A novel 12-gene prognostic signature in breast cancer based on the tumor microenvironment

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Background: The progression of breast cancer (BC) is highly dependent on the tumor microenvironment. Inflammation, stromal cells, and the immune landscape have been identified as significant drivers of BC in multiple preclinical studies. Therefore, this study aimed to clarify the predictive relevance of stromal and immune cell-associated genes in patients suffering from BC.

Methods: We employed the estimation of stromal and immune cells in malignant tumor tissues using expression data (ESTIMATE) algorithm to calculate the stromal and immunological scores, which were then used to evaluate differentially expressed genes (DEGs) in BC samples using The Cancer Genome Atlas (TCGA) database. Univariate analyses were conducted to identify the DEGs linked to survival in BC patients. Next, the prognostic DEGs (with a log-rank $P<0.05$) were used to create a risk signature, and the least absolute shrinkage and selection operator (LASSO) regression method was used to analyze and optimize the risk signature. The following formula was used to compute the prognostic risk score values: Risk score = Gene 1 * β1 + Gene 2 * β2 +… Gene n * βn. The median prognostic risk score values were used to divide BC patients into the low-risk (LR) and high-risk (HR) groups. The patient samples of the validation cohort were then assessed using this formula. We used principal component analysis (PCA) to determine the expression patterns of the different patient groups. Gene Set Enrichment Analysis (GSEA) was used to determine whether there were significant variations between the groups in the evaluated gene sets.

Results: The present study revealed that DEGs linked with survival were closely associated with immunological responses. A prognostic signature was constructed that consisted of 12 genes (*ASCL1*, *BHLHE22*, *C1S*, *CLEC9A*, *CST7*, *EEF1A2*, *FOLR2*, *KLRB1*, *MEOX1*, *PEX5L*, *PLA2G2D*, and *PPP1R16B*). According to their survival, BC patients were separated into LR and HR groups using the identified 12-gene signature. The immunological status and immune cell infiltration were observed differently in the LR and HR groups.

Conclusions: Our results provide novel insights into several microenvironment-linked genes that influence survival outcomes in patients with BC, which suggests that these genes could be candidate therapeutic targets.

Keywords: Breast cancer (BC); tumor microenvironment (TME); gene signature; bioinformatics analyses

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Introduction

Globally, breast cancer (BC) is a highly prevalent form of carcinoma. Over the last two decades, advances in early diagnostic tools and treatments have reduced BC mortality rates by a factor of three when compared to the incidence in 1990 (1,2). However, BC is still a major cause of mortality and threatens women's health throughout the world.

Growing evidence shows that BC tumors are highly heterogeneous. The local tumor microenvironment (TME) is critical for cancer progression, and it is becoming clear that the local TME plays a crucial role in tumor growth (3,4), including BC initiation, progression, metastasis as well as drug resistance(5). This dynamic TME includes endothelial progenitor cells (EPCs), stromal and immunological cells, complex extracellular matrix (ECM), and a wide range of growth factors (GFs) and cytokines (6). Stromal and immunological cells are key cells that promote tumor progression and metastasis. The crosstalk between stromal and immunological cells in the TME has been considered as another key factor in promoting tumor progression. For example, cancer-associated fibroblasts interact with tumor-infiltrating immune cells as well as other immune components over time by secreting various cytokines, growth factors, chemokines, ectoplasmic and other immune molecules, thus creating an immunosuppressive TME that allows cancer cells to evade surveillance by the immune system(7).Various tumor cell characteristics, such as chemotaxis and survival, can be influenced by proteins and the microenvironment of the cells. Recently, several immunomodulatory pharmacological methods have been reported for the treatment of BC (8,9). In order to improve the prognosis of BC and provide reliable information to guide individual treatment strategies, there is an urgent need to screen for reliable TME-related prognostic indicators that can be used clinically for patient management.

The estimation of stromal and immune cells in malignant tumor tissues using expression data (ESTIMATE) algorithm uses datasets of gene expressions to evaluate stromal and immunological cell infiltration in tumor tissues (10). This approach has previously been used to assess the microenvironment composition of colon cancer (11), prostate cancer (12), and glioblastoma (13). Although, there were several reports about the immune cell-associated genes or immune and stroma related genes in patients suffering from BC (14-16), study focus on signature based on both stromal and immunological cell infiltration in BC is still absent to date.

In this study, we used The Cancer Genome Atlas (TCGA) genome expression profiles and the ESTIMATE algorithm to determine immune/stromal scores for BC patients, resulting in the discovery of a group of microenvironment-related genes linked to the overall survival (OS) of BC patients. The genes were then used to create a gene signature associated with patient survival outcomes and investigate the importance of this profile to the immunological response and immune cell infiltration. In conclusion, our findings shed new light on the BC microenvironment, also suggest possible prognostic and therapeutically important gene targets in these cancers.

We present the following article in accordance with the TRIPOD reporting checklist (available at https://atm.amegroups.com/article/view/10.21037/atm-21-6748/rc).

Methods

Sample datasets

TCGA database was used to obtain raw mRNA expression data as well as clinical information from BC patients. A total of 1,069 BC samples (combined set) were randomly separated into training and validation sets of equal size. The validation set was used for validating the findings of the training set. Because all of the data in this report was derived from public sources, no ethical oversight was necessary. The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013).

Evaluation of differentially expressed genes (DEGs) according to the immune/stromal scores

The sample stromal and immunological scores were estimated using the ESTIMATE algorithm. The ESTIMATE R program (www.bioconductor.org/packages/release/BiocViews.html) was used to generate stromal, immune, and ESTIMATE scores by Gene Set Enrichment Analysis (GSEA). Patients were separated into low-risk (LR) and high-risk (HR) groups based on whether their immune/stromal scores were above or below the median value. To discover the immune/stromal score-related DEGs, the expression profiles of BC patients with a high immunological/stromal score were compared to those of BC patients with a low score. The data were then analyzed using the "edgeR" package (www.bioconductor.org/packages/release/bioc/html/edgeR.html), with DEGs classified as those that met the following criteria: false discovery rate (FDR) <0.05 and |log2 fold change| >1.

Functional enrichment analysis of DEGs

Functional enrichment analyses were carried out to evaluate key cascades in which the identified genes were enriched. The "org.Hs.eg.db" package (www.bioconductor.org/packages/release/data/annotation/html/org.Hs.eg.db.html) was initially used to convert gene symbols into entrez IDs, after which Gene Ontology (GO) analyses were conducted using the "clusterProfiler", "ggplot2", and "enrichplot" packages (www.bioconductor.org/packages/release/BiocViews.html), with FDR <0.05 as the significance threshold. A Kyoto Gene and Genome Encyclopedia (KEGG) pathway enrichment analysis was also conducted. A P<0.05 was considered statistically significant.

Development and validation of a DEG (survival-associated) prognostic signature

Univariate Cox regression analyses were carried out to find DEGs associated with the survival of BC patients by using the "survival" R package (www.bioconductor.org/packages/survival). Next, the prognostic DEGs (with a log-rank P<0.05) were used to create a risk signature, and the least absolute shrinkage and selection operator (LASSO) regression method was used to analyze and optimize the risk signature. The following formula was used to compute the prognostic risk score values: Risk score = Gene 1 * β1 + Gene 2 * β2 +… Gene n * βn. The β symbol represents a regression coefficient calculated from the training dataset for each gene of interest. After that, the median prognostic risk score values were used to divide BC patients into the LR and HR groups. The patient samples of the validation cohort were then assessed using this formula. The prognostic relevance of the signature risk score was determined using univariate analyses of patients in both cohorts, followed by multivariate analysis to determine its independent prognostic value in these two cohorts.

Bioinformatics analysis

We used principal component analysis (PCA) to determine the expression patterns of the different patient groups. Gene set enrichment analysis (GSEA) was used to determine whether there were significant variations between the groups in the evaluated gene sets. We focused on two gene sets (immune system process, M13664, and immunological response, M19817) from the Molecular Signatures Database v4.0 (http://www.broadinstitute.org/gsea/msigdb/index.jsp). We also used the Molecular Signatures Database (MSigDB) derived from the KEGG gene sets. To establish significance, we used a normalized enrichment score (NES) <0.05 and an FDR <0.05.

Immune infiltration analysis

The cell-type identification by estimating relative subsets of RNA transcripts (CIBERSORT) R v.12 (www.bioconductor.org/packages/release/BiocViews.html) was utilized to transform the gene expression profiling of BC into the fraction of 22 tumor-infiltrating immune cells in the given samples. One-tailed *t*-tests were used to compare the characteristics between groups.

Statistical analysis

Statistical evaluations were conducted using R v3.6.3 (http://www.Rproject.org). The "glmnet" software was used to run the LASSO regression analysis. After weighting by gene-specific regression coefficient (β) values, the final gene signature was specified as the accumulative individual gene expression. Kaplan-Meier (K-M) curves and log-rank tests were used to evaluate the rate of OS. Uni- and multivariate Cox regression analyses were carried out to evaluate the prognostic markers. The survival receiver operator curve (ROC) program was used for the ROC analysis (time-dependent). A P value <0.05 was considered statistically significant.

Results

Cohort characteristics

TCGA gene expression data were obtained from 1,069 patients suffering from BC, as represented in *Table 1*. A total of 17.12%, 56.88%, 22.45%, and 2.05% of patients had stage I, II, III, and IV tumors, respectively, and the median patient age was 58.08 years.

Association of clinical features with stromal/immune scores

The ESTIMATE algorithm was employed to evaluate the stromal, immune, and ESTIMATE scores ranging between −2,065.59–2,109.48, −1,277.91–3,672.57, and −2,916.86–5,355.63, respectively (*Figure 1* and Table S1).

Table 1 Clinical characteristics of the combined, training, and validation cohorts

Characteristics	Combined cohort, n=1,069	Training cohort, n=535	Validation cohort, n=534
Age (year)	58.08±12.75	57.71±14.51	58.45±11.72
T stage			
T1	279 (26.10)	146 (27.29)	133 (24.91)
T2	617 (57.72)	305 (57.01)	312 (58.43)
T3	132 (12.35)	65 (12.15)	67 (12.55)
T4	38 (3.55)	18 (3.36)	20 (3.75)
Tx	3 (0.28)	1 (0.19)	2 (0.37)
N stage			
N0	502 (46.96)	257 (48.04)	245 (45.88)
N1	357 (33.40)	178 (33.27)	179 (33.52)
N2	120 (11.23)	51 (9.53)	69 (12.92)
N3	73 (6.83)	43 (8.34)	30 (5.62)
Nx	17 (1.59)	6 (1.12)	11 (2.06)
M stage			
M0	1,036 (96.91)	517 (96.64)	519 (97.19)
M1	22 (2.06)	14 (2.62)	8 (1.50)
Mx	11 (1.03)	4 (0.75)	7 (1.31)
TNM stage			
Stage I	183 (17.12)	93 (17.38)	90 (16.85)
Stage II	608 (56.88)	307 (57.38)	301 (56.37)
Stage III	240 (22.45)	113 (21.12)	127 (23.78)
Stage IV	22 (2.05)	14 (2.62)	8 (1.50)
Other	16 (1.50)	8 (1.50)	8 (1.50)

Next, score distributions were evaluated among the various tumor stages, including T, N, M, and TNM, to identify the relationship between stromal/immune scores and the pathologic features of patients with BC. The results revealed that the stromal/immune scores were significantly associated with the T and TNM stages. Elevated stromal scores were significantly correlated with higher T ($P<0.05$) and TNM stages, while elevated immune scores were associated with lower T ($P<0.05$) and TNM stages (all $P<0.05$). However, both scores (stromal and immune) were not significantly associated with the N or M stages (all $P>0.05$), as depicted in *Figure 1A*.

The patients were categorized into LR and HR groups according to the median score values (median stromal score =529.92; median immune score =634.34; median ESTIMATE score =1,206.08) to identify the prognostic relevance of the immune and stromal scores. According to the K-M analyses, the OS rate was longer in patients with high immune scores than those with low immune scores ($P=0.022$), as depicted in *Figure 1C-1E*.

Evaluation of DEGs according to the immune/stromal scores

We used the RNA-seq data from the identified BC patients in TCGA database to see if there was any correlation between the gene expression levels and the immune/stromal scores calculated earlier. To find the immune (or stromal)

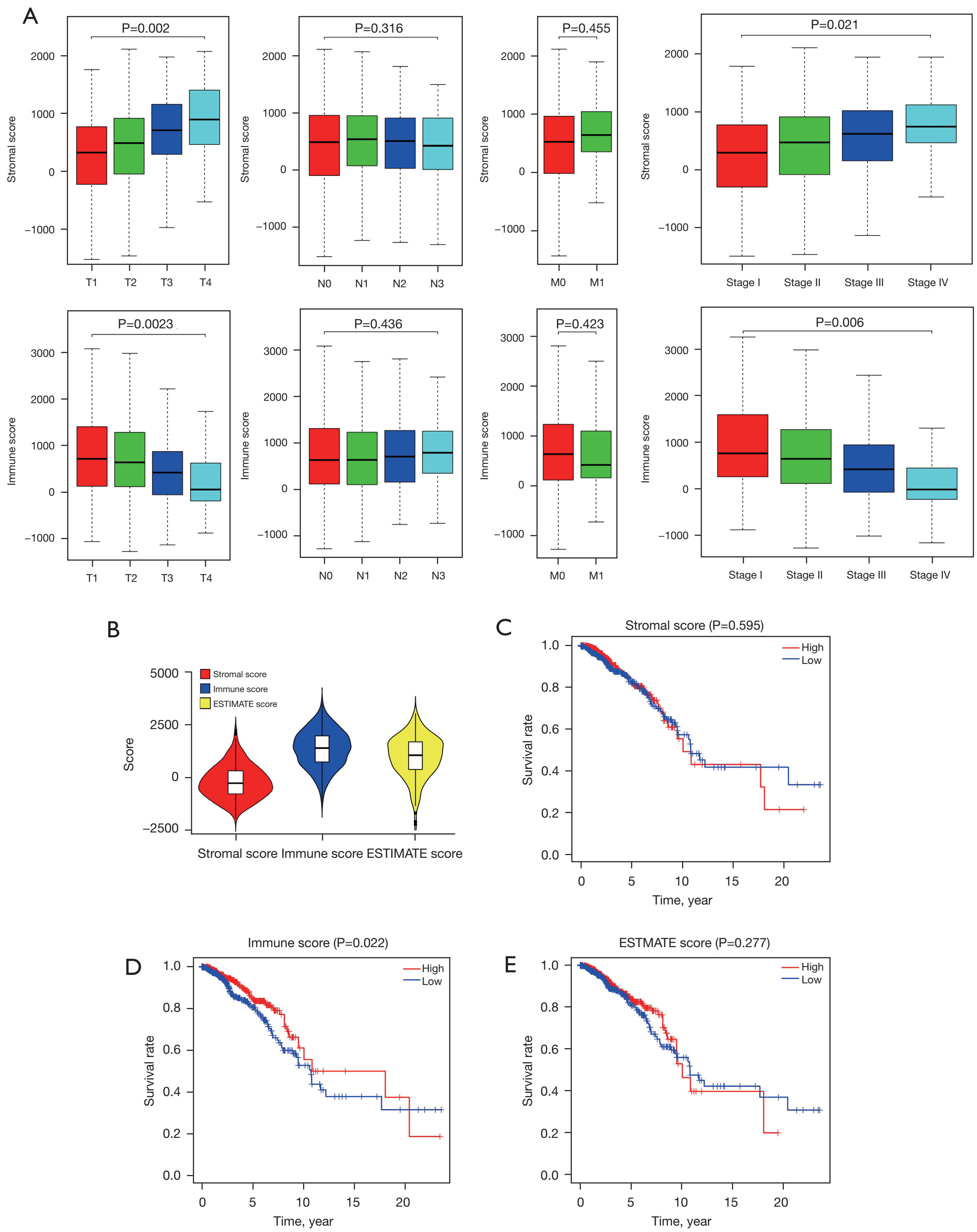

Figure 1 The relationship between patient clinical characteristics and stromal/immune scores in the combined cohort. (A) Stromal and immune scores among BC patients with different stages (T, N, M, and TNM) of the disease. (B) The violin plot of the stromal, immune, and ESTIMATE scores. (C-E) Kaplan-Meier plots demonstrating OS outcomes between low- and high-score groups. BC, breast cancer; ESTIMATE, estimation of stromal and immune cells in malignant tumor tissues using expression data; OS, overall survival.

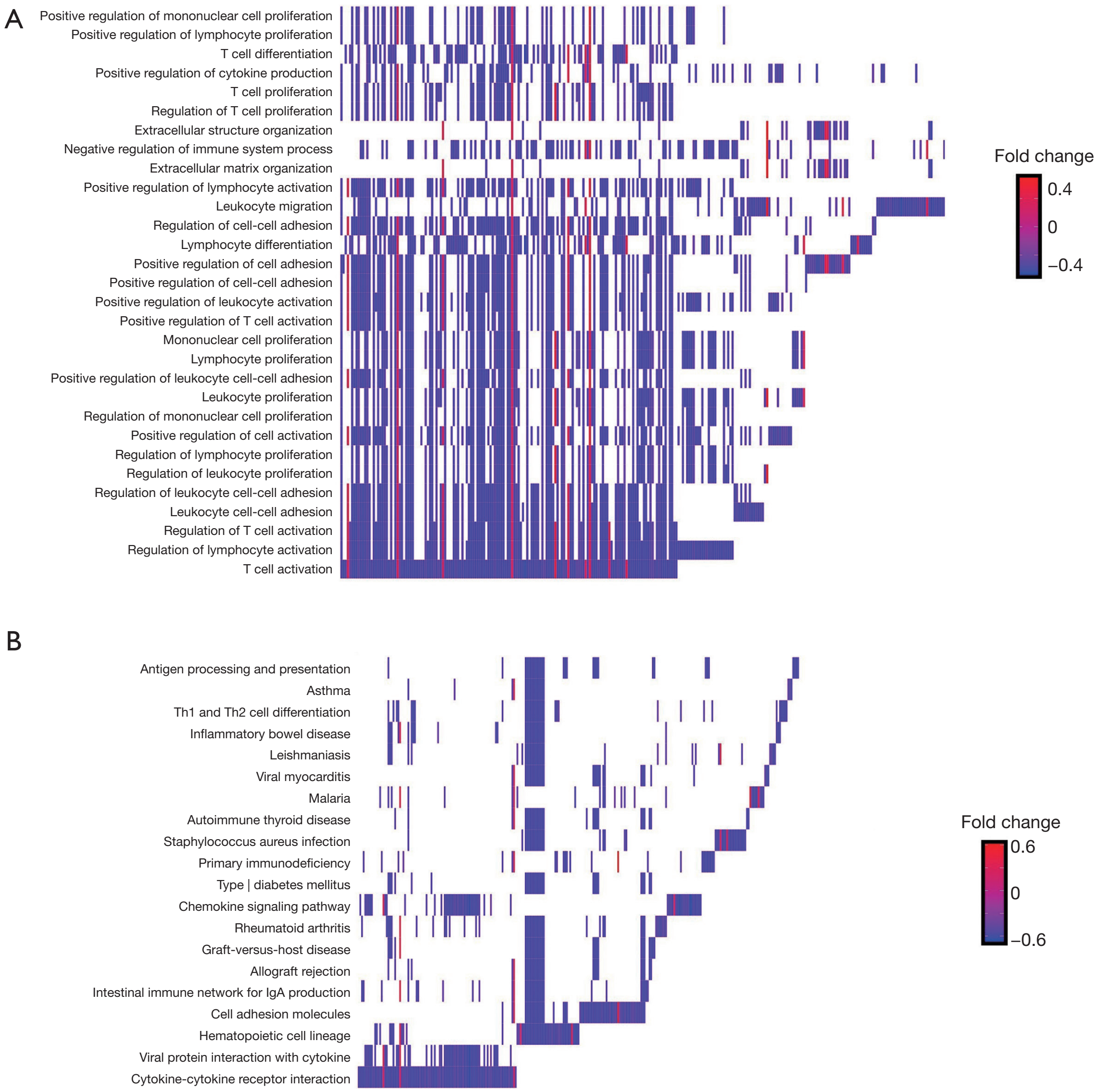

Figure 2 GO and KEGG pathway enrichment analysis results for DEGs. (A) and (B) show GO and KEGG pathway enrichment analysis of DEGs, respectively. The FDR approach was employed to alter the P values. GO, gene ontology; KEGG, kyoto gene and genome encyclopedia; DEGs, differentially expressed genes; FDR, false discovery rate.

score-related DEGs, researchers compared the expression patterns of BC patients with high immune (or stromal) scores to those with low scores. We found 764 stromal score-related DEGs (n=626; n=138) and 829 immune score-related DEGs (n=726; n=103) in the high- and low-score groups, respectively (|log2 fold change|>1 and FDR <0.05) (Tables S2,S3).

Functional enrichment analyses highlight the roles of the DEGs

GO and KEGG analyses were performed to evaluate the immune and stromal score-related DEGs that were enriched (*Figure 2*). With respect to GO, DEGs were primarily enriched in T cell activation, regulation of T cell activation, lymphocyte differentiation, and regulation of

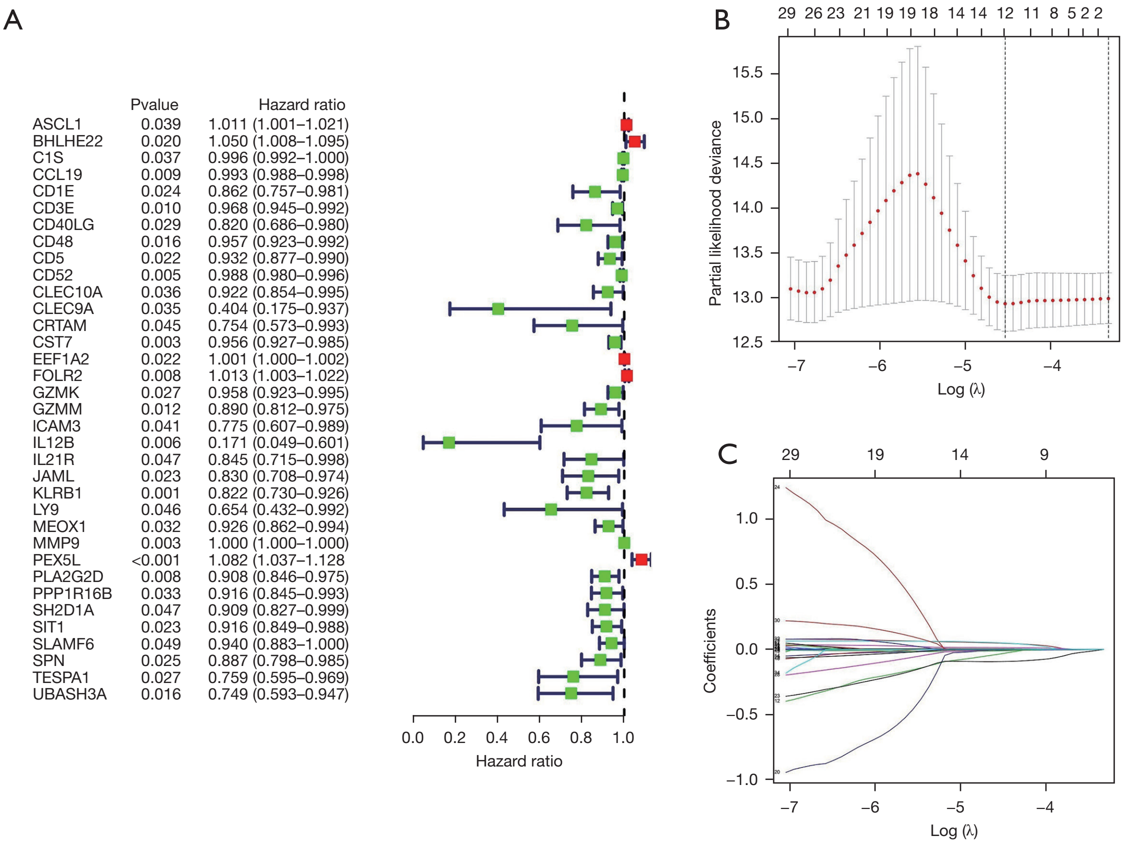

Figure 3 Generation and validation of a 12-gene signature risk score model. (A) Survival-associated DEGs. (B) A coefficient distribution map for a logarithmic (λ) sequence was generated as appropriate. (C) Selection of the optimal BC-related parameters in the LASSO model (λ). DEGs, differentially expressed genes; BC, breast cancer; LASSO, least absolute shrinkage and selection operator.

lymphocyte activation. We also conducted a KEGG analysis that revealed that these DEGs were primarily associated with cytokine-cytokine receptor interaction, chemokine signaling pathway, Th1 and Th2 cell differentiation, and primary immunodeficiency.

Construction of a prognostic signature based on DEGs

We first identified 35 prognostic DEGs as candidates for the development of a gene risk signature based on the BC patient survival data from the training cohort (*Figure 3A*). Ultimately, 12 genes were chosen for inclusion in this signature using a LASSO Cox regression technique (*Table 2*, *Figure 3B,3C*). The predictive significance of the signature-derived risk scores was next investigated for the training cohort by stratifying patients into LR and HR groups using the cohort's median risk score (0.92985) (*Figure 4A,4B*).

LR BC patients had a considerably longer OS than HR BC patients (16.4±2.07 *vs.* 11.16±1.23 years, P<0.001), which was in line with our predictions. Importantly, we discovered that in the validation cohort, LR patients had a longer OS than HR patients (16.57±1.32 *vs.* 12.62±1.32 years; P=0.002) (*Figure 4C,4D*). Multivariate Cox regression models were used to evaluate the independent risk factors in the two cohorts. Multivariate analysis included several clinicopathological factors as well as the 12-gene signature scores, revealing that age (Training set: HR =1.028, 95 % CI: 1.008–1.049, P=0.007; Validation set: HR =1.046, 95% CI: 1.025–1.068, P<0.001) and the 12-gene signature score (Training set: HR =1.192, 95% CI: 1.111–1.28, P<0.001; Validation set: HR =1.512, 95% CI: 1.286–1.779, P<0.001) were independent prognostic indicators both in the training and validation cohorts, as depicted in *Figure 4E,4F*.

We used a ROC analysis to test the predictive value of our 12-gene signature risk model against that of other clinicopathologic parameters, such as age, T, N, M, and TNM stage. Compared to the other clinicopathologic feature curves in the training and validation cohorts, the 12-

Table 2 12-gene signature

Gene symbol	Gene ID	Description	Coefficient
ASCL1	429	Achaete-Scute family bHLH transcription factor 1	0.00349
BHLHE22	27319	Basic Helix-Loop-Helix Family Member E22	0.04779
C1S	716	Complement component C1s activity	–0.00067
CLEC9A	283420	C-Type Lectin Domain Containing 9A	–0.03476
CST7	8530	Cystatin F	–0.00614
EEF1A2	1917	Eukaryotic Translation Elongation Factor 1 Alpha 2	0.00033
FOLR2	2350	Folate Receptor Beta	0.01399
KLRB1	3820	Killer Cell Lectin Like Receptor B1	–0.09338
MEOX1	4222	Mesenchyme Homeobox 1	–0.01082
PEX5L	51555	Peroxisomal Biogenesis Factor 5 Like	0.05008
PLA2G2D	26279	Phospholipase A2 Group IID	–0.00362
PPP1R16B	26051	Protein Phosphatase 1 Regulatory Subunit 16B	–0.004

gene signature curve had the highest AUC value (Training set: AUC =0.806; Validation set: AUC =0.776). As a result, this 12-gene signature risk score could be more accurate than other clinical factors in identifying BC patients (*Figure 4G,4H*).

HR and LR BC patients exhibit differences in immune status and infiltration

A PCA analysis was used to determine the variations in distribution patterns between the LR and HR groups using the 12-gene signature risk scores. The LR and HR groups were distributed into two separate clusters, as depicted in *Figure 5A*. Additionally, a GSEA functional annotation technique was used, revealing that LR samples were highly enriched for immune response pathway-related genes compared with HR samples (*Figure 5B*). When tumor samples from LR and HR BC patients were classified according to their 12-gene signature risk scores, variations were observed in the immunological status of these tumor samples. Additionally, samples from the LR group were enriched for immunological cascades, including the cytokine-cytokine receptor interaction, Notch signaling, primary immunodeficiency, JAK-STAT, Toll-like receptor, and T cell receptor signaling. On the other hand, the enriched cascades were primarily connected with the TGF-signaling cascades in the HR group, as depicted in *Figure 5C*. An immune cell-based study was performed, which suggested an elevation in the numbers of M1 macrophages, plasma cells, naive/memory B cells, activated $CD4^+$ memory T cells, $CD8^+$ T cells, resting NK cells, and follicular helper T cells in the LR group patients. In comparison, HR patients showed elevated levels of M2 macrophages, M0 macrophages, and regulatory T cells (Tregs), as shown in *Figure 5D,5E*.

Discussion

BC is a form of rapidly progressing cancer with a poor prognosis that can be profoundly impacted by the TME. According to previous research, both immunological and stromal cells are key components of the TME and can have a significant impact on tumor growth and proliferation, as well as therapeutic responsiveness (17). A growing body of evidence suggests that the TME promotes BC growth and development, as well as influencing tumor invasion and metastasis. While alterations in immune cells, soluble molecules, and the ECM have all been shown to promote cancer growth, the link between TME-related genes and BC prognosis remains unknown. Therefore, extensive research is needed to assess the genome profiling correlated with existing tumor sequencing datasets to better understand the interaction between BC cells and the TME. In present study, we, as the first, constructed a 12-gene signature (*ASCL1*, *BHLHE22*, *C1S*, *CLEC9A*, *CST7*, *EEF1A2*, *FOLR2*, *KLRB1*, *MEOX1*, *PEX5L*, *PLA2G2D*, and

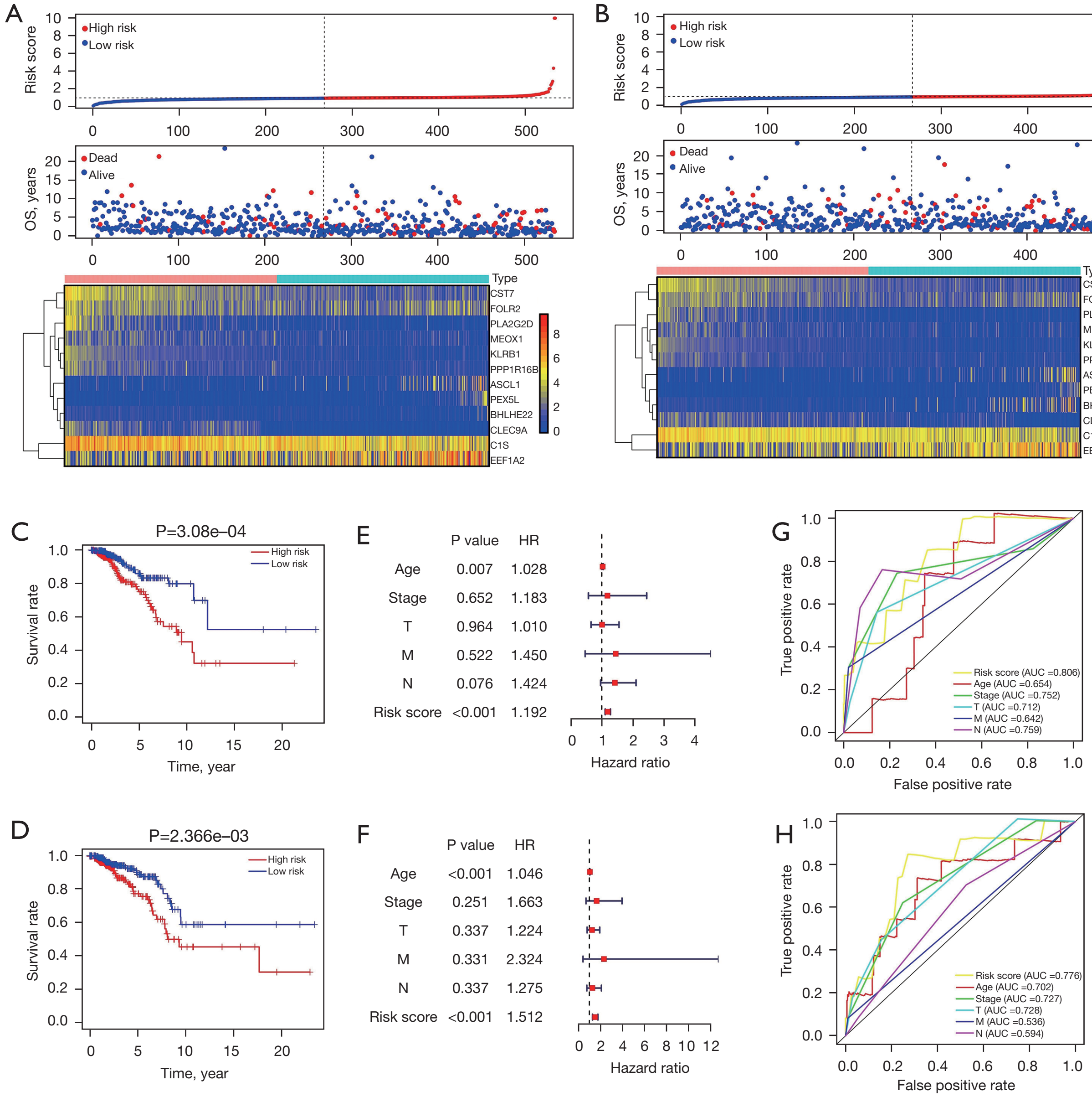

Figure 4 The risk score, survival time, and 12-gene expression (heatmap) distributions in the training (A) and validation cohorts (B). In the heatmap, rows represent genes, while columns correspond to individual patients. Survival analysis of LR and HR BC patients as shown by the Kaplan-Meier analysis of BC patients' OS in the HR and LR subgroups of the training (C) and validation cohorts (D). Multivariate independent prognostic analysis of 12-gene signature risk score and other clinical features in the training (E) and validation cohorts (F). Time-dependent ROC analysis comparing the 12-gene signature risk model and other clinicopathologic features as tools for predicting the OS of BC patients in the training (G) and validation cohorts (H). HR, high risk; LR, low risk; BC, breast cancer; OS, overall survival; ROC, receiver operating characteristic curve, AUC, area under the cure.

PPP1R16B) based on both stromal and immunological cell infiltration in BC. According to their survival, BC patients were separated into LR and HR groups using the identified 12-gene signature. The immunological status and immune cell infiltration were observed differently in the LR and HR groups.

