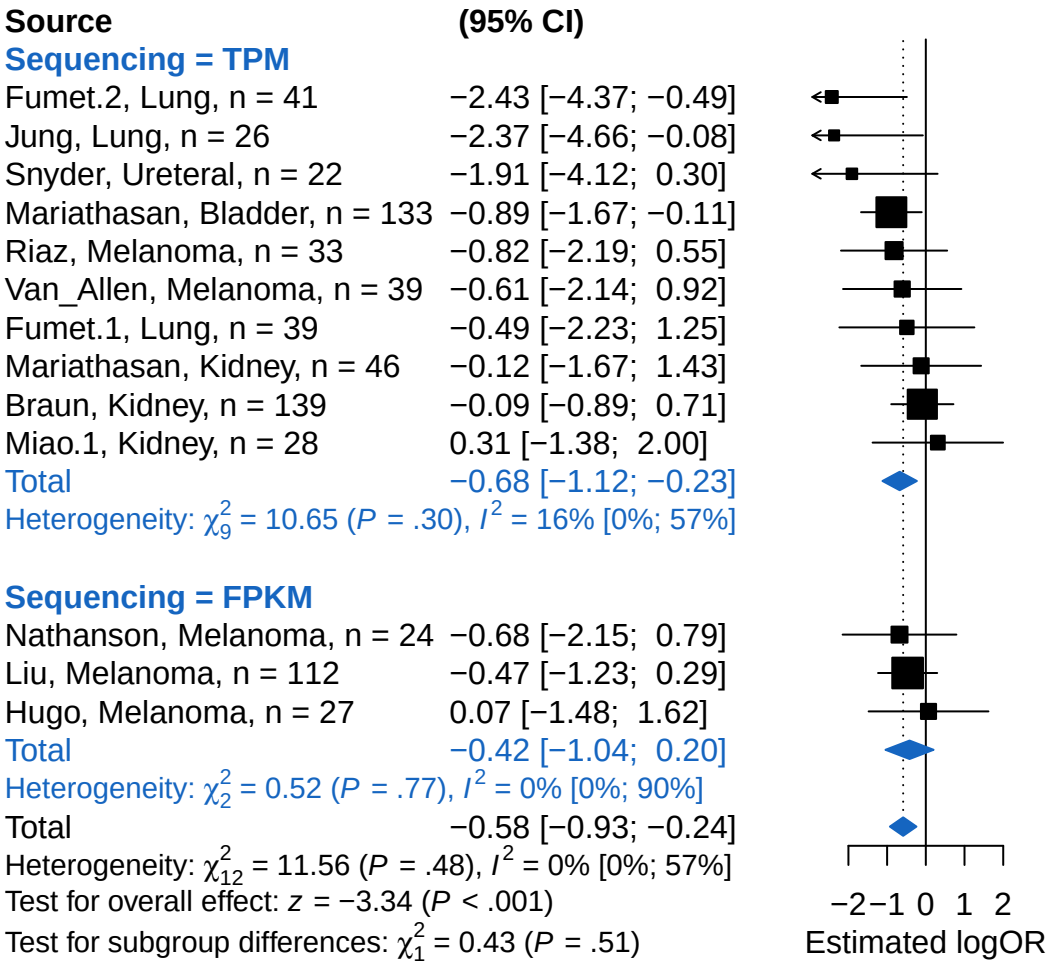
Source
(95% CI)
Sequencing = TPM
Fumet.2, Lung, n = 41 −2.43 [−4.37; −0.49]
Jung, Lung, n = 26 −2.37 [−4.66; −0.08]
Snyder, Ureteral, n = 22 −1.91 [−4.12; 0.30]
Mariathasan, Bladder, n = 133 −0.89 [−1.67; −0.11]
Riaz, Melanoma, n = 33 −0.82 [−2.19; 0.55]
Van_Allen, Melanoma, n = 39 −0.61 [−2.14; 0.92]
Fumet.1, Lung, n = 39 −0.49 [−2.23; 1.25]
Mariathasan, Kidney, n = 46 −0.12 [−1.67; 1.43]
Braun, Kidney, n = 139 −0.09 [−0.89; 0.71]
Miao.1, Kidney, n = 28 0.31 [−1.38; 2.00]
Total −0.68 [−1.12; −0.23]
Heterogeneity: χ^2_9 = 10.65 (P = .30), I^2 = 16% [0%; 57%]
Sequencing = FPKM
Nathanson, Melanoma, n = 24 −0.68 [−2.15; 0.79]
Liu, Melanoma, n = 112 −0.47 [−1.23; 0.29]
Hugo, Melanoma, n = 27 0.07 [−1.48; 1.62]
Total −0.42 [−1.04; 0.20]
Heterogeneity: χ^2_2 = 0.52 (P = .77), I^2 = 0% [0%; 90%]
Total −0.58 [−0.93; −0.24]
Heterogeneity: χ^2_{12} = 11.56 (P = .48), I^2 = 0% [0%; 57%]
Test for overall effect: z = −3.34 (P < .001)
Test for subgroup differences: χ^2_1 = 0.43 (P = .51)
−2 −1 0 1 2
Estimated logOR