



# Clinical Evaluation and Potential Impact of a Semi-Quantitative Multiplex Molecular Assay for the Identification of Pathogenic Bacteria and Viruses in Lower Respiratory Specimens\*

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## Rationale

Rapid identification of organisms causing lower respiratory tract infections (LRTIs) is central to appropriate antimicrobial utilization; however, culture methods are slow and insensitive, and molecular tests are not available or are not routinely ordered. We evaluated the FilmArray Pneumonia Panel (FA-Pneumo) (BioFire Diagnostics, Salt Lake City, UT) for detection of respiratory pathogens in bronchoalveolar lavage (BAL) specimens.

## Methods and Instrumentation

A total of 259 BAL specimens were collected from inpatients aged 18 years and older with symptoms of respiratory tract infection at 8 hospitals in the US. All specimens were tested using the FA-Pneumo assay, which identifies 18 bacterial agents (15 reported semi-quantitatively when the target genomic is present at or above 10<sup>3.5</sup> copies/mL) in addition 8 viral agents (reported qualitatively). Select resistance mechanisms including *mecA/C*, CTX-M, KPC, VIM, IMP, NDM, and OXA-48 are also detected. In this study, identification results for LRTI were compared to standard of care (SOC) methods including bacterial culture and PCR based on clinician order. Chart review was conducted to determine type and duration of antibiotic (abx) therapy for each subject.

**The FilmArray® Pneumonia Panel**  
Sample Type: Sputum, Endotracheal Aspirate, and Bronchoalveolar Lavage

**Panel Menu** 34 Targets in One Test

- Bacteria**
  - Semi-Quantitative Bacteria
  - Acinetobacter calcoaceticus-tosamanni* complex
  - Serratia marcescens*
  - Proteus* spp.
  - Klebsiella pneumoniae* group
  - Enterobacter aerogenes*
  - Enterobacter cloacae*
  - Escherichia coli*
  - Haemophilus influenzae*
  - Moraxella catarrhalis*
  - Pseudomonas aeruginosa*
  - Staphylococcus aureus*
  - Streptococcus pneumoniae*
  - Klebsiella oxytoca*
  - Streptococcus pyogenes*
  - Streptococcus agalactiae*
- Atypical Bacteria**
  - Qualitative Bacteria
  - Legionella pneumophila*
  - Mycoplasma pneumoniae*
  - Chlamydia pneumoniae*
- Antimicrobial Resistance Genes**
  - meaC* and *MFEJ*
  - KPC
  - NDM
  - QacB-like
  - CTX-M
  - VIM
  - IMP
- Viruses**
  - Influenza A
  - Influenza B
  - Respiratory Syncytial Virus
  - Human Rhinovirus/Enterovirus
  - Human Metapneumovirus
  - Parainfluenza virus
  - Adenovirus
  - Coronavirus
  - Middle East Respiratory Syndrome Coronavirus

**Workflow**

Time to Results ~65 min  
2 min hands on time

## Conclusions

- FA-Pneumo detects potential pathogens in **60-70% more** specimens than culture
  - Not subject to NOF overgrowth, fastidious growth requirements, pre-treatment with Abx
- FA-Pneumo detects **additional pathogens** not high on differential
  - Viral agent detected in 20% of specimens
  - Only 22% of positive specimens has a corresponding SOC order
- Results are **clinically actionable**
  - Potential Abx adjustment in >60% of patients 3-4 days earlier
  - 50% of potential Abx adjustments were discontinuation or narrowing

**Table 1. Comparison of FA-Pneumo and bacterial culture in BAL (n=259)**

Organism	SOC+/FA+	SOC+/FA-	SOC-/FA+	SOC-/FA-	Total	PPA	NPA
<i>A. baumannii</i>	1	0	0	258	259	100%	100%
<i>Enterobacter</i>	10	0	5	244	259	100%	98.0%
<i>E. coli</i>	2	0	3	254	259	100%	98.8%
<i>H. influenzae</i>	4	0	19	236	259	100%	92.6%
<i>K. oxytoca</i>	2	0	6	251	259	100%	97.7%
<i>K. pneumoniae</i>	8	0	4	247	259	100%	98.4%
<i>M. catarrhalis</i>	2	0	8	249	259	100%	96.9%
<i>Proteus</i>	2	0	3	254	259	100%	98.8%
<i>P. aeruginosa</i>	17	2	6	234	259	89.5%	97.5%
<i>S. marcescens</i>	3	0	0	256	259	100%	100%
<i>S. agalactiae</i>	1	0	5	253	259	100%	98.1%
<i>S. pneumoniae</i>	2	0	3	254	259	100%	98.8%
<i>S. pyogenes</i>	0	0	1	258	259	100%	99.6%
<i>S. aureus</i>	21	1	21	216	259	95.5%	91.1%
<b>Total</b>	<b>75</b>	<b>3</b>	<b>84</b>	<b>3464</b>	<b>3626</b>	<b>96.1%</b>	<b>97.6%</b>

