Source	(95% CI)
Sequencing = TPM	
Miao.1, Kidney, n = 33	−0.21 [−0.94; 0.52]
Mariathasan, Lymph_node, n = 26	−0.17 [−0.91; 0.57]
Mariathasan, Ureteral, n = 26	−0.01 [−0.75; 0.73]
Braun, Kidney, n = 178	0.05 [−0.26; 0.36]
Mariathasan, Kidney, n = 67	0.05 [−0.40; 0.50]
Mariathasan, Bladder, n = 194	0.06 [−0.21; 0.33]
Van_Allen, Melanoma, n = 42	0.08 [−0.57; 0.73]
Riaz, Melanoma, n = 51	0.19 [−0.32; 0.70]
Snyder, Ureteral, n = 25	0.35 [−0.43; 1.13]
Fumet.2, Lung, n = 43	0.46 [−0.21; 1.13]
Total	0.08 [−0.07; 0.23]
Heterogeneity: $\chi_9^2 = 3.06$ ($P = .96$), $I^2 = 0\%$ [0%; 62%]	
Sequencing = FPKM	
Liu, Melanoma, n = 121	0.12 [−0.29; 0.53]
Nathanson, Melanoma, n = 24	0.15 [−0.69; 0.99]
Hugo, Melanoma, n = 27	1.10 [−0.06; 2.26]
Total	0.22 [−0.14; 0.57]
Heterogeneity: $\chi_2^2 = 2.48$ ($P = .29$), $I^2 = 19\%$ [0%; 92%]	
Total	0.10 [−0.04; 0.24]
Heterogeneity: $\chi_{12}^2 = 6.05$ ($P = .91$), $I^2 = 0\%$ [0%; 57%]	
Test for overall effect: $z = 1.38$ ($P = .17$)	
Test for subgroup differences: $\chi_1^2 = 0.51$ ($P = .47$)	

−0.5 0 0.5 1 1.5
D.Index estimate