

Source	(95% CI)
<b>Sequencing = TPM</b>	
Van_Allen, Melanoma, n = 42	-0.85 [-1.50; -0.20]
Snyder, Ureteral, n = 25	-0.53 [-1.35; 0.29]
Riaz, Melanoma, n = 51	-0.42 [-1.03; 0.19]
Fumet.2, Lung, n = 43	-0.33 [-0.94; 0.28]
Mariathanas, Bladder, n = 194	-0.32 [-0.59; -0.05]
Mariathanas, Lymph_node, n = 26	-0.26 [-1.02; 0.50]
Mariathanas, Kidney, n = 67	-0.18 [-0.69; 0.33]
Hwang, Lung, n = 21	-0.09 [-0.85; 0.67]
Miao.1, Kidney, n = 33	-0.07 [-0.76; 0.62]
Braun, Kidney, n = 178	0.05 [-0.28; 0.38]
Mariathanas, Ureteral, n = 26	0.54 [-0.30; 1.38]
Total	-0.22 [-0.39; -0.05]
Heterogeneity: $\chi^2_{10} = 11.22$ ( $P = .34$ ), $I^2 = 11\%$ [0%; 51%]	

<b>Sequencing = FPKM</b>	
Nathanson, Melanoma, n = 24	-0.56 [-1.27; 0.15]
Liu, Melanoma, n = 121	-0.24 [-0.65; 0.17]
Hugo, Melanoma, n = 27	0.14 [-0.90; 1.18]
Total	-0.27 [-0.61; 0.06]
Heterogeneity: $\chi^2_2 = 1.27$ ( $P = .53$ ), $I^2 = 0\%$ [0%; 90%]	
Total	-0.23 [-0.37; -0.09]
Heterogeneity: $\chi^2_{13} = 12.56$ ( $P = .48$ ), $I^2 = 0\%$ [0%; 55%]	
Test for overall effect: $z = -3.12$ ( $P = .002$ )	
Test for subgroup differences: $\chi^2_1 = 0.07$ ( $P = .79$ )	

