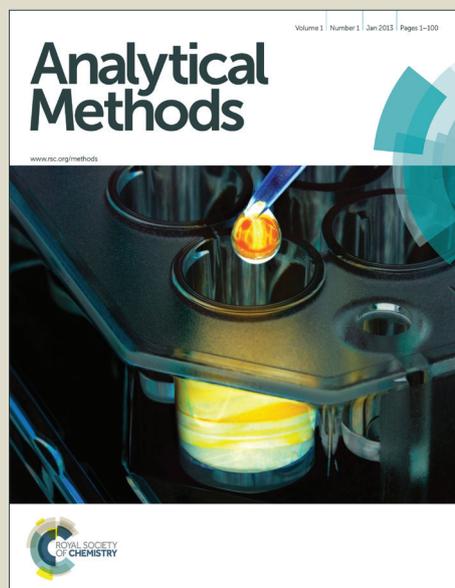


Analytical Methods

Accepted Manuscript



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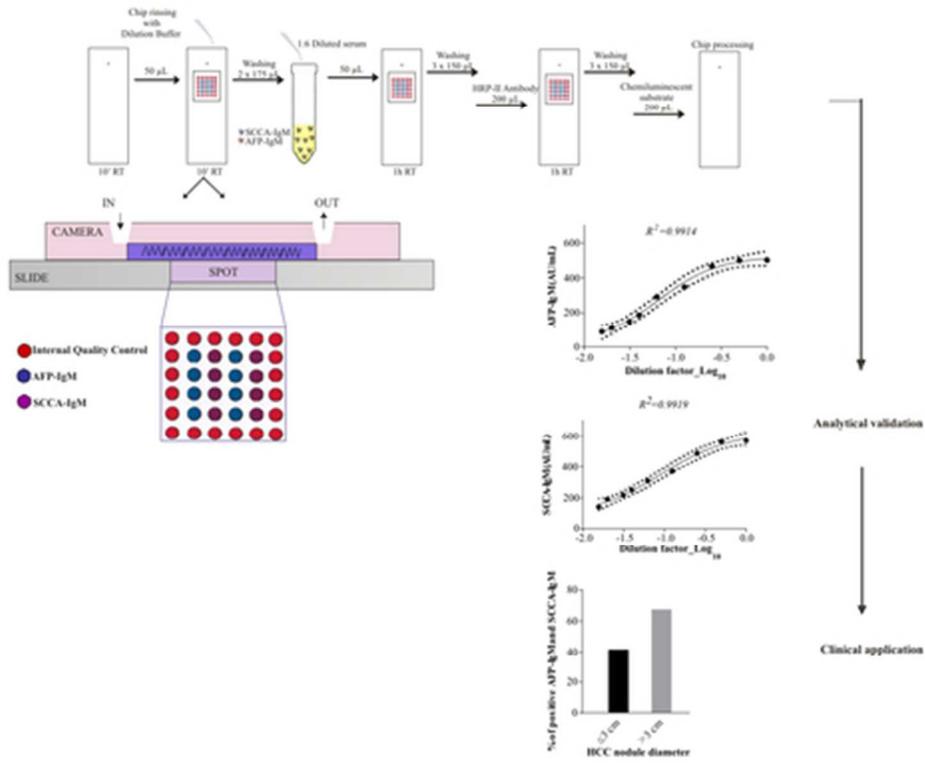


TABLE OF CONTENTS

This contribution demonstrates that a novel Biochip with ink-jet spotted antibodies for the chemiluminescent detection of AFP-IgM and SCCA-IgM is analytically reliable and has potential clinical application. 39x32mm (300 x 300 DPI)

1
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4 1 *Full Title:* Analytical Validation of a Biochip prototype for integrated analysis of AFP-IgM
5
6 2 and SCCA-IgM serum biomarkers in patients with liver cirrhosis and hepatocellular
7
8 3 carcinoma.

9
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13 **TABLE OF CONTENTS**

14 This contribution demonstrates that a novel Biochip with ink-jet spotted antibodies for the
15 chemiluminescent detection of AFP-IgM and SCCA-IgM is analytically reliable and has
16 potential clinical application.

17

1
2
3 **18 ABSTRACT**
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5 *19 Aim:* This study evaluates the analytical and clinical performances of a new technology,
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7
8 *20 CompleXima HCC Biochip*, for the simultaneous serum measurement of alpha-fetoprotein-
9
10 *21 IgM (AFP-IgM) and squamous cell carcinoma antigen-IgM (SCCA-IgM).*

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12 *22 Methods:* AFP- and SCCA-IgM were measured by both ELISA and CompleXima HCC
13
14
15 *23 Biochip* in 39 blood donors and in 174 patients (102 liver cirrhosis -LC- and 72 hepatocellular
16
17 *24 carcinoma -HCC-).*

18
19
20 *25 Results:* The intra-assay coefficients of variation were lower than 12% and inter-assay were
21
22 *26 comprised* between 14% and 21%. The linearity interval for CompleXima HCC Biochip was
23
24 *27 50-300 AU/mL* for AFP-IgM and SCCA-IgM. The comparison between the prototype and the
25
26
27 *28 ELISA test* was studied by using Bland-Altman method and Passing-Bablok regression
28
29 *29 analyses.* Passing-Bablok showed that the Biochip under-estimated AFP-IgM (Intercept A: -
30
31 *30 165.06; 95% CI: -313.11 to -51.32)* and overestimated SCCA-IgM (Intercept A: 26.83; 95%
32
33 *31 CI: 14.47-35.86)* with respect to ELISAs. Both biomarkers were higher in LC and HCC with
34
35 *32 respect* to controls ($p < 0.001$) with no difference between LC and HCC ($p = 0.864$ for AFP-IgM
36
37 *33 and* $p = 0.214$ for SCCA-IgM). The thresholds for AFP-IgM and SCCA-IgM were calculated
38
39 *34 by means* of ROC curves, fixing the specificity at 95%. Sensitivity for AFP-IgM and SCCA-
40
41 *42 IgM* associated with CompleXima in detecting patients with liver diseases were 47% and
42
43 *35 46%,* respectively. The combined evaluation of macrocomplexes with CompleXima in
44
45 *36 diagnosing* HCC with respect to LC was associated with a sensitivity of 51.4% and a
46
47 *37 specificity* of 48%.

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49
50 *38 Conclusions:* AFP-IgM and SCCA-IgM increase in chronic liver disease. The prototype
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53 *39 CompleXima HCC Biochip* allows their measuring with a good analytical reproducibility.
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41 INTRODUCTION

42 Hepatocellular carcinoma (HCC) represents the sixth most common cancer in the world
43 (about 700000 new cases yearly) and the third cause of cancer-related death¹. Although non-
44 alcoholic steatohepatitis associated with obesity, insulin resistance, and type 2 diabetes has
45 recently emerged as a risk factor for HCC², in more than 90% of the cases HCC develops
46 within an established chronic liver disease, namely liver cirrhosis (LC). The most relevant
47 causes of HCC, viral hepatitis B and C and alcohol abuse, in most instances first determine
48 LC, which might evolve in established HCC through a multistep process including early stage
49 neoplasia (early HCC)³⁻⁷. Since a delayed diagnosis of HCC is associated with a worse
50 prognosis⁸, the need of identifying patients with HCC as earlier as possible is advised in order
51 to improve treatment options and ameliorate survival.

