Am J Cancer Res 2021;11(11):5388-5401
www.ajcr.us /ISSN:2156-6976/ajcr0135816

Original Article

Development of KAM score to predict metastasis and worse survival in breast cancer

Kerry-Ann McDonald[1*], Masanori Oshi[1,2*], Tsutomu Kawaguchi[1,3*], Qianya Qi[4], Xuan Peng[4], Akimitsu Yamada[2], Mateusz Opyrchal[9], Song Liu[4], Song Yao[5], Eigo Otsuji[3], Li Yan[4], Itaru Endo[2], Kazuaki Takabe[1,2,6,7,8]

*[1]Department of Surgical Oncology, Roswell Park Comprehensive Cancer Center, Buffalo, NY 14263, USA; [2]Department of Gastroenterological Surgery, Yokohama City University Graduate School of Medicine, Yokohama, Kanagawa 236-0027, Japan; [3]Department of Surgery, Kyoto Prefectural University of Medicine, Kyoto 602-8566, Japan; [4]Department of Biostatistics & Bioinformatics, Roswell Park Comprehensive Cancer Center, Buffalo, NY 14263, USA; [5]Department of Cancer Prevention and Control, Roswell Park Comprehensive Cancer Center, Buffalo, NY 14263, USA; [6]Department of Surgery, University at Buffalo Jacobs School of Medicine and Biomedical Sciences, The State University of New York, Buffalo, NY 14203, USA; [7]Department of Breast Surgery and Oncology, Tokyo Medical University, Tokyo 160-8402, Japan; [8]Department of Surgery, Niigata University Graduate School of Medical and Dental Sciences, Niigata 950-2181, Japan; [9]Department of Medical Oncology, Roswell Park Comprehensive Cancer Center, Buffalo, NY 14263, USA. *Equal contributors.*

Received May 29, 2021; Accepted September 9, 2021; Epub November 15, 2021; Published November 30, 2021

Abstract: Some may think that prediction of metastasis is meaningless since metastatic breast cancer is currently incurable. We argue that effective identification of developing metastasis will enable us to design and conduct clinical trials specifically targeting those patients at high risk. The current study sought to generate the KAM score by 4 genes (*BRSK2, EYA1, SIGLEC15,* and *AGTR1*) overexpressed in primary breast cancer that developed metastasis to bone compared with matched controls without metastasis longer than 10 years. A high KAM score was prognostic of poor overall (OS), disease free survival (DFS), and disease specific survival (DSS) in the METABRIC, and OS in the GSE96058 cohorts. A high KAM score was significantly associated with clinical aggressiveness, such as high American Joint Committee Cancer (AJCC) stage, lymph node metastasis, Nottingham pathological grade, and triple negative breast cancer (TNBC). Subgroup analysis revealed that a high KAM score was associated with worse OS in ER-positive/HER2-negative breast cancer in both cohorts. A high KAM breast cancer enriched all 5 cell proliferation-related gene sets of the Hallmark collection and interferon (IFN)-γ response gene sets. Furthermore, a high KAM breast cancer was significantly infiltrated with a high fraction of not only anti-cancer but also pro-cancer immune cells and associated with high level of cytolytic activity. Finally, a high KAM breast cancer was significantly associated with lung metastasis. In conclusion, we developed KAM score using 4 gene expressions that predict lung metastasis and patient survival in breast cancer.

Keywords: Breast cancer, gene sets, KAM score, metastasis, survival, tumor microenvironment

Introduction

Breast cancer is often diagnosed early before there is any evidence of distant spread. Nevertheless, 20-30% of women with early breast cancer will eventually develop distant metastasis [1-3]. Approximately 70% of all patients with metastatic breast cancer have bony involvement [1-3], which is the most frequent site where local and systemic treatment options are often palliative. However, with the advent of newer systemic therapies, patients with metastatic breast cancer are seeing more meaningful improvements in survival, with median overall survival (OS) approaching 2 years [4].

Currently, a patient's risk of metastasis is often estimated by various clinical and pathologic variables. Clinical staging utilizing tumor size, grade, nodal status, and molecular phenotypes have been developed to evaluate the risk of distant spread and prognosis. Specifically, patients with larger tumors, positive lymph nodes, intermediate to high grade disease, and either human epidermal growth factor receptor

2 (HER2) overexpression or triple negative breast cancers (TNBC) have worse survival and higher chance of metastatic spread [3, 5, 6].

There are prognostic markers for patients with metastatic breast cancer that can provide information on outcomes. For example, the presence of circulating tumor cells (CTCs) >5 CTCs/7.5 ml in whole blood has been associated with a poorer prognosis in metastatic patients compared to patients with undetectable or <5 CTCs/7.5 ml in the blood independent of therapy [7]. Tumor markers, including CA15-3 and CA27.29, are well characterized assays that detect circulating Mucin-1 (MUC-1) antigen in peripheral blood and are used to assess response to therapy [8].

With the advent of gene profiling technologies there has been a shift towards a genomic approach to prognostication [9]. Understanding the genomic drivers of cancer progression and metastasis is an area of active research [10, 11]. The current study sought to generate the KAM score by genes overexpressed in primary breast cancer that developed metastasis to bone, which correlates with survival. Those genes that were identified were used as the basis of the KAM score. Using two large publicly available datasets, the Molecular Taxonomy of Breast Cancer International Consortium (METABRIC) and GSE96058 dataset, we found that a high KAM score was associated with worse survival in breast cancer, particularly, estrogen receptor (ER)-positive breast cancers.

Materials and methods

Patients

The derivation cohort consists of twenty patients; ten patients who developed bone metastasis (bone metastasis group), and age, stage, and subtype matched patients without metastasis for more than five years (control group); all selected from 2007-2014 at Roswell Park Comprehensive Cancer Center (Buffalo, NY). Fresh frozen primary tumor samples from these cohorts were used for the analyses (Table S1). This study was approved by the Institutional Review Board of Roswell Park Comprehensive Cancer Center, and each subject provided signed informed consent.

One thousand nine hundred three and 3,273 breast cancer patients were included in the METABRIC [12] and GSE96058 [13] cohorts, respectively. METABRIC cohort has clinical patient data about age at diagnosis, AJCC stage, tumor size, lymph node metastasis status, Nottingham pathological grade, and patient prognosis; overall survival (OS), disease-free survival (DFS), and disease-specific survival (DSS). GSE96058 cohort has clinical patient data about age at diagnosis, AJCC-T, -N, Nottingham pathological grade, and OS. To investigate the association of the KAM score with metastasis, we obtained GSE2034 [14] and GSE2603 [15] dataset, which have metastatic site-specific disease-free outcome, though the Gene Expression Omnibus (GEO) repository of the US National Institutes of Health (http://www.ncbi.nlm.ih.gov/geo/), as we previously reported [16-18]. Patients were divided into two groups, low and high KAM scores, using median cut-off within each cohort.

Study design

The 20 primary tumor samples in the derivation cohort represent a unique sample set, such that each control was well matched to the corresponding bone metastasis sample (Table S1). Majority of the tumor samples were ER/PR receptor positive and HER2 negative. We then performed RNA sequencing (RNA-Seq) on all 20 samples using the TruSeq Stranded Total RNA kit (Illumina Inc.) and gene expression data was generated as previously described in our publications [19-24]. Up-regulated genes and Down-regulated genes in bone metastasis group compared to control are shown as Tables S2 and S3, respectively.

This led to the identification of six genes in the bone metastasis group: three genes which were significantly upregulated and three genes which were significantly downregulated. Of these genes, the four genes (*BRSK2, EYA1, SIGLEC15,* and *AGTR1*) with the highest absolute values of $\log_2$FoldChange were used to generate the KAM score. Using a bioinformatics approach, the KAM score was developed using the expression value of those four genes. The METABRIC and GSE96058 dataset was used to evaluate the clinical and prognostic significance of the KAM score. We then sought to analyze which gene sets were enriched in patients with high and low KAM scores using Gene Set Enrichment Analysis (GSEA) [25, 26], which defines the biologic significance of the KAM score (**Figure 1**), as we previously reported [27-31].

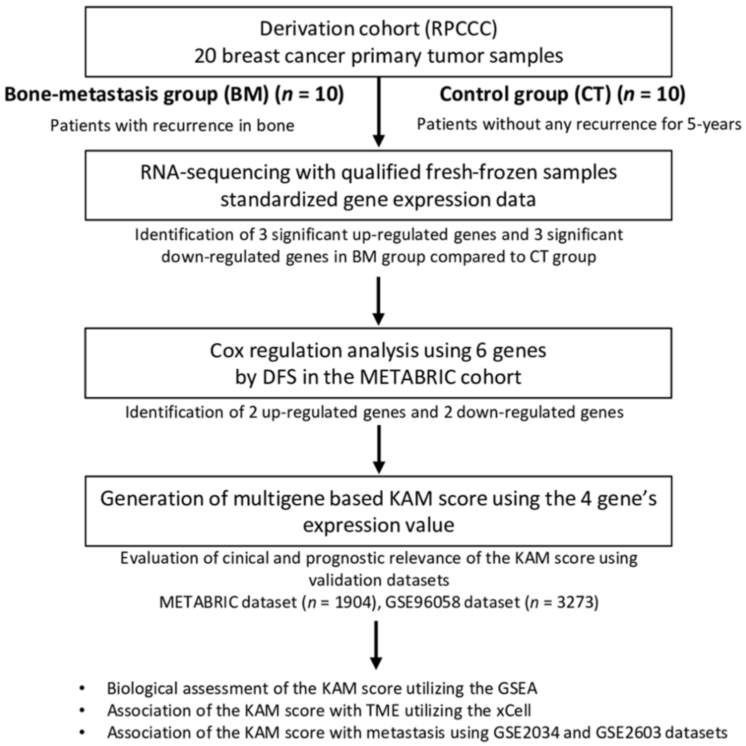

Figure 1. Investigational design. Schematic shown to depict the process by which the KAM score was generated.

Gene expression analysis with RNA-Seq

Following the standard RNA-Seq analysis pipeline [39], we conducted statistical tests to compare the quantitative differences in each gene's expression levels between the bone metastasis and control groups. The Benjamini-Hochberg (BH) method was used for multiple test adjustments of the test *P*-values. Genes that had adjusted *P*-values less than 0.05 and had at least two-fold change was selected as the top three up-regulated genes and top three down-regulated genes, corresponding to a 4 time increase or decrease of gene expression among the two groups, respectively.

Development of the multigene based KAM score

The top three upregulated and top three down-regulated genes were selected as the basis of the KAM score. KAM is defined as low and high based on the expression value of those genes, as a weighed sum of the standardized gene expression levels. The weights were the hazard ratio by fitting a univariate Cox proportional model for each gene [9]. KAM score which is defined as:

$$KAM - BM = \sum_{i=1}^{6} HR_i * SGE_i$$

Where KAM = (HR1*BRSK2) + (HR2*EYA1) + ..., SGE_i is standardized gene expression using z-score transformation for gene i, and HR_i is the hazard ratio by fitting a univariate Cox proportional hazards model for gene i.

Fraction of immune infiltration

Comparison of low and high KAM score with immune infiltration in the tumor microenvironment was reported using the xCell algorithm, which calculates the fraction of 65 cell types of immune and stromal cells, as we previously reported [32-36].

Statistical analysis

All statistical analyses were performed using R software (https://www.r-project.org/) and Bioconductor (https://www.bioconductor.org/). The Kaplan-Meier method with logrank tests and Cox proportional hazards models were used to compare KAM low and high groups. Hazard ratios (HR) and 95% confidence intervals (CI) were provided when fitting the multivariate Cox models of KAM scores and other clinic-pathological features. Patients were divided into two groups, low and high KAM scores, using median cut-off within each cohort. In all analyses, a two-sided $P<0.05$ was considered statistically significant.

Results

Establishment of a KAM score as a prognostic marker for breast cancer

The KAM score was generated by the strategy demonstrated in **Figure 1**. In the derivation cohort, we found the top three up-regulated genes and top three down-regulated genes in the primary breast cancer with bone metastasis group compared to the control primary breast cancer without metastasis group (ad-

Table 1. Bone-metastasis related genes. Identification of three significantly up-regulated genes and three significantly down-regulated genes in bone metastasis group compared to control group

Gene	Function	baseMean	$\log_2$FoldChange	*P*-value	Adjusted *P*-value
BRSK2	Enhance Akt activity	89.82717234	2.816787516	8.21184E-08	0.001858093
EYA1	Transcriptional factor	59.05437494	2.509600832	7.63539E-07	0.008234741
CHST9	Cell-cell interaction	200.1213678	2.3607326	6.81379E-06	0.025695952
CHST9	Cell-cell interaction	200.1213678	2.3607326	6.81379E-06	0.025695952
SIGLEC15	Modulate RANKL signaling pathway	269.7393653	-2.461130924	1.0918E-06	0.008234741
RP11	Pre-mRNA splicing-factor gene	37.82871493	-1.277626147	1.07966E-06	0.010163194
AGTR1	Promote cell apoptosis	1784.142356	-2.438374538	3.70454E-06	0.016764516

Selection criteria, adjusted *P*-value <0.05.

justed $P<0.05$) (**Table 1**). The upregulated genes were BR serine/threonine kinase 2 (*BRSK2*), Drosophila Eyes Absent Homologue 1 (*EYA1*), and Carbohydrate N-acetylgalactosamine 4-0 sulfotransferase 9 (*CHST9*). The downregulated genes included Sialic Acid Binding Ig Like Lectin 15 (*SIGLEC15*), Retinitis pigmentosa 11 (*RP11*), and Angiotensin II receptor type 1 (*AGTR1*). In order to generate a score with high clinical relevance, we analyzed the association of expression of each gene and the likelihood of metastasis using disease-free survival (DFS) in the METABRIC cohort. Of these genes, high expression of the two up-regulated genes; *BRSK2* (HR=1.11, adjusted *P*-value <0.001) and *EYA1* (HR=1.02, adjusted *P*-value <0.001), were significantly associated with worse DFS, and high expression of the two down-regulated genes; *SIGLEC15* (HR=0.69, adjusted *P*-value <0.001) and *AGTR1* (HR=0.86, adjusted *P*-value <0.001), were associated with better DFS. From these results, the four genes (*BRSK2, EYA1, SIGLEC15,* and *AGTR1*) with the highest absolute values of $\log_2$FoldChange were used to generate the KAM score.

A high KAM score was significantly associated with worse survival and tumor aggressiveness in breast cancer

To validate the prognostic value of the KAM score, we compared low and high KAM score by Kaplan-Meier analyses of disease-free survival (DFS), disease-specific survival (DSS), and overall survival (OS) in the METABRIC cohort, as well as OS in the GSE96058 cohort. We found that the KAM score has been shown to be associated with survival; with higher scores associated with worse survival in all the tested cohorts (**Figure 2**; DFS: Hazard Ratio (HR) =1.50, 95% Confidence Interval (CI); 1.27-1.77, DSS: HR=1.50, 95% CI; 1.28-1.75, OS: HR=1.27, 95% CI; 1.12-1.42 in the METABRIC, and OS: HR=1.46, 95% CI; 1.22-1.76, in the GSE96058, all $P<0.001$). Thus, we expect that the KAM score will associate with clinical cancer aggressiveness. To test our expectation, we investigated the association of the KAM score with clinical parameters, including American Joint Committee on Cancer (AJCC) stage, node metastasis status, Nottingham pathological grade, and breast cancer subtype. We found that high KAM score was significantly associated with high AJCC stage ($P<0.001$) in the METABRIC and node metastasis positive, high grade, and TNBC, consistently in both cohorts (**Figure 2**). These results suggest that the KAM score reflected clinical tumor aggressiveness.

