Source (95% CI)

Sequencing = TPM

Hwang, Lung, n = 21-0.97 [-2.19; 0.25] -0.82 [-1.47; -0.17] Riaz, Melanoma, n = 51Van_Allen, Melanoma, n = 42 -0.78 [-1.47; -0.09] -0.30[-0.55; -0.05]Mariathasan, Bladder, n = 194Fumet.2, Lung, n = 43-0.19 [-0.78; 0.40] Miao.1, Kidney, n = 33-0.16 [-0.89; 0.57] Mariathasan, Lymph_node, n = 26 -0.13 [-0.86; 0.60]-0.03 [-0.52; 0.46] Mariathasan, Kidney, n = 67Snyder, Ureteral, n = 250.08 [-0.68; 0.84] Braun, Kidney, n = 1780.13 [-0.20; 0.46] Mariathasan, Ureteral, n = 260.84 [0.02; 1.66] -0.18 [-0.41; 0.05] Total Heterogeneity: $\chi_{10}^2 = 19.22 \ (P = .04), \ I^2 = 48\% \ [0\%; 74\%]$

Sequencing = FPKM

