## (95% CI) Source Sequencing = TPM Van\_Allen, Melanoma, n = 42

-0.61 [-1.10; -0.12] Riaz, Melanoma, n = 51 -0.42 [-0.81; -0.03] Snyder, Ureteral, n = 25-0.38 [-0.87; 0.11] Mariathasan, Lymph\_node, n = 26 - 0.37 [-0.90; 0.16]

Mariathasan, Bladder, n = 194-0.15 [-0.33; 0.03] Braun, Kidney, n = 178-0.02 [-0.22; 0.18]

Fumet.2, Lung, n = 43-0.02 [-0.45; 0.41]

Mariathasan, Kidney, n = 670.03 [-0.26; 0.32] Mariathasan, Ureteral, n = 260.11 [-0.34; 0.56]

Miao.1, Kidney, n = 330.23 [-0.20; 0.66] -0.12 [-0.24; 0.00]

Total Heterogeneity:  $\chi_0^2 = 13.85 (P = .13), I^2 = 35\% [0\%; 69\%]$ 

## Sequencing = FPKM

Hugo, Melanoma, n = 27 -0.58 [-1.23; 0.07] -0.13 [-0.38; 0.12] Liu, Melanoma, n = 121 Nathanson, Melanoma, n = 24-0.07 [-0.60; 0.46] -0.17 [-0.39; 0.05] Total

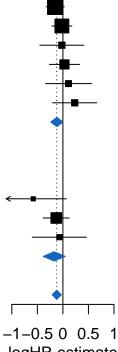
Heterogeneity:  $\chi_2^2 = 1.78 \ (P = .41), \ I^2 = 0\% \ [0\%; 90\%]$ 

-0.12 [-0.21; -0.03] Total

Heterogeneity:  $\chi_{12}^2 = 15.86 \ (P = .20), \ I^2 = 24\% \ [0\%; 61\%]$ 

Test for overall effect: z = -2.65 (P = .008)

Test for subgroup differences:  $\chi_1^2 = 0.17$  (P = .68)



logHR estimate