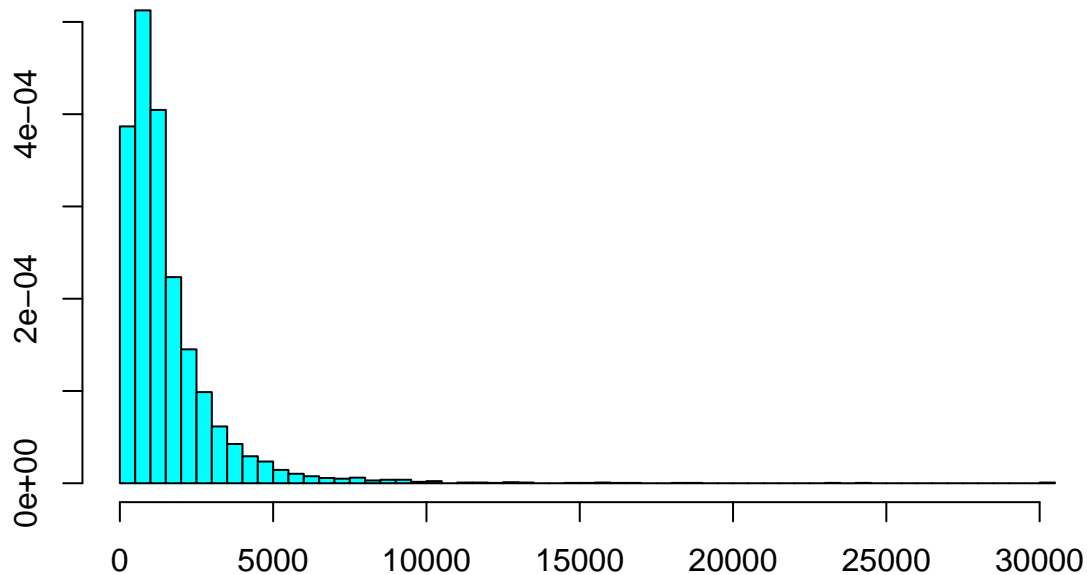# Stems/ha (faib)

faib_vri_true_m1_df$stemsha_L