Genetic variants in \textit{ELOVL2} and \textit{HSD17B12} predict melanoma-specific survival

Wei Dai\textsuperscript{1,2,3,10}, Hongliang Liu\textsuperscript{2,3,10}, Xinyuan Xu\textsuperscript{2,3}, Ge Jie\textsuperscript{2,3}, Sheng Luo\textsuperscript{4}, Dakai Zhu\textsuperscript{5}, Christopher I. Amos\textsuperscript{5}, Shenying Fang\textsuperscript{6}, Jeffrey E. Lee\textsuperscript{6}, Xin Li\textsuperscript{7,8}, Hongmei Nan\textsuperscript{7,8}, Chunying Li\textsuperscript{1*}, and Qingyi Wei\textsuperscript{2,3,9*}

\textsuperscript{1}Department of Dermatology, Xijing Hospital, Fourth Military Medical University, Xi’an, Shaanxi, China;  
\textsuperscript{2}Duke Cancer Institute, Duke University Medical Center, Durham, NC 27710, USA;  
\textsuperscript{3}Department of Population Health Sciences, Duke University School of Medicine, Durham, NC 27710, USA;  
\textsuperscript{4}Department of Biostatistics and Bioinformatics, Duke University School of Medicine, Durham, NC 27710, USA;  
\textsuperscript{5}Institute for Clinical and Translational Research, Baylor College of Medicine, Houston, TX 77030, USA;  
\textsuperscript{6}Department of Surgical Oncology, The University of Texas M. D. Anderson Cancer Center, Houston, TX 77030, USA;  
\textsuperscript{10}These authors contributed equally to this work.
7 Department of Epidemiology, Fairbanks School of Public Health, Indiana University, Indianapolis, IN 46202, USA;

8 Channing Division of Network Medicine, Department of Medicine, Brigham and Women's Hospital, Boston, MA 02115, USA;

9 Department of Medicine, Duke University School of Medicine, Durham, NC 27710, USA.

10 These authors contributed equally to this work.

Corresponding author: Chunying Li, Department of Dermatology, Xijing Hospital, Fourth Military Medical University, Xi’an, Shaanxi, China; E-mail: lichying@fmmu.edu.cn; and Qingyi Wei, Duke Cancer Institute, Duke University Medical Center and Department of Medicine, Duke School of Medicine, 905 S LaSalle Street, Durham, North Carolina 27710, USA. E-mail: qingyi.wei@duke.edu

Short title: Genetic Variants in Fatty Acid Synthesis Pathway and CMSS

Key words: cutaneous melanoma, fatty acid synthesis, single-nucleotide polymorphism, genome-wide association study, melanoma-specific survival
**Abbreviations:** CI, confidence interval; CM, cutaneous melanoma; CMSS, cutaneous melanoma-specific survival; *ELOVL2*, elongation of very long-chain fatty acids 2; FASN, fatty acid synthase; FPRP, false positive report probability; GWAS, genome-wide association study; HR$_{adj}$, adjusted hazards ratio; *HSD17B12*, hydroxysteroid 17-beta dehydrogenase 12; LD, linkage disequilibrium; NHS, the Nurses’ Health Study; HPFS, the Health Professionals Follow-up Study; SNP, single-nucleotide polymorphism.

**The appropriate article category:** Cancer Epidemiology

**Novelty and Impact:** An increased fatty acid synthesis provides metabolic substrates for energy storage, membrane building and signaling transduction, which has been strongly associated with cancer prognosis. The authors analyzed associations between variants in genes in the fatty acid synthesis pathway and cutaneous melanoma-specific survival by using datasets from two published genome-wide association studies. They found that *ELOVL2* rs3734398 and *HSD17B12* rs11037684 were significantly associated with cutaneous melanoma-specific survival, suggesting their potential roles as prognostic factors for melanoma patients.
Abstract

Fatty acids play a key role in cellular bioenergetics, membrane biosynthesis and intracellular signaling processes and thus may be involved in cancer development and progression. In the present study, we comprehensively assessed associations of 14,522 common single-nucleotide polymorphisms (SNPs) in 149 genes of the fatty-acid synthesis pathway with cutaneous melanoma disease-specific survival (CMSS). The dataset of 858 cutaneous melanoma (CM) patients from a published genome-wide association study (GWAS) by The University of Texas M.D. Anderson Cancer Center was used as the discovery dataset, and the identified significant SNPs were validated by a dataset of 409 CM patients from another GWAS from the Nurses’ Health and Health Professionals Follow-up Studies. We found 40 noteworthy SNPs associated with CMSS in both discovery and validation datasets after multiple comparison correction by the false positive report probability method, because more than 85% of the SNPs were imputed. By performing functional prediction, linkage disequilibrium analysis, and stepwise Cox regression selection, we identified two independent SNPs of ELOVL2 rs3734398 T>C and HSD17B12 rs11037684 A>G that predicted CMSS, with an allelic hazards ratio of 0.66 (95% confidence interval=0.51-0.84 and \( P=8.34 \times 10^{-4} \)) and 2.29 (1.55-3.39 and \( P=3.61 \times 10^{-5} \)), respectively. Finally, the ELOVL2 rs3734398 variant CC
genotype was found to be associated with a significantly increased mRNA expression level. These SNPs may be potential markers for CM prognosis, if validated by additional larger and mechanistic studies.
Introduction

