

Source	(95% CI)
Sequencing = TPM	
Braun, Kidney, n = 178	-0.42 [-0.81; -0.03]
Mariathasan, Ureteral, n = 26	-0.17 [-1.11; 0.77]
Mariathasan, Kidney, n = 67	-0.16 [-0.73; 0.41]
Miao.1, Kidney, n = 33	0.14 [-0.72; 1.00]
Snyder, Ureteral, n = 25	0.30 [-0.66; 1.26]
Riaz, Melanoma, n = 51	0.32 [-0.35; 0.99]
Mariathasan, Bladder, n = 194	0.33 [-0.02; 0.68]
Fumet.2, Lung, n = 43	0.47 [-0.33; 1.27]
Mariathasan, Lymph_node, n = 26	0.78 [-0.18; 1.74]
Van_Allen, Melanoma, n = 42	1.02 [0.24; 1.80]
Total	0.20 [-0.09; 0.49]
Heterogeneity: $\chi^2_9 = 18.02$ ($P = .03$), $I^2 = 50\%$ [0%; 76%]	

Sequencing = FPKM	
Liu, Melanoma, n = 121	0.32 [-0.19; 0.83]
Nathanson, Melanoma, n = 24	0.50 [-0.50; 1.50]
Hugo, Melanoma, n = 27	1.00 [-0.23; 2.23]
Total	0.43 [0.01; 0.86]
Heterogeneity: $\chi^2_2 = 1.02$ ($P = .60$), $I^2 = 0\%$ [0%; 90%]	
Total	0.25 [0.00; 0.50]
Heterogeneity: $\chi^2_{12} = 20.62$ ($P = .06$), $I^2 = 42\%$ [0%; 70%]	
Test for overall effect: $z = 1.95$ ($P = .05$)	
Test for subgroup differences: $\chi^2_1 = 0.78$ ($P = .38$)	

