

Source	(95% CI)
<b>Sequencing = TPM</b>	
Mariathasan, Ureteral, n = 26	-0.35 [-1.29; 0.59]
Mariathasan, Kidney, n = 67	-0.21 [-0.78; 0.36]
Van_Allen, Melanoma, n = 42	-0.17 [-0.91; 0.57]
Fumet.2, Lung, n = 43	-0.04 [-0.82; 0.74]
Hwang, Lung, n = 21	-0.04 [-1.10; 1.02]
Braun, Kidney, n = 178	0.07 [-0.32; 0.46]
Mariathasan, Bladder, n = 194	0.20 [-0.15; 0.55]
Riaz, Melanoma, n = 51	0.21 [-0.46; 0.88]
Snyder, Ureteral, n = 25	0.28 [-0.68; 1.24]
Mariathasan, Lymph_node, n = 26	0.47 [-0.47; 1.41]
Miao.1, Kidney, n = 33	0.99 [ 0.05; 1.93]
Total	0.11 [-0.08; 0.29]
Heterogeneity: $\chi^2_{10} = 7.32$ ( $P = .70$ ), $I^2 = 0\%$ [0%; 60%]	

<b>Sequencing = FPKM</b>	
Liu, Melanoma, n = 121	0.13 [-0.38; 0.64]
Hugo, Melanoma, n = 27	0.24 [-0.92; 1.40]
Nathanson, Melanoma, n = 24	1.13 [ 0.09; 2.17]
Total	0.39 [-0.20; 0.98]
Heterogeneity: $\chi^2_2 = 2.89$ ( $P = .24$ ), $I^2 = 31\%$ [0%; 93%]	
Total	0.14 [-0.03; 0.31]
Heterogeneity: $\chi^2_{13} = 10.96$ ( $P = .61$ ), $I^2 = 0\%$ [0%; 55%]	
Test for overall effect: $z = 1.60$ ( $P = .11$ )	
Test for subgroup differences: $\chi^2_1 = 0.83$ ( $P = .36$ )	

