

Source	(95% CI)
Sequencing = TPM	
Van_Allen, Melanoma, n = 42	-1.08 [-1.79; -0.37]
Riaz, Melanoma, n = 51	-0.72 [-1.39; -0.05]
Mariathasan, Lymph_node, n = 26	-0.66 [-1.48; 0.16]
Hwang, Lung, n = 21	-0.46 [-1.36; 0.44]
Mariathasan, Bladder, n = 194	-0.39 [-0.66; -0.12]
Snyder, Ureteral, n = 25	-0.30 [-1.14; 0.54]
Fumet.2, Lung, n = 43	-0.28 [-0.91; 0.35]
Miao.1, Kidney, n = 33	-0.05 [-0.79; 0.69]
Mariathasan, Kidney, n = 67	-0.03 [-0.54; 0.48]
Braun, Kidney, n = 178	0.14 [-0.19; 0.47]
Mariathasan, Ureteral, n = 26	0.40 [-0.42; 1.22]
Total	-0.28 [-0.52; -0.04]
Heterogeneity: $\chi^2_{10} = 18.06$ ($P = .05$), $I^2 = 45\%$ [0%; 73%]	

Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-0.82 [-1.62; -0.02]
Liu, Melanoma, n = 121	-0.31 [-0.72; 0.10]
Hugo, Melanoma, n = 27	0.20 [-0.80; 1.20]
Total	-0.34 [-0.69; 0.00]
Heterogeneity: $\chi^2_2 = 2.51$ ($P = .28$), $I^2 = 20\%$ [0%; 92%]	
Total	-0.29 [-0.49; -0.09]
Heterogeneity: $\chi^2_{13} = 20.82$ ($P = .08$), $I^2 = 38\%$ [0%; 67%]	
Test for overall effect: $z = -2.81$ ($P = .005$)	
Test for subgroup differences: $\chi^2_1 = 0.09$ ($P = .76$)	

