

Source	(95% CI)
Sequencing = TPM	
Riaz, Melanoma, n = 51	-0.46 [-1.05; 0.13]
Mariathasan, Lymph_node, n = 26	-0.32 [-1.26; 0.62]
Snyder, Ureteral, n = 25	-0.29 [-1.05; 0.47]
Mariathasan, Kidney, n = 67	-0.17 [-0.66; 0.32]
Mariathasan, Bladder, n = 194	-0.08 [-0.35; 0.19]
Braun, Kidney, n = 178	-0.06 [-0.37; 0.25]
Miao.1, Kidney, n = 33	0.02 [-0.78; 0.82]
Van_Allen, Melanoma, n = 42	0.30 [-0.33; 0.93]
Fumet.2, Lung, n = 43	0.45 [-0.26; 1.16]
Mariathasan, Ureteral, n = 26	1.68 [0.68; 2.68]
Total	-0.03 [-0.19; 0.13]
Heterogeneity: $\chi^2_9 = 17.44$ ($P = .04$), $I^2 = 48\%$ [0%; 75%]	

Sequencing = FPKM	
Liu, Melanoma, n = 121	-0.15 [-0.58; 0.28]
Nathanson, Melanoma, n = 24	-0.15 [-1.05; 0.75]
Hugo, Melanoma, n = 27	0.08 [-0.88; 1.04]
Total	-0.12 [-0.48; 0.24]
Heterogeneity: $\chi^2_2 = 0.19$ ($P = .91$), $I^2 = 0\%$ [0%; 90%]	
Total	-0.04 [-0.19; 0.10]
Heterogeneity: $\chi^2_{12} = 17.82$ ($P = .12$), $I^2 = 33\%$ [0%; 65%]	
Test for overall effect: $z = -0.59$ ($P = .55$)	
Test for subgroup differences: $\chi^2_1 = 0.19$ ($P = .66$)	

