

Bayesian networks

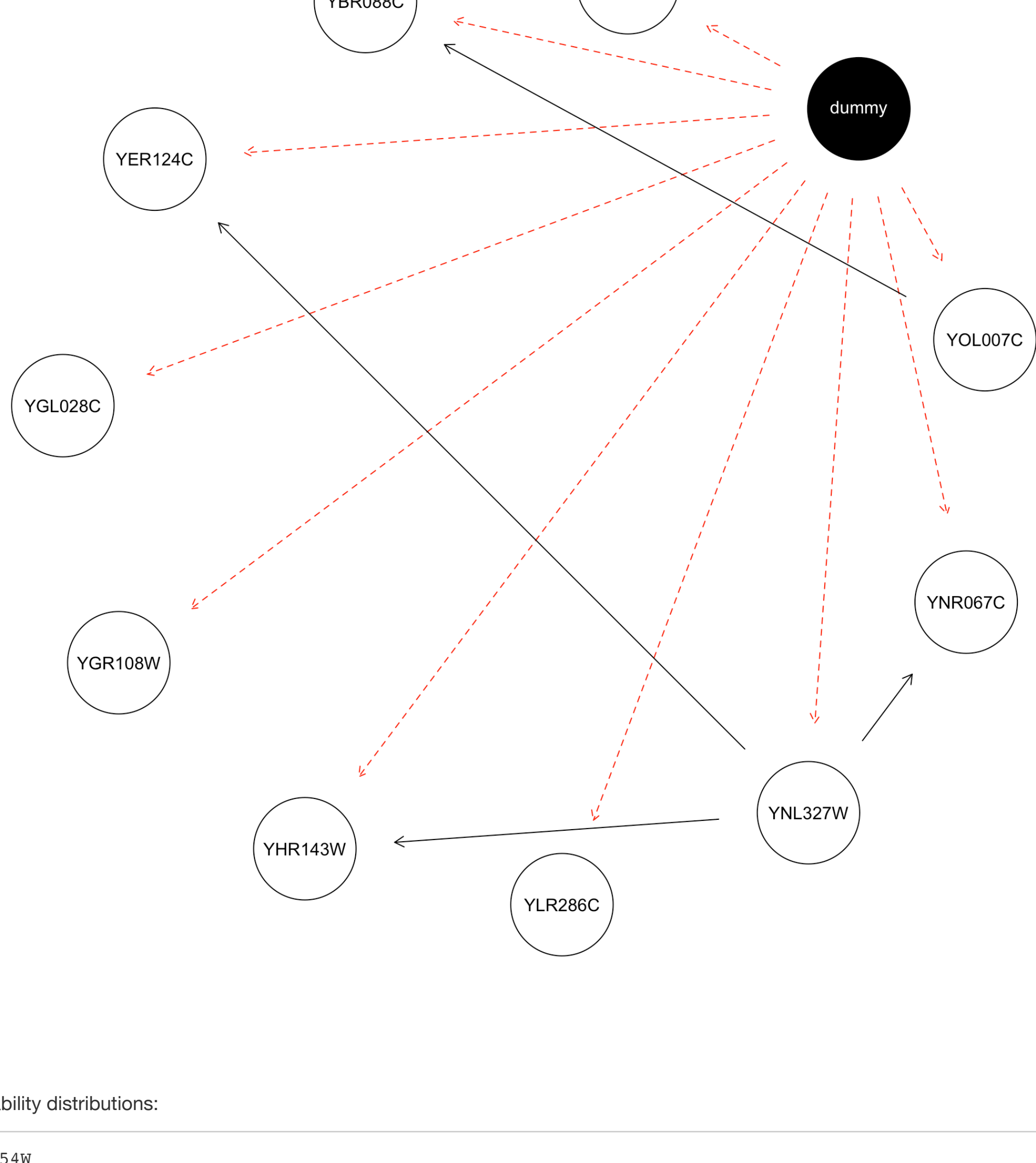
1

10 most variant genes:

```
## [1] "YBR054W" "YBR088C" "YER124C" "YGL028C" "YGR108W" "YHR143W" "YLR286C"
## [8] "YNL327W" "YNR067C" "YOL007C"
```

2

Prior structure:



