

1 **Prognostic role of TLR4 and TLR2 in hepatocellular carcinoma**

2 **Running head: Prognostic role of TLR4 and TLR2 in hepatocellular carcinoma**

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15 **Word count:** 2467

16 Keywords: Toll-like receptors, TLR4, TLR2, HCC

17

18 **Introduction**

19 Hepatocellular carcinoma (HCC) is the second most common cause of cancer mortality [1]. The overall 5-
20 year survival of HCC is only 8%; with curative surgery, the survival rate increases up to 40% [2]. However,
21 only 15-30% of newly diagnosed HCC cases can be treated with curative intent surgery [2] and new
22 prognostic markers are needed for clinical decision-making.

23 Toll-like receptors (TLR) are innate immunity receptors which recognize pathogen-associated molecular
24 patterns and enable rapid responses against invading pathogens [3]. The expression of TLR4 has been
25 associated with an enhanced ability of invasion and metastasis and poor prognosis in HCC [4,5]. The
26 promoting role of TLR2 in cell proliferation, lymph node metastasis, tumour invasion and correlation to
27 TNM stages in HCC has been observed [6,7].

28 The aim of this study was to investigate the prognostic role of TLR4 and TLR2 in HCC patients in the
29 population of Northern Finland.

30 **Materials and methods**

31

32 Study design and data collection

33 The study was a retrospective cohort study in a single tertiary care institution in Northern Finland. Design
34 and data collection has been reported earlier [8]. A total of 273 patients with histologically confirmed HCC
35 were treated in Oulu University Hospital between January 1983 and March 12, 2018. Of these, representative
36 paraffin-embedded tumour samples were available from 203 patients for analysis and were included in the
37 cohort. The 8th edition of TNM classification was used in staging. Patient survival data was acquired from
38 Statistics Finland. The Oulu University Hospital Ethics Committee approved the study and the need to obtain
39 informed consent from the study patients was waived by the Finnish National Authority for Medicolegal
40 Affairs (VALVIRA).

41

42 Detailed description of used immunohistochemistry and tissue microarray has been presented in
43 Supplementary material.

44

45 Immunohistochemical staining of TLR4 and TLR2 was evaluated by two independent investigators (V.K.
46 and N.K.), blinded from the clinical data. Cytoplasm intensity, cytoplasm percentage (e.g. percentage of cells
47 with detectable cytoplasmic expression), nuclei percentage and membrane percentage were evaluated.
48 Median values were used as cut-offs for further analysis. For more accurate description, see Supplementary
49 material. Examples of TLR4 and TLR2 cytoplasm intensity and nuclear staining are presented in
50 Supplementary Figure 1.

51

52 Outcomes

53 Primary outcomes of the study were 5-year overall survival and disease-specific survival. These were
54 defined as death from any cause (overall survival) or HCC (disease-specific survival) during the interval
55 between the date of surgery and the end of 5-year follow-up.

56

57 Statistical analysis

58 For categorical data analysis χ^2 -test was used. The threshold for significance was set at $P < 0.05$. In all
59 continuous variables, median and interquartile range are presented. Mann-Whitney U was used when
60 comparing continuous variables. Cohen's kappa was calculated to analyze interobserver agreement where
61 values between 0.01–0.20 indicate none to slight, 0.21–0.40 fair, 0.41–0.60 moderate, 0.61–0.80 substantial,
62 and 0.81–1.00 almost perfect agreement [9]. If interobserver difference was less than one point in intensity
63 or less than 30% in the proportion of positive cells, agreement was reached. Groups were defined according
64 to median values. Kaplan-Meier method was used to compare survival between groups and log-rank test was
65 used to analyze statistical differences between groups. Cox regression analysis was used to perform
66 multivariable analysis between groups with the following covariates: sex (female/male), age (continuous),
67 comorbidities (Charlson Comorbidity Index 0-1, 2 or higher), cirrhosis (no/yes), Child-Pugh index (A, B or
68 C), year of operation/diagnosis (1983-2005, 2006-2018), tumour grade (1-2, 3) and stage (1, 2 or higher). In
69 adjusted model 2, treatment (surgery, local ablation, transarterial chemoembolization, palliative treatment)
70 was added. Statistical analysis was performed with IBM SPSS statistics 24.0 (IBM Corp., Armonk, NY).

