Creating dataset:

Now, run script.

Here's the script:

Let's check our calculations:

Compare to univariate results:

We can see that our method is more powerful than both univariate and multivariate approahces:

```
lf.mash=read.table("lipid_data_signedzlfsr.txt")[,-1]
lf.bma=read.table("lipid_data_signedz_bmaonlylfsr.txt")[,-1]
lf.ash=read.table("lipids_univariateashtspec.lfsr.txt")
thresh=0.05
sum(lf.mash<thresh)
```

```
## [1] 65080
```

```
sum(lf.ash<thresh)
```

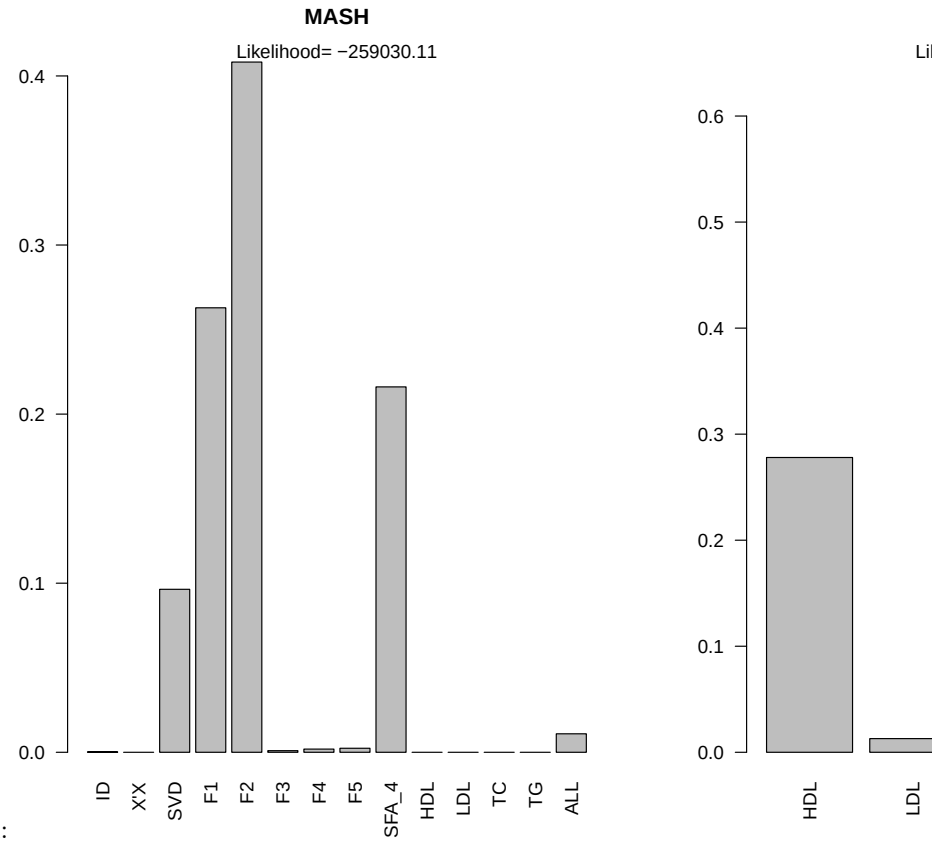
```
## [1] 15710
```

```
sum(lf.bma<thresh)
```

```
## [1] 30226
```

And much better than joint method like BMA. After training on 40,000 snps and testing on a unique set of 40,000 aditional snps, we learn the test set likelihood:

```
sum(log(test.lik%*%pis.train))
cat total.lik.bma.lite
-315326.50
cat total.lik.mash
 -259030.11
```



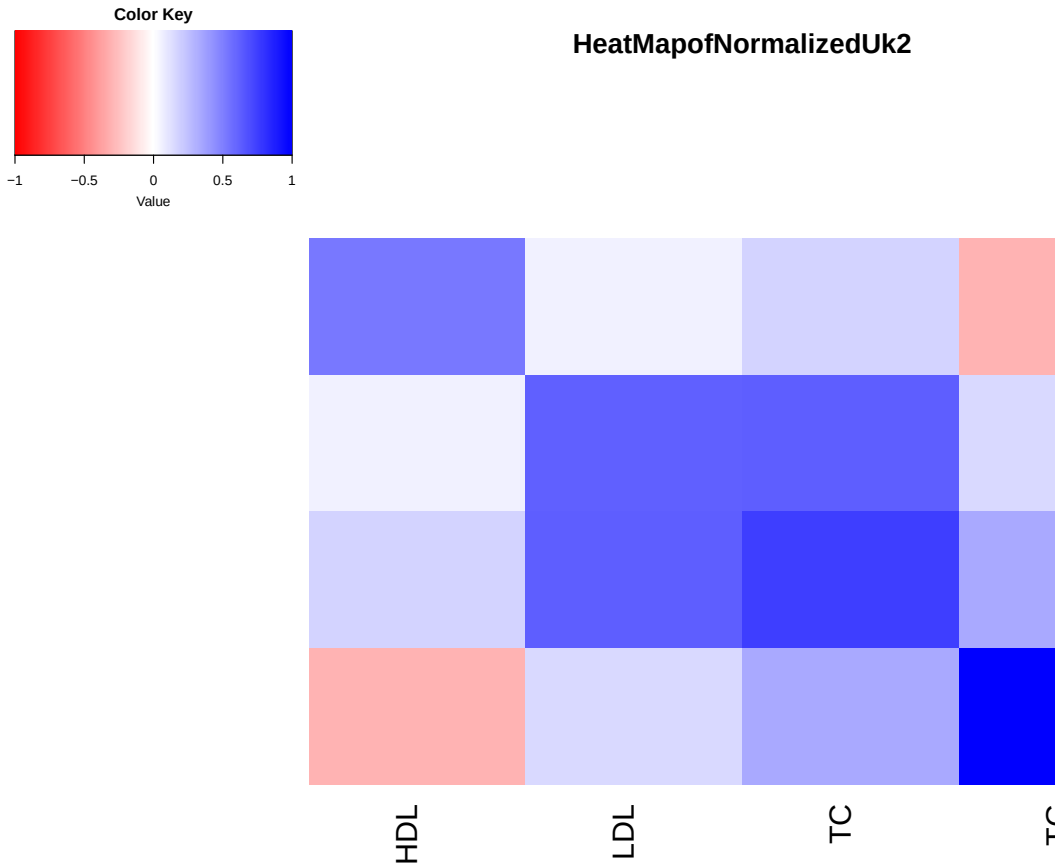
Let's look at the covariance patterns captured:
We can see that the new matrices occupy a majority of the weight, whereas BMA is limited by the 'consistent'

```
sum(colSums(pi.mat[,1:9]))
```

```
## [1] 0.9890654
```

