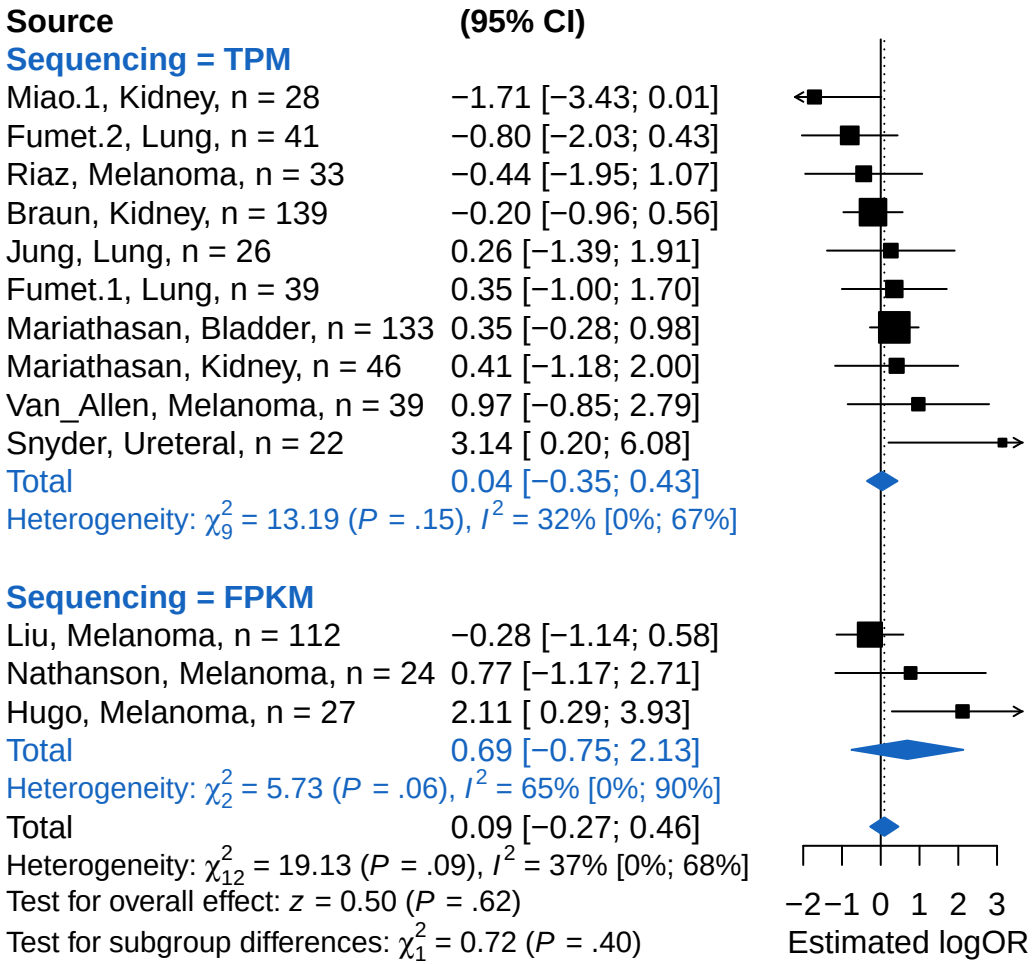
Source
(95% CI)
Sequencing = TPM
Miao.1, Kidney, n = 28 −1.71 [−3.43; 0.01]
Fumet.2, Lung, n = 41 −0.80 [−2.03; 0.43]
Riaz, Melanoma, n = 33 −0.44 [−1.95; 1.07]
Braun, Kidney, n = 139 −0.20 [−0.96; 0.56]
Jung, Lung, n = 26 0.26 [−1.39; 1.91]
Fumet.1, Lung, n = 39 0.35 [−1.00; 1.70]
Mariathasan, Bladder, n = 133 0.35 [−0.28; 0.98]
Mariathasan, Kidney, n = 46 0.41 [−1.18; 2.00]
Van_Allen, Melanoma, n = 39 0.97 [−0.85; 2.79]
Snyder, Ureteral, n = 22 3.14 [0.20; 6.08]
Total 0.04 [−0.35; 0.43]
Heterogeneity: χ^2_9 = 13.19 (P = .15), I^2 = 32% [0%; 67%]
Sequencing = FPKM
Liu, Melanoma, n = 112 −0.28 [−1.14; 0.58]
Nathanson, Melanoma, n = 24 0.77 [−1.17; 2.71]
Hugo, Melanoma, n = 27 2.11 [0.29; 3.93]
Total 0.69 [−0.75; 2.13]
Heterogeneity: χ^2_2 = 5.73 (P = .06), I^2 = 65% [0%; 90%]
Total 0.09 [−0.27; 0.46]
Heterogeneity: χ^2_{12} = 19.13 (P = .09), I^2 = 37% [0%; 68%]
Test for overall effect: z = 0.50 (P = .62)
Test for subgroup differences: χ^2_1 = 0.72 (P = .40)
−2 −1 0 1 2 3
Estimated logOR