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Original Article

A microRNA signature containing miR-1258 and miR-193a predicts survival in HER2-negative breast cancer

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Abstract: Human epidermal growth factor receptor 2 (HER2)-negative breast cancer is one type of breast cancer named by its cells, which lack HER2 expression. At present, there is no definite prognostic evaluation method for this type of breast cancer. Increasing evidence has shown that microRNAs (miRNAs) may play an important role in the occurrence and development of breast cancer. miRNA expression and clinical data of HER2-negative breast cancer patients collected from The Cancer Genome Atlas (TCGA) database were analyzed. Between HER2-negative breast cancer tumor tissues and matched normal tissues, a total of 64 differentially expressed miRNAs were identified using the cut-off criteria of $P < 0.05$ and $|\log2FC| > 1.5$. Of these miRNAs, 36 were downregulated, and 28 were upregulated. Kaplan-Meier survival analysis revealed 34 miRNAs that were closely related to survival (P-value < 0.05). The intersection of the 34 miRNAs and 64 differentially expressed miRNAs revealed 20 miRNAs. After log-rank tests were performed based on survival curves, 7 miRNAs were identified. The prognostic value of these 7 miRNAs was evaluated with the Cox proportional hazards model using multiple logistic regression (LR) with forward stepwise selection of variables. Finally, 2 miRNAs (miR-1258 and miR-193a) were identified as independent risk factors associated with survival in the model. Gene Ontology (GO) and KEGG pathway enrichment analyses showed that miR-1258 and miR-193a are important factors in the processes of HER2-negative breast cancer. These findings suggest that the 2-miRNA signature may serve as a prognostic biomarker for HER2-negative breast cancer.

Keywords: MicroRNA, breast cancer, HER2-negative, miR-193a, miR-1258, drug resistance

Introduction

MicroRNAs (miRNAs) were found in 1993 and are a class of noncoding RNAs [1]. These RNAs, though only 22-26 nucleotides (nt) in length, play a key regulatory role in gene expression. Complex structures enable them to integrate target miRNAs to induce cleavage or translational repression [2]. Genetic mutations and epigenetic modifications are root causes of breast cancer; therefore, miRNAs play important roles in the carcinogenesis and development of breast cancer. Many miRNA expression levels are altered in tumor tissues, making them ideal markers. In fact, miRNA biomarkers have been one of the hotspots in cancer research over the past decade [3].

Previous studies have found miRNA biomarkers for breast cancer, such as miR-21, miR-155, and miR-222 [4]. However, large sample studies are lacking, especially those combined with clinical data. In 2006, the National Cancer Institute (NCI) and the National Human Genome Research Institute (NHGRI) launched The Cancer Genome Mapping (TCGA) project, which contains data from more than 10,000 patients and covers 33 types of cancer [5, 6].

The data used in this study were composed of small miRNA-seq of tissues and clinical information downloaded from the TCGA database. These data were analyzed in four steps: (1) the identification of miRNAs differentially expressed between tumor tissues and normal tissues; (2) screening of the miRNAs obtained in the first step using the Kaplan-Meier survival method, which yielded a total of 7 specific miRNAs; (3) statistical analysis was used to identify miRNAs that can predict patient survival; and (4) the

Gene Ontology (GO) and KEGG pathways related to these miRNAs were screened.

Materials and methods

HER2-negative breast cancer miRNA-seq dataset and clinical information

The miRNA-seq dataset and clinical information were downloaded from the TCGA data portal (1988-Jan. 28, 2016). The clinical data of each patient were derived from a variety of methods used to detect HER-2 levels; therefore, "patient margin status" was used as a standard to determine the HER-2 status of patients. Finally, we established a miRNA-seq database containing tumor tissues (n = 507) and matched normal tissues (n = 55). All of the miRNA-expression data were reported as "reads-per-million-miRNA-mapped" that were normalized by log2 transformation. This miRNA-seq database was analyzed for differential miRNA expression.

In the survival analysis of clinical data, we set the following inclusion criteria: (1) complete follow-up data were available for 1-60 months (30-3650 days); (2) the clinical data were complete (patients with incomplete or uncertain clinical data were excluded; and (3) miRNA-seq data integrity was validated. Finally, survival analysis included 400 cases meeting these criteria (Table S4). To incorporate as many data as possible, differential miRNA expression and survival analyses were performed independently.

Screening of differentially expressed miRNAs

We used the limma package in R language (R version 3.5.1, limma version 3.36.5) to screen differentially expressed miRNAs between tumor tissues and normal tissues. The fold change (FC) indicates the degree of differential expression of the miRNA. A log |FC| > 1.5 and a *P*-value < 0.05 after FDR (false discovery rate) adjustment were established as cut-off criteria.

Survival analysis and the establishment of a prognostic model

In the process of survival analysis and the establishment of a prognostic model, we used the following tools: (1) Survival package (version 2.43-1) in R language and (2) Statistical Package for the Social Sciences (SPSS) (version 22.0, IBM Corp., NY, USA). Four hundred patients were sorted according to the differentially expressed miRNA level and divided into high and low groups based on the median level. In the first step, we identified 34 miRNAs that were closely related to survival by the R program. Each of them was evaluated separately with the Kaplan-Meier method (*P*-value < 0.05). Then, we obtained the intersection of the 34 miRNAs and 64 differentially expressed miRNAs. After the intersection (20 miRNAs) was evaluated with log-rank tests based on survival curves, 7 miRNAs were eliminated. The prognostic value of these 7 miRNAs was tested by the Cox proportional hazards model using multiple logistic regression with forward stepwise (LR) selection of variables. Finally, miR-1258 and miR-193a were found to be independent risk factors associated with survival in the model. We calculated a risk score for each patient. This score was based on the expression levels of miR-1258 and miR-193a, as determined by miRNA's Cox regression coefficient [7]. In total, 400 patients were divided into either the high-risk group (n = 200) or the low-risk group (n = 200) based on the risk score. A risk score based on the expression levels of the 2 miRNAs determined using each miRNA's Cox regression coefficient was calculated for each patient [risk score = (0.669 × expression of miR-193a)-(0.788 × expression of miR-1258)]. The predictive power of the 2-miRNA signature and clinical features was analyzed using univariate/multivariate Cox regression and the Kaplan-Meier method, which could assess their influence on survival. A *P*-value < 0.05 was considered statistically significant. Data are reported as the mean values with standard deviations.

KEGG pathways and Gene Ontology analysis

TargetScan7.2 [8] and miRDB [9, 10] are online miRNA databases that were used to predict the target genes of the 2 prognostic miRNAs in our study. The overlapping set of the target genes from 2 databases was made into a gene list for each miRNA. We created Venn diagrams from the gene lists. We also analyzed the overlapping genes using the Database for Annotation, Visualization and Integrated Discovery (DAVID, v6.8) (https://david.ncifcrf.gov/). This database

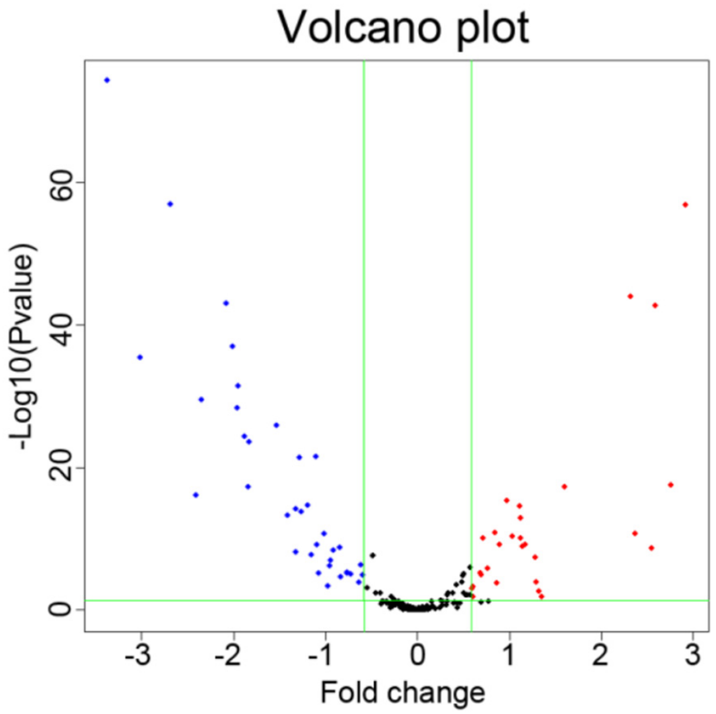

Figure 1. Volcano plot of differentially expressed miRNAs. Red dots represent upregulated miRNAs, while blue dots represent downregulated miRNAs.

integrates biological data and analysis tools. Users can extract bioinformatics expediently from large-scale gene lists of interest. DAVID's tools can implement numerous functions, including gene function enrichment. The role of enrichment analysis is to help biologists understand the biological role of gene sets [11, 12]. Gene Ontology (GO) and KEGG pathway enrichment analyses were performed to determine the biological processes and pathways involving target genes. The cut-off criteria for the KEGG and GO pathways were $P < 0.1$ and gene count ≥ 3.

Results

Identification of differentially expressed miRNAs in HER2-negative breast cancer

The HER2-negative breast cancer miRNA-seq data from 562 samples included 507 tumor tissues and 55 matched normal tissues. A total of 64 differentially expressed miRNAs were identified using the cut-off criteria $P < 0.05$ and $|\log_2 FC| > 1.5$. Of these miRNAs, 36 were down-regulated, and 28 were up-regulated (**Figure 1**, Table S1).

Identification of miRNAs linked to survival in HER2-negative breast cancer

A total of 400 patients who met the inclusion criteria were enrolled in our study. Thirty-four miRNAs were identified based on the survival analysis of these patients' miRNA-seq and clinical data (Table S2). Each of the 34 miRNAs was significantly associated with survival. The intersection of these 34 miRNAs and 64 differentially expressed miRNAs revealed 20 miRNAs: miR-193a, miR-10b, miR-1258, miR-125a, miR-148b, miR-130b, miR-1270-2, miR-103-2, miR-181b-1, miR-127, miR-1307, miR-1301, miR-190b, miR-10a, miR-150, miR-192, miR-1909, miR-1277, miR-1270-1, and miR-1262. After log-rank statistical tests, 7 miRNAs (miR-193a, miR-1258, miR-1270-2, miR-103-2, miR-1307, miR-190b, and miR-1262) were identified based on the cut-off criteria ($P < 0.05$) (Table S3). Then, the prognostic value of these 7 miRNAs was evaluated with the Cox proportional hazards model using multiple logistic regression (LR) with forward stepwise selection of variables. Omnibus tests of model coefficients showed that the model based on miR-193a and miR-1258 yielded the lowest log likelihood ratio (-2 Log Likelihood = 213.881) (Supplmentary Data). This finding indicated that this 2-miRNA combination yielded the best statistical performance. Finally, 2 miRNAs (miR-1258 and miR-193a) were considered independent risk factors associated with survival in the model (**Figure 2A**, **2B**). Among these miRNAs, miR-193a is a risk factor, whereas miR-1258 is a protective factor. A risk score based on the expression levels of the 2 miRNAs determined using each miRNA's Cox regression coefficient was calculated for each patient [risk score = (0.669 × expression of miR-193a)-(0.788 × expression of miR-1258)]. In total, 400 patients were divided into a high-risk group (n = 200, Risk score = 5.17~8.02) and a low-risk group (n = 200, Risk score = 3.04~5.16) based on the risk score. Compared with the low-risk group, the high-risk group exhibited poor survival out-

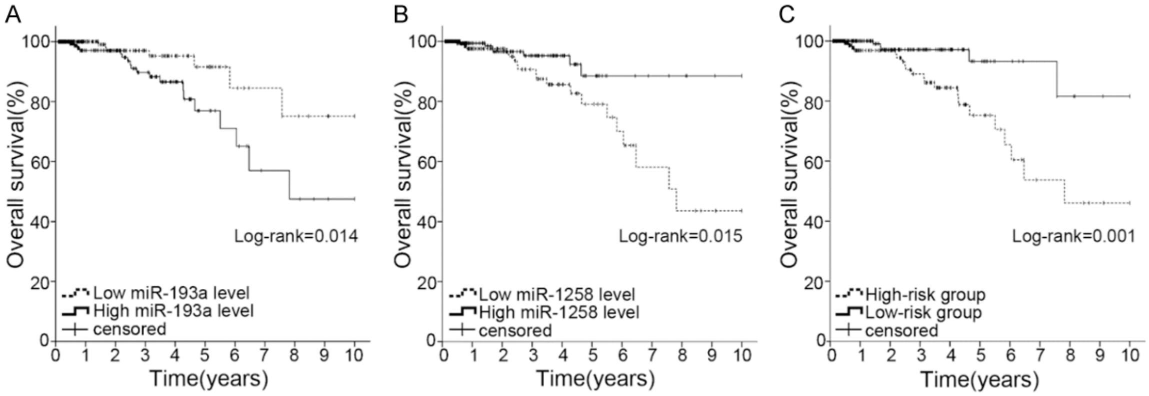

Figure 2. Kaplan-Meier curve with the log-rank test for miRNAs and the miRNA signature: (A) miR-193a; (B) miR-1258; and (C) 2-miRNA signature. The patients were divided into a high-risk group (n=200, Risk score=5.17~8.02) and a low-risk group (n=200, Risk score=3.04~5.16) according to the risk score. Risk score=(0.669 × expression of miR-193a)-(0.788 × expression of miR-1258).

