Source	(95% CI)
Sequencing = FPKM	
Liu, Melanoma, n = 121	−0.26 [−0.69; 0.17]
Nathanson, Melanoma, n = 24	0.19 [−0.67; 1.05]
Hugo, Melanoma, n = 27	0.51 [−0.51; 1.53]
Total	−0.02 [−0.48; 0.44]

Heterogeneity: $\chi^2_2 = 2.33$ ($P = .31$), $I^2 = 14\%$ [0%; 91%]

Sequencing = TPM	
Mariathasan, Kidney, n = 67	−0.26 [−0.71; 0.19]
Riaz, Melanoma, n = 51	−0.03 [−0.60; 0.54]
Miao.1, Kidney, n = 33	0.01 [−0.79; 0.81]
Mariathasan, Bladder, n = 194	0.06 [−0.21; 0.33]
Braun, Kidney, n = 178	0.21 [−0.10; 0.52]
Mariathasan, Ureteral, n = 26	0.27 [−0.61; 1.15]
Mariathasan, Lymph_node, n = 26	0.38 [−0.35; 1.11]
Fumet.2, Lung, n = 43	0.43 [−0.28; 1.14]
Van_Allen, Melanoma, n = 42	0.43 [−0.16; 1.02]
Snyder, Ureteral, n = 25	0.69 [−0.15; 1.53]
Total	0.13 [−0.02; 0.29]

Heterogeneity: $\chi^2_9 = 7.71$ ($P = .56$), $I^2 = 0\%$ [0%; 62%]

Total	0.10 [−0.04; 0.24]

Heterogeneity: $\chi^2_{12} = 11.24$ ($P = .51$), $I^2 = 0\%$ [0%; 57%]

Test for overall effect: $z = 1.40$ ($P = .16$)

Test for subgroup differences: $\chi^2_1 = 0.39$ ($P = .53$)

−0.5 0 0.5 1 1.5

D.Index estimate