Source	(95% CI)	
Sequencing = TPM		
Riaz, Melanoma, n = 51	−0.28 [−0.97; 0.41]	
Mariathasan, Kidney, n = 67	−0.21 [−0.78; 0.36]	
Miao.1, Kidney, n = 33	−0.04 [−0.90; 0.82]	
Mariathasan, Ureteral, n = 26	0.05 [−0.87; 0.97]	
Fumet.2, Lung, n = 43	0.17 [−0.63; 0.97]	
Braun, Kidney, n = 178	0.25 [−0.14; 0.64]	
Mariathasan, Bladder, n = 194	0.26 [−0.09; 0.61]	
Mariathasan, Lymph_node, n = 26	0.53 [−0.43; 1.49]	
Van_Allen, Melanoma, n = 42	0.64 [−0.10; 1.38]	
Snyder, Ureteral, n = 25	1.16 [0.10; 2.22]	
Total	0.20 [0.01; 0.39]	

Heterogeneity: $\chi_9^2 = 9.41$ ($P = .40$), $I^2 = 4\%$ [0%; 64%]

Sequencing = FPKM		
Nathanson, Melanoma, n = 24	−0.27 [−1.25; 0.71]	
Liu, Melanoma, n = 121	−0.20 [−0.71; 0.31]	
Hugo, Melanoma, n = 27	0.17 [−0.97; 1.31]	
Total	−0.16 [−0.58; 0.26]	

Heterogeneity: $\chi_2^2 = 0.4$ ($P = .82$), $I^2 = 0\%$ [0%; 90%]

Total	0.14 [−0.04; 0.31]	

Heterogeneity: $\chi_{12}^2 = 12.17$ ($P = .43$), $I^2 = 1\%$ [0%; 57%]
Test for overall effect: $z = 1.56$ ($P = .12$)
Test for subgroup differences: $\chi_1^2 = 2.36$ ($P = .12$)

−0.5 0 0.5 1 1.5
logHR estimate