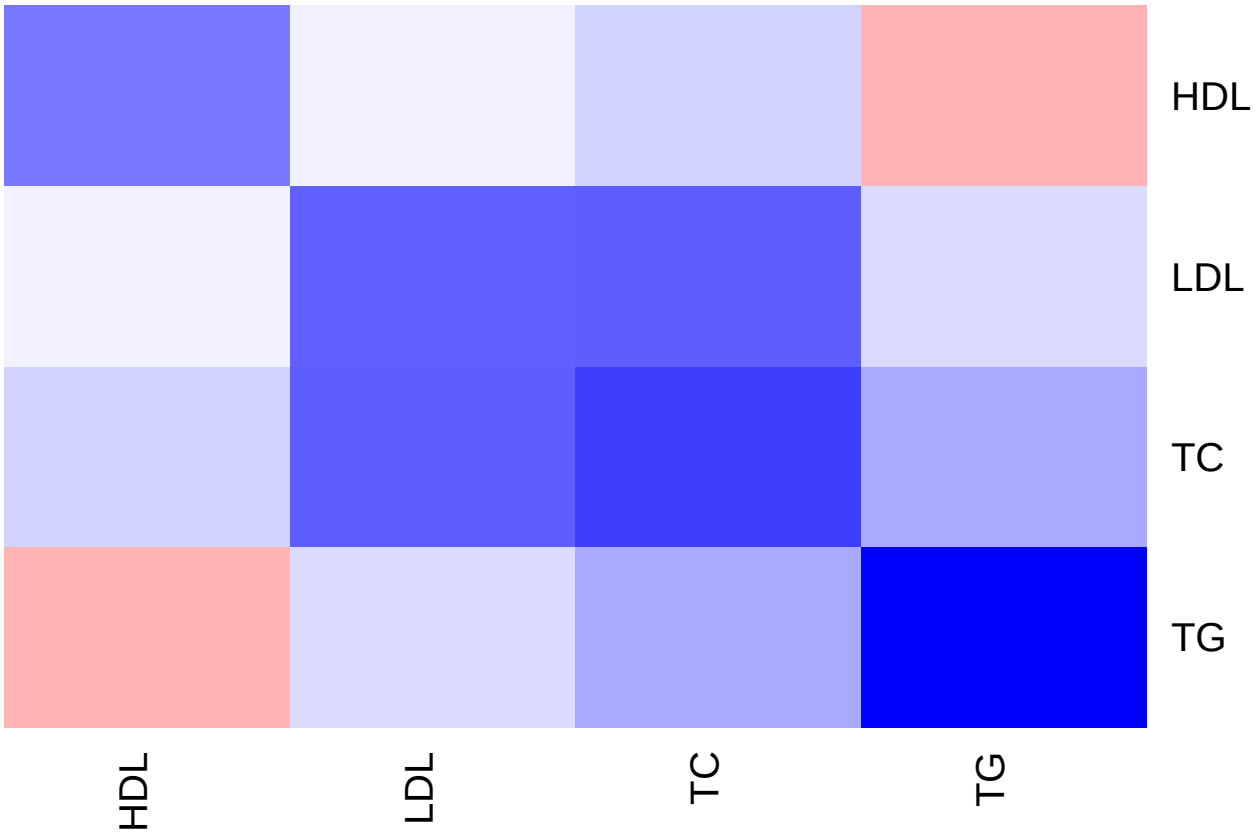
```
colSums(pi.bma.mat)[5]
```

```
##       ALL
## 0.6508965
```

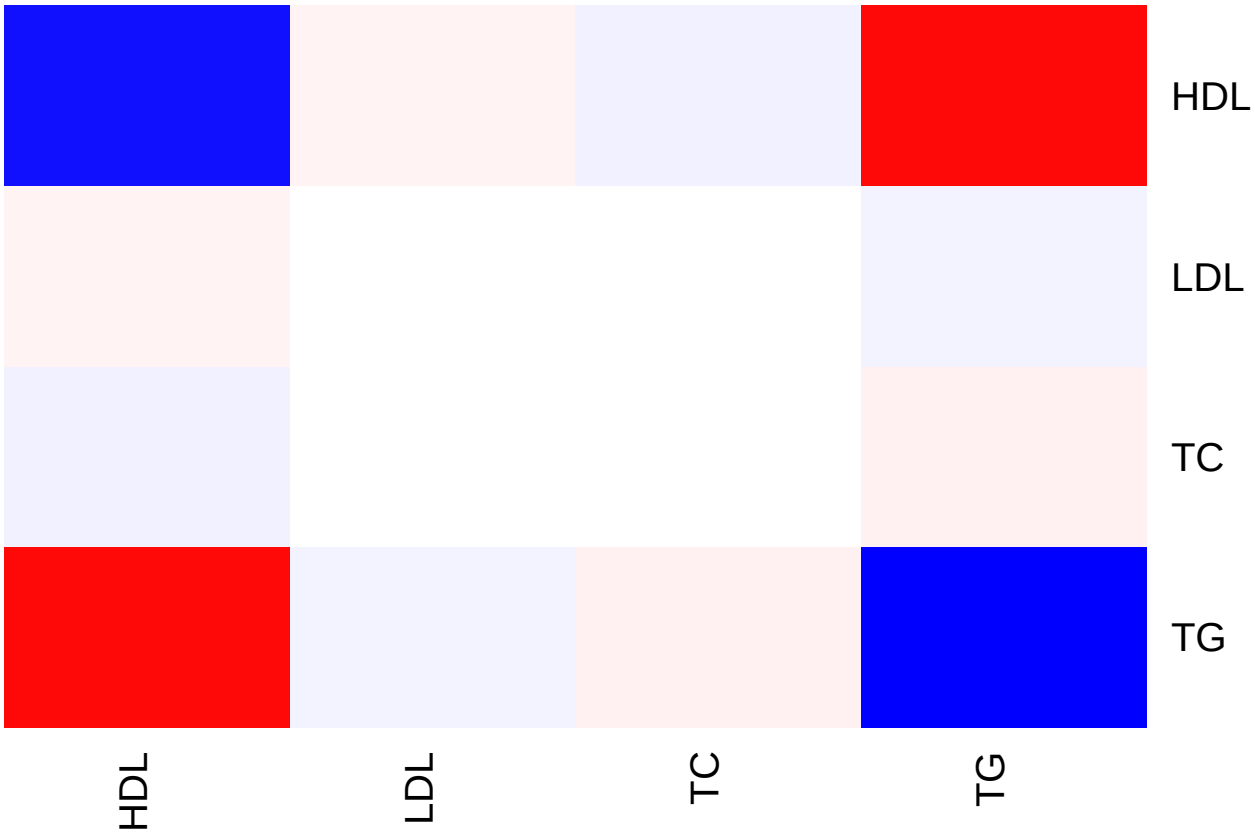


In fact, let's examine the patterns.

