

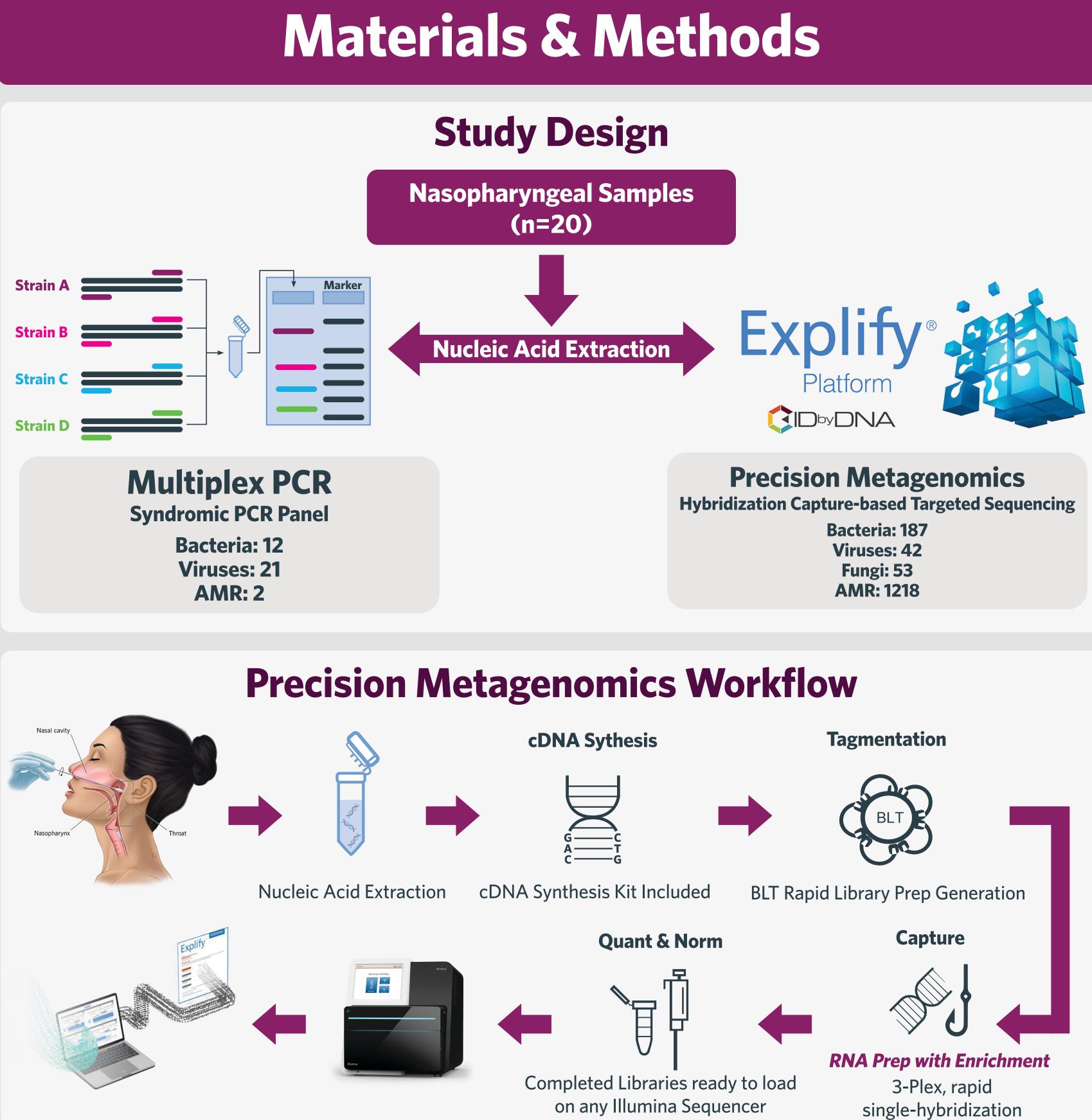
The Human Advantage

## Introduction

- Pulmonary infections are the major cause of morbidity and mortality worldwide.
- Co-infection of bacteria, fungi, viruses, and parasites is common in Pulmonary infections.
- Rapid and accurate pathogen identification enables targeted therapy.
- Metagenomic Next generation sequencing (mNGS) is a powerful emerging tool in clinical diagnosis to overcome the limitations of routine microbiological and PCR methods.
- Precision Metagenomics uses a targeted sequencing of clinically relevant targets using the hybridization capture-based targeted regions.
- The approach may improve diagnostic accuracy for guiding antibiotic prescriptions.

## Objective

- To evaluate microbial diversity in respiratory infection using precision metagenomic sequencing.
- To Compare the analytical power of PCR and NGS-based method to diagnose Respiratory pathogens.
- To explore the analytical and clinical advantage of precision metagenomics over the syndromic PCR panel in respiratory infection.



