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# Corrigendum: Microbiological diagnostic performance of metagenomic next-generation sequencing compared with conventional culture for patients with community-acquired pneumonia

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## KEYWORDS

metagenomic next-generation sequencing, culture, community-acquired pneumonia, conventional microbiological test, pathogen detection

## A corrigendum on

### Microbiological diagnostic performance of metagenomic next-generation sequencing compared with conventional culture for patients with community-acquired pneumonia

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## Error in Figure/Table Legend

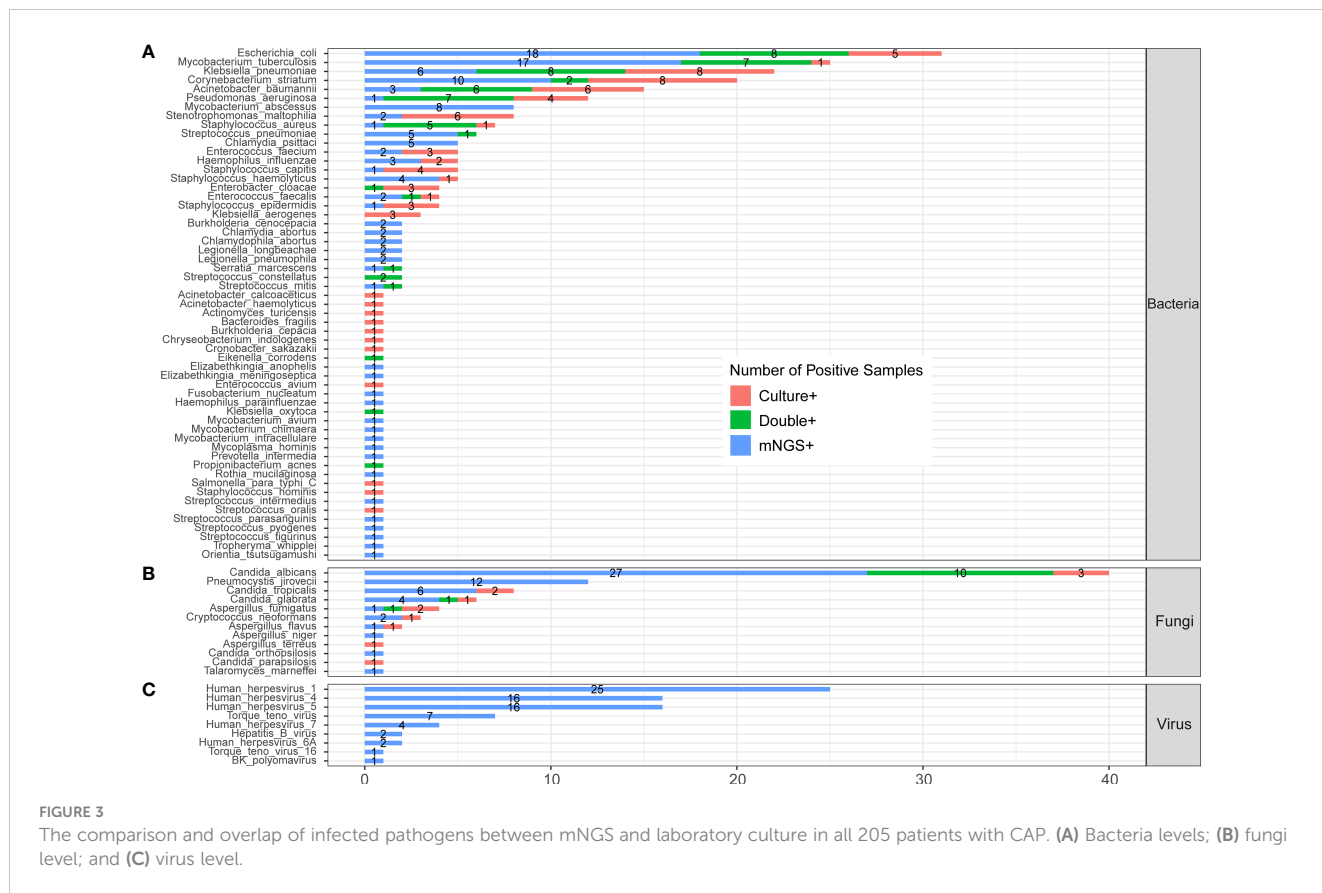
In the published article, there was an error in the legend for [Figure 3](#) as published. “(C) protozoa level” was included in legend of [Figure 3](#), which should be deleted. The corrected legend appears below.

**Figure 3** The comparison and overlap of infected pathogens between mNGS and laboratory culture in all 205 patients with CAP. (A) Bacteria levels; (B) fungi level; and (C) virus level.

