| Source | (95% CI) |
|---|---|
| **Sequencing = FPKM** | |
| Nathanson, Melanoma, n = 24 | −0.91 [−2.34; 0.52] |
| Liu, Melanoma, n = 121 | −0.90 [−1.86; 0.06] |
| Hugo, Melanoma, n = 27 | 1.34 [−1.38; 4.06] |
| Total | −0.73 [−1.49; 0.04] |
| Heterogeneity: $\chi^2_2 = 2.4$ ($P = .30$), $I^2 = 17\%$ [0%; 91%] | |
| | |
| **Sequencing = TPM** | |
| Riaz, Melanoma, n = 51 | −0.74 [−1.90; 0.42] |
| Fumet.2, Lung, n = 43 | −0.71 [−2.08; 0.66] |
| Miao.1, Kidney, n = 33 | −0.63 [−2.10; 0.84] |
| Braun, Kidney, n = 178 | −0.38 [−0.93; 0.17] |
| Mariathasan, Bladder, n = 194 | −0.31 [−0.82; 0.20] |
| Mariathasan, Lymph_node, n = 26 | −0.23 [−1.74; 1.28] |
| Van_Allen, Melanoma, n = 42 | −0.07 [−1.52; 1.38] |
| Mariathasan, Kidney, n = 67 | 0.16 [−1.00; 1.32] |
| Snyder, Ureteral, n = 25 | 0.60 [−0.56; 1.76] |
| Mariathasan, Ureteral, n = 26 | 2.70 [ 1.15; 4.25] |
| Total | −0.06 [−0.54; 0.41] |
| Heterogeneity: $\chi^2_9 = 17.99$ ($P = .04$), $I^2 = 50\%$ [0%; 76%] | |
| Total | −0.17 [−0.58; 0.24] |
| Heterogeneity: $\chi^2_{12} = 22.10$ ($P = .04$), $I^2 = 46\%$ [0%; 72%] | |
| Test for overall effect: $z = -0.81$ ($P = .42$) | |
| Test for subgroup differences: $\chi^2_1 = 2.09$ ($P = .15$) | |



−1 0 1 2 3
logHR estimate