High KAM score is associated with worse survival in ER-positive/HER2-negative breast cancer

Since different breast cancer subtypes are known to have different prognosis, we next investigated the association of the KAM score with prognosis within each subgroup. A high KAM score was significantly associated with worse DFS, DSS, and OS for ER-positive/HER2-negative breast cancer in the METABRIC cohort (**Figure 3**; DFS: HR=1.41, 95% CI; 1.15-1.73, DSS: HR=1.47, 95% CI; 1.20-1.80, OS: HR=1.27, 95% CI; 1.11-1.47, all $P<0.001$) and OS in the GSE96058 cohorts (**Figure 3**; HR=1.40, 95% CI; 1.12-1.75, $P=0.003$). On the other hand, no statistical significance was found between low or high KAM score in TNBC in neither of the cohorts (DFS: HR=1.01, 95% CI; 0.68-1.50, HR=1.05, 95% CI; 0.73-1.52, OS: HR=1.21, 95% CI; 0.89-1.65, in the

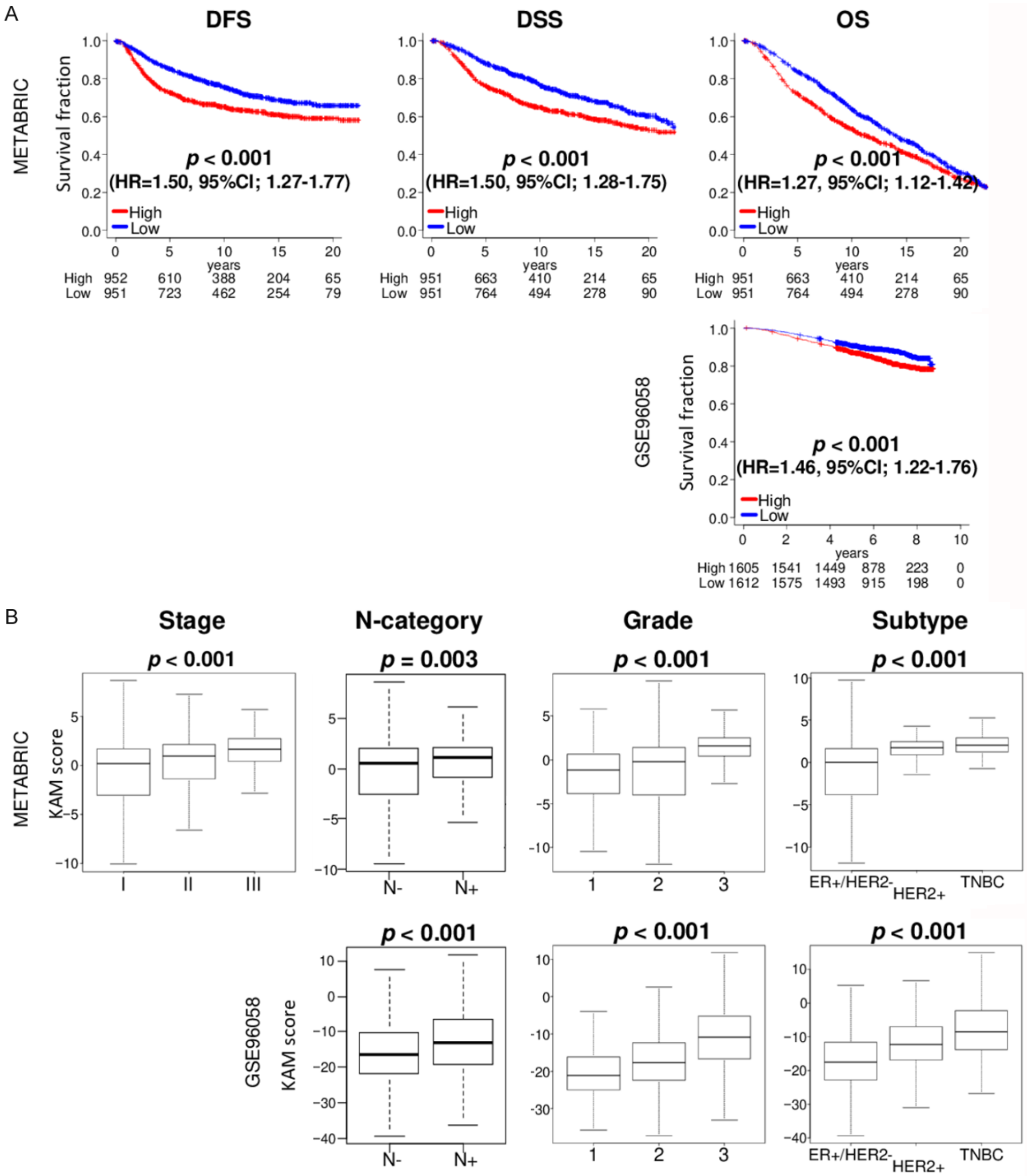

Figure 2. Association of the KAM score with patient survival and clinicopathological aggressiveness in the METABRIC and GSE96058 cohorts. A. Kaplan-Meier survival curve of disease-free survival (DFS), disease-specific survival (DSS), and overall survival (OS) between low (blue line) and high (red line) KAM score in breast cancer. *P*-values were calculated by log rank test. B. Boxplots of low and high KAM score by American Joint Committee Cancer stage in the METABRIC cohort, node metastasis status (N-category), Nottingham histological grade, and breast cancer subtypes in both cohorts. Median cut-off within each cohort was used to dive low and high KAM score group. *P*-values were calculated by Mann-Whitney U test.

METABRIC, and OS: HR=1.00, 95% CI; 0.97-1.04 in the GSE96058). This data demonstrates that the KAM score is associated with worse survival in ER-positive/HER2-negative breast cancers.

KAM score serves as an independent prognostic marker of survival in breast cancer

To investigate if the prognostic value of the KAM score is independent of various other

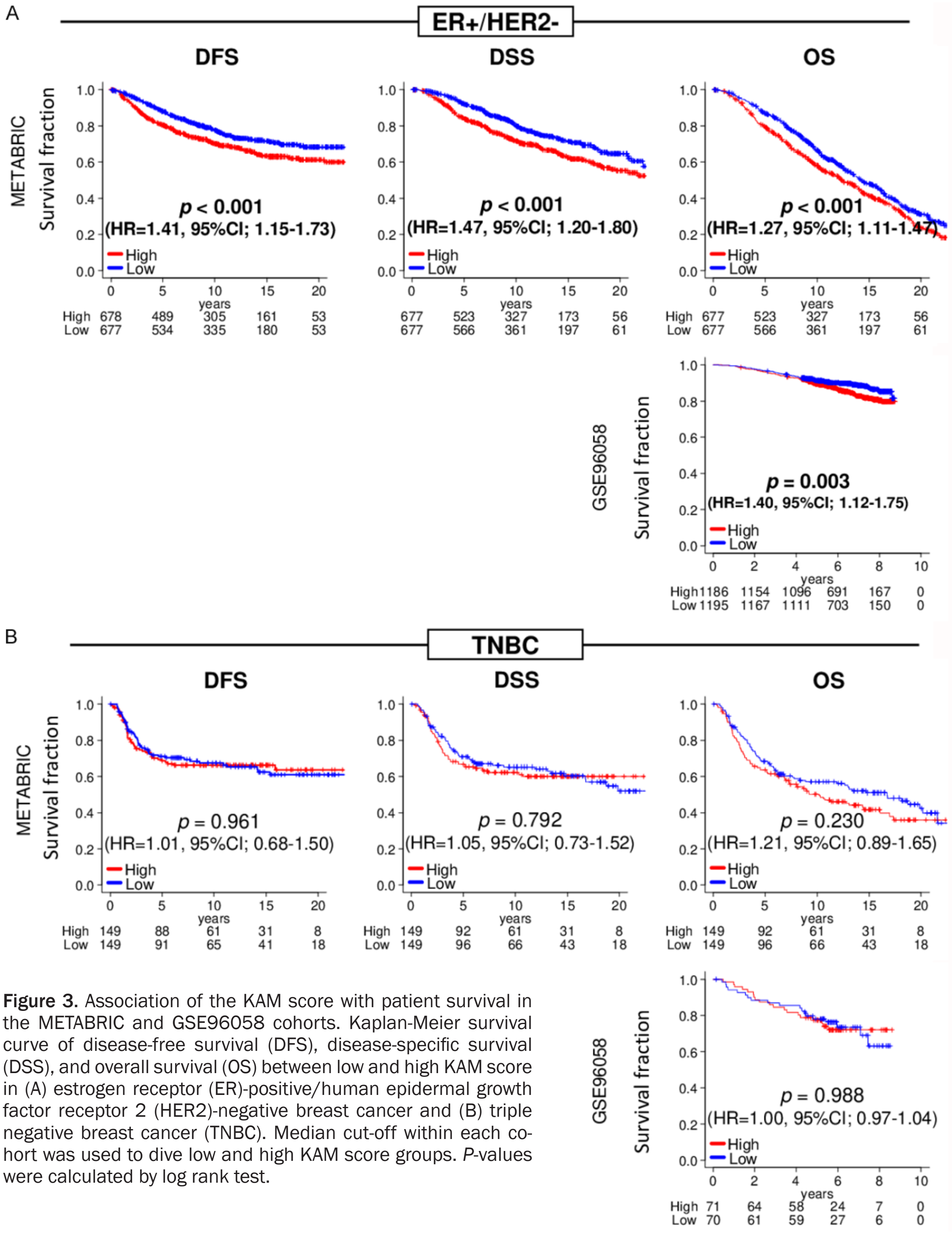

Figure 3. Association of the KAM score with patient survival in the METABRIC and GSE96058 cohorts. Kaplan-Meier survival curve of disease-free survival (DFS), disease-specific survival (DSS), and overall survival (OS) between low and high KAM score in (A) estrogen receptor (ER)-positive/human epidermal growth factor receptor 2 (HER2)-negative breast cancer and (B) triple negative breast cancer (TNBC). Median cut-off within each cohort was used to dive low and high KAM score groups. *P*-values were calculated by log rank test.

clinical and pathological factors, we performed multivariate Cox regression analyses using factors which showed significance in univariate Cox regression analyses in the METABRIC (factors; age at diagnosis (>65 y.o. vs. 65 y.o. >), tumor size (>20 mm vs. 20 mm >), node metastasis (positive vs. negative), Nottingham pathological grade (grade 3 vs. grade 1/2), subtypes (TNBC vs. others), and KAM score) and GSE96058 cohorts. We used OS, DFS,

Table 2. KAM score serves as an independent prognostic marker of bone metastasis in breast cancer. Multivariate cox proportional hazards model of KAM score and other clinic-pathological features

METABRIC		Univariate				Multivariate			
OS		HR	95% CI	*p*		HR	95% CI	*p*	
Age	>65 vs. 65>	2.12	1.88-2.39	<0.001	*	2.12	1.87-2.41	<0.001	*
Tumor size	>20 vs. 20>	1.75	1.55-1.99	<0.001	*	1.47	1.29-1.67	<0.001	*
node metastasis	Positive vs. Negative	1.67	1.48-1.88	<0.001	*	1.55	1.37-1.76	<0.001	*
pathological grade	G3 vs. G1/2	1.33	1.17-1.49	<0.001	*	1.20	1.05-1.36	0.007	*
subtype	TNBC vs. Others	1.04	0.88-1.23	0.636					
score		1.03	1.01-1.04	0.001	*	1.02	1.00-1.03	0.038	*
METABRIC		Univariate				Multivariate			
DFS		HR	95% CI	*P*		HR	95% CI	*P*	
Age	>65 vs. 65>	1.05	0.88-1.24	0.603					
Tumor size	>20 vs. 20>	1.76	1.48-2.09	<0.001	*	1.48	1.24-1.77	<0.001	*
node metastasis	Positive vs. Negative	2.14	1.81-2.54	<0.001	*	1.87	1.57-2.23	<0.001	*
pathological grade	G3 vs. G1/2	1.62	1.37-1.92	<0.001	*	1.31	1.10-1.57	0.003	*
subtype	TNBC vs. Others	1.22	0.98-1.52	0.068					
score		1.06	1.03-1.08	<0.001	*	1.04	1.01-1.06	0.002	*
METABRIC		Univariate				Multivariate			
DSS		HR	95% CI	*P*		HR	95% CI	*P*	
Age	>65 vs. 65>	1.13	0.96-1.33	0.131					
Tumor size	>20 vs. 20>	1.92	1.62-2.27	<0.001	*	1.60	1.34-1.90	<0.001	*
node metastasis	Positive vs. Negative	2.27	1.93-2.67	<0.001	*	1.92	1.62-2.27	<0.001	*
pathological grade	G3 vs. G1/2	1.80	1.53-2.12	<0.001	*	1.43	1.20-1.71	<0.001	*
subtype	TNBC vs. Others	1.37	1.12-1.68	0.002	*	1.01	0.81-1.26	0.915	
score		1.03	1.01-1.04	0.001	*	1.03	1.01-1.06	0.004	*
GSE96058		Univariate				Multivariate			
OS		HR	95% CI	*P*		HR	95% CI	P	
Age	>65 vs. 65>	3.77	3.07-4.65	<0.001	*	3.93	3.14-4.91	<0.001	*
Tumor size	T3/4 vs. T0/1/2	3.17	2.20-4.56	<0.001	*	2.00	1.30-3.08	0.002	*
node metastasis	Positive vs. Negative	1.87	1.51-2.33	<0.001	*	1.67	1.31-2.13	<0.001	*
pathological grade	G3 vs. G1/2	1.75	1.46-2.10	<0.001	*	1.45	1.17-1.81	<0.001	*
subtype	TNBC vs. Others	2.36	1.69-3.30	<0.001	*	1.87	1.32-2.65	<0.001	*
score		1.02	1.01-1.03	<0.001	*	1.01	1.00-1.02	0.016	*

*CI, confidence interval; HR, hazard ratio; OS, overall survival; DFS, disease-free survival; DSS, disease-specific survival.

and DSS with clinical factors in the METABRIC cohort, and OS with clinical factors (age at diagnosis (>65 y.o. vs. 65 y.o. >), AJCC T-category (T3/4 vs. T0/1/2), node metastasis (positive vs. negative), Nottingham pathological grade (grade 3 vs. grade 1/2), subtypes (TNBC vs. others), and KAM score) in the GSE96058 cohorts. We found that the KAM score was an independent prognostic factor compared to several clinical factors in any of the cohorts (**Table 2**). These results suggest that patients with a high KAM score are at higher risk of death independent of all other clinical and pathological variables.

Breast cancers with high KAM score significantly enriched cell proliferation-related and interferon (IFN)-γ response gene sets in breast cancer

To investigate the biological functions that relate the KAM score to be associated with poor prognosis, we compared low and high KAM score utilizing Gene Set Enrichment Analysis (GSEA) with MSigDB Hallmark gene sets correction in the METABRIC and GSE96058 cohorts. We found that breast cancers with high KAM score were associated with significant enrichment of all the cell proliferation-related gene sets in Hallmark collection; E2F targets, G2M checkpoint, Mitotic spindle, MYC targets v1 and v2, and also other pro-cancer gene sets; Mtorc1 signaling, unfolded protein response, and DNA repair, consistently in both cohorts (**Figure 4**). Furthermore, they also enriched IFN-γ response in breast cancer. These results suggest that high KAM score was significantly associated with cell proliferation and immune activity in breast cancer.

Breast cancers with high KAM score were significantly infiltrated with multiple immune cells and associated with high level of cytolytic activity

Given that breast cancers with high KAM score enriched IFN-γ response gene set as shown in **Figure 4**, it was of interest to investigate the association of the KAM score with the fraction of immune cells in the tumor microenvironment (TME). We used xCell algorithm, which allowed us to estimate the fraction of several immune cell types in the TME. We found that high KAM score was significantly associated with a high infiltrating fraction of not only anti-cancer immune cells, including $CD8^+$ T cells, $CD4^+$ memory T cells, T helper type 1 (Th1) cells, and M1 macrophages (**Figure 5A**), but also pro-cancer immune cells, including regulatory T cells, T helper type 2 (Th2) cells, and M2 macrophages, consistently in both METABRIC and GSE96058 cohorts (**Figure 5B**). Furthermore, they were significantly associated with high level of cytolytic activity score (CYT) in both cohorts (**Figure 5C**). These results suggest that breast cancers with high KAM score are significantly associated with high immune cell infiltration and cytolytic activity.

High KAM score was significantly associated with lung metastasis in breast cancer

Since the KAM score was established based on the gene expression differences between primary breast cancer that developed bone metastasis and those that did not, and because it is a prognostic biomarker of breast cancer where distant metastasis is the major cause of death, we hypothesized that the KAM score is predictive of the development of distant metastasis. We used gene expression data of primary breast cancer with associated clinical data on metastases of two independent cohorts; GSE2034 [14] and GSE2603 [15], and analyzed the association of the KAM score of the primary tumor with the time it took to develop metastasis in breast cancer. We found that although the KAM score was not associated with bone metastasis, it was significantly associated with lung metastasis consistently in both cohorts (**Figure 6**; P= 0.046 and 0.004, respectively).

Discussion

The current study sought to generate the KAM score by genes overexpressed and downregulated in primary breast cancer that developed metastasis to bone, which correlates with survival. mRNA-sequencing was performed on 20 fresh frozen primary tumor samples, including ten patients that developed bone metastasis and ten matched controls that did not. Two publicly available datasets, METABRIC and GSE96058, were used to validate the prognostic relevance of the KAM score. A high KAM score was prognostic of poor OS, DFS, and DSS in the METABRIC, and OS in the GSE96058 cohorts. A high KAM score was significantly associated with clinical aggressiveness, such as high AJCC stage, node metastasis, Nottingham grade, and TNBC subtype. Subgroup analysis revealed that a high KAM score was associated with worse OS in ER-positive/HER2-negative breast cancer in both cohorts. A high KAM breast cancer is enriched with cell proliferation-related gene sets and IFN-γ response gene sets. Furthermore, a high KAM breast cancer is infiltrated with a high fraction of not only anti-cancer but also pro-cancer immune cells and associated with high level of cytolytic activity. Finally, a high KAM score is significantly associated with lung metastasis in breast cancer.

The KAM score was established by four genes. These genes have been shown to correlate with aggressive behavior including invasion and metastasis. *BRSK2* is responsible for enhancing Akt activity, which plays a role in cell growth and tumor proliferation [37-39]. *EYA1* serves as an *H2AX* phosphatase that is essential to driving breast cancer cell proliferation [40]. *SIGLEC15* modulates the *RANKL* signaling pathway, which is a critical factor involved in the regulation of bone resorption and metastasis [41]. While AGTR1 promotes cell apoptosis [42].