# **Deciphering the Microbiology of Respiratory Infection Using Precision Metagenomics Analysis**

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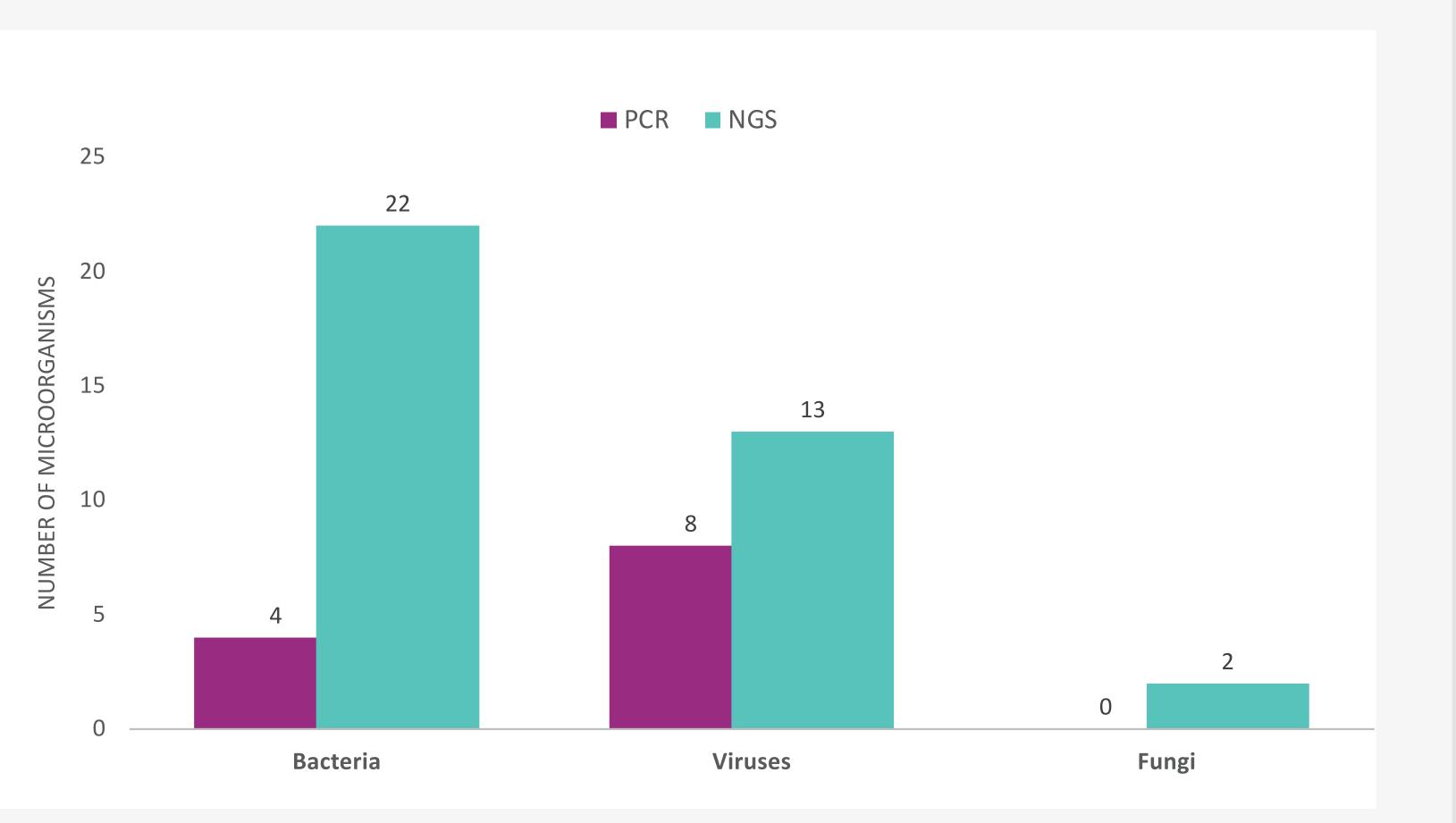
### **Targets Included on NGS & PCR Panels** Fungus AMR Control Total **'US** 10 292 53 1218 36

Panels Detail	Bacteria	Vir
Total Organisms Targeted in Capture- based NGS Panel	187	42
Total Organisms Targeted in Syndromic PCR Panel	12	2

