Source (95% CI)

Sequencing = FPKM

Heterogeneity: $\chi_2^2 = 2.61$ (P = .27), $I^2 = 23\%$ [0%; 92%]

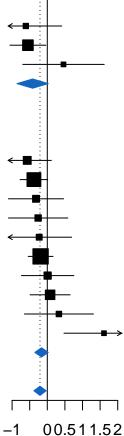
Sequencing = TPM

Riaz, Melanoma, n = 51 -0.57 [-1.26; 0.12] -0.38 [-0.77; 0.01] Braun, Kidney, n = 178Fumet.2, Lung, n = 43-0.32 [-1.10; 0.46] -0.26 [-1.10; 0.58] Miao.1, Kidney, n = 33Mariathasan, Lymph_node, n = 26 - 0.23 [-1.15; 0.69]Mariathasan, Bladder, n = 194-0.19 [-0.54; 0.16] Van Allen, Melanoma, n = 420.01 [-0.73; 0.75] 0.08 [-0.49; 0.65] Mariathasan, Kidney, n = 67Snyder, Ureteral, n = 250.33 [-0.65; 1.31] Mariathasan, Ureteral, n = 261.61 [0.47; 2.75] -0.16 [-0.35; 0.03] Total Heterogeneity: $\chi_9^2 = 14$ (P = .12), $I^2 = 36\%$ [0%; 69%] Total -0.21 [-0.38; -0.03]

Heterogeneity: $\chi_{12}^2 = 17.82 \ (P = .12), \ I^2 = 33\% \ [0\%; 65\%]$

Test for overall effect: z = -2.34 (P = .02)

Test for subgroup differences: $\chi_1^2 = 1.06 \ (P = .30)$



–1 00.511.52 logHR estimate