Source   **(95% CI)**

Sequencing = TPM

Source	(95% CI)
Miao.1, Kidney, n = 28	−2.38 [−4.81; 0.05]
Riaz, Melanoma, n = 33	−0.34 [−2.32; 1.64]
Braun, Kidney, n = 139	−0.28 [−1.06; 0.50]
Fumet.2, Lung, n = 41	−0.24 [−1.83; 1.35]
Fumet.1, Lung, n = 39	0.16 [−1.53; 1.85]
Van_Allen, Melanoma, n = 39	0.16 [−1.88; 2.20]
Mariathasan, Bladder, n = 133	0.24 [−0.43; 0.91]
Jung, Lung, n = 26	0.37 [−1.20; 1.94]
Snyder, Ureteral, n = 22	0.93 [−0.62; 2.48]
Mariathasan, Kidney, n = 46	0.96 [−0.69; 2.61]
Total	0.08 [−0.32; 0.47]

Heterogeneity: $\chi^2_9 = 7.7$ ($P = .56$), $I^2 = 0\%$ [0%; 62%]

Sequencing = FPKM

Source	(95% CI)
Liu, Melanoma, n = 112	−0.13 [−1.23; 0.97]
Nathanson, Melanoma, n = 24	0.87 [−1.03; 2.77]
Hugo, Melanoma, n = 27	3.92 [0.45; 7.39]
Total	0.99 [−0.89; 2.87]

Heterogeneity: $\chi^2_2 = 5.08$ ($P = .08$), $I^2 = 61\%$ [0%; >89%]

Total   0.12 [−0.24; 0.48]

Heterogeneity: $\chi^2_{12} = 13.15$ ($P = .36$), $I^2 = 9\%$ [0%; 47%]

Test for overall effect: $z = 0.67$ ($P = .50$)

Test for subgroup differences: $\chi^2_1 = 0.88$ ($P = .35$)

−2   0 1 2 3 4

Estimated logOR