We assessed the prognostic value of TME-associated genes using TCGA database. We discovered that BC patients

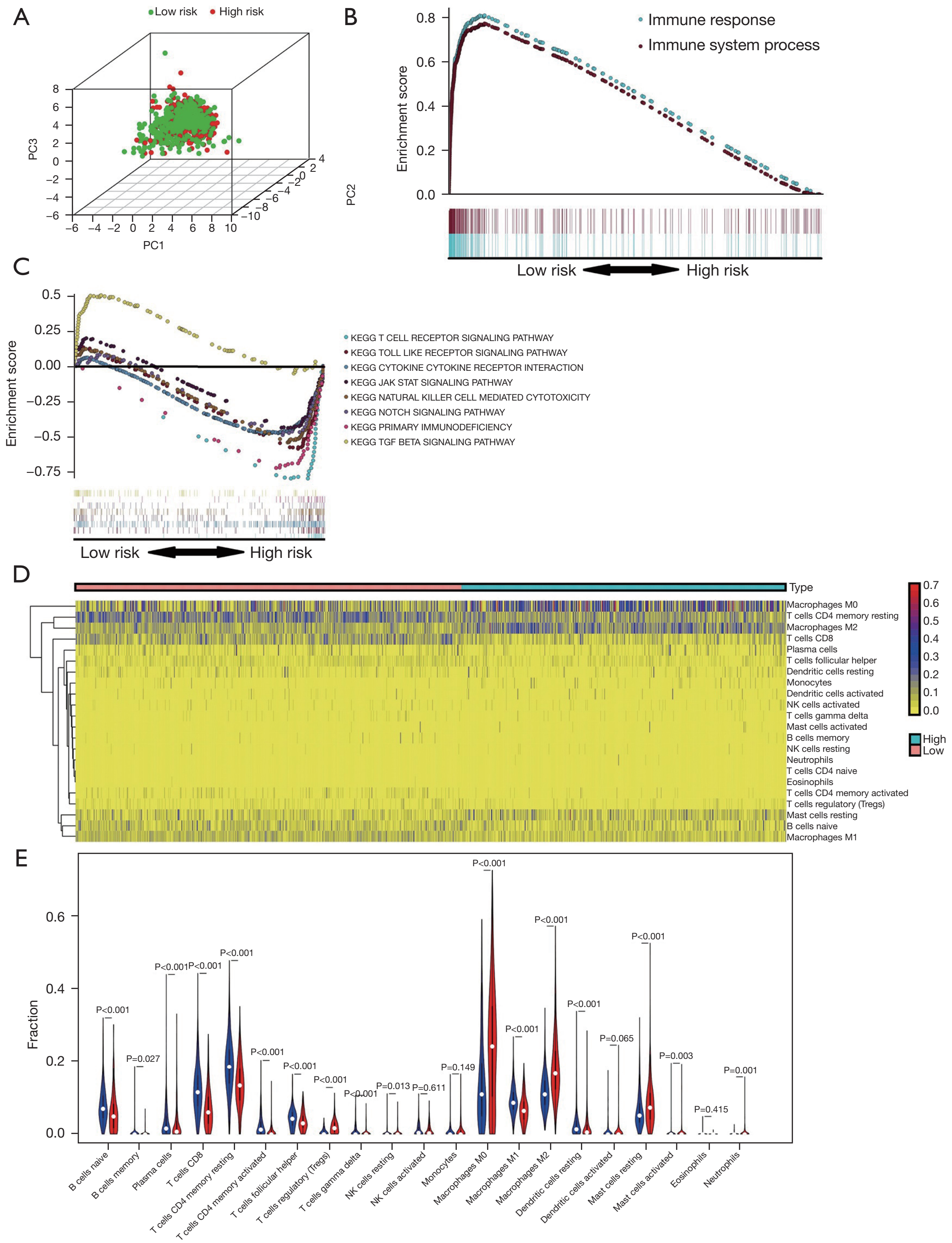

Figure 5 HR and LR BC patients demonstrate differences in immune status. (A) Principal components analysis between LR and HR groups based on the 12-gene signature risk score model. (B) Functional annotation of the 12-gene signature in the Immune response set and the Immune system process set in a GSEA analysis. (C) KEGG enrichment analysis. (D) Estimated immune cell populations as determined using the CIBERSORT algorithm. (E) Violin plots demonstrating the immune cell populations in the LR (blue) and HR (red) groups. P values have been identified based on the Wilcoxon Test. HR, high risk; LR, low risk; BC, breast cancer; GSEA, gene set enrichment analysis; KEGG, kyoto gene and genome encyclopedia; CIBERSORT, cell-type identification by estimating relative subsets of RNA transcripts.

with elevated immune scores had a considerably longer OS rate than those with lower immune scores. DEGs were found to be linked to immune and stromal scores as well as survival. The above genes were used to create a predictive risk profile that assessed differences in OS and immunological cell infiltration between LR and HR BC patients. Our work provides a comprehensive and accurate tool for assessing the TME and survival outcomes of BC patients. Our results thus hold great promise for identifying innovative molecular targets for immunotherapy and, hence, the improvement of treatment strategies available to BC patients.

TME-related genes have a significant impact on clinical outcomes in a variety of solid tumors. In this study, we used a gene signature risk model to incorporate a subset of survival-associated DEGs. Patients were divided into LR and HR groups using risk scores obtained from this model, with additional analyses revealing considerable variations in the OS rates of the patients in these two risk cohorts that corresponded to an elevated AUC value. Among the 12 genes included in this prognostic risk signature, some have previously been shown to be correlated with BC tumorigenesis. For example, eukaryotic translation elongation factor 1-alpha 2 (EEF1A2) has been reported as a putative oncogene owing to its pronounced expression in BC (18). One prior report indicated that EEF1A2 induced Akt-dependent actin remodeling and enhanced the invasion of BC cells (19). Furthermore, Sun *et al.* confirmed that mesenchyme homeobox 1 (MEOX1) is a critical molecular target involved in regulating breast cancer stem cells and mesenchymal-like cell proliferation. MEOX1 has been linked with poor survival, lymph node metastasis, and tumor stage in BC patients (20). And others have been reported to be associated with other tumors or diseases. ASCL1 is a transcription factor and required for neural differentiation, which is also essential for the development of pulmonary neuroendocrine cells (21,22). BHLHE22 was found to be involved in the development of psychiatric disease (23). C1S is part of the complement system family, while CLEC9A is a surface marker on tumor-associated macrophage. FOLR2 is expressed in macrophages, placental and hematopoietic cells (24). Expressing KLRB1 (encoding CD161, a surface marker on NK cells and several T cell subsets) was reported to be associated with favorable outcomes in pan-cancer (25). PLA2G2D, a metabolism- and immune-related molecule, was identified to be a biomarker for immune cell infiltration and patient survival in cervical squamous cell carcinoma (26). While upregulated expression of PLA2G2D was reported to be associated with adaptive resistance to immune checkpoint blockade (pembrolizumab) (27).

In addition, the immunological phenotypes identified in the HR and LR groups were shown to be considerably varied. According to the GSEA, LR patient samples had gene expression patterns that were enriched for genes related to the immune system. While TME composition is of great interest to researchers, immune cells in the BC TME vary greatly and are linked to patient outcomes. Tumor-infiltrating lymphocytes (TILs), especially CD8$^+$ T cells, are important mediators of tumor immune surveillance. Normally, antigen and co-stimulatory molecule exposure activate the effector CD8$^+$ T cells, allowing them to lyse tumor cells and inhibit tumor growth. In patients with BC, T cell infiltration plays an important role. CD8$^+$ T cell monitoring is useful in tracking the course of cancer and the prognosis of patients. Our results are consistent with these prior findings, as LR patients exhibited an increased CD8$^+$ T cell profile. Although the involvement of Tregs in BC prognosis has often been the subject of research, controversy remains regarding the specific prognostic impact of these cells and whether they are beneficial or harmful. According to Shang *et al.* (28), Treg infiltration was reportedly linked to a favorable prognosis in estrogen receptor (ER)- but not ER+ BC patients. We observed significant Treg enrichment in HR patients. The role of B cells in BC remains poorly understood. Our results demonstrated enrichment of B cells in LR patients, indicating a negative correlation between these cells and risk. However, the precise mechanistic role of B cells remains to be defined in this prognostic context.

Tumor-associated macrophages (TAMs) also play a regulatory role in tumor cell-immune system interactions (29,30). TAMs have traditionally been divided into two groups: M1 and M2. Because of their anti-inflammatory, angiogenic, and ECM-remodeling actions, M2 macrophage infiltration within tumors has been associated with a poorer prognosis. In samples from HR BC patients, M2 macrophages were shown to be abundant.

However, we only have a rudimentary understanding of the balance between M1 and M2 phenotypes. The JAK/STAT signaling cascades are among the most significant polarization regulators. According to the GSEA data, signaling cascades, such as JAK/STAT signaling were shown to be elevated in the LR group. IFN-γ triggers STAT1 and produces M1 macrophage polarization, with the IFN-γ/JAK/STAT1 signaling cascade serving as a critical regulator of the M1 phenotype. According to previous research, the activation of the IL-6/JAK/STAT3 signaling cascade is thought to be the primary mediator of macrophage M2 polarization.

The current study has some shortcomings. For one, this was an in silico analysis and as such, all conclusions were correlative. Additional and *in vivo* functional analyses will thus be needed to validate and expand upon these results. In addition, while we made efforts to verify the microenvironment-associated DEGs and subsequently assess their prognostic significance in BC patients, further large-scale prospective studies will be necessary to validate this hypothesis. It is also worth noting that the immune signature discovered in this study is based on an assessment of immunological cell infiltration within tumors derived from algorithmic analyses of RNA-sequenced data. To establish the accuracy of the immune infiltration data and examine the cell-to-cell interactions that may emerge within these tumors and affect BC development or prognosis, more in-depth studies will be required in the future.

Conclusions

To assess the BC TME, we performed an extensive bioinformatics analysis for gene expression in BC patients based on TCGA. Using this method, we were able to identify microenvironment-associated DEGs and subsequently assess their prognostic significance in BC patients. To fully validate their association with patient OS, future clinical studies of the functional roles of the identified genes will be required. Taken together, our findings shed light on the complicated interplay between BC stromal cells and immunological cells in the TME, possibly pointing to novel therapeutic possibilities for future clinical trials.

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Footnote

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Conflicts of Interest: All authors have completed the ICMJE uniform disclosure form (available at https://atm.amegroups.com/article/view/10.21037/atm-21-6748/coif). The authors have no conflicts of interest to declare.

Ethical Statement: The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved. The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013).

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Table S1 Stromal Score, Immune Score, and ESTIMATE Score

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-A2-A0T5-01A-21R-A084-07	361.8755	116.516	478.3916
TCGA-A2-A0EM-01A-11R-A034-07	737.4148	125.7191	863.1339
TCGA-BH-A0BJ-01A-11R-A056-07	918.8147	729.4806	1648.295
TCGA-A7-A0DC-01B-04R-A22O-07	80.78604	-446.069	-365.283
TCGA-D8-A146-01A-31R-A115-07	1129.168	645.8598	1775.028
TCGA-B6-A0X7-01A-11R-A10J-07	691.0138	-123.354	567.6598
TCGA-A2-A0EU-01A-22R-A056-07	210.5296	-44.8378	165.6918
TCGA-AO-A0J9-01A-11R-A034-07	1394.553	1791.937	3186.49
TCGA-A2-A0YG-01A-21R-A109-07	-183.985	58.6547	-125.331
TCGA-E2-A1B4-01A-11R-A12P-07	-30.6976	-289.616	-320.314
TCGA-C8-A130-01A-31R-A115-07	508.0449	269.0979	777.1428
TCGA-OL-A5RW-01A-11R-A28M-07	-224.903	547.8998	322.9967
TCGA-E2-A14U-01A-11R-A22K-07	-529.411	-146.224	-675.635
TCGA-EW-A6SB-01A-12R-A32P-07	-465.344	2283.752	1818.408
TCGA-A2-A3XV-01A-21R-A239-07	210.2683	467.1782	677.4465
TCGA-A2-A3XW-01A-11R-A239-07	529.9273	1329.916	1859.843
TCGA-AC-A3HN-01A-11R-A213-07	1424.561	1306.89	2731.451
TCGA-A8-A09R-01A-11R-A00Z-07	778.5743	1030.722	1809.296
TCGA-A2-A3KD-01A-12R-A213-07	252.3715	264.3228	516.6943
TCGA-AO-A0JG-01A-31R-A084-07	622.2924	1283.13	1905.422
TCGA-B6-A1KI-01A-11R-A14M-07	635.4534	-383.228	252.2255
TCGA-E9-A2JT-01A-22R-A18M-07	999.6288	3153.895	4153.524
TCGA-BH-A0DV-01A-21R-A12P-07	1806.537	959.1447	2765.682
TCGA-BH-A0HA-01A-11R-A12P-07	1358.034	1185.065	2543.098
TCGA-A8-A084-01A-21R-A00Z-07	150.3536	-127.875	22.47875
TCGA-AC-A3EH-01A-22R-A22K-07	244.4624	286.9589	531.4213
TCGA-C8-A12Y-01A-11R-A12D-07	382.3806	347.3721	729.7527
TCGA-AN-A0XP-01A-11R-A109-07	483.9926	49.43273	533.4253
TCGA-A8-A07B-01A-11R-A00Z-07	574.7005	4.713155	579.4137
TCGA-E2-A14N-01A-31R-A137-07	-644.536	861.1031	216.5675
TCGA-AO-A1KS-01A-11R-A13Q-07	259.8816	220.593	480.4747
TCGA-A8-A07F-01A-11R-A00Z-07	434.6468	477.2505	911.8974
TCGA-GM-A3XL-01A-11R-A22U-07	-598.119	1476.801	878.6814
TCGA-S3-A6ZG-01A-22R-A32P-07	145.3673	556.5355	701.9028
TCGA-AC-A2QH-01B-04R-A22O-07	67.16175	-901.699	-834.538
TCGA-AR-A24S-01A-11R-A169-07	1476.478	1627.385	3103.863
TCGA-E2-A574-01A-11R-A29R-07	-1189.05	-741.069	-1930.12
TCGA-EW-A1PG-01A-11R-A144-07	847.732	145.5475	993.2795
TCGA-D8-A1XR-01A-11R-A14M-07	128.4862	-97.4491	31.03715
TCGA-AR-A1AP-01A-11R-A12P-07	609.0522	854.332	1463.384
TCGA-D8-A73X-01A-11R-A32P-07	643.7873	273.1571	916.9444
TCGA-EW-A1J1-01A-11R-A13Q-07	72.74654	939.4384	1012.185

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-AO-A12D-01A-11R-A115-07	1153.618	1706.319	2859.937
TCGA-BH-A0DI-01A-21R-A12P-07	1551.649	1121.563	2673.212
TCGA-E2-A10C-01A-21R-A10J-07	147.3146	1288.139	1435.453
TCGA-GM-A3XG-01A-31R-A24H-07	-143.655	-220.076	-363.731
TCGA-AR-A1AT-01A-11R-A12P-07	544.9239	1745.438	2290.362
TCGA-B6-A40B-01A-11R-A239-07	465.2434	277.3508	742.5942
TCGA-A8-A07J-01A-11R-A00Z-07	1715.338	1539.943	3255.281
TCGA-AO-A0JJ-01A-11R-A056-07	1360.918	1710.694	3071.612
TCGA-E9-A1R0-01A-22R-A16F-07	728.3165	617.1971	1345.514
TCGA-B6-A400-01A-11R-A239-07	411.8958	988.1592	1400.055
TCGA-E9-A3QA-01A-61R-A22K-07	339.648	2235.786	2575.434
TCGA-D8-A27G-01A-11R-A16F-07	1027.899	992.0367	2019.936
TCGA-AR-A2LH-01A-31R-A18M-07	781.1572	2081.253	2862.411
TCGA-BH-A202-01A-11R-A14M-07	525.8503	1054.462	1580.312
TCGA-A2-A0T2-01A-11R-A084-07	137.8387	525.3759	663.2146
TCGA-D8-A1XQ-01A-11R-A14M-07	619.707	1526.191	2145.898
TCGA-A8-A08Z-01A-21R-A00Z-07	1547.362	1198.675	2746.037
TCGA-BH-A1EU-01A-11R-A137-07	1490.766	1883.253	3374.019
TCGA-B6-A0RG-01A-11R-A056-07	75.47074	-353.736	-278.266
TCGA-GM-A2DM-01A-11R-A180-07	-339.439	659.2388	319.8
TCGA-LL-A5YN-01A-11R-A28M-07	282.8581	2379.386	2662.244
TCGA-E2-A1LB-01A-11R-A144-07	408.0456	45.74156	453.7872
TCGA-AQ-A1H2-01A-11R-A13Q-07	-151.667	296.7351	145.0681
TCGA-D8-A1Y1-01A-21R-A14M-07	1109.297	682.2302	1791.527
TCGA-AO-A12A-01A-21R-A115-07	745.3168	641.4136	1386.73
TCGA-AN-A0XN-01A-21R-A109-07	1763.775	1297.679	3061.454
TCGA-PE-A5DE-01A-11R-A27Q-07	661.7617	2569.01	3230.772
TCGA-A8-A075-01A-11R-A084-07	585.9835	1008.529	1594.512
TCGA-LL-A441-01A-11R-A24H-07	390.171	2270.998	2661.169
TCGA-BH-A0W3-01A-11R-A109-07	-414.636	87.9287	-326.707
TCGA-A2-A04V-01A-21R-A034-07	777.8492	439.788	1217.637
TCGA-V7-A7HQ-01A-11R-A33J-07	233.9656	431.396	665.3616
TCGA-BH-A28Q-01A-11R-A16F-07	486.9517	189.8219	676.7736
TCGA-BH-A1FH-01A-12R-A13Q-07	1637.287	436.6379	2073.925
TCGA-E9-A1NE-01A-21R-A14M-07	1074.461	2422.051	3496.512
TCGA-C8-A26V-01A-11R-A16F-07	118.9315	426.295	545.2266
TCGA-AC-A6IW-01A-12R-A33J-07	-128.132	2346.01	2217.879
TCGA-A1-A0SJ-01A-11R-A084-07	542.7676	191.6562	734.4238
TCGA-XX-A899-01A-11R-A36F-07	1234.232	1926.136	3160.368
TCGA-A2-A0SY-01A-31R-A084-07	1205.578	1261.003	2466.581
TCGA-A2-A0CS-01A-11R-A115-07	661.6039	509.7883	1171.392
TCGA-BH-A1F6-01A-11R-A13Q-07	440.3261	1285.562	1725.888

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-A8-A07W-01A-11R-A00Z-07	388.4326	570.3982	958.8308
TCGA-BH-A0HP-01A-12R-A084-07	768.0473	694.2077	1462.255
TCGA-B6-A0IJ-01A-11R-A034-07	-165.631	1963.972	1798.341
TCGA-E2-A1LS-01A-12R-A157-07	-349.069	-258.425	-607.494
TCGA-A2-A0CY-01A-12R-A034-07	-1029.71	-480.293	-1510
TCGA-A7-A26G-01A-21R-A169-07	1581.4	1366.099	2947.498
TCGA-EW-A424-01A-11R-A24H-07	423.2034	-293.974	129.2295
TCGA-B6-A409-01A-11R-A24H-07	-115.004	437.6168	322.6128
TCGA-WT-AB44-01A-11R-A41B-07	632.333	496.1537	1128.487
TCGA-EW-A6SC-01A-12R-A32P-07	1012.236	776.2925	1788.529
TCGA-AR-A256-01A-11R-A169-07	-84.4778	391.5988	307.121
TCGA-E2-A1IG-01A-11R-A144-07	908.3135	223.4988	1131.812
TCGA-EW-A1J5-01A-11R-A13Q-07	501.9921	1600.229	2102.221
TCGA-AR-A1AU-01A-11R-A12P-07	550.7963	89.10184	639.8981
TCGA-AC-A8OP-01A-11R-A36F-07	463.3341	391.3467	854.6808
TCGA-A8-A09Z-01A-11R-A00Z-07	-103.45	1214.572	1111.122
TCGA-BH-A18V-06A-11R-A213-07	272.8575	2513.511	2786.368
TCGA-OL-A66P-01A-11R-A31O-07	1071.928	2659.712	3731.64
TCGA-GM-A5PV-01A-11R-A28M-07	-572.953	550.8572	-22.0963
TCGA-B6-A0WW-01A-11R-A109-07	366.9796	-66.8262	300.1534
TCGA-A2-A04R-01A-41R-A109-07	25.77812	-578.823	-553.044
TCGA-A2-A1FW-01A-11R-A13Q-07	287.9343	-116.673	171.2618
TCGA-C8-A137-01A-11R-A115-07	101.3988	-589.126	-487.727
TCGA-AR-A24X-01A-11R-A169-07	580.9309	198.9324	779.8634
TCGA-BH-A0B2-01A-11R-A10J-07	1514.663	1822.69	3337.353
TCGA-C8-A12K-01A-21R-A115-07	556.8192	2421.228	2978.048
TCGA-BH-A0HB-01A-11R-A056-07	484.0993	1254.427	1738.526
TCGA-E9-A1NH-01A-11R-A14D-07	1229.968	669.7852	1899.753
TCGA-E2-A1LA-01A-11R-A144-07	670.4923	1790.947	2461.439
TCGA-A2-A0EV-01A-11R-A034-07	961.3979	1086.084	2047.481
TCGA-A2-A0SX-01A-12R-A084-07	854.3795	1999.044	2853.423
TCGA-A2-A04Y-01A-21R-A034-07	406.7688	1334.534	1741.303
TCGA-A2-A1FZ-01A-51R-A14D-07	1119.632	832.2423	1951.874
TCGA-E2-A573-01A-11R-A29R-07	-50.7302	1887.077	1836.347
TCGA-A7-A26I-01B-06R-A22O-07	1463.973	725.3403	2189.313
TCGA-C8-A138-01A-11R-A115-07	1113.166	1728.463	2841.629
TCGA-A8-A095-01A-11R-A00Z-07	275.2889	240.2848	515.5737
TCGA-EW-A1P3-01A-11R-A144-07	420.2453	423.5587	843.8041
TCGA-D8-A27H-01A-11R-A16F-07	639.7175	302.074	941.7916
TCGA-BH-A1FC-01A-11R-A13Q-07	-49.1757	1567.677	1518.501
TCGA-B6-A0WX-01A-11R-A109-07	1015.845	932.006	1947.852
TCGA-D8-A143-01A-11R-A115-07	-376.788	574.1614	197.3738

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-B6-A0WY-01A-11R-A109-07	687.9765	522.7469	1210.723
TCGA-A1-A0SK-01A-12R-A084-07	-1406.32	-1277.91	-2684.23
TCGA-A8-A06Q-01A-11R-A034-07	-1015.94	-478.796	-1494.74
TCGA-AC-A6NO-01A-12R-A33J-07	-49.4157	-184.465	-233.881
TCGA-A2-A0YC-01A-11R-A109-07	673.3218	590.4945	1263.816
TCGA-E9-A1R6-01A-11R-A14D-07	151.7173	-121.44	30.27686
TCGA-A1-A0SE-01A-11R-A084-07	625.7867	-39.9417	585.845
TCGA-BH-A1EY-01A-11R-A13Q-07	1330.253	1534.707	2864.96
TCGA-AC-A6IV-01A-12R-A33J-07	1719.387	1882.093	3601.48
TCGA-E2-A1LG-01A-21R-A14M-07	-1030.22	241.6964	-788.519
TCGA-AO-A12C-01A-11R-A10J-07	1125.79	-92.2491	1033.541
TCGA-GM-A4E0-01A-12R-A266-07	1572.667	1964.752	3537.418
TCGA-B6-A0IQ-01A-11R-A034-07	-648.453	415.7192	-232.734
TCGA-E9-A1ND-01A-11R-A144-07	669.3226	2250.225	2919.548
TCGA-A2-A3XS-01A-11R-A22U-07	127.9893	868.3823	996.3716
TCGA-EW-A1OX-01A-11R-A144-07	-1309.35	-1182.02	-2491.36
TCGA-D8-A1XK-01A-21R-A14M-07	-436.216	940.1244	503.9082
TCGA-AR-A24L-01A-11R-A169-07	1000.082	95.95828	1096.041
TCGA-A8-A07Z-01A-11R-A00Z-07	-283.818	627.8333	344.0156
TCGA-BH-A0C0-01A-21R-A056-07	391.4934	2297.431	2688.924
TCGA-S3-AA14-01A-11R-A41B-07	762.4901	-76.9662	685.5239
TCGA-E2-A1BC-01A-11R-A12P-07	901.1329	-184.434	716.6985
TCGA-AC-A8OR-01A-21R-A41B-07	-944.32	250.4118	-693.908
TCGA-E2-A15M-01A-11R-A12D-07	1661.271	2043.78	3705.051
TCGA-B6-A0RL-01A-11R-A084-07	-2065.59	-851.28	-2916.86
TCGA-BH-AB28-01A-31R-A41B-07	522.7143	985.512	1508.226
TCGA-AN-A0XO-01A-11R-A109-07	268.1636	-695.441	-427.278
TCGA-B6-A0X4-01A-11R-A109-07	-1263.07	-937.952	-2201.02
TCGA-A8-A093-01A-11R-A00Z-07	646.9976	-356.164	290.8335
TCGA-D8-A1JL-01A-11R-A13Q-07	1019.591	1744.865	2764.456
TCGA-LL-A5YP-01A-21R-A28M-07	1163.543	967.609	2131.152
TCGA-A2-A0CP-01A-11R-A034-07	1043.887	419.4613	1463.348
TCGA-EW-A1J6-01A-11R-A13Q-07	-118.2	1224.481	1106.282
TCGA-E2-A14R-01A-11R-A115-07	-381.033	1394.596	1013.563
TCGA-EW-A1OV-01A-11R-A144-07	944.881	2656.988	3601.869
TCGA-A2-A0CX-01A-21R-A00Z-07	1022.41	982.3927	2004.802
TCGA-A7-A13E-01A-11R-A277-07	-31.1087	-523.689	-554.798
TCGA-A8-A08F-01A-11R-A00Z-07	847.1192	1482.767	2329.886
TCGA-A7-A13E-01A-11R-A12P-07	-207.958	-415.458	-623.416
TCGA-E9-A1RG-01A-11R-A14D-07	295.3415	724.7952	1020.137
TCGA-E2-A15E-06A-11R-A12D-07	-507.233	606.8605	99.6278
TCGA-A1-A0SQ-01A-21R-A144-07	-86.1776	165.9144	79.73678

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-EW-A1PD-01A-11R-A144-07	841.7623	62.31857	904.0809
TCGA-BH-A0HN-01A-11R-A10U-07	-719.199	22.39037	-696.808
TCGA-E2-A1IU-01A-11R-A14D-07	-162.535	342.4605	179.9251
TCGA-BH-A0BO-01A-23R-A12D-07	1349.32	1182.797	2532.117
TCGA-E2-A1IJ-01A-11R-A144-07	1547.484	1517.192	3064.677
TCGA-A2-A0ES-01A-11R-A115-07	1029.688	717.593	1747.281
TCGA-AO-A12B-01A-11R-A10J-07	-476.558	-35.3909	-511.949
TCGA-BH-A0E9-01B-11R-A115-07	365.8746	518.0013	883.8759
TCGA-BH-A0BP-01A-11R-A115-07	1167.502	351.6442	1519.146
TCGA-E2-A153-01A-12R-A12D-07	1528.418	714.3235	2242.741
TCGA-PL-A8LZ-01A-31R-A36F-07	1156.856	2070.839	3227.695
TCGA-E9-A5UP-01A-11R-A28M-07	-1229.37	214.0843	-1015.29
TCGA-AC-A2FG-01A-11R-A17B-07	354.592	185.3607	539.9527
TCGA-AR-A5QN-01A-12R-A28M-07	637.5483	680.986	1318.534
TCGA-AR-A252-01A-11R-A169-07	1268.562	2454.741	3723.304
TCGA-A8-A08C-01A-11R-A00Z-07	-29.1073	-69.8781	-98.9855
TCGA-D8-A1X8-01A-11R-A14M-07	871.0312	908.3257	1779.357
TCGA-A8-A06X-01A-21R-A00Z-07	297.5506	580.1077	877.6583
TCGA-LL-A50Y-01A-11R-A266-07	39.87822	978.4835	1018.362
TCGA-AN-A049-01A-21R-A00Z-07	776.368	797.5021	1573.87
TCGA-E2-A14W-01A-11R-A12D-07	-441.193	-667.629	-1108.82
TCGA-LD-A9QF-01A-32R-A41B-07	1450.655	2702.04	4152.695
TCGA-D8-A1J8-01A-11R-A13Q-07	775.6169	1538.27	2313.887
TCGA-C8-A275-01A-21R-A16F-07	480.5224	1818.837	2299.36
TCGA-A2-A0YD-01A-11R-A109-07	1482.062	1228.6	2710.663
TCGA-D8-A1JH-01A-11R-A13Q-07	1244.314	973.0456	2217.36
TCGA-D8-A1X9-01A-12R-A157-07	888.3113	757.4187	1645.73
TCGA-E9-A2JS-01A-11R-A180-07	224.2512	37.33185	261.5831
TCGA-AC-A3W5-01A-11R-A22K-07	1464.596	1794.904	3259.5
TCGA-BH-A0C7-01B-11R-A115-07	192.5979	363.468	556.0659
TCGA-AQ-A0Y5-01A-11R-A14M-07	1075.909	335.6985	1411.608
TCGA-A7-A0CD-01A-11R-A00Z-07	71.0026	-277.182	-206.179
TCGA-A8-A08A-01A-11R-A32Y-07	634.6686	778.2095	1412.878
TCGA-A7-A26E-01A-11R-A277-07	1151.604	430.6097	1582.213
TCGA-A8-A09V-01A-11R-A034-07	601.0987	-354.256	246.8428
TCGA-A8-A09K-01A-11R-A00Z-07	-635.614	759.4953	123.881
TCGA-EW-A1IW-01A-11R-A13Q-07	659.6737	578.3143	1237.988
TCGA-C8-A1HF-01A-11R-A137-07	945.2386	1554.357	2499.596
TCGA-AO-A0JI-01A-21R-A056-07	-505.374	-131.136	-636.51
TCGA-D8-A3Z6-01A-11R-A239-07	506.7844	48.90931	555.6937
TCGA-AO-A126-01A-11R-A10J-07	1101.996	622.5388	1724.535
TCGA-E9-A1N3-01A-12R-A157-07	-545.368	-598.082	-1143.45

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-AN-A04A-01A-21R-A034-07	966.894	229.357	1196.251
TCGA-E9-A3X8-01A-31R-A22U-07	940.6986	1521.968	2462.667
TCGA-D8-A27N-01A-11R-A16F-07	1184.871	1152.74	2337.611
TCGA-AR-A0U2-01A-11R-A109-07	-302.459	427.6234	125.1645
TCGA-AO-A0JA-01A-11R-A056-07	1235.396	805.6188	2041.015
TCGA-D8-A147-01A-11R-A115-07	-71.7452	914.9718	843.2266
TCGA-D8-A1JJ-01A-31R-A14M-07	896.9031	498.0246	1394.928
TCGA-EW-A1IX-01A-12R-A144-07	1173.113	529.0541	1702.168
TCGA-A8-A09N-01A-11R-A00Z-07	315.5094	213.6354	529.1447
TCGA-A7-A0CH-01A-21R-A00Z-07	362.8301	-15.2656	347.5645
TCGA-E2-A1IE-01A-11R-A13Q-07	-359.751	-738.322	-1098.07
TCGA-A7-A5ZX-01A-12R-A29R-07	748.17	-9.17635	738.9937
TCGA-A2-A4S3-01A-21R-A266-07	14.63644	997.394	1012.03
TCGA-BH-A1EO-01A-11R-A137-07	1762.219	1118.919	2881.137
TCGA-D8-A4Z1-01A-21R-A266-07	750.1418	450.6213	1200.763
TCGA-GI-A2C9-01A-11R-A21T-07	343.457	554.6482	898.1052
TCGA-Z7-A8R5-01A-42R-A41B-07	619.4029	1605.758	2225.161
TCGA-EW-A1P7-01A-21R-A144-07	1162.052	2643.359	3805.412
TCGA-A7-A13G-01B-04R-A22O-07	605.4785	110.9201	716.3985
TCGA-OL-A66O-01A-11R-A31O-07	-187.004	-297.803	-484.807
TCGA-A8-A083-01A-21R-A00Z-07	-784.433	-177.329	-961.762
TCGA-A2-A0D3-01A-11R-A115-07	-192.06	471.7465	279.687
TCGA-E9-A54X-01A-11R-A266-07	-1780.33	-1063.68	-2844.01
TCGA-D8-A1XU-01A-11R-A14M-07	944.911	517.51	1462.421
TCGA-A8-A07I-01A-11R-A00Z-07	1035.246	812.1313	1847.377
TCGA-E9-A54Y-01A-11R-A466-07	-1135.78	119.9451	-1015.84
TCGA-EW-A2FR-01A-11R-A21T-07	1639.411	782.6616	2422.073
TCGA-S3-A6ZH-01A-22R-A32P-07	-471.72	181.8559	-289.864
TCGA-BH-A18J-01A-11R-A12D-07	667.179	157.8159	824.995
TCGA-D8-A1JD-01A-11R-A13Q-07	1109.967	786.6338	1896.601
TCGA-BH-A0HF-01A-11R-A056-07	1098.827	1070.458	2169.285
TCGA-BH-A1FL-01A-11R-A13Q-07	149.3124	-123.863	25.44899
TCGA-BH-A1FG-01A-11R-A13Q-07	-69.5993	118.75	49.15071
TCGA-BH-A0E7-01A-11R-A034-07	39.3071	-470.015	-430.708
TCGA-BH-A1FR-01A-11R-A13Q-07	11.334	679.1332	690.4672
TCGA-BH-A18L-01A-32R-A12D-07	-663.499	-211.824	-875.323
TCGA-A7-A3IZ-01A-11R-A213-07	-379.409	-161.605	-541.014
TCGA-E2-A15P-01A-11R-A115-07	328.356	-77.2418	251.1141
TCGA-A8-A0A9-01A-11R-A00Z-07	518.4433	449.8194	968.2627
TCGA-A8-A06T-01A-11R-A00Z-07	330.2796	495.2692	825.5489
TCGA-E2-A15G-01A-11R-A12D-07	-155.832	-50.7488	-206.581
TCGA-OL-A5RZ-01A-11R-A28M-07	-492.286	-327.783	-820.07

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-AR-A0TQ-01A-11R-A084-07	296.1889	1234.756	1530.945
TCGA-B6-A1KN-01A-11R-A13Q-07	305.4478	233.7023	539.1501
TCGA-E2-A1II-01A-11R-A144-07	72.37907	2480.916	2553.295
TCGA-AN-A03X-01A-21R-A00Z-07	1435.065	678.4071	2113.473
TCGA-A8-A08I-01A-11R-A00Z-07	-4.22019	2248.734	2244.514
TCGA-E2-A107-01A-11R-A10J-07	-491.631	-19.4475	-511.078
TCGA-A2-A0SW-01A-11R-A084-07	785.1372	1738.339	2523.476
TCGA-A7-A26F-01B-04R-A22O-07	1326.332	1413.063	2739.395
TCGA-D8-A1X6-01A-11R-A14M-07	256.4846	901.6953	1158.18
TCGA-AR-A254-01A-21R-A169-07	1247.876	1548.961	2796.837
TCGA-D8-A1XD-01A-11R-A14D-07	486.3181	-755.25	-268.932
TCGA-E9-A1NG-01A-21R-A14M-07	1888.971	1294.951	3183.922
TCGA-GM-A2DN-01A-11R-A180-07	674.9074	1947.084	2621.992
TCGA-A7-A6VX-01A-12R-A33J-07	582.5163	177.2964	759.8127
TCGA-E2-A1BD-01A-11R-A12P-07	352.6932	36.68973	389.3829
TCGA-E2-A154-01A-11R-A115-07	308.8831	-337.97	-29.0872
TCGA-A7-A13D-01B-04R-A277-07	104.4985	-650.299	-545.8
TCGA-EW-A2FS-01A-11R-A17B-07	125.8324	831.4449	957.2773
TCGA-OL-A66J-01A-11R-A29R-07	806.8557	474.6893	1281.545
TCGA-BH-A0DG-01A-21R-A12P-07	1395.844	1186.16	2582.004
TCGA-B6-A0IK-01A-12R-A056-07	5.711782	423.4338	429.1455
TCGA-EW-A3E8-01B-11R-A24H-07	897.4978	1715.145	2612.643
TCGA-E2-A14P-01A-31R-A12D-07	-400.485	666.5173	266.0323
TCGA-E9-A1N6-01A-11R-A144-07	948.1762	431.411	1379.587
TCGA-BH-A18G-01A-11R-A12D-07	186.3325	488.8252	675.1577
TCGA-A8-A0A2-01A-11R-A034-07	695.8743	663.9198	1359.794
TCGA-C8-A12N-01A-11R-A115-07	1088.538	766.5044	1855.043
TCGA-E9-A1N5-01A-11R-A14D-07	1145.997	1084.947	2230.945
TCGA-LL-A9Q3-01A-11R-A41B-07	327.642	925.4558	1253.098
TCGA-E9-A1R5-01A-11R-A14M-07	608.1203	-65.5964	542.5239
TCGA-AO-A0J8-01A-21R-A034-07	503.1499	894.6839	1397.834
TCGA-D8-A1XV-01A-11R-A14M-07	-622.492	-450.871	-1073.36
TCGA-BH-A0BV-01A-11R-A00Z-07	970.1175	1087.952	2058.069
TCGA-AO-A1KP-01A-11R-A13Q-07	-486.84	-683.072	-1169.91
TCGA-BH-A0HO-01A-11R-A034-07	499.0569	865.3911	1364.448
TCGA-UL-AAZ6-01A-11R-A41B-07	-761.013	62.19552	-698.818
TCGA-E9-A1N8-01A-11R-A144-07	-718.558	-488.607	-1207.17
TCGA-MS-A51U-01A-31R-A266-07	820.0385	679.6545	1499.693
TCGA-AR-A2LO-01A-31R-A18M-07	827.5023	1457.04	2284.543
TCGA-C8-A1HG-01A-11R-A137-07	485.5804	1462.483	1948.063
TCGA-BH-A0H0-01A-11R-A056-07	-464.408	-191.536	-655.943
TCGA-UU-A93S-01A-21R-A41B-07	-776.773	380.9216	-395.852

