Source	(95% CI)
Sequencing = TPM	
Van_Allen, Melanoma, n = 42	−1.10 [−1.84; −0.36]
Hwang, Lung, n = 21	−0.85 [−2.30; 0.60]
Mariathasan, Lymph_node, n = 26	−0.59 [−1.39; 0.21]
Riaz, Melanoma, n = 51	−0.45 [−0.98; 0.08]
Mariathasan, Bladder, n = 194	−0.36 [−0.67; −0.05]
Fumet.2, Lung, n = 43	−0.35 [−1.08; 0.38]
Snyder, Ureteral, n = 25	−0.20 [−1.18; 0.78]
Mariathasan, Kidney, n = 67	−0.02 [−0.55; 0.51]
Miao.1, Kidney, n = 33	0.02 [−0.71; 0.75]
Braun, Kidney, n = 178	0.17 [−0.16; 0.50]
Mariathasan, Ureteral, n = 26	0.61 [−0.43; 1.65]
Total	−0.24 [−0.48; 0.00]
Heterogeneity: χ^2_{10} = 17.17 (P = .07), I^2 = 42% [0%; 71%]	
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	−0.74 [−1.56; 0.08]
Liu, Melanoma, n = 121	−0.23 [−0.68; 0.22]
Hugo, Melanoma, n = 27	0.12 [−0.98; 1.22]
Total	−0.29 [−0.67; 0.08]
Heterogeneity: χ^2_{2} = 1.75 (P = .42), I^2 = 0% [0%; 90%]	
Total	−0.25 [−0.45; −0.05]
Heterogeneity: χ^2_{13} = 19.11 (P = .12), I^2 = 32% [0%; 64%]	
Test for overall effect: z = −2.40 (P = .02)	
Test for subgroup differences: χ^2_{1} = 0.05 (P = .82)	

−1.5 −0.5 0.5 1 1.5

logHR estimate