

Source	(95% CI)
Sequencing = FPKM	
Hugo, Melanoma, n = 27	-0.50 [-1.64; 0.64]
Nathanson, Melanoma, n = 24	-0.45 [-1.35; 0.45]
Liu, Melanoma, n = 121	-0.08 [-0.47; 0.31]
Total	-0.17 [-0.51; 0.17]
Heterogeneity: $\chi^2_2 = 0.9$ ($P = .64$), $I^2 = 0\%$ [0%; 90%]	

Sequencing = TPM	
Van_Allen, Melanoma, n = 42	-0.34 [-0.93; 0.25]
Snyder, Ureteral, n = 25	-0.21 [-0.97; 0.55]
Mariathasan, Bladder, n = 194	-0.06 [-0.33; 0.21]
Mariathasan, Kidney, n = 67	-0.03 [-0.48; 0.42]
Fumet.2, Lung, n = 43	0.06 [-0.61; 0.73]
Mariathasan, Lymph_node, n = 26	0.06 [-0.78; 0.90]
Mariathasan, Ureteral, n = 26	0.13 [-0.63; 0.89]
Braun, Kidney, n = 178	0.24 [-0.09; 0.57]
Total	0.01 [-0.16; 0.17]
Heterogeneity: $\chi^2_7 = 3.92$ ($P = .79$), $I^2 = 0\%$ [0%; 68%]	
Total	-0.03 [-0.17; 0.12]
Heterogeneity: $\chi^2_{10} = 5.68$ ($P = .84$), $I^2 = 0\%$ [0%; 60%]	
Test for overall effect: $z = -0.33$ ($P = .74$)	
Test for subgroup differences: $\chi^2_1 = 0.86$ ($P = .35$)	

