

Source	(95% CI)
Sequencing = TPM	
Van_Allen, Melanoma, n = 42	-0.89 [-1.52; -0.26]
Hwang, Lung, n = 21	-0.58 [-1.56; 0.40]
Mariathasan, Lymph_node, n = 26	-0.57 [-1.35; 0.21]
Riaz, Melanoma, n = 51	-0.48 [-1.03; 0.07]
Mariathasan, Bladder, n = 194	-0.37 [-0.64; -0.10]
Fumet.2, Lung, n = 43	-0.33 [-0.92; 0.26]
Snyder, Ureteral, n = 25	-0.18 [-1.08; 0.72]
Mariathasan, Kidney, n = 67	0.02 [-0.47; 0.51]
Miao.1, Kidney, n = 33	0.14 [-0.57; 0.85]
Braun, Kidney, n = 178	0.20 [-0.11; 0.51]
Mariathasan, Ureteral, n = 26	0.42 [-0.46; 1.30]
Total	-0.22 [-0.45; 0.01]
Heterogeneity: $\chi^2_{10} = 18.56$ ($P = .05$), $I^2 = 46\%$ [0%; 73%]	

Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-0.70 [-1.52; 0.12]
Liu, Melanoma, n = 121	-0.33 [-0.74; 0.08]
Hugo, Melanoma, n = 27	0.25 [-0.79; 1.29]
Total	-0.33 [-0.68; 0.02]
Heterogeneity: $\chi^2_2 = 1.97$ ($P = .37$), $I^2 = 0\%$ [0%; 90%]	
Total	-0.24 [-0.43; -0.04]
Heterogeneity: $\chi^2_{13} = 21.02$ ($P = .07$), $I^2 = 38\%$ [0%; 67%]	
Test for overall effect: $z = -2.36$ ($P = .02$)	
Test for subgroup differences: $\chi^2_1 = 0.27$ ($P = .60$)	