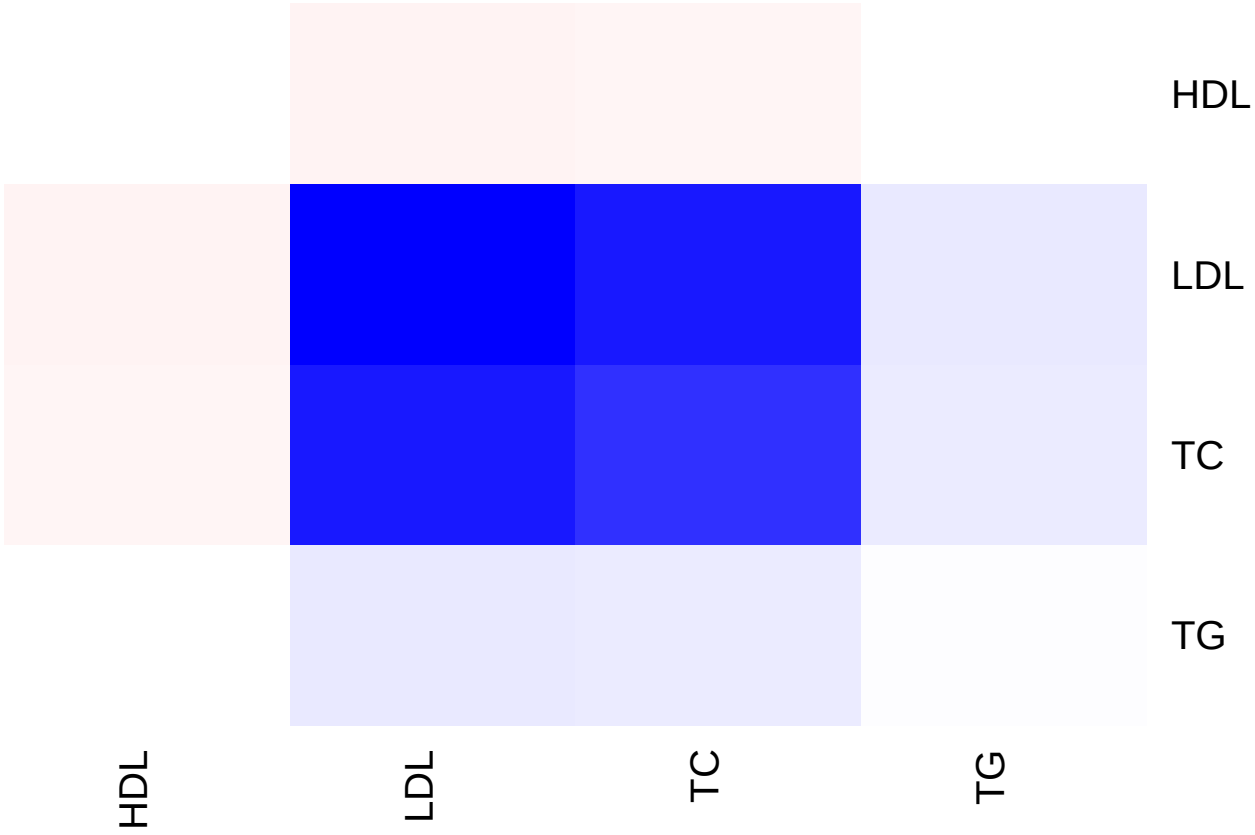
HeatMapofNormalizedUk3



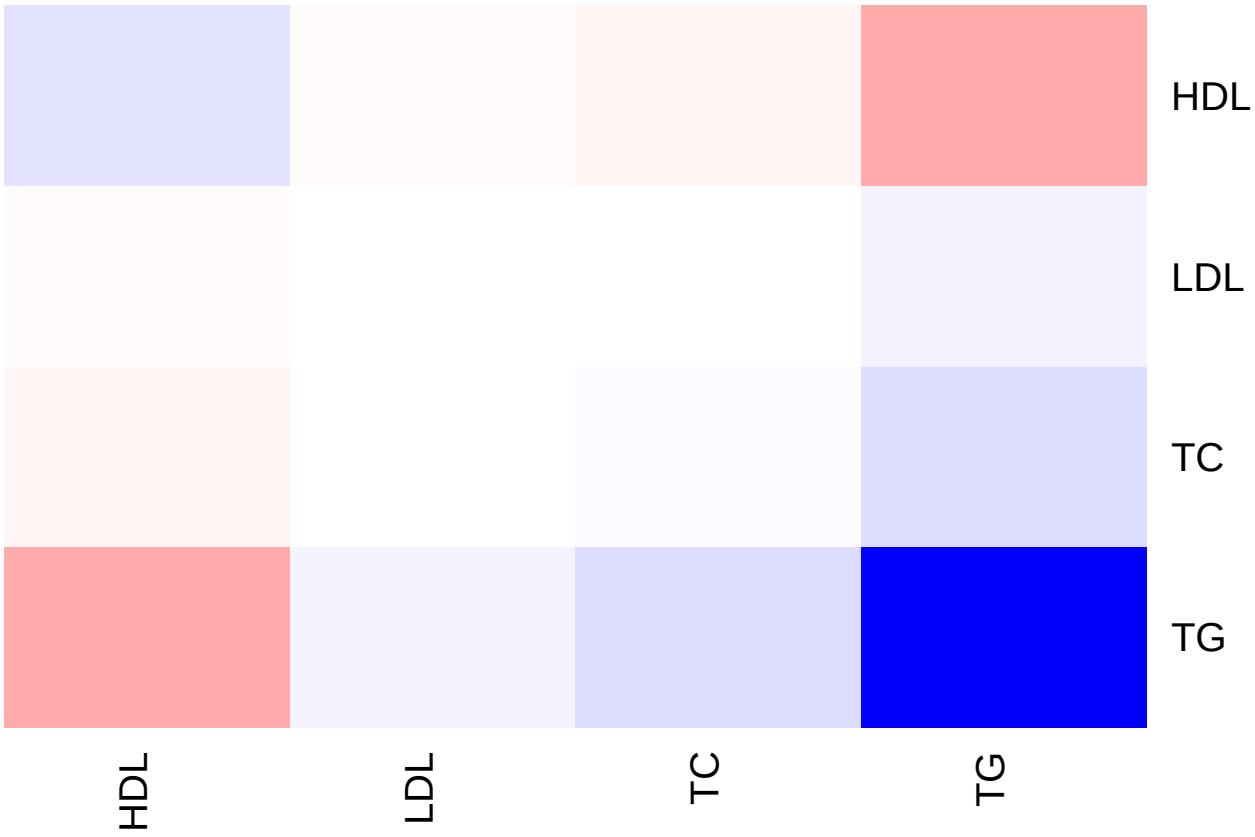
HeatMapofNormalizedUk4



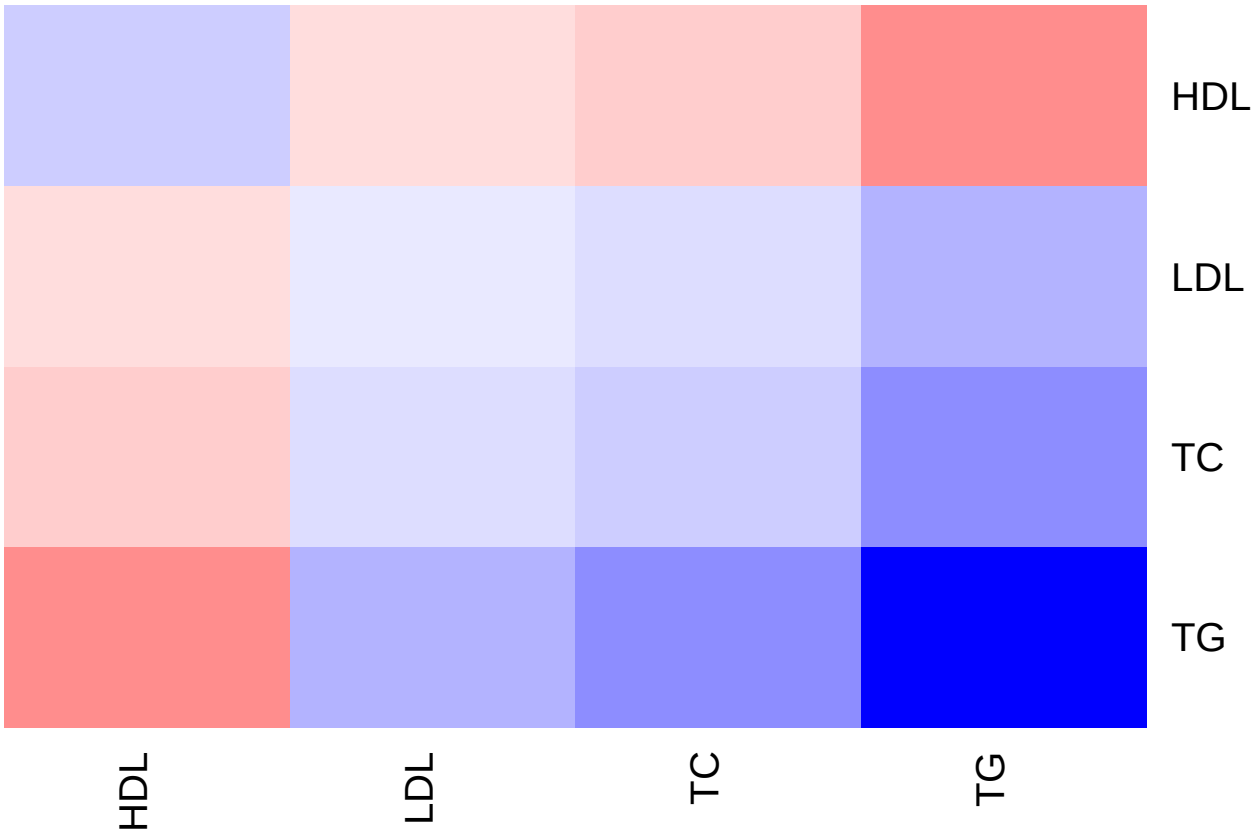
HeatMapofNormalizedUk5