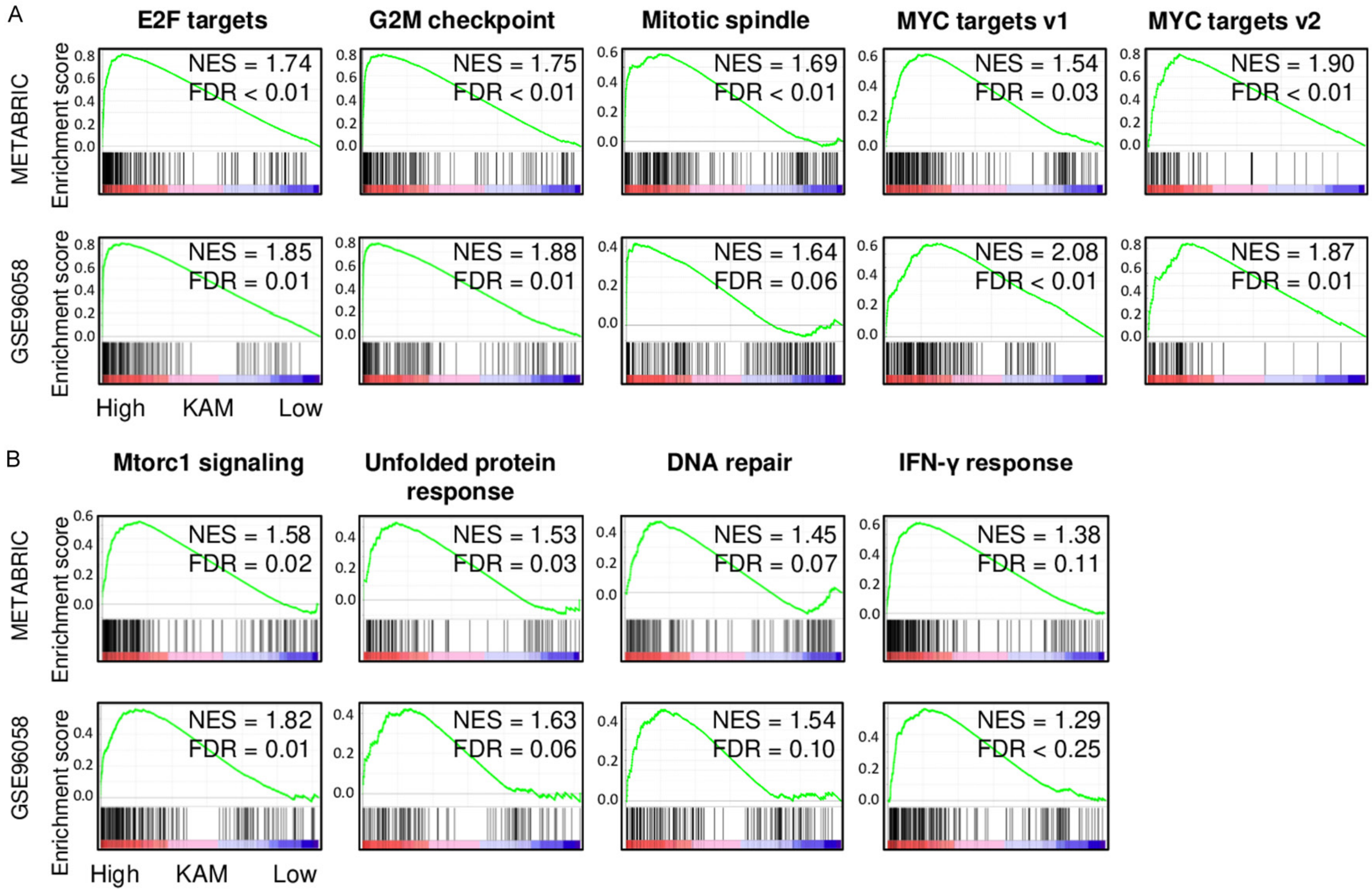

Figure 4. High KAM score significantly enriched pro-cancer-related gene sets. The gene set enrichment analysis (GSEA) with Hallmark collection gene sets were conducted to anlyze which pathway is significantly enriched to high KAM score breast cancer consistently in both GSE96058 and METABRIC cohorts. (A) Cell proliferation-related gene sets; E2F targets, G2M checkpoint, Mitotic spindle, MYC targets v1 and v2, and (B) other pro-cancer-related gene sets; Mtorc1 signaling, Unfolded protein response, DNA repair, and interferon (IFN)-γ response Median KAM score of each cohort was used as cut-offs to dived low and high KAM score groups. Molecular Signatures Database (MSigDB) package were used. Statistical significance was determined to a false discovery rate (FDR) of 0.25, as recommended by the GSEA software. NES, normalized enrichment score.

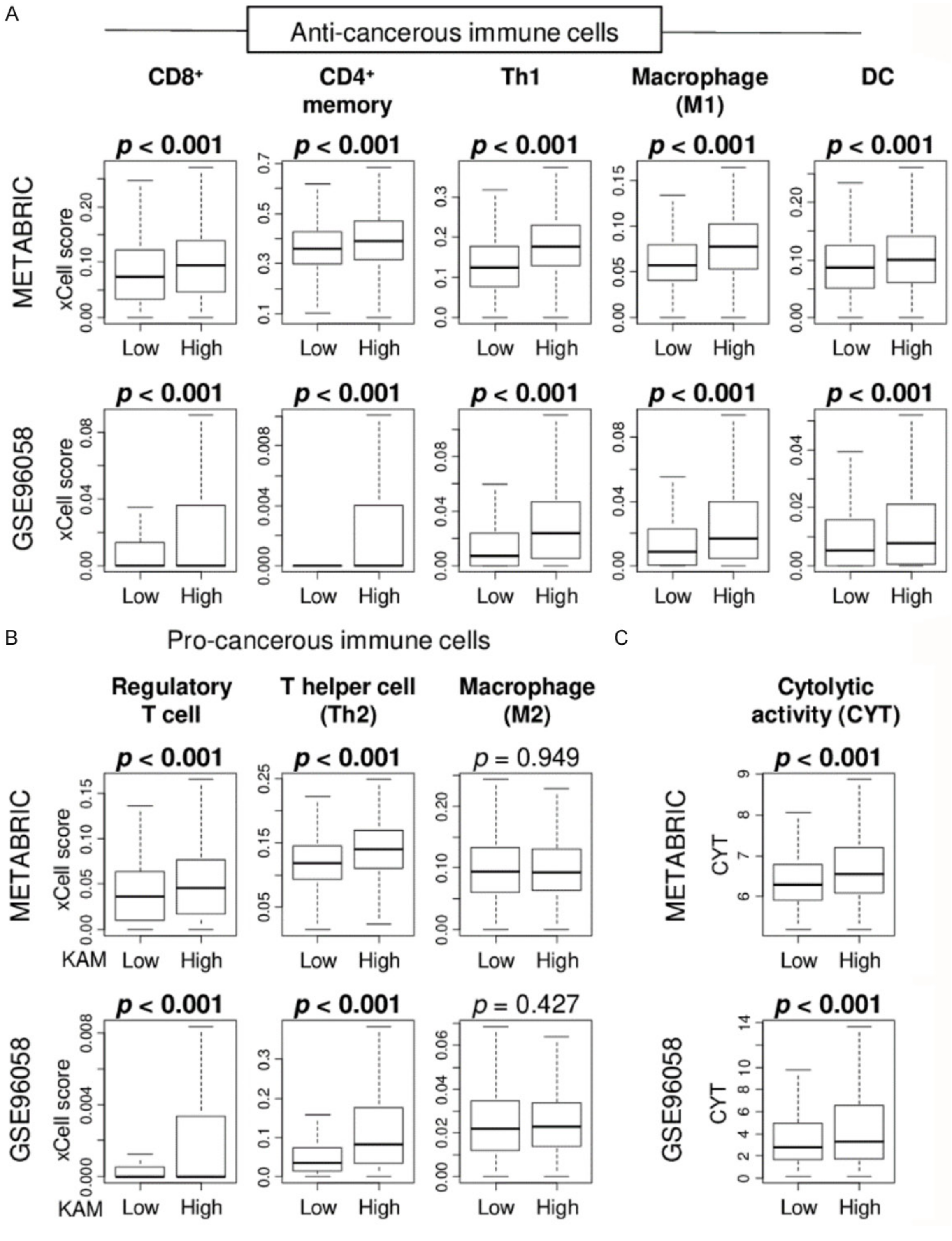

Figure 5. The association of the KAM score with tumor immune microenvironment in the METABRIC and GSE96058 cohorts. Boxplots of the fraction of (A) anti-cancer immune cells; CD8$^+$ T cells, CD4$^+$ memory T cells, T helper type 1 (Th1) cells, M1 macrophages, and dendritic cells (DC), (B) pro-cancer immune cells; regulatory T cells, T helper type 2 (Th2) cells, and M2 macrophages, and (C) levels of cytolytic activity (CYT) score by low and high KAM score in breast cancer. Median KAM value within each cohort was used as cut-offs to dive low and high KAM score groups. Fraction levels of each immune cells were calculated by xCell algorithm. CYT was calculated using gene expression of granzyme A (*GZMA*) and perforin (*PRF1*) in each cohort. *P*-values were calculated by Mann-Whitney U test.

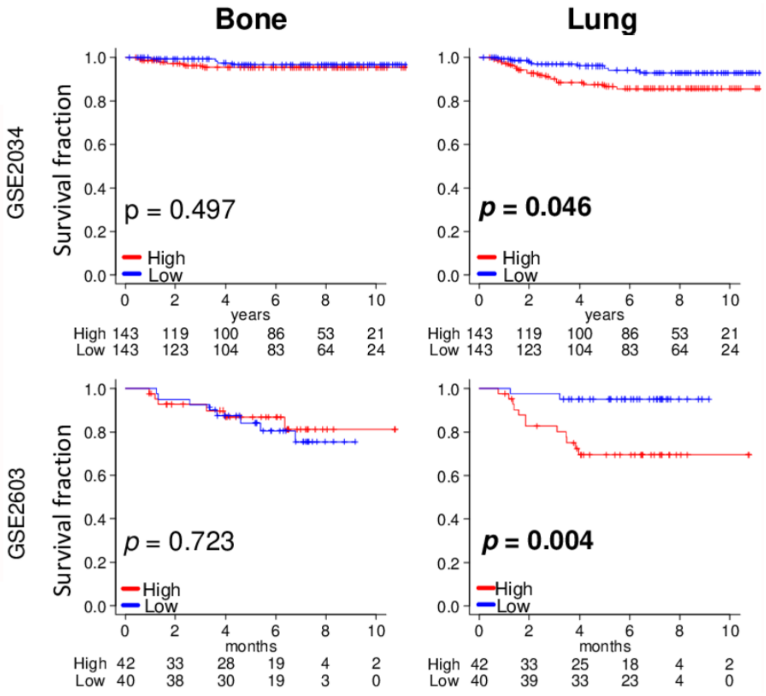

Figure 6. Association between the KAM score and metastasis in breast cancer. The Kaplan-Meier survival curve depict bone or lung metastasis-free survival based on KAM score (High: red line vs. Low: blue line) of the primary tumor in the GSE2034 and GSE2603 cohorts. Median cut-off within each cohort was used to dive low and high KAM score groups. *P*-value was calculated by logrank test.

The evidence provided in this study demonstrates that the KAM score is an independent marker of survival in breast cancer, particularly ER-positive/HER2-negative subtypes. It is known that bone metastasis is more frequent in ER positive than ER-negative breast cancers [43-45]. Interestingly, the KAM score was not significantly associated with TNBC. Possible explanations are that TNBC have lower rates of bone only metastasis [45], and a majority of the patients in the derivation cohort were ER-positive which may have created a bias toward that particular group.

In regard to the biological significance of the KAM score, we found that high KAM was associated with the upregulation of several cell proliferation-related gene sets. The fact that KAM was associated with enrichment of cell proliferation but did not associate with triple negative subtype, suggests that the KAM score may be able to identify aggressive cancers in non-TNBC subtypes. High KAM is also associated with genes that promote tumor growth, such MTORC1 signaling, unfolded protein response, and DNA repair pathways. Based on this association, high KAM is associated with tumor promoting gene sets. After further validation by a prospective study, we anticipate that the KAM score will be used by oncologists as a prognostic marker associated with clinical outcome. We are aware that some may think that prediction of metastasis is meaningless since metastatic breast cancer is incurable. We argue that if we can effectively identify patients who have a high likelihood of developing metastasis and poor survival with the KAM score, we should be able to conduct a clinical trial specifically targeting those patients at high risk. Further, the KAM score should help identify patients who should be treated with adjuvant therapy that would otherwise be missed.

Although this study demonstrates novelty, it does have limitations. This was a pilot study to identify generalizable genes that form the basis of a computational score that is associated with survival in patients with breast cancer. The analytical endpoints such as DFS and OS in the METABARIC and GSE96058 cohorts are general prognostic endpoints and not specific to bone or any other type of metastasis. Since bone is the most common metastatic site in breast cancer, those patients were selected to form the derivation cohort and basis of the KAM score. Further, since Recurrence score of Oncotype DX or any other prognostic indexes were not available in the cohorts analyzed, it was not possible to analyze their relationship with KAM score. We expect that the true clinical relevance of KAM score will be further clarified once its correlation and comparison with other prognostic indexes are performed in a future prospective study. This study was also performed on banked frozen tissue and omitted patients who had poor quality RNA or no banked tissue, thus potential sources of selection bias may exist.

In conclusion, we developed the KAM score using genes overexpressed in primary breast cancer that developed metastasis to bone, and demonstrated that KAM correlates with survival and lung metastasis.

Acknowledgements

This work was supported by US National Institutes of Health/National Cancer Institute grant R01CA160688, R01CA250412, R37CA-248018, US Department of Defense BCRP grant W81XWH-19-1-0674, as well as the Edward K. Duch Foundation and Paul & Helen Ellis Charitable Trust to K.T., and US National Cancer Institute cancer center support grant P30-CA016056 to Roswell Park Comprehensive Cancer Center.

Disclosure of conflict of interest

None.

Address correspondence to: Dr. Kazuaki Takabe, Breast Oncology and Surgery, Roswell Park Cancer Institute, Elm & Carlton Streets, Buffalo, NY 14263, USA. Tel: 716-845-2367; Fax: 716-845-5705; E-mail: Kazuaki.Takabe@roswellpark.org

References

[1] Kennecke H, Yerushalmi R, Woods R, Cheang MC, Voduc D, Speers CH, Nielsen TO and Gelmon K. Metastatic behavior of breast cancer subtypes. J Clin Oncol 2010; 28: 3271-3277.

[2] Pulido C, Vendrell I, Ferreira AR, Casimiro S, Mansinho A, Alho I and Costa L. Bone metastasis risk factors in breast cancer. Ecancermedicalscience 2017; 11: 715.

[3] Delpech Y, Bashour SI, Lousquy R, Rouzier R, Hess K, Coutant C, Barranger E, Esteva FJ, Ueno NT, Pusztai L and Ibrahim NK. Clinical nomogram to predict bone-only metastasis in patients with early breast carcinoma. Br J Cancer 2015; 113: 1003-1009.

[4] Greenberg PA, Hortobagyi GN, Smith TL, Ziegler LD, Frye DK and Buzdar AU. Long-term follow-up of patients with complete remission following combination chemotherapy for metastatic breast cancer. J Clin Oncol 1996; 14: 2197-2205.

[5] Werkoff G, Lambaudie E, Fondrinier E, Levêque J, Marchal F, Uzan M, Barranger E, Guillemin F, Darai E, Uzan S, Houvenaeghel G, Rouzier R and Coutant C. Prospective multicenter comparison of models to predict four or more involved axillary lymph nodes in patients with breast cancer with one to three metastatic sentinel lymph nodes. J Clin Oncol 2009; 27: 5707-5712.

[6] Rouzier R, Pusztai L, Delaloge S, Gonzalez-Angulo AM, Andre F, Hess KR, Buzdar AU, Garbay JR, Spielmann M, Mathieu MC, Symmans WF, Wagner P, Atallah D, Valero V, Berry DA and Hortobagyi GN. Nomograms to predict pathologic complete response and metastasis-free survival after preoperative chemotherapy for breast cancer. J Clin Oncol 2005; 23: 8331-8339.

[7] Bidard FC, Peeters DJ, Fehm T, Nolé F, Gisbert-Criado R, Mavroudis D, Grisanti S, Generali D, Garcia-Saenz JA, Stebbing J, Caldas C, Gazzaniga P, Manso L, Zamarchi R, de Lascoiti AF, De Mattos-Arruda L, Ignatiadis M, Lebofsky R, van Laere SJ, Meier-Stiegen F, Sandri MT, Vidal-Martinez J, Politaki E, Consoli F, Bottini A, Diaz-Rubio E, Krell J, Dawson SJ, Raimondi C, Rutten A, Janni W, Munzone E, Carañana V, Agelaki S, Almici C, Dirix L, Solomayer EF, Zorzino L, Johannes H, Reis-Filho JS, Pantel K, Pierga JY and Michiels S. Clinical validity of circulating tumour cells in patients with metastatic breast cancer: a pooled analysis of individual patient data. Lancet Oncol 2014; 15: 406-414.

[8] Harris L, Fritsche H, Mennel R, Norton L, Ravdin P, Taube S, Somerfield MR, Hayes DF and Bast RC Jr. American Society of Clinical Oncology 2007 update of recommendations for the use of tumor markers in breast cancer. J Clin Oncol 2007; 25: 5287-5312.

[9] Balachandran VP, Arora A, Gönen M, Ito H, Turcotte S, Shia J, Viale A, Snoeren N, van Hooff SR, Rinkes IH, Adam R, Kingham TP, Allen PJ, DeMatteo RP, Jarnagin WR and D'Angelica MI. A validated prognostic multigene expression assay for overall survival in resected colorectal cancer liver metastases. Clin Cancer Res 2016; 22: 2575-2582.

[10] Oshi M, Newman S, Murthy V, Tokumaru Y, Yan L, Matsuyama R, Endo I and Takabe K. ITPKC as a prognostic and predictive biomarker of neoadjuvant chemotherapy for triple negative breast cancer. Cancers (Basel) 2020; 12: 2758.

[11] Oshi M, Angarita FA, Tokumaru Y, Yan L, Matsuyama R, Endo I and Takabe K. High expression of NRF2 is associated with increased tumor-infiltrating lymphocytes and cancer immunity in ER-positive/HER2-negative breast cancer. Cancers (Basel) 2020; 12: 3856.

[12] Curtis C, Shah SP, Chin SF, Turashvili G, Rueda OM, Dunning MJ, Speed D, Lynch AG, Samarajiwa S, Yuan Y, Gräf S, Ha G, Haffari G, Bashashati A, Russell R, McKinney S; METABRIC Group, Langerød A, Green A, Provenzano E, Wishart G, Pinder S, Watson P, Markowetz F, Murphy L, Ellis I, Purushotham A, Børresen-Dale AL, Brenton JD, Tavaré S, Caldas C and Aparicio S. The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature 2012; 486: 346-352.

[13] Brueffer C, Vallon-Christersson J, Grabau D, Ehinger A, Häkkinen J, Hegardt C, Malina J, Chen Y, Bendahl PO, Manjer J, Malmberg M, Larsson C, Loman N, Rydén L, Borg Å and Saal LH. Clinical value of RNA sequencing-based classifiers for prediction of the five conventional breast cancer biomarkers: a report from the population-based multicenter Sweden cancerome analysis network-breast initiative. JCO Precis Oncol 2018; 2: PO.17.00135.

[14] Wang Y, Klijn JG, Zhang Y, Sieuwerts AM, Look MP, Yang F, Talantov D, Timmermans M, Meijer-van Gelder ME, Yu J, Jatkoe T, Berns EM, Atkins D and Foekens JA. Gene-expression profiles to predict distant metastasis of lymph-node-negative primary breast cancer. Lancet 2005; 365: 671-679.

[15] Minn AJ, Gupta GP, Siegel PM, Bos PD, Shu W, Giri DD, Viale A, Olshen AB, Gerald WL and Massagué J. Genes that mediate breast cancer metastasis to lung. Nature 2005; 436: 518-524.

[16] Oshi M, Katsuta E, Yan L, Ebos JML, Rashid OM, Matsuyama R, Endo I and Takabe K. A novel 4-gene score to predict survival, distant metastasis and response to neoadjuvant therapy in breast cancer. Cancers (Basel) 2020; 12: 1148.

