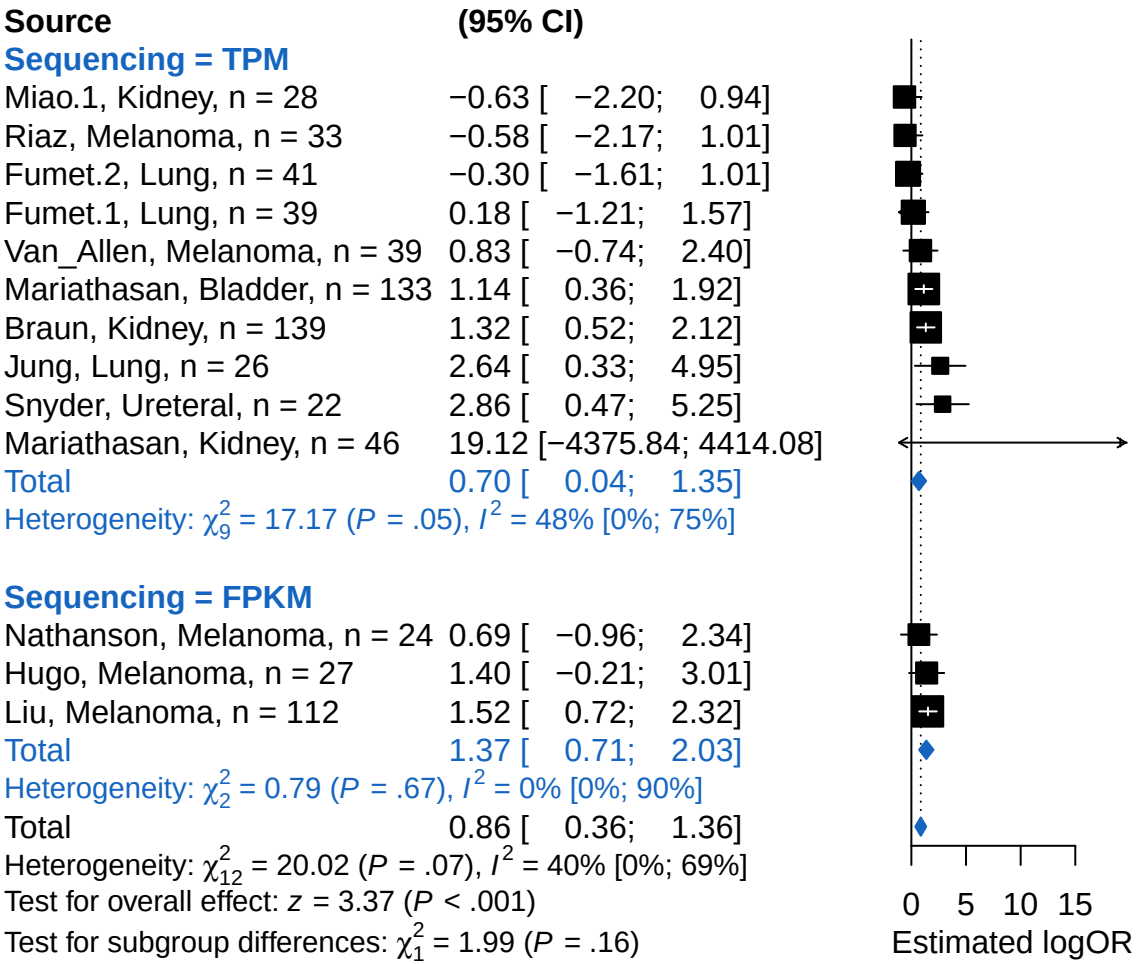
Source
(95% CI)
Sequencing = TPM
Miao.1, Kidney, n = 28 −0.63 [−2.20; 0.94]
Riaz, Melanoma, n = 33 −0.58 [−2.17; 1.01]
Fumet.2, Lung, n = 41 −0.30 [−1.61; 1.01]
Fumet.1, Lung, n = 39 0.18 [−1.21; 1.57]
Van_Allen, Melanoma, n = 39 0.83 [−0.74; 2.40]
Mariathasan, Bladder, n = 133 1.14 [0.36; 1.92]
Braun, Kidney, n = 139 1.32 [0.52; 2.12]
Jung, Lung, n = 26 2.64 [0.33; 4.95]
Snyder, Ureteral, n = 22 2.86 [0.47; 5.25]
Mariathasan, Kidney, n = 46 19.12 [−4375.84; 4414.08]
Total 0.70 [0.04; 1.35]
Heterogeneity: χ^2_9 = 17.17 (P = .05), I^2 = 48% [0%; 75%]
Sequencing = FPKM
Nathanson, Melanoma, n = 24 0.69 [−0.96; 2.34]
Hugo, Melanoma, n = 27 1.40 [−0.21; 3.01]
Liu, Melanoma, n = 112 1.52 [0.72; 2.32]
Total 1.37 [0.71; 2.03]
Heterogeneity: χ^2_2 = 0.79 (P = .67), I^2 = 0% [0%; 90%]
Total 0.86 [0.36; 1.36]
Heterogeneity: χ^2_{12} = 20.02 (P = .07), I^2 = 40% [0%; 69%]
Test for overall effect: z = 3.37 (P < .001)
Test for subgroup differences: χ^2_1 = 1.99 (P = .16)
0
5
10
15
Estimated logOR