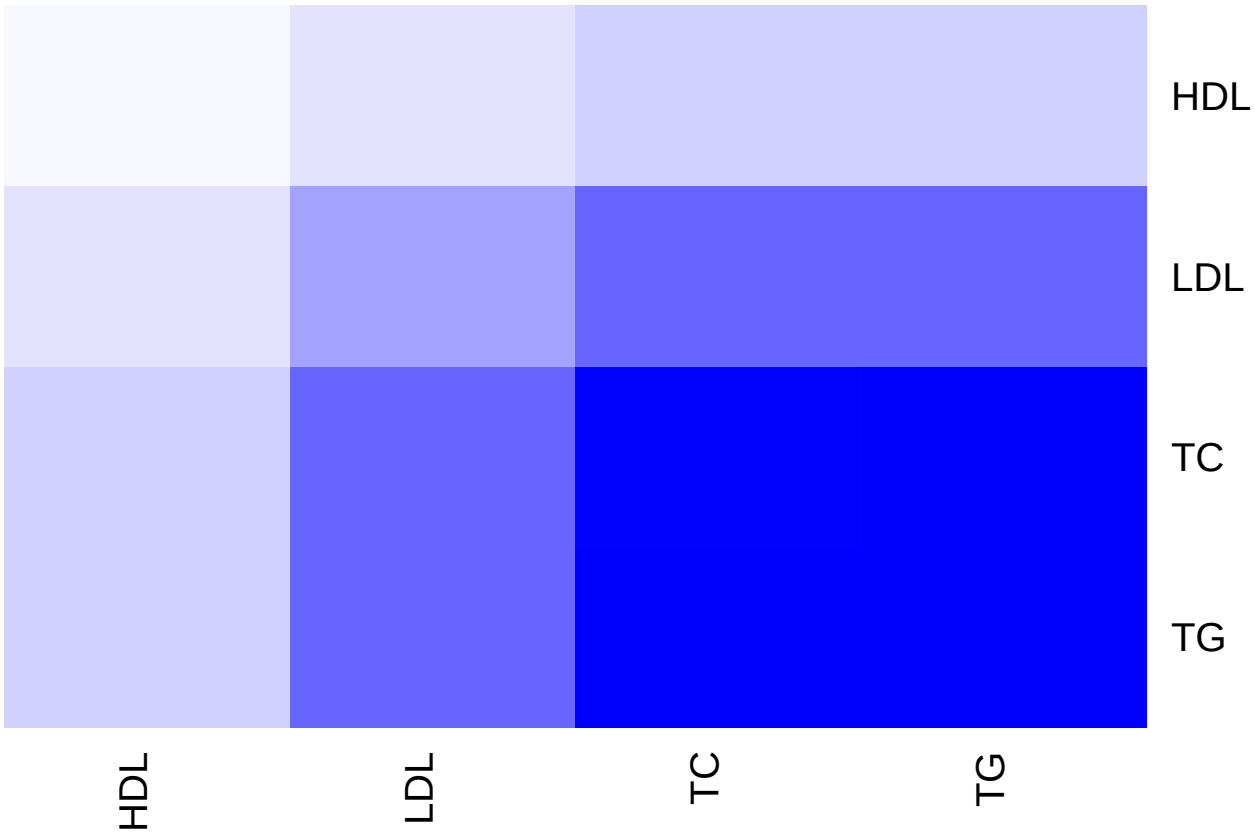
HeatMapofNormalizedUk6



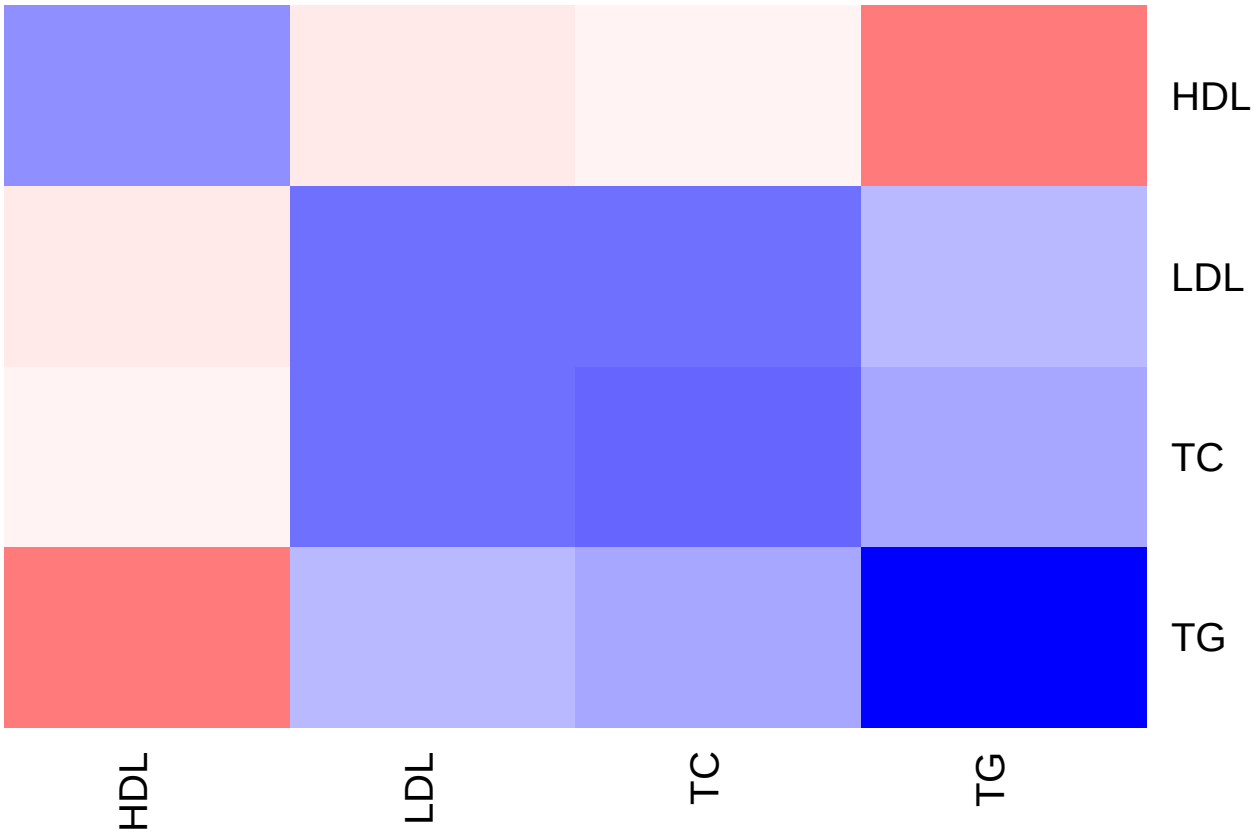
HeatMapofNormalizedUk7

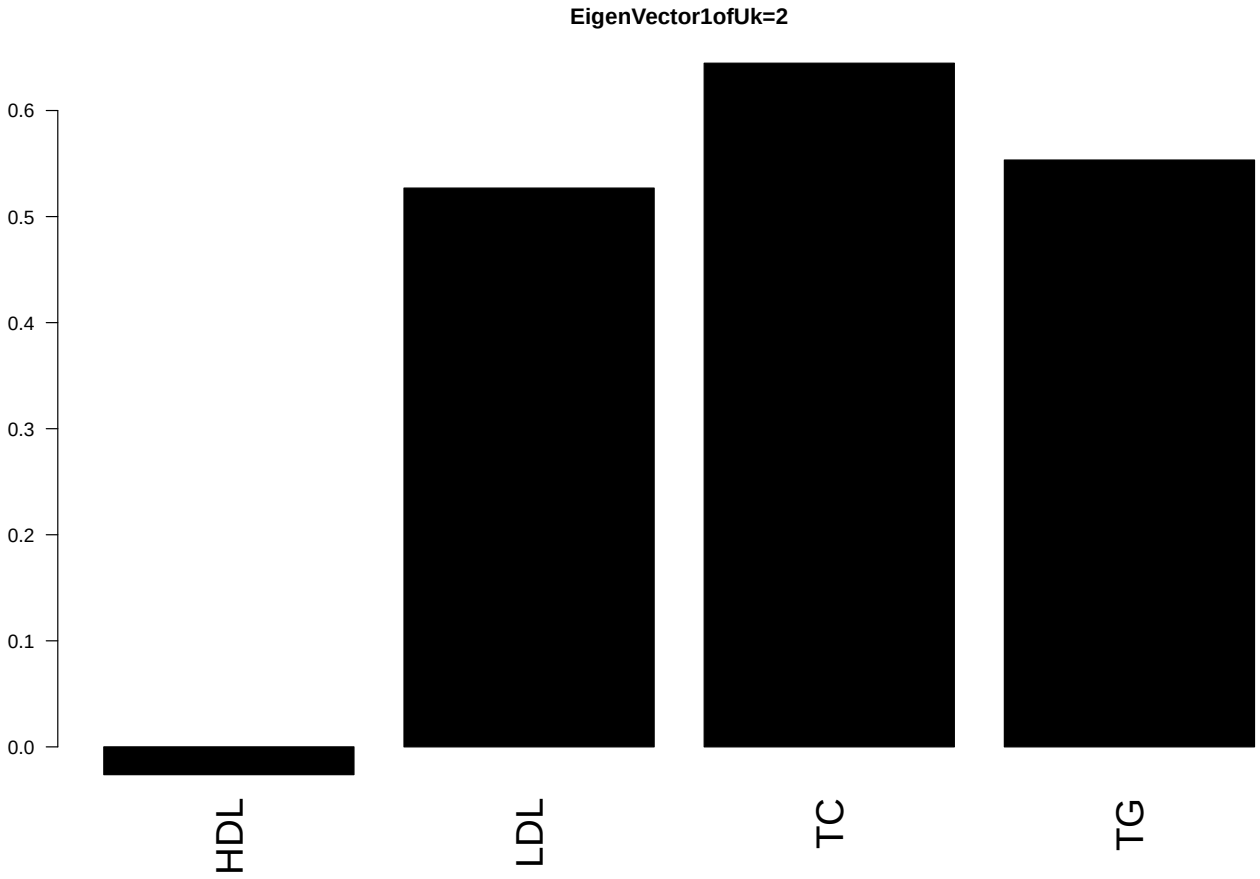


HeatMapofNormalizedUk8



HeatMapofNormalizedUk9

