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Publication Date

2015-07-22

DOI

10.1038/ncomms8539

Peer reviewed



Published in final edited form as:

Nat Commun. ; 6: 7539. doi:10.1038/ncomms8539.

Genome-wide association study identifies variants at 16p13 associated with survival in multiple myeloma patients

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Author Contributions: Study conception: EZ, ED, CV; collection of the data: EZ, ED, KC, DC, PB, JC, CD, MD, AG, KJ, AJ, SK, DA, HM, TM, JML, VR, JS, AJV, MW, JW, NC, FC, CV; performed genotyping: AM, RD, AL BJ; analysis of the data: DH, DS, DC, BA, YZ; drafting of the manuscript: EZ, ED; critical revision of the manuscript: EZ, ED, DH, AM, DS, KC, DC, BA, PB, GB, YZ, JC, RD, CD, MD, LF, AG, SH, KJ, AJ, SK, DA, MG, LCA, BJ, AL, HM, TM, JML, VR, JS, AJV, MW, JW, SS, NC, FC, CV

Competing Financial Interests The authors declare no conflicts of interest.

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Abstract

Here we perform the first genome wide association study (GWAS) of multiple myeloma (MM) survival. In a meta-analysis of 306 MM patients treated at UCSF and 239 patients treated at the Mayo clinic, we find a significant association between SNPs near the gene *FOPNL* on chromosome 16p13 and survival (rs72773978; $p=6 \times 10^{-10}$). Patients with the minor allele are at increased risk for mortality (HR 2.65; 95% CI: 1.94 – 3.58) relative to patients homozygous for the major allele. We replicate the association in the IMMEnSE cohort including 772 patients, and a University of Utah cohort including 318 patients (rs72773978 $p=0.044$). Using publically available data, we find that the minor allele was associated with increased expression of *FOPNL* and increased expression of *FOPNL* was associated with higher expression of centrosomal genes and with shorter survival.. Polymorphisms at the *FOPNL* locus are associated with survival among MM patients.

INTRODUCTION

Multiple myeloma (MM) is an incurable hematological malignancy of plasma cells. Approximately 22,000 new cases are diagnosed each year in the United States and over 10,000 deaths occur annually¹. Family history is a strong risk factor for MM². Recent genome-wide association studies (GWAS) reported 8 loci associated with susceptibility to MM³⁻⁵.

A variety of clinical features and biomarkers are associated with MM prognosis⁶. Chromosomal abnormalities are also associated with prognosis; deletions at 17p, 13q, amplifications at 1q and translocations t(4;14) and t(14;16) have been associated with a poor prognosis, while hyperdiploidy is associated with a favorable prognosis⁷⁻⁹. Gene expression signatures of the myeloma cells also predict survival¹⁰⁻¹⁴.

Germline genetic variants are associated with survival among patients with esophageal¹⁵, breast^{16,17}, pancreatic^{18,19} and small cell lung cancer²⁰. We performed the first GWAS of MM survival, by conducting a meta-analysis of two studies from the University of California San Francisco (UCSF) and the Mayo Clinic. We found a locus on chromosome 16 associated with survival. We replicated the findings in the IMMEnSE consortium and the University of Utah cohort. The top SNPs were at the *FOPNL* locus. Using publically available

data of gene expression from peripheral blood of normal individuals, we found that the risk alleles at the top SNPs were associated with increased expression of *FOPNL*. We also found that increased expression of *FOPNL* was associated with higher “centrosome index”, a gene expression correlate of centrosome amplification in multiple myeloma cells which has been associated with poor survival.

RESULTS

Identifying a Locus for Survival

We performed a GWAS of overall survival among MM patients in cohorts (Table 1) from UCSF (n=306) and Mayo Clinic (n=239) separately. One *locus* mapping to chromosome 16p13.11 (Hg19) showed a suggestive association in both the UCSF ($p=8.4 \times 10^{-7}$; proportional hazards model) and the Mayo Clinic studies ($p=1.1 \times 10^{-4}$; proportional hazards model). In a meta-analysis of these GWAS, the locus was genome-wide significant (Figure 1a) with the strongest evidence at 2 SNPs in perfect linkage disequilibrium rs72773978 and rs117863986 ($p=6.0 \times 10^{-10}$ for both; meta-analysis p value is calculated using inverse variance based weighting). We found no significant deviation from the proportional hazards assumption for the top SNP in either the UCSF ($p=0.74$; p values calculated by testing whether scaled Schoenfeld residuals vary with time) or Mayo clinic studies ($p=0.95$). We identified 131 SNPs at this locus associated with survival at $p<5 \times 10^{-8}$ (Supplementary Data 1); these SNPs had approximately 5–7% minor allele frequency and were in tight linkage disequilibrium ($r^2>0.8$) with the top SNPs (figure 1b). Of the 131 top SNPs, 17 were genotyped in the UCSF dataset and 1 was genotyped in the Mayo Clinic dataset (SupplementaryData 1). The remaining SNPs were imputed, but had very high imputation quality scores (Information >0.9 or $r^2>0.9$). We directly genotyped 8 additional SNPs in the Mayo clinic dataset, including one of the top 2 SNPs, rs117863986, and found consistently strong levels of association with the genotyped SNPs (rs117863986 HR: 2.26; 95% CI: 1.46 – 3.40; $p=0.00021$; proportional hazards model) and other SNPs (Supplementary Table 1).

