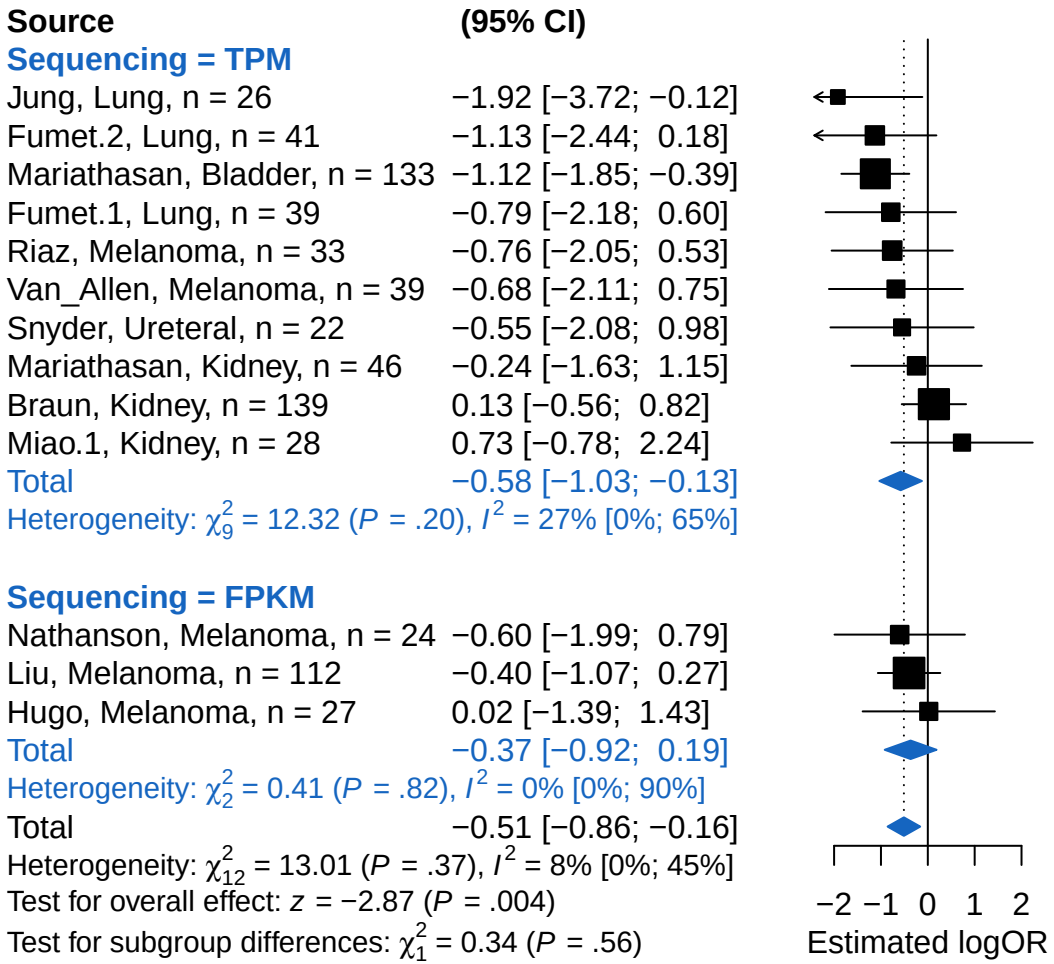
Source
(95% CI)
Sequencing = TPM
Jung, Lung, n = 26 −1.92 [−3.72; −0.12]
Fumet.2, Lung, n = 41 −1.13 [−2.44; 0.18]
Mariathasan, Bladder, n = 133 −1.12 [−1.85; −0.39]
Fumet.1, Lung, n = 39 −0.79 [−2.18; 0.60]
Riaz, Melanoma, n = 33 −0.76 [−2.05; 0.53]
Van_Allen, Melanoma, n = 39 −0.68 [−2.11; 0.75]
Snyder, Ureteral, n = 22 −0.55 [−2.08; 0.98]
Mariathasan, Kidney, n = 46 −0.24 [−1.63; 1.15]
Braun, Kidney, n = 139 0.13 [−0.56; 0.82]
Miao.1, Kidney, n = 28 0.73 [−0.78; 2.24]
Total −0.58 [−1.03; −0.13]
Heterogeneity: χ^2_9 = 12.32 (P = .20), I^2 = 27% [0%; 65%]
Sequencing = FPKM
Nathanson, Melanoma, n = 24 −0.60 [−1.99; 0.79]
Liu, Melanoma, n = 112 −0.40 [−1.07; 0.27]
Hugo, Melanoma, n = 27 0.02 [−1.39; 1.43]
Total −0.37 [−0.92; 0.19]
Heterogeneity: χ^2_2 = 0.41 (P = .82), I^2 = 0% [0%; 90%]
Total −0.51 [−0.86; −0.16]
Heterogeneity: χ^2_{12} = 13.01 (P = .37), I^2 = 8% [0%; 45%]
Test for overall effect: z = −2.87 (P = .004)
Test for subgroup differences: χ^2_1 = 0.34 (P = .56)
−2 −1 0 1 2
Estimated logOR