

Source	(95% CI)
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-1.36 [-2.46; -0.26]
Liu, Melanoma, n = 121	-0.70 [-1.21; -0.19]
Hugo, Melanoma, n = 27	0.07 [-1.09; 1.23]
Total	-0.69 [-1.12; -0.27]
Heterogeneity: $\chi^2_2 = 3.09$ ($P = .21$), $I^2 = 35\%$ [0%; 79%]	

Sequencing = TPM	
Van_Allen, Melanoma, n = 42	-1.10 [-1.88; -0.32]
Mariathasan, Lymph_node, n = 26	-0.89 [-1.85; 0.07]
Snyder, Ureteral, n = 25	-0.83 [-1.81; 0.15]
Riaz, Melanoma, n = 51	-0.65 [-1.34; 0.04]
Mariathasan, Bladder, n = 194	-0.61 [-0.96; -0.26]
Mariathasan, Kidney, n = 67	-0.46 [-1.05; 0.13]
Miao.1, Kidney, n = 33	-0.25 [-1.09; 0.59]
Fumet.2, Lung, n = 43	-0.17 [-0.95; 0.61]
Mariathasan, Ureteral, n = 26	0.38 [-0.58; 1.34]
Braun, Kidney, n = 178	0.50 [0.09; 0.91]
Total	-0.38 [-0.72; -0.03]
Heterogeneity: $\chi^2_9 = 27.35$ ($P = .001$), $I^2 = 67\%$ [36%; 83%]	
Total	-0.44 [-0.74; -0.13]
Heterogeneity: $\chi^2_{12} = 32.92$ ($P < .001$), $I^2 = 64\%$ [34%; 80%]	
Test for overall effect: $z = -2.83$ ($P = .005$)	
Test for subgroup differences: $\chi^2_1 = 1.27$ ($P = .26$)	

