

Source	(95% CI)
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-1.03 [-2.07; 0.01]
Liu, Melanoma, n = 121	-0.18 [-0.69; 0.33]
Hugo, Melanoma, n = 27	0.47 [-0.73; 1.67]
Total	-0.26 [-0.90; 0.38]
Heterogeneity: $\chi^2_2 = 3.63$ ($P = .16$), $I^2 = 45\%$ [0%; 84%]	

Sequencing = TPM	
Van_Allen, Melanoma, n = 42	-0.75 [-1.49; -0.01]
Snyder, Ureteral, n = 25	-0.63 [-1.59; 0.33]
Mariathasan, Lymph_node, n = 26	-0.45 [-1.39; 0.49]
Riaz, Melanoma, n = 51	-0.34 [-1.03; 0.35]
Hwang, Lung, n = 21	-0.30 [-1.38; 0.78]
Miao.1, Kidney, n = 33	-0.22 [-1.06; 0.62]
Fumet.2, Lung, n = 43	-0.18 [-0.96; 0.60]
Mariathasan, Bladder, n = 194	-0.15 [-0.50; 0.20]
Mariathasan, Kidney, n = 67	-0.09 [-0.66; 0.48]
Braun, Kidney, n = 178	-0.01 [-0.40; 0.38]
Mariathasan, Ureteral, n = 26	0.09 [-0.85; 1.03]
Total	-0.19 [-0.38; -0.01]
Heterogeneity: $\chi^2_{10} = 4.82$ ($P = .90$), $I^2 = 0\%$ [0%; 60%]	
Total	-0.20 [-0.37; -0.03]
Heterogeneity: $\chi^2_{13} = 8.49$ ($P = .81$), $I^2 = 0\%$ [0%; 55%]	
Test for overall effect: $z = -2.31$ ($P = .02$)	
Test for subgroup differences: $\chi^2_1 = 0.04$ ($P = .84$)	

