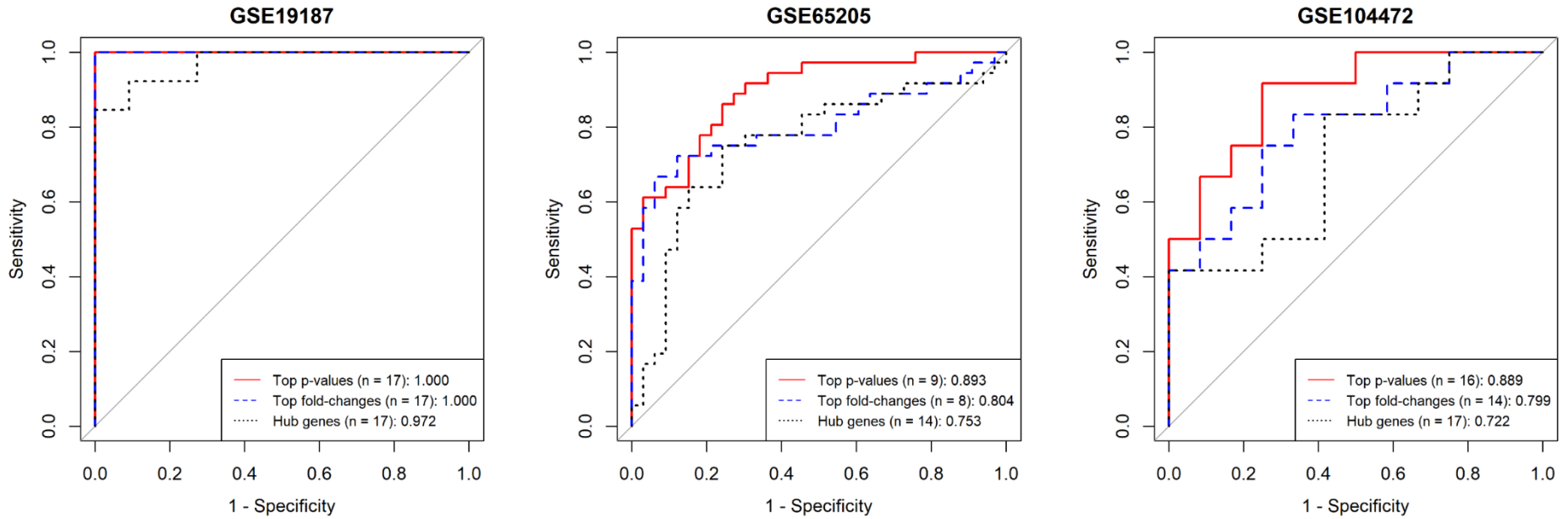


Figure E5 – Replication of prediction analysis in the independent cohorts



Replication performed using the logistic regression models derived from the discovery cohort (EVAPR), including the genes selected and their regression coefficients. Red continuous line = top 17 genes by p-value; blue dashed line = top 17 genes by effect size; black dotted line = 17 “hub” genes. See Table E10 for classification tables.