| Source | (95% CI) |
|---|---|
| **Sequencing = TPM** | |
| Braun, Kidney, n = 178 | −0.23 [−0.56; 0.10] |
| Riaz, Melanoma, n = 51 | −0.11 [−0.64; 0.42] |
| Fumet.2, Lung, n = 43 | 0.19 [−0.44; 0.82] |
| Mariathasan, Kidney, n = 67 | 0.24 [−0.17; 0.65] |
| Mariathasan, Lymph_node, n = 26 | 0.45 [−0.22; 1.12] |
| Miao.1, Kidney, n = 33 | 0.45 [−0.29; 1.19] |
| Mariathasan, Bladder, n = 194 | 0.47 [ 0.18; 0.76] |
| Mariathasan, Ureteral, n = 26 | 0.63 [−0.13; 1.39] |
| Snyder, Ureteral, n = 25 | 0.66 [−0.20; 1.52] |
| Van_Allen, Melanoma, n = 42 | 0.93 [ 0.32; 1.54] |
| Total | 0.31 [ 0.07; 0.55] |
| Heterogeneity: $\chi^2_9 = 19.16$ (P = .02), $I^2 = 53\%$ [4%; 77%] | |
| | |
| **Sequencing = FPKM** | |
| Nathanson, Melanoma, n = 24 | 0.24 [−0.54; 1.02] |
| Hugo, Melanoma, n = 27 | 0.66 [−0.36; 1.68] |
| Liu, Melanoma, n = 121 | 0.66 [ 0.25; 1.07] |
| Total | 0.58 [ 0.24; 0.92] |
| Heterogeneity: $\chi^2_2 = 0.89$ (P = .64), $I^2 = 0\%$ [0%; 90%] | |
| Total | 0.35 [ 0.14; 0.57] |
| Heterogeneity: $\chi^2_{12} = 22.76$ (P = .03), $I^2 = 47\%$ [0%; 72%] | |
| Test for overall effect: z = 3.27 (P = .001) | |
| Test for subgroup differences: $\chi^2_1 = 1.58$ (P = .21) | |

−0.5 0 0.5 1

logHR estimate