

Source	(95% CI)
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-0.57 [-1.57; 0.43]
Liu, Melanoma, n = 121	0.25 [-0.26; 0.76]
Hugo, Melanoma, n = 27	1.09 [-0.13; 2.31]
Total	0.21 [-0.55; 0.97]
Heterogeneity: $\chi^2_2 = 4.38$ ($P = .11$), $I^2 = 54\%$ [0%; 87%]	

Sequencing = TPM	
Mariathasan, Bladder, n = 194	-0.14 [-0.49; 0.21]
Fumet.2, Lung, n = 43	-0.09 [-0.87; 0.69]
Miao.1, Kidney, n = 33	-0.03 [-0.89; 0.83]
Van_Allen, Melanoma, n = 42	0.15 [-0.59; 0.89]
Braun, Kidney, n = 178	0.17 [-0.22; 0.56]
Mariathasan, Kidney, n = 67	0.17 [-0.40; 0.74]
Mariathasan, Ureteral, n = 26	0.29 [-0.65; 1.23]
Riaz, Melanoma, n = 51	0.32 [-0.37; 1.01]
Mariathasan, Lymph_node, n = 26	0.35 [-0.59; 1.29]
Snyder, Ureteral, n = 25	1.67 [0.49; 2.85]
Total	0.12 [-0.07; 0.31]
Heterogeneity: $\chi^2_9 = 9.93$ ($P = .36$), $I^2 = 9\%$ [0%; 66%]	
Total	0.13 [-0.04; 0.31]
Heterogeneity: $\chi^2_{12} = 14.44$ ($P = .27$), $I^2 = 17\%$ [0%; 56%]	
Test for overall effect: $z = 1.48$ ($P = .14$)	
Test for subgroup differences: $\chi^2_1 = 0.05$ ($P = .82$)	

