Source	(95% CI)	
Sequencing = TPM		
Van_Allen, Melanoma, n = 42	−0.92 [−1.68; −0.16]	
Mariathasan, Lymph_node, n = 26	−0.78 [−1.74; 0.18]	
Riaz, Melanoma, n = 51	−0.74 [−1.43; −0.05]	
Hwang, Lung, n = 21	−0.72 [−1.82; 0.38]	
Fumet.2, Lung, n = 43	−0.68 [−1.50; 0.14]	
Miao.1, Kidney, n = 33	−0.30 [−1.14; 0.54]	
Mariathasan, Bladder, n = 194	−0.16 [−0.51; 0.19]	
Snyder, Ureteral, n = 25	−0.16 [−1.12; 0.80]	
Mariathasan, Kidney, n = 67	−0.12 [−0.69; 0.45]	
Braun, Kidney, n = 178	0.08 [−0.31; 0.47]	
Mariathasan, Ureteral, n = 26	0.64 [−0.32; 1.60]	
Total	−0.28 [−0.53; −0.04]	

Heterogeneity: $\chi^2_{10} = 14.32$ ($P = .16$), $I^2 = 30\%$ [0%; 66%]

Sequencing = FPKM		
Nathanson, Melanoma, n = 24	−0.89 [−1.91; 0.13]	
Liu, Melanoma, n = 121	−0.56 [−1.07; −0.05]	
Hugo, Melanoma, n = 27	0.71 [−0.51; 1.93]	
Total	−0.35 [−1.12; 0.42]	

Heterogeneity: $\chi^2_2 = 4.39$ ($P = .11$), $I^2 = 54\%$ [0%; 87%]

Total — −0.31 [−0.54; −0.09]

Heterogeneity: $\chi^2_{13} = 19.63$ ($P = .10$), $I^2 = 34\%$ [0%; 65%]

Test for overall effect: $z = −2.73$ ($P = .006$)

Test for subgroup differences: $\chi^2_1 = 0.03$ ($P = .87$)

−1   0 0.5 1

logHR estimate