| Source | (95% CI) | |
|---|---|---|
| **Sequencing = FPKM** | | |
| Liu, Melanoma, n = 121 | −1.06 [−1.98; −0.14] | |
| Nathanson, Melanoma, n = 24 | −1.00 [−2.49; 0.49] | |
| Hugo, Melanoma, n = 27 | 1.03 [−1.03; 3.09] | |
| Total | −0.67 [−1.63; 0.29] | |
| Heterogeneity: $\chi_2^2 = 3.41$ ($P = .18$), $I^2 = 41\%$ [0%; 82%] | | |
| | | |
| **Sequencing = TPM** | | |
| Miao.1, Kidney, n = 33 | −0.99 [−2.68; 0.70] | |
| Riaz, Melanoma, n = 51 | −0.94 [−2.14; 0.26] | |
| Snyder, Ureteral, n = 25 | −0.41 [−1.94; 1.12] | |
| Van_Allen, Melanoma, n = 42 | −0.41 [−1.63; 0.81] | |
| Mariathasan, Bladder, n = 194 | −0.27 [−0.86; 0.32] | |
| Mariathasan, Lymph_node, n = 26 | −0.23 [−1.82; 1.36] | |
| Braun, Kidney, n = 178 | −0.08 [−0.71; 0.55] | |
| Fumet.2, Lung, n = 43 | 0.04 [−1.39; 1.47] | |
| Mariathasan, Kidney, n = 67 | 0.24 [−0.72; 1.20] | |
| Mariathasan, Ureteral, n = 26 | 1.68 [ 0.13; 3.23] | |
| Total | −0.16 [−0.47; 0.16] | |
| Heterogeneity: $\chi_9^2 = 9.2$ ($P = .42$), $I^2 = 2\%$ [0%; 63%] | | |
| Total | −0.25 [−0.54; 0.04] | |
| Heterogeneity: $\chi_{12}^2 = 14.97$ ($P = .24$), $I^2 = 20\%$ [0%; 58%] | | |
| Test for overall effect: $z = −1.71$ ($P = .09$) | | |
| Test for subgroup differences: $\chi_1^2 = 0.99$ ($P = .32$) | | |

−1.5   0   1   2

logHR estimate