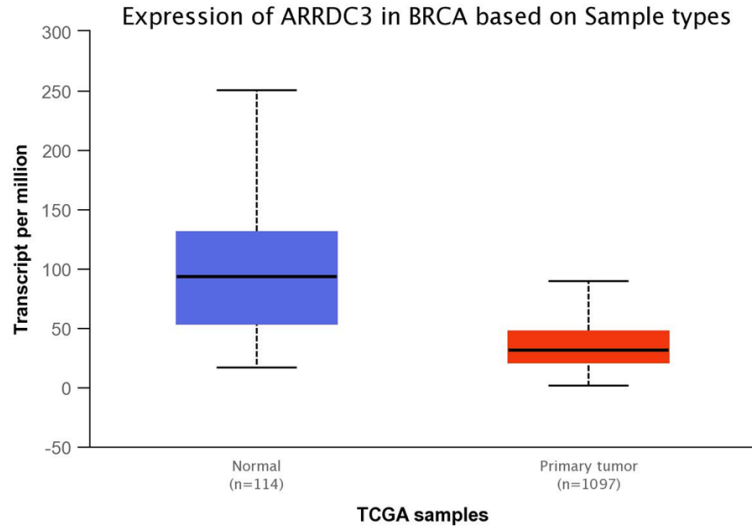
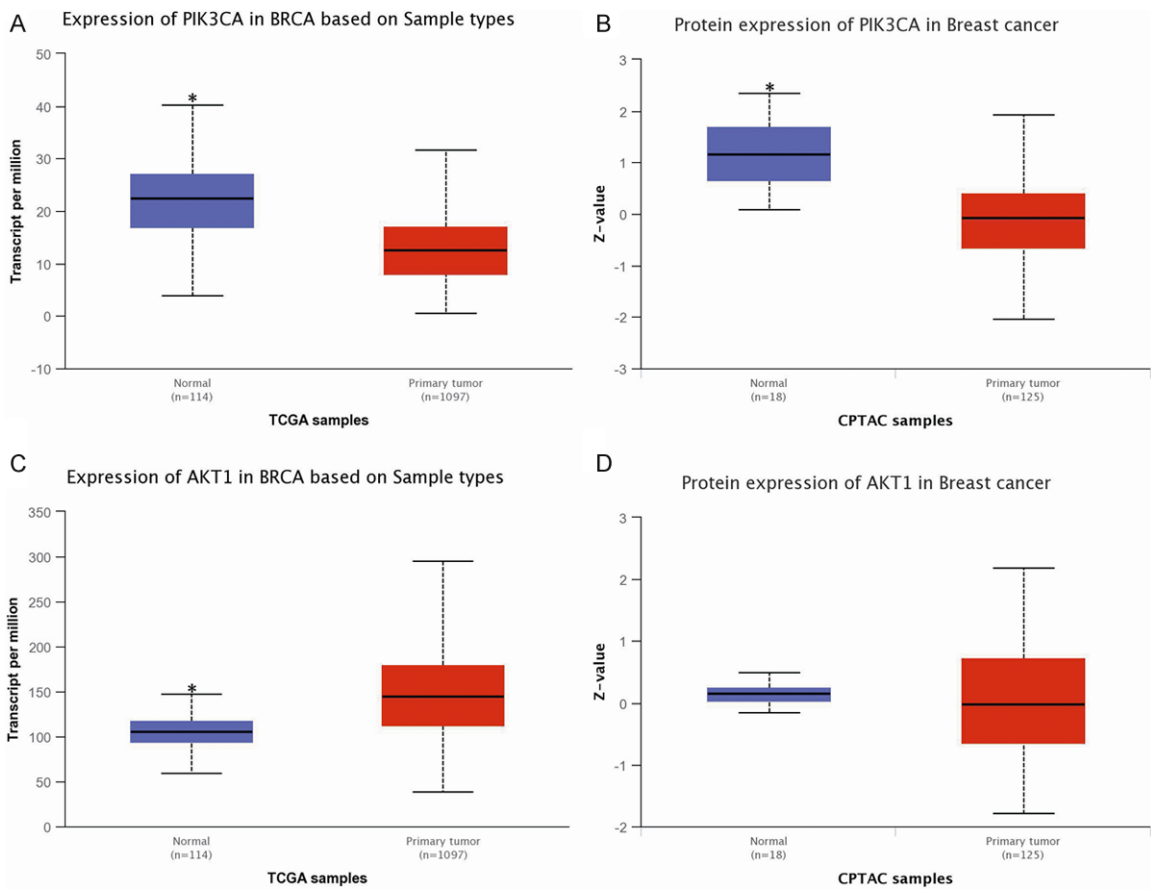


ARRDC3 was regulated by methylation and SRF factor and inhibited breast cancer



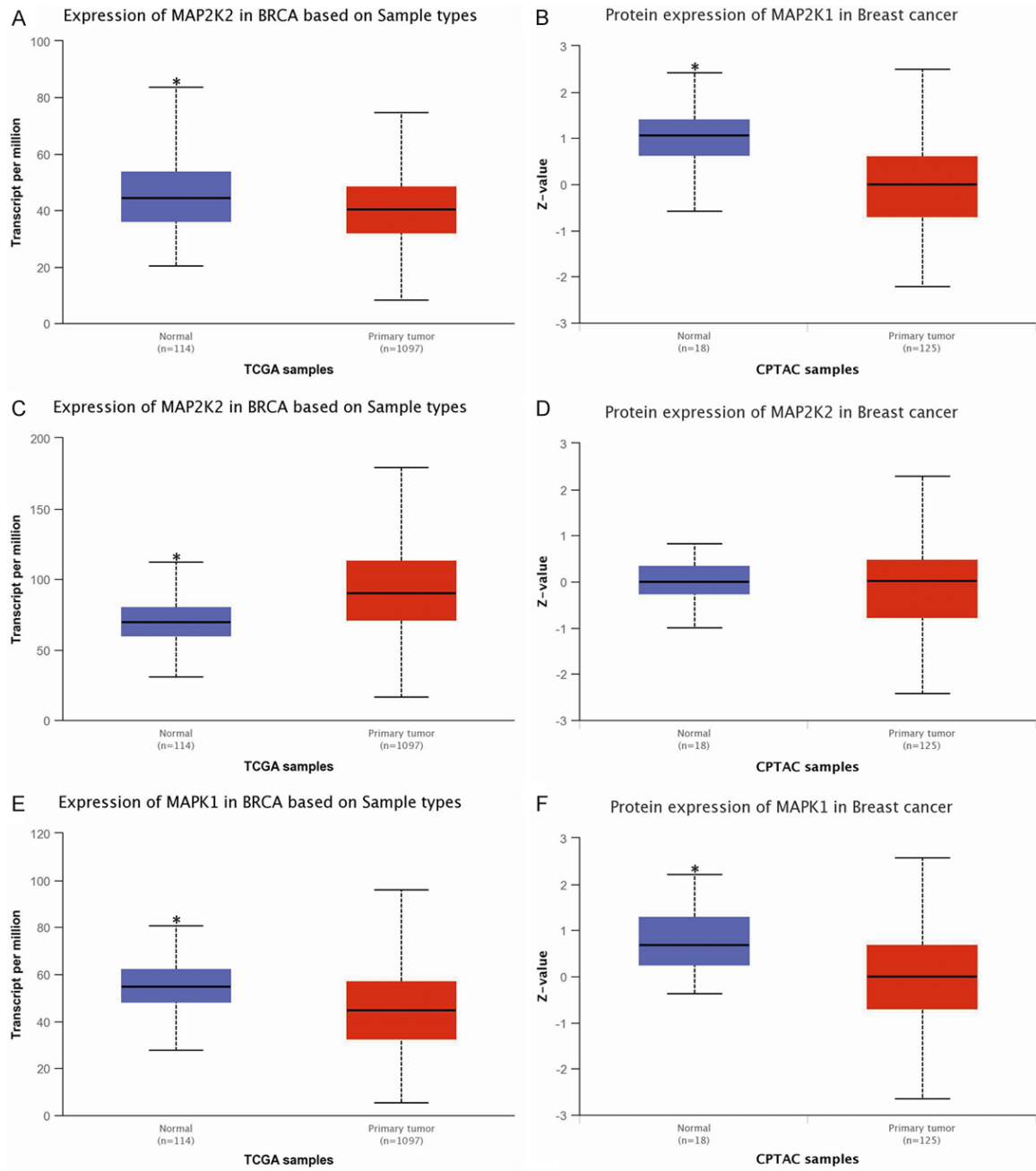
Supplementary Figure 1. Expression of ARRDC3 in breast invasive carcinoma from TCGA database under NIH national cancer institute. The result showed that ARRDC3 was inhibited in primary tumor tissue related to that in normal tissue.



