

Source	(95% CI)
Sequencing = TPM	
Mariathanan, Lymph_node, n = 26	-0.80 [-1.66; 0.06]
Van_Allen, Melanoma, n = 42	-0.80 [-1.43; -0.17]
Snyder, Ureteral, n = 25	-0.73 [-1.57; 0.11]
Riaz, Melanoma, n = 51	-0.40 [-0.99; 0.19]
Mariathanan, Bladder, n = 194	-0.27 [-0.54; 0.00]
Fumet.2, Lung, n = 43	-0.26 [-0.83; 0.31]
Miao.1, Kidney, n = 33	0.11 [-0.67; 0.89]
Mariathanan, Kidney, n = 67	0.21 [-0.26; 0.68]
Braun, Kidney, n = 178	0.31 [-0.02; 0.64]
Mariathanan, Ureteral, n = 26	0.36 [-0.40; 1.12]
Total	-0.18 [-0.44; 0.09]
Heterogeneity: $\chi^2_9 = 21.3$ ($P = .01$), $I^2 = 58\%$ [15%; 79%]	

Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-0.61 [-1.41; 0.19]
Hugo, Melanoma, n = 27	-0.56 [-1.58; 0.46]
Liu, Melanoma, n = 121	-0.52 [-0.91; -0.13]
Total	-0.54 [-0.87; -0.21]
Heterogeneity: $\chi^2_2 = 0.04$ ($P = .98$), $I^2 = 0\%$ [<0%; <90%]	
Total	-0.25 [-0.48; -0.02]
Heterogeneity: $\chi^2_{12} = 26.25$ ($P = .010$), $I^2 = 54\%$ [14%; 76%]	
Test for overall effect: $z = -2.13$ ($P = .03$)	
Test for subgroup differences: $\chi^2_1 = 2.77$ ($P = .10$)	

