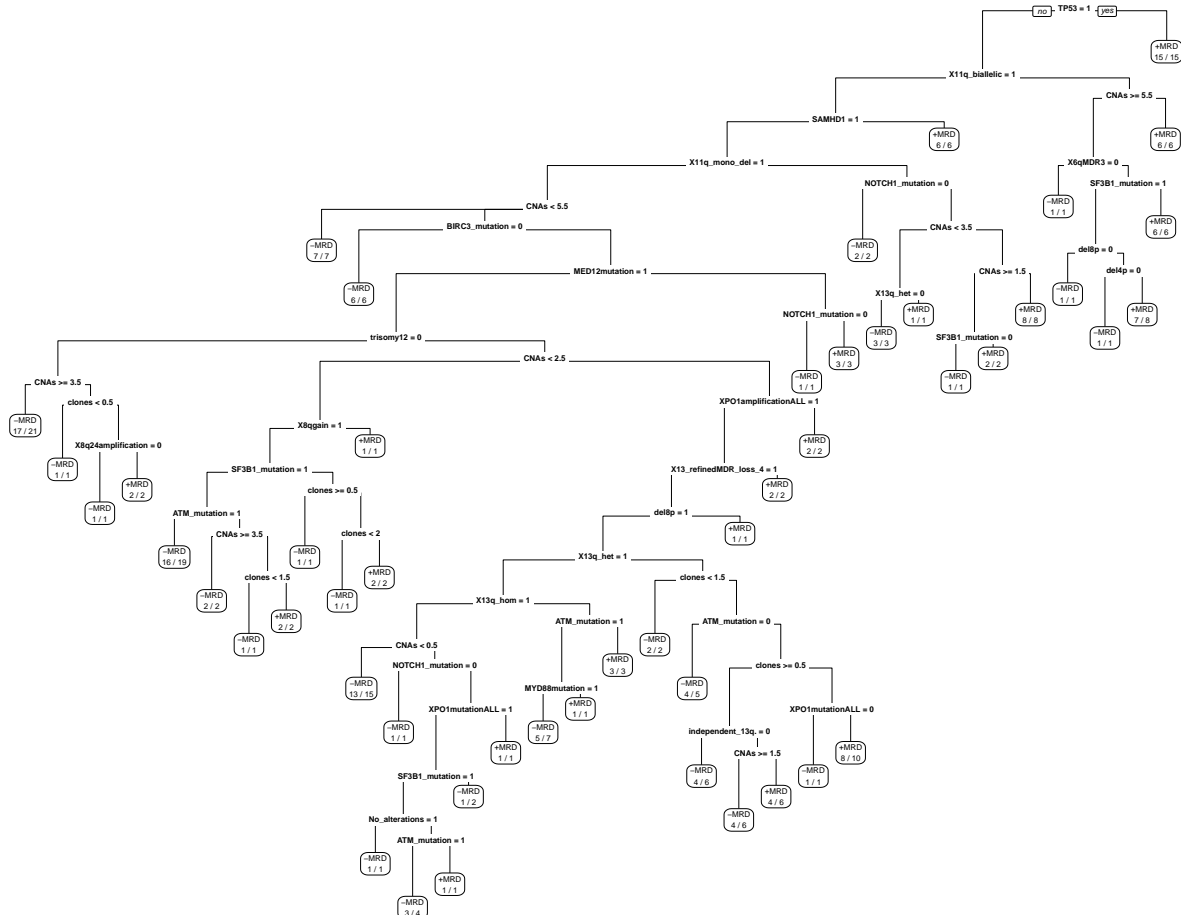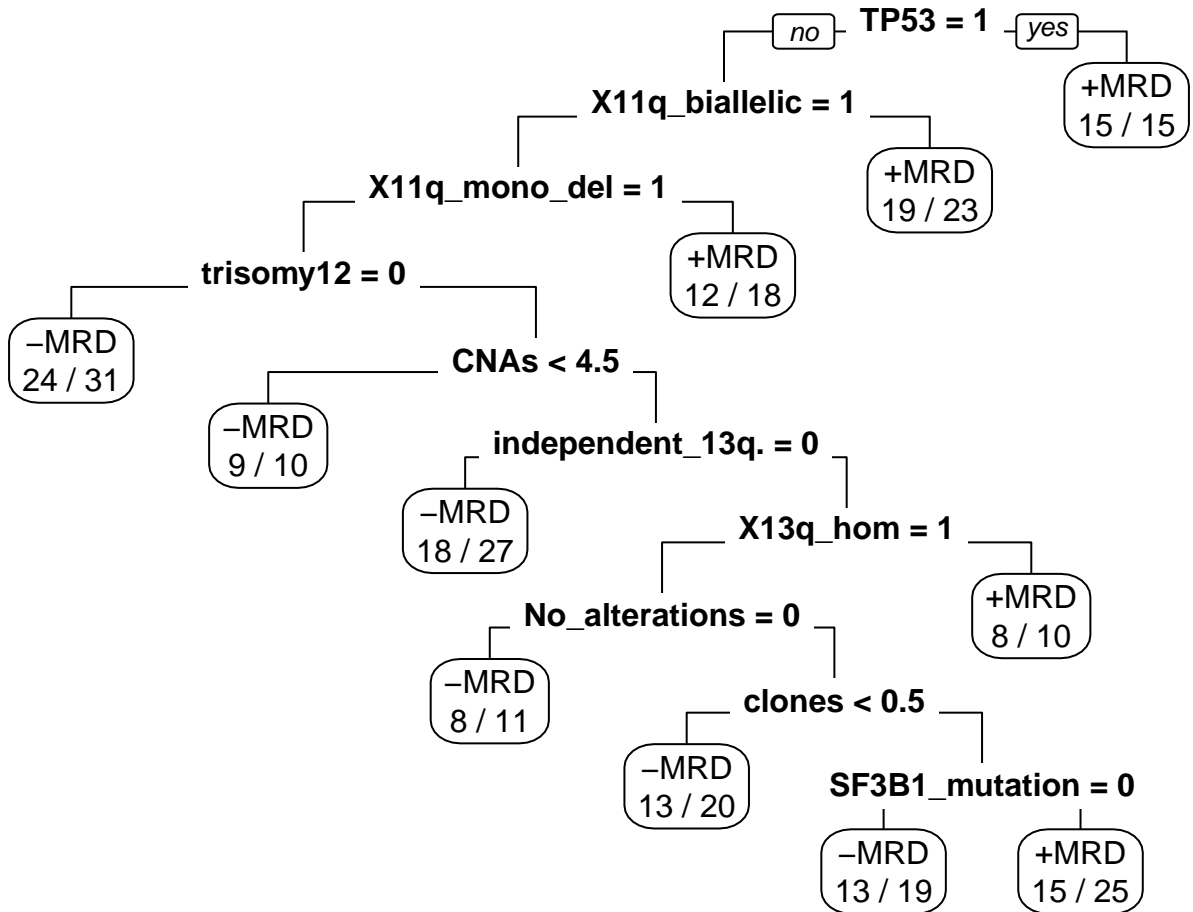**2c) tree1: Only our genetic findings**
cp=0.001, endgroup=1, MissClassErr~11%

This is the best tree with only genetics, but highly specific to our data!

2c) tree2:Only our genetic findings
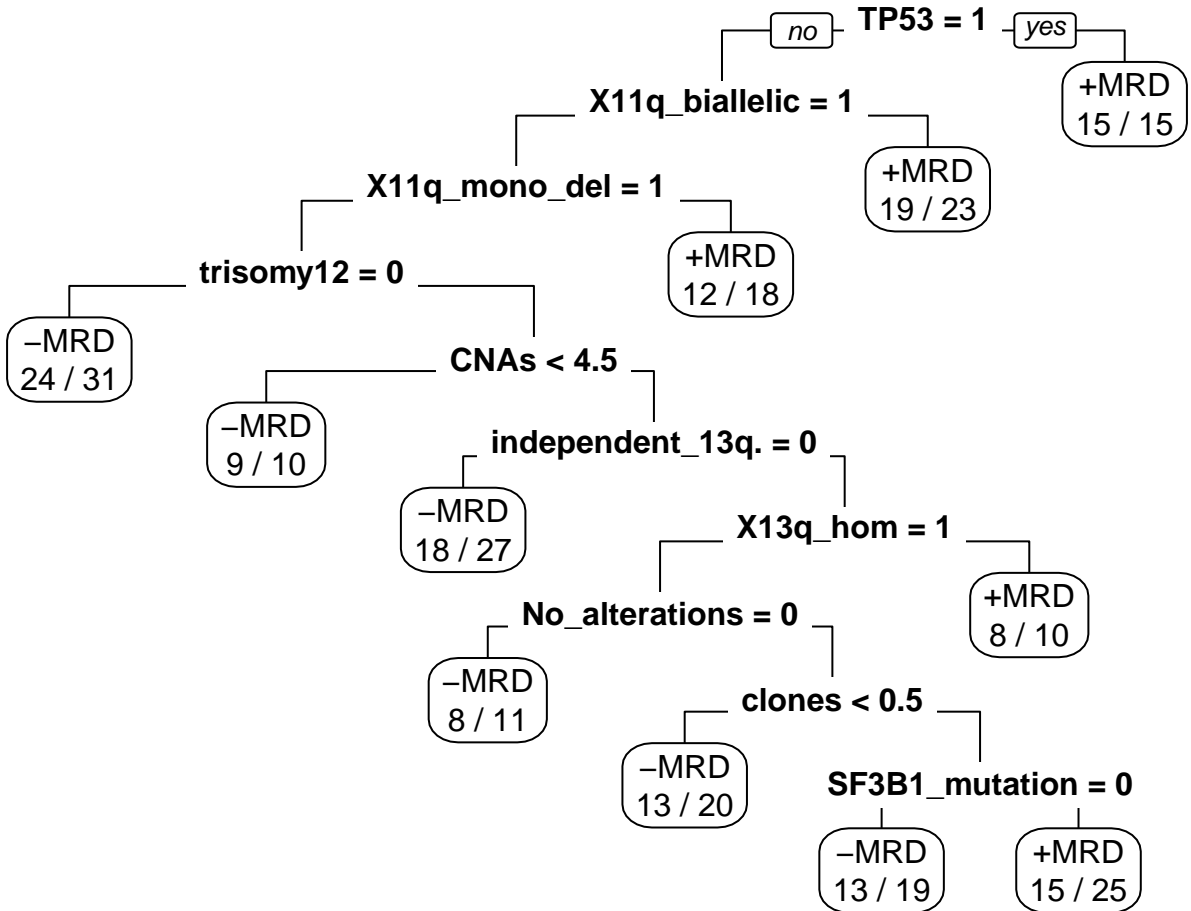## cp=0.01, endgroup=8, MissClassErr~27%

