Source	(95% CI)	
Sequencing = TPM		
Fumet.2, Lung, n = 41	−2.45 [−4.16; −0.74]	
Mariathasan, Kidney, n = 46	−2.35 [−4.53; −0.17]	
Snyder, Ureteral, n = 22	−1.69 [−3.63; 0.25]	
Jung, Lung, n = 26	−1.55 [−3.41; 0.31]	
Mariathasan, Bladder, n = 133	−1.43 [−2.21; −0.65]	
Riaz, Melanoma, n = 33	−1.29 [−2.88; 0.30]	
Van_Allen, Melanoma, n = 39	−0.96 [−2.53; 0.61]	
Miao.1, Kidney, n = 28	−0.63 [−2.20; 0.94]	
Fumet.1, Lung, n = 39	−0.33 [−1.72; 1.06]	
Braun, Kidney, n = 139	−0.06 [−0.80; 0.68]	
Total	−1.08 [−1.63; −0.53]	

Heterogeneity: $\chi_9^2 = 13.54$ ($P = .14$), $I^2 = 34\%$ [0%; 68%]

Sequencing = FPKM		
Nathanson, Melanoma, n = 24	−1.44 [−3.18; 0.30]	
Liu, Melanoma, n = 112	−1.26 [−2.04; −0.48]	
Hugo, Melanoma, n = 27	−0.44 [−1.97; 1.09]	
Total	−1.14 [−1.79; −0.49]	

Heterogeneity: $\chi_2^2 = 1.01$ ($P = .60$), $I^2 = 0\%$ [0%; 90%]

Total	−1.06 [−1.49; −0.63]	

Heterogeneity: $\chi_{12}^2 = 14.77$ ($P = .25$), $I^2 = 19\%$ [0%; 57%]

Test for overall effect: $z = −4.84$ ($P < .001$)

Test for subgroup differences: $\chi_1^2 = 0.02$ ($P = .90$)

Estimated logOR