



Single-cell landscape revealed immune characteristics associated with disease phases in brucellosis patients

Yi Wang¹, Siyuan Yang², Bing Han², Xiufang Du³, Huali Sun⁴, Songnian Hu⁵, et al.

¹Experimental Research Center, Capital Institute of Pediatrics, Beijing, China

²Beijing Ditan Hospital, Capital Medical University, Beijing, China

³The Third People's Hospital of Lifen City, Linfen, Shanxi, China

⁴The Affiliated Hospital of Qingdao University, Qingdao, Shandong, China

⁵ Institute of Microbiology, Chinese Academy of Sciences



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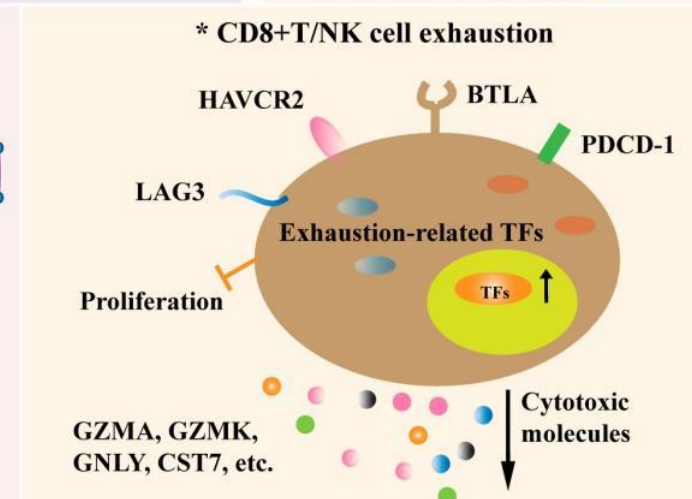
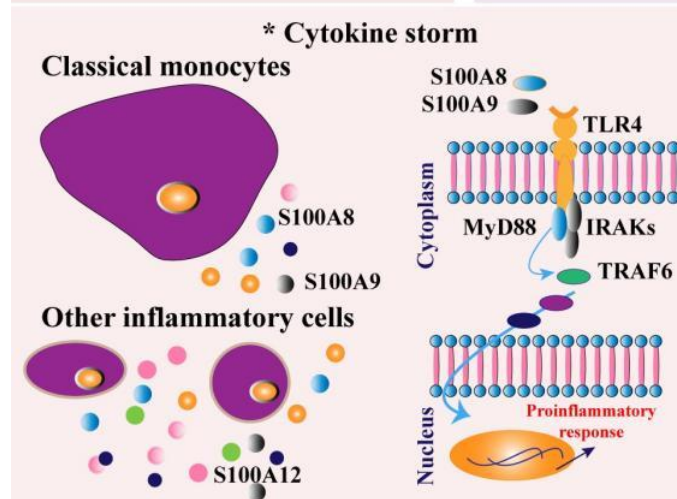
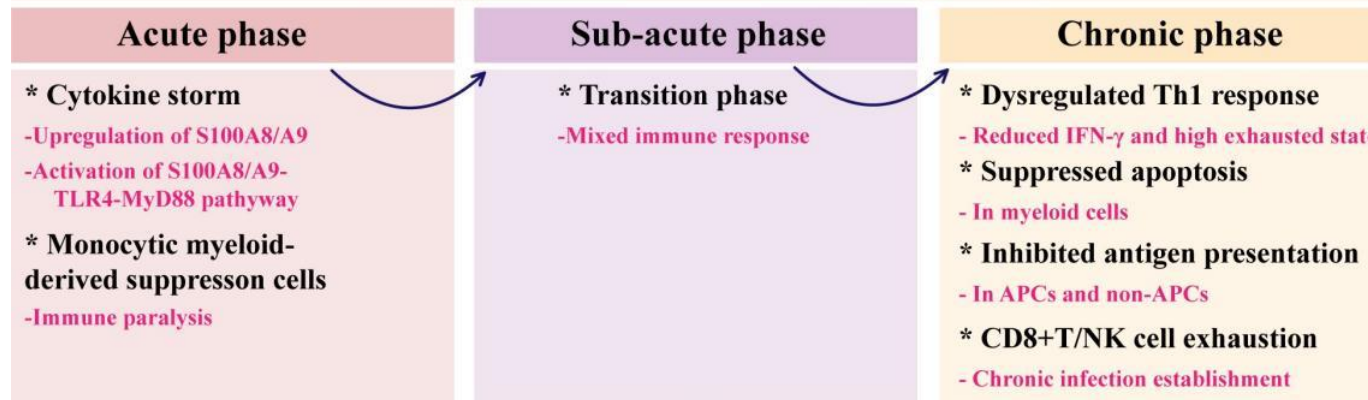
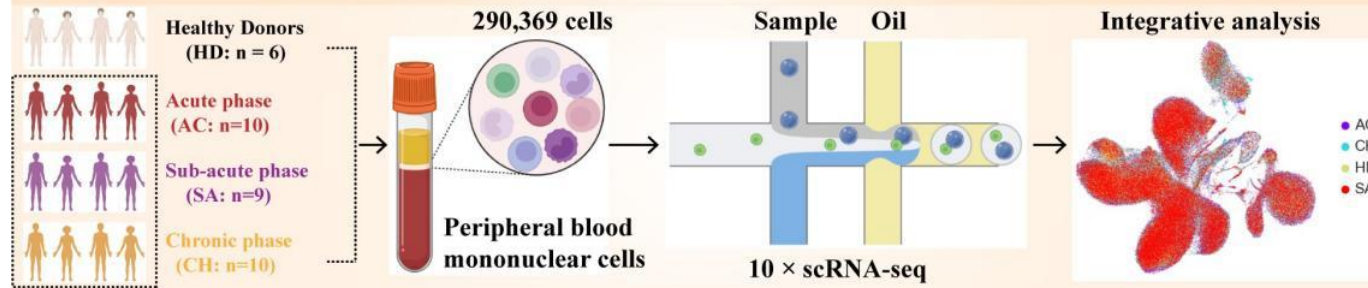
Introduction

