Source (95% CI)

Sequencing = WES

Nathanson, Melanoma, n = 64 - 1.42 [-2.34; -0.50]-1.32 [-2.65; 0.01] Hugo, Melanoma, n = 38-0.67 [-1.16; -0.18] Liu, Melanoma, n = 144 -0.64[-1.44; 0.16]Miao.2, Melanoma, n = 47-0.58 [-2.79; 1.63] Miao.2, Bladder, n = 27-0.49 [-1.41; 0.43] Snyder, Ureteral, n = 25 Van_Allen , Melanoma, n = 112 -0.45 [-0.90; 0.00]Braun, Kidney, n = 249-0.38[-1.46; 0.70]-0.06 [-0.65; 0.53] Riaz, Melanoma, n = 68Miao.2, Lung, n = 340.06 [-1.76; 1.88] 0.81 [-3.95; 5.57] Miao.1, Kidney, n = 35-0.54[-0.77; -0.30]Total Heterogeneity: $\chi_{10}^2 = 8.68 \ (P = .56), \ I^2 = 0\% \ [0\%; 60\%]$

Sequencing = TGS

-1.40 [-4.05; 1.25] Mariathasan, Ureteral, n = 21-1.03 [-2.25; 0.19] Samstein, Ureteral, n = 51 -0.77 [-1.36; -0.18] Samstein, Bladder, n = 158 -0.67 [-1.18; -0.16] Samstein, Colon, n = 129 -0.67 [-1.16; -0.18] Samstein, Unknown, n = 122 Samstein, Kidney, n = 156 -0.63 [-1.37; 0.11] Mariathasan, Bladder, n = 158 -0.53 [-1.14; 0.08]-0.51 [-1.29; 0.27] Samstein, Stomach, n = 46-0.41 [-0.74; -0.08] Samstein, Lung, n = 355Samstein, Melanoma, n = 214 -0.37 [-0.84; 0.10] Mariathasan, Kidney, n = 58-0.34[-1.24; 0.56]Samstein, HNC, n = 145 -0.33[-0.82; 0.16]Samstein, Esophagus, n = 83-0.14[-1.18; 0.90]-0.04 [-0.92; 0.84] Samstein, Breast, n = 46Samstein, Brain, n = 117 -0.02 [-0.61; 0.57] Samstein, Eye, n = 220.41 [-1.75; 2.57] -0.46 [-0.61; -0.30] Total Heterogeneity: $\chi_{15}^2 = 8.6 \ (P = .90), \ I^2 = 0\% \ [0\%; 52\%]$ -0.48[-0.61; -0.35]Total Heterogeneity: $\chi_{26}^2 = 17.58 \ (P = .89), \ I^2 = 0\% \ [0\%; 43\%]$ Test for overall effect: z = -7.28 (P < .001)Test for subgroup differences: $\chi_1^2 = 0.30 \ (P = .58)$

-1.50 logHR estimate