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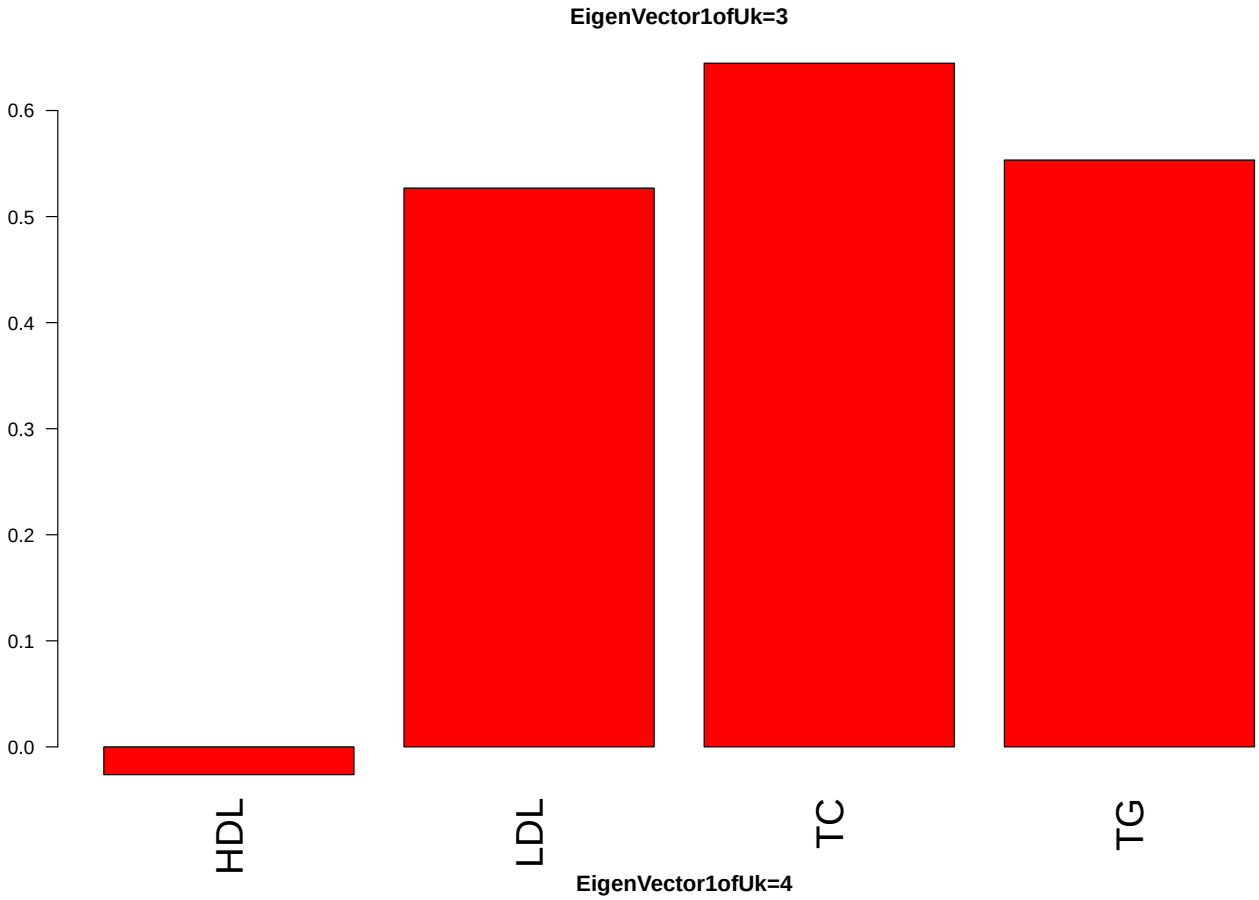
0.5
0.4
0.3
0.2
0.1
0.0
HDL
LDL
TC
TG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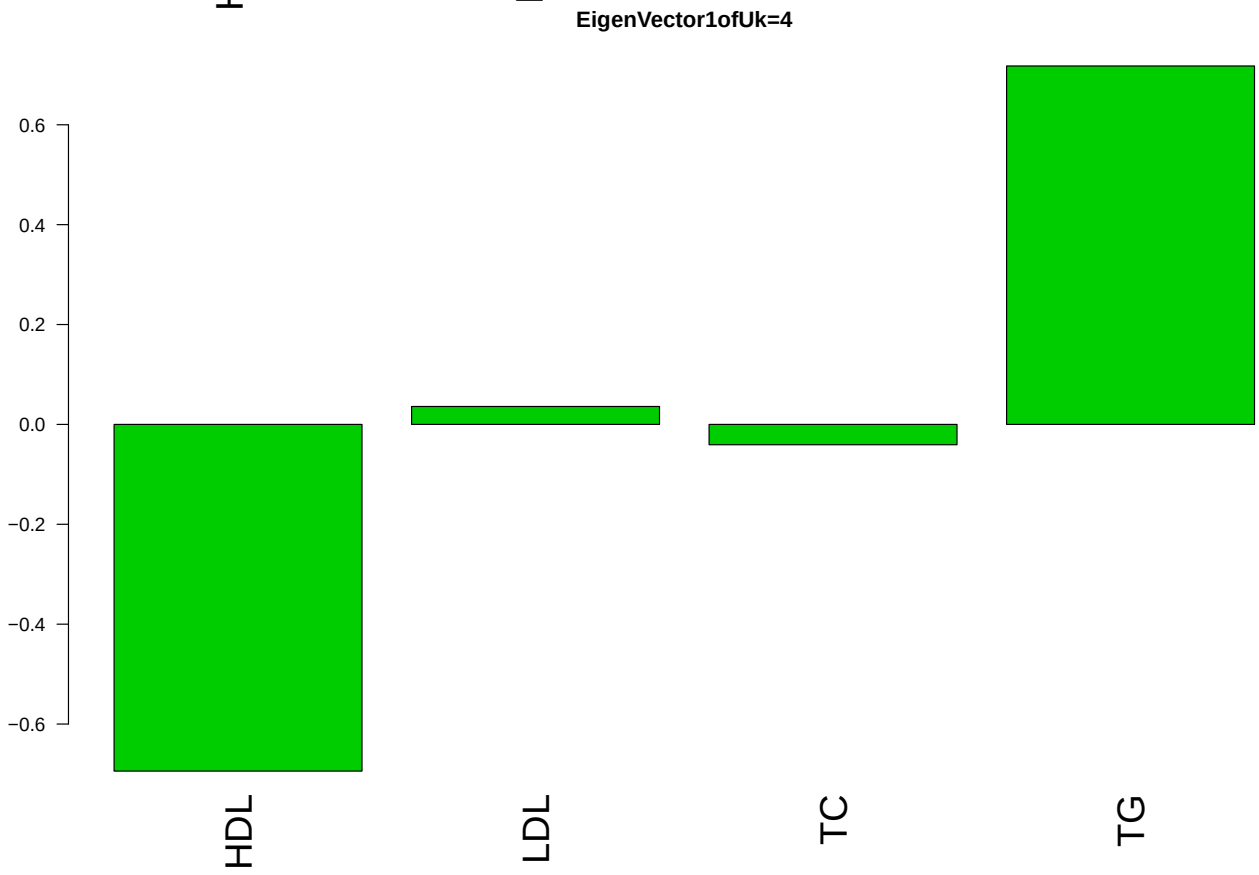