Cutaneous melanoma (CM) has the highest mortality rate among all skin cancers, ranking the fifth most common cancer among males and the sixth among females in the United States. In 2018, an estimated 91,270 new CM cases will be diagnosed in the United States (in addition to 87,290 in situ cases), and the CM incidence rate continues to rise \(^1\). Although many CM patients are considered having an \textit{in situ} or localized disease, these low-risk cases also comprise a substantial fraction of the overall burden of lethal CM \(^2\). CM patients can be classified to having a relative low, average or high risk of recurrence and death according to the American Joint Committee on Cancer; however an estimated 10-20\% of the cases will develop an outcome different from the predicted one \(^3\). Therefore, the identification of alternative prognosis biomarkers is needed.

CM is a disorder of uncontrolled melanocytic cell growth and proliferation, in which cellular metabolism is programmed \(^4\). For example, high levels of carbon flux through aerobic glycolysis accumulate metabolic intermediates as sources of cellular building blocks, and an increased fatty acid synthesis provides metabolic substrates for energy storage, membrane building and signaling transduction, which have been shown to be strongly associated with cancer prognosis \(^5\). Furthermore, lipogenic enzymes in the fatty acid synthesis, such as the ATP citrate lyase \(^6\), fatty acid synthase (FASN) \(^7\) and
stearoyl-CoA desaturase, have emerged as potential therapeutic targets in cancer treatment. Chemical inhibition or genetic knock-down of these key enzymes lead to a reduced proliferation and survival of cancer cells in xenograft tumor models. Interestingly, one study found that inhibition of fatty acid desaturation also increased the chemosensitivity of cancer cells that had an induced apoptosis by the mitochondrial pathway, suggesting an important role of the fatty acid metabolism in cancer cell survival and drug resistance. In melanocytes and melanoma cells, fatty acids regulate the degradation of tyrosinase, a critical enzyme associated with melanin biosynthesis. It has also been reported that alterations in the fatty acid synthesis in melanoma cells helped the cells evade apoptosis and sustain survival after ultraviolet A exposure.

Given the importance of fatty acid synthesis in cancer development and progression, we aimed to identify novel genetic variants in the fatty acid synthesis pathway genes in their association with survival of CM patients by using two published genome-wide association study (GWAS) datasets, which may provide a new clue to novel cancer therapies with interruption of the fatty acid metabolism.

**Materials and Methods**

**Study populations**
In the present study, we used 858 CM patients from The University of Texas MD Anderson Cancer Center (MDACC) study as a discovery dataset and 409 CM patients from the Nurses’ Health Study (NHS) and the Health Professionals Follow-up Studies (HPFS) as a validation dataset, and the published GWAS data were available for both discovery and validation studies. Detailed descriptions of subject selection and data collection for both discovery and validation studies were described elsewhere\textsuperscript{12,13}. The approval to perform the present study was granted by Institutional Review Boards at both MD Anderson and Brigham and Women’s Hospital with a written informed consent obtained from all participants.

**Gene selection and single-nucleotide polymorphism (SNP) genotyping**

We selected 149 fatty acid synthesis pathway genes that are located on the autosomes according to the databases of the Molecular Signatures Database v6.2 of Gene Set Enrichment Analysis website (Table S1). In the MDACC dataset, genomic DNA extracted from the whole blood was genotyped by the Illumina HumanOmni-Quad\_v1\_0\_B array using the National Center for Biotechnology Information Database of Genotypes and Phenotypes (accession: phs000187.v1.p1). Genome-wide imputation was performed by using the MACH software based on the 1000 Genomes Project phase I v2 CEU. In brief, the typed or imputed common SNPs (with minor allele frequency $\geq 0.05$, genotyping success rate $\geq 95\%$, and
Hardy-Weinberg equilibrium $P$ value $\geq 0.00001$, and from imputation for those SNPs with $r^2 \geq 0.8$) within genes in the fatty acid synthesis pathway or their ± 2 kilobase flanking regions were selected for association analysis. Meanwhile, in the NHS/HPFS study, genotyping was performed using the Illumina HumanHap550 array, HumanHap610 array and Affymetrix 6.0 array. Imputation analysis was based on genotyped SNPs and haplotype information from the 1000 Genomes Phase III data using the program MACH. We selected the SNPs by the same standard used in the discovery dataset.

