**Supplementary Table 1. Multi-target interpretation algorithms for CHAMPS database**

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| **BPAR\_1** | **BOP1\_1** | **BOP2\_1** | **Interpretation** |
| Positive | Negative | Negative | *Bordetella* spp. (*B. parapertussis/B. bronchiseptica*) \* |
| Positive | Negative | Positive | *B. parapertussis* |
| Negative | Positive | Negative | *Bordetella* spp. (*B. pertussis/B. holmesii*) \*\* |
| Negative | Positive | Positive | *B. pertussis* |
| Negative | Negative | Positive | Presence of pertussis toxin gene |
| Negative | Negative | Negative | Negative for *Bordetella* spp. |
| Positive | Positive | Positive | *Bordetella* spp. (*B. parapertussis/B. bronchiseptica/B. pertussis/B. holmesii)* \*\*\* |
| Positive | Positive | Negative | *Bordetella* spp. (*B. parapertussis/B. bronchiseptica/B. pertussis/B. holmesii)* \*\*\* |

\* Most probable interpretation is *B. parapertussis* but *B. bronchiseptica* cannot be excluded.

\*\* In the absence of the pertussis toxin (BOP2\_1), BOP1\_1 could be positive from the presence of *B. pertussis* or *B. holmesii*

\*\*\* The *Bordetella* species cannot be definitively determined, and the presence of a mixed *Bordetella* species specimen cannot be excluded.

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| **CLDP\_1** | **CLDA\_1** | **CLDB\_1** | **Interpretation** |
| Positive | Negative | Negative | Non-toxigenic *C. difficile\** |
| Negative | Positive | Negative | toxigenic *C. difficile* with the toxin A gene *tcdA\** |
| Negative | Positive | Positive | toxigenic *C. difficile* with the toxin A gene *tcdA* and the toxin B gene *tcdB\** |
| Negative | Negative | Positive | toxigenic *C. difficile* with the toxin B gene *tcdB\** |
| Negative | Negative | Negative | Negative for *C. difficile* |

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| **CODI\_1** | **COUP\_1** | **CTOX\_1** | **Interpretation** |
| Positive | Negative | Negative | Non-toxigenic *C. diphtheriae* |
| Positive | Negative | Positive | toxigenic *C. diphtheriae* |
| Positive | Positive | Negative | Mixed non-toxigenic *C. diphtheriae* and *C. ulcerans/pseudotuberculosis* |
| Positive | Positive | Positive | Mixed *C. diphtheriae* and *C. ulcerans/pseudotuberculosis* with the presence of the diphtheria toxin gene |
| Negative | Negative | Positive | Presence of the diphtheria toxin gene |
| Negative | Positive | Negative | Non-toxigenic *C. ulcerans/pseudotuberculosis* |
| Negative | Positive | Positive | toxigenic *C. ulcerans/pseudotuberculosis* |
| Negative | Negative | Negative | Negative for *Corynebacterium* |

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| **HIAT\_1** | **HITB\_2** | **Interpretation** |
| Positive | Negative | *H. influenzae* serotype A,C,D,E,F, or NT |
| Positive | Positive | *H. influenzae* serotype B\* |
| Negative | Positive | *H. influenzae* serotype B\* |
| Negative | Negative | Negative for *H. influenzae* |

\*Cross-reactivity with serotype A strains may occur.

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| **MRSN\_1** | **MRSU\_1** | **Interpretation** |
| Positive | Negative | MERS coronavirus |
| Positive | Positive | MERS coronavirus |
| Negative | Positive | MERS coronavirus |
| Negative | Negative | Negative for MERS coronavirus |

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| **SALS\_1** | **SATY\_1** | **SAPA\_1** | **Interpretation** |
| Positive | Negative | Negative | *Salmonella* spp. |
| Positive | Negative | Positive | *Salmonella enterica subspe*ciees *paratyphi A* |
| Positive | Positive | Negative | *Salmonella enterica* subspecies *typhi* |
| Positive | Positive | Positive | Mixed *Salmonella enterica* subspecies *paratyphi A/typhi* |
| Negative | Negative | Positive | *Salmonella enterica* subspecies *paratyphi A* |
| Negative | Positive | Negative | *Salmonella enterica* subspecies *typhi* |
| Negative | Positive | Positive | Mixed *Salmonella enterica* subspecies *paratyphi A/typhi* |
| Negative | Negative | Negative | Negative for *Salmonella* spp. |

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| **VICH\_1** | **VTOX\_1** | **Interpretation** |
| Positive | Negative | non-toxigenic *V. cholerae* |
| Positive | Positive | toxigenic *V. cholerae* |
| Negative | Positive | Presence of the cholera toxin gene |
| Negative | Negative | Negative for *V. cholerae* |

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| **Code** | **Pathogen detected** | **Target** | **Interpretation** |
| ECSH\_1 | *Escherichia coli/Shigella* | *uidA* | *Escherichia coli/Shigella* spp. |
| STX1\_1 | Shiga toxin/Shiga-like toxin 1 | *stx1* | Presence of Shiga toxin carried by *Shigella dysenteriae* and/or Shiga-like toxin 1 carried by *Escherichia, Citrobacter, Aeromonas, Enterobacter* |
| STX2\_1 | Shiga-like toxin 2 | *stx2* | Presence of Shiga-like toxin 2 carried by *Escherichia, Citrobacter, Aeromonas, Enterobacter*  genus |
| EAE1\_1 | *Escherichia coli* | *aaiC* | *Escherichia coli* carrying the *aaiC* virulence gene |
| EAE2\_1 | *Escherichia coli* | *aatA* | *Escherichia coli* carrying the *aatA* virulence gene |
| EPE2\_1 | *Escherichia coli* | *bfpA* | *Escherichia coli* carrying the *bfpA* virulence gene |
| EPE1\_1 | *Escherichia coli* | *eae* | *Escherichia coli* carrying the *eae* virulence gene |
| ETLT\_1 | *Escherichia coli* (heat-labile enterotoxin) | *LT* | *Escherichia coli* carrying the heat-labile enterotoxin gene |
| ETST\_1 | *Escherichia coli* (heat-stable enterotoxin) | *STh/STp* | *Escherichia coli* carrying the heat-stable enterotoxin gene |
| EIES\_1 | *Escherichia coli/Shigella* | *ipaH* | *Escherichia coli/Shigella* spp. carrying the *ipaH* virulence gene |