S3 Table. Comparison of clinical features between patients who received neoadjuvant therapy with detectable and undetectable MRD

Clinical feature	Detectable MRD	Undetectable MRD	p-value
No.	10	33	
Age (yr)[a)]			0.470
Mean ± SEM	45.00±2.662	48.06±2.157	
Stage (AJCC 8)[b)]			0.391
I	0	2 (6.1)	
II	3 (30.0)	16 (48.5)	
III	7 (70.0)	15 (45.5)	
Tumor size[b)]			0.664
T1	0	4 (12.1)	
T2	7 (70.0)	20 (60.6)	
T3	2 (20.0)	3 (9.1)	
T4	1 (10.0)	6 (18.2)	
Node[b)]			0.771
N0	2 (20.0)	8 (24.2)	
N1	3 (30.0)	14 (42.4)	
N2	1 (10.0)	3 (9.1)	
N3	4 (40.0)	8 (24.2)	
Molecular type			0.354
HR+HER–	2 (20.0)	15 (45.5)	
HER2+	4 (40.0)	8 (24.2)	
TNBC	4 (40.0)	10 (30.3)	
Clinical risk			0.877
High	6 (60.0)	15 (45.5)	
Median	4 (40.0)	15 (45.5)	
Low	0	2 (6.1)	
Unknown	0	1 (3.0)	

Values are presented as number (%) unless otherwise indicated. Fisher's exact test and T-test were used for categorical variables and for continuous variables, respectively. p-values shown reflect a comparison between patients with detectable molecular residual disease (MRD) and patients with detectable MRD. $p < 0.05$ were considered significant. AJCC, American Joint Committee on Cancer; HER2, human epidermal growth factor receptor 2; HR, hormone receptor; MRD, molecular residual disease; TNBC, triple-negative breast cancer. [a)]Data meet the normal distribution and the data are described by the mean±standard error of the mean (SEM), [b)]The stage, tumor size, and lymph node status were determined before neoadjuvant therapy.