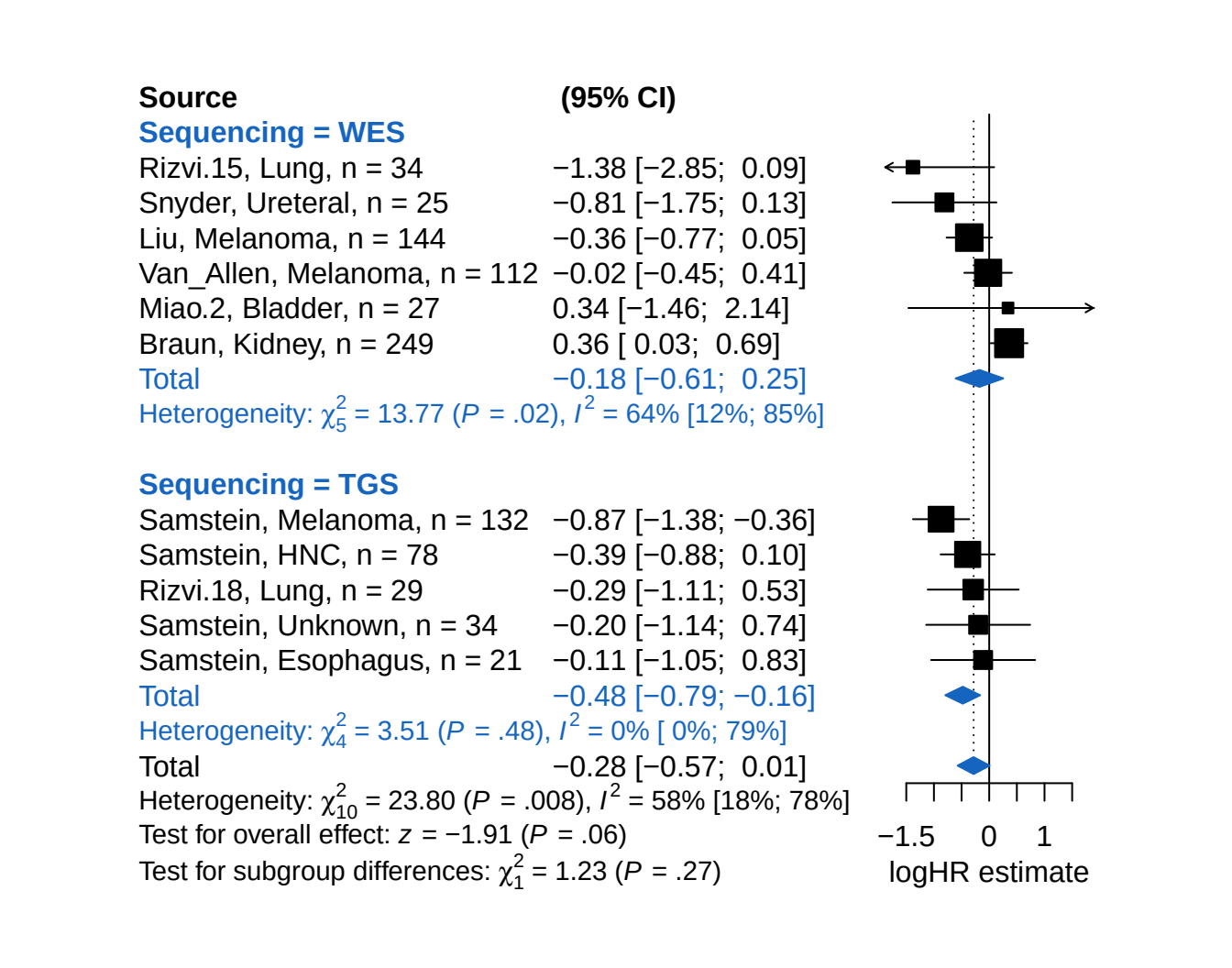
Source
(95% CI)
Sequencing = WES
Rizvi.15, Lung, n = 34
−1.38 [−2.85; 0.09]
Snyder, Ureteral, n = 25
−0.81 [−1.75; 0.13]
Liu, Melanoma, n = 144
−0.36 [−0.77; 0.05]
Van_Allen, Melanoma, n = 112
−0.02 [−0.45; 0.41]
Miao.2, Bladder, n = 27
0.34 [−1.46; 2.14]
Braun, Kidney, n = 249
0.36 [0.03; 0.69]
Total
−0.18 [−0.61; 0.25]
Heterogeneity: χ^2_5 = 13.77 (*P* = .02), I^2 = 64% [12%; 85%]
Sequencing = TGS
Samstein, Melanoma, n = 132
−0.87 [−1.38; −0.36]
Samstein, HNC, n = 78
−0.39 [−0.88; 0.10]
Rizvi.18, Lung, n = 29
−0.29 [−1.11; 0.53]
Samstein, Unknown, n = 34
−0.20 [−1.14; 0.74]
Samstein, Esophagus, n = 21
−0.11 [−1.05; 0.83]
Total
−0.48 [−0.79; −0.16]
Heterogeneity: χ^2_4 = 3.51 (*P* = .48), I^2 = 0% [0%; 79%]
Total
−0.28 [−0.57; 0.01]
Heterogeneity: χ^2_{10} = 23.80 (*P* = .008), I^2 = 58% [18%; 78%]
Test for overall effect: *z* = −1.91 (*P* = .06)
Test for subgroup differences: χ^2_1 = 1.23 (*P* = .27)
−1.5
0
1
logHR estimate