Source	(95% CI)
Sequencing = TPM	
Fumet.2, Lung, n = 41	−2.63 [−4.94; −0.32]
Jung, Lung, n = 26	−1.38 [−3.38; 0.62]
Riaz, Melanoma, n = 33	−1.16 [−2.75; 0.43]
Miao.1, Kidney, n = 28	−0.92 [−3.00; 1.16]
Snyder, Ureteral, n = 22	−0.78 [−3.09; 1.53]
Van_Allen, Melanoma, n = 39	−0.63 [−2.43; 1.17]
Mariathasan, Bladder, n = 133	−0.47 [−1.31; 0.37]
Braun, Kidney, n = 139	−0.08 [−1.06; 0.90]
Mariathasan, Kidney, n = 46	0.11 [−1.58; 1.80]
Fumet.1, Lung, n = 39	0.62 [−1.28; 2.52]
Total	−0.51 [−0.98; −0.05]

Heterogeneity: $\chi_9^2 = 7.44$ ($P = .59$), $I^2 = 0\%$ [0%; 62%]

Sequencing = FPKM	
Liu, Melanoma, n = 112	−1.08 [−2.06; −0.10]
Nathanson, Melanoma, n = 24	−0.48 [−2.11; 1.15]
Hugo, Melanoma, n = 27	0.32 [−1.56; 2.20]
Total	−0.71 [−1.48; 0.05]

Heterogeneity: $\chi_2^2 = 1.78$ ($P = .41$), $I^2 = 0\%$ [0%; 90%]

Total	−0.57 [−0.97; −0.17]

Heterogeneity: $\chi_{12}^2 = 9.41$ ($P = .67$), $I^2 = 0\%$ [0%; 57%]
Test for overall effect: $z = −2.80$ ($P = .005$)
Test for subgroup differences: $\chi_1^2 = 0.19$ ($P = .66$)

−3 −1 0 1 2 3
Estimated logOR