FA: FA-Pneumo; SOC: Standard of care

**Table 2. Comparison of FA-Pneumo and viral NAAT in BAL (n=259)**

Target	FA positive	SOC Order	SOC Agree	FA No Bacteria
hRV/EV	17	6/17 (35%)	6/6 (100%)	7/17 (41%)
CoV	9	2/9 (22%)	2/2 (100%)	7/9 (78%)
FluA	5	0/5 (0%)	n/a	3/5 (60%)
PIV	3	1/3 (33%)	1/1 (100%)	2/3 (66%)
FluB	2	1/2 (50%)	1/1 (100%)	1/2 (50%)
RSV	2	0/2 (0%)	n/a	2/2 (100%)
hMPV	1	0/1 (0%)	n/a	0/1 (0%)
AdV	1	0/1 (0%)	n/a	1/1 (100%)
<i>Legionella</i>	1	0/1 (0%)	n/a	1/1 (100%)
<i>Mycoplasma</i>	1	0/1 (0%)	n/a	1/1 (100%)
CoV+hMPV	1	1/1 (100%)	1 (100%)	0/1 (0%)
hRV/EV+PIV	3	0/3 (0%)	n/a	1/3 (33%)
hRV/EV+CoV	1	0/1 (0%)	n/a	0/1 (0%)
hMPV+FluA+CoV	1	0/1 (0%)	n/a	1/1 (100%)
None Detected	211	79/211 (37%)	76/79 (96.2%)	129/211 (61%)

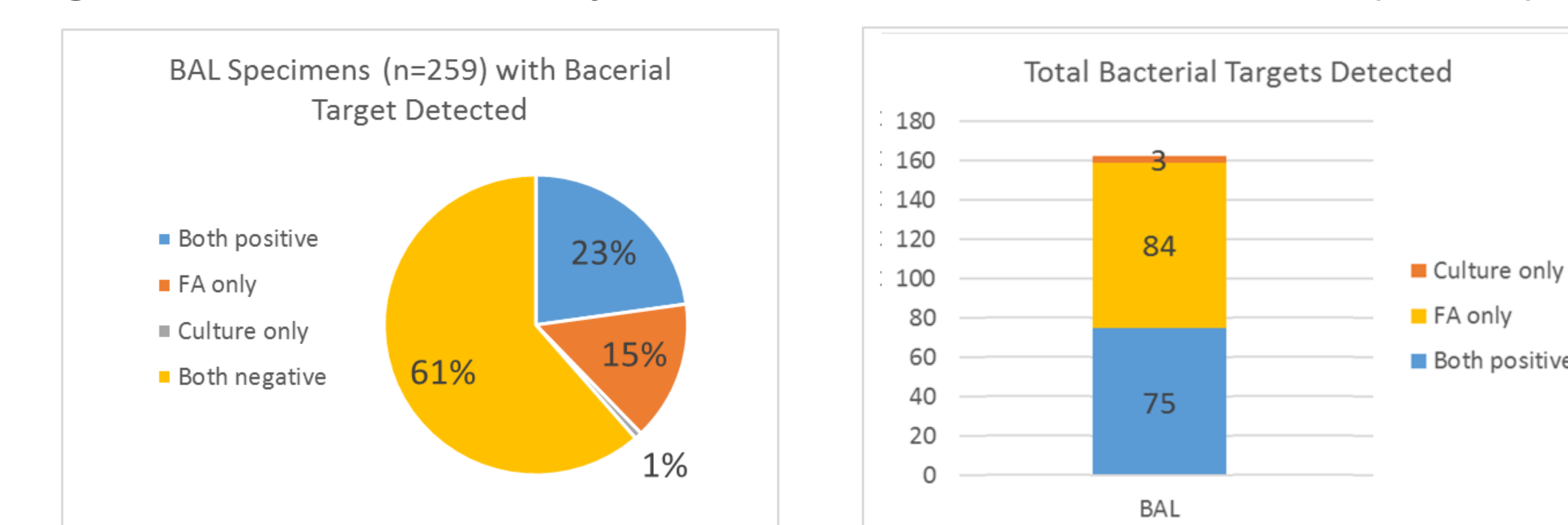
FA: FA-Pneumo; SOC: Standard of care. **Only 22% of positive specimens had an appropriate SOC order.**

