

1 **Assessment of the Clinical Utility of Plasma** 2 **Metagenomic Next-Generation Sequencing in a** 3 **Pediatric Hospital Population**

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28 Summary: We evaluate the test performance characteristics and clinical utility of plasma metagenomic next-
29 generation sequencing in a pediatric hospital cohort and demonstrate sensitivity and specificity of 53% and 79%,
30 with 14% of tests impacting antimicrobial management.

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42 **Abstract**

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44 **Background.** Metagenomic next-generation sequencing (mNGS) of plasma cell-free DNA (cfDNA) is commercially available,
45 but its role in the workup of infectious diseases is unclear.

46 **Methods.** To understand the clinical utility of plasma mNGS, we retrospectively reviewed patients tested at a pediatric
47 institution over 2 years to evaluate the clinical relevance of the organism(s) identified and impact on antimicrobial
48 management. We also investigated the effect of pre-test antimicrobials and interpretation of molecules of microbial cfDNA
49 per microliter (MPM) plasma.

50 **Results.** 29/59 (49%) mNGS tests detected organism(s), and 28/51 (55%) organisms detected were clinically relevant.
51 Median MPM of clinically relevant organisms was 1533 versus 221 for irrelevant organisms ($p=0.01$). mNGS test sensitivity
52 and specificity were 53% and 79%, respectively, with a positive predictive value (PPV) of 72% and negative predictive value
53 (NPV) of 50%. 14% of tests impacted clinical management by changing antimicrobial therapy. Immunocompromised status
54 was the only patient characteristic that trended towards a significant clinical impact ($p=0.056$). No patients with culture-
55 negative endocarditis had organisms identified by mNGS. There were no significant differences in antimicrobial pre-test
56 duration between tests with clinically relevant organism(s) versus those that returned negative, nor was the MPM different
57 between pre-treated and un-treated organisms, suggesting that 10 days of antimicrobial therapy as observed in this cohort
58 did not sterilize testing; however, no pre-treated organisms identified resulted in a new diagnosis impacting clinical
59 management

60 **Conclusions:** Plasma mNGS demonstrated higher utility for immunocompromised patients, but given the low PPV and NPV,
61 cautious interpretation and Infectious Diseases consultation are prudent.

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65 **Introduction:**

66 Next-generation sequencing (NGS) describes high-throughput sequencing methods in which millions of DNA
67 fragments can be independently and simultaneously sequenced. Cell-free DNA (cfDNA) in the bloodstream was
68 first described in 1948¹. CfDNA primarily originates from apoptotic human cells; inflammation, autoimmune
69 disease, trauma, and cancer increase cfDNA levels²⁻³. NGS of cfDNA has been previously described for
70 noninvasive diagnosis of fetal abnormalities⁴⁻⁶, cancer monitoring⁷⁻¹⁰, and transplant rejection¹¹⁻¹⁵. Its adoption in
71 these fields raised the prospect of diagnosing infections through sequencing of microbial cfDNA by metagenomic
72 NGS (mNGS) followed by bioinformatic taxonomic classification.

73 mNGS, sometimes called shotgun sequencing, has been applied to various clinical sample types including
74 cerebrospinal fluid, blood, respiratory samples, gastrointestinal fluid, and ocular fluid¹⁶. mNGS testing is
75 “hypothesis-free,” unlike many contemporary molecular diagnostic infectious disease tests. Potential strengths
76 include the ability to diagnose polymicrobial infections and quantitative reporting of cfDNA molecules detected.
77 As blood traverses the entire body, it is hypothesized that even protected sites of infection may shed enough
78 pathogen nucleic acid into blood for detection¹⁷. This pathogen-agnostic method is in contrast to targeted
79 nucleic acid amplification tests (NAAT) that use specific primers, limiting detection to suspected targets. Because
80 the vast majority of mNGS cfDNA reads will reflect the human host, sample processing methods for human DNA
81 depletion are needed, supplemented by post-processing bioinformatic removal. Due to the amplification of
82 background human DNA, mNGS is generally less sensitive than targeted approaches and requires greater
83 sequencing depth for organism identification¹⁸⁻¹⁹.

