

Source

(95% CI)

Sequencing = WES

Riaz, Melanoma, n = 68	-0.99 [-2.17; 0.19]
Liu, Melanoma, n = 144	-0.98 [-1.63; -0.33]
Hugo, Melanoma, n = 38	-0.65 [-1.77; 0.47]
Nathanson, Melanoma, n = 64	-0.56 [-1.52; 0.40]
Miao.2, Melanoma, n = 47	-0.46 [-1.32; 0.40]
Van_Allen, Melanoma, n = 112	-0.39 [-0.98; 0.20]
Snyder, Ureteral, n = 25	-0.24 [-1.38; 0.90]
Miao.2, Lung, n = 34	0.87 [-0.52; 2.26]
Total	-0.54 [-0.85; -0.23]
Heterogeneity: $\chi^2_7 = 6.87$ ($P = .44$), $I^2 = 0\%$ [0%; 68%]	

Sequencing = TGS

Mariathasan, Bladder, n = 158	-0.98 [-1.88; -0.08]
Samstein, Ureteral, n = 51	-0.89 [-2.12; 0.34]
Samstein, Colon, n = 129	-0.87 [-1.50; -0.24]
Samstein, HNC, n = 145	-0.76 [-1.47; -0.05]
Samstein, Unknown, n = 122	-0.67 [-1.28; -0.06]
Samstein, Esophagus, n = 83	-0.63 [-1.59; 0.33]
Samstein, Melanoma, n = 214	-0.51 [-1.00; -0.02]
Samstein, Stomach, n = 46	-0.39 [-1.49; 0.71]
Samstein, Lung, n = 355	-0.33 [-0.60; -0.06]
Samstein, Brain, n = 117	-0.29 [-1.19; 0.61]
Samstein, Bladder, n = 158	-0.06 [-0.51; 0.39]
Total	-0.47 [-0.66; -0.28]
Heterogeneity: $\chi^2_{10} = 8.72$ ($P = .56$), $I^2 = 0\%$ [0%; 60%]	
Total	-0.48 [-0.64; -0.32]
Heterogeneity: $\chi^2_{18} = 15.85$ ($P = .60$), $I^2 = 0\%$ [0%; 49%]	
Test for overall effect: $z = -5.90$ ($P < .001$)	
Test for subgroup differences: $\chi^2_1 = 0.14$ ($P = .71$)	