Analysis of the genome wide distribution of association statistics (Supplementary Figure 1a) revealed minimal deviation from the expectation under the null ($\lambda=1.002$). After removing SNPs from a 200KB region around the top locus on chromosome 16, we found no evidence for additional signal genome wide (Supplementary Figure 1b) although some other loci had some suggestive signals with p values $5 \times 10^{-7} - 1 \times 10^{-7}$ (Supplementary Data 1).

The UCSF study had a median time of 7.6 months (interquartile range 5.7–8.9 months) between date of diagnosis and date of ascertainment. Therefore, we considered whether this delay affected our results. First, we adjusted for the time difference between date of diagnosis and ascertainment in the proportional hazards models and found no attenuation (Supplementary Table 2). We also considered models stratified by the delay between date of diagnosis and ascertainment (Supplementary Table 2). We found that the effect was consistent among patients enrolled between 0 to 5.9 months after diagnosis (HR 3.23; 95% CI: 1.28 – 8.17; $p=0.013$; proportional hazards model) those enrolled between 6 and 11.9 months after diagnosis (HR 3.04; 95% CI: 1.67 – 5.55; $p=0.00028$; proportional hazards model) and those enrolled from 12 to 23.9 months (HR 5.06; 95% CI: 1.18 – 21.79; $p=0.029$;

proportional hazards model). Thus, we concluded that the delay between diagnosis and ascertainment within the first two years was unlikely to affect the association between the SNP and overall survival. We also considered models that adjusted for the difference between date of diagnosis and ascertainment in the Mayo study and found no change in the association as expected (Supplementary Table 2), since nearly all of the participants were ascertained within 1 month of diagnosis.

We searched for additional SNPs that were associated independently of the top SNP by performing conditional analyses including rs72773978 and other SNPs within 100 KB of that SNP. We performed survival analyses for all SNPs that were either in no LD ($R^2 < 0.1$) or in modest LD (R^2 0.1–0.5) with RS72773978, adjusting for the effect of PC's and for the effect of RS72773978. We found no other significant associations in the locus after adjusting for multiple hypothesis testing.

Median survival was decreased by approximately 2.7 years among patients who were either heterozygous or homozygous for the rare variant (T allele) of rs72773978 compared to patients homozygous for the common variant in both the UCSF and Mayo Clinic cohorts (Figure 2). In models that adjusted for age, gender and genetic ancestry, approximately 10–14% of patients had an increased risk of death (hazard ratio ~2.6; table 2) in the meta-analysis of these 2 datasets.

We also performed a separate analysis of individuals who genetically clustered with Caucasians in the UCSF dataset (Supplementary Figure 2). We repeated the meta-analysis of the Mayo Clinic data with the UCSF Caucasian only sample (Supplementary Table 3), and found the association with rs72773978 remained significant ($p = 2.4 \times 10^{-9}$; proportional hazards model). The UCSF cohort included African American patients (N=25) and patients of Latino (N=27) or other patients who clustered with those of mixed ancestry (N=24). In an analysis of these patients, we also found a nominally significant association between shorter survival and the minor allele (HR 2.43; 95% CI: 1.09 – 5.39; $p = 0.029$ proportional hazards model).

We also examined whether the top SNPs that we identified were associated with susceptibility to MM in our two studies. We found no significant difference in genotype frequencies between cases and controls (Supplementary Table 4).

Relationship to Stage at Diagnosis and Treatment

We evaluated the effect of the genotype on survival after adjustment for clinical stage. In analyses that adjusted for stage using either the ISS definition or the Durie-Salmon staging system, rs72773978 genotype remained a strong predictor of survival (Table 2). Among the participants in the Mayo Clinic on whom LDH levels were available (N=154), we saw a consistent level of association (HR: 2.25; 95% CI: 1.26 – 4.03; $p = 0.006$; proportional hazards model).

Since MM treatment has improved significantly in the last decade, we used data available from both cohorts to determine whether the SNP effect varied by initial treatment (Supplementary Table 5). We found a consistent effect of the SNP regardless of the type of

treatment initiated (Table 3) and no evidence of interaction between treatment and the SNP in either the UCSF ($p=0.9$; p for interaction derived using proportional hazards model) or Mayo Clinic ($p=0.52$; p for interaction derived using proportional hazards model) cohorts.

Among patients in the Mayo Clinic study, 134 (56%) were treated by both high dose chemotherapy (HDC) followed by autologous stem-cell rescue. We adjusted for HDC in the proportional hazards models and found that although HDC was a strong predictor of longer survival in the cohort, there was only mild attenuation of the SNP association with survival (Supplementary Table 6). Since nearly all (97%) of the UCSF patients received HDC, the same analysis could not be done within the UCSF study.

