Source (95% CI) Sequencing = TPM Hwang, Lung, n = 21-1.16 [-2.36; 0.04]

Van_Allen, Melanoma, n = 42 **-1.01** [**-1.77**; **-0.25**] Mariathasan, Lymph_node, n = 26 - 0.85 [-1.81; 0.11]Riaz, Melanoma, n = 51-0.51 [-1.20; 0.18] Fumet.2, Lung, n = 43-0.40 [-1.20; 0.40] Mariathasan, Bladder, n = 194-0.29 [-0.64; 0.06] Snyder, Ureteral, n = 25-0.29 [-1.25; 0.67]

-0.19 [-0.76; 0.38] Mariathasan, Kidney, n = 67Miao.1, Kidney, n = 33-0.08 [-0.94; 0.78]

Braun, Kidney, n = 1780.07 [-0.32; 0.46] Mariathasan, Ureteral, n = 260.71 [-0.27; 1.69]

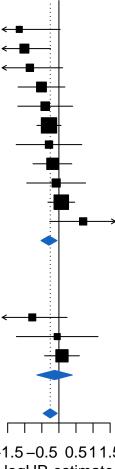
Total -0.29 [-0.52; -0.05] Heterogeneity: $\chi_{10}^2 = 14.69$ (P = .14), $I^2 = 32\%$ [0%; 67%]

Sequencing = FPKM

Nathanson, Melanoma, n = 24-0.78 [-1.80; 0.24] -0.05 [-1.25; 1.15] Hugo, Melanoma, n = 27Liu, Melanoma, n = 121 0.09 [-0.42; 0.60] Total -0.13 [-0.64; 0.39]Heterogeneity: $\chi_2^2 = 2.24 (P = .33), I^2 = 11\% [0\%; 91\%]$

rotal -0.25 [-0.46; -0.05]Heterogeneity: $\chi_{13}^2 = 17.50 (P = .18), I^2 = 26\% [0\%; 61\%]$ Test for overall effect: z = -2.42 (P = .02)

Test for subgroup differences: $\chi_1^2 = 0.32$ (P = .57)



-1.5 - 0.5 0.511.5logHR estimate