

Source	(95% CI)
Sequencing = TPM	
Mariathasan, Ureteral, n = 26	-0.28 [-1.06; 0.50]
Hwang, Lung, n = 21	-0.12 [-0.92; 0.68]
Fumet.2, Lung, n = 43	-0.10 [-0.75; 0.55]
Braun, Kidney, n = 178	-0.09 [-0.40; 0.22]
Mariathasan, Kidney, n = 67	-0.01 [-0.50; 0.48]
Riaz, Melanoma, n = 51	0.09 [-0.48; 0.66]
Snyder, Ureteral, n = 25	0.14 [-0.68; 0.96]
Van_Allen, Melanoma, n = 42	0.22 [-0.45; 0.89]
Mariathasan, Bladder, n = 194	0.25 [-0.02; 0.52]
Mariathasan, Lymph_node, n = 26	0.49 [-0.27; 1.25]
Miao.1, Kidney, n = 33	1.03 [0.03; 2.03]
Total	0.10 [-0.06; 0.26]
Heterogeneity: $\chi^2_{10} = 8.77$ ($P = .55$), $I^2 = 0\%$ [0%; 60%]	

Sequencing = FPKM	
Liu, Melanoma, n = 121	0.12 [-0.27; 0.51]
Hugo, Melanoma, n = 27	0.33 [-0.69; 1.35]
Nathanson, Melanoma, n = 24	1.35 [0.43; 2.27]
Total	0.53 [-0.21; 1.27]
Heterogeneity: $\chi^2_2 = 5.8$ ($P = .06$), $I^2 = 66\%$ [0%; 90%]	
Total	0.14 [-0.01; 0.28]
Heterogeneity: $\chi^2_{13} = 15.78$ ($P = .26$), $I^2 = 18\%$ [0%; 55%]	
Test for overall effect: $z = 1.88$ ($P = .06$)	
Test for subgroup differences: $\chi^2_1 = 1.22$ ($P = .27$)	

