| Source | (95% CI) |
|---|---|
| **Sequencing = TPM** | |
| Miao.1, Kidney, n = 33 | −0.48 [−1.19; 0.23] |
| Mariathasan, Kidney, n = 67 | −0.17 [−0.62; 0.28] |
| Braun, Kidney, n = 178 | −0.01 [−0.32; 0.30] |
| Riaz, Melanoma, n = 51 | 0.00 [−0.51; 0.51] |
| Mariathasan, Bladder, n = 194 | 0.04 [−0.23; 0.31] |
| Van_Allen, Melanoma, n = 42 | 0.10 [−0.53; 0.73] |
| Fumet.2, Lung, n = 43 | 0.19 [−0.44; 0.82] |
| Mariathasan, Lymph_node, n = 26 | 0.21 [−0.53; 0.95] |
| Snyder, Ureteral, n = 25 | 0.35 [−0.38; 1.08] |
| Mariathasan, Ureteral, n = 26 | 1.16 [ 0.18; 2.14] |
| Total | 0.04 [−0.11; 0.19] |

Heterogeneity: $\chi_9^2 = 9.21$ ($P = .42$), $I^2 = 2\%$ [0%; 63%]

| | |
|---|---|
| **Sequencing = FPKM** | |
| Liu, Melanoma, n = 121 | −0.32 [−0.75; 0.11] |
| Nathanson, Melanoma, n = 24 | −0.12 [−1.02; 0.78] |
| Hugo, Melanoma, n = 27 | 0.67 [−0.35; 1.69] |
| Total | −0.07 [−0.59; 0.45] |

Heterogeneity: $\chi_2^2 = 3.08$ ($P = .21$), $I^2 = 35\%$ [0%; 79%]

| | |
|---|---|
| Total | 0.01 [−0.13; 0.15] |

Heterogeneity: $\chi_{12}^2 = 13.27$ ($P = .35$), $I^2 = 10\%$ [0%; 48%]
Test for overall effect: $z = 0.11$ ($P = .91$)
Test for subgroup differences: $\chi_1^2 = 0.16$ ($P = .69$)

−0.50 0.5 1 1.5
D.Index estimate