

Source	(95% CI)
<b>Sequencing = FPKM</b>	
Hugo, Melanoma, n = 27	-0.87 [-2.09; 0.35]
Liu, Melanoma, n = 121	-0.79 [-1.32; -0.26]
Nathanson, Melanoma, n = 24	-0.46 [-1.46; 0.54]
Total	-0.74 [-1.17; -0.30]
Heterogeneity: $\chi^2_2 = 0.38$ ( $P = .83$ ), $I^2 = 0\%$ [0%; 90%]	

<b>Sequencing = TPM</b>	
Mariathasan, Lymph_node, n = 26	-0.71 [-1.67; 0.25]
Snyder, Ureteral, n = 25	-0.65 [-1.63; 0.33]
Van_Allen, Melanoma, n = 42	-0.50 [-1.24; 0.24]
Miao.1, Kidney, n = 33	-0.38 [-1.26; 0.50]
Riaz, Melanoma, n = 51	-0.28 [-0.97; 0.41]
Mariathasan, Bladder, n = 194	-0.23 [-0.58; 0.12]
Fumet.2, Lung, n = 43	-0.18 [-0.96; 0.60]
Mariathasan, Ureteral, n = 26	-0.07 [-1.01; 0.87]
Mariathasan, Kidney, n = 67	0.32 [-0.25; 0.89]
Braun, Kidney, n = 178	0.50 [0.11; 0.89]
Total	-0.12 [-0.40; 0.16]
Heterogeneity: $\chi^2_9 = 15.92$ ( $P = .07$ ), $I^2 = 43\%$ [0%; 73%]	
Total	-0.25 [-0.52; 0.02]
Heterogeneity: $\chi^2_{12} = 24.30$ ( $P = .02$ ), $I^2 = 51\%$ [7%; 74%]	
Test for overall effect: $z = -1.79$ ( $P = .07$ )	
Test for subgroup differences: $\chi^2_1 = 5.38$ ( $P = .02$ )	

