Source	(95% CI)
Sequencing = TPM	
Van_Allen, Melanoma, n = 42	−1.48 [−2.28; −0.68]
Snyder, Ureteral, n = 25	−1.15 [−2.33; 0.03]
Mariathasan, Bladder, n = 194	−0.77 [−1.08; −0.46]
Mariathasan, Lymph_node, n = 26	−0.77 [−1.55; 0.01]
Fumet.2, Lung, n = 43	−0.72 [−1.70; 0.26]
Mariathasan, Kidney, n = 67	−0.41 [−0.90; 0.08]
Riaz, Melanoma, n = 51	−0.41 [−1.02; 0.20]
Miao.1, Kidney, n = 33	−0.28 [−1.10; 0.54]
Mariathasan, Ureteral, n = 26	−0.06 [−1.04; 0.92]
Braun, Kidney, n = 178	0.32 [−0.09; 0.73]
Total	−0.52 [−0.86; −0.18]
Heterogeneity: $\chi_9^2 = 26.8$ ($P = .002$), $I^2 = 66\%$ [34%; 83%]	
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	−0.98 [−1.90; −0.06]
Liu, Melanoma, n = 121	−0.93 [−1.42; −0.44]
Hugo, Melanoma, n = 27	−0.40 [−1.50; 0.70]
Total	−0.87 [−1.27; −0.47]
Heterogeneity: $\chi_2^2 = 0.82$ ($P = .66$), $I^2 = 0\%$ [0%; 90%]	
Total	−0.58 [−0.86; −0.29]
Heterogeneity: $\chi_{12}^2 = 30.71$ ($P = .002$), $I^2 = 61\%$ [28%; 79%]	
Test for overall effect: $z = −3.97$ ($P < .001$)	
Test for subgroup differences: $\chi_1^2 = 1.71$ ($P = .19$)	

−1 0 1
logHR estimate