Source	(95% CI)
Sequencing = TPM	
Riaz, Melanoma, n = 51	−1.00 [−2.06; 0.06]
Mariathasan, Lymph_node, n = 26	−0.46 [−2.28; 1.36]
Snyder, Ureteral, n = 25	−0.31 [−1.56; 0.94]
Mariathasan, Kidney, n = 67	−0.27 [−1.13; 0.59]
Miao.1, Kidney, n = 33	−0.25 [−1.15; 0.65]
Braun, Kidney, n = 178	−0.16 [−0.67; 0.35]
Mariathasan, Bladder, n = 194	−0.08 [−0.57; 0.41]
Fumet.2, Lung, n = 43	0.49 [−0.65; 1.63]
Van_Allen, Melanoma, n = 42	0.64 [−0.54; 1.82]
Mariathasan, Ureteral, n = 26	3.00 [1.18; 4.82]
Total	−0.08 [−0.34; 0.19]
Heterogeneity: $\chi^2_9 = 16.99$ ($P = .05$), $I^2 = 47\%$ [0%; 74%]	
Sequencing = FPKM	
Liu, Melanoma, n = 121	−0.30 [−1.04; 0.44]
Nathanson, Melanoma, n = 24	−0.21 [−1.78; 1.36]
Hugo, Melanoma, n = 27	0.27 [−1.26; 1.80]
Total	−0.19 [−0.81; 0.42]
Heterogeneity: $\chi^2_2 = 0.43$ ($P = .81$), $I^2 = 0\%$ [0%; 90%]	
Total	−0.10 [−0.34; 0.15]
Heterogeneity: $\chi^2_{12} = 17.54$ ($P = .13$), $I^2 = 32\%$ [0%; 65%]	
Test for overall effect: $z = -0.77$ ($P = .44$)	
Test for subgroup differences: $\chi^2_1 = 0.12$ ($P = .73$)	

−1 0 1 2 3
logHR estimate