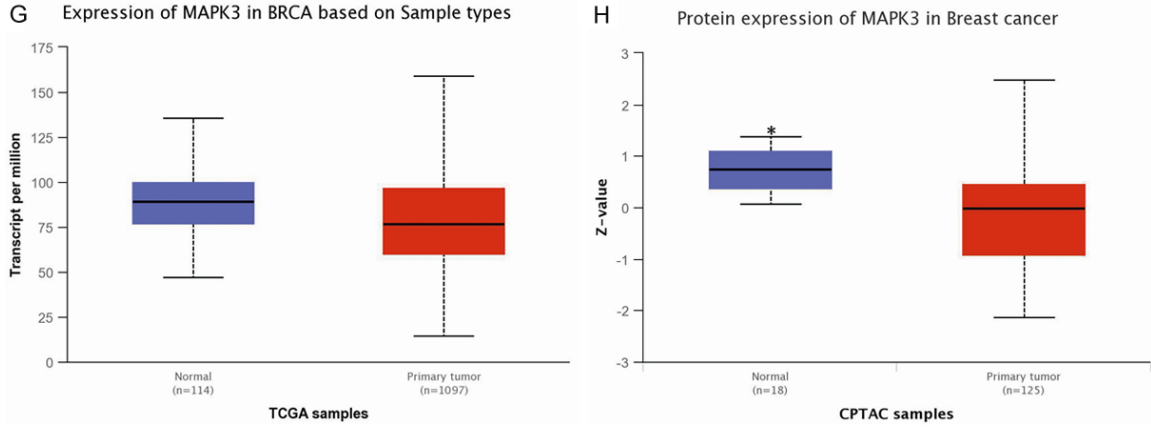
Supplementary Figure 2. The status of the PI3K/Akt signal pathway in breast cancer. A. Expression of PIK3CA in breast invasive carcinoma from the TCGA database. The box plot indicated that PIK3CA mRNA was inhibited in primary tumor tissue than that in normal tissue. B. Protein expression of PIK3CA in breast cancer from the CPTAC database (Clinical Proteomic Tumor Analysis Consortium) under NIH national cancer institute. The plot showed that the protein of PIK3CA was inhibited in the primary tumor tissue than that in normal tissue. C. Expression of AKT1

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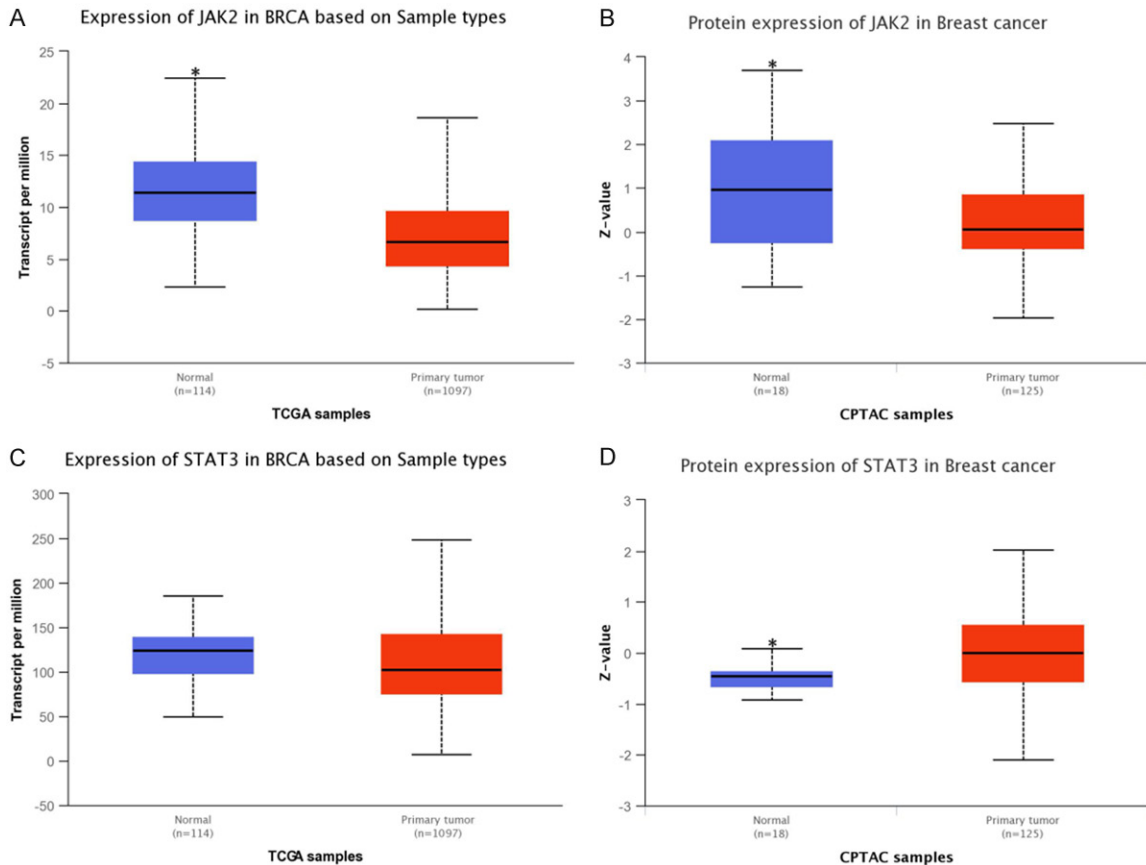
in breast invasive carcinoma from the TCGA database. The box plot indicated that AKT1 mRNA was enhanced in primary tumor tissue than that in normal tissue. D. Protein expression of AKT1 in breast cancer from the CPTAC database. No significant difference was found between them.



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Supplementary Figure 3. The MEK1/2-ERK1/2 signal pathway was analyzed in breast cancer. A. Expression of MAP2K1 in breast invasive carcinoma from the TCGA database. The result indicated that MAP2K1 mRNA was reduced in primary tumor tissue than that in normal tissue. B. Protein expression of MAP2K1 in breast cancer from the CPTAC database. The plot revealed that the protein of MAP2K1 was decreased in primary tumor tissue than that in normal tissue. C. Expression of MAP2K2 in breast invasive carcinoma from the TCGA database. The box plot demonstrated that MAP2K2 mRNA was increased in primary tumor tissue than that in normal tissue. D. Protein expression of MAP2K2 in breast cancer from the CPTAC database. No