52 The association between LC and HCC represents the basis for preventive strategies,
53 which contemplate only one biomarker, serum alpha-fetoprotein (AFP). AFP is a 70 kDa
54 oncofetal antigen proposed in the mid '60 as HCC tumor marker⁹. In normal adults' sera low
55 levels of AFP are detectable. AFP increases during pregnancy¹⁰ but the highest levels are
56 found in the presence of HCC, supporting its use as HCC tumor marker, as stated by several
57 European associations for the study of the liver (EASL, ESMO, EGTM) and by the US
58 National Academy for Clinical Biochemistry (NACB)^{1,11}. However, the limitations in both
59 sensitivity and specificity of AFP have prompted the American Association for the Study of
60 Liver Diseases (AASLD) to rule out AFP from current guidelines for HCC^{12,13}.

61 The discovery and clinical validation of new sensitive and specific biomarkers for the
62 early detection of HCC is strongly advised to overcome AFP limitations or improve AFP
63 clinical utility¹¹⁻¹³. Among the most promising biomarkers of HCC, squamous cell carcinoma
64 antigen (SCCA), a 45-55 kDa member of the serpin family of ovalbumin-serine protease
65 inhibitors, deserves major interest. Two main variants of this antigen have been correlated
66 with HCC, SCCA1, originally identified in squamous cell carcinoma of the uterine cervix¹⁴,

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3 67 and SCCA2. These SCCA isoforms are produced by two tandemly arranged genes located on
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5 68 chromosome 18q21¹⁵; they share a 98% and 92% homology in nucleotide and amino acid
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8 69 sequences, their main difference being found in the reactive site loop (RSL) amino acid
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10 70 sequence responsible for the proteolytic activity. Overall, SCCA is expressed in stratified
11
12 71 squamous epithelia and it is over-expressed in squamous cell carcinoma¹⁶. In HCC patients,
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14 72 the high expression levels of SCCA found in tumoral, not in peritumoral tissues, and in sera
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16 73 have prompted us to suggest this marker as useful for the detection of this cancer type^{17,18}.

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19 74 Both AFP and SCCA are detectable in HCC sera as free antigens, but, as demonstrated
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21 75 for other tumor markers in different cancer settings, they may enter in IgM
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23 76 macrocomplexes¹⁹⁻²⁷. The pathophysiological mechanism underlying the appearance in cancer
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25 77 patients' sera of tumor antigen-IgM macrocomplexes is not completely understood, although
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27 78 it has been suggested that they might be the expression of a physiological mechanism aimed
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29 79 at clear tumor antigens, mainly when they are abnormally glycosylated and/or at high
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31 80 levels^{28,29}. Irrespective of the pathophysiological significance of macrocomplexes, in HCC
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33 81 AFP-IgM in association with AFP determination was suggested to be useful for early
34
35 82 diagnosis^{23,30} and for tumor size prediction³¹, while SCCA-IgM serum levels were shown to
36
37 83 have a prognostic role in patients with chronic HCV-related hepatitis³² and were suggested to
38
39 84 be HCC risk predictors in patients with LC³³. More recently serum SCCA-IgM values were
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41 85 proposed to be useful for prognosis, since low values were correlated with a lower HCC risk³⁴
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43 86 and a longer overall survival³⁵.

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45
46 87 The serum determination of IgM macrocomplexes is actually performed by established
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48 88 ELISA assays, and recently our group demonstrated that SCCA-IgM ELISA determination is
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50 89 not affected by endogenous immunoglobulins, such as IgM with rheumatoid factor activity,
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52 90 supporting the reliability of this detection method³⁶. However, to be cost-effective ELISA
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54 91 assays should be run when the number of samples to be analysed completely fulfill the
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56 92 microtiter ELISA plate. The specific clinical context for which AFP-IgM and SCCA-IgM

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3 93 serum determinations appear to be appropriate might restrict the number of samples to be
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5 94 analysed, especially among non-referral centres. As a consequence the time spent to collect
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8 95 enough samples before performing ELISA determinations might increase the overall turn
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10 96 around time thus unmeeting the clinical needs. A laboratory system which allows individual
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12 97 sample handling providing a reliable and simultaneous measurement of AFP-IgM and SCCA-
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15 98 IgM macrocomplexes in a short time, appears therefore advised. Nanotechnology may be a
16
17 99 reliable tool to address this issue.

100 In recent years the introduction of nanotechnology in diagnostics provided several
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102 miniaturized devices which allow the simultaneous detection of hundreds to thousands of
103
104 targets, including nucleic acids and proteins³⁷. Micro-array systems, mainly designed to detect
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106 nucleic acids, such as the FDA approved Amplichip CYP450, allowed transferability of
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108 complex genetic-based analyses in clinical medicine because they offer the advantage to
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110 handle complexity in a reliable, easy and rapid way^{37,38}. Lab-on-chip miniaturized devices to
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112 replace ELISA immunoassays have also been developed in order to simultaneously test
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114 several proteins for each patient just using small amounts of biological fluids. We developed a
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116 multiplex chip designed system to simultaneously detect AFP-IgM and SCCA-IgM, which
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118 novelty is mainly represented by a miniaturized glass surface which is deposited with
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120 antibodies by means of the precise ink-jet technology, usually employed for ink printers. Our
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122 aims were to investigate the analytical and clinical performances of this novel chip technology
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124 (CompleXima HCC Biochip) in comparison with commercially available ELISAs.

125 **MATERIALS AND METHODS**

126 *Study design*

127 The analytical and clinical performances of CompleXima HCC Biochip were verified using
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129 retrospective collected patients and control sera, following the experimental steps illustrated
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131 in Figure 1.

132 *Patients*

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3 119 Sera from a total of 174 patients, including 102 LC and 72 HCC, stored in the Liver Bio bank
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6 120 of the Department of Medicine, University of Padova, were analysed. The study was
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8 121 approved by the Ethics Committee for Experimentation of Azienda Ospedaliera di Padova
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10 122 (protocol n. 1958P; approved on February 8th 2010). Participants provided their written
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12 123 informed consent for the study. Patients characteristics are detailed in Table 1. Thirty-nine
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14 124 blood donors (23 males, 16 females, mean age \pm SD: 45 \pm 8.5) were also included as controls.
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16 125 HCC diagnosis was done when focal lesions >2 cm in diameter were found by US scan and
17
18 126 confirmed with CT or MR and it was always histologically confirmed (US-guided fine-needle
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20 127 biopsy). Whole blood was collected in Vacutainer tubes (BD Diagnostics, USA) from all
21
22 128 cases and controls and centrifuged for 15' at 2000 x g to obtain sera, which were aliquoted
23
24 129 and stored at -20°C until use. Samples were collected before any pharmacological or surgical
25
26 130 treatment.

131 *Laboratory techniques*

132 **ELISA for AFP-IgM and SCCA-IgM.**

133 Circulating macrocomplexes AFP-IgM and SCCA-IgM were measured by the commercial
134 ELISA kits Hepa AFP-IC and Hepa-IC respectively (Xeptagen S.p.A., Venezia, Italy)
135 according to manufacturer's instructions. In these assays, rabbit oligoclonal anti-human AFP
136 or anti-human SCCA antibodies were used as capture antibodies. The amount of AFP-IgM
137 and SCCA-IgM was expressed in arbitrary units per mL (AU/mL) as described elsewhere^{23,39}.

