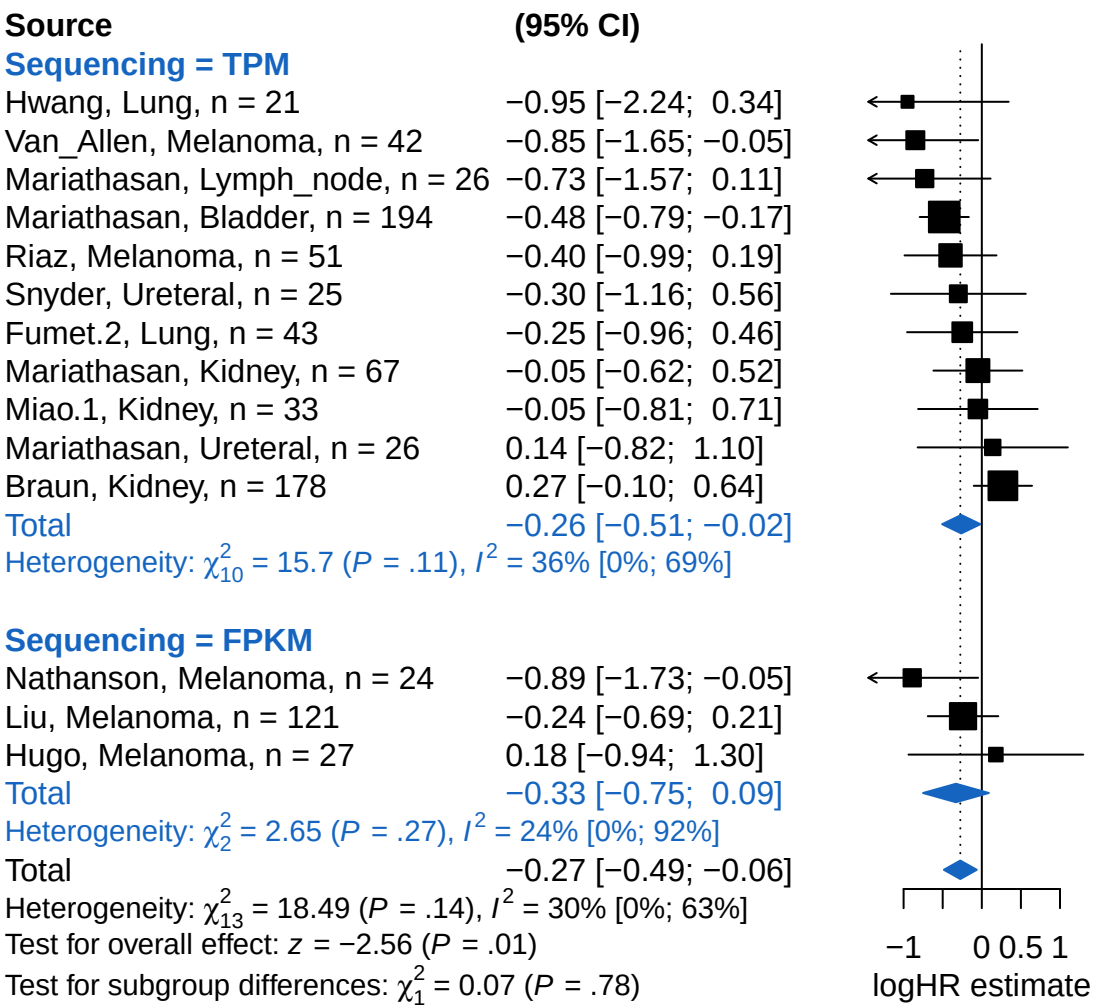
Source
(95% CI)
Sequencing = TPM
Hwang, Lung, n = 21 −0.95 [−2.24; 0.34]
Van_Allen, Melanoma, n = 42 −0.85 [−1.65; −0.05]
Mariathasan, Lymph_node, n = 26 −0.73 [−1.57; 0.11]
Mariathasan, Bladder, n = 194 −0.48 [−0.79; −0.17]
Riaz, Melanoma, n = 51 −0.40 [−0.99; 0.19]
Snyder, Ureteral, n = 25 −0.30 [−1.16; 0.56]
Fumet.2, Lung, n = 43 −0.25 [−0.96; 0.46]
Mariathasan, Kidney, n = 67 −0.05 [−0.62; 0.52]
Miao.1, Kidney, n = 33 −0.05 [−0.81; 0.71]
Mariathasan, Ureteral, n = 26 0.14 [−0.82; 1.10]
Braun, Kidney, n = 178 0.27 [−0.10; 0.64]
Total −0.26 [−0.51; −0.02]
Heterogeneity: χ^2_{10} = 15.7 (P = .11), I^2 = 36% [0%; 69%]
Sequencing = FPKM
Nathanson, Melanoma, n = 24 −0.89 [−1.73; −0.05]
Liu, Melanoma, n = 121 −0.24 [−0.69; 0.21]
Hugo, Melanoma, n = 27 0.18 [−0.94; 1.30]
Total −0.33 [−0.75; 0.09]
Heterogeneity: χ^2_2 = 2.65 (P = .27), I^2 = 24% [0%; 92%]
Total −0.27 [−0.49; −0.06]
Heterogeneity: χ^2_{13} = 18.49 (P = .14), I^2 = 30% [0%; 63%]
Test for overall effect: z = −2.56 (P = .01)
Test for subgroup differences: χ^2_1 = 0.07 (P = .78)
−1 0 0.5 1
logHR estimate