Source	(95% CI)	
Sequencing = FPKM		
Hugo, Melanoma, n = 27	−1.14 [−2.67; 0.39]	
Liu, Melanoma, n = 121	−0.78 [−1.37; −0.19]	
Nathanson, Melanoma, n = 24	−0.69 [−1.77; 0.39]	
Total	−0.80 [−1.29; −0.31]	
Heterogeneity: χ^2_2 = 0.23 (P = .89), I^2 = 0% [0%; 90%]		
Sequencing = TPM		
Mariathasan, Lymph_node, n = 26	−1.08 [−2.35; 0.19]	
Snyder, Ureteral, n = 25	−1.05 [−2.30; 0.20]	
Van_Allen, Melanoma, n = 42	−0.90 [−1.76; −0.04]	
Riaz, Melanoma, n = 51	−0.60 [−1.52; 0.32]	
Fumet.2, Lung, n = 43	−0.45 [−1.39; 0.49]	
Mariathasan, Bladder, n = 194	−0.45 [−0.86; −0.04]	
Miao.1, Kidney, n = 33	0.14 [−1.08; 1.36]	
Mariathasan, Kidney, n = 67	0.32 [−0.33; 0.97]	
Braun, Kidney, n = 178	0.42 [−0.01; 0.85]	
Mariathasan, Ureteral, n = 26	0.47 [−0.61; 1.55]	
Total	−0.24 [−0.61; 0.14]	
Heterogeneity: χ^2_9 = 20.51 (P = .02), I^2 = 56% [11%; 78%]		
Total	−0.35 [−0.69; −0.02]	
Heterogeneity: χ^2_{12} = 26.44 (P = .009), I^2 = 55% [15%; 76%]		
Test for overall effect: z = −2.10 (P = .04)		
Test for subgroup differences: χ^2_1 = 3.22 (P = .07)		

−1.5 −0.5 0.5 1 1.5
logHR estimate