Source	(95% CI)	
Sequencing = TPM		
Fumet.2, Lung, n = 41	−2.43 [−3.98; −0.88]	
Mariathasan, Kidney, n = 46	−1.80 [−3.33; −0.27]	
Jung, Lung, n = 26	−1.34 [−2.75; 0.07]	
Mariathasan, Bladder, n = 133	−1.29 [−1.96; −0.62]	
Snyder, Ureteral, n = 22	−1.10 [−2.45; 0.25]	
Riaz, Melanoma, n = 33	−0.91 [−2.01; 0.19]	
Van_Allen, Melanoma, n = 39	−0.80 [−1.98; 0.38]	
Braun, Kidney, n = 139	−0.44 [−1.05; 0.17]	
Fumet.1, Lung, n = 39	−0.37 [−1.43; 0.69]	
Miao.1, Kidney, n = 28	−0.15 [−1.42; 1.12]	
Total	−0.93 [−1.31; −0.55]	

Heterogeneity: $\chi^2_9 = 11.38$ ($P = .25$), $I^2 = 21\%$ [0%; 61%]

Sequencing = FPKM		
Liu, Melanoma, n = 112	−1.03 [−1.72; −0.34]	
Nathanson, Melanoma, n = 24	−0.80 [−2.02; 0.42]	
Hugo, Melanoma, n = 27	−0.37 [−1.60; 0.86]	
Total	−0.86 [−1.40; −0.32]	

Heterogeneity: $\chi^2_2 = 0.85$ ($P = .65$), $I^2 = 0\%$ [0%; 90%]

Total   −0.89 [−1.18; −0.61]

Heterogeneity: $\chi^2_{12} = 12.25$ ($P = .43$), $I^2 = 2\%$ [0%; 57%]

Test for overall effect: $z = -6.07$ ($P < .001$)

Test for subgroup differences: $\chi^2_1 = 0.04$ ($P = .83$)

−2 −1 0 1 2
Estimated logOR