71

72

73 **Results**

74

75 Patients

76 Of 203 HCC patients, 37 (18.2%) were treated with surgery, 21 (10.3%) with local ablation (radiofrequency
77 ablation or percutaneous ethanol injection), 34 with transarterial chemoembolization (TACE) and 111
78 (54.7%) with best supportive care or palliative treatment. Median age was 71 years (IQR 64-79) with male
79 dominance (71.9%). Median follow-up time was 0.8 years (IQR 0.2-2.0). Most patients (60.6%) had Child
80 Pugh score A. Median tumour size was 65.5mm (IQR 40.0-100.0) and 11 (5.7%) patients had tumour stage
81 II or higher. The overall 5-year survival of the patients in the study cohort was 14.0% and disease-specific
82 survival 22.8%.

83

84 TLR4 and TLR2 stainings

85 Cytoplasmic, nuclear and membrane staining of TLR4 and TLR2, including good interobserver agreement in
86 hepatocellular carcinoma, has been described in Supplementary material.

87

88 TLR4 correlation with clinicopathological variables

89 TLR4 cytoplasm intensity was not associated with any clinicopathological variables. In TLR4 nuclei
90 percentage, differences between groups were observed in BMI ($p=0.004$), treatment method ($p<0.001$),
91 tumour recurrence ($p=0.009$), local tumour recidivism ($p<0.001$), alcohol consumption ($p=0.018$) and
92 cirrhosis ($p=0.034$). The baseline characteristics of TLR4 groups are presented in Supplementary Table 1.

93

94 TLR2 correlation with clinicopathological variables

95 TLR2 cytoplasm intensity was associated with given treatment ($p=0.028$), year of treatment ($p=0.002$) and
96 tumour unifocality ($p=0.033$), TLR2 nuclei percentage was associated with given treatment ($p=0.002$) and
97 local recidivism ($p=0.020$).

98

99 **Outcomes**

100

101 TLR4 and TLR2, 5-year survival

102

103 *Overall and disease-specific 5-year survival, TLR4 cytoplasm intensity*

104 Overall 5-year survival was 11.9% in strong TLR4 cytoplasm intensity group and 18.3% in weak TLR4
105 cytoplasm intensity group, $p=0.050$ (Figure 1A). Disease-specific 5-year survival was 14.3% in strong TLR4
106 cytoplasm intensity group and in weak TLR4 cytoplasm intensity group 33.7%, $p=0.004$ (Figure 1B).

107

108 *Overall and disease-specific 5-year survival, TLR4 percentage of positive nuclei*

109 Overall 5-year survival was 7.5% in high TLR4 nuclei percentage group and 22.7% in low TLR4 nuclei
110 percentage group, $p=0.019$ (Figure 1C). Disease-specific 5-year survival was 12.1% in high TLR4 nuclei
111 percentage group and 35.8% in low TLR4 nuclei percentage group, $p=0.009$ (Figure 1D).

112

113 *Overall and disease-specific 5-year survival, TLR2 cytoplasm intensity staining*

114 Overall 5-year survival was 14.4% in strong TLR2 cytoplasm intensity group and 15.2% in weak TLR2
115 cytoplasm intensity group, $p=0.986$. Disease-specific 5-year survival was 23.2% in strong TLR2 cytoplasm
116 intensity group and 24.3% in weak TLR2 cytoplasm intensity group, $p=0.873$.

117

118 *Overall and disease-specific 5-year survival, TLR2 percentage of positive nuclei*

119 Overall 5-year survival was 27.9% in high TLR2 nuclei percentage group and 14.0%, in low TLR2 nuclei
120 percentage group, $p=0.238$. Disease-specific 5-year survival was 49.6% in high TLR2 nuclei percentage
121 group and 22.5% in low TLR2 nuclei percentage group was, $p=0.130$.

