Source	(95% CI)
Sequencing = TPM	
Snyder, Ureteral, n = 25	−0.40 [−0.89; 0.09]
Hwang, Lung, n = 21	−0.39 [−1.13; 0.35]
Riaz, Melanoma, n = 51	−0.18 [−0.51; 0.15]
Mariathasan, Lymph_node, n = 26	−0.13 [−0.68; 0.42]
Braun, Kidney, n = 178	−0.08 [−0.30; 0.14]
Van_Allen, Melanoma, n = 42	−0.04 [−0.41; 0.33]
Mariathasan, Ureteral, n = 26	0.10 [−0.37; 0.57]
Mariathasan, Bladder, n = 194	0.13 [−0.05; 0.31]
Miao.1, Kidney, n = 33	0.19 [−0.26; 0.64]
Mariathasan, Kidney, n = 67	0.23 [−0.04; 0.50]
Fumet.2, Lung, n = 43	0.39 [−0.06; 0.84]
Total	0.03 [−0.09; 0.15]

Heterogeneity: $\chi^2_{10} = 13.43$ ($P = .20$), $I^2 = 26\%$ [0%; 63%]

Sequencing = FPKM	
Hugo, Melanoma, n = 27	−0.20 [−0.77; 0.37]
Liu, Melanoma, n = 121	−0.05 [−0.30; 0.20]
Nathanson, Melanoma, n = 24	0.30 [−0.21; 0.81]
Total	−0.01 [−0.22; 0.20]

Heterogeneity: $\chi^2_2 = 1.95$ ($P = .38$), $I^2 = 0\%$ [0%; 90%]

Total	0.02 [−0.08; 0.12]

Heterogeneity: $\chi^2_{13} = 15.55$ ($P = .27$), $I^2 = 16\%$ [0%; 55%]
Test for overall effect: $z = 0.48$ ($P = .63$)
Test for subgroup differences: $\chi^2_1 = 0.10$ ($P = .76$)

−0.5 0 0.5
logHR estimate