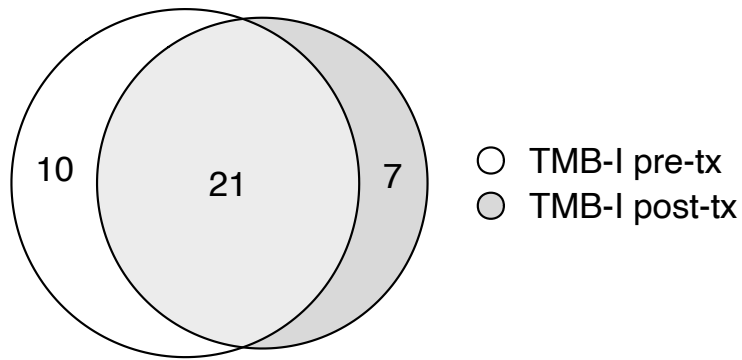


# Supplementary Figure S4

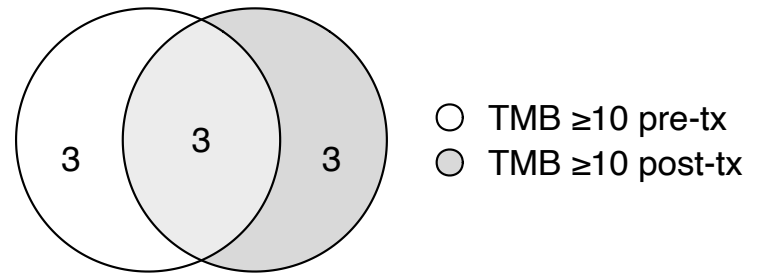
**A**



		Post-tx 1°/met TMB			
		Low	Int	High	Total
Pre-tx 1° TMB	Low	24 (80%)	6 (20%)	0 (0%)	30
	Int	10 (32%)	21 (68%)	0 (0%)	31
	High	0 (0%)	1 (100%)	0 (0%)	1
	Total	34 (55%)	28 (45%)	0 (0%)	62

$p = 0.32$  by McNemar's test (low-int vs. high)

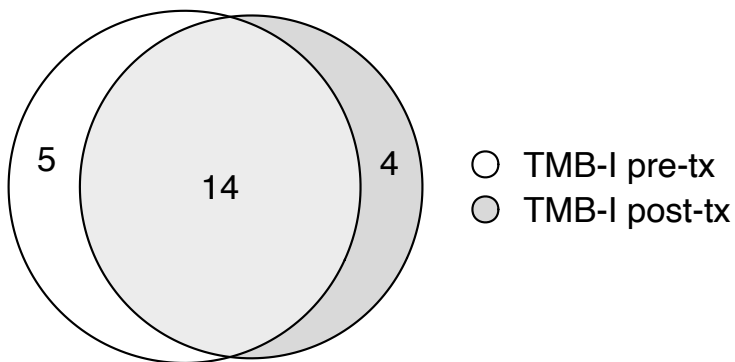
**B**



		Post-tx 1°/met TMB		
		<10	≥10	Total
Pre-tx 1° TMB	<10	53 (95%)	3 (5%)	56
	≥10	3 (50%)	3 (50%)	6
	Total	56 (90%)	6 (10%)	62

$p = 1$  by McNemar's test

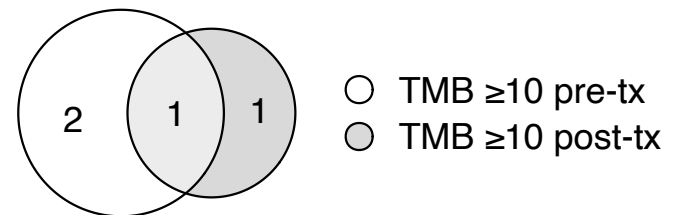
**C**



		Post-tx 1° TMB			
		Low	Int	High	Total
Pre-tx 1° TMB	Low	12 (75%)	4 (25%)	0	16
	Int	5 (26%)	14 (74%)	0	19
	High	0	0	0	0
	Total	17 (49%)	18 (51%)	0	35

$p = 0.74$  by McNemar's test (low vs. int-high)

**D**

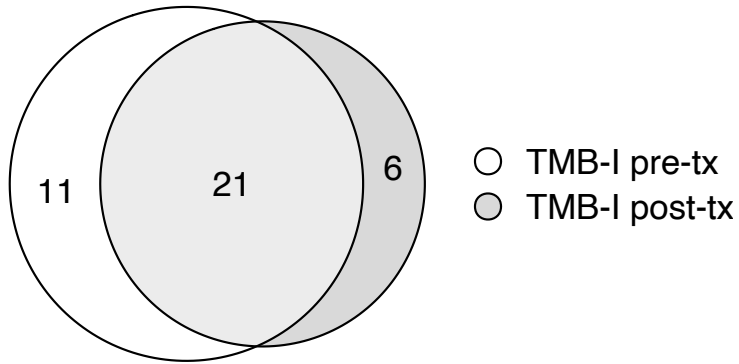


		Post-tx 1° TMB		
		<10	≥10	Total
Pre-tx 1° TMB	<10	31 (97%)	1 (3%)	32
	≥10	2 (67%)	1 (33%)	3
	Total	33 (94%)	2 (6%)	35