138 **AFP-IgM and SCCA-IgM determination using CompleXima Biochip.**

139 CompleXima HCC Biochip prototype has been developed by Xeptagen S.p.A. and Olivetti I-
140 Jet (Torino, Italy). It is based on the contemporary chemiluminescent serum detection of AFP-
141 IgM and SCCA-IgM using a biochip technology. CompleXima HCC Biochip was prepared
142 using a positively charged 2.1x2.1 mm silica surface which was covered with a regular
143 distribution of 36 antibodies spots, each with a diameter of 127 μ m and a surface area of 12.6
144 μ m². Spotting was realized by using an ink-jet method under patent. The external ring, made

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3 145 of 20 individual spots of rabbit IgG anti-human IgM, represented the internal quality control
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5 146 (IQC). The remaining 16 spots inside the IQC ring were replicates of synthetic anti-AFP-IgM
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8 147 and anti-SCCA-IgM (8 replicated spots/each analyte). The silica surface was included in a
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10 148 microfluidic reaction chamber, with in and out accesses. The manufacture's suggested
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12 149 original protocol for CompleXima HCC Biochip analysis included the following analytical
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15 150 steps: direct addition to the reaction chamber of 1:6 diluted sera in PBS-non fat milk,
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17 151 incubation at room temperature (RT) for 1 hr, two washings with PBS-Tween and addition of
18
19 152 the secondary antibody (goat IgG anti-human IgM-HRP), incubation at RT for 1 hr, two
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21 153 washings, addition of the chemiluminescent HRP substrate and chip reading. The detection
22
23 154 and transduction signal systems were based on a CCD (Charge Coupled Device) digital
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25 155 camera and they were part of an integrated system (called Biochip reader) which included the
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27
28 156 CCD Hamamatsu ORCA 05GX, a netbook and a chip housing system. CCD images, which
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30 157 were black and white with a 1344x1024 pixel resolution, were acquired and processed by a
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32 158 dedicated software. Instrument sensitivity was supported by a 16 bit electronics. The
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34 159 dedicated software, on the basis of IQC ring results, selected and distinguished valid from
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36 160 invalid analyses. The concentration and the intra-chip CV for AFP-IgM and SCCA-IgM were
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38 161 calculated by the dedicated software. The CompleXima HCC Biochip returned quantitative
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40 162 results above 50 AU/mL and below 600 AU/mL.

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46 163 The original protocol was optimized as follow and detailed in Supplementary figure 1:
47
48 164 any chip was kept RT for 10', then rinsed with 50 μ L of dilution buffer for 10', washed twice
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50 165 with 175 μ L of washing buffer before adding diluted sera (1:6). All incubations were
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52 166 performed in a humid chamber. All subsequent washings (150 μ L/each) were repeated three
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54 167 instead of two times.

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58 168 AFP-IgM and SCCA-IgM were measured in all serum samples by both ELISAs and by using
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60 169 the CompleXima HCC Biochip. To obtain CompleXima HCC Biochip results in individual
170 sera, all samples were subjected to a first run to distinguish those with AFP-IgM and SCCA-

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3 171 IgM results below or above the upper detection limit of the system (600 AU/mL), the latter
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5 172 requiring further dilution before analysis. All sera were then properly diluted and analysed in
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8 173 triplicate. The mean of these three replicates was used to assign CompleXima HCC Biochip
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10 174 AFP-IgM and SCCA-IgM values for any given patient and were used for comparison with
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13 175 ELISA results.

15 176 **AFP determination.**

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17 177 AFP levels were measured using an automated method (ARCHITECT AFP, Abbott
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19 178 Diagnostics, Sligo, Ireland), which is a two-step assay based on CMIA (Chemiluminescent
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21 179 Microparticle ImmunoAssay) technology.

24 180 *Statistical analysis*

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27 181 Bland-Altman method and Passing-Bablok regression were used to evaluate the agreement
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29 182 between CompleXima HCC Biochip and ELISA assays^{40,41}. For these comparisons ELISAs
30
31 183 and Biochip results of the whole studied subjects (n=213) were included. AFP-IgM and
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33 184 SCCA-IgM thresholds were assessed by Receiver Operating Characteristics (ROC) curve
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35 185 analysis. Statistical analysis was performed using the nonparametric Mann–Whitney Rank
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37 186 Sum Test. Logistic regression models and statistical analysis were performed with statistic
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39 187 software STATA (version 10). Statistical significance was considered when $p < 0.05$.

43 188 **RESULTS**

44
45 189 Overall 1089 Biochips were used in this study to evaluate the performance of CompleXima
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47 190 HCC Biochip prototype. Among them, 34% were marked as invalid by the software since the
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49 191 IQC did not met the established criteria, due to heterogeneity among spots or to the presence
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51 192 of bubble airs.

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54
55 193 Table 2 reports intra-assay coefficients of variation (CV_{intra}) of CompleXima HCC
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57 194 Biochip, which were calculated using a series of 8 different HCC serum samples with high,
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59 195 medium and low concentration levels of AFP-IgM and SCCA-IgM. The inter-assay
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196 coefficient of variation (CV_{inter}), which was calculated by means of 20 repeated measures of

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3 197 the same sample in different days, was 14% for AFP-IgM (mean \pm SD, 310 \pm 42 AU/mL) and
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5 198 21% for SCCA-IgM (mean \pm SD, 463 \pm 95 AU/mL).
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8 199 Sera with high levels of AFP-IgM or SCCA-IgM were selected to define the linearity
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10 200 interval of CompleXima HCC Biochip. Serial dilutions of sera with the dilution buffer were
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12 201 performed and analysed. As shown in Figure 2, values above 300 AU/mL were outside the
13
14 202 linearity for both AFP-IgM and SCCA-IgM.
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17 203 To verify the agreement between ELISAs and CompleXima HCC Biochip results, two
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19 204 statistical approaches were used: the Bland-Altman method and the Passing Bablock
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21 205 regression analysis. Both approaches assume uncertainty of the new (CompleXima HCC
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23 206 Biochip) and the control (ELISA) test. Bland-Altman plot allows to detect the presence of a
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25 207 proportional bias⁴⁰, while Passing Bablock regression analysis is the only method that adjusts
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27 208 for non-normal data as frequently observed in practice⁴¹. Figure 3 shows the Bland-Altman
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29 209 plot results of AFP-IgM and SCCA-IgM values obtained with CompleXima HCC Biochip in
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31 210 comparison with those obtained with the respective ELISAs. Passing-Bablok regression
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33 211 analyses showed that the Biochip prototype underestimated AFP-IgM (Intercept A: -165.06;
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35 212 95% CI: -313.11 to -51.32) and overestimated SCCA-IgM (Intercept A: 26.83; 95% CI: 14.47
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37 213 to 35.86) with respect to ELISAs.
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43 214 Figure 4 shows AFP-IgM (upper panel) and SCCA-IgM (lower panel) measured with
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45 215 CompleXima HCC Biochip in controls, LC and HCC patients. The levels of both markers
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47 216 were significantly higher in LC and HCC patients with respect to controls ($p < 0.001$ for AFP-
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49 217 IgM and SCCA-IgM; Mann-Whitney Rank Sum Test). However, no difference between LC
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51 218 and HCC was observed ($p = 0.864$ and $p = 0.214$ for AFP-IgM and SCCA-IgM, respectively;
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53 219 Mann-Whitney Rank Sum Test).
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57 220 ROC curve analysis for AFP-IgM and SCCA-IgM measured with CompleXima HCC
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59 221 Biochip and ELISAs, and for AFP serum levels were performed (Fig. 5). The thresholds were
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222 identified by fixing the specificity at 95%; corresponding sensitivities in distinguishing