Replication

We replicated the association of top SNPs from the UCSF and Mayo Clinic meta-analysis in a replication meta-analysis of 1,090 MM cases, including 772 European MM patients from the IMMEnSE consortium and 318 from the Utah cohort (Supplementary Table 7). We selected 2 SNPs for replication including rs72773978, one of the top associated SNPs from the meta-analysis and rs12598966, a SNP resulting in an amino acid substitution in the *FOPNL* gene. We performed a meta-analysis of all of the replication studies and found a significant association between rs72773978 and survival in the replication cohorts adjusted by age and sex (HR 1.34; 95% CI: 1.01 – 1.74; $p=0.044$; proportional hazards model) with survival shorter by approximately 1.2 years among carriers of the minor allele (figure 2c). There was no evidence of heterogeneity of effect within the replication studies ($p=0.14$; chi-squared test for heterogeneity). The other SNP, rs12598966, was not significantly associated with survival in the replication.

We noted a slightly stronger effect size in analyses that adjusted for stage. However, the change in effect size was not due to negative confounding between stage and the SNP, but rather to the fact that the cohorts with missing data on stage were the ones with an inconsistent point estimate (Supplementary Table 3). In a meta-analysis that did not adjust for ISS stage but just included participants without missing data on ISS stage, we saw approximately the same effect size (HR 1.71; 95% CI: 1.18 – 2.47; $p=0.005$; proportional hazards model) as in the meta-analysis that adjusted for ISS stage (supplementary table 7.)

Analysis of Function

The top SNPs were in a region that overlapped the entire *FOPNL* gene and a portion of the *MYH11* gene (figure 1b). In addition, known drug transporters, *ABCC1* and *ABCC6*, are located about 50kb and 300kb away, respectively. One of the top SNPs, rs12598966, is located in the coding sequence of *FOPNL*, and leads to a non-synonymous amino acid substitution: E->K at amino acid 156; however, this SNP was not significantly associated with survival in the replication and was not predicted to have a deleterious effect on protein function (SIFT score =0.89 and Polyphen 2 score=0.275). Next, we investigated the top 145 SNPs (all in tight LD ($r^2>0.8$) with rs72773978) for an effect on gene expression using GENEVAR²¹. The top 2 SNPs, rs72773978 and rs117863986, were not included in the database, but six other SNPs in strong LD ($r^2=1$) with rs72773978 are present in the database and are associated with expression of *FOPNL* (Supplementary Table 8). The minor

allele of these SNPs predicted higher expression of *FOPNL*. There was no significant association between these SNPs and expression of other genes within 1 MB of the locus.

We identified 13 SNPs in LD with rs72773978 as being potentially functional (Supplementary Table 9). Six of these SNPs are in the 3' UTR of the *FOPNL* gene and, therefore, may be involved in transcript stability. Seven SNPs were identified as being in sites of open chromatin and thus may be involved in transcriptional regulation.

Since the top SNPs were associated with gene expression, we hypothesized that expression of *FOPNL* may be associated with survival among MM patients. In particular, higher expression of *FOPNL* is associated with the minor allele of the top SNPs from the GWAS and should also be associated with shorter survival. We used publically available data on gene expression (GSE2658) and survival from 414 MM cases to test this hypothesis¹³. As predicted, we found a significant association between higher expression of *FOPNL* and worse survival (Supplementary Table 10). *FOPNL* is known to localize to the centrosome and the pericentriolar satellites. Since centrosome amplification is known to be a predictor of poor prognosis, we evaluated the association between *FOPNL* expression and the centrosome index (CI), a previously validated gene expression signature of centrosome amplification. We found a very strong correlation (supplementary table 11) between higher *FOPNL* expression and increased CI in the study we analyzed for survival (GSE2658) and in two additional studies (GSE19784 and GSE26760).

DISCUSSION

We performed a GWAS for survival among MM patients and identified SNPs at chromosome 16p13 that were strongly associated with mortality. The SNPs were in the region of the *FOPNL* gene and a subset of the SNPs were associated with *FOPNL* expression levels, with the minor allele predicting higher expression²². We also found that *FOPNL* expression was associated with poorer survival using data from a previous study¹³. Thus, our results strongly suggest that *FOPNL* is a gene involved in myeloma progression.

FOPNL is known to be associated with centrosome function^{23,24}. Centrosome amplification is common in MM and is associated with poor prognosis^{25,26}. Furthermore, inhibition of centrosomal clustering may be effective in treatment of MM^{27,28}. We found that germline variation that affects a gene involved in centrosomal function may also contribute to disease progression. Furthermore, we found an association between *FOPNL* expression and centrosome index in 3 datasets of gene expression from myeloma samples. However, our results implicating *FOPNL* as the causal gene at this locus rely on the synthesis of several datasets. We were not able to directly correlate the SNPs with gene expression, centrosome index and survival in the same dataset. It is possible that another gene/s at this locus may be responsible for the effect we observe, or that the effect is mediated by *FOPNL*, but that it is not through a mechanism related to centrosome amplification. Additional studies of this gene and centrosomal function will help to further define the mechanism underlying the association that we identified.

Our results imply that germline genetic variation is associated with survival among patients with MM. Other GWAS have identified loci that affect survival in other cancer types^{15–18,20}. At least one of the known loci for MM susceptibility is associated with the risk for a particular subtype of MM⁴ which may also have an effect on prognosis.

MM is a heterogeneous disease with substantial variation in prognosis among different patients. Identifying patients who are at higher risk of progression may be of importance in treating these patients more aggressively earlier in their disease. Our results identify *FOPNL* genotype as a predictor of survival, and we found that the association remains significant after adjustment for stage at diagnosis. However, the effect size we observed in the replication cohorts was substantially attenuated compared to the effect size in the discovery cohorts. This difference is most likely due to “winner's curse” – a tendency for the initial study to over-estimate the true effect size²⁹. Thus, the replication cohorts in our study are more likely to represent the true effect size in future studies.

