## Source (95% CI) Sequencing = TPM -2.33[-4.29; -0.37]Jung, Lung, n = 26Fumet.2, Lung, n = 41-2.06 [-3.73; -0.39] -1.20 [-3.32; 0.92] Snyder, Ureteral, n = 22Riaz, Melanoma, n = 33 -0.80 [-2.05; 0.45] Mariathasan, Bladder, n = 133 - 0.62 [-1.27; 0.03]Braun, Kidney, n = 139-0.28 [-1.02; 0.46] Van\_Allen, Melanoma, n = 39 -0.27 [-1.72; 1.18]Mariathasan, Kidney, n = 46-0.23 [-1.60; 1.14] Miao.1, Kidney, n = 280.34 [-1.21; 1.89] -0.59 [-0.97; -0.22] Total Heterogeneity: $\chi_8^2 = 8.96 \ (P = .35), \ I^2 = 11\% \ [0\%; 69\%]$ Sequencing = FPKM Nathanson, Melanoma, n = 24 - 0.44 [-1.81; 0.93]-0.36 [-1.09; 0.37] Liu, Melanoma, n = 112 Hugo, Melanoma, n = 27-0.30 [-1.63; 1.03] Total -0.36 [-0.94; 0.21] Heterogeneity: $\chi_2^2 = 0.02 \ (P = .99), \ I^2 = 0\% \ [<0\%; <90\%]$

Heterogeneity:  $\chi_{11}^2 = 9.41$  (P = .58),  $I^2 = 0\%$  [0%; 58%]

Test for overall effect: z = -3.27 (P = .001)

Test for subgroup differences:  $\chi_1^2 = 0.43$  (P = .51)

Total

-0.53 [-0.84; -0.21]

-2-1 0 1 2

Estimated logOR