Source	(95% CI)

Sequencing = TPM

Mariathasan, Ureteral, n = 26	−1.40 [−4.16; 1.36]
Miao.1, Kidney, n = 33	−0.55 [−2.47; 1.37]
Mariathasan, Kidney, n = 67	−0.44 [−1.56; 0.68]
Van_Allen, Melanoma, n = 42	0.27 [−1.10; 1.64]
Fumet.2, Lung, n = 43	0.31 [−1.12; 1.74]
Mariathasan, Bladder, n = 194	0.45 [−0.12; 1.02]
Snyder, Ureteral, n = 25	0.72 [−0.32; 1.76]
Braun, Kidney, n = 178	0.90 [0.25; 1.55]
Riaz, Melanoma, n = 51	1.34 [0.14; 2.54]
Mariathasan, Lymph_node, n = 26	1.60 [−0.40; 3.60]
Total	0.54 [0.21; 0.86]

Heterogeneity: $\chi^2_9 = 10.54$ ($P = .31$), $I^2 = 15\%$ [0%; 56%]

Sequencing = FPKM

Nathanson, Melanoma, n = 24	−0.41 [−2.66; 1.84]
Liu, Melanoma, n = 121	−0.09 [−1.09; 0.91]
Hugo, Melanoma, n = 27	0.34 [−2.05; 2.73]
Total	−0.08 [−0.93; 0.77]

Heterogeneity: $\chi^2_2 = 0.2$ ($P = .90$), $I^2 = 0\%$ [0%; 90%]

Total	0.45 [0.13; 0.77]

Heterogeneity: $\chi^2_{12} = 12.51$ ($P = .41$), $I^2 = 4\%$ [0%; 58%]
Test for overall effect: $z = 2.72$ ($P = .006$)
Test for subgroup differences: $\chi^2_1 = 1.76$ ($P = .18$)

−1 0 1 2
logHR estimate