Source	(95% CI)
Sequencing = TPM	
Braun, Kidney, n = 178	−0.18 [−0.49; 0.13]
Riaz, Melanoma, n = 51	−0.05 [−0.58; 0.48]
Fumet.2, Lung, n = 43	0.22 [−0.37; 0.81]
Mariathasan, Kidney, n = 67	0.31 [−0.10; 0.72]
Mariathasan, Lymph_node, n = 26	0.42 [−0.31; 1.15]
Mariathasan, Bladder, n = 194	0.49 [0.22; 0.76]
Miao.1, Kidney, n = 33	0.53 [−0.21; 1.27]
Snyder, Ureteral, n = 25	0.64 [−0.14; 1.42]
Van_Allen, Melanoma, n = 42	0.89 [0.32; 1.46]
Mariathasan, Ureteral, n = 26	1.06 [0.06; 2.06]
Total	0.35 [0.11; 0.60]
Heterogeneity: χ^2_9 = 20.15 (P = .02), I^2 = 55% [9%; 78%]	
Sequencing = FPKM	
Nathanson, Melanoma, n = 24	0.23 [−0.55; 1.01]
Hugo, Melanoma, n = 27	0.65 [−0.41; 1.71]
Liu, Melanoma, n = 121	0.66 [0.27; 1.05]
Total	0.58 [0.25; 0.91]
Heterogeneity: χ^2_2 = 0.94 (P = .62), I^2 = 0% [0%; 90%]	
Total	0.39 [0.18; 0.60]
Heterogeneity: χ^2_{12} = 23.38 (P = .02), I^2 = 49% [3%; 73%]	
Test for overall effect: z = 3.62 (P < .001)	
Test for subgroup differences: χ^2_1 = 1.17 (P = .28)