84 A commercially available plasma cfDNA mNGS test from Karius Inc., (Redwood City, CA), available since 2016,
85 reports molecules of microbial cfDNA per microliter (MPM) plasma. This laboratory is certified under the Clinical
86 Laboratory Improvement Amendments of 1988, although the test has not been approved by the Federal Drug
87 Administration. A recent company publication describes clinical and analytical test validation for detection of

88 1250 human pathogens²⁰. The limit of detection of the Karius test is 41 MPM and organisms are reported if
89 cfDNA from the organism is detected at statistically significant levels relative to negative controls run in parallel.
90 For all reported organisms, a reference interval (MPM) is provided, based on abundances seen in samples from
91 asymptomatic adult controls²⁰. The relationship between MPM and microbe concentrations in blood [e.g.
92 colony-forming units (CFUs)] is not well understood. Publications have described ongoing MPM detection for
93 weeks after clearance of the organism on blood culture while on appropriate antimicrobial therapy²¹.

94 Despite potential strengths of cfDNA detection by mNGS, notable limitations exist. One obvious limitation is that
95 the test will not detect RNA viruses. Importantly, uncertainty remains regarding how to assess if detected
96 organism DNA (DNAemia) indicates a pathogen contributing to patient disease versus sample contamination or
97 transient bacteremia from colonizing flora. In the clinical validation study by Karius Inc.²⁰, 350 patients who
98 presented with sepsis alert criteria were tested and diagnostic sensitivity of 92.9% and specificity of 62.7% were
99 reported in comparison to a composite reference standard, including all microbiological data and clinical
100 history²⁰. Sensitivity was 84.8% in comparison to standard microbiological testing alone. A recent study of 100
101 plasma mNGS tests sent from a pediatric hospital determined a sensitivity and specificity of the test for
102 detection of organisms that impacted clinical decision-making of 92% and 64% respectively²².

103 At our hospital, clinicians have postulated that plasma mNGS may be useful in the following clinical scenarios: 1)
104 culture-negative infections due to antibiotic pretreatment and/or fastidious or non-culturable organisms, and 2)
105 deep-seated and difficult-to-sample infections such as invasive fungal infections, pneumonia, or osteomyelitis.
106 The purpose of this study was to assess test performance characteristics and explore how mNGS findings
107 impacted clinical management.

108 **Methods**

109 We retrospectively reviewed medical records of all patients for whom commercial plasma mNGS testing was
110 sent at Boston Children's Hospital from October 2017 through October 2019. This study was approved by our
111 institutional review board. Tests required approval from the directors of the Infectious Diseases (ID) Diagnostic
112 Laboratory as well as an ID clinical consultation. The approval process involved a discussion about the utility of
113 testing between the ID team and laboratory director when the diagnosis was not evident from initial testing.
114 There were no fixed criteria and this study was conducted to help inform institutional guideline development
115 based on identification of patient subsets in which the test was found to be the most clinically impactful. We
116 assessed patient demographics, underlying comorbidities, ordering team, site of infection, duration of
117 antimicrobial use prior to test, final clinical diagnoses, and reported MPM if testing returned positive for any
118 organism. Patients were classified as immunocompromised if they had an underlying immunodeficiency,
119 malignancy on active chemotherapy, hematopoietic stem cell or solid organ transplant, or other conditions
120 requiring immunosuppression.

121 Clinical relevance of organisms identified from plasma mNGS was assessed relative to final overall diagnosis
122 (infection versus no infection). Presence of an infection was determined by the treating clinical team and
123 incorporated the clinical presentation that prompted mNGS testing and all microbiologic testing performed
124 (including mNGS findings). A subgroup of clinically relevant organisms was “confirmed positive” if they
125 correlated with a non-mNGS microbiological result (e.g. PCR or culture); however, in some cases, the clinical
126 team made diagnoses on the basis of clinical picture and mNGS findings (Table 1A). These definitions of infection
127 are consistent with prior studies that have evaluated the performance characteristics of mNGS^{22,23}. In the
128 absence of a gold standard for this novel technology, our composite reference standard nonetheless reflects
129 how clinicians interpreted and acted on results, and we surmise this is the most clinically meaningfully definition
130 of “infection”. Clinical relevance and confirmed positives were determined by expert opinions of two pediatric
131 ID physicians not involved in the patient's care at time of testing (R.L. and F.A.) with a tie-breaker opinion of a
132 third (T.S.) if discordant.

133 A novel aspect of our study was to assess the relationship of MPM to determination of a clinically relevant
134 organism. We additionally considered whether there was antimicrobial use active against the organism by
135 reviewing susceptibility data obtained via concurrent routine microbiological methods, when possible, and by
136 assessing whether the patient clinically improved on empiric therapy, suggesting that it was appropriate.