- Brucellosis is caused by Brucella, which affects livestock worldwide and is one of the most important zoonotic diseases in humans. Despite extensive efforts to control the spread of brucellosis, it still remains prevalent in many parts of the world. In epidemic areas, the incidence rate of human brucellosis is still very high, and it is estimated that more than 500000 people are newly infected every year. In East Asia, China has the highest burden of brucellosis, with a rising incidence rate and expanding geographical scope. Therefore, brucellosis remains an important disease that cannot be ignored and continues to cause significant health, veterinary, and economic issues
- Brucellosis patients present with a wide range of clinical manifestations, from asymptomatic to mild/moderate disease, and some patients may develop severe diseases involving multiple organs, even leading to death. Brucellosis can be divided into three stages based on the severity and duration of symptoms: acute phase, subacute phase, and chronic phase. Especially, the reactivation and chronic nature of Brucella infection, as well as the secretive intracellular life cycle of the pathogen, make this infection difficult to eradicate and require lengthy antibiotic treatment. Therefore, understanding the host's immune response during the disease is extremely important for better designing appropriate treatment interventions for brucellosis patients. However, a detailed investigation into the immune response to human brucellosis is still lacking
- Single cell transcriptome sequencing is a powerful technique for breaking down host immune responses, which has been used for various infectious diseases but has not yet been applied to brucellosis. We described high-resolution transcriptomic changes in peripheral blood immune cells at different disease stages and emphasized the relationship between disease stages and host immune response

