

1 **Detection of bacterial co-infections and prediction of fatal outcomes in COVID-19 patients**
2 **presenting to the emergency department using a 29 mRNA host response classifier.**

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30 **Abstract**

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32 Objective

33 Clinicians in the emergency department (ED) face challenges in concurrently assessing patients
34 with suspected COVID-19 infection, detecting bacterial co-infection, and determining illness
35 severity since current practices require separate workflows. Here we explore the accuracy of the
36 IMX-BVN-3/IMX-SEV-3 29 mRNA host response classifiers in simultaneously detecting
37 SARS-CoV-2 infection, bacterial co-infections, and predicting clinical severity of COVID-19.

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39 Methods

40 161 patients with PCR-confirmed COVID-19 (52.2% female, median age 50.0 years, 51%
41 hospitalized, 5.6% deaths) were enrolled at the Stanford Hospital ED. RNA was extracted (2.5
42 mL whole blood in PAXgene Blood RNA) and 29 host mRNAs in response to the infection were
43 quantified using Nanostring nCounter.

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45 Results

46 The IMX-BVN-3 classifier identified SARS-CoV-2 infection in 151 patients with a sensitivity of
47 93.8%. Six of 10 patients undetected by the classifier had positive COVID tests more than 9 days
48 prior to enrolment and the remaining oscillated between positive and negative results in
49 subsequent tests. The classifier also predicted that 6 (3.7%) patients had a bacterial co-infection.
50 Clinical adjudication confirmed that 5/6 (83.3%) of the patients had bacterial infections, i.e.
51 *Clostridioides difficile* colitis (n=1), urinary tract infection (n=1), and clinically diagnosed
52 bacterial infections (n=3) for a specificity of 99.4%. 2/101 (2.8%) patients in the IMX-SEV-3

53 Low and 7/60 (11.7%) in the Moderate severity classifications died within thirty days of
54 enrollment.

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56 Conclusions

57 IMX-BVN-3/IMX-SEV-3 classifiers accurately identified patients with COVID-19, bacterial co-
58 infections, and predicted patients' risk of death. A point-of-care version of these classifiers,
59 under development, could improve ED patient management including more accurate treatment
60 decisions and optimized resource utilization.

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72 **Introduction**

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74 Clinicians in the Emergency Department (ED) face major challenges in accurately
75 assessing patients with suspected infections including SARS-CoV-2, bacterial co-infections, as
76 well as predicting clinical outcomes. Bacterial co-infections (at presentation) and
77 superinfections (after presentation)^{1,2} often cause worse outcomes than the primary viral
78 infection³; this phenomenon was prevalent in the H1N1 influenza pandemic⁴, with 20% - 30%
79 bacterial coinfections in patients with severe influenza^{5,6}. However, current evidence for
80 COVID-19 portrays a different scenario. Recent studies have shown rates of bacterial co-
81 infection in COVID-19 of between 3.2% and 5.5%^{1,7-9}, with rates of secondary or superinfection
82 in hospitalized patients increasing to 6.1% - 15%^{1,7,10,11}. Despite the relatively low prevalence of
83 bacterial co-infections in COVID-19, empiric antibiotics for community or hospital acquired
84 bacterial pneumonia or bacteremia are often prescribed in severely ill patients due to the inability
85 to accurately or rapidly detect bacterial co-infection at presentation^{1,12,13}.

86

87 Existing diagnostic tests have major limitations. Gold standard bacterial cultures often
88 take days to result, are limited by the ability of the organism to grow in the culture medium, and
89 require a large sample volume when testing complex patient samples like blood^{14,15}.
90 Additionally, false negatives can result from insufficient culture duration, or antimicrobial
91 treatment prior to sample collection¹⁶. False negative culture results can have devastating
92 consequences for patients. Alternate testing methods involve polymerase chain reaction based
93 (PCR) targeted amplification of bacterial nucleic acids directly from the patient's blood sample.
94 These are not routinely used in the acute setting, are limited by turnaround time and the panel of

95 targets they can detect, and are influenced by the inherent issues of PCR – lack of sensitivity in
96 detecting low bacterial loads, sensitivity to protocols and threshold decisions adopted, and the
97 presence of inhibitory molecules in complex samples such as blood¹⁷.

