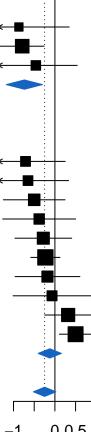
Source (95% CI) Sequencing = FPKM Hugo, Melanoma, n = 27-0.87 [-2.09; 0.35] Liu, Melanoma, n = 121 -0.79 [-1.32; -0.26] Nathanson, Melanoma, n = 24-0.46 [-1.46; 0.54] -0.74 [-1.17; -0.30] Total Heterogeneity: $\chi_2^2 = 0.38 \ (P = .83), \ I^2 = 0\% \ [0\%; 90\%]$ Sequencing = TPM Mariathasan, Lymph node, n = 26 - 0.71 [-1.67; 0.25]Snyder, Ureteral, n = 25-0.65 [-1.63; 0.33] Van_Allen, Melanoma, n = 42 -0.50 [-1.24; 0.24] -0.38 [-1.26; 0.50] -0.28 [-0.97; 0.41]

Miao.1, Kidney, n = 33Riaz, Melanoma, n = 51 Mariathasan, Bladder, n = 194-0.23 [-0.58; 0.12] Fumet.2, Lung, n = 43-0.18 [-0.96; 0.60] -0.07 [-1.01; 0.87] Mariathasan, Ureteral, n = 26Mariathasan, Kidney, n = 670.32 [-0.25; 0.89] Braun, Kidney, n = 1780.50 [0.11; 0.89] -0.12 [-0.40; 0.16] Total Heterogeneity: $\chi_9^2 = 15.92 \ (P = .07), \ I^2 = 43\% \ [0\%; 73\%]$ -0.25 [-0.52; 0.02] Total Heterogeneity: $\chi_{12}^2 = 24.30 \ (P = .02), \ I^2 = 51\% \ [7\%; 74\%]$ Test for overall effect: z = -1.79 (P = .07)

Test for subgroup differences: $\chi_1^2 = 5.38 \ (P = .02)$



0 0.5 1 -1 logHR estimate