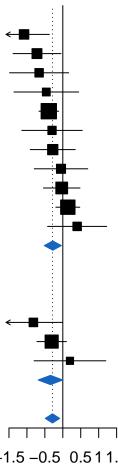
## Source (95% CI)

## **Sequencing = TPM**

Van_Allen, Melanoma, n = 42	-1.08 [-1.79; -0.37]
Riaz, Melanoma, n = 51	-0.72 [-1.39; -0.05]
Mariathasan, Lymph_node, $n = 26$	-0.66 [-1.48; 0.16]
Hwang, Lung, n = 21	-0.46 [-1.36; 0.44]
Mariathasan, Bladder, n = 194	-0.39 [-0.66; -0.12]
Snyder, Ureteral, n = 25	-0.30 [-1.14; 0.54]
Fumet.2, Lung, n = 43	-0.28 [-0.91; 0.35]
Miao.1, Kidney, n = 33	-0.05 [-0.79; 0.69]
Mariathasan, Kidney, n = 67	-0.03 [-0.54; 0.48]
Braun, Kidney, n = 178	0.14 [-0.19; 0.47]
Mariathasan, Ureteral, n = 26	0.40 [-0.42; 1.22]
Total	-0.28 [-0.52; -0.04]
Heterogeneity: $\chi_{40}^2 = 18.06 \ (P = .05)$ .	$I^2 = 45\% [0\%; 73\%]$

## Sequencing = FPKM

-0.82 [-1.62; -0.02] Nathanson, Melanoma, n = 24 -0.31 [-0.72; 0.10] Liu, Melanoma, n = 121 Hugo, Melanoma, n = 270.20 [-0.80; 1.20] Total -0.34 [-0.69; 0.00]Heterogeneity:  $\chi_2^2 = 2.51 (P = .28), I^2 = 20\% [0\%; 92\%]$ Iotal -0.29 [-0.49; -0.09]Heterogeneity:  $\chi_{13}^2 = 20.82 (P = .08), I^2 = 38\% [0\%; 67\%]$ Test for overall effect: z = -2.81 (P = .005)Test for subgroup differences:  $\chi_1^2 = 0.09 \ (P = .76)$ 



-1.5 - 0.5 0.511.5D.Index estimate