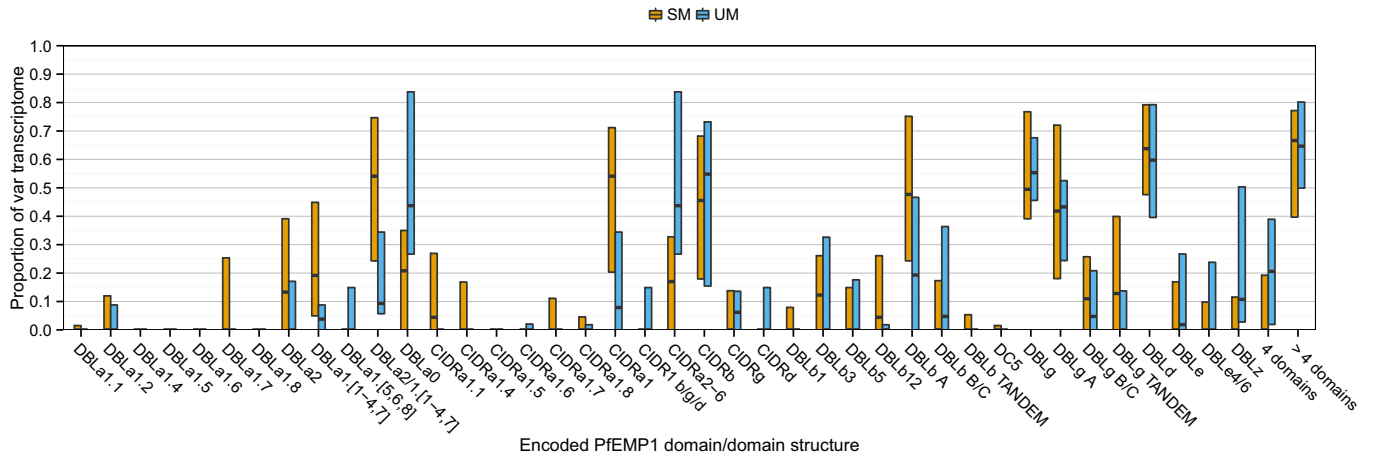
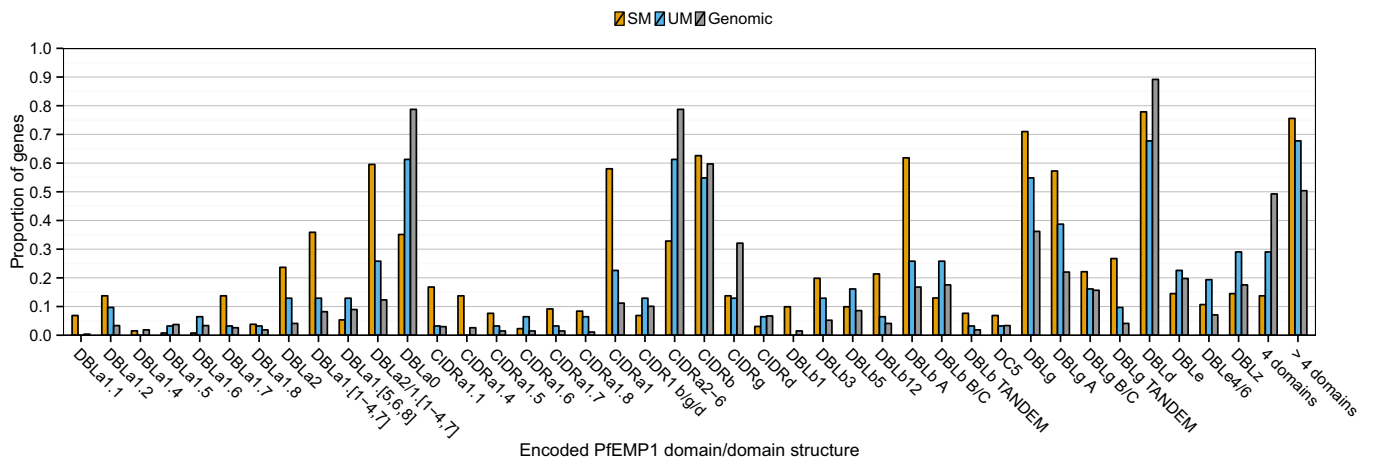


# Expanded View Figures

Transcription of var gene features in SM vs UM patients



Prevalence of var gene features



**Figure EV1. Prevalence and transcript levels of var genes encoding specified PfEMP1 features.**

Upper panel: Patient-wise *var* transcript proportions of encoded domain types/domain compositions, compared by patient group [uncomplicated malaria (UM),  $n = 8$  and severe malaria (SM),  $n = 36$ ]. Boxplots show median and IQR. Lower panel: Proportion of transcripts/genes encoding specific domain types/domain compositions within patient groups [UM ( $n = 31$  genes), SM ( $n = 131$  genes)] and the average *Plasmodium falciparum* genome [distribution based on seven genomes ( $n = 268$  genes)].