137 We further evaluated the effect of mNGS testing on overall patient care to specifically assess the added value of
138 plasma mNGS testing over standard microbiological workup, and defined “clinical impact” if testing resulted in
139 1) new organism(s) with new targeted antimicrobial therapy, 2) new organism(s) with de-escalation of antibiotic
140 therapy, or 3) negative testing thus motivating teams to de-escalate antimicrobial therapy. Cases in which
141 redundant organisms were identified on plasma mNGS and standard microbiological testing were only
142 considered to have clinical impact if there was a change in antimicrobial management on the basis of the plasma
143 mNGS result. For example, if the mNGS resulted in a diagnosis sooner than standard microbiological workup and
144 affected antimicrobial management, this was considered to have a clinical impact. Clinical impact was
145 adjudicated by the research team. Standard microbiological testing was defined as routine microbiological
146 testing/NAAT performed either in our Infectious Diseases Diagnostic Laboratory or in reference laboratories.
147 Logic gates of possible scenarios to determine clinical impact dependent on plasma mNGS, standard
148 microbiological testing, and antimicrobial change are demonstrated in Table 1B.

149 Statistical analysis:

150 Demographic data were summarized using descriptive statistics. Test characteristics (sensitivity, specificity,
151 negative and positive predictive value) for mNGS findings were calculated using two different methods (labeled
152 as counting by test versus result) as illustrated in Figure 1 and Figure 2. Method 1 counted all mNGS results
153 from one plasma sample as one test ($n = 59$). If the mNGS test sent identified a clinically relevant organism,
154 whether or not the organism was a confirmed positive, the test result was considered a “true” positive.
155 However, mNGS tests often identified multiple organisms, and in many of these instances, both clinically

156 relevant and clinically irrelevant organisms (not related to any known or suspected infection in the patient) were
157 reported. By method 1, the mNGS test would be classified as a true positive based on identification of a clinically
158 relevant organism even if clinically irrelevant organism(s) were also identified. Method 1 therefore does not fully
159 account for the “noise” of co-identified clinically irrelevant organisms. To account for this “noise”, we used
160 Method 2 where we counted each organism identified so each organism result was assessed independently (n=81). Method 2 provides more granular detail for mNGS findings by separately assessing the clinical relevance of
161 each organism identified.

163 Comparative analysis was conducted by the Fisher’s exact test or chi-square test as appropriate and continuous
164 data were compared using the Wilcoxon rank sums test and Kruskal-Wallis test for group medians. MPM
165 performance in determination of clinically relevant organisms was assessed by receiver operating characteristics
166 (ROC) analysis and area under the curve (AUC). An optimal cutoff score was found using the Youden index.
167 Statistical tests were performed using Stata 15.1 software (Stata Corporation, College Station, TX, USA) and
168 GraphPad v.8 software (GraphPad Software, San Diego, CA, USA) with p-values ≤ 0.05 as the significance
169 threshold.

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171 **Results:**

172 A total of 59 plasma NGS tests were sent on 54 patients during the study period. Table 2 summarizes patient
173 characteristics, ordering teams, primary sites of infection, and final diagnoses of patients. Of the 5 tests that
174 were re-sent on patients, two revealed new diagnoses (one with clinical impact) and all tests were sent at least a
175 month apart with new or worsening clinical symptoms. The most common final diagnoses of patients on whom
176 plasma mNGS was sent was no clear diagnosis (e.g. prolonged fever that could be due to infection or drug fever,
177 but resolved without determination of specific etiology; 25%). Half of these patients were thought to ultimately
178 have no infection at all, while the others were treated empirically for presumed infection. Autoimmune
179 conditions were identified in 17% of patients and endocarditis in 14%. While cardiology teams ordered the

180 second largest number of tests, no organisms were identified via mNGS on any of the culture-negative
181 endocarditis cases and redundant organisms were identified in three cases by standard microbiological workup.
182 In one case of culture-positive endocarditis, plasma mNGS identified discordant organisms that were deemed
183 clinically irrelevant; *E.coli* and *H. influenzae* were identified on plasma mNGS but PCR of the eventually
184 explanted valve identified *Streptococcus gordonii*, which also grew from an initial blood culture and was
185 preliminarily considered a possible contaminant. No ordering team, primary site of infection, underlying
186 comorbidities, or final patient diagnosis was noted to have a statistically significant association with clinical
187 impact.

