

Source	(95% CI)
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-0.61 [-1.63; 0.41]
Liu, Melanoma, n = 121	-0.55 [-1.06; -0.04]
Hugo, Melanoma, n = 27	0.46 [-0.70; 1.62]
Total	-0.42 [-0.86; 0.03]
Heterogeneity: $\chi^2_2 = 2.61$ ($P = .27$), $I^2 = 23\%$ [0%; 92%]	

Sequencing = TPM	
Riaz, Melanoma, n = 51	-0.57 [-1.26; 0.12]
Braun, Kidney, n = 178	-0.38 [-0.77; 0.01]
Fumet.2, Lung, n = 43	-0.32 [-1.10; 0.46]
Miao.1, Kidney, n = 33	-0.26 [-1.10; 0.58]
Mariathasan, Lymph_node, n = 26	-0.23 [-1.15; 0.69]
Mariathasan, Bladder, n = 194	-0.19 [-0.54; 0.16]
Van_Allen, Melanoma, n = 42	0.01 [-0.73; 0.75]
Mariathasan, Kidney, n = 67	0.08 [-0.49; 0.65]
Snyder, Ureteral, n = 25	0.33 [-0.65; 1.31]
Mariathasan, Ureteral, n = 26	1.61 [0.47; 2.75]
Total	-0.16 [-0.35; 0.03]
Heterogeneity: $\chi^2_9 = 14$ ($P = .12$), $I^2 = 36\%$ [0%; 69%]	
Total	-0.21 [-0.38; -0.03]
Heterogeneity: $\chi^2_{12} = 17.82$ ($P = .12$), $I^2 = 33\%$ [0%; 65%]	
Test for overall effect: $z = -2.34$ ($P = .02$)	
Test for subgroup differences: $\chi^2_1 = 1.06$ ($P = .30$)	