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3 223 healthy subjects from patients with advanced liver disease, including both LC and HCC, were
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5 224 calculated and they are reported in Table 3. The established cut-off values (60 AU/mL for
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8 225 AFP-IgM and 139 AU/mL for SCCA-IgM) were used to categorize as positive or negative
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10 226 each individual value of AFP-IgM and SCCA-IgM. We then ascertained sensitivity and
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12 227 specificity of their combined evaluation in diagnosing HCC with respect to LC, considering
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14 228 positive those patients having positive findings of at least one test: positive results were found
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16 229 in 37/72 HCC (sensitivity=51.4%), while negative results were found in 49/102 LC
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18 230 (specificity=48%). A logistic regression model was developed, by including LC and HCC
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20 231 patients and leaving out controls, and considering the presence or absence of HCC as
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22 232 outcome. The model, adjusted for age and gender, included among predictors AFP-IgM and
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24 233 SCCA-IgM, measured with ELISA or with CompleXima HCC Biochip, AFP and disease
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26 234 aetiology. Table 4 reports the results of the analysis.

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29 235 None of the studied biomarkers, including macrocomplexes measured by both ELISA
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31 236 and Biochip and AFP, was correlated in patients with HCC with the number of nodules nor
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33 237 with their diameter (data not shown). However when AFP-IgM and SCCA-IgM Biochip
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35 238 results were evaluated together according to the above described criteria and cut-off, positive
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37 239 findings were more frequently encountered in HCC patients with nodule diameter above than
38
39 240 in those with nodule diameter below 3 cm (chi-square=3.725; $p<0.05$).

241 **DISCUSSION**

242 In this work we evaluated a prototype device, namely CompleXima HCC Biochip, for the
243
244 243 simultaneous measurement of serum AFP-IgM and SCCA-IgM, two emerging biomarkers
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246 244 suggested to be of utility for early HCC detection^{23,24}. This lab-on-chip technology combines
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248 245 AFP-IgM and SCCA-IgM immunoassays with chemiluminescence detection and
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250 246 microfluidics in one platform. The micro-chip presented in this study shares with other
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252 247 integrated microchip-based systems, designed for the detection of the serum tumor markers
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254 248 AFP and PSA^{42,43,44}, portability, simplicity and rapid processing, which render them attractive

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3 249 for future applications as low-cost point of care testing. However, before commercialization
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5 250 of these new products proof-of-principle studies in a laboratory environment are mandatory⁴⁵.
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8 251 In this study both analytical and clinical performances of the Biochip were evaluated, in
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10 252 agreement with the requirements of the International Standard for Medical Laboratories
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12 253 Accreditation (ISO 15189: 2012)^{46,47}. Analytically, intra-assay coefficients of variation were
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14 254 lower than 12% for low, medium and high SCCA-IgM or AFP-IgM levels, which fits with an
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16 255 overall good performance. The intra-assay coefficients of variation showed a decreasing trend
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18 256 from low to high concentration, and this probably depends on the fact that in the low and
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20 257 medium concentration ranges some measurements were very close or equal to the lower limit
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22 258 of detection (50 AU/mL), thus being more error-prone. Inter-assay was slightly higher than
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24 259 intra-assay variability and this is probably dependent on the fact that, differently from intra-
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26 260 assay experiments, Biochips for inter-assay might be of different lots. In the evaluation
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28 261 process of CompleXima HCC Biochip we compared the results with those obtained with the
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30 262 ELISAs by Bland-Altman method and Passing-Bablok regression, showing that the two
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32 263 methods were not perfectly aligned. On average, AFP-IgM was underestimated while SCCA-
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34 264 IgM was overestimated by CompleXima HCC Biochip compared to ELISAs, and this was
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36 265 indicated by the Bland-Altman differences mean value (-52,6 AU/mL for AFP-IgM and +35.8
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38 266 AU/mL for SCCA-IgM). Moreover the AFP-IgM underestimation and SCCA-IgM
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40 267 overestimation by CompleXima HCC Biochip varied largely along the increasing X-axis,
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42 268 indicating dose-dependence and this was further confirmed by the Passing-Bablok analyses.
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44 269 These discrepancies might probably depend on differences in the standard curve used to
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46 270 calculate ELISAs and CompleXima HCC Biochip results. In the former case the standard
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48 271 curve is always run together with samples, while in the latter case this is not possible and the
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50 272 standard curve is necessarily included in the software for data analysis.

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60 273 To establish whether the differences between ELISAs or CompleXima HCC Biochip
274 AFP-IgM and/or SCCA-IgM measurements might have a different impact in the clinical

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3 275 assessment of LC and HCC we studied a series of patients with chronic liver diseases
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5 276 including LC and HCC. In the majority of healthy subjects both macrocomplexes levels
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8 277 detected by CompleXima HCC Biochip were below 50 AU/mL (39/39 for AFP-IgM and
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10 278 30/39 for SCCA-IgM), and this rendered the cut-off almost equal to the lower detection limit
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12 279 of the system, differently from what observed with ELISAs which measurable results in
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14 280 healthy controls allowed to calculate the threshold level at 120 AU/mL for AFP-IgM and 156
15
16 281 AU/mL for SCCA-IgM. While both biomarkers levels were higher in patients than in
17
18 282 controls, no differences were found between LC and HCC (Fig. 3) and this clearly indicates
19
20 283 that they cannot be used alone in the first clinical assessment of a patient suspected of having
21
22 284 or not HCC. Surprisingly, as presented in Figure 4, ROC curves analyses demonstrated that
23
24 285 the results obtained with CompleXima HCC Biochip discriminated better patients with a
25
26 286 diseased liver from controls than the ELISAs being 60 AU/mL and 139 AU/mL the 95%
27
28 287 specificity associated cut-offs for AFP-IgM and SCCA-IgM, respectively (Table 3). These
29
30 288 cut-offs were, however, associated with a low sensitivity (47% and 46%, respectively).
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32 289 Noteworthy, sensitivity values associated with CompleXima HCC Biochip were slightly
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34 290 better than those obtained with the ELISAs (20% for both AFP-IgM and SCCA-IgM).
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36 291 Sensitivity and specificity associated with the combined evaluation of AFP-IgM and SCCA-
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38 292 IgM in diagnosing HCC with respect to LC were 51.4% and 48%, respectively. However, as
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40 293 emerged by the binary logistic regression analysis presented in Table 4, the only significant
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42 294 predictor able to discriminate LC from HCC was AFP ($p=0.009$).