3

Local probability distributions:

```
## $YBR054W
##          s2 Intercept:YBR054W
##          1.42234485          0.02649351
##
## $YBR088C
##          s2 Intercept:YBR088C          YOL007C
##          0.228734538          0.008498828          0.826678327
##
## $YER124C
##          s2 Intercept:YER124C          YNL327W
##          1.023258845          -0.008715885          0.525497198
##
## $YGL028C
##          s2 Intercept:YGL028C
##          1.455174903          -0.009350649
##
## $YGR108W
##          s2 Intercept:YGR108W
##          0.92446915          0.06779221
##
## $YHR143W
##          s2 Intercept:YHR143W          YNL327W
##          0.7985400886          -0.0001363054          0.4141461457
##
## $YLR286C
##          s2 Intercept:YLR286C
##          1.9945786136          -0.0007792208
##
## $YNL327W
##          s2 Intercept:YNL327W
##          1.41701617          -0.02616883
##
## $YNR067C
##          s2 Intercept:YNR067C          YNL327W
##          0.4623560200          -0.0006759902          0.8972450401
##
## $YOL007C
##          s2 Intercept:YOL007C
##          1.09477190          -0.01090909
##
## $dummy
## 1
## 1
```

Local probability distribution for gene YBR088C:

```
##          s2 Intercept:YBR088C          YOL007C
##          0.228734538          0.008498828          0.826678327
```

4

```
prior0 <- jointprior(G0, 5) # equivalent to imaginary sample size = 5
```

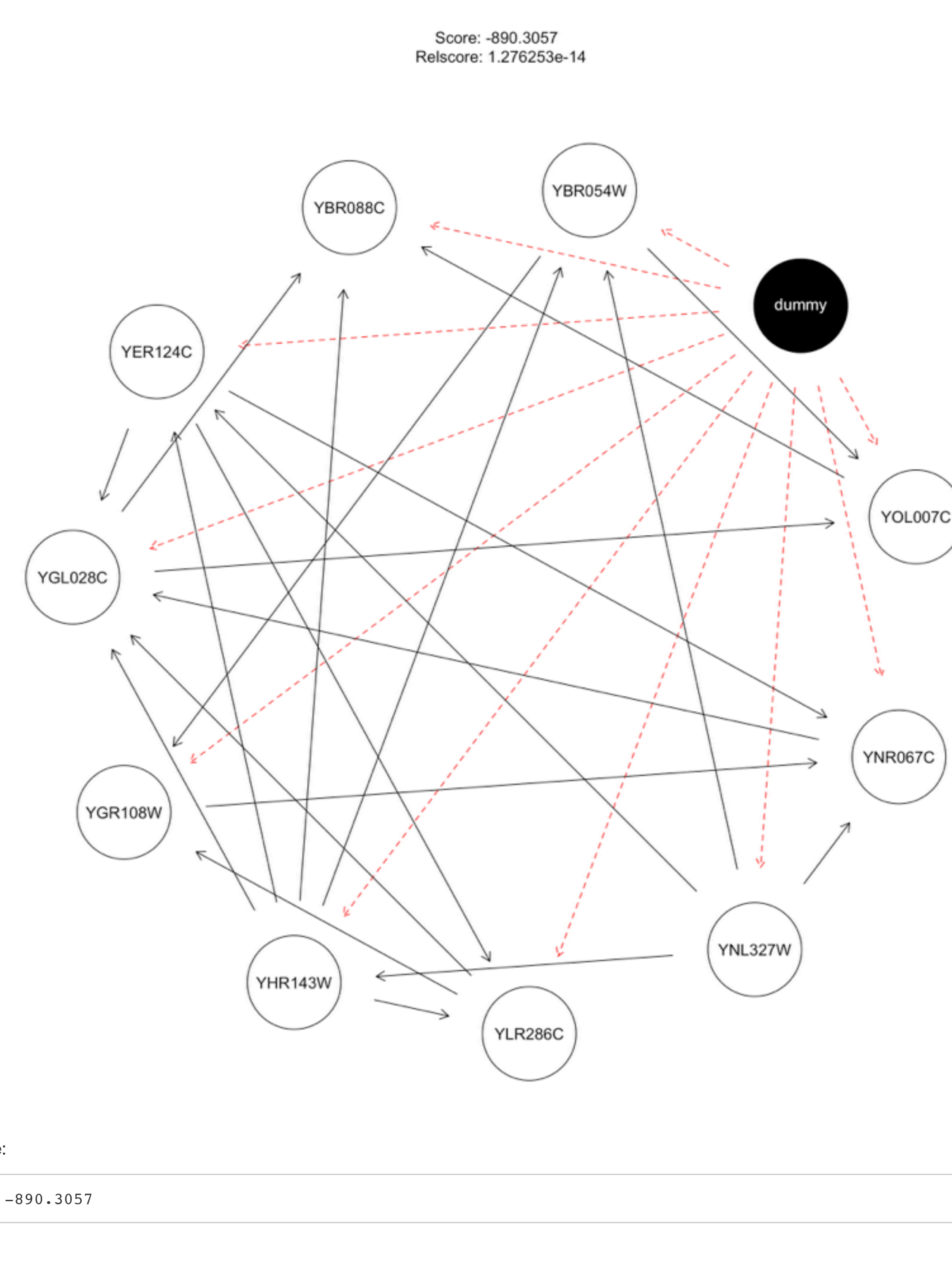
5

Initial BN score:

```
## [1] -1101.865
```

6

BN* network:



