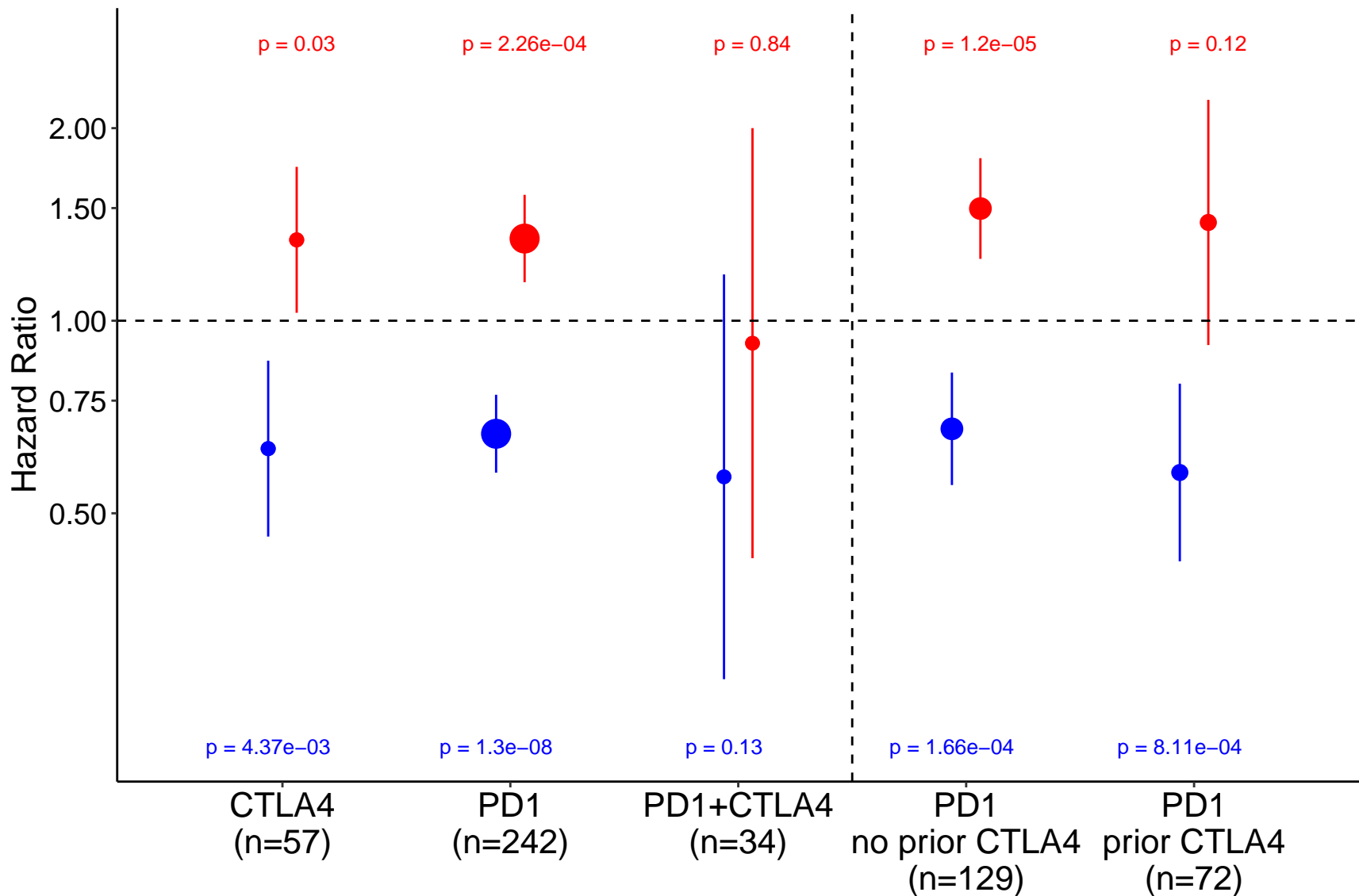


MAP4K1+AGER



as.numeric(cohort_n) ● 50 ● 100 ● 150 ● 200

gene ● MAP4K1 ● AGER