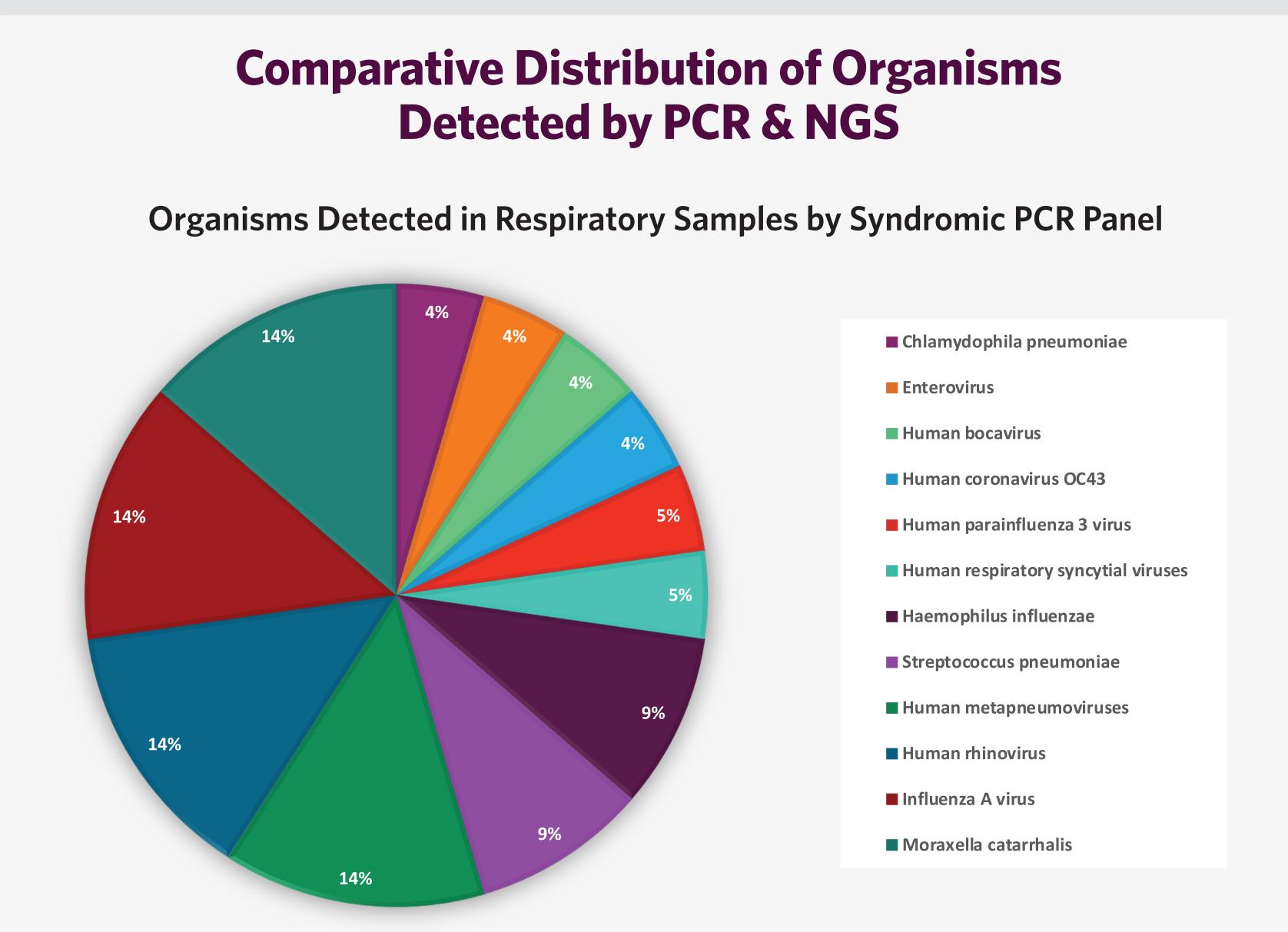
### **Comparative Analysis of Upper Respiratory Track Microbial Community Using PCR & NGS**

