Source	(95% CI)	
Sequencing = TPM		
Mariathasan, Ureteral, n = 26	−0.62 [−1.58; 0.34]	
Miao.1, Kidney, n = 33	−0.22 [−0.89; 0.45]	
Mariathasan, Kidney, n = 67	−0.18 [−0.67; 0.31]	
Fumet.2, Lung, n = 43	0.17 [−0.52; 0.86]	
Van_Allen, Melanoma, n = 42	0.17 [−0.42; 0.76]	
Mariathasan, Bladder, n = 194	0.22 [−0.07; 0.51]	
Braun, Kidney, n = 178	0.41 [0.08; 0.74]	
Snyder, Ureteral, n = 25	0.47 [−0.35; 1.29]	
Riaz, Melanoma, n = 51	0.56 [0.01; 1.11]	
Mariathasan, Lymph_node, n = 26	0.75 [−0.15; 1.65]	
Total	0.21 [0.04; 0.39]	

Heterogeneity: $\chi^2_9 = 11.63$ ($P = .24$), $I^2 = 23\%$ [0%; 62%]

Sequencing = FPKM		
Nathanson, Melanoma, n = 24	−0.22 [−1.12; 0.68]	
Liu, Melanoma, n = 121	−0.09 [−0.48; 0.30]	
Hugo, Melanoma, n = 27	0.21 [−0.73; 1.15]	
Total	−0.07 [−0.41; 0.27]	

Heterogeneity: $\chi^2_2 = 0.46$ ($P = .80$), $I^2 = 0\%$ [0%; 90%]

Total	0.16 [−0.01; 0.32]	

Heterogeneity: $\chi^2_{12} = 14.43$ ($P = .27$), $I^2 = 17\%$ [0%; 56%]

Test for overall effect: $z = 1.83$ ($P = .07$)

Test for subgroup differences: $\chi^2_1 = 2.15$ ($P = .14$)

−1   0 0.5 1 1.5
D.Index estimate