

1 **Supplementary Information**

2 **Table S1. Weight of 21 CpG sites used to construct BEpiC.**

<b>CpG site</b>	<b>Weight</b>
cg02497785	3.48959
cg05632420	-7.83183
cg06144905	23.5599
cg06458239	15.084
cg07477282	27.5761
cg08169949	9.73108
cg10060631	40.7263
cg13158894	5.61094
cg14055004	-11.5602
cg14676592	31.3012
cg14961391	-2.25925
cg15571405	-2.78215
cg15909319	20.4423
cg16867657	6.59828
cg17940694	13.0678
cg18879828	-4.58564
cg19925755	67.2318
cg23606718	30.6746
cg25894658	12.8717
cg26304119	1.56453
cg26830108	39.6635

3

4 **Table S2. The proportion of breast cancer subtype in the tumor**  
 5 **stage.**

<b>Clinical features</b>	<b>Development</b>	<b>Homeostasis</b>	<b>Mitosis</b>
<b>T stage</b>			
T1	59 (27.19%)	88 (29.83%)	52 (19.05%)
T2	121 (55.76%)	162 (54.92%)	168 (61.54%)
T3	32 (14.75%)	39 (13.22%)	40 (14.65%)
T4	5 (2.30%)	6 (2.03%)	13 (4.76%)
<b>N stage</b>			
N0	94 (27.06%)	139 (29.73%)	120 (18.98%)
N1	77 (55.50%)	103 (54.73%)	91 (61.31%)
N2	27 (14.68%)	34 (13.18%)	34 (14.60%)
N3	16 (2.29%)	18 (2.03%)	23 (4.74%)
<b>M stage</b>			

M0	166 (98.22%)	243 (97.59%)	208 (98.11%)
M1	3 (1.78%)	6 (2.41%)	4 (1.89%)
<b>TNM Stage</b>			
stage i-ii	160 (74.42%)	217 (74.31%)	190 (70.37%)
stage iii-iv	53 (25.58%)	69 (25.68%)	77 (29.63%)

6

7 **Supplementary Figure 1**

8 **Expression levels of age-associated gene VS methylation levels of**  
9 **age-associated CpG in gene promoter regions. (A-L)** Correlation analysis

10 between methylation level and expression level of AQP5, AURKB, EXO1,  
11 FTH1, IL7R, KDM6B, MAPT, PARVA.

12 **Supplementary Figure 2**

13 **Correlation analysis of epigenetic age between BEpiC and the Horvath**  
14 **clock.** Epigenetic age predicted by BEpiC and Hovarth clock in Dataset1 **(A)**  
15 and GSE108213 **(B)**.

16 **Supplementary Figure 3**

17 **Three breast cancer subtypes identified by BEpiC based on epigenetic**  
18 **age. (A-C)** Functional enrichment of up-regulated genes in three breast cancer  
19 subtypes. **(D)** Progression-free survival for patients of three breast cancer  
20 subtypes.

21 **Supplementary Figure 4**

22 **Gene mutation frequency in three breast cancer subtypes. Red, yellow,**  
23 **and blue block represent development, homeostasis, and mitotic**  
24 **subtypes, respectively.**

25 **Supplementary Figure 5**

26 **Kaplan–Meier curve for patients taking tamoxifen in development,**  
27 **homeostasis, and mitosis subtype.**

## 28 **Supplementary Figure 6**

29 **The immune characteristics of breast cancer subtypes. (A)** Differences in  
30 immune cell inferred by CIBERSORT among breast cancer subtypes (tested  
31 using Kruskal-Wallis test, \* represent  $p < 0.05$ , \*\* represent  $p < 0.01$ , \*\*\*  
32 represent  $p < 0.001$ , \*\*\*\* represent  $p < 0.0001$ ). **(B)** Stromal score calculated by  
33 “estimate” package in development, homeostasis, and mitosis subtype. **(C)**  
34 Comparison of Tumor mutation burden among pam50 molecular subtypes  
35 (tested using Kruskal-Wallis test, \* represent  $p < 0.05$ , \*\* represent  $p < 0.01$ , \*\*\*  
36 represent  $p < 0.001$ , \*\*\*\* represent  $p < 0.0001$ ).