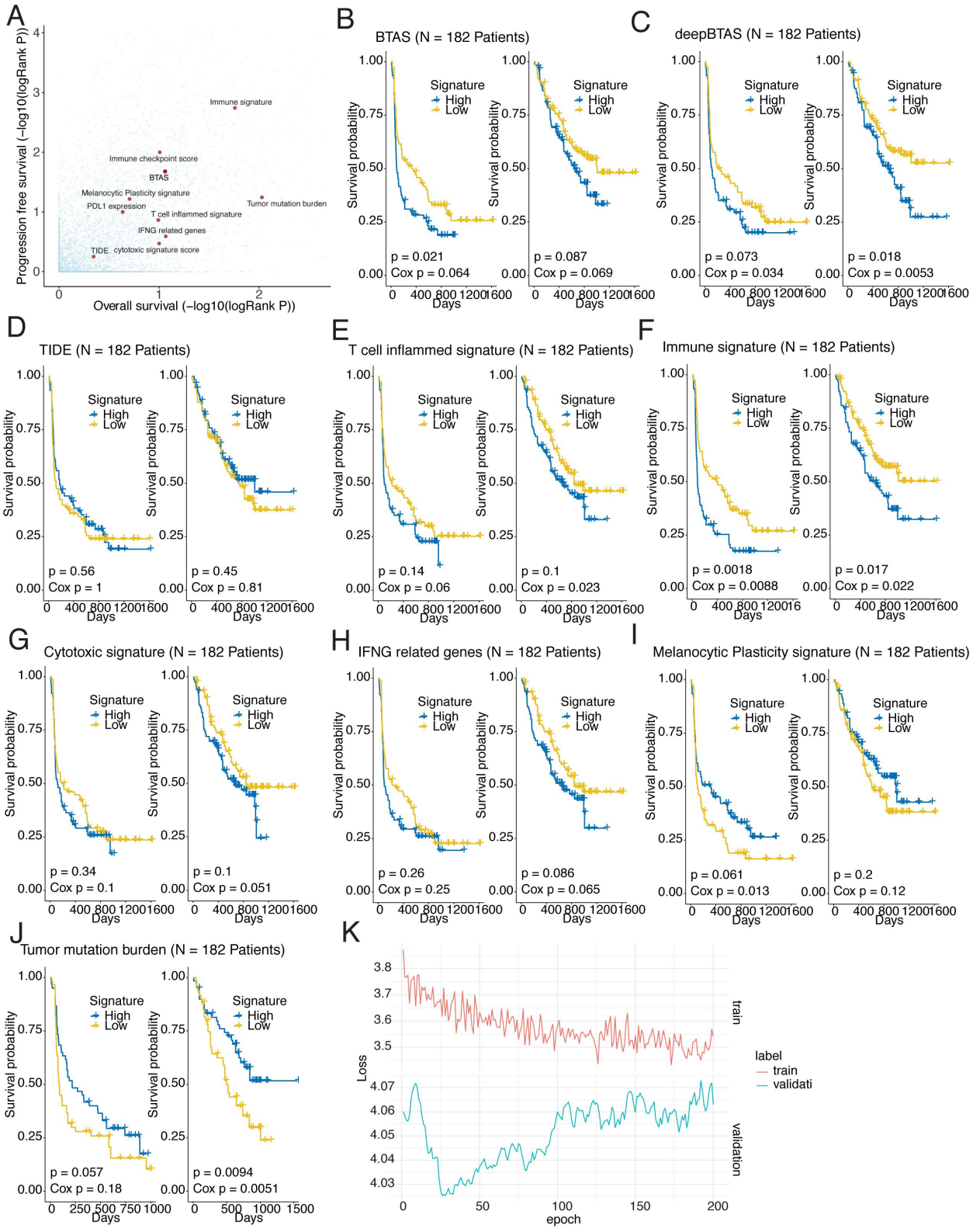

Fig. S10. Machine learning evaluation of immune-metabolic targets in predicting patient response to anti-PD1 monotherapy.

(**A**) Survival stratification performance of BTAS score versus seven other previously published biomarkers for melanoma patients receiving anti-PD1 only. (**B-J**) Kaplan–Meier plots showing progression-free survival and overall survival differences for patients receiving anti-PD1 between the low-risk and high-risk groups defined by the median value of signatures. Signatures displayed are: (**B**) BTAS, (**C**) deepBTAS, (**D**) TIDE (7), (**E**) T-cell inflamed (10), (**F**) Immune (11), (**G**) Cytotoxic(12), (**H**) IFNG (13), (**I**) Melanocytic plasticity (14), and (**J**) Tumor mutation burden. (**K**) deepBTAS training (top) and validation loss (bottom) on TCGA data with training epochs. Validation loss decreased till epoch 24, which is used for early stop criteria and the final model.