

Source	(95% CI)
Sequencing = FPKM	
Liu, Melanoma, n = 121	-0.42 [-0.93; 0.09]
Nathanson, Melanoma, n = 24	-0.20 [-1.18; 0.78]
Hugo, Melanoma, n = 27	0.10 [-1.04; 1.24]
Total	-0.31 [-0.73; 0.11]
Heterogeneity: $\chi^2_2 = 0.73$ ($P = .70$), $I^2 = 0\%$ [0%; 90%]	

Sequencing = TPM	
Riaz, Melanoma, n = 51	-0.35 [-1.04; 0.34]
Snyder, Ureteral, n = 25	-0.26 [-1.22; 0.70]
Van_Allen, Melanoma, n = 42	-0.14 [-0.88; 0.60]
Miao.1, Kidney, n = 33	-0.02 [-0.88; 0.84]
Mariathasan, Bladder, n = 194	0.04 [-0.31; 0.39]
Braun, Kidney, n = 178	0.10 [-0.29; 0.49]
Mariathasan, Lymph_node, n = 26	0.19 [-0.75; 1.13]
Fumet.2, Lung, n = 43	0.31 [-0.47; 1.09]
Mariathasan, Kidney, n = 67	0.35 [-0.22; 0.92]
Mariathasan, Ureteral, n = 26	0.59 [-0.37; 1.55]
Total	0.08 [-0.11; 0.27]
Heterogeneity: $\chi^2_9 = 4.77$ ($P = .85$), $I^2 = 0\%$ [0%; 62%]	
Total	0.01 [-0.16; 0.18]
Heterogeneity: $\chi^2_{12} = 8.17$ ($P = .77$), $I^2 = 0\%$ [0%; 57%]	
Test for overall effect: $z = 0.12$ ($P = .90$)	
Test for subgroup differences: $\chi^2_1 = 2.67$ ($P = .10$)	