Table 1. Univariate/multivariate Cox regression analysis in HER2-negative breast cancer patients

	Univariate analysis		Multivariate analysis	
	P value	HR (95% CI)	*P* value	HR (95% CI)
Age (≥ 60 vs. < 60)	0.081	1.993 (0.917-4.328)	0.004	6.102 (1.765-21.096)
Histological type (IDC vs. ILC vs. Other)	0.401	/	0.470	/
Tumor size (T1-2 vs. T3-4)	0.149	2.056 (0.773-5.466)	0.065	4.038 (0.915-17.814)
Lymph node status (N0-1 vs. N2-3)	0.003	3.547 (1.453-8.656)	0.033	7.372 (1.177-46.155)
Metastasis (M0-x vs. M1)	0.012	8.636 (1.138-65.515)	0.009	23.531 (2.213-250.251)
Pathological stage (G1-2 vs. G3-4)	0.017	2.702 (2.044-17.335)	0.295	0.345 (0.047-2.534)
2-miRNA signature (low risk vs. high risk)	0.003	4.350 (1.638-11.553)	0.004	6.102 (1.765-21.096)

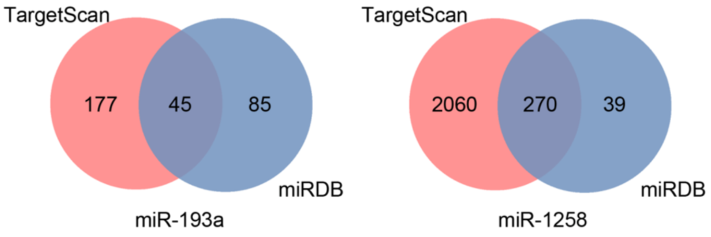

Figure 3. The Venn diagrams show overlapping target genes that were predicted using TargetScan and miRDB online tools.

comes, as assessed using the Kaplan-Meier method (**Figure 2C**).

Univariate and multivariate Cox regression analyses were performed to test the efficacy of the 2-miRNA signature (high-risk group vs. low-risk group) on survival by considering the following clinical features: age at initial pathological diagnosis (< 60 vs. ≥ 60), histological type (IDC vs. ILC vs. other), tumor size (T1-2 vs. T3-4), lymph node status (N0-1 vs. N2-3), metastasis (M0/Mx vs. M1), and pathological stage (G1-2 vs. G3-4). In univariate analysis, the 2-miRNA signature (HR = 4.35, P = 0.003), metastasis (HR = 8.636, P = 0.012), lymph node status (HR = 3.547, P = 0.003) and pathological stage (HR = 2.702, P = 0.017) were associated with survival in HER2-negative breast cancer patients. In multivariate analysis, the 2-miRNA signature (HR = 6.102, P = 0.004), age at initial pathological diagnosis (HR = 2.424, P = 0.035), metastasis (HR = 23.531, P = 0.009), and lymph node status (HR = 7.372, P = 0.033) were identified as independent prognostic factors (**Table 1**).

KEGG pathways and Gene Ontology analysis

We identified 45 overlapping genes of miR-193a and 270 overlapping genes of miR-1258 (**Figure 3**). GO results revealed that these overlapping genes were enriched in 53 GO accessions involving cell structure, cell movement, cellular energy metabolism, signaling pathways

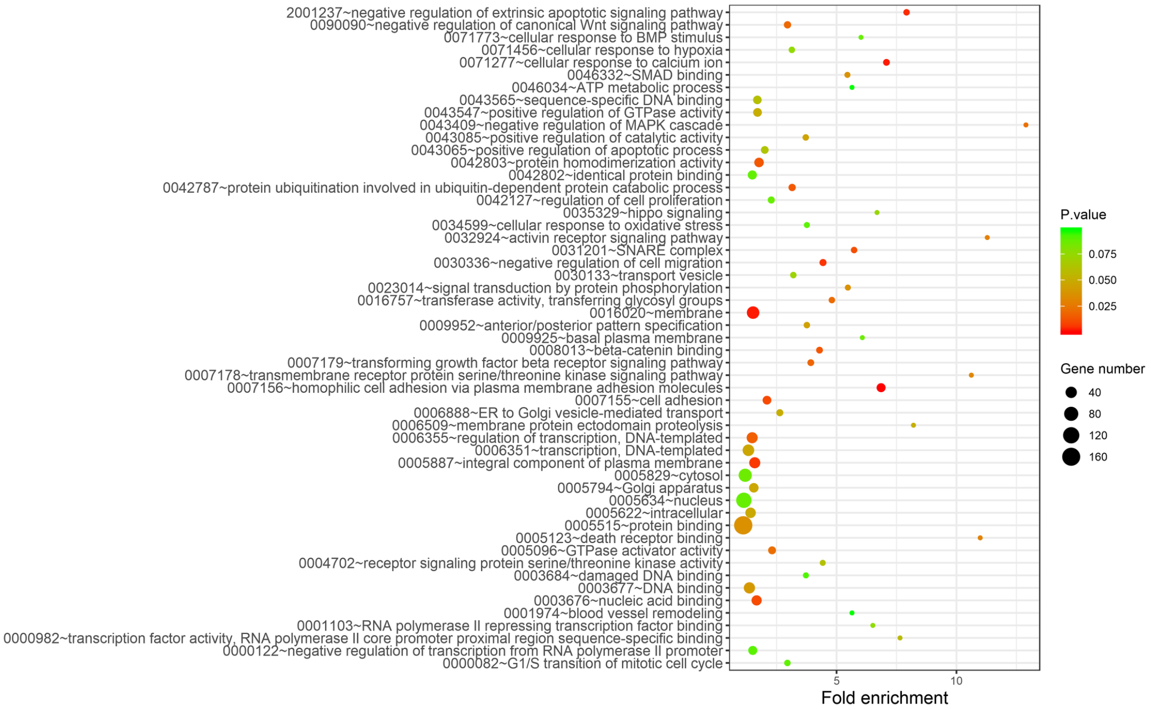

Figure 4. Gene ontology analysis of 2-miRNA signature target genes.

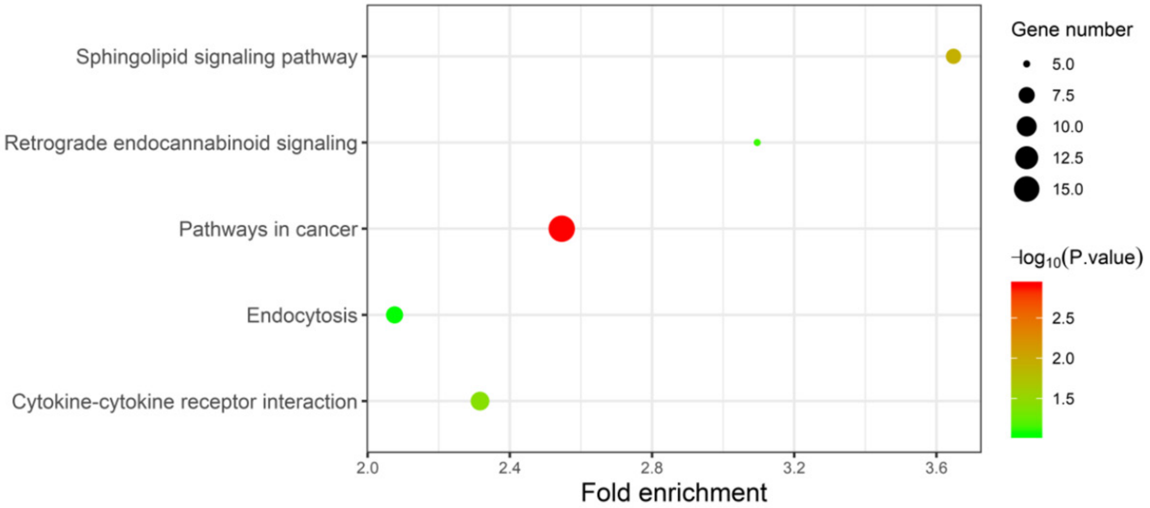

Figure 5. KEGG pathway analysis of 2-miRNA signature target genes.

such as MAPK/Wnt/Hippo, the regulation of transcription, DNA-templated and so on (**Figure 4**). KEGG pathways were enriched in 5 pathways: pathways in cancer, the sphingolipid signaling pathway, cytokine-cytokine receptor interaction, retrograde endocannabinoid signaling, and endocytosis (**Figure 5**).

Discussion

In this study, a 2-miRNA signature associated with HER2-negative breast cancer patient survival was identified. In a multivariate Cox model, this signature was identified as an independent prognostic factor influencing HER2-negative breast cancer patient survival (HR = 6.102, 95% CI 1.765-21.096). KEGG and GO analyses of the target genes of the 2 miRNAs showed that these miRNAs play important roles in cell migration, regulation of the apoptotic signaling pathway, pathways in cancer and so on. All the above results demonstrate that miR-1258 and miR-193a are important factors in the processes of HER2-negative breast cancer. Most likely due to the small sample size (n = 400), we obtained a slightly wider 95% confidence interval (CI). The results display a wide 95% CI interval that was not uncommon in similar studies [13].

miR-193a has been observed in many cancers, such as osteosarcoma, epithelium ovarian cancer, esophageal carcinoma and intrahepatic cholangiocarcinoma. In different cancers, the expression of miR-193a in tumor tissues and its effect on tumor growth are different [14-17]. In breast cancer, research focusing on miR-193a is lacking, especially research on the relationship between miR-193a and patient survival. In our study, the expression of miR-193a was found to be decreased in breast cancer tissues compared with common tissues, which is consistent with previous research [18, 19]. Recent animal experiments have found that primary colon tumors, liver metastases, and immature colon tissue cells excrete miR-193a through exosomes [20], which may be one of the reasons why the expression of miR-193a in tumors is lower than that in normal tissues. In most studies, miR-193a mainly acted as a tumor suppressor [21, 22]. It was found that miR-193a-3p regulates the proliferation and apoptosis of BC cells by regulating PTP1B [23]. One study showed that miR-193a reduced Wilms' tumor 1 (WT1) expression and repressed luciferase reporter activity by binding to WT1 coding region sequences [18]. We noticed that all the above results were derived from cell or animal experiments. Our research first demonstrated that miR-193a was an independent risk factor associated with survival in HER2-negative breast cancer patients. We hypothesized that miR-193a may increase the drug resistance of cancer cells. It has been reported that the targeting regulation of miRNA with apoptotic inhibitors and the negative regulation of cell cycle regulators affect drug action and eventually lead to drug resistance [24, 25]. A study showed that miR-193a partially reversed the antiproliferative effects of lapatinib in SKBR3-cells and that miR-193a contributed to the cytotoxic activity of ATRA and/or lapatinib [26]. All the data used in our research was obtained from the real world, where the patient was treated with various drugs. There may be a complex relationship between miRNAs, drugs and the behavior of cancer cells, which requires additional data and experiments.

