Source	(95% CI)	
Sequencing = TPM		
Van_Allen, Melanoma, n = 42	−0.61 [−1.10; −0.12]	
Riaz, Melanoma, n = 51	−0.42 [−0.81; −0.03]	
Snyder, Ureteral, n = 25	−0.38 [−0.87; 0.11]	
Mariathasan, Lymph_node, n = 26	−0.37 [−0.90; 0.16]	
Mariathasan, Bladder, n = 194	−0.15 [−0.33; 0.03]	
Braun, Kidney, n = 178	−0.02 [−0.22; 0.18]	
Fumet.2, Lung, n = 43	−0.02 [−0.45; 0.41]	
Mariathasan, Kidney, n = 67	0.03 [−0.26; 0.32]	
Mariathasan, Ureteral, n = 26	0.11 [−0.34; 0.56]	
Miao.1, Kidney, n = 33	0.23 [−0.20; 0.66]	
Total	−0.12 [−0.24; 0.00]	

Heterogeneity: χ^2_9 = 13.85 (P = .13), I^2 = 35% [0%; 69%]

Sequencing = FPKM		
Hugo, Melanoma, n = 27	−0.58 [−1.23; 0.07]	
Liu, Melanoma, n = 121	−0.13 [−0.38; 0.12]	
Nathanson, Melanoma, n = 24	−0.07 [−0.60; 0.46]	
Total	−0.17 [−0.39; 0.05]	

Heterogeneity: χ^2_2 = 1.78 (P = .41), I^2 = 0% [0%; 90%]

Total   −0.12 [−0.21; −0.03]

Heterogeneity: χ^2_{12} = 15.86 (P = .20), I^2 = 24% [0%; 61%]

Test for overall effect: z = −2.65 (P = .008)

Test for subgroup differences: χ^2_1 = 0.17 (P = .68)

−1 −0.5 0 0.5 1
logHR estimate