Source	(95% CI)	
Sequencing = TPM		
Miao.1, Kidney, n = 33	−1.34 [−3.83; 1.15]	
Van_Allen, Melanoma, n = 42	−1.12 [−2.83; 0.59]	
Mariathasan, Bladder, n = 194	−0.64 [−1.37; 0.09]	
Fumet.2, Lung, n = 43	−0.60 [−2.11; 0.91]	
Riaz, Melanoma, n = 51	−0.59 [−2.12; 0.94]	
Mariathasan, Lymph_node, n = 26	−0.52 [−1.91; 0.87]	
Braun, Kidney, n = 178	−0.16 [−0.77; 0.45]	
Mariathasan, Kidney, n = 67	0.11 [−1.20; 1.42]	
Snyder, Ureteral, n = 25	0.25 [−1.20; 1.70]	
Mariathasan, Ureteral, n = 26	3.46 [1.23; 5.69]	
Total	−0.28 [−0.64; 0.08]	
Heterogeneity: χ^2_9 = 14.79 (P = .10), I^2 = 39% [0%; 71%]		
Sequencing = FPKM		
Nathanson, Melanoma, n = 24	−0.96 [−2.72; 0.80]	
Liu, Melanoma, n = 121	−0.72 [−1.86; 0.42]	
Hugo, Melanoma, n = 27	1.73 [−1.45; 4.91]	
Total	−0.58 [−1.50; 0.33]	
Heterogeneity: χ^2_2 = 2.27 (P = .32), I^2 = 12% [0%; 91%]		
Total	−0.32 [−0.65; 0.02]	
Heterogeneity: χ^2_{12} = 17.42 (P = .13), I^2 = 31% [0%; 64%]		
Test for overall effect: z = −1.87 (P = .06)		
Test for subgroup differences: χ^2_1 = 0.36 (P = .55)		

−1 0 1 2 3
logHR estimate