Source	(95% CI)
Sequencing = TPM	
Van_Allen, Melanoma, n = 42	−0.67 [−1.43; 0.09]
Mariathasan, Bladder, n = 194	−0.09 [−0.44; 0.26]
Mariathasan, Kidney, n = 67	0.02 [−0.55; 0.59]
Fumet.2, Lung, n = 43	0.08 [−0.70; 0.86]
Mariathasan, Lymph_node, n = 26	0.09 [−0.83; 1.01]
Braun, Kidney, n = 178	0.14 [−0.25; 0.53]
Snyder, Ureteral, n = 25	0.31 [−0.65; 1.27]
Mariathasan, Ureteral, n = 26	0.40 [−0.54; 1.34]
Total	0.01 [−0.20; 0.21]

Heterogeneity: $\chi^2_7 = 4.86$ ($P = .68$), $I^2 = 0\%$ [0%; 68%]

Source	(95% CI)
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	−0.53 [−1.57; 0.51]
Hugo, Melanoma, n = 27	−0.35 [−1.51; 0.81]
Liu, Melanoma, n = 121	−0.30 [−0.81; 0.21]
Total	−0.35 [−0.77; 0.08]

Heterogeneity: $\chi^2_2 = 0.15$ ($P = .93$), $I^2 = 0\%$ [0%; 90%]

Total	−0.06 [−0.24; 0.12]

Heterogeneity: $\chi^2_{10} = 7.14$ ($P = .71$), $I^2 = 0\%$ [0%; 60%]

Test for overall effect: $z = -0.64$ ($P = .52$)

Test for subgroup differences: $\chi^2_1 = 2.13$ ($P = .14$)

−1   0 0.5 1

logHR estimate