Source	(95% CI)
Sequencing = TPM	
Van_Allen, Melanoma, n = 42	−1.15 [−1.91; −0.39]
Snyder, Ureteral, n = 25	−0.42 [−1.32; 0.48]
Mariathasan, Lymph_node, n = 26	−0.38 [−1.09; 0.33]
Hwang, Lung, n = 21	−0.33 [−1.39; 0.73]
Riaz, Melanoma, n = 51	−0.31 [−0.84; 0.22]
Fumet.2, Lung, n = 43	−0.30 [−0.99; 0.39]
Mariathasan, Bladder, n = 194	−0.25 [−0.54; 0.04]
Mariathasan, Kidney, n = 67	−0.10 [−0.59; 0.39]
Miao.1, Kidney, n = 33	0.01 [−0.68; 0.70]
Braun, Kidney, n = 178	0.09 [−0.24; 0.42]
Mariathasan, Ureteral, n = 26	0.36 [−0.46; 1.18]
Total	−0.19 [−0.37; −0.01]
Heterogeneity: $\chi^2_{10} = 11.98$ ($P = .29$), $I^2 = 17\%$ [0%; 57%]	
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	−0.78 [−1.54; −0.02]
Liu, Melanoma, n = 121	−0.25 [−0.68; 0.18]
Hugo, Melanoma, n = 27	0.30 [−0.78; 1.38]
Total	−0.31 [−0.67; 0.06]
Heterogeneity: $\chi^2_2 = 2.76$ ($P = .25$), $I^2 = 27\%$ [0%; 92%]	
Total	−0.21 [−0.37; −0.05]
Heterogeneity: $\chi^2_{13} = 15.13$ ($P = .30$), $I^2 = 14\%$ [0%; 53%]	
Test for overall effect: $z = −2.61$ ($P = .009$)	
Test for subgroup differences: $\chi^2_1 = 0.30$ ($P = .58$)	

−1.5 −0.5 0.5 1 1.5

logHR estimate