[17] Oshi M, Takahashi H, Tokumaru Y, Yan L, Rashid OM, Matsuyama R, Endo I and Takabe K. G2M cell cycle pathway score as a prognostic biomarker of metastasis in estrogen receptor (ER)-positive breast cancer. Int J Mol Sci 2020; 21: 2921.

[18] Oshi M, Takahashi H, Tokumaru Y, Yan L, Rashid OM, Nagahashi M, Matsuyama R, Endo I and Takabe K. The E2F pathway score as a predictive biomarker of response to neoadjuvant therapy in ER+/HER2- breast cancer. Cells 2020; 9: 1643.

[19] Young J, Kawaguchi T, Yan L, Qi Q, Liu S and Takabe K. Tamoxifen sensitivity-related microRNA-342 is a useful biomarker for breast cancer survival. Oncotarget 2017; 8: 99978-99989.

[20] Kim SY, Kawaguchi T, Yan L, Young J, Qi Q and Takabe K. Clinical relevance of microRNA expressions in breast cancer validated using the cancer genome atlas (TCGA). Ann Surg Oncol 2017; 24: 2943-2949.

[21] Ramanathan R, Olex AL, Dozmorov M, Bear HD, Fernandez LJ and Takabe K. Angiopoietin pathway gene expression associated with poor breast cancer survival. Breast Cancer Res Treat 2017; 162: 191-198.

[22] Kawaguchi T, Yan L, Qi Q, Peng X, Gabriel EM, Young J, Liu S and Takabe K. Overexpression of suppressive microRNAs, miR-30a and miR-200c are associated with improved survival of breast cancer patients. Sci Rep 2017; 7: 15945.

[23] McDonald KA, Kawaguchi T, Qi Q, Peng X, Asaoka M, Young J, Opyrchal M, Yan L, Patnaik S, Otsuji E and Takabe K. Tumor heterogeneity correlates with less immune response and worse survival in breast cancer patients. Ann Surg Oncol 2019; 26: 2191-2199.

[24] Sporn JC, Katsuta E, Yan L and Takabe K. Expression of MicroRNA-9 is associated with overall survival in breast cancer patients. J Surg Res 2019; 233: 426-435.

[25] Subramanian A, Kuehn H, Gould J, Tamayo P and Mesirov JP. GSEA-P: a desktop application for gene set enrichment analysis. Bioinformatics 2007; 23: 3251-3253.

[26] Subramanian A, Tamayo P, Mootha VK, Mukherjee S, Ebert BL, Gillette MA, Paulovich A, Pomeroy SL, Golub TR, Lander ES and Mesirov JP. Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. Proc Natl Acad Sci U S A 2005; 102: 15545-15550.

[27] Oshi M, Kim TH, Tokumaru Y, Yan L, Matsuyama R, Endo I, Cherkassky L and Takabe K. Enhanced DNA repair pathway is associated with cell proliferation and worse survival in hepatocellular carcinoma (HCC). Cancers (Basel) 2021; 13: 323.

[28] Oshi M, Newman S, Tokumaru Y, Yan L, Matsuyama R, Endo I, Katz MHG and Takabe K. High G2M pathway score pancreatic cancer is associated with worse survival, particularly after margin-positive (R1 or R2) resection. Cancers (Basel) 2020; 12: 2871.

[29] Oshi M, Newman S, Tokumaru Y, Yan L, Matsuyama R, Endo I, Nagahashi M and Takabe K. Intra-tumoral angiogenesis is associated with inflammation, immune reaction and metastatic recurrence in breast cancer. Int J Mol Sci 2020; 21: 6708.

[30] Oshi M, Newman S, Tokumaru Y, Yan L, Matsuyama R, Endo I and Takabe K. Inflammation is associated with worse outcome in the whole cohort but with better outcome in triple-negative subtype of breast cancer patients. J Immunol Res 2020; 2020: 5618786.

[31] Oshi M, Tokumaru Y, Angarita FA, Yan L, Matsuyama R, Endo I and Takabe K. Degree of early estrogen response predict survival after endocrine therapy in primary and metastatic ER-positive breast cancer. Cancers (Basel) 2020; 12: 3557.

[32] Oshi M, Asaoka M, Tokumaru Y, Angarita FA, Yan L, Matsuyama R, Zsiros E, Ishikawa T, Endo I and Takabe K. Abundance of regulatory T cell (Treg) as a predictive biomarker for neoadjuvant chemotherapy in triple-negative

breast cancer. Cancers (Basel) 2020; 12: 3038.

[33] Oshi M, Asaoka M, Tokumaru Y, Yan L, Matsuyama R, Ishikawa T, Endo I and Takabe K. CD8 T cell score as a prognostic biomarker for triple negative breast cancer. Int J Mol Sci 2020; 21: 6968.

[34] Oshi M, Newman S, Tokumaru Y, Yan L, Matsuyama R, Kalinski P, Endo I and Takabe K. Plasmacytoid dendritic cell (pDC) infiltration correlate with tumor infiltrating lymphocytes, cancer immunity, and better survival in triple negative breast cancer (TNBC) more strongly than conventional dendritic cell (cDC). Cancers (Basel) 2020; 12: 3342.

[35] Oshi M, Tokumaru Y, Asaoka M, Yan L, Satyananda V, Matsuyama R, Matsuhashi N, Futamura M, Ishikawa T, Yoshida K, Endo I and Takabe K. M1 macrophage and M1/M2 ratio defined by transcriptomic signatures resemble only part of their conventional clinical characteristics in breast cancer. Sci Rep 2020; 10: 16554.

[36] Oshi M, Huyser MR, Le L, Tokumaru Y, Yan L, Matsuyama R, Endo I and Takabe K. Abundance of microvascular endothelial cells is associated with response to chemotherapy and prognosis in colorectal cancer. Cancers (Basel) 2021; 13: 1477.

[37] Kusakai G, Suzuki A, Ogura T, Kaminishi M and Esumi H. Strong association of ARK5 with tumor invasion and metastasis. J Exp Clin Cancer Res 2004; 23: 263-268.

[38] Suzuki A, Lu J, Kusakai G, Kishimoto A, Ogura T and Esumi H. ARK5 is a tumor invasion-associated factor downstream of Akt signaling. Mol Cell Biol 2004; 24: 3526-3535.

[39] Saiyin H, Na N, Han X, Fang Y, Wu Y, Lou W and Yang X. BRSK2 induced by nutrient deprivation promotes Akt activity in pancreatic cancer via downregulation of mTOR activity. Oncotarget 2017; 8: 44669-44681.

[40] Wu K, Li Z, Cai S, Tian L, Chen K, Wang J, Hu J, Sun Y, Li X, Ertel A and Pestell RG. EYA1 phosphatase function is essential to drive breast cancer cell proliferation through cyclin D1. Cancer Res 2013; 73: 4488-4499.

[41] Kameda Y, Takahata M, Komatsu M, Mikuni S, Hatakeyama S, Shimizu T, Angata T, Kinjo M, Minami A and Iwasaki N. Siglec-15 regulates osteoclast differentiation by modulating RANKL-induced phosphatidylinositol 3-kinase/Akt and Erk pathways in association with signaling Adaptor DAP12. J Bone Miner Res 2013; 28: 2463-2475.

[42] Plummer S, Tower C, Alonso P, Morgan L, Baker P, Broughton-Pipkin F and Kalsheker N. Haplotypes of the angiotensin II receptor genes AGTR1 and AGTR2 in women with normotensive pregnancy and women with preeclampsia. Hum Mutat 2004; 24: 14-20.

[43] Coleman RE and Rubens RD. The clinical course of bone metastases from breast cancer. Br J Cancer 1987; 55: 61-66.

[44] Wu Q, Li J, Zhu S, Wu J, Chen C, Liu Q, Wei W, Zhang Y and Sun S. Breast cancer subtypes predict the preferential site of distant metastases: a SEER based study. Oncotarget 2017; 8: 27990-27996.

[45] Han HH, Lee SH, Kim BG, Lee JH, Kang S and Cho NH. Estrogen receptor status predicts late-onset skeletal recurrence in breast cancer patients. Medicine (Baltimore) 2016; 95: e2909.

Table S1. Clinicopathologic variables of derivation cohort

	Age (years)	TNM Stage	ER status	PR status	HER2 status
Bone Metastasis 1	47	3C	Positive	Positive	Negative
Control 1	39	3A	Positive	Positive	Negative
Bone Metastasis 2	48	1A	Positive	Positive	Negative
Control 2	48	1A	Positive	Positive	Negative
Bone Metastasis 3	50	3C	Positive	Positive	Negative
Control 3	49	3A	Positive	Positive	Negative
Bone Metastasis 4	53	2A	Positive	Negative	Negative
Control 4	60	2A	Positive	Negative	Negative
Bone Metastasis 5	57	3B	Positive	Positive	Negative
Control 5	53	3A	Positive	Positive	Negative
Bone Metastasis 6	67	3C	Positive	Negative	Negative
Control 6	56	3A	Positive	Negative	Negative
Bone Metastasis 7	68	2A	Positive	Positive	Negative
Control 7	67	2A	Positive	Positive	Negative
Bone Metastasis 8	73	1A	Positive	Positive	Negative
Control 8	85	1A	Positive	Positive	Negative
Bone Metastasis 9	77	2A	Negative	Negative	Negative
Control 9	65	2A	Negative	Negative	Negative
Bone Metastasis 10	59	2B	Negative	Negative	Negative
Control 10	60	2B	Negative	Negative	Negative

Table S2. Up-regulated genes in bone metastasis group compared to control by DEG analysis

	Gene	baseMean	log$_2$FoldChange	*P*-value	Adjusted *P*-value
ENSG00000174672.15	BRSK2	89.82717	2.816787516	8E-08	0
ENSG00000104313.17	EYA1	59.05437	2.509600832	8E-07	0.01
ENSG00000154080.13	CHST9	200.1214	2.3607326	7E-06	0.03
ENSG00000145087.12	STXBP5L	37.10362	2.21309657	3E-05	0.06
ENSG00000179008.8	C14orf39	37.27581	2.068965708	5E-05	0.08
ENSG00000163817.15	SLC6A20	60.71181	2.045518199	6E-05	0.08
ENSG00000119283.15	TRIM67	11.39039	1.979981565	0.0002	0.15
ENSG00000149596.6	JPH2	124.9867	1.955710086	3E-05	0.06
ENSG00000233622.1	CYP2T1P	267.9482	1.848360155	0.0005	0.19
ENSG00000118156.12	ZNF541	29.91668	1.846078487	4E-05	0.06
ENSG00000186377.7	CYP4X1	1984.89	1.846052902	0.0004	0.19
ENSG00000262585.1	RP11-353N14.5	20.51921	1.841471918	0.0005	0.19
ENSG00000258692.2	SALL4P7	19.73168	1.821288906	0.0006	0.19
ENSG00000237517.9	DGCR5	24.05256	1.804404865	0.0001	0.11
ENSG00000239791.1	AC002310.7	6.197058	1.792808585	0.0007	0.23
ENSG00000023839.10	ABCC2	129.4426	1.786097174	0.0002	0.16
ENSG00000259604.5	RP11-66B24.1	4.799733	1.769845054	0.0008	0.23
ENSG00000002746.14	HECW1	55.24888	1.764098811	0.0002	0.16
ENSG00000127249.14	ATP13A4	403.5116	1.757692739	0.0003	0.19
ENSG00000167889.12	MGAT5B	53.33375	1.752703498	0.0008	0.23
ENSG00000238042.5	RP11-815M8.1	14.40026	1.748027862	0.0005	0.19
ENSG00000235721.1	AC013268.3	16.82309	1.74697407	0.0005	0.19
ENSG00000228021.7	RP11-383C5.3	17.04038	1.734111255	0.0009	0.23
ENSG00000069188.16	SDK2	213.8548	1.731418643	0.0002	0.15
ENSG00000182352.8	C17orf77	3.284721	1.727848996	0.0009	

ENSG00000171798.17	KNDC1	38.97552	1.725102037	0.0008	0.23
ENSG00000129455.15	KLK8	5.132723	1.699908916	0.0013	0.25
ENSG00000229299.2	RP4-583P15.10	4.820431	1.683233141	0.0014	0.25
ENSG00000186603.5	HPDL	38.70433	1.678789937	0.0013	0.25
ENSG00000094755.16	GABRP	1054.258	1.677032001	0.0014	0.25
ENSG00000186326.3	RGS9BP	17.49927	1.675886149	0.0004	0.19
ENSG00000137561.4	TTPA	48.18416	1.663660285	0.0014	0.25
ENSG00000105376.4	ICAM5	15.79378	1.650704394	0.0014	0.25
ENSG00000158125.9	XDH	114.781	1.646657796	0.001	0.25
ENSG00000067840.12	PDZD4	58.92909	1.634435809	0.0002	0.16
ENSG00000267034.1	RP11-384O8.1	10.32452	1.628911177	0.0016	0.26
ENSG00000070985.13	TRPM5	2.496255	1.628332828	0.0021	
ENSG00000250917.1	RP4-785G19.5	7.501362	1.627786229	0.0016	0.26
ENSG00000227964.1	LINC01429	13.87786	1.623898637	0.0017	0.27
ENSG00000268529.1	CYP2T3P	7.282139	1.618259044	0.0016	0.26
ENSG00000265702.1	RP11-156L14.1	18.64748	1.616792156	0.0023	0.29
ENSG00000172000.7	ZNF556	18.35464	1.593329453	0.001	0.25
ENSG00000108684.14	ASIC2	3.904438	1.582129491	0.0022	
ENSG00000260428.2	SCX	28.30611	1.57966872	1E-04	0.11
ENSG00000213225.7	NOC2LP1	3.977051	1.578284272	0.0028	
ENSG00000236069.1	RP5-1011O1.3	11.95993	1.575999496	0.0026	0.31
ENSG00000225077.2	LINC00337	3.631236	1.575368712	0.0018	
ENSG00000104321.10	TRPA1	100.0853	1.573657177	0.0025	0.3
ENSG00000173698.17	ADGRG2	41.96084	1.566760127	0.001	0.25
ENSG00000185467.7	KPNA7	8.688589	1.559088301	0.0033	0.33
ENSG00000264462.1	MIR3648-2	64.08621	1.55466966	0.0021	0.29
ENSG00000261115.5	TMEM178B	312.4258	1.550245934	0.0027	0.31
ENSG00000181656.6	GPR88	15.16634	1.54549076	0.0033	0.33
ENSG00000229867.1	STEAP3-AS1	3.476438	1.535413429	0.0024	
ENSG00000235961.5	PNMA6A	24.9007	1.534554817	0.0017	0.26
ENSG00000235749.2	RP11-634B7.4	8.985838	1.5293323	0.0035	0.33
ENSG00000237763.9	AMY1A	27.09399	1.528665088	0.0016	0.26
ENSG00000026559.13	KCNG1	66.86969	1.52733184	0.0034	0.33
ENSG00000275708.1	MIR3648-1	61.63556	1.523778364	0.0026	0.31
ENSG00000176769.9	TCERG1L	2.978407	1.509730435	0.0044	
ENSG00000019102.11	VSIG2	86.16585	1.500011931	0.0046	0.35
ENSG00000253154.1	CTA-392E5.1	133.5904	1.497026643	0.0036	0.33
ENSG00000261123.1	RP11-304L19.3	8.496929	1.492997354	0.0031	0.33
ENSG00000129993.14	CBFA2T3	234.2306	1.487574957	0.0022	0.29
ENSG00000158477.6	CD1A	30.67528	1.487406508	0.004	0.34
ENSG00000138650.8	PCDH10	30.26131	1.481141094	0.0036	0.33
ENSG00000047457.13	CP	2413.532	1.477393512	0.0046	0.35
ENSG00000164520.11	RAET1E	36.89206	1.47434555	0.0052	0.36
ENSG00000253802.1	CTA-392C11.1	2.810379	1.472600274	0.0037	
ENSG00000227195.9	MIR663AHG	373.2087	1.472333551	0.0025	0.3
ENSG00000104267.9	CA2	1276.867	1.469781945	0.0009	0.23
ENSG00000183206.17	POTEC	100.1348	1.469215755	0.0055	0.37
ENSG00000264548.1	RP13-516M14.2	6.635674	1.465510769	0.0047	0.35
ENSG00000157103.10	SLC6A1	47.65355	1.463988818	0.0007	0.23

