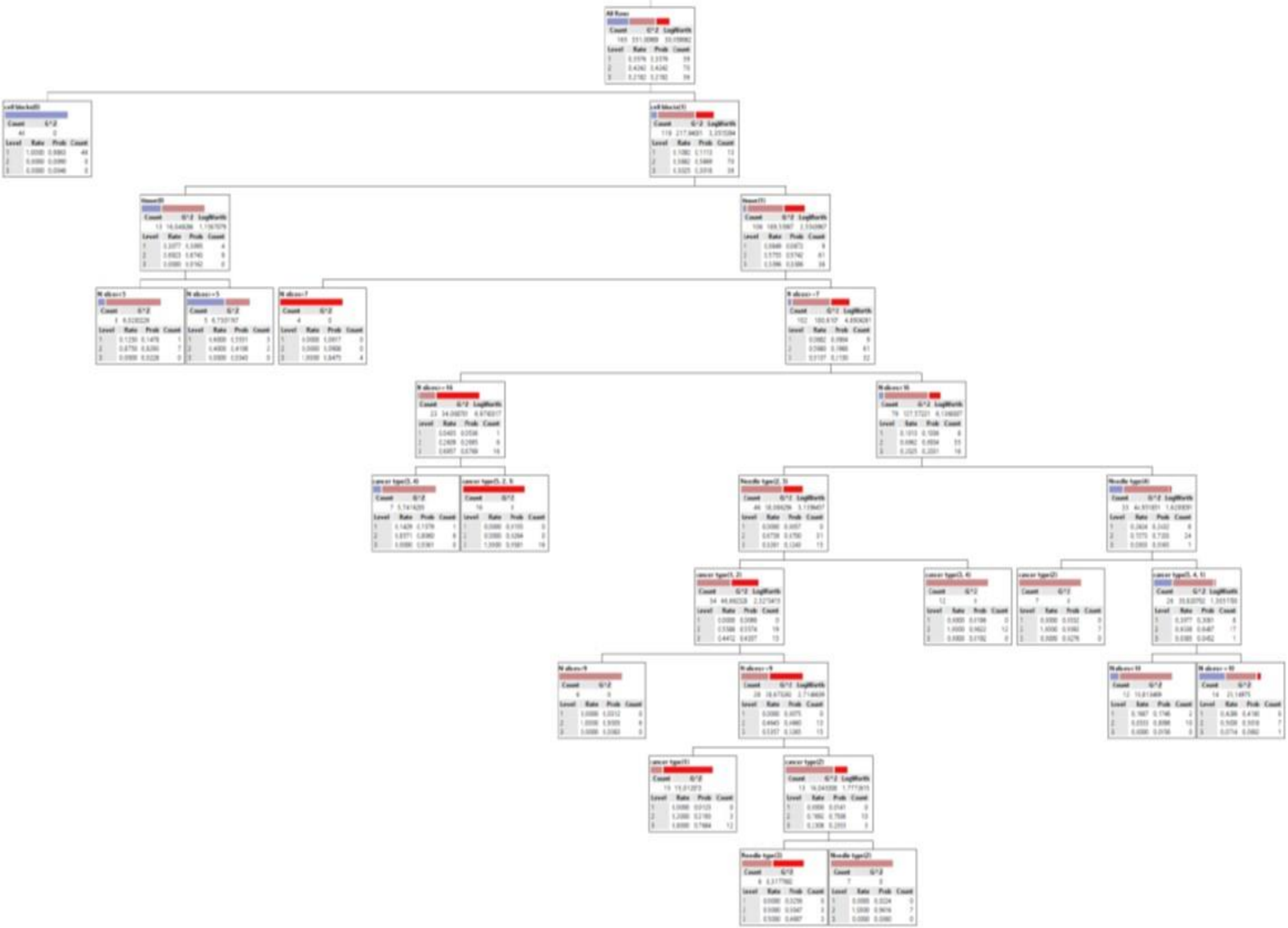
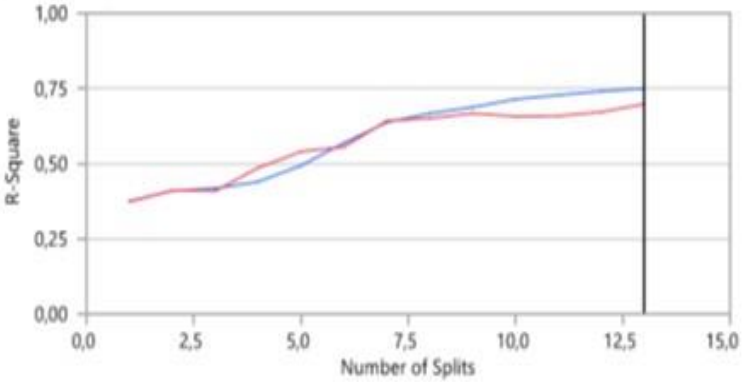

