| Source | (95% CI) | |
|---|---|---|
| **Sequencing = FPKM** | | |
| Nathanson, Melanoma, n = 24 | −1.06 [−2.10; −0.02] | |
| Liu, Melanoma, n = 121 | −0.57 [−1.08; −0.06] | |
| Hugo, Melanoma, n = 27 | 0.09 [−1.11; 1.29] | |
| Total | −0.57 [−1.00; −0.14] | |
| Heterogeneity: $\chi^2_2$ = 2.03 ($P$ = .36), $I^2$ = 1% [0%; 90%] | | |
| | | |
| **Sequencing = TPM** | | |
| Riaz, Melanoma, n = 51 | −0.77 [−1.48; −0.06] | |
| Van_Allen, Melanoma, n = 42 | −0.63 [−1.37; 0.11] | |
| Mariathasan, Lymph_node, n = 26 | −0.60 [−1.54; 0.34] | |
| Fumet.2, Lung, n = 43 | −0.47 [−1.27; 0.33] | |
| Snyder, Ureteral, n = 25 | −0.35 [−1.31; 0.61] | |
| Miao.1, Kidney, n = 33 | −0.25 [−1.09; 0.59] | |
| Mariathasan, Bladder, n = 194 | −0.18 [−0.53; 0.17] | |
| Mariathasan, Kidney, n = 67 | 0.01 [−0.56; 0.58] | |
| Braun, Kidney, n = 178 | 0.20 [−0.19; 0.59] | |
| Mariathasan, Ureteral, n = 26 | 1.09 [ 0.07; 2.11] | |
| Total | −0.18 [−0.44; 0.08] | |
| Heterogeneity: $\chi^2_9$ = 15.34 ($P$ = .08), $I^2$ = 41% [0%; 72%] | | |
| Total | −0.25 [−0.50; −0.01] | |
| Heterogeneity: $\chi^2_{12}$ = 20.58 ($P$ = .06), $I^2$ = 42% [0%; 70%] | | |
| Test for overall effect: $z$ = −2.04 ($P$ = .04) | | |
| Test for subgroup differences: $\chi^2_1$ = 2.32 ($P$ = .13) | | |

logHR estimate