Source	(95% CI)
Sequencing = TPM	
Van_Allen, Melanoma, n = 42	−1.29 [−2.21; −0.37]
Hwang, Lung, n = 21	−0.96 [−2.51; 0.59]
Mariathasan, Lymph_node, n = 26	−0.79 [−1.69; 0.11]
Snyder, Ureteral, n = 25	−0.54 [−1.62; 0.54]
Riaz, Melanoma, n = 51	−0.53 [−1.16; 0.10]
Mariathasan, Bladder, n = 194	−0.36 [−0.67; −0.05]
Fumet.2, Lung, n = 43	−0.29 [−1.17; 0.59]
Mariathasan, Kidney, n = 67	−0.10 [−0.67; 0.47]
Miao.1, Kidney, n = 33	−0.09 [−0.95; 0.77]
Braun, Kidney, n = 178	0.21 [−0.20; 0.62]
Mariathasan, Ureteral, n = 26	0.40 [−0.56; 1.36]
Total	−0.29 [−0.56; −0.03]

Heterogeneity: $\chi^2_{10} = 15.56$ ($P = .11$), $I^2 = 36\%$ [0%; 68%]

Source	(95% CI)
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	−0.83 [−1.65; −0.01]
Liu, Melanoma, n = 121	−0.35 [−0.84; 0.14]
Hugo, Melanoma, n = 27	0.27 [−0.96; 1.50]
Total	−0.40 [−0.80; 0.00]

Heterogeneity: $\chi^2_{2} = 2.22$ ($P = .33$), $I^2 = 10\%$ [0%; 91%]

Total	−0.31 [−0.53; −0.09]

Heterogeneity: $\chi^2_{13} = 18.17$ ($P = .15$), $I^2 = 28\%$ [0%; 62%]
Test for overall effect: $z = −2.75$ ($P = .006$)
Test for subgroup differences: $\chi^2_{1} = 0.18$ ($P = .67$)

−1.5 −0.5 0.5 1 1.5
logHR estimate