

Table S1 Logistic regression of factors associated with nodal complete response

Variables	Category	Patient (N)	Univariate analysis			Multivariate analysis		
			OR	95% CI	P value	OR	95% CI	P value
Age	≥50/<50 years	107/107	1.286	0.729–2.279	0.386			
Sex	Female/Male	68/146	0.832	0.444–1.530	0.560			
T stage	T3–4/T1–2	144/70	1.054	0.578–1.951	0.865			
N stage	N2–3/N1	95/119	0.378	0.203–0.686	0.002	0.574	0.279–1.167	0.127
Clinical stage	III–IVA/II	181/33	0.354	0.164–0.753	0.007	0.608	0.252–1.452	0.264
IC regimen	TPF/TP	96/118	0.755	0.422–1.337	0.338			
Targeted therapy	Yes/No	158/56	0.645	0.344–1.219	0.173			
Multiple nodes	Yes/No	82/132	0.206	0.098–0.403	<0.001	0.238	0.110–0.486	<0.001
Nodal necrosis	Yes/No	72/142	0.273	0.130–0.537	<0.001	0.273	0.124–0.565	0.001
Extranodal extension	Yes/No	7/207	0.319	0.017–1.919	0.295			
Bulky node	Yes/No	16/198	0.261	0.040–0.970	0.081	0.200	0.029–0.814	0.046

Table S2 Hazard ratios of prognostic factors for progression-free survival

Variables	Category	Patients (N)	Univariate analysis			Multivariate analysis		
			HR	95% CI	P value	HR	95% CI	P value
Age	≥50/<50 years	107/107	1.091	0.626–1.900	0.759			
Sex	Female/Male	68/146	0.713	0.379–1.341	0.294			
T stage	T3–4/T1–2	140/70	2.367	1.150–4.871	0.019	2.449	1.189–5.044	0.015
N stage	N2–3/N1	95/119	1.532	0.878–2.672	0.133			
Clinical stage	III–IVA/II	181/33	2.249	0.809–6.251	0.120			
IC regimen	TPF/TP	96/118	1.035	0.593–1.805	0.903			
Nodal complete response	Yes/No	72/142	0.389	0.189–0.800	0.010	0.467	0.219–0.997	0.049
Multiple nodes	Yes/No	82/132	1.705	0.979–2.969	0.060	1.294	0.724–2.310	0.384
Nodal necrosis	Yes/No	72/142	1.871	1.074–3.259	0.027	1.571	0.889–2.778	0.120
Extranodal extension	Yes/No	7/207	1.209	0.293–4.987	0.793			
Bulky node	Yes/No	16/198	0.826	0.257–2.653	0.748			

Table S3 Baseline characteristics after PSM between the modified and control cohorts

Characteristic	Optimized group (N=60)	Standard group (N=60)	P value
Age, mean (SD), years	48.83 (14.61)	48.25 (13.45)	0.82
Age			0.71
<50 years	28 (46.7%)	26 (43.3%)	
≥50 years	32 (53.3%)	34 (56.7%)	
Gender			0.57
Male	39 (65.0%)	36 (60.0%)	
Female	21 (35.0%)	24 (40.0%)	
T classification			0.85
T1–2	22 (36.7%)	21 (35.0%)	
T3–4	38 (63.3%)	39 (65.0%)	
N classification			0.85
N1	38 (63.3%)	39 (65.0%)	
N2–3	22 (36.7%)	21 (35.0%)	
Clinical stage			0.58
II–III	34 (56.7%)	38 (63.3%)	
IVA	26 (43.3%)	22 (36.7%)	
Induction chemotherapy cycles			>0.99
2	53 (88.3%)	53 (88.3%)	
3	7 (11.7%)	7 (11.7%)	
Induction chemotherapy regimen			0.71
TP	34 (56.7%)	36 (60.0%)	
TPF	26 (43.3%)	24 (40.0%)	
Targeted therapy			0.84
Yes	43 (71.7%)	44 (73.3%)	
No	17 (28.3%)	16 (26.7%)	

Survival curves based on these matched cohorts are shown in *Figure 4*.

