Source	(95% CI)
Sequencing = TPM	
Mariathasan, Lymph_node, n = 26	−1.19 [−2.17; −0.21]
Van_Allen, Melanoma, n = 42	−0.90 [−1.59; −0.21]
Riaz, Melanoma, n = 51	−0.75 [−1.40; −0.10]
Hwang, Lung, n = 21	−0.51 [−1.51; 0.49]
Fumet.2, Lung, n = 43	−0.41 [−1.06; 0.24]
Mariathasan, Bladder, n = 194	−0.24 [−0.51; 0.03]
Miao.1, Kidney, n = 33	−0.21 [−0.95; 0.53]
Mariathasan, Kidney, n = 67	−0.12 [−0.61; 0.37]
Snyder, Ureteral, n = 25	0.03 [−0.75; 0.81]
Braun, Kidney, n = 178	0.13 [−0.18; 0.44]
Mariathasan, Ureteral, n = 26	1.15 [0.27; 2.03]
Total	−0.25 [−0.55; 0.05]

Heterogeneity: $\chi^2_{10} = 25.21$ (P = .005), $I^2 = 60\%$ [23%; 80%]

Sequencing = FPKM	
Nathanson, Melanoma, n = 24	−0.65 [−1.53; 0.23]
Liu, Melanoma, n = 121	−0.46 [−0.87; −0.05]
Hugo, Melanoma, n = 27	0.21 [−0.81; 1.23]
Total	−0.41 [−0.76; −0.06]

Heterogeneity: $\chi^2_2 = 1.76$ (P = .41), $I^2 = 0\%$ [0%; 90%]

Total	−0.27 [−0.51; −0.03]

Heterogeneity: $\chi^2_{13} = 28.30$ (P = .008), $I^2 = 54\%$ [16%; 75%]

Test for overall effect: $z = -2.20$ (P = .03)

Test for subgroup differences: $\chi^2_1 = 0.46$ (P = .50)

−1.5 −0.5 0.5 1 1.5

D.Index estimate