98

99 There is therefore an unmet medical need to identify viral and bacterial infection using
100 rapid point-of-care tests in the ED to determine presence and severity of infection and inform the
101 use of antimicrobials. In the absence of such diagnostics, clinical decision making needs to
102 balance antimicrobial stewardship with delivery of appropriate empiric care, including escalation
103 of therapy in patients with suspected bacterial co-infections and/or suspected sepsis, and to
104 predict severity for level of care decisions, and optimal use of healthcare resources.

105

106 The machine-learning supported host response mRNA classifier IMX-BVN-2 has
107 recently been described to accurately identify systemic as well as localized bacterial infections
108 and also viral infections other than COVID-19¹⁸. A separate classifier, IMX-SEV-2, has been
109 developed to predict the illness severity (Galtung et al, in revision). The identity and biological
110 functions of the 29 host mRNAs have recently been published¹⁹, and the classifiers have been
111 further updated (IMX-BVN-3 and IMX-SEV-3) based on additional clinical study data.

112

113 The aim of this study was to investigate the accuracy of IMX-BVN-3 and IMX-SEV-3
114 classifiers to detect SARS-CoV-2 infection, detect bacterial co-infections and predict the severity
115 in patients with confirmed COVID-19.

116

117 **Methods**

118

119 *Patient enrollment and specimen collection*

120 One hundred sixty-one patients with PCR-confirmed COVID-19 infection at presentation
121 were enrolled at the Emergency Department of Stanford University Hospital, USA under the IRB
122 approved protocols 55650 and 55924. 2.5 mL of whole blood was collected in PAXgene Blood
123 RNA tubes (PreAnalytiX) within 12 hours of presenting to the ED and frozen following the
124 instructions of the manufacturer.

125 Clinical data collected, in the form of a structured questionnaire, included presence of
126 symptoms, past medical history, medications, hospital length of stay (hours and days), CRP,
127 procalcitonin, LDH, and ferritin levels, and neutrophil, lymphocyte, monocyte, eosinophil, and
128 basophil counts. In addition, we determined the patient's clinical outcomes in the form of
129 disposition from the Emergency Department, need for mechanical ventilation, and death.

130

131 *PAXgene sample processing*

132 PAXgene Blood RNA (PreAnalytiX, Hombrechtikon, Switzerland) tubes were shipped to
133 Inflammatrix Inc. (Burlingame, CA) under a sponsored research agreement where RNA was
134 extracted using a protocol previously described²⁰ and 29 host mRNAs were quantified using the
135 nCounter FLEX instrument (Nanostring, Seattle, WA).

136

137 *IMX-BVN-3 and IMX-SEV-3 classifiers*

138 Quantification results for the 29 host mRNAs were analyzed using the BVN-3 and SEV-3
139 host response classifiers. The classifiers generate numerical scores for the likelihood of bacterial
140 infection and the likelihood of viral infection that each fall into 4 diagnostic (Very unlikely,

141 Unlikely, Possible, Very likely bacterial and/or viral infection) and a score for the condition's
142 severity that falls into three prognostic interpretation bands (Low, Moderate, and High severity).

143

144 *SARS-CoV-2 RNA quantification*

145 Plasma and nasopharyngeal viral RNA levels in Cycle threshold (Ct) and absolute
146 copies/uL were determined for 89/161 COVID-19 positive patients co-enrolled in our previous
147 study²¹ to correlate viral load with the likelihood scores. Briefly, RNA was extracted from 140
148 μ L of samples using the QIAamp Viral RNA Mini Kit (Qiagen, Germany) and quantified using
149 the |Q| Triplex Assay with the qPCR platform QuantStudio 5 (Applied Biosystems by Thermo
150 Fisher Scientific) and dPCR using the array-based |Q| assay simultaneously.