ENSG00000267013.5	CTD-2171N6.1	75.84918	1.462337976	0.0045	0.35
ENSG00000177519.3	RPRM	2.254338	1.458030187	0.0058	
ENSG00000272468.1	RP1-86C11.7	16.87339	1.455214747	0.0048	0.36
ENSG00000253525.1	CTD-2114J12.1	28.22731	1.45443178	0.0047	0.35
ENSG00000262413.1	RP11-498C9.3	3.872625	1.4537197	0.0039	
ENSG00000163060.7	TEKT4	4.701105	1.453395243	0.0028	
ENSG00000239265.5	CLRN1-AS1	4.643809	1.45158949	0.0062	
ENSG00000188290.10	HES4	373.4963	1.447524576	0.0009	0.23
ENSG00000069696.6	DRD4	6.772787	1.433022611	0.0011	0.25
ENSG00000109956.12	B3GAT1	27.83672	1.432756251	0.0031	0.33
ENSG00000171033.12	PKIA	387.9466	1.431127204	0.0038	0.34
ENSG00000244383.1	FAM3D-AS1	2.037908	1.430939978	0.007	
ENSG00000123838.10	C4BPA	5.870886	1.430155649	0.007	0.4
ENSG00000272588.1	RP11-440L14.4	6.959911	1.430025781	0.0035	0.33
ENSG00000255583.2	RP11-415I12.2	8.395773	1.429548948	0.0067	0.4
ENSG00000149294.16	NCAM1	104.5913	1.428128576	0.0012	0.25
ENSG00000164532.10	TBX20	10.91665	1.426793812	0.0071	0.4
ENSG00000259925.1	CTA-363E6.2	1.929942	1.419489151	0.0066	
ENSG00000272264.1	RP11-92K15.3	40.17172	1.419074224	0.0025	0.3
ENSG00000100427.15	MLC1	24.01831	1.418958388	0.0075	0.4
ENSG00000187634.11	SAMD11	242.499	1.416111365	0.0019	0.28
ENSG00000278996.1	CH507-513H4.1	117.2274	1.41494834	0.0005	0.19
ENSG00000162174.12	ASRGL1	228.3758	1.414193453	0.0012	0.25
ENSG00000162873.14	KLHDC8A	18.16173	1.413082864	0.001	0.25
ENSG00000254275.6	LINC00824	16.26877	1.411328002	0.0061	0.39
ENSG00000205078.5	SYCE1L	29.73183	1.406230202	0.0023	0.29
ENSG00000196277.15	GRM7	18.74268	1.404185989	0.0078	0.4
ENSG00000106278.11	PTPRZ1	99.01832	1.402500443	0.0078	0.4
ENSG00000099617.3	EFNA2	2.26509	1.400384009	0.0074	
ENSG00000185838.13	GNB1L	232.3704	1.399775497	0.0022	0.29
ENSG00000205488.8	CALML3-AS1	36.08624	1.396242107	0.0018	0.27
ENSG00000124939.5	SCGB2A1	128.278	1.390956312	0.0088	0.41
ENSG00000280429.1	AF001548.3	1.43076	1.388262278	0.0072	
ENSG00000163064.6	EN1	100.7401	1.387696507	0.0063	0.39
ENSG00000203685.9	STUM	275.8036	1.385392385	0.0085	0.41
ENSG00000276077.4	CH507-254M2.2	15.02938	1.384030372	0.0018	0.27
ENSG00000214216.10	IQCJ	17.39265	1.38109766	0.0073	0.4
ENSG00000279255.1	LA16c-380A1.2	4.482586	1.378697761	0.0073	
ENSG00000276547.1	PCDHGB5	326.4745	1.375652899	0.0028	0.32
ENSG00000077935.16	SMC1B	101.5288	1.374446667	0.0095	0.43
ENSG00000220008.3	LINGO3	4.281672	1.370284711	0.0098	
ENSG00000148677.6	ANKRD1	32.42132	1.370189472	0.0082	0.41
ENSG00000242798.1	RP11-506M12.1	5.834276	1.366569053	0.0068	0.4
ENSG00000223764.2	RP11-54O7.3	82.21401	1.365974771	0.0036	0.33
ENSG00000181195.10	PENK	21.06147	1.361564402	0.0103	0.44
ENSG00000261150.2	EPPK1	8332.078	1.359657408	0.0006	0.19
ENSG00000102385.12	DRP2	46.67519	1.358109593	0.0019	0.28
ENSG00000232320.6	AC009299.5	5.070275	1.357296574	0.0104	0.44
ENSG00000267801.1	RP11-552F3.9	45.87999	1.353456078	0.0052	0.36

ENSG00000264570.1	SNX19P3	18.31602	1.351725476	0.0078	0.4
ENSG00000231686.1	RP1-203P18.1	8.241165	1.348850213	0.0021	0.29
ENSG00000105880.4	DLX5	9.664089	1.348028393	0.0043	0.35
ENSG00000159184.7	HOXB13	21.57241	1.344059464	0.0098	0.43
ENSG00000205143.2	ARID3C	2.485063	1.343373801	0.0114	
ENSG00000236871.7	LINC00106	9.703967	1.339315037	0.0085	0.41
ENSG00000146147.14	MLIP	6.641623	1.335692965	0.0115	0.44
ENSG00000180422.3	LINC00304	3.715248	1.329267028	0.0121	
ENSG00000103175.10	WFDC1	116.023	1.327402905	0.0091	0.42
ENSG00000175745.11	NR2F1	863.7796	1.324832025	0.0081	0.41
ENSG00000131584.18	ACAP3	1075.646	1.320461886	2E-05	0.06
ENSG00000145536.15	ADAMTS16	280.1434	1.31820245	0.0028	0.32
ENSG00000257883.1	RP11-497G19.1	26.54228	1.315575646	0.0109	0.44
ENSG00000275340.1	FGD5P1	11.25078	1.315195227	0.0045	0.35
ENSG00000159307.18	SCUBE1	258.7202	1.314394495	0.0107	0.44
ENSG00000102290.21	PCDH11X	11.91038	1.312446426	0.007	0.4
ENSG00000103260.8	METRN	1124.267	1.312406762	0.0042	0.35
ENSG00000233012.2	HDAC1P2	11.77241	1.308591581	0.0076	0.4
ENSG00000169710.8	FASN	24535.69	1.303518146	0.0028	0.32
ENSG00000130649.9	CYP2E1	38.80552	1.299913448	0.0059	0.38
ENSG00000165061.14	ZMAT4	19.36809	1.298078499	0.0105	0.44
ENSG00000164488.11	DACT2	4.706575	1.297264866	0.0134	
ENSG00000146216.11	TTBK1	9.319423	1.295450817	0.0127	0.47
ENSG00000237742.6	RP11-624M8.1	4.817318	1.294903924	0.0146	0.47
ENSG00000255693.1	RP11-766N7.3	5.967989	1.292212858	0.0063	0.39
ENSG00000237372.2	UNQ6494	6.494194	1.289316677	0.0049	0.36
ENSG00000260265.1	RP11-44F21.5	11.11763	1.288541771	0.012	0.45
ENSG00000127578.6	WFIKKN1	22.42869	1.287590186	0.0103	0.44
ENSG00000248890.1	HHIP-AS1	3.891005	1.286800188	0.0062	
ENSG00000072182.12	ASIC4	2.830218	1.285983545	0.013	
ENSG00000281538.1	RP4-669P10.20	5.59347	1.285740986	0.0081	0.41
ENSG00000179041.3	RRS1	1141.617	1.285736795	0.0014	0.25
ENSG00000178773.14	CPNE7	498.7747	1.284144379	0.0128	0.47
ENSG00000167614.13	TTYH1	31.63252	1.283700068	0.0115	0.44
ENSG00000254248.1	RP11-320N21.2	2.884477	1.282158637	0.0132	
ENSG00000182103.4	FAM181B	45.21554	1.281589285	0.0146	0.47
ENSG00000279177.1	CH507-338C24.2	3.652607	1.28080134	0.0147	
ENSG00000133937.4	GSC	52.64899	1.277234449	0.0045	0.35
ENSG00000261226.1	RP11-830F9.7	13.91368	1.272753561	0.0118	0.45
ENSG00000178947.8	SMIM10L2A	47.78078	1.272632901	0.0027	0.32
ENSG00000131094.3	C1QL1	9.665818	1.272037227	0.0131	0.47
ENSG00000283288.1	AC138517.6	9.100642	1.271452542	0.0159	0.49
ENSG00000278919.1	AP006285.2	18.06379	1.270487821	0.0077	0.4
ENSG00000175520.8	UBQLN3	2.75508	1.270248919	0.0156	
ENSG00000125848.9	FLRT3	419.5361	1.269841565	0.0133	0.47
ENSG00000130950.13	NUTM2F	1.805985	1.269442449	0.012	
ENSG00000260653.5	RP11-114G11.5	9.910197	1.268372197	0.015	0.48
ENSG00000116254.17	CHD5	8.804639	1.267196384	0.0065	0.4
ENSG00000004777.18	ARHGAP33	267.4992	1.266402807	0.0028	0.32

ENSG00000162631.18	NTNG1	60.632	1.266365452	0.017	0.5
ENSG00000133392.17	MYH11	1582.058	1.259787117	0.0071	0.4
ENSG00000101542.9	CDH20	7.081775	1.259512494	0.0161	0.49
ENSG00000226332.2	RP11-157P1.4	18.39703	1.259420012	0.0119	0.45
ENSG00000249661.1	TNRC18P1	787.7333	1.259089658	0.0119	0.45
ENSG00000240280.6	TCAM1P	7.133885	1.25898462	0.0138	0.47
ENSG00000167034.9	NKX3-1	297.9173	1.258393774	0.011	0.44
ENSG00000104490.17	NCALD	876.0388	1.250866918	0.0049	0.36
ENSG00000135374.9	ELF5	556.5207	1.249134072	0.0171	0.5
ENSG00000280441.2	CH507-528H12.1	115.4304	1.247697022	0.0021	0.29
ENSG00000115138.10	POMC	29.7893	1.247669446	0.0049	0.36
ENSG00000160957.12	RECQL4	756.4483	1.245944461	0.0008	0.23
ENSG00000225756.1	DBH-AS1	14.60692	1.245037646	0.005	0.36
ENSG00000251381.7	LINC00958	15.89324	1.243012787	0.0091	0.42
ENSG00000129744.2	ART1	6.845261	1.241800182	0.0185	0.51
ENSG00000164626.8	KCNK5	473.9431	1.241509861	0.0153	0.48
ENSG00000185347.17	C14orf80	368.9693	1.240227446	0.001	0.25
ENSG00000261670.1	RP11-1C8.5	12.63411	1.239932067	0.0155	0.48
ENSG00000128408.8	RIBC2	121.19	1.239183378	0.002	0.29
ENSG00000184454.6	NCMAP	306.1232	1.236685354	0.0177	0.51
ENSG00000137809.16	ITGA11	2754.975	1.236490134	0.0035	0.33
ENSG00000145113.21	MUC4	10.96763	1.233486844	0.0199	0.52
ENSG00000258175.1	RP11-412H8.2	3.760611	1.230926083	0.0163	
ENSG00000233296.1	AC092159.2	3.182753	1.229297926	0.0205	
ENSG00000101115.12	SALL4	150.6225	1.22927992	0.0042	0.35
ENSG00000109906.13	ZBTB16	290.5309	1.229068891	0.0138	0.47
ENSG00000262484.1	CCER2	5.803766	1.226978101	0.0096	0.43
ENSG00000280424.1	CITF22-92A6.2	3.617953	1.224598707	0.0156	
ENSG00000279039.1	CTC-260E6.3	32.82675	1.224097455	0.0151	0.48
ENSG00000185189.16	NRBP2	1130.308	1.223708161	0.0001	0.12
ENSG00000121101.15	TEX14	41.8221	1.222680447	0.0133	0.47
ENSG00000258101.2	RP11-977B10.2	8.296019	1.221621643	0.0069	0.4
ENSG00000273230.1	RP11-1246C19.1	22.1308	1.221049999	0.0032	0.33
ENSG00000156466.9	GDF6	17.40835	1.217588862	0.0035	0.33
ENSG00000236740.6	RP11-411K7.1	17.70633	1.214981891	0.0201	0.52
ENSG00000124107.5	SLPI	1659.841	1.214912945	0.0215	0.52
ENSG00000101194.17	SLC17A9	247.1003	1.214705879	0.0039	0.34
ENSG00000168528.11	SERINC2	2904.562	1.212031783	0.0021	0.29
ENSG00000168594.15	ADAM29	5.506515	1.210546819	0.0219	0.52
ENSG00000267119.1	RPL10P15	227.4779	1.209589551	0.0065	0.4
ENSG00000187642.9	PERM1	11.42524	1.209362593	0.0087	0.41
ENSG00000184986.10	TMEM121	139.8981	1.20926835	0.0009	0.23
ENSG00000114124.2	GRK7	3.775065	1.208007318	0.0179	
ENSG00000120075.5	HOXB5	6.091525	1.207843663	0.0071	0.4
ENSG00000270547.5	LINC01235	221.7106	1.206902845	0.0102	0.44
ENSG00000132975.7	GPR12	1.80764	1.206556167	0.0222	
ENSG00000233806.7	LINC01237	106.9483	1.202633587	0.0082	0.41
ENSG00000183114.7	FAM43B	16.94543	1.200290806	0.0084	0.41
ENSG00000228330.1	RP11-730A19.5	2.039395	1.199068527	0.0236	

ENSG00000182378.13	PLCXD1	281.8158	1.198580586	0.0039	0.34
ENSG00000255178.1	RP11-686G23.2	3.591686	1.198482143	0.0151	
ENSG00000137709.9	POU2F3	116.4115	1.197413777	0.0054	0.37
ENSG00000233682.3	RP11-13P5.2	12.41513	1.196273458	0.0159	0.49
ENSG00000236833.1	AC024560.2	2.276858	1.196263153	0.0241	
ENSG00000273108.1	RP11-416N2.4	7.383899	1.196246748	0.0156	0.48
ENSG00000262888.1	RP11-462G12.2	3.027513	1.194779306	0.0242	
ENSG00000176956.12	LY6H	19.99902	1.194702946	0.0213	0.52
ENSG00000145526.11	CDH18	6.068548	1.193621135	0.0243	0.54
ENSG00000164403.14	SHROOM1	1150.885	1.193563872	0.0195	0.51
ENSG00000184058.12	TBX1	293.9568	1.193531288	0.0234	0.53
ENSG00000109758.8	HGFAC	6.133854	1.193348721	0.0226	0.53
ENSG00000113249.12	HAVCR1	12.71683	1.192175599	0.0085	0.41
ENSG00000260139.6	CSPG4P13	19.75946	1.19114861	0.004	0.35
ENSG00000171551.11	ECEL1	25.57267	1.188312297	0.0135	0.47
ENSG00000203585.3	RP11-542B15.1	19.22549	1.187781061	0.0038	0.34
ENSG00000170044.8	ZPLD1	19.7422	1.186239852	0.0109	0.44
ENSG00000255318.1	RP11-655M14.13	2.015388	1.184249365	0.0244	
ENSG00000259439.2	RP11-89K21.1	55.76639	1.183118467	0.0255	0.55
ENSG00000234665.8	RP11-262H14.3	19.06917	1.182948036	0.0216	0.52
ENSG00000184270.4	HIST2H2AB	1070.248	1.182607157	0.0044	0.35
ENSG00000184702.17	SEPT5	927.8882	1.18131494	0.0051	0.36
ENSG00000211683.3	KB-1572G7.3	4.746735	1.180953888	0.0197	0.52
ENSG00000219433.2	BTBD10P2	7.51618	1.180451884	0.0203	0.52
ENSG00000197599.12	CCDC154	14.4529	1.179251213	0.0115	0.44
ENSG00000156853.12	ZNF689	1066.363	1.17814237	0.0063	0.39
ENSG00000260934.1	CTA-363E6.7	5.383789	1.178110742	0.0255	0.55
ENSG00000099953.9	MMP11	8790.213	1.174328976	0.0094	0.43
ENSG00000164776.9	PHKG1	45.27832	1.174186907	0.0049	0.36
ENSG00000263718.2	RP11-285E9.6	1.518663	1.173401576	0.0259	
ENSG00000112175.7	BMP5	33.06852	1.171290983	0.0259	0.55
ENSG00000262380.1	CTB-193M12.3	7.415501	1.170685275	0.0232	0.53
ENSG00000129910.7	CDH15	5.476226	1.168036174	0.0261	0.55
ENSG00000258593.2	CTD-3051D23.4	3.724292	1.164828123	0.0204	
ENSG00000169750.8	RAC3	1001.544	1.163997236	0.0104	0.44
ENSG00000103253.17	HAGHL	393.6626	1.163146768	0.0067	0.4
ENSG00000148123.14	PLPPR1	31.47997	1.160693875	0.0282	0.56
ENSG00000182272.11	B4GALNT4	912.3607	1.160597837	0.0052	0.36
ENSG00000225614.2	ZNF469	781.1357	1.159020007	0.0052	0.36
ENSG00000236816.2	ANKRD20A7P	10.67121	1.158816424	0.0241	0.54
ENSG00000169682.17	SPNS1	62.92155	1.154972568	0.0005	0.19
ENSG00000187583.10	PLEKHN1	103.2272	1.154957273	0.0063	0.39
ENSG00000254718.6	CTD-2184C24.2	2.303164	1.153400089	0.0295	
ENSG00000196427.13	NBPF4	143.3431	1.153191641	0.0295	0.57
ENSG00000261349.1	RP3-465N24.5	17.94681	1.153045424	0.0181	0.51
ENSG00000256663.1	RP11-424C20.2	105.9275	1.152486788	0.0177	0.51
ENSG00000131773.13	KHDRBS3	346.7765	1.152454892	0.0013	0.25
ENSG00000142235.8	LMTK3	271.5078	1.152231171	0.014	0.47
ENSG00000197774.12	EME2	661.7859	1.151681668	0.003	0.33

ENSG00000182378.13_PAR_Y	PLCXD1	286.2284	1.151051151	0.0069	0.4
ENSG00000157856.10	DRC1	3.276373	1.150525584	0.0148	
ENSG00000246334.2	PRR7-AS1	4.907035	1.15049182	0.0296	0.58
ENSG00000236670.1	KRT18P5	29.28897	1.150491054	0.0108	0.44
ENSG00000262903.1	RP11-235E17.6	11.84116	1.150449067	0.0132	0.47
ENSG00000255153.1	TOLLIP-AS1	34.79888	1.149941489	0.01	0.43
ENSG00000148204.11	CRB2	7.20552	1.149674793	0.02	0.52
ENSG00000127564.16	PKMYT1	588.7136	1.148863802	0.0104	0.44
ENSG00000187013.4	C17orf82	10.7509	1.148842894	0.0256	0.55
ENSG00000256596.1	RP11-522N14.2	5.359978	1.148550504	0.0298	0.58
ENSG00000134363.11	FST	392.5247	1.148418367	0.0138	0.47
ENSG00000178828.6	RNF186	2.444677	1.146806131	0.023	
ENSG00000239405.1	TMED10P2	4.406779	1.144804194	0.031	
ENSG00000147234.10	FRMPD3	157.7611	1.144129858	0.0194	0.51
ENSG00000156968.8	MPV17L	1083.245	1.142648508	0.017	0.5
ENSG00000070031.3	SCT	5.809022	1.142446415	0.0276	0.56
ENSG00000136542.8	GALNT5	1142.917	1.141944804	0.0168	0.5
ENSG00000177595.17	PIDD1	321.1323	1.141455526	0.0013	0.25
ENSG00000204950.3	LRRC10B	96.50903	1.139471818	0.0268	0.56
ENSG00000178462.11	TUBAL3	36.66907	1.139190794	0.0238	0.54
ENSG00000189166.6	TNRC18P3	12.11146	1.137739689	0.0153	0.48
ENSG00000099889.13	ARVCF	989.9101	1.137329605	0.0052	0.36
ENSG00000244242.1	IFITM10	75.0899	1.136542187	0.0243	0.54
ENSG00000008710.18	PKD1	3194.202	1.136200155	0.0003	0.16
ENSG00000205683.11	DPF3	43.99123	1.135679022	0.024	0.54
ENSG00000182585.9	EPGN	31.47039	1.135148376	0.0324	0.58
ENSG00000270020.1	RP11-46309.9	4.498678	1.135050466	0.0304	
ENSG00000143512.12	HHIPL2	45.95587	1.134104954	0.026	0.55
ENSG00000169894.17	MUC3A	4.715597	1.133491779	0.0257	
ENSG00000165238.16	WNK2	862.9217	1.132707497	0.0178	0.51
ENSG00000247095.2	MIR210HG	60.64939	1.132586348	0.0038	0.34
ENSG00000243967.4	NBPF5P	42.8717	1.132197574	0.0328	0.58
ENSG00000236017.8_PAR_Y	ASMTL-AS1	24.34191	1.129340758	0.0138	0.47
ENSG00000160886.13	LY6K	218.0189	1.127925867	0.0327	0.58
ENSG00000168916.15	ZNF608	1090.038	1.127458966	0.0052	0.36
ENSG00000279013.1	RP11-254A24.2	13.56617	1.126221073	0.0277	0.56
ENSG00000169836.4	TACR3	5.489326	1.125038182	0.034	0.59
ENSG00000130675.14	MNX1	41.729	1.124730507	0.0313	0.58
ENSG00000121207.11	LRAT	61.69455	1.124108195	0.0307	0.58
ENSG00000163623.9	NKX6-1	18.65788	1.123298519	0.0209	0.52
ENSG00000183186.7	C2CD4C	20.11814	1.122155001	0.0183	0.51
ENSG00000180279.6	MGC45922	2.391965	1.119279731	0.0319	
ENSG00000184709.7	LRRC26	93.84834	1.118565008	0.0299	0.58
ENSG00000214676.4	RPL9P16	15.09889	1.117914774	0.024	0.54
ENSG00000163993.6	S100P	1356.778	1.116278472	0.0341	0.59
ENSG00000116985.11	BMP8B	178.109	1.116084562	0.0005	0.19
ENSG00000105219.8	CNTD2	126.8526	1.115291845	0.0277	0.56
ENSG00000266074.8	BAHCC1	602.2837	1.114820566	0.013	0.47
ENSG00000230992.3	FAM201B	1.989821	1.113431035	0.0344	

