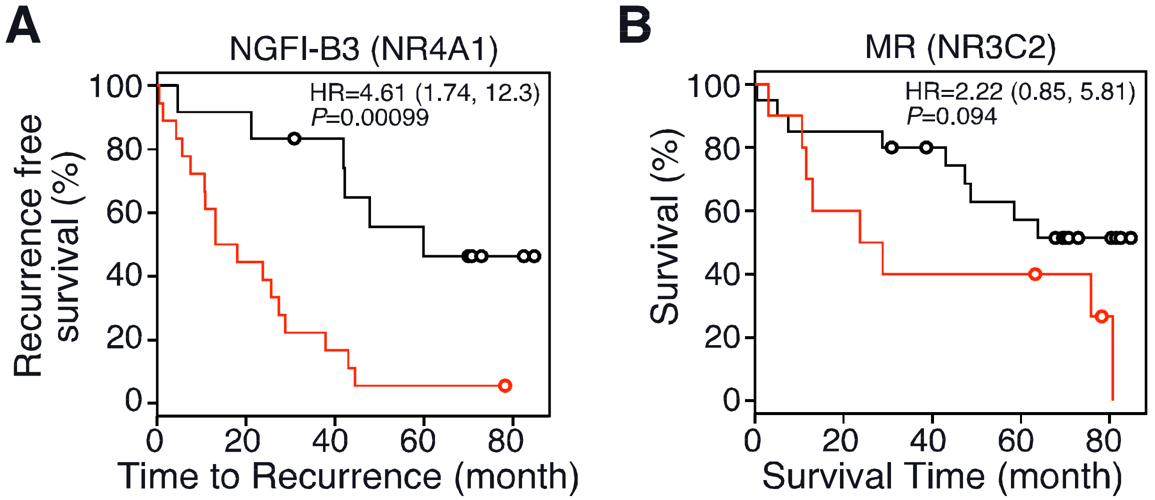

Figure S9. Identification of NRs as prognostic biomarkers in normal lung tissue from lung cancer patients.
Kaplan-Meier plots of time to recurrence and survival are shown for NGFI-B and MR, respectively. Note that these two plots are identical to those obtained when using the entire 48 NR gene set. (A) LOOCV of recursive-partitioning tree model of the MDACC QPCR data in normal tissues shows that NGFI-B is the single gene left in the predictive model for disease progression (HR = 4.61, 95% CI 1.74 to 12.3; *P* = 0.00099). (B) Similar LOOCV analysis shows MR is a single-gene predictor of the entire 48 NR gene set as associated with patient survival (HR = 2.22, 95% CI 0.85 to 5.81; *P* = 0.094). Red and black lines represent high- and low-risk groups, respectively. Open circles indicate censored samples.