Source	(95% CI)
Sequencing = TPM	
Van_Allen, Melanoma, n = 39	−1.58 [−3.64; 0.48]
Mariathasan, Kidney, n = 46	−1.53 [−3.27; 0.21]
Mariathasan, Bladder, n = 133	−0.60 [−1.42; 0.22]
Riaz, Melanoma, n = 33	−0.51 [−2.20; 1.18]
Fumet.1, Lung, n = 39	−0.10 [−1.81; 1.61]
Fumet.2, Lung, n = 41	0.09 [−1.50; 1.68]
Snyder, Ureteral, n = 22	0.09 [−1.85; 2.03]
Braun, Kidney, n = 139	0.57 [−0.39; 1.53]
Jung, Lung, n = 26	0.69 [−1.45; 2.83]
Miao.1, Kidney, n = 28	0.92 [−1.61; 3.45]
Total	−0.21 [−0.72; 0.30]

Heterogeneity: $\chi^2_9 = 9.11$ ($P = .43$), $I^2 = 1\%$ [0%; 63%]

Sequencing = FPKM	
Liu, Melanoma, n = 112	−0.75 [−1.69; 0.19]
Nathanson, Melanoma, n = 24	−0.48 [−2.44; 1.48]
Hugo, Melanoma, n = 27	1.15 [−0.93; 3.23]
Total	−0.32 [−1.32; 0.68]

Heterogeneity: $\chi^2_2 = 2.67$ ($P = .26$), $I^2 = 25\%$ [0%; 92%]

Total	−0.25 [−0.68; 0.18]

Heterogeneity: $\chi^2_{12} = 12.03$ ($P = .44$), $I^2 = 0\%$ [0%; 57%]

Test for overall effect: $z = -1.14$ ($P = .25$)

Test for subgroup differences: $\chi^2_1 = 0.04$ ($P = .84$)

−2 −1 0 1 2
Estimated logOR