Source	(95% CI)
Sequencing = FPKM	
Hugo, Melanoma, n = 27	−2.28 [−4.53; −0.03]
Liu, Melanoma, n = 112	−1.18 [−2.10; −0.26]
Nathanson, Melanoma, n = 24	−0.24 [−2.02; 1.54]
Total	−1.13 [−1.90; −0.36]
Heterogeneity: $\chi^2_2 = 1.97$ ($P = .37$), $I^2 = 0\%$ [0%; 90%]	
Sequencing = TPM	
Van_Allen, Melanoma, n = 39	−2.13 [−4.17; −0.09]
Snyder, Ureteral, n = 22	−1.85 [−4.24; 0.54]
Fumet.2, Lung, n = 41	−1.40 [−3.24; 0.44]
Riaz, Melanoma, n = 33	−1.36 [−3.50; 0.78]
Jung, Lung, n = 26	−1.23 [−3.27; 0.81]
Mariathasan, Bladder, n = 133	−1.17 [−2.05; −0.29]
Fumet.1, Lung, n = 39	−1.05 [−3.01; 0.91]
Braun, Kidney, n = 139	−0.08 [−0.88; 0.72]
Mariathasan, Kidney, n = 46	0.15 [−1.52; 1.82]
Miao.1, Kidney, n = 28	2.34 [−0.07; 4.75]
Total	−0.74 [−1.36; −0.13]
Heterogeneity: $\chi^2_9 = 14.56$ ($P = .10$), $I^2 = 38\%$ [0%; 71%]	
Total	−0.84 [−1.32; −0.35]
Heterogeneity: $\chi^2_{12} = 17.50$ ($P = .13$), $I^2 = 31\%$ [0%; 65%]	
Test for overall effect: $z = −3.36$ ($P < .001$)	
Test for subgroup differences: $\chi^2_1 = 0.60$ ($P = .44$)	

−2 −1 0 1 2

Estimated logOR