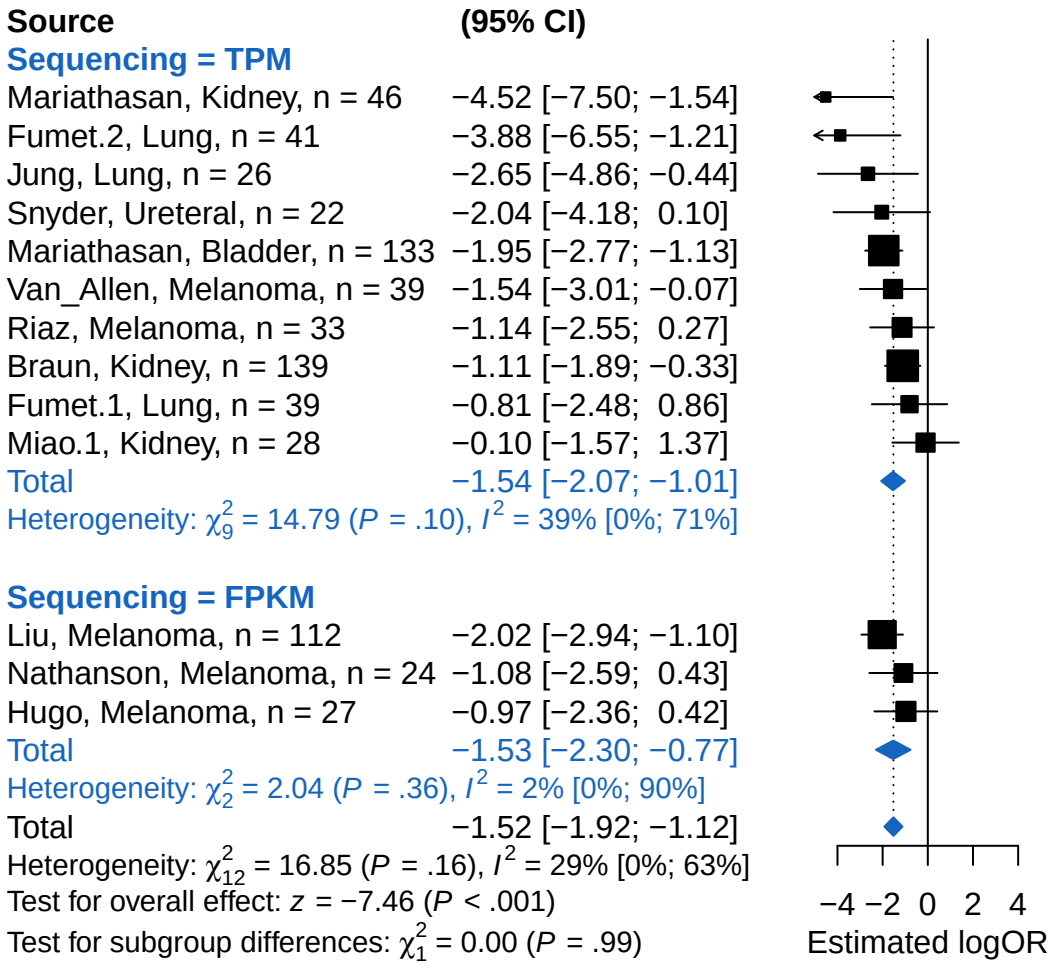
Source (95% CI)
Sequencing = TPM
Mariathasan, Kidney, n = 46 −4.52 [−7.50; −1.54]
Fumet.2, Lung, n = 41 −3.88 [−6.55; −1.21]
Jung, Lung, n = 26 −2.65 [−4.86; −0.44]
Snyder, Ureteral, n = 22 −2.04 [−4.18; 0.10]
Mariathasan, Bladder, n = 133 −1.95 [−2.77; −1.13]
Van_Allen, Melanoma, n = 39 −1.54 [−3.01; −0.07]
Riaz, Melanoma, n = 33 −1.14 [−2.55; 0.27]
Braun, Kidney, n = 139 −1.11 [−1.89; −0.33]
Fumet.1, Lung, n = 39 −0.81 [−2.48; 0.86]
Miao.1, Kidney, n = 28 −0.10 [−1.57; 1.37]
Total −1.54 [−2.07; −1.01]
Heterogeneity: χ^2_9 = 14.79 (P = .10), I^2 = 39% [0%; 71%]
Sequencing = FPKM
Liu, Melanoma, n = 112 −2.02 [−2.94; −1.10]
Nathanson, Melanoma, n = 24 −1.08 [−2.59; 0.43]
Hugo, Melanoma, n = 27 −0.97 [−2.36; 0.42]
Total −1.53 [−2.30; −0.77]
Heterogeneity: χ^2_2 = 2.04 (P = .36), I^2 = 2% [0%; 90%]
Total −1.52 [−1.92; −1.12]
Heterogeneity: χ^2_{12} = 16.85 (P = .16), I^2 = 29% [0%; 63%]
Test for overall effect: z = −7.46 (P < .001)
Test for subgroup differences: χ^2_1 = 0.00 (P = .99)
−4 −2 0 2 4
Estimated logOR