

Source	(95% CI)
Sequencing = FPKM	
Hugo, Melanoma, n = 27	-0.76 [-1.94; 0.42]
Liu, Melanoma, n = 121	-0.11 [-0.62; 0.40]
Nathanson, Melanoma, n = 24	0.66 [-0.36; 1.68]
Total	-0.05 [-0.61; 0.51]
Heterogeneity: $\chi^2_2 = 3.32$ ($P = .19$), $I^2 = 40\%$ [0%; 81%]	

Sequencing = TPM	
Riaz, Melanoma, n = 51	-0.33 [-1.02; 0.36]
Miao.1, Kidney, n = 33	-0.22 [-1.06; 0.62]
Mariathasan, Lymph_node, n = 26	-0.21 [-1.13; 0.71]
Braun, Kidney, n = 178	-0.14 [-0.53; 0.25]
Snyder, Ureteral, n = 25	-0.12 [-1.08; 0.84]
Mariathasan, Kidney, n = 67	0.01 [-0.56; 0.58]
Van_Allen, Melanoma, n = 42	0.06 [-0.68; 0.80]
Mariathasan, Bladder, n = 194	0.15 [-0.20; 0.50]
Hwang, Lung, n = 21	0.16 [-1.00; 1.32]
Fumet.2, Lung, n = 43	0.42 [-0.36; 1.20]
Mariathasan, Ureteral, n = 26	0.42 [-0.54; 1.38]
Total	0.01 [-0.18; 0.20]
Heterogeneity: $\chi^2_{10} = 4.52$ ($P = .92$), $I^2 = 0\%$ [0%; 60%]	
Total	-0.00 [-0.17; 0.17]
Heterogeneity: $\chi^2_{13} = 7.93$ ($P = .85$), $I^2 = 0\%$ [0%; 55%]	
Test for overall effect: $z = -0.01$ ($P > .99$)	
Test for subgroup differences: $\chi^2_1 = 0.04$ ($P = .84$)	

