

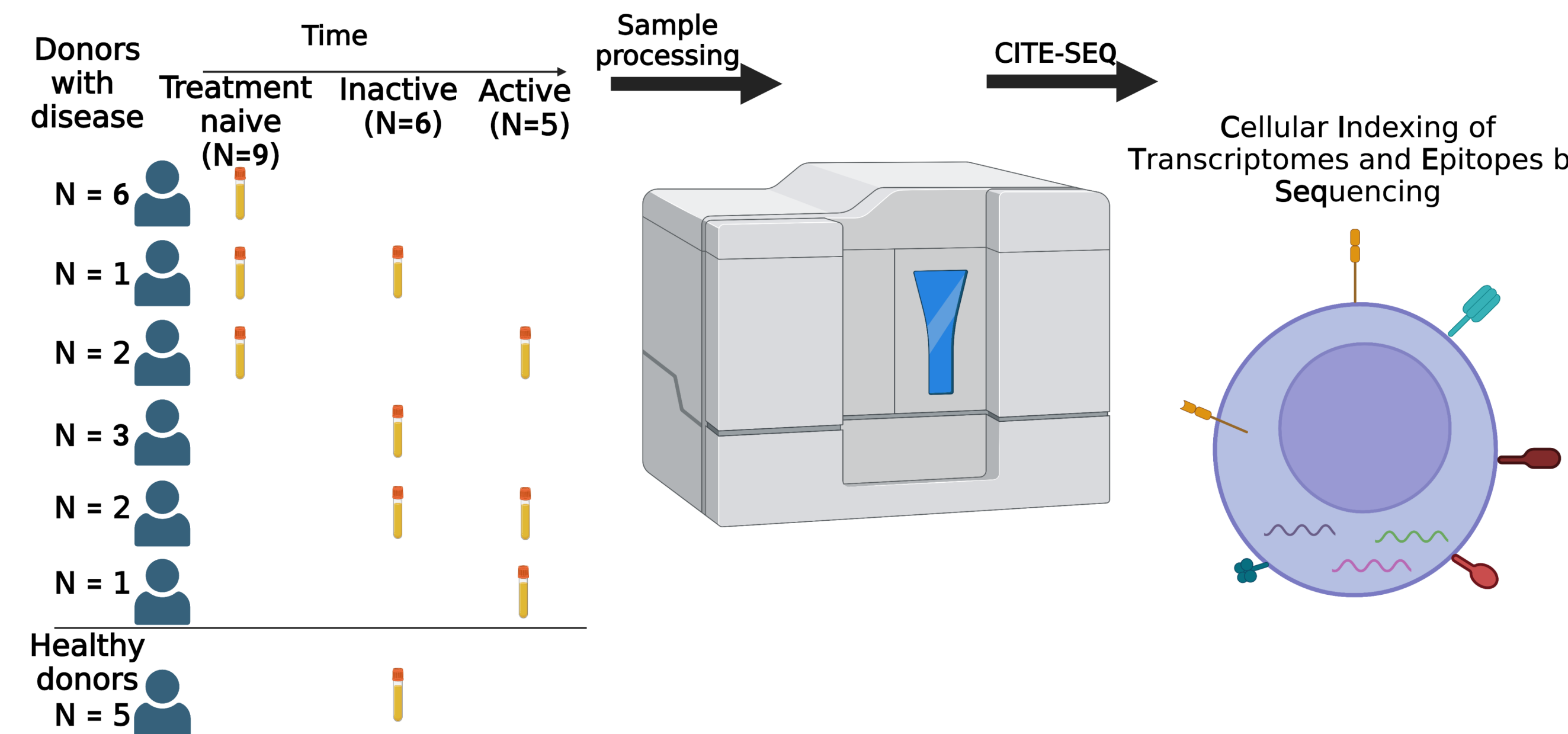
Analysis of Patients with Juvenile Dermatomyositis Compared to Healthy Controls Using CITE-seq Identifies Differences in Cell Composition and Gene and Epitope Expression

