Source	(95% CI)
Sequencing = FPKM	
Hugo, Melanoma, n = 27	−0.76 [−2.56; 1.04]
Nathanson, Melanoma, n = 24	−0.65 [−1.79; 0.49]
Liu, Melanoma, n = 121	−0.14 [−0.83; 0.55]
Total	−0.32 [−0.88; 0.24]
Heterogeneity: $\chi^2_2 = 0.82$ ($P = .66$), $I^2 = 0\%$ [0%; 90%]	
Sequencing = TPM	
Van_Allen, Melanoma, n = 42	−0.32 [−1.32; 0.68]
Snyder, Ureteral, n = 25	−0.25 [−1.35; 0.85]
Mariathasan, Bladder, n = 194	−0.10 [−0.51; 0.31]
Mariathasan, Kidney, n = 67	0.02 [−0.65; 0.69]
Mariathasan, Lymph_node, n = 26	0.02 [−1.06; 1.10]
Fumet.2, Lung, n = 43	0.06 [−0.88; 1.00]
Mariathasan, Ureteral, n = 26	0.15 [−1.05; 1.35]
Braun, Kidney, n = 178	0.40 [−0.13; 0.93]
Total	0.03 [−0.21; 0.28]
Heterogeneity: $\chi^2_7 = 3.03$ ($P = .88$), $I^2 = 0\%$ [0%; 68%]	
Total	−0.03 [−0.25; 0.20]
Heterogeneity: $\chi^2_{10} = 5.15$ ($P = .88$), $I^2 = 0\%$ [0%; 60%]	
Test for overall effect: $z = -0.22$ ($P = .83$)	
Test for subgroup differences: $\chi^2_1 = 1.30$ ($P = .25$)	

logHR estimate

−1   0 0.5 1