**Statistical methods**

The cutaneous melanoma-specific survival (CMSS) time was calculated from the time of diagnosis until death from CM. Statistically associations between SNPs and CMSS were assessed by multivariable Cox proportional hazards regression analyses using the GenABEL package of R software with adjustment for age, sex, Breslow thickness, regional/distant metastasis, ulceration and mitotic rate in the MDACC dataset $^{14}$. In the validation analysis from the NHS/HPFS study, only age and sex were available for adjustment.

We used the false positive report probability (FPRP) method to correct for multiple testing, because more than 85% of SNPs included in the present study were imputed and thus in linkage disequilibrium (LD) with other genotyped SNPs. Three factors
determine the magnitude of FPRP: the level of $P$ values, the prior probability of a true association of the tested genetic variant with a disease, and the statistical power to detect the odds or hazards ratios of the alternative hypothesis at the given condition. Only the significant results with an FPRP value < 0.2 in both discovery and validation datasets were considered noteworthy. We also used a prior probability of 0.1 to detect a hazards ratio (HR) of 2.0 for an association with variant genotypes or minor alleles of the SNPs with $P < 0.05$.

To evaluate the effects of genetic variants on the cumulative probability of CMSS, Kaplan-Meier survival curves and log-rank tests were performed. The establishment of the number of risk genotypes was used to estimate the joint effect of the multi-genetic variants. In the present study, we calculated a genotype score from the number of risk genotypes and performed multivariable Cox regression models to assess the association between the genotype score and CMSS. To assess the SNPs of interest and cumulative incidence of CM-specific death, where death from other causes other than CM was modeled as a competing event. A Fine-Gray competing risk regression model was performed for univariate and multivariable regression analyses, which calculates subdistribution HR from Cox proportional hazards model. For the meta-analysis, fixed-effects models were used, because no heterogeneity was found between two studies ($Q$ test $P > 0.100$ and $I^2 < 25.0\%$). We used receiver operating characteristic (ROC) curve to illustrate the ability of area under the curve (AUC) in
predicting CMSS, which were calculated with timeROC package of R software to assess the accuracy of genetic variants’ continuing effect over the time. Additionally, we performed linear regression analysis for trends in the association between selected SNP and the mRNA expression levels of each corresponding gene as obtained from RNAseq data from the 1000 Genomes Project 16, 17 (including 373 samples from European descendants) and the GTEx Portal 18 (http://www.gtexportal.org/home/). The rest analyses were performed using SAS software Version 9.4 (SAS Institute, Cary, NC), if not specified otherwise.

Results

Subject Characteristics

In the MDACC dataset, there were slightly more male patients (496, 57.8%) than female patients with an age range between 17 and 94 years at diagnosis (a median age of 53 years); 56.8% of these cases were older than 50 years; and 82.6% (709) had been classified as no regional/distant metastasis. Univariate Cox regression analysis suggested that age, sex, stage, Breslow thickness, ulceration and mitotic rate were significantly associated with CMSS. For the NHS/HPFS study, the dataset only had age, sex, survival outcome and genotype data with an age range between 34 and 87 years at diagnosis (a median age of 60 years), and the majority of the cases were over 50 years.
old (337, 82.4%) with more female patients (271, 66.3%). The patients from the MDACC dataset had a relatively shorter median follow-up time of 81.1 months with a range between 4.7 to 175.3 months, compared to 179.0 months with a range between 5.0 to 453.0 months for NHS/HPFS patients (Table S2).

**Associations between SNPs in the fatty acid synthesis pathway genes and CMSS**

Figure 1 provides a flowchart of study design to illustrate the present study. To assess the associations of 2,161 genotyped and 12,361 imputed SNPs of the fatty acid synthesis pathway genes with CMSS, we performed the single locus analysis by using multivariate Cox proportional hazards regression in the MDACC dataset with adjustments for age, sex, regional/distant metastasis, Breslow thickness, ulceration, and mitotic rate. A Manhattan plot showing the associations between 14,522 SNPs and CMSS is presented in Figure S1. As a result, 1,042 SNPs were significantly associated with CMSS at \( P < 0.05 \) in an additive genetic model, of which 538 SNPs were still considered noteworthy after the multiple test correction by FPRP, which took into account of the fact that the vast majority of the SNPs under investigation were imputed with a LD approach. Among the 538 SNPs, 40 were validated in the NHS/HPFS dataset and remained significantly associated with CMSS at \( P < 0.05 \) after the correction by an
FPRP < 0.2. On the basis of the *in silico* functional prediction by using SNPinfo (http://snpinfo.niehs.nih.gov/snpinfo/snpfunc.html) and RegulomeDB (http://www.regulomedb.org/), 13 of these 40 SNPs were predicted to be putatively functional, including two SNPs in *ELOVL2* (the elongation of very long-chain fatty acids 2 gene) and eleven SNPs in *HSD17B12* (the hydroxysteroid 17-beta dehydrogenase 12 gene) (Table S3). In the subsequent meta-analysis of the two datasets, the 13 SNPs in *ELOVL2* and *HSD17B12* remained significant in associations with CMSS (Table 1) without heterogeneity between the two datasets ($P_{het} > 0.05$ for both).