**Table 3. Impact of FA-Pneumo on antibiotic prescribing**

Potential Change, no.	Antimicrobials	Patients	Hours
Appropriate de-escalation	206	122 (48%)	18,284.07
Appropriate escalation	5	5 (2%)	184.66
Inappropriate de-escalation*	6	6 (2%)	-
Inappropriate escalation**	42	42 (17%)	-
No change	-	78 (31%)	-
Unable to assess	-	16	-

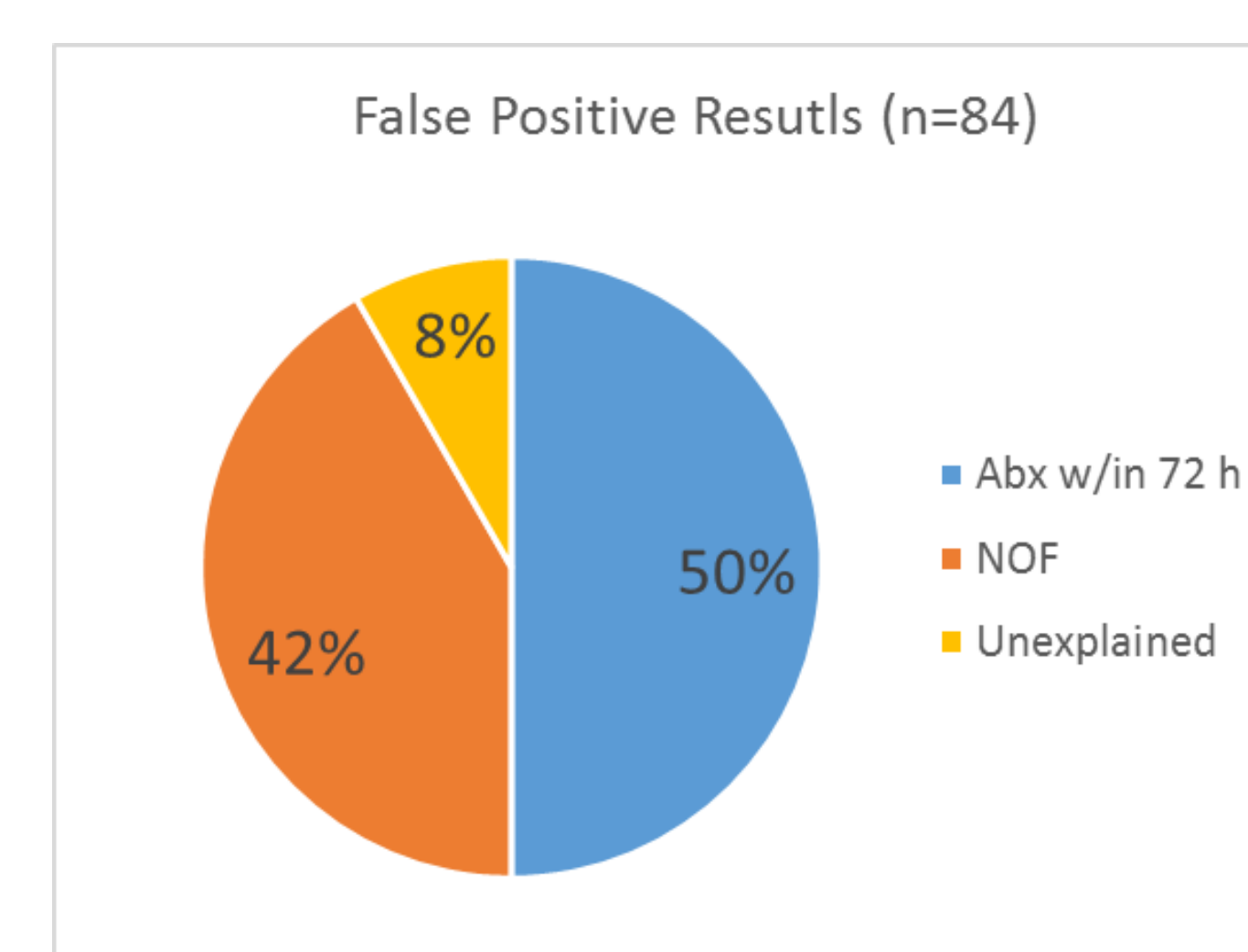
\* Organisms (n=3) or resistance mechanisms (n=3) identified by SOC but not by FA-Pneumo  
\*\* Organisms identified by FA-Pneumo but not by SOC. May represent normal oral flora (NOF) or true pathogen

