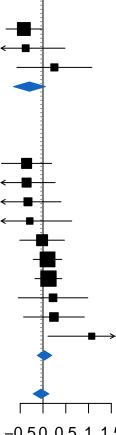| Source	(95% CI)
Sequencing = FPKM	
Liu, Melanoma, n = 121	−0.42 [−0.81; −0.03]
Nathanson, Melanoma, n = 24	−0.38 [−1.24; 0.48]
Hugo, Melanoma, n = 27	0.25 [−0.57; 1.07]
Total	−0.30 [−0.65; 0.05]
Heterogeneity: $\chi^2_2 = 2.11$ ($P = .35$), $I^2 = 5\%$ [0%; 90%]	
Sequencing = TPM	
Riaz, Melanoma, n = 51	−0.36 [−0.91; 0.19]
Van_Allen, Melanoma, n = 42	−0.36 [−0.99; 0.27]
Miao.1, Kidney, n = 33	−0.33 [−1.06; 0.40]
Snyder, Ureteral, n = 25	−0.29 [−1.21; 0.63]
Mariathasan, Kidney, n = 67	−0.02 [−0.51; 0.47]
Braun, Kidney, n = 178	0.10 [−0.21; 0.41]
Mariathasan, Bladder, n = 194	0.12 [−0.17; 0.41]
Mariathasan, Lymph_node, n = 26	0.22 [−0.54; 0.98]
Fumet.2, Lung, n = 43	0.24 [−0.43; 0.91]
Mariathasan, Ureteral, n = 26	1.07 [0.11; 2.03]
Total	0.03 [−0.13; 0.19]
Heterogeneity: $\chi^2_9 = 10.55$ ($P = .31$), $I^2 = 15\%$ [0%; 56%]	
Total	−0.04 [−0.21; 0.13]
Heterogeneity: $\chi^2_{12} = 16.04$ ($P = .19$), $I^2 = 25\%$ [0%; 61%]	
Test for overall effect: $z = -0.48$ ($P = .63$)	
Test for subgroup differences: $\chi^2_1 = 2.86$ ($P = .09$)	

−0.5 0 0.5 1 1.5

D.Index estimate