BN* score:

```
## [1] -890.3057
```

7

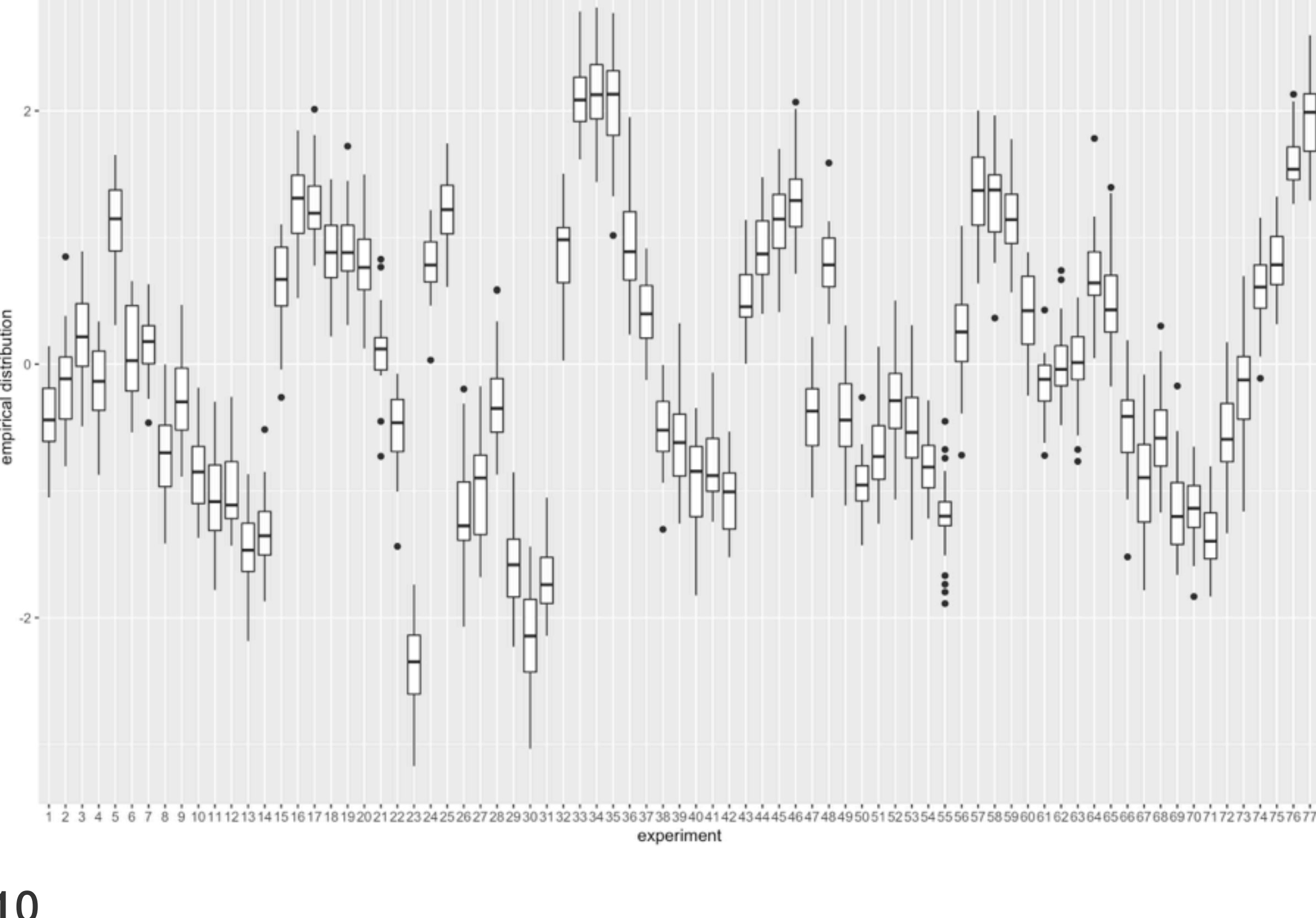
Genes variances:

```
## YBR054W YBR088C YER124C YGL028C YGR108W YHR143W YLR286C YNL327W
## 1.4410599 0.9897524 1.4331767 1.4743219 0.9366332 1.0552875 2.0208231 1.4356611
## YNR067C YOL007C
## 1.6242167 1.1091768
```

