Supplementary Table 16. Comparison between clinicopathologic characteristic of NSCLCs with oncogenic / likely oncogenic *MET* tyrosine kinase domain (TKD) mutations without concurrent other drivers to NSCLCs with *MET* exon 14 alterations in cohort #2.

	***MET* TKD mutant NSCLC (N=78)**	***MET* exon 14 altered NSCLC (N=2,036)**	**P**
Age			
Median (range)	70 (36-89+)	76 (41-89+)	**< 0.0001**
Sex			
Female	23 (29.0%)	1140 (56.0%)	**< 0.0001**
Male	55 (71.0%)	896 (44.0%)	
Ancestry[#]			
EUR	56 (72.0%)	1,658 (81.5%)	**0.005**
AFR	12 (15.0%)	132 (6.5%)	
AMR	8 (10.0%)	134 (6.4%)	
EAS	1 (1.5%)	102 (5.1%)	
SAS	1 (1.5%)	8 (0.5%)	
NA	0	2	
Histology			
Adenocarcinoma	49 (63.0%)	1,288 (63.0%)	0.6
Squamous Cell Carcinoma	8 (10.0%)	286 (14.0%)	
NOS*	19 (24.0%)	399 (20.0%)	
Other	2 (3.0%)	63 (3.0%)	
PD-L1 TPS			
<1%	5 (14.0%)	116 (14.0%)	0.4
1-49%	5 (14.0%)	194 (23.0%)	
≥50%	26 (72.0%)	526 (63.0%)	
NA	42	1200	
Concurrent *MET* amplification			
Yes	8 (10.0%)	228 (11.0%)	1.0
No	70 (90.0%)	1811 (89.0%)	
TMB mut/Mb			
Median (range)	9.8 (0-131)	3.8 (0-80)	**< 0.0001**

Abbreviations: TMB, tumor mutation burden; TPS, tumor proportion score; NA, not available.
[#] Ancestry was available for N=2,034 patients with METex14-altered NSCLC. AFR, african continental ancestry group; AMR, admixed American; EAS, east asian continental ancestry group; EUR, european continental ancestry group; SAS, south asian.
* NOS includes liquid biopsy cases where tissue was not available for review