Source (95% CI)

Sequencing = FPKM

Liu, Melanoma, n = 121 -0.42 [-0.93; 0.09] Nathanson, Melanoma, n = 24 -0.20 [-1.18; 0.78] Hugo, Melanoma, n = 270.10 [-1.04; 1.24]

Total -0.31 [-0.73; 0.11] Heterogeneity: $\chi^2_2 = 0.73$ (P = .70), $I^2 = 0\%$ [0%; 90%]

Sequencing = TPM

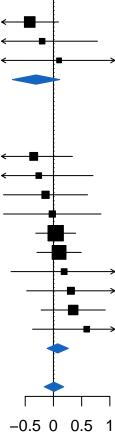
Riaz, Melanoma, n = 51 -0.35 [-1.04; 0.34] Snyder, Ureteral, n = 25-0.26 [-1.22; 0.70] -0.14[-0.88; 0.60]Van_Allen, Melanoma, n = 42 Miao.1, Kidney, n = 33-0.02 [-0.88; 0.84] Mariathasan, Bladder, n = 1940.04 [-0.31; 0.39] Braun, Kidney, n = 1780.10 [-0.29; 0.49] Mariathasan, Lymph_node, $n = 26 \ 0.19 \ [-0.75; 1.13]$ Fumet.2, Lung, n = 430.31 [-0.47; 1.09] Mariathasan, Kidney, n = 670.35 [-0.22; 0.92] Mariathasan, Ureteral, n = 260.59 [-0.37; 1.55] 0.08 [-0.11; 0.27] Total

Heterogeneity: $\chi_9^2 = 4.77 \ (P = .85), \ I^2 = 0\% \ [0\%; 62\%]$

Total 0.01 [-0.16; 0.18] Heterogeneity: χ^2_{12} = 8.17 (P = .77), I^2 = 0% [0%; 57%]

Test for overall effect: z = 0.12 (P = .90)

Test for subgroup differences: $\chi_1^2 = 2.67$ (P = .10)



logHR estimate