**Figure 1. Qualitative comparison of FA-Pneumo and culture (n=259)**



FilmArray detected a bacterial target in **71% more BAL** specimens than routine culture, equating to a **108% increase** in total bacterial detections.

**Figure 2. Discordance: FA-Pneumo positive/Culture negative**

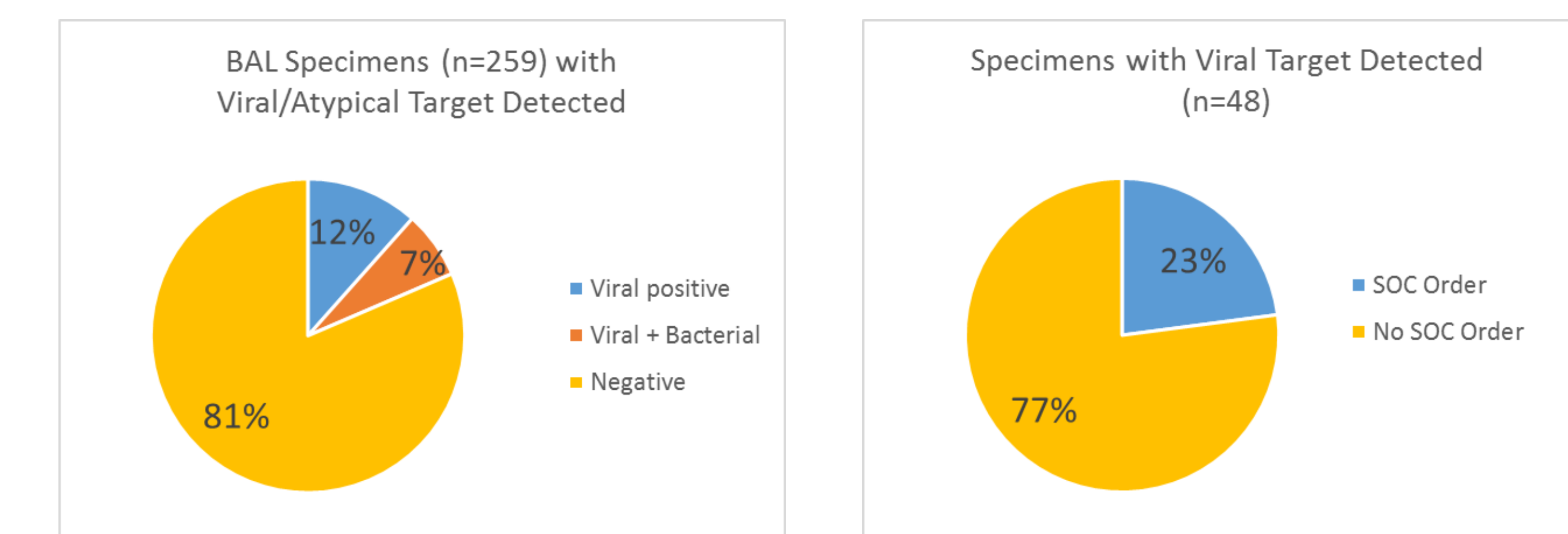


**Unexplained**  
5/7 (71%) quantified at 10<sup>4</sup>/mL by FA-Pneumo  
▪ (3) *S. aureus*, (1) *K. pneumoniae*, (1) *P. aeruginosa*  
▪ All ~10<sup>3</sup>/mL in culture  
Not reported, below "significance" threshold by culture

**NOF**  
14/35 (40%) quantified at 10<sup>4</sup>/mL by FA-Pneumo  
15/35 (43%) contained ≥ 1 more predominant target(s)  
▪ Failed to reach "significance" criteria for reporting by culture