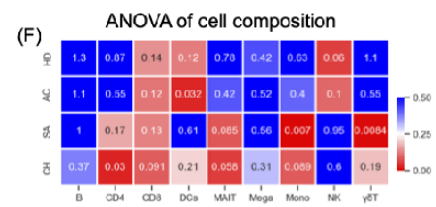
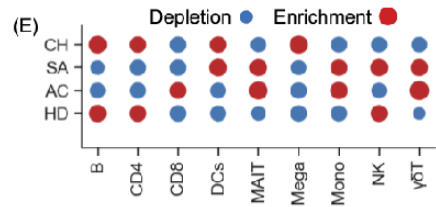
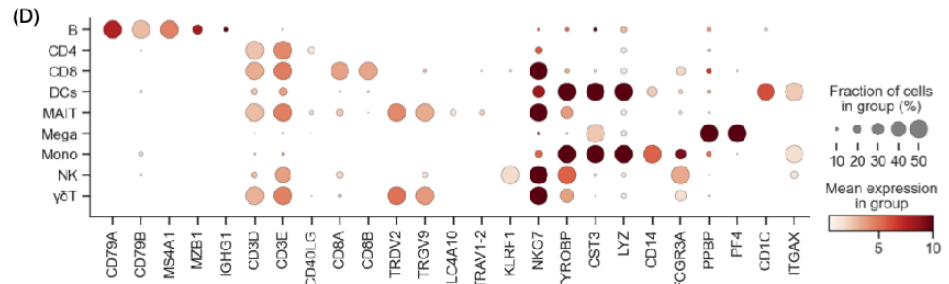
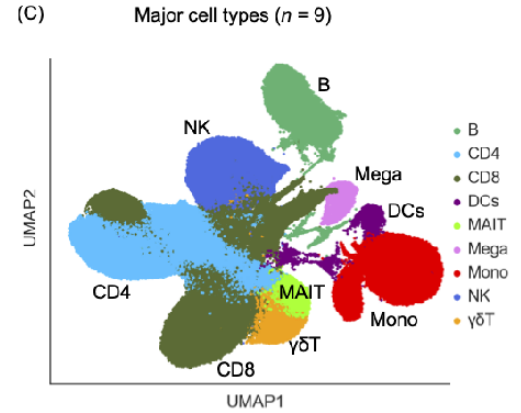
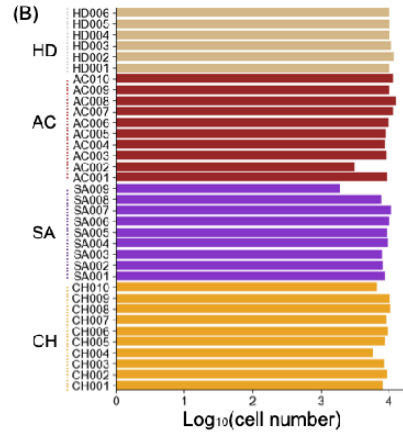
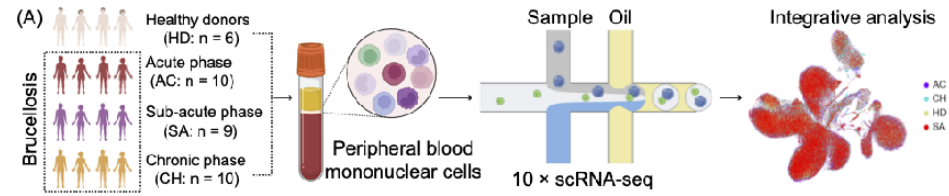


