Source	(95% CI)
Sequencing = TPM	
Miao.1, Kidney, n = 33	−0.75 [−1.61; 0.11]
Mariathasan, Kidney, n = 67	−0.46 [−1.05; 0.13]
Riaz, Melanoma, n = 51	−0.30 [−0.99; 0.39]
Fumet.2, Lung, n = 43	−0.07 [−0.85; 0.71]
Mariathasan, Bladder, n = 194	−0.04 [−0.39; 0.31]
Mariathasan, Lymph_node, n = 26	0.02 [−0.92; 0.96]
Van_Allen, Melanoma, n = 42	0.05 [−0.69; 0.79]
Braun, Kidney, n = 178	0.10 [−0.29; 0.49]
Snyder, Ureteral, n = 25	0.47 [−0.51; 1.45]
Mariathasan, Ureteral, n = 26	0.74 [−0.22; 1.70]
Total	−0.05 [−0.24; 0.14]
Heterogeneity: $\chi^2_9 = 9.25$ ($P = .41$), $I^2 = 3\%$ [0%; 63%]	
Sequencing = FPKM	
Liu, Melanoma, n = 121	−0.37 [−0.88; 0.14]
Nathanson, Melanoma, n = 24	−0.20 [−1.20; 0.80]
Hugo, Melanoma, n = 27	0.77 [−0.39; 1.93]
Total	−0.10 [−0.68; 0.49]
Heterogeneity: $\chi^2_2 = 3.13$ ($P = .21$), $I^2 = 36\%$ [0%; 80%]	
Total	−0.07 [−0.25; 0.10]
Heterogeneity: $\chi^2_{12} = 12.72$ ($P = .39$), $I^2 = 6\%$ [0%; 59%]	
Test for overall effect: $z = −0.82$ ($P = .41$)	
Test for subgroup differences: $\chi^2_1 = 0.02$ ($P = .88$)	

−1   0 0.5 1
logHR estimate