

Source	(95% CI)
Sequencing = TPM	
Mariathasan, Ureteral, n = 26	-0.74 [-1.70; 0.22]
Miao.1, Kidney, n = 33	-0.24 [-1.10; 0.62]
Mariathasan, Kidney, n = 67	-0.20 [-0.77; 0.37]
Mariathasan, Lymph_node, n = 26	-0.04 [-0.98; 0.90]
Van_Allen, Melanoma, n = 42	-0.04 [-0.78; 0.70]
Snyder, Ureteral, n = 25	0.06 [-0.90; 1.02]
Fumet.2, Lung, n = 43	0.09 [-0.69; 0.87]
Mariathasan, Bladder, n = 194	0.09 [-0.26; 0.44]
Braun, Kidney, n = 178	0.55 [0.14; 0.96]
Riaz, Melanoma, n = 51	0.61 [-0.08; 1.30]
Total	0.10 [-0.14; 0.34]
Heterogeneity: $\chi^2_9 = 11.44$ ($P = .25$), $I^2 = 21\%$ [0%; 61%]	

Sequencing = FPKM	
Liu, Melanoma, n = 121	-0.06 [-0.57; 0.45]
Hugo, Melanoma, n = 27	0.18 [-0.96; 1.32]
Nathanson, Melanoma, n = 24	0.74 [-0.30; 1.78]
Total	0.13 [-0.33; 0.59]
Heterogeneity: $\chi^2_2 = 1.85$ ($P = .40$), $I^2 = 0\%$ [0%; 90%]	
Total	0.11 [-0.09; 0.32]
Heterogeneity: $\chi^2_{12} = 13.31$ ($P = .35$), $I^2 = 10\%$ [0%; 48%]	
Test for overall effect: $z = 1.10$ ($P = .27$)	
Test for subgroup differences: $\chi^2_1 = 0.01$ ($P = .92$)	

