

Source	(95% CI)
Sequencing = TPM	
Van_Allen, Melanoma, n = 42	-1.12 [-1.85; -0.39]
Mariathasan, Lymph_node, n = 26	-0.70 [-1.43; 0.03]
Snyder, Ureteral, n = 25	-0.69 [-1.53; 0.15]
Mariathasan, Bladder, n = 194	-0.57 [-0.86; -0.28]
Riaz, Melanoma, n = 51	-0.51 [-1.04; 0.02]
Fumet.2, Lung, n = 43	-0.46 [-1.11; 0.19]
Mariathasan, Kidney, n = 67	-0.36 [-0.83; 0.11]
Miao.1, Kidney, n = 33	-0.10 [-0.84; 0.64]
Braun, Kidney, n = 178	0.18 [-0.15; 0.51]
Mariathasan, Ureteral, n = 26	0.50 [-0.26; 1.26]
Total	-0.36 [-0.64; -0.09]
Heterogeneity: $\chi^2_9 = 23.33$ ($P = .005$), $I^2 = 61\%$ [23%; 81%]	

Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-0.85 [-1.59; -0.11]
Liu, Melanoma, n = 121	-0.60 [-1.03; -0.17]
Hugo, Melanoma, n = 27	0.06 [-0.96; 1.08]
Total	-0.58 [-0.93; -0.23]
Heterogeneity: $\chi^2_2 = 2.03$ ($P = .36$), $I^2 = 1\%$ [0%; 90%]	
Total	-0.40 [-0.63; -0.17]
Heterogeneity: $\chi^2_{12} = 26.90$ ($P = .008$), $I^2 = 55\%$ [17%; 76%]	
Test for overall effect: $z = -3.40$ ($P < .001$)	
Test for subgroup differences: $\chi^2_1 = 0.89$ ($P = .35$)	