ENSG00000105464.3	GRIN2D	34.76503	1.112327308	0.0166	0.5
ENSG00000120088.14	CRHR1	2.357442	1.112149534	0.0204	
ENSG00000100726.14	TELO2	928.8155	1.11157137	0.0006	0.2
ENSG00000182685.7	BRICD5	75.3689	1.110293333	0.003	0.33
ENSG00000185652.11	NTF3	7.400222	1.109809059	0.0305	0.58
ENSG00000142549.9	IGLON5	2.461237	1.10946244	0.0341	
ENSG00000261971.6	MMP25-AS1	85.50555	1.108461949	0.0037	0.33
ENSG00000260742.1	RP11-366L5.1	14.11209	1.107065956	0.0145	0.47
ENSG00000237149.5	ZNF503-AS2	25.36464	1.106160699	0.0263	0.55
ENSG00000147697.8	GSDMC	67.76907	1.104604543	0.0333	0.59
ENSG00000162004.16	CCDC78	127.0928	1.103420112	0.0231	0.53
ENSG00000137843.11	PAK6	104.3802	1.103040687	0.0144	0.47
ENSG00000122787.14	AKR1D1	3.756731	1.102661177	0.0368	
ENSG00000277215.1	SPANXA2-OT1	3.471808	1.10226078	0.0253	
ENSG00000129990.14	SYT5	10.37837	1.102030044	0.0379	0.6
ENSG00000132938.19	MTUS2	15.18955	1.101152394	0.0224	0.53
ENSG00000267383.6	CTC-260E6.6	111.1065	1.100349035	0.0027	0.31
ENSG00000213937.3	CLDN9	7.513045	1.098531781	0.035	0.59
ENSG00000171094.15	ALK	17.09932	1.097699718	0.0321	0.58
ENSG00000198467.13	TPM2	2544.55	1.097596779	0.0011	0.25
ENSG00000162591.15	MEGF6	969.5838	1.097586009	0.0016	0.26
ENSG00000280344.1	AC009166.7	2.43326	1.09712118	0.0382	
ENSG00000015592.16	STMN4	3.098537	1.097074349	0.0388	
ENSG00000113924.11	HGD	269.3717	1.097067932	0.0284	0.56
ENSG00000267432.5	DNAH17-AS1	1.363651	1.096095822	0.0358	
ENSG00000187730.7	GABRD	47.88618	1.094932818	0.0135	0.47
ENSG00000218631.1	RP3-395C13.1	2.77845	1.094669102	0.0353	
ENSG00000262877.4	RP11-1055B8.4	49.74733	1.094430441	0.0272	0.56
ENSG00000245526.9	LINC00461	2.495502	1.091919823	0.0238	
ENSG00000184156.15	KCNQ3	378.9707	1.09161182	0.0129	0.47
ENSG00000254024.1	KB-1562D12.1	32.50363	1.091445937	0.0242	0.54
ENSG00000260152.2	RP11-69H7.4	3.798366	1.091293118	0.0395	
ENSG00000219992.2	RP11-420L9.2	1.148138	1.088501756	0.0292	
ENSG00000260576.1	EIF5A2P1	6.436396	1.088488344	0.0291	0.57
ENSG00000235597.1	LINC01102	3.526797	1.087801176	0.0404	
ENSG00000257890.1	RP11-114F10.2	2.099492	1.087467023	0.0384	
ENSG00000166342.18	NETO1	25.59045	1.085599679	0.04	0.61
ENSG00000221882.2	OR3A2	1.540866	1.085342249	0.0409	
ENSG00000261069.3	RP11-701H24.4	789.0368	1.0845167	0.0213	0.52
ENSG00000228709.1	AP001065.15	3.185427	1.083684293	0.041	
ENSG00000242611.2	AC093627.8	7.326518	1.083375855	0.0409	0.61
ENSG00000251667.1	BRCC3P1	3.808945	1.081782172	0.0381	
ENSG00000256612.7	CYP2B7P	2060.235	1.08142319	0.041	0.61
ENSG00000140511.11	HAPLN3	508.286	1.080992406	0.0098	0.43
ENSG00000135333.13	EPHA7	125.0211	1.080620772	0.0334	0.59
ENSG00000253953.2	PCDHGB4	234.9402	1.080249025	0.0198	0.52
ENSG00000134376.14	CRB1	12.77671	1.079977971	0.033	0.58
ENSG00000171812.11	COL8A2	1783.428	1.079488985	0.0039	0.34
ENSG00000261732.1	LA16c-431H6.6	19.96955	1.079092565	0.0032	0.33

ENSG00000169692.12	AGPAT2	1380.929	1.078784074	0.0027	0.32
ENSG00000153930.11	ANKFN1	28.44334	1.078028037	0.0255	0.55
ENSG00000237886.1	NALT1	9.263784	1.07685301	0.0214	0.52
ENSG00000262580.5	RP11-334C17.5	207.9326	1.075772748	0.011	0.44
ENSG00000280273.1	AF131216.1	1.918836	1.075699812	0.0388	
ENSG00000253549.5	CA3-AS1	12.40349	1.074533187	0.0241	0.54
ENSG00000149591.16	TAGLN	9826.206	1.074143859	0.0077	0.4
ENSG00000157470.11	FAM81A	106.8847	1.073761174	0.0133	0.47
ENSG00000236829.9	Z97634.3	21.11718	1.073107741	0.017	0.5
ENSG00000225138.7	CTD-2228K2.7	132.5341	1.072014484	0.0083	0.41
ENSG00000130702.14	LAMA5	5057.356	1.071757387	0.0146	0.47
ENSG00000260949.1	KB-1836B5.1	11.70059	1.071624066	0.0313	0.58
ENSG00000235026.5	DPP10-AS1	8.091157	1.071406194	0.0256	0.55
ENSG00000178821.12	TMEM52	29.21685	1.070471451	0.0327	0.58
ENSG00000143194.12	MAEL	3.886135	1.070255564	0.0429	
ENSG00000205018.2	RP11-830F9.6	4.748206	1.070015845	0.0323	0.58
ENSG00000103449.11	SALL1	44.29728	1.069975835	0.0142	0.47
ENSG00000159251.6	ACTC1	1.546438	1.069731718	0.0297	
ENSG00000243137.7	PSG4	4.228171	1.069610853	0.0379	
ENSG00000232422.1	KNOP1P4	2.760598	1.069602609	0.0437	
ENSG00000197565.15	COL4A6	119.7478	1.069345574	0.0247	0.54
ENSG00000230411.1	OR3D1P	1.577792	1.068582702	0.0288	
ENSG00000259485.1	CTD-2147F2.1	7.832927	1.068298692	0.036	0.59
ENSG00000268864.4	CTB-167G5.6	2.366055	1.06734904	0.0412	
ENSG00000249275.1	RP11-364P22.2	2.670841	1.067276781	0.0439	
ENSG00000014257.15	ACPP	109.5033	1.066941256	0.0148	0.48
ENSG00000006047.12	YBX2	133.0039	1.066161926	0.0235	0.53
ENSG00000144596.12	GRIP2	27.45617	1.066051807	0.0106	0.44
ENSG00000267909.2	CCDC177	3.126463	1.065747363	0.0446	
ENSG00000261616.1	RP11-6O2.3	15.46711	1.064871891	0.0406	0.61
ENSG00000232176.1	RP11-146N23.1	7.547869	1.064423197	0.0299	0.58
ENSG00000261143.1	ADAMTS7P3	5.733698	1.062933937	0.0167	0.5
ENSG00000260977.1	RP11-333I13.1	11.0432	1.06255473	0.0186	0.51
ENSG00000254610.2	RP5-903G2.2	16.01334	1.062331391	0.0319	0.58
ENSG00000261342.1	AC006538.1	17.56275	1.061523618	0.0372	0.6
ENSG00000236017.8	ASMTL-AS1	26.25817	1.060826305	0.02	0.52
ENSG00000128965.11	CHAC1	66.05153	1.060762338	0.0099	0.43
ENSG00000135312.6	HTR1B	6.958607	1.060712584	0.0432	0.62
ENSG00000250891.1	CTD-2281M20.1	7.559429	1.060678052	0.0452	0.63
ENSG00000228594.3	FNDC10	220.6349	1.060504466	0.0111	0.44
ENSG00000082126.17	MPP4	8.0785	1.06005393	0.0045	0.35
ENSG00000231574.5	KCCAT211	21.99812	1.058719522	0.0457	0.63
ENSG00000279613.1	RP13-638C3.5	3.065622	1.056843375	0.0353	
ENSG00000112309.10	B3GAT2	9.446247	1.05665537	0.0399	0.61
ENSG00000279930.1	LA16c-312E8.4	18.27875	1.05656103	0.0452	0.63
ENSG00000151623.14	NR3C2	807.0701	1.056297662	0.0206	0.52
ENSG00000280195.1	XX-FW83563B9.5	43.96086	1.055915302	0.0002	0.15
ENSG00000168702.17	LRP1B	236.5543	1.055547482	0.0463	0.63
ENSG00000228918.3	LINC01344	17.77368	1.053985753	0.0471	0.63

ENSG00000244257.5	PKD1P1	85.949	1.052543316	0.0038	0.34
ENSG00000167680.15	SEMA6B	297.0131	1.052058717	0.0075	0.4
ENSG00000237818.1	RPS3AP29	7.044997	1.05172896	0.0394	0.61
ENSG00000250241.5	RP11-9G1.3	6.373558	1.051700533	0.0436	0.62
ENSG00000183378.11	OVCH2	4.937038	1.05041444	0.0466	0.63
ENSG00000188293.5	IGFL1	4.464588	1.048937656	0.045	
ENSG00000182676.4	PPP1R27	1.951508	1.047786783	0.0412	
ENSG00000281641.2	SAMD12-AS1	21.99359	1.047668203	0.0113	0.44
ENSG00000257194.2	RP11-567C2.1	1.553503	1.0474426	0.0482	
ENSG00000197558.11	SSPO	129.3368	1.047169475	0.0151	0.48
ENSG00000183570.16	PCBP3	30.0698	1.047123211	0.0185	0.51
ENSG00000232480.1	TGFB2-AS1	3.086025	1.046381849	0.0446	
ENSG00000065534.18	MYLK	4619.986	1.045639875	0.0041	0.35
ENSG00000243978.8	RGAG1	13.54273	1.045580336	0.0323	0.58
ENSG00000283538.1	RP11-180P8.1	3.168526	1.044739155	0.0487	
ENSG00000106113.18	CRHR2	1.859699	1.043954806	0.0483	
ENSG00000264963.2	RN7SL440P	4.642906	1.043623977	0.0265	
ENSG00000236269.1	ENO1-IT1	10.48417	1.043577614	0.022	0.52
ENSG00000267605.5	CTD-3220F14.1	84.87134	1.043365482	0.0013	0.25
ENSG00000180902.17	D2HGDH	533.2823	1.042717667	0.0014	0.25
ENSG00000279138.1	KB-1742H10.3	11.89786	1.042087005	0.0475	0.63
ENSG00000142233.11	NTN5	9.141252	1.042016365	0.0394	0.61
ENSG00000242612.6	DECR2	438.1005	1.041843096	0.0002	0.16
ENSG00000115255.10	REEP6	573.9524	1.039863925	0.0187	0.51
ENSG00000147206.16	NXF3	4.441981	1.039849904	0.0426	
ENSG00000142149.8	HUNK	293.1765	1.039440157	0.0307	0.58
ENSG00000071909.18	MYO3B	58.24992	1.03925449	0.0423	0.62
ENSG00000178404.9	CEP295NL	61.14811	1.039137559	0.0318	0.58
ENSG00000269356.1	RP11-120K24.4	11.14138	1.038549285	0.0472	0.63
ENSG00000104369.4	JPH1	447.704	1.038382527	0.0213	0.52
ENSG00000171388.11	APLN	199.4748	1.036849982	0.0066	0.4
ENSG00000064886.13	CHI3L2	652.0762	1.036386883	0.0434	0.62
ENSG00000171316.11	CHD7	5195.093	1.036206776	0.0167	0.5
ENSG00000265369.3	PCAT18	252.8185	1.03426902	0.0455	0.63
ENSG00000224886.2	RP11-119F19.4	18.28938	1.033821786	0.0105	0.44
ENSG00000149639.14	SOGA1	7379.15	1.03357422	0.0095	0.43
ENSG00000099364.16	FBXL19	980.9377	1.03320996	0.0019	0.28
ENSG00000277440.1	RP11-295D4.5	6.450003	1.032761189	0.0342	0.59
ENSG00000095587.8	TLL2	27.16445	1.032184203	0.0162	0.49
ENSG00000230838.1	LINC01614	245.9512	1.031847573	0.0149	0.48
ENSG00000180900.17	SCRIB	3215.439	1.031654075	0.005	0.36
ENSG00000178752.15	ERFE	7.129961	1.031205533	0.0264	0.56
ENSG00000274333.4	RP11-717F1.2	490.4234	1.029822084	0.0054	0.36
ENSG00000164929.16	BAALC	207.6101	1.028314768	0.0411	0.61
ENSG00000261093.1	CTD-3126B10.1	5.296101	1.028010941	0.0171	0.5
ENSG00000232679.1	RP11-400N13.3	32.87491	1.027162182	0.0492	0.63
ENSG00000249413.2	RP11-25H12.1	4.229327	1.026562366	0.0496	
ENSG00000177106.14	EPS8L2	2282.504	1.025837408	0.0008	0.23
ENSG00000144730.16	IL17RD	1867.097	1.025174541	0.0288	0.57

ENSG00000280119.1	AC093642.1	161.0767	1.024943247	0.0402	0.61
ENSG00000026036.21	RTEL1-TNFRSF6B	82.36922	1.024074941	0.0088	0.41
ENSG00000241547.1	ACTG1P20	14.00196	1.02318656	0.0171	0.5
ENSG00000137270.10	GCM1	6.003522	1.022942487	0.049	0.63
ENSG00000182185.18	RAD51B	589.183	1.022376402	0.0108	0.44
ENSG00000262663.1	RP11-497H17.1	8.064617	1.021929751	0.041	0.61
ENSG00000168427.8	KLHL30	7.098094	1.021592156	0.0215	0.52
ENSG00000140873.15	ADAMTS18	151.0366	1.021516758	0.0445	0.62
ENSG00000072163.19	LIMS2	150.728	1.020784277	0.0012	0.25
ENSG00000256116.1	RP11-783K16.14	11.65381	1.019902133	0.0162	0.49
ENSG00000224367.6	OACYLP	5.028356	1.018468931	0.0416	0.61
ENSG00000213347.10	MXD3	346.8041	1.018255446	0.0037	0.33
ENSG00000223704.1	LINC01422	39.51535	1.017313224	0.0165	0.5
ENSG00000278934.1	CTD-2006M22.2	13.28598	1.017192533	0.0245	0.54
ENSG00000007174.17	DNAH9	3.872812	1.017182327	0.0471	
ENSG00000261659.2	LA16c-313D11.12	72.66948	1.016410427	0.0063	0.39
ENSG00000230650.1	AC112229.1	51.66141	1.015965468	0.0369	0.59
ENSG00000107281.9	NPDC1	1615.807	1.015330972	0.0107	0.44
ENSG00000185760.15	KCNQ5	179.6946	1.015305959	0.0371	0.6
ENSG00000261888.1	AC144831.1	24.42615	1.015090592	0.0271	0.56
ENSG00000239704.10	CDRT4	17.20896	1.014229001	0.0371	0.6
ENSG00000280402.1	RP11-20I23.10	9.963088	1.014058733	0.0392	0.6
ENSG00000238045.9	AC009133.12	34.84287	1.013070164	0.0106	0.44
ENSG00000244480.1	AC005154.7	14.47768	1.012904289	0.01	0.43
ENSG00000105664.10	COMP	2619.455	1.012860391	0.0318	0.58
ENSG00000255240.5	RP11-142C4.6	77.35861	1.012600972	0.0375	0.6
ENSG00000127586.16	CHTF18	586.9548	1.011792389	0.0072	0.4
ENSG00000183458.13	RP11-958N24.1	777.4681	1.011661563	0.0042	0.35
ENSG00000278903.3	CH507-145C22.1	75.38039	1.011124775	0.0081	0.41
ENSG00000230267.7	HERC2P4	46.75976	1.01057055	0.0377	0.6
ENSG00000142408.3	CACNG8	11.13763	1.010287675	0.0406	0.61
ENSG00000204442.3	FAM155A	83.27037	1.009213752	0.0407	0.61
ENSG00000278997.1	RP11-131M11.2	15.68529	1.007931352	0.0059	0.38
ENSG00000189320.8	FAM180A	140.5851	1.005149484	0.0251	0.54
ENSG00000104427.11	ZC2HC1A	977.2421	1.004365492	0.0146	0.47
ENSG00000217275.2	RP1-34B20.4	56.62284	1.004167242	0.047	0.63
ENSG00000274272.1	RP11-44M6.7	34.91743	1.003474144	0.0114	0.44
ENSG00000197562.9	RAB40C	897.8078	1.002504083	0.0015	0.25
ENSG00000242419.5	PCDHGC4	27.9542	1.002111449	0.0131	0.47
ENSG00000103326.11	CAPN15	1134.204	1.001576622	0.0043	0.35
ENSG00000164877.18	MICALL2	643.6163	1.001565294	0.0083	0.41
ENSG00000095713.13	CRTAC1	29.81263	1.00128344	0.0454	0.63
ENSG00000205746.9	RP11-1212A22.1	142.6339	1.001051868	0.0104	0.44
ENSG00000143452.15	HORMAD1	18.46789	1.000944519	0.0114	0.44
ENSG00000237161.4	RP11-32B5.1	33.26006	1.000387377	0.0249	0.54