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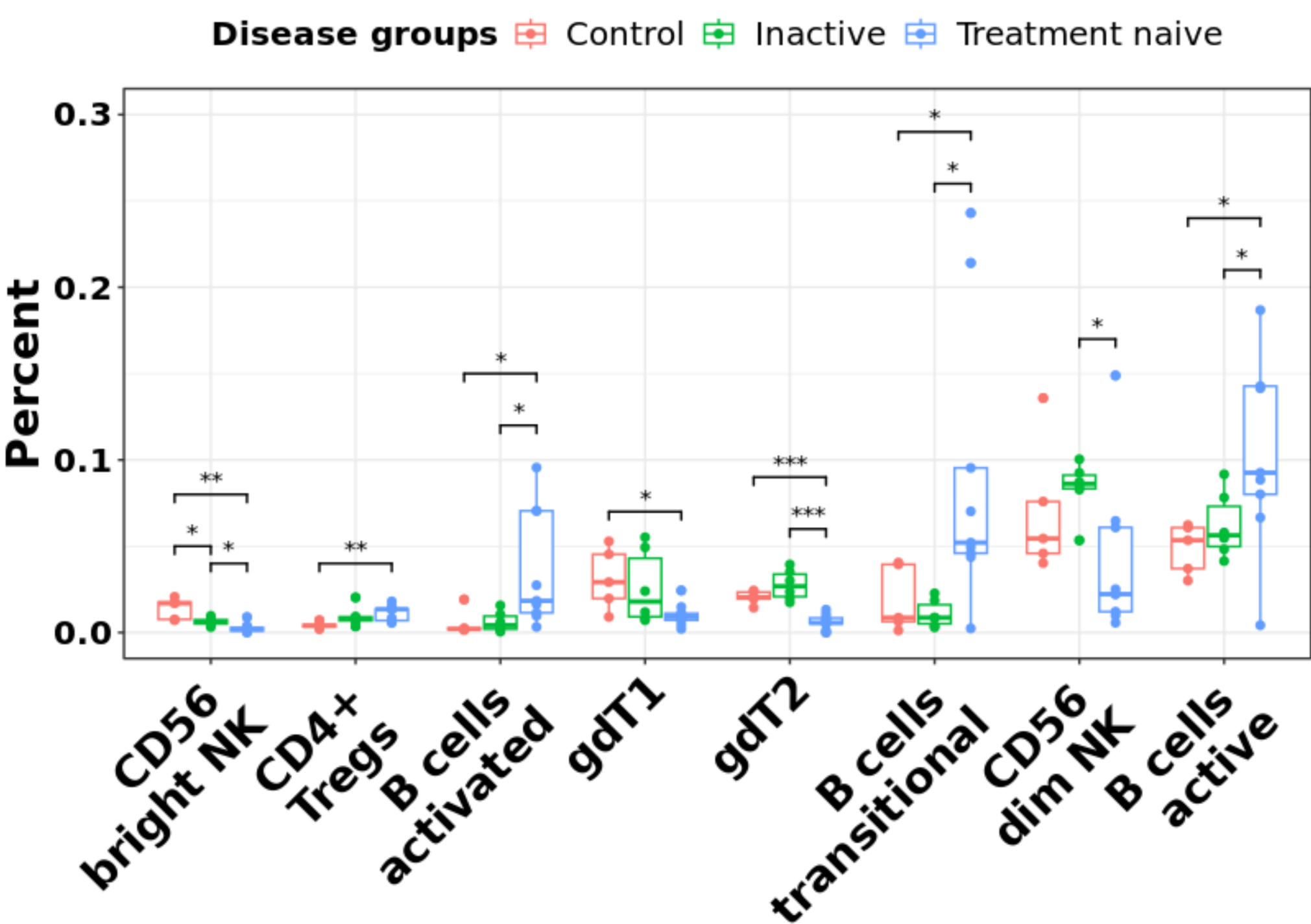
BACKGROUND

Juvenile dermatomyositis is a rare and serious autoimmune condition, and much remains unknown about the pathogenesis. Increasing knowledge of immune dysregulation with detailed immunophenotyping at the cellular level could lead to identification of new therapeutic targets and insight into disease mechanisms.

