

| Source | (95% CI) |
|--|----------------------|
| Sequencing = TPM | |
| Van_Allen, Melanoma, n = 42 | -1.42 [-2.38; -0.46] |
| Hwang, Lung, n = 21 | -1.02 [-2.73; 0.69] |
| Mariathasan, Lymph_node, n = 26 | -0.83 [-1.75; 0.09] |
| Snyder, Ureteral, n = 25 | -0.54 [-1.58; 0.50] |
| Riaz, Melanoma, n = 51 | -0.52 [-1.13; 0.09] |
| Mariathasan, Bladder, n = 194 | -0.38 [-0.69; -0.07] |
| Fumet.2, Lung, n = 43 | -0.24 [-1.08; 0.60] |
| Miao.1, Kidney, n = 33 | -0.12 [-0.94; 0.70] |
| Mariathasan, Kidney, n = 67 | -0.05 [-0.62; 0.52] |
| Braun, Kidney, n = 178 | 0.19 [-0.20; 0.58] |
| Mariathasan, Ureteral, n = 26 | 0.50 [-0.46; 1.46] |
| Total | -0.29 [-0.57; -0.02] |
| Heterogeneity: $\chi^2_{10} = 17.48$ ($P = .06$), $I^2 = 43\%$ [0%; 72%] | |

| | |
|--|----------------------|
| Sequencing = FPKM | |
| Nathanson, Melanoma, n = 24 | -0.82 [-1.64; 0.00] |
| Liu, Melanoma, n = 121 | -0.36 [-0.85; 0.13] |
| Hugo, Melanoma, n = 27 | 0.24 [-0.96; 1.44] |
| Total | -0.40 [-0.80; 0.00] |
| Heterogeneity: $\chi^2_2 = 2.13$ ($P = .35$), $I^2 = 6\%$ [0%; 90%] | |
| Total | -0.31 [-0.53; -0.08] |
| Heterogeneity: $\chi^2_{13} = 20.06$ ($P = .09$), $I^2 = 35\%$ [0%; 66%] | |
| Test for overall effect: $z = -2.67$ ($P = .008$) | |
| Test for subgroup differences: $\chi^2_1 = 0.19$ ($P = .66$) | |

