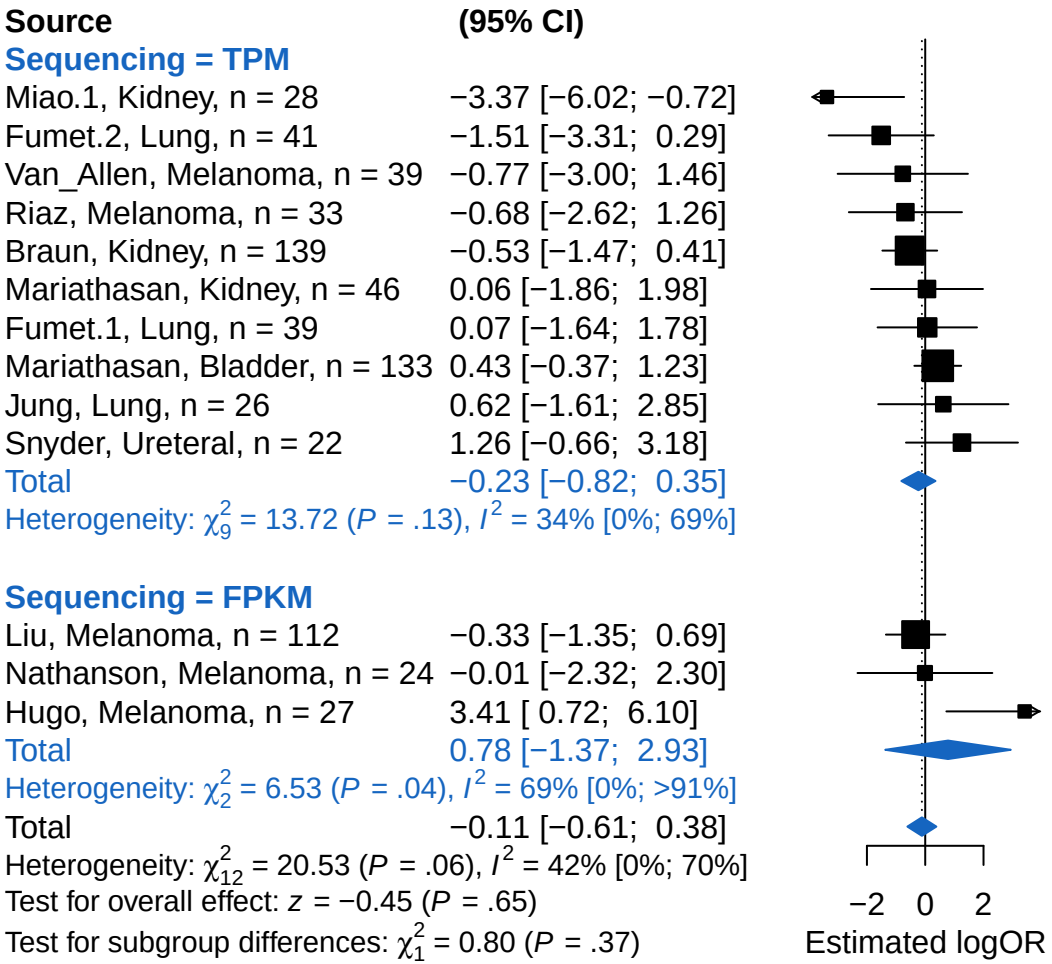
Source
(95% CI)
Sequencing = TPM
Miao.1, Kidney, n = 28 −3.37 [−6.02; −0.72]
Fumet.2, Lung, n = 41 −1.51 [−3.31; 0.29]
Van_Allen, Melanoma, n = 39 −0.77 [−3.00; 1.46]
Riaz, Melanoma, n = 33 −0.68 [−2.62; 1.26]
Braun, Kidney, n = 139 −0.53 [−1.47; 0.41]
Mariathasan, Kidney, n = 46 0.06 [−1.86; 1.98]
Fumet.1, Lung, n = 39 0.07 [−1.64; 1.78]
Mariathasan, Bladder, n = 133 0.43 [−0.37; 1.23]
Jung, Lung, n = 26 0.62 [−1.61; 2.85]
Snyder, Ureteral, n = 22 1.26 [−0.66; 3.18]
Total −0.23 [−0.82; 0.35]
Heterogeneity: χ^2_9 = 13.72 (P = .13), I^2 = 34% [0%; 69%]
Sequencing = FPKM
Liu, Melanoma, n = 112 −0.33 [−1.35; 0.69]
Nathanson, Melanoma, n = 24 −0.01 [−2.32; 2.30]
Hugo, Melanoma, n = 27 3.41 [0.72; 6.10]
Total 0.78 [−1.37; 2.93]
Heterogeneity: χ^2_2 = 6.53 (P = .04), I^2 = 69% [0%; >91%]
Total −0.11 [−0.61; 0.38]
Heterogeneity: χ^2_{12} = 20.53 (P = .06), I^2 = 42% [0%; 70%]
Test for overall effect: z = −0.45 (P = .65)
Test for subgroup differences: χ^2_1 = 0.80 (P = .37)
−2
0
2
Estimated logOR