Source	(95% CI)
Sequencing = TPM	
Fumet.2, Lung, n = 41	−2.00 [−3.72; −0.28]
Jung, Lung, n = 26	−1.89 [−3.87; 0.09]
Van_Allen, Melanoma, n = 39	−0.96 [−2.47; 0.55]
Snyder, Ureteral, n = 22	−0.91 [−2.71; 0.89]
Riaz, Melanoma, n = 33	−0.90 [−2.19; 0.39]
Mariathasan, Bladder, n = 133	−0.78 [−1.49; −0.07]
Mariathasan, Kidney, n = 46	−0.23 [−1.70; 1.24]
Braun, Kidney, n = 139	−0.20 [−0.93; 0.53]
Fumet.1, Lung, n = 39	−0.11 [−1.60; 1.38]
Miao.1, Kidney, n = 28	0.13 [−1.34; 1.60]
Total	−0.61 [−0.99; −0.24]

Heterogeneity: $\chi^2_9 = 7.72$ ($P = .56$), $I^2 = 0\%$ [0%; 62%]

Sequencing = FPKM	
Liu, Melanoma, n = 112	−0.48 [−1.21; 0.25]
Nathanson, Melanoma, n = 24	−0.46 [−1.85; 0.93]
Hugo, Melanoma, n = 27	−0.15 [−1.62; 1.32]
Total	−0.42 [−1.01; 0.17]

Heterogeneity: $\chi^2_2 = 0.16$ ($P = .92$), $I^2 = 0\%$ [0%; 90%]

Total −0.56 [−0.87; −0.25]

Heterogeneity: $\chi^2_{12} = 8.17$ ($P = .77$), $I^2 = 0\%$ [0%; 57%]

Test for overall effect: $z = −3.49$ ($P < .001$)

Test for subgroup differences: $\chi^2_1 = 0.29$ ($P = .59$)

−2 −1 0 1 2

Estimated logOR