8

```
# perturbed data
perturbed_data = list()
for (i in 1:30) {
  p_genes = data.frame(genes)
  for (gene in colnames(p_genes)) {
    p_genes[gene] = p_genes[gene] + rnorm(nrow(p_genes), mean=0, sd=sqrt(genes.vars[gene] / 10))
  }
  perturbed_data[[i]] = p_genes
}
```

9

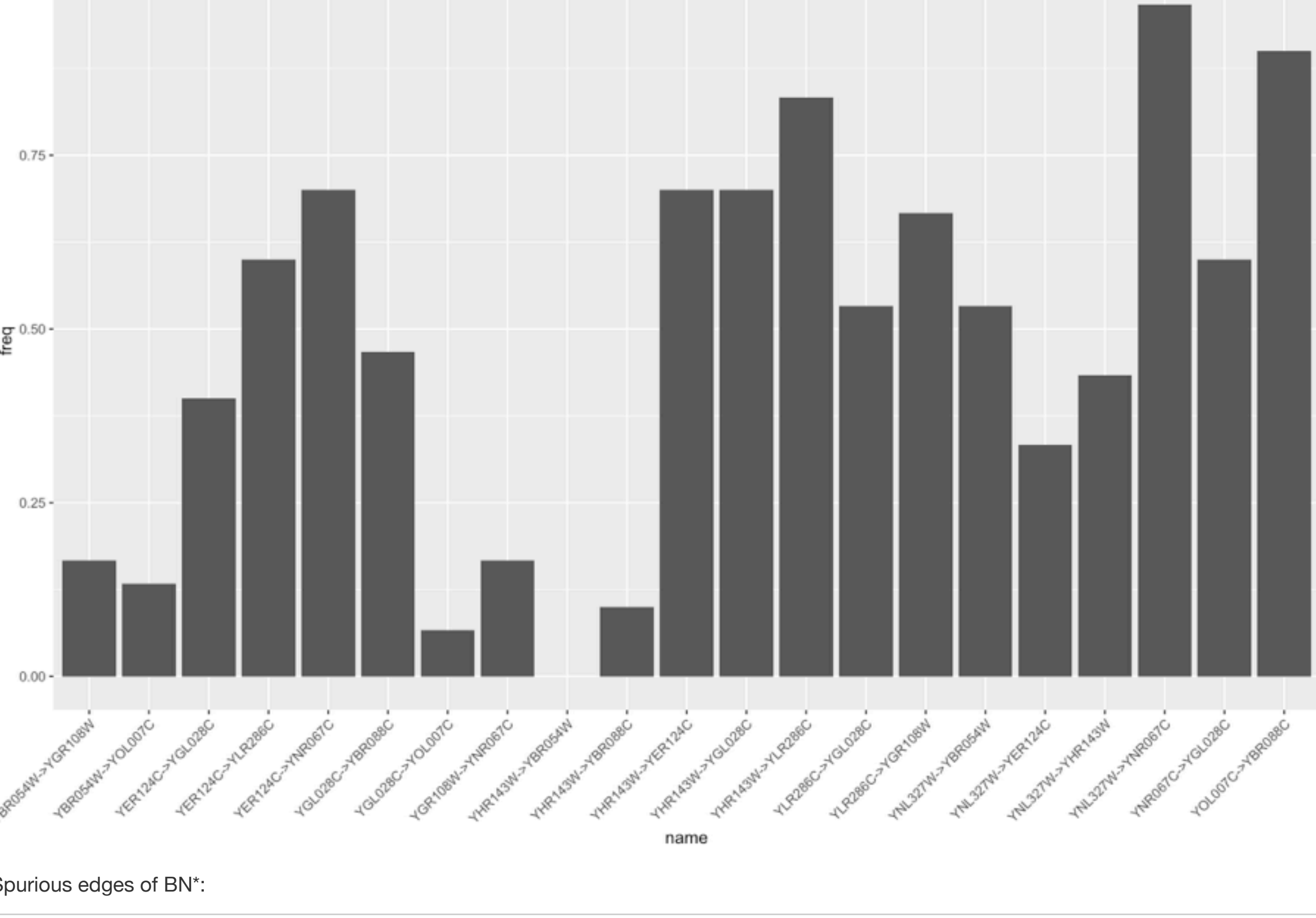


10

PBN5 network:



