

Source	(95% CI)
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-0.94 [-1.76; -0.12]
Liu, Melanoma, n = 121	-0.33 [-0.74; 0.08]
Hugo, Melanoma, n = 27	0.24 [-0.74; 1.22]
Total	-0.37 [-0.84; 0.09]
Heterogeneity: $\chi^2_2 = 3.37$ ($P = .19$), $I^2 = 41\%$ [0%; 82%]	

Sequencing = TPM	
Van_Allen, Melanoma, n = 42	-0.91 [-1.60; -0.22]
Riaz, Melanoma, n = 51	-0.61 [-1.26; 0.04]
Snyder, Ureteral, n = 25	-0.54 [-1.27; 0.19]
Mariathanas, Lymph_node, n = 26	-0.49 [-1.29; 0.31]
Mariathanas, Bladder, n = 194	-0.42 [-0.69; -0.15]
Fumet.2, Lung, n = 43	-0.33 [-0.94; 0.28]
Mariathanas, Kidney, n = 67	-0.17 [-0.66; 0.32]
Miao.1, Kidney, n = 33	-0.05 [-0.76; 0.66]
Braun, Kidney, n = 178	0.16 [-0.17; 0.49]
Mariathanas, Ureteral, n = 26	0.57 [-0.19; 1.33]
Total	-0.26 [-0.50; -0.02]
Heterogeneity: $\chi^2_9 = 17.89$ ($P = .04$), $I^2 = 50\%$ [0%; 76%]	
Total	-0.28 [-0.49; -0.08]
Heterogeneity: $\chi^2_{12} = 21.65$ ($P = .04$), $I^2 = 45\%$ [0%; 71%]	
Test for overall effect: $z = -2.68$ ($P = .007$)	
Test for subgroup differences: $\chi^2_1 = 0.18$ ($P = .67$)	