**Genetic variants in the fatty acid synthesis pathway genes as independent death predictors**

We further performed LD analysis of the 13 SNPs in *ELOVL2* and *HSD17B12* and found that two SNPs of *ELOVL2* were in a high LD and that 11 SNPs of *HSD17B12* were also a high LD (Figure S2). In consideration of $P$ values, LD and predicted functions, we selected *ELOVL2* rs3734398 (genotyped) and *HSD17B12* rs11037684 (genotyped) as the independent tagSNPs for further analysis.

An initial stepwise Cox regression analyses of selected clinical variables from the MDACC dataset suggested these two SNPs were independent predictors of CMSS.
(Table S4). In multivariate Cox regression analysis using an additive model, we evaluated the effects of these two significant SNPs on death risk with adjustment for clinicopathological covariates (i.e., age, sex, Breslow thickness, regional/distant metastasis, ulceration of tumor, and tumor cell mitotic rate) in the MDACC dataset but only for age and sex in the NHS/HPFS dataset. In the MDACC study, we observed a statistically significant protective effect of the \( ELOVL2 \) rs3734398 C allele (\( P_{\text{trend}} = 0.027 \)) but a risk effect of the \( HSD17B12 \) rs11037684 G allele (\( P_{\text{trend}} = 0.007 \)) on CM-specific survival. Similar results were observed for the \( ELOVL2 \) rs3734398 C allele in the NHS/HPFS dataset (\( P_{\text{trend}} = 0.005 \)) and the combined dataset of both MDACC and NHS/HPFS (\( P_{\text{trend}} = 0.003 \)). Similarly, the risk effect of the \( HSD17B12 \) rs11037684 G allele was observed in the NHS/HPFS dataset (\( P_{\text{trend}} = 0.002 \)) and the combined dataset of both MDACC and NHS/HPFS (\( P_{\text{trend}} = 0.002 \)) (Table 2). To further visualize the HR effects, we used Kaplan-Meier survival curves for the associations between CMSS and risk genotypes of \( ELOVL2 \) rs3734398 and \( HSD17B12 \) rs11037684 in the combined dataset of both MDACC and NHS/HPFS (Figure 2a and 2b).

In the Fine-Gray competing-risks regression model, the cumulative incidence of an event of interest was calculated in the presence of competing risks (death not caused by CM). During the follow-up time, 38 and 91 patients died of causes other than CM in
the MDACC and NHS/HPFS datasets, respectively. In multivariate competing risks regression models, *ELOVL2* rs3734398 was a statistically significant predictor of CMSS, after accounting for the postdiagnosis mortality in both datasets (with subdistribution HR of 0.72 in the MDACC dataset and 0.53 in the NHS/HPFS dataset, respectively); similarly, *HSD17B12* rs11037684 was also a significant predictor in the MDACC dataset (subdistribution HR = 1.93 and $P = 0.014$) and NHS/HPFS dataset (subdistribution HR = 2.56 and $P = 0.002$). In the subsequent meta-analyses, for both rs3734398 and rs11037684, the direction, magnitude, and significance of subdistribution HR of CMSS were consistent with the cause-specific HR (Table S5). Furthermore, regional association plots for the MDACC dataset were generated for *ELOVL2* and *HSD17B12*, including the 200-kb regions flanking the neighborhoods of these two genes (Figure S3).

**Survival of CM patients with combined risk genotypes**

To better estimate the joint effect of the two tagSNPs on risk of death, we combined the risk genotypes (those associated with an increased death risk) of *ELOVL2* rs3734398 TT and *HSD17B12* rs11037684 AG+GG into one variable as a genetic score. We then categorized all the patients into three groups with 0, 1 and 2 risk genotype. As illustrated
in Table 2, we observed a risk-genotype dose-response effect; that is, the effect on CMSS increased as the number of risk genotypes increased in the MDACC dataset ($P_{\text{trend}} = 0.007$), the NHS/HPFS dataset ($P_{\text{trend}} < 0.0001$) and the combined dataset of both MDACC and NHS/HPFS ($P_{\text{trend}} < 0.0001$) after adjustments for covariates where appropriate. We next dichotomized all patients into the 0 risk genotype group and the 1-2 risk genotypes group and found that, compared with the 0 risk genotype group, the 1-2 risk genotypes group had a higher CM-death risk in the MDACC dataset (adjusted hazards ratio [HR$_{\text{adj}}$] = 1.66, 95% CI = 1.09-2.53 and $P = 0.019$), the NHS/HPFS dataset (2.82, 1.56-5.10 and 0.0006) and the combined dataset of both MDACC and NHS/HPFS (1.79, 1.29-2.50 and 0.0005). Figure 2c shows the Kaplan-Meier curves for the associations between risk genotypes and CMSS.

