## Source (95% CI)

## Sequencing = FPKM

Hugo, Melanoma, n = 27-0.84 [-1.92; 0.24] -0.22 [-0.61; 0.17] Liu, Melanoma, n = 121 Nathanson, Melanoma, n = 24 -0.07 [-0.95; 0.81] -0.26 [-0.60; 0.08] Total

Heterogeneity:  $\chi_2^2 = 1.33 \ (P = .51), \ I^2 = 0\% \ [0\%; 90\%]$ 

## Sequencing = TPM

Van Allen, Melanoma, n = 42 -0.75[-1.36; -0.14]Riaz, Melanoma, n = 51-0.65 [-1.20; -0.10] Mariathasan, Lymph\_node, n = 26 - 0.61 [-1.53; 0.31]Snyder, Ureteral, n = 25-0.51 [-1.27; 0.25] Mariathasan, Bladder, n = 194-0.23 [-0.50; 0.04] Fumet.2, Lung, n = 43-0.08 [-0.81; 0.65] Braun, Kidney, n = 178-0.03 [-0.34; 0.28] Mariathasan, Kidney, n = 67 0.04 [-0.45; 0.53] Mariathasan, Ureteral, n = 260.28 [-0.48; 1.04] Miao.1, Kidney, n = 330.40 [-0.31; 1.11]

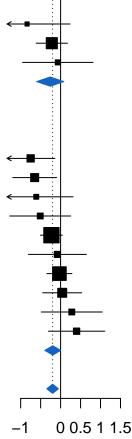
Total -0.20 [-0.40; 0.00] Heterogeneity:  $\chi_9^2 = 13.59 (P = .14), I^2 = 34\% [0\%; 68\%]$ 

-0.20 [-0.35; -0.05] Total

Heterogeneity:  $\chi_{12}^2 = 15.06 \ (P = .24), \ I^2 = 20\% \ [0\%; 58\%]$ 

Test for overall effect: z = -2.70 (P = .007)

Test for subgroup differences:  $\chi_1^2 = 0.10 \ (P = .75)$ 



D.Index estimate