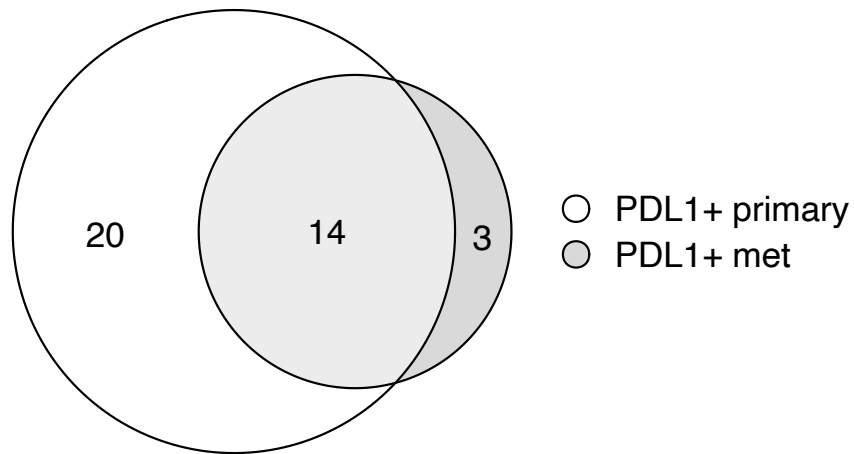


Supplementary Figure S2

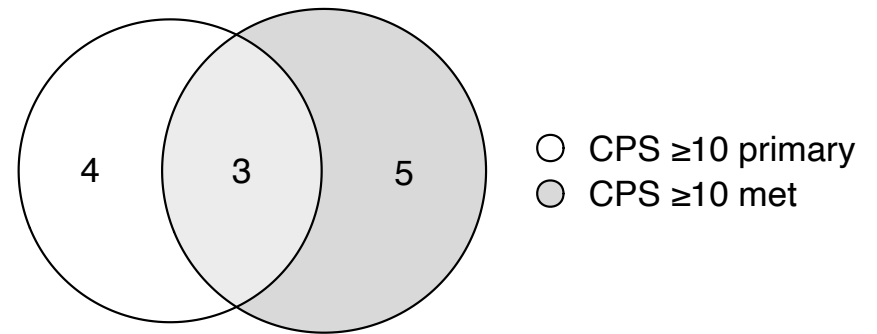
A



		Baseline met PD-L1		
		Negative	Positive	Total
Baseline 1° PD-L1	Negative	23 (88%)	3 (12%)	26
	Positive	20 (59%)	14 (41%)	34
	Total	43 (72%)	17 (28%)	60

$p = 3.9 \times 10^{-4}$ by McNemar's test

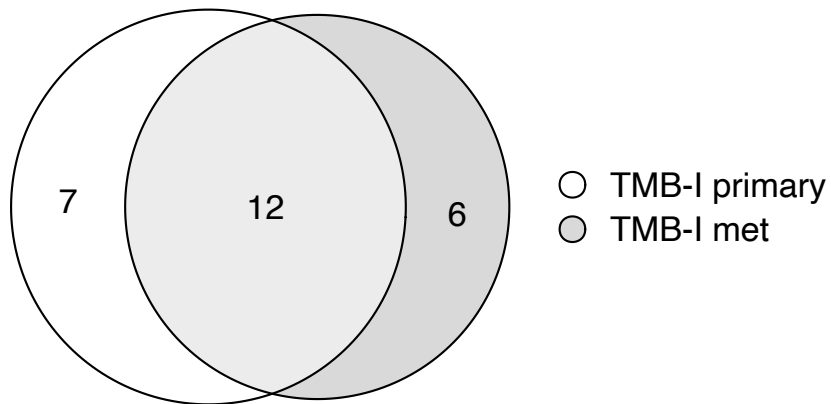
B



		Baseline met PD-L1		
		CPS <10	CPS ≥10	Total
Baseline 1° PD-L1	CPS <10	48 (91%)	5 (9%)	53
	CPS ≥10	4 (57%)	3 (43%)	7
	Total	52 (87%)	8 (13%)	60

$p = 0.74$ by McNemar's test

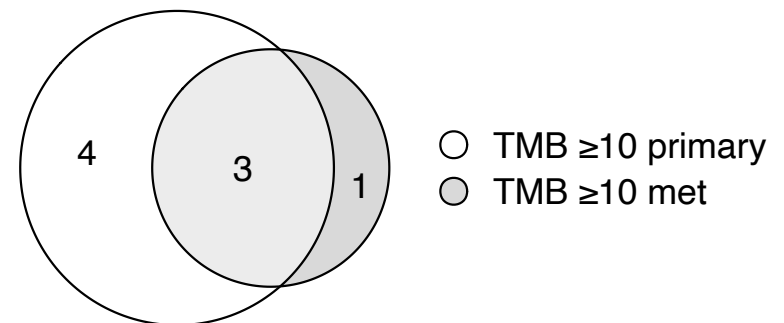
C



		Baseline met TMB			
		Low	Int	High	Total
Baseline 1° TMB	Low	17 (77%)	5 (23%)	0 (0%)	22
	Int	7 (37%)	12 (63%)	0 (0%)	19
	High	1 (50%)	1 (50%)	0 (0%)	2
	Total	25 (58%)	18 (42%)	0 (0%)	43

$p = 0.16$ by McNemar's test (low-int vs. high)

D



		Baseline met TMB		
		<10	≥10	Total
Baseline 1° TMB	<10	37 (97%)	1 (3%)	38
	≥10	4 (80%)	1 (20%)	5
	Total	41 (95%)	2 (5%)	43

$p = 0.18$ by McNemar's test

Supplementary Figure S2. Comparison of PD-L1 expression and TMB in primary vs. metastatic tumors, excluding MSI-H tumors. (A) PD-L1-status of paired baseline primary and baseline metastatic tumors, excluding MSI-H tumors (62%, 37/60 concordance; $p = 3.9 \times 10^{-4}$ by McNemar's test). (B) PD-L1 expression of paired baseline primary and baseline metastatic tumors with threshold PD-L1 CPS of 10, excluding MSI-H tumors (85%, 51/60 concordance; $p = 0.74$ by McNemar's test). (C) TMB-levels of paired baseline primary and baseline metastatic tumors, excluding MSI-H tumors (67%, 29/43 concordance; $p = 0.16$ for low-int vs. high, $p = 0.41$ for low vs. int-high by McNemar's test). (D) TMB of paired baseline primary and baseline metastatic tumors with threshold TMB of 10 mut/Mb, excluding MSI-H tumors (88%; 38/43 concordance; $p = 0.18$ by McNemar's test). In all tables, the number of tumors is shown, with the percentage of tumors by row indicated in parentheses. 1°, primary tumor; met, metastatic tumor; int, intermediate.