A

Biomarker accuracy to classify ICB responders and non-responders

	AUC
deepBTAS	0.603
BTAS	0.585
Tumor mutation burden	0.564
Melanocytic Plasticity signature	0.55
T cell inflamed signature	0.591
Immune signature	0.602
PDL1 expression	0.551
Cytotoxic signature	0.578
TIDE	0.521
IFNG related genes	0.554
Immune checkpoint score	0.569

B

BTAS/biomarker association with progression-free survival

	BTAS	Biomarker
IFNG related genes	0.004	0.007
TIDE	4e−04	0.7
Cytotoxic signature	3e−04	0.5
PDL1 expression	3e−04	0.9
Immune signature	3e−04	0.9
T cell inflamed signature	3e−04	0.8
Melanocytic Plasticity signature	0.001	0.03
Tumor mutation burden	0.002	0.7

C

BTAS/biomarker association with overall survival

	BTAS	Biomarker
IFNG related genes	0.04	0.02
TIDE	0.007	0.7
Cytotoxic signature	0.006	0.3
PDL1 expression	0.006	0.6
Immune signature	0.005	0.3
T cell inflamed signature	0.006	0.9
Melanocytic Plasticity signature	0.02	0.003
Tumor mutation burden	0.03	0.1

D

deepBTAS/biomarker association with progression-free survival

	deepBTAS	Biomarker
IFNG related genes	0.004	0.03
TIDE	1e−04	0.8
Cytotoxic signature	6e−05	0.4
PDL1 expression	7e−05	0.8
Immune signature	8e−05	1
T cell inflamed signature	7e−05	0.8
Melanocytic Plasticity signature	3e−04	0.03
Tumor mutation burden	5e−04	0.6

E

deepBTAS/biomaker association with overall survival

	deepBTAS	Biomarker
IFNG related genes	0.003	0.1
TIDE	1e−04	0.8
Cytotoxic signature	7e−05	0.2
PDL1 expression	9e−05	0.5
Immune signature	8e−05	0.3
T cell inflamed signature	1e−04	0.7
Melanocytic Plasticity signature	5e−04	0.004
Tumor mutation burden	0.002	0.1

F

Biomarker performance improvement with BTAS addition (LRT P)

	PFS	OS
Immune signature	3e−04	0.005
Cytotoxic signature	3e−04	0.006
PDL1 expression	3e−04	0.006
T cell inflamed signature	3e−04	0.006
TIDE	4e−04	0.007
Melanocytic Plasticity signature	1e−03	0.020
Tumor mutation burden	2e−03	0.030
IFNG related genes	4e−03	0.040

Fig. S12. deepBTAS improve the performance of current ICB biomarkers.

(**A**) Predictive power of BTAS and deepBTAS versus other previously published ICB biomarkers in terms of AUCs to predict ICB response. (**B-E**) Significance of association of BTAS/deepBTAS with progression-free survival (PFS) or overall survival (OS) while accounting for levels of different biomarkers (Rows). Association estimated using a multivariable cox proportional hazard model with BTAS and biomarker. P-values displayed are significance of associations calculated using Wald's test. (**F**) Performance improvement (OS and PFS) with addition of BTAS to biomarkers (Rows). An improvement quantified as (p-value of) increase in likelihood of multivariate model containing a biomarker and BTAS over model containing the biomarker alone.