concerns that the GC SNP may not influence in 25-
77	hydroxyvitamin D's biological activity in a predictable way [31, 38, 39]. Nonetheless, we
78	conducted a sensitivity analyses to examine the effect of excluding this SNP. When the GC
79	SNP was excluded, our results were unchanged (the association with ovarian cancer of the
80	combined effect of the 3 SNPs was very similar to that obtained using just 2 SNPs, see
81	Supplementary Table 5).
82	
83	Another potential limitation of our analysis is residual pleiotropy. We found no
84	evidence for SNP-confounder association based on the subset of participants with available

2 3 4	485	confounder information (Supplementary Table 6) although we cannot rule out association	IS
5 6 7	486	with unmeasured confounders. Approach such as Egger regression [40] can potentially be	
8 9 10	487	applied to further test the MR assumptions but these require more SNPs than the two	
11 12 13	488	employed here.	
14 15 16	489		
17 18 19	490	Interpretation of findings	
20 21 22	491	Observation of a larger magnitude of association (OR=1.54) with high grade serous cancer	
23 24 25	492	for lower 25(OH) concentration suggests that the association of circulating 25(OH)D with	
26 27 28	493	risk of ovarian cancer may be confined to the high grade serous type, although the	
29 30	494	confidence limits of the two ORs are overlapping and high-grade serous cancer is contained	۶d
32 33	495	within all ovarian cancer. The results for histological subtypes other than high grade serou	IS
34 35 36	496	carcinoma are shown in Figure 3 (for association of each individual SNP, see Supplementa	ry
37 38 39	497	Table 3), and there is no evidence for association for non-serous disease. For all non high-	
40 41 42	498	grade serous cancers combined, the odds ratio was 1.12 (0.89-1.41).	
43 44 45	499		
46 47 48	500	The association of lower circulating vitamin D (25(OH)D) levels to risk of epithelial	
49 50 51	501	ovarian cancer appear to be consistent with a recent MR study [31] looking at all-cancer	
52 53 54	502	mortality. Vitamin D activating enzymes and vitamin D receptors are present in many	
55 56 57	503	tissues, with the regulation of 1-3% of gene expression in these tissues attributable to	
58 59 60			28

504	vitamin D [35]. Studies have also shown that vitamin D is involved in the regulation of cell
505	processes (proliferation, differentiation and apoptosis) in several cell types that are central
506	to the development of cancer [14, 41-43]. Thus, our findings warrant further investigations
507	on the biological role of vitamin D (specifically, 25(OH)D) in mortality as well as risk of
508	ovarian cancer.
509	
510	In conclusion, we demonstrate an association between low 25(OH)D concentration
511	and risk of ovarian cancer in women of European ancestry, with our MR approach providing
512	estimates which are unaffected by the confounding or biases present in observational
513	studies. Whilst our results cannot guarantee causality, placed in the context of other
514	epidemiological studies, they provide additional evidence supportive of a causal link
515	between vitamin D and risk of ovarian cancer.
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27	635	
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33	636	Funding
34		
35		
36	60 -	
37	637	This work was supported by The COGS project which is funded through a European
38		
39	620	Commission's Seventh Framework Programme Grant (agreement number 222175 HEALTH
40	030	Commission's Seventh Framework Programme Grant (agreement number 225175 nEALTH
41		
42	639	F2 2009-223175): the Genetic Associations and Mechanisms in Oncology (GAME- ON): A NCI
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46	640	Cancer Post-GWAS Initiative (U19-CA148112); the Ovarian Cancer Association Con-sortium
47		
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10	641	is supported by a grant from the Ovarian Cancer Re-search Fund thanks to donations by the

- family and friends of Kathryn Sladek Smith (PPD/RPCI.07). Funding of the constituent studies
- was provided by the California Cancer Research Program (00-01389V-20170, N01-CN25403,
- 2II0200); the Canadian Institutes of Health Research (MOP-86727); Cancer Australia; Cancer

