Source	(95% CI)
Sequencing = FPKM	
Liu, Melanoma, n = 121	−0.35 [−0.96; 0.26]
Nathanson, Melanoma, n = 24	0.04 [−1.14; 1.22]
Hugo, Melanoma, n = 27	0.53 [−0.67; 1.73]
Total	−0.12 [−0.63; 0.38]
Heterogeneity: $\chi^2_2 = 1.75$ ($P = .42$), $I^2 = 0\%$ [0%; 90%]	
Sequencing = TPM	
Mariathasan, Kidney, n = 67	−0.35 [−0.92; 0.22]
Riaz, Melanoma, n = 51	−0.13 [−0.82; 0.56]
Miao.1, Kidney, n = 33	−0.08 [−1.00; 0.84]
Mariathasan, Bladder, n = 194	0.09 [−0.20; 0.38]
Fumet.2, Lung, n = 43	0.24 [−0.49; 0.97]
Braun, Kidney, n = 178	0.26 [−0.15; 0.67]
Mariathasan, Ureteral, n = 26	0.31 [−0.59; 1.21]
Mariathasan, Lymph_node, n = 26	0.43 [−0.37; 1.23]
Van_Allen, Melanoma, n = 42	0.75 [−0.15; 1.65]
Snyder, Ureteral, n = 25	0.86 [−0.08; 1.80]
Total	0.15 [−0.03; 0.33]
Heterogeneity: $\chi^2_9 = 8.82$ ($P = .45$), $I^2 = 0\%$ [0%; 62%]	
Total	0.11 [−0.06; 0.28]
Heterogeneity: $\chi^2_{12} = 11.66$ ($P = .47$), $I^2 = 0\%$ [0%; 57%]	
Test for overall effect: $z = 1.31$ ($P = .19$)	
Test for subgroup differences: $\chi^2_1 = 0.96$ ($P = .33$)	

−0.5 0 0.5 1
logHR estimate