

Source	(95% CI)
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-0.62 [-1.50; 0.26]
Liu, Melanoma, n = 121	-0.49 [-0.90; -0.08]
Hugo, Melanoma, n = 27	0.41 [-0.47; 1.29]
Total	-0.30 [-0.83; 0.23]
Heterogeneity: $\chi^2_2 = 3.64$ ($P = .16$), $I^2 = 45\%$ [0%; 84%]	

Sequencing = TPM	
Riaz, Melanoma, n = 51	-0.44 [-1.03; 0.15]
Miao.1, Kidney, n = 33	-0.40 [-1.22; 0.42]
Van_Allen, Melanoma, n = 42	-0.20 [-0.79; 0.39]
Snyder, Ureteral, n = 25	-0.16 [-1.04; 0.72]
Mariathanas, Lymph_node, n = 26	-0.14 [-0.90; 0.62]
Mariathanas, Bladder, n = 194	-0.08 [-0.35; 0.19]
Braun, Kidney, n = 178	-0.04 [-0.37; 0.29]
Fumet.2, Lung, n = 43	0.10 [-0.57; 0.77]
Mariathanas, Kidney, n = 67	0.13 [-0.32; 0.58]
Mariathanas, Ureteral, n = 26	0.88 [0.12; 1.64]
Total	-0.05 [-0.20; 0.11]
Heterogeneity: $\chi^2_9 = 9.29$ ($P = .41$), $I^2 = 3\%$ [0%; 64%]	
Total	-0.10 [-0.26; 0.05]
Heterogeneity: $\chi^2_{12} = 15.81$ ($P = .20$), $I^2 = 24\%$ [0%; 60%]	
Test for overall effect: $z = -1.27$ ($P = .20$)	
Test for subgroup differences: $\chi^2_1 = 0.82$ ($P = .36$)	

