

## Source

(95% CI)

### Sequencing = TGS

Samstein, Esophagus, n = 21	-1.00 [-2.27; 0.27]
Samstein, Melanoma, n = 132	-0.75 [-1.24; -0.26]
Samstein, HNC, n = 78	-0.50 [-1.21; 0.21]
Rizvi.18, Lung, n = 29	-0.37 [-1.25; 0.51]
Samstein, Unknown, n = 34	-0.30 [-1.18; 0.58]
<b>Total</b>	<b>-0.60 [-0.93; -0.27]</b>
Heterogeneity: $\chi^2_4 = 1.52$ ( $P = .82$ ), $I^2 = 0\%$ [0%; 79%]	

### Sequencing = WES

Snyder, Ureteral, n = 25	-0.35 [-1.47; 0.77]
Liu, Melanoma, n = 144	-0.34 [-0.81; 0.13]
Van_Allen, Melanoma, n = 112	-0.08 [-0.59; 0.43]
Miao.2, Melanoma, n = 38	1.03 [-0.48; 2.54]
<b>Total</b>	<b>-0.17 [-0.50; 0.15]</b>
Heterogeneity: $\chi^2_3 = 3.15$ ( $P = .37$ ), $I^2 = 5\%$ [0%; 85%]	
<b>Total</b>	<b>-0.38 [-0.62; -0.15]</b>
Heterogeneity: $\chi^2_8 = 7.96$ ( $P = .44$ ), $I^2 = 0\%$ [0%; 65%]	
Test for overall effect: $z = -3.20$ ( $P = .001$ )	
Test for subgroup differences: $\chi^2_1 = 3.29$ ( $P = .07$ )	