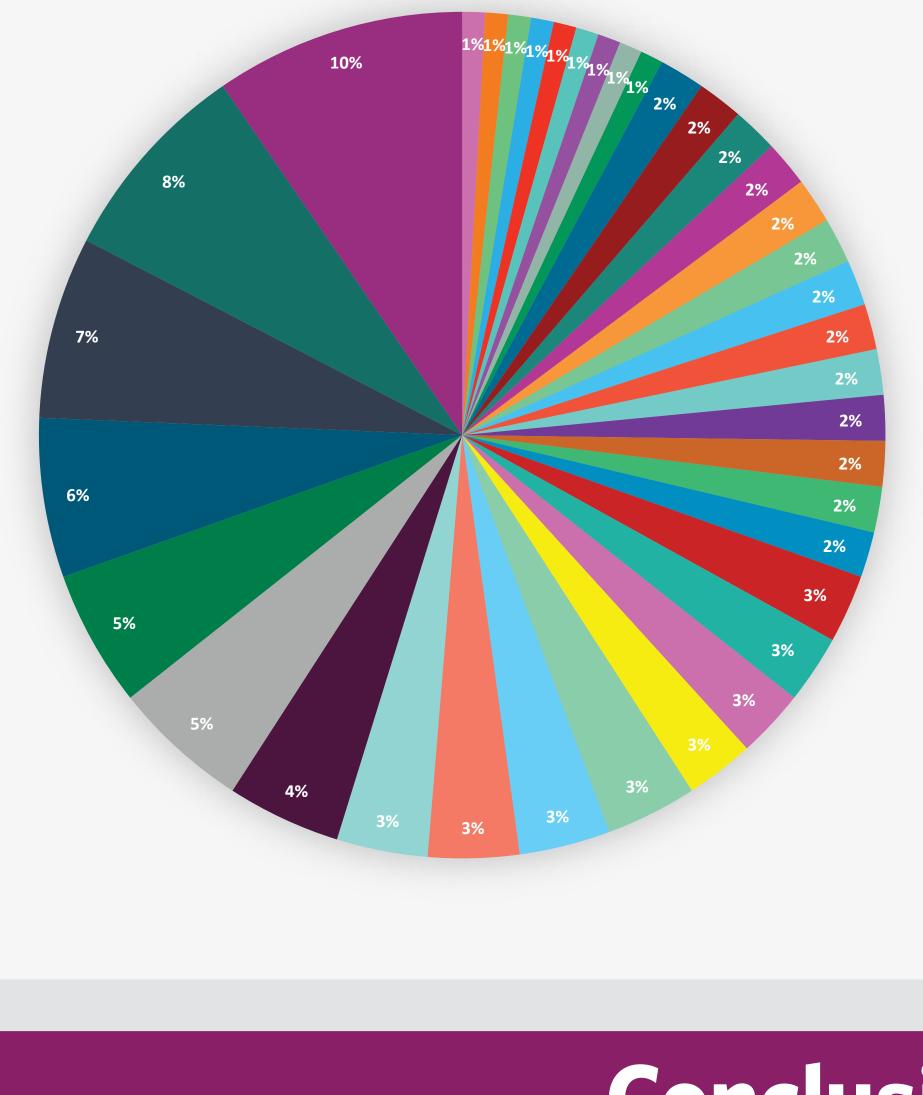
Results	Bacteria	Virus	Fungi	Total
Detected by PCR	4	8	-	12
PCR (+) & NGS (-)	0	0		
PCR (-) & NGS (+)	18	5	2	25
Detected by NGS	22	13	2	37

### Number of Bacterial, Viral, and Fungal Species **Detected by PCR and NGS**



## Results





- diagnostic test.

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### THE HUMAN ADVANTAGE IN LABORATORY

### **Organisms Detected in Respiratory Samples Using Explify Precision Metagenomic Analysis**

- Gemella hae molysans
- Haem ophilus para influenza
- Human parainfluenza virus
- Influenza A virus (H1N1)
- Pseudomonas stutzeri
- Alternaria alternata
- Fusarium proliferatum
- Prevotella melaninogenica
- Rothia mucilaginosa ■ Staphylococcus a ure us
- Streptococcus mitis
- Corynebacterium propinguu
- Human rhinovirus A
- Influenza A virus (H3N2)
- Haem ophilus influenzae
- Stenotrophomonas maltoph
- Elizabethkingia meningoseptic
- Eli zabethki ngi a an ophelis

- Haem ophilus hae molyticus
- Human herpesvirus 6 (HHV-6)
- Hum an rhi novirus C
- Neisseria flavescens
- Actinomyces graevenitzii
- Campylobacter concisus
- Human parainfluenza virus 3
- Respiratory syncytial virus B
- SARS-CoV-2 (2019-nCoV)
- Streptococcus intermedius
- Veillonella parvula
- Human metapneumovirus
- Ochrobactrum anthropi
- Corynebacterium pseudodiphtheriticum 🛛 Human coronavirus OC43
  - Streptococcus pneumoniae
  - Pseudomonas a eruginosa
  - Moraxella catarrhalis
  - Dolosigranulum pigrum

## Conclusion

• Precision metagenomics has a broader detection range compared to PCR. • Precision metagenomic analysis using the Explify platform exclusively identified 25 microorganisms (5 Viruses, 18 Bacteria, and 2 Fungi) not included in PCR panel.

• NGS can potentially alter the landscape of infection diagnosis significantly. Due to the lack of pathogen targeting, a single workflow may be used for all specimens, regardless of symptom, potentially expanding to non-viral pathogens, resulting in a pan-microbial