

Source	(95% CI)
Sequencing = TPM	
Snyder, Ureteral, n = 25	-0.99 [-2.11; 0.13]
Van_Allen, Melanoma, n = 42	-0.97 [-1.85; -0.09]
Mariathasan, Lymph_node, n = 26	-0.56 [-1.50; 0.38]
Fumet.2, Lung, n = 43	-0.50 [-1.42; 0.42]
Riaz, Melanoma, n = 51	-0.49 [-1.14; 0.16]
Mariathasan, Bladder, n = 194	-0.46 [-0.81; -0.11]
Mariathasan, Kidney, n = 67	-0.13 [-0.74; 0.48]
Miao.1, Kidney, n = 33	-0.05 [-0.91; 0.81]
Braun, Kidney, n = 178	0.37 [-0.06; 0.80]
Mariathasan, Ureteral, n = 26	0.55 [-0.43; 1.53]
Total	-0.27 [-0.57; 0.03]
Heterogeneity: $\chi^2_9 = 17.68$ ($P = .04$), $I^2 = 49\%$ [0%; 75%]	

Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-0.97 [-1.85; -0.09]
Liu, Melanoma, n = 121	-0.39 [-0.90; 0.12]
Hugo, Melanoma, n = 27	0.35 [-0.87; 1.57]
Total	-0.43 [-0.89; 0.02]
Heterogeneity: $\chi^2_2 = 3.05$ ($P = .22$), $I^2 = 34\%$ [0%; 79%]	
Total	-0.30 [-0.56; -0.04]
Heterogeneity: $\chi^2_{12} = 21.42$ ($P = .04$), $I^2 = 44\%$ [0%; 71%]	
Test for overall effect: $z = -2.27$ ($P = .02$)	
Test for subgroup differences: $\chi^2_1 = 0.34$ ($P = .56$)	

