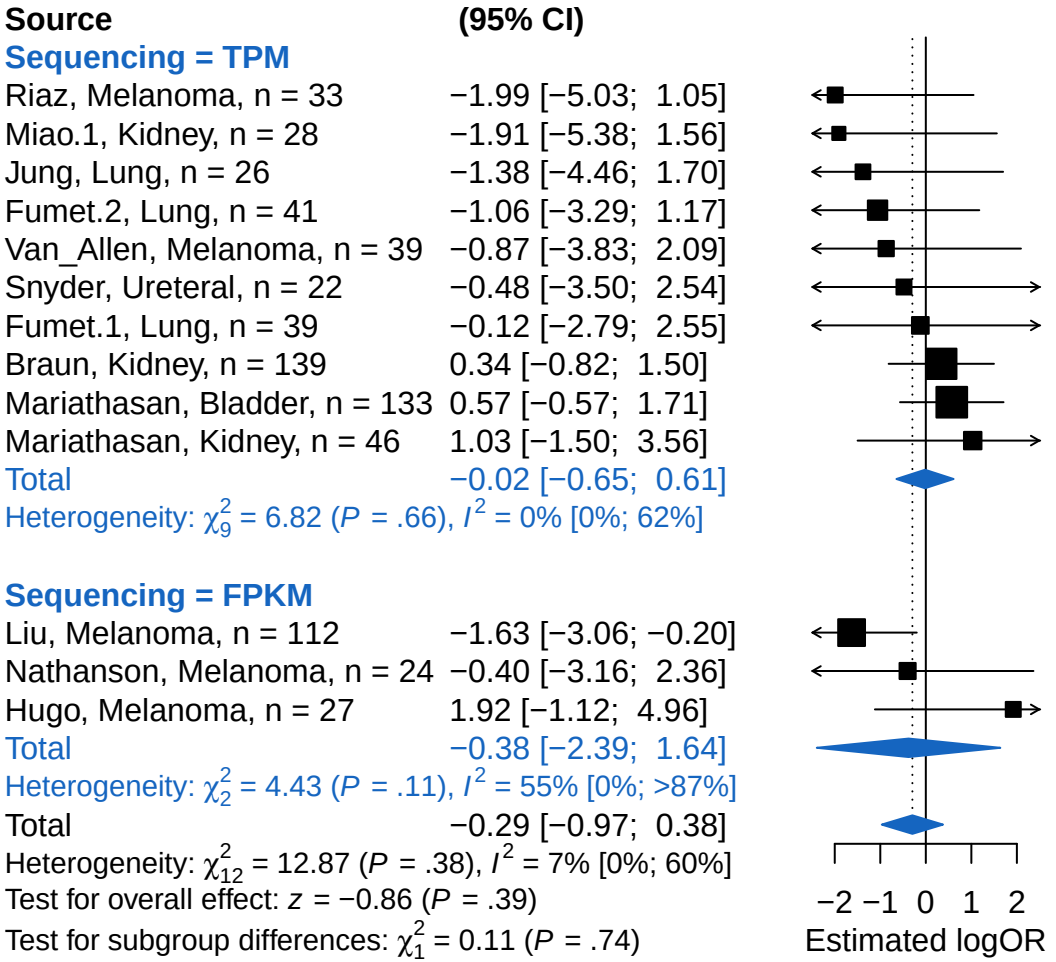
Source
(95% CI)
Sequencing = TPM
Riaz, Melanoma, n = 33 −1.99 [−5.03; 1.05]
Miao.1, Kidney, n = 28 −1.91 [−5.38; 1.56]
Jung, Lung, n = 26 −1.38 [−4.46; 1.70]
Fumet.2, Lung, n = 41 −1.06 [−3.29; 1.17]
Van_Allen, Melanoma, n = 39 −0.87 [−3.83; 2.09]
Snyder, Ureteral, n = 22 −0.48 [−3.50; 2.54]
Fumet.1, Lung, n = 39 −0.12 [−2.79; 2.55]
Braun, Kidney, n = 139 0.34 [−0.82; 1.50]
Mariathasan, Bladder, n = 133 0.57 [−0.57; 1.71]
Mariathasan, Kidney, n = 46 1.03 [−1.50; 3.56]
Total −0.02 [−0.65; 0.61]
Heterogeneity: χ^2_9 = 6.82 (*P* = .66), I^2 = 0% [0%; 62%]
Sequencing = FPKM
Liu, Melanoma, n = 112 −1.63 [−3.06; −0.20]
Nathanson, Melanoma, n = 24 −0.40 [−3.16; 2.36]
Hugo, Melanoma, n = 27 1.92 [−1.12; 4.96]
Total −0.38 [−2.39; 1.64]
Heterogeneity: χ^2_2 = 4.43 (*P* = .11), I^2 = 55% [0%; >87%]
Total −0.29 [−0.97; 0.38]
Heterogeneity: χ^2_{12} = 12.87 (*P* = .38), I^2 = 7% [0%; 60%]
Test for overall effect: *z* = −0.86 (*P* = .39)
Test for subgroup differences: χ^2_1 = 0.11 (*P* = .74)
−2 −1 0 1 2
Estimated logOR