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645	Council Victoria; Cancer Council Queensland; Cancer Council New South Wales; Cancer
646	Council South Australia; Cancer Council Tasmania; Cancer Foundation of Western Australia;
647	the Cancer Institute of New Jersey; Cancer Research UK (C490/A6187, C490/A10119,
648	C490/A10124); the Danish Cancer Society (94-222-52); the ELAN Program of the University
649	of Erlangen-Nuremberg; the Eve Appeal; the Helsinki University Central Hospital Research
650	Fund; Helse Vest; the Norwegian Cancer Society; the Norwegian Research Council; the
651	Ovarian Cancer Research Fund; Nationaal Kankerplan of Belgium; the L & S Milken
652	Foundation; the Polish Ministry of Science and Higher Education (4 PO5C 028 14, 2 PO5A
653	068 27); the Roswell Park Cancer Institute Alliance Foundation; the US National Cancer
654	Institute (K07-CA095666, K07-CA80668, K07-CA143047, K22-CA138563, N01-CN55424, N01-
655	PC67001, N01-PC067010, N01-PC035137, P01-CA017054, P01-CA087696, P30-CA072720,
656	P30-CA15083, P30-CA008748, P50-CA159981, P50-CA105009, P50-CA136393, R01-
657	CA149429, R01-CA014089, R01-CA016056, R01-CA017054, R01-CA049449, R01-CA050385,
658	R01-CA054419, R01-CA058598, R01-CA058860, R01-CA061107, R01-CA061132, R01-
659	CA063678, R01-CA063682, R01-CA067262, R01-CA071766, R01-CA074850, R01-CA080978,
660	R01-CA083918, R01-CA087538, R01-CA092044, R01-CA095023, R01-CA122443, R01-
661	CA112523, R01-CA114343, R01-CA126841, R01-CA136924, R03-CA113148, R03-CA115195,
662	U01-CA069417, U01-CA071966, UM1-CA186107, UM1-CA176726 and Intramural research
663	funds); the NIH/National Center for Research Resources/General Clinical Research Center
	11

2 3 4	664	(MO1-RR000056); the US Army Medical Research and Material Command (DAMD17-01-1-
5 6 7	665	0729, DAMD17-02-1-0666, DAMD17-02-1-0669, W81XWH-07-0449, W81XWH-10-1-02802);
8 9 10	666	the US Public Health Service (PSA-042205); the National Health and Medical Research
11 12 13	667	Council of Australia (199600 and 400281); the German Federal Ministry of Education and
14 15 16	668	Research of Germany Programme of Clinical Biomedical Research (01GB 9401); the State of
17 18 10	669	Baden-Wurttemberg through Medical Faculty of the University of Ulm (P.685); the German
20 21	670	Cancer Research Center; the Minnesota Ovarian Cancer Alliance; the Mayo Foundation; the
22 23 24	671	Fred C. and Katherine B. Andersen Foundation; the Lon V. Smith Foundation (LVS-39420);
25 26 27	672	the Oak Foundation; Eve Appeal; the OHSU Foundation; the Mermaid I project; the Rudolf-
28 29 30	673	Bartling Foundation; the UK National Institute for Health Research Biomedical Research
31 32 33	674	Centres at the University of Cambridge, Imperial College London, University College Hospital
34 35 36	675	'Womens Health Theme' and the Royal Marsden Hospital; and Work Safe BC 14.
37 38 39	676	Investigator-specific funding: JS and GC thank the University of Queensland and QIMR
40 41 42	677	Berghofer Medical Research Institute for scholarship support. YL was supported by the
43 44 45	678	NHMRC Early Career Fellowship. GCT, REN and PMW are supported by the National Health
46 47 48	679	and Medical Research Council. SM acknowledges funding support from an Australian
49 50 51	680	Research Council Future Fellowship.
52 53 54 55 56 57	681	

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682 Acknowledgements

683	We acknowledge with appreciation all the individuals who participated in the OCAC studies,
684	and the many hospital directors and staff, gynaecologists, general practitioners and
685	pathology services who provided assistance with confirmation of diagnoses, and the many
686	research assistants and interviewers for assistance with the studies. For the OCAC studies,
687	we thank: D.Bowtell, A. deFazio, D. Gertig, A. Green, P. Parsons, N. Hayward, P. Webb and
688	D. Whiteman (AUS); G. Peuteman, T. Van Brussel and D. Smeets (BEL); L. Gacucova (HMO);
689	P. Schurmann, F. Kramer, W. Zheng, T. W. Park, Simon, K. Beer-Grondke and D. Schmidt
690	(HJO); S. Windebank, C. Hilker and J. Vollenweider (MAY); the state cancer registries of AL,
691	AZ, AR, CA, CO, CT, DE, FL, GA, HI,ID,IL,IN,IA,KY,LA,ME, MD,MA,MI,NE,NH,NJ,NY,NC,ND,
692	OH,OK,OR,PA,RI,SC,TN,TX,VA,WA and WYL(NHS); L. Paddock, M. King, L. Rodriguez-
693	Rodriguez, A. Samoila and Y. Bensman (NJO); M. Sherman, A. Hutchinson, N. Szeszenia-
694	Dabrowska, B. Peplonska, W. Zatonski, A. Soni, P. Chao and M. Stagner (POL); C. Luccarini, P.
695	Harrington the SEARCH team and ECRIC (SEA); I. Jacobs, M. Widschwendter, E. Wozniak, N.
696	Balogun, A. Ryan, C. Karpinskyj and J. Ford (UKO); Carole Pye (UKR); A. Amin Al Olama, J.
697	Dennis, E. Dicks, K. Michilaidou and K. Kuchenbaker (COGS).
698	

