Source	(95% CI)	

Sequencing = TGS
Samstein, Esophagus, n = 21 −1.54 [−3.87; 0.79]
Samstein, Melanoma, n = 108 −1.23 [−2.03; −0.43]
Samstein, Unknown, n = 29 −1.05 [−2.85; 0.75]
Samstein, HNC, n = 72 −0.94 [−2.25; 0.37]
Rizvi.18, Lung, n = 29 −0.69 [−2.45; 1.07]
Total −1.11 [−1.70; −0.53]
Heterogeneity: $\chi^2_4 = 0.5$ ($P = .97$), $I^2 = 0\%$ [0%; 79%]

Sequencing = WES
Riaz, Melanoma, n = 42 −1.07 [−2.74; 0.60]
Liu, Melanoma, n = 133 −0.79 [−1.55; −0.03]
Miao.2, Melanoma, n = 43 −0.77 [−2.02; 0.48]
Nathanson, Melanoma, n = 64 −0.61 [−1.90; 0.68]
Hugo, Melanoma, n = 38 −0.49 [−1.94; 0.96]
Snyder, Ureteral, n = 22 −0.41 [−2.25; 1.43]
Van_Allen, Melanoma, n = 104 −0.22 [−1.45; 1.01]
Total −0.65 [−1.11; −0.19]
Heterogeneity: $\chi^2_6 = 0.99$ ($P = .99$), $I^2 = 0\%$ [<0%; <71%]
Total −0.83 [−1.19; −0.47]
Heterogeneity: $\chi^2_{11} = 2.97$ ($P > .99$), $I^2 = 0\%$ [<0%; <58%]
Test for overall effect: $z = -4.51$ ($P < .001$)
Test for subgroup differences: $\chi^2_1 = 1.48$ ($P = .22$)

−2 −1 0 1 2
Estimated logOR