Highlights

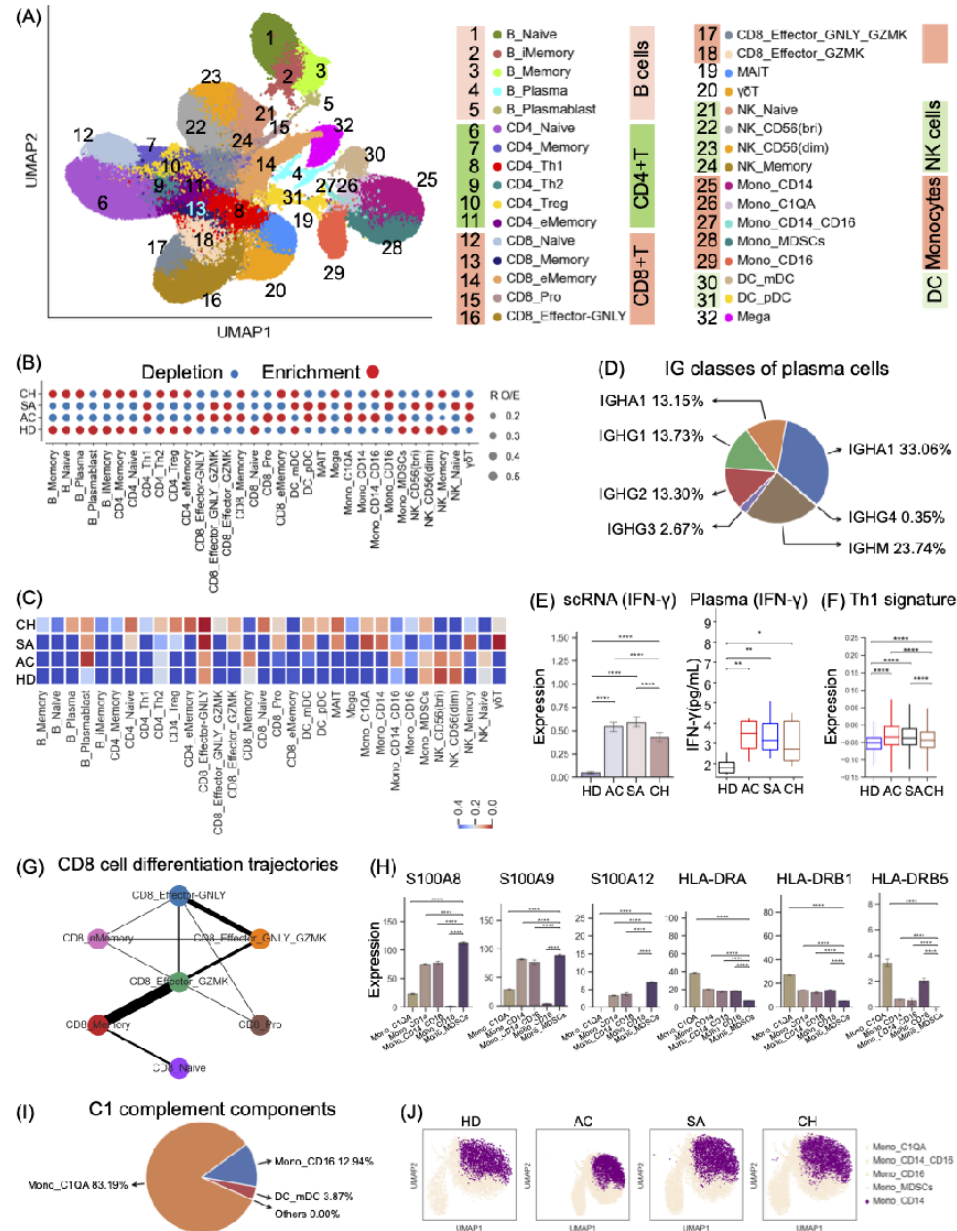
Single-cell immune landscape associated with disease phases in brucellosis patients