122

123

124 *TLR4 cytoplasm intensity, percentage of positive nuclei, cox regression analysis*

125 For results of multivariable analysis see Table 1. In both adjusted models, TLR4 cytoplasm intensity was
126 associated with 5-year disease-specific mortality (model 1 HR 1.95, 95% CI 1.30-2.92, model 2 HR 1.53,
127 95% CI 1.02-2.28), Table 1. TLR4 percentage of positive nuclei associated with risk for 5-year overall (HR
128 1.52, 95% CI 1.06-2.16) and disease-specific (HR 1.78, 95% CI 1.19-2.68) mortality in model 1, Table 1.

129

130 Multivariable analysis was not performed in TLR2 due to non-significant differences in crude survival
131 between groups.

132

133

134

135 **Discussion**

136

137 The results of this study suggest that TLR4 expression is a prognostic factor in HCC. Strong cytoplasmic
138 TLR4 intensity and high TLR4 nuclei percentage were associated with poor 5-year overall and disease-
139 specific survival. In multivariable analysis, strong cytoplasmic TLR4 intensity remained prognostic in both
140 models.

141

142 The strengths of this study are homogenous study population and single geographical area where the
143 diagnosis and treatment occurred in same hospital, minimizing the selection bias. Full access to patient
144 records was available, so we were not restricted to register data, which is often the case in large scale studies.
145 We were able to perform regression analysis with previously recognized confounding factors in adjusted
146 model 1 where both TLR4 cytoplasm intensity and nuclear percentage were independently prognostic. To

147 include the effect of the given treatment, adjusted model 2 was performed. However, treatment strongly
148 overlaps with other covariates such as stage, cirrhosis and Child-Pugh index, but to avoid false positive
149 results, adjusted model 2 was used as the primary analysis despite the possibility of over-adjustment.
150 However, despite strong adjustment, TLR4 cytoplasm expression remained prognostic. The long time period
151 of 35 years (1983-2018) may cause confounding due to the improvements in HCC treatment and staging
152 over the years. Nevertheless, limitations were taken into account by adjusting with relevant confounding
153 factors. To our knowledge, the present study is the largest to examine TLR4 and TLR2 in HCC. We have
154 previously validated the used TLR antibodies with Western blot from human liver [10] suggesting that
155 immunostaining in the current study should work as intended. However, validation studies with other patient
156 cohorts and methods are still needed.

157

158 In previous studies, TLR4 expression has been linked to early recurrence, poor disease-specific survival and
159 associated with higher microvascular invasion [4]. Also negative results have been reported [6,11]. TLR4 in
160 nuclei has been previously observed for example in esophageal cancer, for example, also associating with
161 survival [12].

162 TLR2 expression in cytoplasm and cell nuclei have been previously reported [13]. TLR2 has been associated
163 with grade of differentiation, stage and disease-free survival [6]. Suppression of TLR2 has resulted in lower
164 tumour cell proliferation, invasion and migration [7]. In most cited studies, TLR2 expression levels were
165 higher in HCC and correlated with poor prognosis, but we were unable to repeat this finding which can be
166 due to different etiology in Western and Eastern populations (alcohol vs. hepatitis infection).

167

168 The relationship between inflammatory response and cancer progression has been known for years [14]. In
169 several animal models inflammatory cells and cytokines, such as NF- κ B, TNF- α and various interleukins,
170 have shown the ability to promote carcinogenesis with their anti-apoptotic effects, induction of oxidative
171 damage to DNA, and the induction of tissue repair response [14–17]. Toll-like receptors are known for their
172 role in host defense, but increasing evidence suggests also a role in cancer progression [15]. Infection, or

173 injury can induce inflammation, which can promote tumorigenesis through chronic tissue damage and the
174 subsequent induction of tissue repair [15]. The unregulated TLR-regulated tissue repair response can drive
175 tumour growth and progression in a positive feedback of unregulated tissue injury and repair, which can
176 trigger TLR-dependent inflammatory responses [15]. Multiple mechanisms for TLRs role in cancer
177 promotion have been suggested [5,15,18–20]. Also, the potential role of TLRs in cancer immunotherapy has
178 gained a lot of interest [21]. The underlying mechanism behind nuclear translocation of TLR4 and the
179 correlation with prognosis is unclear. TLR4 contains several sequences indicating nuclear localization [22].
180 Alternatively, nuclear carrier proteins might be related to nuclear translocation, but no such proteins have
181 been identified. Translocation of membrane-bound TLRs to nucleus might be due to an increased amount of
182 these proteins and related to signaling activity [12].