This is a fairly general reasonable tree,
parameters deducted from where all error curves coerce into one point.
Please check if it makes sense in a clinical setting

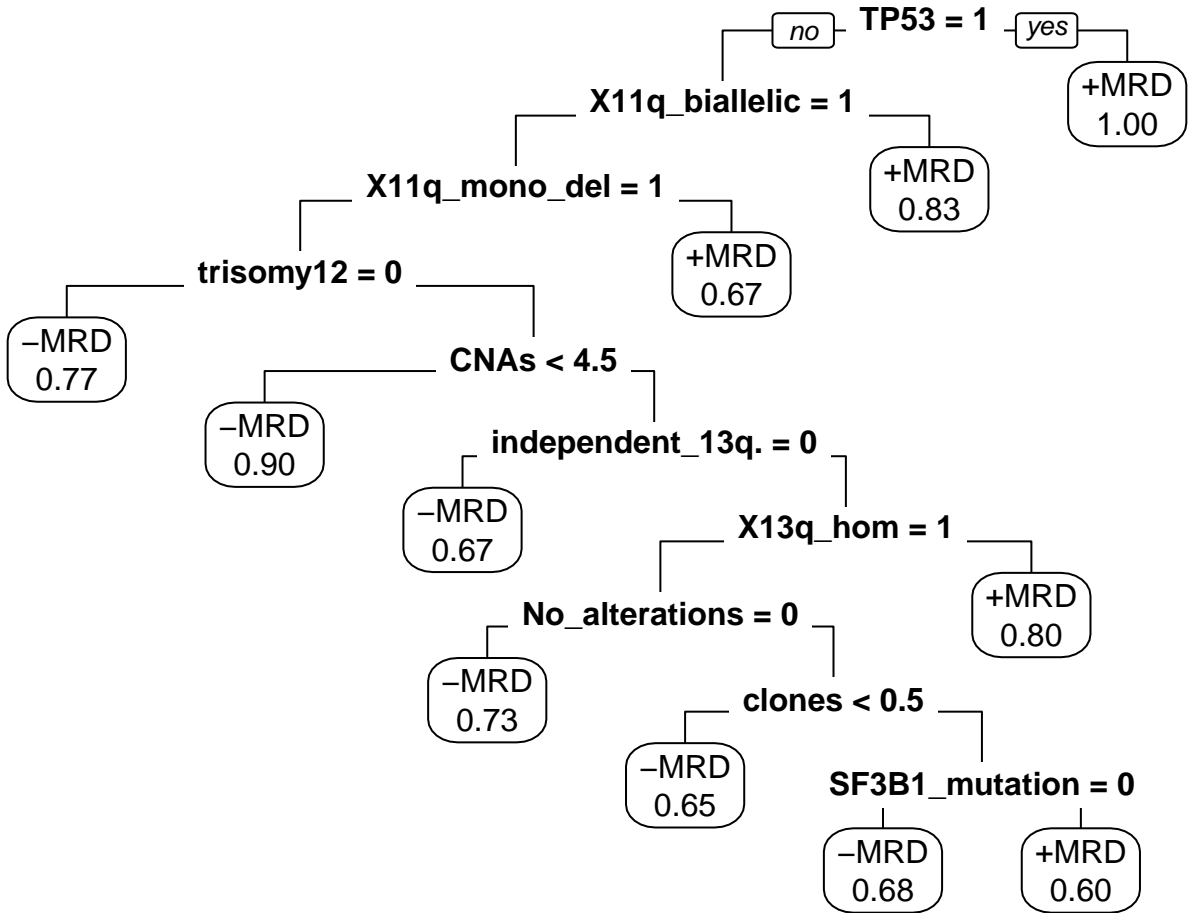This gives an overview about tree aesthetics:

There are around 100 more options to costumise the tree, just give me any ideas you have, and I'll implement them!

