

Source	(95% CI)
<b>Sequencing = TPM</b>	
Van_Allen, Melanoma, n = 42	-1.15 [-1.76; -0.54]
Snyder, Ureteral, n = 25	-1.01 [-1.97; -0.05]
Mariathanan, Lymph_node, n = 26	-0.85 [-1.69; -0.01]
Mariathanan, Bladder, n = 194	-0.65 [-0.92; -0.38]
Fumet.2, Lung, n = 43	-0.39 [-1.02; 0.24]
Riaz, Melanoma, n = 51	-0.38 [-0.95; 0.19]
Mariathanan, Kidney, n = 67	-0.35 [-0.78; 0.08]
Miao.1, Kidney, n = 33	-0.24 [-0.95; 0.47]
Mariathanan, Ureteral, n = 26	-0.03 [-0.89; 0.83]
Braun, Kidney, n = 178	0.24 [-0.09; 0.57]
Total	-0.44 [-0.72; -0.16]
Heterogeneity: $\chi^2_9 = 26.81$ ( $P = .002$ ), $I^2 = 66\%$ [34%; 83%]	

<b>Sequencing = FPKM</b>	
Nathanson, Melanoma, n = 24	-0.81 [-1.65; 0.03]
Liu, Melanoma, n = 121	-0.68 [-1.05; -0.31]
Hugo, Melanoma, n = 27	-0.44 [-1.58; 0.70]
Total	-0.68 [-1.01; -0.35]
Heterogeneity: $\chi^2_2 = 0.26$ ( $P = .88$ ), $I^2 = 0\%$ [0%; 90%]	
Total	-0.48 [-0.72; -0.24]
Heterogeneity: $\chi^2_{12} = 29.50$ ( $P = .003$ ), $I^2 = 59\%$ [25%; 78%]	
Test for overall effect: $z = -3.98$ ( $P < .001$ )	
Test for subgroup differences: $\chi^2_1 = 1.19$ ( $P = .27$ )	

