

Source	(95% CI)
Sequencing = FPKM	
Hugo, Melanoma, n = 27	-0.84 [-1.92; 0.24]
Liu, Melanoma, n = 121	-0.22 [-0.61; 0.17]
Nathanson, Melanoma, n = 24	-0.07 [-0.95; 0.81]
Total	-0.26 [-0.60; 0.08]
Heterogeneity: $\chi^2_2 = 1.33$ ($P = .51$), $I^2 = 0\%$ [0%; 90%]	

Sequencing = TPM	
Van_Allen, Melanoma, n = 42	-0.75 [-1.36; -0.14]
Riaz, Melanoma, n = 51	-0.65 [-1.20; -0.10]
Mariathasan, Lymph_node, n = 26	-0.61 [-1.53; 0.31]
Snyder, Ureteral, n = 25	-0.51 [-1.27; 0.25]
Mariathasan, Bladder, n = 194	-0.23 [-0.50; 0.04]
Fumet.2, Lung, n = 43	-0.08 [-0.81; 0.65]
Braun, Kidney, n = 178	-0.03 [-0.34; 0.28]
Mariathasan, Kidney, n = 67	0.04 [-0.45; 0.53]
Mariathasan, Ureteral, n = 26	0.28 [-0.48; 1.04]
Miao.1, Kidney, n = 33	0.40 [-0.31; 1.11]
Total	-0.20 [-0.40; 0.00]
Heterogeneity: $\chi^2_9 = 13.59$ ($P = .14$), $I^2 = 34\%$ [0%; 68%]	
Total	-0.20 [-0.35; -0.05]
Heterogeneity: $\chi^2_{12} = 15.06$ ($P = .24$), $I^2 = 20\%$ [0%; 58%]	
Test for overall effect: $z = -2.70$ ($P = .007$)	
Test for subgroup differences: $\chi^2_1 = 0.10$ ($P = .75$)	