Table S3. Down-regulated genes in bone metastasis group compared to control by DEG analysis

	Gene	baseMean	log$_2$FoldChange	*P*-value	Adjusted *P*-value
ENSG00000197046.11	SIGLEC15	269.7394	-2.461130924	1E-06	0.01
ENSG00000144891.17	AGTR1	1784.142	-2.438374538	4E-06	0.02
ENSG00000077522.12	ACTN2	68.44627	-2.203559041	3E-05	0.06
ENSG00000169760.17	NLGN1	193.7407	-2.079829912	9E-05	0.1
ENSG00000143369.14	ECM1	5661.309	-2.042139254	6E-05	0.08
ENSG00000170956.16	CEACAM3	10.68951	-2.00023343	8E-05	0.1
ENSG00000157150.4	TIMP4	51.98775	-1.957100268	3E-05	0.06
ENSG00000122145.14	TBX22	2.18445	-1.946962933	0.0002	
ENSG00000182885.16	ADGRG3	29.71701	-1.895495744	0.0003	0.16
ENSG00000211459.2	MT-RNR1	19135.47	-1.893637148	6E-05	0.08
ENSG00000251141.5	RP11-53O19.1	154.8029	-1.87620856	0.0001	0.12
ENSG00000267259.1	CTD-2008P7.9	173.0711	-1.856430949	0.0001	0.12
ENSG00000262902.1	MTCO1P40	48.7523	-1.852597867	0.0004	0.19
ENSG00000166415.14	WDR72	110.9155	-1.838914938	0.0005	0.19
ENSG00000163464.7	CXCR1	30.63731	-1.836584456	0.0005	0.19
ENSG00000164742.14	ADCY1	1765.658	-1.832062779	0.0004	0.19
ENSG00000180871.7	CXCR2	43.45797	-1.800440438	0.0004	0.19
ENSG00000119508.17	NR4A3	806.037	-1.79075605	0.0002	0.15
ENSG00000175920.15	DOK7	151.067	-1.788152032	0.0005	0.19
ENSG00000145832.12	SLC25A48	79.4811	-1.743062993	0.001	0.25
ENSG00000249574.1	AC226118.1	13.05003	-1.733437169	0.0008	0.23
ENSG00000117322.16	CR2	66.41054	-1.718883051	0.0009	0.23
ENSG00000250337.5	LINC01021	7.893234	-1.70095407	0.0014	0.25
ENSG00000175697.10	GPR156	108.8864	-1.684058489	0.0012	0.25
ENSG00000269028.3	MTRNR2L12	136.9896	-1.67954279	0.0002	0.15
ENSG00000114115.9	RBP1	862.7017	-1.667074277	0.0004	0.19
ENSG00000187045.16	TMPRSS6	93.91109	-1.666371359	0.0014	0.25
ENSG00000144908.13	ALDH1L1	84.3225	-1.660258046	0.0013	0.25
ENSG00000187912.11	CLEC17A	16.85302	-1.647130639	0.0008	0.23
ENSG00000144331.18	ZNF385B	142.35	-1.639415498	0.0012	0.25
ENSG00000249203.1	RP11-473L15.3	27.07397	-1.633792945	0.0016	0.26
ENSG00000250329.1	KDELC1P1	54.39017	-1.62891369	2E-05	0.06
ENSG00000171557.16	FGG	23.89121	-1.626025179	0.0017	0.27
ENSG00000107165.12	TYRP1	32.00633	-1.624747822	0.0021	0.29
ENSG00000104921.14	FCER2	6.33189	-1.623036298	0.0019	0.28
ENSG00000272405.1	RP11-284F21.10	176.0519	-1.6168553	0.0023	0.29
ENSG00000113739.10	STC2	5813.296	-1.612871117	0.0012	0.25
ENSG00000089199.9	CHGB	100.4333	-1.611560668	0.0017	0.26
ENSG00000175352.10	NRIP3	682.5293	-1.609740476	0.0008	0.23
ENSG00000127241.16	MASP1	24.62433	-1.607872191	0.0025	0.3
ENSG00000159712.10	ANKRD18CP	33.79838	-1.598353062	0.0021	0.29
ENSG00000227531.1	RP11-202G18.1	4.367853	-1.584168686	0.0028	
ENSG00000164619.8	BMPER	79.33456	-1.583934311	0.0014	0.25
ENSG00000153234.13	NR4A2	889.318	-1.582763351	7E-05	0.09
ENSG00000189221.9	MAOA	636.6987	-1.582602412	0.0003	0.19
ENSG00000143502.14	SUSD4	1157.125	-1.577470101	0.0005	0.19
ENSG00000225472.1	RP11-120J1.1	15.93184	-1.575606383	0.003	0.33

ENSG00000139547.7	RDH16	120.9626	-1.573308736	0.0016	0.26
ENSG00000262406.2	MMP12	233.1482	-1.565513112	0.0022	0.29
ENSG00000262119.1	RP11-483C6.1	78.2447	-1.558208825	0.0015	0.25
ENSG00000269416.5	LINC01224	4.374415	-1.546891041	0.0033	
ENSG00000196604.12	POTEF	296.424	-1.545685467	0.0011	0.25
ENSG00000119866.20	BCL11A	500.6693	-1.541973932	0.0023	0.3
ENSG00000269984.1	RP11-362K14.5	3.300505	-1.540543992	0.0029	
ENSG00000188573.7	FBLL1	25.18135	-1.536760153	0.0035	0.33
ENSG00000235438.7	ESRRAP2	5.317674	-1.528532563	0.0019	0.28
ENSG00000180178.10	FAR2P1	159.9476	-1.525837487	0.0023	0.29
ENSG00000198178.10	CLEC4C	17.08568	-1.488863501	0.0042	0.35
ENSG00000230489.1	VAV3-AS1	3.869846	-1.488537975	0.005	
ENSG00000239402.3	CYP4F62P	6.495477	-1.488081118	0.005	0.36
ENSG00000176697.18	BDNF	20.69506	-1.488038613	0.0049	0.36
ENSG00000007908.15	SELE	284.0767	-1.48774094	0.0021	0.29
ENSG00000166920.11	C15orf48	994.0358	-1.478975738	0.0016	0.26
ENSG00000259723.1	RP5-823G15.5	8.901287	-1.478581091	0.0021	0.29
ENSG00000263826.1	RP11-573D15.9	13.06848	-1.478471164	0.0016	0.26
ENSG00000211950.2	IGHV1-24	154.3414	-1.475265664	0.0052	0.36
ENSG00000226380.8	MIR29A	429.4883	-1.467502052	0.0003	0.16
ENSG00000196932.11	TMEM26	751.6708	-1.463273923	0.0032	0.33
ENSG00000073756.11	PTGS2	278.895	-1.461735667	0.0026	0.31
ENSG00000166509.10	CLEC3A	721.6858	-1.45911101	0.0059	0.38
ENSG00000226051.6	ZNF503-AS1	7.751871	-1.457271431	0.006	0.39
ENSG00000146476.10	ARMT1	6433.239	-1.44726766	0.0012	0.25
ENSG00000164796.17	CSMD3	20.9388	-1.442837468	0.0066	0.4
ENSG00000167676.4	PLIN4	1101.106	-1.439242948	0.0044	0.35
ENSG00000236525.1	AC007278.2	4.091148	-1.435983982	0.0055	
ENSG00000151364.16	KCTD14	113.8503	-1.41975616	0.0029	0.32
ENSG00000124171.8	PARD6B	5407.39	-1.413593037	0.0017	0.26
ENSG00000106013.14	ANKRD7	9.094627	-1.413059568	0.0036	0.33
ENSG00000203279.3	RP11-498P14.5	9.089607	-1.404664725	0.0057	0.37
ENSG00000253187.2	HOXA10-AS	17.53335	-1.403744491	0.0031	0.33
ENSG00000132832.10	LINC01260	2.681145	-1.403493035	0.0056	
ENSG00000008056.12	SYN1	15.10761	-1.397483359	0.0068	0.4
ENSG00000106484.14	MEST	3149.257	-1.396019338	0.003	0.33
ENSG00000244211.3	PDZK1P1	10.09808	-1.394102058	0.0083	0.41
ENSG00000173175.14	ADCY5	563.8546	-1.391035782	0.0075	0.4
ENSG00000279923.1	CTD-2008E3.1	8.754708	-1.390962235	0.0005	0.19
ENSG00000159212.12	CLIC6	230.4603	-1.390578094	0.0046	0.35
ENSG00000153064.11	BANK1	219.4327	-1.390372254	0.0043	0.35
ENSG00000136244.11	IL6	76.21202	-1.381480019	0.0061	0.39
ENSG00000254349.5	MIR2052HG	8.832048	-1.379119432	0.0094	0.43
ENSG00000266903.1	CTB-171A8.1	19.1571	-1.368408317	0.0049	0.36
ENSG00000050628.20	PTGER3	1235.74	-1.367255988	0.0019	0.28
ENSG00000108176.14	DNAJC12	2133.935	-1.359842476	0.0079	0.4
ENSG00000101425.12	BPI	11.14099	-1.357089205	0.0043	0.35
ENSG00000124721.17	DNAH8	27.55096	-1.35483373	0.008	0.41
ENSG00000211689.7	TRGC1	78.42511	-1.349220844	0.0052	0.36

ENSG00000250490.1	FLJ33360	6.319569	-1.348831224	0.0044	0.35
ENSG00000171757.15	LRRC34	65.40633	-1.344117128	0.0028	0.32
ENSG00000203497.2	PDCD4-AS1	28.37984	-1.343248851	0.0014	0.25
ENSG00000250230.2	RP11-855O10.2	7.415065	-1.342311258	0.0102	0.44
ENSG00000187595.15	ZNF385C	44.33474	-1.341048063	0.0018	0.27
ENSG00000273175.1	RP11-11N7.4	2.612801	-1.340299281	0.0115	
ENSG00000237407.1	KB-1183D5.14	1.669363	-1.337819862	0.011	
ENSG00000165449.11	SLC16A9	250.1551	-1.334972432	0.008	0.4
ENSG00000275291.1	U1	6.968553	-1.334561043	0.0115	0.44
ENSG00000137648.17	TMPRSS4	209.2098	-1.333437872	0.0102	0.44
ENSG00000259920.1	RP11-2E11.5	2.6924	-1.332807815	0.0112	
ENSG00000263426.2	RN7SL471P	341.0194	-1.332217375	0.0074	0.4
ENSG00000233327.10	USP32P2	21.85051	-1.331374581	0.001	0.25
ENSG00000259600.2	RP11-925D8.3	4.676088	-1.328908272	0.0123	
ENSG00000201183.1	RNVU1-3	4.398578	-1.326000686	0.0105	
ENSG00000187475.5	HIST1H1T	43.8159	-1.325842083	0.0036	0.33
ENSG00000125245.12	GPR18	37.97747	-1.325833907	0.0079	0.4
ENSG00000069482.6	GAL	32.84228	-1.32435023	0.0107	0.44
ENSG00000204049.1	RP11-126H7.4	60.75929	-1.322466264	0.0079	0.4
ENSG00000115590.13	IL1R2	33.48461	-1.320185401	0.0049	0.36
ENSG00000156738.17	MS4A1	404.1017	-1.318600326	0.0111	0.44
ENSG00000081985.10	IL12RB2	152.9195	-1.318593458	0.0068	0.4
ENSG00000137948.18	BRDT	10.02528	-1.314952802	0.0096	0.43
ENSG00000273210.1	AP001437.1	4.637409	-1.31389233	0.0107	
ENSG00000105613.9	MAST1	37.09433	-1.306879574	0.0097	0.43
ENSG00000221562.1	RNU6ATAC10P	6.049849	-1.306471061	0.0035	0.33
ENSG00000229953.1	RP11-284F21.7	22.34536	-1.306333354	0.0138	0.47
ENSG00000163221.8	S100A12	5.393335	-1.305189415	0.0139	0.47
ENSG00000272767.1	JMJD1C-AS1	24.60742	-1.304322248	0.0004	0.19
ENSG00000269486.2	CTC-360G5.9	21.48466	-1.303293881	0.0031	0.33
ENSG00000154479.12	CCDC173	24.06287	-1.295874876	0.0072	0.4
ENSG00000261575.2	RP11-259G18.1	7.1953	-1.291724197	0.0113	0.44
ENSG00000110675.12	ELMOD1	20.49552	-1.291080443	0.0142	0.47
ENSG00000134962.6	KLB	47.32772	-1.289088913	0.0051	0.36
ENSG00000114771.13	AADAC	1.147092	-1.284923927	0.0141	
ENSG00000132872.11	SYT4	15.03527	-1.283388225	0.0125	0.46
ENSG00000133488.14	SEC14L4	2.178626	-1.279766902	0.0149	
ENSG00000108852.14	MPP2	258.1987	-1.279156672	0.0055	0.37
ENSG00000121454.5	LHX4	7.088394	-1.278698413	0.0093	0.43
ENSG00000105509.10	HAS1	25.55688	-1.278508555	0.0152	0.48
ENSG00000280060.1	RP11-5G9.6	37.82871	-1.277626147	2E-06	0.01
ENSG00000100095.18	SEZ6L	77.93519	-1.271375976	0.0141	0.47
ENSG00000171049.8	FPR2	48.76788	-1.267528963	0.0087	0.41
ENSG00000132677.12	RHBG	16.62952	-1.266348661	0.0098	0.43
ENSG00000118432.12	CNR1	85.15734	-1.264997309	0.0113	0.44
ENSG00000188211.8	NCR3LG1	441.9721	-1.263922206	0.0074	0.4
ENSG00000175877.3	WBSCR28	3.342518	-1.262068038	0.0168	
ENSG00000134548.9	SPX	13.19038	-1.259721907	0.014	0.47
ENSG00000234699.1	RP11-225H22.4	4.246563	-1.257175036	0.0143	

ENSG00000100453.12	GZMB	103.1001	-1.255899092	0.0122	0.46
ENSG00000078596.10	ITM2A	1336.127	-1.255866425	0.0064	0.4
ENSG00000204682.5	CASC10	41.62743	-1.25369954	0.0046	0.35
ENSG00000279236.1	RP11-120K19.3	24.49024	-1.252802666	0.0004	0.19
ENSG00000248323.5	LUCAT1	34.44219	-1.25249429	0.0148	0.48
ENSG00000211959.2	IGHV4-39	501.7384	-1.251378682	0.0142	0.47
ENSG00000144040.12	SFXN5	951.4813	-1.250892413	0.0005	0.19
ENSG00000275126.1	HIST1H4L	352.6581	-1.250574213	0.0114	0.44
ENSG00000163421.8	PROK2	1.749192	-1.250085803	0.0167	
ENSG00000003989.16	SLC7A2	12007.33	-1.249720051	0.0138	0.47
ENSG00000108759.3	KRT32	9.181997	-1.248928293	0.0174	0.51
ENSG00000276842.1	RP11-713N11.6	3.082667	-1.247729208	0.0146	
ENSG00000248050.1	RP11-422N16.3	4.217568	-1.242776051	0.0173	
ENSG00000279733.1	RP11-685B24.1	9.257721	-1.239441726	0.0116	0.45
ENSG00000176928.5	GCNT4	239.3617	-1.235160427	0.0089	0.42
ENSG00000279075.1	RP11-480D4.7	4.089957	-1.234877134	0.0197	
ENSG00000275720.1	CTB-75G16.3	4.203019	-1.234355934	0.0131	
ENSG00000146038.11	DCDC2	198.8448	-1.232847964	0.0189	0.51
ENSG00000261334.1	RP11-65J3.14	6.314285	-1.232561009	0.0086	0.41
ENSG00000004846.16	ABCB5	55.31754	-1.232062132	0.0197	0.52
ENSG00000179915.22	NRXN1	33.41781	-1.229841499	0.0113	0.44
ENSG00000100721.10	TCL1A	24.4764	-1.229677283	0.0185	0.51
ENSG00000165186.10	PTCHD1	138.2852	-1.228662793	0.0184	0.51
ENSG00000006128.11	TAC1	40.23885	-1.228187096	0.0207	0.52
ENSG00000115556.13	PLCD4	255.5051	-1.226051204	0.0127	0.47
ENSG00000251149.1	MTND5P5	2.084147	-1.225743512	0.0196	
ENSG00000184068.2	RP5-821D11.7	8.244342	-1.224817536	0.0051	0.36
ENSG00000151834.15	GABRA2	5.42916	-1.223574063	0.0206	0.52
ENSG00000175426.10	PCSK1	46.55527	-1.220441987	0.0128	0.47
ENSG00000130988.12	RGN	35.60825	-1.220008572	0.0184	0.51
ENSG00000231419.6	LINC00689	13.87675	-1.21752041	0.0154	0.48
ENSG00000210082.2	MT-RNR2	60918.69	-1.215333629	0.0031	0.33
ENSG00000186281.12	GPAT2	69.22544	-1.212003973	0.0076	0.4
ENSG00000144130.11	NT5DC4	2.550498	-1.209788154	0.0226	
ENSG00000186431.18	FCAR	31.4803	-1.208875138	0.0138	0.47
ENSG00000172139.14	SLC9C1	9.586948	-1.208627471	0.01	0.43
ENSG00000234184.5	RP5-887A10.1	4.967833	-1.208529062	0.0219	0.52
ENSG00000174827.13	PDZK1	187.9649	-1.208141742	0.0209	0.52
ENSG00000122679.8	RAMP3	483.4346	-1.206340621	0.0046	0.35
ENSG00000256870.2	SLC5A8	24.13361	-1.205812518	0.0203	0.52
ENSG00000269933.1	RP3-333A15.2	12.43795	-1.204228627	0.0194	0.51
ENSG00000187867.8	PALM3	17.74131	-1.203248363	0.0083	0.41
ENSG00000141469.16	SLC14A1	43.89749	-1.202844059	0.0065	0.4
ENSG00000196565.12	HBG2	3.541872	-1.201644435	0.0229	
ENSG00000273363.1	RP11-285G1.14	8.307958	-1.198188157	0.002	0.28
ENSG00000188916.8	FAM196A	129.6019	-1.196190863	0.0193	0.51
ENSG00000272417.1	CTD-219904.6	10.45159	-1.195660172	0.0103	0.44
ENSG00000198576.3	ARC	44.99967	-1.193088893	0.0181	0.51
ENSG00000111713.2	GYS2	2.406517	-1.192213573	0.0222	

