Source	(95% CI)	
Sequencing = TPM		
Van_Allen, Melanoma, n = 42	−1.03 [−1.72; −0.34]	
Riaz, Melanoma, n = 51	−0.67 [−1.30; −0.04]	
Snyder, Ureteral, n = 25	−0.39 [−1.19; 0.41]	
Fumet.2, Lung, n = 43	−0.27 [−0.92; 0.38]	
Mariathasan, Bladder, n = 194	−0.27 [−0.54; 0.00]	
Miao.1, Kidney, n = 33	−0.23 [−0.96; 0.50]	
Mariathasan, Lymph_node, n = 26	−0.22 [−0.95; 0.51]	
Mariathasan, Kidney, n = 67	−0.09 [−0.64; 0.46]	
Braun, Kidney, n = 178	0.25 [−0.08; 0.58]	
Mariathasan, Ureteral, n = 26	0.90 [0.06; 1.74]	
Total	−0.20 [−0.48; 0.08]	
Heterogeneity: $\chi_9^2 = 21.78$ ($P = .010$), $I^2 = 59\%$ [17%; 79%]		
Sequencing = FPKM		
Nathanson, Melanoma, n = 24	−0.82 [−1.74; 0.10]	
Liu, Melanoma, n = 121	−0.60 [−1.01; −0.19]	
Hugo, Melanoma, n = 27	0.43 [−0.59; 1.45]	
Total	−0.42 [−1.01; 0.17]	
Heterogeneity: $\chi_2^2 = 3.89$ ($P = .14$), $I^2 = 49\%$ [0%; 85%]		
Total	−0.25 [−0.50; 0.00]	
Heterogeneity: $\chi_{12}^2 = 28.77$ ($P = .004$), $I^2 = 58\%$ [23%; 77%]		
Test for overall effect: $z = -1.92$ ($P = .05$)		
Test for subgroup differences: $\chi_1^2 = 0.46$ ($P = .50$)		

−1.5 −0.5 0.5 1 1.5

D.Index estimate