

Source	(95% CI)
Sequencing = TPM	
Van_Allen, Melanoma, n = 42	-1.26 [-2.00; -0.52]
Riaz, Melanoma, n = 51	-0.71 [-1.38; -0.04]
Mariathasan, Lymph_node, n = 26	-0.70 [-1.52; 0.12]
Hwang, Lung, n = 21	-0.66 [-1.70; 0.38]
Mariathasan, Bladder, n = 194	-0.39 [-0.66; -0.12]
Snyder, Ureteral, n = 25	-0.39 [-1.23; 0.45]
Fumet.2, Lung, n = 43	-0.27 [-0.88; 0.34]
Miao.1, Kidney, n = 33	-0.11 [-0.87; 0.65]
Mariathasan, Kidney, n = 67	0.01 [-0.50; 0.52]
Braun, Kidney, n = 178	0.13 [-0.20; 0.46]
Mariathasan, Ureteral, n = 26	0.54 [-0.34; 1.42]
Total	-0.31 [-0.57; -0.04]
Heterogeneity: $\chi^2_{10} = 20.95$ ($P = .02$), $I^2 = 52\%$ [5%; 76%]	

Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-0.89 [-1.73; -0.05]
Liu, Melanoma, n = 121	-0.32 [-0.73; 0.09]
Hugo, Melanoma, n = 27	0.23 [-0.79; 1.25]
Total	-0.35 [-0.70; -0.01]
Heterogeneity: $\chi^2_2 = 2.84$ ($P = .24$), $I^2 = 30\%$ [0%; 93%]	
Total	-0.31 [-0.53; -0.09]
Heterogeneity: $\chi^2_{13} = 24.02$ ($P = .03$), $I^2 = 46\%$ [0%; 71%]	
Test for overall effect: $z = -2.78$ ($P = .006$)	
Test for subgroup differences: $\chi^2_1 = 0.04$ ($P = .83$)	