188 Fifty-one organisms were identified from all testing combined (29 bacteria, 15 DNA viruses, 7 fungi, 1 parasite),
189 55% of which were considered clinically relevant. Table 2 summarizes the proportion of organisms identified
190 that resulted in clinical impact or were determined to be redundant or clinically irrelevant.

191 In eight cases, testing led to clinical impact with a change (addition or de-escalation) in antimicrobial therapy.
192 Seven out of the eight cases were immunocompromised patients and all of the five mNGS cases where a new
193 organism was identified and new diagnosis was made impacting clinical management were in
194 immunocompromised hosts (described in Supplementary Figure 1). Underlying immunodeficiency and overall
195 immunocompromised status were the only variables found to trend towards a significant clinical impact
196 although they did not reach our statistical threshold of 0.05 (p=0.08 and 0.06 respectively). While unexpected
197 false positive and negative test results could lead to unnecessary investigations or treatment, we did not
198 observe this in our cohort.

199 The sensitivity and specificity of plasma mNGS by test sent (method 1, n = 59) were 53% and 79%, respectively,
200 with a positive predictive value (PPV) of 72% and negative predictive value (NPV) of 50% (Figure 2). Eight mNGS
201 tests (14%) identified only clinically irrelevant organisms, and five mNGS tests deemed clinically relevant co-
202 identified irrelevant organisms. When each organism identified was analyzed independently (method 2, n = 81),

203 sensitivity/specificity were 46/75% with a PPV of 55% and NPV of 50% (Figure 2; organism and test assignments
204 are described in Supplementary Dataset 1).

205 Testing was collected after a median of 8 days into clinical workup and median of 9 days of antimicrobial
206 therapy, with median turnaround time (from time of receipt of sample by testing laboratory, to report) of 1 day,
207 which is clinically actionable. For patients with plasma mNGS testing that returned negative in the setting of
208 presumed infection treated empirically (“possibly sterilized” tests, n=15), antimicrobial therapy had been
209 administered for a median of 8 days (mean 9.5, standard deviation 8.9) prior to test collection. Surprisingly, we
210 found that the duration of pre-test therapy for patients with organisms detected on mNGS that should have
211 been sterilized by the antimicrobial(s) in use (n = 27 organisms), was similar [median 10 days of therapy (p-value
212 0.59); mean 19, standard deviation 30]. For cases of presumed infection where both plasma mNGS and standard
213 microbiological workup were negative, the majority of these infections were deep-seated infections (4
214 pulmonary infections, 2 osteomyelitis, 1 septic arthritis, 2 intrabdominal, 1 sepsis); four patients were diagnosed
215 with culture-negative endocarditis.

216 We also assessed the relationship of MPM to identification of a clinically relevant organism. The median MPM
217 for clinically relevant organisms was 1533 [interquartile range (IQR) 340-11309] in contrast to clinically irrelevant
218 organisms (median MPM 221; IQR 62-717), which was a statistically significant difference (p=0.01). The median
219 MPM for organisms with no pre-test antimicrobial therapy active against the organism was 407 (IQR 68-5852),
220 compared to organisms with a covering antimicrobial (MPM 527; IQR 215-6267), which was not a statistically
221 significant difference (p=0.78). While median MPMs did vary by organism type (Table 2), differences were not
222 statistically significant (p=0.48 for bacteria versus fungi versus virus). A ROC curve for MPM data for distinction
223 between clinically relevant and irrelevant organisms yielded an AUC of 0.75 (95% CI 0.611 to 0.887). An optimal
224 cutoff of 390 MPM by Youden index was 74% sensitive (95% CI 55%-87%), and 73% specific (95% CI 52%-87%)
225 with a likelihood ratio of 2.7 (Figure 3).