In our study, we demonstrated that miR-1258 is a protective factor associated with the survival of HER2-negative breast cancer patients and that its expression in tumor tissue is decreased compared with that in normal tissue. This conclusion is consistent with two previous studies on breast cancer [27, 28]. In fact, miR-1258 has been widely researched in multiple cancers, and almost all studies have confirmed that miR-1258 can inhibit the growth of cancer cells [25-29], but its biological function and underlying mechanism in cancer progression are unclear, especially in breast cancer. A study on lung cancer showed that miR-1258 inhibited the progression of NSCLC by targeting the GRB2/Ras/Erk pathway [29]. Another study indicated that miR-1258 inhibited PI3K/AKT and Erk signaling pathway activity in oral squamous cell carcinoma [30]. However, our study showed that its target genes are not enriched in these pathways. Thus, the mechanism of miR-1258 in breast cancer must be investigated further.

In the KEGG and gene ontology analyses, we obtained further insight into the biological activities of miR-193a and miR-1258. Target genes were significantly enriched in pathways involved in cancer, the regulation of transcription, the regulation of cell migration, cytokine-cytokine receptor interaction, the process of apoptosis, the Wnt signaling pathway, cellular energy metabolism and so on. We found that multiple signaling pathways of target gene enrichment are associated with chemotherapeutic drug resistance.

A change in the signal transduction pathway is one of the pathogenetic mechanisms of breast cancer [31]. The MAPK signaling pathway includes extracellular signal-regulated kinase, c-Jun N-terminal kinase and p38 MAPK [32]. The MAPK signaling pathway plays an important role in many physiological processes, especially in inducing cell injury [33]. The activation of MAPK leads to the phosphorylation of p38, the activation of transcription factors and the promotion of apoptosis [34]. An analysis based on the GEO database showed that microRNAs and their target genes related to breast cancer resistance were enriched in the MAPK and Wnt signaling pathways [35]. Some studies further strengthened that microRNAs can affect the sensitivity of breast cancer cells to chemotherapeutic drugs by regulating the MARP signaling pathway [36, 37].

The activation of Wnt signaling and gene regulation mediated by microRNAs are causal factors that together drive tumorigenesis. Anton et al. [38] overexpressed 470 microRNAs in HEK293 cells and screened target genes downstream of the Wnt pathway by gene chip technology. The results showed that 38 candidate microRNAs were related to the expression of target genes downstream of Wnt. It has been reported that the abnormal activation of Wnt signaling pathway downstream target genes (such as LEF1, TCF, and P53) can enhance the expression of drug-resistant proteins in cancer cells and ultimately lead to changes in the biological behavior of cancer cells, such as increased drug resistance and metastasis ability [39]. miR-193a, as a risk factor, may increase drug resistance in breast cancer cells through Wnt signaling pathway activation.

Many studies support the role of the Hippo pathway as a tumor suppressor pathway in diverse human cancers, including breast cancer [40, 41]. TAZ/YAP is an important transcriptional factor downstream of the Hippo signaling pathway. Recent studies have shown that TAZ/YAP is associated with drug resistance in breast cancer. TAZ makes breast cancer cells resistant to paclitaxel by activating the cyr61/ctgf promoter [42]. The resistance of BC cells and stem cells expressing TAZ to adriamycin and paclitaxel was higher than that of control cells [43]. Other studies have shown that Yap expression can lead to the resistance of BC cells to paclitaxel and cisplatin [44]. The phosphorylation of ER alpha is one of the mechanisms of endocrine resistance in breast cancer. LATS2 can make breast cancer patients resistant to tamoxifen, fulvestrant or letrozole by activating the transcription of ER alpha [45].

In conclusion, this study identified two microRNAs as potential prognostic factors for HER2-negative breast cancer patients. The results obtained in the TCGA samples need to be verified in a larger sample size, and the molecular mechanism of these microRNAs in the development of breast cancer needs to be further studied.

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Disclosure of conflict of interest

None.

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Table S1. Analysis of differentially expressed miRNAs in HER2-negative breast cancer

miRNA	adj.P.Val	logFC	AveExpr	t	*P*.Value	B	threshold
hsa-mir-139	8.52E-75	-3.367486563	5.550905298	-21.8378401	3.38E-77	165.1578609	blue
hsa-mir-144	4.15E-36	-3.017544033	5.23151513	-13.80975897	1.32E-37	74.32438615	blue
hsa-mir-145	1.73E-57	-2.686343886	10.34161486	-18.38842333	1.38E-59	124.7298281	blue
hsa-mir-1247	7.43E-17	-2.407744141	4.228645706	-8.930137291	5.90E-18	29.4217559	blue
hsa-mir-133a-1	3.95E-30	-2.349405781	1.08072246	-12.42734014	1.57E-31	60.41500328	blue
hsa-mir-10b	1.24E-43	-2.074858317	16.01229663	-15.47775141	2.45E-45	92.03998401	blue
hsa-mir-125b-1	1.43E-37	-2.00574305	9.551286554	-14.14452178	3.98E-39	77.80493143	blue
hsa-let-7c	5.64E-29	-1.959519943	11.09969202	-12.14545628	2.46E-30	57.67923905	blue
hsa-mir-100	4.01E-32	-1.944844872	11.53614265	-12.89995322	1.43E-33	65.0812882	blue
hsa-mir-125b-2	4.22E-25	-1.880730136	4.154292955	-11.18618753	2.18E-26	48.65444955	blue
hsa-mir-1-2	6.35E-18	-1.83345275	1.681420486	-9.247654309	4.61E-19	31.94140602	blue
hsa-mir-1258	3.05E-24	-1.830480642	0.139745247	-10.96280551	1.69E-25	46.6199981	blue
hsa-mir-195	1.55E-26	-1.530113935	5.453117667	-11.54934139	7.36E-28	52.01726198	blue
hsa-mir-1468	5.99E-14	-1.404014217	2.37538593	-8.017820134	6.18E-15	22.55937129	blue
hsa-mir-130a	5.98E-15	-1.319023635	5.898598122	-8.339030626	5.69E-16	24.90991163	blue
hsa-mir-129-2	7.82E-09	-1.314257992	0.189594482	-6.173526104	1.27E-09	10.5504883	blue
hsa-mir-140	3.78E-22	-1.276378239	9.436929687	-10.41072572	2.40E-23	41.70817937	blue
hsa-mir-126	1.43E-14	-1.263736351	11.408701	-8.216797904	1.42E-15	24.00686812	blue
hsa-mir-143	1.97E-15	-1.19096433	15.33480017	-8.496699792	1.72E-16	26.09010362	blue
hsa-mir-1271	1.77E-08	-1.151616939	1.38773579	-6.030289578	2.95E-09	9.730024188	blue
hsa-mir-193a	3.04E-22	-1.100039928	8.919817617	-10.4425297	1.81E-23	41.98651961	blue
hsa-mir-154	6.10E-10	-1.086598926	2.496604099	-6.617511399	8.47E-11	13.19975035	blue
hsa-mir-129-1	6.67E-06	-1.067460339	0.051214602	-4.876800237	1.40E-06	3.753734485	blue
hsa-mir-101-2	1.83E-11	-1.01285283	5.243751581	-7.186349723	2.10E-12	16.82245967	blue
hsa-mir-150	0.0004184	-0.969870354	9.044082054	-3.899507732	0.000107921	-0.393945971	blue
hsa-mir-1295	5.59E-07	-0.948487829	0.018777801	-5.388418307	1.04E-07	6.263801097	blue
hsa-mir-134	1.05E-07	-0.939027444	8.32495268	-5.705361181	1.87E-08	7.931938019	blue
hsa-mir-1262	3.80E-09	-0.910488195	-0.393214922	-6.298547589	6.03E-10	11.2803588	blue
hsa-mir-190	1.74E-09	-0.840762375	2.007856392	-6.435235483	2.62E-10	12.09286808	blue
hsa-mir-10a	1.86E-05	-0.828326169	14.49066241	-4.638651204	4.36E-06	2.66378001	blue
hsa-mir-127	5.28E-06	-0.764792227	9.602477925	-4.936420659	1.05E-06	4.034463302	blue
hsa-mir-1296	6.57E-06	-0.7624291	2.494415761	-4.887775219	1.33E-06	3.805175936	blue
hsa-mir-1249	9.56E-06	-0.717216994	1.095470442	-4.794468937	2.09E-06	3.371229693	blue
hsa-mir-133b	0.000137307	-0.636009678	-0.458210385	-4.179814591	3.38E-05	0.70712404	blue
hsa-mir-125a	4.14E-07	-0.615980816	9.98214817	-5.44894726	7.56E-08	6.575760151	blue
hsa-let-7b	1.12E-05	-0.589625252	14.49009451	-4.754099959	2.53E-06	3.185872476	blue
hsa-mir-181d	0.001010479	0.599166464	4.323536282	3.662948153	0.000272669	-1.266760174	red
hsa-mir-148a	0.000498607	0.602013505	15.28514829	3.851854093	0.000130588	-0.573941591	red
hsa-mir-18a	0.015892657	0.60729567	2.795431895	2.811064925	0.005108354	-3.974539957	red
hsa-mir-181c	6.65E-06	0.686720349	6.46024297	4.881359671	1.37E-06	3.775092354	red
hsa-mir-15b	1.01E-05	0.68938642	7.528508838	4.779563613	2.24E-06	3.302622391	red
hsa-mir-128-1	9.13E-11	0.715961126	6.168875043	6.923576231	1.20E-11	15.11762098	red
hsa-mir-191	1.51E-06	0.761200355	9.683099008	5.189205209	2.94E-07	5.259358879	red
hsa-mir-128-2	1.28E-11	0.840389801	5.560716448	7.244266078	1.43E-12	17.20534101	red
hsa-mir-188	0.000142944	0.860082083	1.059169553	4.166612091	3.57E-05	0.653647803	red
hsa-mir-103-2	6.10E-10	0.895433661	3.15981178	6.621801615	8.24E-11	13.22612258	red
hsa-mir-148b	5.23E-16	0.978049842	7.309269193	8.675004031	4.36E-17	27.44531235	red
hsa-mir-1307	4.95E-11	1.035639083	10.20874266	7.026660675	6.09E-12	15.78006761	red
hsa-mir-181b-1	2.36E-15	1.113749161	8.332420908	8.467346391	2.15E-16	25.86908586	red
hsa-mir-130b	7.39E-11	1.121830614	4.201001964	6.960748969	9.38E-12	15.35555187	red

hsa-mir-192	1.47E-13	1.123909127	8.55552718	7.889349635	1.57E-14	21.63980882	red
hsa-mir-155	1.20E-09	1.147611291	8.211349377	6.500386925	1.76E-10	12.48544889	red
hsa-mir-181b-2	7.29E-10	1.173047161	1.961826146	6.584486517	1.04E-10	12.99723471	red
hsa-mir-142	4.20E-08	1.277929527	10.60900147	5.871958813	7.34E-09	8.842842251	red
hsa-mir-196a-2	0.000136138	1.295150086	4.358327643	4.185628116	3.30E-05	0.730721947	red
hsa-mir-187	0.002063032	1.325174762	3.062240566	3.467617164	0.000564878	-1.948163332	red
hsa-mir-1269	0.013895145	1.352409327	1.452942689	2.86266782	0.004356018	-3.830139743	red
hsa-mir-1301	6.35E-18	1.599723985	3.625284932	9.243006235	4.79E-19	31.90405031	red
hsa-mir-182	1.19E-44	2.316198114	14.95572933	15.71182415	1.89E-46	94.59483665	red
hsa-mir-196a-1	1.92E-11	2.369780505	8.114862209	7.174296596	2.28E-12	16.74309887	red
hsa-mir-184	2.18E-09	2.548131603	2.807972407	6.39411685	3.38E-10	11.84685944	red
hsa-mir-141	2.11E-43	2.59187846	10.39899259	15.41224551	5.02E-45	91.32776997	red
hsa-mir-190b	2.83E-18	2.758879869	2.816646423	9.355641629	1.91E-19	32.81316671	red
hsa-mir-183	1.73E-57	2.916297708	13.44503591	18.35359572	2.06E-59	124.3287641	red

