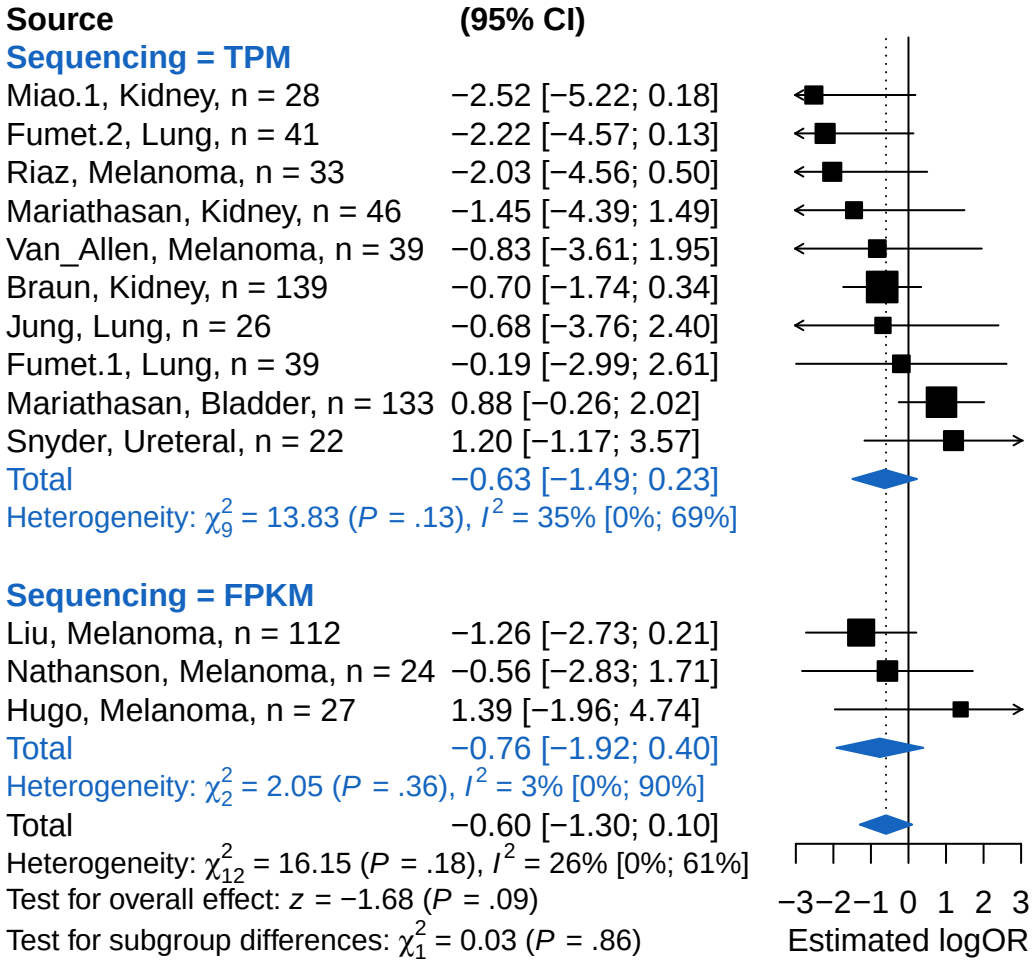
Source
(95% CI)
Sequencing = TPM
Miao.1, Kidney, n = 28
−2.52 [−5.22; 0.18]
Fumet.2, Lung, n = 41
−2.22 [−4.57; 0.13]
Riaz, Melanoma, n = 33
−2.03 [−4.56; 0.50]
Mariathasan, Kidney, n = 46
−1.45 [−4.39; 1.49]
Van_Allen, Melanoma, n = 39
−0.83 [−3.61; 1.95]
Braun, Kidney, n = 139
−0.70 [−1.74; 0.34]
Jung, Lung, n = 26
−0.68 [−3.76; 2.40]
Fumet.1, Lung, n = 39
−0.19 [−2.99; 2.61]
Mariathasan, Bladder, n = 133
0.88 [−0.26; 2.02]
Snyder, Ureteral, n = 22
1.20 [−1.17; 3.57]
Total
−0.63 [−1.49; 0.23]
Heterogeneity: χ^2_9 = 13.83 (P = .13), I^2 = 35% [0%; 69%]
Sequencing = FPKM
Liu, Melanoma, n = 112
−1.26 [−2.73; 0.21]
Nathanson, Melanoma, n = 24
−0.56 [−2.83; 1.71]
Hugo, Melanoma, n = 27
1.39 [−1.96; 4.74]
Total
−0.76 [−1.92; 0.40]
Heterogeneity: χ^2_2 = 2.05 (P = .36), I^2 = 3% [0%; 90%]
Total
−0.60 [−1.30; 0.10]
Heterogeneity: χ^2_{12} = 16.15 (P = .18), I^2 = 26% [0%; 61%]
Test for overall effect: z = −1.68 (P = .09)
Test for subgroup differences: χ^2_1 = 0.03 (P = .86)
−3 −2 −1 0 1 2 3
Estimated logOR