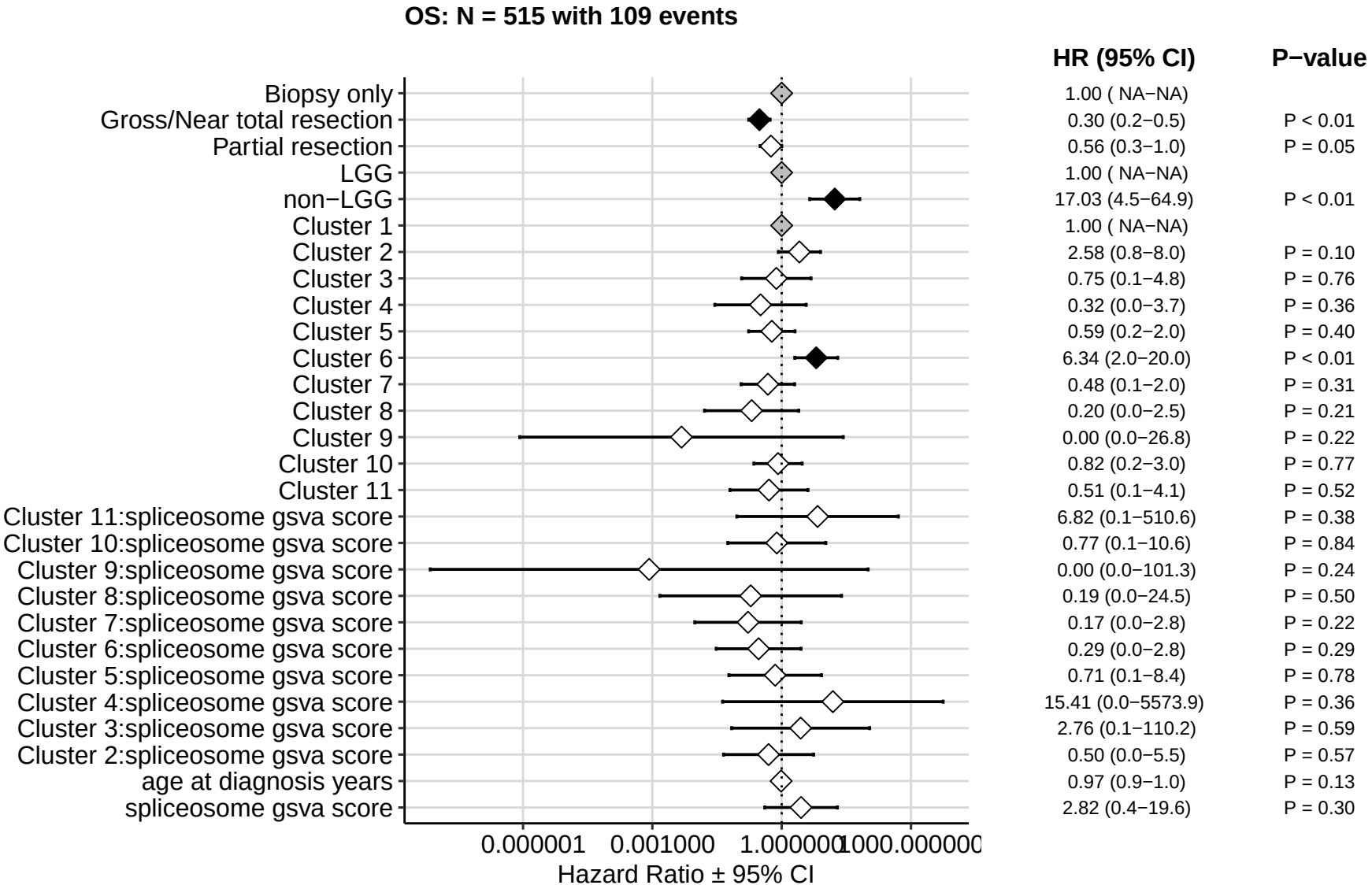
OS: N = 515 with 109 events
HR (95% CI)
P−value
Biopsy only 1.00 (NA−NA)
Gross/Near total resection 0.30 (0.2−0.5) P < 0.01
Partial resection 0.56 (0.3−1.0) P = 0.05
LGG 1.00 (NA−NA)
non−LGG 17.03 (4.5−64.9) P < 0.01
Cluster 1 1.00 (NA−NA)
Cluster 2 2.58 (0.8−8.0) P = 0.10
Cluster 3 0.75 (0.1−4.8) P = 0.76
Cluster 4 0.32 (0.0−3.7) P = 0.36
Cluster 5 0.59 (0.2−2.0) P = 0.40
Cluster 6 6.34 (2.0−20.0) P < 0.01
Cluster 7 0.48 (0.1−2.0) P = 0.31
Cluster 8 0.20 (0.0−2.5) P = 0.21
Cluster 9 0.00 (0.0−26.8) P = 0.22
Cluster 10 0.82 (0.2−3.0) P = 0.77
Cluster 11 0.51 (0.1−4.1) P = 0.52
Cluster 11:spliceosome gsva score 6.82 (0.1−510.6) P = 0.38
Cluster 10:spliceosome gsva score 0.77 (0.1−10.6) P = 0.84
Cluster 9:spliceosome gsva score 0.00 (0.0−101.3) P = 0.24
Cluster 8:spliceosome gsva score 0.19 (0.0−24.5) P = 0.50
Cluster 7:spliceosome gsva score 0.17 (0.0−2.8) P = 0.22
Cluster 6:spliceosome gsva score 0.29 (0.0−2.8) P = 0.29
Cluster 5:spliceosome gsva score 0.71 (0.1−8.4) P = 0.78
Cluster 4:spliceosome gsva score 15.41 (0.0−5573.9) P = 0.36
Cluster 3:spliceosome gsva score 2.76 (0.1−110.2) P = 0.59
Cluster 2:spliceosome gsva score 0.50 (0.0−5.5) P = 0.57
age at diagnosis years 0.97 (0.9−1.0) P = 0.13
spliceosome gsva score 2.82 (0.4−19.6) P = 0.30
0.000001
0.001000
1.000000
1000.000000
Hazard Ratio ± 95% CI