

Supplementary table 1: Associations between immune microenvironment and TNBC biological variables

	TILs					CD3					CD8				
	≤ 10		> 10		p	≤ 658.41		> 658.41		p	≤ 73.81		> 73.81		p
	n	%	n	%		n	%	n	%		n	%	n	%	
AR/FOXA1 (1% cut-off)	0.010					0.024					0.474				
AR+/FOXA1+	51	42.9	6	18.2		34	44.7	20	27.0		30	38.5	24	32.9	
Other	68	57.1	27	81.8		42	55.3	54	73.0		48	61.5	49	67.1	
Basal-like phenotype	0.353					0.509					0.668				
No	52	42.3	11	33.3		32	41.6	28	36.4		32	41.0	29	37.7	
Yes	71	57.7	22	66.7		45	58.4	49	63.6		46	59.0	48	62.3	
BRCA1 promoter methylation	0.224					0.070					0.671				
No	98	80.3	24	70.6		63	82.9	55	70.5		58	75.3	61	78.2	
Yes	24	19.7	10	29.4		13	17.1	23	29.5		19	24.7	17	27.8	
PIK3CA mutations	0.681					0.168					0.038				
None	106	85.5	30	88.2		64	82.0	70	89.7		64	81.0	72	92.3	
Exon 9/Exon 20	18	14.5	4	11.8		14	18.0	8	10.3		15	19.0	6	7.7	

	PD-L1 _{TC}					PD-L1 _{SC}					PD-1 _{SC}				
	$< 1\%$		$\geq 1\%$		p	≤ 10		> 10		p	≤ 10		> 10		P
	n	%	n	%		n	%	n	%		n	%	n	%	
AR/FOXA1 (1% cut-off)	0.001					0.097					0.351				
AR+/FOXA1+	40	48.2	15	22.1		39	41.5	16	28.1		36	39.1	18	31.6	
Other	43	51.8	53	77.9		55	58.5	41	71.9		56	60.9	39	68.4	
Basal-like phenotype	0.013					0.107					0.552				
No	41	48.8	20	29.0		43	44.8	18	31.6		35	37.2	24	42.1	
Yes	43	51.2	49	71.0		53	55.2	39	68.4		59	62.8	33	57.9	
BRCA1 promoter methylation	0.030					0.161					0.041				
No	70	84.3	48	69.6		78	81.3	40	71.4		77	82.8	39	68.4	
Yes	13	15.7	21	30.4		18	18.7	16	28.6		16	17.2	18	31.6	
PIK3CA mutations	0.064					0.048					0.284				
None	68	81.0	64	91.4		79	81.4	53	93.0		79	83.2	51	89.5	
Exon 9/Exon 20	16	19.0	6	8.6		18	18.6	4	7.0		16	16.8	6	10.5	

Footnote: Basal-like phenotype was considered in the case of positive staining for cytokeratin 5/6 and/or EGFR ($>10\%$ of tumor cells stained in IHC); AR: androgen receptor; FOXA1: Forkhead box protein A1; TILs: tumor-infiltrating lymphocytes; PD-L1: programmed cell death ligand 1; PD-1: programmed cell death 1; TC: tumor cells; SC: stromal cells.