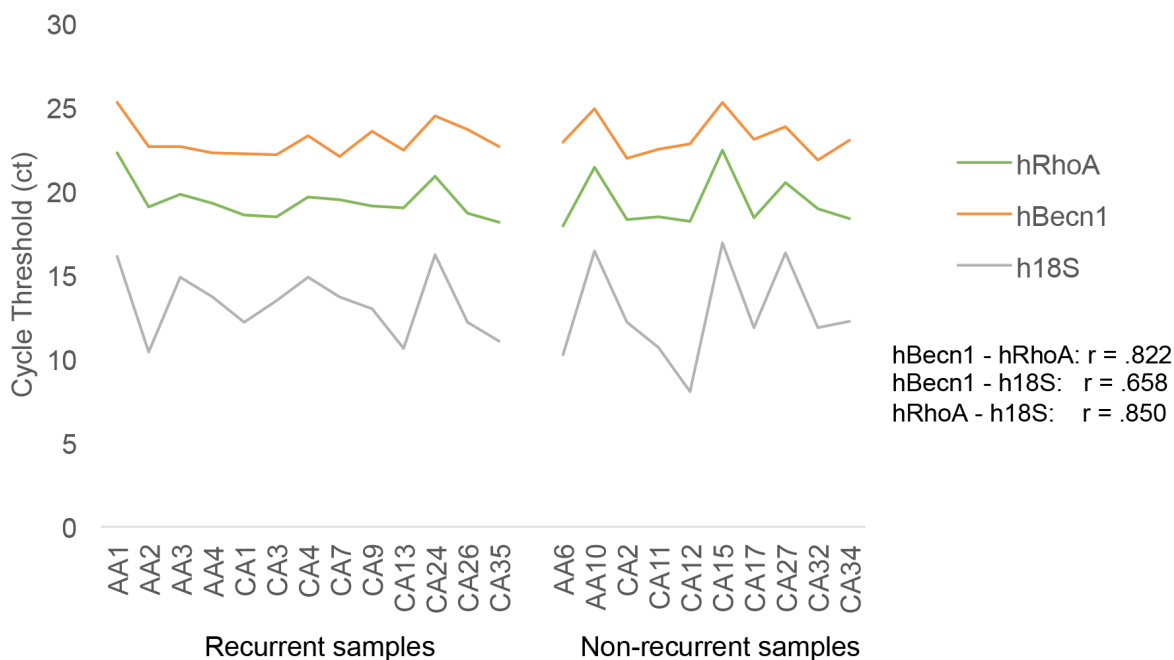


**Supplementary Figure S2: Expression of stromal markers in validation set samples.** **A.** Non-normalized expression of smooth muscle alpha-actin (ACTA1), vimentin (VIM), and beclin-1 (BECN1). Expression was quantified via RT-PCR. **B.** Relative expression of smooth muscle alpha-actin and vimentin normalized to beclin-1.



**Supplementary Figure S3: Expression of reference genes in validation set samples.** Expression of reference genes beclin-1 (BECN1), Ras homolog gene family member A (RHOA), and 18S ribosomal RNA (18S) was quantified via RT-PCR. Pearson’s correlational coefficients were calculated between these three genes using expression across all samples in the validation set.

**Supplementary Table S1: RT-PCR data derived from human prostate cancer specimens.** Raw data represent threshold cycle (Ct) values generated by Taq-Man Low Density Array (TLDA) RT-PCR. Data in sheets 3 and 4 have been normalized to BECN1. In the sheet “Training set normalized data”, the data has also been imputed using the “nondetects” R package as described in Methods.

See Supplementary File 1