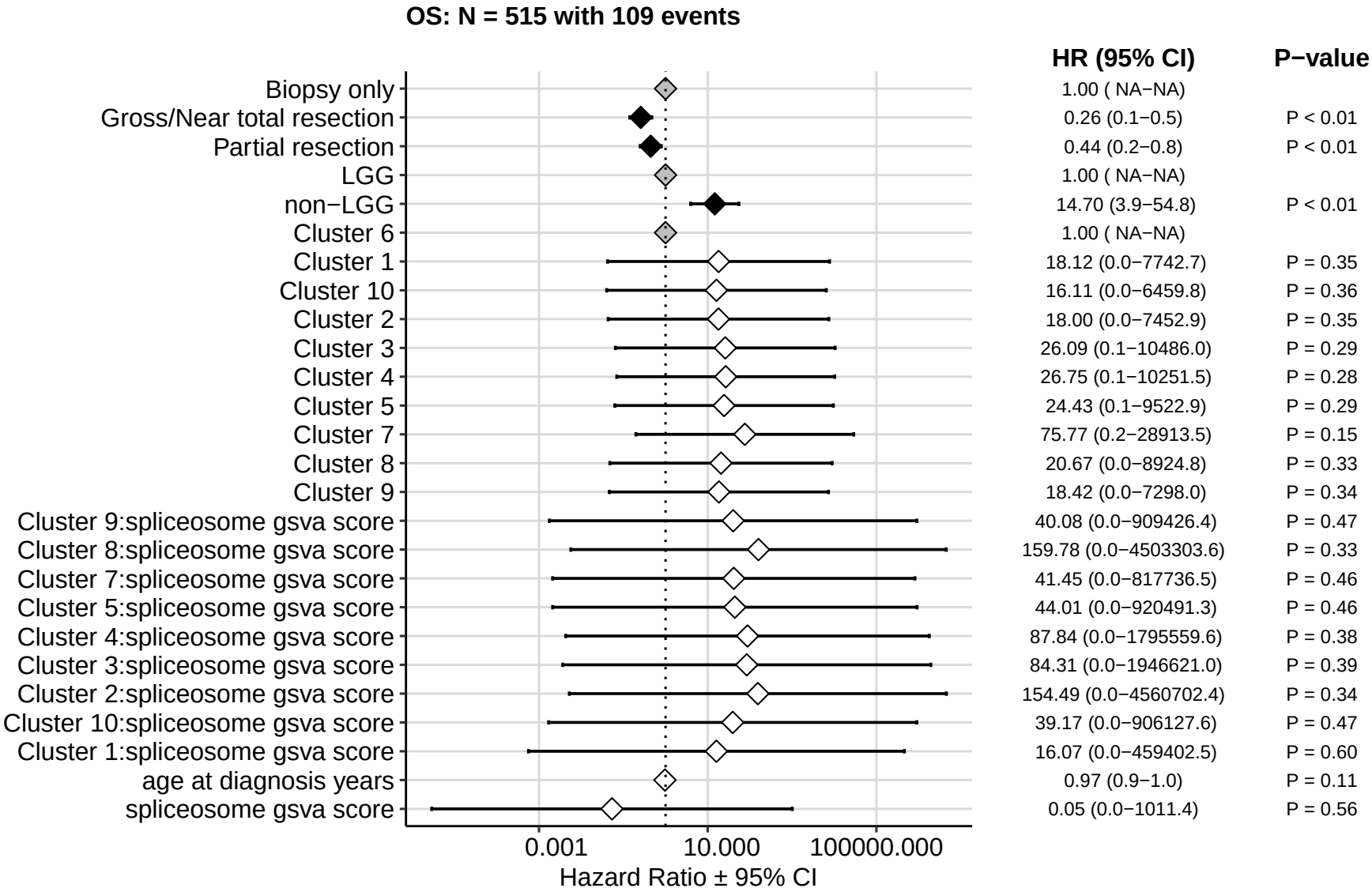
OS: N = 515 with 109 events
HR (95% CI)
P−value
Biopsy only
1.00 (NA−NA)
Gross/Near total resection
0.26 (0.1−0.5)
P < 0.01
Partial resection
0.44 (0.2−0.8)
P < 0.01
LGG
1.00 (NA−NA)
non−LGG
14.70 (3.9−54.8)
P < 0.01
Cluster 6
1.00 (NA−NA)
Cluster 1
18.12 (0.0−7742.7)
P = 0.35
Cluster 10
16.11 (0.0−6459.8)
P = 0.36
Cluster 2
18.00 (0.0−7452.9)
P = 0.35
Cluster 3
26.09 (0.1−10486.0)
P = 0.29
Cluster 4
26.75 (0.1−10251.5)
P = 0.28
Cluster 5
24.43 (0.1−9522.9)
P = 0.29
Cluster 7
75.77 (0.2−28913.5)
P = 0.15
Cluster 8
20.67 (0.0−8924.8)
P = 0.33
Cluster 9
18.42 (0.0−7298.0)
P = 0.34
Cluster 9:spliceosome gsva score
40.08 (0.0−909426.4)
P = 0.47
Cluster 8:spliceosome gsva score
159.78 (0.0−4503303.6)
P = 0.33
Cluster 7:spliceosome gsva score
41.45 (0.0−817736.5)
P = 0.46
Cluster 5:spliceosome gsva score
44.01 (0.0−920491.3)
P = 0.46
Cluster 4:spliceosome gsva score
87.84 (0.0−1795559.6)
P = 0.38
Cluster 3:spliceosome gsva score
84.31 (0.0−1946621.0)
P = 0.39
Cluster 2:spliceosome gsva score
154.49 (0.0−4560702.4)
P = 0.34
Cluster 10:spliceosome gsva score
39.17 (0.0−906127.6)
P = 0.47
Cluster 1:spliceosome gsva score
16.07 (0.0−459402.5)
P = 0.60
age at diagnosis years
0.97 (0.9−1.0)
P = 0.11
spliceosome gsva score
0.05 (0.0−1011.4)
P = 0.56
0.001
10.000
100000.000
Hazard Ratio ± 95% CI