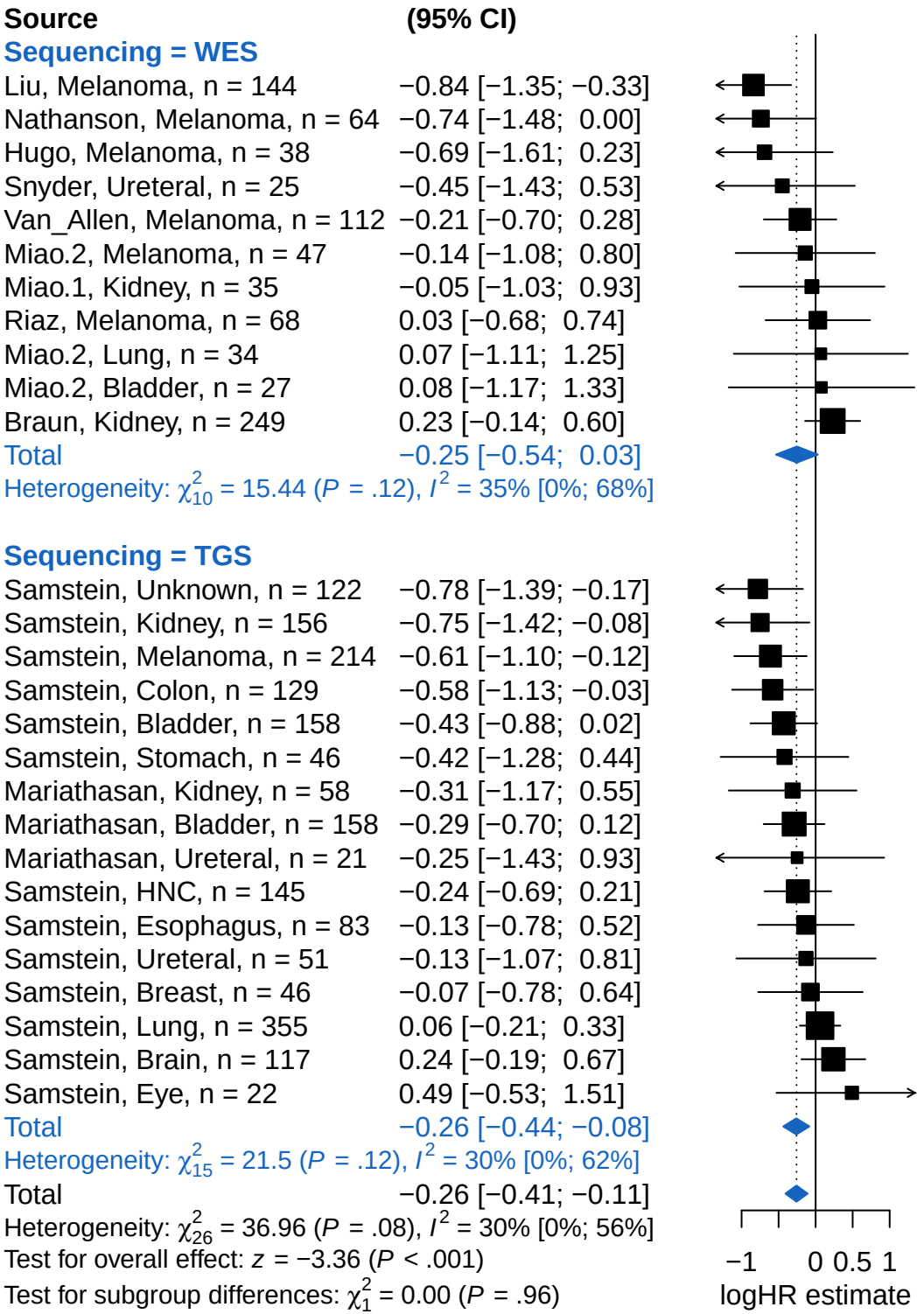
Source
(95% CI)
Sequencing = WES
Liu, Melanoma, n = 144 −0.84 [−1.35; −0.33]
Nathanson, Melanoma, n = 64 −0.74 [−1.48; 0.00]
Hugo, Melanoma, n = 38 −0.69 [−1.61; 0.23]
Snyder, Ureteral, n = 25 −0.45 [−1.43; 0.53]
Van_Allen, Melanoma, n = 112 −0.21 [−0.70; 0.28]
Miao.2, Melanoma, n = 47 −0.14 [−1.08; 0.80]
Miao.1, Kidney, n = 35 −0.05 [−1.03; 0.93]
Riaz, Melanoma, n = 68 0.03 [−0.68; 0.74]
Miao.2, Lung, n = 34 0.07 [−1.11; 1.25]
Miao.2, Bladder, n = 27 0.08 [−1.17; 1.33]
Braun, Kidney, n = 249 0.23 [−0.14; 0.60]
Total −0.25 [−0.54; 0.03]
Heterogeneity: χ^2_{10} = 15.44 (P = .12), I^2 = 35% [0%; 68%]
Sequencing = TGS
Samstein, Unknown, n = 122 −0.78 [−1.39; −0.17]
Samstein, Kidney, n = 156 −0.75 [−1.42; −0.08]
Samstein, Melanoma, n = 214 −0.61 [−1.10; −0.12]
Samstein, Colon, n = 129 −0.58 [−1.13; −0.03]
Samstein, Bladder, n = 158 −0.43 [−0.88; 0.02]
Samstein, Stomach, n = 46 −0.42 [−1.28; 0.44]
Mariathasan, Kidney, n = 58 −0.31 [−1.17; 0.55]
Mariathasan, Bladder, n = 158 −0.29 [−0.70; 0.12]
Mariathasan, Ureteral, n = 21 −0.25 [−1.43; 0.93]
Samstein, HNC, n = 145 −0.24 [−0.69; 0.21]
Samstein, Esophagus, n = 83 −0.13 [−0.78; 0.52]
Samstein, Ureteral, n = 51 −0.13 [−1.07; 0.81]
Samstein, Breast, n = 46 −0.07 [−0.78; 0.64]
Samstein, Lung, n = 355 0.06 [−0.21; 0.33]
Samstein, Brain, n = 117 0.24 [−0.19; 0.67]
Samstein, Eye, n = 22 0.49 [−0.53; 1.51]
Total −0.26 [−0.44; −0.08]
Heterogeneity: χ^2_{15} = 21.5 (P = .12), I^2 = 30% [0%; 62%]
Total −0.26 [−0.41; −0.11]
Heterogeneity: χ^2_{26} = 36.96 (P = .08), I^2 = 30% [0%; 56%]
Test for overall effect: z = −3.36 (P < .001)
Test for subgroup differences: χ^2_1 = 0.00 (P = .96)
−1
0
0.5
1
logHR estimate