183

184 Alcohol consumption leads to the activation of innate immunity via TLRs signaling, and TLR4 signaling
185 seems to contribute with the development of alcohol liver disease [23]. Alcohol ingestion or high fat intake
186 disrupts the protective mucosal barrier due to the overgrowth of intestinal bacteria or disruption of intestinal
187 barrier functions, resulting in higher intake of endotoxins, which leads to activation of TLR signaling
188 cascades that regulate inflammatory response and the release of various cytokines [23,24]. In our study,
189 TLR4 expression associated with cirrhosis and alcohol consumption. Previously, hepatic TLR4 and TLR2
190 expression has been observed to be higher in hepatitis and cirrhosis tissue samples than in HCC [25]. Also,
191 high intake of alcohol leads to increased levels of LPS, which is the key factor for alcohol-induced liver
192 injury and it is known that alcohol is a major risk factor in population of Northern Europe. This might be the
193 explanation why in this study the expression of TLR4, but not TLR2, was found to be a risk factor for poor
194 prognosis [26].

195

196 The results of the present study have clinical and research-related implications. Our study showed that strong
197 cytoplasmic TLR4 expression is an independent factor for poor prognosis in HCC. High TLR4 nuclei
198 expression percentage seems to have prognostic impact in HCC, but in this cohort poor prognosis was seen

199 only in unadjusted analysis, and multivariable analysis when given treatment was not included as a
200 confounder. Replication studies are needed in the future to examine the prognostic role of TLR4 in HCC,
201 especially in different subgroups based on received treatment. Furthermore, optimal cut-offs need to be
202 determined. Based on this study, TLR4 is a useful biomarker for poor prognosis both in surgically resected
203 tissue samples as well as from core biopsies with good interobserver agreement. TLR2 nuclear percentage
204 was detected in 90.6% patients, but only 9.1% had high TLR2 nuclei percentage. The absolute survival
205 difference between high and low TLR2 nuclei percentage was nearly 30%, but without statistical
206 significance. The role of TLR2 nuclear percentage in HCC needs further studies.

207

208 **Conclusion**

209

210 TLR4 cytoplasmic expression is independently prognostic in HCC. Role of TLR4 cytoplasmic and nuclear
211 expression in different treatment subgroups need further studies.

212

213 Additional information

214

215 Authors' contributions

216 **Valtteri Kairaluoma:** investigation, drafted the manuscript, formal analysis, conceptualization,
217 methodology, software, writing - original draft, writing - review & editing, visualization, validation, project
218 administration.

219 **Olli Helminen:** investigation, formal analysis, conceptualization, methodology, software, investigation,
220 writing - review & editing, visualization, resources, funding acquisition, supervision, project administration.

221 **Niko Kemi:** investigation, formal analysis, conceptualization, methodology, software, writing - review &
222 editing, visualization, validation.

223 **Heikki Huhta:** acquired the data, performed the experiments, formal analysis, conceptualization,
224 methodology, software, writing - review & editing, visualization.

225 **Vesa-Matti Pohjanen:** acquired the data, investigation, formal analysis, conceptualization, methodology,
226 software, writing - review & editing, visualization, supervision.

227

228 Ethical approval and consent to participate

229 The study was approved by the Oulu University Hospital Ethics Committee and the hospital district
230 (committee's reference number 81/2008). The need to obtain informed consent from the study patients was
231 waived by the Finnish National Authority for Medicolegal Affairs (VALVIRA, reference number
232 10832/06.01.03.01/2014). The study was performed in accordance with the Declaration of Helsinki.

233

234 Data availability

235 Anonymized data is available from the corresponding author upon request. Sharing the data will require
236 additional ethical approval.

