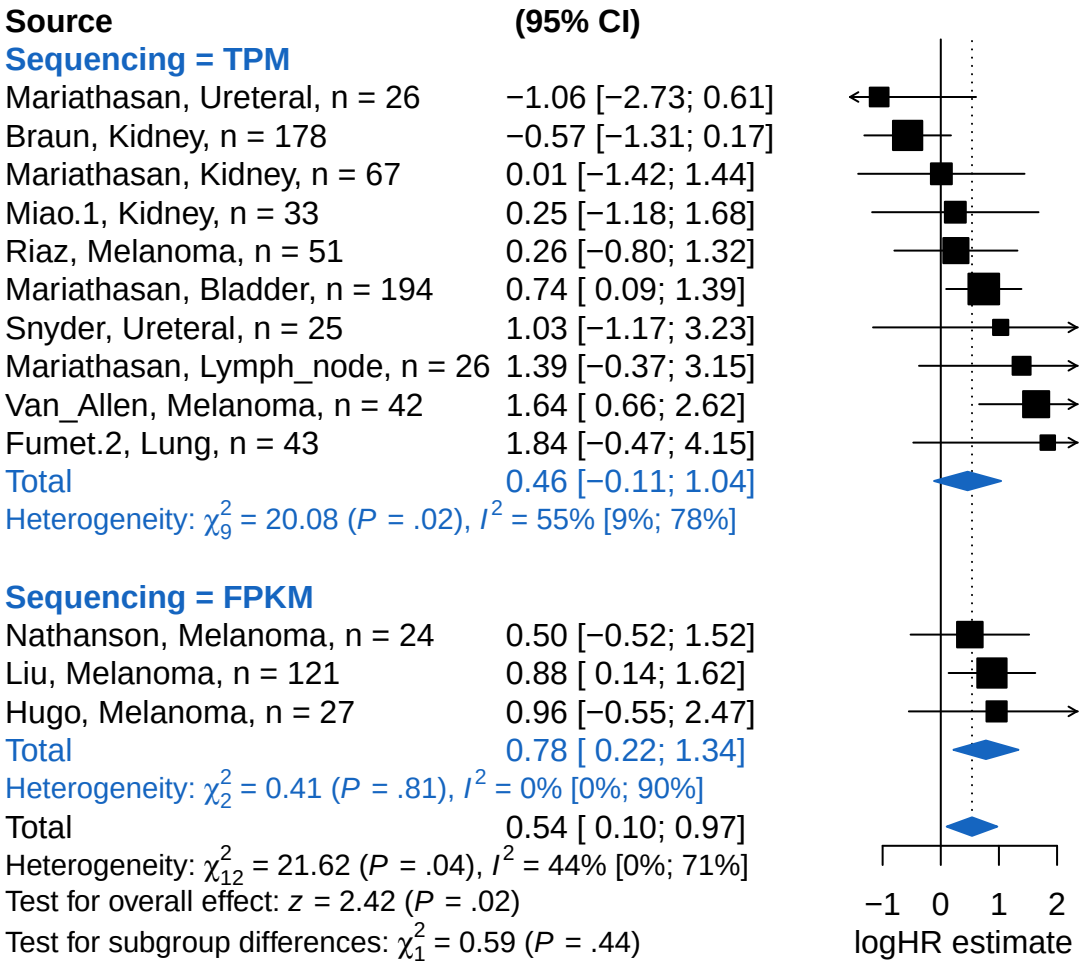
Source
(95% CI)
Sequencing = TPM
Mariathasan, Ureteral, n = 26
−1.06 [−2.73; 0.61]
Braun, Kidney, n = 178
−0.57 [−1.31; 0.17]
Mariathasan, Kidney, n = 67
0.01 [−1.42; 1.44]
Miao.1, Kidney, n = 33
0.25 [−1.18; 1.68]
Riaz, Melanoma, n = 51
0.26 [−0.80; 1.32]
Mariathasan, Bladder, n = 194
0.74 [0.09; 1.39]
Snyder, Ureteral, n = 25
1.03 [−1.17; 3.23]
Mariathasan, Lymph_node, n = 26
1.39 [−0.37; 3.15]
Van_Allen, Melanoma, n = 42
1.64 [0.66; 2.62]
Fumet.2, Lung, n = 43
1.84 [−0.47; 4.15]
Total
0.46 [−0.11; 1.04]
Heterogeneity: χ^2_9 = 20.08 (P = .02), I^2 = 55% [9%; 78%]
Sequencing = FPKM
Nathanson, Melanoma, n = 24
0.50 [−0.52; 1.52]
Liu, Melanoma, n = 121
0.88 [0.14; 1.62]
Hugo, Melanoma, n = 27
0.96 [−0.55; 2.47]
Total
0.78 [0.22; 1.34]
Heterogeneity: χ^2_2 = 0.41 (P = .81), I^2 = 0% [0%; 90%]
Total
0.54 [0.10; 0.97]
Heterogeneity: χ^2_{12} = 21.62 (P = .04), I^2 = 44% [0%; 71%]
Test for overall effect: z = 2.42 (P = .02)
Test for subgroup differences: χ^2_1 = 0.59 (P = .44)
−1
0
1
2
logHR estimate