

Source	(95% CI)
Sequencing = FPKM	
Liu, Melanoma, n = 121	-0.52 [-1.25; 0.21]
Nathanson, Melanoma, n = 24	-0.20 [-1.69; 1.29]
Hugo, Melanoma, n = 27	1.12 [-0.39; 2.63]
Total	-0.03 [-0.97; 0.91]
Heterogeneity: $\chi^2_2 = 3.69$ ($P = .16$), $I^2 = 46\%$ [0%; 84%]	

Sequencing = TPM	
Miao.1, Kidney, n = 33	-0.49 [-1.61; 0.63]
Mariathasan, Kidney, n = 67	-0.33 [-1.04; 0.38]
Riaz, Melanoma, n = 51	-0.10 [-0.92; 0.72]
Braun, Kidney, n = 178	0.03 [-0.46; 0.52]
Mariathasan, Bladder, n = 194	0.03 [-0.34; 0.40]
Van_Allen, Melanoma, n = 42	0.15 [-0.99; 1.29]
Fumet.2, Lung, n = 43	0.28 [-0.72; 1.28]
Mariathasan, Lymph_node, n = 26	0.29 [-0.85; 1.43]
Snyder, Ureteral, n = 25	0.52 [-0.40; 1.44]
Mariathasan, Ureteral, n = 26	1.21 [-0.04; 2.46]
Total	0.06 [-0.17; 0.28]
Heterogeneity: $\chi^2_9 = 6.84$ ($P = .65$), $I^2 = 0\%$ [0%; 62%]	
Total	0.02 [-0.19; 0.23]
Heterogeneity: $\chi^2_{12} = 11.20$ ($P = .51$), $I^2 = 0\%$ [0%; 57%]	
Test for overall effect: $z = 0.23$ ($P = .82$)	
Test for subgroup differences: $\chi^2_1 = 0.03$ ($P = .86$)	