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51 295 In conclusion, with respect to ELISA, CompleXima HCC Biochip allows to perform
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53 296 AFP-IgM and SCCA-IgM determinations in one run and to handle each sample independently
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55 297 from the others. CompleXima HCC Biochip allows to obtain AFP-IgM and SCCA-IgM
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57 298 values characterized by a good analytical reproducibility, although they tended to be under- or
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59 299 overestimated with respect to ELISAs. Future chances for this new Biochip, to further
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300 implement its reproducibility and simplicity, are automation of the whole analytical process

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3 301 and validation of the system for other matrices, such as whole blood, thus allowing the
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5 302 development of a point-of-care testing device. Moreover, due to its power-free design our
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8 303 device can be easily equipped with increasing number of antigens to the grid, thus being
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10 304 suitable for rapid implementation when new diagnostic/prognostic markers of HCC will
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13 305 emerge.

14 306 **Acknowledgements**

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17 307 The authors thank Mr. Flaviano Favaro for AFP measurements.

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22 438 **FIGURE CAPTIONS**

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25 439 **Figure 1. Study design.** The flowchart illustrates the experimental steps followed to validate
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27 440 CompleXima HCC Biochip.

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29 441 **Figure 2. CompleXima HCC Biochip Linearity Interval for SCCA-IgM and AFP-IgM.**
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31 442 Serial dilution of sera with high levels of specific biomarkers-IgM were performed and results
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33 443 are presented. Values above 300 AU/mL were outside the linearity for both AFP-IgM and
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35 444 SCCA-IgM.

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37 445 **Figure 3. Bland-Altman comparison of AFP-IgM and SCCA-IgM values.** Comparison
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39 446 between CompleXima HCC Biochip and ELISA measurements. Upper panel: AFP-IgM
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41 447 results; lower panel: SCCA-IgM results. For any single subject the average between
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43 448 CompleXima HCC Biochip and ELISA results are reported on the X-axis, while the
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45 449 corresponding differences between the two measurements are reported in the Y-axis.
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47 450 Continuous lines indicate mean values, dashed lines show ± 1.96 standard deviation (SD). The
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49 451 comparison included all studied subjects (n=213).

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51 452 **Figure 4. AFP-IgM and SCCA-IgM increase in patients with liver diseases.** AFP-IgM
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53 453 (upper panel) and SCCA-IgM (lower panel) were measured with CompleXima HCC Biochip
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55 454 in 39 controls, in 102 patients with liver cirrhosis (LC) and in 72 patients with hepatocellular

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3 455 carcinoma (HCC). Higher levels of both biomarkers were found in LC and HCC patients with
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6 456 respect to controls.

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8 457 **Figure 5. Receiver Operating Characteristic (ROC) curves analysis for determining**
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10 458 **AFP-IgM and SCCA-IgM thresholds.** The figure illustrates ROC curves of AFP-IgM and
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12 459 SCCA-IgM measured with both CompleXima HCC Biochip (CHIP_AFP-IgM and
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14 460 CHIP_SCCA-IgM) and ELISA (ELISA_AFP-IgM and ELISA_SCCA-IgM). Alpha-
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16 461 fetoprotein (AFP) is also shown. Patients with chronic liver disease (LC and HCC together)
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18 462 were compared to healthy controls. The arrow indicates 95% specificity. The areas under the
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20 463 ROC curves with their respective standard errors (SE) are reported in the bottom table.
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465 **Table 1.** Patients' characteristic included in the study.

		LC	HCC
		n=102	n=72
SEX	males	70	55
	females	32	17
AGE	mean (years)	60.29	67.86
	SD	11.96	10.24
AETIOLOGY	HBV-related	18	9
	HCV-related	44	39
	Alcohol-related	39	22
	Other*	1	2
CHILD-PUGH	A	59	37
	B	33	23
	C	10	12
TUMOR Ø	>2cm >3 cm		32
	≥3cm		24
	missing		16
N° OF NODULES	1		35
	2-3		13
	diffuse		23
	missing		1

466 Notes: *: aetiology autoimmune, cryptogenic, HDV or Primary Biliary Cirrhosis (PBC)

Table 2. CompleXima HCC Biochip Intra-assay coefficients of variation (CV_{intra}) of AFP-IgM and of SCCA-IgM. For both biomarkers and for any detection levels (low, medium and high) 8 samples were analysed in quadruplicate the same day using Biochips of the same batch. To calculate intra-assay CVs, first for each sample the CV from four replicated analyses was obtained. Mean intra-assay CVs were calculated from the eight individual CVs and reported in the table together with the corresponding mean values and standard deviations of AFP-IgM and SCCA-IgM results. AU= Arbitrary Units.

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	AFP-IgM		AFP-IgM		SCCA-IgM		SCCA-IgM	
	concentration		CV_{intra}		concentration		CV_{intra}	
	Mean±SD	Range	Mean	Range	Mean±SD	Range	Mean	Range
	(AU/mL)	(AU/mL)	(%)	(%)	(AU/mL)	(AU/mL)	(%)	(%)
Low	58 ± 14	50-110	10	0-36	96 ± 31	50-153	12	2-29
Medium	101 ± 57	50-224	12	0-21	237 ± 70	103-352	9	3-13
High	304 ± 58	211-447	9	2-22	443 ± 75	294-579	9	3-17

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2 473 **Table 3.** Sensitivity%, specificity%, positive (LR+) and negative (LR-) likelihood ratios of serum biomarkers in distinguishing healthy controls
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4 474 from patients with LC or HCC. The cut-offs were established at a 95% fixed specificity. 95% Confidence intervals are reported in brackets.
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Biomarker	Method	Cut-off	Sensitivity %	Specificity %	LR+	LR-
AFP-IgM	ELISA	319 AU/mL	20 (14-27)	95 (79-98)	2.60 (1.90-3.60)	0.87 (0.30-2.60)
	Biochip	60 AU/mL	47 (40-55)	95 (83-99)	9.19 (7.7-10.9)	0.56 (0.10-2.20)
SCCA-IgM	ELISA	231 AU/mL	20 (14-26)	95 (79-98)	2.54 (1.90-3.50)	0.87 (0.30-2.60)
	Biochip	139 AU/mL	46 (38-54)	95 (83-99)	8.97 (7.50-10.70)	0.57 (0.10-2.20)
AFP		4.2 IU/mL	59 (51-66)	95 (83-99)	11.43	0.44

