Source	(95% CI)

Sequencing = TPM

Fumet.2, Lung, n = 41	−2.27 [−4.13; −0.41]
Jung, Lung, n = 26	−2.11 [−4.21; −0.01]
Snyder, Ureteral, n = 22	−0.98 [−2.88; 0.92]
Riaz, Melanoma, n = 33	−0.94 [−2.25; 0.37]
Mariathasan, Bladder, n = 133	−0.80 [−1.51; −0.09]
Van_Allen, Melanoma, n = 39	−0.73 [−2.26; 0.80]
Mariathasan, Kidney, n = 46	−0.37 [−1.82; 1.08]
Braun, Kidney, n = 139	−0.21 [−0.95; 0.53]
Fumet.1, Lung, n = 39	−0.01 [−1.58; 1.56]
Miao.1, Kidney, n = 28	0.06 [−1.51; 1.63]
Total	−0.64 [−1.02; −0.26]

Heterogeneity: $\chi_9^2 = 8.16$ ($P = .52$), $I^2 = 0\%$ [0%; 62%]

Sequencing = FPKM

Liu, Melanoma, n = 112	−0.54 [−1.28; 0.20]
Nathanson, Melanoma, n = 24	−0.48 [−1.89; 0.93]
Hugo, Melanoma, n = 27	−0.07 [−1.60; 1.46]
Total	−0.46 [−1.06; 0.15]

Heterogeneity: $\chi_2^2 = 0.29$ ($P = .86$), $I^2 = 0\%$ [0%; 90%]

Total	−0.59 [−0.91; −0.26]

Heterogeneity: $\chi_{12}^2 = 8.71$ ($P = .73$), $I^2 = 0\%$ [0%; 57%]
Test for overall effect: $z = -3.57$ ($P < .001$)
Test for subgroup differences: $\chi_1^2 = 0.25$ ($P = .62$)

−2 −1 0 1 2
Estimated logOR