2 3 4 5	699	Competing Interest
6 7 8	700	Mark T Goodman is a consultant for Johnson and Johnson Ltd. Usha Menon has stock
9 10 11	701	ownership and research funding from Abcodia Ltd, a UCL spin-out company with interest in
12 13 14	702	biomarkers and ovarian cancer screening. Peter Fasching conducts research with grants
15 16 17	703	from Amgen and Novartis, and received honoraria from Amgen, Novartis, Roche, Celgene,
18 19 20	704	Nanostring, Genomic Health and TEVA. All remaining authors declare no competing interest.
21 22 23	705	
24 25 26	706	
27 28 29 30	707	Supplementary Material
31 32 33	708	See separate file.
34 35 36	709	
37 38 39	710	
40 41 42	711	
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Table 1: Distribution of cases based on epithelial ovarian carcinoma subtypes

EOC subtypes	Number of Cases	
High-grade Serous	4 121	
Low-grade Serous	363	
Serous of unknown grade	1 344	
Mucinous	662	
Clear Cell	621	
Endometroid	1 350	
Others	1 604	

Table 2: Mendelian randomization results: 25(OH)D concentration and ovarian cancer.

SNPs	EA/NEA	25(OH)D per 25(OH)D decreasing			All epithelial ovarian subtype				Only high grade serous epithelial ovarian subtype			
		allele (nmol/Liter)			(N=10 065 cases)				(N=4 121 cases)			
		β_{zx}	σ_{zx}	R ²	β_{zy}	σ _{zy}	β _{IVW}	σ_{IVW}	β_{zy}	σ_{zy}	β_{IVW}	σ_{IVW}
rs7944926	A/G	-2	0.19	0.40%	0.0153	0.0217	-0.0076	0.0109	0.0418	0.0309	-0.0209	0.0154
rs12794714	A/G	-3	0.22	0.60%	0.0412	0.0189	-0.0137	0.0063	0.0772	0.0270	-0.0257	0.0091
rs2282679	C/A	-2.5	0.70	0.30%	0.0276	0.0205	-0.0110	0.0082	0.0432	0.0292	-0.0173	0.0117
Combined	-	-	-	1.30%			-0.0118	0.0045	-	-	-0.0218	0.0067

EA/NEA refers to the Effect Allele and Non-Effect Allele. β_{zy} denotes the magnitude of association of the SNP-outcome estimate. σ_{zx} is the standard error of the SNP-exposure estimate. β_{zx} denotes the magnitude of association of Z, the SNP instrument on X, the modifiable exposure level (25(OH)D).

 σ_{zy} is the standard error of β_{zy} .

 R^2 is the proportion of variance in 25(OH)D explained by the SNP(s).

 β_{IVW} is the estimate and σ_{IVW} its standard deviation. β_{zy} is presented on the log(OR) scale.

 β_{IVW} is presented on the log(OR) scale for a single unit (1nmol/Liter) change in 25(OH)D – see text for OR scale changes for a 20 unit (nmol/Liter) change in 25(OH)D.

Note: the β_{zx} estimate for rs2282679 is obtained from Mokry et al. and transformed to natural scale (from natural logarithm) using an intercept at e^4 (~54.59) nmol/Litre of 25(OH)D. Standard errors for these estimates were calculated from F-statistics. The variance explained (R^2) for rs12794714 and rs7944926 were obtained directly from Afzal et al. ; whereas the R^2 for rs2822679 was computed from Mokry et al.

<text>



Schematic representation of the Mendelian randomization framework using vitamin D SNPs as instrumental

n randomiz. box 292mm (96 .

Causal OR for 20nmol/Liter change in 25(OH)D on risk of all ovarian cancer and high grade serous subtype



Causal OR of 25(OH)D on all ovarian cancer and high grade serous ovarian cancer 357x194mm (72 x 72 DPI)

57x194m...

Causal OR for 20nmol/Liter change in 25(OH)D towards risk of ovarian cancer by subtypes



Causal OR of 25(OH)D on individual ovarian cancer subtypes 357x194mm (72 x 72 DPI)

357x194mm (72 x 72 DPI)