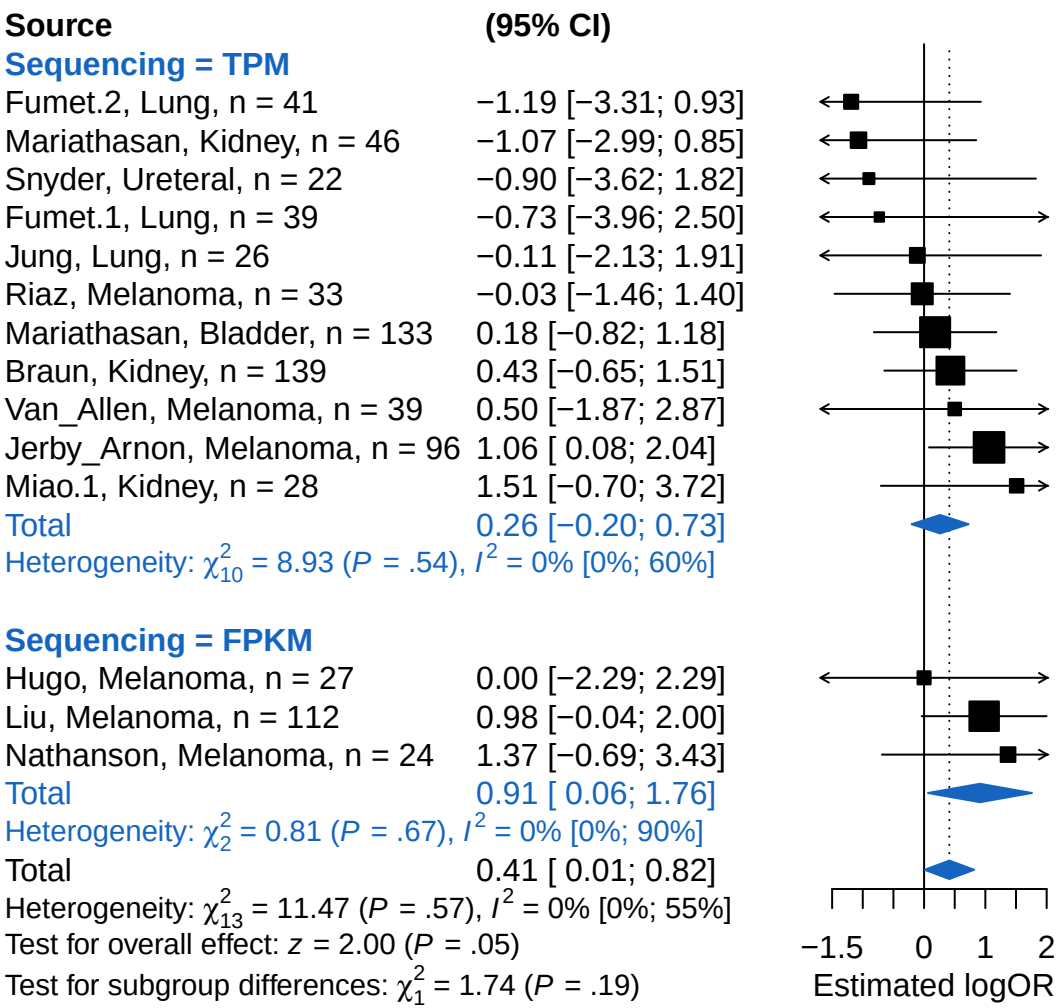
Source
(95% CI)
Sequencing = TPM
Fumet.2, Lung, n = 41
−1.19 [−3.31; 0.93]
Mariathasan, Kidney, n = 46
−1.07 [−2.99; 0.85]
Snyder, Ureteral, n = 22
−0.90 [−3.62; 1.82]
Fumet.1, Lung, n = 39
−0.73 [−3.96; 2.50]
Jung, Lung, n = 26
−0.11 [−2.13; 1.91]
Riaz, Melanoma, n = 33
−0.03 [−1.46; 1.40]
Mariathasan, Bladder, n = 133
0.18 [−0.82; 1.18]
Braun, Kidney, n = 139
0.43 [−0.65; 1.51]
Van_Allen, Melanoma, n = 39
0.50 [−1.87; 2.87]
Jerby_Arnon, Melanoma, n = 96
1.06 [0.08; 2.04]
Miao.1, Kidney, n = 28
1.51 [−0.70; 3.72]
Total
0.26 [−0.20; 0.73]
Heterogeneity: χ^2_{10} = 8.93 (P = .54), I^2 = 0% [0%; 60%]
Sequencing = FPKM
Hugo, Melanoma, n = 27
0.00 [−2.29; 2.29]
Liu, Melanoma, n = 112
0.98 [−0.04; 2.00]
Nathanson, Melanoma, n = 24
1.37 [−0.69; 3.43]
Total
0.91 [0.06; 1.76]
Heterogeneity: χ^2_2 = 0.81 (P = .67), I^2 = 0% [0%; 90%]
Total
0.41 [0.01; 0.82]
Heterogeneity: χ^2_{13} = 11.47 (P = .57), I^2 = 0% [0%; 55%]
Test for overall effect: z = 2.00 (P = .05)
Test for subgroup differences: χ^2_1 = 1.74 (P = .19)
−1.5
0
1
2
Estimated logOR