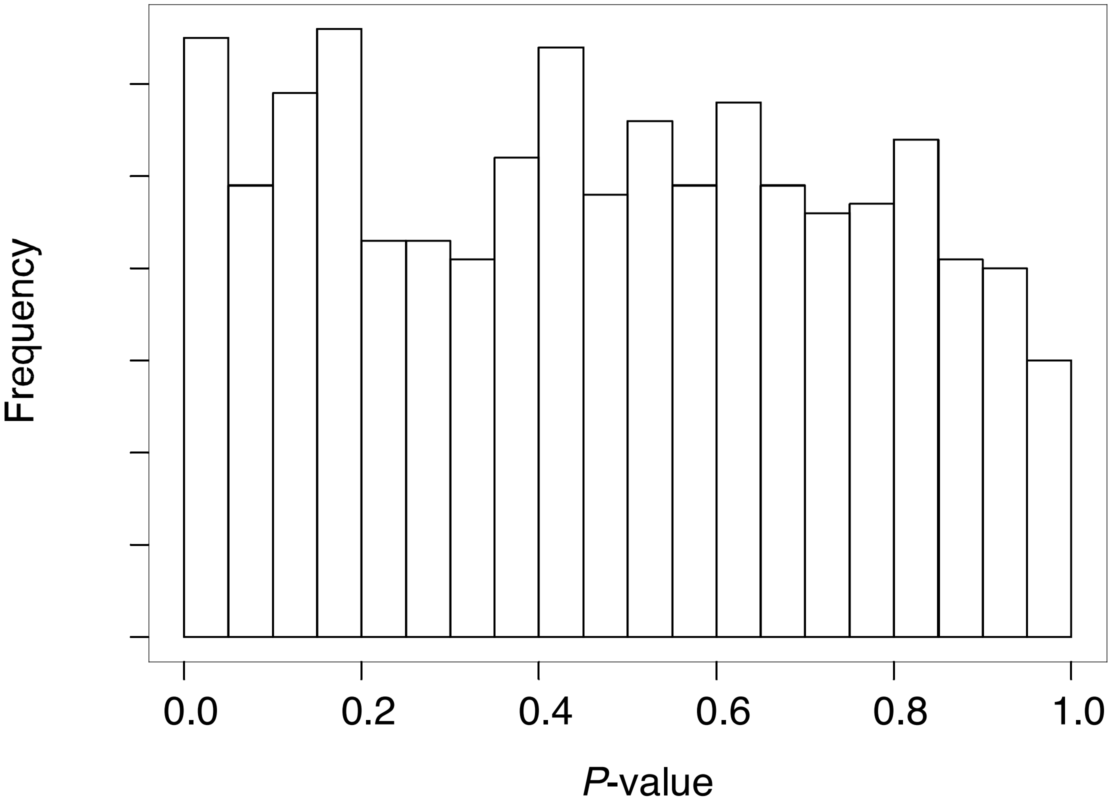

Figure S6. The histograms for *P*-values of 1000 randomly selected lists of 48 genes. The histogram represents the association between the predicted risk groups and survival outcomes. The *P*-values were derived from prediction models built from 1000 random lists each comprising 48 genes in the Consortium training set and validated in the Consortium testing set. Only 28 random lists reach the significance level of 0.018 for the NR signature. Thus, the empirical *P*-value of 0.028 for the permutation test confirms the specificity of the NR signature.