226 **Discussion:**

227 In this study we describe the clinical utilization of plasma mNGS testing at our clinical center and include novel
228 assessments not described in other studies. The sensitivity, specificity, PPV, and NPV of plasma mNGS testing at
229 our hospital were considerably lower than results reported in the main clinical validation study led by the
230 company²⁰ as well as in a recent retrospective description of another pediatric hospital experience²². We
231 surmise that the difference in test performance in part reflects a difference in how mNGS was applied, which
232 was as a tertiary-level test sent in high-stakes scenarios where standard workup was unrevealing. At our
233 institution, due to the considerable cost and unknown clinical utility, mNGS requires approval from the
234 Infectious Diseases Diagnostic Laboratory Director and an ID consultation. We feel that our utilization likely
235 reflects how many clinical centers would use plasma mNGS, in contrast to how this test was validated
236 commercially as a sepsis screen in the emergency department²⁰. This is the first study to account for the “noise”
237 of polymicrobial identification in plasma mNGS in assessment of test performance and to individually assess the
238 clinical relevance of each organism, which substantially impacted the positive predictive value (72% for per-test
239 assessment versus 55% for per-organism assessment). We also included patients with a discordant mNGS
240 finding (where the final clinical diagnosis of infection was made from standard microbiological workup and was
241 not consistent with the mNGS finding) as cases for our calculations, rather than excluding them, in order to
242 provide the most realistic estimates of test performance. Our study uniquely defined additional clinical factors
243 we hypothesized could be relevant to plasma mNGS yield, including days into disease course, pre-test
244 antimicrobial duration, and MPM interpretation.

245 This study illustrates how pretest probability affects testing utility, as the likelihood of plasma mNGS revealing
246 an as-of-yet unidentified organism and new diagnosis after standard workup was low, particularly for
247 immunocompetent patients. Many of our patients ultimately had a non-infectious diagnosis, or a presumed
248 infection treated empirically in the absence of microbiological data, which yielded higher false positives and
249 negatives in comparison to prior studies. Negative mNGS results in patients with culture-negative infections

250 (designated as false negatives) also mostly involved protected sites of infection (pulmonary, intrabdominal,
251 bone), which is suggestive that plasma mNGS may be an inadequate and at worst a misleading proxy for invasive
252 microbiological sampling. Notably, the test had minimal yield for culture-negative endocarditis, despite the
253 adjacency of cardiac valves to blood (only one endocarditis case underwent surgical management and had
254 confirmed endocarditis on pathology, but all cases had presentations that met modified Duke's criteria for
255 endocarditis and improved on therapy). We additionally report that the clinical impact of tests through changes
256 in antimicrobial therapy was low (14%), although notably this was higher than another study that found that
257 only 7% of tests led to a positive clinical impact²¹.

258 A key overall finding was that the negative predictive value in our clinical practice was only 50%. While many
259 providers wanted to use plasma mNGS to “rule-out” an infection, we show that negative tests only predict the
260 absence of an infection as well as a coin flip, and therefore are a poor rule-out screening test. However, we did
261 find a significant association between MPM reported and clinical relevance (Figure 3), suggesting that high
262 MPMs should make providers more confident that the result is meaningful.

263 Given that mNGS was sent several days into the disease course, we also wanted to address the possible impact
264 of empiric pre-test antimicrobials on plasma mNGS yield. While clearance of bloodstream pathogen cfDNA over
265 time is expected, kinetics for specific pathogens will need to be elucidated as mNGS becomes more routine.

266 Counterintuitively, we did not find significant differences in MPM values between organisms treated with an
267 appropriate antimicrobial pre-test and those untreated, even when only considering clinically relevant
268 organisms (dismissing organisms that may have been contaminants and thus unaffected by antimicrobials).

269 Furthermore, we did not find significant differences in antimicrobial duration between “possibly sterilized”
270 mNGS tests and tests where an organism was identified with an active antimicrobial on-board. This suggests that
271 pre-test antimicrobial durations of 10 days (median) as observed in this cohort do not likely substantially affect
272 sterilization of plasma mNGS. The ongoing detectable MPM may be related to slow-to-clear DNAemia from high
273 pathogen burden even though organisms may have been appropriately killed on targeted therapy, a finding that

274 is consistent with prior reports.²² Notably, no identified pre-treated organisms resulted in a novel diagnosis that
275 affected clinical management in our cohort.

276 Limitations of this study include a relatively small sample size, which in turn leads to a small number of patients
277 in each relevant diagnostic sub-category (e.g. culture-negative endocarditis) and for establishment of the MPM
278 cutoff in ROC analysis. Additionally, our gold standard definition of the presence of infection was a composite
279 assessment from the provider team, which included interpretation of all microbiological data including mNGS
280 findings. In the ideal scenario, we would have an independent gold standard of the test under evaluation
281 although there is precedent in the literature for assessing novel and possibly more sensitive technologies this
282 way²³⁻²⁵. In clinical practice, providers routinely incorporate the results of this test with other clinical data and,
283 understanding the limitation that there is no reference standard for mNGS, our goal was to characterize
284 provider response to findings, in the context of all of the information available for the patient.

