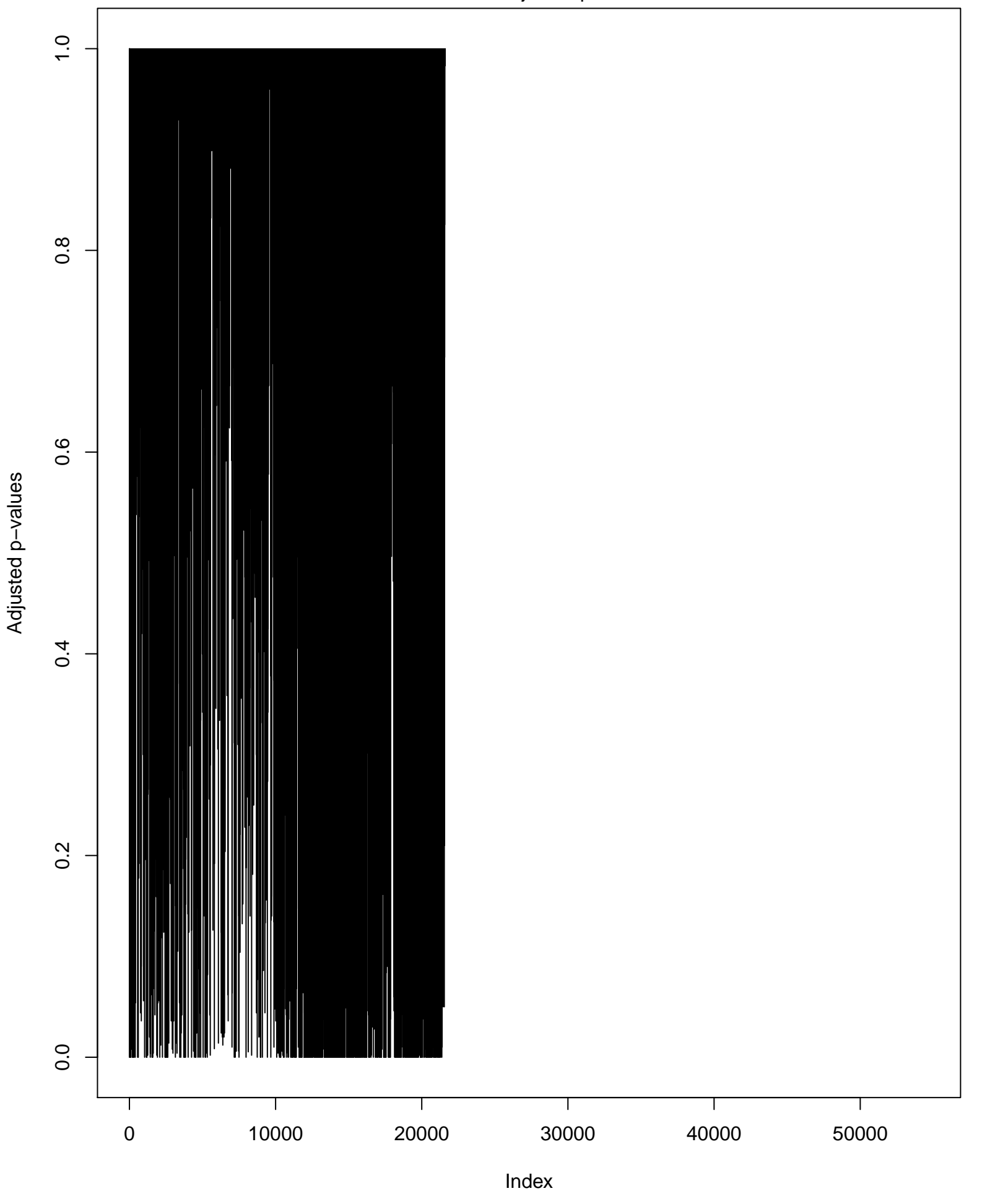


Unordered Adjusted p-values



multtest::MTP(X = t(GeneExpressionScaled), Y = RejectionStatus[, 2], na.rm = TRUE, test = "t.twosamp.unequalvar", robust = FALSE, standardize = TRUE, alternative = "two.sided", typeone = "fdr", fdr.method = "conservative", alp