

Source	(95% CI)
Sequencing = TPM	
Mariathasan, Lymph_node, n = 26	-0.69 [-1.63; 0.25]
Miao.1, Kidney, n = 33	-0.18 [-1.04; 0.68]
Van_Allen, Melanoma, n = 42	-0.10 [-0.84; 0.64]
Mariathasan, Ureteral, n = 26	-0.02 [-0.94; 0.90]
Mariathasan, Bladder, n = 194	-0.01 [-0.36; 0.34]
Mariathasan, Kidney, n = 67	0.23 [-0.34; 0.80]
Braun, Kidney, n = 178	0.24 [-0.15; 0.63]
Snyder, Ureteral, n = 25	0.26 [-0.70; 1.22]
Fumet.2, Lung, n = 43	0.33 [-0.45; 1.11]
Riaz, Melanoma, n = 51	0.38 [-0.31; 1.07]
Total	0.09 [-0.10; 0.28]
Heterogeneity: $\chi^2_9 = 5.59$ ($P = .78$), $I^2 = 0\%$ [0%; 62%]	

Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-0.27 [-1.29; 0.75]
Liu, Melanoma, n = 121	-0.04 [-0.55; 0.47]
Hugo, Melanoma, n = 27	1.04 [-0.18; 2.26]
Total	0.06 [-0.39; 0.51]
Heterogeneity: $\chi^2_2 = 3.05$ ($P = .22$), $I^2 = 34\%$ [0%; 79%]	
Total	0.09 [-0.09; 0.26]
Heterogeneity: $\chi^2_{12} = 8.67$ ($P = .73$), $I^2 = 0\%$ [0%; 57%]	
Test for overall effect: $z = 0.98$ ($P = .33$)	
Test for subgroup differences: $\chi^2_1 = 0.02$ ($P = .90$)	