285 In summary, our major findings included lower sensitivity and specificity of plasma mNGS than prior literature
286 suggests, with only half of the organisms identified as clinically relevant -- emphasizing the need for ID
287 consultation for interpretation. We found higher utility for immunocompromised patients, and less value than
288 expected for endocarditis. Additionally, although we expected that pre-test antimicrobials would decrease the
289 yield of plasma mNGS testing, after 10 days (median) of antimicrobial therapy, the MPM did not differ
290 significantly between treated and untreated organisms nor was overall detection compromised. Despite the
291 insights gained in this study regarding plasma mNGS test performance and utility, further work will be required
292 to understand how to optimally integrate this technology into the infectious diseases diagnostic work up.

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391 Table 1A: Scenarios for clinically relevant (true positive) and clinically irrelevant (false positive/negative)
392 organisms. *Example clinical scenario: concern for contaminant from standard microbiological testing and
393 negative plasma mNGS results are used to clinically confirm suspicion and antibiotics are de-escalated
394 Table 1B: Possible scenarios for determining clinical impact
395 Figure 1: mNGS findings were counted by two separate methods, as illustrated above, for assessment of test
396 characteristics by plasma test sent (Method 1), and by organism detected (Method 2).
397 Table 2: Plasma mNGS Test and Organism Characteristics, Clinical Impact, and Relevance. Patient characteristic
398 p-values assess association of dichotomized categorical variable versus clinical impact by Fisher's exact tests. *p-
399 value to compare MPM medians by organism type did not include "parasite" as there was only one case. [†]No
400 diagnosis refers to no clear final diagnosis assigned by providers: 7 received empiric antimicrobials (assigned as
401 infection), and 8 were ultimately considered to have no infection (no empiric antimicrobials)
402 Figure 2: Testing characteristics calculated by Method 1 (each plasma test sent interpreted as a whole, n=59)
403 and Method 2 (by organism) to discriminate noise in mNGS tests from clinically irrelevant organisms co-
404 identified with relevant pathogens. Infection was defined by composite reference method (provider
405 interpretation of clinical history and all microbiological data including mNGS findings). "Box B" was added to the
406 usual 2x2 contingency table as these are clinically irrelevant organism(s) identified in the setting of an infection
407 diagnosed by non-mNGS findings (i.e. diagnosed by standard microbiological workup). They cannot be included
408 in Box D since mNGS identified organism(s) and cannot be included in Box C as the patient's final diagnosis was
409 infection. Nonetheless these cases contribute to sensitivity and positive predictive value and should not be
410 dropped from calculations.
411 Figure 3: A: Comparison of distribution of MPM results for clinically relevant and irrelevant organisms (lines
412 indicate medians) and B: Analysis of performance of MPM for distinction between clinically relevant and
413 irrelevant organisms by receiver operating characteristic (ROC) curve.
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Clinically Relevant (True positive):	Clinically Irrelevant (False positive or negative):
Confirmed positive and primary etiology of illness: E.g. Patient septic from <i>Enterococcus</i> bacteremia on blood culture, which was also identified on mNGS testing	Pathogens that are likely contaminant : E.g. <i>Staphylococcus epidermidis</i> identified on mNGS but no evidence of bloodstream infection and concurrent blood cultures negative with no treatment
Confirmed positive but not primary reason for hospitalization/severe acute illness: E.g. HSV gingivostomatitis in patient septic from <i>Pseudomonas</i> bacteremia, but HSV (and <i>Pseudomonas</i>) identified on mNGS testing and verified by standard workup (PCR swab and blood culture respectively)	Pathogens that may reflect GI/skin colonization with no obvious manifestation in the patient: e.g. <i>Neisseria sicca</i> co-identified in patient with respiratory failure/sepsis from adenovirus, and not confirmed on blood culture nor treated Pathogens with no known clinical significance : e.g. virus with no known associated infectious clinical manifestation.
Not Confirmed Positive but Consistent with Infectious Diagnosis: E.g. <i>Fusobacterium necrophilum</i> identified in mNGS testing in patient diagnosed with aspiration pneumonia, although standard microbiological workup didn't identify this organism	Pathogens identified on mNGS that were discordant with final clinical diagnosis made on the basis of standard microbiological workup: e.g. <i>Escherichia coli</i> and <i>Haemophilus influenzae</i> on mNGS in setting of <i>Streptococcus gordonii</i> endocarditis identified from blood culture and universal PCR of valve.