All Rows
Count
G^2
LogWorth
Level
Rate
Prob
Count

**Split History**



Validation Data in Red
Training set in blue

**Fit Details**

| | RSquare | N | Number of Splits |
|---|---|---|---|
| Training | 0,750 | 165 | 13 |
| Validation (30%) | 0,698 | 83 | |

**Crossvalidation**

| k-fold | | -2LogLike | RSquare |
|---|---|---|---|
| 10 | Folded | 111,817273 | 0,6814 |
| | Overall | 77,7931251 | 0,7501 |

| Measure | Training | Validation | Definition |
|---|---|---|---|
| Entropy RSquare | 0,7501 | 0,6982 | 1-Loglike(model)/Loglike(0) |
| Nagelkerke RSquare | 0,9051 | 0,8783 | (1-(L(0)/L(model))^(2/n))/(1-L(0)^(2/n)) |
| Mean -Log p | 0,2658 | 0,3214 | ∑ -Log(ρ[j])/n |
| RMSE | 0,2889 | 0,3257 | √ ∑(y[j]-ρ[j])$^2$/n |
| Mean Abs Dev | 0,1808 | 0,2172 | ∑ \|y[j]-ρ[j]\|/n |
| Misclassification Rate | 0,1152 | 0,1687 | ∑ (ρ[j]≠ρMax)/n |
| N | 165 | 83 | n |

**Confusion Matrix**

Training

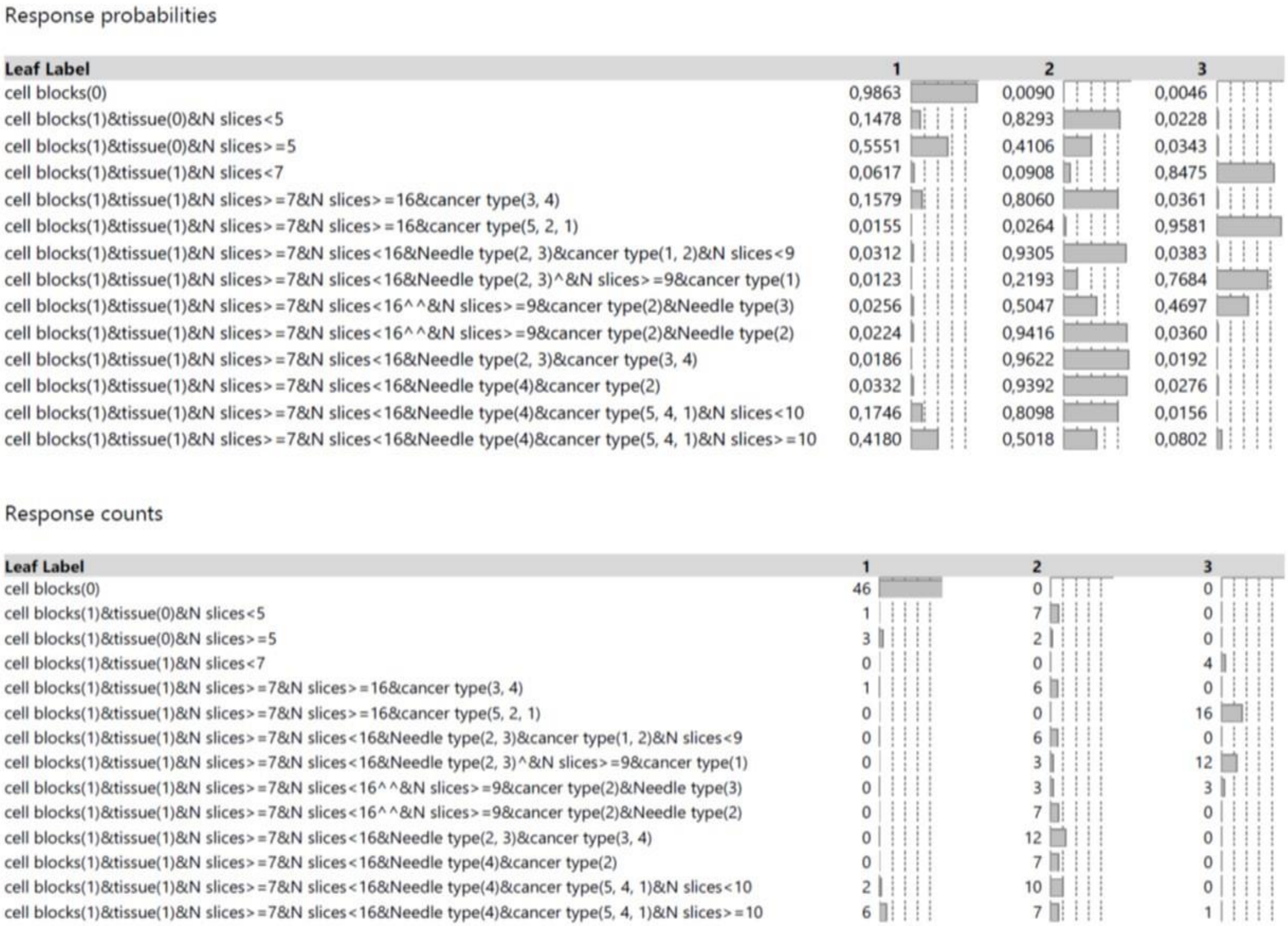
| Actual | Predicted Count | | |
|---|---|---|---|
| lesion size (cm) | 1 | 2 | 3 |
| 1 | 49 | 10 | 0 |
| 2 | 2 | 65 | 3 |
| 3 | 0 | 4 | 32 |