In the published article, there was an error in the legend for [Figure 4](#) as published. “(C) protozoa level” was included in legend of [Figure 4](#), which should be deleted. The corrected legend appears below.

**Figure 4** Infected pathogens detected by mNGS in severe and non-severe patients with CAP. (A) bacteria levels; (B) fungi level; and (C) virus level.

In the published article, there was an error in the legend for [Figure 6](#) as published. “(C) protozoa level” was included in legend of [Figure 6](#), which should be deleted. The corrected legend appears below.



**Figure 6** Infected pathogens detected by mNGS in immunocompetent and immunocompromised patients with severe pneumonia. (A) Bacteria levels; (B) fungi level; and (C) virus level.

**Error in Figure/Table**

In the published article, there was an error in Figure 3 as published. *Orientia tsutsugamushi* was divided in Part C “Protozoa”, which should be moved to Part A “Bacteria”. The corrected Figure 3 and its caption \*\* The comparison and overlap of infected pathogens between mNGS and laboratory culture in all 205 patients with CAP. (A) Bacteria levels; (B) fungi level; and (C) virus level. appear below.

In the published article, there was an error in Figure 4 as published. *Orientia tsutsugamushi* was divided in Part C “Protozoa”, which should be moved to Part A “Bacteria”. The corrected Figure 4 and its caption \*\* Infected pathogens detected by mNGS in severe and non-severe patients with CAP. (A) bacteria levels; (B) fungi level; and (C) virus level. appear below.

In the published article, there was an error in Figure 6 as published. *Orientia tsutsugamushi* was divided in Part C “Protozoa”, which should be moved to Part A “Bacteria”. The corrected Figure 6 and its caption \*\* Infected pathogens detected by mNGS in immunocompetent and immunocompromised patients with severe pneumonia. (A) Bacteria levels; (B) fungi level; and (C) virus level. appear below.

**Incorrect Supplementary Material**

In the published article, there was an error in Supplementary Figure 2. *Orientia tsutsugamushi* was divided in Part C “Protozoa”, which should be moved to Part A “Bacteria”.

**Supplementary Figure 2.** The comparison and overlap of infected pathogens between metagenomic next-generation sequencing (mNGS) and laboratory culture in 186 patients with CAP whose sample type was consistent between two methods. (A) Bacteria levels; (B) Fungi level; (C) Virus level.

In the published article, there was an error in Supplementary Table 2. *Orientia tsutsugamushi* was divided in Part of “Protozoa”, which should be moved to Part of “Bacteria”.

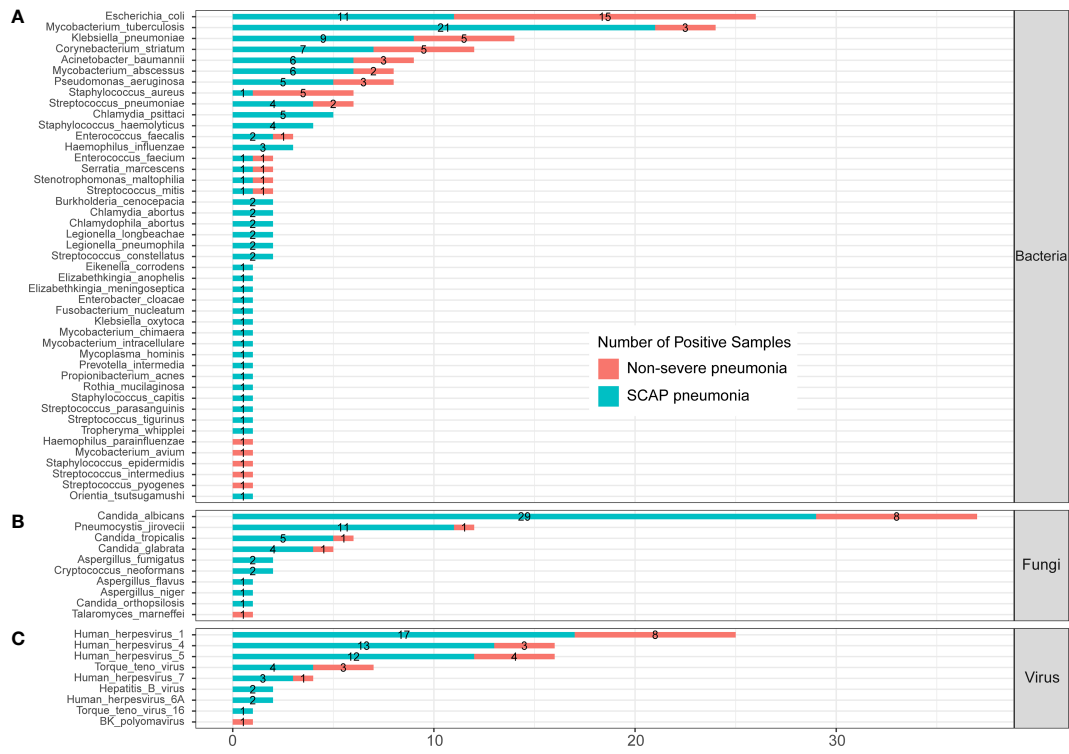
**Supplementary Table 2.** Comparison of pathogens detected by mNGS between non-severe CAP and SCAP groups.