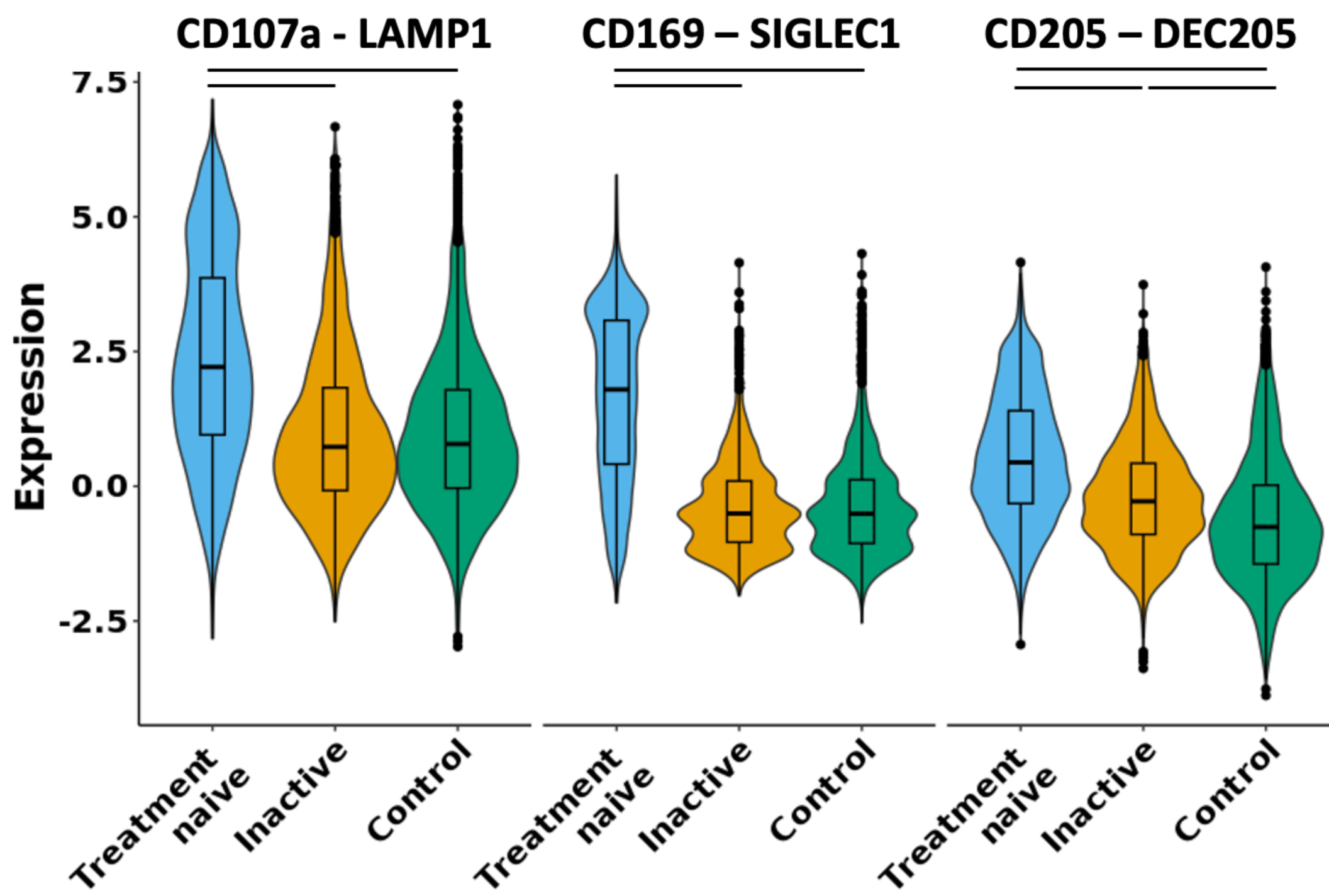
METHODS



RESULTS



In treatment naive disease we found a reduction in innate populations ie gdT and NK cells and an expansion of adaptive populations ie Tregs and activated, transitional and naive B cells. Many of these proportions correlated to disease activity measures (data now shown). *:p<0.05, **:p<0.01, ***:p<0.001



In both treatment naive and inactive disease CD205-expression was increased. CD169 and CD107a were elevated in treatment naive disease only. The expression of these two epitopes correlated to disease activity (data not shown). Marked comparisons have p < 0.001

CONCLUSION

Patients with juvenile dermatomyositis show distinct differences in both immune cell composition and RNA and epitope expression. The strong interferon signature in treatment naive disease indicates a potential bigger role for anti-interferon drugs in treatment. Multiple surface proteins are uniquely expressed in only treatment naive JDM, while others seem to be overexpressed regardless of disease state. These might provide future biomarkers and drug targets. We found multiple differences that remained even in inactive disease. This might indicate that patients with inactive disease should not be considered 'healthy' per se, and future research should investigate, if this gene signature i.e., persists over time and predicts flares or later co-morbidities

Patients with Juvenile Dermatomyositis show Distinct Transcriptomic and Proteomic Signatures, even in an Inactive Disease State, in CD14+ monocytes

