Source	(95% CI)	
Sequencing = TPM		
Miao.1, Kidney, n = 28	−2.65 [−6.10; 0.80]	
Van_Allen, Melanoma, n = 39	−2.39 [−5.27; 0.49]	
Fumet.2, Lung, n = 41	−2.09 [−4.66; 0.48]	
Riaz, Melanoma, n = 33	−1.31 [−3.70; 1.08]	
Braun, Kidney, n = 139	−0.57 [−1.71; 0.57]	
Snyder, Ureteral, n = 22	−0.54 [−3.26; 2.18]	
Jung, Lung, n = 26	−0.10 [−3.06; 2.86]	
Fumet.1, Lung, n = 39	0.19 [−2.20; 2.58]	
Mariathasan, Bladder, n = 133	0.34 [−0.93; 1.61]	
Mariathasan, Kidney, n = 46	1.94 [−0.80; 4.68]	
Total	−0.44 [−1.08; 0.20]	

Heterogeneity: $\chi_9^2 = 10.13$ ($P = .34$), $I^2 = 11\%$ [0%; 52%]

Source	(95% CI)	
Sequencing = FPKM		
Liu, Melanoma, n = 112	−1.01 [−2.36; 0.34]	
Nathanson, Melanoma, n = 24	−0.51 [−3.00; 1.98]	
Hugo, Melanoma, n = 27	1.49 [−1.59; 4.57]	
Total	−0.59 [−1.69; 0.52]	

Heterogeneity: $\chi_2^2 = 2.13$ ($P = .34$), $I^2 = 6\%$ [0%; 90%]

Total −0.47 [−1.02; 0.08]

Heterogeneity: $\chi_{12}^2 = 12.32$ ($P = .42$), $I^2 = 3\%$ [0%; 58%]

Test for overall effect: $z = -1.68$ ($P = .09$)

Test for subgroup differences: $\chi_1^2 = 0.05$ ($P = .82$)

−3   −1 0 1 2 3

Estimated logOR