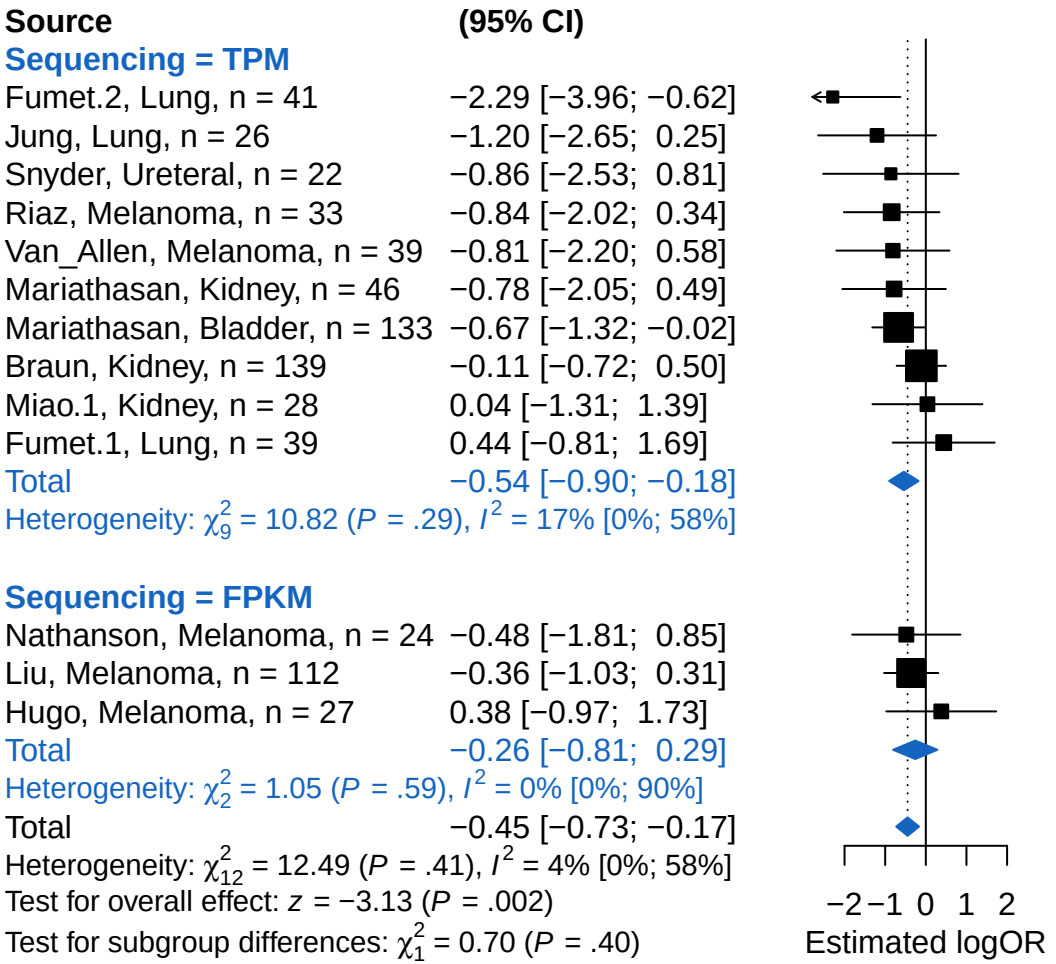
Source
(95% CI)
Sequencing = TPM
Fumet.2, Lung, n = 41 −2.29 [−3.96; −0.62]
Jung, Lung, n = 26 −1.20 [−2.65; 0.25]
Snyder, Ureteral, n = 22 −0.86 [−2.53; 0.81]
Riaz, Melanoma, n = 33 −0.84 [−2.02; 0.34]
Van_Allen, Melanoma, n = 39 −0.81 [−2.20; 0.58]
Mariathasan, Kidney, n = 46 −0.78 [−2.05; 0.49]
Mariathasan, Bladder, n = 133 −0.67 [−1.32; −0.02]
Braun, Kidney, n = 139 −0.11 [−0.72; 0.50]
Miao.1, Kidney, n = 28 0.04 [−1.31; 1.39]
Fumet.1, Lung, n = 39 0.44 [−0.81; 1.69]
Total −0.54 [−0.90; −0.18]
Heterogeneity: χ^2_9 = 10.82 (P = .29), I^2 = 17% [0%; 58%]
Sequencing = FPKM
Nathanson, Melanoma, n = 24 −0.48 [−1.81; 0.85]
Liu, Melanoma, n = 112 −0.36 [−1.03; 0.31]
Hugo, Melanoma, n = 27 0.38 [−0.97; 1.73]
Total −0.26 [−0.81; 0.29]
Heterogeneity: χ^2_2 = 1.05 (P = .59), I^2 = 0% [0%; 90%]
Total −0.45 [−0.73; −0.17]
Heterogeneity: χ^2_{12} = 12.49 (P = .41), I^2 = 4% [0%; 58%]
Test for overall effect: z = −3.13 (P = .002)
Test for subgroup differences: χ^2_1 = 0.70 (P = .40)
−2 −1 0 1 2
Estimated logOR