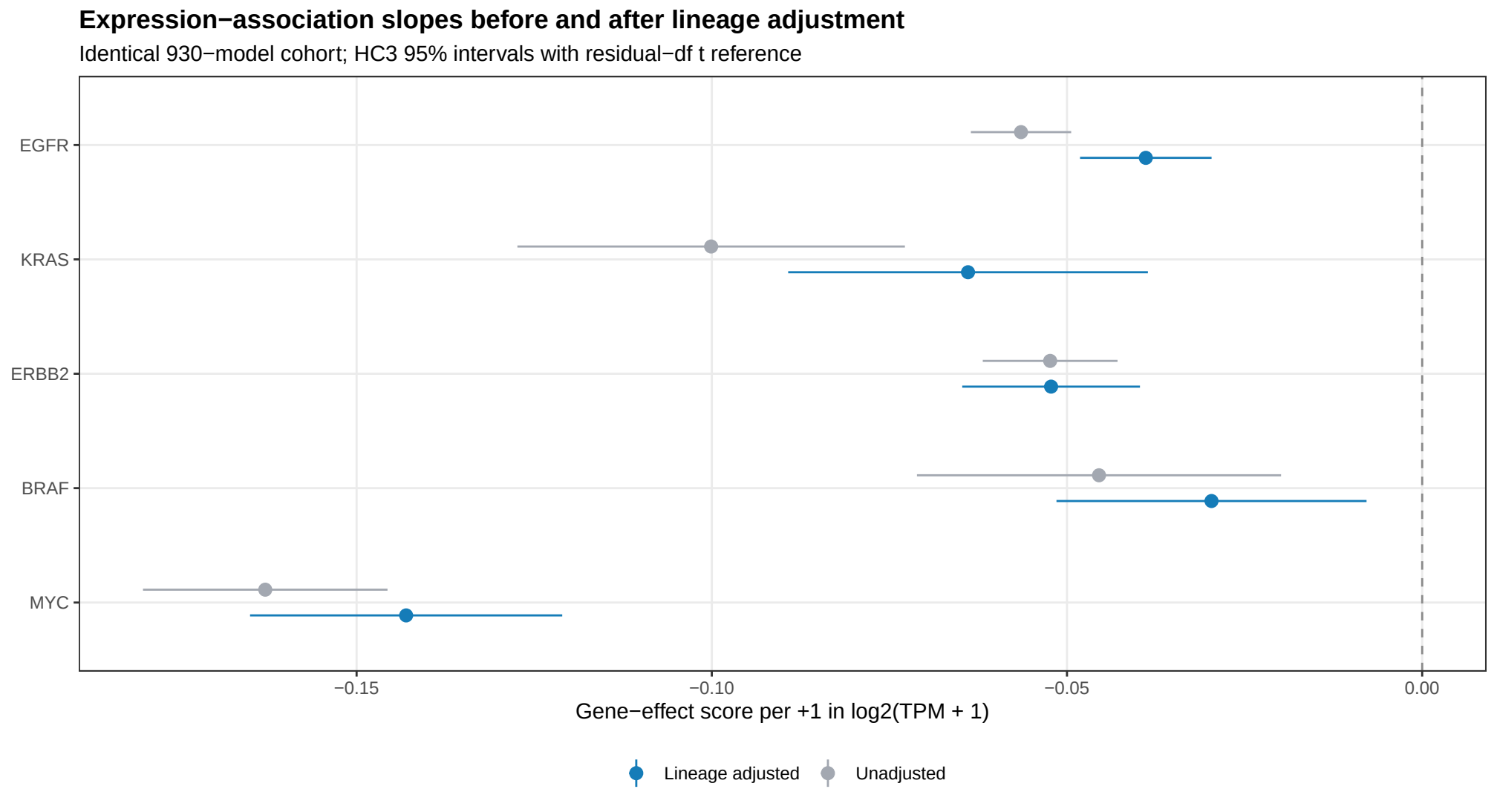
Expression−association slopes before and after lineage adjustment
Identical 930−model cohort; HC3 95% intervals with residual−df t reference
EGFR
KRAS
ERBB2
BRAF
MYC
−0.15
−0.10
−0.05
0.00
Gene−effect score per +1 in log2(TPM + 1)
Lineage adjusted
Unadjusted