Table S2. Survival analysis results of miRNAs in HER2-negative breast cancer (Kaplan-Meier method)

Terms	HR [exp(coef)]	coef	95% CI lower	95% CI upper	Z	*P* value
hsa-mir-193a	2.300474238	0.833115292	0.42121371	1.245016874	3.964238154	7.36E-05
hsa-let-7e	2.247998132	0.810040101	0.344010665	1.276069537	3.406757817	6.57E-04
hsa-mir-10b	0.592636557	-0.523173956	-0.865985715	-0.180362198	-2.991152101	0.00277927
hsa-mir-1258	0.359361375	-1.02342678	-1.734234733	-0.312618827	-2.821971282	0.004772945
hsa-mir-125a	1.823253808	0.600622711	0.168260132	1.032985291	2.722712229	0.006474843
hsa-mir-148b	1.907107815	0.645587862	0.174859862	1.116315862	2.688025692	0.007187587
hsa-mir-1248	1.558171065	0.443512739	0.11686712	0.770158358	2.661199	0.007786292
hsa-mir-1290	72.31660511	4.281053772	1.061786611	7.500320934	2.606404125	0.009149844
hsa-mir-130b	1.495381381	0.402381279	0.088250647	0.716511911	2.510588698	0.012053004
hsa-mir-1270-2	1.736422596	0.551827017	0.119898297	0.983755738	2.504026771	0.012278874
hsa-mir-103-2	1.744923205	0.556710546	0.114289966	0.999131125	2.46627908	0.013652492
hsa-mir-1229	1.462034779	0.37982915	0.064374587	0.695283713	2.35993243	0.018278264
hsa-mir-1246	2.616268287	0.961748985	0.162482832	1.761015137	2.358405102	0.018353652
hsa-mir-181b-1	1.488687779	0.397895047	0.064060492	0.731729602	2.336067221	0.019487738
hsa-mir-127	0.649473112	-0.431593842	-0.79649131	-0.066696374	-2.318208432	0.020437996
hsa-mir-185	1.777107163	0.574986853	0.085280377	1.064693329	2.301283686	0.021375601
hsa-let-7d	1.656539247	0.504730635	0.07263509	0.936826181	2.289433152	0.022054198
hsa-mir-196b	1.292488776	0.256569643	0.033689973	0.479449314	2.256227584	0.024056382
hsa-mir-105-1	1.190284816	0.17419262	0.022323222	0.326062018	2.2480583	0.024572473
hsa-mir-1307	1.364083603	0.31048285	0.035238359	0.585727341	2.210889677	0.027043478
hsa-mir-105-2	1.180947449	0.166317039	0.016357501	0.316276577	2.173755744	0.029723484
hsa-mir-1301	1.445030763	0.368130611	0.033085208	0.703176013	2.153507356	0.031278827
hsa-mir-1237	3.592921919	1.278965776	0.110812142	2.447119411	2.145887994	0.031881916
hsa-mir-190b	0.781909095	-0.246016792	-0.478139467	-0.013894117	-2.07728113	0.03777562
Terms	HR [exp(coef)]	coef	95% CI lower	95% CI upper	Z	*P* value
hsa-mir-17	1.367092886	0.312686504	0.017027426	0.608345582	2.072841091	0.038187071
hsa-mir-10a	0.726745122	-0.319179451	-0.623706145	-0.014652757	-2.054270583	0.03994951
hsa-mir-150	0.788259234	-0.237928267	-0.465016836	-0.010839697	-2.053519617	0.040022209
hsa-mir-1306	1.373324014	0.317234089	0.011562443	0.622905735	2.034102268	0.041941285
hsa-mir-192	1.448062567	0.370226502	0.012838893	0.727614111	2.030374284	0.042318509
hsa-mir-101-1	0.630129439	-0.461830022	-0.907786414	-0.015873631	-2.029728081	0.042384187
hsa-mir-1909	3.965022476	1.377511524	0.041089074	2.713933974	2.0202242	0.043360137
hsa-mir-1277	1.628529134	0.487677236	0.011137934	0.964216537	2.005773323	0.044880438
hsa-mir-1270-1	1.527225075	0.423452412	9.78E-04	0.845926599	1.964502218	0.049471879
hsa-mir-1262	0.392503258	-0.935210442	-1.869814639	-6.06E-04	-1.961235345	0.049851576

Table S3. Log-rank statistical tests on 20 overlapping miRNAs

Terms	HR [exp(coef)]	coef	95% CI lower	95% CI upper	Z	*P* value	Log-rank test
hsa-mir-193a	2.300474238	0.833115292	0.42121371	1.245016874	3.964238154	7.36E-05	0.014
hsa-mir-10b	0.592636557	-0.523173956	-0.865985715	-0.180362198	-2.991152101	0.00277927	0.107
hsa-mir-1258	0.359361375	-1.02342678	-1.734234733	-0.312618827	-2.821971282	0.004772945	0.015
hsa-mir-125a	1.823253808	0.600622711	0.168260132	1.032985291	2.722712229	0.006474843	0.088
hsa-mir-148b	1.907107815	0.645587862	0.174859862	1.116315862	2.688025692	0.007187587	0.071
hsa-mir-130b	1.495381381	0.402381279	0.088250647	0.716511911	2.510588698	0.012053004	0.074
hsa-mir-1270-2	1.736422596	0.551827017	0.119898297	0.983755738	2.504026771	0.012278874	0.015
hsa-mir-103-2	1.744923205	0.556710546	0.114289966	0.999131125	2.46627908	0.013652492	0.006
hsa-mir-181b-1	1.488687779	0.397895047	0.064060492	0.731729602	2.336067221	0.019487738	0.202
hsa-mir-127	0.649473112	-0.431593842	-0.79649131	-0.066696374	-2.318208432	0.020437996	0.090
hsa-mir-1307	1.364083603	0.31048285	0.035238359	0.585727341	2.210889677	0.027043478	0.007
hsa-mir-1301	1.445030763	0.368130611	0.033085208	0.703176013	2.153507356	0.031278827	0.060
hsa-mir-190b	0.781909095	-0.246016792	-0.478139467	-0.013894117	-2.07728113	0.03777562	0.024
hsa-mir-10a	0.726745122	-0.319179451	-0.623706145	-0.014652757	-2.054270583	0.03994951	0.353
hsa-mir-150	0.788259234	-0.237928267	-0.465016836	-0.010839697	-2.053519617	0.040022209	0.105
hsa-mir-192	1.448062567	0.370226502	0.012838893	0.727614111	2.030374284	0.042318509	0.038
hsa-mir-1909	3.965022476	1.377511524	0.041089074	2.713933974	2.0202242	0.043360137	0.084
hsa-mir-1277	1.628529134	0.487677236	0.011137934	0.964216537	2.005773323	0.044880438	0.084
hsa-mir-1270-1	1.527225075	0.423452412	9.78E-04	0.845926599	1.964502218	0.049471879	0.745
hsa-mir-1262	0.392503258	-0.935210442	-1.869814639	-6.06E-04	-1.961235345	0.049851576	0.0502

Table S4. Clinical information and miRNA-seq date for statistics

Terms	Time	Status	hsa-mir-193a	hsa-mir-1258	PI	Risk	Group	Patient age	Age level	AGE	Patient stage M	M	Patient stage N	n level	N	Patient stage T	t level	T	Patient pathologic stage	Stage level	Stage	Histological type	HT
TCGA-OL-A5DA	1357	0	6.704312325	1.828473926	3.044	low	0	61	≥ 60	1	mx	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-D8-A1JJ	274	0	8.588259697	3.231887341	3.199	low	0	54	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AR-A24T	1620	0	7.186508179	2.018251896	3.217	low	0	46	< 60	0	m0	0	n3	n2-3	1	t3	t3-4	1	stage iiic	G3-4	1	ILC	0
TCGA-AQ-A7U7	304	0	8.024859428	2.582978487	3.333	low	0	55	< 60	0	m0	0	n2a	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	ILC	0
TCGA-D8-A27I	186	0	7.884914398	2.427578688	3.362	low	0	58	< 60	0	m0	0	n2a	n2-3	1	t1c	t1-2	0	stage iiia	G3-4	1	ILC	0
TCGA-AR-A1AX	1103	0	8.093935013	2.55117774	3.405	low	0	64	≥ 60	1	m0	0	n0	n0-1	0	t1	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-A2-A25A	2968	0	6.973899364	1.543005824	3.45	low	0	44	< 60	0	m0	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-D8-A1JB	365	0	8.642220497	2.759328604	3.607	low	0	54	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E9-A1RI	48	0	8.141786575	2.222064734	3.696	low	0	43	< 60	0	m0	0	n2	n2-3	1	t1c	t1-2	0	stage iiia	G3-4	1	other	2
TCGA-E2-A1B1	1361	0	8.416133881	2.425773382	3.719	low	0	45	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-BH-A0DX	1442	0	9.228347778	3.091762304	3.737	low	0	62	≥ 60	1	m0	0	n0	n0-1	0	t1b	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-D8-A145	49	0	8.255809784	2.258417368	3.744	low	0	80	≥ 60	1	m0	0	n1a	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-A2-A0CV	1870	0	8.07972908	2.106334448	3.746	low	0	41	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-AC-A3YI	47	0	8.081995964	2.107718945	3.746	low	0	74	≥ 60	1	mx	0	n3a	n2-3	1	t1c	t1-2	0	stage iiic	G3-4	1	ILC	0
TCGA-E2-A1B6	338	0	7.501805782	1.607981682	3.752	low	0	44	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E2-A2P5	326	0	8.427605629	2.328629494	3.803	low	0	78	≥ 60	1	m0	0	n3	n2-3	1	t2	t1-2	0	stage iiic	G3-4	1	ILC	0
TCGA-A2-A1FV	461	0	8.09458828	2.036913395	3.81	low	0	74	≥ 60	1	m0	0	n0 (i+)	n0-1	0	t3	t3-4	1	stage iib	G1-2	0	ILC	0
TCGA-AC-A3OD	35	0	7.210938931	1.278107285	3.817	low	0	68	≥ 60	1	mx	0	n1mi	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-D8-A73U	492	0	7.51935482	1.444328427	3.892	low	0	88	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-D8-A1JG	187	0	9.779685974	3.342283964	3.909	low	0	62	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-A1-A0SF	1463	0	8.013496399	1.830838561	3.918	low	0	54	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-A1-A0SI	635	0	8.338135719	2.104475021	3.92	low	0	52	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-AC-A5EH	63	0	8.791529655	2.476408482	3.93	low	0	76	≥ 60	1	mx	0	n1mi	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-D8-A1JU	106	0	8.663034439	2.341204405	3.951	low	0	51	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-A7-A4SE	371	0	7.56045723	1.399690032	3.955	low	0	54	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AC-A2FF	1686	0	8.614374161	2.293997288	3.955	low	0	40	< 60	0	mx	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-AC-A2FK	1180	0	8.937872887	2.531440973	3.985	low	0	45	< 60	0	m0	0	n3a	n2-3	1	t2	t1-2	0	stage iiic	G3-4	1	ILC	0
TCGA-GM-A3XL	1717	0	8.507378578	2.087397337	4.047	low	0	49	< 60	0	m0	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-EW-A424	322	0	7.165463448	0.940889955	4.052	low	0	51	< 60	0	mx	0	n1	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	ILC	0
TCGA-AR-A24S	1888	0	8.328902245	1.899936199	4.075	low	0	61	≥ 60	1	m0	0	n0	n0-1	0	t1	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-D8-A1J8	256	0	7.984126091	1.60506475	4.077	low	0	77	≥ 60	1	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-BH-A0H3	1149	0	7.936556339	1.55081892	4.088	low	0	46	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-GM-A2DA	3650	0	7.812375069	1.42623353	4.103	low	0	46	< 60	0	m0	0	n1b	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E2-A15P	315	0	8.4516716	1.961361766	4.109	low	0	61	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-E2-A14X	692	0	8.07321167	1.639502168	4.109	low	0	55	< 60	0	m0	0	n2	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-BH-A8G0	199	0	7.830341339	1.419642329	4.12	low	0	54	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-BH-A18J	612	1	8.634421349	2.078167439	4.139	low	0	56	< 60	0	m1	1	n2	n2-3	1	t4b	t3-4	1	stage iv	G3-4	1	IDC	1
TCGA-BH-A0W7	558	0	8.407997131	1.885066748	4.14	low	0	49	< 60	0	m0	0	n0 (i-)	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1

