## Source (95% CI)

## **Sequencing = TPM**

Riaz, Melanoma, n = 33-2.07 [-4.38; 0.24] Miao.1, Kidney, n = 28-1.85 [-3.83; 0.13] -0.95 [-2.79; 0.89] Fumet.2, Lung, n = 41Snyder, Ureteral, n = 22-0.81 [-3.40; 1.78] Braun, Kidney, n = 1390.07 [-0.93; 1.07] Mariathasan, Kidney, n = 460.14[-2.33; 2.61]Fumet.1, Lung, n = 390.45 [-1.94; 2.84] Mariathasan, Bladder,  $n = 133 \ 0.86 \ [-0.30; \ 2.02]$ Jung, Lung, n = 261.27 [-0.81; 3.35] Van\_Allen, Melanoma,  $n = 39 \ 1.48 [-0.81; 3.77]$ -0.04 [-0.74; 0.66] Total Heterogeneity:  $\chi_0^2 = 13.14$  (P = .16),  $I^2 = 31\%$  [0%; 67%]

## **Sequencing = FPKM**

Liu, Melanoma, n = 112 -0.40 [-1.48; 0.68] Nathanson, Melanoma, n = 24 -0.38 [-2.83; 2.07] Hugo, Melanoma, n = 27 0.25 [-1.73; 2.23] Total -0.27 [-1.15; 0.62] Heterogeneity:  $\chi_2^2 = 0.33$  (P = .85),  $I^2 = 0\%$  [0%; 90%] Total -0.06 [-0.56; 0.44] Heterogeneity:  $\chi_{12}^2 = 13.80$  (P = .31),  $I^2 = 13\%$  [0%; 52%] Test for overall effect: z = -0.23 (P = .82) Test for subgroup differences:  $\chi_1^2 = 0.15$  (P = .69)