151

152 *Clinical adjudication of bacterial co-infections*

153 Blood for culturing was collected from 58/161 patients suspected of an infection. Blood
154 culture results and labs were compared against the IMX-BVN-3 bacterial likelihood scores. A
155 thorough chart review was performed on patients with discordant IMX-BVN-3 bacterial
156 likelihood scores and bacterial culture results and other laboratory results to identify any patient
157 with suspected bacterial infection. Bacterial infection was confirmed if the patient had: 1)
158 ED/inpatient primary or relevant discharge diagnoses that included sepsis, septic shock, or any
159 bacterial infections, 2) positive microbiological data for bacterial pathogens collected within 48
160 hours from ED presentation, or 3) infectious disease expert consultation documenting bacterial
161 infection upon hospital admission.

162

163 *Statistical analysis*

164 We calculated the Pearson correlation between the IMX-BVN-3/IMX-SEV-3 viral
165 likelihood scores and severity with the absolute viral load in the nasopharynx and plasma for 89
166 patients described elsewhere²¹, between the bacterial likelihood scores and levels of C-reactive
167 protein, procalcitonin, and lactate dehydrogenase, and the Spearman rank correlation between the
168 Cycle threshold (Ct) and the viral likelihood scores. We compared the viral loads between the
169 true positive and false negative calls of viral infection as well as the severity scores between
170 clinical outcomes using the Wilcoxon rank sum test with continuity correction and adjusted the
171 p-value when comparing multiple outcomes using the Benjamin and Hochberg correction. We
172 also calculated the sensitivity, specificity, and the likelihood ratios of the viral and bacterial
173 classification bands against the PCR COVID-19 positivity and adjudicated bacterial co-
174 infections respectively. Additionally, we also compared the proportions of patients in the severity
175 likelihood bands and their clinical outcomes – disposition from the ED and the need for
176 ventilation/30-day mortality using χ^2 tests with continuity corrections. All analyses were
177 performed in R.

178

179 **Results**

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181 *Patient characteristics*

182 A total of 161 patients were enrolled from April 2020 to February 2021, with median age
183 of 50 years (IQR: 35 - 64). 84/161 (52.2%) were women. 158/161 (98.1%) were symptomatic on
184 presentation with a median of 6 symptoms (IQR: 4 - 8). Medical history, comorbidities and
185 symptoms at presentation are shown in **Table 1**.

186

187 *Accuracy in predicting COVID-19 infection using host response markers*

188 151/161 (93.8%) of patients positive for COVID-19 by RT-PCR were accurately
189 classified as “Possible” or “Very Likely” viral infection by IMX-BVN-3, corresponding to an
190 overall sensitivity of 93.8% (85.3% and 7.5% for the Very likely and Possible viral bands,
191 respectively; **Table 2**). As all patients were confirmed SARS-CoV-2 positive we did not
192 calculate specificity of the classifier.

193 We further investigated the causes of 10 potentially “false negative” results in BVN-3;
194 six of the 10 patients had first tested positive for SARS-CoV-2 at least 9 days before presentation
195 to the ED, while the remaining four had SARS-CoV-2 PCR test results that were initially
196 positive but oscillated between positive and negative when retested. Of interest, 3 of the 10
197 patients were predicted to have a bacterial superinfection as indicated by the BVN-3 classifier’s
198 bacterial score and 2/3 were clinically adjudicated to have a bacterial infection by expert chart
199 review (see below).

200

201 The viral likelihood score was inversely correlated with the PCR cycle threshold value
202 (Ct) from nasopharyngeal samples collected on admission (Spearman rank correlation: -0.63,
203 $p < 0.001$) and correlated with the absolute viral load (copies/uL) as determined by digital PCR
204 (Pearson correlation: 0.52, $p < 0.001$) (**Figure 1**). Patients with Very Likely or Possible positive
205 BVN-3 viral scores indicating viral infection (“true positives”) had a median viral load of 3,483
206 copies/ μ L in the nasopharyngeal sample (IQR: 155 – 23,539) compared to 3.52 copies/ μ L (IQR:
207 2.82 – 4.9) in the Unlikely and Very Unlikely BVN-3 (“false negative”) patients (p -value =
208 0.009).

