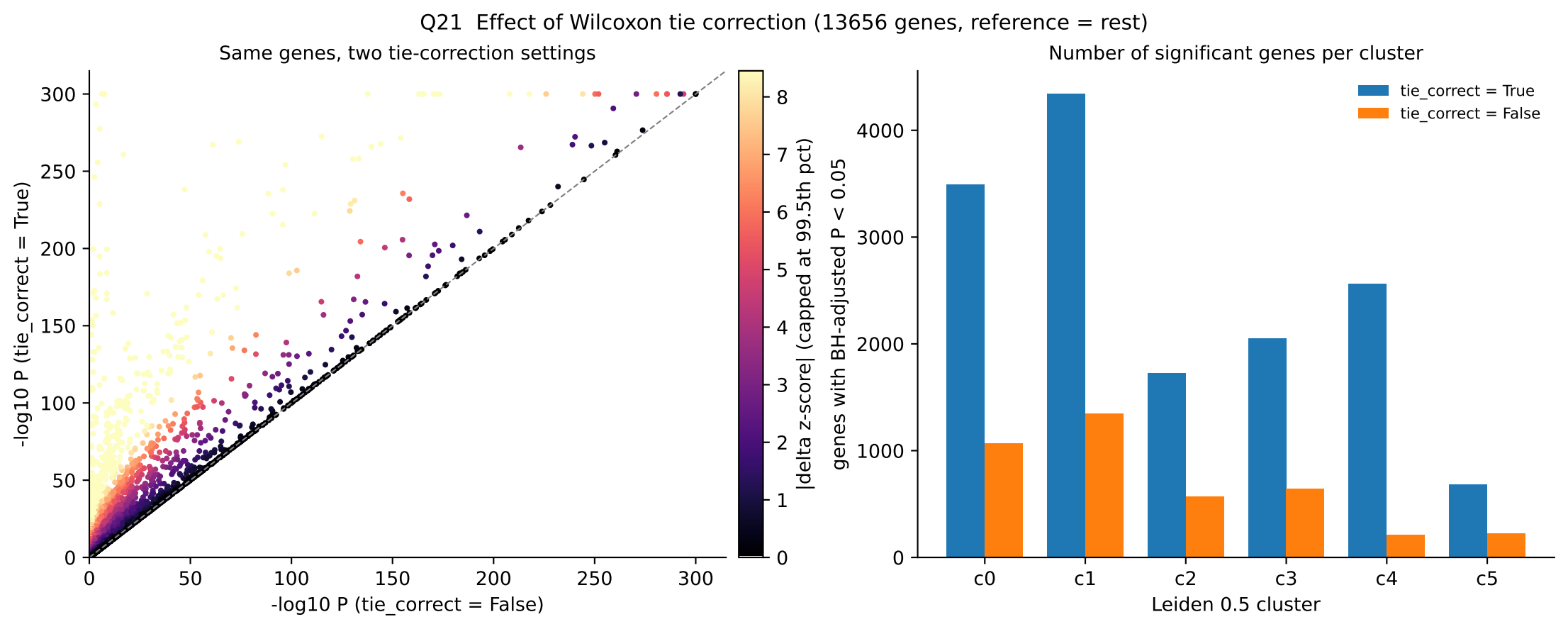

Q21 Effect of Wilcoxon tie correction (13656 genes, reference = rest)
Same genes, two tie-correction settings
-log10 P (tie_correct = True)
-log10 P (tie_correct = False)
|delta z-score| (capped at 99.5th pct)
Number of significant genes per cluster
genes with BH-adjusted P < 0.05
tie_correct = True
tie_correct = False
Leiden 0.5 cluster
c0
c1
c2
c3
c4
c5