

Supplementary Legends

Supplementary Figure Legends

Supplemental Figure S1. Determination of soft thresholding power in WGCNA. A) Analysis of the scale-free fit index for various soft-thresholding powers. B) Analysis of the mean connectivity for various soft-thresholding powers.

Supplemental Figure S2. Cluster of module eigengenes.

Supplemental Figure S3. Heatmap of the correlation between module eigengenes and different subtypes of breast cancer.

Supplemental Figure S4. PPI networks for breast cancer subtypes.

Supplementary Table Legends

Supplemental Table S1. Characteristics of BC cell lines.

Supplemental Table S2. Threshold value for different 50 genes with higher co-expression of SBC.

Supplemental Table S3. Functional Enrichment for Biological Process.

Supplemental Table S4. Functional Enrichment for Cellular Components.

Supplemental Table S5. Functional Enrichment for Molecular Functions.

Supplemental Table S6. Functional Enrichment for Pathways.

Supplemental Table S7. Top 50 highly degree genes for each of SBC.

Supplemental Table S8. Features of the five hub genes for each SBC.

Supplemental Table S9. Features of Basal A network.

Supplemental Table S10. Features of Basal B network.

Supplemental Table S11. Features of Luminal A network.

Supplemental Table S12. Features of Luminal B network.

Supplemental Table S13. Features of Her2ampl network.

Supplemental Table S14. Hub genes in patients for each breast cancer subtype.