Source	(95% CI)
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	−0.89 [−1.71; −0.07]
Liu, Melanoma, n = 121	−0.20 [−0.59; 0.19]
Hugo, Melanoma, n = 27	0.21 [−0.81; 1.23]
Total	−0.30 [−0.75; 0.16]
Heterogeneity: $\chi_2^2 = 3.15$ ($P = .21$), $I^2 = 37\%$ [0%; 80%]	
Sequencing = TPM	
Van_Allen, Melanoma, n = 42	−0.88 [−1.57; −0.19]
Mariathasan, Lymph_node, n = 26	−0.77 [−1.61; 0.07]
Hwang, Lung, n = 21	−0.68 [−1.66; 0.30]
Riaz, Melanoma, n = 51	−0.55 [−1.16; 0.06]
Mariathasan, Bladder, n = 194	−0.39 [−0.66; −0.12]
Fumet.2, Lung, n = 43	−0.30 [−0.95; 0.35]
Snyder, Ureteral, n = 25	−0.20 [−1.02; 0.62]
Mariathasan, Kidney, n = 67	−0.05 [−0.54; 0.44]
Miao.1, Kidney, n = 33	0.09 [−0.60; 0.78]
Mariathasan, Ureteral, n = 26	0.16 [−0.68; 1.00]
Braun, Kidney, n = 178	0.17 [−0.16; 0.50]
Total	−0.26 [−0.48; −0.04]
Heterogeneity: $\chi_{10}^2 = 15.97$ ($P = .10$), $I^2 = 37\%$ [0%; 69%]	
Total	−0.26 [−0.45; −0.07]

Heterogeneity: $\chi_{13}^2 = 19.16$ ($P = .12$), $I^2 = 32\%$ [0%; 64%]

Test for overall effect: $z = -2.69$ ($P = .007$)

Test for subgroup differences: $\chi_1^2 = 0.02$ ($P = .89$)

D.Index estimate