

Source	(95% CI)
Sequencing = TPM	
Mariathanas, Ureteral, n = 26	-0.28 [-1.16; 0.60]
Miao.1, Kidney, n = 33	-0.26 [-1.42; 0.90]
Mariathanas, Lymph_node, n = 26	-0.18 [-1.06; 0.70]
Braun, Kidney, n = 178	0.01 [-0.38; 0.40]
Mariathanas, Bladder, n = 194	0.06 [-0.25; 0.37]
Mariathanas, Kidney, n = 67	0.06 [-0.49; 0.61]
Van_Allen, Melanoma, n = 42	0.06 [-1.08; 1.20]
Riaz, Melanoma, n = 51	0.39 [-0.35; 1.13]
Snyder, Ureteral, n = 25	0.41 [-0.47; 1.29]
Fumet.2, Lung, n = 43	0.78 [-0.22; 1.78]
Total	0.08 [-0.11; 0.26]
Heterogeneity: $\chi^2_9 = 4.54$ ($P = .87$), $I^2 = 0\%$ [0%; 62%]	

Sequencing = FPKM	
Liu, Melanoma, n = 121	0.19 [-0.55; 0.93]
Nathanson, Melanoma, n = 24	0.37 [-0.81; 1.55]
Hugo, Melanoma, n = 27	0.57 [-1.02; 2.16]
Total	0.29 [-0.30; 0.87]
Heterogeneity: $\chi^2_2 = 0.21$ ($P = .90$), $I^2 = 0\%$ [0%; 90%]	
Total	0.10 [-0.08; 0.28]
Heterogeneity: $\chi^2_{12} = 5.19$ ($P = .95$), $I^2 = 0\%$ [0%; 57%]	
Test for overall effect: $z = 1.05$ ($P = .29$)	
Test for subgroup differences: $\chi^2_1 = 0.45$ ($P = .50$)	

