DNA methylation signatures correlate with response to immune checkpoint

inhibitors in metastatic melanoma

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SUPPLEMENTARY TABLE

Sex (n; %)	
Female	4 (50.0%)
Male	4 (50.0%)
Age (years)	
Median	78 (range: 54-81 years)
Mutation status (n; %)	
BRAF	2 (25.0%)
NRAS	2 (25.0%)
cKIT	1 (12.5%)
wt	3 (39.0%)
Baseline ECOG (n; %)	- //>
0	7 (87.5%)
	1 (12.5%)
Baseline LDH (U/L)	0 (05 00()
normal	6 (25.0%)
>ULN Recoling \$100 (ug/L)	2 (75.0%)
Baseline S100 (ug/L)	4 (50.0%)
normai	4 (50.0%) 4 (50.0%)
> ULIN Origin of treatment noive typer tipeue for methylation profiling ($p: \theta'$)	4 (30.0%)
Primary tumor and organ metastatic lesion	1 (12 5%)
Primary tumor and lymph node metastatic lesion	2(25.0%)
Cutaneous and lymph node metastatic lesion	2 (23.0%)
Primary tumor and cutaneous metastatic lesion	1 (12 5%)
Primary tumor, cutaneous and lymph node metastatic lesion	1 (12.5%)
First-line $IO(n; %)$. (12.070)
Nivolumab monotherapy	4 (50.0%)
Pembrolizumab monotherapy	1 (12.5%)
Nivolumab and ipilimumab	3 (39.0%)
iBOR according to iRECIST (n; %)	· · · ·
iCR	1 (12.5%)
iPD (iUPD or iCPD)	7 (87.5%)

Patient's clinical and tumor characteristics from patients with tumor tissue derived from different body sites

Table S1. Patient's clinical and tumor characteristics from patients with tumor tissue derived from different body sites.

Wildtype (wt); lactate dehydrogenase (LDH); upper limit of normal (ULN); not applicable (NA); Eastern Cooperative Oncology Group (ECOG) performance status; Immunotherapy (IO); Response was classified according to immune-based Response Evaluation Criteria in Solid Tumors (iRECIST): best overall response (iBOR), immune complete response (iCR); immune partial response (iPR), immune stable disease (iSD), immune progressive disease (iPD); immune unconfirmed progressive disease (iUPD); immune confirmed progressive disease (iCPD).



Figure S1. Methylation signature-based response to immune checkpoint inhibitors in metastatic melanoma of an independent validation cohort. A) Heatmap demonstrating three clusters based on the top 500 DMPs of the discovery cohort. Responders (R), non-responders (NR). Beta values ranging from 0 (blue) to 1 (red) are shown.