2c) tree3: Only our genetic findings cp=0.01, endgroup=8, MissClassErr~27%

TP53 = 1 — no / yes

+MRD 15 / 15

X11q_biallelic = 1

+MRD 19 / 23

X11q_mono_del = 1

+MRD 12 / 18

trisomy12 = 0

−MRD 24 / 31

CNAs < 4.5

−MRD 9 / 10

independent_13q. = 0

−MRD 18 / 27

X13q_hom = 1

+MRD 8 / 10

No_alterations = 0

−MRD 8 / 11

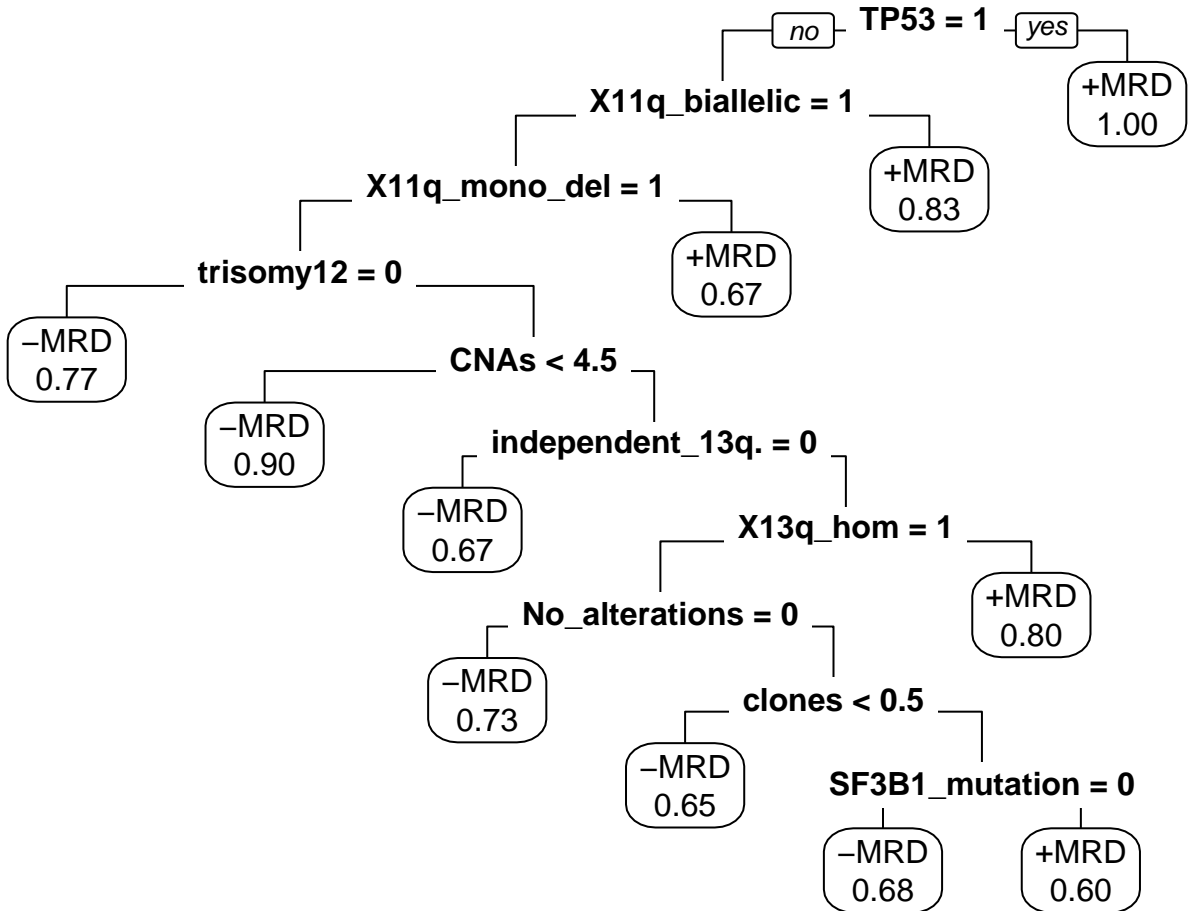clones < 0.5

−MRD 13 / 20

SF3B1_mutation = 0

−MRD 13 / 19

+MRD 15 / 25

All branches same length, total patient numbers displayed

**2c) tree4:Only our genetic findings
cp=0.01, endgroup=8, MissClassErr~27%**

TP53 = 1 — *no* / *yes*

X11q_biallelic = 1

X11q_mono_del = 1

trisomy12 = 0

CNAs < 4.5

independent_13q. = 0

X13q_hom = 1

No_alterations = 0

clones < 0.5

SF3B1_mutation = 0

+MRD 1.00

+MRD 0.83

+MRD 0.67

−MRD 0.77

−MRD 0.90

−MRD 0.67

+MRD 0.80

−MRD 0.73

−MRD 0.65
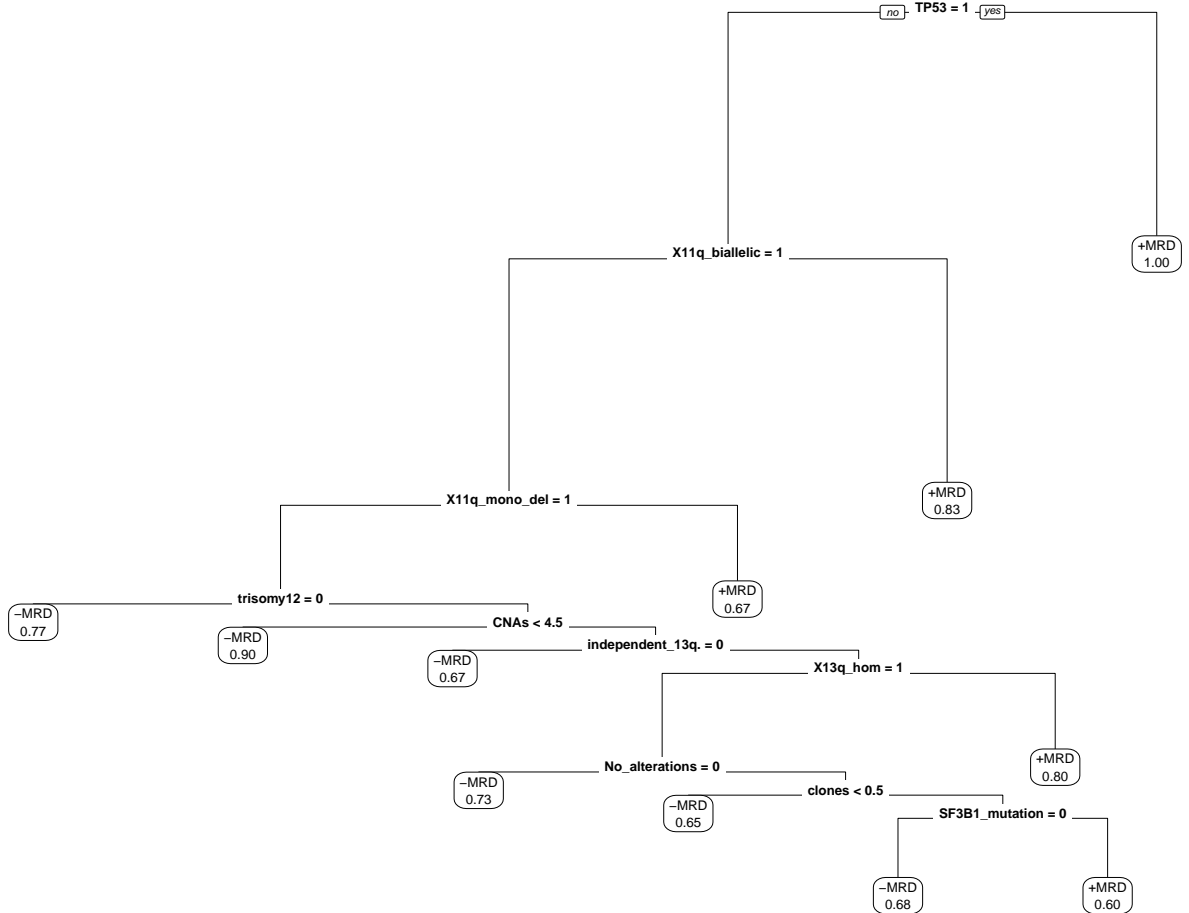
−MRD 0.68

+MRD 0.60

All branches same length, group correct classification rate displayed

2c) tree5:Only our genetic findings
cp=0.01, endgroup=8, MissClassErr~27%
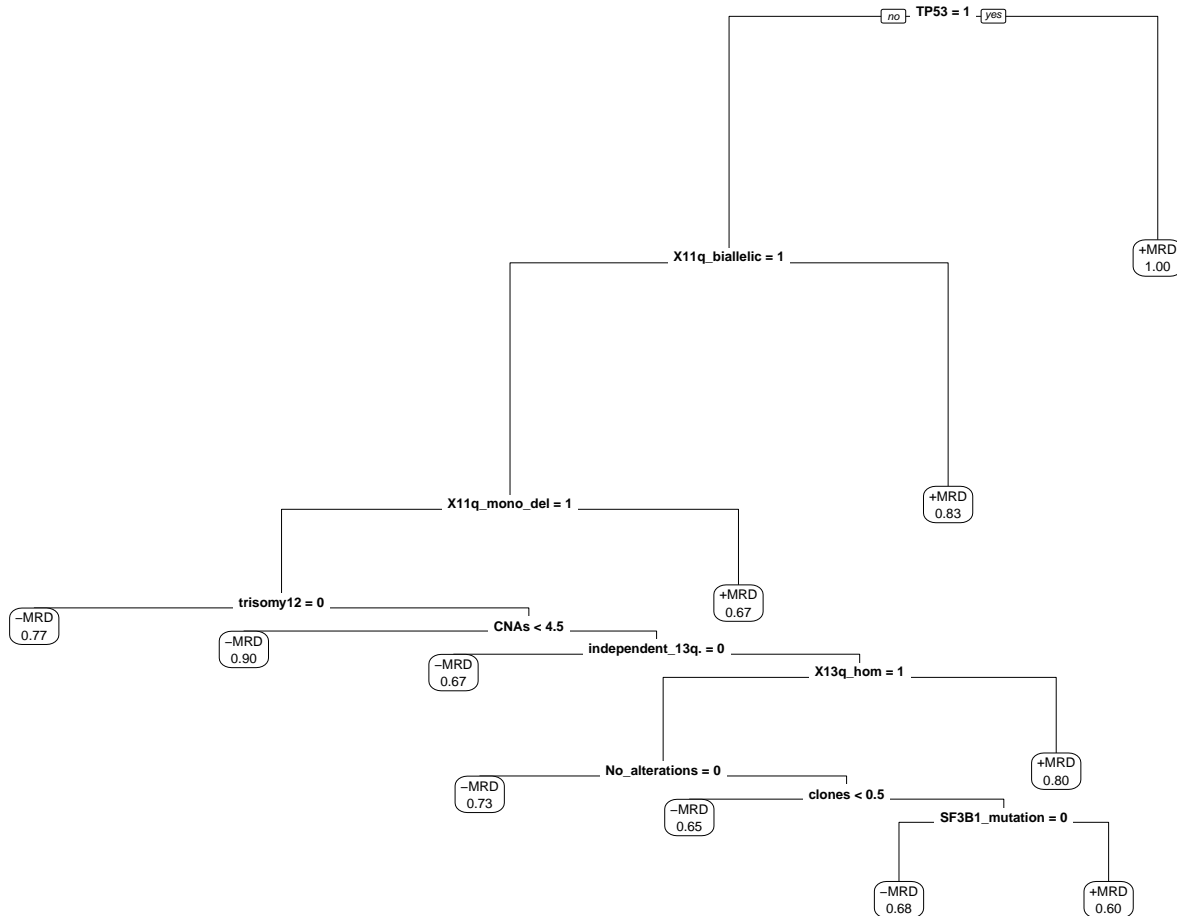

All branches same length, group correct classification rate displayed

2c) tree6:Only our genetic findings
cp=0.01, endgroup=8, MissClassErr~27%

TP53 = 1 — no / yes

+MRD 1.00

X11q_biallelic = 1

+MRD 0.83

X11q_mono_del = 1

+MRD 0.67

trisomy12 = 0

−MRD 0.77

−MRD 0.90

CNAs < 4.5

−MRD 0.67

independent_13q. = 0

X13q_hom = 1

+MRD 0.80

No_alterations = 0

−MRD 0.73

−MRD 0.65

clones < 0.5

SF3B1_mutation = 0

−MRD 0.68

+MRD 0.60

Branch length proportional to fit of model, group correct classification rate displayed

