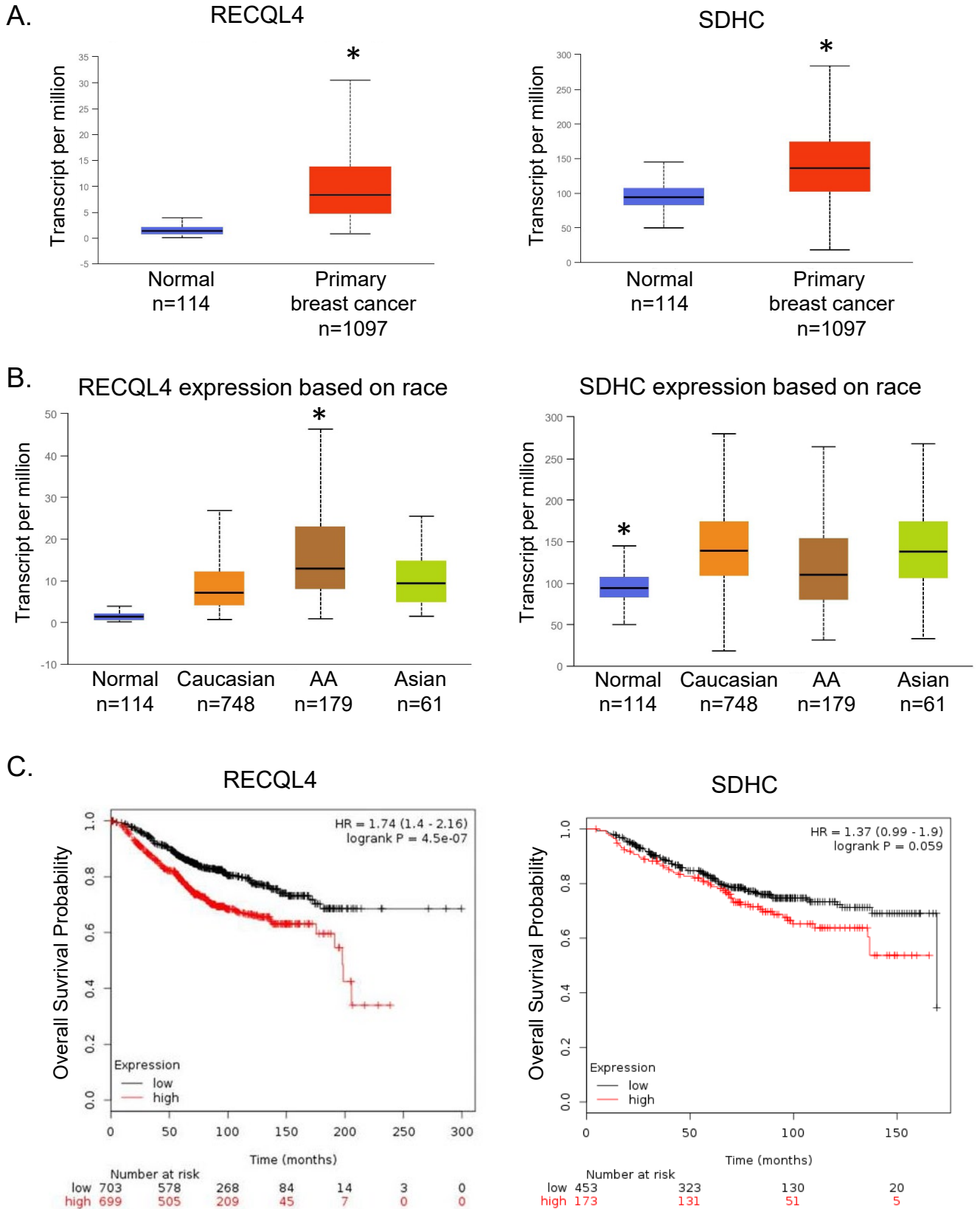


Supplementary Figure 1

TCGA database



Supplementary Figure 1. Analyses of TCGA breast cancer datasets. **A.** Using UALCAN (1), RECQL4 and SDHC transcript is elevated in invasive carcinomas compared with normal breast tissues. **B.** Analyses of both proteins according to race. RECQL4 mRNA is significantly higher in AA women compared to Caucasians and Asians. For SDHC, transcript levels are increased in all races compared with normal tissues. **C.** In silico analysis of transcript expression according to patient overall survival.

1 . Chandrashekar DS, Bashel B, Balasubramanya SAH, Creighton CJ, Rodriguez IP, Chakravarthi BVSK and Varambally S. UALCAN: A portal for facilitating tumor subgroup gene expression and survival analyses. *Neoplasia*. 2017 Aug;19(8):649-658. doi: 10.1016/j.neo.2017.05.002 [PMID:28732212]