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Plasma mNGS Result	Standard Microbiological Testing	Antimicrobial Change due to mNGS Result	Clinical Impact	
-	-	-	Redundant information, antibiotics and clinical plan were not changed (no impact)	-
-	-	+	Clinical impact (e.g. de-escalation) if team used negative mNGS results to de-escalate	+
-	+	-	No additional information (no impact)	-
-	+	+	Clinical impact (e.g. de-escalation) *	+
+	-	-	Not relevant organism (considered contamination or transient unrelated bacteremia)	-
+	-	+	Clinical impact (e.g. new diagnosis and targeted therapy)	+
+	+	-	Redundant information, antibiotics and clinical plan were not changed (e.g. known bacteria identified and no impact)	-
+	+	+	Clinical impact (e.g. different diagnosis and additional therapy)	+

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mNGS findings
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Method 1 [by plasma test], N = 59: counted by each plasma mNGS test sent (all the organisms identified count as one test), and clinically irrelevant and relevant organisms could be co-identified.

10 tests with multiple organisms
19 tests with one organism

30 tests with no organisms

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Method 2 [by result (each organism or absence of organism assessed)], N = 81 results: counted by each organism identified. Each organism is independently evaluated as “clinically relevant” or “clinically irrelevant.”

51 organisms

30 tests with no organisms

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Test Characteristic		Organism Characteristic			
All plasma mNGS tests (n = 59)		All organisms identified (n=51)			
		Median MPM		471	Mean MPM (s.d.) 17139 (54155)
Clinical Impact: n (%)	8 (14%)	Organism type (n):	MPM Range	Median MPM (IQR)	p-value
mNGS test with organism(s)	29 (49%)	Bacteria (29)	3-316000	340 (188-6267)	
New antimicrobial	4 (6.8%)	Virus (15)	33-99538	550 (138-3220)	
Antimicrobial de-escalation	1 (1.7%)	Fungi (6)	104-2655	717 (705-1684)	
Redundant/Irrelevant	24 (41%)	Parasite (1)	5852	5852	
mNGS identified no organisms	30 (51%)				0.48*
Antimicrobial de-escalation	3 (5.1%)				
No change	27 (45%)				
Duration pre-test antimicrobial	Days (median)	Mean Days (s.d.)	Clinically relevant (n=28)	48-316000	1533 (340-11309)
No organism identified but presumed infection	8	9.5 (8.9)	Clinically irrelevant (n=23)	3-18620	221 (62-717)
Organism(s) detected but with antimicrobial on-board	10	19 (29.7)			p-value 0.01
	p-value	0.59			
Patient Characteristics and Relationship to Clinical Impact (n=8 tests)					
Median Patient Age, years (S.D.)	9 (9.4)				
Clinical Impact: n/8 (%)			Clinical Impact: n/8 (%)		
Gender: n/59 tests (%)		p-value	Site of infection: n/59 tests (%)		p-value
Female 21 (36%)	3 (38%)		Pulmonary 18 (31%)	4 (50%)	0.23
Male 38 (64%)	5 (63%)		Cardiac 8 (14%)	0	0.58
		0.60	Fever of unknown origin 11 (19%)	1 (13%)	1
Immune status: n/59 tests (%)			Abdomen 4 (6.8%)	1 (13%)	0.45
Immunocompromised 33 (56%)	7 (87.5%)		CNS 3 (5.1%)	0	1
Immunocompetent 26 (44%)	1 (12.5%)		Multi-site 9 (15.3%)	1 (13%)	1
		0.056	Other 6 (10.2%)	1 (13%)	1
Ordering medical team: n/59 tests (%)			Final Diagnosis : n/59 tests (%)		
Cardiology 16 (27%)	1 (25%)	0.30	Endocarditis 8 (14%)	0	0.58
Hematology/Oncology 23 (39%)	5 (62.5%)	0.14	Culture-negative 4 (6.8%)	0	
Immunology					
ICU 11 (19%)	2 (25%)	0.47	Identified organism 4 (6.8%)	0	
Other 9 (15%)	0		Autoimmune 10 (17%)	0	0.33
Underlying condition: n/59 tests (%)			(steroid-responsive)		
Hematological 7 (11.9%)	1 (13%)	1	Bacteremia 5 (8.5%)	1 (13%)	0.53
Cancer 5 (8.5%)	1(13%)	0.53	Pneumonia 6 (10%)	2 (25%)	0.23
HSCT 12 (20.3%)	1(13%)	1	Fungal Infection 6 (10%)	2 (25%)	0.53
Immunodeficiency 4 (6.8%)	2(25%)	0.085	No diagnosis [†] 15 (25%)	1 (13%)	0.67
Cardiac hardware 14 (24%)	1(12%)	0.67	Other 9 (15%)	2 (25%)	0.60
Rheumatological (on steroids)	3 (5.1%)	0			
Other 14 (24%)	2(25%)	1			