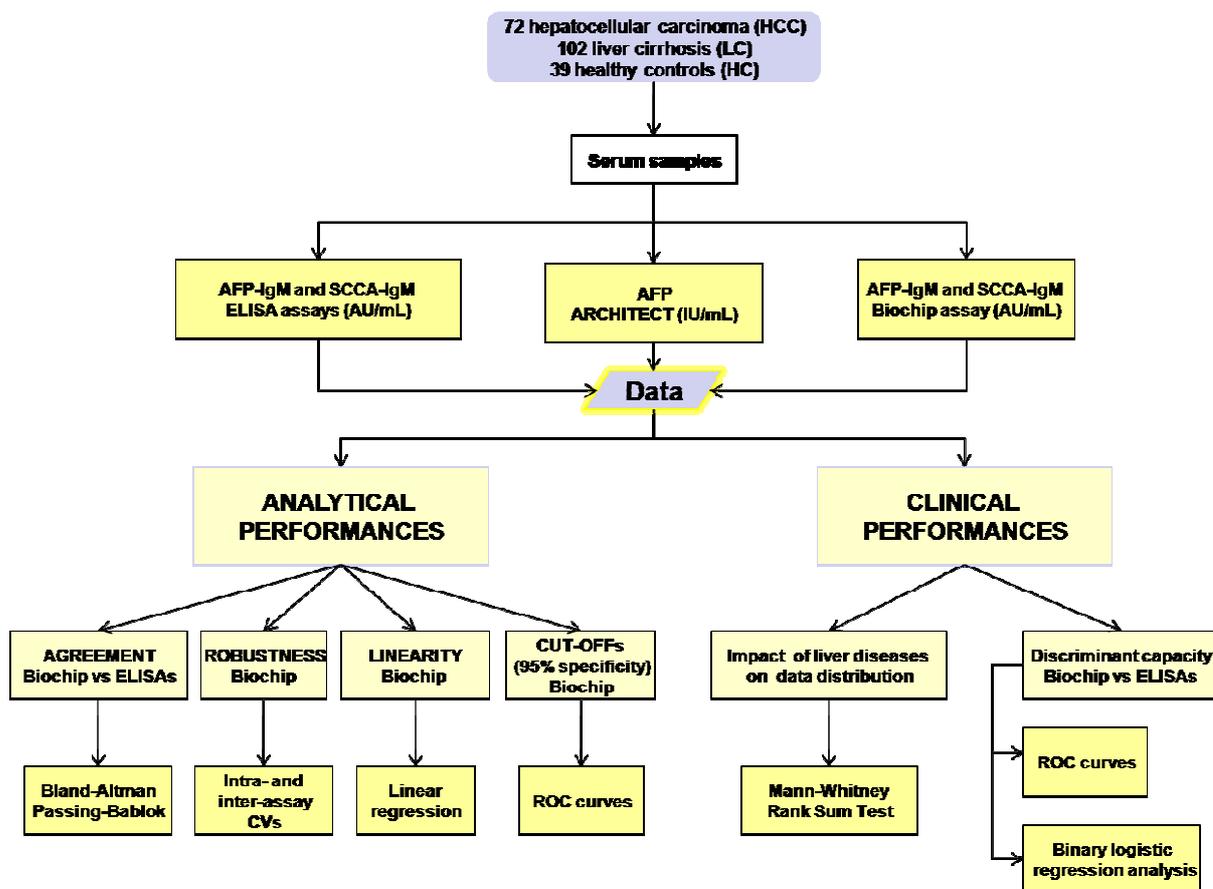
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3 476 **Table 4.** Binary logistic regression analysis. Among patients with LC and HCC, the presence
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5 477 or absence of HCC was considered as outcome variable. Predictors included in the analysis
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7 478 were AFP, AFP-IgM and SCCA-IgM measured with both ELISA and Biochip, age, gender
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10 479 and disease aetiology.
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	Odds Ratio	P value	95% C.I.
AFP (IU/mL)	1.02	0.009	1.00-1.03
ELISA AFP-IgM (AU/mL)	1.00	0.707	0.99-1.00
ELISA SCCA-IgM (AU/mL)	1.00	0.535	0.99-1.00
Biochip AFP-IgM (AU/mL)	0.99	0.852	0.99-1.00
Biochip SCCA-IgM (AU/mL)	0.99	0.797	0.99-1.00
Disease aetiology	1.01	0.973	0.44-2.31
Age (years)	1.08	0.0001	1.04-1.12
Gender	0.21	0.004	0.07-0.61

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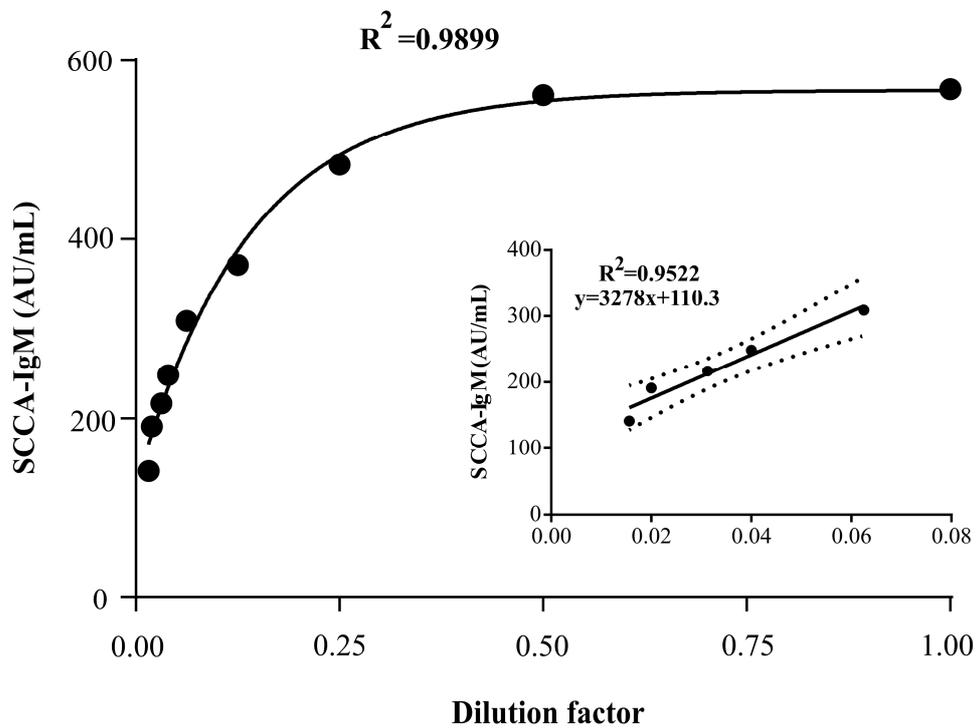
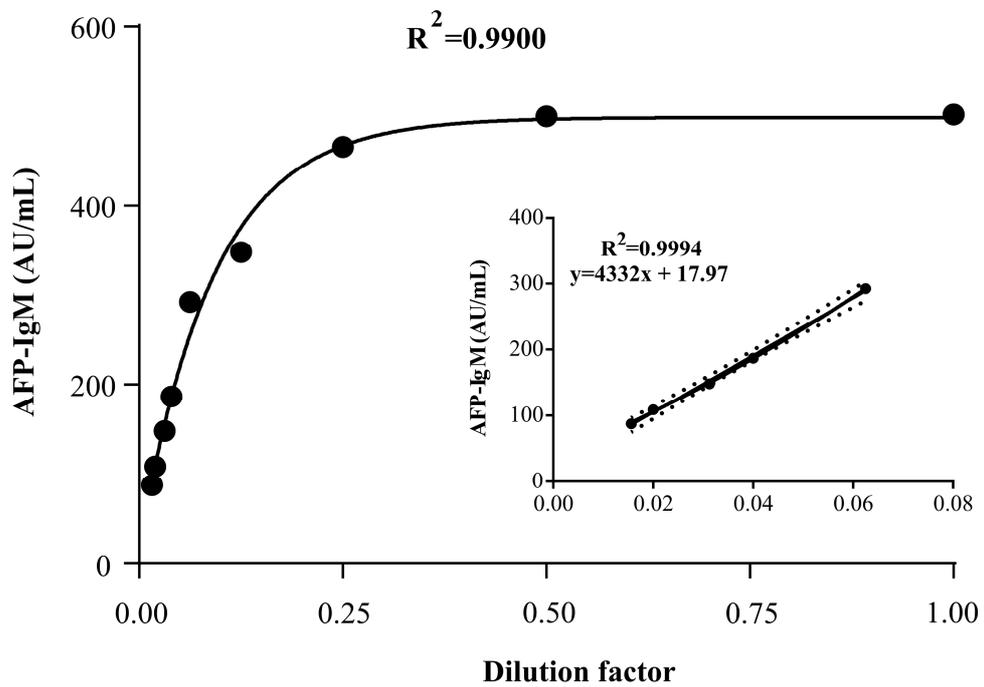
482 **Figure 1**



