



**Figure S5. Kaplan-Meier plots showing the predictive power of the NR gene signature between lung adenocarcinomas and squamous cell carcinomas.**

Independent validation of the 48 NR gene-expression signature was performed using the Consortium cohort (n=442) as a training set and testing it in the microarray data from a cohort of 130 squamous cell carcinomas taken from Raponi et al. (19). (A), and vice versa (B). *P*-values were obtained by the log-rank test. Red and black lines represent predicted high- and low-risk groups, respectively. Open circles indicate censored samples.