Our study has several important limitations. We could not examine the association between SNPs and MM survival by cytogenetic abnormalities since the majority of our patients were diagnosed prior to the common use of cytogenetic and fluorescent in-situ hybridization (FISH) analysis in clinical practice. Therefore, it will be important to examine the utility of this genotype in the setting of cytogenetic and FISH analysis and gene expression signatures. Furthermore, we could not adjust for gene expression patterns which are also known to be associated with survival.

We found no difference between patients who were initially treated with modern vs. older therapies. However, our ability to analyze the SNP by different therapies was limited to the UCSF dataset and we had inadequate power to detect interactions between the SNPs and particular drugs. Furthermore, we only adjusted for the association between initial treatment and survival, and it is likely that many of the patients who were initially treated with older regimens received newer regimens if they survived to the era when these became available. It is possible that the effect that we saw is modified by one regimen or by one class of medications. Additional studies should be done in the context of clinical trials or other cohorts where treatment regimens are more uniform to investigate whether the effect of the locus we identified is modified by particular treatments.

In summary, we found a strong association between a locus on chromosome 16p and MM survival that is likely due to an effect on expression of the *FOPNL* gene. The SNPs we identified may become important clinical predictors of outcome among MM patients.

METHODS

UCSF Study

The UCSF Institutional Review Board (IRB) approved ascertainment of cases and use of existing biospecimens for genetic analysis. All participants gave informed consent. The study included 370 patients treated for MM at UCSF between 1989 and 2010. We excluded 10 samples due to insufficient clinical data. We also excluded 42 participants whose blood was collected 2 years after diagnosis from the survival analysis due to the potential bias

towards long-term survivors among these participants. The median delay between diagnosis and ascertainment among the 42 participants excluded was 2.9 years (interquartile range 2.4 to 4.7 years). The median delay among the participants included was 7.6 months (interquartile range 5.7–8.9 months).

We used white blood cells harvested after mobilization of stem cells with granulocyte colony stimulating factor (GCSF) as a source of DNA. Mobilization of stem cells is performed prior to high dose chemotherapy followed by autologous stem cell transplantation. The patient receives GCSF and then undergoes harvesting of peripheral white blood cells via apheresis several days later^{30,31}. Bone marrow stem cell fraction is monitored via CD34 antibody and apheresis is continued until an adequate number of CD34+ cells have been collected for stem cell rescue. The cells are then stored in liquid nitrogen.

We ascertained date of death using chart reviews and death registry data. Survival time was determined as the date of diagnosis until date of death or last clinic visit for patients who were not known to have died. Clinical stage and initial chemotherapy regimen was determined by chart review. For analysis of treatment, we dichotomized treatments into either newer regimens (including an Imid and/or proteasome Inhibitor) or older regimens (including neither an Imid nor proteasome Inhibitor). Nearly all of the participants in the UCSF study (>97%) received high dose chemotherapy with stem cell rescue (autologous bone marrow transplant).

Mayo Clinic Study

Ascertainment of MM cases and genotyping was approved by the Mayo Clinic Institutional Review Board. The study included incident MM cases seen in the regional practice between 1998 and 2007 and recruited within 6 months of initial diagnosis. Nearly all participants (96%) were recruited within 1 month of diagnosis and the remainder were recruited between 1 and 5.5 months after diagnosis. Eligible cases provided consent and a blood sample for research studies of MM. A total of 243 MM cases were used for analyses. DNA was extracted from stored peripheral blood samples. We ascertained date of death and calculated survival time as described for the UCSF study. Clinical stage was determined by chart review. Clinical data on survival could be ascertained on 239 patients. Initial chemotherapy regimen and use of high dose chemotherapy was determined by chart review. For analysis of treatment, we dichotomized treatments into either newer regimens (including an Imid and/or proteasome Inhibitor) or older regimens (including neither an Imid nor proteasome Inhibitor). Approximately 56% of participants were treated with autologous stem cell transplant.

IMMENSE Study

The International Multiple Myeloma rESEarch (IMMEnSE) consortium is a case-control study recruited from 7 different European and North American countries³². MM cases are defined by a confirmed diagnosis of MM, according to the International Myeloma Working Group (IMWG) criteria³³. For each patient, demographic and clinical parameters at diagnosis and survival were collected by the responsible clinicians in each of the IMMEnSE

centers. The data collected are standardized in a central database kept at the German Cancer Research Center (DKFZ, Heidelberg, Germany). For each subject, a sample of peripheral blood or extracted DNA has been collected and sent to DKFZ. A total of 772 MM cases with survival information available in the IMMEnSE consortium were included in this study.

Utah study

Sampling and genetic analysis was approved by the University of Utah Institutional Review Board. The study included prevalent MM cases in the state of Utah, ascertained up to 2012. Eligible cases provided consent and a blood or saliva sample from which DNA was extracted. Date of diagnosis was confirmed from chart review and Utah Cancer Registry data. Date of death was confirmed from chart review and death registry data. Survival time was determined as the date of diagnosis until date of death, last contact with the study, or last known event in Utah (determined from statewide vital records, driver's license renewals, and voter registrations in the Utah Population Database) for patients who were not known to have died. A total of 318 MM cases with DNA and survival information were available for this study.

