

Source	(95% CI)
<b>Sequencing = TPM</b>	
Mariathasan, Kidney, n = 67	-0.43 [-1.00; 0.14]
Mariathasan, Ureteral, n = 26	-0.38 [-1.32; 0.56]
Fumet.2, Lung, n = 43	-0.35 [-1.15; 0.45]
Braun, Kidney, n = 178	0.12 [-0.27; 0.51]
Snyder, Ureteral, n = 25	0.18 [-0.78; 1.14]
Mariathasan, Bladder, n = 194	0.23 [-0.12; 0.58]
Riaz, Melanoma, n = 51	0.28 [-0.41; 0.97]
Van_Allen, Melanoma, n = 42	0.35 [-0.39; 1.09]
Miao.1, Kidney, n = 33	0.63 [-0.23; 1.49]
Mariathasan, Lymph_node, n = 26	0.87 [-0.09; 1.83]
Total	0.13 [-0.06; 0.32]
Heterogeneity: $\chi^2_9 = 10.64$ ( $P = .30$ ), $I^2 = 15\%$ [0%; 57%]	

<b>Sequencing = FPKM</b>	
Hugo, Melanoma, n = 27	0.23 [-0.91; 1.37]
Nathanson, Melanoma, n = 24	0.54 [-0.46; 1.54]
Liu, Melanoma, n = 121	0.63 [ 0.12; 1.14]
Total	0.56 [ 0.14; 0.98]
Heterogeneity: $\chi^2_2 = 0.4$ ( $P = .82$ ), $I^2 = 0\%$ [0%; 90%]	
Total	0.20 [ 0.00; 0.40]
Heterogeneity: $\chi^2_{12} = 14.38$ ( $P = .28$ ), $I^2 = 17\%$ [0%; 55%]	
Test for overall effect: $z = 1.95$ ( $P = .05$ )	
Test for subgroup differences: $\chi^2_1 = 3.35$ ( $P = .07$ )	

