

Genome-wide screen identifies a novel prognostic signature for breast cancer survival

SUPPLEMENTARY TABLES

Supplementary Table 1: Differential gene expression between breast tumor and normal breast tissue

See Supplementary File 1

Supplementary Table 2: The 795 probe IDs robustly deregulated in breast cancer

See Supplementary File 2

Supplementary Table 3: Genes significantly associated with relapse-free survival in breast cancer patients

See Supplementary File 3

Supplementary Table 4: Significant GO categories associated with 381 genes significantly associated with relapse-free survival in breast cancer

See Supplementary File 4