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-AR-A2LK-01A-11R-A180-07	537.4697	410.2841	947.7538
TCGA-C8-A274-01A-11R-A16F-07	-412.09	-12.6178	-424.707
TCGA-E2-A15A-01A-11R-A12D-07	612.8599	900.2486	1513.108
TCGA-A8-A08B-01A-11R-A00Z-07	-522.119	665.9271	143.8083
TCGA-A8-A06N-01A-11R-A00Z-07	-1517.94	-546.535	-2064.48
TCGA-B6-A1KF-01A-11R-A13Q-07	-192.636	-834.331	-1026.97
TCGA-AR-A24T-01A-11R-A169-07	1513.777	721.9456	2235.722
TCGA-D8-A1X7-01A-11R-A14M-07	425.6273	89.74614	515.3735
TCGA-AC-A3QQ-01B-06R-A22O-07	1032.808	756.4496	1789.257
TCGA-BH-A6R9-01A-21R-A32P-07	2106.169	1964.822	4070.991
TCGA-B6-A0RM-01A-11R-A084-07	-389.169	-345.133	-734.302
TCGA-5T-A9QA-01A-11R-A41B-07	-1463.8	-349.54	-1813.34
TCGA-A8-A085-01A-11R-A00Z-07	199.8931	-685.624	-485.731
TCGA-E2-A159-01A-11R-A115-07	549.1572	1837.364	2386.521
TCGA-AC-A2B8-01A-11R-A17B-07	1284.619	1171.917	2456.536
TCGA-C8-A12Z-01A-11R-A115-07	-84.0037	-310.433	-394.437
TCGA-E9-A229-01A-31R-A157-07	1483.161	953.6353	2436.796
TCGA-PE-A5DC-01A-12R-A27Q-07	-83.6901	123.7811	40.09093
TCGA-AO-A03V-01A-11R-A115-07	-5.01483	-17.5613	-22.5762
TCGA-BH-A1EW-01A-11R-A137-07	446.4243	978.4268	1424.851
TCGA-AC-A2BK-01A-11R-A21T-07	-1321.35	-686.015	-2007.36
TCGA-E2-A1LH-01A-11R-A14D-07	596.9906	2228.104	2825.095
TCGA-BH-A0HK-01A-11R-A056-07	744.0624	538.8814	1282.944
TCGA-AC-A3BB-01A-21R-A19W-07	1237.046	1826.081	3063.127
TCGA-AR-A1AR-01A-31R-A137-07	1090.462	1881.448	2971.911
TCGA-GM-A3NW-01A-21R-A22K-07	-35.2085	298.5093	263.3008
TCGA-AN-A04C-01A-21R-A034-07	-280.731	444.7691	164.0385
TCGA-A2-A25D-01A-12R-A16F-07	564.4129	1974.605	2539.018
TCGA-C8-A273-01A-11R-A16F-07	608.8667	161.6921	770.5589
TCGA-C8-A131-01A-11R-A115-07	570.3256	763.4247	1333.75
TCGA-AC-A2QI-01A-12R-A19W-07	1009.078	1042.318	2051.396
TCGA-AC-A2FM-01A-11R-A19W-07	-92.798	-475.171	-567.969
TCGA-AO-A1KQ-01A-11R-A13Q-07	313.5107	1134.919	1448.43
TCGA-C8-A133-01A-32R-A12D-07	-1180.78	-174.885	-1355.67
TCGA-D8-A1XM-01A-21R-A14M-07	1192.506	1270.396	2462.902
TCGA-AN-A0XL-01A-11R-A10J-07	1108.434	126.2597	1234.694
TCGA-C8-A12T-01A-11R-A115-07	911.0357	442.6516	1353.687
TCGA-E2-A15O-01A-11R-A115-07	-502.745	-35.6848	-538.43
TCGA-OL-A5RU-01A-11R-A28M-07	364.8265	1642.756	2007.583
TCGA-AN-A046-01A-21R-A034-07	903.3392	1515.551	2418.89
TCGA-AN-A0FK-01A-11R-A034-07	54.1933	5.054238	59.24754
TCGA-D8-A27M-01A-11R-A16F-07	1145.803	2035.197	3181

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-A2-A0YF-01A-21R-A109-07	173.4318	638.5214	811.9533
TCGA-A8-A08P-01A-11R-A00Z-07	1046.999	1813.959	2860.958
TCGA-AO-A12H-01A-11R-A115-07	-78.6807	159.2628	80.58207
TCGA-D8-A1XL-01A-11R-A14M-07	209.9127	1671.025	1880.938
TCGA-E9-A1NI-01A-11R-A14D-07	735.979	197.3277	933.3067
TCGA-A2-A0YH-01A-11R-A109-07	1141.447	1698.336	2839.783
TCGA-A2-A04Q-01A-21R-A034-07	1012.099	2765.754	3777.853
TCGA-BH-A42V-01A-11R-A24H-07	765.0166	933.5393	1698.556
TCGA-D8-A1JN-01A-11R-A13Q-07	-927.665	128.0942	-799.571
TCGA-A2-A0CK-01A-11R-A22K-07	508.8867	720.8016	1229.688
TCGA-BH-A0BQ-01A-21R-A115-07	1142.005	1083.591	2225.596
TCGA-BH-A0DK-01A-21R-A056-07	1380.024	1952.503	3332.527
TCGA-AR-A24W-01A-11R-A169-07	708.9092	-147.423	561.4865
TCGA-A8-A07G-01A-11R-A034-07	1208.918	607.3049	1816.223
TCGA-A2-A0CT-01A-31R-A056-07	-167.11	-51.2179	-218.328
TCGA-B6-A0IN-01A-11R-A034-07	997.7566	1524.57	2522.327
TCGA-A2-A0CU-01A-12R-A034-07	242.0714	-147.016	95.05559
TCGA-B6-A0RN-01A-12R-A084-07	691.916	-174.624	517.2917
TCGA-A2-A0SV-01A-11R-A084-07	841.0259	1187.973	2028.999
TCGA-E2-A15K-06A-11R-A12P-07	-1179.49	-133.75	-1313.24
TCGA-A7-A26H-01A-11R-A169-07	1021.029	840.6603	1861.689
TCGA-C8-A12V-01A-11R-A115-07	833.1775	2956.843	3790.02
TCGA-A8-A082-01A-11R-A00Z-07	287.748	353.3295	641.0776
TCGA-E2-A1L6-01A-11R-A13Q-07	480.304	404.5206	884.8246
TCGA-A1-A0SM-01A-11R-A084-07	912.0325	469.8834	1381.916
TCGA-E2-A1B5-01A-21R-A12P-07	849.1319	2645.375	3494.507
TCGA-E2-A2P6-01A-11R-A19W-07	72.17081	423.0387	495.2095
TCGA-D8-A1JI-01A-11R-A13Q-07	-367.765	6.879369	-360.886
TCGA-S3-AA17-01A-11R-A41B-07	576.549	2380.767	2957.316
TCGA-B6-A40C-01A-11R-A239-07	781.2876	653.3194	1434.607
TCGA-A8-A091-01A-11R-A00Z-07	169.177	117.6703	286.8473
TCGA-AC-A7VC-01A-11R-A352-07	954.591	653.3246	1607.916
TCGA-AR-A1AO-01A-11R-A12P-07	1625.519	2693.983	4319.502
TCGA-AO-A1KR-01A-12R-A144-07	-919.954	454.4652	-465.489
TCGA-A8-A06Y-01A-21R-A00Z-07	-849.514	-535.032	-1384.55
TCGA-BH-A1FE-01A-11R-A13Q-07	1194.594	1567.315	2761.909
TCGA-E9-A3HO-01A-11R-A213-07	-155.433	822.8983	667.4657
TCGA-A2-A3Y0-01A-11R-A239-07	-349.147	1429.845	1080.697
TCGA-BH-A0H9-01A-11R-A056-07	-42.3523	-60.3187	-102.671
TCGA-GM-A2DF-01A-11R-A180-07	582.3275	1706.133	2288.461
TCGA-D8-A1JF-01A-11R-A13Q-07	808.0212	534.7868	1342.808

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-E9-A1RH-01A-21R-A169-07	272.8545	129.3158	402.1704
TCGA-AO-A0J2-01A-11R-A034-07	-200.919	1074.81	873.8908
TCGA-B6-A0IP-01A-11R-A034-07	48.37279	371.1902	419.563
TCGA-BH-A0GY-01A-11R-A056-07	426.4957	707.6625	1134.158
TCGA-A7-A6VY-01A-12R-A33J-07	572.1738	1479.049	2051.223
TCGA-E2-A15K-01A-11R-A12P-07	359.651	1261.519	1621.17
TCGA-D8-A1JE-01A-11R-A13Q-07	1456.41	778.9514	2235.361
TCGA-LL-A440-01A-11R-A24H-07	1646.531	1668.589	3315.12
TCGA-BH-A0BR-01A-21R-A115-07	1395.899	1118.376	2514.275
TCGA-D8-A1J9-01A-11R-A13Q-07	835.4996	525.2199	1360.719
TCGA-B6-A0RV-01A-11R-A084-07	125.3533	848.541	973.8943
TCGA-E9-A5UO-01A-11R-A28M-07	-1185.38	-768.869	-1954.25
TCGA-BH-A0C3-01A-21R-A12P-07	1329.285	1225.316	2554.601
TCGA-JL-A3YW-01A-12R-A239-07	1550.597	1735.731	3286.329
TCGA-B6-A0I8-01A-11R-A034-07	198.9268	-455.099	-256.172
TCGA-E2-A10F-01A-11R-A10J-07	1327.489	1319.296	2646.785
TCGA-AN-A0FW-01A-11R-A034-07	378.375	245.0547	623.4298
TCGA-AR-A1AL-01A-21R-A12P-07	982.5787	640.9186	1623.497
TCGA-BH-A1F2-01A-31R-A13Q-07	1087.943	301.727	1389.67
TCGA-BH-A0EB-01A-11R-A034-07	1293.988	1532.985	2826.972
TCGA-B6-A402-01A-11R-A239-07	-428.766	-352.656	-781.422
TCGA-AC-A2FF-01A-11R-A17B-07	1615.571	1478.603	3094.174
TCGA-E2-A15F-01A-11R-A115-07	-109.959	156.5899	46.63054
TCGA-AO-A03R-01A-21R-A034-07	88.29943	1242.222	1330.522
TCGA-E2-A15S-01A-11R-A115-07	-877.33	-800.121	-1677.45
TCGA-BH-A0B5-01A-11R-A12P-07	638.2503	757.0109	1395.261
TCGA-E9-A1RB-01A-11R-A157-07	21.46747	149.4424	170.9098
TCGA-OL-A66N-01A-12R-A31O-07	691.9623	1097.497	1789.459
TCGA-4H-AAAK-01A-12R-A41B-07	1150.833	528.3564	1679.189
TCGA-A7-A0CJ-01A-21R-A00Z-07	-421.907	41.61098	-380.296
TCGA-BH-A0W4-01A-11R-A109-07	531.8684	-265.717	266.1516
TCGA-BH-A0BT-01A-11R-A12P-07	396.2768	533.7987	930.0756
TCGA-C8-A135-01A-11R-A115-07	697.1139	845.9094	1543.023
TCGA-A8-A09X-01A-11R-A00Z-07	1116.332	1736.487	2852.82
TCGA-A2-A04N-01A-11R-A115-07	871.8746	221.6774	1093.552
TCGA-E9-A244-01A-11R-A169-07	7.459725	9.75598	17.2157
TCGA-AN-A0FL-01A-11R-A034-07	-589.75	-254.751	-844.501
TCGA-AN-A0AS-01A-11R-A00Z-07	945.8897	695.586	1641.476
TCGA-BH-A0E1-01A-11R-A056-07	267.0232	-173.582	93.44127
TCGA-D8-A27I-01A-11R-A16F-07	1348.811	1334.623	2683.433
TCGA-C8-A1HE-01A-11R-A13Q-07	134.6316	240.5281	375.1597
TCGA-BH-A0DL-01A-11R-A115-07	106.5185	1909.096	2015.614

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-AQ-A7U7-01A-22R-A352-07	1627.254	2614.509	4241.763
TCGA-E2-A14Q-01A-11R-A12D-07	195.4108	199.6547	395.0655
TCGA-AO-A12E-01A-11R-A10J-07	582.8914	680.6227	1263.514
TCGA-C8-A8HP-01A-11R-A36F-07	439.7177	1769.667	2209.385
TCGA-BH-A1EX-01A-11R-A13Q-07	1077.812	902.1673	1979.979
TCGA-AO-A0JC-01A-11R-A056-07	701.9085	3672.572	4374.48
TCGA-BH-A0BM-01A-11R-A056-07	751.0524	249.7343	1000.787
TCGA-A7-A3RF-01A-11R-A22K-07	-260.699	-451.449	-712.147
TCGA-AQ-A04L-01B-21R-A10J-07	475.1579	134.2401	609.3981
TCGA-AC-A23E-01A-11R-A157-07	1617.035	733.9818	2351.017
TCGA-E2-A572-01A-13R-A31O-07	-620.858	156.1652	-464.693
TCGA-E2-A1LK-01A-21R-A14D-07	-1049.31	139.4484	-909.857
TCGA-BH-A0C1-01B-11R-A12D-07	740.5608	849.7702	1590.331
TCGA-A1-A0SH-01A-11R-A084-07	1514.031	400.4648	1914.496
TCGA-LL-A8F5-01A-11R-A36F-07	19.62501	1103.509	1123.134
TCGA-BH-A1FN-01A-11R-A13Q-07	381.4059	112.5716	493.9775
TCGA-OK-A5Q2-01A-11R-A27Q-07	700.0521	1420.35	2120.402
TCGA-EW-A1OZ-01A-11R-A144-07	653.7616	730.5923	1384.354
TCGA-GM-A3NY-01A-11R-A21T-07	152.2355	317.6782	469.9137
TCGA-BH-A0HU-01A-11R-A034-07	-311.013	7.70059	-303.312
TCGA-A8-A06O-01A-11R-A00Z-07	465.5005	473.4211	938.9216
TCGA-GM-A2DL-01A-11R-A18M-07	1192.773	802.6466	1995.42
TCGA-OL-A66L-01A-12R-A31O-07	894.8982	1394.557	2289.455
TCGA-BH-A5IZ-01A-11R-A27Q-07	-385.122	269.5012	-115.621
TCGA-A2-A0T4-01A-31R-A084-07	1221.45	1232.871	2454.321
TCGA-E2-A1IK-01A-11R-A144-07	-151.314	1174.666	1023.351
TCGA-A8-A09T-01A-11R-A00Z-07	567.5435	336.0982	903.6417
TCGA-E2-A1B6-01A-31R-A12P-07	67.83951	2799.006	2866.845
TCGA-AR-A24O-01A-11R-A169-07	1606.662	1175.783	2782.445
TCGA-D8-A1JM-01A-11R-A13Q-07	-1234.56	141.4302	-1093.13
TCGA-A2-A04P-01A-31R-A034-07	380.1929	1285.486	1665.679
TCGA-D8-A1XS-01A-11R-A14M-07	817.4659	352.2442	1169.71
TCGA-C8-A26Y-01A-11R-A16F-07	-668.467	515.8996	-152.567
TCGA-B6-A2IU-01A-32R-A18M-07	-247.622	-322.476	-570.098
TCGA-AQ-A54O-01A-11R-A266-07	-149.626	613.9511	464.3255
TCGA-AC-A62V-01A-11R-A31O-07	247.0104	255.4636	502.474
TCGA-D8-A1JC-01A-11R-A13Q-07	614.4136	660.1372	1274.551
TCGA-B6-A0IB-01A-11R-A034-07	-668.498	-728.912	-1397.41
TCGA-D8-A1XF-01A-11R-A14D-07	-848.746	-399.854	-1248.6
TCGA-E2-A15E-01A-11R-A12D-07	216.3034	-426.175	-209.872
TCGA-E2-A10A-01A-21R-A115-07	212.2516	278.3571	490.6087
TCGA-AR-A0TV-01A-21R-A084-07	-196.123	1271.524	1075.401

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-AO-A129-01A-21R-A10J-07	277.0341	1586.026	1863.06
TCGA-AO-A0JE-01A-11R-A056-07	1509.47	1738.304	3247.774
TCGA-E2-A155-01A-11R-A12D-07	-503.67	-583.583	-1087.25
TCGA-A2-A0ET-01A-31R-A034-07	-694.436	440.1853	-254.25
TCGA-BH-A0EE-01A-11R-A034-07	-1087.33	742.2632	-345.069
TCGA-BH-A0B0-01A-21R-A115-07	1176.52	1331.177	2507.698
TCGA-BH-A18R-01A-11R-A12D-07	-200.751	376.6011	175.8498
TCGA-BH-A0AZ-01A-21R-A12P-07	1674.43	726.3399	2400.77
TCGA-GI-A2C8-01A-11R-A16F-07	1515.506	1195.235	2710.741
TCGA-GM-A3XN-01A-12R-A22U-07	1215.533	1125.132	2340.665
TCGA-EW-A1IY-01A-11R-A13Q-07	1213.353	1607.799	2821.153
TCGA-AN-A0XT-01A-11R-A109-07	103.5683	-70.3559	33.21241
TCGA-S3-A6ZF-01A-32R-A32P-07	315.5398	805.0783	1120.618
TCGA-OL-A66I-01A-21R-A29R-07	989.126	2677.521	3666.647
TCGA-E2-A9RU-01A-11R-A41B-07	299.3331	517.2123	816.5454
TCGA-E2-A1B1-01A-21R-A12P-07	1508.528	1626.312	3134.84
TCGA-A2-A04W-01A-31R-A115-07	632.4285	300.521	932.9496
TCGA-E2-A14X-01A-11R-A115-07	88.94032	1284.196	1373.136
TCGA-BH-A0DT-01A-21R-A12D-07	745.2452	823.5593	1568.805
TCGA-B6-A0IC-01A-11R-A034-07	-1539.98	-479.891	-2019.87
TCGA-AR-A0TU-01A-31R-A109-07	-687.236	1206.421	519.1851
TCGA-AR-A2LJ-01A-12R-A19W-07	1060.36	1865.057	2925.417
TCGA-E9-A22A-01A-11R-A157-07	1672.066	1583.114	3255.18
TCGA-E2-A1IN-01A-11R-A13Q-07	1114.23	109.2306	1223.46
TCGA-E2-A15R-01A-11R-A115-07	-506.843	-863.543	-1370.39
TCGA-B6-A0WT-01A-11R-A109-07	666.4318	-56.9762	609.4556
TCGA-AR-A2LM-01A-11R-A180-07	1163.349	550.6785	1714.028
TCGA-A2-A0YK-01A-22R-A109-07	1264.906	2135.919	3400.825
TCGA-AR-A0TZ-01A-12R-A084-07	97.28027	-142.661	-45.3807
TCGA-AN-A0XS-01A-22R-A109-07	1131.336	1196.099	2327.435
TCGA-BH-A42U-01A-12R-A24H-07	712.6805	1407.938	2120.618
TCGA-D8-A1Y2-01A-11R-A157-07	1709.525	2239.124	3948.649
TCGA-A2-A0T1-01A-21R-A084-07	1393.135	2146.91	3540.044
TCGA-A8-A07R-01A-21R-A034-07	-635.922	-159.932	-795.854
TCGA-A2-A0CQ-01A-21R-A034-07	-63.7033	755.6686	691.9652
TCGA-B6-A0X1-01A-11R-A109-07	-602.932	1098.577	495.6451
TCGA-EW-A1PE-01A-11R-A144-07	959.8381	1455.833	2415.671
TCGA-E2-A105-01A-11R-A10J-07	-487.449	-357.277	-844.726
TCGA-E2-A3DX-01A-21R-A213-07	1523.438	1987.279	3510.717
TCGA-LL-A442-01A-11R-A24H-07	-327.71	599.6283	271.9179
TCGA-GM-A2DH-01A-11R-A180-07	-41.9396	1608.152	1566.212
TCGA-BH-A0B7-01A-12R-A115-07	1036.709	1688.354	2725.062

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-BH-A1F5-01A-12R-A13Q-07	120.5441	-238.441	-117.897
TCGA-A2-A3XZ-01A-42R-A239-07	92.38918	1883.586	1975.975
TCGA-A7-A0DB-01C-02R-A277-07	1163.98	138.5772	1302.557
TCGA-Z7-A8R6-01A-11R-A41B-07	-98.5055	181.559	83.05344
TCGA-OL-A6VQ-01A-12R-A41B-07	942.2669	670.6117	1612.879
TCGA-BH-A0W5-01A-11R-A109-07	979.7997	2093.378	3073.178
TCGA-AN-A0FJ-01A-11R-A00Z-07	179.1662	6.508184	185.6744
TCGA-BH-A28O-01A-11R-A22K-07	1081.86	548.1975	1630.057
TCGA-AR-A5QP-01A-11R-A28M-07	568.0603	377.7524	945.8126
TCGA-LL-A6FP-01A-11R-A31O-07	-1045.65	-489.328	-1534.97
TCGA-C8-A12X-01A-11R-A115-07	74.77738	357.3881	432.1655
TCGA-B6-A0I6-01A-11R-A034-07	290.093	-80.6433	209.4497
TCGA-AC-A2FE-01A-11R-A19W-07	1122.768	2044.423	3167.192
TCGA-A7-A13F-01A-11R-A12P-07	105.4052	208.7168	314.122
TCGA-AC-A6IX-01A-12R-A32P-07	1144.207	1000.226	2144.433
TCGA-D8-A1JS-01A-11R-A13Q-07	-1014.67	-296.948	-1311.61
TCGA-AC-A6IX-06A-11R-A32P-07	122.5068	1925.096	2047.603
TCGA-B6-A0WZ-01A-11R-A109-07	-2.56319	-275.545	-278.108
TCGA-AR-A0TW-01A-11R-A084-07	161.4651	1208.318	1369.783
TCGA-AO-A0J7-01A-11R-A034-07	-363.883	-482.582	-846.465
TCGA-AN-A0XR-01A-11R-A109-07	-194.177	-301.203	-495.379
TCGA-AQ-A04H-01B-11R-A10J-07	-146.855	-192.393	-339.249
TCGA-A2-A0CW-01A-21R-A115-07	-463.577	543.8826	80.30527
TCGA-E2-A15T-01A-11R-A115-07	-659.168	-568.555	-1227.72
TCGA-E2-A14T-01A-11R-A115-07	-71.8007	309.3122	237.5115
TCGA-AR-A255-01A-11R-A169-07	1169.103	962.3101	2131.413
TCGA-BH-A18H-01A-11R-A12D-07	546.5554	1848.304	2394.859
TCGA-A8-A07P-01A-11R-A00Z-07	583.4555	485.8967	1069.352
TCGA-D8-A1JK-01A-11R-A13Q-07	917.8517	1687.361	2605.213
TCGA-BH-A0DP-01A-21R-A056-07	954.3696	1028.307	1982.676
TCGA-BH-A0H3-01A-11R-A12P-07	1102.593	748.5467	1851.14
TCGA-AR-A0TS-01A-11R-A115-07	635.7285	2182.786	2818.514
TCGA-E9-A22B-01A-11R-A157-07	960.589	503.5976	1464.187
TCGA-A2-A0SU-01A-11R-A084-07	436.689	529.3933	966.0823
TCGA-B6-A0WS-01A-11R-A115-07	911.1775	1450.921	2362.099
TCGA-BH-A0H5-01A-21R-A115-07	822.9571	3071.227	3894.184
TCGA-AR-A251-01A-12R-A169-07	157.8719	262.5329	420.4048
TCGA-BH-A203-01A-12R-A169-07	341.7357	1056.522	1398.258
TCGA-LL-A6FR-01A-12R-A31O-07	401.3968	256.0778	657.4746
TCGA-AR-A0TT-01A-31R-A084-07	1284.974	2562.753	3847.727
TCGA-A2-A3XU-01A-12R-A22U-07	-1136.4	-673.145	-1809.55
TCGA-E9-A1RC-01A-11R-A157-07	-80.1232	-505.341	-585.464

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-OL-A5S0-01A-11R-A28M-07	755.9052	1267.145	2023.05
TCGA-A1-A0SI-01A-11R-A144-07	1336.878	1127.83	2464.707
TCGA-AO-A0JL-01A-11R-A056-07	8.92155	-14.4606	-5.53904
TCGA-C8-A12L-01A-11R-A115-07	-298.575	281.9975	-16.5774
TCGA-A1-A0SD-01A-11R-A115-07	897.9876	448.4575	1346.445
TCGA-BH-A0HL-01A-11R-A10U-07	-1040.79	-1123.32	-2164.11
TCGA-EW-A1P0-01A-11R-A144-07	185.7129	344.6405	530.3534
TCGA-A2-A0T7-01A-21R-A084-07	765.3267	464.0035	1229.33
TCGA-A8-A086-01A-11R-A00Z-07	912.5523	111.7766	1024.329
TCGA-AR-A0TX-01A-11R-A084-07	937.7344	1785.05	2722.785
TCGA-A2-A1FX-01A-11R-A13Q-07	703.9401	621.4645	1325.405
TCGA-A2-A0YL-01A-21R-A109-07	894.5677	730.2851	1624.853
TCGA-AO-A0JB-01A-11R-A32Y-07	298.3392	644.7256	943.0648
TCGA-PE-A5DD-01A-12R-A27Q-07	679.081	884.8451	1563.926
TCGA-A2-A3XX-01A-21R-A239-07	75.7561	777.0301	852.7862
TCGA-A2-A1G1-01A-21R-A13Q-07	945.6563	1441.786	2387.443
TCGA-C8-A12P-01A-11R-A115-07	835.966	634.3436	1470.31
TCGA-A2-A25F-01A-11R-A169-07	2025.063	3330.563	5355.625
TCGA-AR-A1AS-01A-11R-A12P-07	105.9054	103.9979	209.9033
TCGA-BH-A0DX-01A-11R-A115-07	1318.567	1219.951	2538.518
TCGA-BH-A0B3-01A-11R-A056-07	623.6845	1349.342	1973.026
TCGA-A8-A0AB-01A-11R-A034-07	-225.123	-788.358	-1013.48
TCGA-AN-A0FD-01A-11R-A034-07	960.0156	570.4925	1530.508
TCGA-BH-A0E0-01A-11R-A056-07	-690.063	343.1055	-346.957
TCGA-EW-A1P6-01A-11R-A144-07	601.3752	-33.8744	567.5008
TCGA-C8-A1HN-01A-11R-A137-07	25.37219	219.7926	245.1648
TCGA-BH-A1ES-06A-12R-A24H-07	-778.799	-297.407	-1076.21
TCGA-BH-A0DD-01A-31R-A12P-07	-51.5225	61.66404	10.1415
TCGA-AC-A2FK-01A-12R-A180-07	387.5003	624.514	1012.014
TCGA-E9-A227-01A-11R-A157-07	822.152	1377.997	2200.149
TCGA-A7-A4SB-01A-21R-A266-07	66.73792	-412.844	-346.106
TCGA-AN-A0FN-01A-11R-A034-07	2109.483	2164.239	4273.722
TCGA-A2-A0EX-01A-21R-A034-07	995.839	543.7979	1539.637
TCGA-AR-A24M-01A-11R-A169-07	958.1618	290.7916	1248.953
TCGA-A7-A5ZW-01A-12R-A29R-07	1312.818	759.2034	2072.021
TCGA-BH-A0WA-01A-11R-A109-07	187.1007	362.8875	549.9882
TCGA-AR-A24V-01A-21R-A169-07	1544.23	852.8681	2397.098
TCGA-A2-A4S0-01A-21R-A266-07	-513.76	-285.982	-799.742
TCGA-AC-A62Y-01A-11R-A29R-07	634.0315	1285.572	1919.603
TCGA-AR-A1AY-01A-21R-A12P-07	-116.704	6.020758	-110.683
TCGA-E2-A1IF-01A-11R-A144-07	855.2292	547.1291	1402.358
TCGA-C8-A26X-01A-31R-A16F-07	1256.999	2099.988	3356.986

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-BH-A0HW-01A-11R-A034-07	-1159.13	-994.707	-2153.83
TCGA-S3-AA10-01A-21R-A41B-07	297.2685	2313.035	2610.303
TCGA-BH-A201-01A-11R-A14M-07	899.2896	1.501701	900.7913
TCGA-A8-A08T-01A-21R-A00Z-07	378.5585	98.64183	477.2003
TCGA-BH-A0HQ-01A-11R-A034-07	609.6994	44.91707	654.6165
TCGA-AO-A0J4-01A-11R-A034-07	211.2342	1423.836	1635.071
TCGA-D8-A1XC-01A-11R-A14D-07	-948.68	-347.426	-1296.11
TCGA-3C-AALJ-01A-31R-A41B-07	508.1145	1144.377	1652.492
TCGA-BH-A209-01A-11R-A157-07	539.8323	2384.329	2924.161
TCGA-BH-A18P-01A-11R-A12D-07	347.1617	329.8238	676.9855
TCGA-AR-A1AW-01A-21R-A12P-07	1179.695	3087.187	4266.882
TCGA-BH-A1FJ-01A-11R-A13Q-07	-338.83	-564.255	-903.085
TCGA-A2-A0CZ-01A-11R-A034-07	1454.083	1187.103	2641.186
TCGA-A2-A0ST-01A-12R-A084-07	653.3262	3028.762	3682.088
TCGA-AC-A4ZE-01A-11R-A41B-07	-94.4751	-39.3839	-133.859
TCGA-AO-A12G-01A-11R-A10J-07	738.5308	421.1004	1159.631
TCGA-E9-A1RA-01A-11R-A14D-07	384.7664	463.0363	847.8027
TCGA-A1-A0SG-01A-11R-A144-07	647.4868	587.9347	1235.422
TCGA-A7-A4SD-01A-11R-A266-07	495.9436	1399.437	1895.381
TCGA-EW-A6SD-01A-12R-A33J-07	420.6123	1230.251	1650.863
TCGA-E2-A14V-01A-11R-A12D-07	-216.415	-285.371	-501.785
TCGA-E9-A226-01A-21R-A157-07	797.9951	-72.8177	725.1774
TCGA-A8-A09B-01A-11R-A00Z-07	427.4128	72.81319	500.226
TCGA-E2-A156-01A-11R-A12D-07	-727.092	-365.934	-1093.03
TCGA-A8-A08H-01A-21R-A00Z-07	1919.957	2566.119	4486.076
TCGA-BH-A0DQ-01A-11R-A084-07	1368.56	548.5919	1917.152
TCGA-AO-A1KT-01A-11R-A13Q-07	768.1988	539.329	1307.528
TCGA-AC-A8OQ-01A-11R-A41B-07	876.3415	1517.855	2394.197
TCGA-B6-A0X0-01A-21R-A115-07	-737.454	-281.364	-1018.82
TCGA-A7-A4SA-01A-11R-A266-07	793.8767	1650.843	2444.719
TCGA-AC-A3W6-01A-12R-A22K-07	1514.684	1669.29	3183.974
TCGA-E2-A158-01A-11R-A12D-07	-1168.01	-401.355	-1569.36
TCGA-AO-A0J5-01A-11R-A034-07	1308.896	304.502	1613.398
TCGA-A8-A06Z-01A-11R-A00Z-07	-639.718	-155.581	-795.299
TCGA-A8-A09E-01A-11R-A00Z-07	-203.949	-239.803	-443.752
TCGA-AR-A2LR-01A-12R-A18M-07	739.3271	-1.55485	737.7722
TCGA-A2-A0D1-01A-11R-A034-07	-295.214	-366.353	-661.567
TCGA-D8-A1XT-01A-11R-A14M-07	1174.823	882.3971	2057.22
TCGA-WT-AB41-01A-11R-A41B-07	249.0038	2264.202	2513.206
TCGA-AO-A0JF-01A-11R-A056-07	1616.348	1199.019	2815.367
TCGA-BH-A1F0-01A-11R-A137-07	1389.358	2497.862	3887.22
TCGA-D8-A1XJ-01A-11R-A14M-07	366.6069	17.66356	384.2705

