Source Sequencing = WES Nathanson, Melanoma, n = 64 Hugo, Melanoma, n = 38 Miao.2, Melanoma, n = 47 Miao.2, Lung, n = 34 Liu, Melanoma, n = 144 Snyder, Ureteral, n = 25 Van_Allen, Melanoma, n = 112 Miao.2, Bladder, n = 27 Braun, Kidney, n = 249 Riaz, Melanoma, n = 68 Miao.1, Kidney, n = 35 Total Heterogeneity: $\chi_{10}^2$ = 15.04 ( $P$ = .1	-0.91 [-1.77; -0.05] -0.68 [-1.46; 0.10] -0.55 [-1.51; 0.41] -0.54 [-0.91; -0.17] -0.45 [-1.25; 0.35] -0.40 [-0.75; -0.05] -0.36 [-1.30; 0.58] -0.08 [-0.33; 0.17] 0.02 [-0.47; 0.51] 0.19 [-0.55; 0.93] -0.36 [-0.57; -0.15]	
Sequencing = TGS  Samstein, Ureteral, n = 51  Samstein, Unknown, n = 122  Samstein, Stomach, n = 46  Samstein, Bladder, n = 158  Samstein, Colon, n = 129  Samstein, Melanoma, n = 214  Samstein, Kidney, n = 156  Samstein, HNC, n = 145  Mariathasan, Bladder, n = 158  Mariathasan, Ureteral, n = 21  Samstein, Lung, n = 355  Samstein, Esophagus, n = 83  Mariathasan, Kidney, n = 58  Samstein, Breast, n = 46  Samstein, Breast, n = 46  Samstein, Brain, n = 117  Samstein, Eye, n = 22  Total  Heterogeneity: $\chi_{15}^2 = 10.87$ ( $P = .7$ Total  Heterogeneity: $\chi_{26}^2 = 26.15$ ( $P = .4$ Test for overall effect: $z = -6.59$ ( $P$ Test for subgroup differences: $\chi_1^2 = 10.87$	-0.28 [-0.36; -0.20] 5), $I^2 = 1\% [0\%; 43\%]$ $I^2 < .001$	-1 0 0.5 1 1.5 D.Index estimate