$p = 0.56$  by McNemar's test

# Supplementary Figure S4

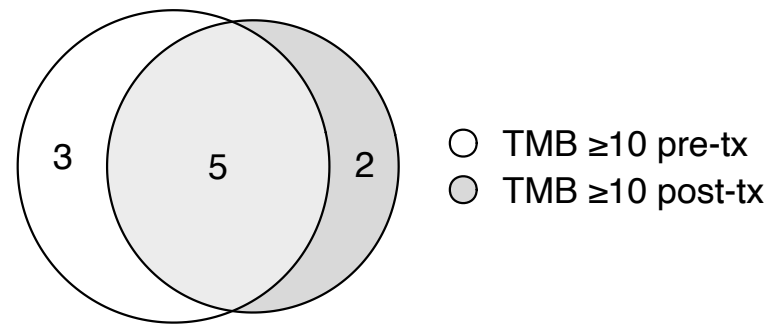
**E**



		Post-tx 1°/met TMB			
		Low	Int	High	Total
Pre-tx 1°/met TMB	Low	29 (83%)	6 (17%)	0 (0%)	35
	Int	11 (34%)	21 (66%)	0 (0%)	32
	High	0 (0%)	0 (0%)	1 (100%)	1
	Total	40 (59%)	27 (40%)	1 (1%)	68

$p = 0.23$  by McNemar's test (low vs. int-high)

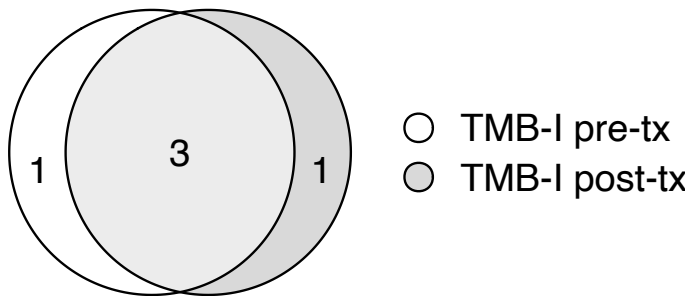
**F**



		Post-tx 1°/met TMB		
		<10	≥10	Total
Pre-tx 1°/met TMB	<10	58 (97%)	2 (3%)	60
	≥10	3 (38%)	5 (62%)	8
	Total	61 (90%)	7 (10%)	68

$p = 0.65$  by McNemar's test

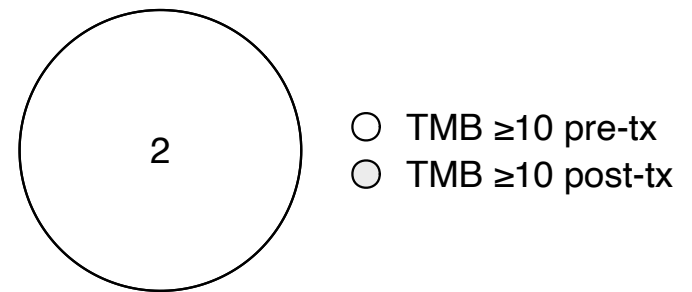
**G**



		Post-tx met TMB			
		Low	Int	High	Total
Pre-tx met TMB	Low	5 (83%)	1 (17%)	0	6
	Int	1 (25%)	3 (75%)	0	4
	High	0	0	0	0
	Total	6 (60%)	4 (40%)	0	10

$p = 1$  by McNemar's test (low vs. int-high)

**H**



		Post-tx met TMB		
		<10	≥10	Total
Pre-tx met TMB	<10	8 (100%)	0 (0%)	8
	≥10	0 (0%)	2 (100%)	2
	Total	8 (80%)	2 (20%)	10

$p = \text{NA}$  by McNemar's test

**Supplementary Figure S4.** Comparison of TMB before vs. after chemotherapy. (A) TMB-levels of paired pre-treatment primary tumors and post-treatment primary or metastatic tumors (73%, 45/62 concordance;  $p = 0.32$  for low-int vs. high,  $p = 0.32$  for low vs. int-high by McNemar's test). (D) TMB of paired pre-treatment primary tumors and post-treatment primary or metastatic tumors with threshold of 10 mut/Mb (90%, 56/62 concordance;  $p = 1$  by McNemar's test). (C) TMB-levels of paired pre- and post-treatment primary tumors (74%, 26/35 concordance;  $p = 0.74$  for low vs. int-high by McNemar's test). (D) TMB of paired pre- and post-treatment primary tumors with threshold TMB of 10 mut/Mb (91%, 32/35 concordance;  $p = 0.56$  by McNemar's test). (E) TMB-levels of paired pre- and post-treatment primary or metastatic tumors (75%, 51/68 concordance;  $p = 0.23$  for low vs. int-high,  $p = \text{NA}$  for low-int vs. high by McNemar's test since 100% concordance creates zero denominator). (F) TMB of paired pre- and post-treatment primary or metastatic tumors with threshold TMB of 10 mut/Mb (93%, 63/68 concordance;  $p = 0.65$  by McNemar's test). (G) TMB-levels of paired pre- and post-treatment metastatic tumors at matching sites (80%, 8/10 concordance;  $p = 1$  for low vs. int-high by McNemar's test). (F) TMB of paired pre- and post-treatment metastatic tumors with threshold TMB of 10 mut/Mb (100%, 10/10 concordance since 100% concordance creates zero denominator;  $p = \text{NA}$  by McNemar's test). 1°, primary tumor; met, metastatic tumor; int, intermediate; tx, treatment; NA, no answer.