significant difference was found between them. E. Expression of MAPK1 in breast invasive carcinoma from the TCGA database. The box plot indicated that MAPK1 mRNA was inhibited in primary tumor tissue than that in normal tissue. F. Protein expression of MAPK1 in breast cancer from the CPTAC database. The plot showed that the protein of MAPK1 was inhibited in the primary tumor tissue than that in normal tissue. G. Expression of MAPK3 in breast invasive carcinoma from the TCGA database. No significant difference was found between them. H. Protein expression of MAPK3 in breast cancer from the CPTAC database. The box plot indicated that MAPK3 was down-regulated in primary tumor tissue than that in normal tissue.



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Supplementary Figure 4. The status of the JAK2/STAT3 signal pathway in breast cancer. A. Expression of JAK2 in breast invasive carcinoma from the TCGA database. The box plot indicated that JAK2 mRNA was inhibited in primary tumor tissue than that in normal tissue. B. Protein expression of JAK2 in breast cancer from the CPTAC database. The plot showed that the protein of JAK2 was inhibited in the primary tumor tissue than that in normal tissue. C. Expression of STAT3 in breast invasive carcinoma from the TCGA database. No significant difference was found between them. And the $P = 0.105$, the result revealed the same variation trend as our results. D. Protein expression of STAT3 in breast cancer from the CPTAC database. The box plot indicated that STAT3 was enhanced in primary tumor tissue than that in normal tissue. The trend was opposite to the above plot. Therefore, based on the two plots, we could speculate that STAT3 was involved in breast cancer development.