## Source (95% CI)

## Sequencing = FPKM

Liu, Melanoma, n = 121 -0.98 [-1.90; -0.06] Nathanson, Melanoma, n = 24 -0.60 [-2.29; 1.09] Hugo, Melanoma, n = 27 0.60 [-1.24; 2.44] Total -0.60 [-1.43; 0.22]

Heterogeneity:  $\chi_2^2 = 2.26$  (P = .32),  $I^2 = 12\%$  [0%; 91%]

## Sequencing = TPM

Van Allen, Melanoma, n = 42 -0.84 [-2.19; 0.51] Riaz, Melanoma, n = 51-0.78 [-2.15; 0.59] Miao.1, Kidney, n = 33-0.75 [-2.51; 1.01] Snyder, Ureteral, n = 25-0.58 [-2.40; 1.24] Mariathasan, Kidney, n = 670.00 [-0.98; 0.98] Braun, Kidney, n = 1780.19 [-0.40; 0.78] Mariathasan, Bladder, n = 1940.20 [-0.33; 0.73] Fumet.2, Lung, n = 430.59 [-0.80; 1.98] Mariathasan, Lymph\_node,  $n = 26 \ 0.60 \ [-1.71; \ 2.91]$ Mariathasan, Ureteral, n = 26 1.71 [ 0.10; 3.32] 0.10 [-0.21; 0.41] Total Heterogeneity:  $\chi_9^2 = 9.64$  (P = .38),  $I^2 = 7\%$  [0%; 65%] Total -0.05 [-0.41; 0.30] Heterogeneity:  $\chi_{12}^2 = 15.29 \ (P = .23), \ I^2 = 22\% \ [0\%; 59\%]$ Test for overall effect: z = -0.29 (P = .78)

Total  $0.10 \ [-0.21; \ 0.41]$ Heterogeneity:  $\chi_9^2 = 9.64 \ (P = .38), \ I^2 = 7\% \ [0\%; \ 65\%]$ Total  $-0.05 \ [-0.41; \ 0.30]$ Heterogeneity:  $\chi_{12}^2 = 15.29 \ (P = .23), \ I^2 = 22\% \ [0\%; \ 59\%]$ Test for overall effect:  $z = -0.29 \ (P = .78)$ Test for subgroup differences:  $\chi_1^2 = 2.46 \ (P = .12)$  logHR estimate