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-E9-A1RD-01A-11R-A157-07	489.222	204.7444	693.9664
TCGA-EW-A3U0-01A-11R-A22K-07	999.9527	2696.632	3696.585
TCGA-AC-A2QJ-01A-12R-A19W-07	1254.487	1956.35	3210.837
TCGA-E9-A1N4-01A-11R-A14M-07	1022.581	1435.724	2458.305
TCGA-C8-A1HO-01A-11R-A13Q-07	-134.2	-218.157	-352.357
TCGA-A8-A08G-01A-11R-A00Z-07	424.749	503.5932	928.3421
TCGA-GM-A2DD-01A-11R-A180-07	1249.25	2302.757	3552.006
TCGA-C8-A26W-01A-11R-A16F-07	660.1169	1095.1	1755.216
TCGA-LQ-A4E4-01A-11R-A266-07	-147.797	-515.605	-663.403
TCGA-C8-A12W-01A-11R-A115-07	990.2119	733.7251	1723.937
TCGA-BH-A18I-01A-11R-A12D-07	1413.6	1260.241	2673.841
TCGA-AC-A62X-01A-11R-A29R-07	-854.854	-283.179	-1138.03
TCGA-A8-A09Q-01A-11R-A00Z-07	906.2845	1477.412	2383.697
TCGA-BH-A0B6-01A-11R-A19W-07	1033.296	2592.293	3625.589
TCGA-BH-A8FY-01A-11R-A36F-07	-695.887	196.7842	-499.103
TCGA-A7-A26E-01B-06R-A277-07	1148.99	453.3545	1602.345
TCGA-D8-A27E-01A-11R-A16F-07	-14.2502	301.6555	287.4053
TCGA-AC-A3W7-01A-11R-A22K-07	559.2791	187.2385	746.5177
TCGA-E2-A15H-01A-11R-A12D-07	127.5582	-142.524	-14.9655
TCGA-B6-A0I2-01A-11R-A034-07	-332.881	2019.57	1686.689
TCGA-B6-A0IE-01A-11R-A034-07	84.362	-45.8996	38.46237
TCGA-AQ-A1H3-01A-31R-A13Q-07	839.4353	715.7597	1555.195
TCGA-BH-A0BC-01A-22R-A084-07	1112.558	1535.932	2648.489
TCGA-AR-A0U4-01A-11R-A109-07	629.5442	2164.562	2794.106
TCGA-LL-A7SZ-01A-32R-A352-07	544.834	2036.24	2581.074
TCGA-A7-A13D-01A-13R-A277-07	41.17683	-385.465	-344.289
TCGA-GM-A2DK-01A-21R-A180-07	807.7075	944.96	1752.667
TCGA-AN-A0FZ-01A-11R-A034-07	158.5832	-351.501	-192.918
TCGA-AN-A0AT-01A-11R-A034-07	-479.205	509.2958	30.09061
TCGA-BH-A0GZ-01A-11R-A056-07	670.5231	152.734	823.2571
TCGA-A7-A26E-01A-11R-A169-07	905.2366	186.3171	1091.554
TCGA-A7-A5ZV-01A-11R-A28M-07	-365.996	583.3078	217.3116
TCGA-A7-A4SC-01A-12R-A266-07	751.5316	641.9556	1393.487
TCGA-AN-A0FT-01A-11R-A034-07	773.5763	641.4723	1415.049
TCGA-A2-A1G0-01A-11R-A13Q-07	975.729	855.5105	1831.24
TCGA-A8-A08X-01A-21R-A00Z-07	1100.633	1375.379	2476.013
TCGA-A7-A13E-01B-06R-A277-07	1289.183	1509.585	2798.768
TCGA-D8-A1XA-01A-11R-A14D-07	254.5209	245.4157	499.9365
TCGA-D8-A27F-01A-11R-A16F-07	461.0445	181.9832	643.0277
TCGA-BH-A208-01A-11R-A157-07	2068.331	762.1649	2830.496
TCGA-A7-A13H-01A-11R-A22K-07	736.7682	1598.352	2335.12
TCGA-E2-A10E-01A-21R-A10J-07	88.57744	298.4154	386.9929

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-A1-A0SO-01A-22R-A084-07	-1129.73	-583.059	-1712.79
TCGA-E9-A22H-01A-11R-A157-07	-85.067	477.937	392.8699
TCGA-D8-A1XZ-01A-11R-A14M-07	682.761	754.1715	1436.933
TCGA-D8-A1XO-01A-11R-A14M-07	1146.792	782.6289	1929.42
TCGA-C8-A1HJ-01A-11R-A13Q-07	-263.133	133.7804	-129.352
TCGA-B6-A0IH-01A-11R-A115-07	963.0788	1045.692	2008.771
TCGA-GM-A2DC-01A-11R-A18M-07	-259.189	5.94529	-253.244
TCGA-A1-A0SB-01A-11R-A144-07	-366.731	-1064.42	-1431.16
TCGA-AO-A03P-01A-11R-A00Z-07	87.27544	-19.8291	67.44632
TCGA-E2-A15L-01A-11R-A12D-07	535.3498	-95.2432	440.1066
TCGA-A2-A25C-01A-11R-A169-07	665.3412	431.3032	1096.644
TCGA-D8-A1X5-01A-11R-A14D-07	784.1902	780.163	1564.353
TCGA-B6-A0RT-01A-21R-A084-07	947.3707	3126.038	4073.409
TCGA-LL-A73Y-01A-11R-A33J-07	725.5302	1136.015	1861.545
TCGA-A2-A0CO-01A-13R-A22K-07	1114.083	1926.567	3040.65
TCGA-A8-A0A7-01A-11R-A00Z-07	1527.586	2753.51	4281.096
TCGA-AO-A03N-01B-11R-A10J-07	410.0172	62.81878	472.8359
TCGA-AR-A0TR-01A-11R-A084-07	-1221.66	-96.8081	-1318.46
TCGA-BH-A1FU-01A-11R-A14D-07	1206.157	1023.288	2229.445
TCGA-C8-A1HM-01A-12R-A137-07	13.77551	2169.838	2183.613
TCGA-AQ-A54N-01A-11R-A266-07	-1433.08	37.30281	-1395.77
TCGA-A2-A0CM-01A-31R-A034-07	681.5476	1728.242	2409.79
TCGA-AR-A2LN-01A-21R-A18M-07	1418.376	909.4092	2327.785
TCGA-BH-A0BD-01A-11R-A034-07	754.0753	1116.901	1870.976
TCGA-A2-A3XT-01A-11R-A22U-07	283.6683	1709.613	1993.281
TCGA-A7-A4SF-01A-11R-A266-07	-137.428	338.0649	200.6367
TCGA-A2-A0T0-01A-22R-A084-07	398.4611	548.1414	946.6025
TCGA-BH-A0AW-01A-11R-A056-07	1136.314	2243.975	3380.289
TCGA-A7-A425-01A-11R-A24H-07	762.0663	971.3269	1733.393
TCGA-D8-A13Z-01A-11R-A115-07	637.8675	1179.137	1817.004
TCGA-LD-A66U-01A-11R-A31O-07	682.2014	1428.589	2110.791
TCGA-A8-A079-01A-21R-A00Z-07	-250.388	263.1151	12.72694
TCGA-EW-A6S9-01A-22R-A33J-07	633.1273	127.0777	760.205
TCGA-BH-A0DO-01B-11R-A12D-07	167.1955	-107.012	60.18328
TCGA-B6-A401-01A-11R-A239-07	459.7458	996.8263	1456.572
TCGA-3C-AAAU-01A-11R-A41B-07	-628.397	-491.601	-1120
TCGA-A7-A2KD-01A-31R-A21T-07	946.0329	1101.539	2047.572
TCGA-AR-A1AX-01A-11R-A12P-07	930.8421	2244.811	3175.654
TCGA-A2-A0YJ-01A-11R-A109-07	-653.773	-338.038	-991.811
TCGA-A8-A08O-01A-21R-A056-07	484.6263	-406.705	77.92116
TCGA-BH-A0B8-01A-21R-A056-07	230.9847	41.26919	272.2539
TCGA-A2-A0D2-01A-21R-A034-07	223.7987	1139.734	1363.533

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-5L-AAT0-01A-12R-A41B-07	1088.982	1299.854	2388.836
TCGA-A2-A0EW-01A-21R-A115-07	1339.088	985.9865	2325.075
TCGA-AR-A0TY-01A-12R-A115-07	-362.611	-203.469	-566.08
TCGA-A2-A3KC-01A-11R-A213-07	1074.267	781.5876	1855.854
TCGA-BH-A0BG-01A-11R-A115-07	116.4027	1594.355	1710.758
TCGA-AR-A24U-01A-11R-A169-07	1268.507	1924.653	3193.16
TCGA-A8-A096-01A-11R-A00Z-07	1407.314	1773.404	3180.718
TCGA-A8-A09G-01A-21R-A00Z-07	162.731	1106.234	1268.965
TCGA-B6-A0WV-01A-11R-A109-07	-704.441	-968.83	-1673.27
TCGA-AR-A1AK-01A-21R-A12P-07	1073.773	1677.362	2751.135
TCGA-A1-A0SF-01A-11R-A144-07	541.2882	927.2839	1468.572
TCGA-BH-A0RX-01A-21R-A084-07	1237.272	2230.181	3467.452
TCGA-E2-A109-01A-11R-A10J-07	275.9186	199.3477	475.2663
TCGA-B6-A0I1-01A-11R-A21T-07	-1148.59	-492.446	-1641.03
TCGA-E9-A22D-01A-11R-A157-07	624.8519	2561.58	3186.432
TCGA-A8-A0AD-01A-11R-A056-07	1008.874	816.7859	1825.66
TCGA-D8-A73W-01A-22R-A352-07	948.6209	1054.234	2002.855
TCGA-E9-A1R7-01A-11R-A14M-07	-304.843	-550.292	-855.136
TCGA-BH-A0W7-01A-11R-A115-07	1191.2	1763.419	2954.619
TCGA-BH-A6R8-01A-21R-A33J-07	-26.8333	934.1934	907.3601
TCGA-AC-A2FB-01A-11R-A17B-07	907.0175	2399.569	3306.587
TCGA-AN-A0XU-01A-11R-A109-07	-610.211	684.122	73.91141
TCGA-E2-A1IH-01A-11R-A13Q-07	1664.305	2010.938	3675.243
TCGA-A7-A6VW-01A-21R-A33J-07	-34.6628	870.6263	835.9635
TCGA-E2-A570-01A-11R-A29R-07	836.755	77.10732	913.8623
TCGA-E2-A56Z-01A-12R-A29R-07	-265.966	-87.0753	-353.041
TCGA-BH-A1EV-01A-11R-A137-07	512.2499	-202.366	309.8842
TCGA-A7-A6VV-01A-22R-A33J-07	935.3193	998.2184	1933.538
TCGA-AN-A0AK-01A-21R-A00Z-07	-410.237	239.2564	-170.981
TCGA-AO-A125-01A-11R-A10J-07	-1419.26	-470.349	-1889.61
TCGA-A8-A0A4-01A-11R-A00Z-07	579.5445	-187.935	391.6093
TCGA-A2-A3XY-01A-11R-A239-07	1089.634	1577.641	2667.275
TCGA-EW-A1OW-01A-21R-A144-07	566.0716	482.024	1048.096
TCGA-A8-A09M-01A-11R-A00Z-07	238.2622	1223.784	1462.046
TCGA-A2-A0EP-01A-52R-A22U-07	1901.568	3083.962	4985.53
TCGA-A7-A426-01A-22R-A24H-07	645.0027	599.1148	1244.118
TCGA-A2-A0CV-01A-31R-A115-07	923.5815	1019.963	1943.545
TCGA-B6-A0RH-01A-21R-A115-07	658.252	298.7831	957.0351
TCGA-GM-A5PX-01A-12R-A28M-07	979.0288	557.6407	1536.669
TCGA-A7-A0CE-01A-11R-A00Z-07	-379.473	-36.0469	-415.52
TCGA-E9-A5FK-01A-11R-A27Q-07	795.9814	2419.77	3215.752
TCGA-OL-A6VR-01A-32R-A33J-07	-864.162	-419.978	-1284.14

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-B6-A0RE-01A-11R-A056-07	-236.415	125.7877	-110.627
TCGA-AO-A03T-01A-21R-A034-07	-252.219	702.8875	450.6681
TCGA-E2-A1L8-01A-11R-A13Q-07	740.505	455.1936	1195.699
TCGA-AR-A24Q-01A-12R-A169-07	825.9828	945.5791	1771.562
TCGA-BH-A0AV-01A-31R-A115-07	1199.454	592.1266	1791.581
TCGA-BH-A0HI-01A-11R-A084-07	713.3177	472.6526	1185.97
TCGA-B6-A0RU-01A-11R-A084-07	225.2625	-152.824	72.43818
TCGA-E9-A1R2-01A-11R-A14D-07	343.9285	458.5513	802.4798
TCGA-BH-A204-01A-11R-A157-07	246.254	-446.021	-199.767
TCGA-AR-A1AJ-01A-21R-A12P-07	1228.745	2640.199	3868.945
TCGA-AN-A0FV-01A-11R-A00Z-07	486.4739	-138.877	347.5971
TCGA-BH-A0BZ-01A-31R-A12P-07	1303.395	1804.42	3107.815
TCGA-E9-A247-01A-11R-A169-07	-288.373	-416.735	-705.108
TCGA-AC-A23C-01A-12R-A169-07	749.6747	884.9533	1634.628
TCGA-A1-A0SN-01A-11R-A144-07	882.1153	1126.598	2008.713
TCGA-A7-A0D9-01A-31R-A056-07	82.8946	-441.306	-358.411
TCGA-AN-A041-01A-11R-A034-07	829.5652	208.9613	1038.526
TCGA-BH-A1FE-06A-11R-A213-07	1182.315	511.6504	1693.965
TCGA-BH-A0B9-01A-11R-A056-07	-678.169	1711.561	1033.392
TCGA-AO-A128-01A-11R-A10J-07	620.8024	3055.547	3676.349
TCGA-AR-A0U0-01A-11R-A109-07	148.7198	1810.755	1959.474
TCGA-C8-A12Q-01A-11R-A115-07	741.4946	777.8372	1519.332
TCGA-S3-AA0Z-01A-11R-A41B-07	-191.799	1117.207	925.4082
TCGA-BH-A1F8-01A-11R-A13Q-07	317.1473	109.4608	426.6081
TCGA-AC-A5XU-01A-11R-A28M-07	531.805	14.44495	546.25
TCGA-AC-A2FO-01A-11R-A180-07	1136.151	1659.959	2796.11
TCGA-A7-A0DB-01A-11R-A00Z-07	871.518	755.4778	1626.996
TCGA-AR-A0TP-01A-11R-A084-07	-617.339	-654.418	-1271.76
TCGA-AO-A03O-01A-11R-A00Z-07	-162.289	906.545	744.2564
TCGA-OL-A66H-01A-11R-A29R-07	593.698	1401.583	1995.281
TCGA-D8-A27R-01A-11R-A16F-07	652.4078	905.3357	1557.743
TCGA-A2-A4RW-01A-21R-A266-07	661.9914	552.3733	1214.365
TCGA-AN-A0G0-01A-11R-A034-07	-91.9706	99.91624	7.945662
TCGA-C8-A134-01A-11R-A115-07	-64.9455	1164.388	1099.443
TCGA-A2-A25A-01A-12R-A16F-07	1371.669	1129.97	2501.639
TCGA-A1-A0SP-01A-11R-A084-07	-27.631	1073.946	1046.315
TCGA-EW-A1OY-01A-11R-A144-07	-114.003	219.8998	105.8971
TCGA-A8-A081-01A-11R-A00Z-07	-344.492	1203.221	858.7284
TCGA-D8-A73U-01A-11R-A33J-07	1595.865	2985.229	4581.094
TCGA-BH-A0BL-01A-11R-A115-07	1486.025	1752.169	3238.193
TCGA-AR-A24P-01A-11R-A169-07	920.2539	351.9361	1272.19
TCGA-D8-A140-01A-11R-A115-07	321.6286	704.2887	1025.917

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-D8-A27L-01A-11R-A16F-07	1162.418	979.6747	2142.093
TCGA-EW-A1PC-01B-11R-A21T-07	-354.512	-346.377	-700.888
TCGA-BH-A18M-01A-11R-A12D-07	1036.823	528.6924	1565.515
TCGA-AR-A5QM-01A-11R-A27Q-07	932.14	1101.055	2033.195
TCGA-E9-A1RI-01A-11R-A169-07	1289.876	449.4842	1739.361
TCGA-A8-A08R-01A-11R-A034-07	569.6026	1474.146	2043.749
TCGA-AN-A0FS-01A-11R-A034-07	881.1838	-16.4002	864.7836
TCGA-BH-A8G0-01A-11R-A352-07	1337.062	1801.328	3138.391
TCGA-C8-A12O-01A-11R-A115-07	1182.415	859.7651	2042.18
TCGA-E9-A1R4-01A-21R-A14D-07	597.5154	1703.144	2300.66
TCGA-AN-A0AJ-01A-11R-A00Z-07	366.2583	1407.873	1774.131
TCGA-BH-A0HY-01A-11R-A056-07	320.8468	-309.316	11.53074
TCGA-AC-A5XS-01A-11R-A29R-07	812.9374	1636.74	2449.678
TCGA-BH-A0AU-01A-11R-A12P-07	688.9994	547.443	1236.442
TCGA-EW-A1P1-01A-31R-A14D-07	1645.574	1519.397	3164.971
TCGA-E9-A22E-01A-11R-A157-07	1910.63	1205.026	3115.656
TCGA-BH-A0E2-01A-11R-A056-07	728.0152	366.7327	1094.748
TCGA-OL-A5RV-01A-12R-A28M-07	45.88011	-67.9637	-22.0836
TCGA-E9-A245-01A-22R-A16F-07	-216.921	-271.127	-488.048
TCGA-D8-A1Y3-01A-11R-A157-07	161.3131	1254.449	1415.762
TCGA-A8-A07L-01A-11R-A00Z-07	219.1686	-334.858	-115.689
TCGA-AC-A23H-01A-11R-A157-07	206.5002	-177.458	29.04187
TCGA-BH-A0HX-01A-21R-A056-07	651.7482	364.9702	1016.718
TCGA-AC-A3QP-01A-11R-A22U-07	1072.898	1334.68	2407.578
TCGA-S3-AA12-01A-11R-A41B-07	-407.213	-283.687	-690.9
TCGA-E2-A1IO-01A-11R-A144-07	1318.252	940.1925	2258.445
TCGA-E9-A22G-01A-11R-A157-07	-947.017	123.9563	-823.06
TCGA-E9-A1NA-01A-11R-A144-07	945.5398	1009.572	1955.111
TCGA-B6-A0IA-01A-11R-A034-07	-841.613	-299.725	-1141.34
TCGA-AC-A3TN-01A-11R-A22K-07	91.51009	144.2376	235.7477
TCGA-AO-A03M-01B-11R-A10J-07	324.9524	1533.292	1858.245
TCGA-E2-A15C-01A-31R-A12D-07	650.4034	267.952	918.3554
TCGA-AR-A0U3-01A-11R-A109-07	-496.348	100.8246	-395.524
TCGA-EW-A1PB-01A-11R-A144-07	147.0918	2455.77	2602.862
TCGA-OL-A66K-01A-11R-A29R-07	621.3392	26.96036	648.2996
TCGA-EW-A1J3-01A-11R-A13Q-07	179.2221	170.4062	349.6283
TCGA-A8-A076-01A-21R-A00Z-07	881.7204	611.911	1493.631
TCGA-B6-A0RQ-01A-11R-A115-07	-110.535	-357.827	-468.362
TCGA-C8-A12U-01A-11R-A115-07	-789.09	895.9795	106.8895
TCGA-A2-A0EQ-01A-11R-A034-07	381.0849	2310.012	2691.097
TCGA-BH-A1FB-01A-11R-A13Q-07	1351.213	1769.579	3120.792
TCGA-BH-A2L8-01A-11R-A18M-07	962.979	2076.272	3039.251

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-BH-A8FZ-01A-11R-A352-07	1103.02	1784.833	2887.853
TCGA-A8-A06R-01A-11R-A00Z-07	1073.294	1063.906	2137.2
TCGA-BH-A18Q-01A-12R-A12D-07	-24.125	796.8441	772.7191
TCGA-E9-A248-01A-11R-A169-07	413.0591	2069.897	2482.956
TCGA-A8-A0A6-01A-12R-A056-07	724.036	1823.306	2547.342
TCGA-LL-A7T0-01A-31R-A352-07	8.281051	710.4948	718.7758
TCGA-EW-A1P4-01A-21R-A144-07	151.469	1573.023	1724.492
TCGA-C8-A3M8-01A-11R-A213-07	180.6251	-218.361	-37.7361
TCGA-A2-A0YE-01A-11R-A109-07	-27.6124	-234.458	-262.07
TCGA-EW-A1P8-01A-11R-A144-07	260.4594	1396.026	1656.486
TCGA-E2-A15A-06A-11R-A12D-07	342.8426	1728.13	2070.972
TCGA-3C-AALK-01A-11R-A41B-07	921.7338	593.955	1515.689
TCGA-OL-A5D7-01A-11R-A27Q-07	-432.471	1779.625	1347.154
TCGA-XX-A89A-01A-11R-A36F-07	1764.481	1737.498	3501.979
TCGA-GM-A2DO-01A-11R-A18M-07	197.35	3073.61	3270.96
TCGA-E2-A14O-01A-31R-A115-07	-123.272	157.2245	33.95272
TCGA-D8-A27P-01A-11R-A16F-07	187.8482	-224.496	-36.6476
TCGA-E2-A1AZ-01A-11R-A12P-07	974.8927	1511.382	2486.275
TCGA-LL-A5YL-01A-12R-A29R-07	466.2993	1192.41	1658.709
TCGA-A2-A1G6-01A-11R-A13Q-07	550.8594	604.3526	1155.212
TCGA-BH-A0EI-01A-11R-A115-07	868.1544	-210.159	657.9953
TCGA-A2-A0T6-01A-11R-A084-07	1670.695	1417.19	3087.885
TCGA-A2-A1FV-01A-11R-A13Q-07	122.5499	-608.74	-486.19
TCGA-E2-A2P5-01A-11R-A19W-07	375.3251	274.5978	649.9229
TCGA-E9-A6HE-01A-11R-A31O-07	718.9059	902.9974	1621.903
TCGA-E2-A108-01A-13R-A10J-07	1942.987	2704.442	4647.43
TCGA-LD-A7W6-01A-81R-A352-07	243.0749	439.3715	682.4464
TCGA-BH-A1ES-01A-11R-A137-07	419.5377	-609.581	-190.043
TCGA-D8-A1JU-01A-11R-A13Q-07	1794.007	1067.397	2861.404
TCGA-E2-A14Z-01A-11R-A115-07	746.0742	1824.092	2570.166
TCGA-A2-A0ER-01A-21R-A034-07	-168.46	171.1949	2.7351
TCGA-OL-A6VO-01A-12R-A33J-07	-473.337	503.6326	30.29553
TCGA-AR-A24K-01A-11R-A169-07	-151.45	-565.872	-717.322
TCGA-B6-A0X5-01A-21R-A109-07	-398.761	-294.71	-693.471
TCGA-A2-A25E-01A-11R-A169-07	149.6723	-12.8447	136.8276
TCGA-B6-A0IM-01A-11R-A034-07	373.5572	-45.2946	328.2626
TCGA-LL-A740-01A-21R-A32P-07	1044.732	683.1956	1727.928
TCGA-LL-A5YM-01A-11R-A28M-07	123.3167	544.0642	667.3809
TCGA-JL-A3YX-01A-11R-A22U-07	-56.2291	-282.849	-339.078
TCGA-D8-A1JA-01A-11R-A13Q-07	758.6791	299.531	1058.21
TCGA-A8-A07S-01A-11R-A034-07	199.5905	215.3809	414.9714
TCGA-A8-A090-01A-11R-A00Z-07	690.7509	822.3706	1513.121

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-A8-A09D-01A-11R-A00Z-07	1498.793	1021.963	2520.756
TCGA-BH-A0AY-01A-21R-A00Z-07	1375.534	1153.168	2528.702
TCGA-B6-A0I5-01A-11R-A034-07	334.4097	698.0978	1032.508
TCGA-AO-A124-01A-11R-A10J-07	-746.365	177.4029	-568.962
TCGA-OL-A97C-01A-32R-A41B-07	490.6302	724.4907	1215.121
TCGA-E9-A249-01A-11R-A169-07	-184.717	130.8408	-53.8763
TCGA-E2-A1LE-01A-12R-A19W-07	1226.15	1513.458	2739.608
TCGA-AR-A2LQ-01A-22R-A18M-07	1713.118	782.3614	2495.479
TCGA-A8-A08L-01A-11R-A00Z-07	157.7085	1116.836	1274.545
TCGA-AR-A24Z-01A-11R-A169-07	-112.733	100.5104	-12.2227
TCGA-AR-A24N-01A-11R-A169-07	554.0422	157.6162	711.6584
TCGA-A8-A07U-01A-11R-A034-07	849.9227	2362.488	3212.411
TCGA-B6-A0RP-01A-21R-A084-07	970.8318	742.3626	1713.194
TCGA-BH-A0BW-01A-11R-A115-07	288.3453	1849.017	2137.362
TCGA-A2-A0YT-01A-11R-A109-07	-162.411	152.3484	-10.0631
TCGA-PL-A8LY-01A-11R-A41B-07	-600.819	275.114	-325.705
TCGA-AC-A3OD-01B-06R-A22O-07	1073.924	2171.455	3245.379
TCGA-BH-A0BF-01A-21R-A12P-07	1769.559	2374.354	4143.913
TCGA-A8-A0A1-01A-11R-A00Z-07	1133.912	1757.1	2891.012
TCGA-5L-AAT1-01A-12R-A41B-07	985.8195	2050.83	3036.649
TCGA-A8-A092-01A-11R-A00Z-07	207.4417	178.9112	386.3528
TCGA-A2-A0CL-01A-11R-A115-07	1377.688	2810.275	4187.963
TCGA-GM-A2DI-01A-31R-A18M-07	1392.171	2664.815	4056.986
TCGA-AN-A0XV-01A-11R-A109-07	793.6113	592.4079	1386.019
TCGA-HN-A2NL-01A-11R-A18M-07	-825.541	616.8804	-208.66
TCGA-E2-A15J-01A-11R-A12P-07	-294.615	-172.522	-467.137
TCGA-E2-A106-01A-11R-A10J-07	-540.817	-574.854	-1115.67
TCGA-D8-A1JG-01B-11R-A13Q-07	865.7544	1347.324	2213.079
TCGA-E9-A1R3-01A-31R-A14M-07	948.7981	995.9155	1944.714
TCGA-BH-A18U-01A-21R-A12D-07	499.5201	516.3812	1015.901
TCGA-E2-A1L9-01A-11R-A13Q-07	1416.114	914.9735	2331.087
TCGA-A7-A3J0-01A-11R-A213-07	-651.251	421.6714	-229.58
TCGA-BH-A0E6-01A-11R-A034-07	-16.7246	875.1611	858.4366
TCGA-AN-A0FX-01A-11R-A034-07	279.9482	-179.387	100.5613
TCGA-A2-A1G4-01A-11R-A13Q-07	-352.643	175.6484	-176.994
TCGA-AO-A0J6-01A-11R-A034-07	-684.298	1313.266	628.9678
TCGA-W8-A86G-01A-21R-A36F-07	215.7305	-445.943	-230.213
TCGA-AC-A2BM-01A-11R-A21T-07	103.0187	761.9579	864.9767
TCGA-C8-A3M7-01A-12R-A21T-07	752.6987	551.0641	1303.763
TCGA-D8-A145-01A-11R-A115-07	877.1933	547.6363	1424.83
TCGA-3C-AALI-01A-11R-A41B-07	234.6229	1145.596	1380.219
TCGA-EW-A1IZ-01A-11R-A13Q-07	252.1322	2435.123	2687.255

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-A2-A0EN-01A-13R-A084-07	1540.088	2151.644	3691.732
TCGA-HN-A2OB-01A-21R-A27Q-07	1250.846	280.1424	1530.988
TCGA-AN-A0FY-01A-11R-A034-07	462.3564	-27.9313	434.425
TCGA-AO-A1KO-01A-31R-A13Q-07	281.6827	46.21256	327.8953
TCGA-C8-A1HL-01A-11R-A137-07	778.2094	396.0358	1174.245
TCGA-BH-A18S-01A-11R-A12D-07	-324.243	108.8449	-215.398
TCGA-C8-A27A-01A-11R-A169-07	-493.582	-424.128	-917.71
TCGA-AN-A04D-01A-21R-A034-07	-1102.63	-778.19	-1880.82
TCGA-BH-A42T-01A-11R-A24H-07	394.0191	812.0634	1206.083
TCGA-E9-A1RF-01A-11R-A157-07	1032.784	1341.461	2374.246
TCGA-BH-A18N-01A-11R-A12D-07	32.59187	-62.5523	-29.9604
TCGA-AN-A0FF-01A-11R-A034-07	604.7918	977.7231	1582.515
TCGA-C8-A12M-01A-11R-A115-07	-334.66	-8.58491	-343.244
TCGA-E2-A15I-01A-21R-A137-07	382.2514	911.8453	1294.097
TCGA-D8-A1XG-01A-11R-A14D-07	-34.7014	-104.309	-139.01
TCGA-C8-A1HI-01A-11R-A137-07	292.5962	73.74994	366.3461
TCGA-EW-A2FV-01A-11R-A17B-07	649.438	1104.496	1753.934
TCGA-B6-A0RS-01A-11R-A084-07	382.2575	1115.728	1497.985
TCGA-BH-A0B4-01A-11R-A00Z-07	1132.78	815.4244	1948.204
TCGA-C8-A278-01A-11R-A169-07	1217.648	1723.384	2941.031
TCGA-A2-A4RY-01A-31R-A266-07	808.5705	797.0441	1605.615
TCGA-A8-A08S-01A-11R-A034-07	84.80927	223.0109	307.8202
TCGA-AR-A2LL-01A-11R-A180-07	280.5886	721.8692	1002.458
TCGA-A2-A04X-01A-21R-A034-07	338.2693	1719.398	2057.667
TCGA-A8-A09A-01A-11R-A00Z-07	898.1088	537.3706	1435.479
TCGA-D8-A142-01A-11R-A115-07	983.989	818.03	1802.019
TCGA-EW-A2FW-01A-11R-A17B-07	121.8171	-162.716	-40.8986
TCGA-AC-A23G-01A-11R-A213-07	1745.625	1097.803	2843.428
TCGA-E2-A1LL-01A-11R-A144-07	-494.739	-145.237	-639.976
TCGA-EW-A6SA-01A-21R-A32P-07	-879.365	-997.372	-1876.74
TCGA-E2-A1IL-01A-11R-A14D-07	605.5253	-185.318	420.2069
TCGA-D8-A1XB-01A-11R-A14D-07	908.4237	-46.1767	862.247
TCGA-AC-A3TM-01A-11R-A22K-07	200.6479	886.3429	1086.991
TCGA-AR-A1AI-01A-11R-A12P-07	-270.289	1803.233	1532.944
TCGA-AC-A8OS-01A-12R-A41B-07	1106.788	1095.774	2202.562
TCGA-OL-A5RX-01A-11R-A28M-07	272.9918	567.7486	840.7404
TCGA-AO-A0J3-01A-11R-A034-07	-951.251	-408.069	-1359.32
TCGA-E9-A295-01A-11R-A16F-07	551.6853	253.8996	805.5849
TCGA-LL-A73Z-01A-11R-A32P-07	923.4781	1368.9	2292.378
TCGA-AR-A250-01A-31R-A169-07	1279.446	953.7778	2233.224
TCGA-A2-A0YI-01A-31R-A10J-07	1132.268	1787.522	2919.79
TCGA-BH-A0DH-01A-11R-A084-07	191.543	479.8495	671.3925

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-D8-A27W-01A-11R-A16F-07	537.6674	565.9388	1103.606
TCGA-AR-A1AN-01A-11R-A12P-07	1136.585	627.1317	1763.717
TCGA-B6-A3ZX-01A-11R-A239-07	198.6427	2502.26	2700.902
TCGA-AR-A1AQ-01A-11R-A12P-07	485.5663	1988.832	2474.399
TCGA-E9-A1NF-01A-11R-A14D-07	1774.905	870.1714	2645.076
TCGA-A7-A0DB-01A-11R-A277-07	1195.261	717.4106	1912.672
TCGA-BH-A0EA-01A-11R-A115-07	885.0061	503.2001	1388.206
TCGA-EW-A1PF-01A-11R-A144-07	1099.357	715.7033	1815.061
TCGA-E9-A3Q9-01A-11R-A21T-07	418.1703	1091.197	1509.368
TCGA-D8-A27K-01A-11R-A16F-07	638.3432	838.2782	1476.621
TCGA-OL-A5RY-01A-21R-A28M-07	1333.745	2388.954	3722.7
TCGA-LD-A74U-01A-13R-A33J-07	1144.366	1060.71	2205.075
TCGA-B6-A408-01A-12R-A24H-07	710.4715	1367.594	2078.066
TCGA-AR-A24R-01A-11R-A169-07	345.4299	663.9052	1009.335
TCGA-EW-A1P5-01A-11R-A144-07	178.3584	994.0958	1172.454
TCGA-GM-A2DB-01A-31R-A18M-07	-430.024	1055.994	625.9693
TCGA-A8-A07C-01A-11R-A034-07	67.34505	845.39	912.7351
TCGA-AR-A1AM-01A-41R-A22K-07	687.7306	706.481	1394.212
TCGA-BH-A0DZ-01A-11R-A00Z-07	1292.436	1094.562	2386.997
TCGA-A2-A259-01A-11R-A16F-07	804.241	957.7424	1761.983
TCGA-A7-A56D-01A-11R-A27Q-07	826.9756	1065.11	1892.086
TCGA-AR-A1AH-01A-11R-A12D-07	-446.507	-379.378	-825.885
TCGA-A8-A09I-01A-22R-A034-07	547.9132	1095.846	1643.76
TCGA-BH-A1FD-01A-11R-A13Q-07	577.8286	295.1973	873.0259
TCGA-AO-A0JD-01A-11R-A056-07	-710.404	485.4039	-225
TCGA-GM-A2DA-01A-11R-A18M-07	1035.633	1597.37	2633.004
TCGA-EW-A1J2-01A-21R-A13Q-07	1236.721	1024.335	2261.056
TCGA-D8-A1XY-01A-11R-A14M-07	1028.686	181.4297	1210.115
TCGA-BH-A1EN-01A-11R-A13Q-07	347.8897	-102.727	245.1629
TCGA-C8-A26Z-01A-11R-A16F-07	134.3686	-395.78	-261.412
TCGA-D8-A1JB-01A-11R-A13Q-07	744.6621	1911.992	2656.654
TCGA-BH-A0DS-01A-11R-A056-07	824.4646	1096.059	1920.523
TCGA-PL-A8LX-01A-11R-A41B-07	-344.266	400.3515	56.08547
TCGA-A2-A0T3-01A-21R-A115-07	-264.529	-436.67	-701.199
TCGA-BH-A1ET-01A-11R-A137-07	655.5713	401.4169	1056.988
TCGA-AN-A03Y-01A-21R-A00Z-07	51.04332	529.9174	580.9608
TCGA-A7-A3IY-01A-21R-A21T-07	984.5914	1380.34	2364.932
TCGA-BH-A18F-01A-11R-A12D-07	975.4634	849.9154	1825.379
TCGA-AO-A03U-01B-21R-A10J-07	1108.084	1986.15	3094.234
TCGA-A8-A07O-01A-11R-A00Z-07	-233.832	767.0534	533.2213
TCGA-LL-A6FQ-01A-11R-A31O-07	17.30215	619.5616	636.8638
TCGA-E9-A24A-01A-11R-A169-07	1151.486	1165.733	2317.219