All SNP positions were annotated using the Genome Reference Consortium GRCh37 (Hg19) version of the human genome.

UCSF

A pilot study of 81 MM samples used an Illumina 660 array genotyped at the UCSF Genomics Core Facility. In a second phase, we genotyped 289 MM samples using an Illumina Omni5 array at Expression Analysis (Durham, NC). Of the 370 participants in the GWAS, 52 participants were excluded from the survival analysis as noted above due to either insufficient clinical data (N=10) or due to >2 year time difference between diagnosis and ascertainment (N=42). Of the remaining 318 samples we dropped 12 since they did not pass quality control for genotyping. Eleven were dropped due to high missing genotype values (>5% missing genotypes per sample) and 1 sample was dropped due to potential contamination, leaving 306 patients. We dropped SNPs that had >5% missing values, or were monomorphic. Imputation was performed using IMPUTE2³⁴ (https://mathgen.stats.ox.ac.uk/impute/impute_v2.html#home) with all samples from 1000 Genomes dataset (Version 2, May 2011 release³⁵) as a reference. Imputed SNPs with Information<0.5 or minor allele frequency (MAF)<0.025 were excluded, leaving 8,036,255 SNPs for analysis.

Mayo Clinic

Cases were genotyped using the Affymetrix 6.0 array. Monomorphic SNPs and those with a call rate < 95% were excluded, leaving 786,950 observed SNPs. Four samples with call rates < 95% and one sample with non-European ancestry according to principal components analysis were excluded, leaving 243 MM cases and 239 with follow-up past date of diagnosis. Imputation was performed with BEAGLE³⁶ (<http://faculty.washington.edu/browning/beagle/beagle.html>), using all samples from version 2 of the 1000 Genomes data

(May 2011 release) as reference. Imputed SNPs with an $r^2 < 0.3$ or MAF < 0.025 were excluded, leaving 7,276,170 SNPs for further analyses.

We selected 2 SNPs for replication in IMMEnSE and Utah samples including one of the top two SNPs from the meta-analysis (rs72773978) and a SNP in high linkage disequilibrium with the top SNP, encoding a non-synonymous amino acid substitution in *FOPNL* (rs12598966). These SNPs were typed using 5' exonuclease (TaqMan) assays (ABI) at the German Cancer Research Center (DKFZ) in Heidelberg (IMMEnSE samples) and at the Genomics Core at the University of Utah (Utah samples). Duplicates of 12% of the samples were interspersed throughout the plates and concordance rate among duplicates was $>99.9\%$.

We performed genome-wide analyses for association with survival using proportional hazards models in the UCSF and Mayo datasets separately. We inferred genetic ancestry using principal components analysis (PCA) in each cohort using SmartPCA³⁷. Each SNP was entered into the model under an assumption of log-additive increased risk, and adjusting for PC's 1–3, age and gender. Imputed SNPs were modeled using the probability of genotypes. We tested the proportional hazards assumption for the top SNPs by calculating the scaled Schoenfeld residuals and testing whether they are significantly associated with time³⁸.

We also performed a subset analysis of Caucasians only in the UCSF dataset. We identified Caucasians based on genetic ancestry (see supplementary figure 2). Individuals who clustered with self-described Caucasians (PC1 >0 , PC2 <0) were included in this subset analysis (N=229).

All analyses were performed in R. For graphing survival results, we used the Kaplan-Meier estimates of the survival function and graphed the results using Stata (Version 10). We graphed the association statistics for all SNPs near the top locus using LocusZoom³⁹.

We used Cox regression models adjusted for age and gender to test the association between SNPs and survival in the IMMEnSE consortium and the Utah cohort.

We performed a meta-analysis of the UCSF and Mayo Clinic results on a total of 6,026,834 SNPs in common from both GWAS that met the allele frequency and imputation quality thresholds. We also conducted a meta-analysis of data on two top SNPs from 7 centers within the IMMEnSE consortium and the Utah study in our replication study. We calculated a fixed effects model for each SNP using METAL⁴⁰. We used Cochran's Q statistic to test for heterogeneity.

To examine the association of SNPs and risk of MM, we compared the genotype frequencies of cases vs. ethnically matched controls from the UCSF (N=298) and the Mayo Clinic (N=295) sites respectively. We used logistic regression models, adjusting for PC1-3 age and gender.

We used the dataset from Grundberg *et al*²² for eQTL analyses, which consists of 856 Caucasian individuals including 154 monozygotic twin pairs, 232 dizygotic twin pairs and 84 singletons. We focused on expression in lymphocytes in this dataset. We used

GENEVAR²¹ to query the top 145 SNPs from the GWAS and identified 6 SNPs, that were also in the Grundberg et al dataset. We queried GENEVAR for beta coefficients and p values for associations between 6 SNPs and the genes within a 1 Mb window including: FOPNL, MYH11, ABCC1, NDE1, KIAA0430, ABCC6, RRN3, NTAN1 KIAA0250, KIAA0251.

