

Source	(95% CI)
Sequencing = TPM	
Van_Allen, Melanoma, n = 42	-1.25 [-2.03; -0.47]
Riaz, Melanoma, n = 51	-0.36 [-1.05; 0.33]
Snyder, Ureteral, n = 25	-0.31 [-1.27; 0.65]
Hwang, Lung, n = 21	-0.27 [-1.33; 0.79]
Mariathasan, Bladder, n = 194	-0.27 [-0.62; 0.08]
Mariathasan, Lymph_node, n = 26	-0.23 [-1.15; 0.69]
Mariathasan, Kidney, n = 67	-0.13 [-0.70; 0.44]
Miao.1, Kidney, n = 33	-0.04 [-0.88; 0.80]
Fumet.2, Lung, n = 43	-0.02 [-0.80; 0.76]
Mariathasan, Ureteral, n = 26	0.13 [-0.81; 1.07]
Braun, Kidney, n = 178	0.14 [-0.25; 0.53]
Total	-0.20 [-0.41; 0.02]
Heterogeneity: $\chi^2_{10} = 11.05$ ($P = .35$), $I^2 = 10\%$ [0%; 49%]	

Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-0.49 [-1.49; 0.51]
Hugo, Melanoma, n = 27	-0.22 [-1.42; 0.98]
Liu, Melanoma, n = 121	-0.15 [-0.66; 0.36]
Total	-0.22 [-0.64; 0.20]
Heterogeneity: $\chi^2_2 = 0.35$ ($P = .84$), $I^2 = 0\%$ [0%; 90%]	
Total	-0.19 [-0.37; -0.01]
Heterogeneity: $\chi^2_{13} = 11.43$ ($P = .57$), $I^2 = 0\%$ [0%; 55%]	
Test for overall effect: $z = -2.12$ ($P = .03$)	
Test for subgroup differences: $\chi^2_1 = 0.01$ ($P = .92$)	