209

210 *Detection of bacterial superinfections using host response markers*

211 The IMX-BVN-3 bacterial score classified 6/161 (3.7%) of patients into the Possible
212 bacterial interpretation band suggesting a bacterial co-infection, and 155/161 (96.3%) were
213 classified as Unlikely or Very Unlikely bacterial infections (**Table 3**). Chart review and clinical
214 adjudication confirmed that 5/6 (83.3%) of the Possible bacterial patients did indeed have
215 superinfections translating into a specificity (ruling in) of 99.4% for identification of bacterial
216 infection: one patient had *Clostridioides difficile* colitis, one had rectal adenocarcinoma with
217 gastrointestinal perforation and abdominopelvic abscess and three had clinically diagnosed
218 superinfections without positive microbiology findings (including blood culture) (**Table 4**). We
219 did not detect evidence for bacterial infections in 52 patients with negative blood culture results
220 translating into a sensitivity of 100% for ruling out bacterial infection in the subgroup of patients
221 where microbiology data were available. The bacterial scores correlated with the levels of C-
222 reactive protein (Pearson correlation: 0.58, $p < 0.001$), procalcitonin (Pearson correlation: 0.4, p -
223 value = 0.003), and lactate dehydrogenase (Pearson correlation: 0.42, $p = 0.003$).

224

225 *Disease severity based on host response markers and association with clinical outcomes*

226 The IMX-SEV-3 test classified 101/161 (62.7%) patients in the Low severity category
227 and 60/161 (37.3%) in the Moderate severity category. No patients were categorized in the High
228 severity category. The calculated severity score was correlated with the absolute viral load in
229 plasma (Pearson correlation: 0.49, p -value = 0.002) and the above bacterial score (Pearson
230 correlation: 0.45, p -value < 0.001). Interestingly, 6/6 (100%) patients classified in the Likely
231 bacterial co-infections category were classified to have Moderate severity. The IMX-SEV-3

232 severity score also correlated with the modified WHO severity score at enrollment for these
233 patients (Pearson correlation: 0.43, p-value < 0.001).

234 In total, 79/161 (49.1%) patients were discharged, 72/161 (44.7%) patients were admitted
235 to the floor, 10/161 (6.2%) were admitted to ICU, 7/161 (4.3%) required mechanical ventilation
236 (**Table 5**), and 9/161 (5.6%) died. As expected, 59.4% patients in the Low severity category
237 were discharged from the ED compared to only 31.7% in the Moderate category (difference,
238 27.7% [95% CI: 11.2% - 44.2%]) (**Figure 2**). Interestingly, more patients in the Moderate
239 category were admitted to the ICU (difference, 11.4% [95% CI: 1% - 21.7%]). Median IMX-
240 SEV-3 severity scores in patients admitted to the ICU were 14.5 (IQR: 13 – 18.25), in those
241 admitted to the floor was 10 (IQR: 8 – 13), and in those discharged it was 8 (IQR: 7 - 10).
242 Wilcoxon rank sum test for each pairwise comparison was significant (adjusted p-value < 0.05).
243 When grouping the need for mechanical ventilation and/or mortality as a severe outcome, 13/161
244 (8.1%) had such a severe outcome from the COVID-19 infection. A greater proportion of
245 patients in the Moderate category had such a severe outcome compared to those in the Low
246 category (15% vs 3.9%, difference, 11.1% [95% CI: 0.09% - 22.2%]), and the patients had a
247 higher median IMX-SEV-3 severity score (12 [IQR: 10 - 14]) than those that didn't (9 [IQR: 7 –
248 11.15], Wilcoxon rank sum test, p-value = 0.07).

249

250 **Discussion**

251

252 As of January 2022, SARS-CoV-2 has infected more than 340 million people globally
253 and resulted in ~5.5 million deaths²². Bacterial co/superinfections are known to occur in patients
254 infected with SARS-CoV-2 at varying prevalence conditional on the severity of the viral
255 infection^{1,7-13,23,24}. Successful detection of the virus requires a high-fidelity PCR test targeting

256 the viral RNA and to date the detection of coinfecting pathogens has depended on either bacterial
257 culture or detecting target nucleic acids in patient samples using PCR. Here we present, to the
258 best of our knowledge, the first host response based simultaneous detection of viral (SARS-CoV-
259 2) infection, co-infection with bacterial pathogens, as well as the stratification of disease severity
260 using the IMX-BVN-3 and IMX-SEV-3 classifiers.