We downloaded gene expression data from Zhan *et al*¹³, Broyl *et al*⁴¹, and Chapman *et al*⁴² from the National Institutes of Health Gene Expression Omnibus (accession number: GSE2658, GSE19784, and GSE26760, respectively). Zhan *et al* consisted of gene expression data from 559 MM samples assayed on Affymetrix U133 arrays; Broyl *et al* consisted of gene expression data from purified CD138+ plasma cells of 320 newly diagnosed myeloma patients using Affymetrix GeneChip U133 plus 2.0 arrays; Chapman *et al* consisted of 304 CD138-purified bone marrow samples from patients with multiple myeloma were analyzed on Affymetrix U133 Plus 2.0 microarrays.

Gene expression and MM outcome Of the samples in the Zhan *et al* dataset, 414 also had available clinical data and were included in the original publication¹³, and therefore, we used the data from these 414 samples in our analyses. We used log-transformed probe intensity values as predictors of survival, entering these as continuous variables into a proportional hazards model. We analyzed each of the two probes for *FOPNL* on the Affymetrix U133 array separately and also considered the average of the two probes as a predictor of overall survival in the proportional hazards model.

Analysis of potential SNP function: We used SIFT⁴³ and Polyphen2⁴⁴ to determine the likelihood that a non-synonymous amino acid substitution has a deleterious effect on protein function. We used FunciSNP⁴⁵ to determine whether any of the SNPs may affect gene expression, including any SNPs with $r^2 > 0.7$ with rs72773928. r^2 values for linkage disequilibrium were calculated in European ancestry samples from 1000 genomes.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgements

This work was supported by the Steve and Nancy Grand Multiple Myeloma Translational Initiative and a grant from Expression Analysis and a grant from the National Cancer Institute (R21CA191896). E Ziv is supported in part by a mid-career award in patient research from the National Cancer Institute (K24169004). Collection of blood samples from Polish patients and controls from Łódź area and DNA extraction was supported by a grant from Polish Ministry of Science and Higher Education (No. NN402178334). DNA extraction from Danish healthy controls was supported by The Research Fund at Region Sjælland, Denmark. The Utah study was supported by LLS 6067-09, CA152336 and CA134674, with data collection made possible, in part, by the Utah Population Database (UPDB) and the Utah Cancer Registry (UCR). Partial support for all datasets within the UPDB is provided by the Huntsman Cancer Institute (HCI) and the HCI Cancer Center Support grant, P30 CA42014. The UCR is supported in part by NIH contract HHSN261201000026C from the NCI SEER Program with additional support from the Utah State Department of Health and the University of Utah. In Utah, Jathine Wong is thanked for support in formatting files and advice on R programming. Several authors (EZ, NC, FC, CV) are members of the International Multiple Myeloma Consortium. The authors are grateful to the leadership and other members of the International Multiple Myeloma Consortium for facilitating this collaborative study.

