

SUPPLEMENTARY TABLES**Supplementary Table 1: The DNA sequence of PCR primers**

Name	Primer	Sequence	Note
NTKL	Forward	5'- CGGAATTCCGGGGGACGATGTGGTTCTT -3'	Primers used for cloning NTKL
	Reverse	5'- CGGAATTCCGACGGTTCAGTCCAGCTTCC -3'	
RT- NTKL	Forward	5'- GCCTGTGCTCTGCGGTCT -3'	Primers used for QPCR
	Reverse	5'- GTGGCAGGAACAGGGGTG -3'	
RT-18s	Forward	5'- CTCTTAGCTGAGTGTCGCC -3'	Primers used for QPCR
	Reverse	5'- CTGATCGTCTTCGAACCTCC -3'	
RT-CHD1L	Forward	5'- GGTGGAGTTGGCATGAACCTT -3'	Primers used for QPCR
	Reverse	5'- CACTCAACTGGAGGTAGCA -3'	
GFP-NTKL	Forward	5'- CGGGATCCCAGGGGACGATGTGGTTCTT -3'	Primers for constructing GFP fused NTKL
	Reverse	5'- CGGAATTCCGTCCAGCTCCGGCTCCCA -3'	
NTKL-UP1	Forward	5'- CTTGCCTCCGCACCTA -3'	Primers used for Chip-PCR
	Reverse	5'- GCACAGGGTTGGAACCTAAA -3'	
NTKL-UP2	Forward	5'- ATGGCTGGAGGTGAGATA -3'	Primers used for Chip-PCR
	Reverse	5'- CAGAACAGGGTGATGGTG -3'	

Supplementary Table 2: Cox proportional hazard regression analyses for 3-year survival

Clinicopathological features	Univariable analysis		Multivariable analysis	
	HR(95%CI)	P	HR (95%CI)	P
NTKL expression				
Without up-regulation	1		1	
With up-regulation	2.83(1.36–5.86)	0.005	2.47(1.08–5.68)	0.033
Differentiation				
Well differentiated	1		1	
Poorly differentiated	3.47(1.47–8.21)	0.005	3.16(0.98–10.21)	NS
Vascular invasion				
Absent	1			
Present	2.79(1.44–1.5.37)	0.020	1.29(0.29–5.68)	NS
Tumor number				
Single	1		1	
Multiple	2.29(1.29–4.06)	0.005	2.07(0.45–9.40)	NS

(Continued)

Clinicopathological features	Univariable analysis		Multivariable analysis	
	HR(95%CI)	P	HR (95%CI)	P
Serum AFP level [\log_{10} (ng/ml)]				
Low	1		1	
High	1.56(1.24–1.95)	0.012	1.94(1.25–3.03)	0.003
Tumor stage (TNM)				
Early	1		1	
Late	2.54(1.40–4.60)	0.002	1.32(0.28–6.21)	NS

CI = confidence interval; HR = hazard ratio; NS = not significant.