

Source	(95% CI)
<b>Sequencing = TPM</b>	
Van_Allen, Melanoma, n = 42	-1.07 [-1.93; -0.21]
Snyder, Ureteral, n = 25	-0.59 [-1.59; 0.41]
Mariathasan, Lymph_node, n = 26	-0.45 [-1.25; 0.35]
Fumet.2, Lung, n = 43	-0.35 [-1.09; 0.39]
Riaz, Melanoma, n = 51	-0.32 [-0.93; 0.29]
Mariathasan, Bladder, n = 194	-0.30 [-0.61; 0.01]
Hwang, Lung, n = 21	-0.28 [-1.32; 0.76]
Mariathasan, Kidney, n = 67	-0.13 [-0.68; 0.42]
Miao.1, Kidney, n = 33	-0.06 [-0.86; 0.74]
Braun, Kidney, n = 178	0.08 [-0.33; 0.49]
Mariathasan, Ureteral, n = 26	0.40 [-0.44; 1.24]
Total	-0.22 [-0.40; -0.04]
Heterogeneity: $\chi^2_{10} = 9.43$ ( $P = .49$ ), $I^2 = 0\%$ [0%; 60%]	

<b>Sequencing = FPKM</b>	
Nathanson, Melanoma, n = 24	-0.78 [-1.56; 0.00]
Liu, Melanoma, n = 121	-0.25 [-0.72; 0.22]
Hugo, Melanoma, n = 27	0.29 [-0.81; 1.39]
Total	-0.31 [-0.69; 0.07]
Heterogeneity: $\chi^2_2 = 2.59$ ( $P = .27$ ), $I^2 = 23\%$ [0%; 92%]	
Total	-0.24 [-0.40; -0.08]
Heterogeneity: $\chi^2_{13} = 12.19$ ( $P = .51$ ), $I^2 = 0\%$ [0%; 55%]	
Test for overall effect: $z = -2.89$ ( $P = .004$ )	
Test for subgroup differences: $\chi^2_1 = 0.17$ ( $P = .68$ )	