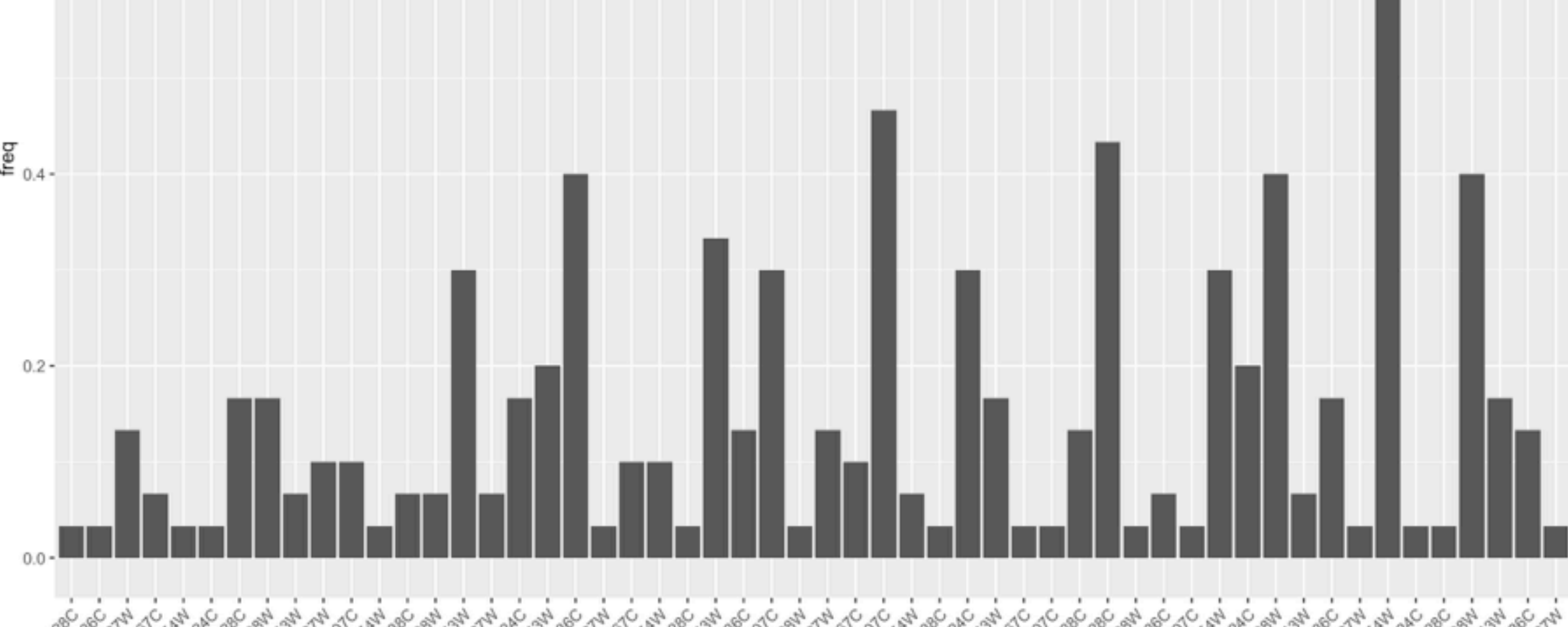
11



Spurious edges of BN*:

```
##          freq          name
## 1 0.00000000 YHR143W->YBR054W
## 3 0.46666667 YGL028C->YBR088C
## 4 0.10000000 YHR143W->YBR088C
## 7 0.33333333 YNL327W->YER124C
## 8 0.40000000 YER124C->YGL028C
## 12 0.16666667 YBR054W->YGR108W
## 14 0.43333333 YNL327W->YHR143W
## 18 0.16666667 YGR108W->YNR067C
## 20 0.13333333 YBR054W->YOL007C
## 21 0.06666667 YGL028C->YOL007C
```

12



Edges that might be missing in BN*:

```
##          freq          name
## 3 0.83333333 YOL007C->YBR054W
## 4 0.40000000 YOL007C->YGR108W
## 5 0.33333333 YGR108W->YHR143W
## 12 0.43333333 YNL327W->YGL028C
## 14 0.40000000 YNR067C->YGR108W
## 16 0.40000000 YGL028C->YLR286C
## 17 0.46666667 YHR143W->YOL007C
```