TCGA-AC-A5XS	47	0	7.544492245	1.150820851	4.14	low	0	74	≥ 60	1	mx	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-D8-A4Z1	223	0	7.885449409	1.439587474	4.141	low	0	68	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	ILC	0
TCGA-BH-A5J0	225	0	7.592204571	1.187735319	4.143	low	0	63	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-BH-A0C1	1339	0	8.205407143	1.678423524	4.167	low	0	61	≥ 60	1	m0	0	n2a	n2-3	1	t3	t3-4	1	stage iiia	G3-4	1	ILC	0
TCGA-E2-A1L7	633	0	7.655369282	1.211277604	4.167	low	0	40	< 60	0	m0	0	n2	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-AR-A2LM	1218	0	7.943893909	1.385086417	4.223	low	0	49	< 60	0	m0	0	n1	n0-1	0	t1	t1-2	0	stage ii	G1-2	0	ILC	0
TCGA-A2-A0ES	1001	0	8.881971359	2.180293798	4.224	low	0	52	< 60	0	m0	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-GM-A2DD	1309	0	8.905488968	2.17519784	4.244	low	0	53	< 60	0	m0	0	n0 (i-)	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-E2-A1B5	774	0	8.465802193	1.795914054	4.248	low	0	46	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-E2-A1LG	350	0	6.984338284	0.531522691	4.254	low	0	50	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-AR-A1AK	1559	0	7.86212635	1.276415706	4.254	low	0	70	≥ 60	1	m0	0	n0	n0-1	0	t1	t1-2	0	stage i	G1-2	0	ILC	0
TCGA-AR-A1AJ	1605	0	8.632853508	1.920543313	4.262	low	0	83	≥ 60	1	m0	0	n0	n0-1	0	t1	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-OL-A66K	1021	0	7.773662567	1.16517818	4.282	low	0	72	≥ 60	1	mx	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-BH-A0E9	1405	0	8.873277664	2.097609043	4.283	low	0	53	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-E9-A243	43	0	8.16685009	1.480222225	4.297	low	0	52	< 60	0	m0	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AR-A255	1059	0	8.191746712	1.494511366	4.303	low	0	62	≥ 60	1	m0	0	n0	n0-1	0	t1	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-AR-A2LE	3650	0	7.803832054	1.161934853	4.305	low	0	69	≥ 60	1	m0	0	n0	n0-1	0	t1	t1-2	0	stage i	G1-2	0	ILC	0
TCGA-GM-A5PV	412	0	8.694237709	1.912259698	4.31	low	0	63	≥ 60	1	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-AR-A24Q	2009	0	8.610416412	1.820239067	4.326	low	0	49	< 60	0	m0	0	n0	n0-1	0	t3	t3-4	1	stage iib	G1-2	0	IDC	1
TCGA-D8-A1JD	273	0	8.196146011	1.462287903	4.331	low	0	41	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-AR-A2LH	616	1	8.096535683	1.374345183	4.334	low	0	55	< 60	0	m0	0	n3	n2-3	1	t3	t3-4	1	stage iii	G3-4	1	ILC	0
TCGA-D8-A27V	73	0	7.651470661	0.963878751	4.359	low	0	62	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-GM-A2DI	1883	0	8.4295578	1.615978956	4.366	low	0	52	< 60	0	m0	0	n0 (i+)	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-GM-A3XG	982	0	8.160068512	1.387145758	4.366	low	0	46	< 60	0	m0	0	n1a	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	ILC	0
TCGA-AR-A2LO	633	0	7.76875782	1.053587556	4.367	low	0	46	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-D8-A27M	145	0	9.248347282	2.305301189	4.371	low	0	59	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-D8-A27L	126	0	8.164271355	1.381189227	4.374	low	0	49	< 60	0	m0	0	n2a	n2-3	1	t1c	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-OL-A66I	714	0	8.512921333	1.674696565	4.375	low	0	36	< 60	0	mx	0	n1mi	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AR-A2LQ	516	0	8.784239769	1.901473522	4.378	low	0	59	< 60	0	m0	0	n0	n0-1	0	t3	t3-4	1	stage iib	G1-2	0	ILC	0
TCGA-BH-A0DV	1374	0	8.428436279	1.594880462	4.382	low	0	54	< 60	0	m0	0	n2a	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-BH-A0BF	782	0	8.125274658	1.328884125	4.389	low	0	56	< 60	0	m0	0	n1mi	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-D8-A3Z5	441	0	8.284176826	1.457912087	4.393	low	0	54	< 60	0	m0	0	n3a	n2-3	1	t2	t1-2	0	stage iiic	G3-4	1	ILC	0
TCGA-D8-A1JF	96	0	8.777215958	1.874160767	4.395	low	0	79	≥ 60	1	m0	0	n2a	n2-3	1	t1c	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-GM-A5PX	551	0	7.846510887	1.081916332	4.397	low	0	65	≥ 60	1	m0	0	n1mi	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-A7-A13H	551	0	8.100128174	1.283409119	4.408	low	0	61	≥ 60	1	mx	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-E2-A14U	838	0	9.193198204	2.159472466	4.449	low	0	74	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	ILC	0
TCGA-5L-AAT1	1471	0	7.563589573	0.774080634	4.45	low	0	63	≥ 60	1	m1	1	n0	n0-1	0	t2	t1-2	0	stage iv	G3-4	1	ILC	0
TCGA-D8-A1XS	50	0	8.14766407	1.26658988	4.453	low	0	48	< 60	0	m0	0	n3a	n2-3	1	t2	t1-2	0	stage iiic	G3-4	1	other	2
TCGA-E2-A1IH	658	0	8.343224525	1.418885589	4.464	low	0	80	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	ILC	0
TCGA-E2-A14S	834	0	7.966282845	1.075225115	4.482	low	0	65	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-BH-A0B6	1732	0	8.326242447	1.376180291	4.486	low	0	47	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-GM-A4E0	1753	0	8.974456787	1.917882323	4.493	low	0	67	≥ 60	1	m0	0	n3a	n2-3	1	t3	t3-4	1	stage iiic	G3-4	1	ILC	0

TCGA-BH-A8FZ	144	0	8.119084358	1.18814075	4.495	low	0	58	< 60	0	m0	0	n0	n0-1	0	t1b	t1-2	0	stage ia	G1-2	0	ILC	0
TCGA-AR-A24M	1991	0	8.725231171	1.694722414	4.502	low	0	38	< 60	0	m0	0	n2	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	other	2
TCGA-OL-A5D6	385	0	8.376480103	1.397358418	4.503	low	0	71	≥ 60	1	mx	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-OL-A5RU	841	0	9.256131172	2.121231556	4.521	low	0	63	≥ 60	1	mx	0	n1	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-BH-A0H5	1080	0	8.70002079	1.647209525	4.522	low	0	45	< 60	0	m0	0	n0 (i-)	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-AC-A2FG	1125	0	8.813105583	1.73014605	4.533	low	0	79	≥ 60	1	mx	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-BH-A42U	3324	0	8.227163315	1.227113843	4.537	low	0	80	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-D8-A27T	136	0	8.083371162	1.102193236	4.539	low	0	53	< 60	0	m0	0	n3a	n2-3	1	t2	t1-2	0	stage iiic	G3-4	1	ILC	0
TCGA-MS-A51U	85	0	8.496385574	1.439669847	4.55	low	0	44	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-AC-A2B8	45	0	8.975340843	1.842463255	4.553	low	0	84	≥ 60	1	m0	0	n0 (i-)	n0-1	0	t3	t3-4	1	stage iib	G1-2	0	ILC	0
TCGA-E2-A14N	1350	0	9.071447372	1.909910917	4.564	low	0	37	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-BH-A0BZ	1492	0	9.505978584	2.277034044	4.565	low	0	59	< 60	0	m0	0	n1a	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	IDC	1
TCGA-EW-A3E8	647	0	8.14336586	1.117078662	4.568	low	0	60	≥ 60	1	mx	0	n0	n0-1	0	t3	t3-4	1	stage iib	G1-2	0	ILC	0
TCGA-GM-A2DO	1623	0	8.482867241	1.39761734	4.574	low	0	54	< 60	0	m0	0	n0 (i-)	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	ILC	0
TCGA-AR-A2LJ	1359	0	8.619842529	1.499749541	4.585	low	0	40	< 60	0	mx	0	n1	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	ILC	0
TCGA-D8-A13Y	264	0	6.86320734	0	4.591	low	0	52	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-OL-A6VO	480	0	7.563552856	0.555085838	4.623	low	0	43	< 60	0	mx	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-AR-A1AW	1072	0	7.851240635	0.796530426	4.625	low	0	65	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-BH-A0DO	525	0	8.623994827	1.448798895	4.628	low	0	78	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-BH-A0BT	1386	0	8.731268883	1.538811803	4.629	low	0	56	< 60	0	m0	0	n1mi	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E2-A576	578	0	7.686409473	0.632777274	4.644	low	0	69	≥ 60	1	mx	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	ILC	0
TCGA-E2-A14Z	518	0	9.081979752	1.809140682	4.65	low	0	64	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-E2-A1BD	317	0	8.920548439	1.66333735	4.657	low	0	53	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-HN-A2NL	79	0	6.963218212	0	4.658	low	0	56	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-BH-A0DI	673	0	8.461247444	1.271337867	4.659	low	0	63	≥ 60	1	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E2-A1IF	956	0	8.759508133	1.509848952	4.67	low	0	74	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-OL-A66N	413	0	8.502440453	1.290024519	4.672	low	0	59	< 60	0	mx	0	n3	n2-3	1	t3	t3-4	1	stage iiic	G3-4	1	ILC	0
TCGA-GM-A2DB	1616	0	8.480732918	1.265486717	4.676	low	0	62	≥ 60	1	m0	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-B6-A1KI	1463	0	8.362722397	1.149082541	4.689	low	0	63	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-HN-A2OB	1849	0	7.989714146	0.804298937	4.711	low	0	45	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-AR-A0TS	1138	0	8.795694351	1.48290813	4.716	low	0	46	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E2-A1II	850	0	7.063110828	0	4.725	low	0	51	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-AR-A1AM	1903	0	8.581820488	1.282062531	4.731	low	0	52	< 60	0	m0	0	n1	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	ILC	0
TCGA-AR-A2LR	620	0	9.013122559	1.648028731	4.731	low	0	49	< 60	0	m0	0	n0	n0-1	0	t1	t1-2	0	stage i	G1-2	0	other	2
TCGA-PE-A5DD	1953	0	7.418836594	0.286631644	4.737	low	0	64	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-A2-A1G6	132	0	8.732152939	1.39514339	4.742	low	0	50	< 60	0	m0	0	n2a	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-E2-A1IK	519	0	8.407551765	1.117802739	4.744	low	0	71	≥ 60	1	m0	0	n1mi	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-OL-A66L	945	0	8.980583191	1.600690246	4.747	low	0	71	≥ 60	1	mx	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-BH-A0DG	713	0	9.313995361	1.846943736	4.776	low	0	30	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AR-A1AL	1485	0	8.69402504	1.308364272	4.785	low	0	60	≥ 60	1	m0	0	n1	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	ILC	0
TCGA-D8-A1XL	319	0	8.708683014	1.319617271	4.786	low	0	34	< 60	0	mx	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-BH-A0DE	948	0	8.650514603	1.259581685	4.795	low	0	62	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1