Stratified analyses for the effect of combined risk genotypes on CMSS

We further conducted stratified analyses to investigate whether the joint effect of risk genotypes on CMSS was modified by clinical-pathologic variables including age, sex, distant/regional metastasis, Breslow thickness, ulceration and mitotic rate in the MDACC dataset and age and sex in the NHS/HPFS dataset. As a result, patients with the 1-2 risk genotypes group, compared with the 0 risk genotype group, showed a substantially
increased risk of CM-associated death in the presence of clinical variables, which were more evident in the subgroups of age ≤ 50, male subjects and those with tumor cell mitotic rate of ≤ 1/mm$^2$ in the MDACC dataset and the subgroups age > 50 and female subjects in the NHS/HPFS dataset. However, no significant interaction was found among all the subgroups (Table S6).

**ROC and AUC estimation for CMSS prediction**

To assess the ability of risk genotypes to predict CMSS, we compared the model with ROC for clinical variables where appropriate to that of ROC for both clinical variables and risk genotypes. Consistently, the AUC of the five-year CMSS improved prediction performance in the MDACC dataset, the NHS/HPFS dataset and the combined dataset of both MDACC and NHS/HPFS with the addition of risk genotypes to the model (Supplementary Figure S4a, 4c and 4e). Only the AUC of the five-year CMSS in the NHS/HPFS dataset significantly increased from 54.05% to 73.51% ($P = 0.022$) with the addition of risk genotypes to the model. In addition, the time-dependent AUC curves were also provided to assess the ability of risk genotypes to predict CMSS through the entire follow-up period in the above-mentioned three datasets (Supplementary Figure S4b, 4d and 4f).
Genotype-phenotype correlation analyses

We further evaluated the correlations between SNPs and their corresponding mRNA expression levels using publically available RNA-seq data of 373 lymphoblastoid cell lines from the 1000 Genomes Project \(^\text{17, 18}\). Notably, the rs3734398 C allele was significantly correlated with mRNA expression levels of \textit{ELOVL2} in an additive model \((P = 0.024, \text{Figure 2d})\). We also performed expression quantitative trait loci (eQTL) analysis using genomic data from the Genotype-Tissue Expression (GTEx) Project (http://www.gtexportal.org/home), which includes \textit{ELOVL2} rs3734398 in transformed fibroblasts from 300 donors. We found that rs3734398 C allele was associated with a significantly increased \textit{ELOVL2} mRNA expression level \((P = 7.3 \times 10^{-7})\) in an additive genetic model (\text{Figure 2e}), which is consistent with our initial findings. However, there was no significant correlation between rs11037684 genotypes and \textit{HSD17B12} mRNA expression levels \((P = 0.911, 0.988\) and 0.547 for additive, dominant and recessive models, respectively) (\text{Figure S5}) in the 1000 Genomes Project nor in the GTEx. No significant associations between selected SNPs and their corresponding mRNA expression levels were observed in the normal skin tissues from the sun exposed lower leg and the unexposed suprapubic (\text{Table S7}) from the GTEx. Using experimental data
from the ENCODE Project (Figure S6), we found the two SNPs (i.e., rs3734398 and rs11037684) to be located in a DNase I hypersensitive site, where the DNase hypersensitivity and histone modification H3K27 acetylation indicated some signals for active enhancer and promoter functions. The evidence from the DNase cluster and transcription factor CHIP-seq data suggests that rs3734398 is located on the SPI1 motif and that rs11037684 is located on the RP58 motif as indicated by the position weight matrix.

Discussion

In the present study, we found that genetic variants \textit{ELOVL2} rs3734398 and \textit{HSD17B12} rs11037684 were likely to independently or jointly modulate the survival of CM patients. We also observed a dose-response effect of their combined risk-genotypes on CMSS. Moreover, the rs3734398 C allele was correlated with an increase in \textit{ELOVL2} mRNA expression level in lymphoblastoid cell lines derived from 373 European descendants from the 1000 Genomes Project. These findings are biologically plausible, because the fatty acid synthesis pathway contributes to membrane biosynthesis, energy storage and the regulation of oncogenic signaling.