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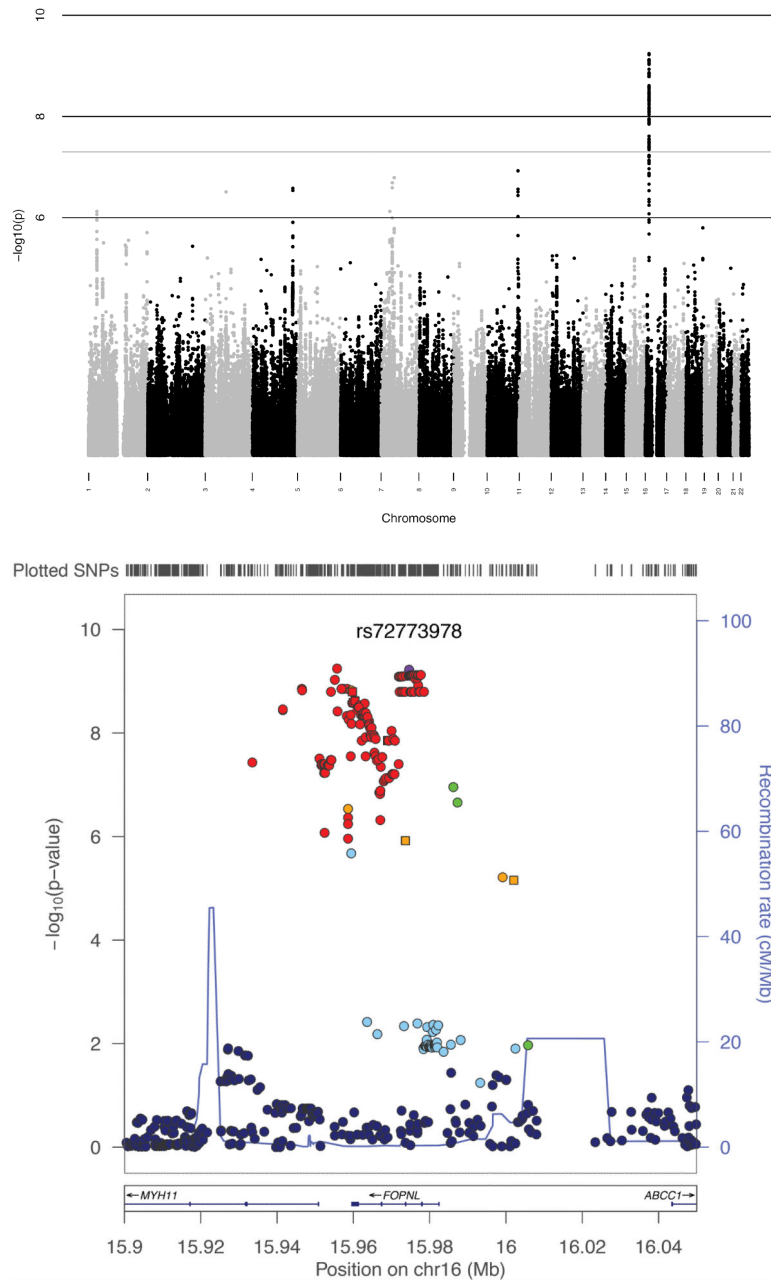
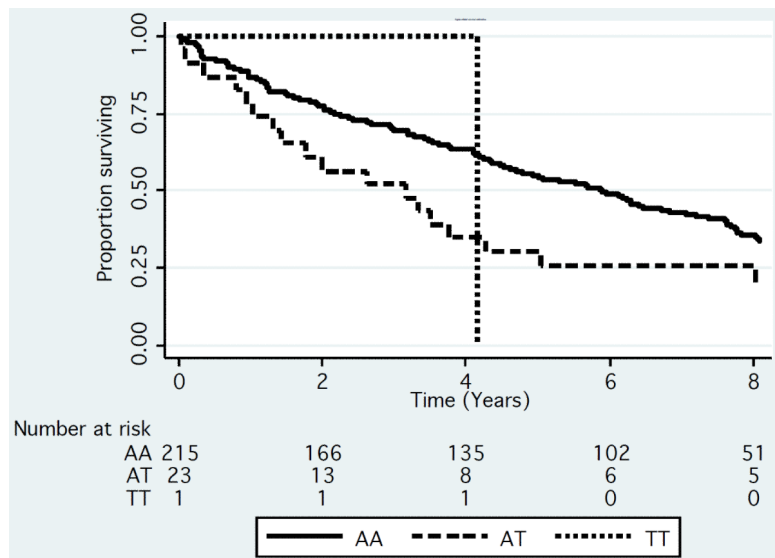
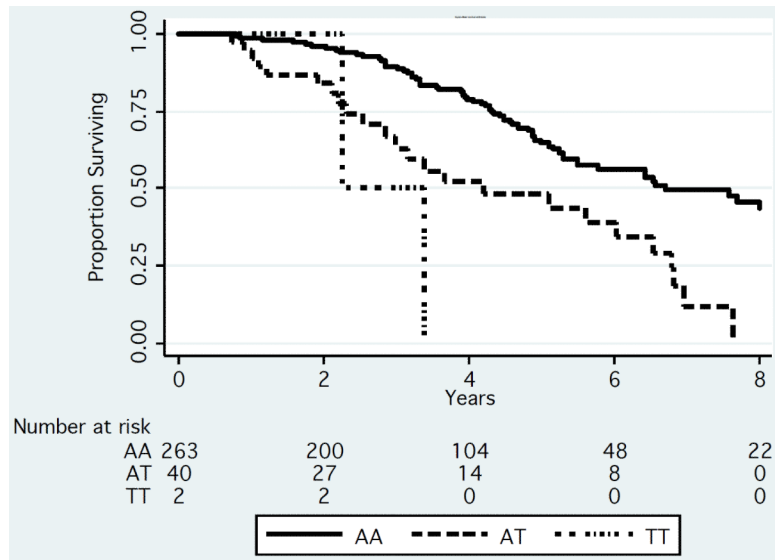


Figure 1. GWAS results for survival among MM patients (a) Manhattan plot of results of genome-wide association analysis for survival in MM patients. Each point represents the negative log p value of the meta-analysis for association with survival using the UCSF and Mayo Clinic data (b) Locuszoom plot for association statistics at the 16p13 region in the meta-analysis of UCSF and Mayo. Each dot represents the negative log p value for the association statistics from the meta-analysis. The top associated SNP (rs72773978) is colored in purple and the remaining SNPs are colored according to linkage disequilibrium values (r^2) with the top SNP.



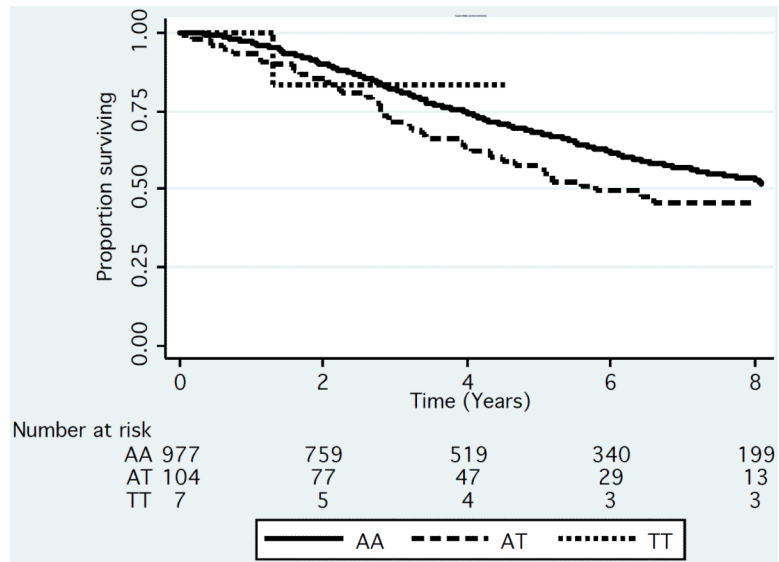


Figure 2. Kaplan-Meier Survivorship plot by genotype for rs72773978 in the UCSF (N=306) (A) Mayo (N=239) (B) and IMMENSE/Utah (N=1080) (C) studies. We plotted the results by genotype. To generate the plots for the discovery datasets, we rounded the imputation results to the nearest whole numbers to infer genotypes of individuals.