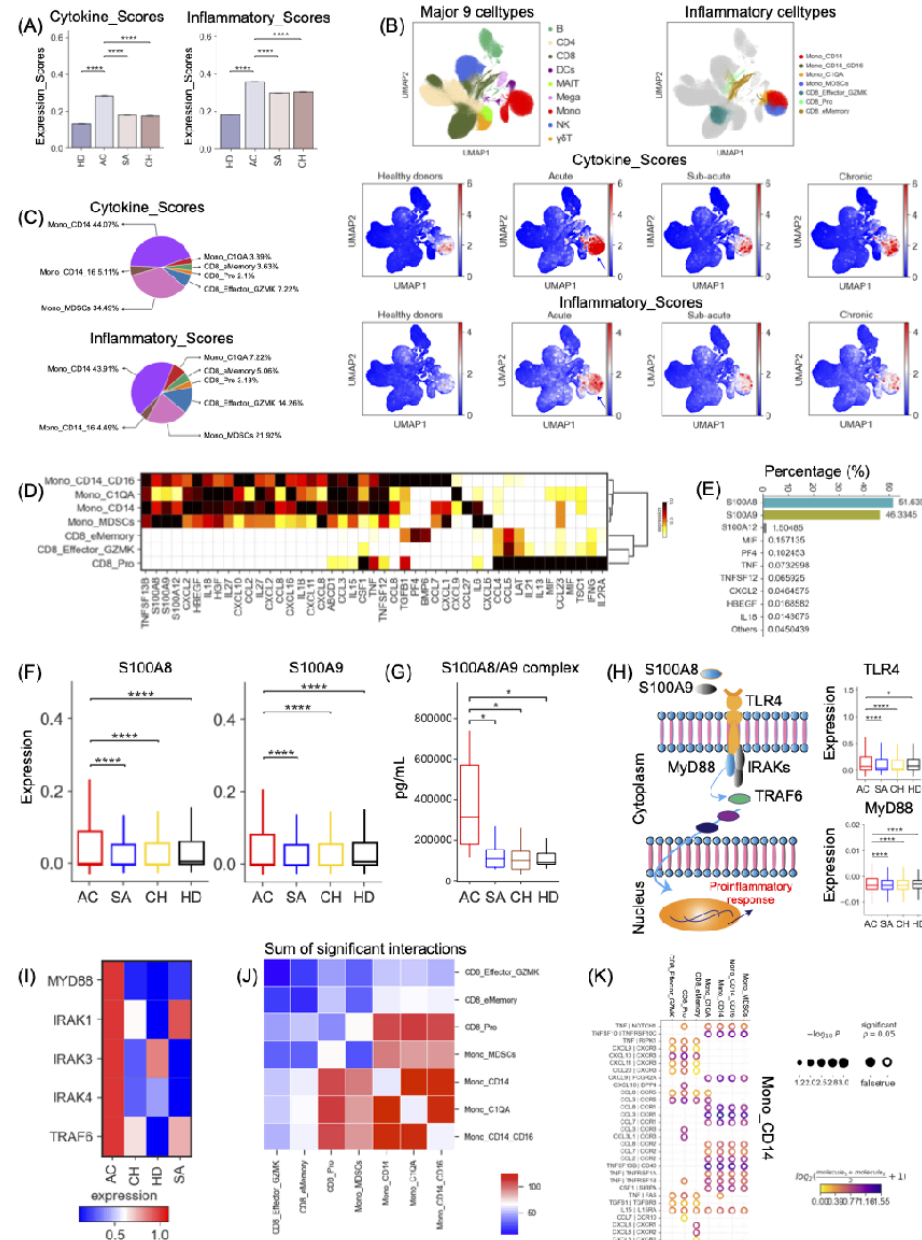
Research result 1- Overview of single-cell transcriptome sequencing data of brucellosis patients.



