## A MULTIOMIC ATLAS OF A NORTHERN KENYAN COHORT

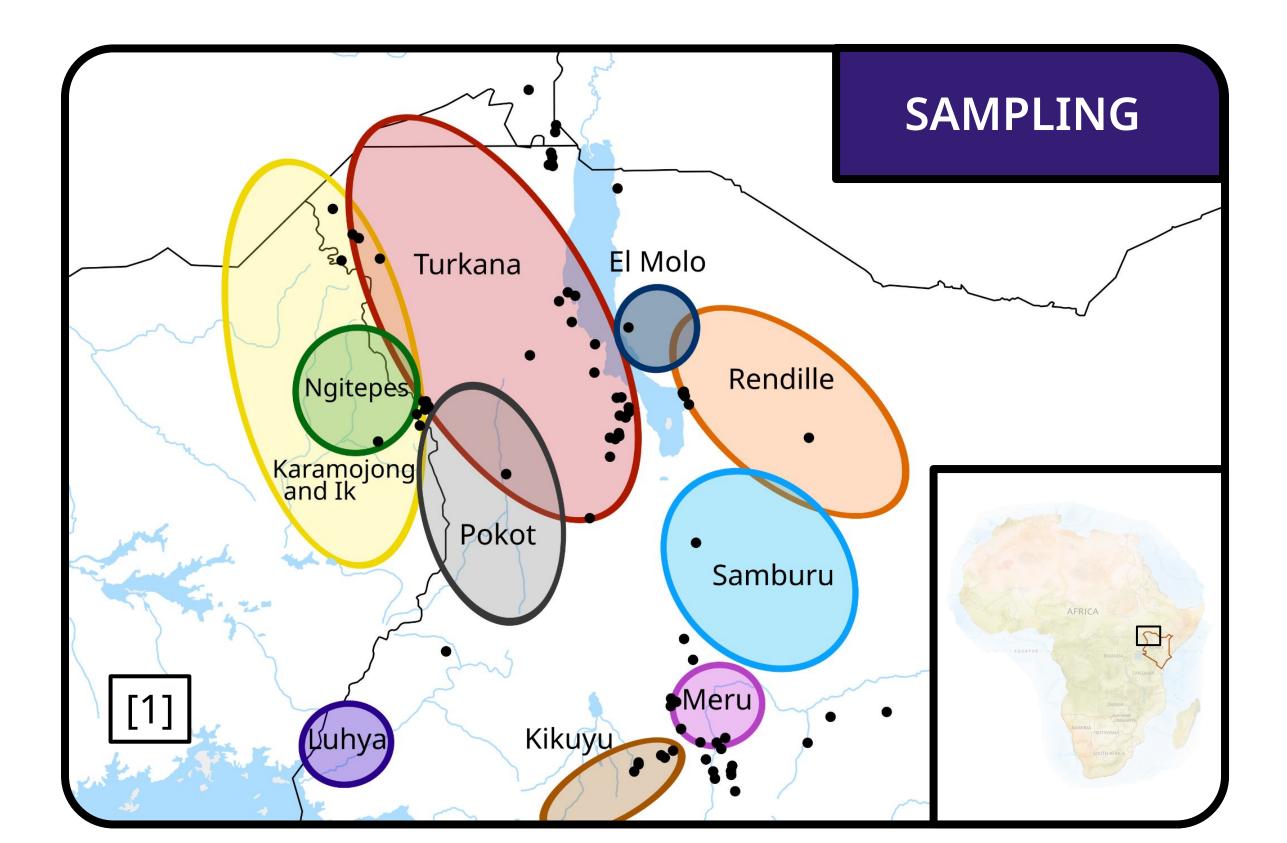
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We are collaborating with communities in northern Kenya to develop a multiomic atlas characterizing inflammatory profiles of communities undergoing rural to urban transitions. By examining individuals across diverse lifestyles with similar genetics, we aim to elucidate how gene by environment interactions contribute to variations in immune function. This will help us understand the role of inflammation in health disparities between rural and urban populations—identifying factors that could be targeted to reduce inflammation-related health risks in communities experiencing rapid urbanization.

## SINGLE CELL PILOT Bulk RNA Seq (n≈400) LPCAT1 Effector memory CD8 T ce **Identify Differentially Expressed Genes** Between Pastoralists Scenario 1: The gene is Naive B cel and Farmers differentially expressed Classical monocyte Plasma cel in a cell-type specific manner Dendritic cel Single Cell RNA Seq (n≈60) T regulatory cell Subsistence LPCAT1 Expression (median counts/cell Naive CD4 T cell Effector memory CD4 T ce Dendritic ce Non-classical monocyte Plasma cell Naive CD4 T cell Naive B cell Measure Cell Type Scenario 2: The gene is Effector memory CD8 T cell Non-classical monocyte Effector memory CD8 T cell Specificity of DE Genes not differentially Effector memory CD4 T cell Naive CD8 T cell expressed in a cell-type Gamma delta T cell specific manner Memory B cell T regulatory cell Subsistence ■ farming pastoralism

## DATA MODALITIES Lifestyle Questionnaire Deep Phenotyping (n=4175) (over 160 traits) Whole Genome (n≈1100) Sequencing Bulk PBMC RNA (n≈1100) Sequencing Single-Cell PBMC (n=299) RNA Sequencing Single-Cell PBMC (n=48)Surface Protein Profiling Circulating Cytokine (n=400)Levels (n=180)Immune history (n≈1100) Microbiomics (n=600)Metabolomics

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[1] Lea AJ, et al. albioRxiv [ 2023 Jan 19:2023.01.17.524066. doi: 10.1101/2023.01.17.524066. [2] Lea AJ, et al. et al (2020) Sci. Adv.6,eabb1430. DOI:10.1126/sciadv.abb1430