261
262 The IMX-BVN-3 classifier detected COVID-19 with 93.8% sensitivity. This is the first
263 report of the successful detection of SARS-CoV-2 using the IMX-BVN-3 host response
264 signature, previously validated in other viral infections^{18,25}, and the imputed false negative rate
265 of the classifier is lower than that of the currently accepted qPCR assays for SARS-CoV-2. A
266 recent systematic review and meta-analysis of 32 studies comprised of 18,000 patients revealed
267 heterologous false negative rates in qPCR ranging from 2%²⁶ – 58%²⁷ with an overall summary
268 estimate of 12%²⁸. Of interest, we observed several specific circumstances in the few patients
269 that showed “false negative” results in IMX-BVN-3: first, the time lag between the initial
270 positive SARS-CoV-2 test result and the presentation to the ED in these patients likely indicates
271 clearing of the virus and waning of the associated viral immune response with subsequent
272 negative results in the classifier; second, low viral loads (<5 copies/ μ L) also contributed to
273 “false-negative” results in the classifier in a few patients. Lastly, two patients with “false
274 negative” classifier results were also found to have bacterial superinfections. As the generation
275 of viral and bacterial scores in the IMX-BVN-3 classifier is interdependent, bacterial scores may
276 have impacted the viral scores and contributed to “false negative” results in addition to the
277 factors mentioned above.

278 Importantly, the IMX-BVN-3 classifier predicted bacterial co-infection within 48h in
279 6/161 patients with a specificity of 99.4%. 5/6 were clinically adjudicated to be bacterially
280 infected. We calculated a prevalence of 8.6% (5/58) for bacterial co-infections in a subset of
281 patients with blood cultures available as part of clinical care; this prevalence is similar to the
282 prevalence reported recently for patients with low or moderate SARS-CoV-2 infection^{1,7-9}.
283 Importantly, the identification of bacterial co-infections was achieved from the same 2.5 mL
284 blood sample that provided the viral result in IMX-BVN-3 without the need for additional
285 sample collection such as bacterial cultures or samples for the amplification of bacterial nucleic
286 acids. The high accuracy of the IMX-BVN-3 classifier could thus be used along the viral result
287 to initiate antimicrobial treatment and other clinical decisions in SARS-CoV-2 positive patients
288 while also contributing to antimicrobial stewardship in the ED.

289 The IMX-SEV-3 classifier categorized patients into Low and Moderate severity
290 categories in our cohort. This host-response dependent classifier predicted severity scores that
291 correlated with a modified WHO score that was designed to describe the need for supplemental
292 oxygen²¹. With a significant difference in the median severity scores of patients admitted to the
293 ICU, admitted to the floor, and those who were discharged, as well as the observed increased
294 proportions of patients in the Moderate severity interpretation band admitted to the ICU and
295 having a severe outcome, the severity score could facilitate level of care decision for patients.
296 However, as the study was not powered to assess the accuracy of the severity readout of the
297 IMX-SEV-3 classifier we only report the nominal results here. Additional studies -including a
298 current large registrational trial conducted for clearance by regulatory agencies in the US and
299 Europe- will report the accuracy of the severity readout in larger COVID-19 and other cohorts.

300 Other limitations of our study include the fact that this study was conducted at a single
301 center and used biobanked blood samples obtained from a limited cohort of 161 patients. As only
302 PCR confirmed COVID-19 positive patients were enrolled we could not determine the IMX-
303 BVN-3 classifier's specificity. We were also unable to clinically adjudicate the entire patient
304 cohort for bacterial infections and thus calculated sensitivity for a subset of patients only. Lastly,
305 since bacterial co- or superinfections are defined based on when the patient presents to the ED^{1,2}
306 and not when in the course of the infection the patient presents, we were unable to determine the
307 timeline of the infection to distinguish between the two. Additionally, the host response-based
308 classifier detects any bacterial infection and, hence, does not allow differentiating between co- or
309 superinfections.