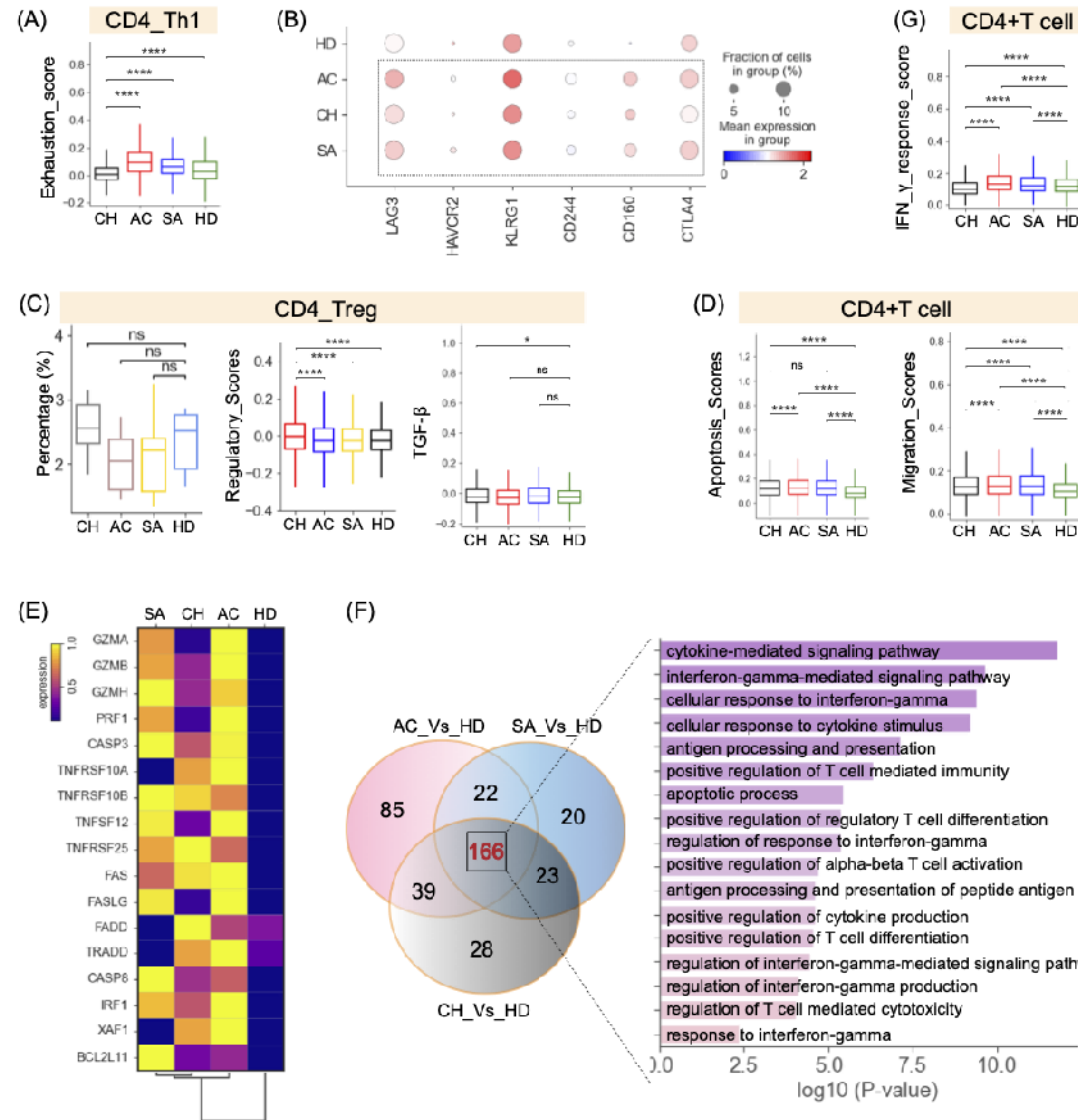
Research result 2- Characteristics of peripheral blood mononuclear cells in acute, subacute, and chronic phases of brucellosis patients