0.5
0.4
0.3
0.2
0.1
0.0
HDL
LDL
TC
TG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0.2
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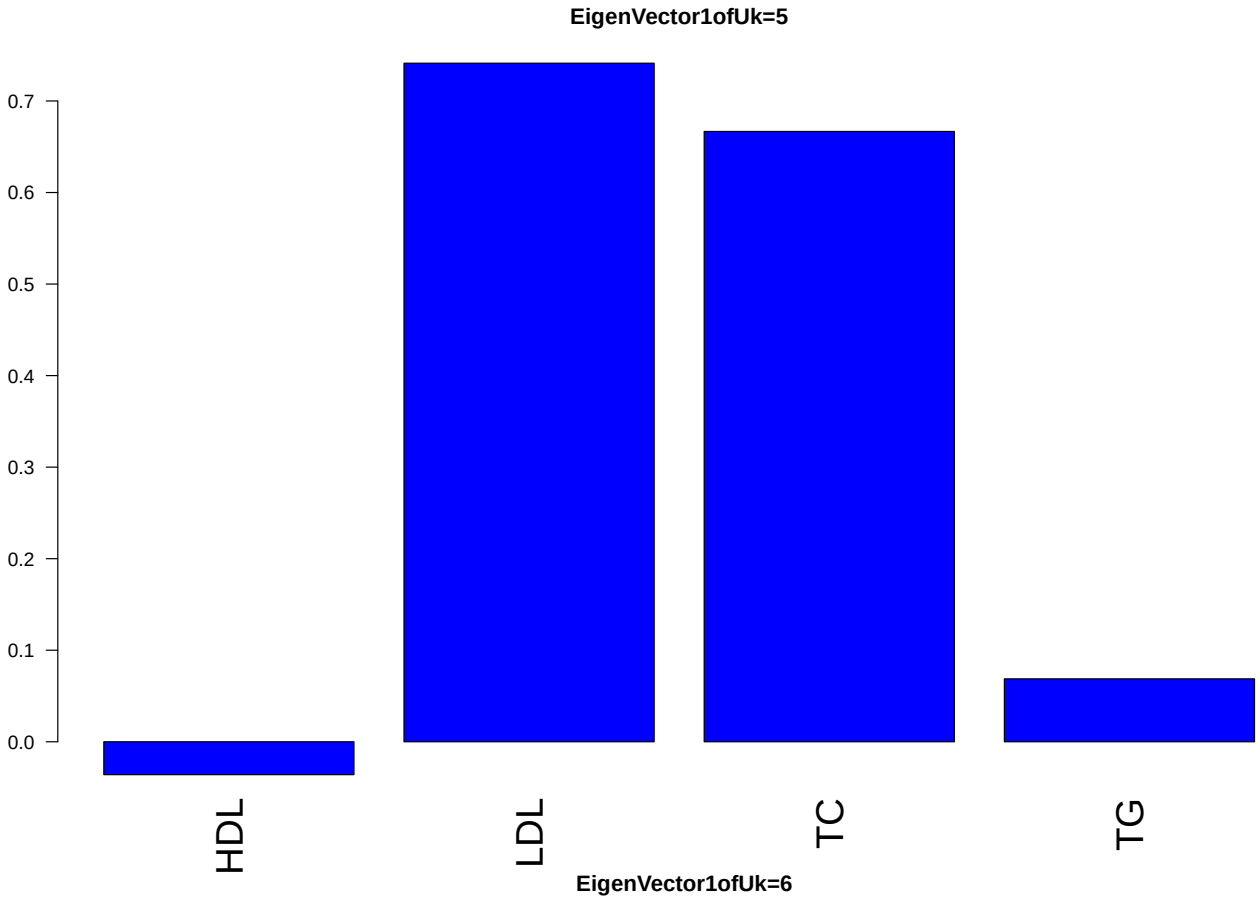
−0.2
−0.4
−0.6
HDL
LDL
TC
TG


