

## Supplementary Figure Legends

**Supplementary Figure S1. Regional plots of 3p24, 11q13, 12p11, 14q13, 16q12/TOX3, 16q12/FTO, 16q23, and 19p13.** The chromosomal position (based on GRCh37) of SNPs on each region against  $-\log_{10} P$ -values for breast cancer in our African American sample. Panel (i) and (ii) show the associations with overall breast cancer. Panel (iii) and (iv) show the associations with ER+ disease and panel (v) and (vi) show the associations with ER- disease. The red arrow denotes the better markers. The blue arrow denotes secondary signals. The purple circle and black arrow denotes the index variant. For panels (i), (iii) and (v), SNPs surrounding the index variant are colored to indicate the LD structure using pairwise  $r^2$  in reference to the SNP from the May 2012 EUR panel of 1000 Genomes. For panels (ii), (iv) and (vi), LD structure was plotted from the May 2012 AFR panel of 1000 Genomes. The plots were generated using LocusZoom (Pruim et al. 2010).

**Supplementary Figure S2. Genome browser views of 3p24, 11q13, 12p11, 14q13, 16q12/TOX3, 16q12/FTO, 16q23, and 19p13.** Genomic browser views with epigenetic chromatin features in breast cells (T47D, MCF7, HCC1954, MDAMB231, HMEC, Breast Myoepithelial, Breast Fibroblast, Breast Luminal epithelial cells) near the better markers or independent signals are generated using the UCSC genome browser. Shown from the top: chromosome coordinates (based on GRCh37), UCSC genes, location of better markers/independent signals from fine-mapping, index SNPs, epigenetic chromatin features (T47D DNaseI, estradiol treated T47D DNaseI, MCF7 DNaseI, estradiol treated MCF7 DNaseI, MCF7 H3K4me3, H3K4me1, H3K27Ac, estradiol treated MCF7 H3K4me3, H3K4me1, H3K27Ac, HCC1954 H3K4me3, H3K4me1, H3K27Ac, MDAMB231 FAIRE, H3K4me3, H3K4me1, H3K27Ac, HMEC FAIRE, DNaseI, H3K4me3, H3K4me1, H3K27Ac, Breast Myoepithelial H3K4me3, H3K4me1, Breast Fibroblast H3K4me3, H3K4me1, H3K27Ac, Breast Luminal epithelial H3K4me1, Layered H3K4me3, H3K4me1, H3K27Ac from 7 cell lines from ENCODE, ChromHMM states in MCF7 and HMEC, the ENCODE master DNaseI hypersensitive site track 125 cell types, the ENCODE layered ChIP-seq track for 161 TFs, T47D ESR1, estradiol treated T47D ESR1, T47D FOXA1, GATA3, MCF7 GATA3 ChIP-seq). For detailed information, see Materials and Methods.