

Source**(95% CI)****Sequencing = TPM**

Mariathasan, Lymph_node, n = 26	-1.21 [-2.21; -0.21]
Fumet.2, Lung, n = 43	-0.92 [-1.74; -0.10]
Van_Allen, Melanoma, n = 42	-0.92 [-1.68; -0.16]
Mariathasan, Bladder, n = 194	-0.73 [-1.08; -0.38]
Riaz, Melanoma, n = 51	-0.68 [-1.37; 0.01]
Miao.1, Kidney, n = 33	-0.41 [-1.27; 0.45]
Mariathasan, Kidney, n = 67	-0.37 [-0.96; 0.22]
Snyder, Ureteral, n = 25	-0.28 [-1.24; 0.68]
Mariathasan, Ureteral, n = 26	-0.15 [-1.09; 0.79]
Braun, Kidney, n = 178	0.18 [-0.21; 0.57]
Total	-0.50 [-0.80; -0.21]
Heterogeneity: $\chi^2_9 = 18.29$ ($P = .03$), $I^2 = 51\%$ [0%; 76%]	

Sequencing = FPKM

Liu, Melanoma, n = 121	-1.03 [-1.56; -0.50]
Nathanson, Melanoma, n = 24	-0.78 [-1.80; 0.24]
Hugo, Melanoma, n = 27	0.12 [-1.02; 1.26]
Total	-0.71 [-1.33; -0.09]
Heterogeneity: $\chi^2_2 = 3.24$ ($P = .20$), $I^2 = 38\%$ [0%; 81%]	
Total	-0.55 [-0.81; -0.28]
Heterogeneity: $\chi^2_{12} = 23.78$ ($P = .02$), $I^2 = 50\%$ [4%; 73%]	
Test for overall effect: $z = -4.05$ ($P < .001$)	
Test for subgroup differences: $\chi^2_1 = 0.36$ ($P = .55$)	