EigenVector1ofUk=5
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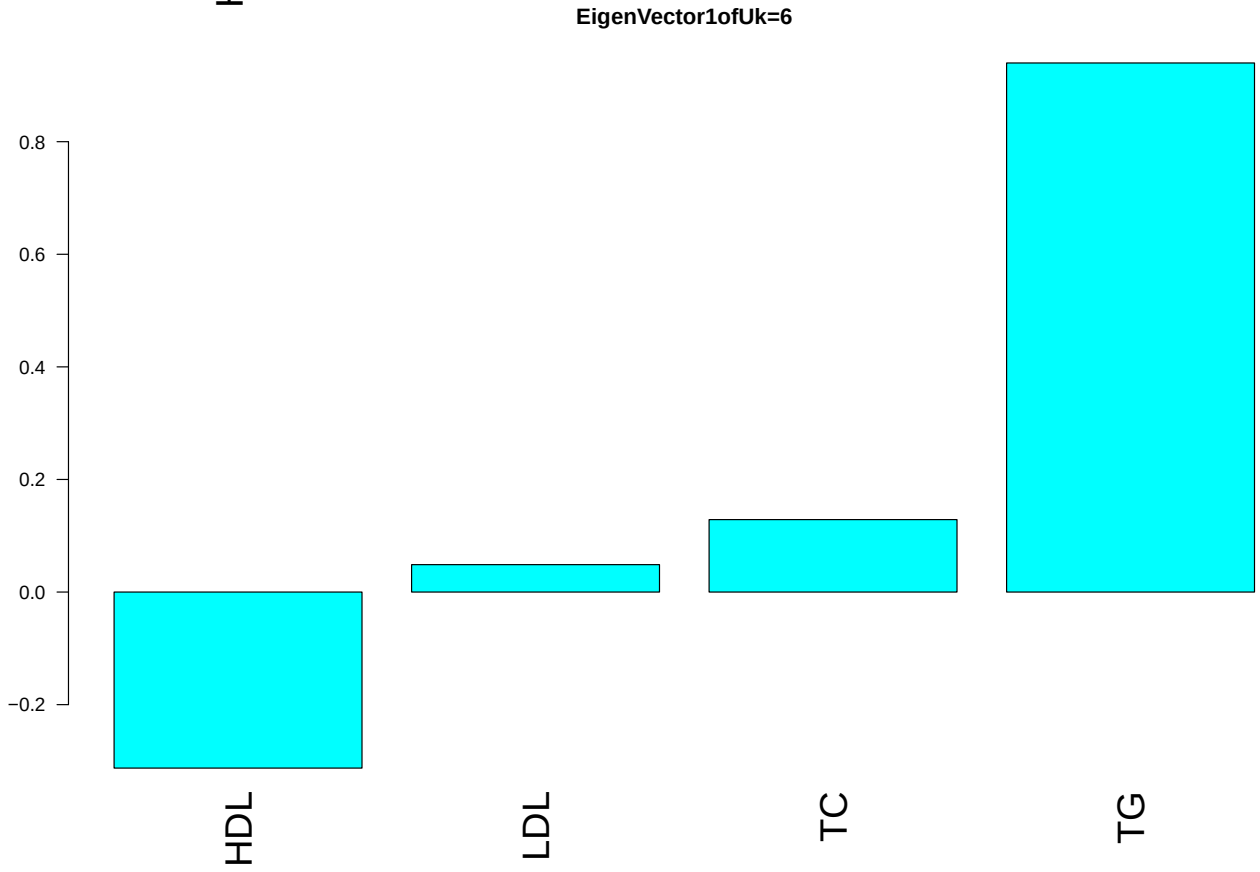
0.5
0.4
0.3
0.2
0.1
0.0
HDL
LDL
TC
TG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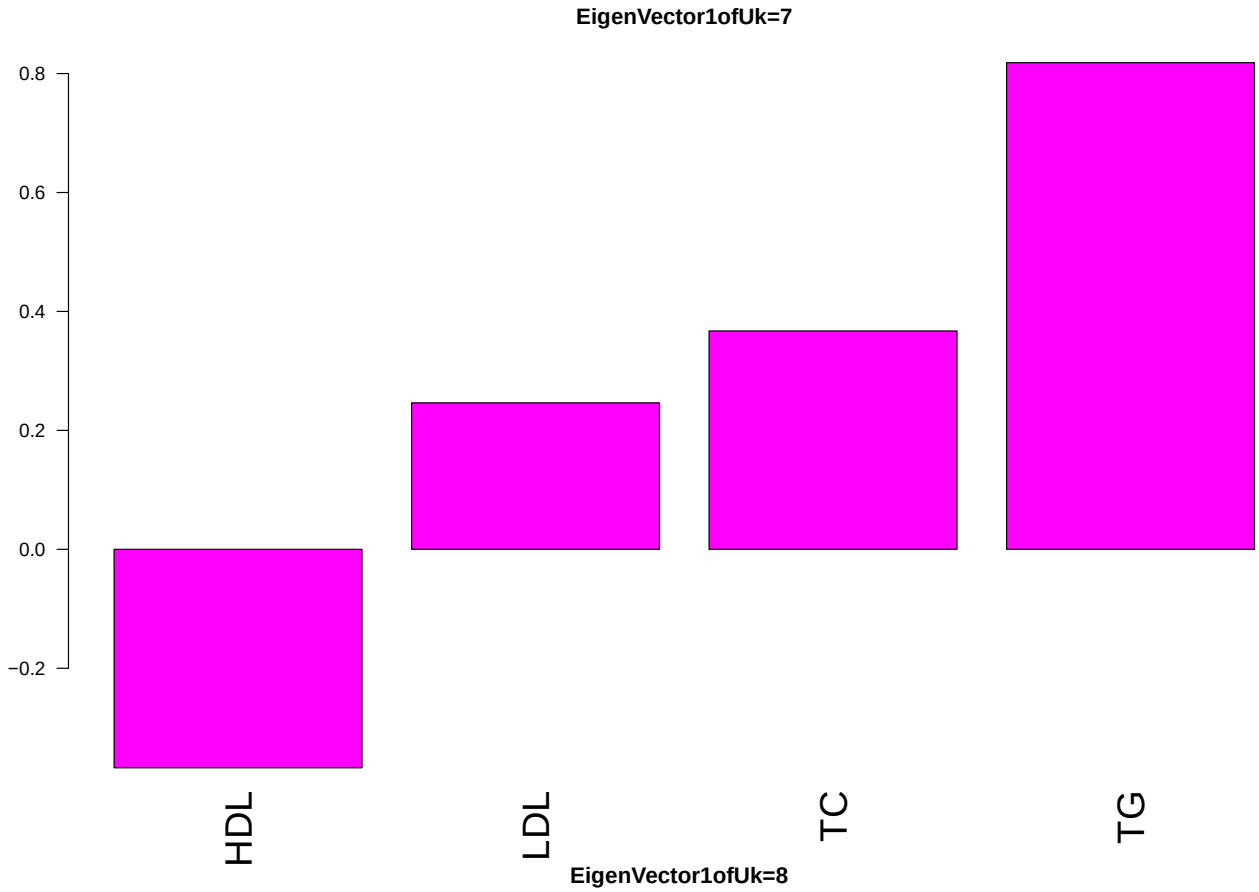
0.6
0.4
0.2
0.0
−0.2
HDL
LDL
TC
TG