2c) tree7:Only our genetic findings
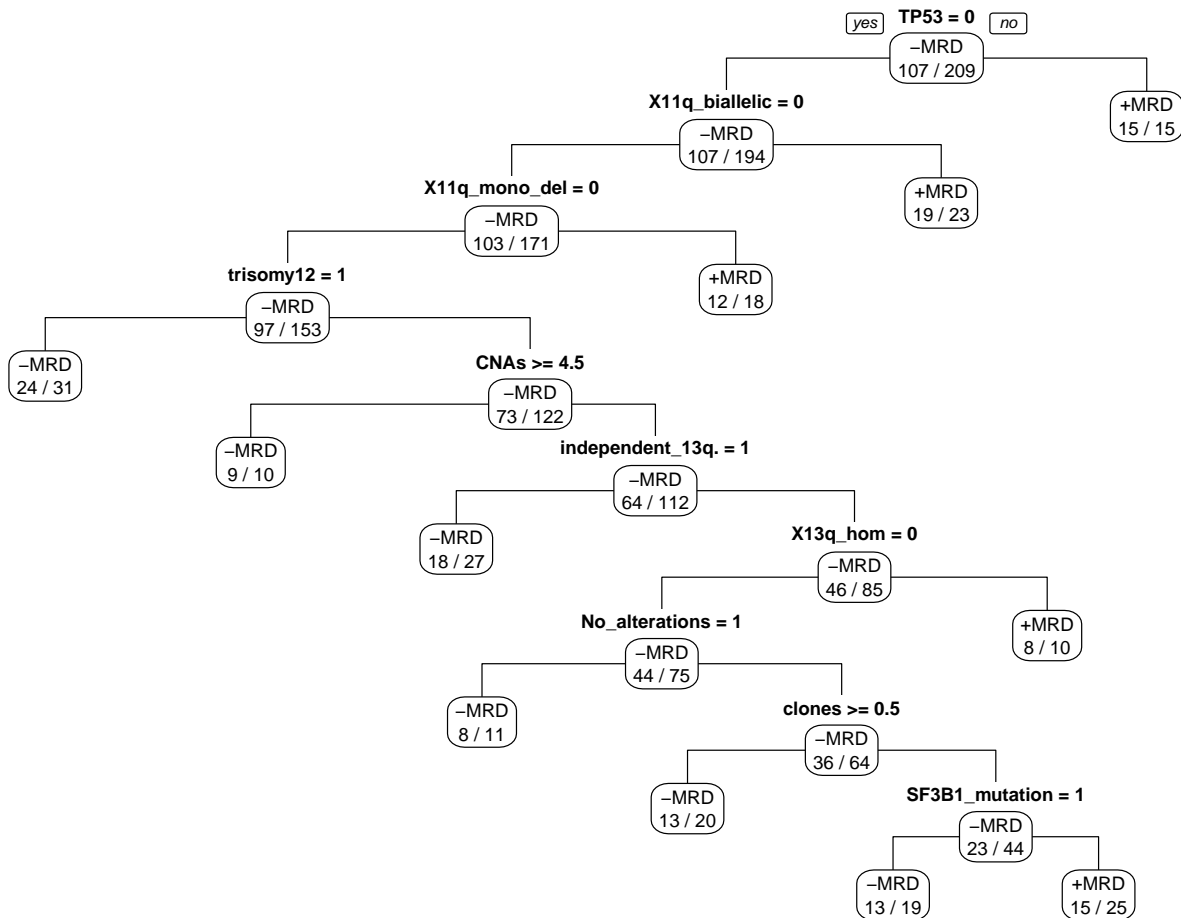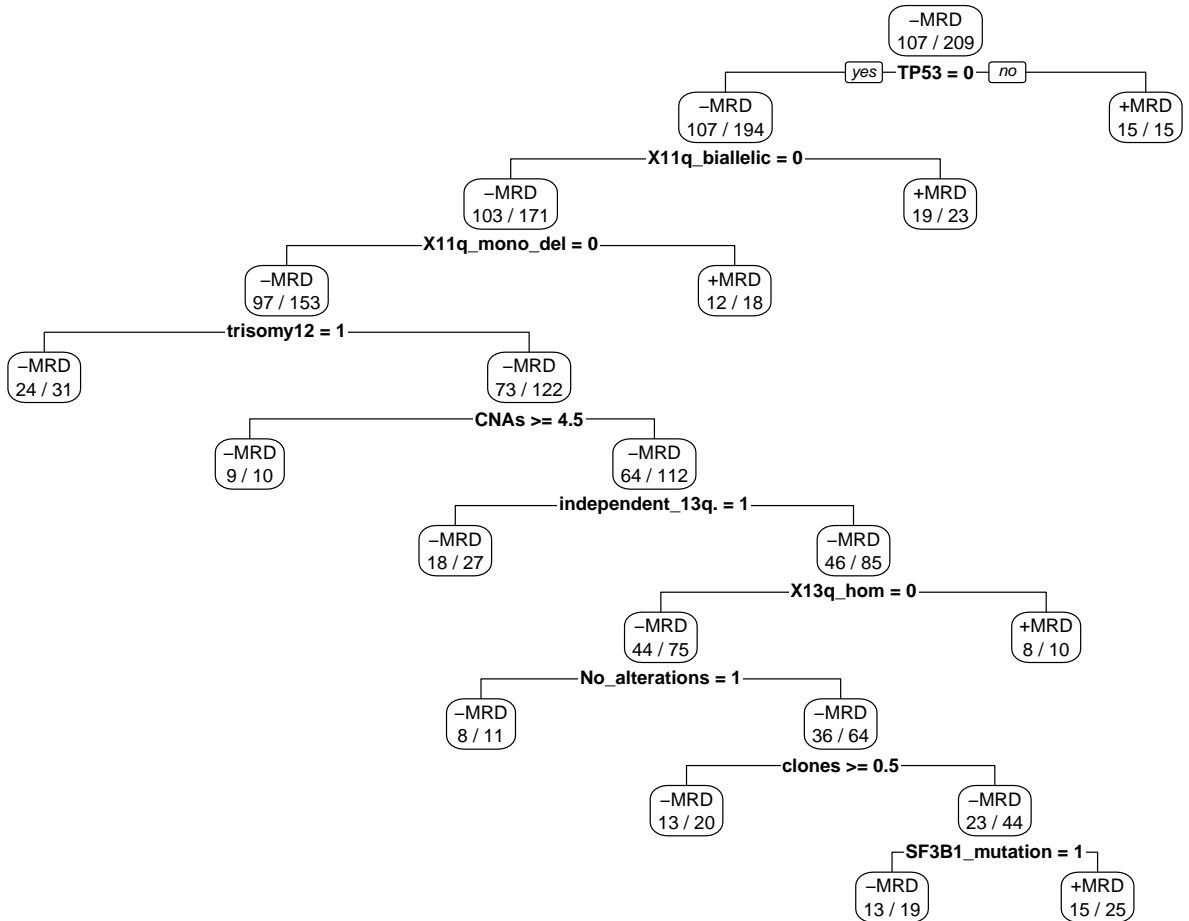**cp=0.01, endgroup=8, MissClassErr~27%**

Branch length proportional to fit of model, group correct classification rate displayed

**2c) tree8:Only our genetic findings
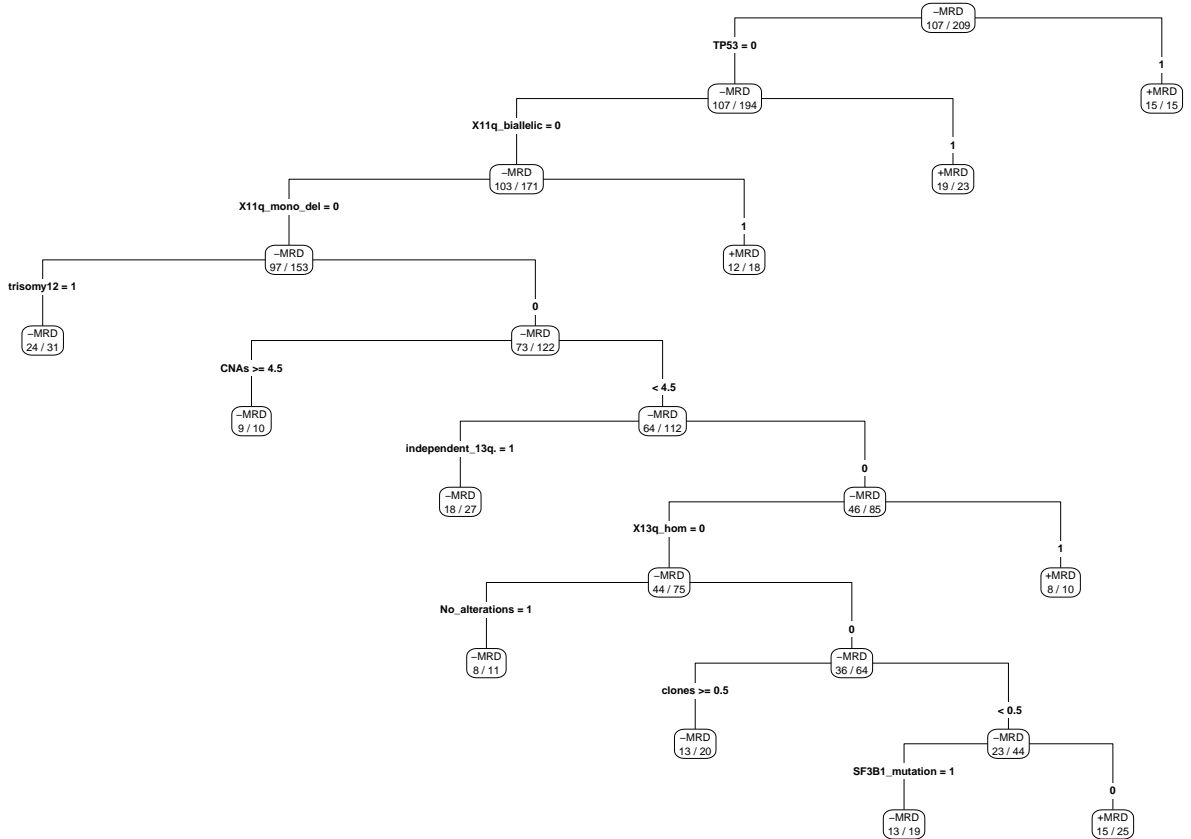cp=0.01, endgroup=8, MissClassErr~27%**

TP53 = 0
yes | no
−MRD
107 / 209

+MRD
15 / 15

X11q_biallelic = 0
−MRD
107 / 194

+MRD
19 / 23

X11q_mono_del = 0
−MRD
103 / 171

+MRD
12 / 18

trisomy12 = 1
−MRD
97 / 153

−MRD
24 / 31

CNAs >= 4.5
−MRD
73 / 122

−MRD
9 / 10

independent_13q. = 1
−MRD
64 / 112

−MRD
18 / 27

X13q_hom = 0
−MRD
46 / 85

+MRD
8 / 10

No_alterations = 1
−MRD
44 / 75

−MRD
8 / 11

clones >= 0.5
−MRD
36 / 64

−MRD
13 / 20

SF3B1_mutation = 1
−MRD
23 / 44

−MRD
13 / 19

+MRD
15 / 25

All branches same length, total patient numbers displayed, individual node labelled (type1)

