Source (95% CI)

Sequencing = FPKM

Nathanson, Melanoma, n = 24-1.36 [-2.46; -0.26] Liu, Melanoma, n = 121 -0.70 [-1.21; -0.19] Hugo, Melanoma, n = 270.07 [-1.09; 1.23] Total -0.69 [-1.12; -0.27] Heterogeneity: $\chi_2^2 = 3.09$ (P = .21), $I^2 = 35\%$ [0%; 79%]

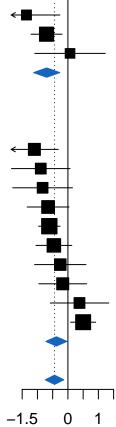
Sequencing = TPM

Van Allen, Melanoma, n = 42 **-1.10** [**-1.88**; **-0.32**] Mariathasan, Lymph_node, n = 26 - 0.89 [-1.85; 0.07]Snyder, Ureteral, n = 25-0.83 [-1.81; 0.15] -0.65 [-1.34; 0.04] Riaz, Melanoma, n = 51Mariathasan, Bladder, n = 194 -0.61 [-0.96; -0.26] Mariathasan, Kidney, n = 67-0.46 [-1.05; 0.13] Miao.1, Kidney, n = 33-0.25 [-1.09; 0.59] -0.17 [-0.95; 0.61] Fumet.2, Lung, n = 43Mariathasan, Ureteral, n = 260.38 [-0.58; 1.34] Braun, Kidney, n = 1780.50 [0.09; 0.91] Total -0.38 [-0.72; -0.03]Heterogeneity: $\chi_9^2 = 27.35 (P = .001), I^2 = 67\% [36\%; 83\%]$ Total -0.44[-0.74; -0.13]

Heterogeneity: $\chi_{12}^2 = 32.92 \ (P < .001), \ I^2 = 64\% \ [34\%; 80\%]$

Test for overall effect: z = -2.83 (P = .005)

Test for subgroup differences: $\chi_1^2 = 1.27$ (P = .26)



logHR estimate