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A Unified Transcriptomic Signature Associated with Severity of Infection, Risk Factors for Severe Outcomes, and Treatments

Stanford researchers have developed a powerful immune-based gene expression signature that accurately predicts severe outcomes and all-cause mortality across high-risk populations, enabling personalized treatment selection and advancing precision medicine in critical illnesses and preventative care.

Many adults, especially those who are older, male, obese, smokers, or have chronic diseases like diabetes and asthma, face increased risk of severe outcomes from critical illnesses such as infections, sepsis, trauma, burns, or acute respiratory disease syndrome (ARDS). These risk factors have been studied largely in isolation, and treatment response in critically ill patients remains highly variable, leading to repeated clinical trial failures.

Stanford researchers have developed a powerful immune-based signature that captures a shared biological pathway across high-risk populations. This signature predicts all-cause mortality with high accuracy surpassing existing diagnostics. It enables patient-specific prognostics for severe outcomes, guides treatment selection and predicts response to monoclonal antibody treatment in asthma patients. This innovation reduces clinical heterogeneity and offers a scalable, actionable tool for personalized critical care and preventive medicine.

Stage of Development:
Pre-clinical

Applications

- Prognostic test for severe outcomes in critical illness
- Personalizes selection of immunomodulatory treatments
- Predicts response to monoclonal antibody treatment in asthma patients
- Predicts risk for all-cause mortality

Advantages

- Comprehensive risk prediction
- Personalized treatments for better outcomes
- Scalable and actionable
- High accuracy
- Better patient stratification

Innovators

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