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Method 1: by mNGS plasma test as a whole	Infection related to mNGS test	Infection not related to mNGS test	No infection at all	
mNGS identifies organism(s)	Box A: TP: True positive (with/without other clinically irrelevant organisms also identified): 21	Box B: FN: False negative (ONLY clinically irrelevant organisms): 4	Box C: FP: False positive (ONLY clinically irrelevant organisms): 4	Positive Predictive Value: TP/(box A+B+C): 72%
mNGS identifies NO organisms	Box D: FN: False negative: 15		Box E: TN: True negative: 15	Negative Predictive Value: TN/(box D+E): 50%
	Sensitivity: TP/(box A+B+D): 53%		Specificity: TN/(box C+E): 79%	

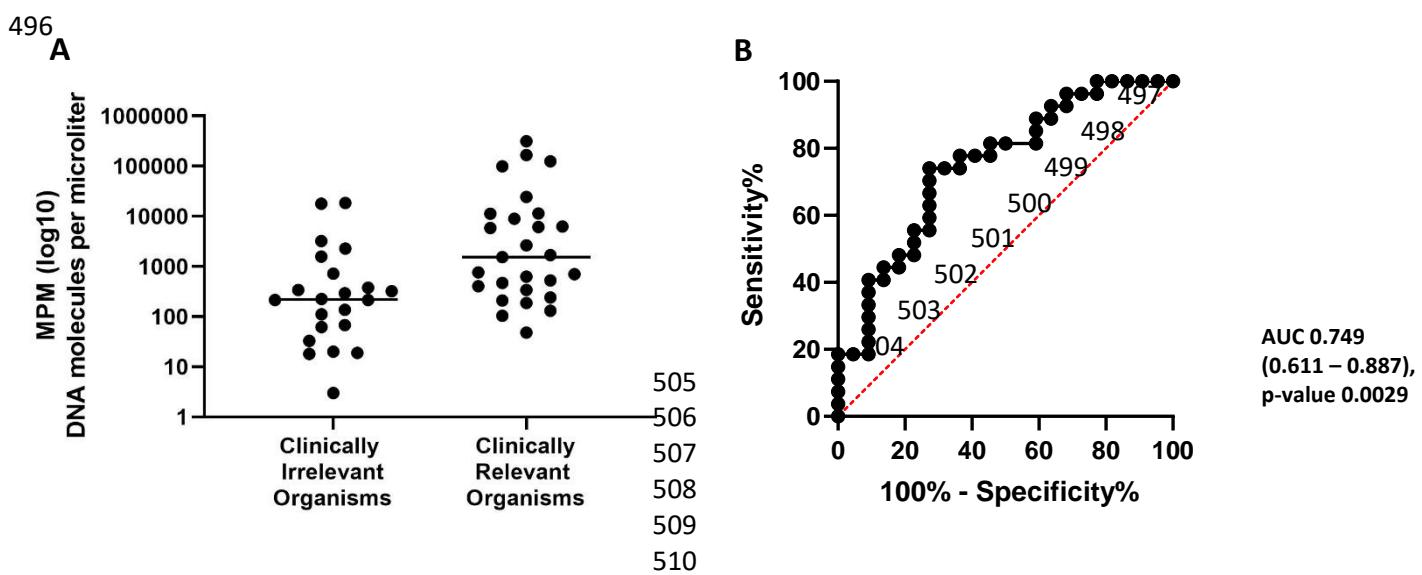
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Method 2: by result (each organism or absence of organism assessed)	Infection related to mNGS organism	Infection not related to mNGS organism	No infection at all	
mNGS identifies organism	Box A: TP: True positive organism: 28	Box B: FN: False negative (clinically irrelevant organism): 18	Box C: FP: False positive (clinically irrelevant organism): 5	Positive Predictive Value: TP/(box A+B+C): 55%
mNGS identifies NO organisms	Box D: FN: False negative: 15		Box E: TN: True negative: 15	Negative Predictive Value: TN/(box D+E): 50%
	Sensitivity: TP/(box A+B+D): 46%		Specificity: TN/(box C+E): 75%	

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