Supplementary Table 2. Univariate analyses of both hypoxia gene signatures using nanoString or RT-PCR analyses. HR = hazard ratio; 95% CI = 95 percent confidence interval.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **Loco-regional control** | | **Distant metastases** | | **Overall survival** | |
|  | **HR (95% CI)** | **p-value** | **HR (95% CI)** | **p-value** | **HR (95% CI)** | **p-value** |
| **All patients** |  |  |  |  |  |  |
| **nanoString** |  |  |  |  |  |  |
| 15-gene signature | 3.55 (1.35-9.35) | **0.010** | 1.27 (0.65-2.46) | 0.485 | 1.47 (0.88-2.47) | 0.141 |
| 26-gene signature | 9.37 (2.22-39.5) | **0.002** | 2.15 (1.01-4.55) | **0.046** | 2.48 (1.39-4.42) | **0.002** |
| **RT-PCR** |  |  |  |  |  |  |
| 15-gene signature | 2.71 (1.16-6.35) | **0.022** | 1.34 (0.69-2.62) | 0.394 | 1.31 (0.79-2.17) | 0.305 |
| 26-gene signature | 6.00 (1.82-19.9) | **0.003** | 2.88 (1.26-6.58) | **0.012** | 2.23 (1.25-4.00) | **0.007** |
| **Patients with HPV16 DNA negative tumors only** | | | |  |  |  |
| **nanoString** |  |  |  |  |  |  |
| 15-gene signature | 4.66 (1.60-13.5) | **0.005** | 1.54 (0.73-3.21) | 0.255 | 1.88 (1.06-3.34) | **0.031** |
| 26-gene signature | 11.3 (1.53-83.7) | **0.017** | 1.51 (0.65-3.51) | 0.338 | 2.05 (1.03-4.08) | **0.040** |
| **RT-PCR** |  |  |  |  |  |  |
| 15-gene signature | 3.91 (1.58-9.71) | **0.003** | 1.90 (0.90-4.00) | 0.091 | 1.84 (1.05-3.22) | **0.033** |
| 26-gene signature | 4.34 (1.03-18.3) | **0.046** | 1.80 (0.69-4.71) | 0.230 | 1.49 (0.75-2.97) | 0.258 |