

S7 Table. Univariate and multivariate analyses in terms of overall survival

Characteristic	Univariate analysis			Multivariate analysis (Model 1) ^{a)}			Multivariate analysis (Model 2) ^{b)}		
	HR	95% CI	p-value	HR	95% CI	p-value	HR	95% CI	p-value
BCL2 group (high vs. low ^{c)})	0.426	0.228-0.797	0.008	0.362	0.149-0.884	0.026	1.102	0.306-3.967	0.882
Tumor size (> 2 cm vs. ≤ 2 cm)	1.453	0.986-2.141	0.059				0.875	0.260-2.942	0.830
Node positivity (yes vs. no)	2.151	1.504-3.076	< 0.001	1.916	0.743-4.941	0.178	3.108	0.926-10.433	0.066
Metastasis (yes vs. no)	4.986	2.975-8.356	< 0.001	12.154	3.184-46.394	< 0.001	21.851	4.511-105.836	< 0.001
ER (positive vs. negative)	0.733	0.509-1.058	0.097				0.146	0.020-1.093	0.061
PR (positive vs. negative)	0.748	0.533-1.048	0.092				1.899	0.309-11.655	0.488
HER2 (positive vs. negative)	1.333	0.836-2.124	0.227				0.850	0.234-3.086	0.805
Sex (female vs. male)	0.835	0.117-5.978	0.857						
Menopausal status (post vs. pre)	2.250	1.337-3.788	0.002	4.512	1.170-17.394	0.029	13.296	2.117-83.509	0.006

HR, hazard ratio; CI, confidence interval; BCL2, B-cell CLL/lymphoma 2; ER, estrogen receptor; PR, progesterone receptor; HER2, human epidermal growth factor receptor 2. ^{a)}BCL2 was adjusted with node positivity, metastasis, and menopausal status which were significant factors by univariate analysis, ^{b)}BCL2 was adjusted with all factors described above, ^{c)}The low BCL2 group was defined as reverse phase protein array (RPPA) low, mRNA sequencing (mRNA-seq) low, methylation high, and copy number alteration linear (CNA lin) low. The high BCL2 group was defined as RPPA high, mRNA-seq high, methylation low, and CNA lin high.