310 In conclusion, once the IMX-BVN-3 and SEV-3 classifiers are introduced as a rapid
311 point of care host RNA detection platform with a turnaround time of less than 30 min (currently
312 in development), results at the point of care could guide decisions about starting or withholding
313 antibiotics allowing escalation of therapy or antimicrobial stewardship but also the initiation of
314 contact precaution measures and/or viral therapy and choosing the appropriate level of care for
315 SARS-CoV-2 positive patients.

316

317

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424

425 **Tables**

426 **Table 1. Patient medical history and symptoms at presentation**

Past medical history	N=161
Lung disease	14.9% (24)
Cancer	6.8% (11)
Diabetes	29.8% (48)
Immunosuppression	9.3% (15)
Heart disease	9.9% (16)
Hypertension	39.1% (63)
ACE/ARB use	21.7% (35)
Stroke	3.7% (6)

Dementia	2.5% (4)
DVT/PE	5.6% (9)
Chronic kidney disease	9.3% (15)
Smoking	21.1% (34)
Symptoms at presentation	
Fever	57.1% (92)
Chills	34.2% (55)
Cough	68.9% (111)
Sore throat	21.1% (34)
Congestion	9.9% (16)
Shortness of breath	62.1% (100)
Chest pain	34.8% (56)
Myalgia	41.6% (67)
Nausea/vomiting/diarrhea	56.5% (91)
Loss of taste	39.8% (64)
Loss of smell	36.6% (59)
Confusion	0 (0)
Headache	39.8% (64)

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429

430 **Table 2. Break down of patients into viral likelihood interpretation bands using IMX-BVN-**

431 **3***

IMX-BVN-3 viral interpretation band	Frequency	Sensitivity for COVID-19 (%)
Very Likely	139	86.3
Possible	12	7.5
Unlikely	5	-
Very Unlikely	5	-

432 *, specificity was not calculated as all patients were confirmed SARS-CoV-2 positive by PCR

433

434

435 **Table 3. Breakdown of patients into bacterial likelihood interpretation bands using IMX-**
436 **BVN-3***

IMX-BVN-3 bacterial interpretation band	Confirmed bacterial infection	No bacterial infection	Percent in band	Sensitivity (%)	Specificity (%)	Likelihood ratio
Very Likely	0	0	0	n.d.	n.d.	n.d.
Possible	5	1	3.7	n.d.	99.4	156
Unlikely	0	59	36.6	100	n.d.	0
Very Unlikely	0	96	59.6	100	n.d.	0

437 n.d., not determined

438 *, complete data to calculate sensitivity were only available in 58 patients

Table 4. Clinical adjudication based on expert chart review in 6 patients with Possible IMX-BVN-3 bacterial scores

ID	IMX-BVN-3 bacterial result	IMX-BVN-3 viral result	IMX-SEV-3 severity result	Clinical characteristics	Microbiology findings	Antimicrobial therapy and other data	Discharge diagnoses	Bacterial infection
0076	Possible	Very Unlikely	Moderate	Septic shock on admission	Positive (<i>C. difficile</i> toxin in stool)	Cefepime, vancomycin, fidaxomicin, metronidazole	Septic shock; <i>C. difficile</i> colitis	Co-infection
0082	Possible	Possible	Moderate	Hypoxic respiratory failure, hypotension	Negative	Cefepime azithromycin, vancomycin	Septic shock; bacterial pneumonia, viral pneumonia	Co-infection (bacterial pneumonia diagnosed clinically)
0281	Possible	Unlikely	Moderate	Abdominal pain	Positive (Urine culture positive for viridans streptococci)	Ertapenem, cefepime, metronidazole	COVID-19; abdominopelvic abscess	Co-infection (gastrointestinal perforation with peritonitis and fecal pathogens in urine)
0397	Possible	Possible	Moderate	Hypoxic respiratory failure, persistent leukocytosis	Negative	Azithromycin, ceftriaxone	Persistent leukocytosis	Co-infection (bacterial infection, improved with antibiotics suspected by ID consult)
0477	Possible	Possible	Moderate	Shortness of breath, hypoxia, SIRS	Negative	Eefepime, caspofungin	Sepsis; Leukemia with graft vs. host disease	Co-infection (bacterial infection, treated with antibiotics suspected by ID consult)
0500	Possible	Very Unlikely	Moderate	Fall	Negative	None used on admission	Asymptomatic COVID-19 infection	Negative