237

238 Declaration of Interest statement

239 Authors declare that they have no conflicts of interest.

240

241 Funding

242 This work was supported by grants from The Finnish Medical Foundation (V.K.) and Georg C. and Mary
243 Ehrnrooth Foundation and Finnish State Research Fund (H.H. and O.H.)

244 Acknowledgements

245 The study benefited from samples/data from Northern Finland Biobank Borealis, Oulu, Finland.

246 We thank Dr. Matti Kairaluoma for his contribution editing the Supplementary Figure 1.

247

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301 levels of endotoxin and markers of monocyte activation. *Sci Rep.* 2017;7:4462.
- 302

303 Table 1. Overall and disease-specific 5-year mortality, TLR4 cytoplasm intensity and TLR4 percentage of
 304 positive nuclei. Hazard ratios (HR) with 95% confidence intervals (CI) of mortality comparing patients with
 305 HCC treated in Oulu University Hospital 1983-2018. Follow-up ended December 31, 2017. In patients
 306 treated in 2018, follow-up ended 30 days after surgery.

307

	Weak TLR4 cytoplasm intensity (n=176) HR (95% CI)	Strong TLR4 cytoplasm intensity (n=176) HR (95% CI)	Low TLR4 nuclei percentage (n=179) HR (95% CI)	High TLR4 nuclei percentage (n=179) HR (95% CI)
5-year overall mortality				
Crude	1 (reference)	1.40 (0.99-1.96)	1 (reference)	1.49 (1.07-2.08)
Adjusted model 1 ^a	1 (reference)	1.56 (1.01-2.23)	1 (reference)	1.52 (1.06-2.16)
Adjusted model 2 ^b	1 (reference)	1.24 (0.87-1.77)	1 (reference)	0.75 (0.50-1.12)
5-year disease specific mortality				
Crude	1 (reference)	1.74 (1.19-2.54)	1 (reference)	1.65 (1.13-2.41)
Adjusted model 1 ^a	1 (reference)	1.95 (1.30-2.92)	1 (reference)	1.78 (1.19-2.68)
Adjusted model 2 ^b	1 (reference)	1.53 (1.02-2.28)	1 (reference)	0.82 (0.52-1.30)

308

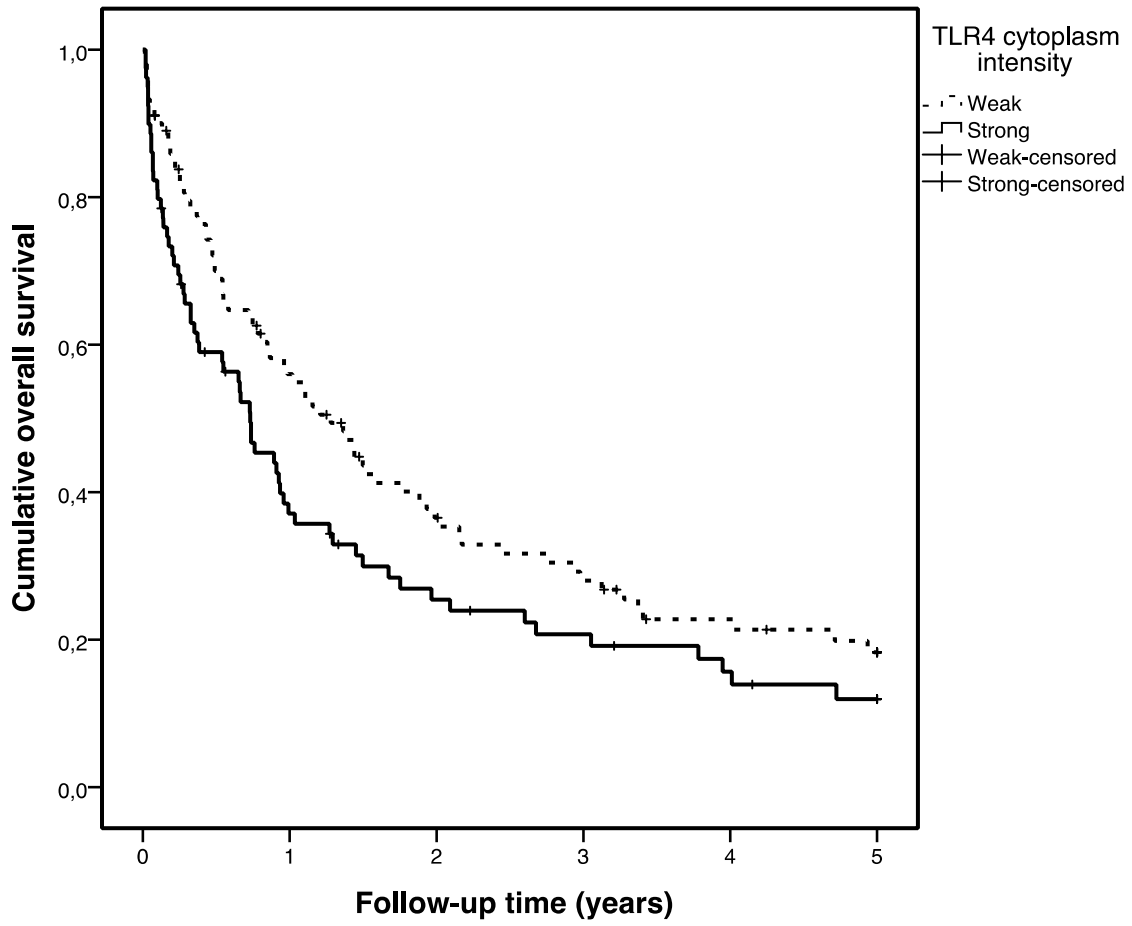
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310 **Figure Legends**