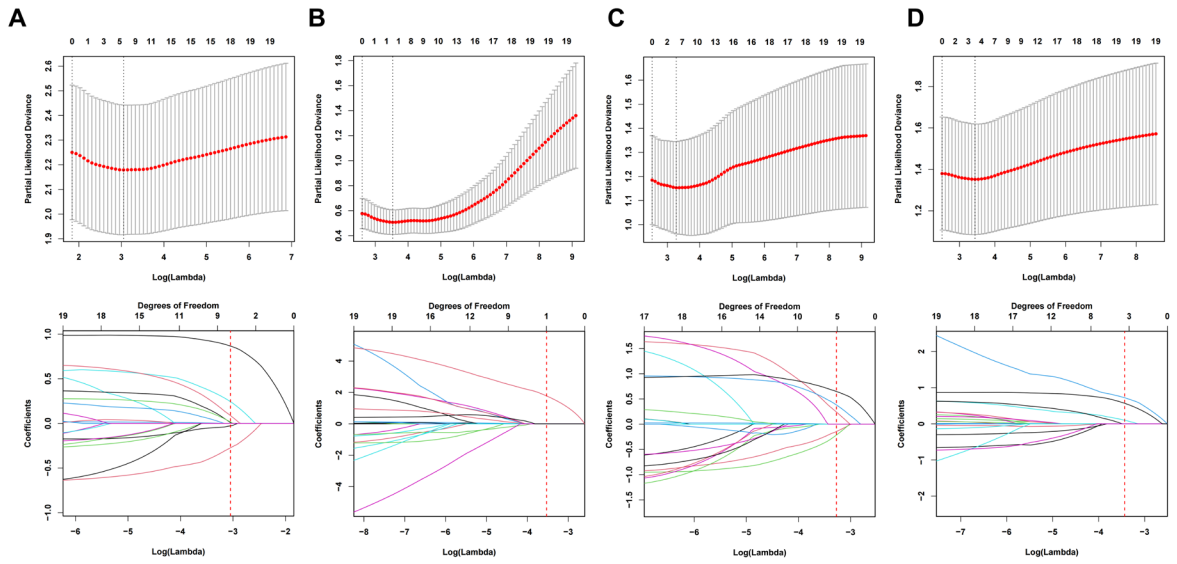


Figure S1 Exploratory LASSO Cox regression analysis for survival outcomes. (A-D) Cross-validation curves and corresponding coefficient paths for OS (A), LRRFS (B), DMFS (C), and PFS (D).

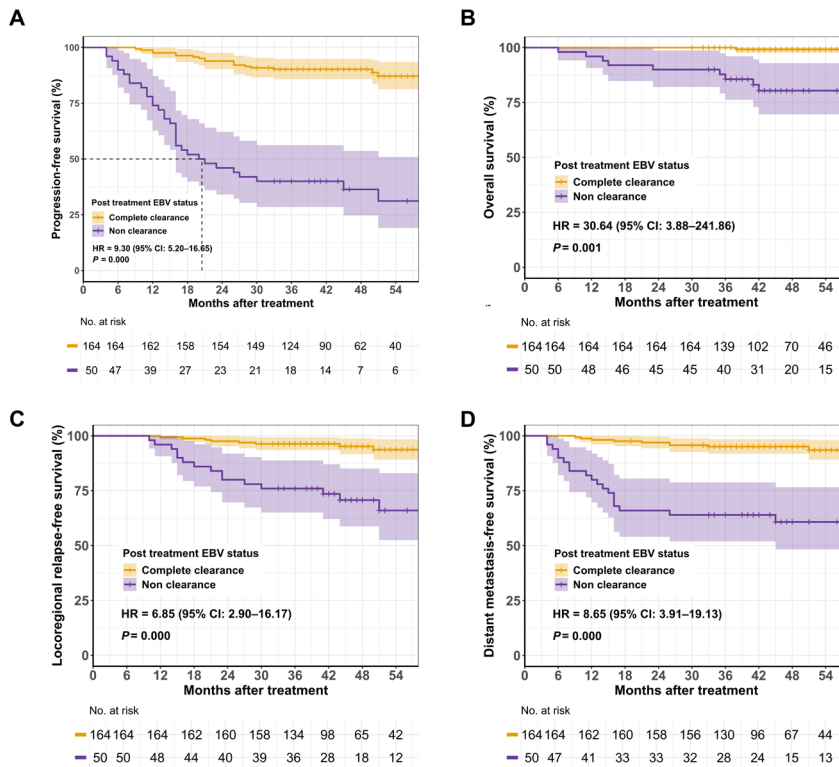


Figure S2 EBV DNA clearance within 12 months and survival outcomes (quantitative analyses in Table 2). (A-D) EBV DNA clearance within 12 months was associated with improved survival outcomes across PFS (A), OS (B), LRRFS (C), and DMFS (D).