Source	(95% CI)	
Sequencing = TPM		
Van_Allen, Melanoma, n = 42	−0.70 [−1.46; 0.06]	
Mariathasan, Lymph_node, n = 26	−0.67 [−1.63; 0.29]	
Riaz, Melanoma, n = 51	−0.50 [−1.17; 0.17]	
Mariathasan, Bladder, n = 194	−0.25 [−0.60; 0.10]	
Snyder, Ureteral, n = 25	−0.24 [−1.20; 0.72]	
Fumet.2, Lung, n = 43	−0.16 [−0.94; 0.62]	
Mariathasan, Kidney, n = 67	0.00 [−0.57; 0.57]	
Braun, Kidney, n = 178	0.10 [−0.29; 0.49]	
Miao.1, Kidney, n = 33	0.57 [−0.27; 1.41]	
Mariathasan, Ureteral, n = 26	0.59 [−0.37; 1.55]	
Total	−0.13 [−0.33; 0.08]	

Heterogeneity: $\chi^2_9 = 11.37\ (P = .25)$, $I^2 = 21\%\ [0\%; 61\%]$

Sequencing = FPKM		
Hugo, Melanoma, n = 27	−0.55 [−1.78; 0.68]	
Liu, Melanoma, n = 121	0.00 [−0.51; 0.51]	
Nathanson, Melanoma, n = 24	0.18 [−0.80; 1.16]	
Total	−0.03 [−0.46; 0.39]	

Heterogeneity: $\chi^2_2 = 0.87\ (P = .65)$, $I^2 = 0\%\ [0\%; 90\%]$

Total   −0.11 [−0.28; 0.06]

Heterogeneity: $\chi^2_{12} = 12.39\ (P = .41)$, $I^2 = 3\%\ [0\%; 58\%]$

Test for overall effect: $z = −1.24\ (P = .21)$

Test for subgroup differences: $\chi^2_1 = 0.15\ (P = .69)$

−1   0 0.5 1

logHR estimate