Source	(95% CI)
Sequencing = TPM	
Hwang, Lung, n = 21	−1.11 [−2.29; 0.07]
Van_Allen, Melanoma, n = 42	−0.97 [−1.73; −0.21]
Mariathasan, Lymph_node, n = 26	−0.94 [−1.88; 0.00]
Mariathasan, Bladder, n = 194	−0.31 [−0.66; 0.04]
Riaz, Melanoma, n = 51	−0.30 [−0.99; 0.39]
Mariathasan, Kidney, n = 67	−0.23 [−0.80; 0.34]
Miao.1, Kidney, n = 33	−0.05 [−0.91; 0.81]
Snyder, Ureteral, n = 25	0.04 [−0.92; 1.00]
Fumet.2, Lung, n = 43	0.10 [−0.68; 0.88]
Braun, Kidney, n = 178	0.25 [−0.14; 0.64]
Mariathasan, Ureteral, n = 26	0.49 [−0.47; 1.45]
Total	−0.22 [−0.48; 0.05]

Heterogeneity: $\chi^2_{10} = 16.95$ ($P = .08$), $I^2 = 41\%$ [0%; 71%]

Sequencing = FPKM	
Nathanson, Melanoma, n = 24	−0.78 [−1.80; 0.24]
Liu, Melanoma, n = 121	−0.39 [−0.90; 0.12]
Hugo, Melanoma, n = 27	0.09 [−1.11; 1.29]
Total	−0.40 [−0.82; 0.03]

Heterogeneity: $\chi^2_{2} = 1.18$ ($P = .55$), $I^2 = 0\%$ [0%; 90%]

Total	−0.24 [−0.47; −0.02]

Heterogeneity: $\chi^2_{13} = 18.98$ ($P = .12$), $I^2 = 32\%$ [0%; 64%]

Test for overall effect: $z = −2.13$ ($P = .03$)

Test for subgroup differences: $\chi^2_{1} = 0.51$ ($P = .48$)

logHR estimate
−1.5 −0.5 0.5 1 1.5