Validation

| Actual | Predicted Count | | |
|---|---|---|---|
| lesion size (cm) | 1 | 2 | 3 |
| 1 | 25 | 6 | 0 |
| 2 | 2 | 27 | 5 |
| 3 | 0 | 1 | 17 |

## Column Contributions

| Term | Number of Splits | G^2 | Portion |
|---|---|---|---|
| cell blocks | 1 | 133,06988 | 0,4870 |
| cancer type | 4 | 54,4381518 | 0,1992 |
| N slices | 5 | 43,1144779 | 0,1578 |
| Needle type | 2 | 30,2616018 | 0,1108 |
| tissue | 1 | 12,332654 | 0,0451 |



## Response probabilities

| Leaf Label | 1 | 2 | 3 |
|---|---|---|---|
| cell blocks(0) | 0,9863 | 0,0090 | 0,0046 |
| cell blocks(1)&tissue(0)&N slices<5 | 0,1478 | 0,8293 | 0,0228 |
| cell blocks(1)&tissue(0)&N slices>=5 | 0,5551 | 0,4106 | 0,0343 |
| cell blocks(1)&tissue(1)&N slices<7 | 0,0617 | 0,0908 | 0,8475 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices>=16&cancer type(3, 4) | 0,1579 | 0,8060 | 0,0361 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices>=16&cancer type(5, 2, 1) | 0,0155 | 0,0264 | 0,9581 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16&Needle type(2, 3)&cancer type(1, 2)&N slices<9 | 0,0312 | 0,9305 | 0,0383 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16&Needle type(2, 3)^&N slices>=9&cancer type(1) | 0,0123 | 0,2193 | 0,7684 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16^^&N slices>=9&cancer type(2)&Needle type(3) | 0,0256 | 0,5047 | 0,4697 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16^^&N slices>=9&cancer type(2)&Needle type(2) | 0,0224 | 0,9416 | 0,0360 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16&Needle type(2, 3)&cancer type(3, 4) | 0,0186 | 0,9622 | 0,0192 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16&Needle type(4)&cancer type(2) | 0,0332 | 0,9392 | 0,0276 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16&Needle type(4)&cancer type(5, 4, 1)&N slices<10 | 0,1746 | 0,8098 | 0,0156 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16&Needle type(4)&cancer type(5, 4, 1)&N slices>=10 | 0,4180 | 0,5018 | 0,0802 |

## Response counts

| Leaf Label | 1 | 2 | 3 |
|---|---|---|---|
| cell blocks(0) | 46 | 0 | 0 |
| cell blocks(1)&tissue(0)&N slices<5 | 1 | 7 | 0 |
| cell blocks(1)&tissue(0)&N slices>=5 | 3 | 2 | 0 |
| cell blocks(1)&tissue(1)&N slices<7 | 0 | 0 | 4 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices>=16&cancer type(3, 4) | 1 | 6 | 0 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices>=16&cancer type(5, 2, 1) | 0 | 0 | 16 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16&Needle type(2, 3)&cancer type(1, 2)&N slices<9 | 0 | 6 | 0 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16&Needle type(2, 3)^&N slices>=9&cancer type(1) | 0 | 3 | 12 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16^^&N slices>=9&cancer type(2)&Needle type(3) | 0 | 3 | 3 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16^^&N slices>=9&cancer type(2)&Needle type(2) | 0 | 7 | 0 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16&Needle type(2, 3)&cancer type(3, 4) | 0 | 12 | 0 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16&Needle type(4)&cancer type(2) | 0 | 7 | 0 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16&Needle type(4)&cancer type(5, 4, 1)&N slices<10 | 2 | 10 | 0 |
| cell blocks(1)&tissue(1)&N slices>=7&N slices<16&Needle type(4)&cancer type(5, 4, 1)&N slices>=10 | 6 | 7 | 1 |

## Legends to the figures

**Figure 5.** Partition report for lesion size. Each terminal node informs for the number of counts, total and particular per category level, the candidate $G^2$ statistic corresponding to a logWorth value ($-\log_{10}$(p value)) and the probability fit contribution per level. Zero $G^2$ values signal a perfect division.

**Figure 6.** Statistical information on the validity and reliability of the partition modeling.

**Figure 7.** Leaf report of the 13 pathways according to the decision tree of the study, in response probabilities and numbers of patients.