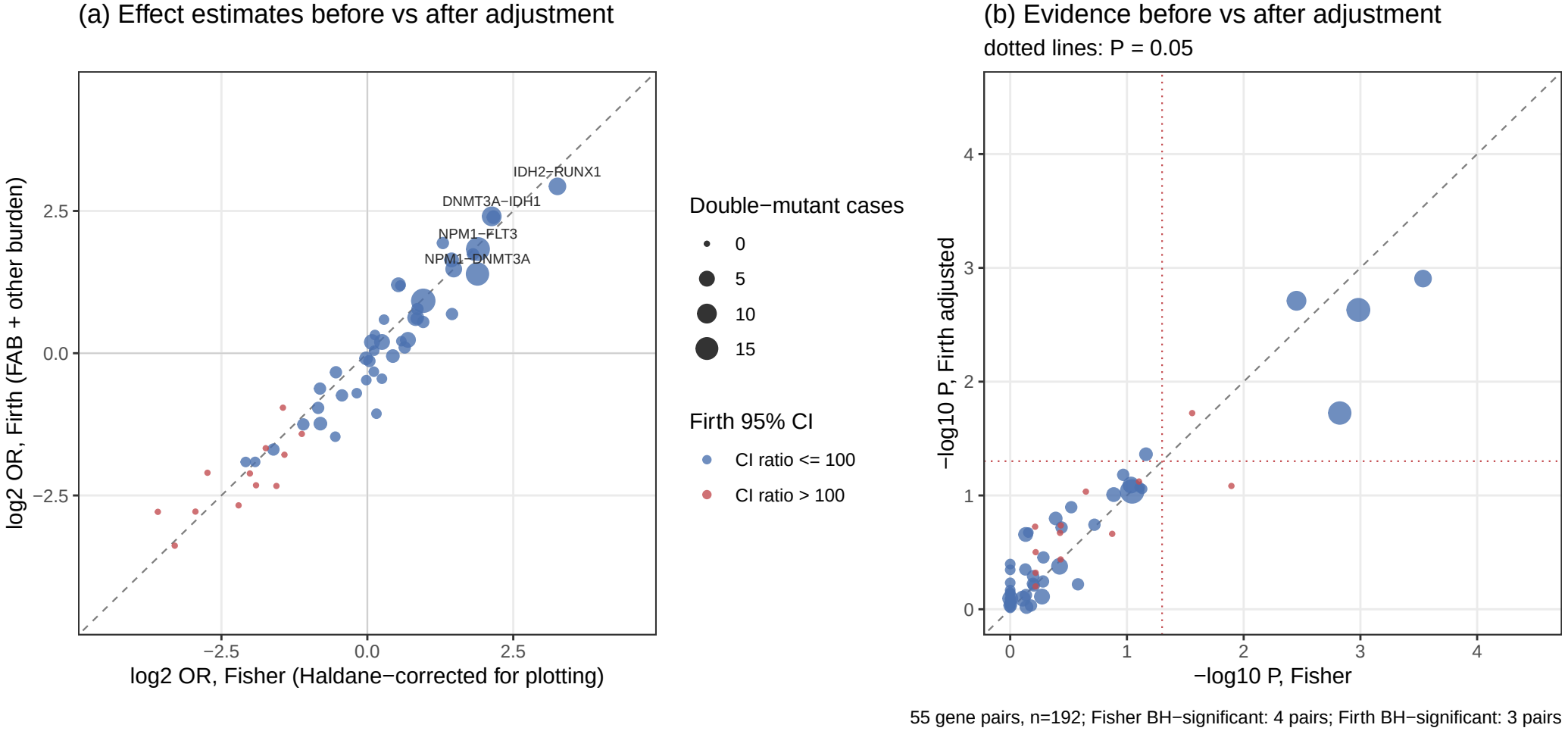

(a) Effect estimates before vs after adjustment
log2 OR, Firth (FAB + other burden)
log2 OR, Fisher (Haldane−corrected for plotting)
IDH2−RUNX1
DNMT3A−IDH1
NPM1−FLT3
NPM1−DNMT3A
Double−mutant cases
0
5
10
15
Firth 95% CI
CI ratio <= 100
CI ratio > 100
(b) Evidence before vs after adjustment
dotted lines: P = 0.05
−log10 P, Firth adjusted
−log10 P, Fisher
55 gene pairs, n=192; Fisher BH−significant: 4 pairs; Firth BH−significant: 3 pairs