**2c) tree9:Only our genetic findings
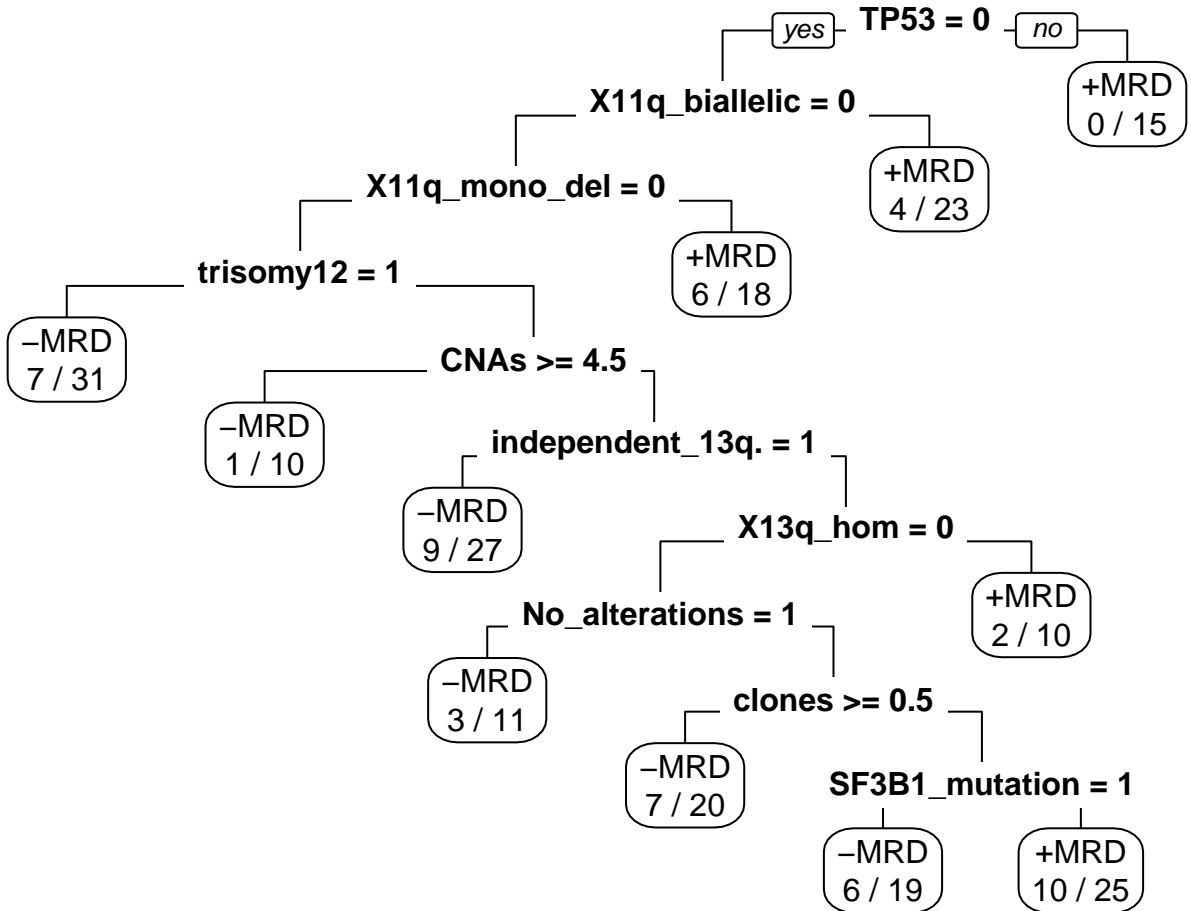cp=0.01, endgroup=8, MissClassErr~27%**

All branches same length, total patient numbers displayed, nodes labelled above split (type2)

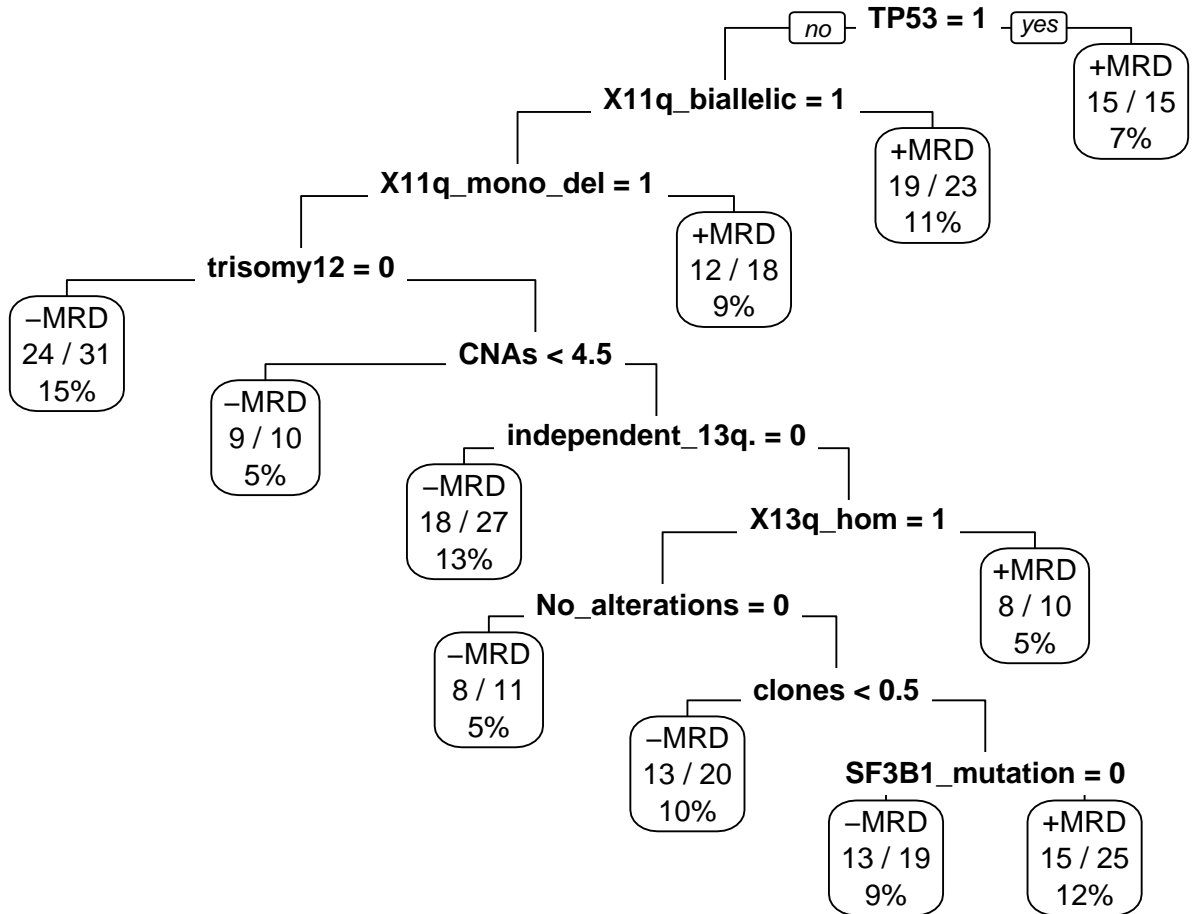**2c) tree10:Only our genetic findings cp=0.01, endgroup=8, MissClassErr~27%**

TP53 = 0

−MRD
107 / 209

1
+MRD
15 / 15

−MRD
107 / 194

X11q_biallelic = 0

1
+MRD
19 / 23

−MRD
103 / 171

X11q_mono_del = 0

1
+MRD
12 / 18

−MRD
97 / 153

trisomy12 = 1

0

−MRD
24 / 31

−MRD
73 / 122

CNAs >= 4.5

< 4.5

−MRD
9 / 10

−MRD
64 / 112

independent_13q. = 1

0

−MRD
18 / 27

−MRD
46 / 85

X13q_hom = 0

1
+MRD
8 / 10

−MRD
44 / 75

No_alterations = 1

0

−MRD
8 / 11

−MRD
36 / 64

clones >= 0.5

< 0.5

−MRD
13 / 20

−MRD
23 / 44

SF3B1_mutation = 1

0

−MRD
13 / 19

+MRD
15 / 25

All branches same length, total patient numbers displayed, nodes and branches labelled (type4)