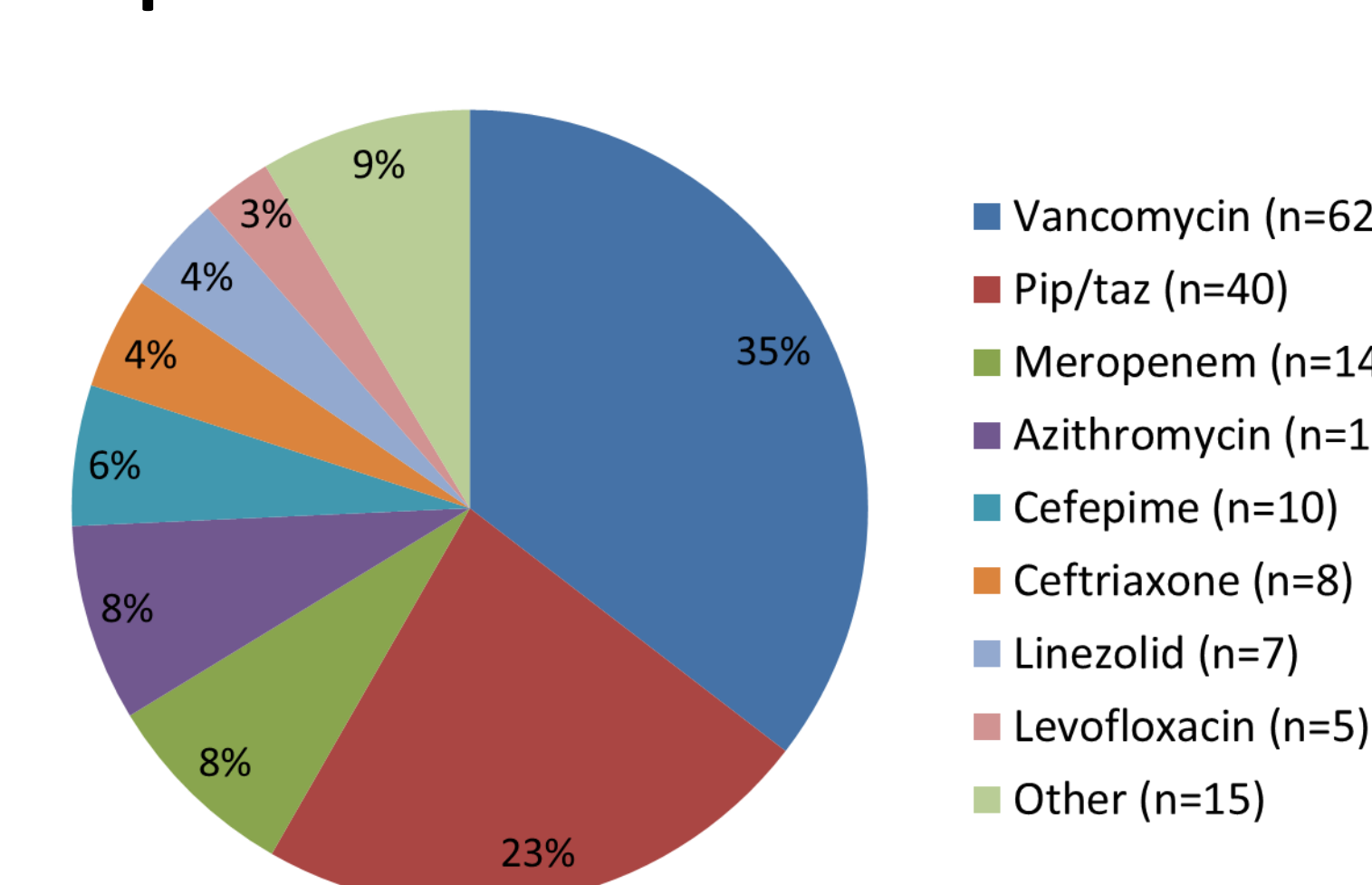
**Abx**  
All received Abx with potential activity against target  
▪ Still useful to detect targets in culture negative specimens  
Narrow broad-spectrum therapy (e.g. H. flu vs. P. aeru)

**Figure 3. Prevalence of viral targets and related standard of care orders**



FilmArray detected a viral target in **19% of BAL** specimens. **77%** of positive specimens **did not have SOC order**.

**Specific antibiotics de-escalated**



- Antibiotic adjustment could be made on **165/243 (68%)** evaluable patients
- FA-Pneumo results enabled an avg. of **1.48 antibiotic interventions/patient**
- FA-Pneumo results enabled **≥18,000 antibiotic hours saved** (avg. 6.2 d/patient, 3.8 d/abx)

\*The assays described in this poster have not been evaluated for IVD use by regulatory agencies