Source	(95% CI)
Sequencing = TPM	
Mariathasan, Lymph_node, n = 26	−1.46 [−2.66; −0.26]
Hwang, Lung, n = 21	−1.13 [−2.93; 0.67]
Van_Allen, Melanoma, n = 42	−1.10 [−2.06; −0.14]
Riaz, Melanoma, n = 51	−0.64 [−1.31; 0.03]
Fumet.2, Lung, n = 43	−0.61 [−1.63; 0.41]
Mariathasan, Bladder, n = 194	−0.33 [−0.70; 0.04]
Miao.1, Kidney, n = 33	−0.25 [−1.27; 0.77]
Mariathasan, Kidney, n = 67	−0.13 [−0.82; 0.56]
Snyder, Ureteral, n = 25	−0.06 [−1.08; 0.96]
Braun, Kidney, n = 178	0.13 [−0.30; 0.56]
Mariathasan, Ureteral, n = 26	1.45 [0.29; 2.61]
Total	−0.31 [−0.67; 0.04]

Heterogeneity: $\chi^2_{10} = 21.37$ ($P = .02$), $I^2 = 53\%$ [7%; 76%]

Sequencing = FPKM	
Nathanson, Melanoma, n = 24	−0.83 [−1.71; 0.05]
Liu, Melanoma, n = 121	−0.63 [−1.20; −0.06]
Hugo, Melanoma, n = 27	0.31 [−1.12; 1.74]
Total	−0.59 [−1.04; −0.14]

Heterogeneity: $\chi^2_{2} = 1.82$ ($P = .40$), $I^2 = 0\%$ [0%; 90%]

Total	−0.35 [−0.64; −0.07]

Heterogeneity: $\chi^2_{13} = 24.91$ ($P = .02$), $I^2 = 48\%$ [3%; 72%]

Test for overall effect: $z = −2.41$ ($P = .02$)

Test for subgroup differences: $\chi^2_{1} = 0.89$ ($P = .35$)

−1 0 1

logHR estimate