ENSG00000226777.7	KIAA0125	101.0609	-1.191914615	0.0216	0.52
ENSG00000255521.1	RP4-607I7.1	12.09411	-1.190964731	0.0211	0.52
ENSG00000197385.5	ZNF860	394.5694	-1.190768944	0.0033	0.33
ENSG00000249159.6	RP11-480D4.2	2.514167	-1.189565612	0.0236	
ENSG00000109424.3	UCP1	7.366865	-1.188147275	0.018	0.51
ENSG00000143473.11	KCNH1	164.2738	-1.188022035	0.0213	0.52
ENSG00000112232.8	KHDRBS2	9.895111	-1.187503358	0.0232	0.53
ENSG00000207205.1	RNVU1-15	59.47069	-1.187481857	0.0128	0.47
ENSG00000275569.1	RP11-930O11.3	2.7506	-1.185656681	0.0229	
ENSG00000227191.8	TRGC2	117.5007	-1.1831828	0.0111	0.44
ENSG00000211829.8	TRDC	78.11936	-1.183045	0.0155	0.48
ENSG00000207370.1	Y_RNA	1.518596	-1.181856319	0.0259	
ENSG00000283511.1	RP11-456N14.6	1.760889	-1.180613107	0.0213	
ENSG00000154864.11	PIEZO2	1831.723	-1.179392025	0.0139	0.47
ENSG00000233013.8	FAM157B	9.963739	-1.17844292	0.011	0.44
ENSG00000245954.6	RP11-18H21.1	11.51967	-1.177190757	0.0216	0.52
ENSG00000100285.9	NEFH	81.28392	-1.176539542	0.0156	0.48
ENSG00000271584.2	RP11-89C3.4	4.693992	-1.175475522	0.0268	
ENSG00000274618.1	HIST1H4F	216.7591	-1.175373708	0.0069	0.4
ENSG00000273733.1	CTC-510F12.7	2.872383	-1.174922787	0.0218	
ENSG00000118849.9	RARRES1	1673.597	-1.173440211	0.0192	0.51
ENSG00000260100.1	RP11-220I1.5	1.791496	-1.172788345	0.0269	
ENSG00000197705.9	KLHL14	22.51257	-1.172465756	0.0175	0.51
ENSG00000206172.8	HBA1	183.6335	-1.170256703	0.0148	0.48
ENSG00000131355.14	ADGRE3	14.28154	-1.166700521	0.0272	0.56
ENSG00000248494.1	LNX1-AS2	5.855261	-1.166483123	0.0167	0.5
ENSG00000234503.1	KB-1592A4.14	6.011148	-1.163914958	0.0282	0.56
ENSG00000072657.8	TRHDE	17.10576	-1.16309583	0.0208	0.52
ENSG00000141314.12	RHBDL3	42.5001	-1.162365184	0.0173	0.51
ENSG00000065325.12	GLP2R	3.406129	-1.158856931	0.029	
ENSG00000173404.4	INSM1	23.35817	-1.157588613	0.0279	0.56
ENSG00000170382.11	LRRN2	562.2848	-1.154259945	0.0108	0.44
ENSG00000214814.7	FER1L6	10.01012	-1.15240016	0.0165	0.5
ENSG00000251665.1	RP11-700H6.2	2.019563	-1.151902308	0.0299	
ENSG00000163534.14	FCRL1	41.03056	-1.151049225	0.0281	0.56
ENSG00000134545.13	KLRC1	38.23652	-1.149372571	0.0121	0.45
ENSG00000120322.3	PCDHB8	93.61015	-1.148565214	0.0151	0.48
ENSG00000269404.6	SPIB	51.41031	-1.142529578	0.0243	0.54
ENSG00000123689.5	G0S2	304.8695	-1.139951201	0.0087	0.41
ENSG00000105996.6	HOXA2	12.5295	-1.137544376	0.0288	0.57
ENSG00000100302.6	RASD2	212.1627	-1.137010535	0.022	0.52
ENSG00000163536.12	SERPINI1	696.0607	-1.136754045	0.0171	0.5
ENSG00000278099.1	U1	2.997861	-1.135364112	0.0319	
ENSG00000277511.1	CTD-2095E4.5	10.25184	-1.135127441	0.0035	0.33
ENSG00000156510.12	HKDC1	7.783661	-1.134389736	0.0298	0.58
ENSG00000188833.9	ENTPD8	56.48165	-1.134288729	0.0271	0.56
ENSG00000101441.4	CST4	16.22688	-1.133602589	0.0323	0.58
ENSG00000147394.18	ZNF185	832.5762	-1.127955046	0.0011	0.25
ENSG00000183908.5	LRRC55	51.18032	-1.126981998	0.0247	0.54

ENSG00000104833.11	TUBB4A	99.5388	-1.126776627	0.0304	0.58
ENSG00000204970.9	PCDHA1	3.42195	-1.125960406	0.0337	
ENSG00000136011.14	STAB2	48.13814	-1.125118604	0.0334	0.59
ENSG00000211972.2	IGHV3-66	83.32201	-1.123328056	0.0317	0.58
ENSG00000203907.9	OOEP	0.971298	-1.12259313	0.0274	
ENSG00000148734.7	NPFFR1	20.21401	-1.121520846	0.0315	0.58
ENSG00000107968.9	MAP3K8	1375.094	-1.119878872	0.0042	0.35
ENSG00000054598.6	FOXC1	229.696	-1.118247394	0.0074	0.4
ENSG00000215417.11	MIR17HG	410.5629	-1.117881803	0.014	0.47
ENSG00000266258.1	RP11-41O4.1	12.93294	-1.115078014	0.0105	0.44
ENSG00000132026.13	RTBDN	4.481682	-1.113998357	0.0358	
ENSG00000279341.1	RP11-720D4.2	1.508532	-1.113102154	0.0329	
ENSG00000248553.1	OR52H2P	5.130319	-1.112137628	0.0324	0.58
ENSG00000210678.1	RNU6ATAC2P	17.65548	-1.111408158	0.0047	0.35
ENSG00000139910.19	NOVA1	590.8164	-1.110979976	0.0247	0.54
ENSG00000112137.17	PHACTR1	451.2505	-1.110690771	0.0005	0.19
ENSG00000249082.2	C5orf66-AS1	7.067412	-1.107621814	0.034	0.59
ENSG00000170927.14	PKHD1	24.45352	-1.106499531	0.0278	0.56
ENSG00000187889.12	C1orf168	141.6495	-1.10591079	0.0276	0.56
ENSG00000211452.10	DIO1	287.7945	-1.102741056	0.0378	0.6
ENSG00000154898.15	CCDC144CP	309.7954	-1.102364978	0.0064	0.4
ENSG00000271856.1	LINC01215	12.87988	-1.101016439	0.0268	0.56
ENSG00000243836.5	WDR86-AS1	14.30222	-1.098304629	0.0271	0.56
ENSG00000204539.3	CDSN	35.58856	-1.097949201	0.0379	0.6
ENSG00000279928.1	FO538757.2	2.161664	-1.09710558	0.0338	
ENSG00000236601.2	RP4-669L17.2	4.203829	-1.096992261	0.0386	
ENSG00000162878.12	PKDCC	221.9124	-1.096302659	0.0044	0.35
ENSG00000173535.13	TNFRSF10C	76.36996	-1.096271299	0.0076	0.4
ENSG00000169429.10	CXCL8	479.1539	-1.095628401	0.025	0.54
ENSG00000260302.1	RP11-973H7.1	2.973423	-1.095247777	0.0391	
ENSG00000143185.3	XCL2	19.9334	-1.094208757	0.0347	0.59
ENSG00000120093.11	HOXB3	606.5976	-1.093746433	0.0277	0.56
ENSG00000128383.12	APOBEC3A	105.645	-1.093172447	0.018	0.51
ENSG00000116260.16	QSOX1	7209.21	-1.092567584	0.0029	0.32
ENSG00000215859.8	RP6-74O6.2	7.042003	-1.090009491	0.0328	0.58
ENSG00000250444.1	CCT5P1	3.014674	-1.089023756	0.0208	
ENSG00000070526.14	ST6GALNAC1	32.15961	-1.086371613	0.033	0.58
ENSG00000151948.11	GLT1D1	18.08216	-1.085160134	0.0319	0.58
ENSG00000279717.1	LLNLF-158E9.1	4.046352	-1.085120759	0.0379	
ENSG00000132185.16	FCRLA	42.27738	-1.084684461	0.0363	0.59
ENSG00000277301.1	RP5-1184F4.7	4.86758	-1.084340808	0.0273	0.56
ENSG00000007038.10	PRSS21	55.09459	-1.084045651	0.0399	0.61
ENSG00000166823.5	MESP1	56.84104	-1.083929402	0.0289	0.57
ENSG00000251363.2	RP11-129M6.1	4.417581	-1.083861101	0.0236	
ENSG00000272701.2	MESTIT1	7.13075	-1.083206875	0.0316	0.58
ENSG00000196684.12	HSH2D	437.5323	-1.082960552	0.0102	0.44
ENSG00000214626.2	POLR3DP1	13.64346	-1.082840856	0.0106	0.44
ENSG00000241351.3	IGKV3-11	883.0757	-1.082495994	0.036	0.59
ENSG00000260578.1	CTD-2541J13.1	27.84569	-1.080590817	0.0203	0.52

ENSG00000248476.1	BACH1-IT1	25.79597	-1.07987496	0.0015	0.25
ENSG00000274292.1	RP11-347I19.7	22.46234	-1.079224373	0.0036	0.33
ENSG00000168004.9	HRASLS5	293.7191	-1.079047661	0.0415	0.61
ENSG00000186998.15	EMID1	150.1095	-1.078808093	0.0179	0.51
ENSG00000163749.17	CCDC158	98.14068	-1.078191424	0.0392	0.6
ENSG00000276174.1	RP11-687E1.2	9.359843	-1.075648463	0.007	0.4
ENSG00000259651.2	MTCO3P23	1.379859	-1.07471756	0.0287	
ENSG00000229278.1	RP11-483F11.7	3.29845	-1.074514093	0.0373	
ENSG00000227684.2	CROCCP4	2.058132	-1.073476322	0.0426	
ENSG00000155906.16	RMND1	1600.289	-1.072462165	0.0083	0.41
ENSG00000156298.12	TSPAN7	158.4532	-1.072087603	0.0193	0.51
ENSG00000233907.1	FLJ31662	5.736492	-1.071868007	0.0363	0.59
ENSG00000138166.5	DUSP5	2008.183	-1.071457958	0.0052	0.36
ENSG00000275322.1	RP11-262A16.1	9.303389	-1.070407763	0.016	0.49
ENSG00000230002.2	ALMS1-IT1	67.37082	-1.070188502	0.0012	0.25
ENSG00000188404.8	SELL	584.6571	-1.069107141	0.0186	0.51
ENSG00000276573.1	RP11-128N14.5	3.93711	-1.067512008	0.0303	
ENSG00000264269.1	RP11-15F12.1	4.028302	-1.067320037	0.0442	
ENSG00000073464.11	CLCN4	246.113	-1.067151962	0.0245	0.54
ENSG00000211787.1	TRAV8-3	5.335642	-1.066961295	0.039	0.6
ENSG00000232811.1	RP11-96K19.2	2.988065	-1.066288563	0.0442	
ENSG00000236296.7	GUSBP5	26.41095	-1.066025517	0.0085	0.41
ENSG00000274274.1	GAGE13	1.97138	-1.062595648	0.0251	
ENSG00000158270.11	COLEC12	3219.625	-1.062490311	0.0242	0.54
ENSG00000116194.12	ANGPTL1	159.1273	-1.061344336	0.0163	0.49
ENSG00000253649.3	PRSS51	7.359974	-1.061037487	0.0409	0.61
ENSG00000164509.13	IL31RA	3.731321	-1.060680401	0.0424	
ENSG00000224614.1	TNK2-AS1	7.778737	-1.05936197	0.0187	0.51
ENSG00000163687.13	DNASE1L3	23.20167	-1.058913886	0.0117	0.45
ENSG00000185933.6	CALHM1	5.714549	-1.057310002	0.0419	0.61
ENSG00000204969.6	PCDHA2	12.82143	-1.056388875	0.0419	0.61
ENSG00000211804.3	TRDV1	9.417754	-1.055379976	0.0468	0.63
ENSG00000272087.1	RP11-379F4.7	12.49961	-1.054828693	0.0378	0.6
ENSG00000174473.15	GALNTL6	21.78703	-1.054149074	0.02	0.52
ENSG00000111405.8	ENDOU	9.38194	-1.053486207	0.0429	0.62
ENSG00000271119.1	CTD-2012J19.3	2.626738	-1.053253851	0.0472	
ENSG00000254164.1	CTB-33O18.2	7.004251	-1.050325422	0.0318	0.58
ENSG00000012223.12	LTF	11636.18	-1.050129509	0.0469	0.63
ENSG00000279885.1	RP11-637N19.1	36.89051	-1.049074261	0.0338	0.59
ENSG00000270069.1	MIR222HG	185.128	-1.046701395	0.0208	0.52
ENSG00000125538.11	IL1B	193.7951	-1.045867844	0.0202	0.52
ENSG00000226835.2	RP11-148B18.1	11.71108	-1.045839424	0.0464	0.63
ENSG00000267365.1	KCNJ2-AS1	9.657278	-1.045124138	0.0218	0.52
ENSG00000275485.1	RP11-261P13.6	5.412578	-1.044920941	0.0367	0.59
ENSG00000123892.11	RAB38	345.4488	-1.043898277	0.0218	0.52
ENSG00000199933.1	RNY1P16	2.689036	-1.041221693	0.0454	
ENSG00000175287.18	PHYHD1	347.8924	-1.040356907	0.0368	0.59
ENSG00000164237.8	CMBL	2065.878	-1.040069506	0.0228	0.53
ENSG00000222724.1	RNU2-63P	39.7742	-1.039530398	0.0367	0.59

ENSG00000009709.11	PAX7	193.79	-1.039476005	0.0348	0.59
ENSG00000147724.11	FAM135B	74.72237	-1.038317353	0.0485	0.63
ENSG00000174514.12	MFSD4A	62.18784	-1.037274031	0.0104	0.44
ENSG00000105997.22	HOXA3	57.36237	-1.034267163	0.0373	0.6
ENSG00000268734.1	CTB-61M7.2	5.150367	-1.032735211	0.05	0.64
ENSG00000260196.1	RP1-239B22.5	42.71027	-1.032119563	0.0369	0.59
ENSG00000240853.3	RN7SL328P	3.615681	-1.03132108	0.0469	
ENSG00000130413.15	STK33	18.46786	-1.030790372	0.0227	0.53
ENSG00000150627.15	WDR17	273.9877	-1.030641771	0.0389	0.6
ENSG00000221676.1	RNU6ATAC	263.9793	-1.030622247	0.0007	0.22
ENSG00000276116.2	FUT8-AS1	65.00139	-1.028633139	0.0134	0.47
ENSG00000197584.11	KCNMB2	3.049933	-1.028342076	0.0453	
ENSG00000170961.6	HAS2	350.2995	-1.02755231	0.0219	0.52
ENSG00000273338.1	RP11-386I14.4	27.19779	-1.025314428	0.0304	0.58
ENSG00000211794.3	TRAV12-3	14.30893	-1.025245575	0.0403	0.61
ENSG00000169908.11	TM4SF1	12915.08	-1.024671472	0.0338	0.59
ENSG00000141293.15	SKAP1	275.8741	-1.024479468	0.0143	0.47
ENSG00000162620.15	LRRIQ3	117.7624	-1.024393682	0.0118	0.45
ENSG00000206828.1	U1	14.81506	-1.023521802	0.0121	0.45
ENSG00000207313.1	SNORA2B	25.65292	-1.022874533	0.0055	0.37
ENSG00000197992.6	CLEC9A	17.395	-1.021748929	0.0351	0.59
ENSG00000280587.1	LINC01348	47.00743	-1.02094448	0.0373	0.6
ENSG00000130487.5	KLHDC7B	86.9262	-1.01868994	0.0367	0.59
ENSG00000080007.7	DDX43	17.55328	-1.018299537	0.0351	0.59
ENSG00000271778.1	RP11-379F4.8	14.05509	-1.017596607	0.0283	0.56
ENSG00000250111.3	AC107982.4	226.3568	-1.015491304	0.0177	0.51
ENSG00000110436.11	SLC1A2	972.3289	-1.012318148	0.0219	0.52
ENSG00000273305.1	RP11-440D17.4	52.028	-1.011616136	0.0205	0.52
ENSG00000271980.1	CTD-2256P15.4	6.448082	-1.010350105	0.0477	0.63
ENSG00000210709.1	RNU6ATAC3P	7.588115	-1.005000401	0.0174	0.51
ENSG00000145687.16	SSBP2	3061.451	-1.004927946	0.0136	0.47