

Source	(95% CI)
Sequencing = TPM	
Mariathasan, Lymph_node, n = 26	-1.27 [-2.25; -0.29]
Van_Allen, Melanoma, n = 42	-0.97 [-1.73; -0.21]
Hwang, Lung, n = 21	-0.82 [-1.92; 0.28]
Riaz, Melanoma, n = 51	-0.55 [-1.24; 0.14]
Mariathasan, Bladder, n = 194	-0.36 [-0.71; -0.01]
Snyder, Ureteral, n = 25	-0.29 [-1.25; 0.67]
Mariathasan, Kidney, n = 67	-0.23 [-0.80; 0.34]
Miao.1, Kidney, n = 33	-0.05 [-0.91; 0.81]
Fumet.2, Lung, n = 43	0.02 [-0.76; 0.80]
Mariathasan, Ureteral, n = 26	0.13 [-0.81; 1.07]
Braun, Kidney, n = 178	0.24 [-0.15; 0.63]
Total	-0.30 [-0.57; -0.04]
Heterogeneity: $\chi^2_{10} = 17.02$ ($P = .07$), $I^2 = 41\%$ [0%; 71%]	

Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-0.78 [-1.80; 0.24]
Liu, Melanoma, n = 121	-0.37 [-0.88; 0.14]
Hugo, Melanoma, n = 27	0.19 [-0.97; 1.35]
Total	-0.37 [-0.79; 0.06]
Heterogeneity: $\chi^2_2 = 1.52$ ($P = .47$), $I^2 = 0\%$ [0%; 90%]	
Total	-0.31 [-0.53; -0.08]
Heterogeneity: $\chi^2_{13} = 18.79$ ($P = .13$), $I^2 = 31\%$ [0%; 63%]	
Test for overall effect: $z = -2.66$ ($P = .008$)	
Test for subgroup differences: $\chi^2_1 = 0.06$ ($P = .81$)	

