

# Wound Pathogen Panel (PCR)

CoreBioLabs PCR	Culture
✓ Results within 24 hours	⚠ Results in 3-14 days
✓ > 99% Sensitivity and Specificity	⚠ Typically can only detect one pathogen
✓ Rapid detection of fastidious organisms such as fungi & anaerobes	⚠ Extended incubation for fungi and anaerobes
✓ NOT affected by antibiotic use	⚠ IS affected by antibiotic use

## Wound Pathogen Panel

CoreBioLabs precisely analyzes wounds for 48 pathogens and 13 resistance markers simultaneously using advanced molecular identification techniques including the QuantStudio 12 Flex by ThermoFisher®. We proudly offer an option for in-house Antibiotic Susceptibility Testing. After positive culture growth, our BD Phoenix® system provides antimicrobial concentrations for detection of emerging resistance. Our provider friendly reporting is portal driven with personalized office flexibility.

### Pathogens + Markers

- |                                                     |                              |
|-----------------------------------------------------|------------------------------|
| Acinetobacter baumannii                             | Microsporium audouinii       |
| Acremonium strictum                                 | Moraxella Catarrhalis        |
| Aspergillus fumigatus                               | Morganella morganii          |
| Aspergillus niger                                   | Neofusicoccum mangiferae     |
| Aspergillus versicolor                              | Prevotella loescheii         |
| Bacteroides fragilis                                | Proteus mirabilis            |
| Candida albicans                                    | Proteus vulgaris             |
| Candida glabrata                                    | Pseudomonas aeruginosa       |
| Candida krusei                                      | Scopulariopsis brevicaulis   |
| Candida parapsilosis                                | Serratia marcescens          |
| Candida tropicalis                                  | Staphylococcus aureus        |
| Citrobacter freundii                                | Staphylococcus Coag-Neg      |
| Clostridium novyi (A, B)                            | Staphylococcus epidermidis   |
| Clostridium perfringens                             | Staphylococcus saprophyticus |
| Clostridium septicum                                | Strep agalactiae (Group B)   |
| Corynebacterium sp                                  | Strep dysgalactiae (Group G) |
| Cutibacterium                                       | Strep pyogenes (Group A)     |
| (Propionibacterium) acnes                           | Strep pneumoniae             |
| Enterobacter aerogenes                              | Trichophyton interdigitale   |
| Enterobacter cloacae                                | Trichophyton rubrum          |
| Enterococcus faecalis                               | <b>Resistance Markers</b>    |
| Enterococcus faecium                                | Carbapenems                  |
| Epidermophyton floccosum                            | ESBL                         |
| Escherichia coli                                    | Fosfomycin                   |
| Fusarium solani                                     | Macrolide                    |
| Herpes simplex virus 1                              | Quinolone                    |
| Herpes simplex virus 2                              | Sulfonamide/ Trimethoprim    |
| Human herpesvirus 3 (HHV3 – Varicella zoster Virus) | Tetracycline                 |
| Kingella kingae                                     | Vancomycin                   |
| Klebsiella oxytoca                                  | AmpC                         |
| Klebsiella pneumoniae                               | Methicillin                  |



"Ninety-seven patients with post-operative SSI whose wound swabs/aspirate were **negative in the conventional aerobic culture** after 72 h of incubation were analysed by 16S rRNA gene specific broad range PCR.

Of the 97 patients, 16S rRNA based **broad range PCR assay could identify the presence of bacterial pathogen in 53 (54.63%) cases**, of which 29 isolates were supposed to be of viable but non-culturable bacteria (VBNC), 07 were of obligatory anaerobes and 13 were of unculturable bacteria, 04 were with poly bacterial infections."<sup>1</sup>



<sup>1</sup> Behera, H. S., Chayani, N., Bal, M., Khuntia, H. K., Pati, S., Das, S., & Ranjit, M. (2021). Identification of population of bacteria from culture negative surgical site infection patients using molecular tool. BMC surgery, 21(1), 28. <https://doi.org/10.1186/s12893-020-01016-y>