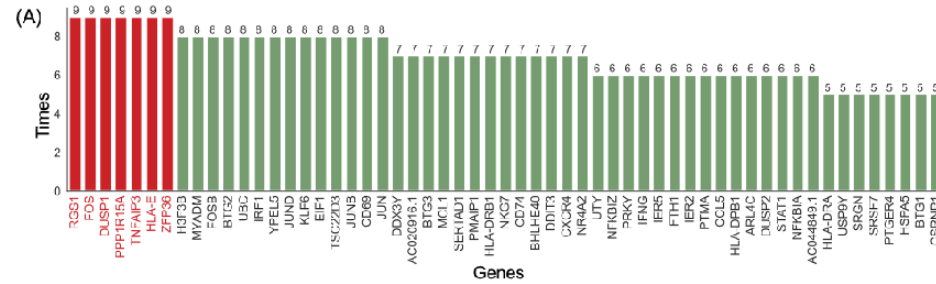
Research result 3-Monocytes are an important potential source of cytokine storm in the acute phase of brucellosis



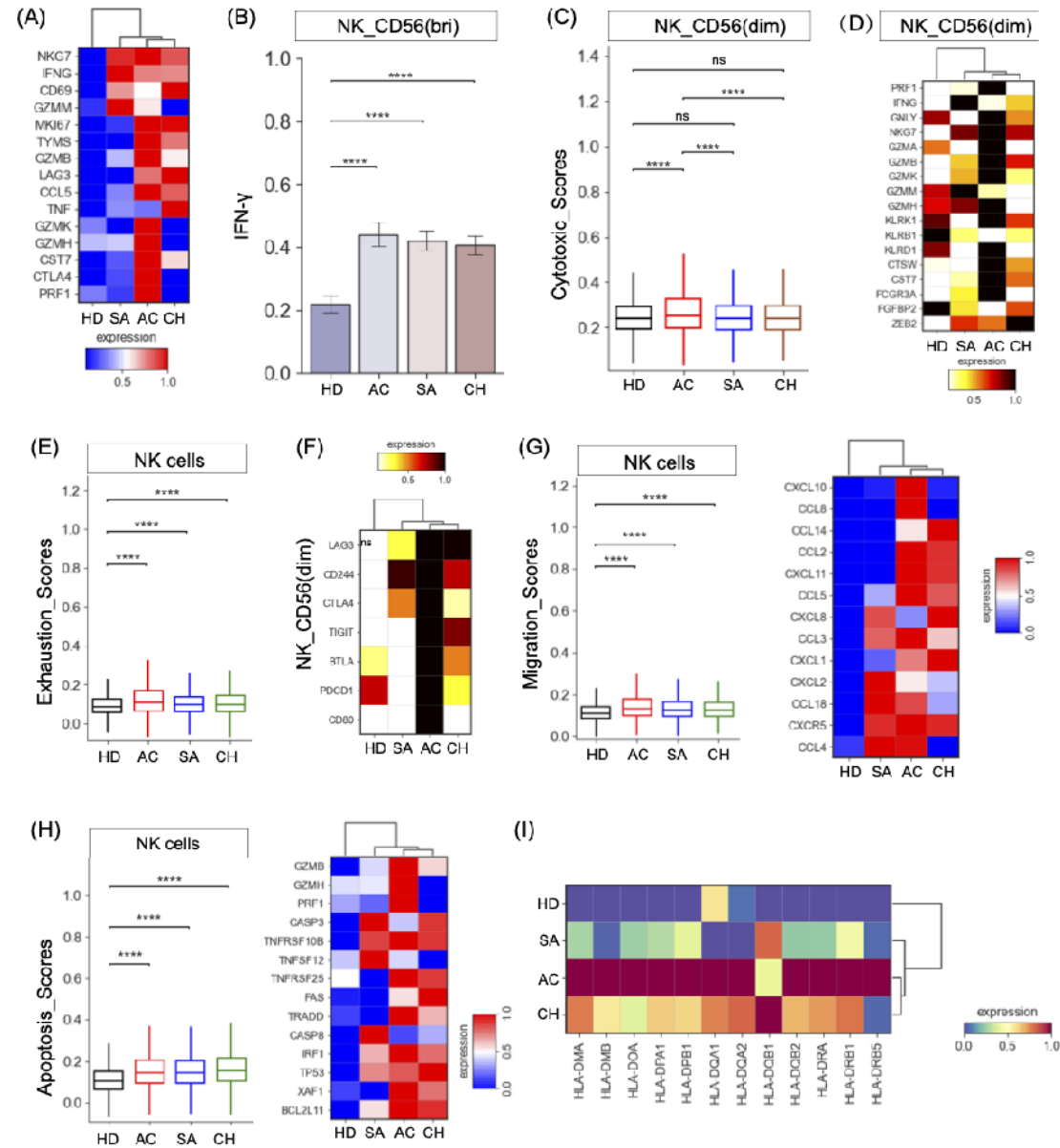
Research result 4-Th1 response imbalance in patients with chronic brucellosis



