Source	(95% CI)
Sequencing = TPM	
Riaz, Melanoma, n = 51	−0.74 [−1.45; −0.03]
Mariathasan, Kidney, n = 67	−0.34 [−0.91; 0.23]
Miao.1, Kidney, n = 33	−0.14 [−0.98; 0.70]
Braun, Kidney, n = 178	−0.12 [−0.51; 0.27]
Mariathasan, Lymph_node, n = 26	−0.10 [−1.04; 0.84]
Mariathasan, Bladder, n = 194	−0.05 [−0.40; 0.30]
Snyder, Ureteral, n = 25	0.06 [−0.90; 1.02]
Fumet.2, Lung, n = 43	0.23 [−0.55; 1.01]
Van_Allen, Melanoma, n = 42	0.55 [−0.19; 1.29]
Mariathasan, Ureteral, n = 26	1.34 [0.36; 2.32]
Total	−0.01 [−0.27; 0.25]

Heterogeneity: $\chi^2_9 = 15.61$ ($P = .08$), $I^2 = 42\%$ [0%; 72%]

Source	(95% CI)
Sequencing = FPKM	
Hugo, Melanoma, n = 27	−0.29 [−1.45; 0.87]
Liu, Melanoma, n = 121	−0.26 [−0.77; 0.25]
Nathanson, Melanoma, n = 24	−0.22 [−1.20; 0.76]
Total	−0.26 [−0.68; 0.16]

Heterogeneity: $\chi^2_2 = 0.01$ ($P > .99$), $I^2 = 0\%$ [<0%; <90%]

Total	−0.08 [−0.25; 0.09]

Heterogeneity: $\chi^2_{12} = 16.43$ ($P = .17$), $I^2 = 27\%$ [0%; 62%]
Test for overall effect: $z = −0.90$ ($P = .37$)
Test for subgroup differences: $\chi^2_1 = 0.94$ ($P = .33$)

−1 0 0.5 1 1.5
logHR estimate