In the published article, there was an error in Supplementary Table 3. *Orientia tsutsugamushi* was divided in Part of “Protozoa”, which should be moved to Part of “Bacteria”.

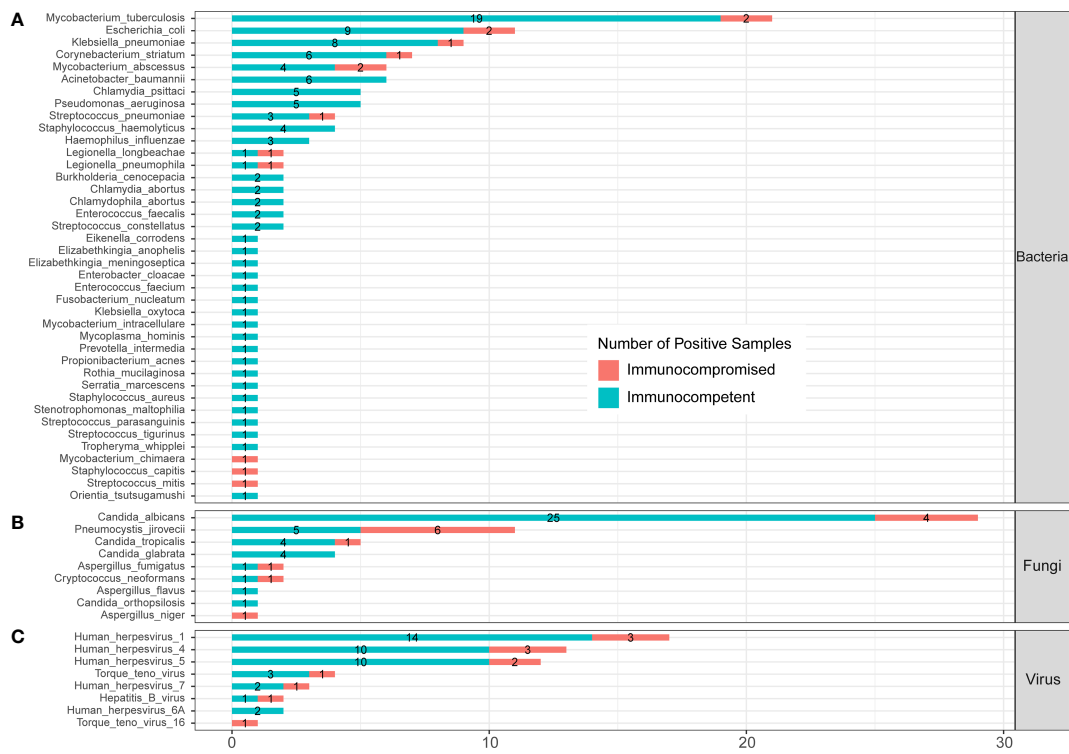
**Supplementary Table 3.** Comparison of pathogens detected by mNGS between immunocompetent and immunocompromised patients with SCAP.

**Text Correction**

In the published article, there was an error. *Orientia tsutsugamushi* was wrongly be categorized as Protozoa, which should be a bacterium. So, the number of detected bacteria and protozoan should be corrected.



**FIGURE 4** Infected pathogens detected by mNGS in severe and non-severe patients with CAP. (A) bacteria levels; (B) fungi level; and (C) virus level.



**FIGURE 6** Infected pathogens detected by mNGS in immunocompetent and immunocompromised patients with severe pneumonia. (A) Bacteria levels; (B) fungi level; and (C) virus level.

A correction has been made to **3 Results, 3.4 Pathogens' profile of all CAP patients according to detection methods**, Paragraph 1. This sentence previously stated:

"The detected pathogens were divided into four kingdoms, namely, bacteria, fungi, protozoa, and viruses. A total of 56 bacteria (Figure 3A), 12 fungi (Figure 3B), 1 protozoan (Figure 3C), and 9 viruses (Figure 3D) were detected by mNGS and the CMT."

