



Supplementary Figure 1. Bimodal distribution of predicted risk scores for developing metastasis generated by the iPAM classifier

Risk scores for 556 samples from the three Decipher GRID validation data sets (MC II, CC, and TJU) with follow-up time were used to generate this histogram. The predicted iPAM risk scores for metastasis showed a bimodal distribution with score range of 0–1 where higher scores represent higher risk of developing metastasis. Based on the distribution, risk scores of 0.4 and 0.6 were selected to stratify risk scores into three groups, low risk group [0–0.4), intermediate risk group [0.4–0.6], and high risk group (0.6–1].