TCGA-D8-A1JH	284	0	8.614850044	1.228833318	4.795	low	0	56	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-AR-A1AR	524	1	8.700772285	1.298594952	4.798	low	0	50	< 60	0	m0	0	n2	n2-3	1	t1	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-OL-A5RZ	313	0	7.495112419	0.266851306	4.804	low	0	57	< 60	0	mx	0	n0	n0-1	0	t1b	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-A7-A6VX	169	0	7.969227314	0.669085741	4.804	low	0	68	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-D8-A1JC	178	0	9.263747215	1.761072993	4.81	low	0	59	< 60	0	m0	0	n2a	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-OL-A5RW	797	0	7.749851704	0.473507464	4.812	low	0	40	< 60	0	mx	0	n1	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E2-A1LA	463	0	8.912524223	1.459139347	4.813	low	0	59	< 60	0	m0	0	n1a	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-D8-A3Z6	185	0	8.924263954	1.466589093	4.815	low	0	56	< 60	0	m0	0	n3a	n2-3	1	t3	t3-4	1	stage iiic	G3-4	1	ILC	0
TCGA-D8-A142	61	0	9.454319	1.898545861	4.829	low	0	74	≥ 60	1	m0	0	n0	n0-1	0	t3	t3-4	1	stage iib	G1-2	0	IDC	1
TCGA-E2-A15C	497	0	8.575097084	1.148755908	4.832	low	0	61	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-E2-A1B4	911	0	8.274359703	0.890425742	4.834	low	0	74	≥ 60	1	m0	0	n2a	n2-3	1	t1c	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-E2-A14Q	974	0	8.137966156	0.771487534	4.836	low	0	50	< 60	0	m0	0	n1mi	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-AQ-A1H3	162	0	8.790895462	1.321522951	4.84	low	0	49	< 60	0	mx	0	n3a	n2-3	1	t2	t1-2	0	stage iiic	G3-4	1	IDC	1
TCGA-E2-A158	450	0	7.234470844	0	4.84	low	0	43	< 60	0	m0	0	n1mi	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-BH-A0BR	1633	0	8.916036606	1.42519021	4.842	low	0	59	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-BH-A18Q	1692	1	8.28741169	0.890054405	4.843	low	0	56	< 60	0	m0	0	n1b	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-OL-A66H	413	0	7.97357893	0.621427953	4.845	low	0	74	≥ 60	1	mx	0	n1mi	n0-1	0	t1c	t1-2	0	stage ib	G1-2	0	other	2
TCGA-D8-A1XR	168	0	8.074830055	0.702778995	4.848	low	0	56	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-BH-A0AZ	867	0	8.495718956	1.050000668	4.856	low	0	47	< 60	0	cm0 (i+)	0	n1a	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	IDC	1
TCGA-A2-A4S3	104	0	8.340307236	0.894771993	4.875	low	0	59	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-AR-A1AO	1325	0	9.036178589	1.481019855	4.878	low	0	47	< 60	0	m0	0	n1	n0-1	0	t1	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-OL-A5RV	733	0	8.356063843	0.90170145	4.88	low	0	43	< 60	0	mx	0	n3	n2-3	1	t2	t1-2	0	stage iiic	G3-4	1	IDC	1
TCGA-AC-A8OP	53	0	7.524414063	0.195610851	4.88	low	0	72	≥ 60	1	mx	0	n0 (i-)	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-D8-A1XO	242	0	8.654829979	1.141381264	4.891	low	0	56	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-LD-A9QF	266	0	9.324118614	1.707920074	4.892	low	0	73	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-AC-A2QH	31	0	8.067434311	0.639633179	4.893	low	0	58	< 60	0	mx	0	n0	n0-1	0	t3	t3-4	1	stage iib	G1-2	0	other	2
TCGA-EW-A6SC	952	0	8.660534859	1.134879947	4.9	low	0	60	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-XX-A899	292	0	8.599254608	1.076329231	4.905	low	0	46	< 60	0	mx	0	n2a	n2-3	1	t1c	t1-2	0	stage iiia	G3-4	1	ILC	0
TCGA-AC-A8OS	70	0	8.753499031	1.207122445	4.905	low	0	71	≥ 60	1	mx	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-D8-A1Y3	125	0	8.6900177	1.151639342	4.906	low	0	61	≥ 60	1	mx	0	n2a	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-BH-A0B7	1733	0	9.86679554	2.114708424	4.934	low	0	42	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-D8-A1XG	75	0	8.879861832	1.27004087	4.94	low	0	86	≥ 60	1	m0	0	n1a	n0-1	0	t4b	t3-4	1	stage iiib	G3-4	1	IDC	1
TCGA-E2-A159	515	0	8.411216736	0.869374692	4.942	low	0	50	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-D8-A73X	368	0	8.132468224	0.629992545	4.944	low	0	53	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	other	2
TCGA-GM-A2DH	1286	0	9.280828476	1.59839952	4.949	low	0	58	< 60	0	m0	0	n0 (i+)	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-A2-A1G1	371	0	8.697769165	1.102627277	4.95	low	0	85	≥ 60	1	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-A2-A04U	671	0	7.404290199	0	4.953	low	0	47	< 60	0	m0	0	n0 (i+)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-GM-A2DN	2352	0	8.901628494	1.26648736	4.957	low	0	58	< 60	0	m0	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AR-A24L	2221	0	7.936450481	0.441191316	4.962	low	0	26	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-BH-A0BG	756	0	9.488158226	1.757283211	4.963	low	0	73	≥ 60	1	m0	0	n0	n0-1	0	t1	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-AC-A2FE	791	0	8.450964928	0.869569004	4.968	low	0	62	≥ 60	1	mx	0	n3a	n2-3	1	t3	t3-4	1	stage iiic	G3-4	1	ILC	0
TCGA-D8-A27N	146	0	8.989034653	1.321711659	4.972	low	0	36	< 60	0	m0	0	n2a	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1

TCGA-AC-A2BM	1162	0	8.965544701	1.299470305	4.974	low	0	41	< 60	0	mx	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E2-A56Z	219	0	7.775541306	0.280826837	4.981	low	0	69	≥ 60	1	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E2-A150	591	0	9.264579773	1.534656286	4.989	low	0	48	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-D8-A1XK	326	0	8.416359901	0.809668839	4.993	low	0	55	< 60	0	mx	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E2-A14Y	688	0	8.46383667	0.838058591	5.002	low	0	35	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E2-A15G	316	0	8.947032928	1.244935155	5.005	low	0	76	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	other	2
TCGA-E2-A1LL	1014	0	8.596923828	0.939100921	5.011	low	0	73	≥ 60	1	mx	0	n2a	n2-3	1	t3	t3-4	1	stage iiia	G3-4	1	IDC	1
TCGA-BH-A18K	2763	1	8.428283691	0.786939204	5.018	low	0	46	< 60	0	m0	0	n0	n0-1	0	t1	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-AR-A2LN	520	0	8.755438805	1.052853227	5.028	low	0	65	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-E2-A570	549	0	8.508002281	0.835677564	5.033	low	0	47	< 60	0	m0	0	n1mi	n0-1	0	t1c	t1-2	0	stage ib	G1-2	0	IDC	1
TCGA-BH-A0BQ	827	0	8.528814316	0.844429851	5.04	low	0	39	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-D8-A1XQ	177	0	8.304536819	0.645990252	5.047	low	0	69	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-A1-A0SN	1196	0	7.552363396	0	5.053	low	0	50	< 60	0	mx	0	n1	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E2-A14R	845	0	8.459001541	0.750188053	5.068	low	0	62	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-XX-A89A	278	0	8.856752396	1.082603216	5.072	low	0	68	≥ 60	1	mx	0	n0	n0-1	0	t3	t3-4	1	stage iib	G1-2	0	ILC	0
TCGA-B6-A2IU	3650	0	8.674161911	0.923143089	5.076	low	0	62	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-GM-A3NW	2982	0	9.004037857	1.17736733	5.096	low	0	63	≥ 60	1	m0	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-EW-A3U0	229	0	8.279994965	0.56043911	5.098	low	0	61	≥ 60	1	m0	0	n1a	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	IDC	1
TCGA-D8-A13Z	210	0	8.976247787	1.141020656	5.106	low	0	51	< 60	0	m0	0	n2a	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-GM-A2DL	2763	0	8.630810738	0.841878891	5.111	low	0	50	< 60	0	m0	0	n0 (i-)	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-BH-AB28	185	0	7.911342144	0.229405746	5.112	low	0	53	< 60	0	m0	0	n1a	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	ILC	0
TCGA-OL-A5RX	513	0	8.603832245	0.808560431	5.119	low	0	51	< 60	0	mx	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-E2-A15K	34	0	8.877385139	1.038835168	5.12	low	0	58	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-BH-A0EI	743	0	8.301211357	0.543471098	5.125	low	0	51	< 60	0	m0	0	n1a	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-BH-A0DT	1170	0	8.725854874	0.903282046	5.126	low	0	41	< 60	0	m0	0	n1a	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-A2-A04W	1918	0	8.682147026	0.863122463	5.128	low	0	50	< 60	0	m0	0	n1mi	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	other	2
TCGA-E9-A6HE	92	0	8.15112114	0.410550594	5.13	low	0	45	< 60	0	mx	0	n3	n2-3	1	t3	t3-4	1	stage iiic	G3-4	1	ILC	0
TCGA-EW-A6SA	510	0	7.670750618	0	5.132	low	0	59	< 60	0	mx	0	n0 (i+)	n0-1	0	t2	t1-2	0	stage ii	G1-2	0	IDC	1
TCGA-A7-A4SC	215	0	8.174604416	0.426542848	5.133	low	0	62	≥ 60	1	mx	0	n0	n0-1	0	t3	t3-4	1	stage iib	G1-2	0	ILC	0
TCGA-E2-A1IN	392	0	8.446913719	0.651155055	5.138	low	0	60	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-BH-A0BP	1481	0	9.216281891	1.301757455	5.14	low	0	76	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-AR-A1AH	2298	0	7.691013813	0	5.145	low	0	51	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-A7-A4SD	168	0	7.703917503	0	5.154	low	0	52	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E2-A15E	518	0	8.807544708	0.936764956	5.154	low	0	40	< 60	0	m0	0	n1a	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-BH-A0BO	1085	0	8.720304489	0.856569886	5.159	low	0	54	< 60	0	m0	0	n0	n0-1	0	t1b	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-E2-A14P	487	0	8.81045723	0.927932918	5.163	low	0	79	≥ 60	1	m0	0	n3	n2-3	1	t2	t1-2	0	stage iiic	G3-4	1	IDC	1
TCGA-E2-A574	605	0	8.439785957	0.602477789	5.171	high	1	44	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E9-A1RF	38	0	8.896080017	0.989371538	5.172	high	1	68	≥ 60	1	m0	0	n2	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-BH-A2L8	168	0	8.320915222	0.49786377	5.174	high	1	45	< 60	0	m0	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-D8-A1JP	167	0	8.869100571	0.952930689	5.183	high	1	73	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-BH-A0AV	1180	0	8.714212418	0.819325626	5.184	high	1	52	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-D8-A1XD	155	0	9.055874825	1.100888133	5.191	high	1	36	< 60	0	m0	0	n2a	n2-3	1	t1c	t1-2	0	stage iiia	G3-4	1	IDC	1

