Summary statistics were from meta-analysis for overall, ER-positive, and ER-negative. Only top 10,000 SNPs included in the csv files.

The meta-analysis combined GWAS results for one BCAC study on women of European ancestry (BCAC-white) and five studies on women of African Ancestry (BCAC-black, AABC, Ghana, Amber, ROOT)

Based on meta-analysis results, we selected the top SNPs with MinFreq >0.005 and MaxFreq <0.995 (see below for definition of MinFreq and MaxFreq).

The summary statistics csv files include the following columns:

# MarkerName - this is the marker name

# Allele1 - the first allele for this marker in the first file (listed in the metal command file) where it occurs

# Allele2 - the second allele for this marker in the first file where it occurs

# Freq1 - weighted average of frequency for allele 1 across all studies

# FreqSE - corresponding standard error for allele frequency estimate

# MinFreq - minimum frequency for allele 1 across all studies

# MaxFreq - maximum frequency for allele 1 across all studies

# Effect - overall estimated effect size for allele1

# StdErr - overall standard error for effect size estimate

# P-value - meta-analysis p-value

# Direction - summary of effect direction for each study, with one '+' or '-' per study

# HetISq - I^2 statistic which measures heterogeneity on scale of 0-100%

# HetChiSq - chi-squared statistic in simple test of heterogeneity

# df - degrees of freedom for heterogeneity statistic

# HetPVal - P-value for heterogeneity statistic