A deregulated fatty acid synthesis can affect drug resistance and cancer risk,
prognosis and recurrence. For example, several studies have shown that overexpression of FASN is associated with a poor prognosis and drug resistance in breast cancer and gastrointestinal stromal tumors as well as associated with a higher risk of recurrence of human cancers, including cancers of the breast, prostate and bladder. Furthermore, blocking the fatty acid synthesis overcomes tumor regrowth and metastasis after withdrawal of the antiangiogenic therapy in breast and colon cancer cells. When restricted to hepatocellular carcinoma patients receiving surgery treatment, genetic variants of FASN could predict recurrence risk. Importantly, evidence also exists that fatty acid synthesis inhibitors may induce apoptosis and also reduce metastases and angiogenesis in melanoma cells. Consistently, CM patients with high expression levels of fatty-acid metabolic signature genes resulted in a significant decrease in survival rates of CM patients, supporting a role of the fatty acid metabolism in CM progression.

We report here some striking significant associations of CMSS with genetic variants in ELOVL2 and HSD17B12. CM patients with an increasing number of risk variant genotypes had a worse survival. Importantly, the risk effect was consistent across different analyses and the majority of subgroup comparisons, suggesting a strong association of a genetic effect on CM survival. We believe that these results are likely
biologically plausible, since the genotype-phenotype correlation demonstrates that
ELOVL2 expression levels may be modulated by rs3734398 T>C change, although
additional investigation is needed to unravel molecular mechanisms underlying the
observed correlation.

ELOVL2 is located on chromosome 6p24.2, encoding for a transmembrane protein
that controls the elongation of polyunsaturated fatty acids (PUFA), which modulates
energy production, and influences inflammation and cell membrane integrity. For
patients with breast cancer, ELOVL2 can hormonally regulate the PUFA synthesis and
thus may have a potential implication on the endocrine therapy. Deletion of ELOVL2
in a mouse model leads to a decrease in Foxp3+ regulatory T cells, suggesting its
potential role in the adaptive immunity. GWAS have identified ELOVL2 variants to be
associated with serum metabolic profile, aging process and DNA methylation.
Recently, ELOVL2 rs3734398 has been reported to be significantly associated with
plasma eicosapentaenoic and docosahexaenoic acid proportions after fish oil
supplement, which provides evidence on personalized dietary recommendations for
reducing cardiovascular disease risk based on the genotype of this SNP. To date,
ELOVL2 has not been reported to be associated with CM progression and prognosis. In
light of our results and in the consideration that PUFAs are involved in crucial biological
functions and that rs3734398 may regulate ELOVL2 expression, it is possible that genetic variants in ELOVL2 may be utilized in managing CM progression and prognosis in the future precision medicine, once validated by additional studies.

HSD17B12, located on chromosome 11p11.2, is a multifunctional isozyme, catalyzing the elongation of long chain fatty acids, particularly the conversion of palmitic to arachidonic acid. The latter is the precursor of prostaglandin E2, an important mediator of inflammation, linking HSD17B12 expression levels to inflammation and cancer. HSD17B12 expression levels were also shown to be associated with adipocyte differentiation as well as embryogenesis and differentiation. HSD17B12 also is believed to act as an oncogene involved in multiple cancers. For example, immunohistochemical analyses indicated that cytoplasmic staining of HSD17B12 was enhanced along with the severity of ovarian cancer, whereas HSD17B12 weak expression was correlated to a better overall survival and a longer time to first tumor recurrence. For breast cancer cases, HSD17B12 expression was significantly higher in tumor tissues than in normal tissues, leading to an increased risk of recurrence and adverse clinical outcome. Furthermore, HSD17B12 variants were found to be significantly associated with risk of biochemical recurrence in patients with localized prostate cancer in one study and with less aggressive form of neuroblastoma in
The present study has some strengths and limitations. A major strength of the present study is the comprehensive analysis of associations between SNPs in all genes involved in the fatty acid synthesis pathway and survival of CM as well as the use of two published GWAS datasets with a relative long median follow-up time and strict quality control procedures. The effects of risk genotypes of the two novel SNPs on CMSS were consistent in two different GWAS datasets. However, a potential weakness was the lack of information about different treatment, which should have been adjusted for the possible effect on CM patients’ outcomes. The samples of the two GWAS studies were not large enough to allow for the false discovery rate test, a more desired multiple test correction method, although the FPRP was more appropriate for highly correlated SNPs under investigations as a result of imputation in the present study. Finally, further functional investigation should be conducted to provide mechanistic insights into the mechanisms underlying the CM-death association with these two novel SNPs.

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Conflicts of interest

The authors declare no conflict of interest.
References


2. Whiteman DC, Baade PD, Olsen CM. More people die from thin melanomas (1 mm) than from thick melanomas (>4 mm) in Queensland, Australia. *J Invest Dermatol* 2015;135: 1190-3.


