

Source	(95% CI)
<b>Sequencing = FPKM</b>	
Nathanson, Melanoma, n = 24	-0.78 [-1.64; 0.08]
Liu, Melanoma, n = 121	0.09 [-0.30; 0.48]
Hugo, Melanoma, n = 27	1.08 [ 0.02; 2.14]
Total	0.09 [-0.85; 1.04]
Heterogeneity: $\chi^2_2 = 7.23$ ( $P = .03$ ), $I^2 = 72\%$ [7%; 92%]	

<b>Sequencing = TPM</b>	
Mariathasan, Lymph_node, n = 26	-0.21 [-1.05; 0.63]
Van_Allen, Melanoma, n = 42	-0.16 [-0.71; 0.39]
Mariathasan, Kidney, n = 67	-0.12 [-0.61; 0.37]
Miao.1, Kidney, n = 33	0.03 [-0.62; 0.68]
Riaz, Melanoma, n = 51	0.05 [-0.52; 0.62]
Mariathasan, Bladder, n = 194	0.06 [-0.23; 0.35]
Braun, Kidney, n = 178	0.24 [-0.07; 0.55]
Fumet.2, Lung, n = 43	0.32 [-0.29; 0.93]
Mariathasan, Ureteral, n = 26	0.32 [-0.54; 1.18]
Snyder, Ureteral, n = 25	0.90 [-0.06; 1.86]
Total	0.10 [-0.05; 0.26]
Heterogeneity: $\chi^2_9 = 6.48$ ( $P = .69$ ), $I^2 = 0\%$ [0%; 62%]	
Total	0.10 [-0.05; 0.24]
Heterogeneity: $\chi^2_{12} = 13.78$ ( $P = .31$ ), $I^2 = 13\%$ [0%; 52%]	
Test for overall effect: $z = 1.33$ ( $P = .18$ )	
Test for subgroup differences: $\chi^2_1 = 0.00$ ( $P = .98$ )	

