Source	(95% CI)
Sequencing = TPM	
Mariathasan, Ureteral, n = 26	−0.45 [−1.23; 0.33]
Braun, Kidney, n = 178	−0.23 [−0.54; 0.08]
Mariathasan, Kidney, n = 67	0.03 [−0.46; 0.52]
Riaz, Melanoma, n = 51	0.08 [−0.51; 0.67]
Miao.1, Kidney, n = 33	0.21 [−0.55; 0.97]
Mariathasan, Bladder, n = 194	0.29 [0.02; 0.56]
Snyder, Ureteral, n = 25	0.29 [−0.45; 1.03]
Fumet.2, Lung, n = 43	0.48 [−0.17; 1.13]
Mariathasan, Lymph_node, n = 26	0.68 [−0.12; 1.48]
Van_Allen, Melanoma, n = 42	1.08 [0.41; 1.75]
Total	0.21 [−0.04; 0.46]

Heterogeneity: $\chi_9^2 = 19.47$ ($P = .02$), $I^2 = 54\%$ [6%; 77%]

Sequencing = FPKM	
Liu, Melanoma, n = 121	0.36 [−0.07; 0.79]
Nathanson, Melanoma, n = 24	0.50 [−0.26; 1.26]
Hugo, Melanoma, n = 27	0.64 [−0.50; 1.78]
Total	0.42 [0.06; 0.77]

Heterogeneity: $\chi_2^2 = 0.26$ ($P = .88$), $I^2 = 0\%$ [0%; 90%]

Total	0.25 [0.04; 0.46]

Heterogeneity: $\chi_{12}^2 = 21.44$ ($P = .04$), $I^2 = 44\%$ [0%; 71%]

Test for overall effect: $z = 2.31$ ($P = .02$)

Test for subgroup differences: $\chi_1^2 = 0.87$ ($P = .35$)

−0.5 0 0.5 1 1.5
D.Index estimate