Figure 1. Study workflow for SNPs in the fatty acid synthesis pathway genes.

Abbreviations: AUC, area under curve; CMSS, cutaneous melanoma-specific survival; 
ELOVL2, elongation of very long-chain fatty acids 2; FPRP, false positive report 
probability; GWAS, genome wide association study; HSD17B12, hydroxysteroid 
dehydrogenase type 12; HWE, Hardy Weinberg equilibrium; MAF, minor allele 
frequency; MDACC, The University of Texas MD Anderson Cancer Center; NHS, the 
Nurses’ Health Study; HPFS, the Health Professionals Follow-up Study; ROC, receiver 
operating characteristic; SNP, single nucleotide polymorphism.

Figure 2. Two independent SNPs predict cutaneous melanoma survival and eQTL 
analysis for ELOVL2 rs3734398. Kaplan-Meier survival curves of CMSS stratified by 
ELOVL2 rs3734398 (a) and HSD17B12 rs11037684 (b), assuming a dominant model in 
the combined dataset of both MDACC and NHS/HPFS. (c) Kaplan-Meier survival 
curves of the combined risk genotypes on CMSS: dichotomized 0 risk genotype group 
and 1-2 risk genotypes group in the combined dataset of both MDACC and NHS/HPFS. 
The table below the Kaplan-Meier curves illustrates the numbers at risk for each time 
point. (d) The eQTL analysis for ELOVL2 rs3734398 in blood cells in the 1,000 
Genomes Project in an additive model. (e) The eQTL analysis from the
Genotype-Tissue Expression project for ELOVL2 rs3734398 in an additive genetic model. Abbreviations: CM, cutaneous melanoma; CMSS, cutaneous melanoma-specific survival; ELOVL2, elongation of very long-chain fatty acids 2; eQTL, expression quantitative trait loci; HSD17B12, hydroxysteroid dehydrogenase type 12; MDACC, The University of Texas MD Anderson Cancer Center; NHS, the Nurses’ Health Study; HPFS, the Health Professionals Follow-up Study; SNP, single-nucleotide polymorphism.
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<td>G&gt;C</td>
<td>ELOVL2</td>
<td>6p24.2</td>
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<td>0.68 (0.51-0.91)</td>
<td>0.019</td>
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<tr>
<td>rs11037683&lt;sup&gt;8&lt;/sup&gt;</td>
<td>A&gt;C</td>
<td>HSD17B12</td>
<td>11p11.2</td>
<td>0.06</td>
<td>2.10 (1.22-3.61)</td>
<td>0.007</td>
</tr>
<tr>
<td>rs11037684&lt;sup&gt;8&lt;/sup&gt;</td>
<td>A&gt;G</td>
<td>HSD17B12</td>
<td>11p11.2</td>
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<td>2.10 (1.22-3.61)</td>
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<tr>
<td>rs11037680&lt;sup&gt;7&lt;/sup&gt;</td>
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<td>HSD17B12</td>
<td>11p11.2</td>
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<td>2.25 (1.31-3.86)</td>
<td>0.003</td>
</tr>
<tr>
<td>rs11037609&lt;sup&gt;7&lt;/sup&gt;</td>
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<td>HSD17B12</td>
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<td>0.003</td>
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<tr>
<td>rs11037611&lt;sup&gt;7&lt;/sup&gt;</td>
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<td>HSD17B12</td>
<td>11p11.2</td>
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<td>2.25 (1.31-3.86)</td>
<td>0.003</td>
</tr>
<tr>
<td>rs6188344&lt;sup&gt;7&lt;/sup&gt;</td>
<td>T&gt;C</td>
<td>HSD17B12</td>
<td>11p11.2</td>
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<td>2.25 (1.31-3.86)</td>
<td>0.003</td>
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<tr>
<td>rs6188345&lt;sup&gt;7&lt;/sup&gt;</td>
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<td>HSD17B12</td>
<td>11p11.2</td>
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<td>2.25 (1.31-3.86)</td>
<td>0.003</td>
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<td>rs17514553&lt;sup&gt;7&lt;/sup&gt;</td>
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<td>0.003</td>
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<td>rs17099114&lt;sup&gt;7&lt;/sup&gt;</td>
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<td>HSD17B12</td>
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<td>2.25 (1.31-3.86)</td>
<td>0.003</td>
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<tr>
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<td>A&gt;C</td>
<td>HSD17B12</td>
<td>11p11.2</td>
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<td>2.25 (1.31-3.86)</td>
<td>0.003</td>
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<tr>
<td>rs77739152&lt;sup&gt;7&lt;/sup&gt;</td>
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<td>HSD17B12</td>
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<td>2.22 (1.29-3.82)</td>
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</table>