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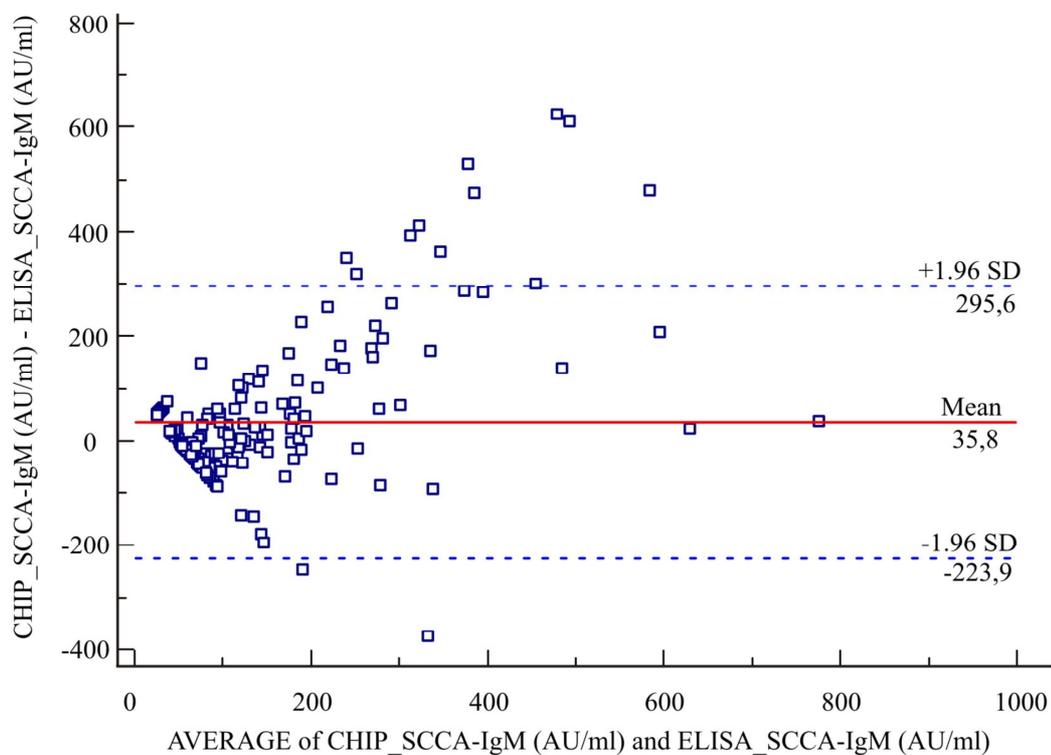
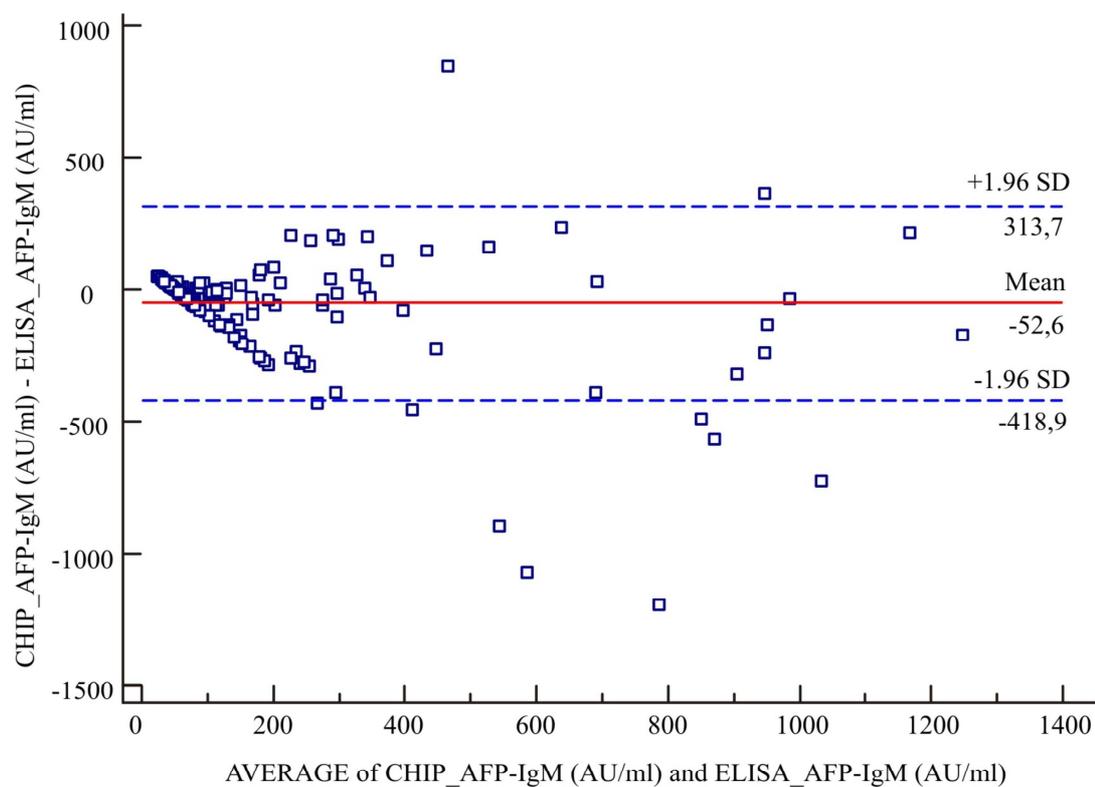
485 **Figure 2**



