Source Sequencing = WES Rizvi.15, Lung, n = 27 Miao.2, Bladder, n = 23 Nathanson, Melanoma, n = 64 Snyder, Ureteral, n = 22 Liu, Melanoma, n = 133 Riaz, Melanoma, n = 42 Hugo, Melanoma, n = 38 Van_Allen, Melanoma, n = 104 Miao.2, Melanoma, n = 43 Miao.1, Kidney, n = 26 Braun, Kidney, n = 198 Total Heterogeneity: $\chi_{10}^2 = 18.25$ ($P = .0$	-1.10 [-2.90; 0.70] -0.80 [-1.51; -0.09] -0.79 [-2.24; 0.66] -0.60 [-1.89; 0.69] -0.13 [-1.21; 0.95] -0.08 [-1.37; 1.21] 0.90 [-0.94; 2.74] 1.00 [0.08; 1.92] -0.45 [-0.97; 0.08]	
Sequencing = TGS Samstein, Melanoma, n = 108 Samstein, HNC, n = 72 Mariathasan, Bladder, n = 111 Rizvi.18, Lung, n = 29 Samstein, Unknown, n = 29 Samstein, Esophagus, n = 21 Total Heterogeneity: $\chi_5^2 = 4.11$ ($P = .53$) Total Heterogeneity: $\chi_{16}^2 = 27.16$ ($P = .07$) Test for overall effect: $z = -3.04$ ($P = .07$) Test for subgroup differences: $\chi_1^2 = 0.07$	-1.16 [-2.26; -0.06] -1.12 [-1.94; -0.30] -0.55 [-2.39; 1.29] -0.55 [-2.39; 1.29] 0.41 [-1.63; 2.45] -1.10 [-1.59; -0.61] 0, $I^2 = 0\%$ [0%; 75%] -0.64 [-1.05; -0.23] 04), $I^2 = 41\%$ [0%; 67%] $I^2 = 0.002$	-2 -1 0 1 2 Estimated logOR