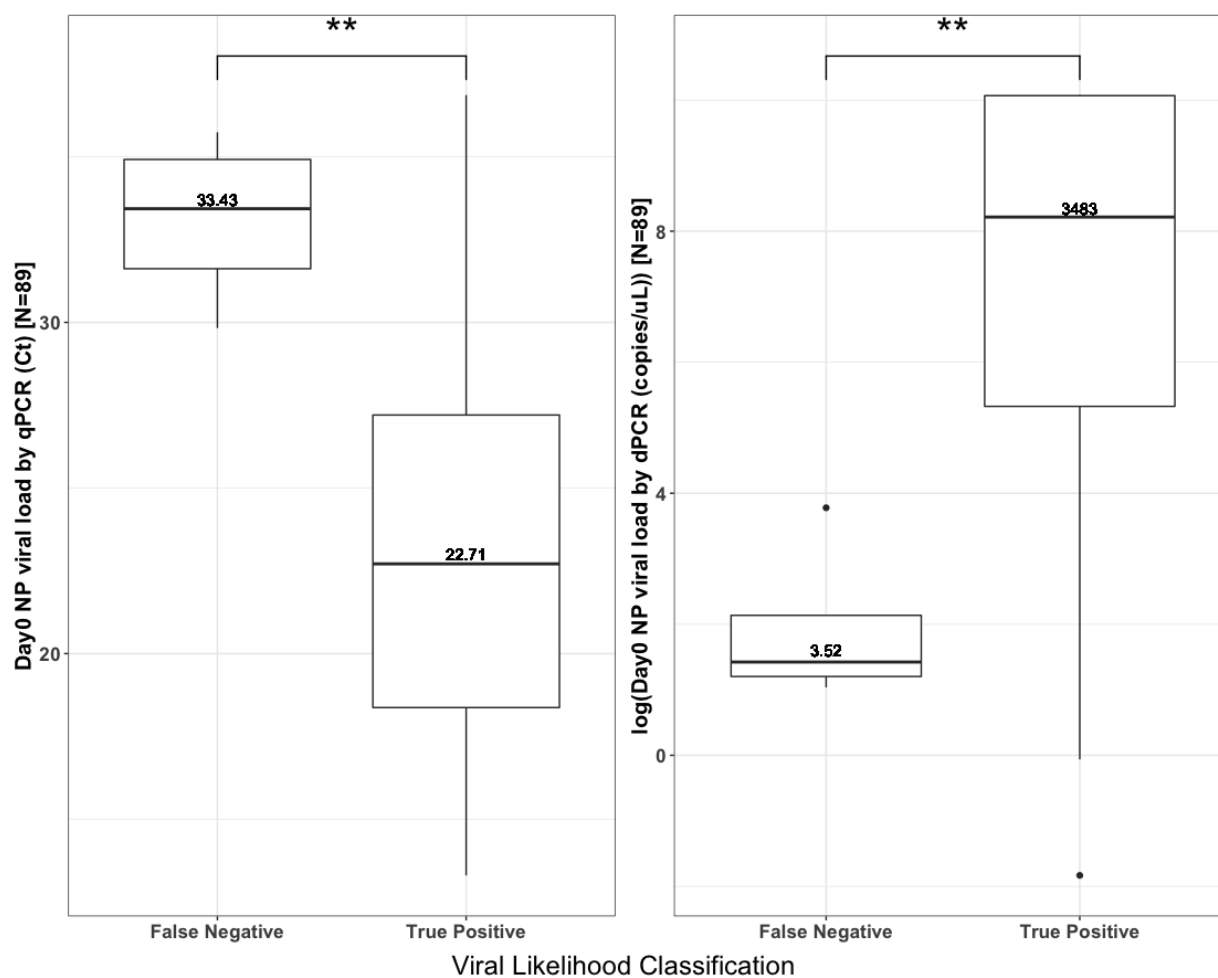
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440 **Table 5. Breakdown of patients into severity interpretation bands using IMX-SEV-3**