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488 **Figure 3**



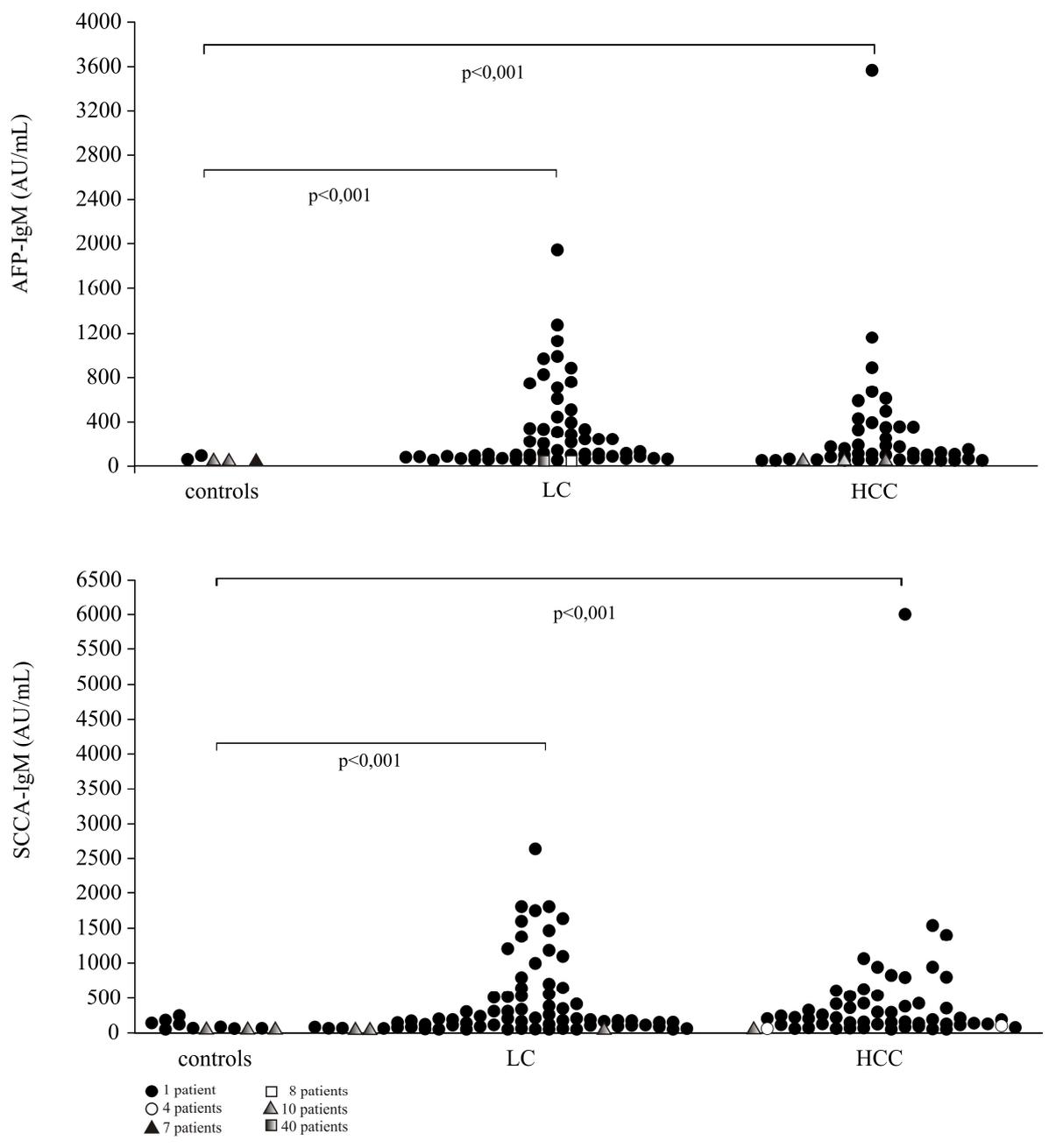
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491 **Figure 4**

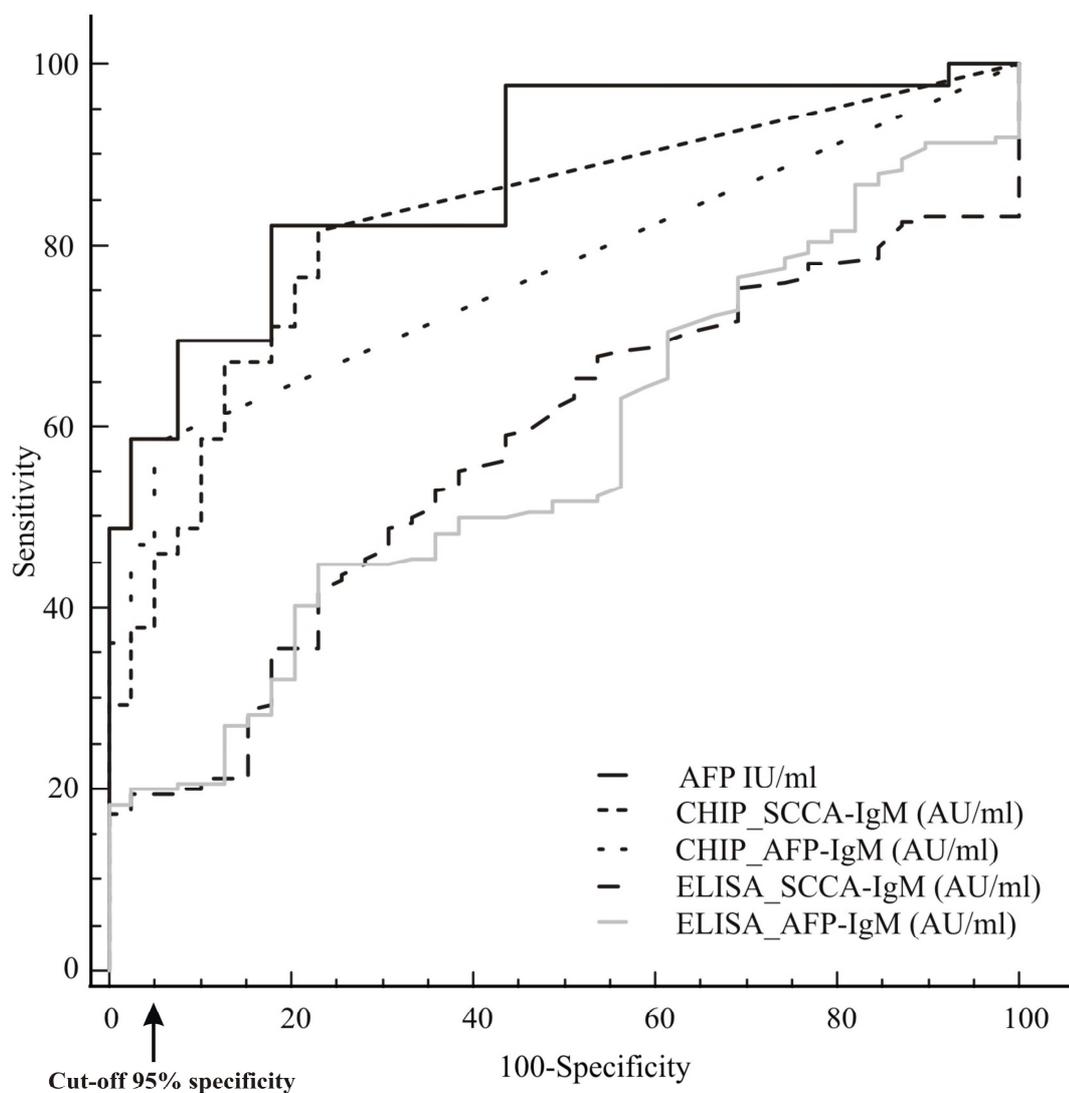


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494 **Figure 5**



	AUC	SE	95% CI
AFP_IU/ml	0,878	0,024	0,826-0,918
CHIP_SCCA-IgM AU/ml	0,827	0,030	0,770-0,876
CHIP_AFP-IgM AU/ml	0,771	0,036	0,709-0,826
ELISA_SCCA-IgM AU/ml	0,575	0,049	0,506-0,642
ELISA_AFP-IgM AU/ml	0,572	0,049	0,502-0,639

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497 Supplementary Figure 1

