Source	(95% CI)

Sequencing = FPKM

Nathanson, Melanoma, n = 24 — −1.36 [−2.46; −0.26]
Liu, Melanoma, n = 121 — −0.47 [−0.98; 0.04]
Hugo, Melanoma, n = 27 — 0.19 [−0.97; 1.35]
Total — −0.54 [−1.20; 0.13]
Heterogeneity: $\chi^2_2 = 3.73$ ($P = .15$), $I^2 = 46\%$ [0%; 84%]

Sequencing = TPM

Van_Allen, Melanoma, n = 42 — −0.94 [−1.70; −0.18]
Snyder, Ureteral, n = 25 — −0.77 [−1.75; 0.21]
Mariathasan, Bladder, n = 194 — −0.46 [−0.81; −0.11]
Mariathasan, Lymph_node, n = 26 — −0.41 [−1.35; 0.53]
Riaz, Melanoma, n = 51 — −0.29 [−0.98; 0.40]
Fumet.2, Lung, n = 43 — −0.18 [−0.96; 0.60]
Mariathasan, Kidney, n = 67 — −0.14 [−0.71; 0.43]
Miao.1, Kidney, n = 33 — −0.07 [−0.91; 0.77]
Braun, Kidney, n = 178 — 0.39 [0.00; 0.78]
Mariathasan, Ureteral, n = 26 — 0.49 [−0.47; 1.45]
Total — −0.21 [−0.50; 0.08]
Heterogeneity: $\chi^2_9 = 18.01$ ($P = .04$), $I^2 = 50\%$ [0%; 76%]
Total — −0.27 [−0.53; −0.01]
Heterogeneity: $\chi^2_{12} = 23.73$ ($P = .02$), $I^2 = 49\%$ [4%; 73%]
Test for overall effect: $z = -2.04$ ($P = .04$)
Test for subgroup differences: $\chi^2_1 = 0.79$ ($P = .37$)

−1.5   0   1

logHR estimate