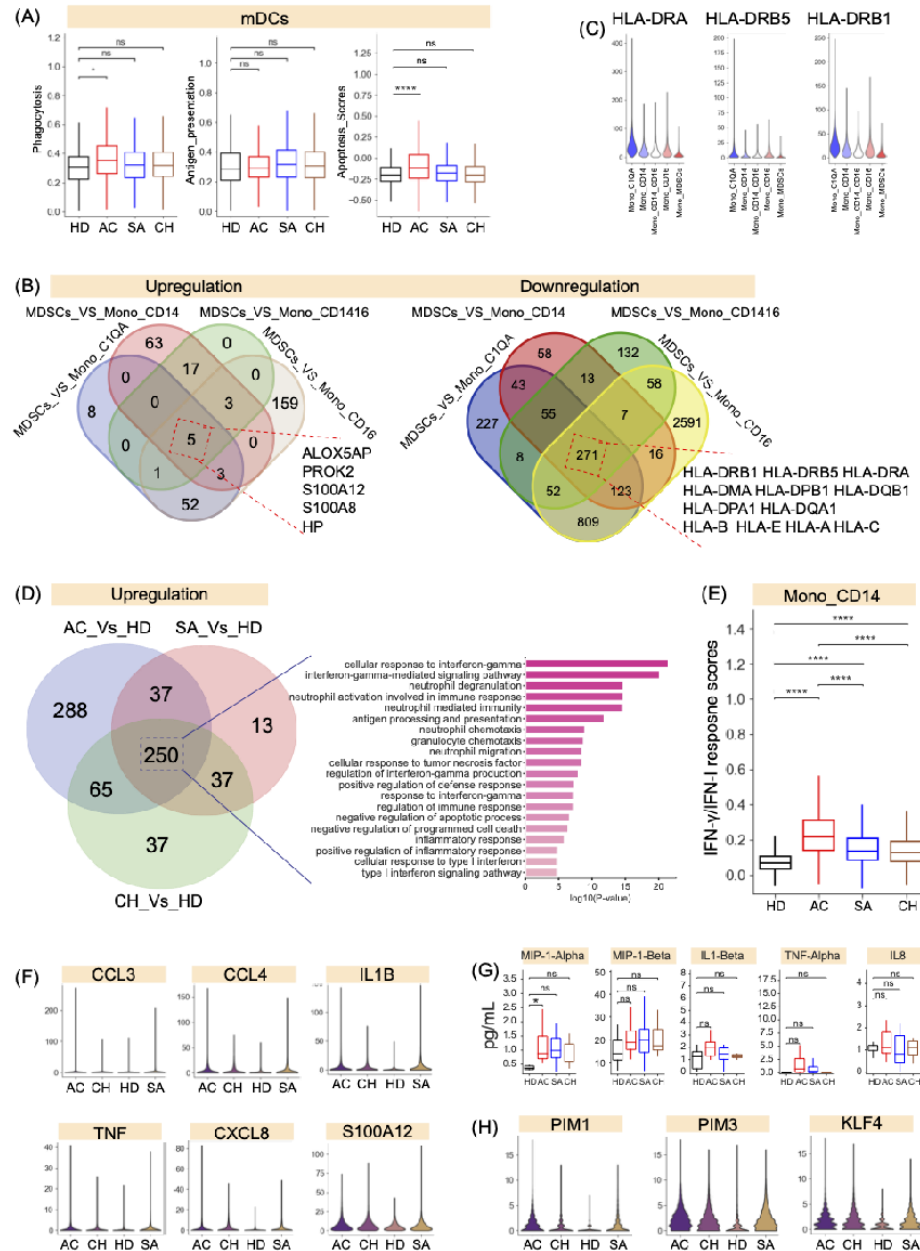
Research result 5-Dysregulated CD8 response in patients with chronic brucellosis



Research result 6-NK cell depletion in patients with brucellosis



Research result 7-Imbalance of immune response in bone marrow cells of patients with brucellosis





Summary

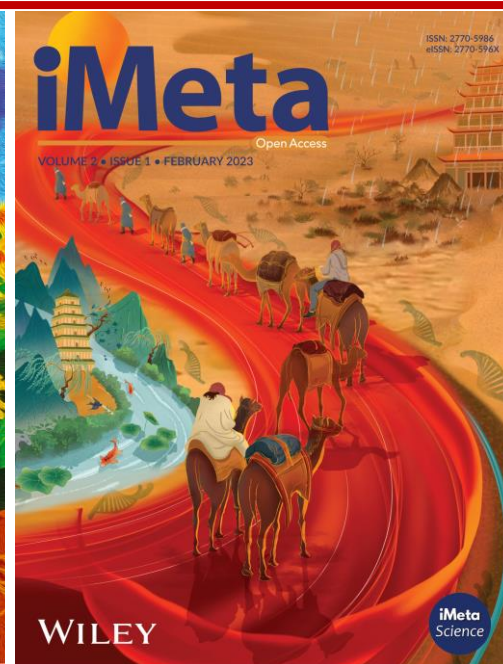
- The first use of single-cell transcriptome sequencing analysis revealed different immune responses in the acute, subacute, and chronic stages of Brucella infection
- The acute infection characteristics of brucellosis are cytokine storm, activation of S100A8/A9 TLR4 MyD88 pathway, and potential role of M-MDSCs driven immune suppression mediation
- The main characteristics of infection in the chronic phase of brucellosis are Th1 immune response imbalance, widespread depletion of T cells and NK cells

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