**Supplementary data**



**Supplementary data Figure 1:** **Relative transcription expression of six hub genes in normal tissues and breast cancer tissues with different breast cancer stages.** **(A)** CDK1, **(B)** FN1, **(C)**AURKA, **(D)** CCNB2, **(E)** BIRC5, and **(F)** TOP2A. *p*-value (*p<0.05)* was used to represent the significance of the correlation between the observed parameters.



**Supplementary data Figure 2:** **Relative transcription expression of six hub genes in normal tissues and breast cancer tissues with different subclasses.** **(A)** CDK1, **(B)** FN1, **(C)**AURKA, **(D)** CCNB2, **(E)** BIRC5, and **(F)** TOP2A. *p*-value (*p<0.05)* was used to represent the significance of the correlation between the observed parameters.



**Supplementary data Figure 3:** **Relative transcription expression of six hub genes in normal individual and breast cancer patients with different age groups.** **(A)** CDK1, **(B)** FN1, **(C)**AURKA, **(D)** CCNB2, **(E)** BIRC5, and **(F)** TOP2A. *p*-value (*p<0.05)* was used to represent the significance of the correlation between the observed parameters.

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**Supplementary data Figure 4:** **Relative transcription expression of six hub genes in normal individual and breast cancer patients with different races.** **(A)** CDK1, **(B)** FN1, **(C)**AURKA, **(D)** CCNB2, **(E)** BIRC5, and **(F)** TOP2A. *p*-value (*p<0.05)* was used to represent the significance of the correlation between the observed parameters.

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**Supplementary data Figure 5: Relative transcription expression of six hub genes in normal individual and breast cancer patients with different menopause status.** **(A)** CDK1, **(B)** FN1, **(C)**AURKA, **(D)** CCNB2, **(E)** BIRC5, and **(F)** TOP2A. *p*-value (*p<0.05)* was used to represent the significance of the correlation between the observed parameters.



 **Supplementary data Figure 6: Relative translation expression of six hub genes in normal individual and breast cancer patients with different menopause status.** **(A)** CDK1, **(B)** FN1, **(C)**AURKA, **(D)** CCNB2, **(E)** BIRC5, and **(F)** TOP2A. Z-value indicates standard deviations from the median documented across samples of a particular group. The log2 values of spectral count ratio, obtained from CPTAC analysis, were first normalized within profile of each type / group of sample profile followed by normalization across the samples. The number of samples in a particular dataset is represented by n.