2c) tree11:Only our genetic findings
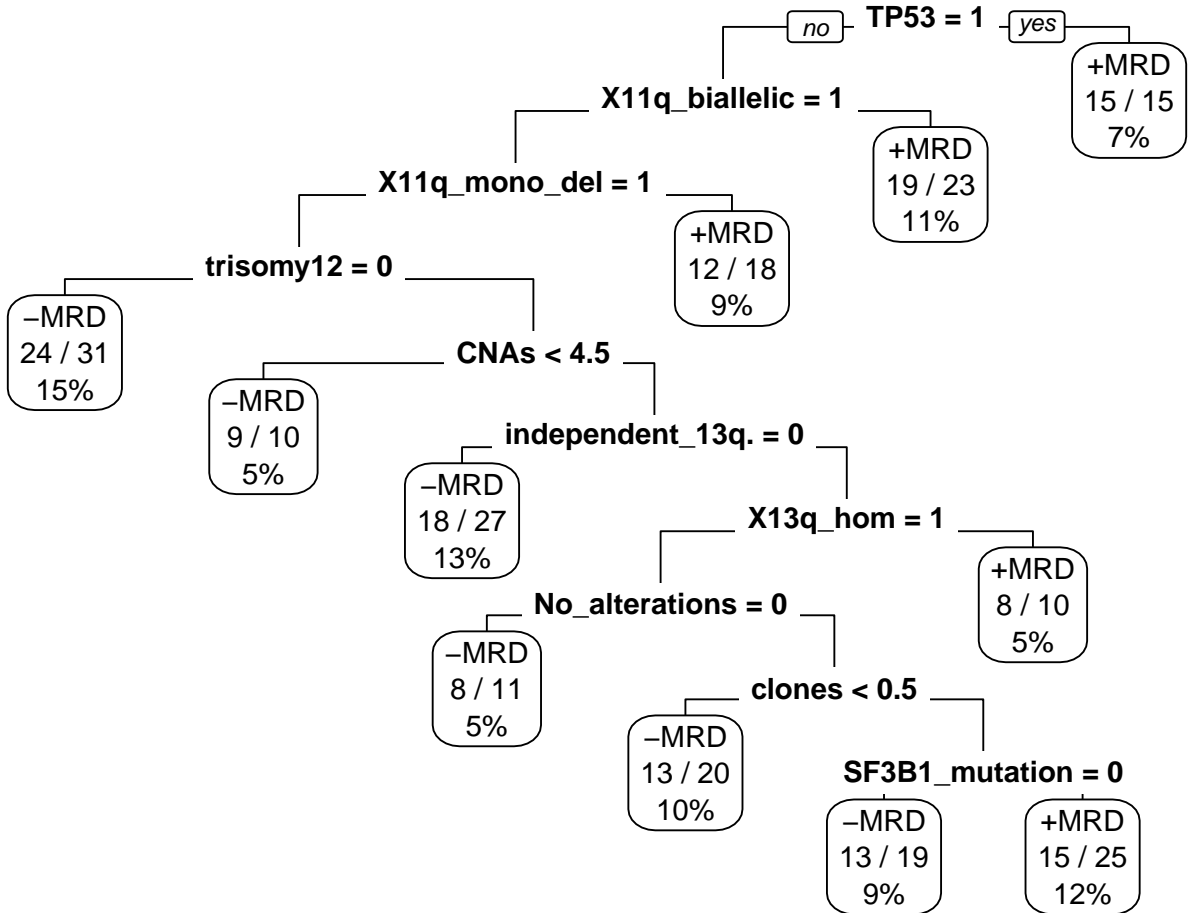**cp=0.01, endgroup=8, MissClassErr~27%**

All branches same length, missclassified patients displayed (extra=3)

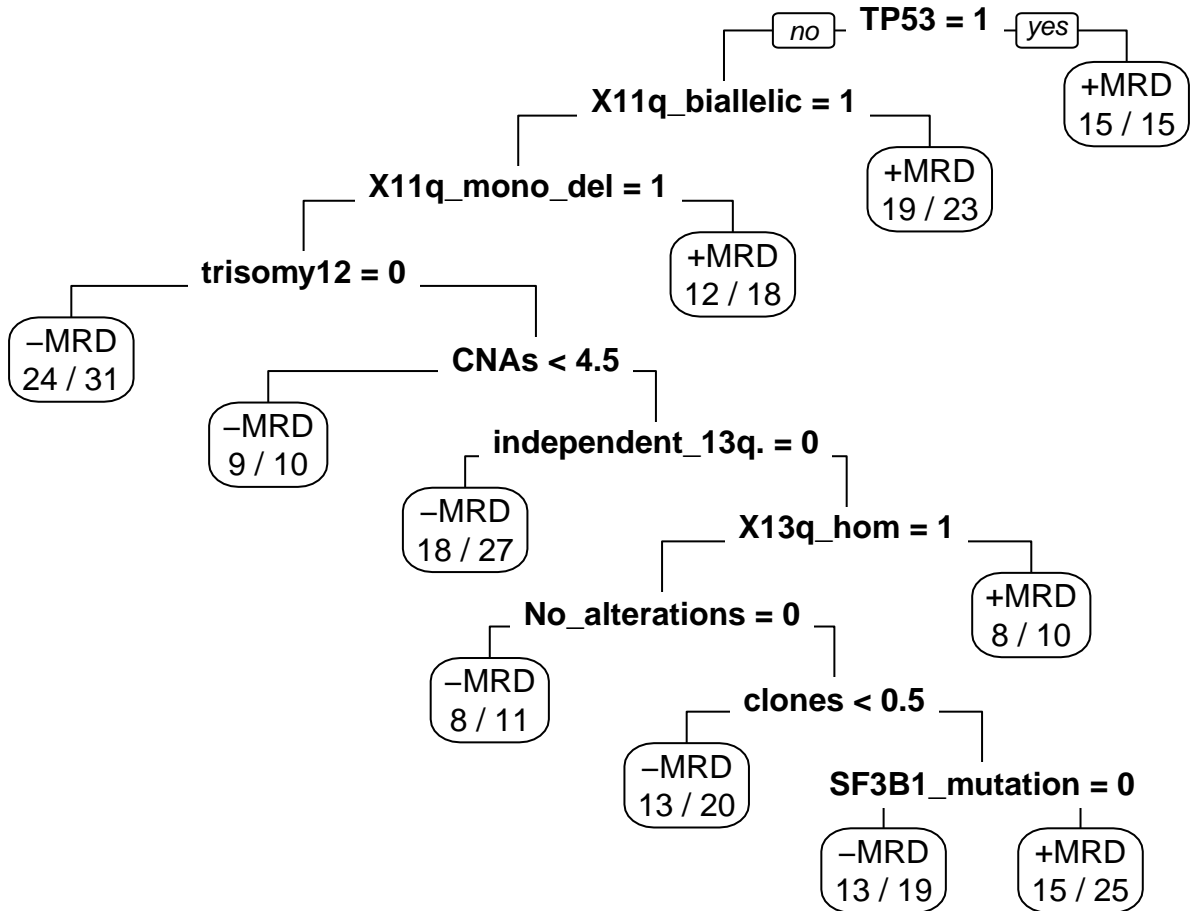**2c) tree12:Only our genetic findings
cp=0.01, endgroup=8, MissClassErr~27%**

TP53 = 1

no   yes

+MRD
15 / 15
7%

X11q_biallelic = 1

+MRD
19 / 23
11%

X11q_mono_del = 1

+MRD
12 / 18
9%

trisomy12 = 0

−MRD
24 / 31
15%

−MRD
9 / 10
5%

CNAs < 4.5

−MRD
18 / 27
13%

independent_13q. = 0

X13q_hom = 1

+MRD
8 / 10
5%

No_alterations = 0

−MRD
8 / 11
5%

clones < 0.5

−MRD
13 / 20
10%

SF3B1_mutation = 0

−MRD
13 / 19
9%

+MRD
15 / 25
12%

All branches same length,
correctly classified patients & total percentage in dataset displayed (extra=102)

