

Source	(95% CI)
<b>Sequencing = TPM</b>	
Miao.1, Kidney, n = 33	-0.41 [-1.23; 0.41]
Van_Allen, Melanoma, n = 42	-0.35 [-0.96; 0.26]
Riaz, Melanoma, n = 51	-0.33 [-0.94; 0.28]
Mariathasan, Bladder, n = 194	-0.29 [-0.58; 0.00]
Fumet.2, Lung, n = 43	-0.25 [-0.84; 0.34]
Braun, Kidney, n = 178	-0.08 [-0.39; 0.23]
Mariathasan, Lymph_node, n = 26	-0.05 [-0.76; 0.66]
Mariathasan, Kidney, n = 67	-0.02 [-0.53; 0.49]
Snyder, Ureteral, n = 25	0.15 [-0.71; 1.01]
Mariathasan, Ureteral, n = 26	1.70 [ 0.68; 2.72]
Total	-0.14 [-0.30; 0.02]
Heterogeneity: $\chi^2_9 = 15.75$ ( $P = .07$ ), $I^2 = 43\%$ [0%; 73%]	

<b>Sequencing = FPKM</b>	
Nathanson, Melanoma, n = 24	-0.37 [-1.11; 0.37]
Liu, Melanoma, n = 121	-0.19 [-0.58; 0.20]
Hugo, Melanoma, n = 27	0.55 [-0.43; 1.53]
Total	-0.14 [-0.47; 0.18]
Heterogeneity: $\chi^2_2 = 2.33$ ( $P = .31$ ), $I^2 = 14\%$ [0%; 91%]	
Total	-0.14 [-0.29; 0.00]
Heterogeneity: $\chi^2_{12} = 18.09$ ( $P = .11$ ), $I^2 = 34\%$ [0%; 66%]	
Test for overall effect: $z = -1.96$ ( $P = .05$ )	
Test for subgroup differences: $\chi^2_1 = 0.00$ ( $P > .99$ )	