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-AC-A5EH-01A-11R-A28M-07	1015.118	872.7366	1887.854
TCGA-AR-A24H-01A-11R-A169-07	-178.575	637.8663	459.2911
TCGA-A8-A099-01A-11R-A00Z-07	298.1725	279.8523	578.0248
TCGA-D8-A27T-01A-11R-A16F-07	1278.63	1204.82	2483.451
TCGA-BH-A0H6-01A-21R-A056-07	659.5788	-151.338	508.2404
TCGA-A7-A0DC-01A-11R-A00Z-07	-946.213	-1011.82	-1958.03
TCGA-OL-A5D8-01A-11R-A27Q-07	26.29124	462.7266	489.0179
TCGA-A2-A0CR-01A-11R-A22K-07	1054.394	2747.267	3801.662
TCGA-EW-A1PA-01A-11R-A144-07	291.735	344.5474	636.2824
TCGA-B6-A0RI-01A-11R-A056-07	779.4208	334.4367	1113.858
TCGA-D8-A1Y0-01A-11R-A14M-07	989.6782	1308.813	2298.491
TCGA-B6-A0RO-01A-22R-A084-07	-423.048	-150.303	-573.351
TCGA-A2-A4S1-01A-21R-A266-07	1494.513	1834.707	3329.22
TCGA-AC-A3YI-01A-21R-A239-07	1170.917	809.808	1980.725
TCGA-A7-A13D-01A-13R-A12P-07	-39.1143	-223.312	-262.427
TCGA-D8-A27V-01A-12R-A17B-07	703.8121	75.96051	779.7726
TCGA-A2-A0D4-01A-11R-A00Z-07	-381.759	-506.206	-887.965
TCGA-B6-A0IG-01A-11R-A034-07	-98.7163	0.791701	-97.9246
TCGA-BH-A0B1-01A-12R-A056-07	627.4291	200.1607	827.5898
TCGA-AC-A7VB-01A-11R-A352-07	-918.916	-863.341	-1782.26
TCGA-A7-A26J-01B-02R-A277-07	1098.731	955.7106	2054.442
TCGA-E2-A10B-01A-11R-A10J-07	597.4535	447.0144	1044.468
TCGA-D8-A141-01A-11R-A115-07	1619.495	2180.746	3800.241
TCGA-C8-A1HK-01A-21R-A13Q-07	-280.329	135.9724	-144.356
TCGA-D8-A3Z5-01A-41R-A24H-07	-66.1206	-27.9168	-94.0374
TCGA-EW-A423-01A-11R-A24H-07	-144.906	997.8827	852.9764
TCGA-AR-A2LE-01A-11R-A180-07	158.2877	211.6336	369.9213
TCGA-A7-A4SE-01A-11R-A266-07	680.8561	337.51	1018.366
TCGA-AO-A12F-01A-11R-A115-07	494.8098	-125.777	369.033
TCGA-A7-A26J-01A-11R-A169-07	753.8377	344.939	1098.777
TCGA-A8-A06P-01A-11R-A00Z-07	1296.46	510.6509	1807.111
TCGA-AC-A3YJ-01A-11R-A22U-07	-229.558	804.0604	574.5026
TCGA-A2-A0EO-01A-11R-A034-07	1277.463	972.183	2249.646
TCGA-E2-A14Y-01A-21R-A12D-07	-578.929	-38.1955	-617.124
TCGA-E2-A152-01A-11R-A12D-07	1006.459	477.3252	1483.784
TCGA-BH-A5J0-01A-11R-A27Q-07	1159.633	1870.244	3029.878
TCGA-D8-A1JP-01A-11R-A13Q-07	1227.168	873.9578	2101.126
TCGA-AO-A03L-01A-41R-A056-07	767.0852	718.1652	1485.25
TCGA-AN-A0XW-01A-11R-A109-07	1579.78	1803.921	3383.701
TCGA-E9-A1QZ-01A-21R-A169-07	820.7735	1840.071	2660.844
TCGA-A8-A097-01A-11R-A034-07	919.9518	666.413	1586.365
TCGA-AR-A1AV-01A-21R-A12P-07	276.5305	40.62765	317.1582

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-BH-A18K-01A-11R-A12D-07	713.7209	205.7447	919.4656
TCGA-AQ-A04J-01A-02R-A034-07	978.9645	1897.641	2876.606
TCGA-OL-A5DA-01A-11R-A27Q-07	38.46988	347.3105	385.7804
TCGA-OL-A5D6-01A-21R-A27Q-07	1012.512	616.9078	1629.42
TCGA-B6-A0IO-01A-11R-A034-07	-525.476	248.7673	-276.709
TCGA-BH-A0H7-01A-13R-A056-07	822.6424	238.4276	1061.07
TCGA-E9-A1N9-01A-11R-A14D-07	373.5142	256.1196	629.6338
TCGA-AN-A0AM-01A-11R-A034-07	331.1679	921.8502	1253.018
TCGA-C8-A27B-01A-11R-A169-07	-132.478	1589.933	1457.455
TCGA-LL-A5YO-01A-21R-A28M-07	738.741	2816.414	3555.155
TCGA-A2-A25B-01A-11R-A169-07	666.632	636.7454	1303.377
TCGA-E9-A1NC-01A-21R-A26B-07	795.3441	1738.732	2534.076
TCGA-E2-A1LI-01A-12R-A157-07	-402.894	963.5521	560.6581
TCGA-E9-A1RE-01A-11R-A157-07	-105.176	-393.775	-498.952
TCGA-D8-A1JT-01A-31R-A13Q-07	-327.704	187.5496	-140.154
TCGA-A8-A06U-01A-11R-A00Z-07	-62.6942	632.5762	569.882
TCGA-C8-A8HR-01A-11R-A36F-07	1415.377	1560.755	2976.132
TCGA-A7-A0CG-01A-12R-A056-07	1229.529	1471.015	2700.545
TCGA-A2-A0D0-01A-11R-A00Z-07	-894.965	947.7314	52.76632
TCGA-D8-A13Y-01A-11R-A115-07	-934.393	-977.274	-1911.67
TCGA-B6-A0I9-01A-11R-A034-07	-369.575	299.1114	-70.4637
TCGA-A2-A04T-01A-21R-A034-07	-265.108	1169.003	903.8949
TCGA-E2-A150-01A-11R-A12D-07	484.1966	1046.641	1530.837
TCGA-AN-A0AR-01A-11R-A00Z-07	-776.076	-373.633	-1149.71
TCGA-C8-A8HQ-01A-11R-A36F-07	1021.922	1136.573	2158.495
TCGA-A8-A094-01A-11R-A00Z-07	735.357	1575.801	2311.158
TCGA-S3-AA15-01A-11R-A41B-07	1370.527	2492.983	3863.51
TCGA-B6-A1KC-01B-11R-A157-07	-282.12	-297.321	-579.441
TCGA-A2-A0YM-01A-11R-A109-07	170.0203	1081.479	1251.499
TCGA-AO-A0JM-01A-21R-A056-07	771.784	492.6522	1264.436
TCGA-AR-A5QQ-01A-11R-A28M-07	499.2073	2213.566	2712.773
TCGA-A8-A08J-01A-11R-A00Z-07	726.563	486.7599	1213.323
TCGA-E2-A1B0-01A-11R-A12P-07	648.7097	807.3876	1456.097
TCGA-S3-AA11-01A-31R-A41B-07	-399.49	-537.685	-937.175
TCGA-BH-A0DE-01A-11R-A115-07	1125.441	1030.508	2155.949
TCGA-BH-A1FM-01A-11R-A13Q-07	803.2553	31.96023	835.2155
TCGA-A8-A09W-01A-11R-A00Z-07	762.6519	573.9067	1336.559
TCGA-D8-A1XW-01A-11R-A14M-07	1144.116	1493.856	2637.972
TCGA-GM-A2D9-01A-11R-A18M-07	543.0226	646.3363	1189.359
TCGA-E2-A15D-01A-11R-A115-07	520.3371	362.2321	882.5692
TCGA-A7-A0DA-01A-31R-A115-07	422.7975	-31.9549	390.8426
TCGA-E2-A576-01A-11R-A31O-07	-46.0453	247.9733	201.928

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-PL-A8LV-01A-21R-A41B-07	-38.1724	1031.531	993.3585
TCGA-A2-A4RX-01A-11R-A266-07	969.7661	892.3097	1862.076
TCGA-E9-A243-01A-21R-A169-07	1341.147	2789.554	4130.701
TCGA-A8-A07E-01A-11R-A034-07	1378.974	888.2013	2267.175
TCGA-E9-A228-01A-31R-A157-07	20.21764	244.6108	264.8284
TCGA-A2-A4S2-01A-12R-A266-07	620.1788	1369.798	1989.977
TCGA-A7-A3J1-01A-11R-A213-07	902.851	1746.58	2649.431
TCGA-EW-A1PH-01A-11R-A14M-07	-306.027	225.041	-80.9857
TCGA-A2-A04U-01A-11R-A115-07	-179.333	-235.656	-414.99
TCGA-C8-A132-01A-31R-A115-07	1089.54	1506.795	2596.335
TCGA-BH-A18T-01A-11R-A12D-07	-352.035	325.0774	-26.9576
TCGA-E2-A1L7-01A-11R-A144-07	346.2563	1446.559	1792.815
TCGA-A7-A26J-01A-11R-A277-07	673.7085	339.6911	1013.4
TCGA-BH-A0BA-01A-11R-A056-07	511.7026	490.2181	1001.921
TCGA-E9-A5FL-01A-11R-A27Q-07	318.9038	598.3258	917.2296
TCGA-BH-A18V-01A-11R-A12D-07	715.345	1291.534	2006.879
TCGA-AN-A0AL-01A-11R-A00Z-07	853.5801	1251.918	2105.498
TCGA-A2-A0EY-01A-11R-A034-07	344.6446	882.5369	1227.181

Table S2 DEGs based upon stromal scores

Gene	conMean	treatMean	logFC	P value	fdr
KCNH6	0.244936	0.051984	-2.23626	1.81E-05	3.29E-05
AEBP1	88.56828	222.7741	1.330719	8.50E-98	1.01E-95
ISM1	2.815568	5.892012	1.065334	8.52E-62	2.30E-60
SEC14L4	0.209085	0.099951	-1.0648	0.010777851	0.014627391
MMP3	4.128772	11.50347	1.478284	4.18E-58	9.65E-57
LRP1	11.24731	28.57202	1.345024	1.47E-122	9.53E-120
SCARF2	2.557794	5.516618	1.108884	4.77E-68	1.63E-66
CPA3	6.46058	14.57038	1.173303	1.31E-47	2.03E-46
KIF26B	1.782467	3.583796	1.007613	6.26E-66	1.94E-64
ANTXRL	0.190947	0.058239	-1.71311	0.016490042	0.021892867
SCARA5	0.384015	1.273912	1.730031	8.32E-31	6.87E-30
PCSK1N	5.329104	1.924885	-1.46912	0.005616738	0.007881505
CCL19	18.43253	39.47377	1.09864	1.07E-22	6.24E-22
MYOCD	0.050427	0.146077	1.534467	2.60E-35	2.53E-34
DNASE1L3	0.273994	0.564663	1.043247	1.36E-29	1.07E-28
TLR4	2.209909	5.009064	1.180554	3.35E-99	4.34E-97
MEDAG	1.937366	5.408507	1.481134	2.80E-83	1.73E-81
CH25H	0.958164	2.315362	1.272893	3.39E-56	7.35E-55
CXCL12	11.30704	29.66187	1.391388	8.30E-112	2.17E-109
LRRTM2	0.106684	0.254597	1.254875	8.17E-43	1.04E-41
C1QTNF7	0.225428	0.736774	1.708555	2.60E-62	7.12E-61
ADIPOQ	2.473261	10.4573	2.080023	7.92E-26	5.32E-25
CELF4	0.484387	0.118051	-2.03674	2.75E-08	6.38E-08
KLK3	0.172468	0.571526	1.72849	1.03E-20	5.38E-20
GLT8D2	3.317327	9.165257	1.466154	2.35E-123	1.60E-120
GIMAP8	2.221345	4.45722	1.00471	7.28E-68	2.45E-66
CTSE	0.160688	0.457464	1.509401	9.12E-08	2.03E-07
SLAMF6	1.459438	3.268533	1.16323	1.20E-36	1.23E-35
SPDYC	10.82922	2.146757	-2.3347	0.014530224	0.019410245
CD69	1.407135	3.287871	1.224394	1.88E-43	2.48E-42
MRGPRF	1.118384	2.952346	1.400446	3.51E-86	2.48E-84
CELF3	0.360735	0.090206	-1.99964	0.000131218	0.000221606
COL10A1	20.71633	65.06779	1.651175	5.69E-69	2.01E-67
BTLA	0.270116	0.622922	1.205473	1.17E-28	8.85E-28
CYP11A1	0.225828	2.206447	3.288428	1.61E-52	3.09E-51
FCRLA	0.440843	0.930342	1.077497	4.64E-26	3.14E-25
MXRA5	21.759	59.08938	1.441287	4.01E-113	1.16E-110
ICAM3	0.450747	0.927922	1.041684	1.35E-40	1.58E-39
CA10	0.08012	0.180581	1.172405	7.96E-05	0.000137408
CALHM5	0.636335	1.635364	1.361754	4.38E-133	7.45E-130
WIPF1	4.852727	10.36226	1.094471	1.47E-111	3.65E-109
COL16A1	8.245005	17.04573	1.047818	2.48E-65	7.59E-64

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
FAM57B	0.72143	0.314475	-1.19792	1.26E-08	3.02E-08
SLC8A2	0.562669	0.134726	-2.06226	0.002678175	0.003912596
FCRL1	0.173452	0.458912	1.403683	4.72E-18	2.14E-17
DPP4	1.218031	3.358975	1.463471	3.00E-96	3.21E-94
PPM1E	0.797705	0.264271	-1.59384	1.00E-11	3.04E-11
CCR5	2.38918	4.847795	1.020813	6.88E-43	8.81E-42
FAP	3.544912	10.0916	1.509334	3.26E-120	1.43E-117
FN1	177.4868	415.7963	1.228166	2.14E-69	7.68E-68
LRCH2	0.290851	0.630024	1.115126	3.25E-105	5.66E-103
KERA	0.350967	0.915955	1.383943	1.13E-85	7.81E-84
IKZF1	1.309711	2.849067	1.121241	3.64E-55	7.66E-54
OGN	5.021205	10.87321	1.114672	2.13E-74	9.36E-73
KRT10	26.45772	12.90371	-1.0359	0.000832003	0.001284586
ZNF366	0.376656	0.830672	1.141033	1.78E-58	4.17E-57
CTSG	0.814063	2.26958	1.479212	1.59E-41	1.93E-40
TM6SF1	0.847183	1.776877	1.068598	2.57E-90	2.15E-88
SRPX	5.297004	11.52635	1.121687	5.76E-92	5.15E-90
KCTD12	10.20215	22.80866	1.160709	1.66E-114	5.36E-112
COL8A2	8.422329	22.71467	1.431333	1.98E-89	1.56E-87
PM20D1	0.068062	0.165133	1.278706	1.29E-37	1.36E-36
FHL5	0.511451	1.157478	1.178317	9.15E-48	1.42E-46
SRPX2	5.797462	12.16319	1.069029	7.18E-85	4.72E-83
CRHBP	0.114369	0.237641	1.055093	2.52E-42	3.17E-41
GABRB2	0.102839	0.222602	1.114077	9.42E-37	9.68E-36
GIMAP6	3.706445	7.52299	1.02127	4.48E-71	1.70E-69
CLDN11	0.956155	1.950133	1.028256	1.34E-33	1.23E-32
MSRB3	4.230526	10.05328	1.248757	9.96E-107	1.83E-104
WISP1	3.023915	8.367162	1.468321	1.72E-119	7.33E-117
IL9R	0.126891	0.266589	1.071033	1.58E-37	1.66E-36
TWIST2	1.399721	3.046965	1.122234	5.47E-69	1.93E-67
FBLN2	20.87396	45.16378	1.113462	7.09E-98	8.53E-96
CD52	16.33177	47.5384	1.541412	4.47E-34	4.15E-33
KLK4	0.90518	2.739022	1.597384	1.16E-74	5.18E-73
LY9	0.230218	0.519904	1.175243	2.52E-38	2.73E-37
CYP2C8	0.56937	0.28254	-1.01091	0.024605598	0.031932129
ANTXR2	2.572935	5.160287	1.004036	9.04E-112	2.32E-109
CAMK4	0.249476	0.500981	1.005857	1.22E-68	4.27E-67
TMEM130	0.379373	0.816214	1.10533	2.64E-52	5.01E-51
LRFN5	0.108615	0.231417	1.09127	2.86E-59	6.92E-58
VCAN	16.38733	46.35644	1.500189	5.44E-112	1.45E-109
TPSAB1	5.855386	13.62819	1.218758	5.27E-35	5.08E-34
NR5A1	0.179008	0.083538	-1.09951	0.030130026	0.038651765

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
SLC9A9	1.160101	2.335385	1.00941	1.06E-83	6.64E-82
NOX4	1.081425	2.567157	1.247238	2.92E-95	3.03E-93
SLC28A1	0.221297	0.10432	-1.08496	1.80E-07	3.92E-07
NETO1	0.112819	0.301558	1.418424	9.31E-20	4.64E-19
FGF7	0.812506	2.263324	1.477993	8.98E-94	8.60E-92
IL33	2.327581	5.628825	1.274002	1.03E-35	1.01E-34
CD5	1.761189	3.711782	1.075563	2.66E-35	2.58E-34
KLK2	0.044092	0.229363	2.379033	2.61E-57	5.81E-56
KCNIP2	0.749495	1.833838	1.290876	2.09E-11	6.20E-11
RTBDN	1.388851	0.380226	-1.86896	1.50E-07	3.29E-07
TSHZ2	0.953989	1.914612	1.005008	1.90E-75	8.77E-74
C1orf105	0.403477	0.064845	-2.63742	0.00104144	0.001591339
HPGDS	0.951947	1.920097	1.012227	1.94E-58	4.53E-57
SLC38A3	1.951338	0.957438	-1.02721	0.003402351	0.004903176
ADAM12	5.700672	17.34209	1.605074	1.75E-110	3.90E-108
CD96	1.048765	2.169694	1.0488	4.94E-37	5.13E-36
TFR2	1.065222	0.525786	-1.01861	3.87E-12	1.21E-11
P4HA3	1.497286	3.782842	1.337121	1.61E-97	1.90E-95
TMEM255A	0.481097	0.978981	1.024953	5.48E-58	1.26E-56
CSDC2	0.445488	1.131046	1.344198	1.06E-58	2.50E-57
GNG2	1.78358	3.883056	1.122417	1.54E-109	3.17E-107
COL3A1	323.5202	1083.454	1.74371	8.31E-122	4.52E-119
ZEB1	2.56072	6.148752	1.263744	2.57E-115	8.75E-113
ADAMTS6	0.306866	0.671304	1.129357	2.37E-72	9.59E-71
IGDCC4	0.410673	0.846618	1.043722	8.50E-62	2.29E-60
CTGF	93.67212	226.3096	1.272606	3.55E-79	1.85E-77
TLL1	0.388504	0.990321	1.349966	2.18E-94	2.13E-92
CLEC4G	0.066849	0.146864	1.135493	3.06E-15	1.16E-14
HSPB6	3.695889	8.793816	1.250568	7.63E-41	8.98E-40
AL845331.2	0.050982	0.108621	1.091242	1.15E-12	3.72E-12
ASPHD1	3.345412	1.443672	-1.21244	8.08E-09	1.97E-08
GNG3	1.311725	0.440552	-1.57408	1.71E-06	3.41E-06
ANTXR1	18.07282	44.39325	1.296519	3.78E-87	2.75E-85
PRSS35	0.155375	0.424908	1.4514	2.11E-34	1.99E-33
HBQ1	0.194411	0.048747	-1.99572	1.80E-12	5.73E-12
LAX1	0.645345	1.485941	1.203233	3.81E-40	4.37E-39
CAMK2B	1.456361	0.704871	-1.04694	0.023579077	0.030681888
SLFN12L	0.220666	0.50025	1.180786	1.97E-38	2.14E-37
C7	2.640374	7.648845	1.5345	2.35E-35	2.29E-34
CLEC2B	2.947153	6.03214	1.033348	2.47E-106	4.47E-104
TEX11	0.067909	0.144251	1.086907	2.34E-47	3.58E-46
TPSD1	1.148653	3.294213	1.51999	8.28E-15	3.05E-14

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
AQP7	0.372455	1.197404	1.684771	1.68E-21	9.21E-21
AKR1B15	1.266191	4.492802	1.827121	5.01E-08	1.14E-07
PGC	0.727679	1.865194	1.357951	0.018921448	0.02493841
BRINP2	3.333084	0.833074	-2.00034	1.53E-05	2.81E-05
TNFSF8	0.69126	1.527324	1.143706	5.41E-71	2.03E-69
FCAMR	0.070303	0.215714	1.617454	0.000154369	0.000258905
KLHL6	0.614977	1.302045	1.082175	9.59E-59	2.28E-57
TCF4	2.221721	4.908811	1.143696	1.69E-121	8.84E-119
PTPRC	4.352418	10.34417	1.248929	5.13E-56	1.10E-54
NID1	15.10688	30.86231	1.03064	2.17E-94	2.13E-92
MMP11	40.57909	84.75469	1.062557	5.71E-35	5.51E-34
AOC3	4.371049	11.56055	1.403158	1.89E-66	6.00E-65
FLRT2	0.25401	0.630463	1.311523	4.55E-99	5.78E-97
ABCA8	0.325096	1.158882	1.833797	1.39E-58	3.27E-57
ZCCHC24	5.184296	11.17964	1.108653	8.93E-92	7.79E-90
AKAP12	2.16732	6.105127	1.494109	1.45E-100	2.01E-98
CA9	5.704306	2.290349	-1.31648	0.000337743	0.000544446
MPEG1	5.628759	12.09719	1.103783	1.71E-63	4.92E-62
EVI2B	5.719385	12.27725	1.102055	2.47E-68	8.59E-67
APLP1	6.612317	2.129753	-1.63447	5.21E-11	1.50E-10
FCRLB	4.80399	1.582998	-1.60157	5.50E-08	1.25E-07
PDGFRA	3.236679	7.363006	1.185781	3.37E-111	8.18E-109
SIGLEC6	0.16053	0.398475	1.311649	2.26E-52	4.29E-51
COL5A1	25.75171	69.29407	1.428063	2.46E-100	3.32E-98
TIMP2	48.62659	106.6482	1.133042	7.18E-114	2.13E-111
ITK	0.489057	1.149129	1.232465	1.44E-39	1.61E-38
FNDC1	7.511947	16.86392	1.166681	6.19E-77	3.01E-75
CYS1	1.207093	3.057541	1.340835	3.40E-90	2.80E-88
IL6	0.863728	2.067188	1.25902	1.80E-19	8.83E-19
TUBB4A	0.825233	0.357197	-1.20808	0.002082591	0.003076519
SLAMF1	0.548368	1.188871	1.116377	1.44E-37	1.52E-36
CD200R1	0.289807	0.617624	1.091636	6.13E-49	1.00E-47
PDIA2	0.627987	0.132763	-2.24188	4.82E-08	1.10E-07
MS4A6E	0.026146	0.150725	2.527258	4.57E-11	1.32E-10
COL12A1	28.15552	73.88848	1.391932	8.50E-77	4.10E-75
TLR10	0.392725	0.815278	1.053771	1.66E-33	1.50E-32
DIRC1	0.112266	0.266436	1.246869	2.91E-55	6.13E-54
TRAT1	0.468075	1.019597	1.123187	8.46E-34	7.77E-33
HTR2B	0.461867	1.186825	1.361556	2.06E-74	9.08E-73
RPL3L	0.494354	0.106217	-2.21853	4.09E-12	1.27E-11
DOCK2	1.302006	2.769112	1.088688	1.07E-62	2.99E-61
ECM2	2.314453	7.290659	1.655378	1.12E-130	1.27E-127

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
RUNX2	1.833327	3.868193	1.077195	9.26E-90	7.45E-88
JAM2	1.817581	3.959234	1.123201	1.97E-86	1.40E-84
ARMH4	0.54487	1.235126	1.180674	1.59E-101	2.28E-99
BRSK2	0.618765	0.245114	-1.33594	0.000143706	0.000241827
AOAH	1.832563	3.702445	1.014616	2.76E-51	4.98E-50
PODN	5.751664	18.20064	1.661938	1.61E-116	5.78E-114
ALPK2	0.156965	0.341008	1.119361	2.78E-48	4.45E-47
HTRA3	18.64694	48.48069	1.378471	2.02E-76	9.63E-75
SH3GL3	0.169217	0.061866	-1.45165	2.14E-05	3.88E-05
ITIH5	0.884258	2.172281	1.296671	4.73E-43	6.12E-42
CASQ2	0.44189	0.914475	1.049257	9.38E-32	7.99E-31
CDK15	0.120904	0.301413	1.317876	3.29E-77	1.63E-75
SLURP1	1.75456	0.694204	-1.33768	0.003060284	0.004438897
FREM1	0.201174	0.546029	1.440531	1.27E-53	2.54E-52
DOCK11	1.95399	4.164363	1.091673	1.54E-86	1.10E-84
VGLL3	0.853127	2.005884	1.233405	1.98E-89	1.56E-87
GZMK	2.384973	5.847128	1.293755	7.02E-36	6.96E-35
MS4A4E	0.153584	0.317802	1.049098	2.05E-34	1.93E-33
IL16	1.108937	2.469009	1.154755	2.65E-94	2.58E-92
DDN	0.257258	0.082448	-1.64166	5.16E-08	1.17E-07
TMEM179	0.504323	0.165407	-1.60833	0.037479264	0.047559483
GXYLT2	2.871213	8.892444	1.63092	2.65E-102	4.06E-100
EEF1A2	75.8926	35.88525	-1.08057	0.000645202	0.001008068
COL8A1	6.73658	18.19668	1.433587	3.24E-91	2.77E-89
PTGER4	1.716715	3.447834	1.006039	1.05E-70	3.92E-69
ABCB5	0.029901	0.081528	1.447096	1.10E-35	1.08E-34
TCEAL7	0.986602	2.096214	1.087246	1.48E-71	5.77E-70
IGF1	0.175739	0.571351	1.700943	1.90E-75	8.77E-74
FST	4.650148	9.353755	1.008269	1.30E-58	3.08E-57
ANGPTL2	10.32445	27.16243	1.395547	1.54E-118	6.00E-116
TFF2	0.721248	0.306779	-1.2333	0.011754135	0.01589846
XCR1	0.158382	0.395927	1.321827	7.41E-33	6.58E-32
RASGRF2	0.716847	1.952952	1.44592	3.35E-127	3.04E-124
DCN	22.08507	76.50543	1.792491	2.40E-145	1.63E-141
CST7	4.681054	9.445094	1.012732	4.40E-48	6.98E-47
TNN	1.136619	3.60731	1.666174	1.58E-60	4.00E-59
FABP4	17.54774	66.38834	1.919645	2.05E-25	1.35E-24
LVRN	0.060611	0.141297	1.221076	3.03E-23	1.81E-22
CCDC36	0.093701	0.243129	1.375582	2.21E-97	2.55E-95
NRTN	1.9742	0.823537	-1.26136	1.23E-10	3.46E-10
PYHIN1	0.452032	0.9662	1.095896	1.23E-34	1.16E-33
CA4	0.117445	0.401257	1.772534	4.15E-17	1.77E-16

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
SFRP4	14.02719	52.07969	1.892495	3.67E-102	5.48E-100
PHGDH	23.29832	10.07963	-1.20878	1.46E-08	3.49E-08
PAH	0.462175	0.189488	-1.28633	0.000788541	0.001220668
LOXL1	10.89372	22.93358	1.073965	6.46E-81	3.57E-79
ADAM33	0.444618	1.3105	1.559481	1.16E-66	3.67E-65
CMA1	0.35103	1.036535	1.562102	2.93E-33	2.63E-32
ACSM5	0.287722	0.614269	1.094196	3.06E-51	5.50E-50
PLIN1	3.603054	13.06485	1.858398	3.74E-22	2.12E-21
BHLHE22	0.357631	0.937879	1.390929	2.63E-85	1.77E-83
ABCC9	0.714953	1.433622	1.003743	5.96E-70	2.19E-68
INHBA	6.823756	15.69425	1.201598	1.16E-70	4.30E-69
ADH1B	2.517512	10.31472	2.034634	1.83E-30	1.50E-29
RUNDC3A	1.790276	0.353958	-2.33853	1.42E-05	2.62E-05
MAB21L1	0.265578	0.637684	1.263707	6.36E-67	2.06E-65
CCL14	0.305743	0.842191	1.461825	1.20E-38	1.31E-37
GSTM5	0.677276	1.719286	1.343993	1.61E-49	2.71E-48
SCN7A	0.169701	0.591407	1.801156	1.16E-52	2.24E-51
WNT2	2.08759	5.219593	1.322099	3.11E-79	1.62E-77
FGF16	0.083529	0.355585	2.089845	6.82E-66	2.11E-64
CLDN18	0.052894	0.147395	1.478517	3.71E-18	1.69E-17
MRC2	15.24852	30.91815	1.019785	1.01E-77	5.01E-76
SERPING1	52.07141	108.5458	1.059741	2.76E-102	4.18E-100
TEX19	0.343354	0.093135	-1.8823	2.14E-06	4.24E-06
VXN	1.211027	0.48132	-1.33116	0.018172641	0.024014288
PRDM1	2.221413	4.572045	1.041362	4.65E-92	4.22E-90
COL1A2	226.2341	718.3252	1.666821	3.28E-115	1.09E-112
GEM	7.274045	16.98512	1.223442	2.28E-60	5.71E-59
ATOH8	0.264283	0.625948	1.243957	1.52E-32	1.33E-31
CEL	2.862412	1.144692	-1.32227	4.80E-09	1.19E-08
MT1G	20.30477	9.559389	-1.08683	0.000762359	0.001182156
CD3E	4.617012	9.414181	1.027876	1.42E-33	1.29E-32
CSAG1	1.861663	0.72086	-1.3688	0.000720514	0.001120589
SLC18A2	0.232129	0.485847	1.065574	9.59E-42	1.17E-40
SULT4A1	0.864419	0.376759	-1.19809	1.80E-06	3.60E-06
SAMD3	0.138743	0.310555	1.162433	1.18E-41	1.44E-40
LAMA4	6.068924	12.50985	1.043551	5.38E-114	1.63E-111
FAM110D	0.960742	1.924691	1.002405	1.43E-25	9.52E-25
MMP19	1.688712	4.273564	1.339516	2.53E-122	1.50E-119
C2CD4B	0.695659	1.498514	1.107081	2.98E-20	1.53E-19
FPR1	1.579053	3.29853	1.062763	1.14E-57	2.59E-56
CACNA1G	0.10027	0.214555	1.097449	5.95E-45	8.26E-44
LILRB5	0.312219	0.677222	1.117069	1.63E-39	1.82E-38

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
PCSK5	0.502481	1.170818	1.220377	1.80E-98	2.22E-96
LIPE	2.491479	5.630245	1.176195	1.99E-13	6.70E-13
AADAC	0.216683	0.594483	1.456053	4.65E-15	1.74E-14
CCR2	0.980888	2.205771	1.169123	2.42E-47	3.69E-46
EPYC	1.033386	3.706323	1.84261	1.03E-31	8.79E-31
BLK	0.248334	0.520665	1.068071	1.76E-17	7.72E-17
CNR2	0.084332	0.195151	1.210437	9.40E-20	4.68E-19
CAVIN2	1.742025	4.548669	1.384679	1.16E-43	1.55E-42
VGF	0.985507	0.347733	-1.50289	1.46E-15	5.66E-15
ONECUT2	0.353889	0.171942	-1.04137	4.39E-05	7.74E-05
DLGAP1	0.93254	0.395225	-1.23849	0.023625256	0.030739038
FSTL1	24.86914	62.07765	1.319717	1.20E-136	3.27E-133
LMO1	0.399867	0.145659	-1.45692	0.000468019	0.000742317
ADAMTS14	0.902465	1.921759	1.090484	9.14E-55	1.90E-53
CILP2	2.367954	5.82397	1.298362	5.72E-56	1.22E-54
ST6GAL2	0.898278	2.453637	1.449687	3.22E-72	1.29E-70
ACTL6B	0.412158	0.027191	-3.92202	3.96E-06	7.68E-06
COL5A3	5.16901	10.90291	1.076753	6.84E-58	1.56E-56
CYR61	48.90063	114.2537	1.224316	1.70E-54	3.49E-53
ARL9	2.301354	1.033598	-1.15481	3.51E-06	6.84E-06
TFEC	0.724558	1.504824	1.054422	3.29E-48	5.23E-47
SLC27A2	11.5402	4.987947	-1.21015	0.001859214	0.002761224
CLMP	4.244493	8.601882	1.01906	1.97E-90	1.65E-88
TGFBR2	13.55915	32.92261	1.279812	3.30E-121	1.60E-118
CIDEC	1.852647	6.997951	1.917345	5.88E-18	2.65E-17
ANGPT4	0.052722	0.128786	1.288504	8.80E-43	1.12E-41
PGPEP1L	0.140393	0.064784	-1.11575	2.75E-07	5.90E-07
CLEC9A	0.124177	0.261588	1.074895	2.89E-28	2.16E-27
CTHRC1	36.41541	76.80803	1.076708	2.10E-85	1.45E-83
DAB2	6.94493	14.22125	1.034016	1.72E-125	1.38E-122
MFAP4	12.62364	41.00961	1.699834	1.51E-78	7.75E-77
EGFL6	1.418883	2.951298	1.056594	1.21E-29	9.57E-29
PLIN4	4.521226	14.96286	1.7266	3.01E-15	1.14E-14
MATN4	0.472251	0.171626	-1.46029	0.000146202	0.000245813
ADAMTS16	0.999533	2.824352	1.498594	8.50E-65	2.52E-63
C1QL4	0.584618	0.23669	-1.3045	0.00238771	0.003507457
PDGFRL	5.908689	15.36716	1.378941	1.72E-100	2.36E-98
PLN	1.394304	3.114189	1.159312	4.19E-63	1.19E-61
FOXI3	0.421244	0.18143	-1.21525	0.00838329	0.011524695
GLDC	2.726753	0.931845	-1.54902	7.59E-06	1.43E-05
COL1A1	368.289	1119.015	1.603319	9.10E-105	1.57E-102
SOHLH1	0.174655	0.072557	-1.26731	0.006028259	0.008423343

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
TLX1	0.897316	0.383159	-1.22767	5.31E-08	1.20E-07
C11orf86	0.63777	0.144763	-2.13934	0.002645933	0.003867985
CYP2A13	0.425204	0.063968	-2.73273	1.08E-05	2.02E-05
SELE	1.501335	3.021533	1.009034	5.84E-28	4.32E-27
FAM189A1	0.212708	0.431954	1.022002	1.57E-23	9.50E-23
NR2F1	3.521436	7.762799	1.140413	1.16E-52	2.23E-51
SCN2B	0.097813	0.266357	1.445265	1.98E-62	5.48E-61
MT3	0.202767	0.082097	-1.30443	1.08E-05	2.01E-05
INMT	0.76475	1.746272	1.191218	2.26E-42	2.84E-41
STAB2	0.057588	0.121842	1.081166	1.02E-16	4.25E-16
CLEC4D	0.067023	0.232641	1.795369	4.98E-10	1.33E-09
GLIS3	0.570327	1.185265	1.055349	3.01E-71	1.15E-69
AP3B2	0.967393	0.416522	-1.21571	4.81E-07	1.01E-06
CNRIP1	1.469268	3.425156	1.221072	4.80E-140	2.18E-136
DHH	0.155387	0.310863	1.000413	1.17E-35	1.15E-34
PGM5	0.630376	1.498453	1.24919	3.22E-54	6.54E-53
CYBB	9.889828	19.99619	1.015707	1.29E-51	2.34E-50
BICC1	1.820694	4.617104	1.3425	1.57E-117	5.78E-115
CNTN1	1.185344	2.714486	1.195374	1.18E-62	3.27E-61
CFH	3.588411	9.327826	1.378196	1.36E-131	1.85E-128
MMP2	49.07799	154.6103	1.655488	4.01E-131	4.96E-128
ITGBL1	2.241135	6.582105	1.554319	3.60E-99	4.62E-97
CD226	0.177876	0.368816	1.05203	6.46E-45	8.95E-44
TNFSF4	1.394779	2.859057	1.035503	8.44E-59	2.01E-57
GPIHBP1	0.866225	2.330757	1.427984	1.42E-34	1.34E-33
TMEM82	0.176952	0.05961	-1.56973	0.004501656	0.006395952
WISP2	2.844927	9.047208	1.669081	2.74E-61	7.23E-60
UBASH3A	0.485068	0.972901	1.004106	8.67E-32	7.39E-31
THSD7B	0.170207	0.378183	1.151797	2.98E-42	3.72E-41
NCAN	1.455371	0.363723	-2.00048	0.0211123	0.027654512
TCL1A	0.621605	1.244251	1.001208	1.01E-11	3.06E-11
CD209	0.569308	1.262595	1.149112	9.44E-37	9.70E-36
RFX8	0.294137	0.619781	1.07527	4.04E-67	1.32E-65
SBSN	5.475512	0.87821	-2.64036	0.002891725	0.00420876
GAS7	2.592191	6.961687	1.425265	8.93E-124	6.75E-121
ACKR4	0.381711	1.035803	1.440195	2.62E-78	1.32E-76
KL	0.270776	0.548446	1.018251	2.03E-47	3.12E-46
NMU	3.464222	1.029932	-1.74998	1.16E-06	2.36E-06
MYOG	0.125669	0.046874	-1.42276	3.83E-06	7.42E-06
ADAMTS12	2.901195	6.788183	1.226378	3.88E-76	1.83E-74
PPP1R16B	1.30209	2.618363	1.007836	3.65E-43	4.75E-42
FBN1	9.708461	31.12972	1.680978	3.42E-122	1.94E-119

