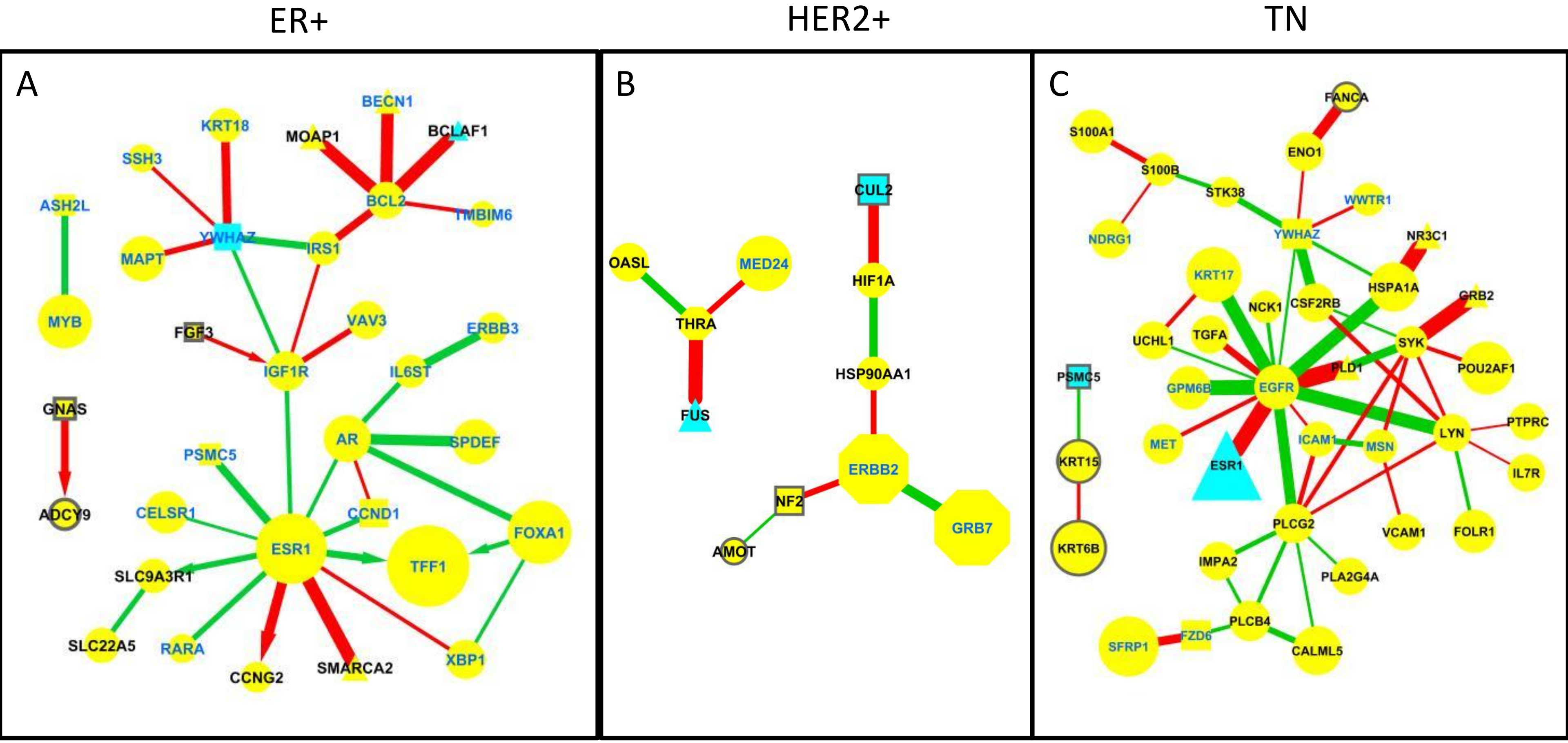

Supplementary Fig 2: Breast cancer driver-networks for three clinical subtypes (ER+: A, HER2+: B, TNBC: 2C), constructed using CNA and gene expression data from Chin et al. Size of a node is proportional to the differential expression level of the corresponding gene. Yellow and blue nodes represent up and down regulation, respectively, from gene expression data. The shapes indicate the type of genomic change, squares representing the seed genes with copy number alterations, circles representing differential expression without copy number alteration, hexagons representing both copy number and gene expression changes, and triangles representing inclusion based on differential co-expression without differential expression. The width and color of an edge connecting two nodes reflect the magnitude and sign of the correlation between two genes within the driver-network. An arrow pointing from one member gene to another indicates a transcriptional or signaling relationship while lines without arrowheads represent protein-protein interactions. Genes that are also present in the driver-networks created from Andre et al. dataset (Fig 2D-F)have blue font color. Genes that are also present in the driver-networks created from Chin et al. dataset (Fig 2A-C) are highlighted with gray node border.