Source	(95% CI)
Sequencing = TPM	
Mariathasan, Ureteral, n = 26	−0.97 [−2.05; 0.11]
Miao.1, Kidney, n = 33	−0.55 [−1.88; 0.78]
Mariathasan, Kidney, n = 67	−0.27 [−0.90; 0.36]
Fumet.2, Lung, n = 43	−0.03 [−0.99; 0.93]
Snyder, Ureteral, n = 25	−0.01 [−1.11; 1.09]
Mariathasan, Bladder, n = 194	0.02 [−0.37; 0.41]
Mariathasan, Lymph_node, n = 26	0.08 [−1.04; 1.20]
Van_Allen, Melanoma, n = 42	0.08 [−0.78; 0.94]
Riaz, Melanoma, n = 51	0.72 [−0.06; 1.50]
Braun, Kidney, n = 178	0.93 [0.38; 1.48]
Total	0.09 [−0.26; 0.44]
Heterogeneity: $\chi^2_9 = 17.39$ ($P = .04$), $I^2 = 48\%$ [0%; 75%]	
Sequencing = FPKM	
Liu, Melanoma, n = 121	0.07 [−0.52; 0.66]
Nathanson, Melanoma, n = 24	0.23 [−0.95; 1.41]
Hugo, Melanoma, n = 27	0.54 [−1.13; 2.21]
Total	0.14 [−0.36; 0.64]
Heterogeneity: $\chi^2_2 = 0.3$ ($P = .86$), $I^2 = 0\%$ [0%; 90%]	
Total	0.12 [−0.17; 0.40]
Heterogeneity: $\chi^2_{12} = 17.69$ ($P = .13$), $I^2 = 32\%$ [0%; 65%]	
Test for overall effect: $z = 0.81$ ($P = .42$)	
Test for subgroup differences: $\chi^2_1 = 0.03$ ($P = .87$)	

logHR estimate