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
CLDN6	2.494945	0.417582	-2.57888	0.033733825	0.043019321
RGS18	0.42491	0.868989	1.032179	3.48E-46	5.07E-45
LEP	0.509573	2.728144	2.420558	1.66E-18	7.76E-18
NID2	3.35112	8.164395	1.284703	2.00E-89	1.56E-87
GLRA3	0.713602	1.773445	1.313363	0.00077772	0.001204602
TENM4	0.666298	1.417226	1.088831	2.91E-85	1.95E-83
GYPE	0.093444	0.190149	1.024964	2.32E-58	5.39E-57
AICDA	0.030415	0.231272	2.926725	7.90E-19	3.76E-18
SLC38A4	0.166782	0.431321	1.370803	1.02E-80	5.54E-79
TREML2	0.089356	0.186616	1.062436	1.25E-27	9.08E-27
BHMT2	0.778829	1.586482	1.026453	1.68E-81	9.50E-80
GZMM	1.307191	2.639437	1.01376	1.76E-21	9.61E-21
ABCD2	0.15145	0.346964	1.195941	7.66E-45	1.05E-43
GLYAT	0.061072	0.233808	1.936749	6.37E-15	2.37E-14
CCDC69	3.089055	6.285219	1.024798	6.39E-45	8.87E-44
GIMAP7	6.704325	13.4454	1.003949	4.85E-45	6.77E-44
ABCB1	0.536773	1.168816	1.122664	8.13E-46	1.17E-44
DPYSL5	0.580468	0.095173	-2.6086	8.85E-05	0.000152131
SPN	1.22719	2.605913	1.08643	4.05E-55	8.49E-54
ZEB2	1.104462	2.641516	1.258022	2.37E-122	1.47E-119
TLR7	1.222782	2.794947	1.192654	2.01E-67	6.66E-66
GPR34	2.604936	5.865366	1.170973	3.97E-82	2.34E-80
GREM1	2.154606	5.522	1.357767	1.82E-65	5.58E-64
GAPT	0.943378	1.989809	1.076722	8.31E-61	2.13E-59
FHL1	3.585038	10.09388	1.49342	2.28E-85	1.56E-83
ASPN	18.63238	82.75899	2.151104	5.23E-95	5.27E-93
MMP13	5.615603	17.57689	1.646167	6.20E-36	6.16E-35
FCRL3	0.298083	0.604608	1.020287	1.79E-23	1.09E-22
GLIS1	0.233295	0.470902	1.013271	2.73E-52	5.17E-51
GAS1	6.156056	14.35206	1.221179	5.49E-93	5.15E-91
TRARG1	1.233954	3.893155	1.657651	1.13E-22	6.54E-22
SH2D1A	0.955894	2.095952	1.132683	7.12E-34	6.57E-33
LGALS12	0.735079	1.719644	1.226139	2.68E-17	1.16E-16
MEOX1	1.304268	2.823749	1.114371	7.33E-24	4.52E-23
MYOM2	0.317077	0.927609	1.548682	2.36E-09	6.01E-09
TMEM273	1.083815	2.348699	1.115743	1.71E-71	6.59E-70
FCRL6	0.332159	0.671702	1.015947	6.71E-30	5.36E-29
SVEP1	0.962158	2.781492	1.531513	5.06E-89	3.83E-87
CD300LG	0.275647	0.93126	1.756361	9.12E-25	5.82E-24
PLPP4	2.674305	6.952018	1.378268	2.82E-69	1.00E-67
KCNK7	0.362313	0.165876	-1.12713	0.012856565	0.017296745
KCNA5	0.147138	0.314816	1.097342	1.25E-28	9.51E-28

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
METTL24	0.135037	0.345559	1.355579	8.81E-72	3.46E-70
ADAMTS2	6.652906	17.85299	1.42411	2.84E-110	6.14E-108
FOLR2	4.283695	10.11357	1.239365	8.68E-48	1.36E-46
JCHAIN	64.51482	164.8194	1.353183	9.31E-33	8.24E-32
COMP	25.80341	66.52678	1.366374	5.06E-54	1.02E-52
CD1E	0.706462	1.501716	1.087929	9.21E-28	6.73E-27
ITGA11	4.247094	11.65115	1.455925	3.69E-68	1.27E-66
EMX2	0.236981	0.533062	1.16953	3.65E-70	1.35E-68
JAML	0.737223	1.599117	1.117102	2.17E-47	3.33E-46
LEPR	0.727178	1.46111	1.006684	1.11E-39	1.24E-38
ADH1A	0.024782	0.062432	1.332972	4.49E-20	2.29E-19
CD40LG	0.552583	1.231953	1.156685	3.92E-36	3.93E-35
SALL1	0.227294	0.473497	1.058792	1.21E-71	4.73E-70
FAT4	0.468926	1.077001	1.199588	7.74E-87	5.60E-85
GPR1	0.3256	1.127263	1.791651	9.06E-82	5.24E-80
IFFO1	1.315919	2.63354	1.000932	1.20E-92	1.12E-90
DBX2	0.050813	0.137277	1.433821	4.94E-45	6.89E-44
SIT1	1.476449	2.97478	1.010652	4.75E-32	4.10E-31
EMILIN1	13.21609	31.97722	1.274749	1.28E-75	5.97E-74
TH	0.314227	0.155956	-1.01067	0.003155591	0.004569345
ANGPTL1	0.474073	1.663547	1.811081	3.02E-82	1.78E-80
CLEC10A	1.102251	2.721491	1.303945	5.13E-31	4.29E-30
IL21R	0.671572	1.378851	1.037853	7.79E-52	1.43E-50
ACVR1C	0.152213	0.359026	1.238002	2.89E-21	1.56E-20
MRVI1	1.623625	3.496862	1.106843	2.00E-96	2.16E-94
TNXB	0.580297	1.753556	1.59542	5.04E-45	7.03E-44
FBN3	0.496456	0.240363	-1.04645	0.001103889	0.001683548
3-Sep	5.258872	2.33447	-1.17166	2.80E-17	1.22E-16
MCTP1	0.651973	1.323839	1.021842	2.22E-69	7.92E-68
P2RY12	0.481577	0.996268	1.048767	5.56E-45	7.74E-44
KCNH2	1.506782	0.553018	-1.44607	6.21E-08	1.40E-07
ABCA6	0.232507	0.736731	1.663862	5.67E-94	5.47E-92
APOA1	1.27782	0.284688	-2.16623	0.021832024	0.028536826
CD248	12.30018	26.21395	1.091655	1.44E-78	7.38E-77
HSD11B1	1.251101	3.254204	1.379107	7.25E-40	8.22E-39
SLC19A3	0.471713	1.383196	1.552025	3.24E-17	1.39E-16
SGIP1	0.47994	1.006364	1.068226	9.82E-67	3.15E-65
ROPN1B	1.967686	0.721074	-1.44828	0.036005496	0.045813239
SPIN2A	0.058612	0.147843	1.334791	8.07E-37	8.31E-36
CPXM1	8.004237	23.13446	1.531208	1.09E-80	5.89E-79
F2RL2	5.646246	13.93021	1.302853	6.92E-53	1.34E-51
CLDN5	1.992881	4.476605	1.167549	1.09E-28	8.32E-28

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
ARSI	1.024252	2.198125	1.101703	3.47E-65	1.05E-63
GFPT2	2.907697	5.942321	1.03115	7.09E-97	8.04E-95
MGARP	0.172875	0.466779	1.433011	9.49E-28	6.92E-27
C2orf70	0.649772	0.309073	-1.07198	4.26E-08	9.75E-08
CCDC80	7.634024	27.18417	1.832251	6.03E-139	2.05E-135
PI16	1.880419	6.304699	1.745373	1.81E-22	1.04E-21
CCL23	0.192142	0.418531	1.123163	2.15E-32	1.87E-31
SLITRK1	0.370406	0.094974	-1.96351	0.001036652	0.0015842
NEXN	1.842856	3.756721	1.02753	5.63E-92	5.07E-90
ANK2	0.482254	1.144863	1.247309	4.92E-76	2.32E-74
CPA1	0.022127	0.071157	1.6852	8.40E-18	3.76E-17
NLRP3	0.576432	1.226724	1.089588	1.34E-72	5.49E-71
LRRC17	3.351968	9.322823	1.475759	1.05E-66	3.37E-65
CORIN	0.356903	1.048974	1.555375	3.26E-62	8.88E-61
PEX5L	0.788032	0.363802	-1.1151	8.55E-05	0.00014714
ARHGAP20	0.210816	0.54964	1.3825	7.88E-97	8.86E-95
PLA2G2D	1.467224	3.166657	1.109871	2.97E-14	1.05E-13
HSPB7	0.65552	1.528017	1.22095	6.45E-46	9.30E-45
GALNT15	0.880987	3.091316	1.811028	3.11E-103	5.04E-101
HIC1	0.866363	1.85743	1.100264	2.25E-78	1.14E-76
CD84	1.550968	3.670711	1.242891	5.77E-64	1.69E-62
PSORS1C2	1.33125	0.613749	-1.11706	0.006045044	0.008444197
RBMS3	0.895212	2.149176	1.263483	1.04E-98	1.31E-96
VCAM1	4.571069	9.984068	1.127096	1.18E-57	2.68E-56
ABCA10	0.173832	0.372451	1.099355	2.43E-25	1.60E-24
PLA2G5	0.270247	0.587568	1.120477	3.89E-53	7.64E-52
XPNPEP2	0.168084	0.507249	1.593512	5.80E-58	1.33E-56
B3GALT2	0.107928	0.258943	1.262566	6.98E-42	8.59E-41
PDK4	7.395936	15.79381	1.094554	5.35E-25	3.46E-24
COL6A3	36.37068	100.2132	1.462224	3.13E-119	1.25E-116
MS4A2	0.484983	1.203817	1.31161	1.59E-49	2.68E-48
SEMA3D	0.360257	0.90468	1.328382	1.17E-76	5.61E-75
CRTAM	0.380608	0.869182	1.191351	4.33E-54	8.76E-53
JCAD	3.246038	6.915707	1.091197	3.71E-121	1.74E-118
PTH1R	0.404766	1.163598	1.523433	4.04E-83	2.44E-81
TAGLN3	0.321949	0.071314	-2.17456	0.022843559	0.029796042
GPR141	0.403549	0.902912	1.16184	1.50E-74	6.62E-73
COL5A2	39.62302	117.727	1.571034	1.76E-114	5.56E-112
TNFRSF17	1.088005	2.204634	1.018854	5.81E-25	3.75E-24
TMEM119	7.818352	22.08482	1.498119	5.87E-111	1.38E-108
GPX3	15.1274	31.54309	1.06016	4.79E-32	4.13E-31
FILIP1L	4.279196	10.09839	1.238714	3.77E-106	6.75E-104

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
CPN2	0.103962	0.212813	1.03353	1.31E-46	1.94E-45
ZFPM2	0.518185	1.328084	1.357807	5.33E-111	1.27E-108
MYT1	1.092954	0.285551	-1.93641	7.38E-06	1.39E-05
MAP1LC3C	0.213667	0.667785	1.644022	2.26E-58	5.26E-57
FIBIN	6.071702	16.70131	1.459789	1.92E-110	4.21E-108
KCNA3	0.293175	0.755368	1.365419	6.73E-47	1.01E-45
HMCN1	1.180521	3.639145	1.624176	1.01E-100	1.42E-98
FCER1A	1.548099	3.801758	1.296169	1.61E-40	1.86E-39
OLFML2B	12.74606	31.52271	1.30634	1.31E-112	3.56E-110
POU5F1B	0.36584	0.155032	-1.23865	0.00063158	0.000988487
PDE1A	0.449143	0.962719	1.099938	1.37E-72	5.61E-71
HSPG2	11.74674	23.97271	1.029132	2.81E-74	1.23E-72
OMD	2.127916	8.824745	2.052114	3.07E-103	5.04E-101
CR2	0.652143	1.645998	1.335701	4.51E-08	1.03E-07
ERG	1.394249	2.795577	1.003658	1.17E-81	6.74E-80
HEPACAM	0.031394	0.107057	1.769824	4.08E-19	1.96E-18
CASS4	0.31397	0.645599	1.040012	4.41E-59	1.06E-57
SYNDIG1	1.356353	4.344002	1.679292	9.01E-81	4.95E-79
OLFML1	2.07629	5.547427	1.417811	2.32E-151	3.16E-147
C7orf61	0.390505	0.18215	-1.10022	0.000152999	0.000256735
CSF2RB	2.290159	5.0456	1.139578	5.88E-60	1.46E-58
SERPINF1	32.42892	85.94985	1.406214	1.03E-127	1.00E-124
DDR2	3.208797	6.559042	1.031452	6.71E-97	7.67E-95
GLI1	0.235779	0.552821	1.229377	7.64E-41	8.99E-40
HGF	0.432188	1.082531	1.324678	3.78E-90	3.10E-88
THY1	17.40804	37.17553	1.094599	1.48E-93	1.41E-91
METTL11B	0.106059	0.269253	1.344092	1.33E-31	1.13E-30
G0S2	9.534128	22.48835	1.238005	5.89E-20	2.97E-19
GPR15	0.151655	0.405314	1.418249	5.34E-24	3.31E-23
LPO	0.190159	0.051782	-1.87668	0.0052259	0.007356592
TMEM132C	0.205961	0.731781	1.829041	6.45E-35	6.20E-34
REEP2	2.253005	1.109192	-1.02234	1.24E-08	2.98E-08
COL14A1	5.724734	21.02912	1.877108	1.06E-85	7.36E-84
TMEM145	2.707647	0.913457	-1.56763	5.47E-11	1.57E-10
LYZ	64.80755	130.3403	1.00805	3.41E-35	3.31E-34
TNFAIP6	5.202276	10.47825	1.010183	2.13E-80	1.14E-78
ASPA	0.142016	0.319913	1.171631	3.40E-46	4.96E-45
MSLNL	0.249464	0.105867	-1.23657	1.90E-09	4.88E-09
MRO	0.233923	0.746971	1.675019	5.93E-34	5.49E-33
TMEM151A	0.294442	0.102064	-1.52851	3.71E-06	7.21E-06
FCER2	0.331626	0.691725	1.060639	1.49E-22	8.61E-22
USH1C	0.284488	0.049699	-2.51707	0.00011915	0.000202356

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
ABI3BP	1.470486	3.55055	1.271749	3.02E-72	1.21E-70
CD3G	0.800306	1.795654	1.165886	5.20E-39	5.75E-38
LRP1B	0.59527	1.319451	1.148321	1.51E-10	4.20E-10
DMBT1	0.165723	1.25341	2.919013	3.60E-15	1.36E-14
BMX	0.278902	0.657028	1.236197	5.77E-42	7.13E-41
OMG	0.115351	0.249758	1.114496	3.53E-21	1.89E-20
LRRC70	0.183883	0.378364	1.040986	4.19E-43	5.45E-42
THBS4	8.839271	20.83456	1.236979	1.39E-46	2.05E-45
VMO1	2.474678	7.568237	1.612716	0.000194006	0.000322246
BNC2	0.516974	1.565981	1.598905	7.36E-126	6.26E-123
FGL2	5.236208	12.11778	1.210532	9.01E-73	3.73E-71
S1PR1	5.034631	10.9527	1.121329	6.41E-64	1.86E-62
C1QTNF6	4.527487	9.21705	1.025595	1.00E-80	5.46E-79
EGR1	52.06311	113.6361	1.126088	2.34E-32	2.04E-31
SLC38A5	1.526549	3.238216	1.084925	6.45E-65	1.92E-63
FBLN1	22.08322	45.05221	1.028647	4.59E-72	1.82E-70
ABCA9	0.277193	0.912496	1.718926	9.36E-72	3.67E-70
SLC24A2	0.253302	0.922327	1.864418	4.11E-77	2.03E-75
PNOC	0.249963	0.5417	1.11578	5.87E-36	5.85E-35
HAS1	0.296332	0.661177	1.157819	5.03E-29	3.88E-28
MS4A1	1.499212	3.220684	1.103163	1.87E-20	9.68E-20
MAST1	0.490363	0.182088	-1.42921	1.16E-15	4.51E-15
EBF1	1.231513	2.692459	1.128493	3.61E-89	2.76E-87
COL6A2	101.9679	240.1029	1.235537	2.21E-83	1.37E-81
CRISPLD2	5.947034	17.32157	1.542328	1.22E-131	1.84E-128
CAV1	12.67735	26.71003	1.075128	1.73E-79	9.09E-78
SPON1	6.15901	17.44062	1.501681	4.66E-110	9.92E-108
GNG13	1.577726	0.745787	-1.08101	1.11E-07	2.46E-07
THEMIS	0.330627	0.749054	1.179864	1.18E-41	1.43E-40
BACH2	0.406501	0.827469	1.025445	1.13E-68	3.97E-67
PRKCB	0.588465	1.412375	1.263093	3.15E-43	4.12E-42
FCRL5	0.266374	0.556447	1.062792	3.01E-22	1.71E-21
PDE2A	0.809476	1.653018	1.030041	9.49E-49	1.54E-47
FCGR3B	0.367833	0.879234	1.257197	4.65E-09	1.15E-08
GIMAP5	0.161278	0.363153	1.171033	3.00E-43	3.92E-42
ELAVL3	0.232079	0.021051	-3.46268	3.33E-09	8.39E-09
GRP	3.859387	8.147288	1.077948	1.88E-41	2.27E-40
BARX2	10.32219	5.143943	-1.0048	1.61E-09	4.16E-09
PRND	0.574521	1.445409	1.331046	2.12E-38	2.30E-37
PODNL1	1.816463	3.907965	1.105286	1.57E-71	6.09E-70
DLL3	0.410981	0.150802	-1.44641	2.02E-08	4.75E-08
MAT1A	1.286743	0.474846	-1.43819	7.75E-08	1.73E-07

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
CLEC4C	0.07399	0.198278	1.422124	3.27E-16	1.32E-15
COL2A1	17.27541	7.473683	-1.20883	5.69E-05	9.94E-05
CORO2B	0.572435	1.280664	1.161708	6.12E-75	2.74E-73
SPARCL1	46.60231	112.5836	1.272524	1.62E-90	1.37E-88
RASL10B	1.909806	0.912027	-1.06628	0.000212377	0.000350791
CPZ	0.137841	0.376989	1.451518	1.74E-72	7.07E-71
KCNJ15	0.206047	0.417911	1.020222	1.32E-65	4.07E-64
CHSY3	0.851307	2.016012	1.243752	2.20E-109	4.47E-107
SLIT3	2.185583	5.30701	1.279881	3.95E-103	6.18E-101
LAMP5	5.173644	10.89779	1.074783	2.21E-57	4.93E-56
NR4A3	0.718384	1.670414	1.217378	6.23E-27	4.40E-26
F13A1	5.276401	18.92928	1.842993	1.19E-110	2.70E-108
ACKR1	5.990046	17.65809	1.55969	5.08E-30	4.08E-29
CD1C	1.042491	2.349374	1.172242	5.09E-33	4.54E-32
FYB1	3.25908	6.798301	1.060709	8.22E-54	1.65E-52
LTBP2	13.87084	28.8785	1.057941	1.02E-85	7.10E-84
NAP1L3	0.834115	1.947558	1.223348	9.79E-100	1.29E-97
SSC5D	2.700384	5.610315	1.054917	3.80E-67	1.25E-65
DMP1	0.074992	0.258167	1.783503	0.000370973	0.000595473
CDH11	6.087292	15.94942	1.389631	2.30E-109	4.61E-107
PLAU	21.88393	44.82204	1.034336	1.87E-52	3.56E-51
MMP8	0.082706	0.178079	1.106456	1.13E-11	3.41E-11
FGF18	0.510552	1.068401	1.065323	2.21E-57	4.93E-56
CBLN4	0.236478	0.492712	1.059037	1.99E-29	1.56E-28
C14orf180	0.125691	0.402144	1.677826	3.29E-18	1.51E-17
HSD17B13	0.072986	0.174421	1.256884	1.53E-33	1.39E-32
LGI2	0.5517	1.159668	1.071756	1.46E-64	4.32E-63
IL12B	0.085986	0.17675	1.039535	8.84E-17	3.71E-16
C6	0.236763	0.695229	1.554042	1.67E-25	1.11E-24
LRRC32	7.038867	15.98535	1.183335	8.33E-107	1.55E-104
FCN1	0.478968	1.031544	1.106805	2.32E-26	1.59E-25
TSPAN11	0.538718	1.096751	1.025632	3.18E-65	9.65E-64
PRSS1	0.732806	0.309397	-1.24397	0.009122935	0.012487252
LILRA4	0.505793	1.063859	1.072689	5.20E-35	5.02E-34
MSLN	16.62659	5.237529	-1.66653	1.57E-05	2.88E-05
LYVE1	0.545518	1.494404	1.453872	2.34E-44	3.17E-43
P2RY13	1.133197	2.323198	1.035714	2.12E-50	3.72E-49
CCR4	0.772858	1.995223	1.368275	7.19E-57	1.58E-55
NTSR2	0.270847	0.023473	-3.52843	7.99E-16	3.15E-15
ADH1C	0.571921	1.213476	1.085257	3.82E-26	2.60E-25
ALDH1A1	5.660941	11.76752	1.055696	2.32E-79	1.22E-77
TBX15	1.166643	2.477731	1.086656	1.44E-98	1.80E-96

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
VWF	11.78163	23.69121	1.007813	8.31E-64	2.41E-62
MRAP	0.136899	0.513173	1.906337	2.06E-20	1.06E-19
PTGDS	6.343909	15.81215	1.317589	2.75E-34	2.58E-33
FLNC	0.975933	2.133898	1.128637	2.91E-84	1.87E-82
F2R	12.72295	26.57116	1.062428	5.30E-89	3.98E-87
TFCP2L1	6.572677	3.266403	-1.00878	6.94E-10	1.84E-09
SGCD	1.068576	2.866268	1.423484	9.85E-97	1.10E-94
COL11A1	13.26381	41.50512	1.645795	3.57E-45	5.01E-44
GRID1	0.352457	0.713098	1.016651	5.97E-84	3.80E-82
ELN	12.21209	29.49115	1.271971	2.59E-55	5.48E-54
SFRP2	126.7616	383.8459	1.59841	1.70E-105	3.00E-103
LRRN4CL	0.446377	1.352934	1.599756	5.22E-76	2.45E-74
NPR1	1.351818	2.746195	1.022533	2.37E-38	2.56E-37
CCNE1	5.022873	2.420482	-1.05322	2.78E-12	8.75E-12
ENHO	7.990382	3.038556	-1.39488	6.07E-13	1.99E-12
DIO2	2.865629	7.019647	1.292547	8.24E-58	1.88E-56
DPYSL3	14.4471	34.06656	1.237576	1.02E-115	3.57E-113
CDK5R2	0.617012	0.062069	-3.31336	0.001203444	0.001826306
COX6A2	0.385174	0.172913	-1.15546	0.010509867	0.014293629
FMR1NB	0.440038	0.044019	-3.32142	0.020123718	0.026448704
FLI1	1.627208	3.34997	1.04175	2.82E-99	3.69E-97
DACT1	2.197908	5.745184	1.386222	7.17E-113	1.99E-110
AXL	7.535407	15.73355	1.062087	1.51E-128	1.58E-125
CILP	12.32775	47.88523	1.957671	1.15E-84	7.50E-83
SLIT2	1.1739	2.82469	1.266784	4.30E-95	4.37E-93
EOMES	0.486819	1.110422	1.189651	2.11E-32	1.84E-31
GLI2	0.388807	0.90961	1.226194	2.77E-91	2.38E-89
MAGEL2	0.142641	0.401591	1.493336	2.99E-100	3.99E-98
ASCL1	3.863548	1.429858	-1.43405	0.005424172	0.007619937
ZNF831	0.147089	0.357387	1.280798	3.87E-38	4.16E-37
PLAC9	2.325955	5.824868	1.324402	3.72E-50	6.46E-49
IL7R	2.708594	7.041039	1.378244	1.21E-48	1.97E-47
MSR1	4.111582	8.482946	1.044872	4.09E-61	1.07E-59
EVI2A	3.081755	6.940376	1.171262	1.36E-95	1.43E-93
SOX17	0.999276	2.064305	1.046702	1.13E-41	1.38E-40
RGS13	0.073889	0.168256	1.187219	2.63E-48	4.21E-47
ENPP2	3.254802	6.590492	1.017816	1.63E-48	2.64E-47
ROS1	0.073575	0.280519	1.930809	1.52E-10	4.23E-10
SPOCK1	4.680589	11.48984	1.295597	7.38E-78	3.72E-76
SELP	1.370387	3.781494	1.464373	1.90E-40	2.18E-39
CHRDL1	2.201697	6.761083	1.618638	7.06E-34	6.52E-33
MMP9	35.39459	96.06222	1.44044	2.25E-08	5.28E-08

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
ADGRA2	3.29402	7.255749	1.139275	1.76E-97	2.05E-95
GAB3	0.594114	1.22047	1.038624	5.75E-82	3.35E-80
CAMK2N2	1.089958	0.481	-1.18016	2.88E-08	6.67E-08
DPEP1	0.412066	0.827402	1.005715	3.35E-42	4.19E-41
SPARC	312.91	841.2864	1.426849	2.86E-121	1.44E-118
SCML4	0.146115	0.332047	1.184287	1.64E-32	1.44E-31
CCL11	0.854299	1.950447	1.190992	1.52E-39	1.70E-38
PLPP7	0.566111	1.226677	1.115598	1.46E-94	1.46E-92
CD300LB	0.272145	0.638461	1.230224	3.36E-49	5.54E-48
VSTM4	1.336686	3.230667	1.273172	6.45E-109	1.27E-106
LMOD1	4.136328	8.583664	1.053243	5.39E-71	2.03E-69
CD28	0.608587	1.327559	1.12524	2.90E-48	4.62E-47
KLRB1	1.118274	2.545909	1.186907	3.37E-42	4.20E-41
HMCN2	0.106526	0.307318	1.528521	3.98E-54	8.07E-53
GPR174	0.465436	1.204738	1.372065	7.78E-36	7.70E-35
ATP6V0D2	0.364091	0.893185	1.29466	8.40E-25	5.37E-24
TBX5	0.511746	1.148968	1.166839	4.09E-95	4.19E-93
TLR8	0.504618	1.08394	1.103022	5.39E-51	9.64E-50
SLC22A3	0.392684	0.789484	1.00754	5.54E-48	8.71E-47
NCKAP1L	2.287054	4.826606	1.077518	2.19E-67	7.24E-66
RFTN2	0.489764	0.980096	1.000836	4.74E-104	7.97E-102
KRTDAP	8.07128	0.84693	-3.25248	7.93E-05	0.000136989
DLGAP3	0.395612	0.180915	-1.12877	9.95E-05	0.000170243
SYT13	18.45142	8.303717	-1.1519	0.000151055	0.000253632
MMRN1	0.580575	1.76835	1.606849	1.61E-43	2.13E-42
COL6A1	91.82498	221.1245	1.2679	9.93E-87	7.15E-85
ARHGAP28	0.422085	0.975142	1.208081	1.83E-96	2.01E-94
C16orf54	1.062089	2.292409	1.10996	3.56E-42	4.44E-41
CYP19A1	0.051638	0.92074	4.156302	1.04E-22	6.06E-22
MYL3	0.196028	0.441893	1.17264	7.49E-92	6.58E-90
CEMIP	1.852437	4.299808	1.214848	7.16E-31	5.93E-30
TMSB15A	6.610548	2.429219	-1.44428	8.24E-08	1.84E-07
ADAMTS5	1.064608	2.198705	1.046331	5.15E-74	2.22E-72
RECK	1.557915	3.853149	1.306421	1.01E-123	7.26E-121
PRSS3	0.444472	0.140418	-1.66236	0.014386857	0.019231945
CLEC17A	0.17535	0.35498	1.017499	1.39E-21	7.64E-21
SLCO2B1	3.186958	6.596754	1.049577	2.80E-75	1.28E-73
PENK	0.201243	0.727917	1.854837	1.68E-28	1.27E-27
HPDL	2.273143	1.037774	-1.1312	3.38E-05	6.01E-05
TMPRSS6	3.14985	1.518859	-1.0523	0.009639446	0.013162463
MUC7	0.175424	0.628501	1.841068	3.56E-07	7.56E-07
FADS6	0.188302	0.032112	-2.55186	2.95E-06	5.78E-06

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
PRDM8	0.223851	0.491611	1.134978	9.05E-91	7.70E-89
PECAM1	14.72296	29.78364	1.016452	3.86E-95	3.98E-93
MYH11	2.938914	6.544446	1.154988	1.22E-40	1.42E-39
PCDHGA12	0.331355	0.694535	1.067668	7.07E-80	3.73E-78
GPR158	0.525924	0.236632	-1.15221	0.018693571	0.024652396
MFAP5	6.90962	19.1193	1.468351	4.79E-85	3.18E-83
TBX18	0.486931	1.142214	1.230043	1.40E-101	2.03E-99
LCN6	0.071742	0.178961	1.318748	2.30E-21	1.25E-20
ELAVL2	1.002201	0.467524	-1.10006	0.000775418	0.001201584
EGR2	3.993135	8.249238	1.046739	1.04E-43	1.39E-42
POSTN	122.6003	337.7909	1.462168	2.00E-93	1.89E-91
CST9L	0.587715	0.276837	-1.08608	0.010900049	0.014788809
TEK	1.800491	3.768683	1.06567	3.00E-71	1.15E-69
PARP15	0.366861	0.795425	1.116493	9.18E-42	1.13E-40
NEURL1	4.340861	2.108994	-1.04143	4.35E-05	7.68E-05
CHIT1	1.206048	4.210135	1.803579	2.40E-15	9.19E-15
PCOLCE	16.8827	40.69438	1.269284	5.99E-90	4.85E-88
VEGFD	0.341527	0.76017	1.15432	5.31E-15	1.98E-14
TMEM252	0.043554	0.108498	1.316797	5.88E-36	5.85E-35
AGXT	0.081498	0.249698	1.615345	4.01E-09	1.00E-08
KLHL4	0.089896	0.250704	1.479657	4.74E-63	1.34E-61
GPD1	2.213281	7.81726	1.820476	4.19E-18	1.91E-17
PRTN3	0.421844	0.16451	-1.35853	0.000541722	0.000852262
CR1	0.093652	0.221032	1.23887	2.86E-31	2.40E-30
TPSB2	7.727632	16.96091	1.134115	4.58E-29	3.54E-28
CRYBA2	0.40755	0.063212	-2.6887	8.65E-08	1.93E-07
LAMA2	2.038473	5.980339	1.552739	3.82E-89	2.90E-87
TSHZ3	1.611	3.625759	1.170327	7.24E-118	2.74E-115
LRRC15	11.04221	39.86284	1.852015	6.73E-98	8.18E-96
HTRA1	69.19381	179.5765	1.375884	6.66E-111	1.53E-108
CD48	3.62074	7.265684	1.004814	2.75E-44	3.72E-43
PDGFRB	18.18703	40.37043	1.150389	4.02E-114	1.24E-111
PCDH7	1.252097	2.845589	1.18438	5.32E-81	2.96E-79
RUNX1T1	0.299432	0.728818	1.283333	5.35E-113	1.52E-110
TMEM213	0.900241	0.385613	-1.22316	0.024354653	0.031621542
SORCS2	1.064212	3.00887	1.499436	1.64E-80	8.84E-79
MXRA8	25.43406	52.00347	1.031846	1.46E-69	5.27E-68
C3orf80	1.21724	2.469936	1.02086	8.12E-81	4.48E-79
MSI1	2.912179	1.276551	-1.18985	5.14E-09	1.27E-08
CIDEA	0.749215	2.306358	1.622165	8.22E-19	3.90E-18
TSPAN7	2.235329	4.564347	1.029921	4.33E-38	4.64E-37
LRTM2	0.739518	0.197325	-1.90601	0.000371613	0.00059636

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
DPT	9.459844	34.01147	1.846133	3.33E-103	5.33E-101
ERVFRD-1	0.059934	0.240765	2.006176	3.90E-28	2.91E-27
FMO1	1.385284	3.174777	1.196474	3.37E-56	7.32E-55
CPED1	1.025133	2.194414	1.098025	2.56E-85	1.74E-83
PRRX1	7.845041	19.97272	1.348178	2.37E-119	9.77E-117
PRSS33	1.41159	0.375432	-1.9107	0.006724023	0.009338005
TERT	0.167503	0.068617	-1.28754	1.55E-15	6.02E-15
CYP1A1	0.05025	0.162623	1.694343	0.02631852	0.033996212
NUGGC	0.189962	0.420819	1.147489	2.73E-41	3.27E-40
GFRA3	1.518352	0.259942	-2.54624	0.008608932	0.011826526
C1QTNF3	3.154058	8.273563	1.391299	3.22E-52	6.06E-51
TESPA1	0.470854	1.029836	1.129064	9.47E-46	1.35E-44
COL6A6	0.167515	0.4444	1.407567	4.71E-54	9.52E-53
DKK3	7.776233	16.0715	1.047361	9.37E-74	4.01E-72
CD36	5.6039	12.19	1.121195	1.43E-24	9.08E-24
ACTL8	4.374555	1.762887	-1.3112	2.33E-07	5.03E-07
FAM131C	0.431519	0.167295	-1.36703	2.34E-11	6.92E-11
NDN	4.547895	9.947947	1.1292	1.43E-102	2.21E-100
SLC1A7	0.118054	0.314545	1.413826	3.92E-79	2.03E-77
PIK3CG	0.606742	1.512947	1.318207	5.14E-67	1.67E-65
SLC1A2	2.565454	1.127468	-1.18613	9.11E-06	1.71E-05
LOX	6.353005	16.39884	1.368083	1.52E-103	2.53E-101
LHFPL6	10.18344	22.02517	1.112928	1.13E-96	1.26E-94
FOS	50.57364	107.135	1.082972	3.67E-27	2.61E-26
C9orf84	0.080297	0.185415	1.20733	6.66E-09	1.63E-08
DACT3	0.722325	1.531938	1.084639	2.45E-86	1.74E-84
PLXNC1	2.83257	6.642928	1.229708	9.42E-110	1.97E-107
PDPN	3.906365	9.276355	1.247731	1.75E-100	2.38E-98
DCSTAMP	0.233543	0.520125	1.15517	3.74E-23	2.23E-22
C8orf86	0.299091	0.097334	-1.61957	4.18E-07	8.82E-07
GRIN2C	0.566263	0.245184	-1.20761	8.11E-05	0.00013978
TEX14	1.388928	0.507279	-1.45312	0.004787185	0.006777569
CTSK	57.55395	177.0593	1.621246	3.94E-135	8.93E-132
SPOCK3	0.042665	0.138093	1.694514	8.79E-13	2.85E-12
PDE1B	0.53296	1.15211	1.112181	3.22E-84	2.06E-82
COL15A1	13.42067	28.48256	1.085622	1.87E-98	2.29E-96
C1S	36.92673	75.49182	1.031655	1.28E-111	3.23E-109
AVPR2	0.306345	0.646522	1.07754	2.43E-25	1.59E-24
LUM	116.3737	369.4877	1.666761	2.99E-133	5.81E-130
OGDHL	0.402885	0.117155	-1.78195	8.42E-05	0.000145057
KCNA1	0.043804	0.111382	1.346375	5.45E-50	9.38E-49
SULT1B1	0.099635	0.325443	1.707679	3.02E-30	2.45E-29

