Source	(95% CI)
Sequencing = TPM	
Mariathasan, Kidney, n = 46	−19.12 [−4414.08; 4375.84]
Fumet.2, Lung, n = 41	−3.23 [−5.43; −1.03]
Jung, Lung, n = 26	−2.64 [−4.95; −0.33]
Mariathasan, Bladder, n = 133	−1.96 [−2.82; −1.10]
Van_Allen, Melanoma, n = 39	−1.52 [−3.24; 0.20]
Riaz, Melanoma, n = 33	−1.11 [−2.70; 0.48]
Braun, Kidney, n = 139	−0.88 [−1.64; −0.12]
Snyder, Ureteral, n = 22	−0.80 [−2.58; 0.98]
Fumet.1, Lung, n = 39	−0.18 [−1.57; 1.21]
Miao.1, Kidney, n = 28	0.86 [−0.73; 2.45]
Total	−1.15 [−1.86; −0.45]
Heterogeneity: χ^2_9 = 17.26 (P = .04), I^2 = 48% [0%; 75%]	
Sequencing = FPKM	
Liu, Melanoma, n = 112	−2.01 [−2.85; −1.17]
Nathanson, Melanoma, n = 24	−0.69 [−2.34; 0.96]
Hugo, Melanoma, n = 27	−0.44 [−1.97; 1.09]
Total	−1.23 [−2.31; −0.14]
Heterogeneity: χ^2_2 = 4.18 (P = .12), I^2 = 52% [0%; 86%]	
Total	−1.17 [−1.73; −0.62]
Heterogeneity: χ^2_{12} = 22.09 (P = .04), I^2 = 46% [0%; 72%]	
Test for overall effect: z = −4.14 (P < .001)	
Test for subgroup differences: χ^2_1 = 0.01 (P = .91)