

Suppl. Table S4: Correlation of TMB with molecular subtypes and genomic alterations

Parameter	Category (n)	Median TMB	P-value [§] (Wilcoxon test)
Molecular subtype (AIMS) [†]	Basal-like (82)	1.49	0.299
	HER2-enriched (50)	1.60	
	other (4)	1.25	
ATM	mut (6)	1.44	0.931
	wt (143)	1.52	
ARID1A	mut (5)	2.46	0.040
	wt (144)	1.47	
BRCA1	mut (20)	1.85	0.091
	wt (129)	1.43	
BRCA2	mut (9)	2.70	0.004
	wt (140)	1.43	
CCNE1	amp (11)	1.30	0.569
	wt (138)	1.53	
NOTCH1	mut (5)	2.50	0.063
	wt (144)	1.50	
MYC	amp (39)	1.43	0.269
	wt (110)	1.56	
PIK3CA	mut/amp (17)	1.39	0.900
	wt (132)	1.56	
PTEN	mut/del (17)	1.87	0.099
	wt (132)	1.47	
TP53	mut (103)	1.65	0.011
	wt (46)	1.14	
HRD-panel [#]	mut/del (45)	1.89	<0.001
	wt (104)	1.37	

[§] *P-values not corrected for multiple testing*

[†] *Molecular subtype from RNA-seq was available only for 136 of the 149 samples with WES (see Supplementary Figure S1).*

[#] *The predefined HRD-panel encompassed: BRCA1, BRCA2, ATM, PALB2, BARD1, DRP1, RAD51B, RAD51C, RAD51D, FAAP20, CHECK2, FAN1, FANCE, FANCM, POLQ, NBN*