Source	(95% CI)

Sequencing = FPKM

Source	(95% CI)	
Nathanson, Melanoma, n = 24	−1.36 [−2.46; −0.26]	
Liu, Melanoma, n = 121	−0.64 [−1.15; −0.13]	
Hugo, Melanoma, n = 27	0.14 [−1.06; 1.34]	
Total	−0.65 [−1.18; −0.12]	

Heterogeneity: $\chi^2_2 = 3.29$ ($P = .19$), $I^2 = 39\%$ [0%; 81%]

Sequencing = TPM

Source	(95% CI)
Hwang, Lung, n = 21	−1.09 [−2.38; 0.20]
Fumet.2, Lung, n = 43	−0.92 [−1.74; −0.10]
Riaz, Melanoma, n = 51	−0.83 [−1.52; −0.14]
Mariathasan, Lymph_node, n = 26	−0.60 [−1.54; 0.34]
Van_Allen, Melanoma, n = 42	−0.35 [−1.09; 0.39]
Mariathasan, Bladder, n = 194	−0.29 [−0.64; 0.06]
Miao.1, Kidney, n = 33	−0.11 [−0.95; 0.73]
Mariathasan, Kidney, n = 67	0.03 [−0.54; 0.60]
Braun, Kidney, n = 178	0.27 [−0.12; 0.66]
Snyder, Ureteral, n = 25	0.30 [−0.66; 1.26]
Mariathasan, Ureteral, n = 26	0.46 [−0.50; 1.42]
Total	−0.22 [−0.50; 0.05]

Heterogeneity: $\chi^2_{10} = 18.07$ ($P = .05$), $I^2 = 45\%$ [0%; 73%]

Total	−0.31 [−0.57; −0.04]

Heterogeneity: $\chi^2_{13} = 25.31$ ($P = .02$), $I^2 = 49\%$ [5%; 72%]

Test for overall effect: $z = −2.28$ ($P = .02$)

Test for subgroup differences: $\chi^2_1 = 1.97$ ($P = .16$)

−1.5   0   1

logHR estimate