EigenVector1ofUk=7
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0.4
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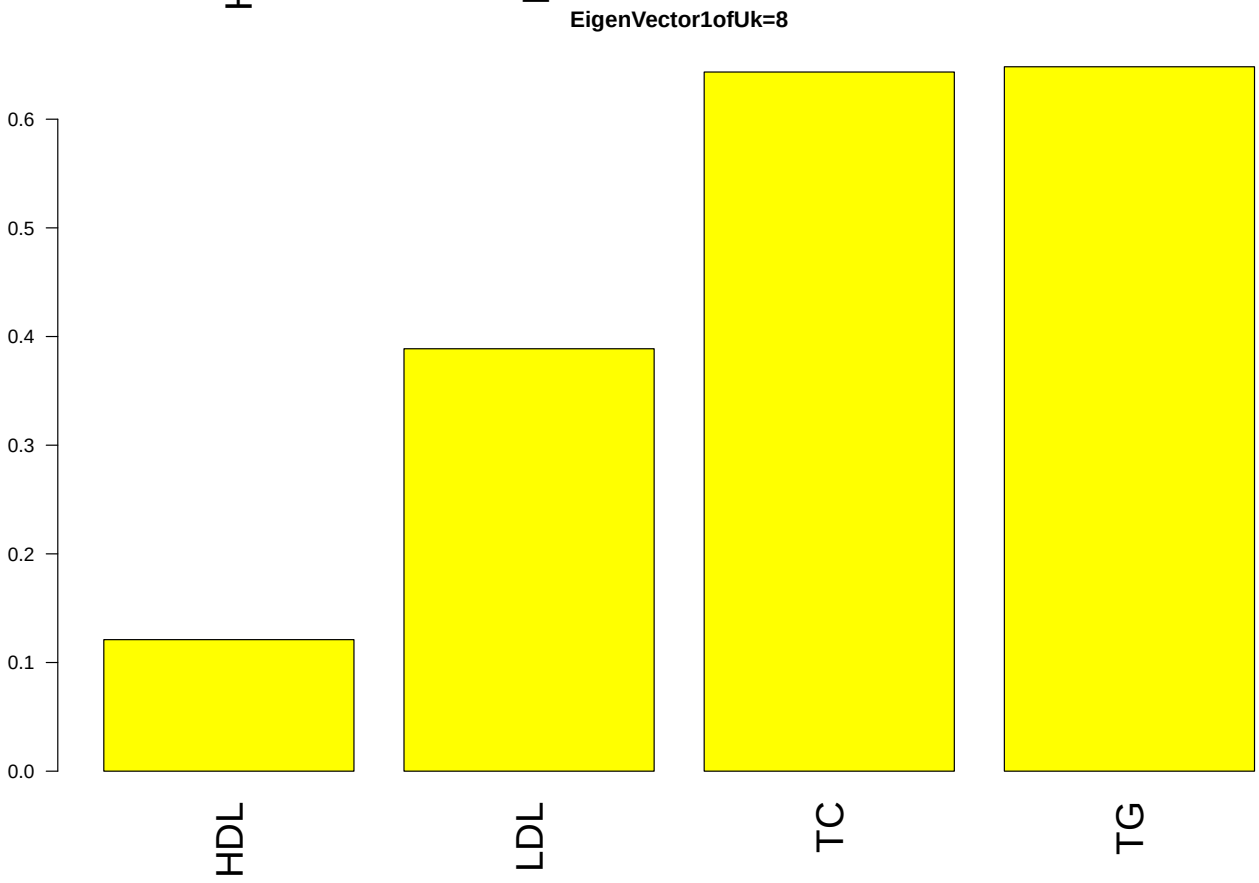
−0.2
HDL
LDL
TC
TG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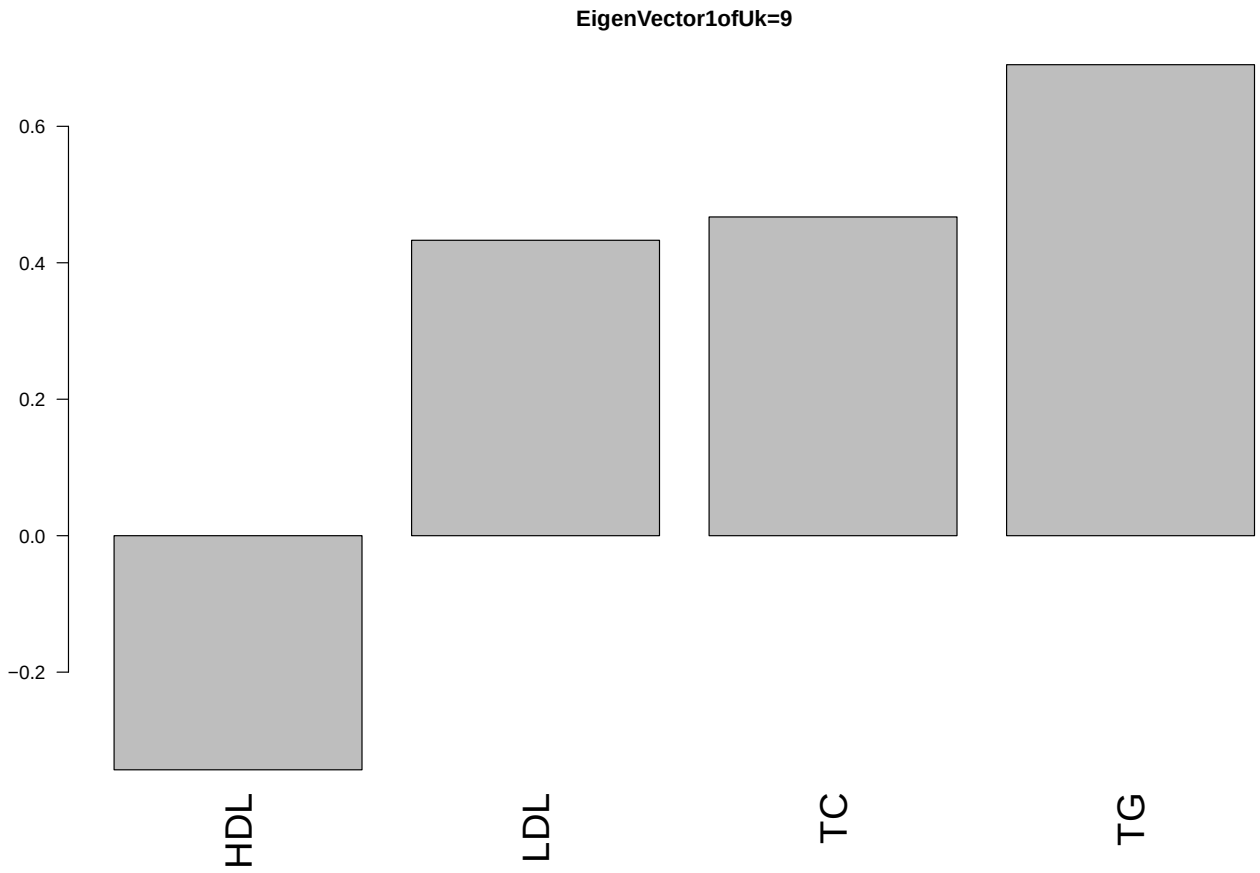
LDL
TC
TG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HDL
LDL
TC
TG