TCGA-C8-A27A	371	0	9.273570061	1.271405339	5.202	high	1	48	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-D8-A141	113	0	8.936400414	0.983924985	5.203	high	1	40	< 60	0	m0	0	n1	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-OL-A5D7	1416	0	7.815629482	0	5.229	high	1	70	≥ 60	1	mx	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AC-A6IV	36	0	9.196909904	1.167366385	5.233	high	1	47	< 60	0	mx	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-AR-A24V	1648	0	9.074800491	1.053401232	5.241	high	1	52	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E2-A15M	235	0	8.792060852	0.804257691	5.248	high	1	66	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-AC-A2FO	1542	0	9.501763344	1.392549276	5.259	high	1	65	≥ 60	1	mx	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-BH-A0DL	1467	0	8.621970177	0.642837465	5.262	high	1	64	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	other	2
TCGA-D8-A1XU	150	0	8.390404701	0.438456863	5.268	high	1	56	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-GM-A3NY	743	0	8.726724625	0.688272536	5.296	high	1	72	≥ 60	1	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-BH-A0HA	856	0	9.075992584	0.974821568	5.304	high	1	31	< 60	0	m0	0	n0 (i-)	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-AR-A254	1212	0	9.131616592	1.019148827	5.306	high	1	50	< 60	0	m0	0	n2	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-A7-A6VY	125	0	8.367227554	0.360969901	5.313	high	1	48	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E2-A15H	42	0	8.331831932	0.325290918	5.318	high	1	38	< 60	0	m0	0	n1mi	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-LL-A5YO	97	0	7.951778412	0	5.32	high	1	50	< 60	0	mx	0	n0	n0-1	0	t1b	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-AC-A3QP	286	0	8.216109276	0.221608654	5.322	high	1	79	≥ 60	1	mx	0	n1mi	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-BH-A6R9	160	0	7.956700325	0	5.323	high	1	61	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	other	2
TCGA-OL-A66O	220	0	9.800347328	1.556028128	5.33	high	1	39	< 60	0	mx	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-AC-A23E	72	0	8.509255409	0.457269639	5.332	high	1	50	< 60	0	mx	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-BH-A1EN	2127	1	8.001235008	0	5.353	high	1	78	≥ 60	1	m0	0	nx	nx	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E2-A1IU	127	0	8.819758415	0.689133584	5.357	high	1	60	≥ 60	1	m0	0	n0 (mol+)	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-BH-A18P	921	1	8.803372383	0.669405103	5.362	high	1	60	≥ 60	1	m0	0	n0	n0-1	0	t1	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-D8-A1XW	118	0	8.468405724	0.378037602	5.367	high	1	53	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-OL-A66P	58	0	9.108762741	0.91569221	5.372	high	1	75	≥ 60	1	mx	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-OL-A5S0	298	0	9.327123642	1.094729304	5.377	high	1	66	≥ 60	1	mx	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-A7-A3J1	75	0	8.316170692	0.233322427	5.38	high	1	63	≥ 60	1	mx	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	ILC	0
TCGA-A2-A3XZ	973	0	8.564442635	0.43939656	5.383	high	1	46	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-BH-A6R8	293	0	8.730293274	0.580120385	5.383	high	1	46	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-D8-A1JE	57	0	8.479441643	0.366921395	5.384	high	1	62	≥ 60	1	m0	0	n1a	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E2-A1L6	1312	0	8.689026833	0.544473529	5.384	high	1	44	< 60	0	m0	0	n1mi	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-A2-A1FW	221	0	9.440172195	1.176508546	5.388	high	1	62	≥ 60	1	m0	0	n2a	n2-3	1	t3	t3-4	1	stage iiia	G3-4	1	IDC	1
TCGA-A2-A0D3	736	0	8.620117188	0.467306644	5.399	high	1	42	< 60	0	m0	0	n0 (i-)	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-D8-A27K	119	0	9.164075851	0.926321328	5.401	high	1	47	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E9-A1R5	42	0	8.844964027	0.650094569	5.405	high	1	63	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-D8-A1Y2	73	0	9.218729019	0.961932898	5.409	high	1	71	≥ 60	1	mx	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-A2-A3XY	786	0	9.549557686	1.240942001	5.411	high	1	49	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-BH-A5IZ	98	0	8.103378296	0	5.421	high	1	51	< 60	0	cm0 (i+)	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-D8-A1J9	248	0	10.42304134	1.969056487	5.421	high	1	48	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-BH-A0AU	746	0	9.459210396	1.137606621	5.432	high	1	45	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-D8-A1JL	265	0	8.859676361	0.621412814	5.437	high	1	72	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AR-A1AN	1330	0	8.129159927	0	5.438	high	1	46	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-GM-A2DF	1299	0	8.828961372	0.591673672	5.44	high	1	53	< 60	0	m0	0	n1a	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1

TCGA-AR-A252	1236	0	9.654634476	1.286313415	5.445	high	1	50	< 60	0	m0	0	n0	n0-1	0	t1	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-AR-A24N	2074	0	8.629296303	0.415327102	5.446	high	1	54	< 60	0	m0	0	n0	n0-1	0	t1	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-AC-A3W7	192	0	8.730671883	0.492743284	5.453	high	1	66	≥ 60	1	mx	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-E2-A573	677	0	8.465589523	0.263790429	5.456	high	1	48	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-E9-A1RG	35	0	8.680361748	0.440871447	5.46	high	1	62	≥ 60	1	m0	0	n2	n2-3	1	t1c	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-A2-A0CW	1750	0	9.847499847	1.428431869	5.462	high	1	67	≥ 60	1	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E2-A150	396	0	8.175821304	0	5.47	high	1	89	≥ 60	1	m0	0	nx	nx	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-BH-A0BS	1641	0	9.130701065	0.808517635	5.471	high	1	55	< 60	0	m0	0	n1c	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	IDC	1
TCGA-BH-A28O	324	0	9.056553841	0.742953062	5.473	high	1	50	< 60	0	m0	0	n3	n2-3	1	t3a	t3-4	1	stage iiic	G3-4	1	ILC	0
TCGA-E2-A15S	274	0	8.927440643	0.631359458	5.475	high	1	34	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-D8-A1XZ	121	0	8.909020424	0.613041222	5.477	high	1	81	≥ 60	1	mx	0	n2a	n2-3	1	t1c	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-E2-A15R	330	0	8.793557167	0.501529872	5.488	high	1	64	≥ 60	1	m0	0	n1a	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E9-A1R3	64	0	8.940176964	0.622253835	5.491	high	1	70	≥ 60	1	m0	0	n3	n2-3	1	t2	t1-2	0	stage iiic	G3-4	1	IDC	1
TCGA-AQ-A1H2	230	0	8.647717476	0.367032081	5.496	high	1	84	≥ 60	1	mx	0	n2a	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-AQ-A0Y5	172	1	10.39227962	1.847038746	5.497	high	1	70	≥ 60	1	mx	0	n2a	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-D8-A73W	244	0	8.878725052	0.559176564	5.499	high	1	79	≥ 60	1	mx	0	n1a	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	other	2
TCGA-BH-A0BL	1340	0	9.069063187	0.717864871	5.502	high	1	35	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-D8-A1JT	123	0	8.255728722	0	5.523	high	1	70	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	other	2
TCGA-AO-A12D	1948	0	9.44465065	1.004503608	5.527	high	1	43	< 60	0	m0	0	n1a	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-D8-A1XB	201	0	8.745893478	0.410854489	5.527	high	1	62	≥ 60	1	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-BH-A0HL	72	0	8.269708633	0	5.532	high	1	56	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E9-A1R7	34	0	9.375757217	0.938249707	5.533	high	1	64	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-BH-A18R	1142	1	8.29445076	0	5.549	high	1	50	< 60	0	m0	0	n1	n0-1	0	t2b	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AC-A3TM	93	0	8.846169472	0.463181973	5.553	high	1	50	< 60	0	m0	0	n1mi	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	ILC	0
TCGA-E2-A153	586	0	9.385015488	0.909972012	5.562	high	1	51	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-AO-A12H	863	0	8.613758087	0.248250589	5.567	high	1	69	≥ 60	1	m0	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	other	2
TCGA-E2-A1IE	983	0	9.557587624	1.038963556	5.575	high	1	61	≥ 60	1	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-BH-A0EA	991	1	9.433574677	0.925302148	5.582	high	1	72	≥ 60	1	m0	0	n1a	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-3C-AALI	3650	0	9.002483368	0.557705104	5.583	high	1	50	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-AC-A3TN	34	0	9.224144936	0.732857823	5.593	high	1	75	≥ 60	1	mx	0	n0	n0-1	0	t3	t3-4	1	stage iib	G1-2	0	ILC	0
TCGA-A7-A26G	210	0	8.378512383	0	5.605	high	1	50	< 60	0	m0	0	n0 (i+)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	other	2
TCGA-AR-A24K	1548	0	8.749916077	0.314874023	5.606	high	1	46	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AC-A8OQ	34	0	8.875937462	0.41209209	5.613	high	1	72	≥ 60	1	mx	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-A7-A26H	65	0	8.890634537	0.421709687	5.616	high	1	72	≥ 60	1	m0	0	n1a	n0-1	0	t1	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-GI-A2C9	711	0	9.33788681	0.796845257	5.619	high	1	58	< 60	0	mx	0	n0	n0-1	0	t3	t3-4	1	stage iib	G1-2	0	IDC	1
TCGA-A1-A0SG	434	0	9.299485207	0.761422276	5.621	high	1	61	≥ 60	1	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	other	2
TCGA-AC-A6NO	51	0	8.702723503	0.25040251	5.625	high	1	43	< 60	0	mx	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-A2-A04N	3153	0	8.956708908	0.461615592	5.628	high	1	66	≥ 60	1	m0	0	n0 (i-)	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-AO-A12B	2359	0	8.42666626	0	5.637	high	1	63	≥ 60	1	m0	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AR-A1AY	615	0	9.118008614	0.585518241	5.639	high	1	65	≥ 60	1	m0	0	n0	n0-1	0	t1	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-E2-A9RU	280	0	8.772389412	0.285712361	5.644	high	1	90	≥ 60	1	mx	0	n3a	n2-3	1	t2	t1-2	0	stage iiic	G3-4	1	IDC	1
TCGA-A7-A13F	196	0	8.436728477	0	5.644	high	1	44	< 60	0	m0	0	n1a	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	IDC	1

