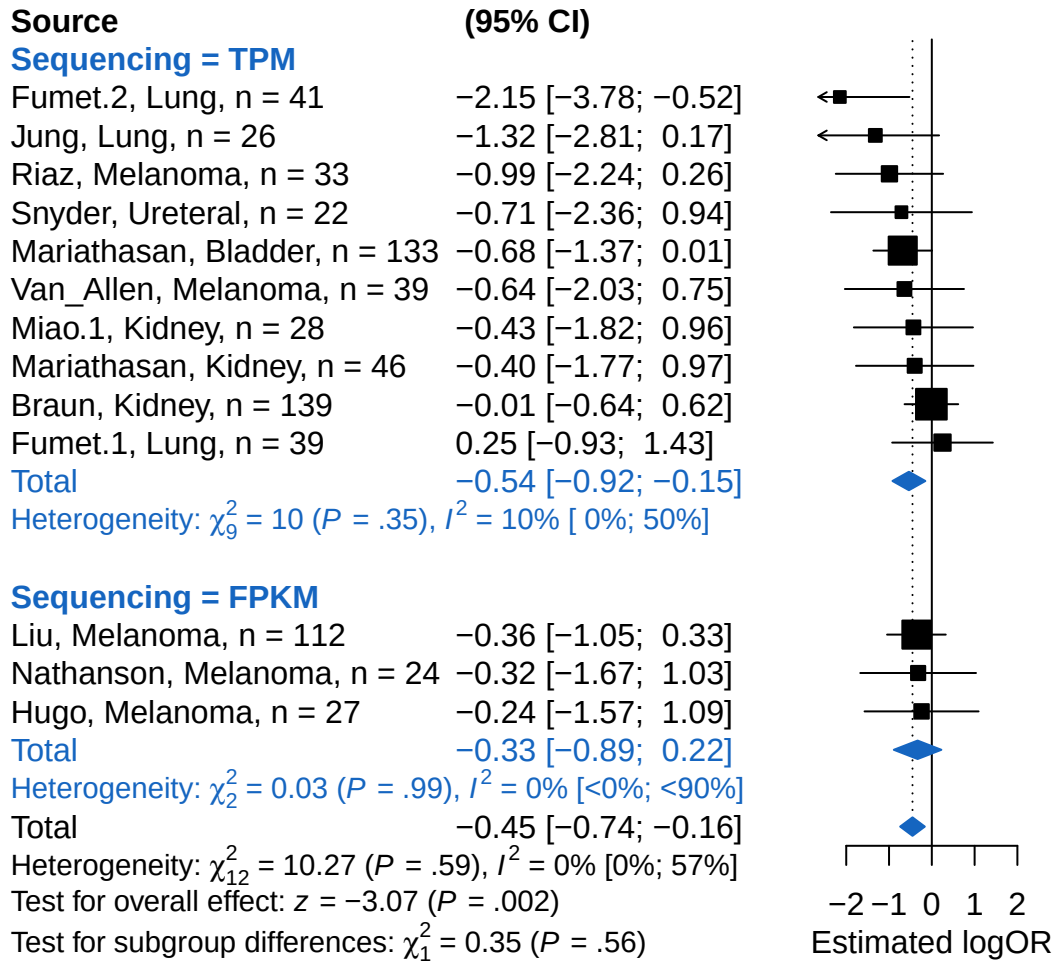
Source
(95% CI)
Sequencing = TPM
Fumet.2, Lung, n = 41 −2.15 [−3.78; −0.52]
Jung, Lung, n = 26 −1.32 [−2.81; 0.17]
Riaz, Melanoma, n = 33 −0.99 [−2.24; 0.26]
Snyder, Ureteral, n = 22 −0.71 [−2.36; 0.94]
Mariathasan, Bladder, n = 133 −0.68 [−1.37; 0.01]
Van_Allen, Melanoma, n = 39 −0.64 [−2.03; 0.75]
Miao.1, Kidney, n = 28 −0.43 [−1.82; 0.96]
Mariathasan, Kidney, n = 46 −0.40 [−1.77; 0.97]
Braun, Kidney, n = 139 −0.01 [−0.64; 0.62]
Fumet.1, Lung, n = 39 0.25 [−0.93; 1.43]
Total −0.54 [−0.92; −0.15]
Heterogeneity: χ^2_9 = 10 (P = .35), I^2 = 10% [0%; 50%]
Sequencing = FPKM
Liu, Melanoma, n = 112 −0.36 [−1.05; 0.33]
Nathanson, Melanoma, n = 24 −0.32 [−1.67; 1.03]
Hugo, Melanoma, n = 27 −0.24 [−1.57; 1.09]
Total −0.33 [−0.89; 0.22]
Heterogeneity: χ^2_2 = 0.03 (P = .99), I^2 = 0% [<0%; <90%]
Total −0.45 [−0.74; −0.16]
Heterogeneity: χ^2_{12} = 10.27 (P = .59), I^2 = 0% [0%; 57%]
Test for overall effect: z = −3.07 (P = .002)
Test for subgroup differences: χ^2_1 = 0.35 (P = .56)
−2 −1 0 1 2
Estimated logOR