Source	(95% CI)
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	−0.97 [−4.60; 2.66]
Liu, Melanoma, n = 112	−0.54 [−2.17; 1.09]
Hugo, Melanoma, n = 27	1.53 [−1.82; 4.88]
Total	−0.26 [−1.62; 1.10]
Heterogeneity: $\chi^2_2 = 1.36$ ($P = .51$), $I^2 = 0\%$ [0%; 90%]	
Sequencing = TPM	
Braun, Kidney, n = 139	−0.04 [−1.24; 1.16]
Mariathasan, Bladder, n = 133	0.54 [−0.71; 1.79]
Riaz, Melanoma, n = 33	0.63 [−1.98; 3.24]
Fumet.2, Lung, n = 41	0.70 [−1.55; 2.95]
Van_Allen, Melanoma, n = 39	1.91 [−1.79; 5.61]
Fumet.1, Lung, n = 39	2.05 [−1.38; 5.48]
Mariathasan, Kidney, n = 46	2.24 [−1.43; 5.91]
Snyder, Ureteral, n = 22	2.47 [−0.55; 5.49]
Total	0.64 [−0.06; 1.35]
Heterogeneity: $\chi^2_7 = 4.51$ ($P = .72$), $I^2 = 0\%$ [0%; 68%]	
Total	0.45 [−0.17; 1.08]
Heterogeneity: $\chi^2_{10} = 7.21$ ($P = .71$), $I^2 = 0\%$ [0%; 60%]	
Test for overall effect: $z = 1.41$ ($P = .16$)	
Test for subgroup differences: $\chi^2_1 = 1.34$ ($P = .25$)	

−1 0 1 2

Estimated logOR