

Source	(95% CI)
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-1.00 [-2.04; 0.04]
Liu, Melanoma, n = 121	-0.37 [-0.88; 0.14]
Hugo, Melanoma, n = 27	0.53 [-0.63; 1.69]
Total	-0.33 [-0.98; 0.31]
Heterogeneity: $\chi^2_2 = 3.73$ ($P = .15$), $I^2 = 46\%$ [0%; 84%]	

Sequencing = TPM	
Mariathasan, Lymph_node, n = 26	-0.96 [-1.92; 0.00]
Hwang, Lung, n = 21	-0.70 [-1.80; 0.40]
Mariathasan, Bladder, n = 194	-0.37 [-0.72; -0.02]
Van_Allen, Melanoma, n = 42	-0.35 [-1.09; 0.39]
Riaz, Melanoma, n = 51	-0.32 [-1.01; 0.37]
Miao.1, Kidney, n = 33	-0.30 [-1.16; 0.56]
Mariathasan, Kidney, n = 67	-0.19 [-0.76; 0.38]
Fumet.2, Lung, n = 43	-0.13 [-0.91; 0.65]
Mariathasan, Ureteral, n = 26	-0.08 [-1.02; 0.86]
Snyder, Ureteral, n = 25	-0.04 [-1.00; 0.92]
Braun, Kidney, n = 178	0.26 [-0.13; 0.65]
Total	-0.21 [-0.44; 0.01]
Heterogeneity: $\chi^2_{10} = 9.91$ ($P = .45$), $I^2 = 0\%$ [0%; 60%]	
Total	-0.24 [-0.44; -0.03]
Heterogeneity: $\chi^2_{13} = 14.10$ ($P = .37$), $I^2 = 8\%$ [0%; 45%]	
Test for overall effect: $z = -2.29$ ($P = .02$)	
Test for subgroup differences: $\chi^2_1 = 0.12$ ($P = .73$)	

