

Source	(95% CI)
<b>Sequencing = TPM</b>	
Van_Allen, Melanoma, n = 42	-1.21 [-1.92; -0.50]
Snyder, Ureteral, n = 25	-0.87 [-1.77; 0.03]
Riaz, Melanoma, n = 51	-0.80 [-1.47; -0.13]
Mariathanas, Lymph_node, n = 26	-0.70 [-1.46; 0.06]
Mariathanas, Bladder, n = 194	-0.57 [-0.84; -0.30]
Fumet.2, Lung, n = 43	-0.45 [-1.08; 0.18]
Mariathanas, Kidney, n = 67	-0.31 [-0.82; 0.20]
Miao.1, Kidney, n = 33	-0.08 [-0.86; 0.70]
Braun, Kidney, n = 178	0.10 [-0.23; 0.43]
Mariathanas, Ureteral, n = 26	0.64 [-0.16; 1.44]
Total	-0.41 [-0.71; -0.11]
Heterogeneity: $\chi^2_9 = 25.33$ ( $P = .003$ ), $I^2 = 64\%$ [30%; 82%]	

<b>Sequencing = FPKM</b>	
Nathanson, Melanoma, n = 24	-1.07 [-1.99; -0.15]
Liu, Melanoma, n = 121	-0.63 [-1.04; -0.22]
Hugo, Melanoma, n = 27	0.10 [-0.98; 1.18]
Total	-0.62 [-0.97; -0.26]
Heterogeneity: $\chi^2_2 = 2.63$ ( $P = .27$ ), $I^2 = 24\%$ [0%; 92%]	
Total	-0.44 [-0.70; -0.19]
Heterogeneity: $\chi^2_{12} = 29.44$ ( $P = .003$ ), $I^2 = 59\%$ [25%; 78%]	
Test for overall effect: $z = -3.39$ ( $P < .001$ )	
Test for subgroup differences: $\chi^2_1 = 0.76$ ( $P = .38$ )	

