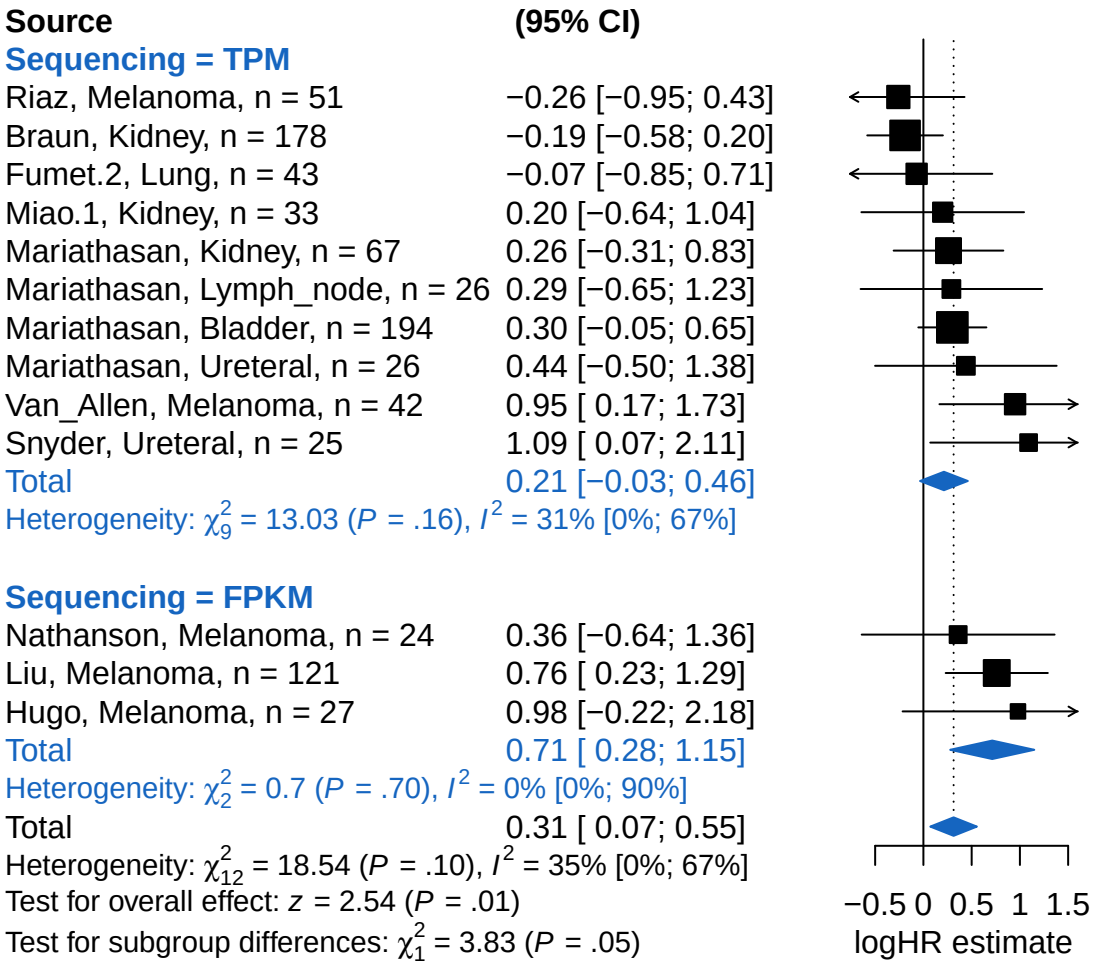
Source
(95% CI)
Sequencing = TPM
Riaz, Melanoma, n = 51
−0.26 [−0.95; 0.43]
Braun, Kidney, n = 178
−0.19 [−0.58; 0.20]
Fumet.2, Lung, n = 43
−0.07 [−0.85; 0.71]
Miao.1, Kidney, n = 33
0.20 [−0.64; 1.04]
Mariathasan, Kidney, n = 67
0.26 [−0.31; 0.83]
Mariathasan, Lymph_node, n = 26
0.29 [−0.65; 1.23]
Mariathasan, Bladder, n = 194
0.30 [−0.05; 0.65]
Mariathasan, Ureteral, n = 26
0.44 [−0.50; 1.38]
Van_Allen, Melanoma, n = 42
0.95 [0.17; 1.73]
Snyder, Ureteral, n = 25
1.09 [0.07; 2.11]
Total
0.21 [−0.03; 0.46]
Heterogeneity: χ^2_9 = 13.03 (P = .16), I^2 = 31% [0%; 67%]
Sequencing = FPKM
Nathanson, Melanoma, n = 24
0.36 [−0.64; 1.36]
Liu, Melanoma, n = 121
0.76 [0.23; 1.29]
Hugo, Melanoma, n = 27
0.98 [−0.22; 2.18]
Total
0.71 [0.28; 1.15]
Heterogeneity: χ^2_2 = 0.7 (P = .70), I^2 = 0% [0%; 90%]
Total
0.31 [0.07; 0.55]
Heterogeneity: χ^2_{12} = 18.54 (P = .10), I^2 = 35% [0%; 67%]
Test for overall effect: z = 2.54 (P = .01)
Test for subgroup differences: χ^2_1 = 3.83 (P = .05)
−0.5 0 0.5 1 1.5
logHR estimate