Source	(95% CI)
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	-0.73 [-1.75; 0.29]
Liu, Melanoma, n = 121	-0.53 [-1.04; -0.02]
Hugo, Melanoma, n = 27	0.55 [-0.67; 1.77]
Total	-0.43 [-0.87; 0.01]
Heterogeneity: $\chi^2_2 = 2.98$ ($P = .23$), $I^2 = 33\%$ [0%; 93%]	
Sequencing = TPM	
Van_Allen, Melanoma, n = 42	-0.58 [-1.32; 0.16]
Mariathasan, Lymph_node, n = 26	-0.45 [-1.39; 0.49]
Mariathasan, Kidney, n = 67	-0.34 [-0.91; 0.23]
Riaz, Melanoma, n = 51	-0.23 [-0.90; 0.44]
Mariathasan, Bladder, n = 194	-0.13 [-0.48; 0.22]
Miao.1, Kidney, n = 33	-0.12 [-0.96; 0.72]
Braun, Kidney, n = 178	0.04 [-0.35; 0.43]
Fumet.2, Lung, n = 43	0.09 [-0.69; 0.87]
Snyder, Ureteral, n = 25	0.20 [-0.76; 1.16]
Mariathasan, Ureteral, n = 26	1.57 [0.41; 2.73]
Total	-0.09 [-0.28; 0.10]
Heterogeneity: $\chi^2_9 = 12.08$ ($P = .21$), $I^2 = 26\%$ [0%; 64%]	
Total	-0.15 [-0.32; 0.03]
Heterogeneity: $\chi^2_{12} = 17.10$ ($P = .15$), $I^2 = 30\%$ [0%; 64%]	
Test for overall effect: $z = -1.67$ ($P = .09$)	
Test for subgroup differences: $\chi^2_1 = 1.87$ ($P = .17$)	

logHR estimate