Abbreviations: SNP, single-nucleotide polymorphism; GWAS, genome-wide association study; MDACC, The University of Texas MD Anderson Cancer Center; NHS/HPFS, the Nurses’ Health Study and Health Professionals Follow-up Study; EAF, effect allele frequency; HR, hazards ratio; CI, confidence interval; FPRP, false positive report probability; P<sub>het</sub>, P value for heterogeneity by Cochrane’s Q test; ELOVL2, elongation of very long-chain fatty acids 2; HSD17B12, hydroxysteroid dehydrogenase type 12;<br><sup>1</sup>Reference allele/effect allele;<br><sup>2</sup>Adjusted for age, sex, Breslow thickness, distant/regional metastasis, ulceration and mitotic rate in the additive model;<br><sup>3</sup>Imputation was used for multiple test correction because 85.1% of the analyzed SNPs in MDACC dataset were imputed with a high level of linkage disequilibrium;<br><sup>4</sup>Adjusted for age and sex in an additive genetic model;<br><sup>5</sup>Meta-analysis in the fix-effect model;<br><sup>6</sup>Compared SNPs in the MDACC dataset.
Imputed SNPs in the MDACC dataset.
Table 2. Associations between two independent SNPs in the fatty acid synthesis pathway genes and CMSS of patients in the MDACC dataset, the NHS/HPFS dataset and the combined dataset of both MDACC and NHS/HPFS

<table>
<thead>
<tr>
<th>Genotype</th>
<th>MDACC (n=858)</th>
<th>NHS/HPFS (n=409)</th>
<th>MDACC + NHS/HPFS (n=1267)</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>Frequency</td>
<td>Multivariate analysis</td>
<td>Frequency</td>
</tr>
<tr>
<td></td>
<td>All Death (%)</td>
<td>P</td>
<td>All Death (%)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>HR (95% CI)</td>
<td></td>
</tr>
<tr>
<td>ELOVL2 rs3734398 T&gt;C</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>TT</td>
<td>310</td>
<td>40 (12.90)</td>
<td>1.00</td>
</tr>
<tr>
<td>TC</td>
<td>385</td>
<td>42 (10.91)</td>
<td>0.86 (0.55-1.35)</td>
</tr>
<tr>
<td>CC</td>
<td>163</td>
<td>13 (7.98)</td>
<td>0.45 (0.23-0.89)</td>
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<td>Trend test</td>
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<td></td>
<td>0.027</td>
</tr>
<tr>
<td>TC+CC</td>
<td>548</td>
<td>55 (10.04)</td>
<td>0.72 (0.47-1.10)</td>
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<tr>
<td>HSD17B12 rs11037684 A&gt;G</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>AA</td>
<td>757</td>
<td>79 (10.44)</td>
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<td>AG</td>
<td>99</td>
<td>16 (16.16)</td>
<td>2.23 (1.28-3.91)</td>
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<tr>
<td>GG</td>
<td>2</td>
<td>0 (0.00)</td>
<td>-</td>
</tr>
<tr>
<td>Trend test</td>
<td></td>
<td></td>
<td>0.007</td>
</tr>
<tr>
<td>AG+GG</td>
<td>101</td>
<td>16 (15.84)</td>
<td>2.21 (1.26-3.86)</td>
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<td>Combined number of risk genotypes</td>
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<tr>
<td>0</td>
<td>489</td>
<td>46 (9.41)</td>
<td>1.00</td>
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<tr>
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<td>327</td>
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<td>1.56 (1.00-2.41)</td>
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<tr>
<td>2</td>
<td>42</td>
<td>7 (16.67)</td>
<td>2.70 (1.18-6.18)</td>
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<tr>
<td>Trend test</td>
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<td></td>
<td>0.007</td>
</tr>
<tr>
<td>0</td>
<td>489</td>
<td>46 (9.41)</td>
<td>1.00</td>
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<tr>
<td>1-2</td>
<td>369</td>
<td>49 (13.28)</td>
<td>1.66 (1.09-2.53)</td>
</tr>
</tbody>
</table>

Abbreviations: SNP, single-nucleotide polymorphism; CMSS, cutaneous melanoma-specific survival; MDACC, The University of Texas MD Anderson Cancer Center; NHS/HPFS, the Nurses’ Health Study and Health Professionals Follow-up Study; HR, hazards ratio; CI, confidence interval; ELOVL2, elongation of very-long-chain fatty acids 2; HSD17B12, hydroxysteroid dehydrogenase type 12; 1Adjusted for age, sex, Breslow thickness, distant/regional metastasis, ulceration and mitotic rate in the MDACC dataset; 2Adjusted for age and sex in the NHS/HPFS dataset; 3Adjusted for age and sex in the combined dataset of both MDACC and NHS/HPFS; 4Risk genotypes include ELOVL2 rs3734398 TT and HSD17B12 rs11037684 AG+GG.