The corrected sentence appears below:

"The detected pathogens were divided into three kingdoms, namely, bacteria, fungi, and viruses. A total of 57 bacteria (Figure 3A), 12 fungi (Figure 3B), and 9 viruses (Figure 3C) were detected by mNGS and the CMT."

In the published article, there was an error. *Orientia tsutsugamushi* was wrongly be categorized as Protozoa, which should be a bacterium. So, the number of detected bacteria and protozoan should be corrected.

A correction has been made to **3 Results, 3.4.1 Profile of bacteria**, Paragraph 1. This sentence previously stated:

"A total of 22 bacteria were only detected by mNGS, including *Mycobacterium abscessus* (*M. abscessus*, n=8), *Chlamydia psittaci* (*C. psittaci*, n=5), *Burkholderia cenocepacia* (n=2), and *Chlamydia abortus* (n=2)."

The corrected sentence appears below:

"A total of 23 bacteria were only detected by mNGS, including *Mycobacterium abscessus* (*M. abscessus*, n=8), *Chlamydia psittaci* (*C. psittaci*, n=5), *Burkholderia cenocepacia* (n=2), and *Chlamydia abortus* (n=2)."

In the published article, there was an error. *Orientia tsutsugamushi* was wrongly be categorized as Protozoa, which should be a bacterium. So, result of protozoa should be deleted.

A correction has been made to **3 Results, 3.4.2 Profile of fungi and protozoa**, sub-title and Paragraph 1. This paragraph previously stated:

"3.4.2 Profile of fungi and protozoa

In the fungi level (Figure 3B), *Candida albicans* (*C. albicans*) detected in 40 patients was the most frequent fungus, and 27 of cases were only detected by mNGS. *Pneumocystis jirovecii* (*P. jirovecii*) was the second common fungus detected in 12 cases by mNGS only. One case was positive of *Orientia tsutsugamushi*, which was detected by mNGS only (Figure 3C)."

The corrected paragraph appears below:

"3.4.2 Profile of fungi

In the fungi level (Figure 3B), *Candida albicans* (*C. albicans*) detected in 40 patients was the most frequent fungus, and 27 of cases were only detected by mNGS. *Pneumocystis jirovecii* (*P. jirovecii*) was the second common fungus detected in 12 cases by mNGS only."

In the published article, there was an error. *Orientia tsutsugamushi* was wrongly be categorized as Protozoa, which should be a bacterium. So, the number of detected bacteria should be corrected.

A correction has been made to **3 Results, 3.5 Comparison of pathogens detected by metagenomic next-generation sequencing**

*between severe and non-severe community-acquired pneumonia patients*, Paragraph 1. These sentences previously stated:

"A total of 44 bacteria were identified by mNGS in 205 CAP patients. There were 14 bacteria found in both severe and non-severe CAP patients, 5 bacteria were found only in infected non-severe patients, and 25 bacteria were only detected in SCAP patients (Figure 4A)."

The corrected sentence appears below:

"A total of 45 bacteria were identified by mNGS in 205 CAP patients. There were 14 bacteria found in both severe and non-severe CAP patients, 5 bacteria were found only in infected non-severe patients, and 26 bacteria were only detected in SCAP patients (Figure 4A)."

In the published article, there was an error. *Orientia tsutsugamushi* was wrongly be categorized as Protozoa, which should be a bacterium. So, the number of detected bacteria should be corrected.

A correction has been made to **3 Results, 3.6 Comparison of pathogens between immunocompromised and immunocompetent patients with severe community-acquired pneumonia**, Paragraph 2. These sentences previously stated:

"A total of 39 bacteria were identified by mNGS from 144 SCAP patients. Among them, 28 bacteria were detected in immunocompetent cases only, 3 bacteria were detected in immunocompromised cases only, and 8 bacteria were found in both immunocompetent and immunocompromised groups."

The corrected sentence appears below:

"A total of 40 bacteria were identified by mNGS from 144 SCAP patients. Among them, 29 bacteria were detected in immunocompetent cases only, 3 bacteria were detected in immunocompromised cases only, and 8 bacteria were found in both immunocompetent and immunocompromised groups."

In the published article, there was an error. *Orientia tsutsugamushi* was wrongly be categorized as Protozoa, which should be a bacterium. So, the word "Protozoa" should be deleted in Conclusions.

A correction has been made to **Conclusions**. These sentences previously stated:

"mNGS is superior in detecting MTB, NTM, viruses, *P. jirovecii*, chlamydia, and protozoa."

The corrected sentence appears below:

"mNGS is superior in detecting MTB, NTM, viruses, *P. jirovecii*, and chlamydia."

The authors apologize for these errors and state that this do not change the scientific conclusions of the article in any way. The original article has been updated.

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