Source Sequencing = WES Rizvi.15, Lung, n = 34 Miao.1, Kidney, n = 35 Jung, Lung, n = 58 Miao.2, Bladder, n = 27 Snyder, Ureteral, n = 25 Liu, Melanoma, n = 144 Van_Allen, Melanoma, n = 112 Braun, Kidney, n = 249 Miao.2, Melanoma, n = 38 Miao.2, Lung, n = 34 Total Heterogeneity: $\chi_9^2 = 14.28$ ( $P = .12$	-0.03 [ -1.03; 0.97] 0.56 [ -0.58; 1.70] 5.91 [ -3.44; 15.26] -0.27 [ -0.51; -0.02]	
Sequencing = TGS Rizvi.18, Lung, n = 29 Samstein, Unknown, n = 34 Samstein, Melanoma, n = 132 Samstein, Esophagus, n = 21 Samstein, HNC, n = 78 Total Heterogeneity: $\chi_4^2 = 3.59 \ (P = .46)$ Total Heterogeneity: $\chi_{14}^2 = 20.13 \ (P = .1)$ Test for overall effect: $z = -3.37 \ (P = .1)$	-0.41 [-1.68; 0.86] $-0.20 [-0.73; 0.33]$ $-0.58 [-0.92; -0.23]$ $0.96 [-0.96; 79%]$ $-0.43 [-0.68; -0.18]$ $0.96 [-0.96; 63%]$ $0.96 [-0.96; 63%]$ $0.96 [-0.96; 63%]$	-2 0 2 4 6 logHR estimate