Table 1

Clinical characteristics of patients in discovery and replication studies

	UCSF (N=306)	Mayo Clinic (N=239)	IMMENSE Cohorts & University of Utah (N=1090)
Age at diagnosis Mean (SD)	55.9 ± 9.0	62.2 ± 11.4	54.4 ± 10.1
Average follow up time Mean years (SD)	3.8 ± 2.5	5.3 ± 3.5	4.8 ± 3.3
Mortality N (%)	103 (33.7)	174 (72.8)	423 (38.5%)
Type of disease (N with data)	292	239	649
IgG Kappa N (%)	127 (43.5)	86 (36.0)	145 (22.3)
IgG Lambda N (%)	44 (15.1)	49 (20.5)	64 (9.9)
IgG light chain not specified N (%)	11 (3.8)	-	173 (26.7)
IgA Kappa N (%)	31 (10.6)	35 (15.0)	35 (5.4)
IgA Lambda N (%)	21 (7.2)	22 (9.1)	33 (5.1)
IgA light chain not specified N (%)	-	-	75 (11.6)
Light chain only N (%)	51 (17.5)	31 (13.0)	86 (13.3)
Other/non-secretory N (%)	7 (2.4)	16 (6.7)	38 (5.9)
ISS Stage (N with data)	140	221	513
1 N (%)	49 (35.0)	86 (38.9)	162 (31.6)
2 N (%)	55 (39.3)	74 (33.5)	165 (32.2)
3 N (%)	36 (25.7)	61 (27.6)	186 (36.3)
Durie-Salmon Stage (N with data)	256	187	633
IA or IB N (%)	39 (15.2)	14 (7.5)	69 (10.9)
IIA or IIB N (%)	40 (15.6)	30 (16.4)	149 (23.5)
IIIA or IIIB N (%)	177 (69.2)	143 (76.5)	415 (65.6)

Table 2

Association of rs72773978 and MM survival

Age, Sex adjusted*				
Study	Allele frequency	HR	95% CI	P- value***
UCSF (n=306)	0.075	3.03	1.95 – 4.73	8.0×10^{-7}
Mayo (n=239)	0.054	2.31	1.51 – 3.53	1.1×10^{-4}
Discovery Meta-analysis (UCSF & Mayo)		2.65	1.94 – 3.58	6.0×10^{-10}
Replication ** (1,090): IMMENSE n=772, Utah n=315		1.34	1.01 – 1.78	0.044
Discovery & Replication Meta-analysis		1.93	1.54 – 2.41	6.7×10^{-9}

Age, Sex, Stage adjusted *			
ISS adjusted			
UCSF (n=140)	4.06	2.04 – 8.05	6.3×10^{-5}
Mayo (n=221)	2.41	1.51 – 3.83	2.2×10^{-4}
Replication ** (n=513)	1.70	1.19 – 2.44	0.004
Salmon-Durie adjusted			
UCSF (n=256)	2.81	1.73 – 4.57	3.2×10^{-5}
Mayo (n=184)	2.75	1.68 – 4.49	5.3×10^{-5}
Replication ** (n=625)	1.46	1.04 – 2.05	0.029

*The UCSF and Mayo Clinic study results are also adjusted by PCA. The IMMENSE data is not due to the lack of availability of GWAS data.

** The IMMENSE results are from a meta-analysis of the individual regions (see supplementary table 3).

*** P values are calculated from proportional hazards models.

Table 3

Effect of SNP by initial treatment among patients in the UCSF and Mayo Clinic cohorts

	HR*	95% CI	P value***
Mayo Clinic			
Old treatments**		N=136, 102 deaths	
RS72773978	1.90	0.98 – 3.83	0.057
New treatments***		N=93, 64 deaths	
RS72773978	2.71	1.56 – 4.70	0.00045
Entire sample adjusted for treatment		N=229, 166 deaths	
RS72773978	2.18	1.43 – 3.32	0.00028
UCSF			
Old treatments**		N= 109 60 deaths	
RS72773978	3.35	1.74 – 6.44	0.00028
New treatments***		N=187, 30 deaths	
RS72773978	3.57	1.71 – 7.43	0.0007
Entire Sample Adjusted for treatment		N=296, 90 deaths	
RS72773978	3.35	2.07 – 5.41	8.2×10^{-7}

* All models are adjusted for age, gender and principal components 1–10.

** Regimens including vincristine/Adriamycin/Dexamethasone or melphalan/prednisone

*** Treatments containing at least on of the following agents: thalidomide, botezomib or lenalidomide

**** P values are calculated from proportional hazards models.