Source	(95% CI)
Sequencing = TPM	
Miao.1, Kidney, n = 33	−0.60 [−1.44; 0.24]
Mariathasan, Ureteral, n = 26	−0.40 [−1.36; 0.56]
Mariathasan, Kidney, n = 67	−0.19 [−0.76; 0.38]
Fumet.2, Lung, n = 43	−0.13 [−0.91; 0.65]
Mariathasan, Bladder, n = 194	0.12 [−0.23; 0.47]
Mariathasan, Lymph_node, n = 26	0.36 [−0.56; 1.28]
Riaz, Melanoma, n = 51	0.42 [−0.27; 1.11]
Braun, Kidney, n = 178	0.46 [0.07; 0.85]
Van_Allen, Melanoma, n = 42	0.53 [−0.21; 1.27]
Snyder, Ureteral, n = 25	0.67 [−0.31; 1.65]
Total	0.16 [−0.06; 0.38]

Heterogeneity: $\chi^2_9 = 11.41$ ($P = .25$), $I^2 = 21\%$ [0%; 61%]

Sequencing = FPKM	
Liu, Melanoma, n = 121	−0.21 [−0.72; 0.30]
Nathanson, Melanoma, n = 24	−0.11 [−1.13; 0.91]
Hugo, Melanoma, n = 27	0.53 [−0.63; 1.69]
Total	−0.09 [−0.52; 0.33]

Heterogeneity: $\chi^2_2 = 1.32$ ($P = .52$), $I^2 = 0\%$ [0%; 90%]

Total	0.12 [−0.08; 0.32]

Heterogeneity: $\chi^2_{12} = 14.00$ ($P = .30$), $I^2 = 14\%$ [0%; 53%]

Test for overall effect: $z = 1.15$ ($P = .25$)

Test for subgroup differences: $\chi^2_1 = 1.09$ ($P = .30$)

−1 −0.5 0 0.5 1

logHR estimate