Source	(95% CI)
Sequencing = TPM	
Van_Allen, Melanoma, n = 42	−0.93 [−1.56; −0.30]
Fumet.2, Lung, n = 43	−0.36 [−0.97; 0.25]
Hwang, Lung, n = 21	−0.35 [−1.27; 0.57]
Riaz, Melanoma, n = 51	−0.30 [−0.87; 0.27]
Mariathasan, Bladder, n = 194	−0.28 [−0.55; −0.01]
Snyder, Ureteral, n = 25	−0.25 [−1.03; 0.53]
Mariathasan, Lymph_node, n = 26	−0.22 [−0.96; 0.52]
Miao.1, Kidney, n = 33	−0.01 [−0.68; 0.66]
Mariathasan, Kidney, n = 67	0.04 [−0.43; 0.51]
Braun, Kidney, n = 178	0.13 [−0.20; 0.46]
Mariathasan, Ureteral, n = 26	0.40 [−0.38; 1.18]
Total	−0.17 [−0.36; 0.02]
Heterogeneity: $\chi^2_{10} = 13.17$ ($P = .21$), $I^2 = 24\%$ [0%; 62%]	
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	−0.86 [−1.66; −0.06]
Liu, Melanoma, n = 121	−0.26 [−0.65; 0.13]
Hugo, Melanoma, n = 27	0.39 [−0.63; 1.41]
Total	−0.30 [−0.80; 0.21]
Heterogeneity: $\chi^2_2 = 3.66$ ($P = .16$), $I^2 = 45\%$ [0%; 84%]	
Total	−0.20 [−0.36; −0.03]
Heterogeneity: $\chi^2_{13} = 17.30$ ($P = .19$), $I^2 = 25\%$ [0%; 60%]	
Test for overall effect: $z = -2.27$ ($P = .02$)	
Test for subgroup differences: $\chi^2_1 = 0.20$ ($P = .65$)	

−1   0 0.5 1 1.5

D.Index estimate