Source (95% CI)

Sequencing = TPM

Snyder, Ureteral, n = 22-0.85 [-1.91; 0.21] Jung, Lung, n = 26-0.77 [-1.77; 0.23] Miao.1, Kidney, n = 28-0.48 [-1.28; 0.32] -0.39 [-0.78; 0.00] Braun, Kidney, n = 139Fumet.1, Lung, n = 39-0.32 [-1.03; 0.39] Riaz, Melanoma, n = 33-0.10 [-0.86; 0.66] Mariathasan, Kidney, n = 460.01 [-0.70; 0.72] Fumet.2, Lung, n = 410.13 [-0.52; 0.78] Mariathasan, Bladder, n = 133 0.20 [-0.19; 0.59] Van_Allen, Melanoma, $n = 39 \ 0.40 \ [-0.44; 1.24]$ -0.14 [-0.38; 0.09] Total Heterogeneity: $\chi_0^2 = 11.07 \ (P = .27), I^2 = 19\% \ [0\%; 59\%]$

Sequencing = FPKM

Liu, Melanoma, n = 112 -0.36 [-0.75; 0.03] Hugo, Melanoma, n = 27 -0.03 [-0.79; 0.73] Nathanson, Melanoma, n = 24 0.72 [-0.24; 1.68] Total -0.02 [-0.59; 0.56] Heterogeneity: $\chi_2^2 = 4.33$ (P = .11), $I^2 = 54\%$ [0%; 87%] Total -0.14 [-0.34; 0.06] Heterogeneity: $\chi_{12}^2 = 15.44$ (P = .22), $I^2 = 22\%$ [0%; 59%] Test for overall effect: z = -1.34 (P = .18) Test for subgroup differences: $\chi_1^2 = 0.16$ (P = .69)

