Supplementary Table S1: Example of the R code used to develop the clinical nomogram. This utilised the 'rms' and 'survival' packages in R.

```
#RMS load data and nomogram construction
nomo <- read.csv("Clinical_train.csv", TRUE)
library(rms)
mod.Cox <- cph(Surv(DFI, CENSR) ~Palpnew + Mitoticrate + Necrosis, nomo,surv=TRUE)
ddist <- datadist(nomo)
options(datadist='ddist')
surv.Cox <- Survival(mod.Cox)
nom.Cox <- nomogram(mod.Cox,fun=list(function(x)surv.Cox(1095,x)),funlabel=c("3-year
DFS"),lp=FALSE)
plot(nom.Cox)


#RMS validation of Cox model using validation dataset
nomo_valid <- read.csv("Clinical_valid.csv", TRUE)
fit_valid <- cph(Surv(DFI,CENSR) ~Palpnew + Mitoticrate + Necrosis, nomo_valid,x=TRUE,
y=TRUE)
validate(fit_valid, method="boot", B=40, bw=FALSE, rule="aic",type="residual", sls=.05, aics=0,
force=NULL, estimates=TRUE, pr=FALSE, dxy=TRUE, u, tol=1e-9)


#RMS nomogram of IHC training data
nomo <- read.csv("IHC_test.csv", TRUE)
library(rms)
mod.Cox <- cph(Surv(DFI, CENSR) ~VEGF + Decorin + Mitoticrate + Age, nomo,surv=TRUE)
ddist <- datadist(nomo)
options(datadist='ddist')
surv.Cox <- Survival(mod.Cox)
nom.Cox <- nomogram(mod.Cox,fun=list(function(x)surv.Cox(1095,x)),funlabel=c("3-year
DFS"),lp=FALSE)
plot(nom.Cox)


#RMS validation of Cox model using IHC_validation dataset
nomo_valid <- read.csv("IHC_test.csv", TRUE)
fit_valid <- cph(Surv(DFI, CENSR) ~VEGF + Decorin + Mitoticrate + Age, nomo_valid,x=TRUE,
y=TRUE)
validate(fit_valid, method="boot", B=40, bw=FALSE, rule="aic", type="residual", sls=.05, aics=0,
force=NULL, estimates=TRUE, pr=FALSE, dxy=TRUE, u, tol=1e-9)
```

Supplementary Table S2. Results from statistical analysis of all patient and tumour characteristics used in the Clinical_train dataset.

	Mean	Median	Signif.	HR (95% CI)
Disease free interval (days)	764.57	655		
Recurrence **Recur = 27 (27%)** **No recur = 75 (73%)**				
Differentiation **1 = 54 (53%)** **2 = 38 (37%)** **3 = 10 (10%)**			p= 0.7	1.2 (0.7 - 2.2)
Mitotic rate **1 = 80 (78%)** **2 = 14 (14%)** **3 = 8 (8%)**			P = 0.03	1.9 (1.1 - 3.2)
Necrosis **0 = 74 (73%)** **1 = 23 (23%)** **2 = 5 (5%)**			P = <0.001	2.8 (1.6 – 5.0)
Grade **1 = 70 (69%)** **2 = 24 (24%)** **3 = 8 (8%)**			P = <0.001	2.6 (1.6 - 4.3)
Age **3 – 16 years**	9.657	9.5		1.0 (0.9 - 1.2)
Size **< 1cm = 6 (6%)** **1-5cm = 57 (56%)** **5cm = 39 (38%)**			P = 0.1	1.0 (0.1 - 5)
Palpable **Mobile = 49 (48%)** **Fixed = 53 (52%)**			P = 0.001	4.4 (1.8 - 11.05)

Supplementary Table S3. Results from statistical analysis of all patient and tumour characteristics used in the IHC dataset.

	Mean	Median	Range	Signif.	HR (95% CI)
Disease free interval (days)	772	655			
Recurrence **Recur = 26 (32%)** **No recur = 56 (68%)**					
VEGF score **Low = 43 (52%)** **High = 39 (47%)**				p= <0.001	8.4 (2.9 - 24.4)
Decorin score **1 = 26 (32%)** **2 = 22 (27%)** **3 = 34 (42%)**				p= 0.7	
Differentiation **1 = 31 (38%)** **2 = 40 (49%)** **3 = 11 (13%)**				p= 0.7	
Mitotic rate **1 = 61 (74%)** **2 = 12 (15%)** **3 = 9 (11%)**				p= 0.6	
Necrosis **0 = 54 (66%)** **1 = 23 (28%)** **2 = 5 (6%)**				p= 0.003	- 1.1 (0.4 - 2.7) 7.2 (1.9 - 27)
Grade **1 = 46 (56%)** **2 = 27 (33%)** **3 = 9 (11%)**				p= 0.5	
Age	9.77	10	12		
Size **< 1cm = 2 (2%)** **1-5cm = 45 (55%)** **>5cm = 21 (26%)**				p= 0.2	
Palpable **Mobile = 32 (39%)** **Fixed = 45 (55%)**				p= 0.03	- 2.7 (1.1 - 8)

Supplementary File S1. Dataset used in the creation of the Clinical Nomogram (Clinical_train.csv)

Supplementary File S2. Dataset used to validate the Clinical Nomogram (Clinical_valid.csv)

Supplementary File S3. Dataset used in the creation of the IHC Nomogram (IHC_test all.csv)