Source	(95% CI)	
Sequencing = TPM		
Miao.1, Kidney, n = 33	−0.55 [−1.47; 0.37]	
Fumet.2, Lung, n = 43	−0.39 [−1.04; 0.26]	
Riaz, Melanoma, n = 51	−0.30 [−0.85; 0.25]	
Braun, Kidney, n = 178	−0.23 [−0.54; 0.08]	
Mariathasan, Lymph_node, n = 26	−0.16 [−1.02; 0.70]	
Mariathasan, Bladder, n = 194	−0.15 [−0.42; 0.12]	
Van_Allen, Melanoma, n = 42	−0.03 [−0.70; 0.64]	
Mariathasan, Kidney, n = 67	0.10 [−0.41; 0.61]	
Snyder, Ureteral, n = 25	0.35 [−0.39; 1.09]	
Mariathasan, Ureteral, n = 26	1.63 [0.73; 2.53]	
Total	−0.04 [−0.29; 0.21]	
Heterogeneity: $\chi^2_9 = 19.19$ ($P = .02$), $I^2 = 53\%$ [4%; 77%]		
Sequencing = FPKM		
Nathanson, Melanoma, n = 24	−0.49 [−1.31; 0.33]	
Liu, Melanoma, n = 121	−0.39 [−0.80; 0.02]	
Hugo, Melanoma, n = 27	0.58 [−0.48; 1.64]	
Total	−0.30 [−0.65; 0.04]	
Heterogeneity: $\chi^2_2 = 3.04$ ($P = .22$), $I^2 = 34\%$ [0%; 79%]		
Total	−0.10 [−0.30; 0.10]	
Heterogeneity: $\chi^2_{12} = 23.30$ ($P = .03$), $I^2 = 48\%$ [2%; 73%]		
Test for overall effect: $z = −0.96$ ($P = .34$)		
Test for subgroup differences: $\chi^2_1 = 1.40$ ($P = .24$)		

D.Index estimate: −1 0 0.5 1 1.5 2