311

312 Figure 1A. Overall 5-year survival, TLR4 cytoplasm intensity

313

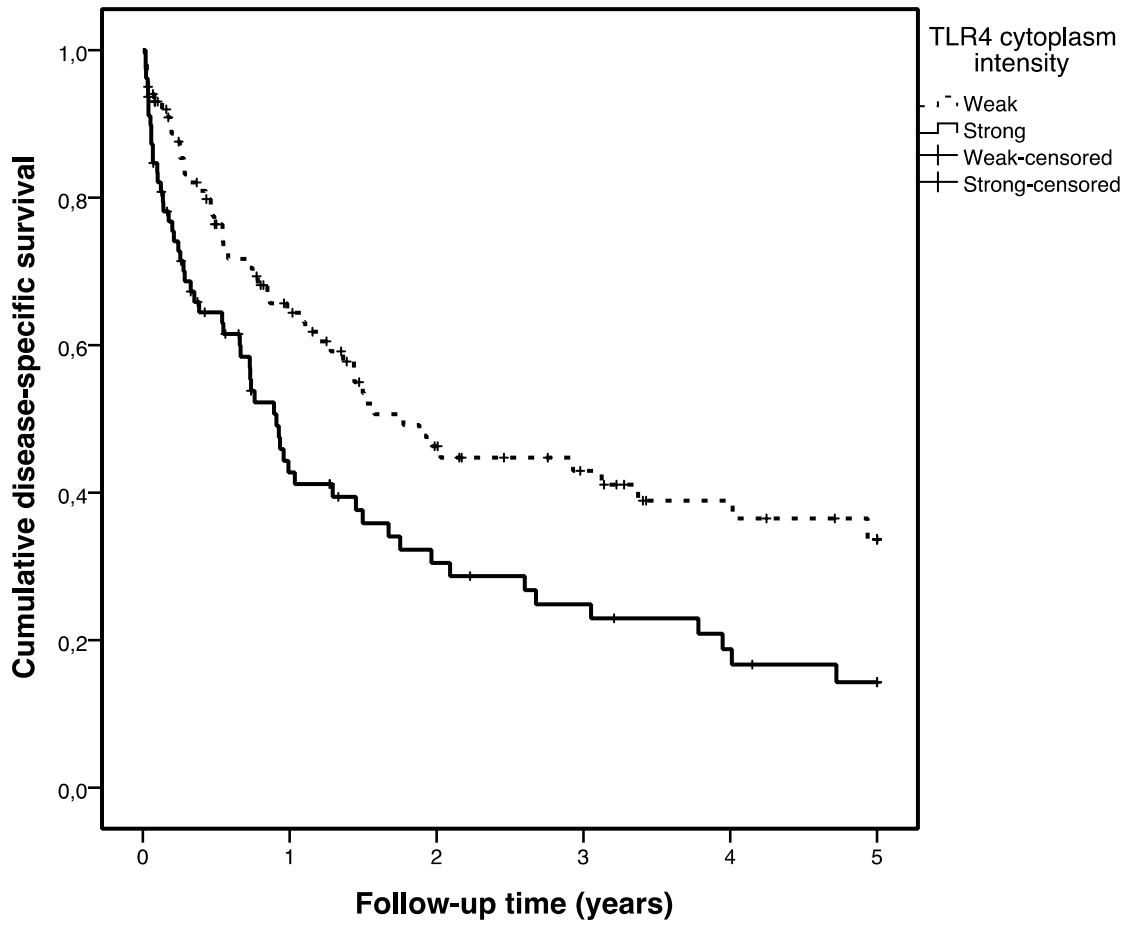


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316 Figure 1B. Disease-specific 