| Source | (95% CI) |
|---|---|
| **Sequencing = TPM** | |
| Van_Allen, Melanoma, n = 42 | −1.40 [−2.44; −0.36] |
| Riaz, Melanoma, n = 51 | −0.69 [−1.45; 0.07] |
| Mariathasan, Lymph_node, n = 26 | −0.62 [−1.62; 0.38] |
| Snyder, Ureteral, n = 25 | −0.57 [−1.90; 0.76] |
| Miao.1, Kidney, n = 33 | −0.47 [−1.67; 0.73] |
| Fumet.2, Lung, n = 43 | −0.43 [−1.59; 0.73] |
| Mariathasan, Bladder, n = 194 | −0.33 [−0.72; 0.06] |
| Mariathasan, Kidney, n = 67 | −0.06 [−0.77; 0.65] |
| Braun, Kidney, n = 178 | 0.42 [−0.11; 0.95] |
| Mariathasan, Ureteral, n = 26 | 1.22 [ 0.10; 2.34] |
| Total | −0.26 [−0.66; 0.14] |

Heterogeneity: $\chi_9^2 = 20.08$ ($P = .02$), $I^2 = 55\%$ [9%; 78%]

| | |
|---|---|
| **Sequencing = FPKM** | |
| Nathanson, Melanoma, n = 24 | −0.91 [−1.95; 0.13] |
| Liu, Melanoma, n = 121 | −0.85 [−1.50; −0.20] |
| Hugo, Melanoma, n = 27 | 0.61 [−0.90; 2.12] |
| Total | −0.69 [−1.21; −0.18] |

Heterogeneity: $\chi_2^2 = 3.26$ ($P = .20$), $I^2 = 39\%$ [0%; 81%]

| | |
|---|---|
| Total | −0.33 [−0.68; 0.03] |

Heterogeneity: $\chi_{12}^2 = 26.17$ ($P = .01$), $I^2 = 54\%$ [14%; 75%]

Test for overall effect: $z = −1.81$ ($P = .07$)

Test for subgroup differences: $\chi_1^2 = 1.73$ ($P = .19$)

−1.5   0   1

logHR estimate