Source (95% CI)

Sequencing = FPKM

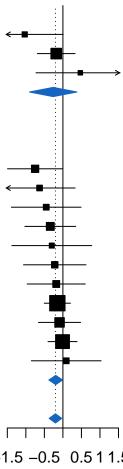
-1.03 [-2.07; 0.01] Nathanson, Melanoma, n = 24-0.18 [-0.69; 0.33] Liu, Melanoma, n = 121 Hugo, Melanoma, n = 270.47 [-0.73; 1.67] -0.26 [-0.90; 0.38] Total Heterogeneity: $\chi_2^2 = 3.63$ (P = .16), $I^2 = 45\%$ [0%; 84%]

Sequencing = TPM

Van_Allen, Melanoma, n = 42 -0.75[-1.49; -0.01]Snyder, Ureteral, n = 25-0.63 [-1.59; 0.33] Mariathasan, Lymph_node, n = 26 - 0.45 [-1.39; 0.49]Riaz, Melanoma, n = 51-0.34 [-1.03; 0.35] Hwang, Lung, n = 21-0.30 [-1.38; 0.78] Miao.1, Kidney, n = 33-0.22 [-1.06; 0.62] Fumet.2, Lung, n = 43-0.18 [-0.96; 0.60] Mariathasan, Bladder, n = 194-0.15 [-0.50; 0.20] Mariathasan, Kidney, n = 67-0.09 [-0.66; 0.48] Braun, Kidney, n = 178-0.01 [-0.40; 0.38] Mariathasan, Ureteral, n = 260.09 [-0.85; 1.03] Total -0.19 [-0.38; -0.01] Heterogeneity: $\chi_{10}^2 = 4.82$ (P = .90), $I^2 = 0\%$ [0%; 60%] -0.20 [-0.37; -0.03] Heterogeneity: $\chi_{13}^2 = 8.49 \ (P = .81), \ I^2 = 0\% \ [0\%; 55\%]$

Test for overall effect: z = -2.31 (P = .02)

Test for subgroup differences: $\chi_1^2 = 0.04$ (P = .84)



-1.5 -0.5 0.5 1 1.5 logHR estimate