2c) tree13:Only our genetic findings
cp=0.01, endgroup=8, MissClassErr~27%
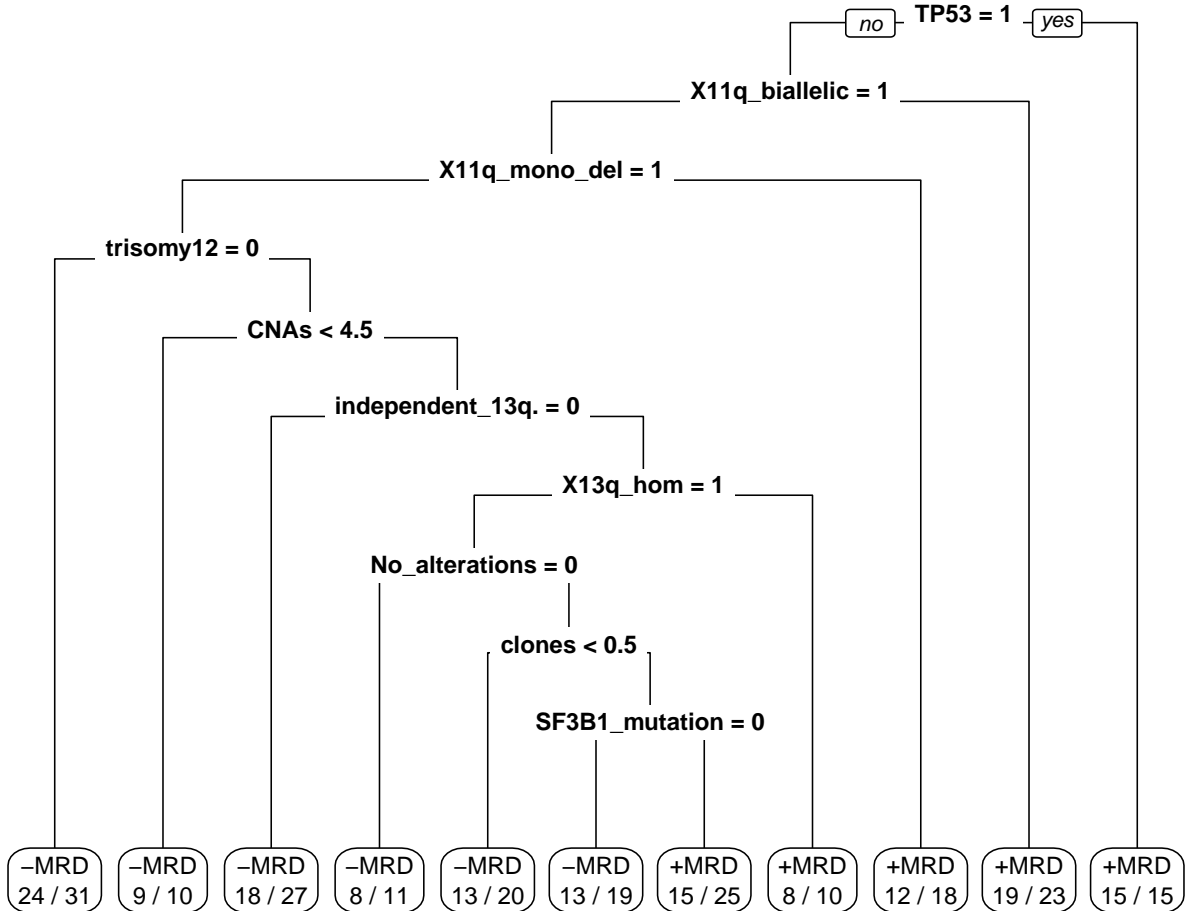
All branches same length,
correctly classified patients & total percentage in dataset displayed (extra=102)

2c) tree14:Only our genetic findings
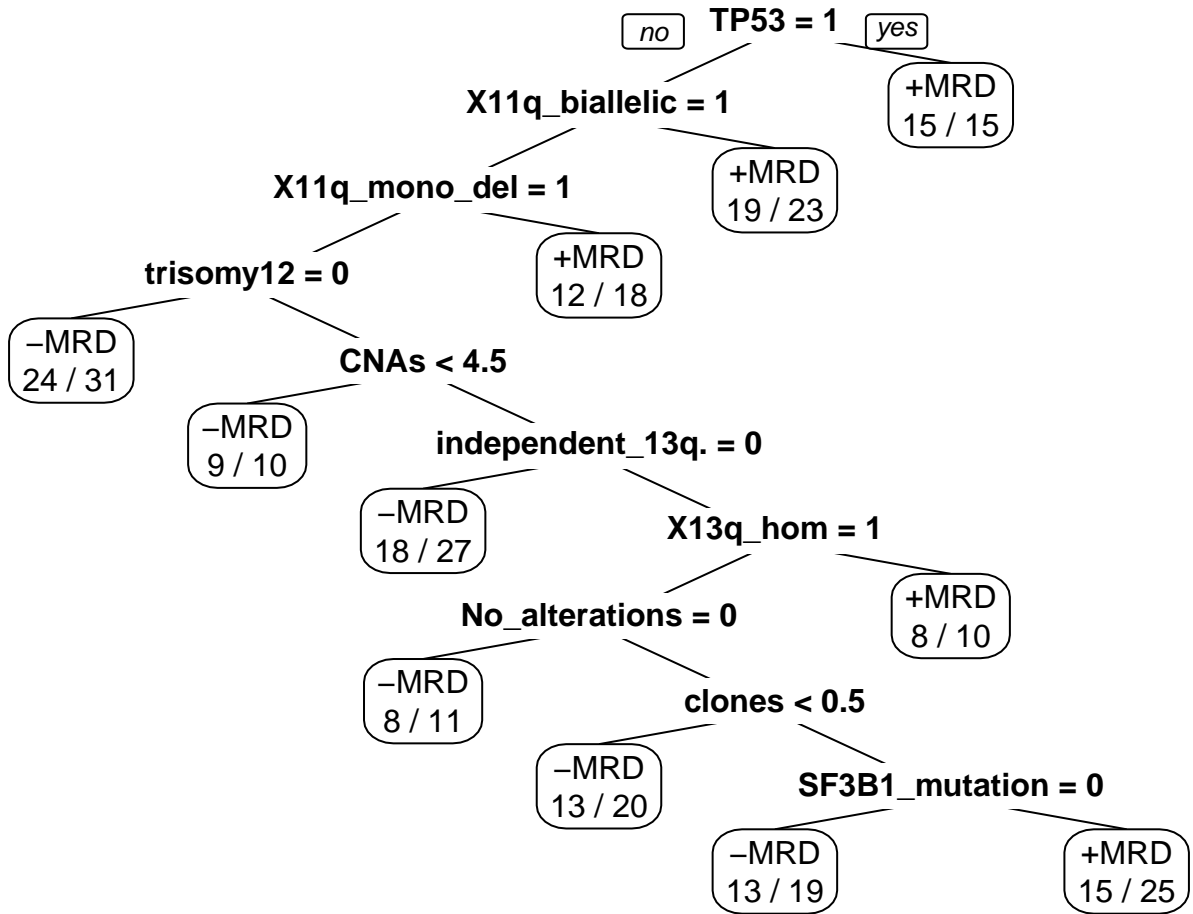# cp=0.01, endgroup=8, MissClassErr~27%

All branches same length, total patient numbers displayed

2c) tree15:Only our genetic findings
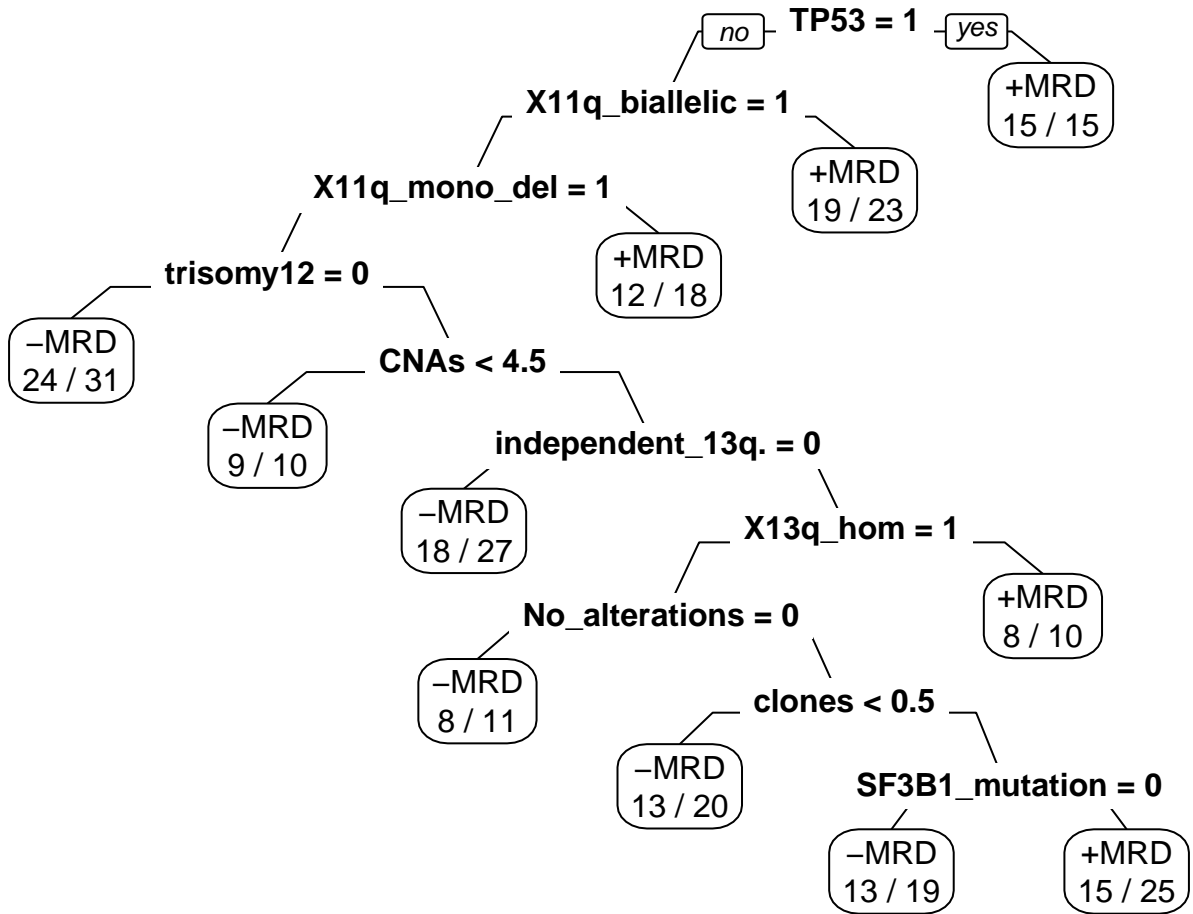## cp=0.01, endgroup=8, MissClassErr~27%

