

Source	(95% CI)
<b>Sequencing = TPM</b>	
Miao.1, Kidney, n = 33	-0.79 [-1.71; 0.13]
Riaz, Melanoma, n = 51	-0.43 [-1.12; 0.26]
Van_Allen, Melanoma, n = 42	-0.33 [-1.07; 0.41]
Mariathasan, Bladder, n = 194	-0.23 [-0.58; 0.12]
Fumet.2, Lung, n = 43	-0.16 [-0.94; 0.62]
Snyder, Ureteral, n = 25	-0.16 [-1.12; 0.80]
Braun, Kidney, n = 178	-0.07 [-0.46; 0.32]
Mariathasan, Kidney, n = 67	0.06 [-0.51; 0.63]
Mariathasan, Lymph_node, n = 26	0.06 [-0.88; 1.00]
Mariathasan, Ureteral, n = 26	0.91 [-0.05; 1.87]
Total	-0.14 [-0.33; 0.05]
Heterogeneity: $\chi^2_9 = 8.47$ ( $P = .49$ ), $I^2 = 0\%$ [0%; 62%]	

<b>Sequencing = FPKM</b>	
Nathanson, Melanoma, n = 24	-0.73 [-1.73; 0.27]
Liu, Melanoma, n = 121	-0.48 [-0.99; 0.03]
Hugo, Melanoma, n = 27	0.72 [-0.44; 1.88]
Total	-0.27 [-0.97; 0.44]
Heterogeneity: $\chi^2_2 = 4.09$ ( $P = .13$ ), $I^2 = 51\%$ [0%; 86%]	
Total	-0.18 [-0.35; -0.01]
Heterogeneity: $\chi^2_{12} = 13.44$ ( $P = .34$ ), $I^2 = 11\%$ [0%; 50%]	
Test for overall effect: $z = -2.03$ ( $P = .04$ )	
Test for subgroup differences: $\chi^2_1 = 0.11$ ( $P = .74$ )	