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
PREX2	0.512404	1.114959	1.121638	4.81E-65	1.44E-63
GIMAP1	1.0652	2.13265	1.001522	1.18E-54	2.43E-53
RARRES2	14.82585	32.12196	1.115445	3.84E-69	1.36E-67
HEG1	5.625239	12.77524	1.183365	1.60E-120	7.26E-118
THBS2	32.38425	91.6077	1.500177	1.27E-101	1.85E-99
WDFY4	0.697652	1.505824	1.109973	1.37E-58	3.23E-57
CYTL1	0.729683	1.569356	1.104832	9.73E-43	1.24E-41
FOSB	6.456207	17.06021	1.401876	1.62E-19	7.95E-19

Table S3 DEGs based upon immune scores

Gene	conMean	treatMean	logFC	P value	fdr
NSG2	2.728889	0.325978	-3.06547	0.00077113	0.001358121
CPLX2	2.414082	0.314533	-2.94019	0.013903927	0.020225331
CNMD	1.051576	0.163392	-2.68615	0.017872377	0.025522893
KCNC1	0.330574	0.056977	-2.53652	1.39E-05	3.11E-05
LMOD2	0.200502	0.03494	-2.52066	0.002133283	0.003507262
TRH	21.80203	4.152237	-2.3925	1.65E-08	5.39E-08
CGA	18.60144	3.687994	-2.33451	0.001563637	0.002628173
CSMD3	0.210856	0.042826	-2.2997	2.94E-05	6.30E-05
RTL9	0.366743	0.075721	-2.276	0.004543666	0.007112594
NELL1	0.932896	0.197731	-2.23818	0.013314072	0.019419519
CYP2A6	38.51201	8.240002	-2.22459	3.16E-07	8.73E-07
UGT2B4	5.81663	1.318364	-2.14143	7.59E-05	0.000153386
ZDHHC22	0.314074	0.076728	-2.03328	0.000270025	0.000506252
SLC5A7	0.204297	0.051331	-1.99276	3.76E-05	7.93E-05
CYP17A1	0.376669	0.099247	-1.9242	0.000894484	0.001560714
RPL3L	0.473993	0.126541	-1.90527	0.00163843	0.002744085
ASCL1	4.174378	1.119588	-1.89859	0.020482352	0.028964839
RUNDC3A	1.689786	0.454267	-1.89523	0.009426403	0.014103006
MYT1	1.082448	0.296037	-1.87045	6.89E-14	3.86E-13
KCNH6	0.232574	0.064325	-1.85424	0.004525178	0.007086809
PRR4	2.118757	0.592475	-1.83839	0.011363716	0.016771319
FAM135B	0.39912	0.114336	-1.80355	1.81E-08	5.88E-08
CELF3	0.348343	0.102576	-1.76381	1.27E-05	2.85E-05
CST9	15.23604	4.584421	-1.73268	5.31E-10	2.05E-09
INSYN2	5.310157	1.738563	-1.61086	2.89E-09	1.03E-08
SYNPO2L	2.336806	0.774807	-1.59263	2.56E-08	8.16E-08
SEZ6L	2.447436	0.812118	-1.59151	0.007724211	0.011704485
GDAP1L1	0.161179	0.05356	-1.58944	3.04E-05	6.50E-05
CHRNB2	1.050718	0.350755	-1.58284	4.74E-05	9.85E-05
LRTM2	0.700936	0.235837	-1.57149	0.013114704	0.01915256
INHA	2.76851	0.932215	-1.57038	4.98E-05	0.00010329
FCRLB	4.754776	1.632123	-1.54263	0.000604089	0.001082773
SERPINC1	0.418512	0.145265	-1.52659	0.004919878	0.007670778
MYOG	0.127913	0.044634	-1.51896	2.12E-07	5.99E-07
CPB1	446.7315	156.7354	-1.51108	5.40E-09	1.86E-08
C8orf86	0.292849	0.103565	-1.49962	1.01E-14	6.09E-14
ATRNL1	1.670195	0.593519	-1.49265	5.80E-06	1.36E-05
WDR72	1.021145	0.363768	-1.4891	0.002015285	0.003330003
SCGN	3.385736	1.206497	-1.48864	0.00020948	0.000398531
RLN2	3.068419	1.111423	-1.46509	2.90E-07	8.06E-07
SLC8A2	0.510237	0.187064	-1.44764	0.002344165	0.003827569
KCNC2	2.280864	0.846008	-1.43084	9.03E-06	2.07E-05

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
PHF21B	0.504652	0.189302	-1.4146	1.58E-07	4.55E-07
NXPH1	3.391889	1.291178	-1.3934	0.010493857	0.015567567
SYT13	19.34318	7.413561	-1.38359	9.56E-08	2.82E-07
KCNJ3	17.78859	6.847611	-1.37728	5.05E-08	1.54E-07
RTBDN	1.272728	0.496139	-1.35911	0.008663226	0.013027721
SMCO3	1.458359	0.569081	-1.35764	0.015459605	0.022342719
PHGR1	3.529591	1.394687	-1.33956	7.00E-08	2.11E-07
PAH	0.463776	0.18789	-1.30354	0.000123769	0.000243232
CYP2A7	12.73642	5.236363	-1.28232	0.000136376	0.000266074
PXDNL	2.750532	1.134218	-1.27801	0.009846075	0.014663813
TMEM145	2.561657	1.059184	-1.27412	3.74E-13	1.97E-12
PEX5L	0.81471	0.337172	-1.2728	1.17E-10	4.86E-10
CDH7	0.213111	0.088206	-1.27266	4.99E-07	1.35E-06
NOVA1	3.879278	1.610373	-1.26839	5.23E-05	0.000107921
SYP	2.272178	0.949057	-1.25951	0.016342399	0.023514663
BRINP2	2.924498	1.240924	-1.23677	2.42E-06	5.99E-06
NTSR2	0.205699	0.088503	-1.21674	0.032645845	0.044748446
COL2A1	17.27513	7.473957	-1.20875	2.28E-09	8.22E-09
CST9L	0.601475	0.263101	-1.19289	4.13E-10	1.61E-09
SLC27A2	11.49557	5.032495	-1.19173	3.24E-08	1.02E-07
VSTM2A	6.427241	2.828086	-1.18437	0.024388033	0.034059943
KRT24	0.601491	0.265788	-1.17827	0.000485485	0.000882329
RP1	0.185142	0.081868	-1.17727	0.000264173	0.000495874
CACNB2	1.009616	0.44651	-1.17704	0.017650787	0.025221815
HEPACAM2	2.522725	1.126542	-1.16308	7.12E-06	1.65E-05
NRCAM	2.640977	1.18083	-1.16127	4.40E-05	9.21E-05
FAM234B	23.35576	10.47959	-1.1562	4.00E-21	3.62E-20
CADM2	0.430231	0.195544	-1.13762	3.91E-12	1.89E-11
ELOVL2	16.22456	7.384002	-1.1357	5.24E-09	1.81E-08
RIMS4	9.093853	4.141138	-1.13486	5.70E-10	2.19E-09
NPC1L1	0.527981	0.241455	-1.12873	1.29E-12	6.51E-12
KRT33A	0.259284	0.118925	-1.12448	9.22E-05	0.000184027
STC2	126.7623	58.14373	-1.12443	8.97E-11	3.78E-10
APLP1	5.987257	2.753686	-1.12053	0.008000043	0.012091189
KLHL41	0.566586	0.261596	-1.11495	0.00027436	0.000514106
PYY	1.42129	0.657762	-1.11156	6.92E-09	2.36E-08
SLC1A2	2.520135	1.172705	-1.10366	4.73E-12	2.26E-11
EEF1A2	76.26907	35.50946	-1.10289	2.31E-14	1.35E-13
RBM24	5.20993	2.435521	-1.09703	4.26E-05	8.91E-05
DCDC1	0.486767	0.229865	-1.08244	2.00E-09	7.25E-09
AFF3	15.63104	7.398875	-1.07904	7.51E-18	5.73E-17
BMPR1B	45.21727	21.41082	-1.07853	2.38E-06	5.90E-06

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
GRIA2	3.915184	1.857686	-1.07557	5.64E-07	1.51E-06
C10orf113	0.342183	0.162657	-1.07294	0.000262464	0.00049293
FAM57B	0.701035	0.334833	-1.06605	9.33E-12	4.32E-11
PRTN3	0.396688	0.18962	-1.06489	1.29E-07	3.75E-07
STH	0.289018	0.138206	-1.06434	2.16E-08	6.95E-08
WDR17	0.523047	0.251158	-1.05835	0.000444123	0.00081135
TMPRSS6	3.153326	1.515389	-1.05719	2.29E-09	8.24E-09
ADAMTS19	0.63702	0.307087	-1.05269	2.65E-07	7.39E-07
MPPED1	0.213485	0.103044	-1.05088	0.003742782	0.00593754
NEURL1	4.34863	2.101239	-1.04932	6.43E-07	1.71E-06
SCUBE1	1.38817	0.671386	-1.04797	0.020885545	0.029499416
SERPINA6	35.01784	16.97602	-1.04459	0.000517383	0.000935828
MS4A8	1.170655	0.568422	-1.04228	9.63E-10	3.60E-09
BSN	0.363356	0.176512	-1.04162	7.22E-12	3.39E-11
LRP2	11.1319	5.408756	-1.04133	1.89E-06	4.74E-06
TMEM82	0.158981	0.077549	-1.03569	0.010797409	0.015989215
DNAJC12	30.90977	15.14134	-1.02957	4.17E-16	2.78E-15
TMPRSS11E	1.379565	0.678235	-1.02436	0.020208214	0.028611691
IGDCC3	0.908454	0.451056	-1.01011	5.46E-06	1.29E-05
VNN3	0.089672	0.179444	1.00081	2.32E-16	1.59E-15
CTSG	1.023617	2.060403	1.00925	2.02E-16	1.38E-15
SAMHD1	15.4686	31.15543	1.01014	1.34E-99	6.60E-98
SLC12A3	0.070932	0.142893	1.010416	1.40E-73	4.00E-72
CD300LG	0.400417	0.806715	1.010555	2.03E-15	1.29E-14
GYPC	4.163223	8.389582	1.010898	1.21E-73	3.45E-72
LIPG	0.312924	0.630775	1.011315	7.85E-33	1.02E-31
TLR4	2.391856	4.827445	1.013129	3.59E-71	9.70E-70
C11orf16	0.144779	0.292254	1.01337	3.41E-07	9.38E-07
GIMAP8	2.210054	4.46849	1.015706	1.27E-75	3.78E-74
IL12RB2	0.460834	0.932988	1.01761	3.10E-45	5.24E-44
DOCK8	2.121543	4.300225	1.019298	6.78E-67	1.73E-65
ACSL5	3.970288	8.051108	1.019944	4.45E-60	9.74E-59
CSAG3	0.249791	0.506849	1.020835	4.53E-12	2.17E-11
C5AR1	3.272868	6.641662	1.020989	1.42E-71	3.88E-70
BATF3	0.44015	0.894802	1.023574	5.72E-72	1.57E-70
NRROS	1.504625	3.062123	1.025128	6.69E-89	2.60E-87
P2RY6	0.994139	2.026326	1.027347	1.92E-71	5.24E-70
S100A7A	1.494377	3.046007	1.027375	3.82E-08	1.19E-07
EPHB6	1.135144	2.31385	1.027419	3.53E-40	5.33E-39
WARS	17.05904	34.77832	1.027651	2.38E-50	4.44E-49
MAL	0.750744	1.53073	1.027826	3.39E-79	1.08E-77
LILRA1	0.182739	0.372617	1.027909	2.17E-65	5.34E-64

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
IFI16	11.19982	22.86692	1.029786	1.13E-85	4.11E-84
TDRD12	0.475181	0.973268	1.034359	0.001548303	0.002603334
TPSD1	1.456181	2.98724	1.036624	0.008429851	0.012701216
GLYAT	0.096603	0.19834	1.037832	3.72E-08	1.16E-07
BMP3	0.070599	0.144998	1.03832	6.33E-05	0.000129345
PRDM1	2.223254	4.570207	1.039587	1.06E-78	3.34E-77
HAPLN3	5.432724	11.17957	1.041117	5.69E-71	1.52E-69
GAPT	0.957449	1.975764	1.045143	2.55E-47	4.45E-46
RGS13	0.079034	0.16312	1.045395	2.99E-29	3.51E-28
BIRC7	0.155378	0.320903	1.04635	1.49E-22	1.42E-21
SLC1A3	1.905253	3.940747	1.048487	6.54E-70	1.72E-68
KLRF1	0.246053	0.509008	1.048717	1.02E-44	1.71E-43
APOBEC3C	6.87736	14.23285	1.049298	2.39E-82	8.31E-81
SOWAHD	0.427735	0.885446	1.049689	2.54E-61	5.74E-60
IFI44L	4.684015	9.705149	1.051005	5.17E-39	7.62E-38
CAMK4	0.244063	0.506384	1.052976	7.90E-60	1.72E-58
RUBCNL	0.698612	1.450203	1.053692	6.61E-67	1.69E-65
C14orf180	0.171605	0.356312	1.054049	1.28E-09	4.74E-09
TF	1.838286	3.818779	1.05475	3.27E-08	1.03E-07
LGI2	0.555935	1.155441	1.055457	1.42E-50	2.65E-49
P2RY14	0.466392	0.970441	1.057099	1.58E-65	3.91E-64
LAT2	1.96848	4.099775	1.058463	1.09E-104	6.03E-103
MIXL1	0.159139	0.33164	1.059335	2.62E-40	3.97E-39
ICAM1	9.274419	19.355	1.061378	1.01E-58	2.16E-57
LCP1	23.18574	48.41775	1.062298	1.59E-73	4.52E-72
MEFV	0.086515	0.181458	1.068613	2.61E-50	4.85E-49
FLI1	1.606163	3.370977	1.069549	1.35E-99	6.63E-98
ALOX5AP	7.175782	15.07118	1.070585	1.50E-79	4.85E-78
MZB1	8.023471	16.85415	1.070805	4.07E-29	4.78E-28
TREML1	0.225493	0.473937	1.071615	1.47E-60	3.25E-59
CYSLTR2	0.206646	0.434417	1.071917	3.83E-63	9.00E-62
HEPHL1	0.132491	0.278611	1.072355	0.003603536	0.005731509
SERPINB9	2.617045	5.506606	1.073225	9.66E-89	3.74E-87
SAMD9L	5.069203	10.66718	1.073348	2.59E-54	5.16E-53
GIMAP6	3.615793	7.613478	1.074244	6.79E-80	2.23E-78
EPYC	1.526004	3.214592	1.074877	4.63E-14	2.63E-13
SLC22A3	0.380521	0.801625	1.07495	3.53E-44	5.86E-43
CPNE5	1.010179	2.1313	1.077122	6.58E-59	1.41E-57
HLA-B	356.8178	752.8702	1.077214	3.33E-74	9.62E-73
IL7	0.300135	0.634984	1.081107	2.51E-51	4.75E-50
MAP1LC3C	0.282915	0.598661	1.081371	4.69E-31	5.80E-30
C2	3.044141	6.453943	1.084146	3.31E-83	1.17E-81

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
S100A9	205.7698	436.4039	1.084633	1.67E-31	2.09E-30
MEOX1	1.319936	2.808109	1.089132	1.22E-28	1.40E-27
OSCAR	1.725058	3.671157	1.08959	3.75E-78	1.17E-76
CMA1	0.443238	0.944494	1.091462	7.70E-16	5.03E-15
TAP2	3.888744	8.289627	1.092003	8.70E-63	2.03E-61
DPT	13.87647	29.6028	1.093093	7.31E-40	1.10E-38
COL4A4	0.241102	0.515337	1.095871	9.31E-46	1.59E-44
HLA-E	123.7002	264.4688	1.09625	1.32E-108	8.13E-107
LYN	3.838819	8.21086	1.096871	1.48E-92	6.25E-91
AGAP2	0.589864	1.262327	1.097631	2.56E-88	9.82E-87
DOK3	1.353008	2.902501	1.101126	3.21E-106	1.86E-104
GPBAR1	0.16178	0.347267	1.102017	1.05E-65	2.61E-64
LGALS9	6.814745	14.64762	1.103935	3.86E-87	1.45E-85
LY86	3.959979	8.516019	1.104687	2.44E-99	1.19E-97
CD300A	2.438561	5.248581	1.105897	7.95E-102	4.11E-100
CELF2	2.134897	4.597909	1.106812	2.95E-79	9.44E-78
ADGRE5	4.433888	9.549683	1.106881	3.40E-86	1.25E-84
CLIC2	2.868779	6.18097	1.107396	1.32E-90	5.36E-89
IL15	0.321184	0.692573	1.108565	1.23E-81	4.22E-80
TSHR	0.071301	0.153827	1.109319	4.94E-48	8.76E-47
CD14	23.43428	50.58969	1.110223	2.23E-73	6.29E-72
LY6D	4.348987	9.391013	1.110601	6.68E-11	2.85E-10
LYL1	0.906892	1.958813	1.110977	2.38E-64	5.73E-63
TEX11	0.066981	0.145177	1.115984	5.54E-45	9.35E-44
MCOLN2	0.812659	1.762798	1.117145	1.22E-64	2.95E-63
CASP1	3.315466	7.19423	1.117629	4.46E-94	1.95E-92
CHRDL1	2.8247	6.139203	1.119954	3.47E-25	3.63E-24
ABI3	2.848489	6.192482	1.120321	4.88E-116	4.18E-114
SLC15A3	3.878231	8.431998	1.120476	2.72E-110	1.82E-108
CCDC69	2.952072	6.421956	1.121285	1.35E-70	3.60E-69
CPA1	0.029329	0.063968	1.125004	7.27E-07	1.92E-06
CLEC7A	2.123307	4.639366	1.127615	1.93E-92	8.06E-91
MILR1	1.523007	3.329235	1.128269	1.99E-109	1.26E-107
PLD4	0.771792	1.687527	1.128626	1.07E-38	1.56E-37
WNT10A	0.389571	0.852652	1.130071	7.71E-75	2.26E-73
LY96	6.261711	13.70789	1.130377	3.49E-110	2.31E-108
SELE	1.417646	3.105072	1.13113	7.09E-39	1.04E-37
CXCR2	0.09745	0.213591	1.132123	1.12E-41	1.74E-40
IFI30	0.276989	0.607863	1.133916	1.23E-79	3.99E-78
PILRA	2.468964	5.420289	1.134464	1.47E-103	7.89E-102
SIGLEC9	0.791121	1.739745	1.136907	3.18E-97	1.46E-95
GLT1D1	0.070043	0.154084	1.137407	1.77E-60	3.91E-59

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
APOBEC3D	1.180195	2.596265	1.137412	1.89E-64	4.55E-63
PRAM1	0.425113	0.935906	1.138518	1.99E-79	6.45E-78
MATK	0.723905	1.594247	1.139003	1.13E-54	2.26E-53
G0S2	9.999633	22.02369	1.139109	8.63E-32	1.09E-30
SEL1L3	3.164518	6.975114	1.140231	3.46E-51	6.52E-50
CARMIL2	0.452781	1.001728	1.145608	2.88E-52	5.51E-51
C4BPA	0.724631	1.60384	1.146211	7.28E-07	1.92E-06
IRF1	5.738171	12.70845	1.147125	1.86E-87	7.02E-86
TRIM22	6.310583	13.97701	1.14721	1.90E-80	6.35E-79
ADGRE2	0.437833	0.970074	1.147714	2.79E-67	7.15E-66
TNFSF18	0.165361	0.366385	1.147741	1.03E-33	1.35E-32
CARD16	1.941866	4.304895	1.148535	1.41E-104	7.74E-103
KRT81	28.19567	62.60873	1.15089	2.11E-08	6.78E-08
VSIR	3.776617	8.391591	1.15185	1.24E-98	5.97E-97
CAPN6	2.858231	6.351328	1.151936	4.02E-15	2.49E-14
GPA33	0.075935	0.168825	1.152689	3.86E-68	9.99E-67
PRSS12	0.616447	1.372842	1.155117	2.54E-10	1.02E-09
PIGR	9.302722	20.73798	1.15655	2.29E-11	1.02E-10
OR52N4	0.06517	0.145285	1.156614	7.48E-41	1.14E-39
CEACAM21	0.508402	1.133444	1.156672	2.36E-82	8.21E-81
HLA-G	1.797553	4.015942	1.159704	9.85E-27	1.07E-25
GSDMA	0.283409	0.633376	1.160174	5.78E-39	8.51E-38
CD68	0.409871	0.916508	1.160977	1.80E-63	4.27E-62
IL18R1	0.45456	1.017294	1.162196	1.37E-74	3.97E-73
TRARG1	1.581955	3.545781	1.164395	7.13E-11	3.03E-10
CH25H	1.009343	2.264275	1.165633	5.97E-44	9.78E-43
ACHE	0.383356	0.861208	1.167678	9.08E-32	1.14E-30
IVL	0.381178	0.85673	1.168374	7.19E-06	1.67E-05
MGAM2	0.311779	0.701028	1.168947	3.75E-06	9.02E-06
LPXN	5.117802	11.5093	1.169204	1.56E-128	2.20E-126
CCL20	0.699452	1.57345	1.169634	1.10E-33	1.44E-32
C1S	34.56428	77.85001	1.171415	6.69E-78	2.09E-76
APOL3	4.216521	9.511335	1.173595	4.07E-82	1.40E-80
CMKLR1	1.929114	4.353126	1.174113	4.64E-89	1.81E-87
FCGR2B	0.838801	1.892858	1.174166	3.68E-87	1.38E-85
IL1B	0.988997	2.232195	1.174425	9.13E-45	1.53E-43
CD1A	0.569387	1.286093	1.175513	1.73E-32	2.23E-31
KBTBD8	0.301596	0.681535	1.176168	2.99E-75	8.81E-74
CDX1	0.16117	0.364334	1.176674	8.15E-40	1.22E-38
ADGRE1	0.232721	0.526101	1.176739	1.81E-76	5.50E-75
RGS1	9.73868	22.03374	1.177917	1.90E-58	4.05E-57
SLC9A9	1.071041	2.424285	1.178546	5.25E-103	2.75E-101

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
GNGT2	0.506531	1.147449	1.179707	1.60E-131	3.12E-129
SNAI3	0.470624	1.067272	1.181282	2.59E-78	8.13E-77
GLYATL2	10.18764	23.11888	1.182252	5.68E-06	1.34E-05
KIF21B	0.517089	1.173734	1.182622	1.39E-68	3.61E-67
APOL1	16.29846	37.06103	1.185167	2.16E-90	8.67E-89
CTSC	5.559414	12.64762	1.185862	4.35E-84	1.56E-82
TMEM273	1.047839	2.38461	1.186337	5.65E-92	2.36E-90
PTGER4	1.574191	3.590101	1.189414	5.35E-90	2.13E-88
C3AR1	5.29832	12.09034	1.190248	1.26E-104	6.93E-103
RUNX3	2.840457	6.498944	1.194083	1.30E-92	5.48E-91
KIF19	0.140739	0.32256	1.196549	1.10E-40	1.68E-39
CPVL	4.057838	9.305414	1.197359	6.38E-105	3.55E-103
SPNS3	0.194281	0.445622	1.197675	1.76E-54	3.52E-53
HVCN1	0.978827	2.249782	1.200659	2.10E-110	1.42E-108
TLR7	1.217115	2.800604	1.202272	2.02E-69	5.27E-68
FXYD7	0.096488	0.222023	1.202296	4.28E-43	6.86E-42
WIPF1	4.604925	10.60962	1.204123	4.17E-115	3.45E-113
FCGR1B	0.174368	0.401882	1.204634	1.49E-81	5.11E-80
SCARA5	0.501713	1.156425	1.204737	3.57E-30	4.29E-29
SLCO2B1	2.957001	6.826296	1.206968	1.99E-93	8.53E-92
HAVCR2	3.17254	7.333054	1.208776	5.53E-118	5.12E-116
EMILIN2	1.56566	3.620029	1.20923	1.23E-94	5.41E-93
LILRA6	0.265357	0.613796	1.209823	7.62E-65	1.85E-63
AKNA	2.229258	5.156894	1.209939	3.94E-103	2.08E-101
KCNAB2	1.391016	3.220194	1.211008	9.54E-115	7.62E-113
GBP6	0.178546	0.414709	1.215804	3.53E-40	5.33E-39
CCL22	1.663371	3.865684	1.216614	1.28E-69	3.37E-68
IL1A	0.105146	0.244458	1.2172	1.72E-19	1.43E-18
GPR150	0.0743	0.172824	1.217871	1.03E-66	2.61E-65
PRDM8	0.214734	0.500711	1.221427	4.73E-82	1.63E-80
PPBP	0.064947	0.151507	1.222042	4.40E-05	9.21E-05
TRAF1	1.643852	3.835383	1.22229	9.08E-85	3.28E-83
CD33	0.37316	0.871272	1.22333	7.80E-115	6.27E-113
CASS4	0.287637	0.671884	1.223963	5.23E-103	2.75E-101
OSM	0.83442	1.952434	1.226427	1.77E-45	3.01E-44
ABI3BP	1.502638	3.518456	1.227445	5.12E-48	9.06E-47
CCL3	2.204605	5.169713	1.229564	4.11E-63	9.63E-62
GPSM3	8.004102	18.79422	1.231478	6.06E-109	3.79E-107
LRRC25	1.663194	3.907079	1.232134	8.93E-121	9.11E-119
SLC26A9	0.146952	0.345284	1.232439	4.11E-20	3.55E-19
FAM20A	1.342258	3.154476	1.232739	2.58E-75	7.61E-74
TNFRSF4	1.404835	3.301915	1.232902	7.85E-60	1.71E-58

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
NFAM1	1.312583	3.085737	1.233207	9.16E-98	4.35E-96
LSP1	7.781112	18.30887	1.234495	2.88E-100	1.43E-98
FCGR1A	1.163663	2.746591	1.238969	9.15E-87	3.40E-85
TRPV2	2.348036	5.549271	1.240844	1.78E-130	3.09E-128
NLRC3	0.69509	1.643526	1.241523	1.75E-82	6.11E-81
TNFAIP3	4.925116	11.65614	1.242861	2.48E-93	1.06E-91
CSF2RA	1.491727	3.530939	1.243068	1.80E-103	9.55E-102
STX11	1.153815	2.731748	1.243412	2.31E-97	1.07E-95
FCGR3A	16.77016	39.75154	1.245115	2.01E-77	6.22E-76
AGXT	0.098203	0.233023	1.246626	6.64E-08	2.00E-07
RAB33A	0.457933	1.086727	1.246781	3.82E-94	1.68E-92
PLA1A	1.119757	2.659386	1.247907	8.69E-46	1.48E-44
LEP	0.95839	2.280136	1.250435	1.90E-11	8.55E-11
RCSD1	2.000945	4.762531	1.251047	7.76E-104	4.22E-102
CD40	3.508589	8.352104	1.251249	3.22E-112	2.32E-110
FMO3	1.27826	3.043196	1.251406	2.38E-24	2.44E-23
KRT86	1.90644	4.539927	1.251788	8.45E-14	4.68E-13
RNASE6	7.770187	18.50439	1.251847	3.08E-115	2.58E-113
CCL4L2	1.877723	4.480599	1.254707	2.39E-63	5.62E-62
MFNG	2.113132	5.042502	1.254756	6.62E-106	3.81E-104
KLRG1	0.420363	1.004718	1.257084	6.55E-66	1.64E-64
TRPM8	0.126489	0.302477	1.257814	7.43E-17	5.26E-16
FABP4	24.73791	59.21112	1.259144	4.84E-14	2.74E-13
SELP	1.5165	3.635645	1.261466	2.42E-34	3.24E-33
FABP7	9.636444	23.13858	1.263727	3.39E-09	1.19E-08
FCER1G	21.9509	52.96642	1.270798	4.02E-123	4.63E-121
HLA-F	9.874743	23.83534	1.271287	1.99E-76	6.01E-75
SIRPB2	0.442301	1.069047	1.273223	4.71E-99	2.28E-97
CSF1R	7.188162	17.39719	1.27516	1.33E-109	8.60E-108
SLC7A7	2.357376	5.706983	1.275547	1.02E-121	1.10E-119
1-Sep	1.490387	3.610018	1.27632	4.46E-64	1.07E-62
PIK3AP1	2.433871	5.89929	1.277288	5.14E-99	2.48E-97
VSIG4	4.678339	11.33972	1.277317	1.90E-63	4.49E-62
FAM92B	0.121409	0.294539	1.27858	1.12E-27	1.26E-26
APOE	77.32314	187.7546	1.279876	1.68E-62	3.90E-61
PNMA5	0.112779	0.273868	1.27998	1.89E-15	1.21E-14
CADM3	0.5659	1.374739	1.280538	3.56E-31	4.40E-30
FPR1	1.422014	3.455287	1.28087	6.13E-80	2.01E-78
CD300C	0.788746	1.917222	1.281385	2.30E-101	1.17E-99
FATE1	0.172696	0.420556	1.284065	9.53E-13	4.87E-12
MMP1	10.75846	26.20053	1.284124	1.09E-10	4.57E-10
NLRP7	0.094597	0.230544	1.28517	6.03E-50	1.11E-48

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
ADA2	6.725749	16.41883	1.287585	2.99E-97	1.38E-95
XPNPEP2	0.196074	0.47931	1.289563	2.39E-50	4.45E-49
TM4SF19	0.194752	0.476834	1.29185	2.24E-11	1.00E-10
GIMAP1	0.927241	2.27036	1.291905	1.84E-91	7.62E-90
BCL11B	0.570256	1.396339	1.291967	1.35E-73	3.87E-72
IL15RA	1.84549	4.519897	1.292286	1.53E-106	8.89E-105
APOC1	27.83079	68.17604	1.292583	1.65E-65	4.07E-64
S100A7	69.09969	169.3087	1.292905	5.95E-11	2.55E-10
SLC2A5	0.522276	1.280369	1.293674	7.98E-67	2.03E-65
PI3	10.94128	26.848	1.295033	6.98E-13	3.60E-12
PI16	2.368824	5.817173	1.296147	2.35E-24	2.40E-23
VAV1	1.733235	4.258705	1.296948	1.39E-110	9.43E-109
FMNL1	2.443226	6.010995	1.298816	6.85E-133	1.48E-130
P2RY13	0.997803	2.458348	1.300862	7.67E-72	2.10E-70
HCK	3.718612	9.163342	1.30111	1.99E-119	1.93E-117
CD180	0.919881	2.267965	1.301879	3.50E-93	1.49E-91
MCEMP1	0.126424	0.312218	1.304279	7.57E-21	6.78E-20
TAP1	19.20395	47.43313	1.304492	3.31E-61	7.47E-60
CCL7	0.417146	1.031011	1.305436	6.19E-23	6.00E-22
SH2D2A	1.103972	2.729954	1.306174	4.05E-80	1.34E-78
CD80	0.267203	0.66089	1.306473	3.33E-73	9.37E-72
EVI2A	2.885238	7.136539	1.306534	1.87E-116	1.61E-114
CD1D	0.543835	1.345643	1.307056	2.98E-86	1.10E-84
PIM2	6.78147	16.8183	1.310362	7.25E-60	1.58E-58
NCF2	3.537107	8.778621	1.311424	1.97E-105	1.11E-103
ADGRG3	0.106191	0.263614	1.31177	8.04E-39	1.18E-37
BATF2	1.691455	4.199822	1.312064	8.24E-43	1.31E-41
NLRP3	0.517485	1.285565	1.312815	4.04E-100	2.00E-98
PLCB2	1.251155	3.111213	1.314216	3.86E-121	4.15E-119
TYROBP	30.90247	76.99359	1.317016	7.99E-123	9.06E-121
RASSF4	1.97494	4.939821	1.32265	2.45E-107	1.46E-105
JCHAIN	65.48074	163.8552	1.323279	5.41E-48	9.56E-47
C1orf162	3.025395	7.577808	1.324657	3.13E-133	7.46E-131
DNASE1L3	0.238878	0.599716	1.328008	1.71E-44	2.86E-43
GIMAP4	8.114773	20.40162	1.330061	4.29E-124	5.06E-122
DERL3	2.99144	7.521325	1.330147	1.93E-47	3.38E-46
IGSF6	2.396136	6.025605	1.330396	1.78E-109	1.14E-107
SIGLEC7	0.49027	1.233203	1.330761	1.02E-108	6.32E-107
GAB3	0.515411	1.299031	1.333641	2.26E-126	2.86E-124
THEMIS2	2.69226	6.786633	1.333878	5.96E-115	4.84E-113
SIGLEC1	1.680399	4.243965	1.336609	1.17E-73	3.35E-72
IL22RA2	0.1812	0.457888	1.337416	3.90E-37	5.55E-36

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
CCL2	7.654475	19.34746	1.337769	2.31E-76	6.95E-75
CCL11	0.793844	2.010792	1.340836	1.46E-49	2.65E-48
CCDC88B	0.929632	2.361138	1.344751	2.52E-70	6.65E-69
AIF1	9.663958	24.62497	1.349436	7.37E-138	2.53E-135
PIK3R5	0.80019	2.041878	1.351482	9.08E-131	1.66E-128
CD8B2	0.219893	0.561248	1.351839	1.57E-19	1.32E-18
SHISAL2A	0.186883	0.477902	1.354583	2.67E-66	6.72E-65
GPR65	0.835928	2.142667	1.357957	2.14E-115	1.80E-113
IL18BP	1.938808	4.980065	1.360995	7.47E-116	6.37E-114
NLRC5	1.987358	5.110503	1.362613	5.80E-91	2.39E-89
IL6	0.819796	2.111042	1.364619	1.40E-36	1.96E-35
ETV7	1.771908	4.56511	1.365346	4.22E-55	8.57E-54
ACKR1	6.609754	17.0395	1.366214	4.25E-29	4.99E-28
LAPTM5	38.71369	99.87358	1.367259	5.84E-145	3.74E-142
MS4A6A	4.002798	10.33631	1.368641	1.19E-129	1.88E-127
ERVFRD-1	0.083913	0.216829	1.369594	2.82E-07	7.86E-07
ITGAX	1.884083	4.869604	1.369942	1.44E-117	1.29E-115
CCL24	0.174072	0.450018	1.370296	3.27E-35	4.48E-34
ITGAL	2.820233	7.310689	1.374193	3.31E-85	1.20E-83
CLEC4A	1.371277	3.555589	1.374568	1.15E-129	1.84E-127
LILRB3	0.247313	0.642121	1.376509	3.74E-112	2.67E-110
SELL	4.668111	12.13138	1.377833	1.72E-98	8.24E-97
INPP5D	1.855621	4.833975	1.381308	1.01E-122	1.12E-120
LIMD2	2.603699	6.797279	1.384394	1.00E-85	3.66E-84
RARRES1	15.82678	41.33833	1.385112	3.57E-42	5.61E-41
TNFAIP8L2	2.373102	6.201352	1.385809	1.41E-131	2.79E-129
C3	36.39676	95.12733	1.38605	1.11E-89	4.36E-88
MMP8	0.072087	0.188679	1.388129	2.55E-12	1.26E-11
TRABD2A	0.1404	0.368019	1.390237	1.70E-92	7.15E-91
PTAFR	2.320355	6.083163	1.390476	4.19E-118	3.93E-116
APBB1IP	2.399474	6.297181	1.391988	7.87E-132	1.58E-129
LAIR1	2.014008	5.291486	1.393603	9.28E-141	4.35E-138
CD274	0.732226	1.929698	1.398014	1.98E-77	6.13E-76
AC119396.1	0.181649	0.479319	1.399837	1.93E-32	2.48E-31
CD70	0.30109	0.794844	1.400479	1.34E-66	3.39E-65
IL10	0.228009	0.601979	1.400621	4.08E-90	1.62E-88
BHLHE22	0.355835	0.939673	1.40095	1.13E-60	2.50E-59
CCR1	2.97572	7.87595	1.404215	2.05E-95	9.16E-94
DPEP2	0.413625	1.096114	1.406001	4.79E-111	3.31E-109
MYO1F	1.458462	3.867157	1.406826	1.79E-143	9.34E-141
PLA2G7	2.520955	6.68632	1.407242	9.90E-62	2.26E-60
SOCS1	1.702924	4.528598	1.411051	6.19E-79	1.97E-77