TCGA-AR-A24W	1550	0	9.367173195	0.788938701	5.645	high	1	55	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-OL-A6VR	848	0	9.29232502	0.718016446	5.651	high	1	48	< 60	0	mx	0	n0	n0-1	0	t1b	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-BH-A18V	1556	1	9.443917274	0.825286627	5.668	high	1	48	< 60	0	m0	0	n1b	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-GM-A3XN	1641	0	9.399993896	0.777132273	5.676	high	1	44	< 60	0	m0	0	n2a	n2-3	1	t1c	t1-2	0	stage iiia	G3-4	1	ILC	0
TCGA-AR-A1AQ	1310	0	8.485261917	0	5.677	high	1	49	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AR-A24X	1465	0	8.488562584	0	5.679	high	1	52	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	other	2
TCGA-E9-A1R6	84	0	8.723937988	0.192695409	5.684	high	1	63	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-A7-A0DA	373	0	8.917995453	0.351975381	5.689	high	1	62	≥ 60	1	m0	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-BH-A0C3	1464	0	9.79355526	1.091817617	5.692	high	1	47	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	other	2
TCGA-AR-A1AI	1881	0	9.567324638	0.884837806	5.703	high	1	47	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	other	2
TCGA-BH-A0C7	1305	0	9.38038826	0.721243978	5.707	high	1	48	< 60	0	m0	0	n1mi	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E9-A1RE	47	0	9.641051292	0.928617418	5.718	high	1	74	≥ 60	1	m0	0	n2	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-AC-A23G	330	0	8.552757263	0	5.722	high	1	76	≥ 60	1	mx	0	n1	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-AR-A24H	3333	0	8.565556526	0	5.73	high	1	65	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-AR-A1AV	1295	0	8.569067001	0	5.733	high	1	68	≥ 60	1	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-AQ-A54O	665	0	8.574037552	0	5.736	high	1	51	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AO-A03V	886	0	8.836987495	0.220955253	5.738	high	1	41	< 60	0	m0	0	n0 (i-)	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-BH-A0DD	1394	0	9.644135475	0.903088391	5.74	high	1	58	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-A2-A3XX	1168	0	9.04607296	0.374154776	5.757	high	1	49	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-D8-A146	344	0	8.618579865	0	5.766	high	1	57	< 60	0	mx	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-B6-A1KF	3088	0	8.655327797	0	5.79	high	1	68	≥ 60	1	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-A1-A0SQ	554	0	9.501366615	0.693806827	5.81	high	1	45	< 60	0	mx	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-AC-A62X	34	0	8.703565598	0	5.823	high	1	72	≥ 60	1	mx	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-D8-A27F	106	0	9.297967911	0.504279792	5.823	high	1	40	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AR-A24R	1746	0	9.202594757	0.418038785	5.827	high	1	45	< 60	0	m0	0	n2	n2-3	1	t1	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-AQ-A54N	78	0	8.710630417	0	5.827	high	1	51	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-D8-A27G	210	0	9.027197838	0.26818645	5.828	high	1	75	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-D8-A1XA	274	0	9.302192688	0.500748038	5.829	high	1	64	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-3C-AALJ	1228	0	9.056752205	0.286033005	5.834	high	1	62	≥ 60	1	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-A7-A13G	208	0	8.723700523	0	5.836	high	1	79	≥ 60	1	mx	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E2-A152	588	0	8.727942467	0	5.839	high	1	56	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-D8-A1XJ	352	0	9.736515999	0.839999139	5.852	high	1	76	≥ 60	1	mx	0	n1a	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	other	2
TCGA-E2-A1LB	972	0	9.544584274	0.676554441	5.852	high	1	41	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E2-A14T	890	0	9.111347198	0.30689916	5.854	high	1	52	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-D8-A1JK	109	0	8.795489311	0	5.884	high	1	90	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-D8-A1JN	217	0	8.808962822	0	5.893	high	1	80	≥ 60	1	mx	0	n3a	n2-3	1	t3	t3-4	1	stage iiic	G3-4	1	ILC	0
TCGA-BH-A18N	1148	1	8.822987556	0	5.903	high	1	88	≥ 60	1	m0	0	n1b	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-A2-A3XT	2238	0	9.329408646	0.415971756	5.914	high	1	45	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-A1-A0SB	259	0	8.853712082	0	5.923	high	1	70	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	other	2
TCGA-GM-A2DM	2331	0	8.869756699	0	5.934	high	1	57	< 60	0	m0	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E2-A15D	316	0	8.875107765	0	5.937	high	1	47	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-A7-A3J0	76	0	8.884467125	0	5.944	high	1	62	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	other	2

TCGA-AO-A12F	1471	0	9.560117722	0.56967777	5.947	high	1	36	< 60	0	m0	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AC-A8OR	40	0	9.188830376	0.243902937	5.955	high	1	75	≥ 60	1	mx	0	n0 (i-)	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	other	2
TCGA-AR-A0TY	1699	1	9.422772408	0.412251443	5.979	high	1	54	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AR-A2LL	224	0	9.311908722	0.314519078	5.982	high	1	70	≥ 60	1	m0	0	n0	n0-1	0	t3	t3-4	1	stage iib	G1-2	0	ILC	0
TCGA-D8-A27E	182	0	9.54009819	0.505337179	5.984	high	1	66	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	other	2
TCGA-BH-A18T	224	1	8.949351311	0	5.987	high	1	70	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E9-A1RC	1224	0	8.951083183	0	5.988	high	1	56	< 60	0	m0	0	n3	n2-3	1	t4b	t3-4	1	stage iiic	G3-4	1	other	2
TCGA-B6-A1KN	3330	0	9.662795067	0.593749583	5.997	high	1	57	< 60	0	m0	0	n1	n0-1	0	t4b	t3-4	1	stage iiib	G3-4	1	IDC	1
TCGA-E2-A1B0	1271	0	9.015973091	0	6.032	high	1	50	< 60	0	m0	0	n2	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-BH-A18M	2207	1	9.01630497	0	6.032	high	1	39	< 60	0	m0	0	n1	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	IDC	1
TCGA-B6-A0X0	3650	0	9.038300514	0	6.047	high	1	54	< 60	0	m0	0	n0 (i-)	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	other	2
TCGA-E2-A1L8	1015	0	9.05447197	0	6.057	high	1	52	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-AC-A3YJ	40	0	9.056530952	0	6.059	high	1	66	≥ 60	1	mx	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	other	2
TCGA-EW-A423	309	0	9.064483643	0	6.064	high	1	75	≥ 60	1	mx	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-D8-A1XT	193	0	9.080913544	0	6.075	high	1	61	≥ 60	1	m0	0	n1a	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-GM-A2DC	1628	0	9.908826828	0.701239407	6.076	high	1	57	< 60	0	m0	0	n1a	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E2-A156	481	0	9.08449173	0	6.078	high	1	61	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-OL-A66J	1658	0	9.681607246	0.496643394	6.086	high	1	80	≥ 60	1	mx	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	ILC	0
TCGA-A7-A13E	287	0	9.10185051	0	6.089	high	1	62	≥ 60	1	mx	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-BH-A0BW	355	0	9.893677711	0.66231221	6.097	high	1	71	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-D8-A1XM	218	0	9.890275955	0.656859756	6.099	high	1	57	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-AR-A1AU	1409	0	9.116843224	0	6.099	high	1	39	< 60	0	m0	0	n2	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-E2-A1LS	239	0	9.427633286	0.262494475	6.1	high	1	46	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-E2-A15T	267	0	9.142344475	0	6.116	high	1	65	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-D8-A1XC	81	0	9.148042679	0	6.12	high	1	85	≥ 60	1	m0	0	n1a	n0-1	0	t4b	t3-4	1	stage iiib	G3-4	1	other	2
TCGA-A7-A6VV	181	0	9.38359642	0.195573166	6.124	high	1	51	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-A2-A25E	2511	0	10.20366573	0.887136936	6.127	high	1	34	< 60	0	m0	0	n2a	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-E2-A10A	352	0	9.189134598	0	6.148	high	1	41	< 60	0	m0	0	n0 (i-)	n0-1	0	t3	t3-4	1	stage iib	G1-2	0	IDC	1
TCGA-EW-A6SB	760	0	9.191628456	0	6.149	high	1	62	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage ii	G1-2	0	IDC	1
TCGA-E2-A15J	464	0	9.207045555	0	6.16	high	1	51	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-BH-A18U	1563	1	9.229512215	0	6.175	high	1	72	≥ 60	1	m0	0	n2a	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-A7-A5ZV	210	0	9.637470245	0.332114428	6.186	high	1	62	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	other	2
TCGA-D8-A1XV	147	0	9.251106262	0	6.189	high	1	84	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	other	2
TCGA-AC-A2QJ	69	0	9.58050251	0.26437071	6.201	high	1	48	< 60	0	m0	0	n0	n0-1	0	t4b	t3-4	1	stage iiib	G3-4	1	other	2
TCGA-AC-A2BK	1172	0	9.780333519	0.433054596	6.202	high	1	78	≥ 60	1	mx	0	n2a	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-BH-A18G	61	0	9.283856392	0	6.211	high	1	81	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	IDC	1
TCGA-E2-A14O	1173	0	9.882958412	0.504513621	6.214	high	1	76	≥ 60	1	m0	0	n1a	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	IDC	1
TCGA-D8-A143	172	0	9.551047325	0.195085451	6.236	high	1	51	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-AR-A24Z	1574	0	9.466517448	0.11249996	6.244	high	1	57	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-BH-A0E2	376	0	10.23531628	0.75776577	6.25	high	1	49	< 60	0	m0	0	n2a	n2-3	1	t2	t1-2	0	stage iiia	G3-4	1	IDC	1
TCGA-BH-A18S	2009	1	9.815919876	0.387730867	6.261	high	1	79	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	other	2
TCGA-GM-A2DK	1896	0	9.852236748	0.411287397	6.267	high	1	58	< 60	0	m0	0	n0 (i-)	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1

TCGA-AR-A256	2854	1	9.386221886	0	6.279	high	1	45	< 60	0	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E2-A15A	502	0	9.422997475	0	6.304	high	1	45	< 60	0	m0	0	n3a	n2-3	1	t2	t1-2	0	stage iiic	G3-4	1	IDC	1
TCGA-AC-A4ZE	152	0	9.670698166	0.170275033	6.336	high	1	63	≥ 60	1	m0	0	n0	n0-1	0	t3	t3-4	1	stage iib	G1-2	0	ILC	0
TCGA-AC-A23H	81	0	9.69005394	0.182421476	6.339	high	1	90	≥ 60	1	m0	0	nx	nx	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-BH-A18L	811	1	9.488788605	0	6.348	high	1	50	< 60	0	m0	0	n1mi	n0-1	0	t3	t3-4	1	stage iiia	G3-4	1	IDC	1
TCGA-AR-A1AT	1272	1	9.531912804	0	6.377	high	1	62	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-BH-A8FY	295	1	9.536643982	0	6.38	high	1	87	≥ 60	1	m0	0	n0 (i+)	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	ILC	0
TCGA-D8-A1X5	171	0	9.55644989	0	6.393	high	1	81	≥ 60	1	mx	0	n3a	n2-3	1	t2	t1-2	0	stage iiic	G3-4	1	IDC	1
TCGA-D8-A1X6	236	0	9.577465057	0	6.407	high	1	80	≥ 60	1	mx	0	n2a	n2-3	1	t3	t3-4	1	stage iiia	G3-4	1	IDC	1
TCGA-D8-A1X7	85	0	9.661418915	0	6.463	high	1	40	< 60	0	mx	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	other	2
TCGA-D8-A1JS	105	0	9.676546097	0	6.474	high	1	77	≥ 60	1	m0	0	n0	n0-1	0	t1c	t1-2	0	stage ia	G1-2	0	other	2
TCGA-B6-A1KC	1326	0	9.752690315	0	6.525	high	1	67	≥ 60	1	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E9-A3Q9	31	0	9.797823906	0	6.555	high	1	78	≥ 60	1	m0	0	n3	n2-3	1	t3	t3-4	1	stage iiic	G3-4	1	ILC	0
TCGA-AR-A1AS	1150	0	9.842622757	0	6.585	high	1	54	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-BH-A0B0	1428	0	9.846500397	0	6.587	high	1	56	< 60	0	m0	0	n0	n0-1	0	t1c	t1-2	0	stage i	G1-2	0	IDC	1
TCGA-E2-A1LK	266	1	9.974945068	0	6.673	high	1	84	≥ 60	1	m0	0	n3a	n2-3	1	t4b	t3-4	1	stage iiic	G3-4	1	IDC	1
TCGA-AC-A2FM	792	1	10.86990547	0.714758039	6.709	high	1	87	≥ 60	1	m0	0	n1mi	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	ILC	0
TCGA-A2-A3XU	912	1	10.05895615	0	6.729	high	1	35	< 60	0	m0	0	n1mi	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-E2-A15L	331	0	10.64011478	0.382830977	6.817	high	1	65	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	ILC	0
TCGA-E2-A155	553	0	10.23097897	0	6.845	high	1	58	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-EW-A6SD	1010	0	10.59033489	0.187694281	6.937	high	1	32	< 60	0	m0	0	n1a	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1
TCGA-AC-A7VB	74	0	10.41584587	0	6.968	high	1	51	< 60	0	mx	0	n1a	n0-1	0	t1c	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-A2-A25F	114	0	11.63388443	0.991439641	7.002	high	1	66	≥ 60	1	m0	0	n0 (i-)	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-E2-A1LE	879	1	11.61052895	0.201982543	7.608	high	1	71	≥ 60	1	m0	0	n3a	n2-3	1	t2	t1-2	0	stage iiic	G3-4	1	IDC	1
TCGA-B6-A0I1	2361	1	11.45239353	0	7.662	high	1	73	≥ 60	1	m0	0	n0	n0-1	0	t2	t1-2	0	stage iia	G1-2	0	IDC	1
TCGA-C8-A137	34	0	12.57151699	0.499164641	8.017	high	1	34	< 60	0	m0	0	n1	n0-1	0	t2	t1-2	0	stage iib	G1-2	0	IDC	1