5-year survival, TLR4 cytoplasm intensity

317



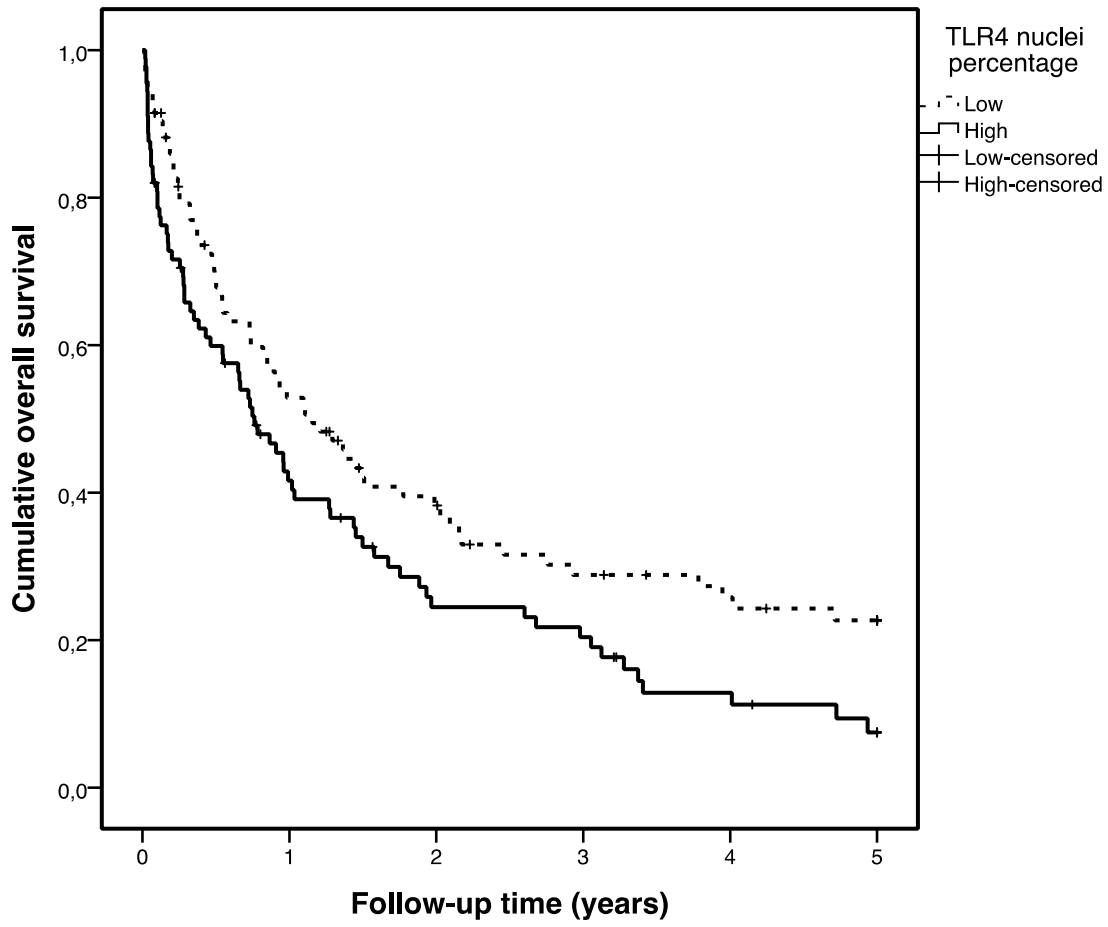
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321 Figure 1C. Overall 5-year survival, TLR4 nuclei percentage