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
HLA-DMA	15.76589	41.99059	1.413259	8.07E-131	1.49E-128
CD300E	0.346579	0.923108	1.413314	5.95E-62	1.37E-60
PPP1R16B	1.068852	2.851181	1.415497	3.99E-73	1.12E-71
TSPAN32	0.170758	0.456326	1.418109	3.13E-74	9.07E-73
S100A8	42.36826	113.5952	1.422847	5.58E-35	7.57E-34
GPR84	0.563762	1.511664	1.42298	6.48E-70	1.71E-68
LST1	2.223523	5.971214	1.425177	4.67E-132	9.51E-130
GNG8	0.241501	0.648599	1.425297	9.74E-45	1.63E-43
SPI1	6.379661	17.15413	1.427005	1.03E-135	3.00E-133
EPSTI1	2.629633	7.074613	1.42779	1.31E-96	5.95E-95
TNFSF8	0.600634	1.617787	1.429464	2.04E-101	1.04E-99
CD300LF	0.768277	2.07313	1.432111	2.61E-124	3.14E-122
SIGLEC14	0.82717	2.234006	1.433378	1.04E-73	3.00E-72
MS4A4A	2.481477	6.70899	1.434897	1.45E-110	9.83E-109
SELPLG	6.437585	17.46849	1.440164	2.23E-140	1.01E-137
FOLR2	3.87263	10.5239	1.442283	2.65E-69	6.92E-68
CLEC4G	0.057474	0.156222	1.442621	2.92E-33	3.81E-32
TRIM55	0.198054	0.53876	1.443753	3.50E-12	1.70E-11
IL32	7.826902	21.30714	1.444824	8.78E-87	3.28E-85
IL16	0.961029	2.616651	1.44507	3.37E-107	2.00E-105
PIK3CD	1.703144	4.644648	1.447369	8.72E-119	8.35E-117
CLEC9A	0.103395	0.282333	1.449237	4.29E-56	8.89E-55
MNDA	3.141132	8.580019	1.449696	2.64E-122	2.92E-120
CXCL1	1.066856	2.915685	1.450469	2.77E-25	2.90E-24
ASB2	0.209757	0.573961	1.452235	1.21E-90	4.94E-89
GMFG	5.408415	14.82527	1.454781	9.65E-135	2.56E-132
SIGLEC10	1.231834	3.386419	1.458953	1.14E-113	8.61E-112
FAM78A	1.019279	2.802502	1.459167	1.11E-143	6.01E-141
GIMAP7	5.372128	14.7752	1.459612	6.74E-94	2.93E-92
BTK	1.17079	3.221649	1.460317	4.33E-138	1.56E-135
EGFL6	1.163364	3.206357	1.462633	2.18E-36	3.06E-35
ARHGAP30	3.438403	9.487228	1.464248	3.75E-134	9.10E-132
CD86	2.158199	5.955658	1.464433	4.81E-135	1.30E-132
PARVG	0.822132	2.276955	1.469664	6.31E-138	2.22E-135
RAC2	8.727129	24.18842	1.470738	4.83E-107	2.85E-105
IPCEF1	0.203351	0.563767	1.471127	1.24E-93	5.34E-92
P2RX5	0.215504	0.597997	1.472427	1.01E-52	1.94E-51
CYTH4	1.529391	4.244253	1.472553	2.45E-139	1.01E-136
CXorf21	0.976862	2.717795	1.47621	2.15E-114	1.68E-112
CCR8	0.339464	0.946427	1.479232	2.28E-71	6.21E-70
ITGAD	0.10497	0.292965	1.480753	3.27E-51	6.16E-50
NCF4	2.617373	7.309393	1.481632	2.60E-143	1.31E-140

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
SAMSN1	1.609922	4.499169	1.482668	2.99E-129	4.63E-127
PDE6G	0.325891	0.915147	1.489616	4.56E-99	2.22E-97
FPR3	6.13306	17.228	1.490076	8.23E-91	3.37E-89
C1QC	44.10048	123.8825	1.490106	5.73E-121	6.06E-119
SLA	1.54323	4.344529	1.493247	3.87E-133	8.92E-131
FGR	1.489968	4.216522	1.500772	2.63E-130	4.46E-128
CFP	0.206596	0.585845	1.503704	4.44E-61	9.98E-60
RGS18	0.337057	0.956685	1.505053	1.48E-101	7.61E-100
PSMB9	6.784775	19.27521	1.506373	5.49E-90	2.18E-88
HCRTR2	0.057519	0.163529	1.507445	3.07E-05	6.56E-05
LILRA5	0.384453	1.093482	1.508049	3.16E-90	1.27E-88
GP1BA	0.307578	0.876228	1.510352	5.31E-40	7.98E-39
ARHGAP15	0.553357	1.576585	1.510522	6.40E-133	1.41E-130
CD300LB	0.236346	0.674196	1.512269	1.50E-67	3.85E-66
APOBEC3G	1.416778	4.043881	1.513127	2.09E-108	1.28E-106
AQP9	0.685554	1.957944	1.513998	1.51E-27	1.68E-26
HTRA4	0.190965	0.545555	1.514418	2.42E-73	6.82E-72
PIK3CG	0.549393	1.570192	1.515029	2.51E-80	8.36E-79
MYO1G	0.666113	1.908759	1.518795	5.58E-110	3.64E-108
ARHGAP25	1.512422	4.336038	1.519517	2.69E-145	1.89E-142
ABCD2	0.128654	0.369719	1.522933	2.12E-76	6.40E-75
VNN1	0.4791	1.377289	1.523433	8.77E-73	2.45E-71
CD72	0.758925	2.182865	1.524193	1.85E-109	1.18E-107
VCAM1	3.737038	10.8166	1.53328	4.44E-74	1.28E-72
TNFRSF1B	5.870949	16.99466	1.533416	5.31E-147	3.93E-144
LILRB5	0.253963	0.735374	1.533858	2.30E-68	5.96E-67
POU2F2	0.553728	1.606914	1.537042	3.52E-115	2.93E-113
PDCD1LG2	1.011863	2.939686	1.538648	5.76E-107	3.39E-105
IL2RB	2.648194	7.701101	1.540056	8.75E-111	5.97E-109
FCGR3B	0.319027	0.927953	1.540375	2.01E-21	1.83E-20
MMP12	2.05997	6.001652	1.542737	9.24E-19	7.45E-18
CD74	328.7308	959.866	1.545926	1.32E-134	3.44E-132
LCP2	2.082452	6.084416	1.546836	4.63E-152	9.30E-149
ARRDC5	0.087941	0.257063	1.547513	4.55E-84	1.63E-82
CLDN16	0.064098	0.187681	1.549938	4.79E-18	3.70E-17
CTSS	12.71293	37.39482	1.556541	7.97E-121	8.24E-119
CSF3	0.051423	0.151291	1.556836	6.95E-11	2.96E-10
TNFSF13B	2.555604	7.521146	1.557288	2.25E-108	1.37E-106
SRGN	27.32365	80.57723	1.560222	9.49E-138	3.18E-135
CD163	4.596869	13.59259	1.564097	3.46E-88	1.32E-86
VNN2	0.470984	1.39515	1.566669	4.24E-95	1.88E-93
HLA-DMB	5.017561	14.90156	1.570405	4.03E-145	2.70E-142

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
HCLS1	4.465497	13.27215	1.571509	6.48E-153	1.52E-149
TBX10	0.432545	1.287687	1.573861	0.000803925	0.001411813
CD84	1.311611	3.909636	1.575695	2.22E-105	1.25E-103
FGL2	4.350769	13.00163	1.57935	1.83E-112	1.34E-110
HLA-DPA1	26.46526	79.27484	1.582763	6.87E-129	1.01E-126
CD4	7.498467	22.49005	1.584619	2.09E-154	5.87E-151
HLA-DPB1	43.50944	130.5614	1.585328	1.52E-136	4.85E-134
PHKG1	0.633816	1.902184	1.585521	3.07E-08	9.69E-08
HLA-DQB2	4.906605	14.73766	1.58671	3.01E-71	8.16E-70
TOX	0.512217	1.548202	1.595766	1.44E-90	5.83E-89
JSRP1	0.381592	1.154004	1.596544	3.05E-32	3.90E-31
KLRC1	0.08953	0.27097	1.597688	7.80E-76	2.33E-74
CLEC12A	0.227977	0.692821	1.603596	1.51E-90	6.10E-89
CD200R1	0.224479	0.682834	1.604955	4.18E-101	2.11E-99
GPR55	0.12664	0.38572	1.606823	1.89E-75	5.62E-74
DCSTAMP	0.186223	0.567359	1.607229	1.28E-39	1.91E-38
TFEC	0.550628	1.678441	1.607972	3.81E-110	2.51E-108
CD209	0.452233	1.37946	1.608966	7.28E-71	1.94E-69
FGD2	0.385128	1.17502	1.609275	1.68E-130	2.96E-128
LILRB1	0.713254	2.17747	1.610164	6.06E-139	2.30E-136
SIRPB1	0.16986	0.520434	1.615367	5.82E-62	1.34E-60
CCL23	0.150212	0.460385	1.615835	1.08E-67	2.79E-66
HLA-DRB1	155.2191	475.9225	1.61642	4.67E-133	1.06E-130
FPR2	0.0609	0.187207	1.62011	3.18E-67	8.14E-66
IKZF3	1.101902	3.393023	1.622575	4.19E-81	1.42E-79
MPEG1	4.339699	13.38393	1.624835	8.61E-123	9.69E-121
CYTIP	1.983161	6.130623	1.628232	1.40E-119	1.37E-117
FOXP3	1.213175	3.757957	1.631161	8.13E-101	4.08E-99
SCIMP	0.549126	1.700994	1.63117	1.73E-127	2.29E-125
GPR18	0.347792	1.078382	1.632573	2.71E-95	1.21E-93
HLA-DOA	4.162829	12.91502	1.633414	1.56E-120	1.58E-118
ITGB2	7.117906	22.13959	1.637104	1.20E-135	3.37E-133
BIN2	1.372589	4.272628	1.638224	2.51E-147	2.21E-144
ITGB7	0.428389	1.333549	1.638277	1.54E-88	5.93E-87
PATL2	0.157316	0.489734	1.63833	1.38E-82	4.83E-81
FERMT3	4.033852	12.56807	1.639533	9.33E-149	1.01E-145
GIMAP5	0.12731	0.397059	1.641003	8.19E-90	3.22E-88
CTSE	0.150036	0.468097	1.641499	1.95E-15	1.24E-14
C1QB	37.84303	118.2799	1.644105	2.27E-123	2.64E-121
KRT2	0.056583	0.176892	1.644428	1.83E-17	1.36E-16
P2RY10	0.821348	2.569825	1.645604	9.54E-91	3.90E-89
HLA-DRA	285.763	894.1829	1.645751	7.99E-145	4.89E-142

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
TXK	0.113666	0.355856	1.646499	2.99E-63	7.04E-62
BIRC3	2.57086	8.049611	1.646668	3.13E-82	1.08E-80
PTPN22	0.61479	1.931845	1.651814	1.18E-115	9.98E-114
TAGAP	1.290242	4.070469	1.657553	1.99E-117	1.79E-115
DOCK2	0.979411	3.091126	1.658146	2.57E-134	6.33E-132
LILRB4	1.829003	5.782417	1.660615	1.67E-129	2.61E-127
WAS	2.408691	7.620902	1.661712	9.85E-155	3.46E-151
NCKAP1L	1.707635	5.404981	1.66229	2.24E-144	1.31E-141
CLECL1	0.214109	0.679014	1.665097	1.17E-97	5.52E-96
P2RX1	0.198162	0.629497	1.667519	1.20E-64	2.91E-63
RIPOR2	0.61865	1.966485	1.668424	1.65E-78	5.20E-77
SULT1B1	0.10171	0.323372	1.668732	3.99E-14	2.28E-13
IL9R	0.094105	0.299315	1.669322	2.27E-80	7.58E-79
CD226	0.130251	0.416356	1.676521	1.70E-109	1.09E-107
C1QA	39.33399	125.844	1.677789	8.23E-126	1.03E-123
CXorf65	0.136229	0.437042	1.681738	3.20E-65	7.83E-64
CYBB	7.08854	22.79243	1.684994	2.56E-112	1.86E-110
CCL8	1.823721	5.880063	1.688947	5.81E-60	1.27E-58
TNFRSF8	0.195198	0.632428	1.695963	7.26E-113	5.34E-111
LILRB2	0.791109	2.577837	1.704213	1.51E-142	7.30E-140
HLA-DQB1	14.06281	45.85692	1.705254	8.43E-106	4.84E-104
EBI3	1.021709	3.333353	1.70599	7.06E-110	4.58E-108
GRAP2	0.308035	1.005684	1.707011	9.67E-104	5.19E-102
PSORS1C2	0.455297	1.488122	1.708612	0.006514528	0.009990932
WDFY4	0.515299	1.687849	1.711705	5.11E-122	5.62E-120
HLA-DRB5	50.62613	166.0396	1.713573	6.82E-90	2.69E-88
STAT4	0.470021	1.547382	1.719032	5.22E-112	3.71E-110
GPR183	3.391108	11.25802	1.731124	9.20E-114	6.99E-112
P2RY8	0.844293	2.805906	1.732651	3.57E-114	2.76E-112
CIITA	0.982035	3.267814	1.734479	1.28E-117	1.16E-115
RUFY4	0.148619	0.498734	1.746656	3.46E-55	7.06E-54
PRKCQ	0.389876	1.30971	1.748159	2.94E-102	1.52E-100
TRAF3IP3	0.579291	1.947248	1.749076	2.76E-120	2.77E-118
TMEM150B	0.300469	1.01032	1.749525	4.27E-100	2.11E-98
KLRK1	0.05591	0.188005	1.7496	3.33E-66	8.34E-65
KLHL6	0.438752	1.477953	1.752123	1.06E-124	1.29E-122
EVI2B	4.115023	13.87872	1.753902	8.95E-144	5.03E-141
RASAL3	1.106488	3.73569	1.755387	2.18E-131	4.09E-129
CEACAM4	0.070216	0.237468	1.757858	9.22E-84	3.27E-82
HTR3A	0.109756	0.37143	1.758795	3.50E-18	2.71E-17
CD53	9.80268	33.33192	1.765656	2.46E-161	3.46E-157
FYB1	2.284396	7.771229	1.76633	6.09E-124	7.14E-122

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
MEI1	0.276629	0.943238	1.769669	1.73E-105	9.80E-104
XCL1	0.229175	0.781693	1.770154	4.88E-91	2.01E-89
LAMP3	1.865129	6.379882	1.774254	6.65E-81	2.24E-79
UTS2	0.074851	0.256122	1.774741	2.46E-53	4.79E-52
ADGRG5	0.204986	0.703689	1.779412	2.93E-82	1.01E-80
SPOCK2	2.430739	8.363947	1.782789	1.41E-116	1.23E-114
IRF8	1.831791	6.308502	1.784042	2.07E-134	5.30E-132
IL10RA	1.919089	6.621414	1.786717	1.42E-147	1.33E-144
KLRD1	0.09091	0.314366	1.789943	2.02E-97	9.39E-96
AOAH	1.23863	4.295308	1.794016	3.55E-136	1.08E-133
CCL4	1.572836	5.464184	1.796638	5.05E-117	4.50E-115
MAP4K1	1.055384	3.668859	1.797563	1.91E-124	2.31E-122
HCST	2.770915	9.643491	1.799193	1.72E-111	1.21E-109
FCRL6	0.22393	0.779736	1.799938	2.65E-95	1.18E-93
HLA-DQA2	9.061418	31.55652	1.800129	1.98E-53	3.86E-52
CARD17	0.170896	0.595701	1.801468	1.20E-61	2.75E-60
GBP1	7.768416	27.07945	1.801506	1.12E-94	4.95E-93
IL4I1	2.100103	7.325673	1.802501	1.22E-95	5.49E-94
APOBEC3H	0.300332	1.058619	1.817556	6.28E-112	4.44E-110
CD28	0.426534	1.509284	1.823132	3.88E-110	2.54E-108
IL2RA	0.617433	2.190411	1.826848	8.66E-104	4.67E-102
CARD11	0.806924	2.862746	1.826895	1.05E-135	3.00E-133
HLA-DQA1	9.804146	35.00756	1.836203	1.14E-128	1.66E-126
LILRA4	0.342844	1.226514	1.83894	1.16E-74	3.37E-73
CASP5	0.058804	0.210558	1.840225	5.01E-63	1.17E-61
ACY3	0.76692	2.749067	1.841793	4.85E-38	7.02E-37
GFI1	0.250216	0.899995	1.846743	2.46E-108	1.49E-106
CD37	2.513035	9.043413	1.847437	1.21E-151	2.13E-148
CALHM6	2.619007	9.435149	1.849025	1.41E-114	1.12E-112
JAK3	1.017678	3.666297	1.849043	3.78E-120	3.74E-118
CORO1A	4.947004	17.83368	1.849977	8.99E-133	1.92E-130
PTCRA	0.08714	0.315484	1.856164	2.54E-86	9.36E-85
ZC3H12D	0.155456	0.563357	1.857538	1.29E-113	9.68E-112
ACAP1	0.717599	2.603969	1.859462	7.87E-111	5.40E-109
CCL21	6.302648	22.87745	1.859896	1.02E-40	1.56E-39
TNFRSF13C	0.392336	1.425986	1.8618	5.22E-39	7.69E-38
HK3	0.636577	2.31461	1.862363	2.49E-79	8.03E-78
RASGRP2	0.387618	1.411249	1.864264	3.15E-80	1.04E-78
CD244	0.138569	0.504528	1.864327	5.59E-114	4.27E-112
PLEK	3.981504	14.53125	1.867774	3.05E-147	2.53E-144
TBC1D10C	0.81057	2.966032	1.871526	3.54E-104	1.93E-102
NCF1	0.392232	1.437563	1.873845	1.52E-128	2.16E-126

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
SASH3	3.153664	11.61662	1.881089	7.77E-160	5.46E-156
SLAMF8	2.522517	9.292544	1.88121	6.60E-122	7.20E-120
GPR15	0.118853	0.438056	1.881936	1.09E-34	1.48E-33
CD69	1.001709	3.692566	1.88216	6.15E-103	3.21E-101
CD1C	0.720947	2.670339	1.889058	2.02E-62	4.69E-61
MMP9	27.9422	103.5012	1.88913	2.69E-31	3.34E-30
TNFSF14	0.178452	0.661049	1.889222	5.00E-109	3.16E-107
CSF2RB	1.557112	5.777326	1.89153	8.39E-119	8.08E-117
CCR7	1.512651	5.636606	1.897748	9.17E-106	5.24E-104
TMC8	1.194898	4.471193	1.903772	2.54E-134	6.33E-132
KLRB1	0.772492	2.891068	1.904011	1.56E-105	8.88E-104
ZBP1	0.387241	1.450676	1.905423	3.91E-90	1.56E-88
CXCL5	0.35897	1.346109	1.906859	1.55E-16	1.07E-15
CCL17	0.735642	2.764512	1.909949	2.30E-65	5.66E-64
IKZF1	0.873493	3.284498	1.910804	1.62E-136	5.06E-134
SPN	0.804732	3.027609	1.911598	1.14E-138	4.24E-136
XIRP1	0.150752	0.569775	1.918217	1.73E-63	4.10E-62
ARHGAP9	0.808487	3.080628	1.929928	2.31E-151	3.61E-148
CD8B	0.793738	3.03439	1.934671	1.63E-98	7.82E-97
HLA-DOB	1.027149	3.952845	1.944246	7.92E-80	2.59E-78
SIGLEC12	0.109856	0.422963	1.944913	6.28E-28	7.10E-27
CCL25	0.072468	0.27968	1.948369	1.62E-22	1.54E-21
KCNJ10	0.1093	0.421938	1.948735	1.09E-53	2.15E-52
DOK2	1.344184	5.18939	1.948834	7.31E-136	2.19E-133
CD1E	0.454002	1.753721	1.949648	2.49E-65	6.11E-64
GBP4	4.079801	15.91592	1.9639	1.19E-96	5.41E-95
CLLU1OS	0.102689	0.404284	1.97709	1.46E-26	1.58E-25
LGALS2	1.13529	4.476765	1.979396	1.45E-87	5.50E-86
BCL2A1	2.193047	8.685402	1.985656	1.06E-97	5.00E-96
C16orf54	0.666152	2.687633	2.012413	2.69E-130	4.51E-128
TIMD4	0.164707	0.667094	2.017985	1.57E-64	3.78E-63
IL12RB1	0.370429	1.511853	2.029048	3.16E-151	4.04E-148
VMO1	1.961646	8.080345	2.042352	1.93E-24	1.97E-23
JAML	0.454647	1.881184	2.048823	4.73E-128	6.52E-126
SLFN12L	0.139308	0.581462	2.061409	8.66E-104	4.67E-102
PSTPIP1	0.485927	2.034006	2.065511	3.25E-139	1.31E-136
IL21R	0.394556	1.655368	2.06885	6.25E-120	6.15E-118
TESPA1	0.288674	1.211688	2.069505	2.04E-112	1.49E-110
STAP1	0.317869	1.346143	2.082328	2.08E-81	7.10E-80
SNX20	0.602676	2.562436	2.088062	2.92E-155	1.37E-151
TLR10	0.229803	0.977907	2.089302	4.64E-84	1.66E-82
XCR1	0.105406	0.448808	2.090136	1.72E-90	6.92E-89

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
APOBEC3A	0.241446	1.029593	2.092299	1.83E-53	3.58E-52
CST7	2.672764	11.44977	2.098914	4.07E-132	8.41E-130
CCR5	1.365963	5.869168	2.103237	7.01E-148	7.04E-145
CR1	0.05936	0.255262	2.104409	4.32E-73	1.21E-71
CCR4	0.52214	2.245489	2.10452	6.90E-107	4.05E-105
SP140	0.357501	1.539744	2.106671	3.61E-133	8.46E-131
C11orf21	0.109233	0.472142	2.111816	4.89E-108	2.95E-106
CXCR6	0.482678	2.0904	2.114646	4.31E-121	4.59E-119
LAG3	0.789612	3.422886	2.115997	2.39E-79	7.71E-78
THEMIS	0.202011	0.877439	2.118867	3.39E-110	2.25E-108
KCNA3	0.196154	0.852214	2.119227	1.70E-89	6.65E-88
PTPRC	2.738553	11.95513	2.126144	2.00E-131	3.80E-129
PTPN7	0.686195	3.019085	2.137422	3.10E-151	4.04E-148
TLR8	0.293878	1.2943	2.138881	2.15E-113	1.61E-111
SAMD3	0.083015	0.366182	2.14112	7.44E-123	8.51E-121
CD48	1.99152	8.891968	2.158633	4.00E-150	4.69E-147
CCR2	0.582173	2.603768	2.16108	3.49E-112	2.51E-110
TNFRSF9	0.213978	0.964232	2.171917	1.14E-116	9.98E-115
CD6	0.699663	3.170452	2.179956	3.98E-129	6.03E-127
IL18RAP	0.096591	0.439605	2.186252	1.44E-107	8.64E-106
KLK14	2.916702	13.30816	2.189902	0.000984031	0.001706004
GPR25	0.040325	0.184934	2.19727	1.10E-48	1.97E-47
ICAM3	0.246301	1.131999	2.200376	6.29E-121	6.60E-119
NCR3	0.18823	0.873579	2.214438	1.48E-101	7.61E-100
PTGDS	3.925659	18.22604	2.214994	1.08E-63	2.58E-62
CLEC4E	0.299555	1.393186	2.217496	1.16E-93	5.01E-92
NUGGC	0.107989	0.502644	2.218652	1.72E-87	6.51E-86
CD8A	1.460698	6.803574	2.219635	1.43E-114	1.13E-112
LYZ	34.45826	160.6349	2.220864	4.64E-105	2.59E-103
PARP15	0.205176	0.956818	2.221386	4.00E-111	2.77E-109
CD7	0.777276	3.626996	2.222277	6.69E-115	5.40E-113
CLEC10A	0.674511	3.14846	2.222734	2.29E-85	8.32E-84
TNIP3	0.081258	0.379624	2.223992	1.98E-97	9.22E-96
TMIGD2	0.086992	0.407824	2.228994	1.68E-86	6.23E-85
CXCL10	17.85152	83.84436	2.231667	3.90E-88	1.48E-86
LAIR2	0.119289	0.566434	2.247446	7.73E-90	3.04E-88
CRTAM	0.216757	1.032738	2.252325	1.21E-139	5.33E-137
KLHDC7B	2.556513	12.23784	2.2591	1.06E-41	1.64E-40
GZMH	0.85945	4.137055	2.267119	7.69E-109	4.78E-107
CTSW	1.110158	5.358009	2.270932	1.26E-111	8.83E-110
FCN1	0.258971	1.251144	2.272388	1.36E-97	6.37E-96
CD79B	1.143646	5.534794	2.274889	1.16E-79	3.78E-78

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
CD96	0.547952	2.669604	2.284503	5.76E-129	8.52E-127
IRF4	0.442578	2.157243	2.285186	1.48E-97	6.90E-96
CLEC17A	0.090223	0.439953	2.285786	9.00E-62	2.06E-60
PLAC8	0.242532	1.192623	2.297889	1.47E-93	6.28E-92
CD247	0.536154	2.650495	2.305542	1.60E-130	2.85E-128
ZNF683	0.438206	2.16758	2.306404	2.71E-105	1.52E-103
CCL18	2.100773	10.41627	2.309848	7.13E-52	1.36E-50
VPREB3	0.591471	2.94	2.313438	1.70E-43	2.75E-42
IL7R	1.630233	8.117458	2.31595	8.95E-107	5.22E-105
SLA2	0.41529	2.075603	2.32134	2.39E-135	6.60E-133
TNFRSF17	0.546996	2.744668	2.32703	5.60E-61	1.25E-59
XCL2	0.344063	1.728255	2.328571	5.48E-101	2.76E-99
CXCL11	2.786998	14.0878	2.337663	2.34E-83	8.28E-82
FUT7	0.100588	0.510666	2.34392	2.28E-111	1.59E-109
CD40LG	0.292571	1.491496	2.349901	2.83E-110	1.88E-108
PRKCB	0.327929	1.672442	2.350501	9.94E-126	1.24E-123
PENK	0.150912	0.778157	2.366358	1.13E-09	4.20E-09
MARCO	1.059976	5.47911	2.36991	5.69E-44	9.35E-43
LCK	1.069391	5.531834	2.370969	1.69E-128	2.35E-126
UBASH3A	0.23506	1.22246	2.378689	2.35E-127	3.06E-125
FASLG	0.229015	1.19407	2.38237	1.49E-108	9.15E-107
CD5	0.87347	4.597901	2.396145	1.84E-131	3.54E-129
SLAMF7	1.419632	7.481632	2.397836	7.08E-118	6.51E-116
PNOC	0.125856	0.665583	2.402839	2.58E-76	7.72E-75
PRF1	0.84572	4.479172	2.404979	3.26E-129	4.99E-127
LAX1	0.338	1.792732	2.407064	5.63E-94	2.45E-92
CCL5	9.755549	51.86385	2.410435	7.14E-128	9.65E-126
CD27	1.371251	7.305437	2.413478	4.73E-118	4.41E-116
IL12B	0.04145	0.221206	2.415933	2.06E-88	7.92E-87
S1PR4	0.466799	2.491182	2.415956	2.83E-120	2.82E-118
UBD	3.139272	16.78631	2.418783	2.03E-72	5.61E-71
GPR171	0.329591	1.776984	2.430682	4.73E-115	3.89E-113
GNLY	0.632314	3.425065	2.437418	1.09E-102	5.66E-101
GZMA	2.481537	13.46392	2.439793	8.34E-130	1.35E-127
IL2RG	3.681922	20.05697	2.445573	3.53E-147	2.76E-144
PAX5	0.124347	0.679575	2.450261	7.49E-59	1.61E-57
ZAP70	0.391871	2.148626	2.454963	3.12E-118	2.94E-116
GZMM	0.603181	3.342179	2.470125	1.40E-104	7.69E-103
SIT1	0.680083	3.769711	2.470672	1.94E-132	4.08E-130
CD2	3.263507	18.17974	2.477836	2.27E-139	9.69E-137
ADAMDEC1	1.289364	7.193976	2.48013	6.21E-77	1.90E-75
CTLA4	0.362666	2.027524	2.483006	3.14E-114	2.44E-112

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
CD3G	0.38948	2.20574	2.501641	1.24E-128	1.78E-126
AIM2	0.382315	2.166142	2.502294	5.20E-109	3.26E-107
EOMES	0.239469	1.357327	2.502857	2.05E-114	1.61E-112
CCL13	0.576998	3.273173	2.504051	5.82E-84	2.07E-82
TREML2	0.041321	0.234564	2.505021	1.53E-88	5.90E-87
LTA	0.201381	1.143801	2.505833	5.65E-117	5.00E-115
SCML4	0.071172	0.406856	2.51514	1.08E-116	9.49E-115
TBX21	0.165363	0.946595	2.517109	7.61E-130	1.25E-127
POU2AF1	0.403348	2.310413	2.518053	4.61E-72	1.27E-70
MS4A6E	0.026163	0.150708	2.526186	4.15E-12	2.00E-11
BANK1	0.205982	1.186854	2.526554	2.26E-76	6.81E-75
LY9	0.110426	0.63948	2.533821	9.25E-125	1.14E-122
SLAMF1	0.255608	1.481103	2.534665	2.04E-130	3.50E-128
ZNF831	0.073937	0.430407	2.54133	5.93E-115	4.84E-113
PYHIN1	0.207402	1.210389	2.54497	3.56E-130	5.89E-128
AC136428.1	0.234799	1.380948	2.556159	4.24E-44	7.02E-43
CXCR3	0.813501	4.790686	2.558016	5.78E-133	1.29E-130
CD3E	2.017282	12.00923	2.573659	4.89E-137	1.60E-134
CD1B	0.112801	0.673503	2.577901	6.19E-69	1.61E-67
PDCD1	0.313487	1.873529	2.57928	1.04E-117	9.47E-116
ITK	0.234743	1.402985	2.579344	1.59E-126	2.03E-124
OR2I1P	1.440637	8.613051	2.579818	2.44E-81	8.32E-80
GPR174	0.238965	1.430801	2.581953	1.21E-97	5.67E-96
IGLL5	6.649046	39.979	2.588023	2.25E-58	4.79E-57
NKG7	2.440551	14.76835	2.59723	3.12E-124	3.72E-122
KIR2DL4	0.043435	0.263735	2.602148	1.05E-65	2.61E-64
FAM129C	0.074225	0.454484	2.614248	6.45E-61	1.44E-59
ROS1	0.049541	0.30451	2.6198	0.000283684	0.000530658
TNFRSF13B	0.059102	0.365627	2.629106	1.97E-73	5.59E-72
CD3D	2.123914	13.20874	2.636695	5.07E-139	1.98E-136
TIGIT	0.359398	2.240623	2.640246	7.14E-128	9.65E-126
ICOS	0.257932	1.608969	2.641077	5.20E-114	3.99E-112
SH2D1A	0.418491	2.632386	2.653103	2.17E-127	2.85E-125
CCL19	7.899773	49.98754	2.661686	2.93E-69	7.63E-68
SLAMF6	0.644465	4.082037	2.663115	1.11E-130	1.99E-128
ZBED2	0.157458	0.999064	2.665614	1.19E-93	5.14E-92
CD38	0.269294	1.732079	2.685249	2.71E-100	1.35E-98
CD52	8.482918	55.37312	2.706553	4.24E-127	5.47E-125
LTB	2.020641	13.35687	2.724697	5.29E-98	2.52E-96
GZMK	1.074322	7.155418	2.735609	7.11E-121	7.41E-119
SIRPG	0.326951	2.178715	2.736331	4.61E-129	6.89E-127
BTLA	0.114988	0.77777	2.757867	3.11E-113	2.30E-111

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
TIFAB	0.043913	0.299204	2.768418	2.16E-113	1.61E-111
FCRL5	0.103987	0.718541	2.788673	1.68E-70	4.45E-69
SPIB	0.403624	2.868219	2.82907	2.26E-84	8.14E-83
CHIT1	0.666338	4.748873	2.83326	2.75E-37	3.93E-36
FCRLA	0.166665	1.204025	2.852839	1.65E-86	6.13E-85
CR2	0.275467	2.021995	2.875826	7.24E-42	1.13E-40
TRAT1	0.178223	1.308927	2.876628	8.69E-121	8.92E-119
CLEC4C	0.03222	0.239973	2.896829	3.24E-77	9.98E-76
IDO1	1.499219	11.19081	2.900031	4.36E-94	1.91E-92
GBP5	0.918153	6.89248	2.908216	8.92E-119	8.47E-117
CNR2	0.031987	0.247403	2.951326	7.27E-78	2.26E-76
CD79A	2.146012	17.02748	2.988135	1.50E-78	4.74E-77
CLEC4D	0.032602	0.267	3.033801	2.06E-60	4.54E-59
BLK	0.082816	0.685885	3.049989	1.09E-72	3.03E-71
FCRL2	0.046213	0.383003	3.050996	1.47E-72	4.08E-71
CXCL9	9.174485	76.14552	3.05306	1.20E-100	6.02E-99
FCRL3	0.095955	0.806371	3.071017	1.71E-103	9.12E-102
GZMB	0.665798	5.59977	3.072211	5.47E-108	3.29E-106
IFNG	0.070838	0.699267	3.303254	6.92E-96	3.13E-94
CD19	0.161633	1.660855	3.361128	5.15E-81	1.74E-79
IGLL1	0.034445	0.378258	3.457023	1.76E-32	2.26E-31
FCAMR	0.023444	0.262488	3.484953	3.42E-28	3.91E-27
MS4A1	0.362738	4.35511	3.585709	2.37E-80	7.91E-79
FCRL1	0.045721	0.586412	3.680998	1.58E-73	4.50E-72
DMBT1	0.098058	1.320953	3.751802	0.0010808	0.001863609
PLA2G2D	0.315815	4.315992	3.772539	1.43E-95	6.43E-94
FCER2	0.063118	0.95975	3.926535	3.84E-72	1.06E-70
KRT1	0.897951	14.29212	3.99244	6.96E-07	1.84E-06
TCL1A	0.108973	1.755959	4.010215	2.22E-82	7.75E-81
AICDA	0.01164	0.250014	4.424884	4.41E-43	7.05E-42
LOR	0.053887	2.216532	5.362215	7.23E-18	5.53E-17