

Source	(95% CI)
Sequencing = TPM	
Snyder, Ureteral, n = 25	-0.63 [-1.47; 0.21]
Riaz, Melanoma, n = 51	-0.31 [-0.90; 0.28]
Hwang, Lung, n = 21	-0.20 [-1.34; 0.94]
Braun, Kidney, n = 178	-0.13 [-0.46; 0.20]
Mariathasan, Lymph_node, n = 26	-0.06 [-0.90; 0.78]
Van_Allen, Melanoma, n = 42	-0.02 [-0.61; 0.57]
Mariathasan, Bladder, n = 194	0.21 [-0.08; 0.50]
Mariathasan, Ureteral, n = 26	0.21 [-0.57; 0.99]
Mariathasan, Kidney, n = 67	0.30 [-0.13; 0.73]
Miao.1, Kidney, n = 33	0.31 [-0.45; 1.07]
Fumet.2, Lung, n = 43	0.60 [-0.09; 1.29]
Total	0.07 [-0.11; 0.24]
Heterogeneity: $\chi^2_{10} = 10.79$ ($P = .37$), $I^2 = 7\%$ [0%; 63%]	

Sequencing = FPKM	
Hugo, Melanoma, n = 27	-0.39 [-1.33; 0.55]
Liu, Melanoma, n = 121	-0.09 [-0.48; 0.30]
Nathanson, Melanoma, n = 24	0.47 [-0.47; 1.41]
Total	-0.06 [-0.39; 0.28]
Heterogeneity: $\chi^2_2 = 1.71$ ($P = .42$), $I^2 = 0\%$ [0%; 90%]	
Total	0.05 [-0.10; 0.20]
Heterogeneity: $\chi^2_{13} = 12.97$ ($P = .45$), $I^2 = 0\%$ [0%; 55%]	
Test for overall effect: $z = 0.61$ ($P = .54$)	
Test for subgroup differences: $\chi^2_1 = 0.41$ ($P = .52$)	

