

Figure S1. Volcanic map analysis of miRNAs sequencing data of 110 paracancerous tissues and 1200 breast cancer tissue samples in TCGA database. A total of 1260 differentially expressed miRNAs were screened, of which 310 miRNAs were downregulated and 200 miRNAs were upregulated. Compared with adjacent cancer tissues, miR-92b-3p is significantly upregulated in tumor tissues.

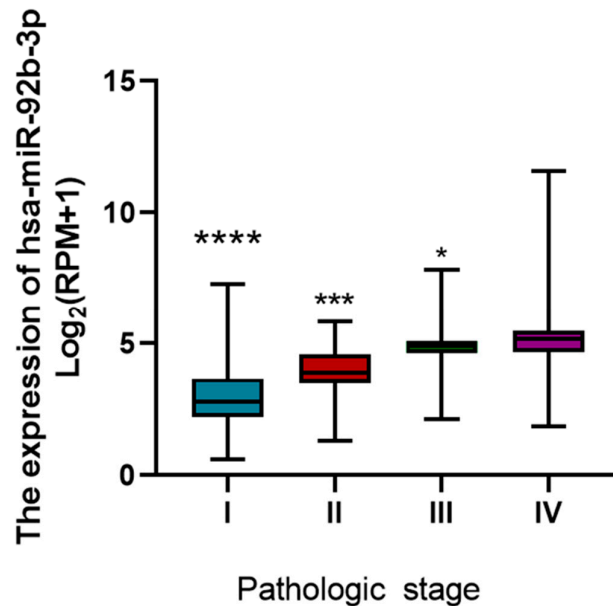


Figure S2. The expression level of miR-92b-3p in stage I-III breast cancer patients (n = 912) was compared with that in stage IV breast cancer patients (n=288) in TCGA database. The difference in * $p < 0.05$, *** $p < 0.001$, **** $p < 0.0001$.

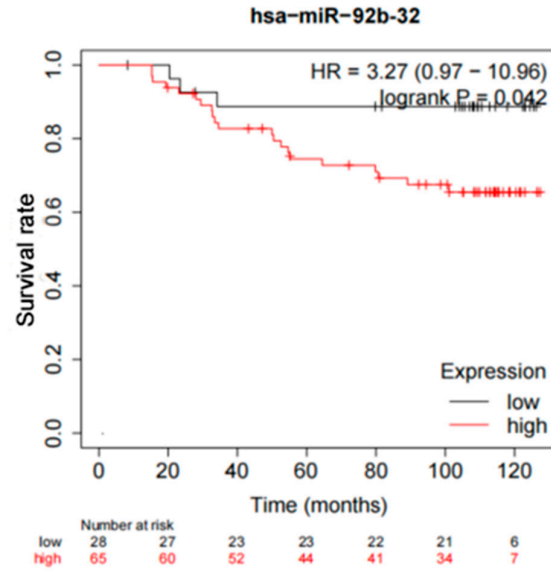


Figure S3. patient survival curves of 110 paracancerous tissues and 1200 breast cancer tissues in TCGA database. According to the median value of mir-92b-3p expression in TCGA database, breast cancer tissues were divided into high expression group and low expression group.