IMX-SEV-3 interpretation band	Percent in band	Discharged	Admitted		Mechanical ventilation	30-day mortality	Ventilation and/or 30-day mortality
			to floor	to ICU			
High	0	0	0	0	0	0	0
Moderate	37.3	19	33	8	4	7	9
Low	62.7	60	39	2	3	2	4

441 **Figures**

442



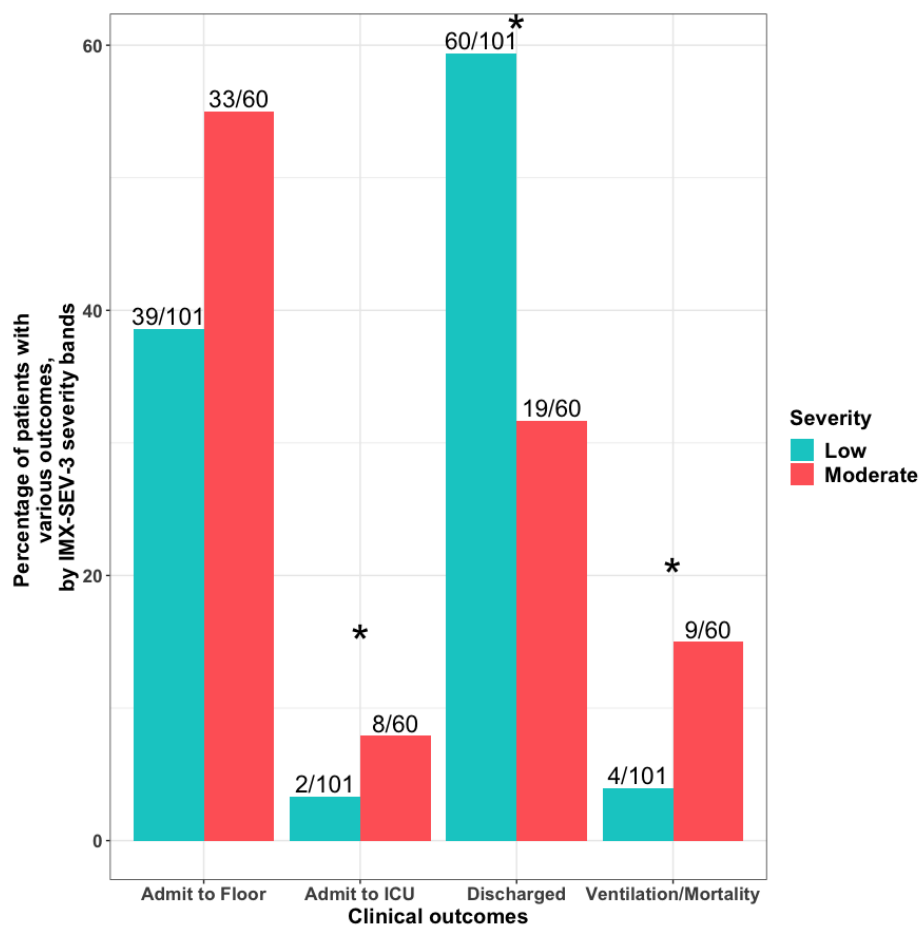
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444 Figure 1. Difference in the nasopharyngeal SARS-CoV-2 load between “false negative”
445 (Unlikely or Very unlikely viral BVN-3 scores) and “true positive” (Possible or Very Likely
446 BVN-3 scores) for 89 patients. qPCR measured viral loads in cycle threshold (Ct) (*left*) and
447 dPCR measured absolute viral loads in copies/μL (*right*). ** represents p-value < 0.001.

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451

452 Figure 2. Proportions of patients with different clinical outcomes, including the disposition from
453 the ED as well as the need for ventilation or 30-day mortality, by the severity likelihood
454 predicted by the IMX-SEV-3 classifier. Overall, more patients in the Low category were
455 discharged (difference in proportions, 27.7% [95% CI: 11.2% - 44.2%]) and more patients in the
456 Moderate category were admitted to the ICU or required ventilation/succumbed to the infection,
457 difference in proportions of 11.4% [95% CI: 1% - 21.7%] and 11.1% [95% CI: 0.09% - 22.2%]
458 respectively. * represents p-value < 0.05.