All branches same length, total patient numbers displayed, 'fallen leaves'

2c) tree16:Only our genetic findings
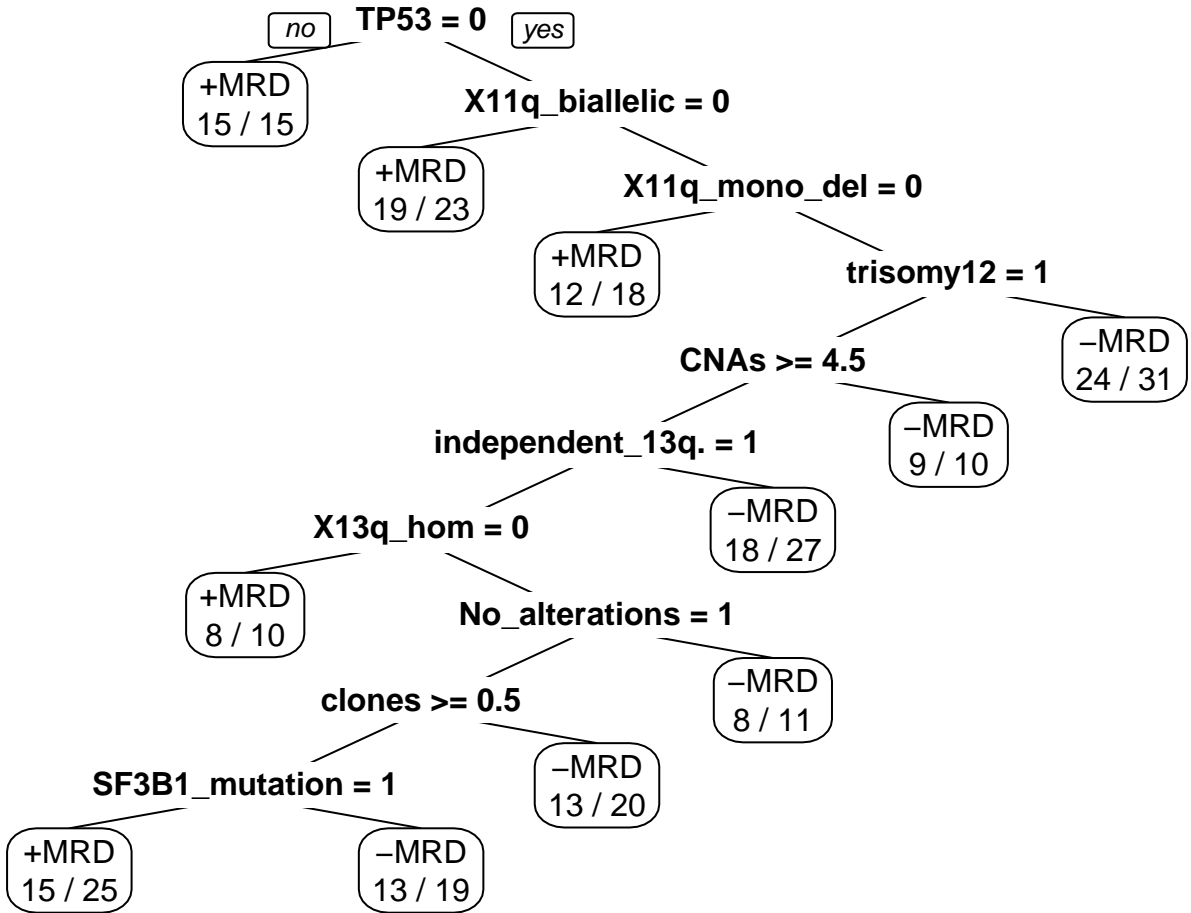# cp=0.01, endgroup=8, MissClassErr~27%

All branches same length, total patient numbers displayed, 'branch=0'

2c) tree17:Only our genetic findings
cp=0.01, endgroup=8, MissClassErr~27%

TP53 = 1

no

yes

+MRD
15 / 15

X11q_biallelic = 1

+MRD
19 / 23

X11q_mono_del = 1

+MRD
12 / 18

trisomy12 = 0

−MRD
24 / 31

CNAs < 4.5

−MRD
9 / 10

independent_13q. = 0

−MRD
18 / 27

X13q_hom = 1

No_alterations = 0

+MRD
8 / 10

−MRD
8 / 11

clones < 0.5

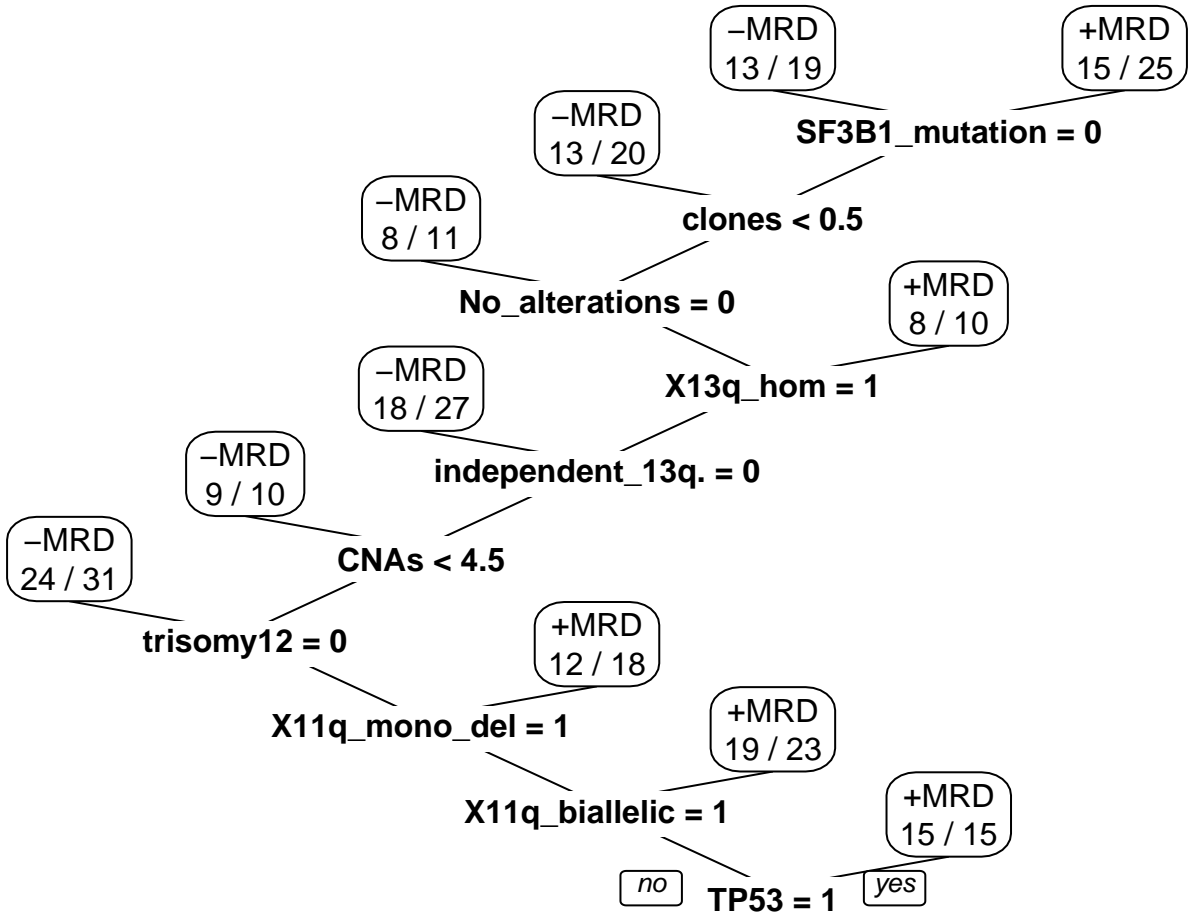−MRD
13 / 20

SF3B1_mutation = 0

−MRD
13 / 19

+MRD
15 / 25

All branches same length, total patient numbers displayed, 'branch=0.8'

**2c) tree18:Only our genetic findings
cp=0.01, endgroup=8, MissClassErr~27%**

All branches same length, total patient numbers displayed, 'xflip=TRUE'

2c) tree19:Only our genetic findings
cp=0.01, endgroup=8, MissClassErr~27%

−MRD 13 / 19

+MRD 15 / 25

SF3B1_mutation = 0

−MRD 13 / 20

clones < 0.5

−MRD 8 / 11

No_alterations = 0

+MRD 8 / 10

X13q_hom = 1

−MRD 18 / 27

independent_13q. = 0

−MRD 9 / 10

CNAs < 4.5

−MRD 24 / 31

trisomy12 = 0

+MRD 12 / 18

X11q_mono_del = 1

+MRD 19 / 23

X11q_biallelic = 1

+MRD 15 / 15

no **TP53 = 1** yes

All branches same length, total patient numbers displayed, 'yflip=TRUE'