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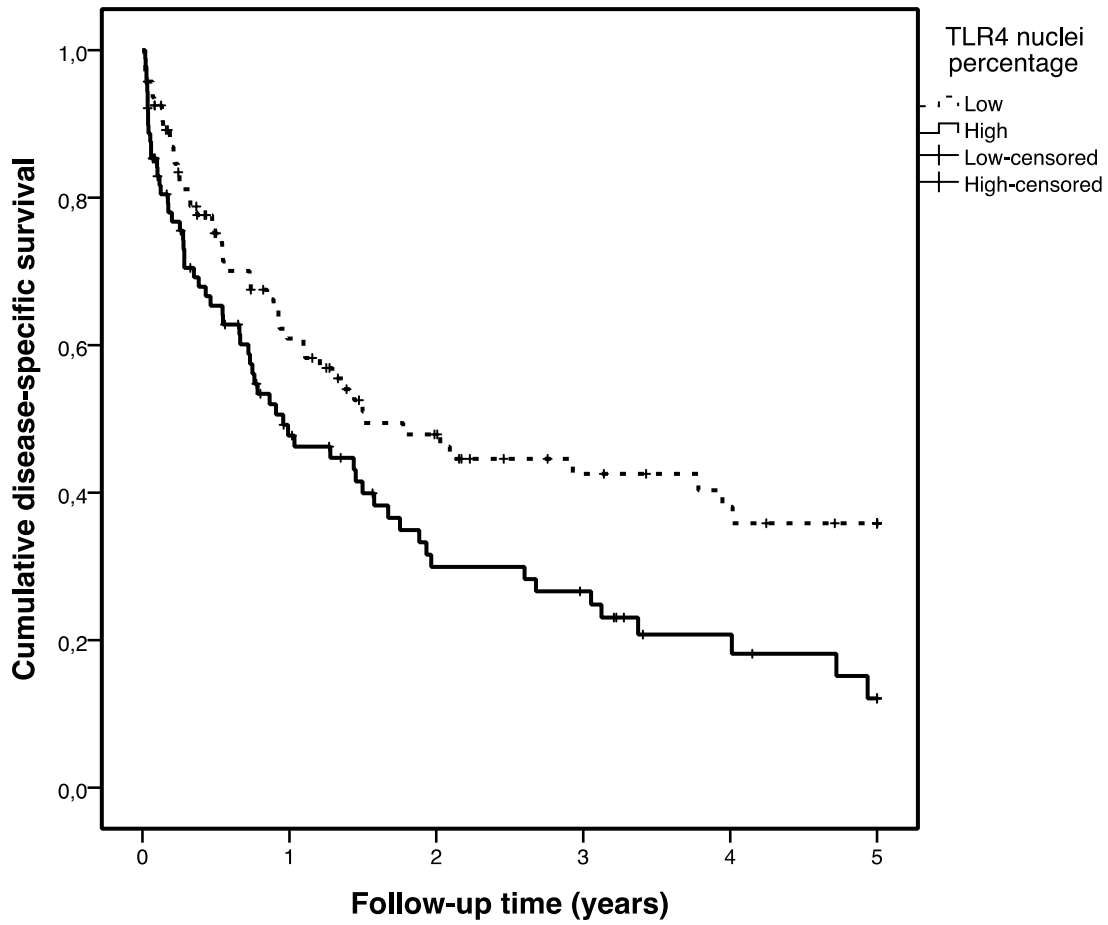


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324

325 Figure 1D. Disease-specific 5-year survival, TLR4 nuclei percentage

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327